



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 07:18 PM UTC

PDB ID : 7OPD / pdb_00007opd
EMDB ID : EMD-13016
Title : Pol II-CSB-CRL4CSA-UVSSA-SPT6-PAF (Structure 5)
Authors : Kokic, G.; Cramer, P.
Deposited on : 2021-05-31
Resolution : 3.00 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
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

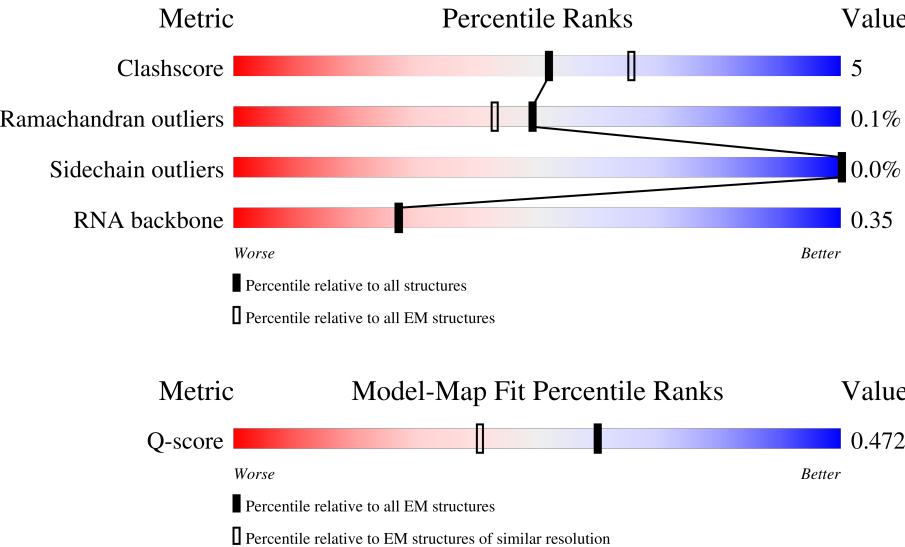
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	
2	B	1174	
3	C	275	

Continued on next page...

Continued from previous page...

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	1729	
14	N	47	
15	P	45	
16	R	40	
17	S	1179	
18	T	47	
19	U	666	
20	V	531	
21	Y	305	
22	Z	531	
23	a	396	
24	b	1496	
25	c	712	
26	d	1143	
27	e	762	
28	f	108	

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 64227 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 II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1412	Total	C	N	O	S	0	0
			11179	7033	2002	2074	70		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1131	Total	C	N	O	S	0	0
			9052	5727	1592	1669	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 RPOL4c 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
			1720	1089	300	323	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			657	418	113	121	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
			949	587	169	182	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
			533	345	90	92	6		

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

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
			388	241	75	66	6		

- Molecule 13 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	810	Total	C	N	O	S	0	0
			6648	4226	1155	1234	33		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q7KZ85
M	-1	ASN	-	expression tag	UNP Q7KZ85
M	0	ALA	-	expression tag	UNP Q7KZ85

- Molecule 14 is a DNA chain called NTS.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	35	Total	C	N	O	P	0	0
			727	344	142	206	35		

- Molecule 15 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	21	Total	C	N	O	P	0	0
			454	204	89	140	21		

- Molecule 16 is a protein called LEO1 helix.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	R	40	Total	C	N	O	0	0
			160	80	40	40		

- Molecule 17 is a protein called RNA polymerase-associated protein CTR9 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	S	890	Total	C	N	O	0	0
			3560	1780	890	890		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1174	GLU	-	expression tag	UNP Q6PD62
S	1175	ASN	-	expression tag	UNP Q6PD62
S	1176	LEU	-	expression tag	UNP Q6PD62
S	1177	TYR	-	expression tag	UNP Q6PD62
S	1178	PHE	-	expression tag	UNP Q6PD62
S	1179	GLN	-	expression tag	UNP Q6PD62

- Molecule 18 is a DNA chain called TS.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	47	Total	C	N	O	P	0	0
			947	453	159	288	47		

- Molecule 19 is a protein called RNA polymerase-associated protein LEO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	U	104	Total	C	N	O	0	0
			416	208	104	104		

- Molecule 20 is a protein called RNA polymerase II-associated factor 1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	V	217	Total	C	N	O	0	0
			868	434	217	217		

- Molecule 21 is a protein called WD repeat-containing protein 61.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Y	300	Total	C	N	O	0	0
			1200	600	300	300		

- Molecule 22 is a protein called Parafibromin.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Z	43	Total	C	N	O	0	0
			172	86	43	43		

- Molecule 23 is a protein called DNA excision repair protein ERCC-8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	365	Total	C	N	O	S	0	0
			2849	1775	507	548	19		

- Molecule 24 is a protein called DNA excision repair protein ERCC-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	520	Total	C	N	O	S	0	0
			4261	2746	748	746	21		

There are 4 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	538	ARG	LYS	conflict	UNP Q03468

- Molecule 25 is a protein called UV-stimulated scaffold protein A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	c	141	Total	C	N	O	0	0
			564	282	141	141		

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 26 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	1096	Total	C	N	O	S	0	0
			7443	4562	1354	1493	34		

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 27 is a protein called Cullin-4A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	e	711	Total	C	N	O	0	0
			2845	1422	711	712		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	-2	SER	-	expression tag	UNP Q13619
e	-1	ASN	-	expression tag	UNP Q13619
e	0	ALA	-	expression tag	UNP Q13619

- Molecule 28 is a protein called E3 ubiquitin-protein ligase RBX1.

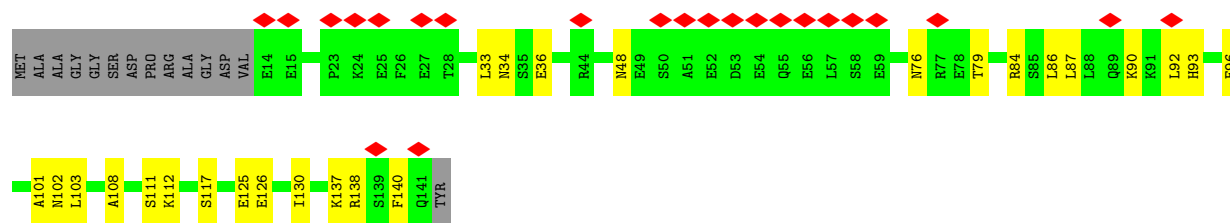
Mol	Chain	Residues	Atoms				AltConf	Trace
28	f	21	Total	C	N	O	0	0
			84	42	21	21		

- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn).

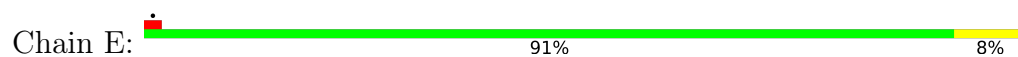
Mol	Chain	Residues	Atoms		AltConf
29	A	2	Total	Zn	0
			2	2	
29	B	1	Total	Zn	0
			1	1	
29	C	1	Total	Zn	0
			1	1	
29	I	2	Total	Zn	0
			2	2	
29	J	1	Total	Zn	0
			1	1	
29	L	1	Total	Zn	0
			1	1	

- Molecule 30 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

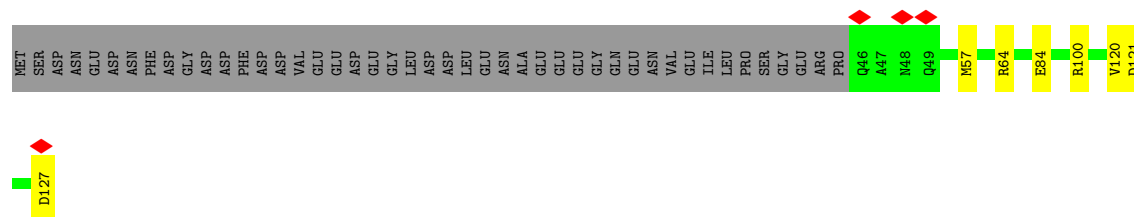
Mol	Chain	Residues	Atoms		AltConf
30	A	1	Total	Mg	0
			1	1	



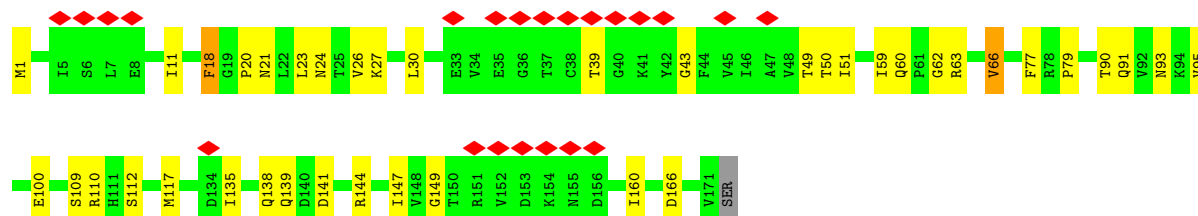
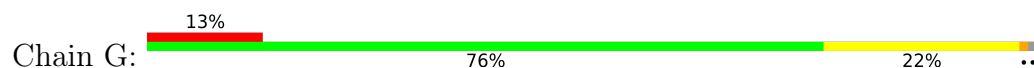
- Molecule 5: DNA-directed RNA polymerase II subunit E



