



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:50 AM UTC

PDB ID : 8B3D / pdb_00008b3d
EMDB ID : EMD-15825
Title : Structure of the Pol II-TCR-ELOF1 complex.
Authors : Kokic, G.; Cramer, P.
Deposited on : 2022-09-16
Resolution : 2.60 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:

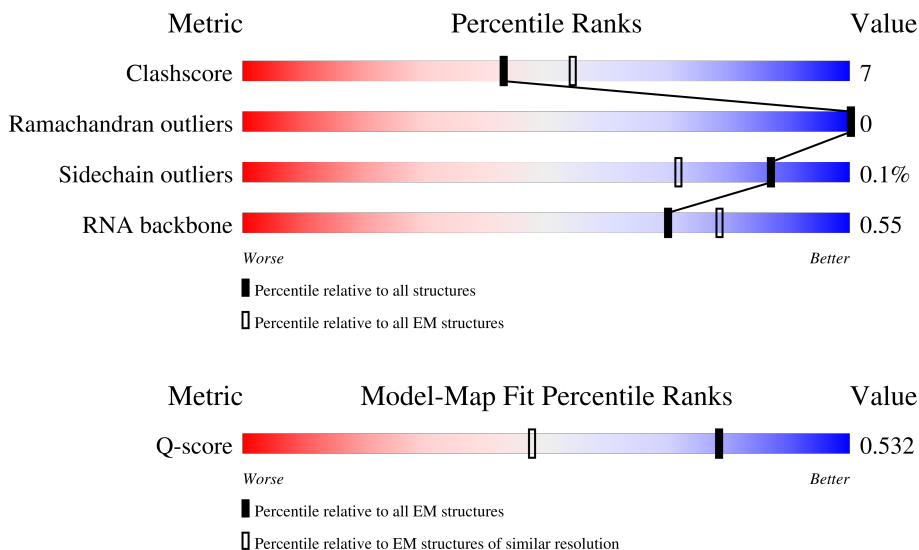
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.60 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	1970	 5% 59% 11% 28%
2	B	1167	 5% 82% 14% 5%
3	C	275	 5% 81% 12% 5%

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Mol	Chain	Length	Quality of chain
4	D	142	78% 73% 15% 10%
5	E	210	84% 15%
6	F	127	5% 54% 9% 35%
7	G	254	41% 52% 13% 33%
8	H	150	87% 10% ..
9	I	125	16% 70% 22% 6%
10	J	67	93% 7%
11	K	117	81% 16% ..
12	L	58	59% 17% 21%
13	M	83	12% 73% 23%
14	N	52	10% 17% 60% 23%
15	P	10	80% 10% 10%
16	T	52	8% 21% 79%
17	a	396	78% 14% 8%
18	b	1493	28% 7% 65%
19	c	709	34% 33% 63%
20	d	1140	61% 7% 31%

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 95808 atoms, of which 46954 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	1409	22460	7022	11299	1998	2070	71	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	TYR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	THR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	TYR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	THR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	B	1130	18131	5725	9083	1591	1668	64	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	C	260	4120	1309	2031	359	415	6	0	0

- Molecule 4 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	D	128	1985	636	972	172	201	4	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	E	209	3457	1089	1737	300	323	8	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	F	82	1341	418	684	113	121	5	0	0

- Molecule 7 is a protein called RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
7	G	171	2665	867	1331	216	243	8	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
8	H	148	2333	750	1147	194	237	5	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	I	117	1827	587	878	169	182	11	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	J	67	1086	345	553	90	92	6	0	0

- Molecule 11 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	115	Total	C	H	N	O	S	0	0
			1862	593	942	152	173	2		

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	46	Total	C	H	N	O	S	0	0
			781	241	393	75	66	6		

- Molecule 13 is a protein called Transcription elongation factor 1 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	64	Total	C	H	N	O	S	0	0
			968	312	463	81	105	7		

- Molecule 14 is a DNA chain called NTS.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	40	Total	C	H	N	O	P	0	0
			913	393	84	162	234	40		

- Molecule 15 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	10	Total	C	H	N	O	P	0	0
			330	98	110	45	67	10		

- Molecule 16 is a DNA chain called TS.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	T	52	Total	C	H	N	O	P	0	0
			1078	476	87	160	303	52		

- Molecule 17 is a protein called DNA excision repair protein ERCC-8.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	a	365	Total	C	H	N	O	S	0	0
			5624	1775	2775	507	548	19		

- Molecule 18 is a protein called DNA excision repair protein ERCC-6.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
18	b	520	8561	2746	4302	746	746	21	0	0

- Molecule 19 is a protein called UV-stimulated scaffold protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
19	c	264	3910	1237	1911	390	363	9	0	0

- Molecule 20 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
20	d	781	12321	3916	6160	1038	1173	34	0	0

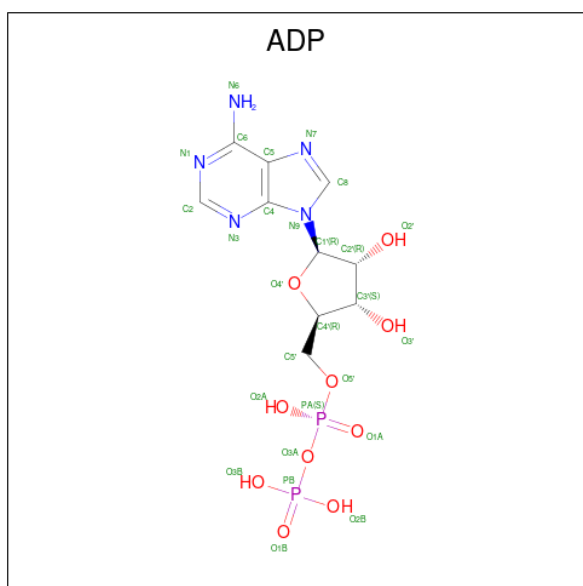
- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
21	A	2	Total	Zn	0
			2	2	
21	B	1	Total	Zn	0
			1	1	
21	C	1	Total	Zn	0
			1	1	
21	I	2	Total	Zn	0
			2	2	
21	J	1	Total	Zn	0
			1	1	
21	L	1	Total	Zn	0
			1	1	
21	M	1	Total	Zn	0
			1	1	
21	c	1	Total	Zn	0
			1	1	

- Molecule 22 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

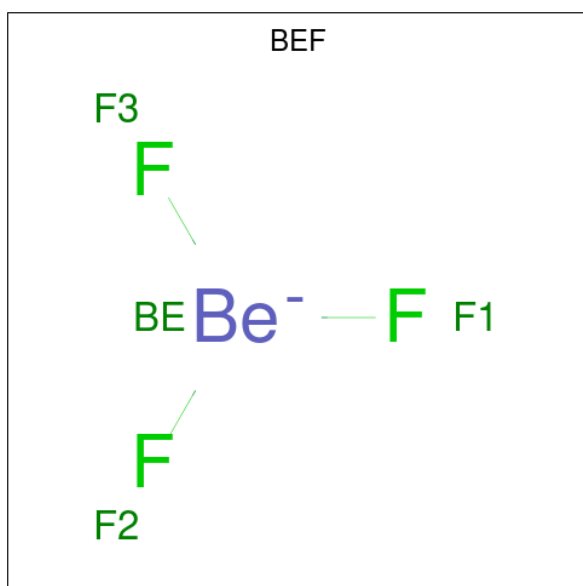
Mol	Chain	Residues	Atoms		AltConf
22	A	1	Total	Mg	0
			1	1	
22	b	1	Total	Mg	0
			1	1	

- Molecule 23 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
23	b	1	39	10	12	5	10	2	0

- Molecule 24 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3).

