



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:05 PM UTC

PDB ID : 9BZ0 / pdb_00009bz0
EMDB ID : EMD-45050
Title : Structure of an STK19-containing TC-NER complex
Authors : Mevissen, T.E.T.; Kuemmecke, M.; Farnung, L.; Walter, J.C.
Deposited on : 2024-05-24
Resolution : 1.90 Å(reported)
Based on initial models : ., 8B3F

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:

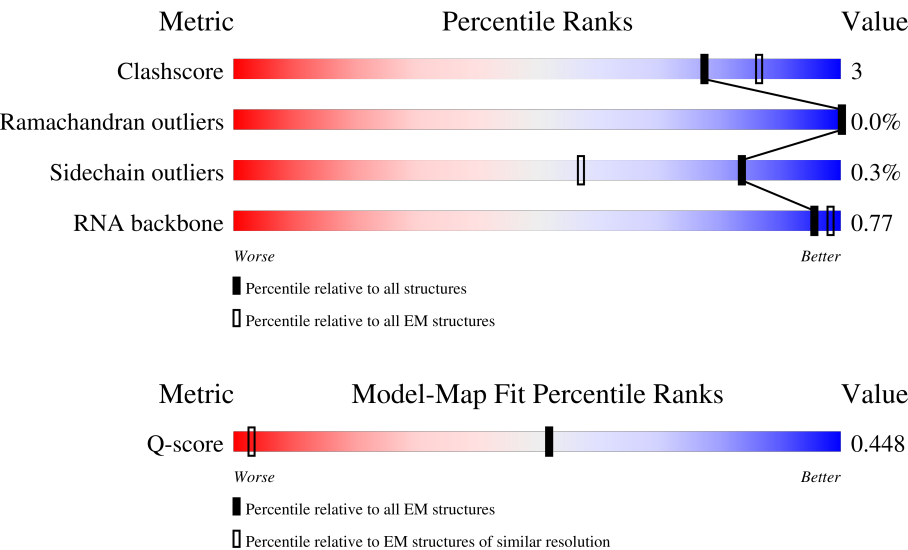
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 1.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	1185 (1.40 - 2.40)

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	1984	67%5%28%
2	B	1251	84%6%10%
3	C	275	87%8%5%

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Mol	Chain	Length	Quality of chain
4	D	142	
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	85	
14	N	90	
15	P	10	
16	T	90	
17	a	396	
18	b	1496	
19	c	712	
20	d	1143	
21	e	105	
22	f	254	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 54687 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1425	Total	C	N	O	S	0	0
			11289	7096	2018	2103	72		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1129	Total	C	N	O	S	0	0
			9038	5719	1587	1668	64		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	260	Total	C	N	O	S	0	0
			2089	1309	359	415	6		

- Molecule 4 is a protein called RNA polymerase Rpb4/RPC9 core domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	128	Total	C	N	O	S	0	0
			1013	636	172	201	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			658	418	113	122	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1334	867	216	243	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	117	Total	C	N	O	S	0	0
			950	587	169	183	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			534	345	90	93	6		

- Molecule 11 is a protein called RNA polymerase II subunit J.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	115	Total	C	N	O	S	0	0
			920	593	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	N	O	S	0	0
			389	241	75	67	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	64	Total	C	N	O	S	0	0
			505	312	81	105	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-1	SER	-	expression tag	UNP A0A2K5RSX0
M	0	ASN	-	expression tag	UNP A0A2K5RSX0
M	1	ALA	-	expression tag	UNP A0A2K5RSX0

- Molecule 14 is a DNA chain called DNA (35-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	35	Total	C	N	O	P	0	0
			732	346	146	205	35		

- Molecule 15 is a RNA chain called RNA (5'-R(P*AP*UP*CP*GP*AP*GP*AP*GP*GP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	10	Total	C	N	O	P	0	0
			220	98	45	67	10		

- Molecule 16 is a DNA chain called DNA (49-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	49	Total	C	N	O	P	0	0
			984	472	161	302	49		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	386	Total	C	N	O	S	0	0
			3017	1880	529	589	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	621	Total	C	N	O	S	0	0
			5065	3238	895	909	23		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-2	SER	-	expression tag	UNP Q03468
b	-1	ASN	-	expression tag	UNP Q03468
b	0	ALA	-	expression tag	UNP Q03468
b	1213	GLY	ARG	variant	UNP Q03468

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Chain	Residue	Modelled	Actual	Comment	Reference
b	1413	ARG	GLN	variant	UNP Q03468

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	243	Total	C	N	O	S	0	0
			1865	1162	364	331	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	-2	SER	-	expression tag	UNP Q2YD98
c	-1	ASN	-	expression tag	UNP Q2YD98
c	0	ALA	-	expression tag	UNP Q2YD98

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	1140	Total	C	N	O	S	0	0
			8918	5642	1503	1724	49		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-2	SER	-	expression tag	UNP Q16531
d	-1	ASN	-	expression tag	UNP Q16531
d	0	ALA	-	expression tag	UNP Q16531

- Molecule 21 is a protein called DET1- and DDB1-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	e	53	Total	C	N	O	S	0	0
			429	271	76	80	2		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	-2	SER	-	expression tag	UNP Q9BW61
e	-1	ASN	-	expression tag	UNP Q9BW61
e	0	ALA	-	expression tag	UNP Q9BW61

- Molecule 22 is a protein called Inactive serine/threonine-protein kinase 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	f	232	Total	C	N	O	S	0	0
			1817	1161	324	326	6		

- Molecule 23 is ZINC ION (CCD ID: ZN) (formula: Zn).

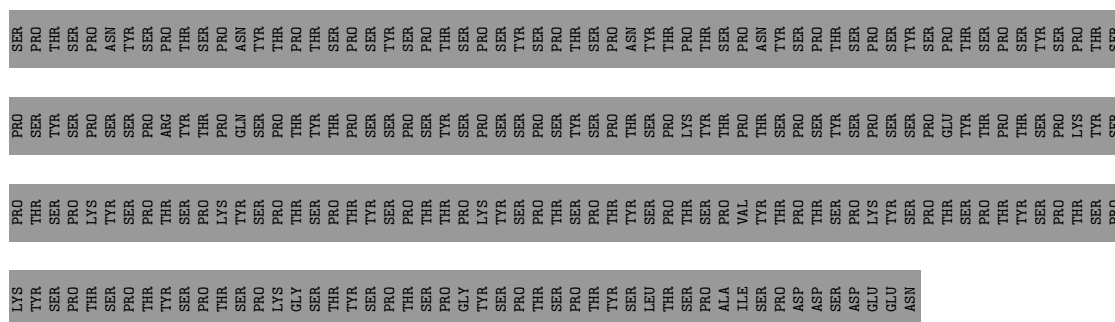
Mol	Chain	Residues	Atoms		AltConf
23	A	2	Total	Zn	0
			2	2	
23	B	1	Total	Zn	0
			1	1	
23	C	1	Total	Zn	0
			1	1	
23	I	2	Total	Zn	0
			2	2	
23	J	1	Total	Zn	0
			1	1	
23	L	1	Total	Zn	0
			1	1	
23	M	1	Total	Zn	0
			1	1	
23	c	1	Total	Zn	0
			1	1	

- Molecule 24 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

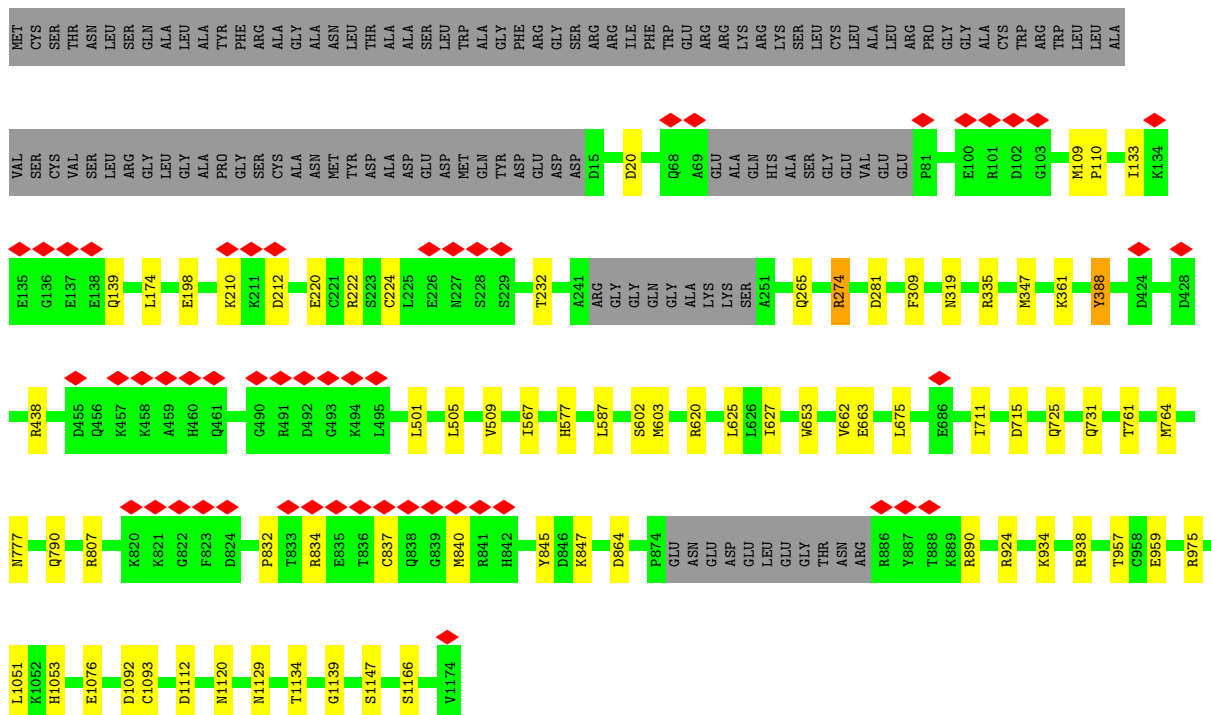
- Molecule 25 is water.

