



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:19 AM UTC

PDB ID : 6YUF / pdb_00006yuf
EMDB ID : EMD-10930
Title : Cohesin complex with loader gripping DNA
Authors : Higashi, T.L.; Eickhoff, P.; Sousa, J.S.; Costa, A.; Uhlmann, F.
Deposited on : 2020-04-27
Resolution : 3.94 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

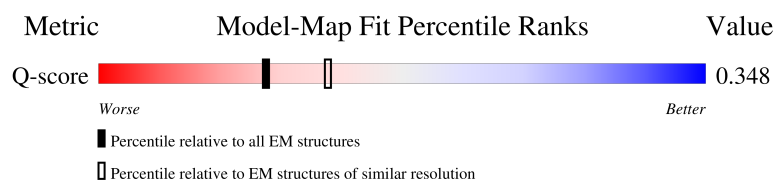
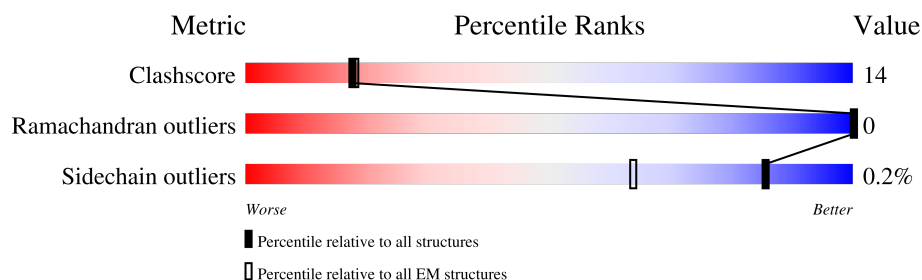
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.94 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	7757 (3.44 - 4.43)

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	B	628	
2	D	1587	
3	A	1228	
4	C	1194	

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Mol	Chain	Length	Quality of chain
5	X	32	 72% 28%
6	Y	32	 84% 16%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 19528 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cohesin subunit rad21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	152	Total	C	N	O	S	0	0
			1195	758	206	225	6		

- Molecule 2 is a protein called Sister chromatid cohesion protein mis4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	1272	Total	C	N	O	S	0	0
			10247	6604	1687	1910	46		

- Molecule 3 is a protein called Structural maintenance of chromosomes protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	384	Total	C	N	O	S	0	0
			3047	1932	521	587	7		

- Molecule 4 is a protein called Structural maintenance of chromosomes protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	456	Total	C	N	O	S	0	0
			3665	2294	644	714	13		

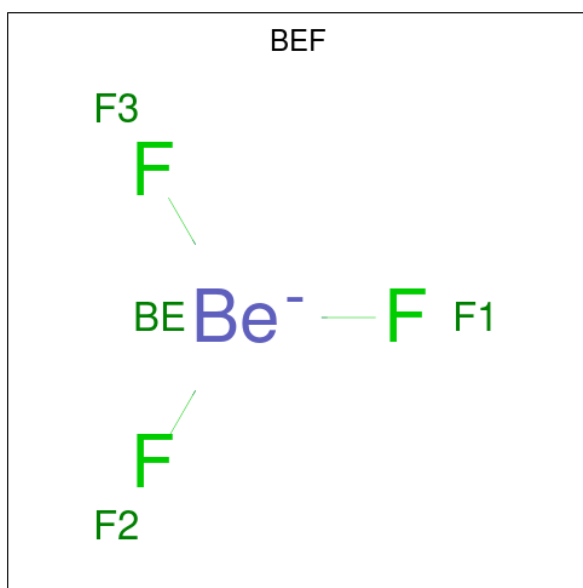
- Molecule 5 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	32	Total	C	N	O	P	0	0
			658	312	129	185	32		

- Molecule 6 is a DNA chain called DNA (32-MER).

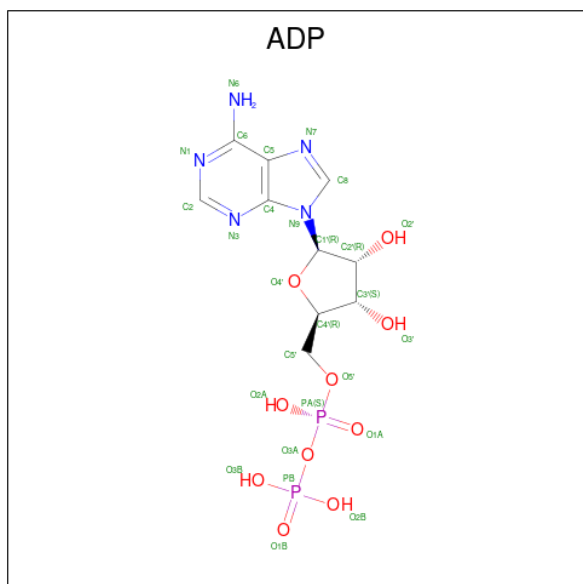
Mol	Chain	Residues	Atoms					AltConf	Trace
6	Y	32	Total	C	N	O	P	0	0
			654	313	110	199	32		

- Molecule 7 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3).



Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	Be	F	0
			4	1	3	
7	C	1	Total	Be	F	0
			4	1	3	

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$).



Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

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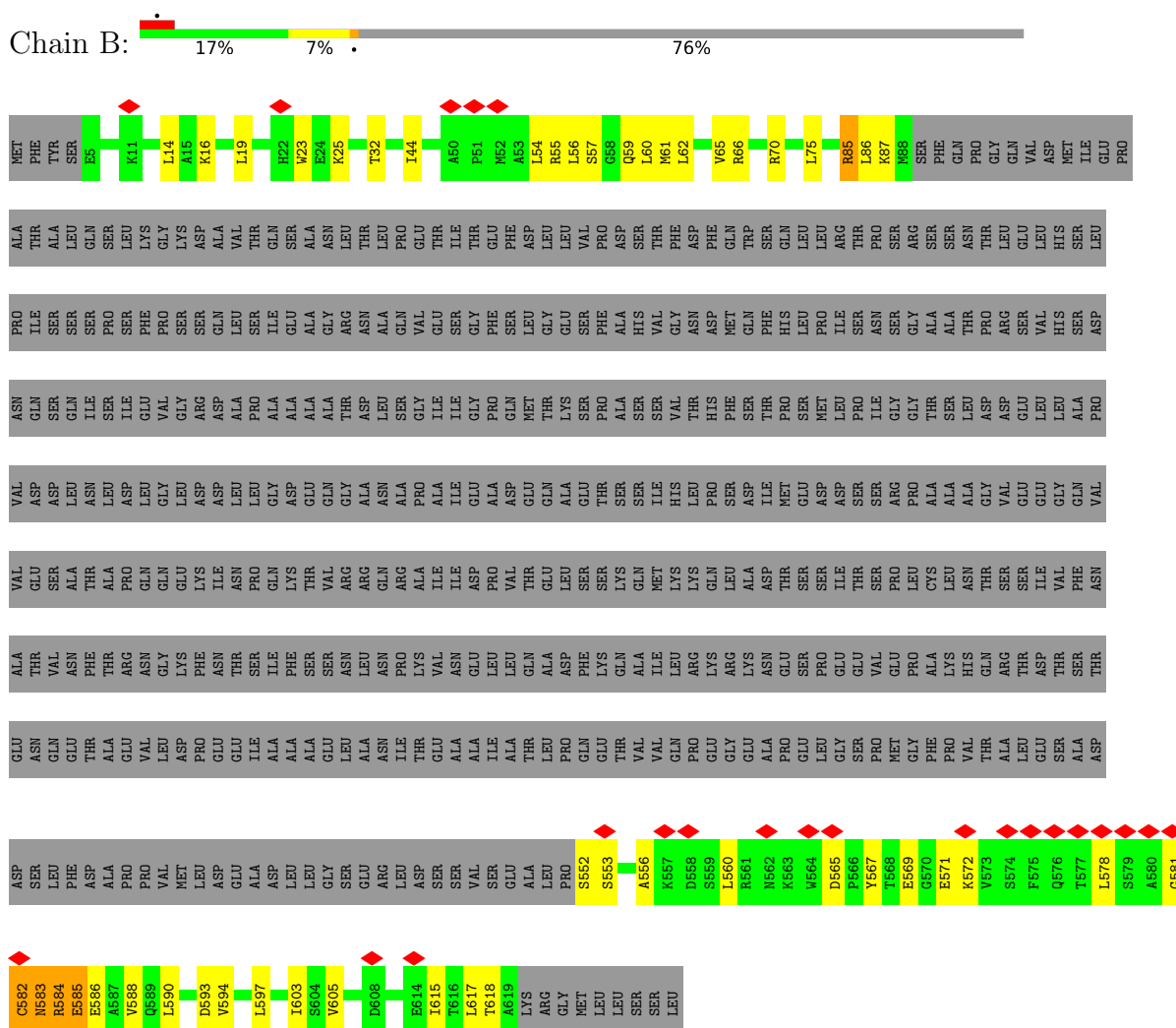
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
8	C	1	27	10	5	10	2	0

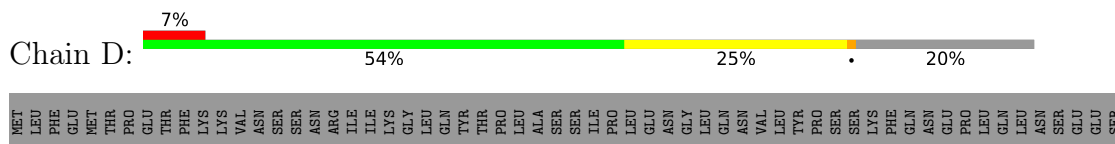
3 Residue-property plots

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.