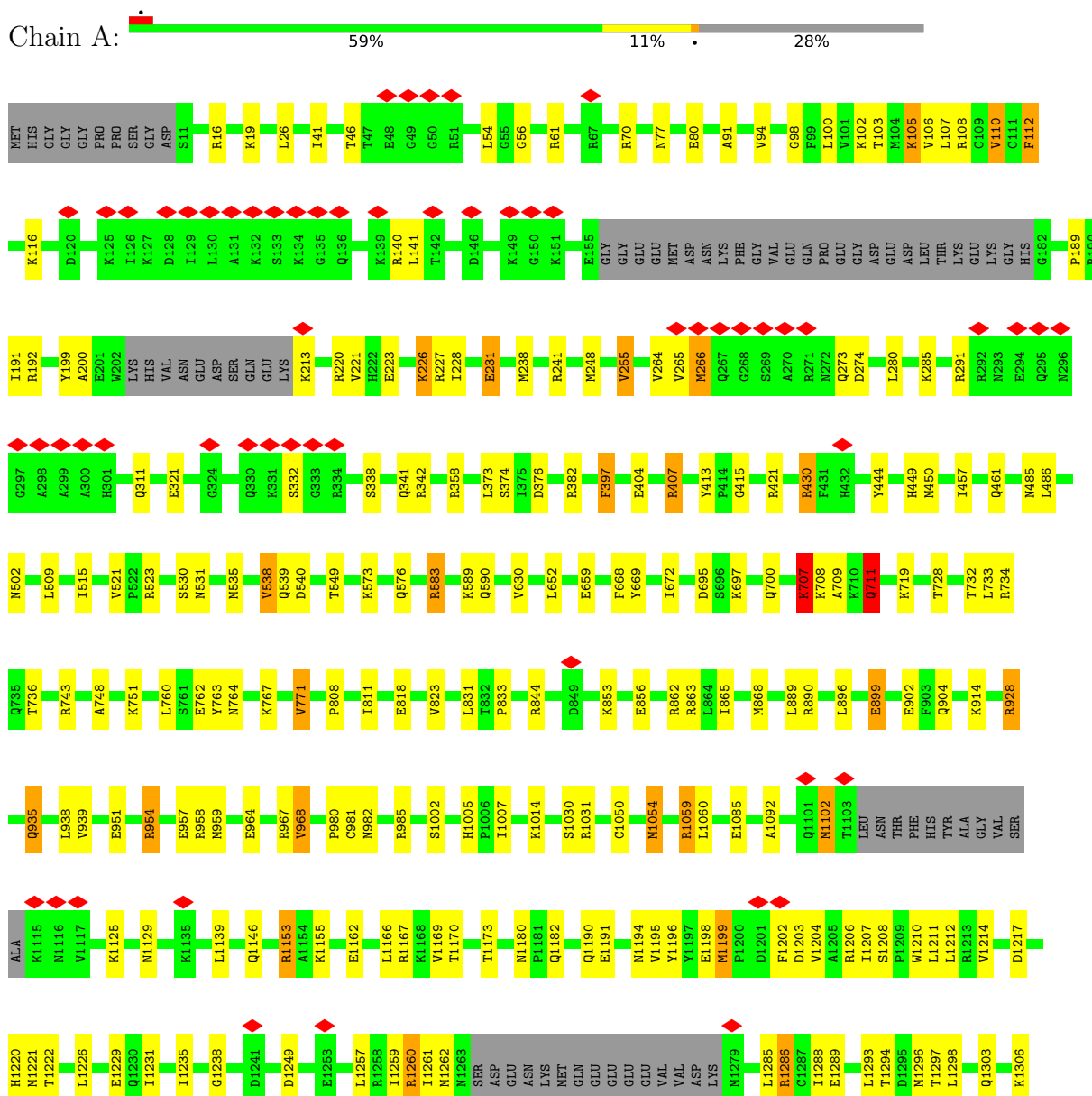


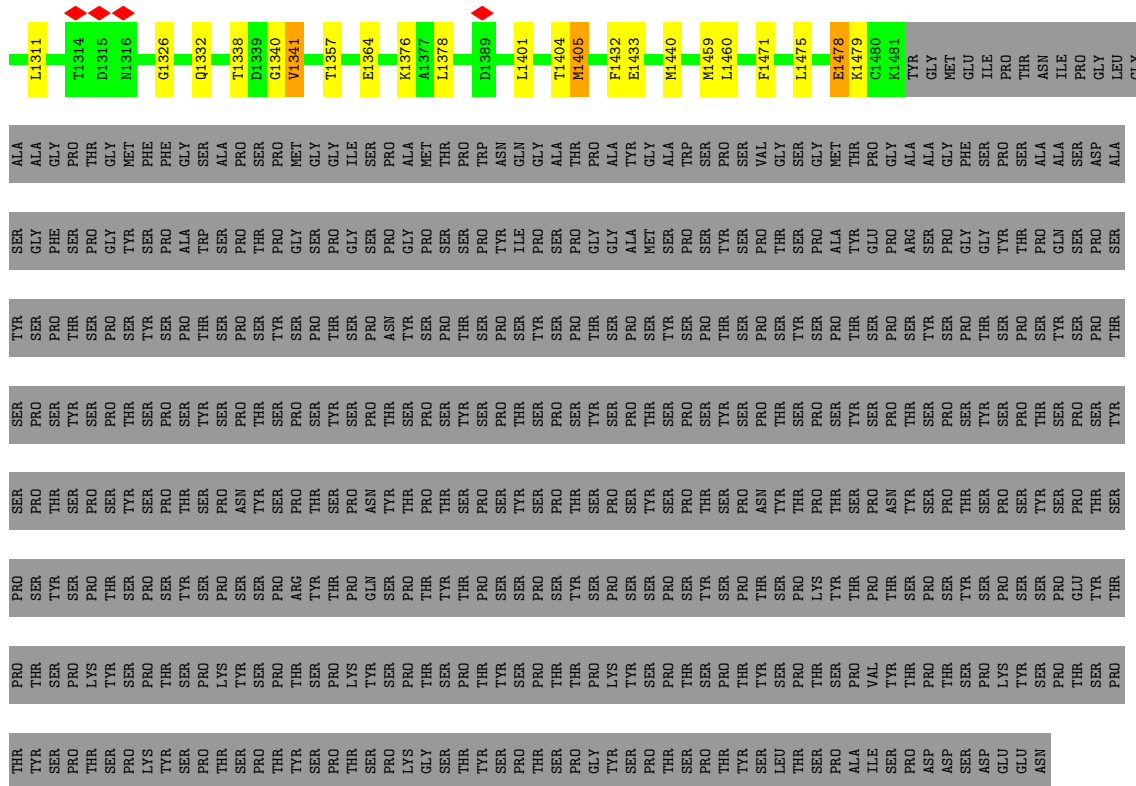
Mol	Chain	Residues	Atoms			AltConf
			Total	Be	F	
24	b	1	4	1	3	0

3 Residue-property plots [i](#)

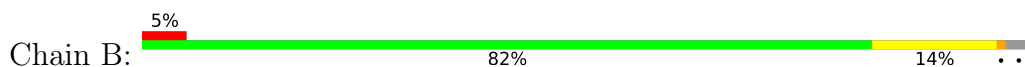
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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-directed RNA polymerase subunit



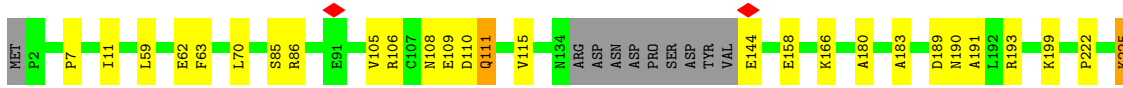
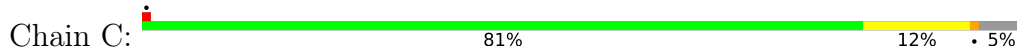


• Molecule 2: DNA-directed RNA polymerase subunit beta

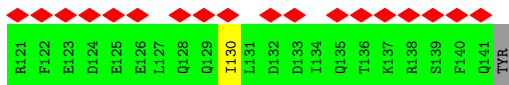
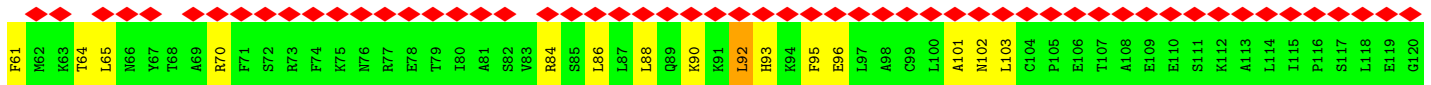
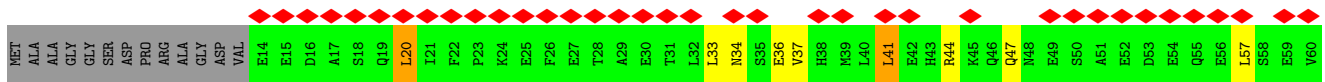
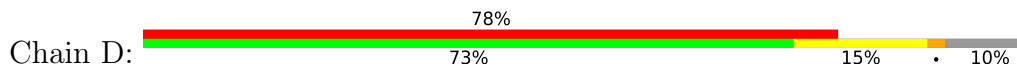




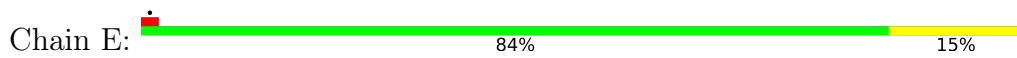
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3



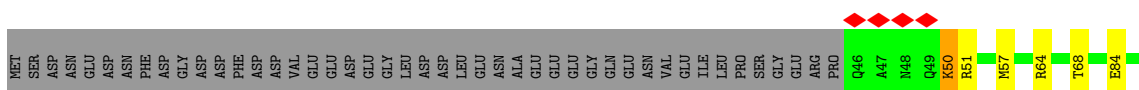
• Molecule 4: RNA polymerase II subunit D



• Molecule 5: DNA-directed RNA polymerase II subunit E

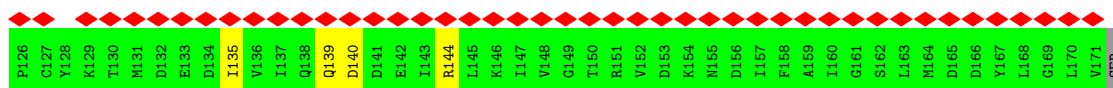
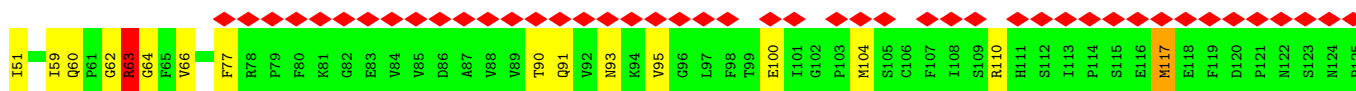
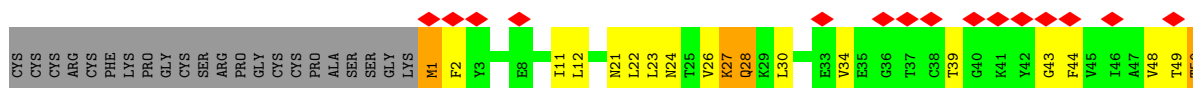
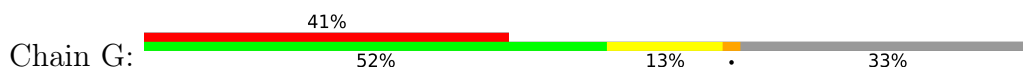


• Molecule 6: DNA-directed RNA polymerase II subunit F

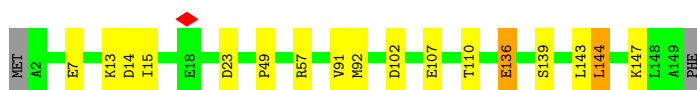
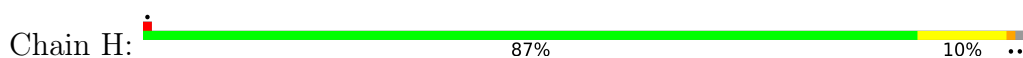




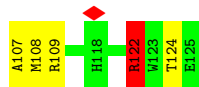
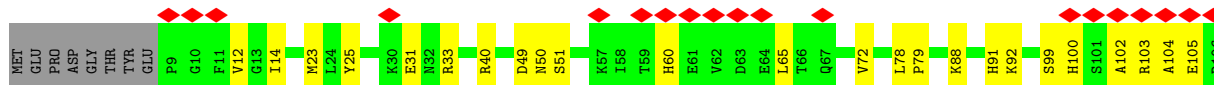
- Molecule 7: RPB7



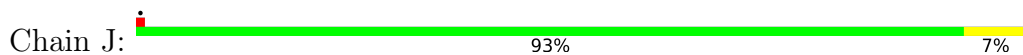
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



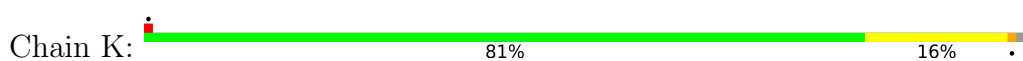
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

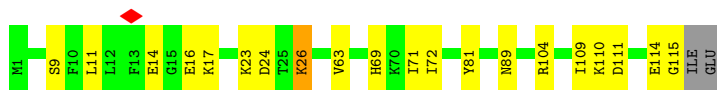


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 11: RNA_pol_L_2 domain-containing protein