Mol	Chain	Residues	Atoms		AltConf
25	A	2	Total	O	0
			2	2	



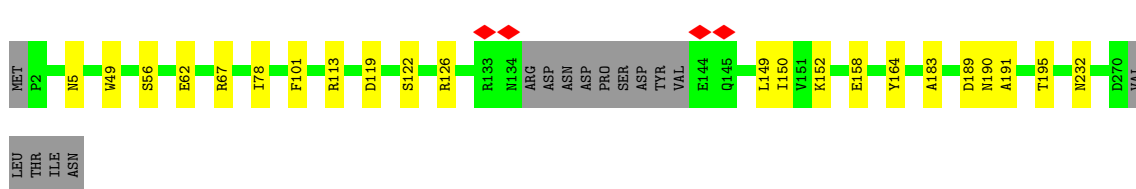
• Molecule 2: DNA-directed RNA polymerase subunit beta

Chain B: 84% 6% 10%



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

Chain C: 87% 8% 5%



• Molecule 4: RNA polymerase Rpb4/RPC9 core domain-containing protein

Chain D: 11% 82% 10%



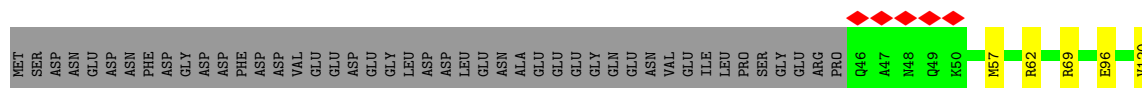
- Molecule 5: DNA-directed RNA polymerase II subunit E

Chain E: 95%



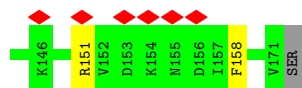
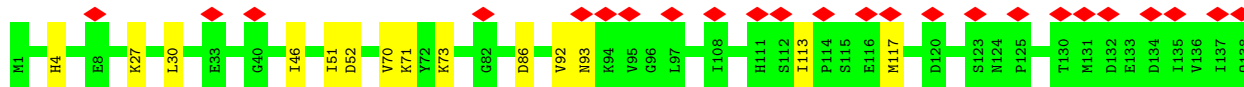
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F: 6% 61% 35%



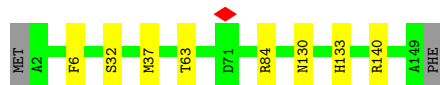
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7

Chain G: 17% 90% 9%



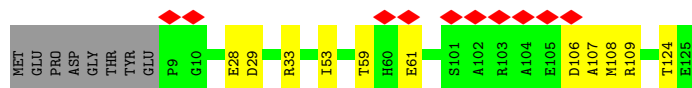
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 93% 5%

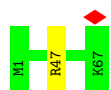


- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

Chain I: 8% 85% 9% 6%



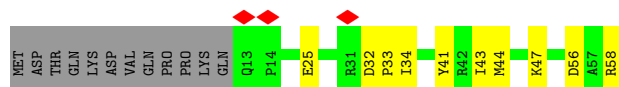
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



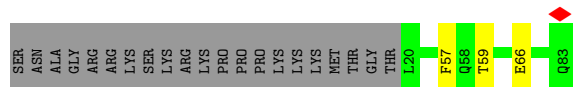
- Molecule 11: RNA polymerase II subunit J



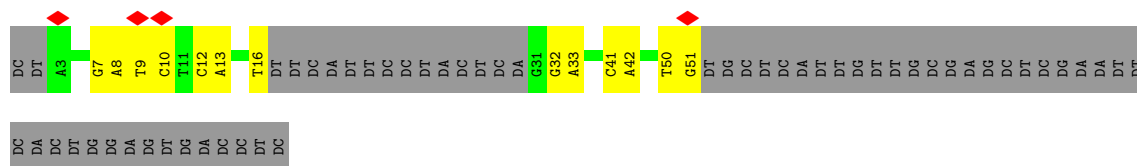
- Molecule 12: RNA polymerase II subunit K



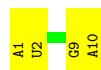
- Molecule 13: Transcription elongation factor 1 homolog



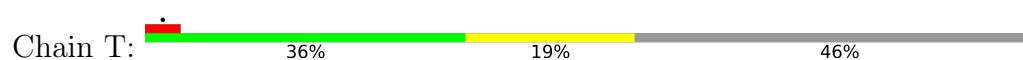
- Molecule 14: DNA (35-MER)

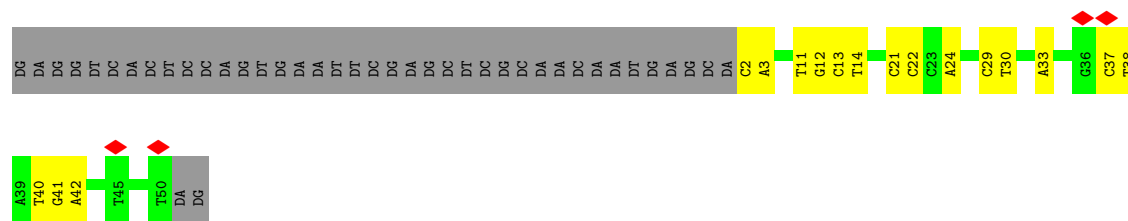


- Molecule 15: RNA (5'-R(P*AP*UP*CP*GP*AP*GP*AP*GP*GP*A)-3')

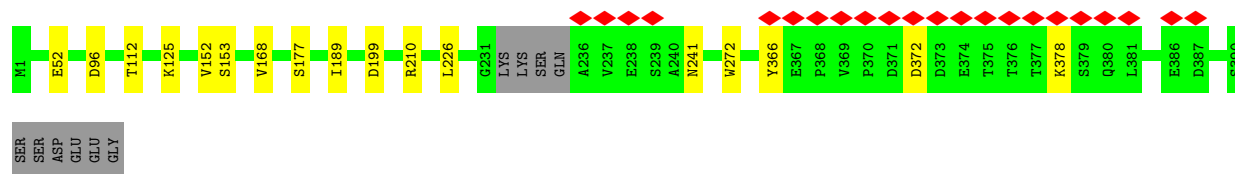
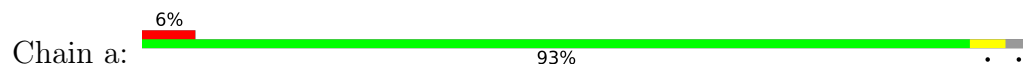


- Molecule 16: DNA (49-MER)