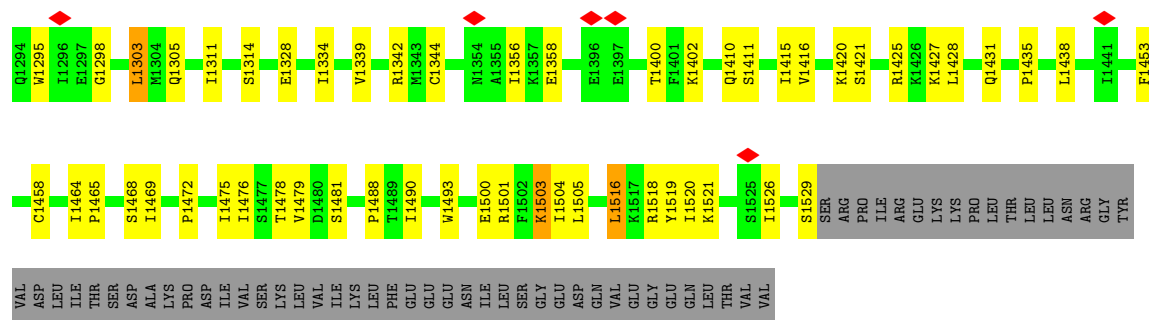
• Molecule 1: Cohesin subunit rad21



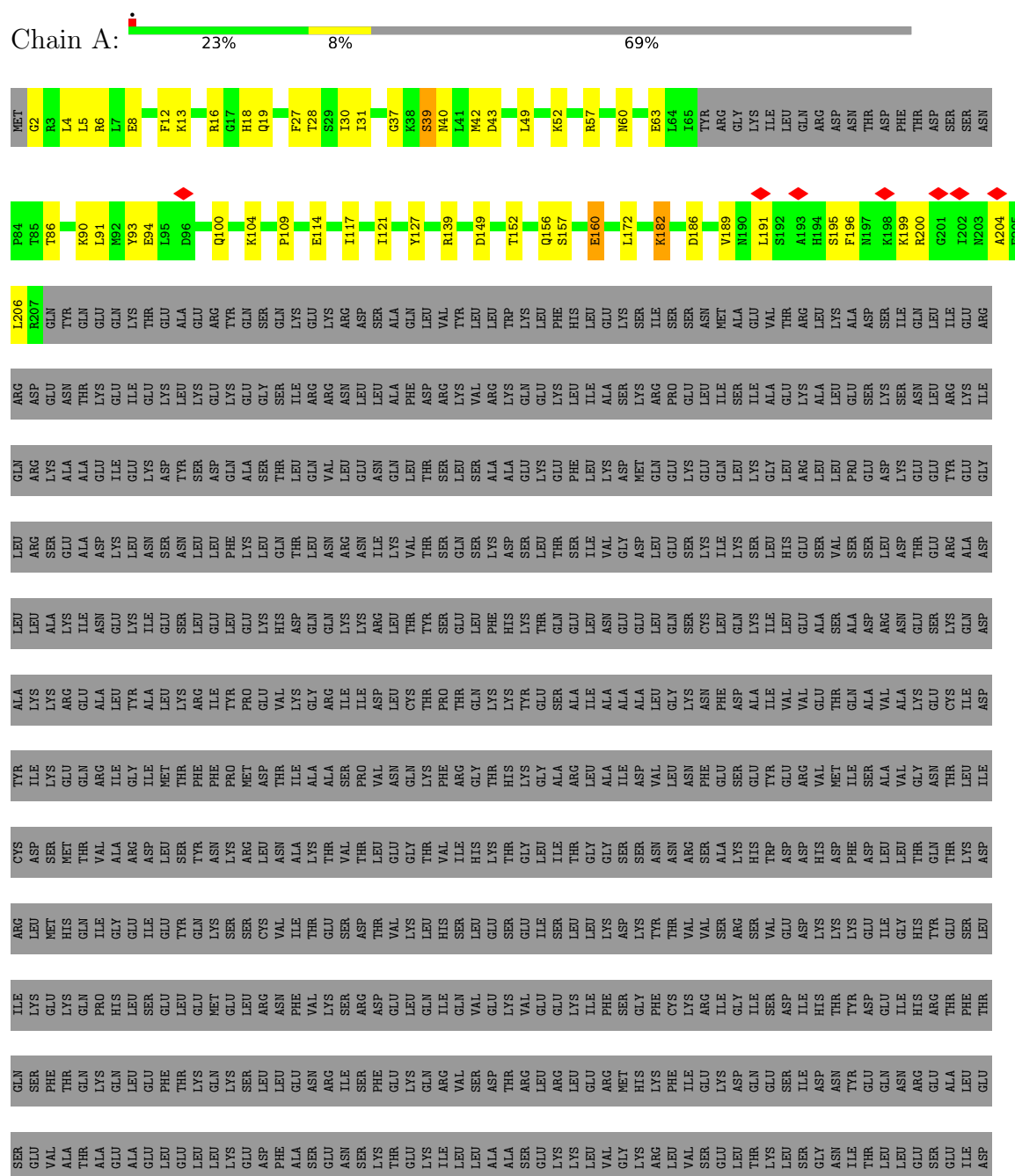
• Molecule 2: Sister chromatid cohesion protein mis4

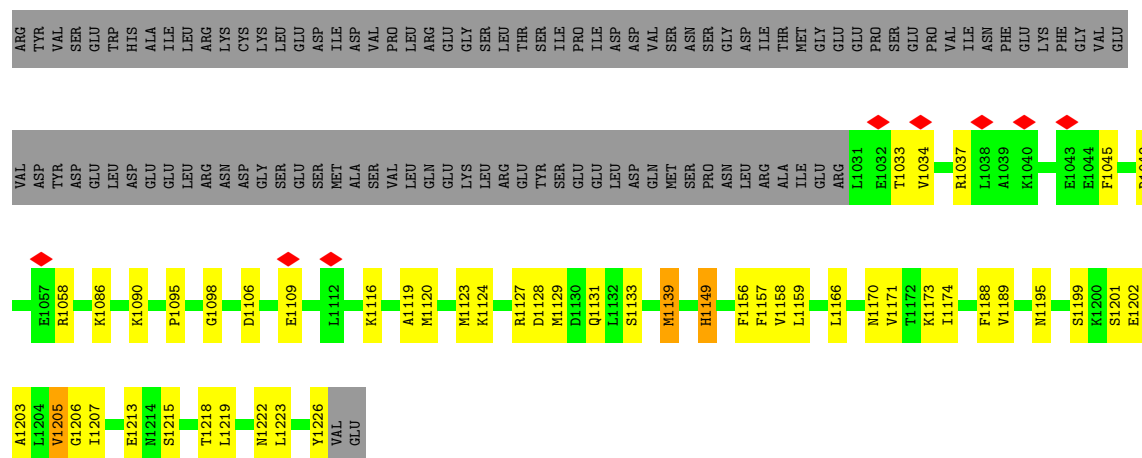


I1208	D1209	M1210	M1211	S1212	R1213	L1221	F1222	I1223	S1224	F1225	L1226	M1227	T1230	N1239	E1242	L1246	S1249	L1251	E1252	D1259	L1260	D1265	Q1266	K1267	L1268	S1269	I1270	K1271	G1272	K1273	Q1274	N1275	V1276	GLN	SER	ASN	LYS	SER	VAL	SER	ASP	GLN	D1182	D1183	A1184	L1188	F1192	Q1193	K1194	L1195	L1196	R1204	K1293													
F1114	T1115	R1116	L1117	N1118	E1121	K1124	C1130	S1133	L1134	R1138	N1143	F1144	Q1145	M1147	V1148	R1149	L1150	I1151	L1153	I1154	R1159	D1162	L1163	N1164	R1165	I1166	N1167	D1168	D1169	W1170	K1171	H1172	S1178	D1182	D1183	A1184	L1188	F1192	Q1193	K1194	L1195	L1196	R1204	K1293																						
VAL	ASP	GLU	SER	T1016	I1019	L1020	M1024	S1025	T1026	L1027	F1028	V1029	S1031	F1034	L1037	F1038	D1039	L1040	S1041	H1044	L1045	L1046	K1047	L1050	S1054	L1073	K1077	E1078	I1079	F1083	L1084	R1085	S1086	S1089	L1095	A1101	T1102	L1103	M1104	E1105	I1106	V1107	S1112	L1113																						
D905	E906	I910	L918	E919	K920	W922	N928	E937	F941	L942	E943	K944	Q945	K946	L947	R948	V949	Q950	Y951	I954	C958	R965	L969	S972	S979	K980	E981	E982	I983	N984	T987	L988	Q991	I992	R993	L994	L995	L999	I1004	E1009	ASP	GLN																								
F791	Q792	A793	S794	L795	R796	T797	K798	C799	L800	R801	I802	S803	N804	Q805	S811	I812	L813	E728	A729	I730	K731	I732	R733	D734	N735	I736	T737	K738	N739	A740	Q741	K742	K743	S744	F748	GLN	GLY	PRO	SER	PRO	PHE	LYS	ALA	ASP	GLU	N759	D760	I763	F774	K778	F779	S782	S790													
F586	A587	L588	S589	T590	L511	I512	Q513	S514	I517	Q518	N519	L520	F521	I522	D523	R524	G525	T526	I525	V526	Q527	S528	E529	S530	K531	S532	T533	E534	A535	K536	A637	L638	V645	V648	L651	F652	D653	L654	S655	L656	K659	P663	D670	I671	I672	T675	I678	T679	R680	L681	S582	D583														
Y504	S505	V509	R510	L511	I512	Q513	S514	I517	Q518	N519	L520	F521	I522	D523	R524	G525	T526	I525	V526	Q527	S528	E529	S530	K531	S532	T533	E534	A535	K536	A637	L638	V645	V648	L651	F652	D653	L654	S655	L656	K659	P663	D670	I671	I672	T675	I678	T679	R680	L681	S582	D583															
H389	L390	L394	V397	A398	R399	V400	N402	S405	V418	I419	R420	I421	V422	Y423	P426	S446	F449	K450	L451	T457	L458	Q459	P466	R469	D470	F471	I472	I473	E474	E475	S476	L477	T478	N479	F480	L483	R487	T492	Y493	R494	K499	Q502	Y503																							
LEU	PRO	VAL	ALA	TYR	SER	ILE	ILE	ASN	HIS	ASP	SER	THR	F320	D324	F325	I326	L327	T329	T330	A331	V333	L334	F335	V340	P341	S342	F343	L346	Q347	S351	L355	H360	T366	E369	A370	I371	I374	V375	Q376	S377	K378	E386																								
D241	F242	S243	S244	N245	I249	K250	R251	L252	THR	THR	PRO	PRO	LYS	LYS	ARG	GLN	LEU	MET	GLU	PRO	GLU	ASP	I259	S260	THR	S261	H262	A263	I264	E265	K266	L267	V268	M269	A270	I271	P272	T273	L274	S275	R276	L277	V218	L219	L220	K221	Q222	L223	Q224	E285	D225	T226	R227	L228	L229	I230	S231	V232	V233	I234	E235	A236	E237	N238	S239	E240
SER	GLU	ILE	LEU	ASN	GLN	THR	LYS	VAL	ASP	PHE	PRO	GLY	ALA	THR	PHE	LEU	VAL	CYS	ASN	ASP	SER	GLU	LYS	THR	ASN	ALA	ALA	GLY	PHE	LEU	ALA	LEU	THR	PRO	ARG	SER	VAL	SER	ASN	SER	GLN	SER	LYS	SER	ARG	VAL	PHE	ASN	SER	ASP	VAL	GLN														