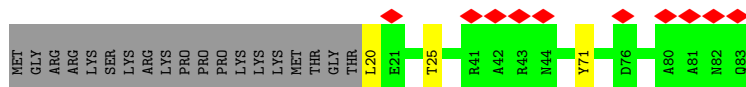




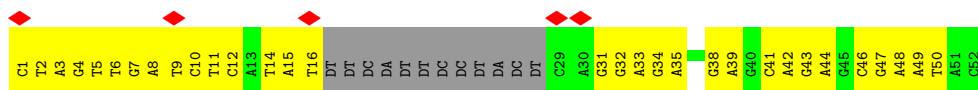
- Molecule 12: RNA polymerase II subunit K



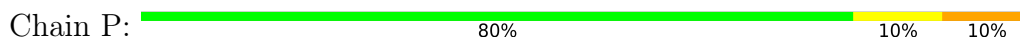
- Molecule 13: Transcription elongation factor 1 homolog



- Molecule 14: NTS



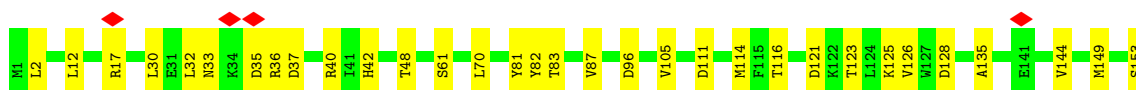
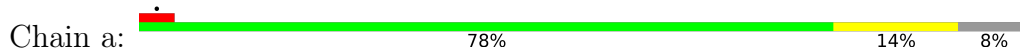
- Molecule 15: RNA

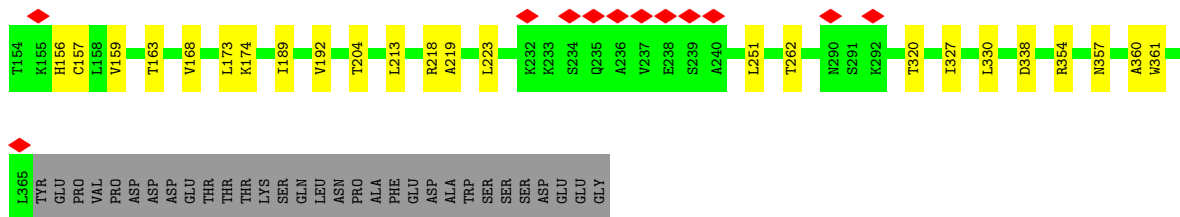


- Molecule 16: TS

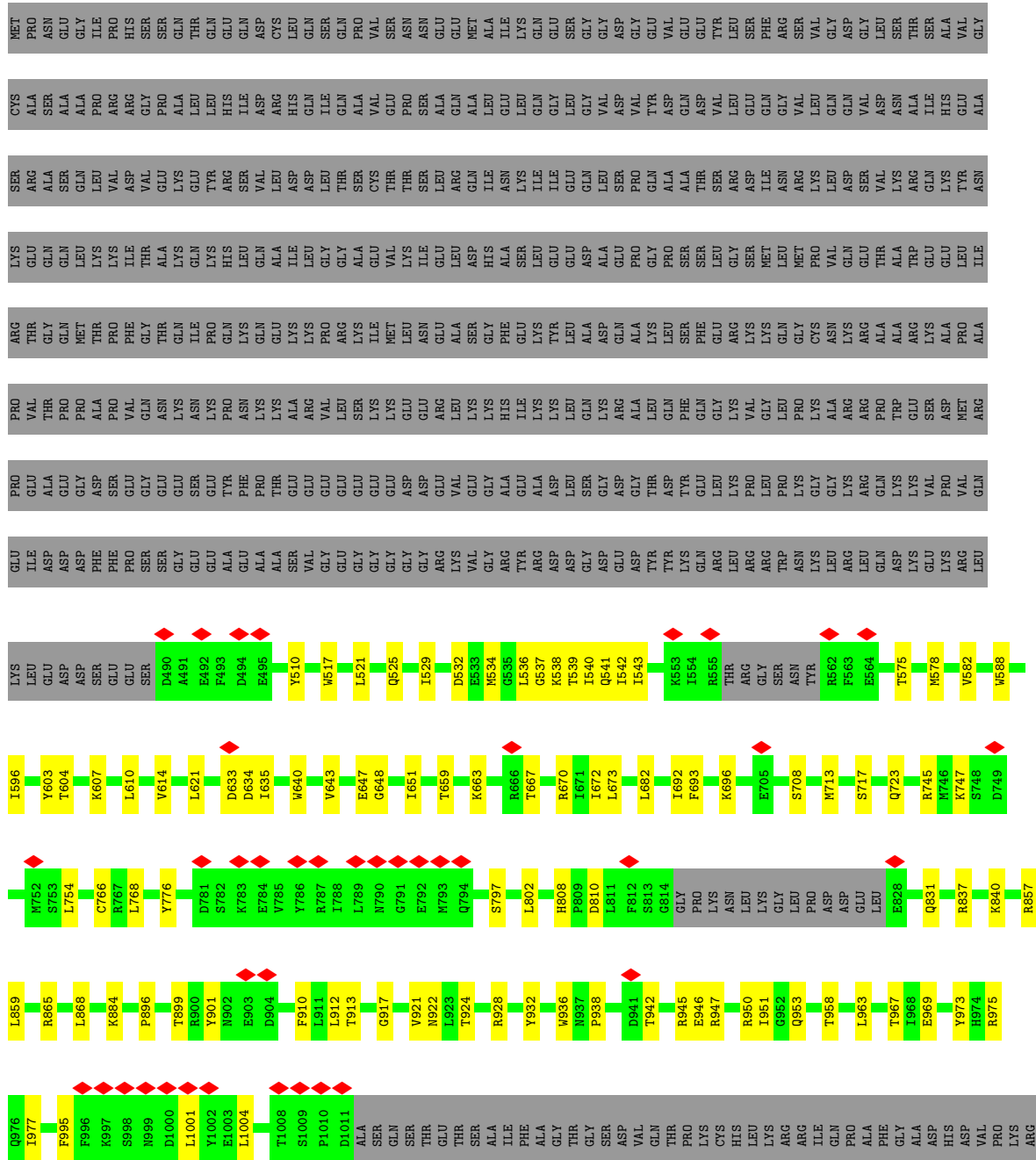


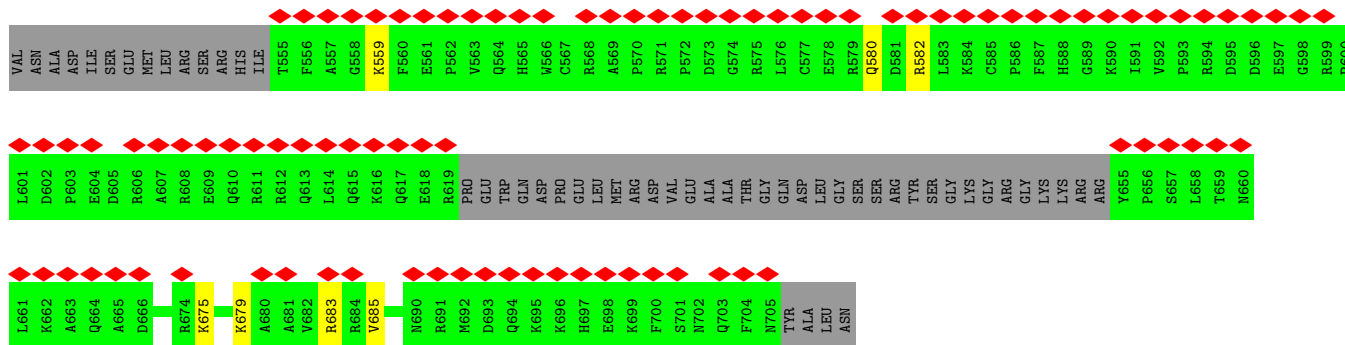
- Molecule 17: DNA excision repair protein ERCC-8