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



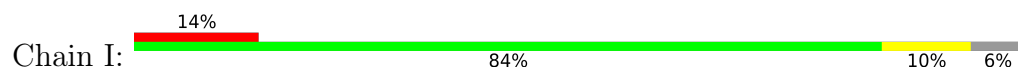
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



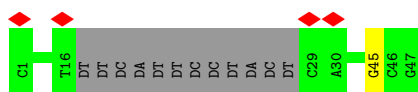
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



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





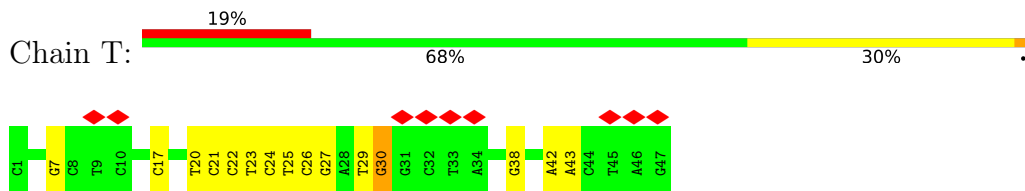


A C A A U C U A U A C C C A A U U U G A A A C C A G A A A U A30 A31 A32 A33 A34 A35 A36 A37 A38 A39 A40 A41 A42 A43 A44 A45 A46 A47 A48 A49 A50

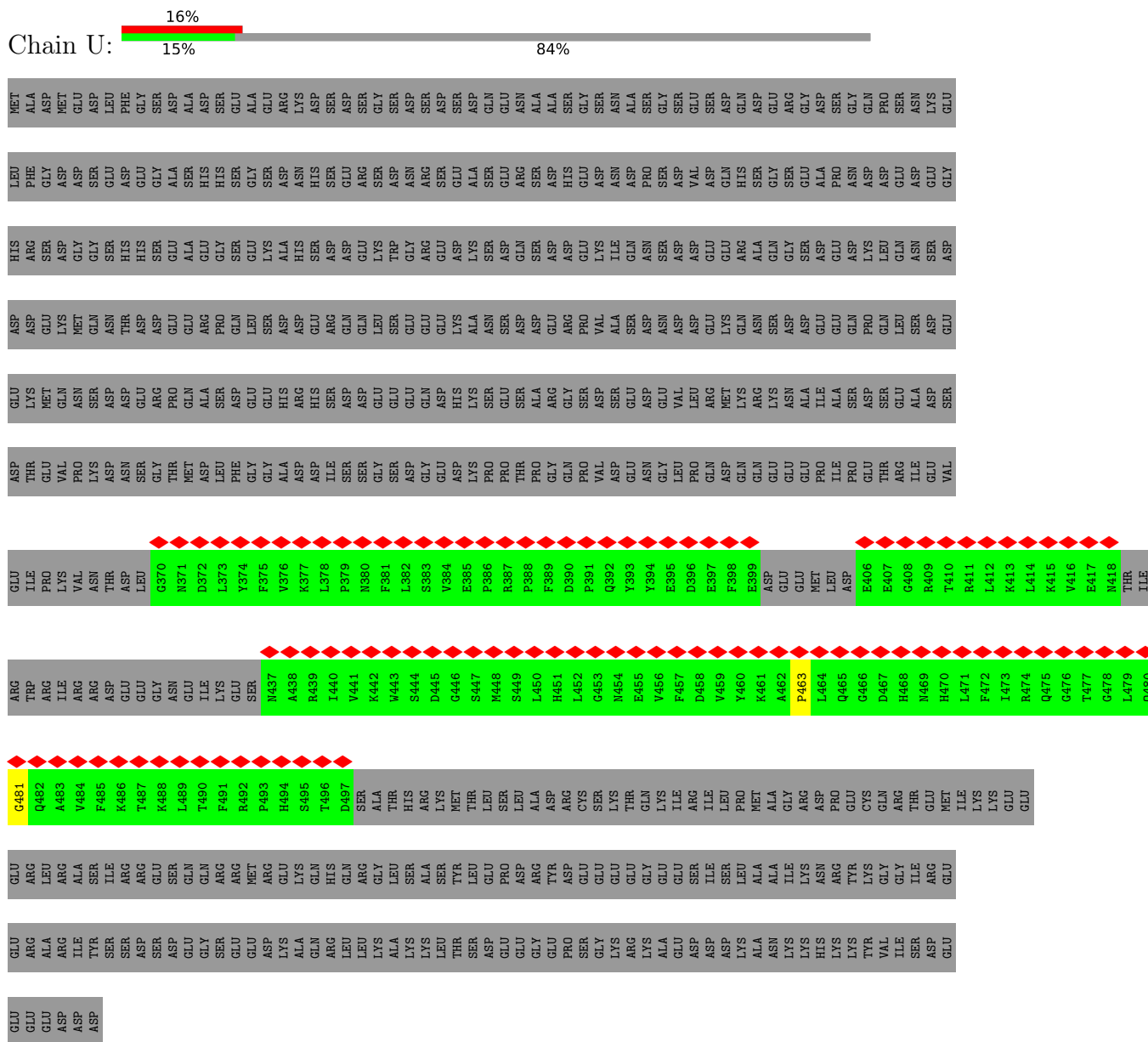
A horizontal bar chart showing the distribution of 40 categories, labeled x1 through x40. The categories are grouped into four sets of 10. The first set (x1-x10) has a total height of 10, with x1-x4 at height 1 and x5-x10 at height 2. The second set (x11-x20) has a total height of 10, with x11-x14 at height 1 and x15-x20 at height 2. The third set (x21-x30) has a total height of 10, with x21-x24 at height 1 and x25-x30 at height 2. The fourth set (x31-x40) has a total height of 10, with x31-x34 at height 1 and x35-x40 at height 2. The bars are colored in a repeating pattern of red, green, and yellow.

GLU	SER	GLU	GLU	ARG	ASP	SER	ARG	ES350	E665	Q128	MET
SER	GLU	ARG	GLY	ASP	GLY	SER	LYS	L851	A666	E141	R3
GLU	PRO	LYS	HIS	ASP	LYS	LYS	LYS	L852	R667	G142	G4
GLU	ARG	PRO	ARG	GLU	GLY	GLY	GLY	R853	D668	D143	S5
SER	PRO	ASN	ARG	THR	GLY	GLU	GLY	Q854	V669		T6
ASN	SER	ASN	ASN	ASN	PHE	ASN	PHE	K855	F670	D146	E7
GLY	GLY	ASP	SER	GLY	ASP	GLY	ASP	L856	A671		T8
ASN	SER	SER	ASN	PRO	GLU	PRO	GLU	L857	Q672	Q158	P9
ALA	GLU	ASN	ALA	LYS	VAL	LYS	VAL	K858	V673		L10
SER	GLN	SER	GLN	PRO	GLN	PRO	GLN	Q859	R674	N161	R11
ARG	ASP	ASP	ASP	LYS	ASP	LYS	ASP	Q860	E675		D12
ASP	ASN	ASP	ASN	ARG	ASP	ARG	ASP	E861	A676	P197	T13
SER	GLU	GLU	GLU	ARG	THR	ARG	THR	E862	T677	G205	D14
GLU	SER	ASP	ASP	PRO	ASP	PRO	ASP	K863	A678		E15
HIS	VAL	GLU	GLU	PRO	ASP	PRO	ASP	R864		V209	V16
GLY	GLY	GLN	GLN	LYS	ASP	LYS	ASP	L865	L687		E17
SER	SER	SER	SER	ALA	LEU	ALA	LEU	R866		E247	E18
ASP	GLY	LYS	LYS	GLU	PRO	GLU	PRO	R867	Y691		L19
ASP	LYS	ARG	LYS	LYS	LYS	LYS	LYS	E867	V692	G254	D20
SER	CYS	SER	CYS	LYS	LYS	LYS	LYS	K868	Q693		F21
GLU	HIS	ALA	ALA	LYS	ALA	LYS	LYS	E869	Q694	F279	D22
ASN	GLY	SER	SER	GLY	PRO	GLY	LYS	Q870	K695	D284	Q23
VAL	VAL	GLY	VAL	LYS	LYS	LYS	LYS	E871	Q696		L24
GLU	GLU	SER	SER	GLU	ARG	GLU	ARG	K872	V697	G382	P25
ASN	ASN	ASP	ASP	ARG	LYS	ARG	LYS	K873	L698		E26
SER	GLU	GLU	GLU	PRO	LEU	GLY	GLY	L874	S699	S388	Q27
ASN	GLY	ASN	ASN	PRO	GLY	GLY	GLY	L875	A700	P409	D28
PRO	GLN	ALA	ALA	SER	SER	SER	SER	E876	V701	D410	
ALA	ASN	ALA	ASN	MET	GLU	GLU	GLU	Q877	Q702		Q36
SER	LYS	LYS	LYS	LYS	GLN	LYS	GLN	R878	M703	E413	
PRO	SER	GLY	SER	GLY	GLY	GLY	GLY	A879		L416	L43
ALA	ALA	SER	SER	ILE	ASP	LYS	ASP	Q880	M706		N44
GLU	GLU	GLU	GLU	LYS	GLU	GLU	GLU	Y881		K444	L45
SER	ALA	SER	ALA	SER	GLY	LYS	GLY	E882	F711		A46
ASP	GLY	ASP	GLY	LYS	GLU	GLY	GLU	V883		Y507	
HIS	SER	HIS	SER	ILE	ILE	GLY	GLY	K884	K729	E512	G55
GLU	PRO	SER	ARG	GLU	GLU	GLU	GLU	T885	C730		
GLU	GLU	ARG	ARG	SER	ARG	LYS	ARG	T886	G731	L535	
ARG	GLY	ARG	GLY	SER	LYS	SER	LYS	K887	D771	A539	M72
SER	SER	SER	ARG	ASP	LYS	ASP	LYS	I888	E772		L73
ASP	GLN	ASP	GLN	ASP	LYS	ASP	LYS	L889	K773	K586	D74
ASN	ASN	ASN	SER	SER	ARG	SER	ARG	M890	S774	K587	V75
GLY	GLY	GLY	GLY	ASP	ARG	ASP	ARG	F891			R76
SER	SER	SER	GLN	GLU	HIS	GLU	HIS		G600	I591	D77
GLY	GLY	GLY	GLY	ASP	PRO	ASP	PRO	T892			
GLN	GLN	SER	SER	LYS	LYS	LYS	LYS	GLY	R804		X80
GLY	ASP	GLY	ASP	LEU	GLY	GLY	GLY	THR	F805	A644	
SER	SER	ASP	SER	LYS	GLU	GLU	GLU	THR	D806	A649	A90
GLY	GLY	GLY	GLY	ILE	GLU	GLU	GLU				