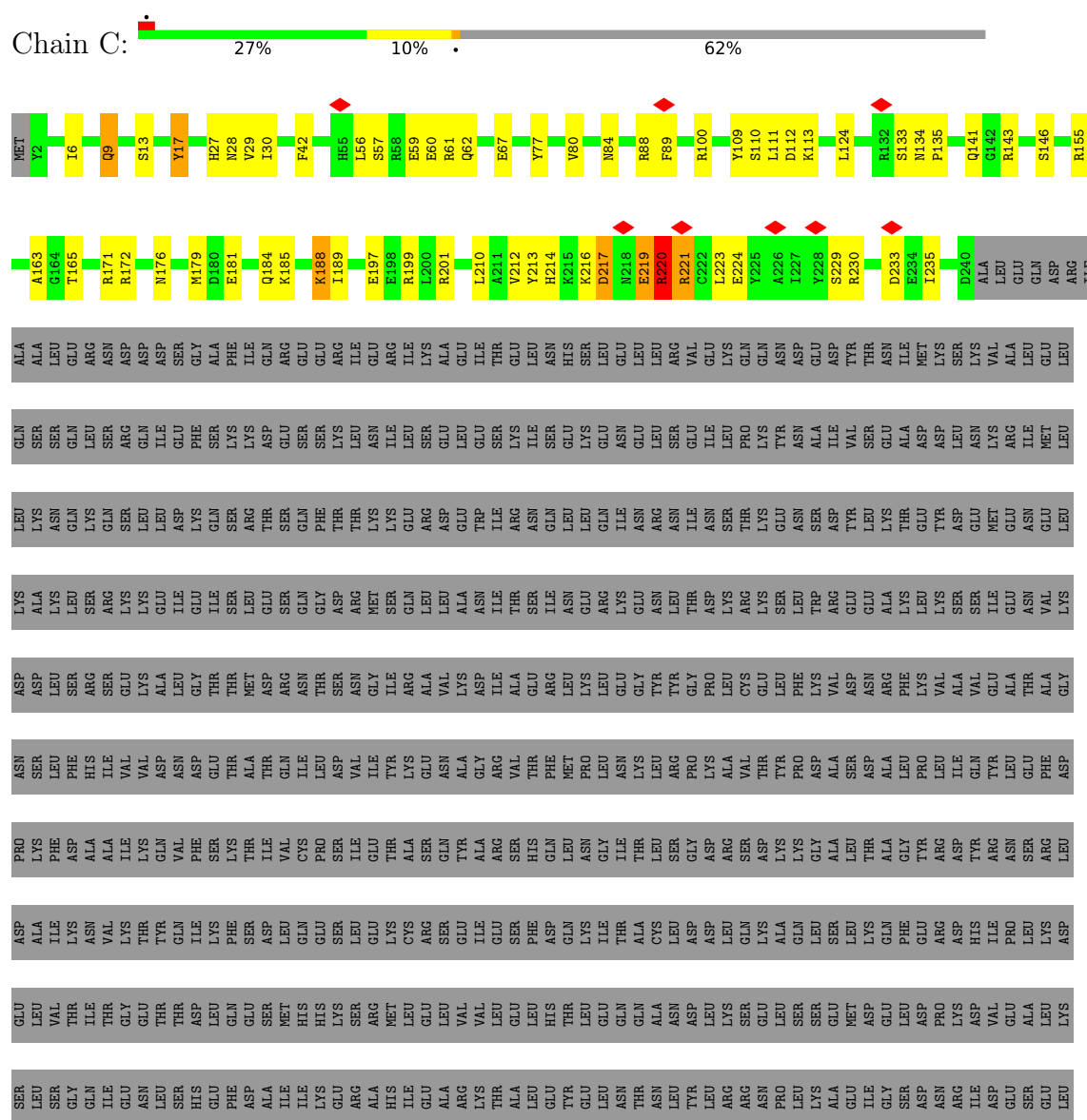


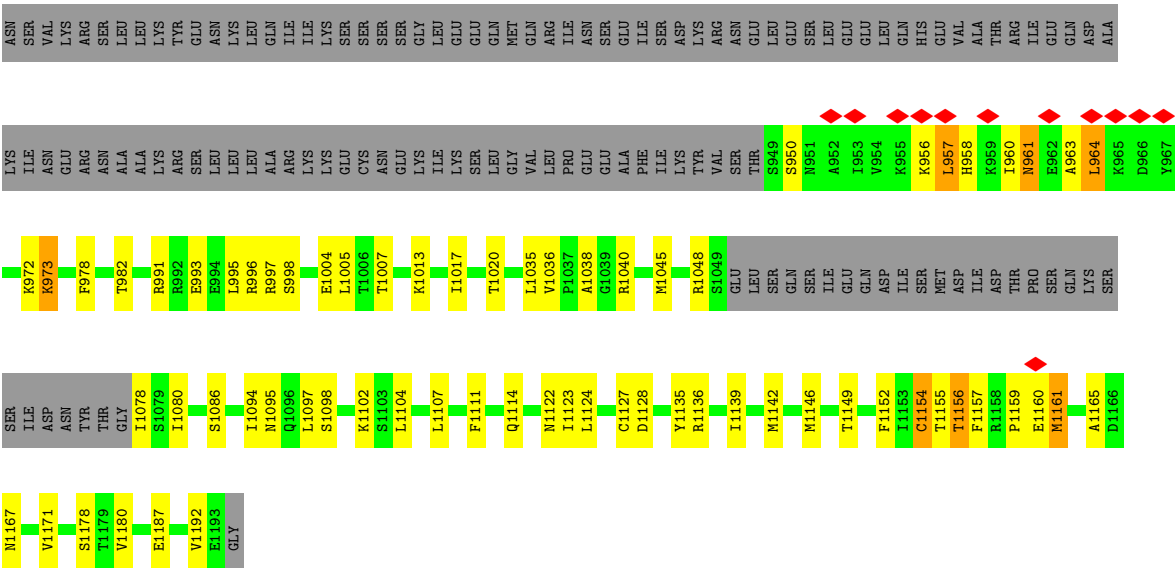
• Molecule 3: Structural maintenance of chromosomes protein 1





• Molecule 4: Structural maintenance of chromosomes protein 3

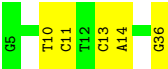
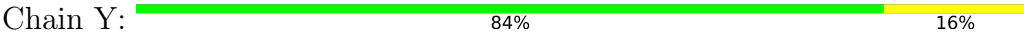




• Molecule 5: DNA (32-MER)



• Molecule 6: DNA (32-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	255148	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	33.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	4.069	Depositor
Minimum map value	-1.652	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	392.40002, 392.40002, 392.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

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

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	B	0.73	1/1211 (0.1%)	1.16	7/1634 (0.4%)
2	D	0.66	18/10425 (0.2%)	0.88	22/14086 (0.2%)
3	A	0.70	4/3100 (0.1%)	0.85	10/4170 (0.2%)
4	C	0.94	16/3717 (0.4%)	1.10	35/4996 (0.7%)
5	X	0.37	0/740	0.48	0/1139
6	Y	0.40	0/730	0.57	0/1125
All	All	0.71	39/19923 (0.2%)	0.92	74/27150 (0.3%)

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
1	B	0	1
2	D	0	3
4	C	0	2
All	All	0	6

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	9	GLN	CD-NE2	-25.17	0.80	1.33
4	C	9	GLN	CB-CG	-14.25	1.09	1.52
2	D	1520	ILE	CG1-CD1	-13.20	1.00	1.51
3	A	152	THR	CB-CG2	-11.36	1.15	1.52
4	C	9	GLN	CG-CD	-10.97	1.24	1.52

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	220	ARG	NE-CZ-NH2	16.52	134.07	119.20
4	C	220	ARG	NE-CZ-NH1	-15.65	105.84	121.50
4	C	9	GLN	CG-CD-NE2	-14.96	93.95	116.40
2	D	1211	MET	CG-SD-CE	-14.57	68.85	100.90
4	C	9	GLN	CG-CD-OE1	10.97	142.74	120.80

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	85	ARG	Sidechain
4	C	220	ARG	Sidechain
2	D	1178	SER	Peptide
2	D	722	LYS	Peptide
2	D	744	SER	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1195	0	1238	52	0
2	D	10247	0	10549	319	0
3	A	3047	0	3045	70	0
4	C	3665	0	3668	93	0
5	X	658	0	358	8	0
6	Y	654	0	365	4	0
7	A	4	0	0	0	0
7	C	4	0	0	1	0
8	A	27	0	11	4	0
8	C	27	0	11	1	0
All	All	19528	0	19245	525	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 14.