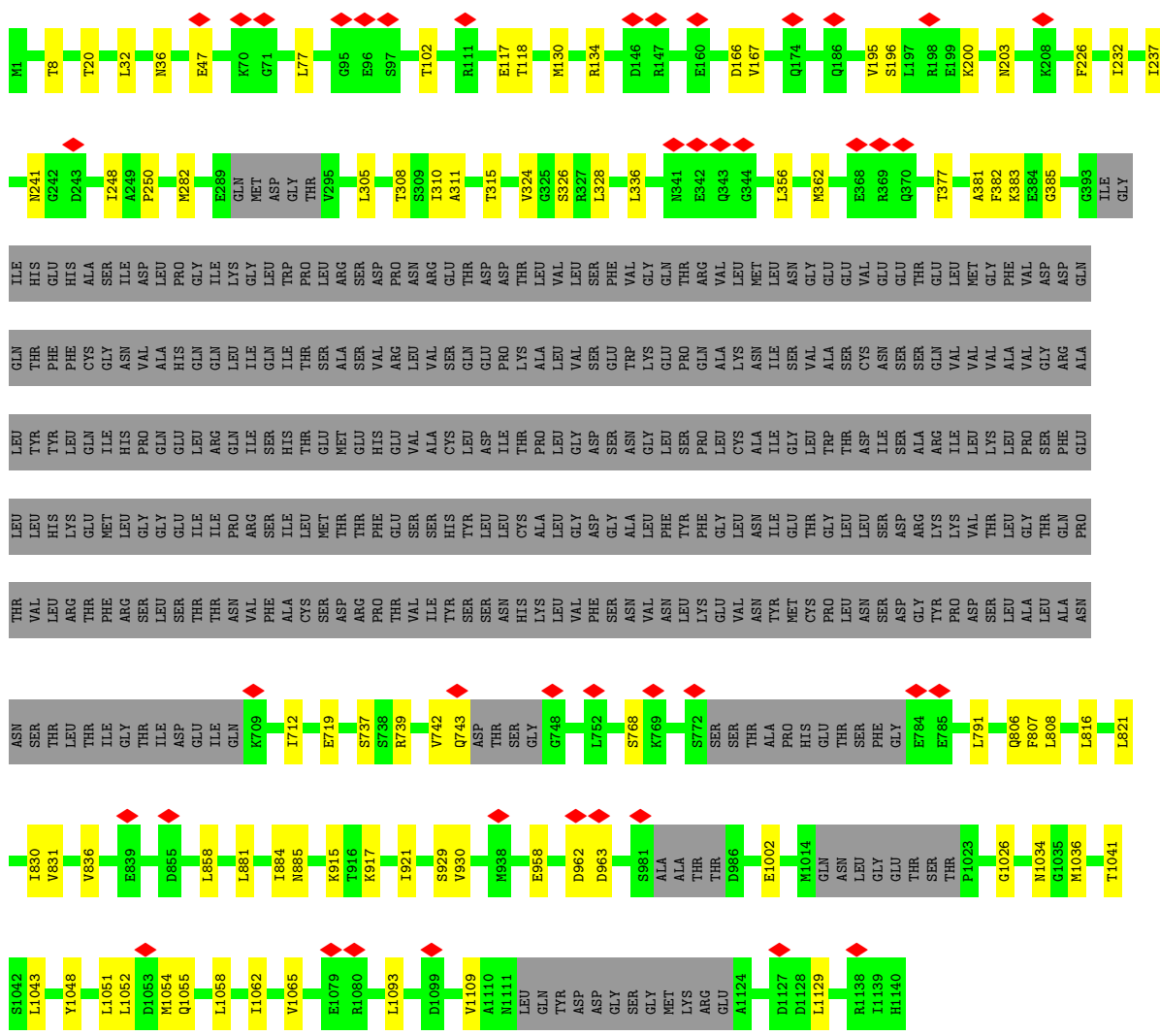


• Molecule 18: DNA excision repair protein ERCC-6





● Molecule 20: DNA damage-binding protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	544306	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	144	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.182	Depositor
Minimum map value	-0.120	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00912	Depositor
Map size (\AA)	440.99997, 440.99997, 440.99997	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	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: BEF, ADP, 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	A	0.50	9/11364 (0.1%)	1.08	130/15342 (0.8%)
2	B	0.49	5/9229 (0.1%)	0.87	66/12458 (0.5%)
3	C	0.53	1/2132 (0.0%)	1.02	22/2896 (0.8%)
4	D	0.55	2/1027 (0.2%)	1.15	17/1384 (1.2%)
5	E	0.61	1/1751 (0.1%)	1.19	29/2366 (1.2%)
6	F	0.41	0/667	0.96	5/901 (0.6%)
7	G	0.54	1/1365 (0.1%)	1.27	19/1853 (1.0%)
8	H	0.40	0/1207	0.69	5/1628 (0.3%)
9	I	0.50	0/972	1.12	13/1316 (1.0%)
10	J	0.38	0/542	1.00	3/730 (0.4%)
11	K	0.57	2/939 (0.2%)	1.13	15/1271 (1.2%)
12	L	0.79	2/394 (0.5%)	1.57	13/524 (2.5%)
13	M	0.17	0/515	0.33	0/700
14	N	0.19	0/932	0.32	0/1435
15	P	0.37	0/247	0.35	0/384
16	T	0.28	0/1102	0.42	0/1682
17	a	0.21	0/2908	0.45	0/3939
18	b	0.19	0/4362	0.42	0/5890
19	c	0.24	0/2034	0.49	0/2715
20	d	0.19	0/6268	0.43	1/8466 (0.0%)
All	All	0.43	23/49957 (0.0%)	0.86	338/67880 (0.5%)

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	A	0	9
2	B	0	6
3	C	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	1
6	F	0	1
7	G	0	2
9	I	0	2
12	L	0	1
17	a	0	1
All	All	0	28

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	1	MET	CB-CG	-8.21	1.27	1.52
11	K	26	LYS	CG-CD	-5.97	1.34	1.52
11	K	26	LYS	CD-CE	-5.93	1.34	1.52
3	C	111	GLN	CG-CD	-5.79	1.37	1.52
12	L	35	ARG	CZ-NH1	-5.76	1.24	1.32

The worst 5 of 338 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1286	ARG	CG-CD-NE	22.17	160.77	112.00
1	A	958	ARG	CG-CD-NE	21.44	159.16	112.00
7	G	28	GLN	CA-CB-CG	18.44	150.98	114.10
1	A	711	GLN	CA-CB-CG	18.21	150.52	114.10
1	A	105	LYS	CA-CB-CG	17.35	148.80	114.10

There are no chirality outliers.

5 of 28 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	PHE	Sidechain
1	A	397	PHE	Sidechain
1	A	407	ARG	Sidechain
1	A	430	ARG	Sidechain
1	A	538	VAL	Peptide

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	11161	11299	11297	153	0
2	B	9048	9083	9084	103	0
3	C	2089	2031	2031	21	0
4	D	1013	972	972	19	0
5	E	1720	1737	1737	13	0
6	F	657	684	684	9	0
7	G	1334	1331	1333	26	0
8	H	1186	1147	1147	9	0
9	I	949	878	879	21	0
10	J	533	553	553	4	0
11	K	920	942	942	9	0
12	L	388	393	393	4	0
13	M	505	463	463	2	0
14	N	829	84	450	63	0
15	P	220	110	109	2	0
16	T	991	87	553	71	0
17	a	2849	2775	2777	39	0
18	b	4259	4302	4302	71	0
19	c	1999	1911	1916	32	0
20	d	6161	6160	6159	50	0
21	A	2	0	0	0	0
21	B	1	0	0	0	0
21	C	1	0	0	0	0
21	I	2	0	0	0	0
21	J	1	0	0	0	0
21	L	1	0	0	0	0
21	M	1	0	0	0	0
21	c	1	0	0	0	0
22	A	1	0	0	0	0
22	b	1	0	0	0	0
23	b	27	12	12	2	0
24	b	4	0	0	1	0
All	All	48854	46954	47793	634	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 7.

The worst 5 of 634 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:41:DC:C5'	19:c:679:LYS:HE3	1.71	1.21
14:N:41:DC:H5''	19:c:679:LYS:CE	1.82	1.09
19:c:12:LEU:HD22	19:c:64:ILE:HD11	1.34	1.09
14:N:41:DC:H5''	19:c:679:LYS:HE3	1.34	1.00
16:T:11:DT:H2''	16:T:12:DG:H5'	1.42	0.99

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1399/1970 (71%)	1348 (96%)	51 (4%)	0	100	100
2	B	1122/1167 (96%)	1072 (96%)	50 (4%)	0	100	100
3	C	256/275 (93%)	248 (97%)	8 (3%)	0	100	100
4	D	126/142 (89%)	117 (93%)	9 (7%)	0	100	100
5	E	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
6	F	80/127 (63%)	75 (94%)	5 (6%)	0	100	100
7	G	169/254 (66%)	159 (94%)	10 (6%)	0	100	100
8	H	146/150 (97%)	141 (97%)	5 (3%)	0	100	100
9	I	115/125 (92%)	106 (92%)	9 (8%)	0	100	100
10	J	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
11	K	113/117 (97%)	109 (96%)	4 (4%)	0	100	100
12	L	44/58 (76%)	40 (91%)	4 (9%)	0	100	100
13	M	62/83 (75%)	61 (98%)	1 (2%)	0	100	100
17	a	363/396 (92%)	343 (94%)	20 (6%)	0	100	100
18	b	512/1493 (34%)	486 (95%)	26 (5%)	0	100	100
19	c	258/709 (36%)	247 (96%)	11 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	d	765/1140 (67%)	730 (95%)	35 (5%)	0	100	100
All	All	5802/8483 (68%)	5542 (96%)	260 (4%)	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	
1	A	1241/1749 (71%)	1241 (100%)	0	100	100
2	B	992/1021 (97%)	989 (100%)	3 (0%)	86	94
3	C	237/252 (94%)	237 (100%)	0	100	100
4	D	108/126 (86%)	108 (100%)	0	100	100
5	E	191/192 (100%)	191 (100%)	0	100	100
6	F	71/111 (64%)	71 (100%)	0	100	100
7	G	147/217 (68%)	147 (100%)	0	100	100
8	H	129/131 (98%)	129 (100%)	0	100	100
9	I	105/112 (94%)	105 (100%)	0	100	100
10	J	56/56 (100%)	56 (100%)	0	100	100
11	K	104/106 (98%)	104 (100%)	0	100	100
12	L	43/55 (78%)	43 (100%)	0	100	100
13	M	59/76 (78%)	59 (100%)	0	100	100
17	a	320/348 (92%)	319 (100%)	1 (0%)	86	94
18	b	466/1297 (36%)	466 (100%)	0	100	100
19	c	196/608 (32%)	196 (100%)	0	100	100
20	d	685/999 (69%)	685 (100%)	0	100	100
All	All	5150/7456 (69%)	5146 (100%)	4 (0%)	87	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	301	VAL
2	B	331	THR
2	B	393	LEU
17	a	32	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
20	d	156	ASN
20	d	261	HIS
20	d	952	ASN
2	B	1094	GLN
2	B	1053	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	9/10 (90%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	10	A

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	BEF	b	1502	-	0,3,3	-	-	-	-	-
23	ADP	b	1501	22	28,29,29	1.38	4 (14%)	43,45,45	1.86	10 (23%)

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
23	ADP	b	1501	22	-	3/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	b	1501	ADP	C5-C4	4.42	1.47	1.39
23	b	1501	ADP	C5-C6	2.54	1.48	1.41
23	b	1501	ADP	C5-N7	-2.34	1.34	1.39
23	b	1501	ADP	C8-N7	2.32	1.36	1.31

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	b	1501	ADP	C5-C4-N3	-5.68	118.90	126.72
23	b	1501	ADP	N3-C4-N9	4.66	135.09	127.17
23	b	1501	ADP	C2-N3-C4	3.85	121.23	111.83
23	b	1501	ADP	N3-C2-N1	-3.79	122.84	128.58
23	b	1501	ADP	C4-C5-N7	-3.29	106.82	110.58