- Molecule 18: TS

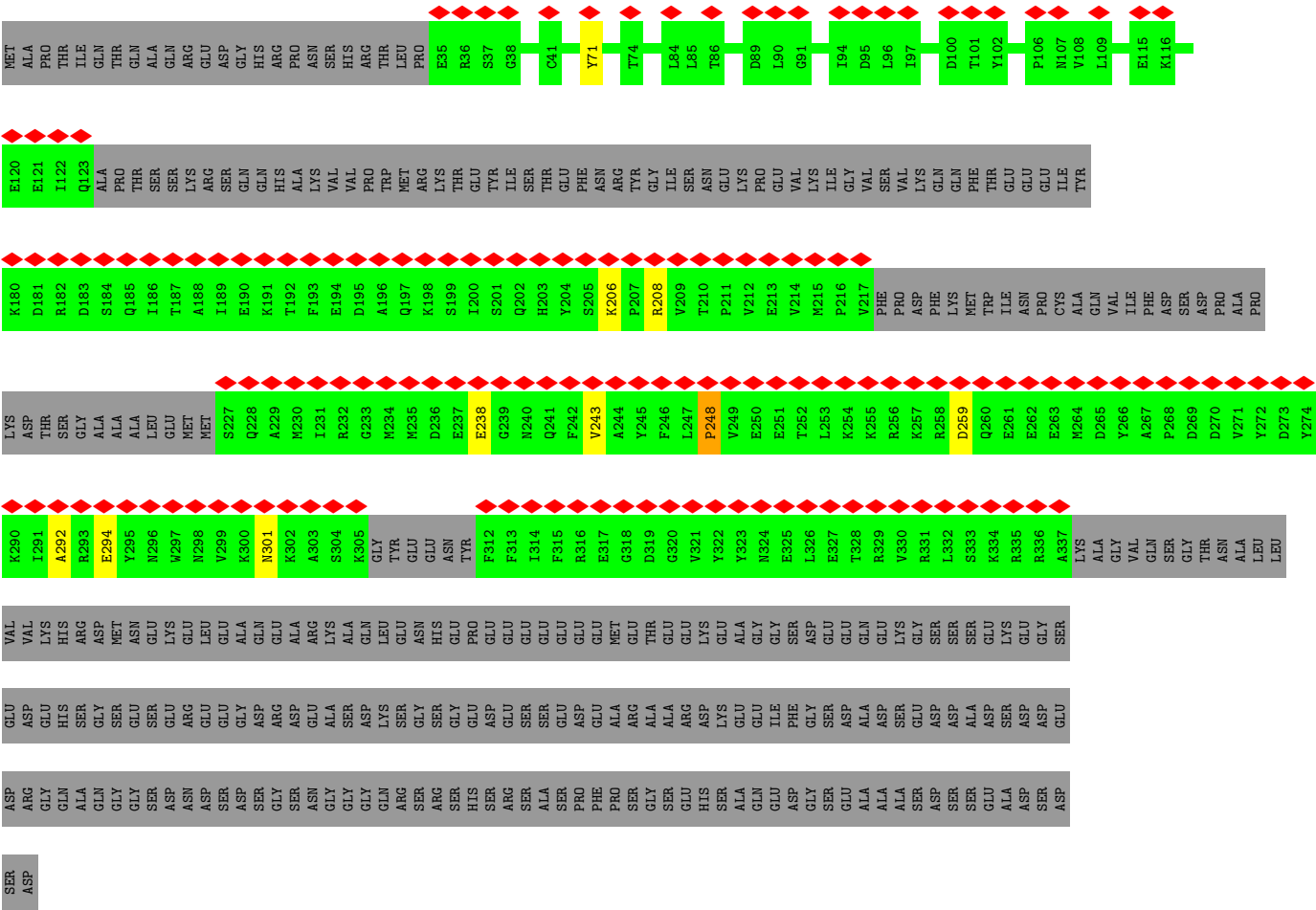


- Molecule 19: RNA polymerase-associated protein LEO1



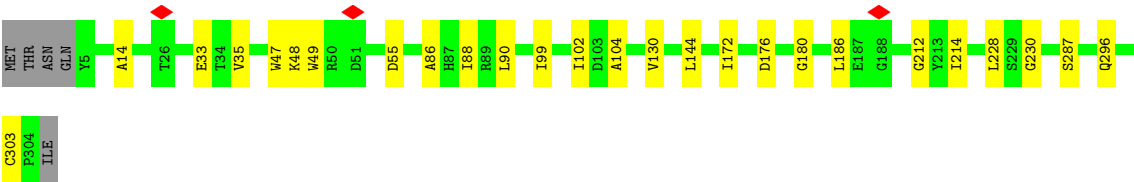
- Molecule 20: RNA polymerase II-associated factor 1 homolog





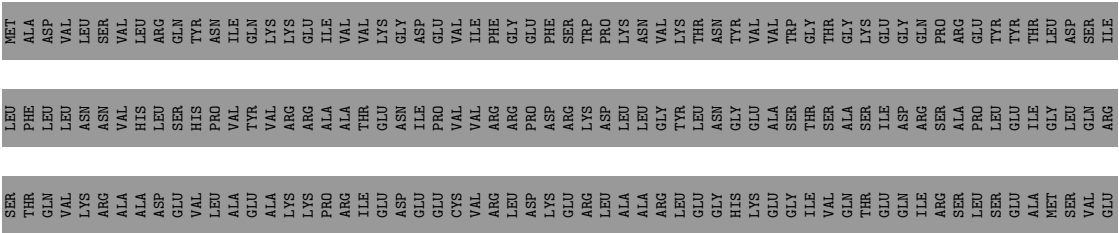
• Molecule 21: WD repeat-containing protein 61

Chain Y: 90% 9% .