The worst 5 of 525 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:D:290:ILE:HD11	2:D:346:LEU:CD1	1.66	1.25
2:D:268:TYR:HB2	2:D:332:LEU:CD2	1.73	1.18
2:D:290:ILE:CD1	2:D:346:LEU:HD12	1.73	1.16
2:D:290:ILE:HD11	2:D:346:LEU:HD12	1.01	1.00
2:D:268:TYR:HB2	2:D:332:LEU:HD21	0.99	0.96

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	148/628 (24%)	137 (93%)	11 (7%)	0	100	100
2	D	1262/1587 (80%)	1148 (91%)	114 (9%)	0	100	100
3	A	378/1228 (31%)	351 (93%)	27 (7%)	0	100	100
4	C	450/1194 (38%)	402 (89%)	48 (11%)	0	100	100
All	All	2238/4637 (48%)	2038 (91%)	200 (9%)	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	B	132/539 (24%)	128 (97%)	4 (3%)	36	57
2	D	1186/1480 (80%)	1185 (100%)	1 (0%)	88	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	330/1102 (30%)	330 (100%)	0	100	100
4	C	407/1082 (38%)	407 (100%)	0	100	100
All	All	2055/4203 (49%)	2050 (100%)	5 (0%)	85	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	582	CYS
1	B	583	ASN
1	B	584	ARG
1	B	585	GLU
2	D	299	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	1193	GLN
3	A	60	ASN
4	C	1114	GLN
2	D	1336	GLN
3	A	194	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](#)

4 ligands are modelled in this entry.

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	BEF	C	1201	8	0,3,3	-	-	-		
7	BEF	A	1301	8	0,3,3	-	-	-		
8	ADP	A	1302	7	28,29,29	2.00	4 (14%)	43,45,45	1.62	8 (18%)
8	ADP	C	1202	7	28,29,29	2.01	4 (14%)	43,45,45	1.76	8 (18%)

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
8	ADP	A	1302	7	-	8/16/32/32	0/3/3/3
8	ADP	C	1202	7	-	8/16/32/32	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	1202	ADP	PA-O5'	7.80	1.89	1.59
8	A	1302	ADP	PA-O5'	7.78	1.89	1.59
8	A	1302	ADP	PA-O3A	-3.43	1.55	1.59
8	C	1202	ADP	PA-O3A	-3.36	1.55	1.59
8	A	1302	ADP	O2'-C2'	-3.25	1.34	1.43

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	1202	ADP	O2A-PA-O3A	7.33	127.09	107.27
8	A	1302	ADP	O3A-PA-O1A	5.44	127.06	110.70
8	C	1202	ADP	O5'-PA-O1A	-4.02	93.02	108.94
8	A	1302	ADP	O2A-PA-O5'	-3.20	93.06	107.57
8	A	1302	ADP	O5'-PA-O1A	-2.82	97.77	108.94

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

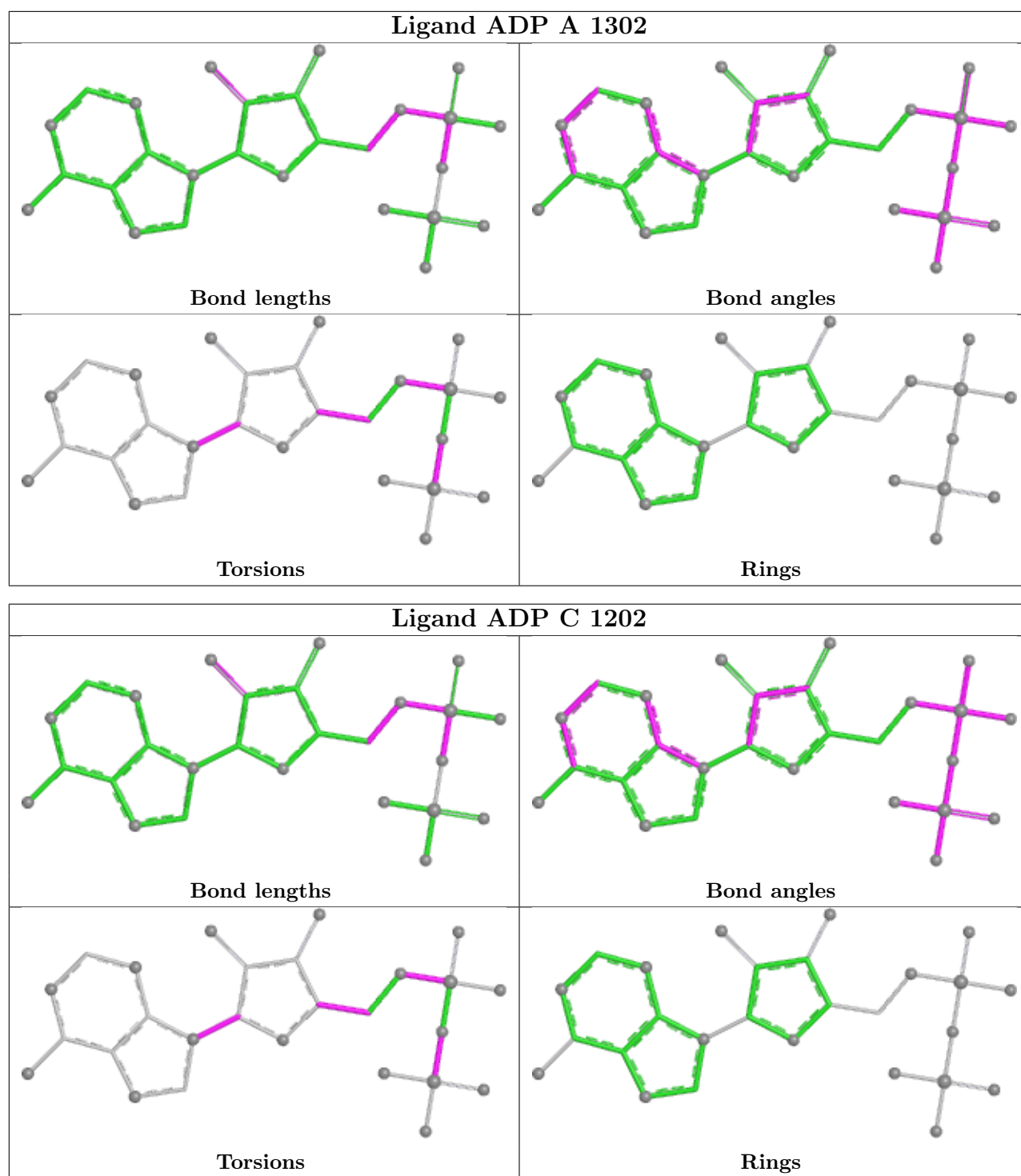
Mol	Chain	Res	Type	Atoms
8	A	1302	ADP	PA-O3A-PB-O2B
8	A	1302	ADP	C5'-O5'-PA-O1A
8	A	1302	ADP	C5'-O5'-PA-O2A
8	A	1302	ADP	C3'-C4'-C5'-O5'
8	C	1202	ADP	PA-O3A-PB-O2B

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1201	BEF	1	0
8	A	1302	ADP	4	0
8	C	1202	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	602:SER	C	603:LEU	N	1.20

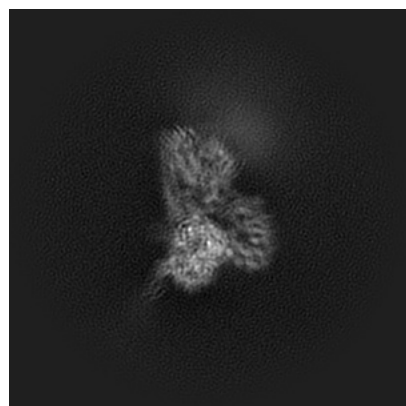
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10930. These allow visual inspection of the internal detail of the map and identification of artifacts.

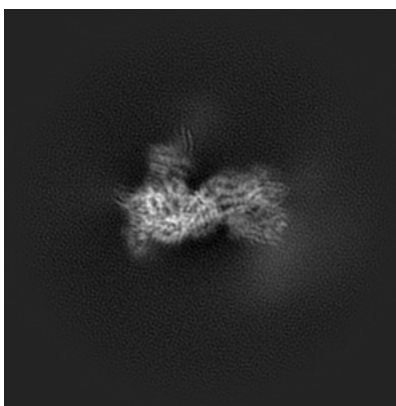
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