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	b	1501	ADP	PB-O3A-PA-O2A

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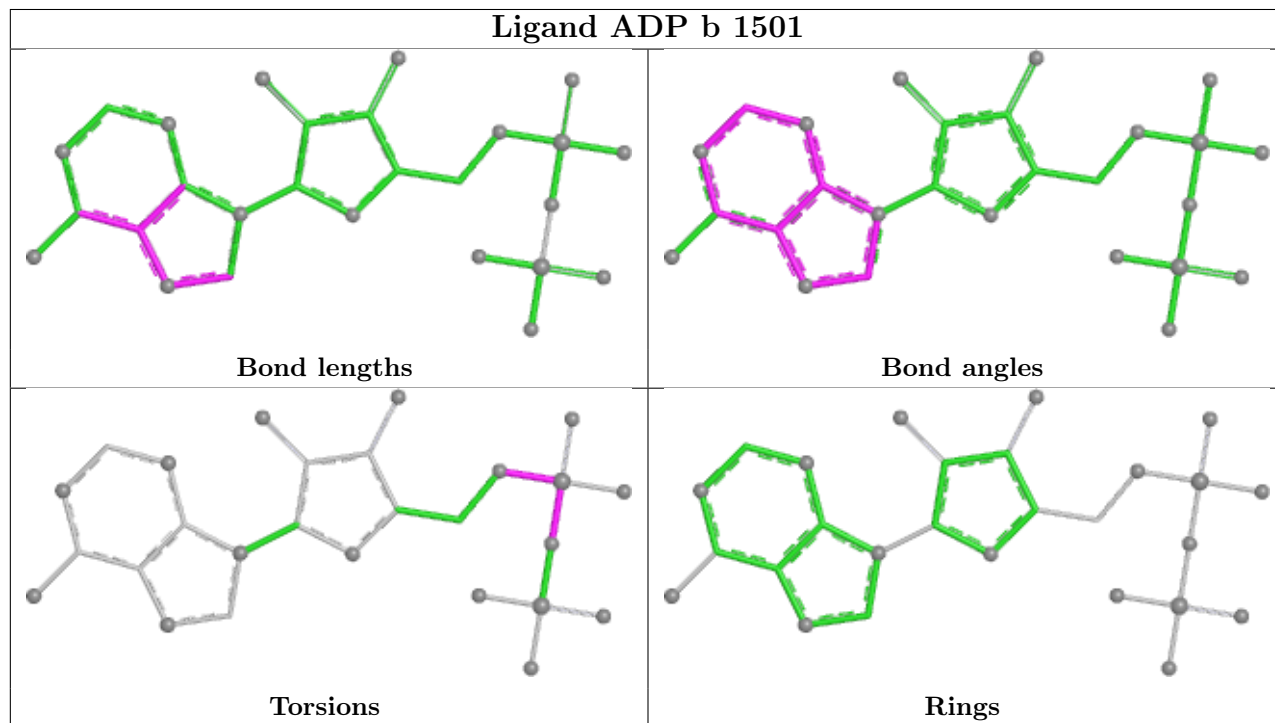
Mol	Chain	Res	Type	Atoms
23	b	1501	ADP	C5'-O5'-PA-O1A
23	b	1501	ADP	PB-O3A-PA-O1A

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	b	1502	BEF	1	0
23	b	1501	ADP	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

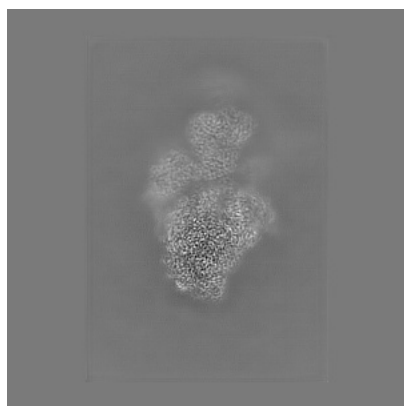
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15825. These allow visual inspection of the internal detail of the map and identification of artifacts.

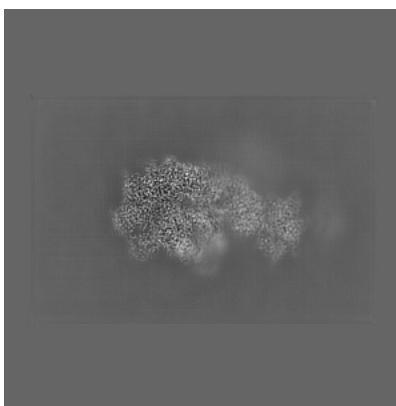
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

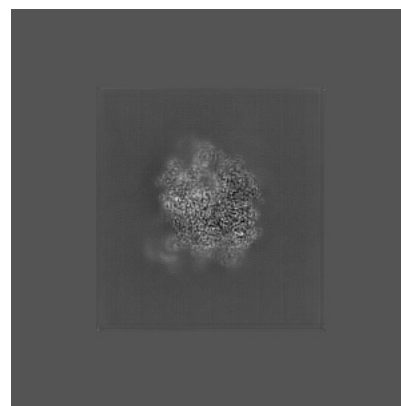
6.1.1 Primary map



X

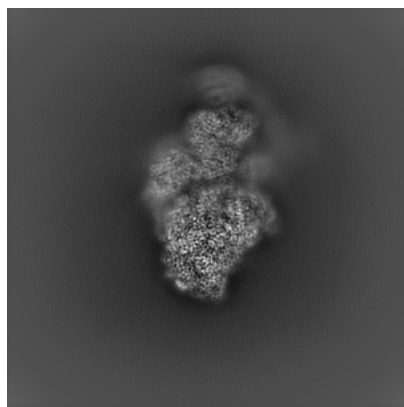


Y

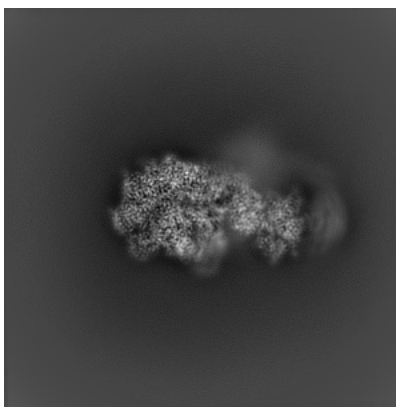


Z

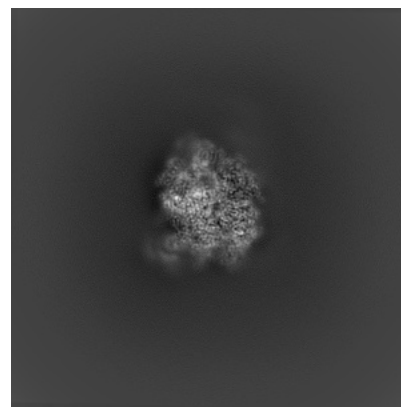
6.1.2 Raw map



X



Y

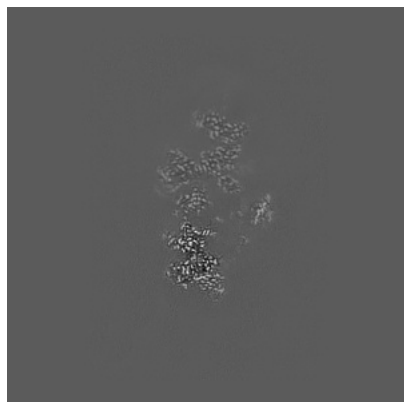


Z

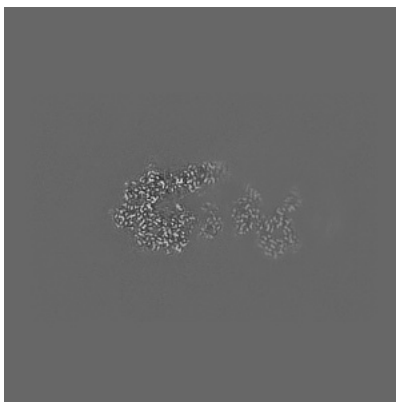
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

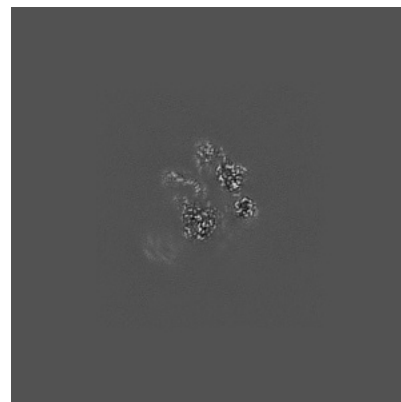
6.2.1 Primary map



X Index: 210

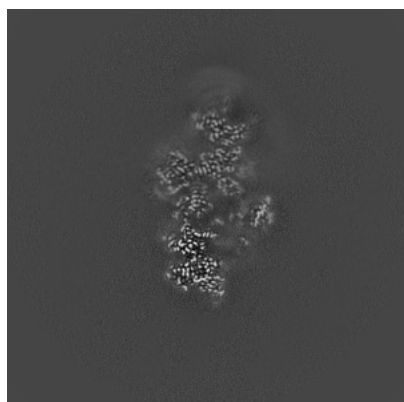


Y Index: 210

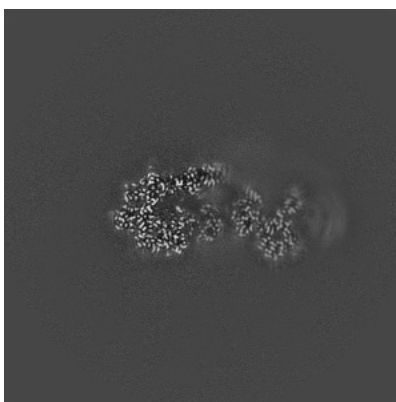


Z Index: 210

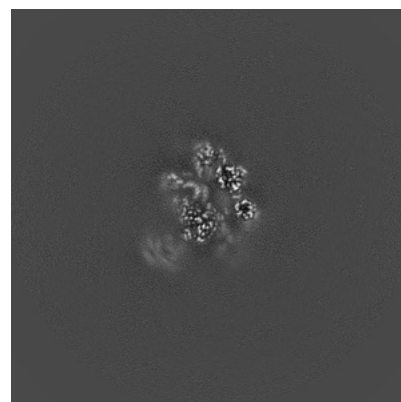
6.2.2 Raw map



X Index: 210



Y Index: 210

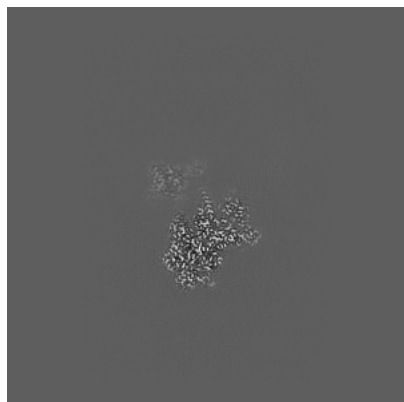


Z Index: 210

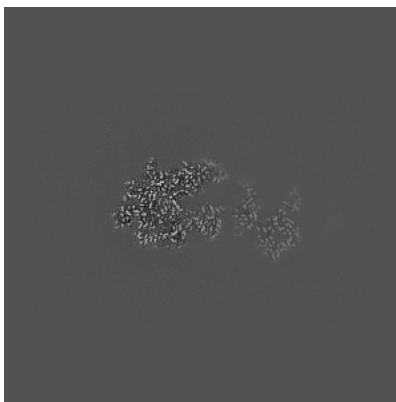
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