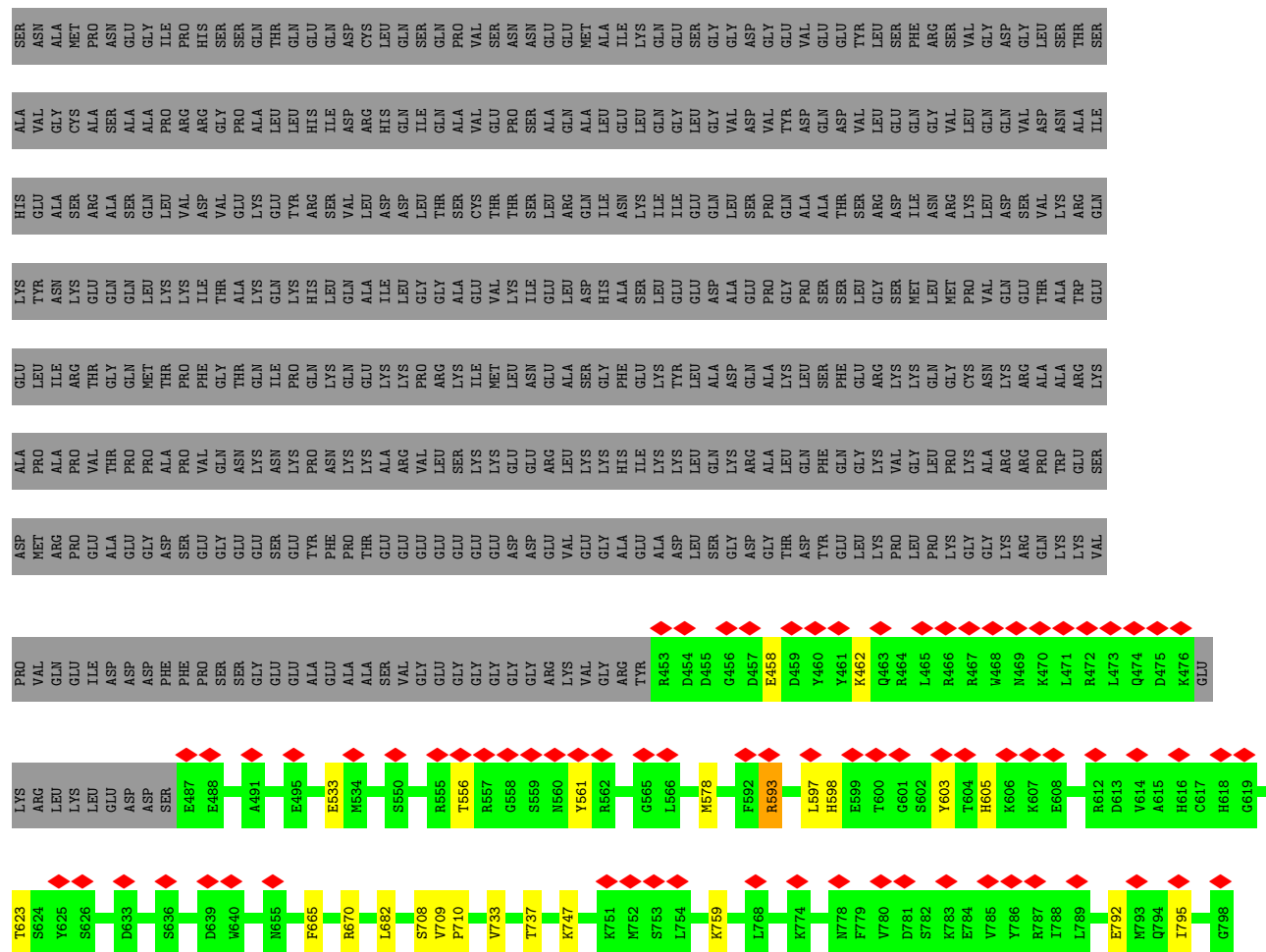


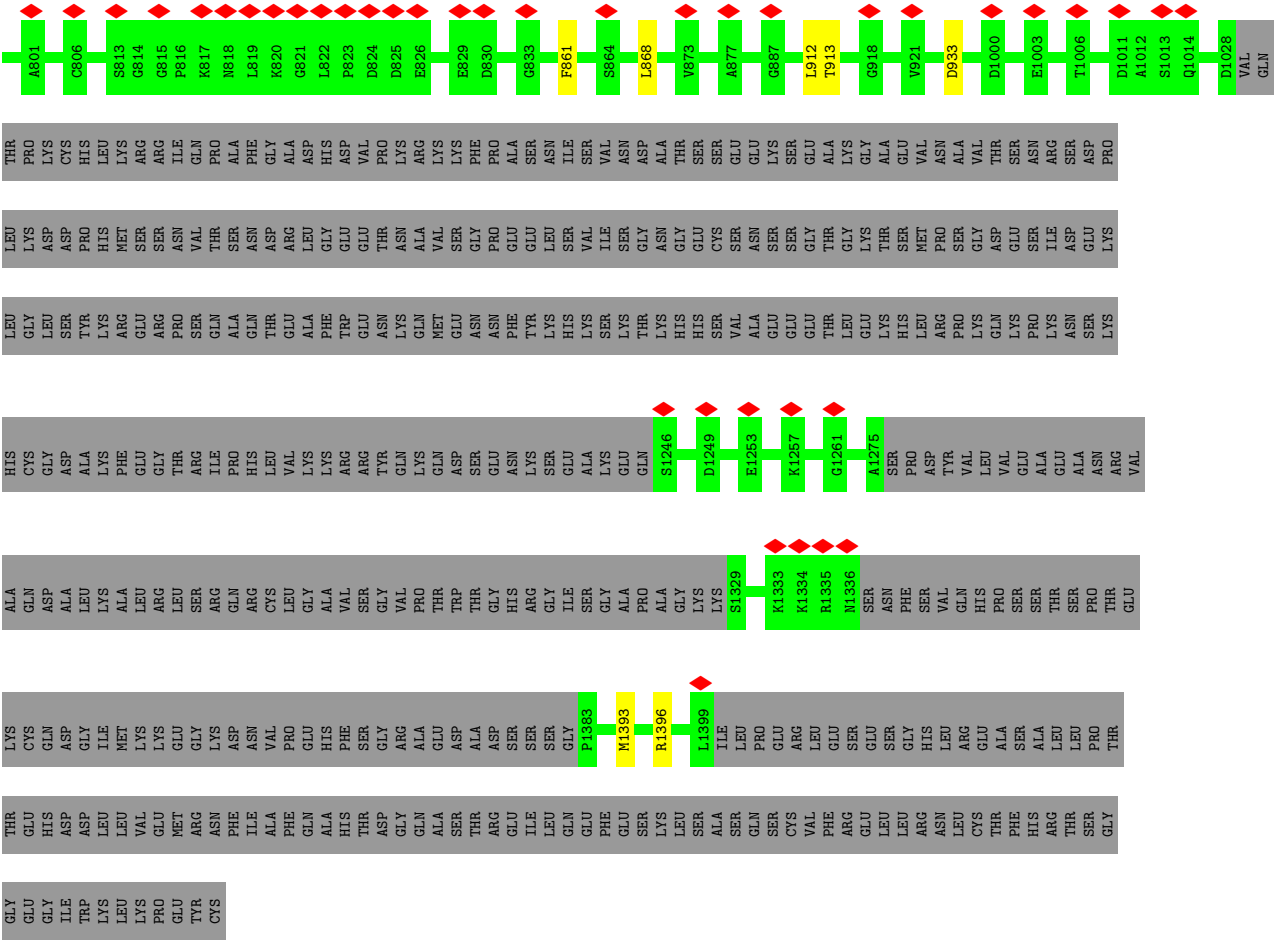


• Molecule 17: DNA excision repair protein ERCC-8

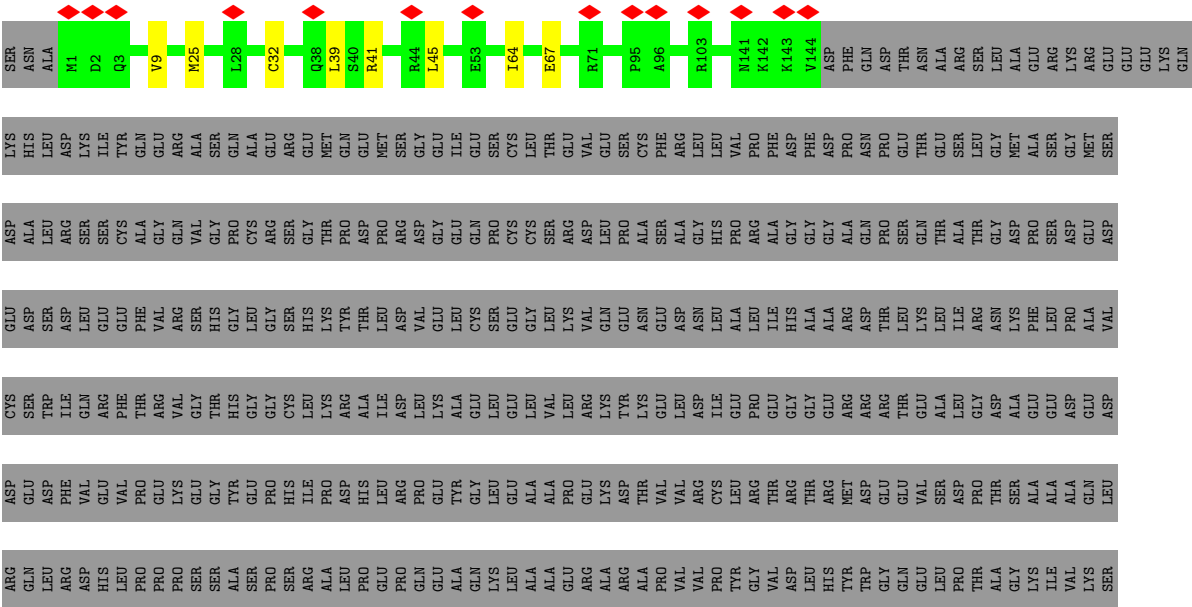


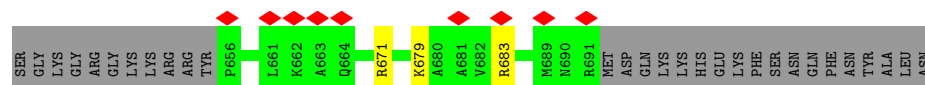
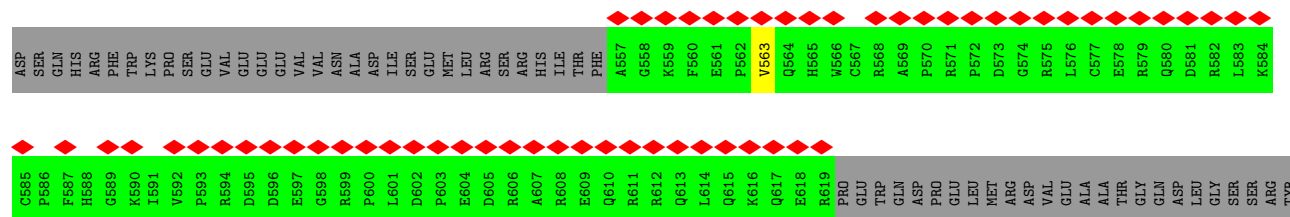
• Molecule 18: DNA excision repair protein ERCC-6



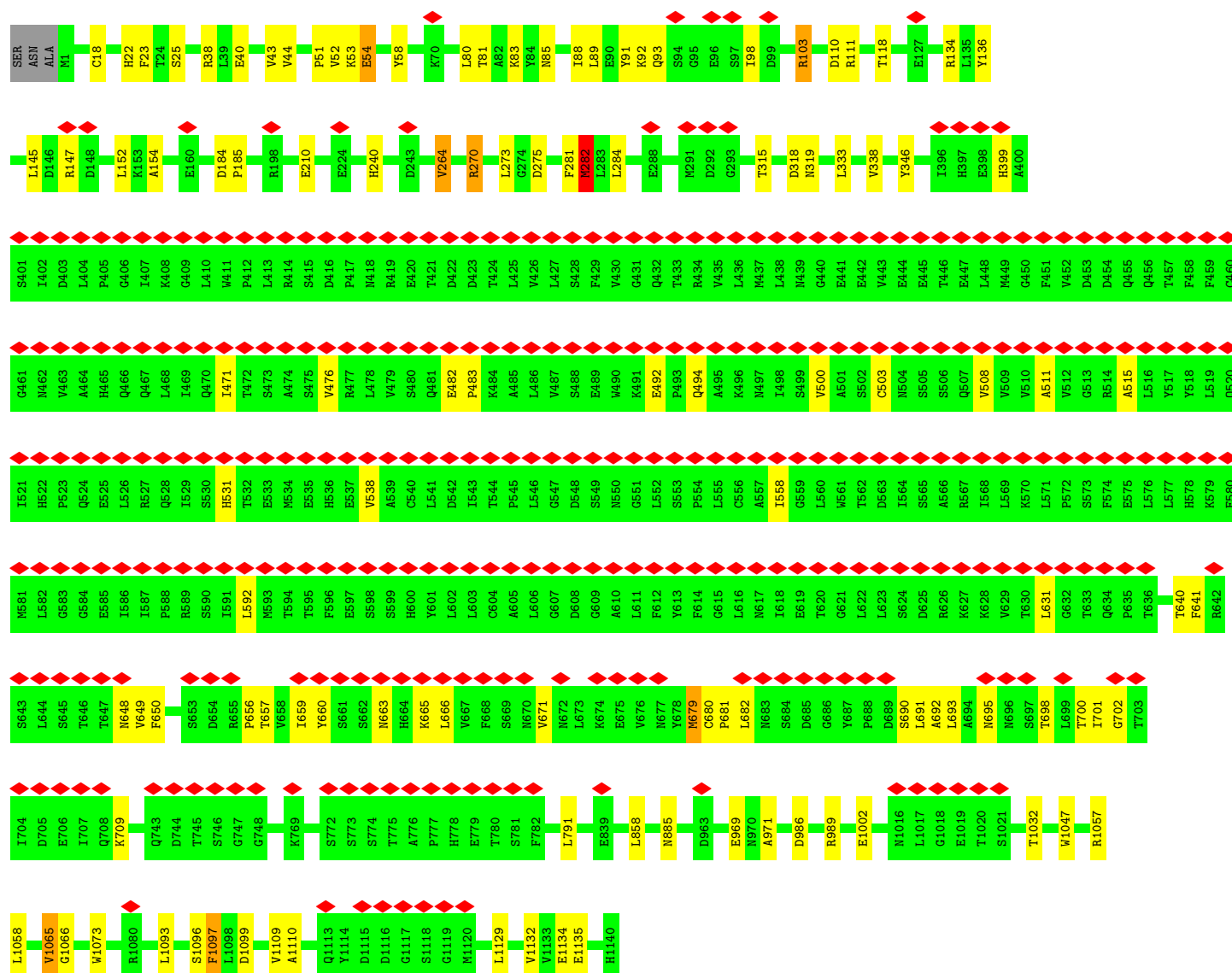
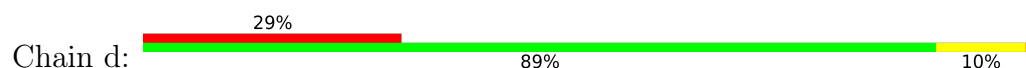


● Molecule 19: UV-stimulated scaffold protein A



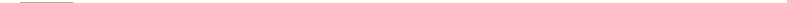


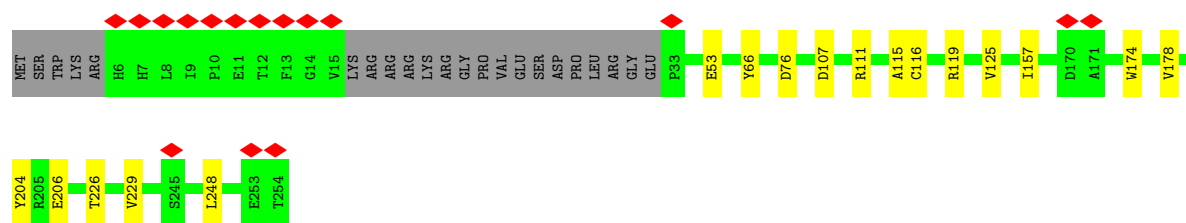
• Molecule 20: DNA damage-binding protein 1



• Molecule 21: DET1- and DDB1-associated protein 1

GLU	LEU	GLY	GLU	SER	SER	ALA	PRO	PRO	ARG	LYS	VAL	ALA	ARG	THR	ASP	SER	PRO	ASP	MET	HIS	GLU	ASP	THR																																
SER	ASN	ALA	H1	A2	D3	F4	L5	Y11	H20	A21	D22	S23	V24	C25	K26	A27	S28	N29	R30	R31	P32	Y36	Q45	I46	I47	V48	T49	E50	K51	T52	H53	L1E	LEU	LEU	ARG	TYR	LEU	HIS	GLN	GLN	TRP	ASP	LYS	LYS	ASN	ALA	ALA	LYS	LYS	ARG	ASP	GLN	GLU	GLN	THR

- Chain f: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	484012	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52.4	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	142.479	Depositor