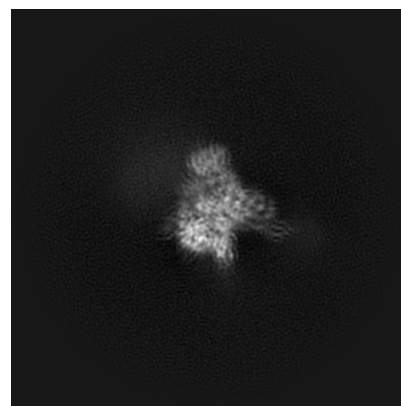
6.1.1 Primary map



X

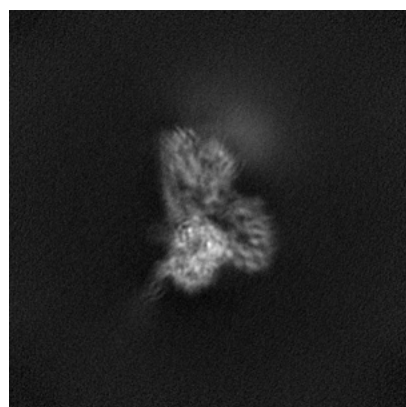


Y

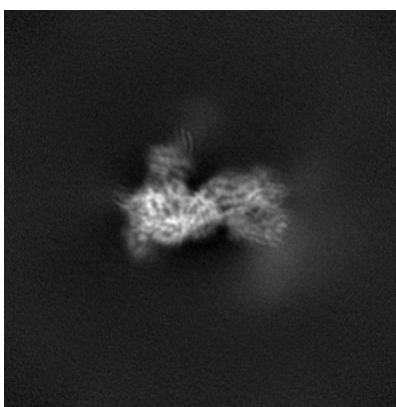


Z

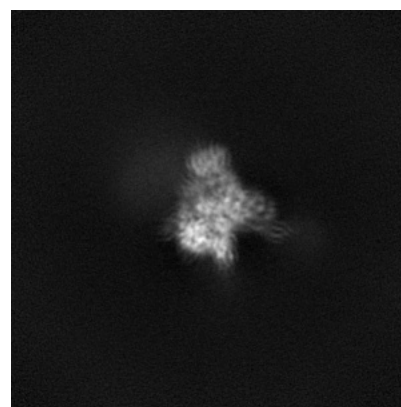
6.1.2 Raw map



X



Y

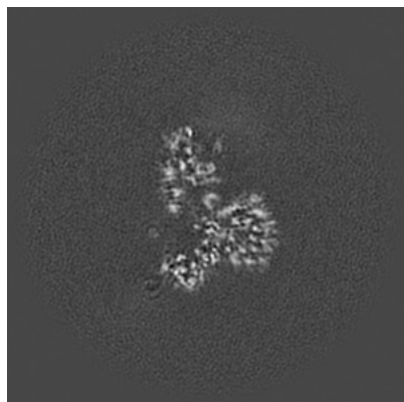


Z

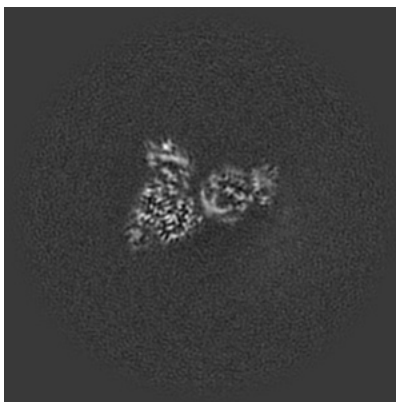
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

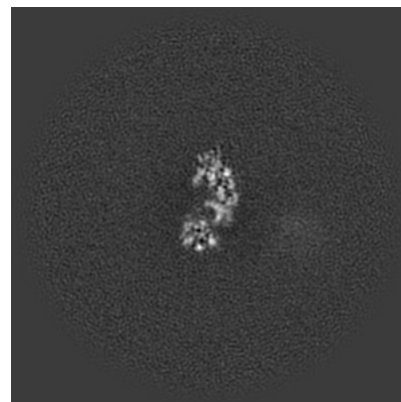
6.2.1 Primary map



X Index: 180

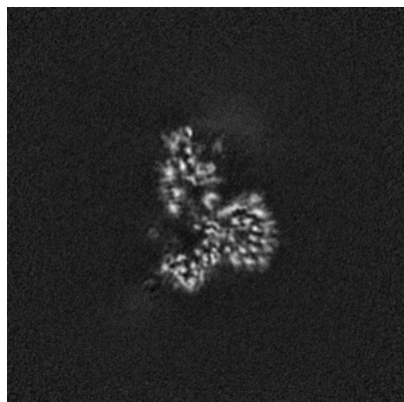


Y Index: 180

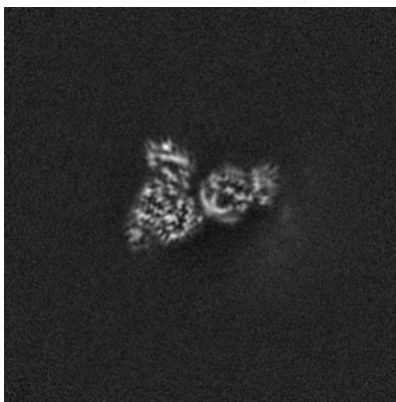


Z Index: 180

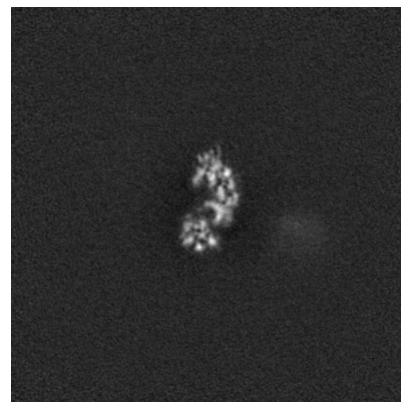
6.2.2 Raw map



X Index: 180



Y Index: 180

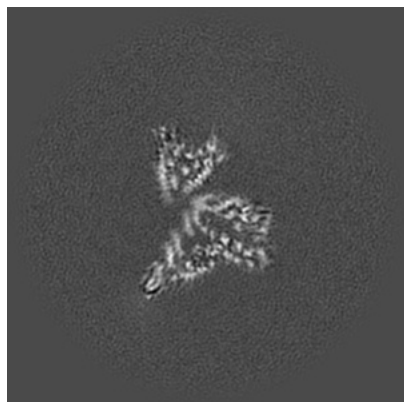


Z Index: 180

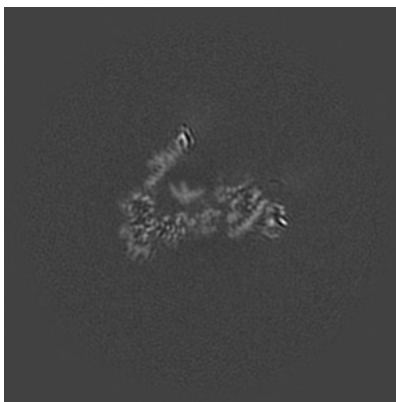
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

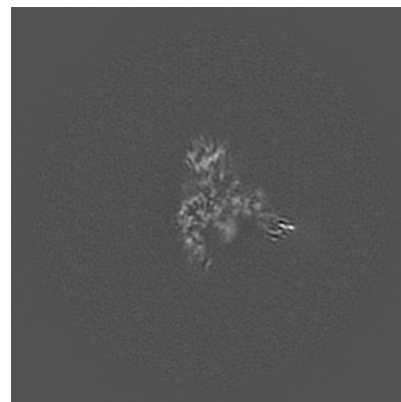
6.3.1 Primary map



X Index: 188

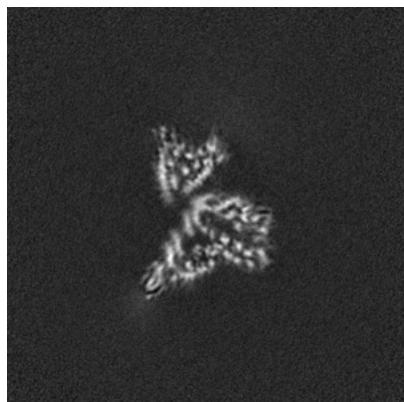


Y Index: 163

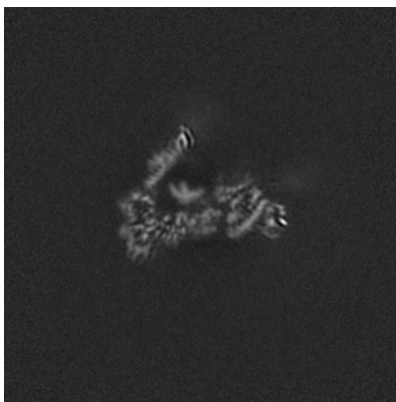


Z Index: 160

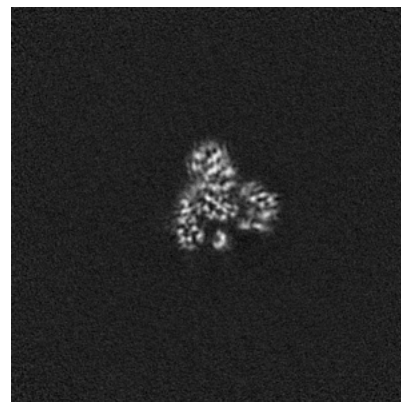
6.3.2 Raw map



X Index: 188



Y Index: 163

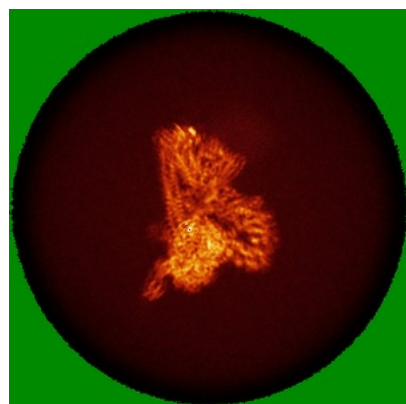


Z Index: 140

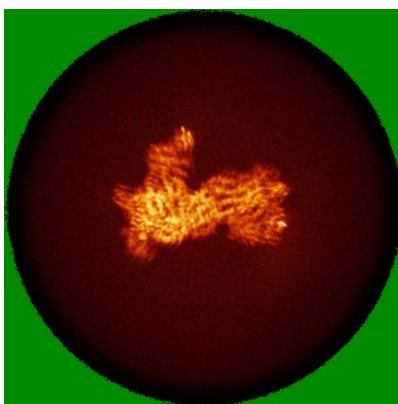
The images above show the largest variance slices of the map in three orthogonal directions.