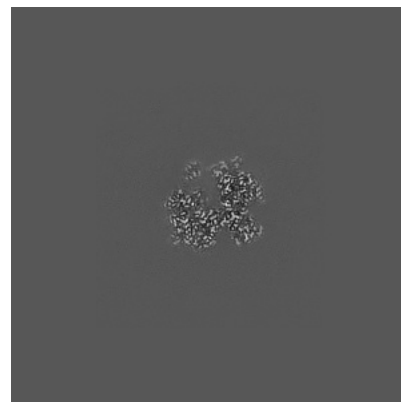
6.3.1 Primary map



X Index: 236

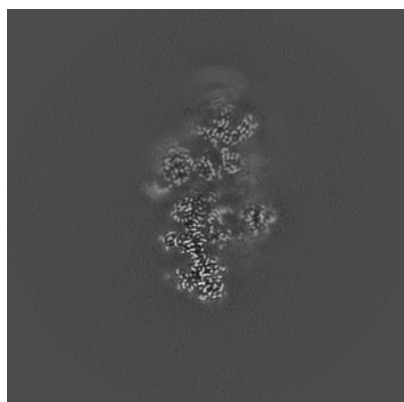


Y Index: 206

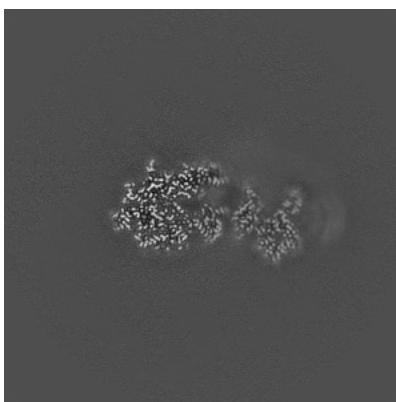


Z Index: 173

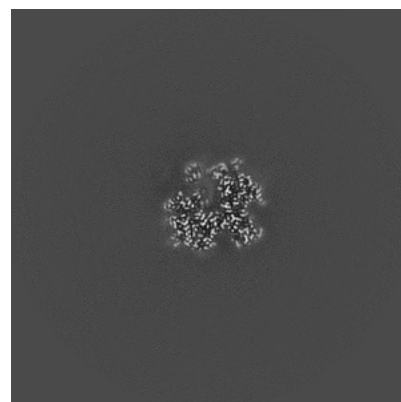
6.3.2 Raw map



X Index: 202



Y Index: 207

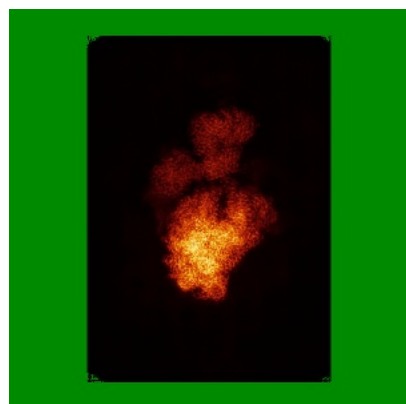


Z Index: 173

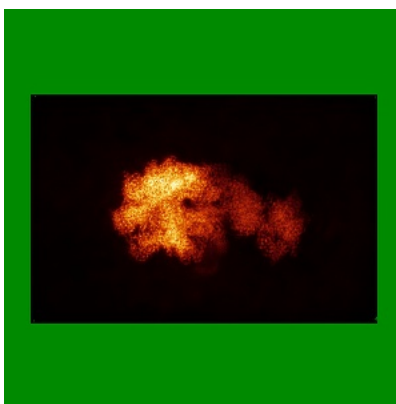
The images above show the largest variance slices of the map in three orthogonal directions.

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

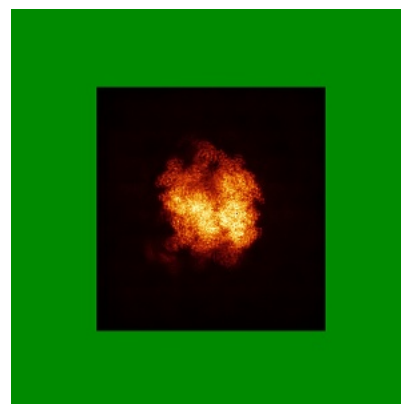
6.4.1 Primary map



X

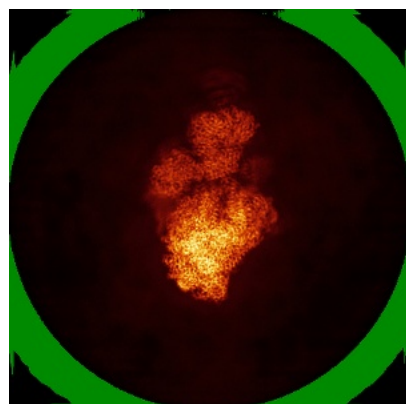


Y

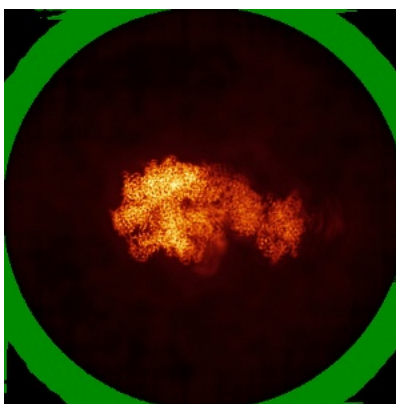


Z

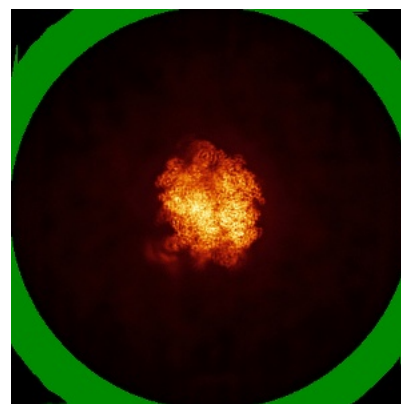
6.4.2 Raw map



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.

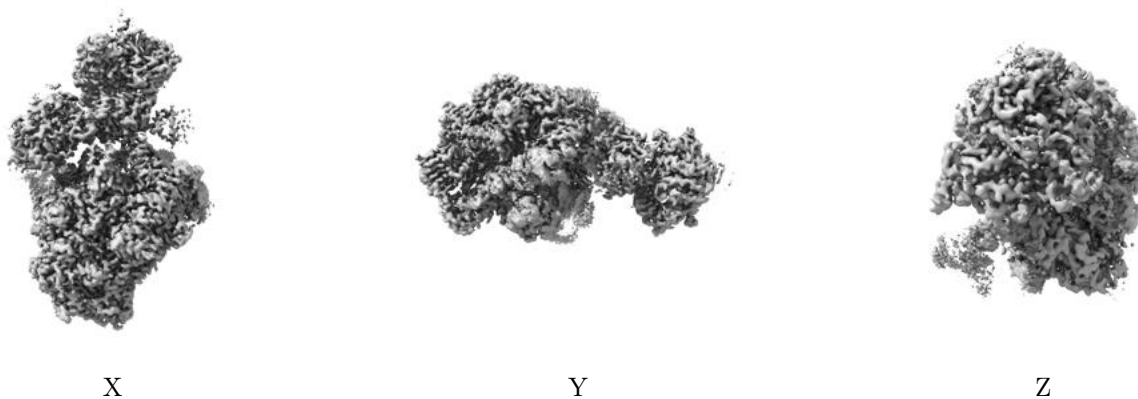
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00912. 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.

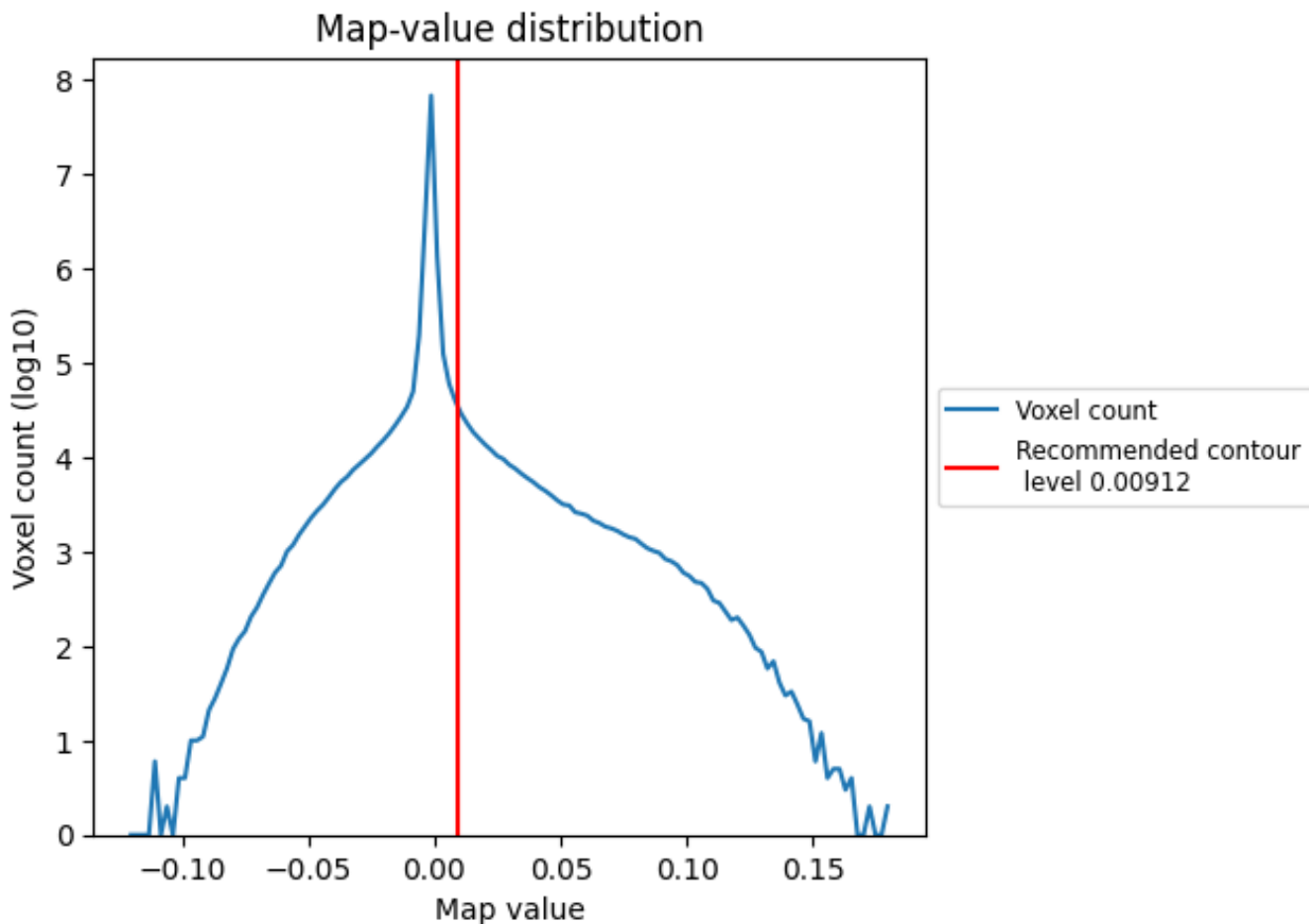
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