Minimum map value	-0.208	Depositor
Average map value	0.017	Depositor
Map value standard deviation	1.349	Depositor
Recommended contour level	3.06	Depositor
Map size (Å)	439.92, 439.92, 439.92	wwPDB
Map dimensions	468, 468, 468	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.94000006, 0.94000006, 0.94000006	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.32	0/11493	0.60	1/15515 (0.0%)
2	B	0.35	0/9219	0.59	1/12444 (0.0%)
3	C	0.32	0/2132	0.55	0/2896
4	D	0.14	0/1027	0.43	0/1384
5	E	0.37	0/1752	0.56	0/2366
6	F	0.31	0/668	0.54	0/901
7	G	0.18	0/1365	0.48	0/1853
8	H	0.29	0/1207	0.52	0/1628
9	I	0.33	0/973	0.56	0/1316
10	J	0.32	0/543	0.62	0/730
11	K	0.30	0/939	0.48	0/1271
12	L	0.31	0/395	0.66	0/524
13	M	0.34	0/515	0.50	0/700
14	N	0.49	0/824	1.08	0/1270
15	P	0.51	0/247	0.76	1/384 (0.3%)
16	T	0.50	0/1096	1.11	1/1685 (0.1%)
17	a	0.45	0/3082	0.56	0/4182
18	b	0.54	0/5180	0.60	0/6982
19	c	0.21	0/1899	0.54	0/2540
20	d	0.41	0/9083	0.62	3/12306 (0.0%)
21	e	0.17	0/439	0.55	0/593
22	f	0.51	0/1853	0.60	0/2509
All	All	0.38	0/55931	0.61	7/75979 (0.0%)