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

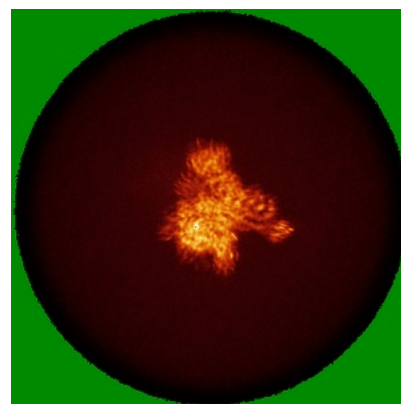
6.4.1 Primary map



X

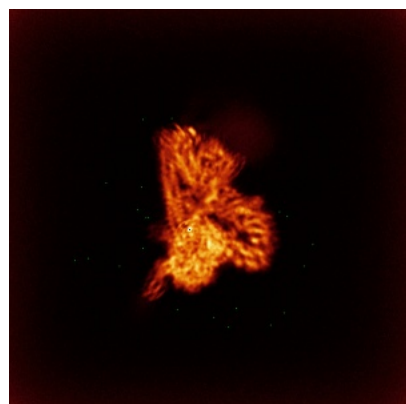


Y

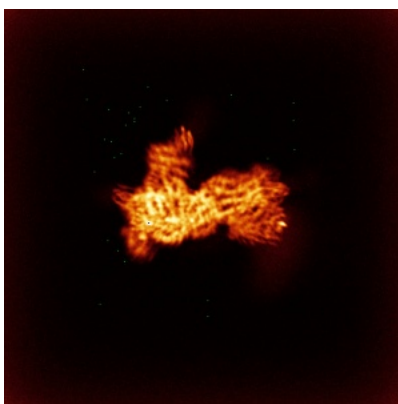


Z

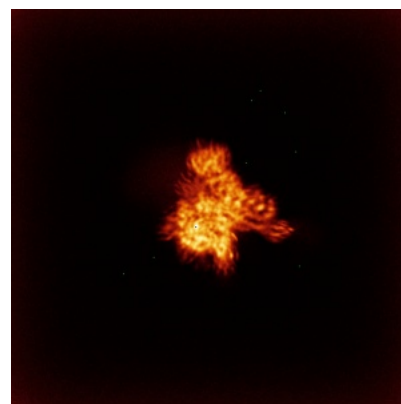
6.4.2 Raw map



X



Y

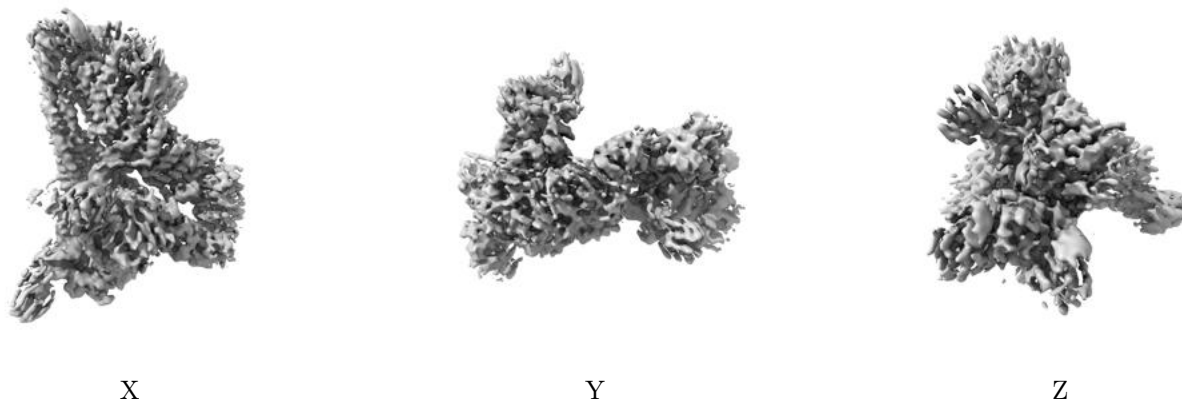


Z

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.

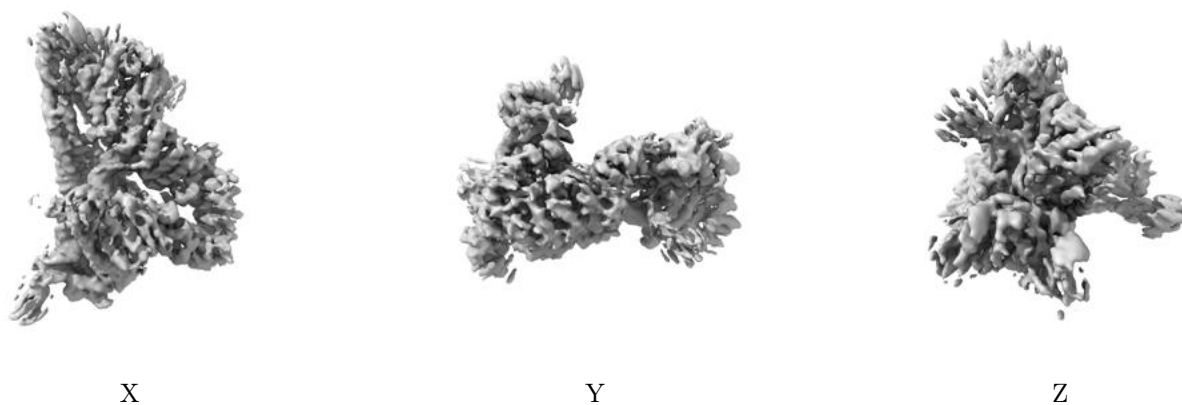
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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.

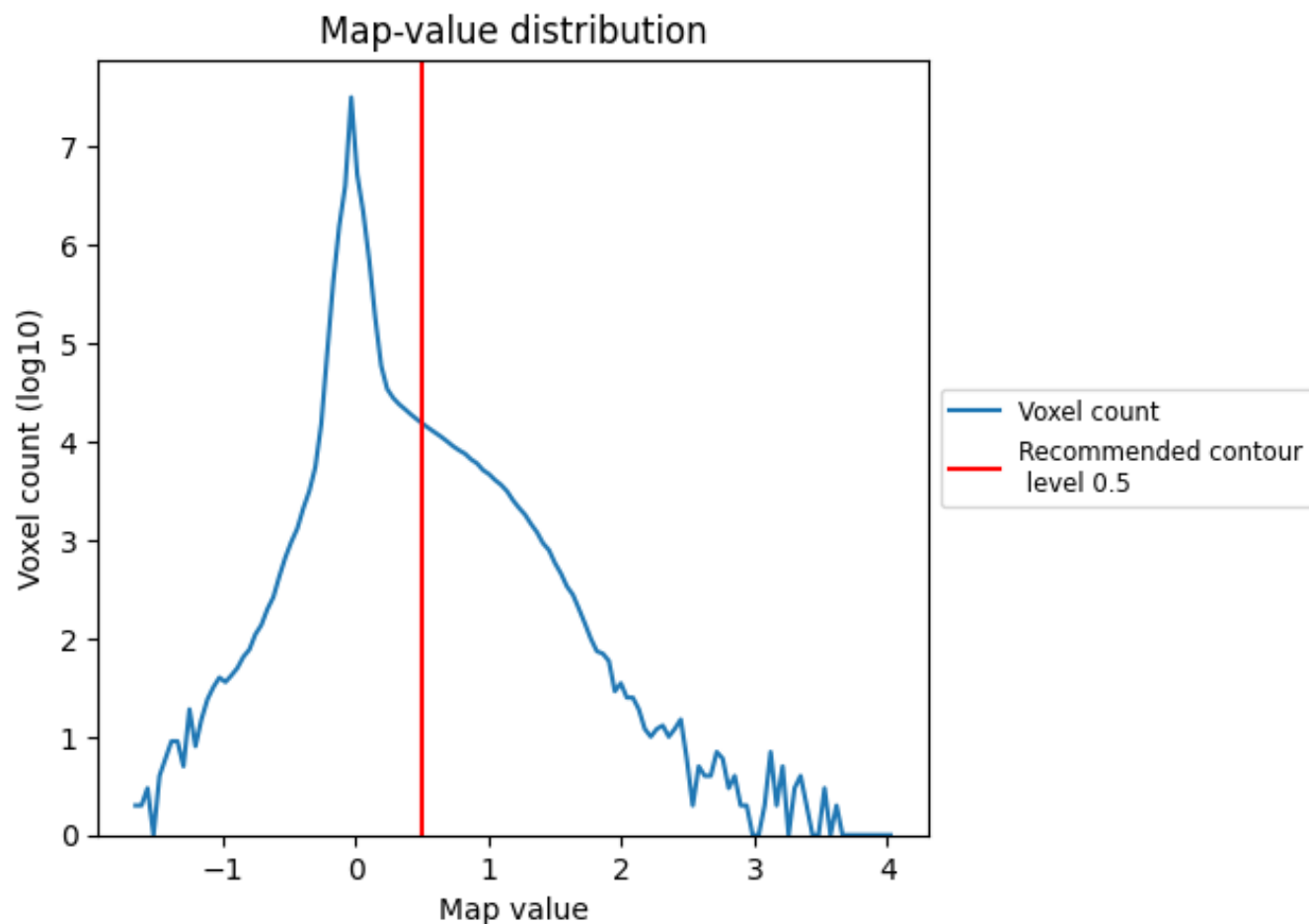
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