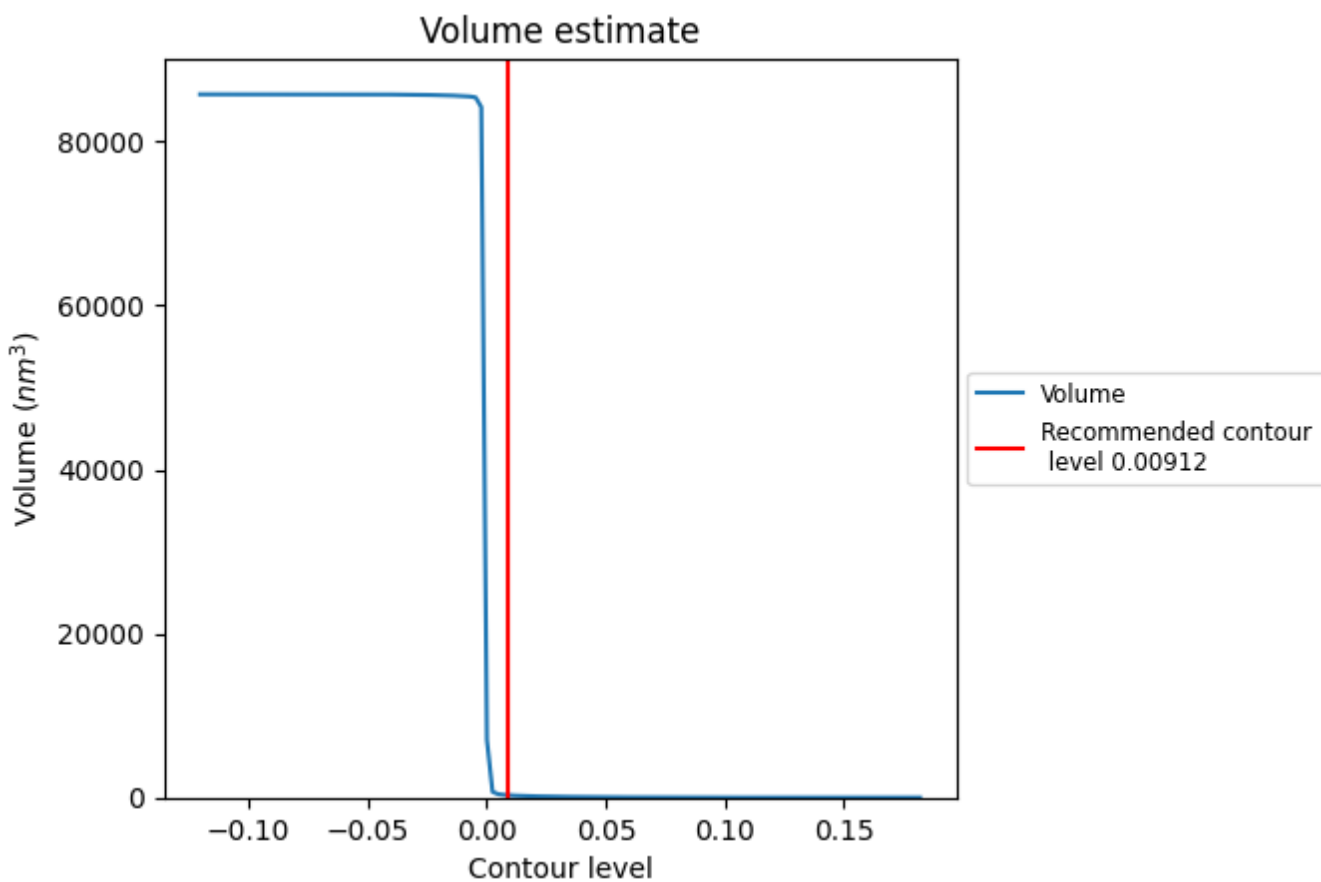
This section contains the results of statistical analysis of the map.

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.

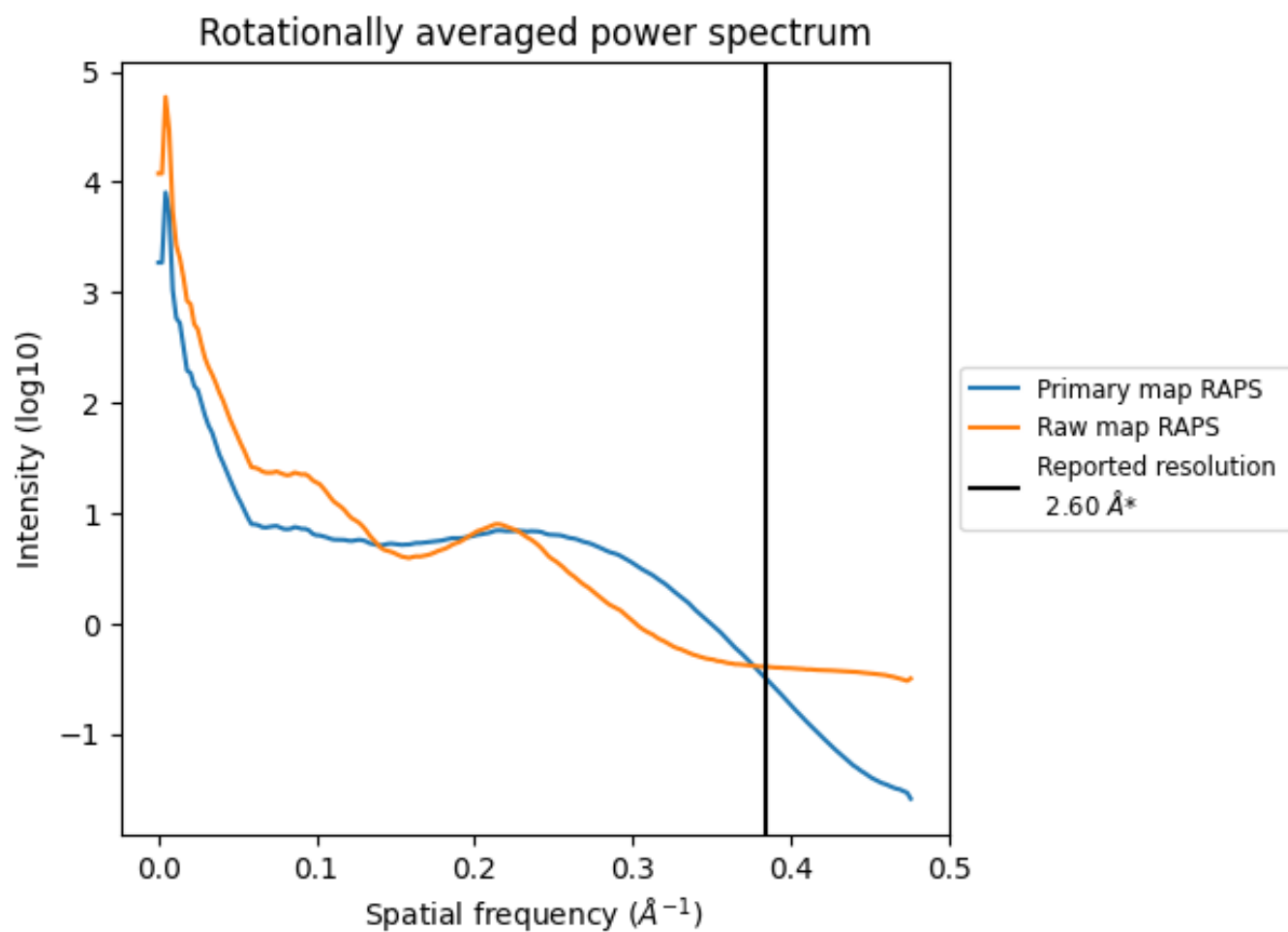
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 287 nm³; this corresponds to an approximate mass of 259 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