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	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
15	P	0	1
18	b	0	1
20	d	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	d	270	ARG	N-CA-C	12.29	125.87	108.54
15	P	9	G	O3'-P-O5'	-7.61	92.58	104.00
1	A	499	ASP	CA-CB-CG	6.96	119.56	112.60
20	d	282	MET	N-CA-C	5.63	118.41	107.71
20	d	1066	GLY	N-CA-C	-5.48	107.54	115.27

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	967	ARG	Sidechain
2	B	274	ARG	Sidechain
15	P	10	A	Sidechain
18	b	593	ARG	Sidechain
20	d	103	ARG	Sidechain

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	A	11289	0	11411	69	0
2	B	9038	0	9072	48	0
3	C	2089	0	2031	12	0
4	D	1013	0	972	7	0
5	E	1721	0	1737	5	0
6	F	658	0	684	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1334	0	1333	9	0
8	H	1186	0	1147	5	0
9	I	950	0	879	9	0
10	J	534	0	553	1	0
11	K	920	0	942	3	0
12	L	389	0	393	6	0
13	M	505	0	463	2	0
14	N	732	0	394	15	0
15	P	220	0	109	2	0
16	T	984	0	556	18	0
17	a	3017	0	2909	10	0
18	b	5065	0	5081	19	0
19	c	1865	0	1839	12	0
20	d	8918	0	8881	79	0
21	e	429	0	427	13	0
22	f	1817	0	1851	10	0
23	A	2	0	0	0	0
23	B	1	0	0	0	0
23	C	1	0	0	0	0
23	I	2	0	0	0	0
23	J	1	0	0	0	0
23	L	1	0	0	0	0
23	M	1	0	0	0	0
23	c	1	0	0	0	0
24	A	1	0	0	0	0
24	b	1	0	0	0	0
25	A	2	0	0	0	0
All	All	54687	0	53664	310	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 3.

The worst 5 of 310 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:50:DT:H2'	14:N:51:DG:C8	1.79	1.18
14:N:50:DT:C2'	14:N:51:DG:C8	2.38	1.06
19:c:41:ARG:O	19:c:45:LEU:HD13	1.66	0.95
16:T:2:DC:O2	16:T:3:DA:C6	2.29	0.86
16:T:2:DC:C2	16:T:3:DA:C6	2.65	0.85

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	A	1417/1984 (71%)	1370 (97%)	46 (3%)	1 (0%)	48	40
2	B	1121/1251 (90%)	1086 (97%)	35 (3%)	0	100	100
3	C	256/275 (93%)	247 (96%)	9 (4%)	0	100	100
4	D	126/142 (89%)	120 (95%)	6 (5%)	0	100	100
5	E	207/210 (99%)	206 (100%)	1 (0%)	0	100	100
6	F	80/127 (63%)	77 (96%)	3 (4%)	0	100	100
7	G	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
8	H	146/150 (97%)	141 (97%)	5 (3%)	0	100	100
9	I	115/125 (92%)	109 (95%)	6 (5%)	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%)	41 (93%)	3 (7%)	0	100	100
13	M	62/85 (73%)	61 (98%)	1 (2%)	0	100	100
17	a	382/396 (96%)	367 (96%)	15 (4%)	0	100	100
18	b	611/1496 (41%)	587 (96%)	24 (4%)	0	100	100
19	c	237/712 (33%)	230 (97%)	7 (3%)	0	100	100
20	d	1138/1143 (100%)	1083 (95%)	55 (5%)	0	100	100
21	e	51/105 (49%)	45 (88%)	6 (12%)	0	100	100
22	f	228/254 (90%)	221 (97%)	7 (3%)	0	100	100
All	All	6568/8869 (74%)	6329 (96%)	238 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1274	GLU

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	1256/1763 (71%)	1254 (100%)	2 (0%)	87	90
2	B	991/1084 (91%)	989 (100%)	2 (0%)	87	90
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	147/153 (96%)	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	59/77 (77%)	59 (100%)	0	100	100
17	a	339/348 (97%)	339 (100%)	0	100	100
18	b	553/1298 (43%)	553 (100%)	0	100	100
19	c	186/610 (30%)	186 (100%)	0	100	100
20	d	999/1001 (100%)	988 (99%)	11 (1%)	65	67
21	e	49/95 (52%)	48 (98%)	1 (2%)	48	46
22	f	194/214 (91%)	193 (100%)	1 (0%)	81	84
All	All	5817/7784 (75%)	5800 (100%)	17 (0%)	84	88

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	d	1097	PHE

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Mol	Chain	Res	Type
22	f	178	VAL
20	d	147	ARG
20	d	264	VAL
20	d	282	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	168	ASN
20	d	991	HIS
9	I	67	GLN
20	d	990	GLN
20	d	234	GLN

5.3.3 RNA [i](#)

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

There are no RNA backbone outliers to report.

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 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

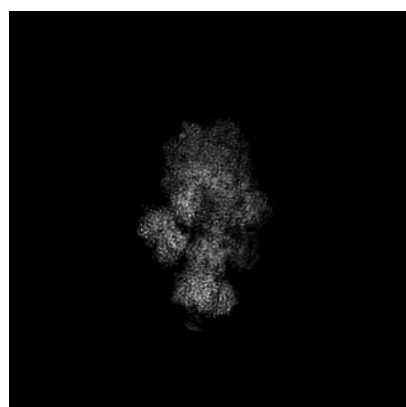
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45050. These allow visual inspection of the internal detail of the map and identification of artifacts.

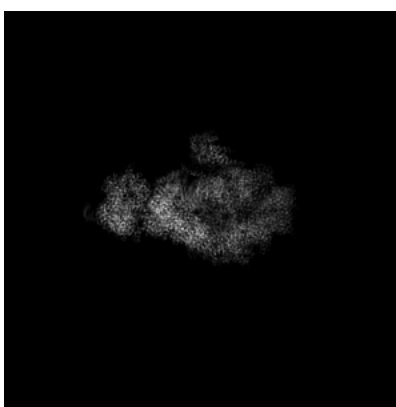
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

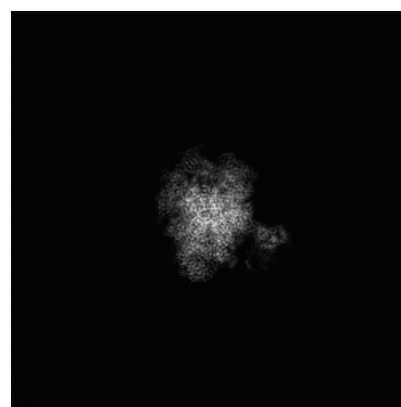
6.1.1 Primary map



X



Y

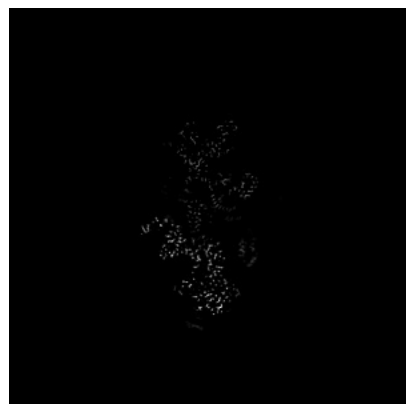


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 234



Y Index: 234



Z Index: 234

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

6.3 Largest variance slices [i](#)

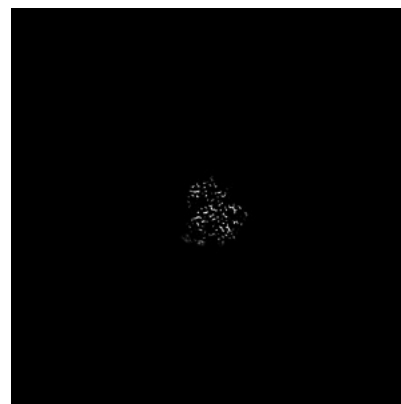
6.3.1 Primary map



X Index: 218



Y Index: 219

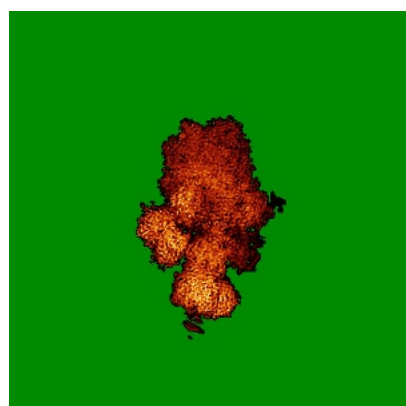


Z Index: 132

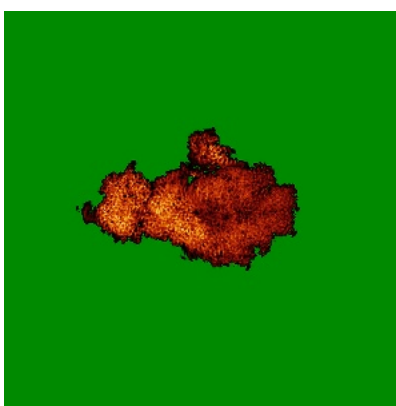
The images above show the largest variance slices of the map in three orthogonal directions.