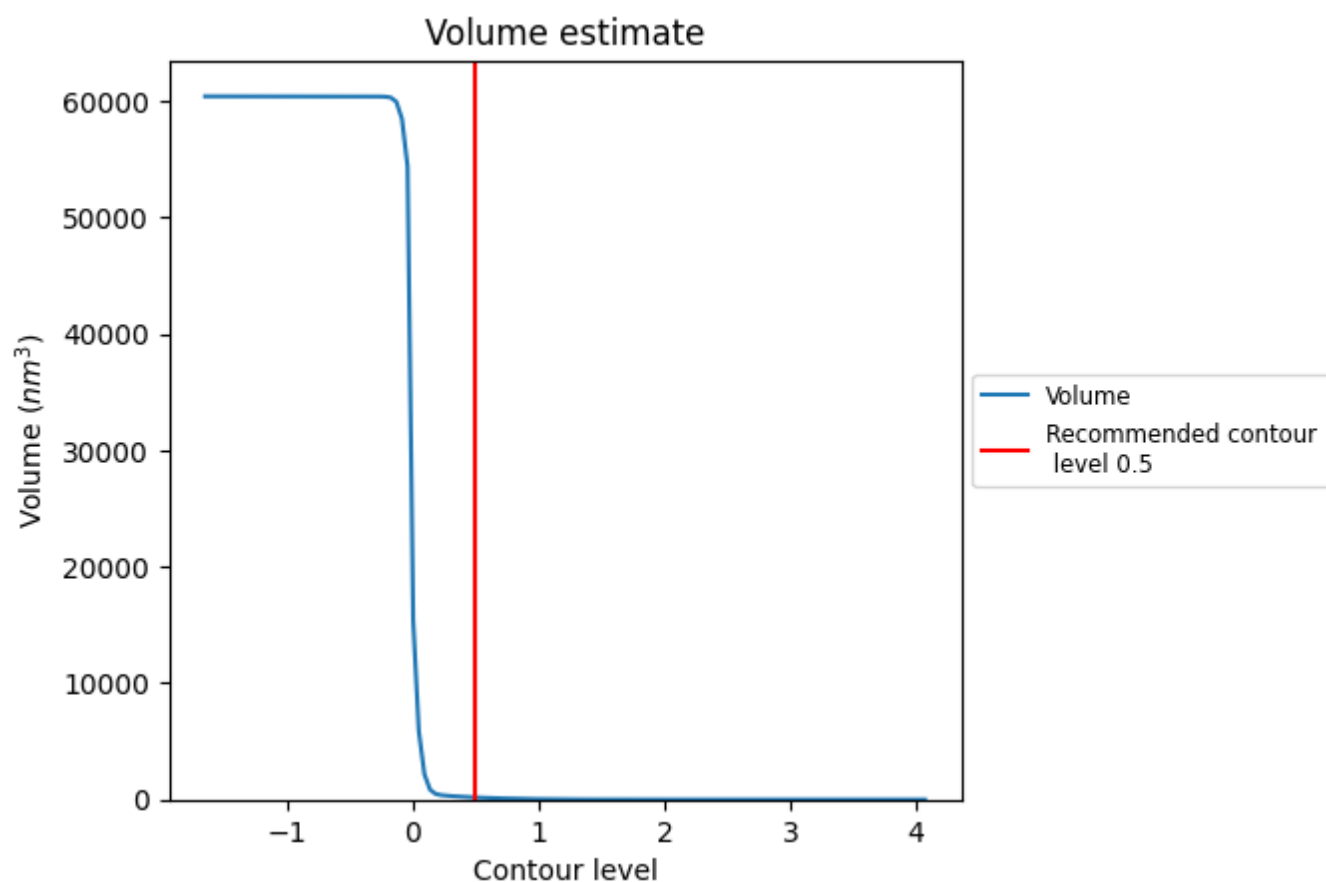
This section contains the results of statistical analysis of the map.

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.

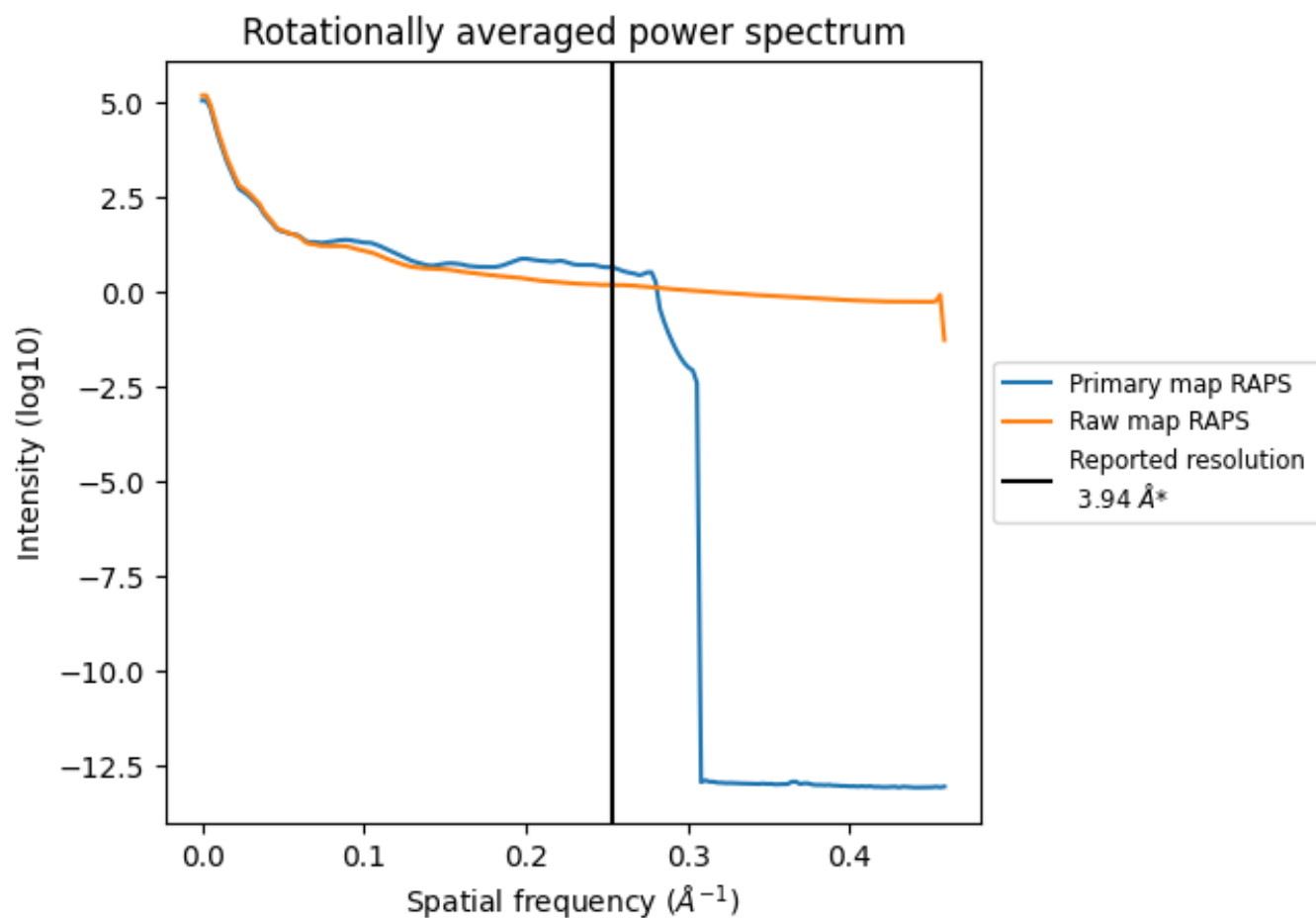
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm³; this corresponds to an approximate mass of 161 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 ⓘ

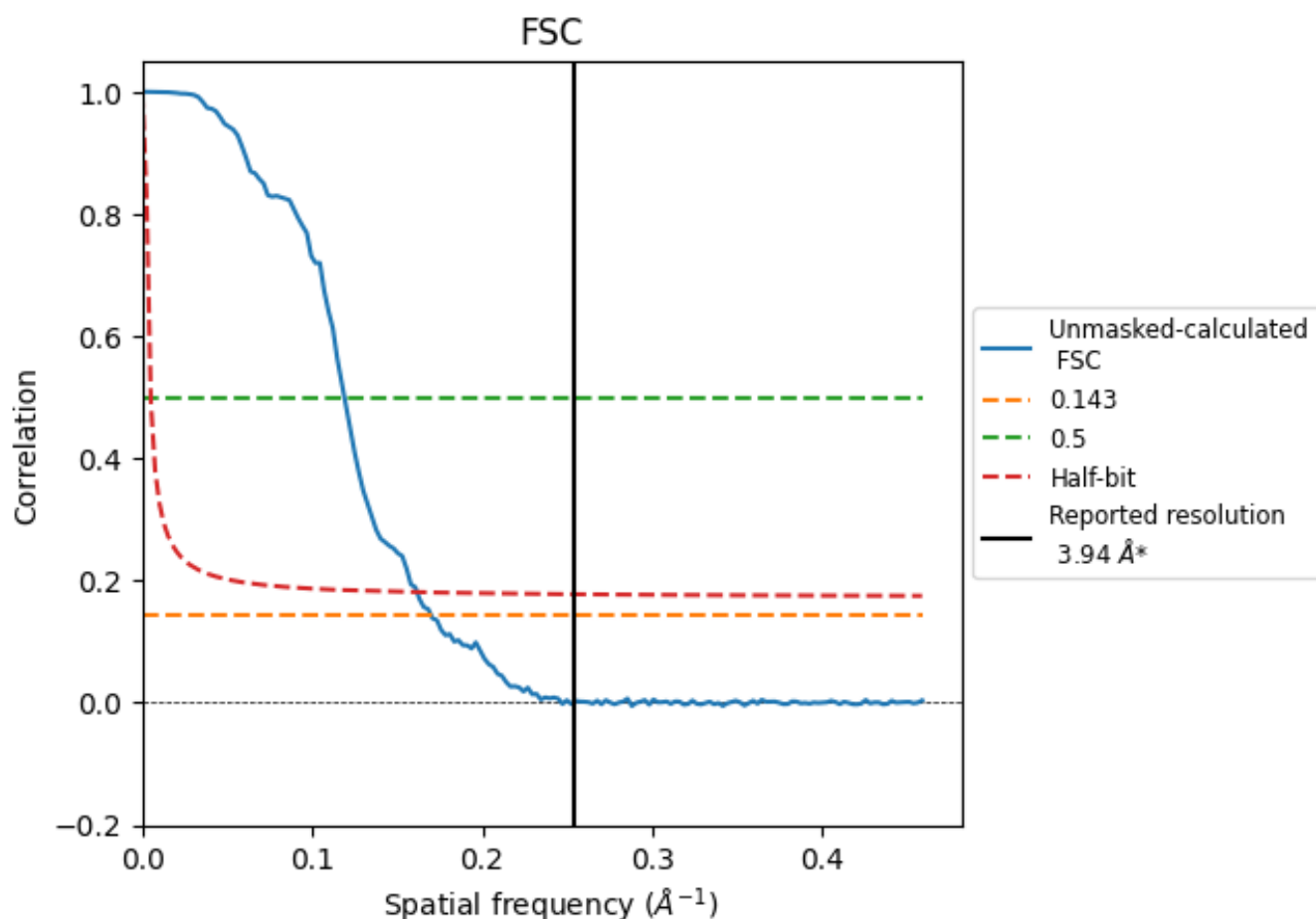


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 0.254 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