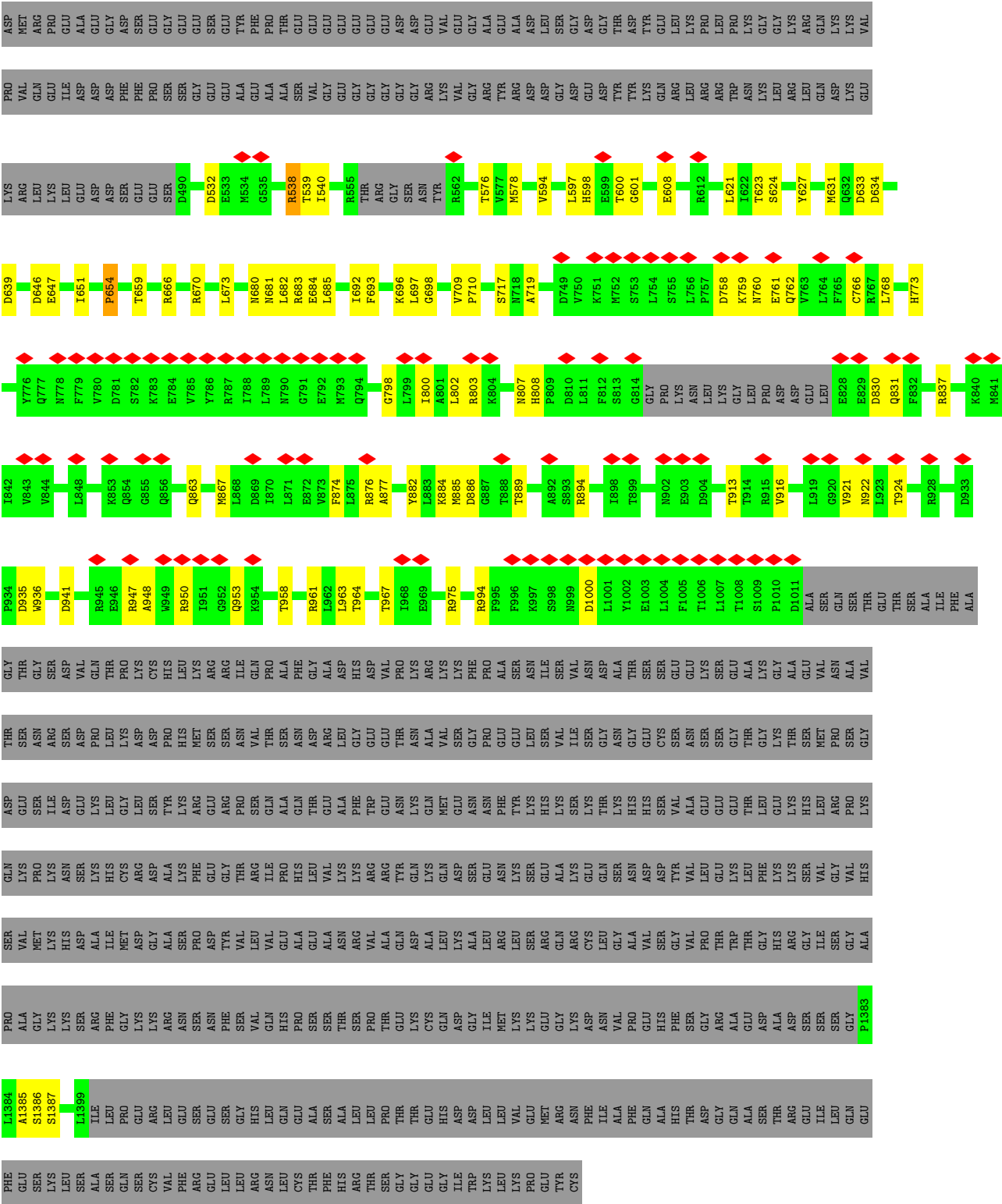


• Molecule 22: Parafibromin

Chain Z: 7% 92% .





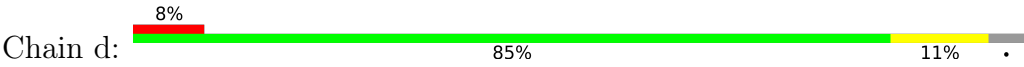


● Molecule 25: UV-stimulated scaffold protein A

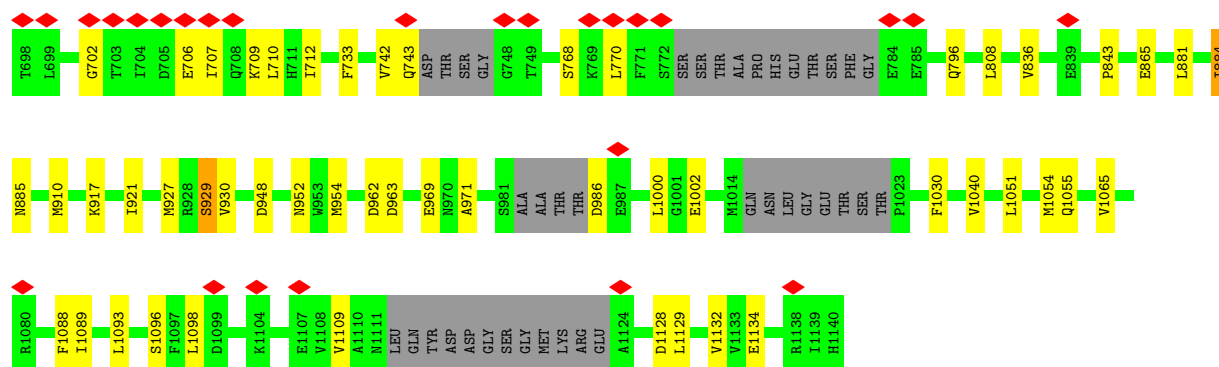


SER	ASN	ALA	MET	ASP	Q3	K4	L5	S6	K7	L8	V9	E10	E11	L12	T13	T14	S15	G16	E17	P18	R19	L20	N21	P22	E23	K24	M25	K26	E27	L28	K29	K30	I31	C32	K33	S34	S35	E36	E37	Q38	L39	S40	R41	A42	Y43	R44	L45	L46	I47	A48	Q49	L50	T51	Q52	E53	H54	A55	E56	I57	
R58	L59	S60	A61	F62	Q63	I64	V65	E66	E67	L68	F69	E10	V70	R71	S72	H73	Q74	F75	R76	M77	L78	V79	W80	S81	N82	F83	Q84	E85	F86	L87	E88	L89	T90	L91	G92	T93	D94	P95	A96	Q97	P98	L99	P100	P101	P102	R103	E104	A105	A106	Q107	R108	L109	R110	Q111	A112	T113	T114	R115	A116	V117
E118	G119	W120	N121	E122	K123	F124	G125	E126	A127	Y128	K129	L130	L131	A132	L133	G134	Y135	H136	F137	L138	R139	H140	N141	K142	K143	VAL	ASP	PHE	GLN	ASP	THR	ASN	ALA	ARG	SER	LEU	ALA	GLU	ARG	LEU	GLU	GLU	LYS	GLN	LYS	HIS	LEU	ASP	LYS	ILE	TYR	GLN	TYR	GLN	TYR	GLN	PRO			
ALA	GLU	ARG	MET	GLU	GLN	MET	GLY	GLY	ILE	GLU	CYS	THR	THR	GLU	VAL	CYS	PHE	ALA	ARG	LEU	VAL	PRO	PRO	PHE	ASP	ASP	ASN	PRO	PRO	GLU	THR	LEU	GLY	MET	GLY	MET	ASP	ALA	ARG	LEU	ARG	GLU	CYS	GLN	ALA	GLY	GLN	VAL	GLN	GLY	VAL	PRO								
CYS	ARG	SER	GLY	THR	PRO	GLU	ASP	GLY	GLN	PRO	CYS	CYS	SER	ARG	ASP	ALA	ALA	ALA	ALA	GLY	ARG	ARG	ALA	GLY	GLY	GLN	GLN	GLY	SER	GLN	THR	ALA	GLY	ASP	GLU	ASP	ALA	SER	ASP	LEU	ARG	GLU	GLU	PHE	THR	VAL	ARG	GLY	HIS	GLY										
LEU	GLY	SER	HIS	TYR	THR	ASP	ASP	VAL	LEU	CYS	GLU	GLY	LEU	LYS	VAL	GLN	ASN	GLU	ASN	LEU	ALA	LEU	LEU	ILE	HIS	ALA	ASP	THR	LEU	LYS	THR	ASN	LYS	PHE	VAL	ASP	CYS	SER	TRP	ILE	GLN	ARG	GLU	PHE	THR	ARG	VAL	GLY	THR	HIS										
GLY	GLY	CYS	LEU	ARG	ALA	ILE	LEU	ASP	GLU	LEU	GLU	VAL	VAL	ARG	LYS	TYR	LYS	GLU	ILE	GLY	GLU	PRO	GLU	GLY	GLY	ARG	ARG	GLY	THR	ALA	GLY	ASP	ALA	GLU	ASP	ASP	GLU	ASP	PHE	VAL	GLU	VAL	PRO	THR	ARG	GLY	GLY	TYR												
GLU	PRO	HIS	ILE	PRO	ASP	HIS	PRO	HIS	GLY	PRO	ARG	ALA	ALA	PRO	VAL	THR	LYS	THR	VAL	VAL	LEU	ARG	VAL	VAL	THR	GLY	ASP	GLY	GLU	VAL	THR	ALA	LYS	ALA	GLU	GLU	ASP	GLN	ASP	ARG	HIS	ASP	GLU	VAL	GLY	GLY	GLY	ALA												
SER	PRO	SER	ARG	ALA	LEU	PRO	GLN	GLU	ALA	LEU	ALA	ALA	ALA	GLU	PRO	GLY	ALA	PRO	VAL	VAL	TYR	GLY	VAL	VAL	GLY	TRP	GLY	GLN	GLU	GLY	LEU	THR	ALA	THR	ALA	LYS	SER	GLN	HIS	ARG	PHE	THR	LYS	PRO	PRO	ARG	GLY	VAL	GLU											
GLU	VAL	VAL	ASN	ALA	PRO	GLU	ILE	ASP	GLU	ARG	GLN	ARG	ARG	THR	PHE	ALA	GLY	LYS	GLU	GLU	ASN	HIS	TRP	PRO	VAL	VAL	TRP	GLY	GLN	GLY	LEU	CYS	GLY	THR	ALA	GLY	ASP	GLN	PHE	GLY	LYS	ILE	VAL	PRO	ARG	ASP	GLU	GLU												
GLY	ARG	PRO	LEU	PRO	ASP	ASP	GLU	ARG	GLN	ARG	GLY	GLN	HIS	GLN	GLN	GLN	ARG	PRO	TRP	ASP	PRO	PRO	GLY	GLY	VAL	VAL	GLY	GLY	ALA	GLY	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LYS	ILE	VAL	PRO	ARG	ASP	ASP	GLU	GLU	SER											
LEU	THR	LEU	ALA	ALA	ASP	THR	ALA	ALA	GLU	ARG	GLN	GLY	GLN	GLN	GLN	GLN	ARG	ALA	GLU	GLU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL				