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

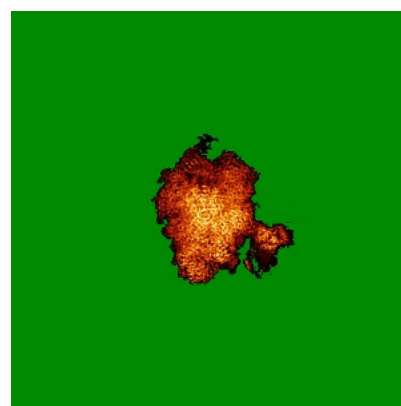
6.4.1 Primary map



X



Y



Z

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](#)

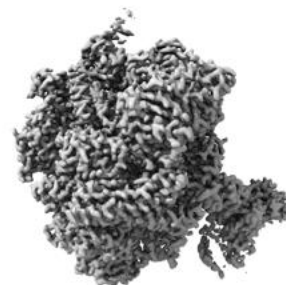
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

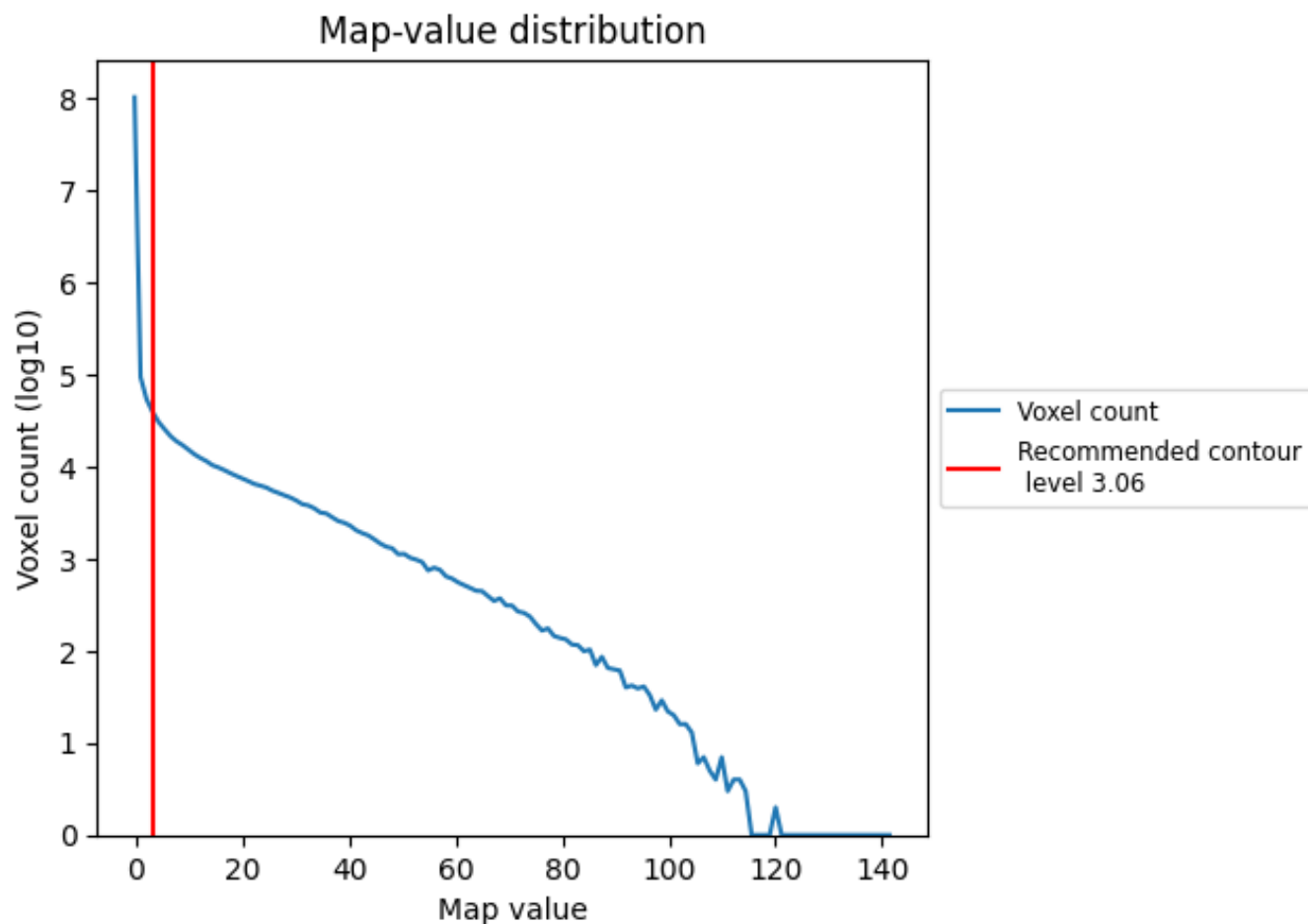
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

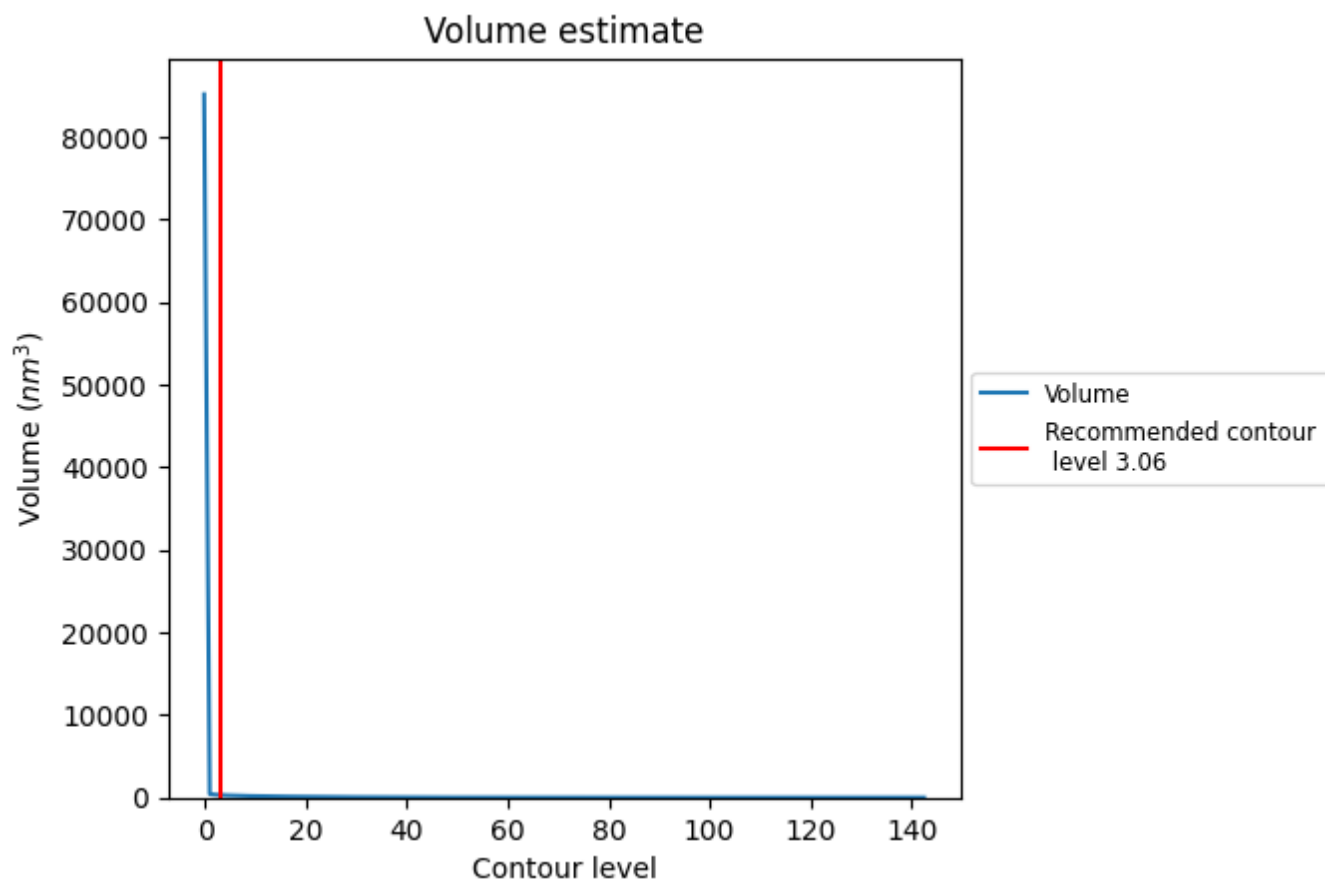
This section contains the results of statistical analysis of the map.