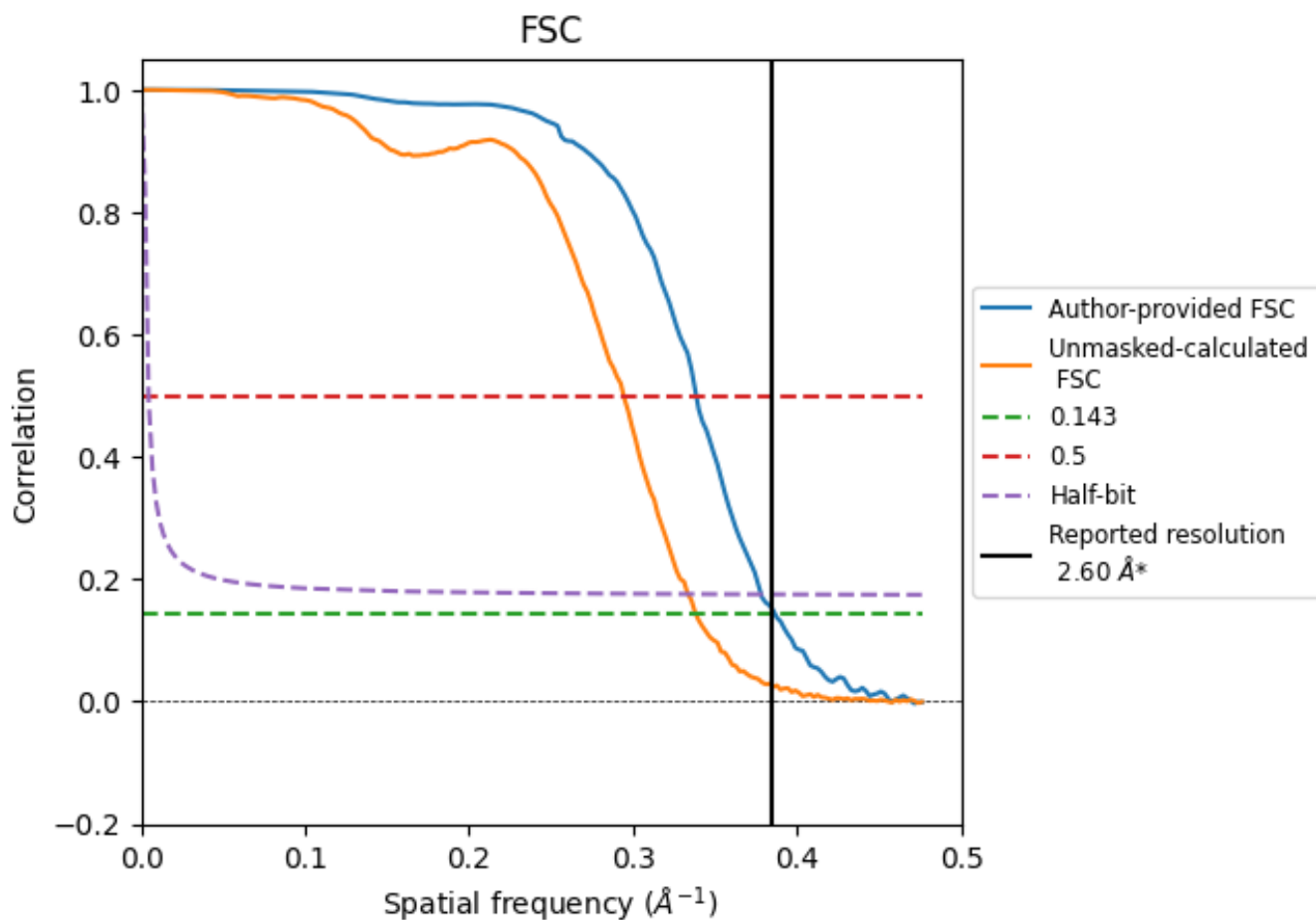


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

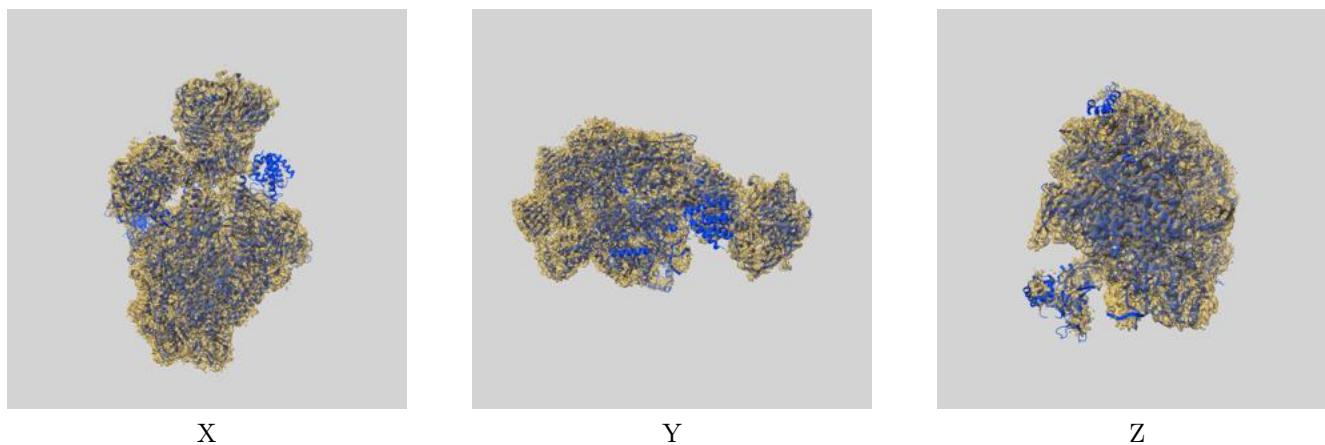
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.59	2.95	2.64
Unmasked-calculated*	2.96	3.40	3.00

*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 2.96 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

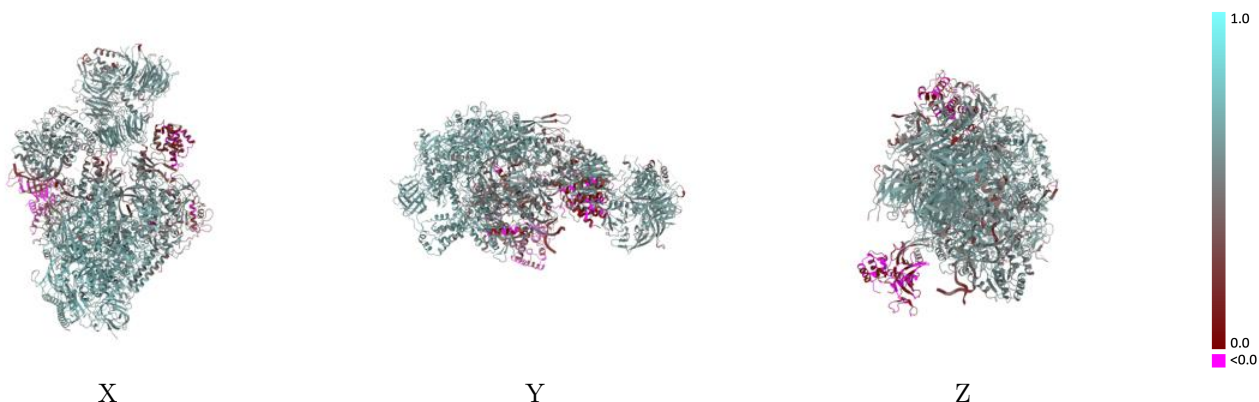
This section contains information regarding the fit between EMDB map EMD-15825 and PDB model 8B3D. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



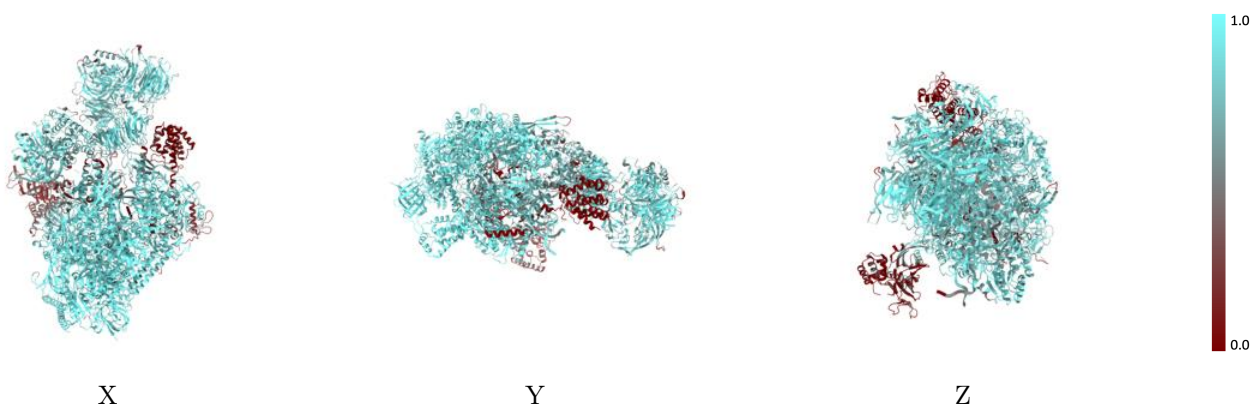
The images above show the 3D surface view of the map at the recommended contour level 0.00912 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



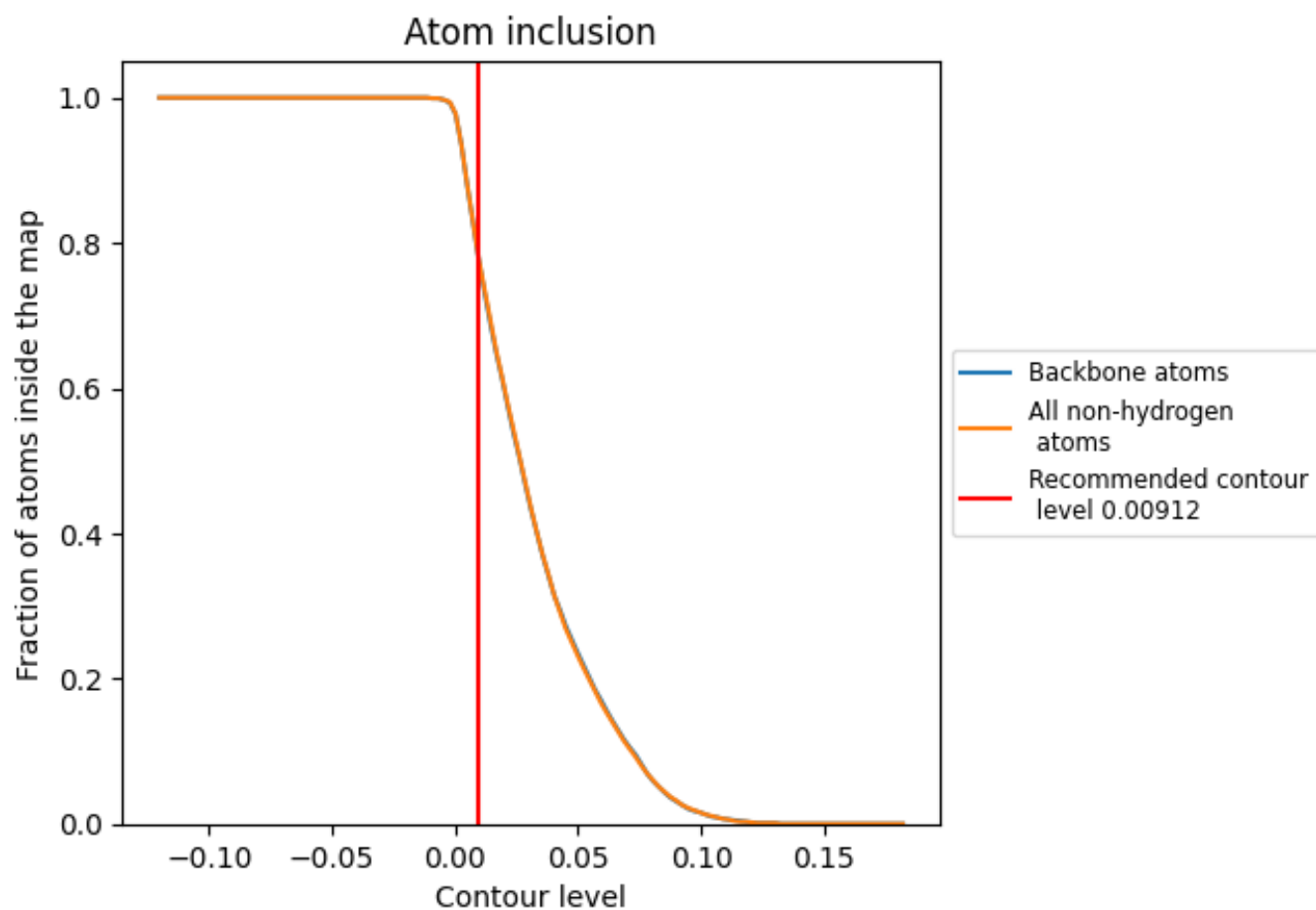
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00912).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (0.00912) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.5320
A	 0.8690	 0.5780
B	 0.8870	 0.5940
C	 0.9310	 0.6250
D	 0.1550	 0.0350
E	 0.8810	 0.5270
F	 0.8920	 0.6000
G	 0.3650	 0.1960
H	 0.9350	 0.6150
I	 0.7550	 0.4910
J	 0.9410	 0.6430
K	 0.9320	 0.6250
L	 0.8390	 0.5290
M	 0.6490	 0.4530
N	 0.6920	 0.4340
P	 0.9550	 0.6520
T	 0.8170	 0.4740
a	 0.8470	 0.5770
b	 0.7660	 0.5240
c	 0.1030	 0.2010
d	 0.8110	 0.5550