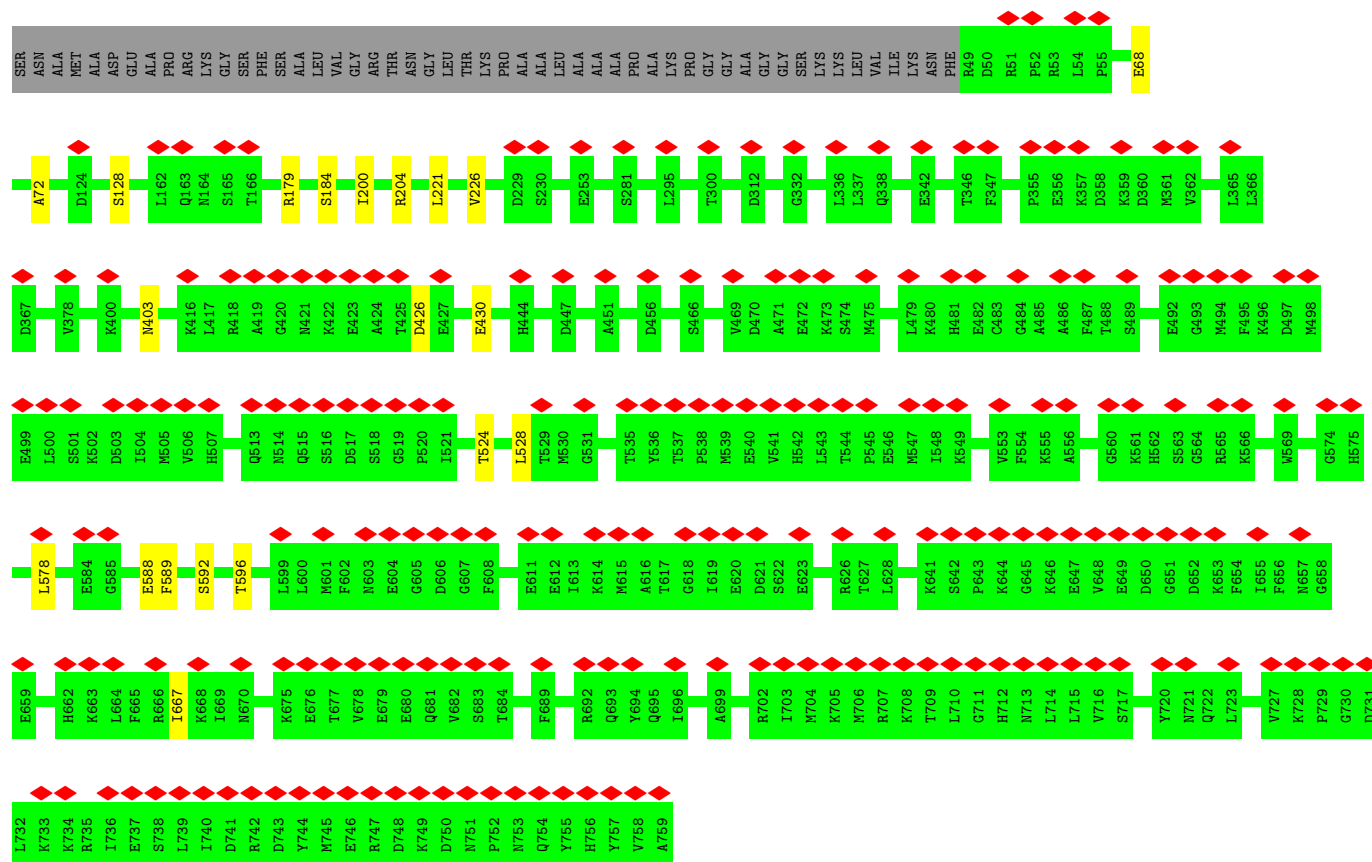
● Molecule 26: DNA damage-binding protein 1



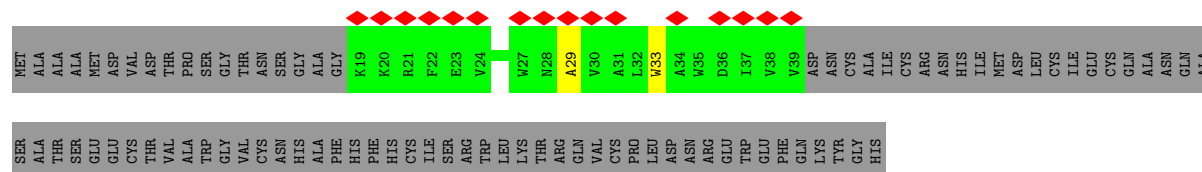
SER	ASN	ALA	M1	V6	C18	V19	L31	L32	I33	A34	K35	R38	V43	T45	A46	E47	V52	K53	E54	I61	M64	K70	G71	E72	I79	L80	T81	A82	K83	E96	T102	R103	E117	T118	G119	M130	R134	D146	R147	V164	I165								
F169	L170	C179	V195	S196	K200	V207	K208	E213	S217	F226	I232	S236	I237	N241	G242	D243	I248	A249	P250	L273	G274	D275	R279	M282	L283	L284	L285	E289	GLN	MET	ASP	GLY	THR	V295	T296	L297	R301	L305	T308	S309									
I310	A311	T315	V324	G325	S326	R327	L328	E342	V347	L356	V365	D366	L367	E368	R369	A381	F382	K383	E384	G385	I390	R391	N392	G395	I396	H397	E398	R399	A400	S401	I402	D403	L404	P405	G406	L413	D422	D423	T424	L425	V426	L427	L438	N439	G440	E441	E442		
V443	E444	G547	D548	S549	N550	E585	E597	S598	D625	R626	K627	G632	S643	L644	S645	T646	D654	R655	S661	S662	N663	H664	K665	L666	V667	F668	S669	N670	V671	N672	L673	K674	E675	V676	N677	L682	N683	S684	D685	G686	Y687	P688	D689	S690	L691	A694	N695	N696	S697



• Molecule 27: Cullin-4A



• Molecule 28: E3 ubiquitin-protein ligase RBX1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100000	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 ($e^-/\text{\AA}^2$)	40.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.167	Depositor
Minimum map value	-0.117	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	440.99997, 440.99997, 440.99997	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	0.24	0/11382	0.41	0/15368
2	B	0.24	0/9233	0.39	0/12463
3	C	0.27	0/2132	0.42	0/2896
4	D	0.93	0/1027	0.81	0/1384
5	E	0.21	0/1751	0.35	0/2366
6	F	0.23	0/667	0.36	0/901
7	G	1.22	2/1365 (0.1%)	0.85	1/1853 (0.1%)
8	H	0.23	0/1207	0.37	0/1628
9	I	0.20	0/972	0.40	0/1316
10	J	0.24	0/542	0.37	0/730
11	K	0.23	0/939	0.34	0/1271
12	L	0.26	0/394	0.42	0/524
13	M	1.76	34/6770 (0.5%)	1.05	6/9119 (0.1%)
14	N	1.05	0/817	0.57	0/1258
15	P	2.14	18/510 (3.5%)	0.82	1/793 (0.1%)
17	S	0.32	0/3559	0.76	2/4447 (0.0%)
18	T	1.90	13/1056 (1.2%)	0.79	2/1624 (0.1%)
19	U	0.33	0/413	0.66	0/511
20	V	0.34	0/864	0.80	2/1073 (0.2%)
21	Y	0.33	0/1199	0.76	0/1497
22	Z	0.36	0/171	0.86	0/212
23	a	1.93	16/2908 (0.6%)	0.95	1/3939 (0.0%)
24	b	1.13	2/4364 (0.0%)	0.73	0/5893
25	c	0.11	0/563	0.27	0/702
26	d	0.30	0/7551	0.45	1/10076 (0.0%)
27	e	0.34	0/2844	0.85	1/3552 (0.0%)
28	f	0.22	0/83	0.81	0/102
All	All	0.88	85/65283 (0.1%)	0.65	17/87498 (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
13	M	0	1
16	R	0	1
23	a	0	1
26	d	0	2
27	e	0	1
All	All	0	7