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.

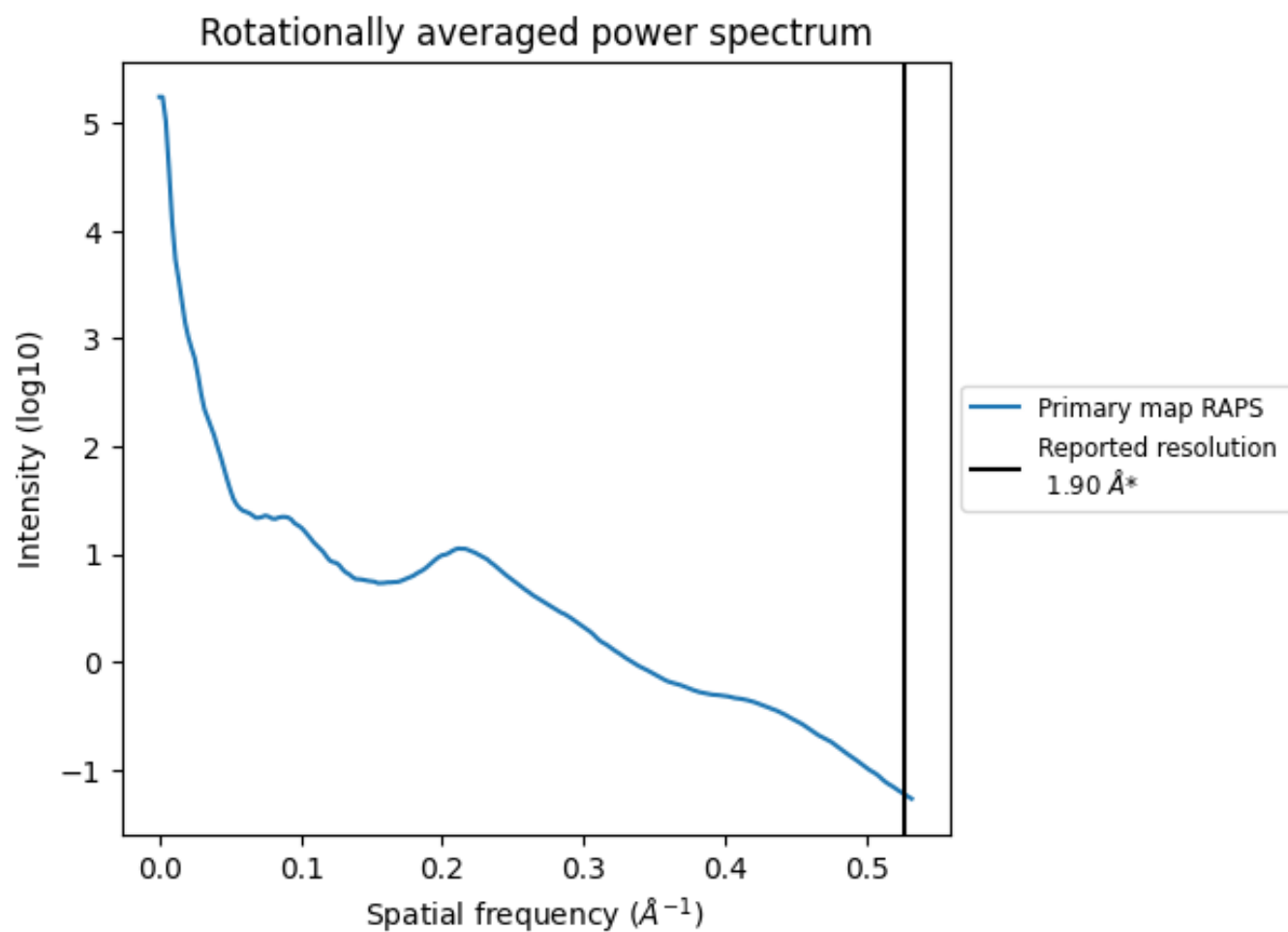
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 306 nm^3 ; this corresponds to an approximate mass of 276 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 ⓘ

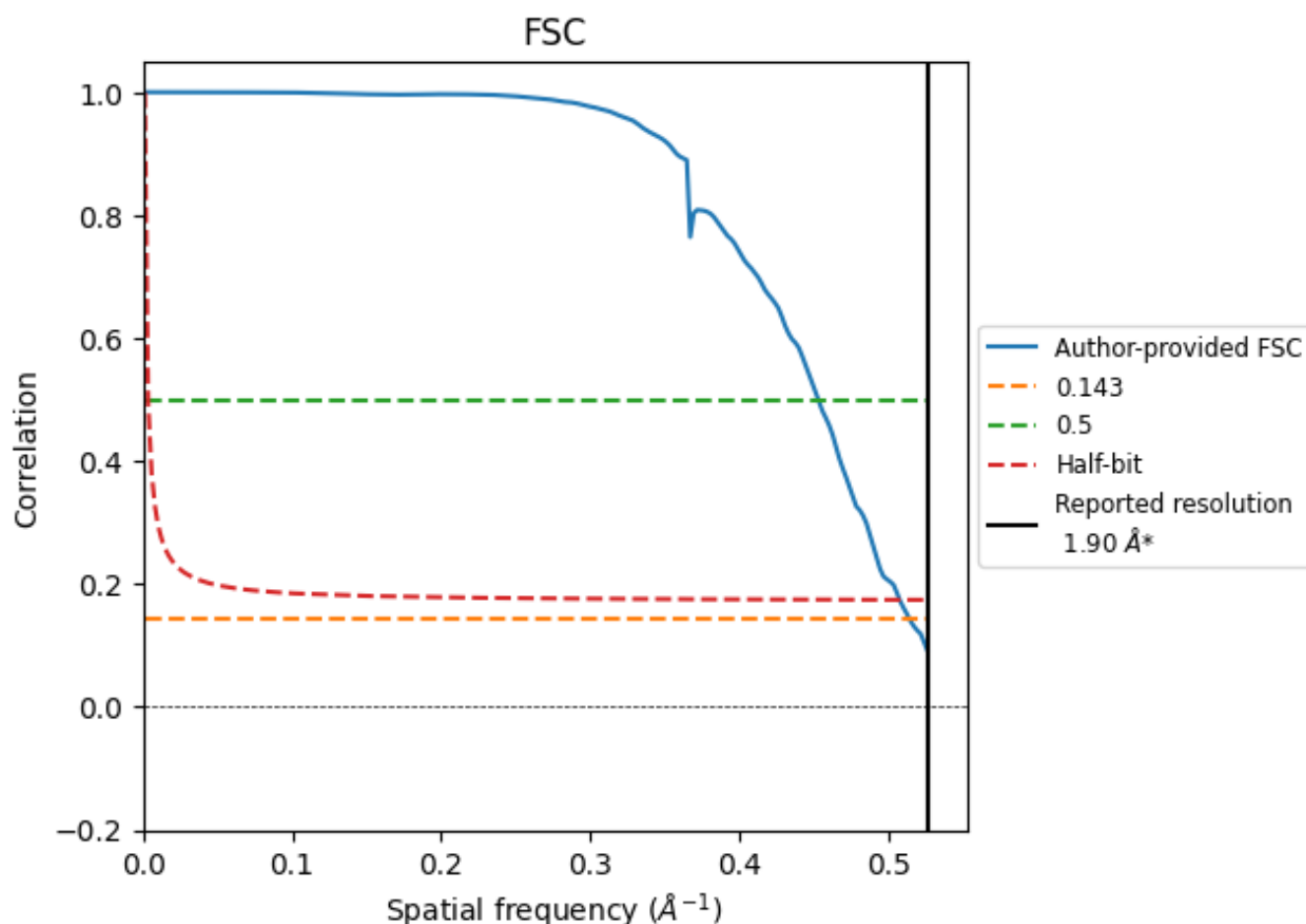


*Reported resolution corresponds to spatial frequency of 0.526 Å⁻¹

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 0.526 Å⁻¹

8.2 Resolution estimates [i](#)

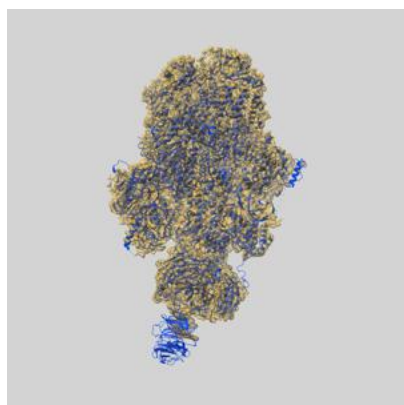
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.90	-	-
Author-provided FSC curve	1.95	2.21	1.97
Unmasked-calculated*	-	-	-