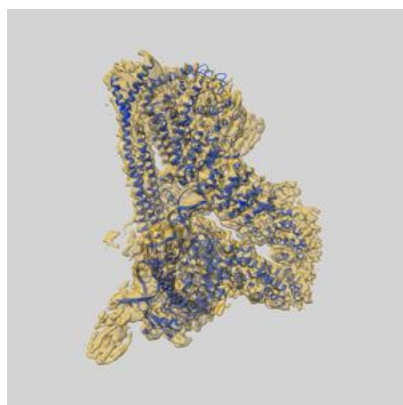
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.89	8.41	6.19

*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 5.89 differs from the reported value 3.94 by more than 10 %

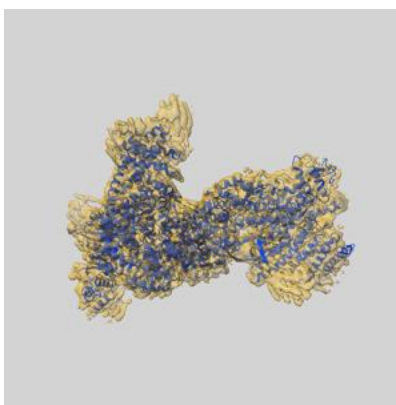
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10930 and PDB model 6YUF. Per-residue inclusion information can be found in section [3](#) on page [7](#).

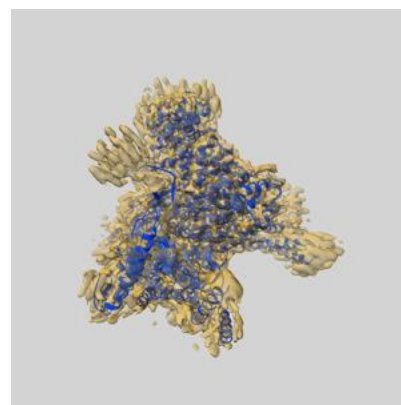
9.1 Map-model overlay [i](#)



X



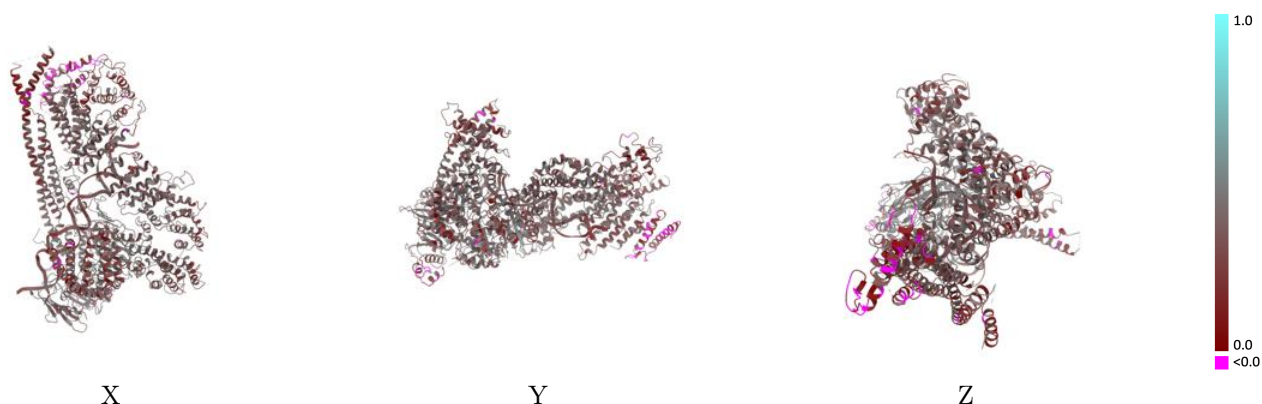
Y



Z

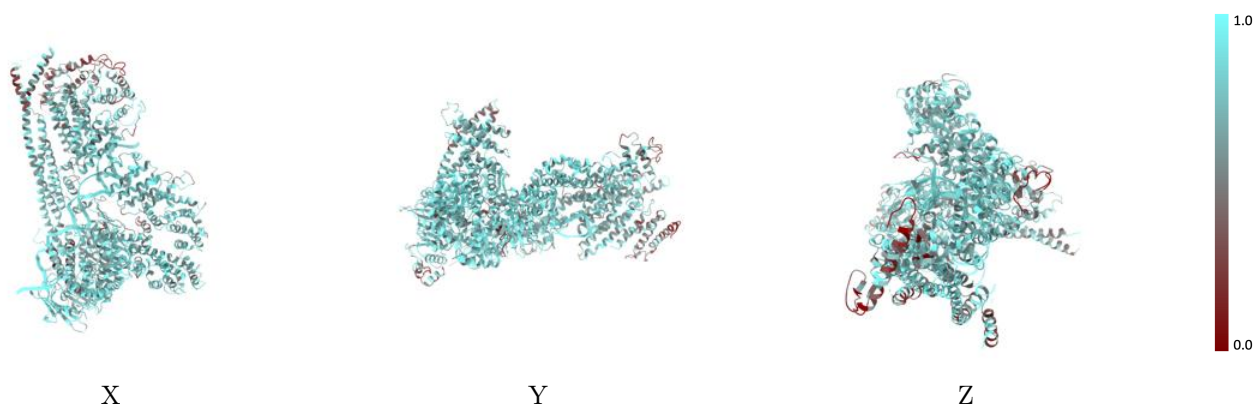
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



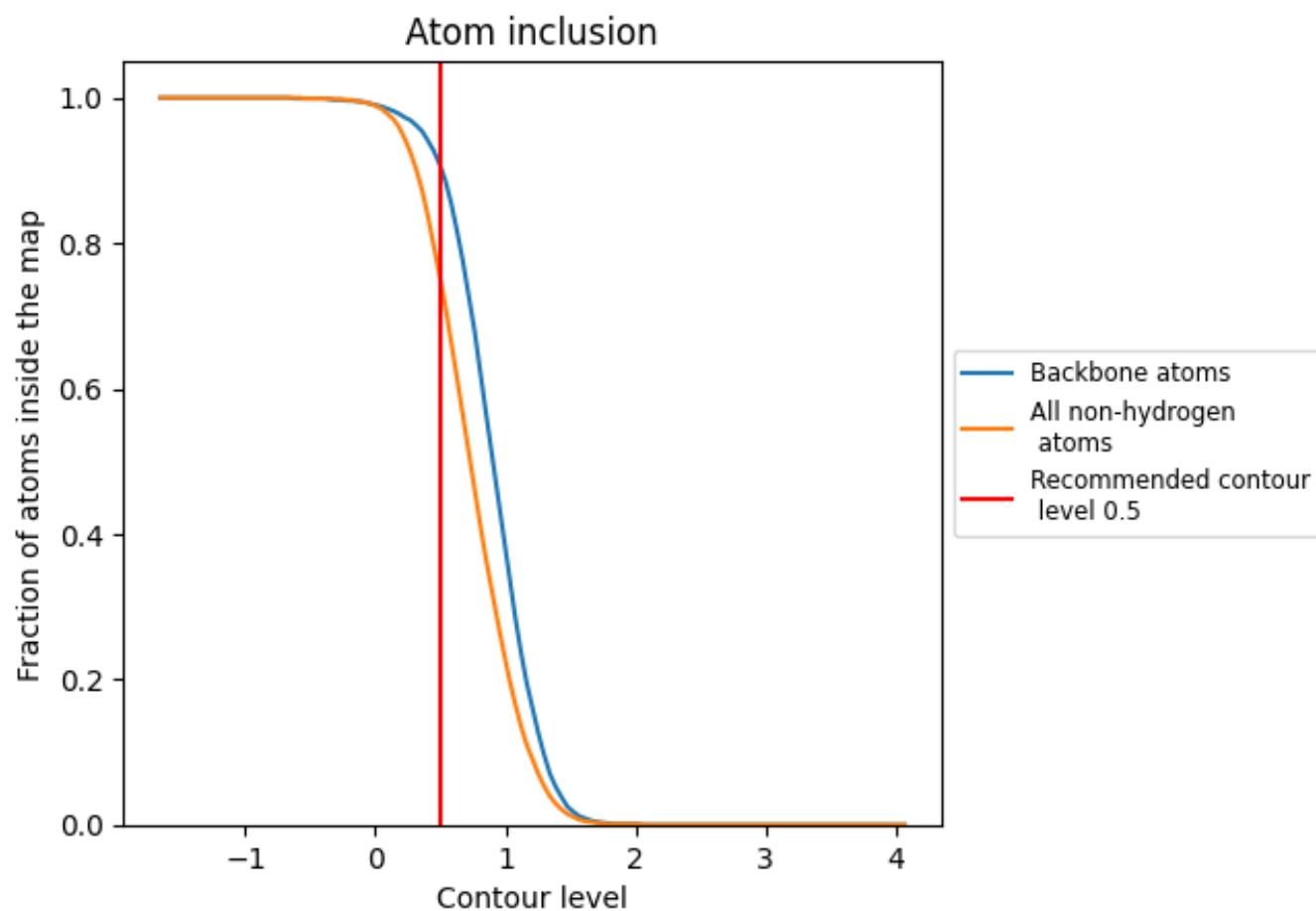
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 75% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7500	0.3480
A	0.8000	0.3990
B	0.6830	0.3130
C	0.7820	0.3820
D	0.7100	0.3290
X	0.9090	0.3100
Y	0.9220	0.3230