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	a	19	ARG	CB-CG	-8.38	1.27	1.52
23	a	215	ASP	CA-CB	-8.07	1.42	1.53
23	a	312	TYR	CA-CB	-8.02	1.28	1.53
13	M	912	GLN	CB-CG	-7.90	1.28	1.52
15	P	50	A	P-OP1	-7.42	1.34	1.49

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	1014	ARG	NE-CZ-NH1	-7.79	113.71	121.50
27	e	128	SER	N-CA-C	-7.67	103.27	114.39
13	M	1014	ARG	NE-CZ-NH2	7.07	125.57	119.20
13	M	724	GLN	N-CA-CB	6.31	120.06	110.28
17	S	772	GLU	CA-C-N	5.91	132.33	121.70

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	538	VAL	Peptide
13	M	575	CYS	Peptide
16	R	11	UNK	Peptide
23	a	174	LYS	Peptide
26	d	35	LYS	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	A	11179	0	11313	105	0
2	B	9052	0	9087	60	0
3	C	2089	0	2031	14	0
4	D	1013	0	972	21	0
5	E	1720	0	1737	14	0
6	F	657	0	684	5	0
7	G	1334	0	1333	26	0
8	H	1186	0	1147	7	0
9	I	949	0	879	9	0
10	J	533	0	553	5	0
11	K	920	0	942	7	0
12	L	388	0	393	2	0
13	M	6648	0	6644	142	0
14	N	727	0	393	1	0
15	P	454	0	210	12	0
16	R	160	0	2	3	0
17	S	3560	0	940	8	0
18	T	947	0	519	14	0
19	U	416	0	111	0	0
20	V	868	0	212	3	0
21	Y	1200	0	341	15	0
22	Z	172	0	44	2	0
23	a	2849	0	2778	44	0
24	b	4261	0	4302	71	0
25	c	564	0	143	1	0
26	d	7443	0	6536	95	0
27	e	2845	0	753	10	0
28	f	84	0	20	2	0
29	A	2	0	0	0	0
29	B	1	0	0	0	0
29	C	1	0	0	0	0
29	I	2	0	0	0	0
29	J	1	0	0	0	0
29	L	1	0	0	0	0
30	A	1	0	0	0	0
All	All	64227	0	55019	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 5.

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)
26:d:392:ASN:OD1	26:d:710:LEU:CD2	1.82	1.28
1:A:114:CYS:SG	1:A:184:CYS:HB3	1.83	1.18
26:d:392:ASN:OD1	26:d:710:LEU:HD23	1.41	1.13
24:b:975:ARG:NH2	24:b:1000:ASP:OD1	1.92	1.02
26:d:392:ASN:OD1	26:d:710:LEU:HD21	1.58	1.00

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	1402/1970 (71%)	1366 (97%)	36 (3%)	0	100	100
2	B	1123/1174 (96%)	1076 (96%)	47 (4%)	0	100	100
3	C	256/275 (93%)	249 (97%)	7 (3%)	0	100	100
4	D	126/142 (89%)	118 (94%)	8 (6%)	0	100	100
5	E	207/210 (99%)	204 (99%)	3 (1%)	0	100	100
6	F	80/127 (63%)	75 (94%)	5 (6%)	0	100	100
7	G	169/172 (98%)	158 (94%)	11 (6%)	0	100	100
8	H	146/150 (97%)	142 (97%)	4 (3%)	0	100	100
9	I	115/125 (92%)	111 (96%)	4 (4%)	0	100	100
10	J	65/67 (97%)	65 (100%)	0	0	100	100
11	K	113/117 (97%)	111 (98%)	2 (2%)	0	100	100
12	L	44/58 (76%)	40 (91%)	4 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	M	788/1729 (46%)	710 (90%)	76 (10%)	2 (0%)	36	70
17	S	888/1179 (75%)	842 (95%)	46 (5%)	0	100	100
19	U	98/666 (15%)	82 (84%)	14 (14%)	2 (2%)	6	28
20	V	209/531 (39%)	174 (83%)	31 (15%)	4 (2%)	6	30
21	Y	298/305 (98%)	278 (93%)	20 (7%)	0	100	100
22	Z	41/531 (8%)	40 (98%)	1 (2%)	0	100	100
23	a	363/396 (92%)	336 (93%)	27 (7%)	0	100	100
24	b	512/1496 (34%)	470 (92%)	42 (8%)	0	100	100
25	c	139/712 (20%)	136 (98%)	3 (2%)	0	100	100
26	d	1082/1143 (95%)	1004 (93%)	78 (7%)	0	100	100
27	e	709/762 (93%)	652 (92%)	57 (8%)	0	100	100
28	f	19/108 (18%)	18 (95%)	1 (5%)	0	100	100
All	All	8992/14145 (64%)	8457 (94%)	527 (6%)	8 (0%)	49	80

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	V	248	PRO
19	U	481	GLY
19	U	463	PRO
20	V	238	GLU
20	V	259	ASP

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	A	1242/1749 (71%)	1242 (100%)	0	100	100
2	B	992/1027 (97%)	992 (100%)	0	100	100
3	C	237/252 (94%)	237 (100%)	0	100	100
4	D	108/126 (86%)	108 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	722/1524 (47%)	721 (100%)	1 (0%)	88	93
23	a	320/348 (92%)	320 (100%)	0	100	100
24	b	466/1299 (36%)	465 (100%)	1 (0%)	87	92
26	d	690/1001 (69%)	690 (100%)	0	100	100
All	All	5623/8242 (68%)	5621 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	572	ASP
24	b	538	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
11	K	36	ASN
13	M	979	HIS
26	d	261	HIS
13	M	948	HIS
13	M	1007	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	20/45 (44%)	9 (45%)	1 (5%)

5 of 9 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	31	U
15	P	32	A
15	P	33	U
15	P	34	A
15	P	35	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	P	32	A

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 9 ligands modelled in this entry, 9 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

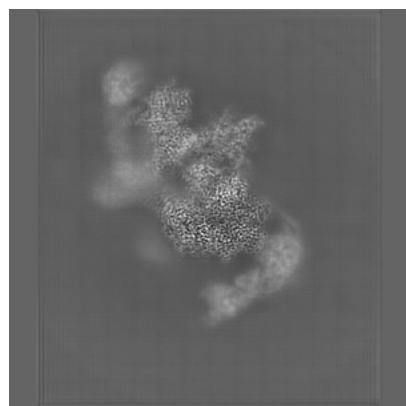
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13016. These allow visual inspection of the internal detail of the map and identification of artifacts.

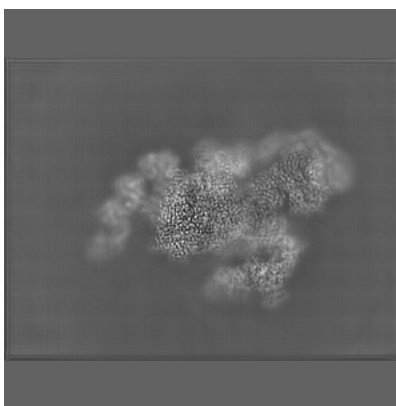
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