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

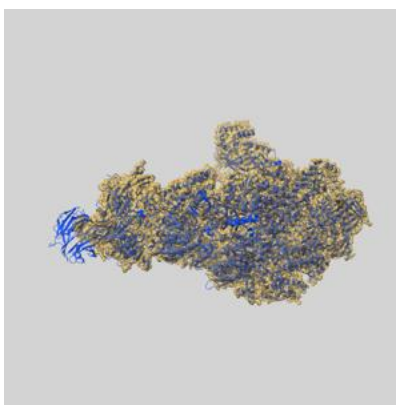
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45050 and PDB model 9BZ0. Per-residue inclusion information can be found in section [3](#) on page [9](#).

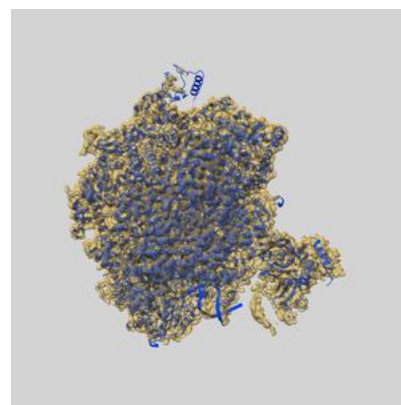
9.1 Map-model overlay [i](#)



X



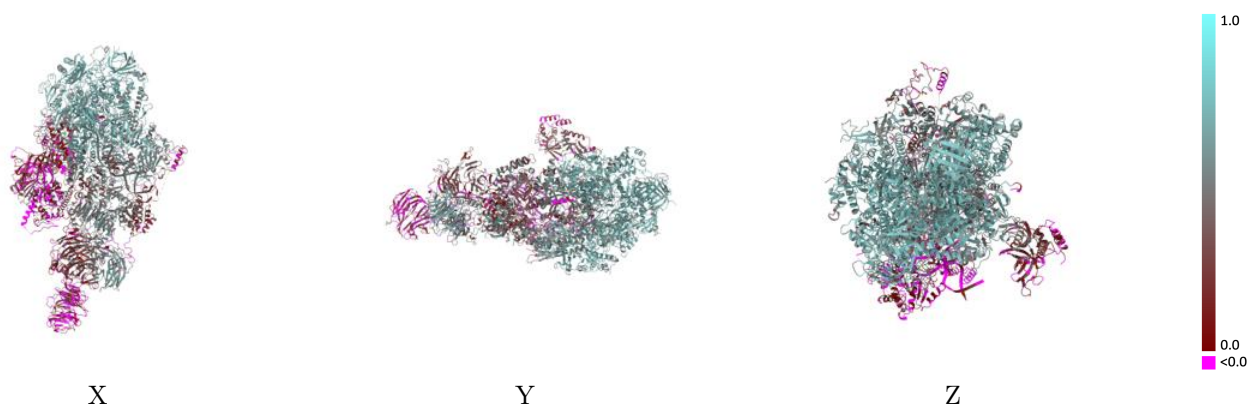
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.06 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](#)

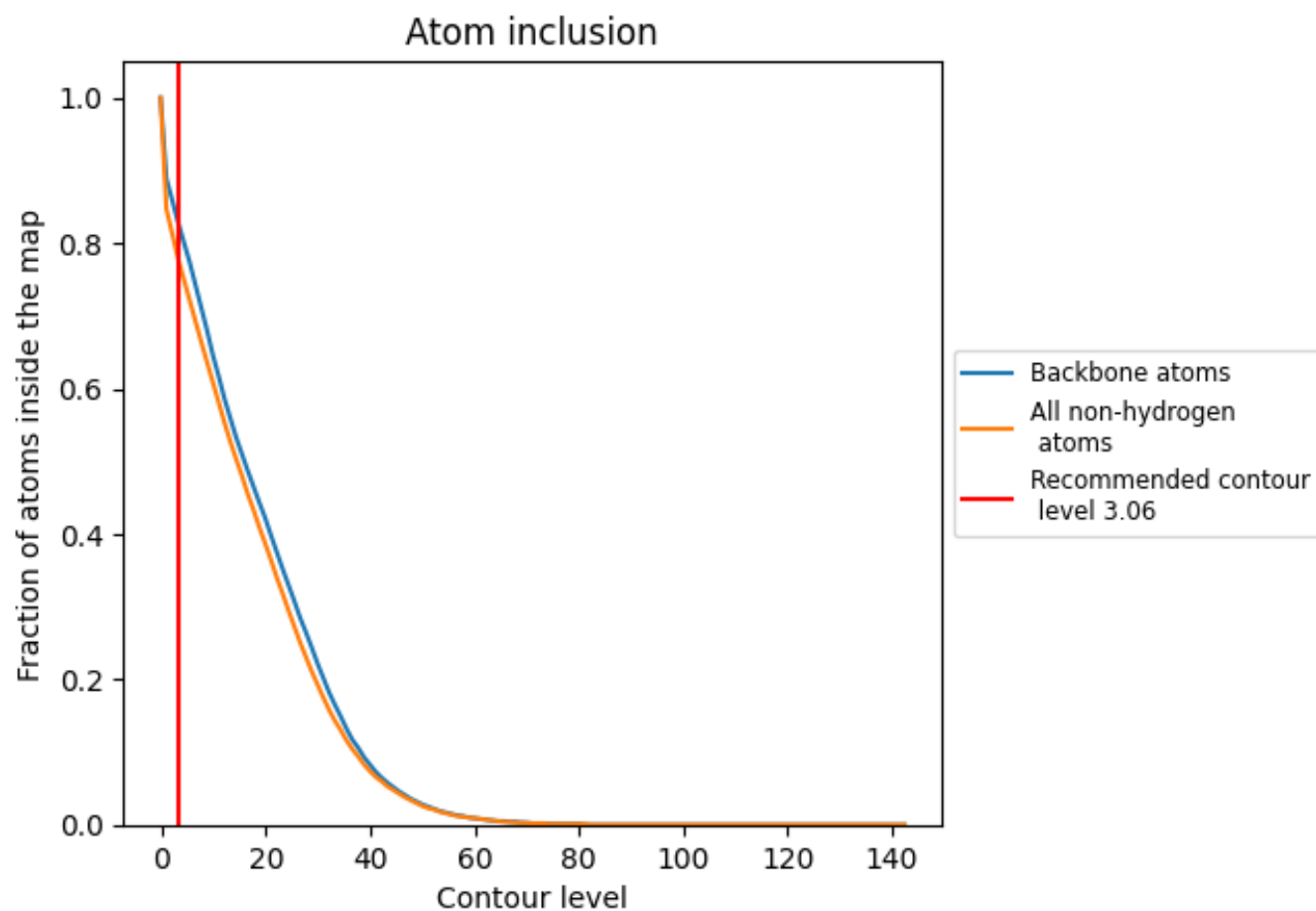


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 78% 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 (3.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.4480
A	 0.8680	 0.5810
B	 0.8880	 0.6130
C	 0.8980	 0.6430
D	 0.6710	 0.1430
E	 0.9040	 0.5940
F	 0.8700	 0.5870
G	 0.6780	 0.2670
H	 0.9030	 0.6370
I	 0.8270	 0.5440
J	 0.9120	 0.6590
K	 0.9180	 0.6540
L	 0.7830	 0.5240
M	 0.8640	 0.5220
N	 0.7250	 0.2710
P	 0.9550	 0.6300
T	 0.7730	 0.3400
a	 0.8810	 0.4870
b	 0.6620	 0.1040
c	 0.5420	 0.2750
d	 0.6180	 0.2740
e	 0.5360	 0.2360
f	 0.7940	 0.3990