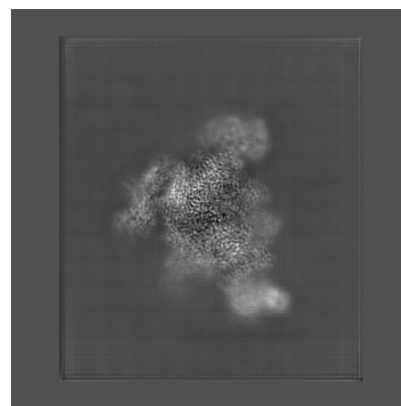
6.1.1 Primary map



X

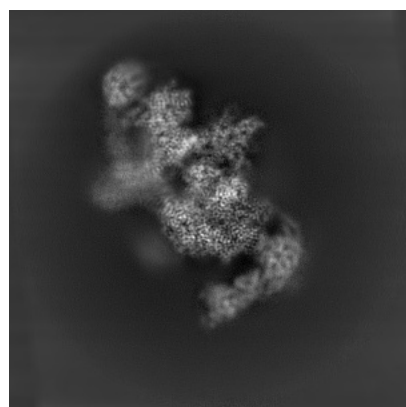


Y

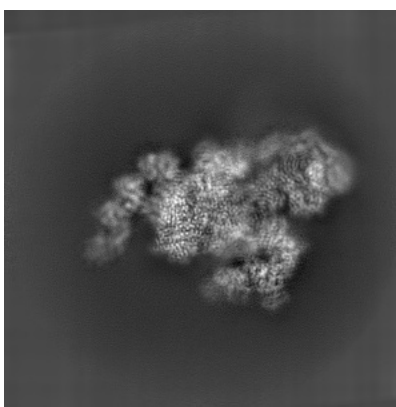


Z

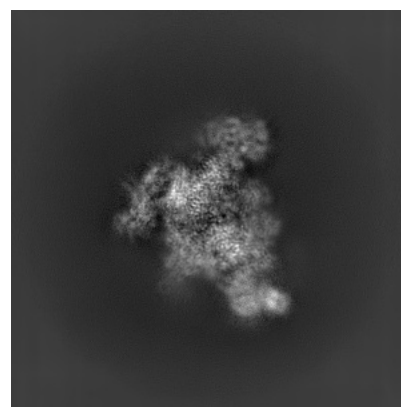
6.1.2 Raw map



X



Y

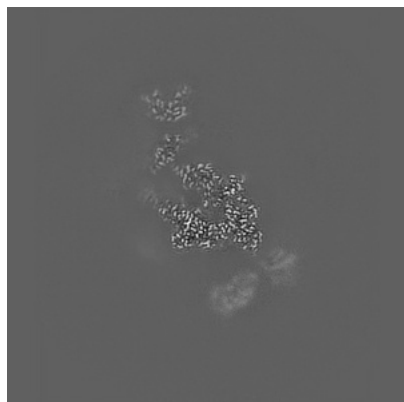


Z

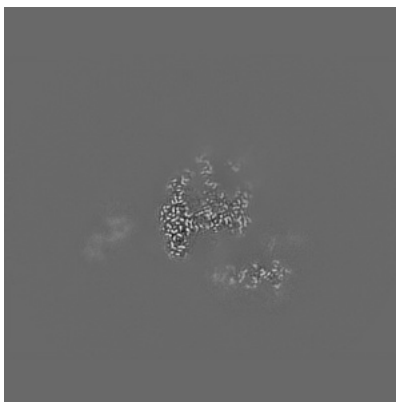
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

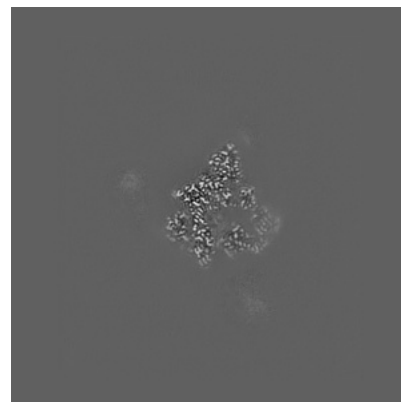
6.2.1 Primary map



X Index: 210

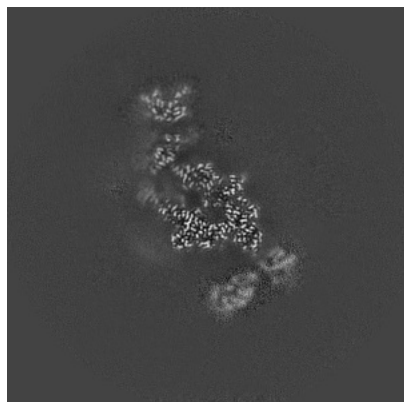


Y Index: 210

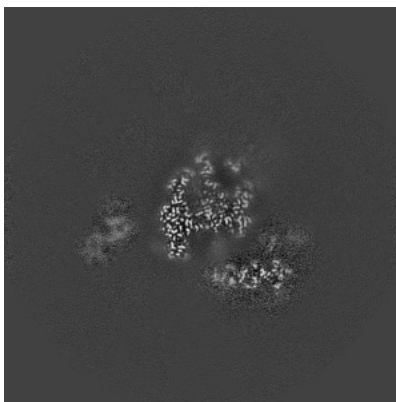


Z Index: 210

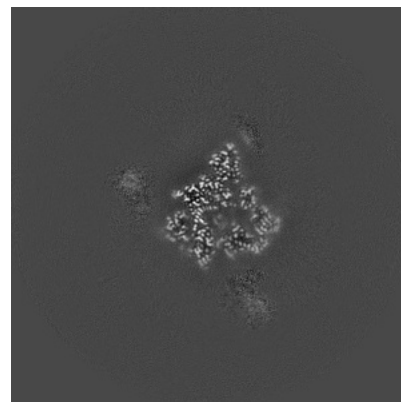
6.2.2 Raw map



X Index: 210



Y Index: 210

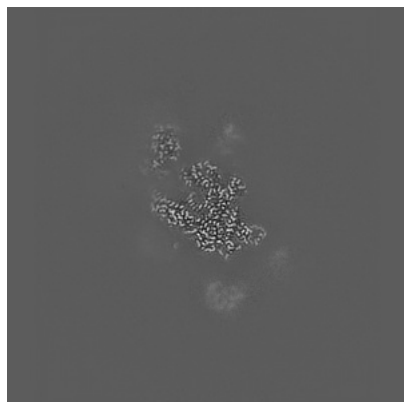


Z Index: 210

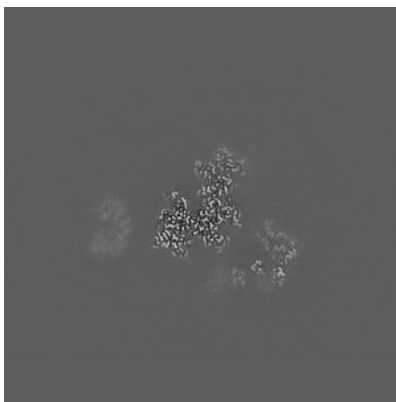
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

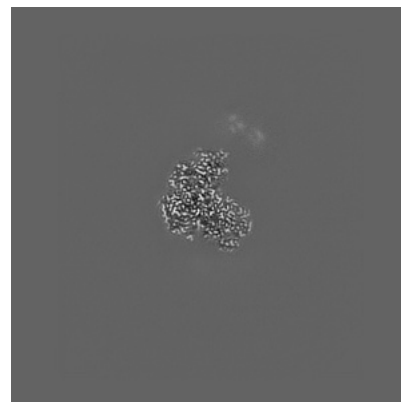
6.3.1 Primary map



X Index: 197

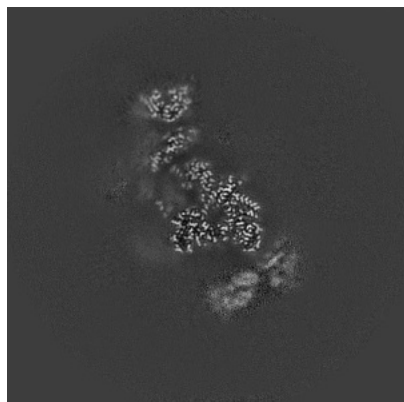


Y Index: 222

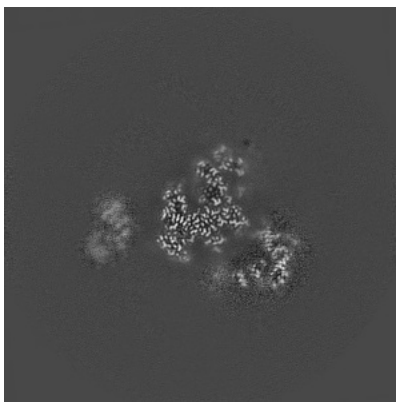


Z Index: 183

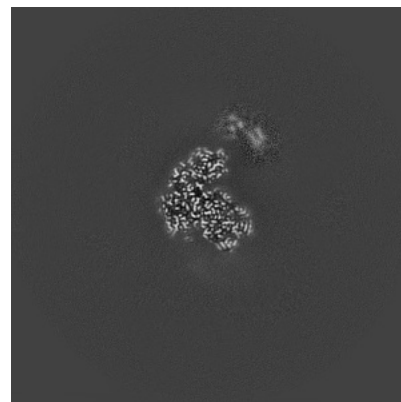
6.3.2 Raw map



X Index: 213



Y Index: 218

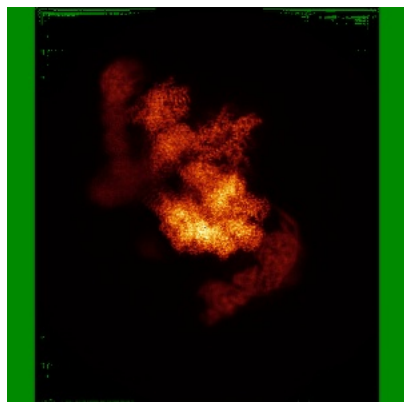


Z Index: 181

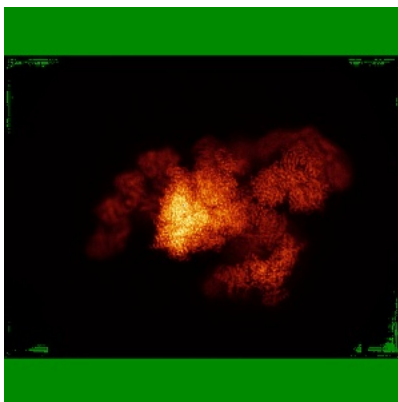
The images above show the largest variance slices of the map in three orthogonal directions.

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

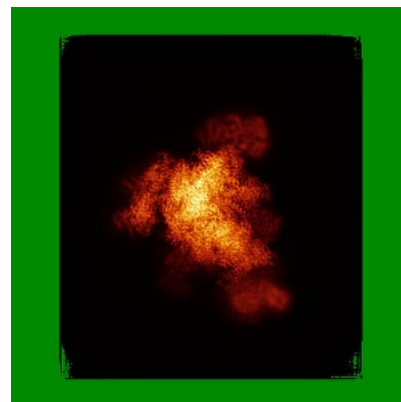
6.4.1 Primary map



X

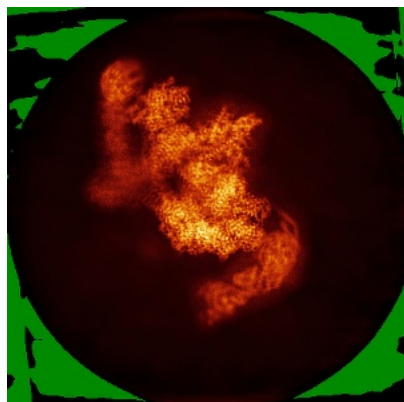


Y

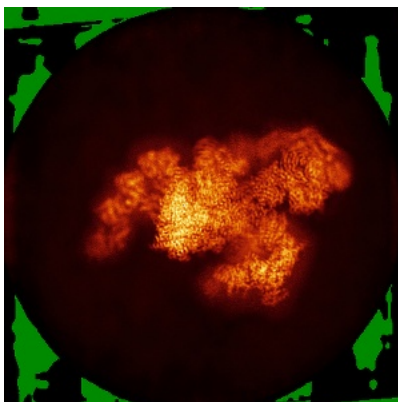


Z

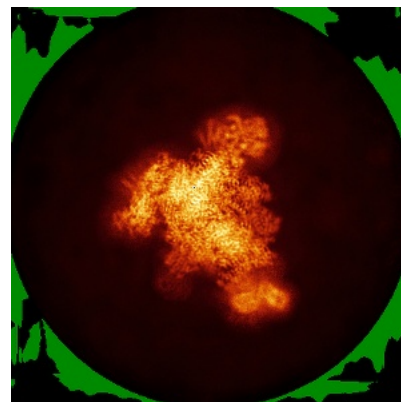
6.4.2 Raw map



X



Y

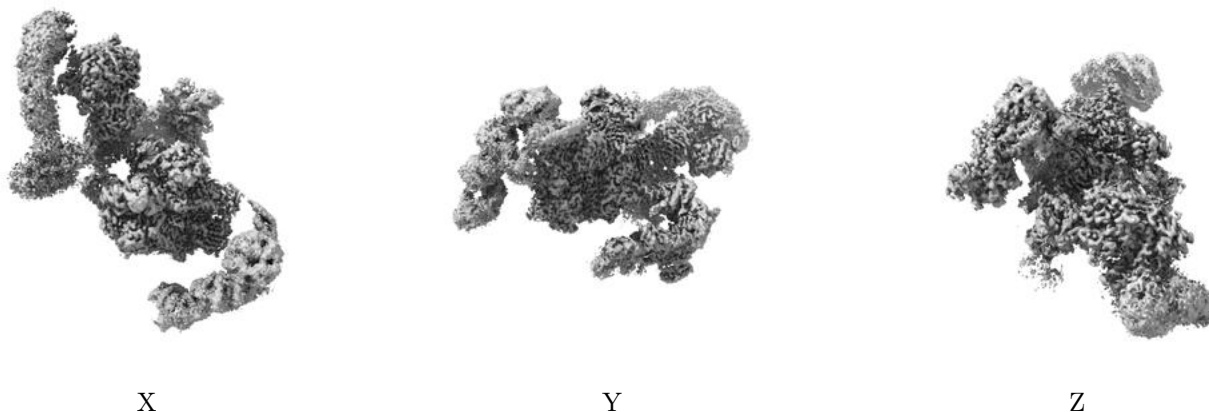


Z

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.

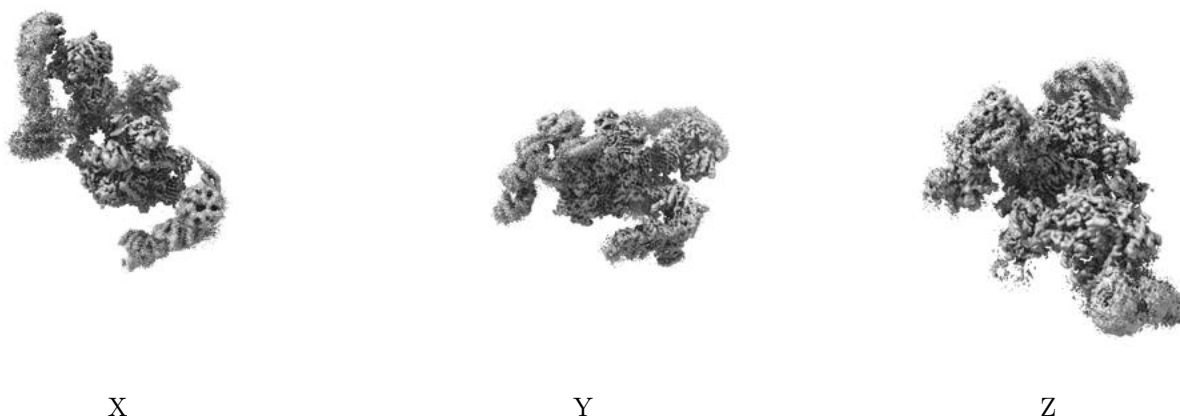
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

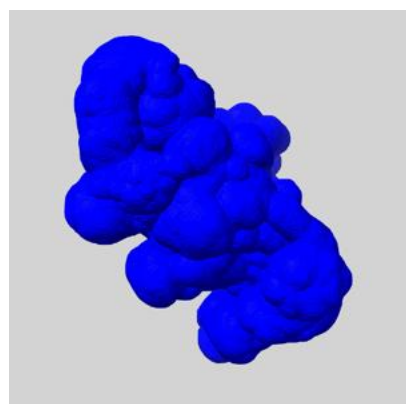
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

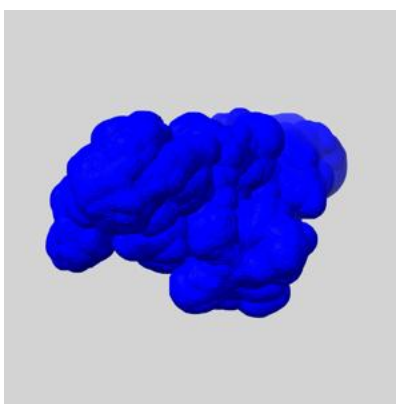
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

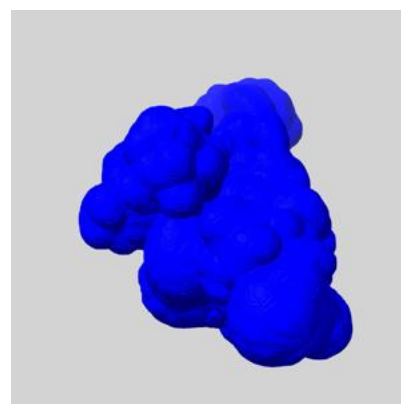
6.6.1 emd_13016_msk_1.map [i](#)



X

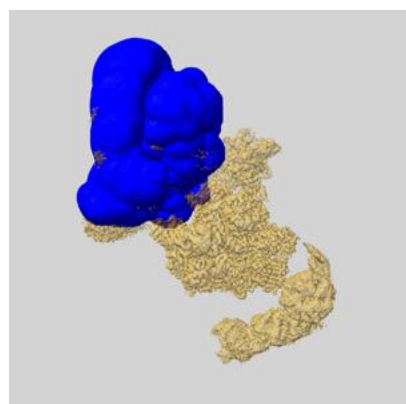


Y

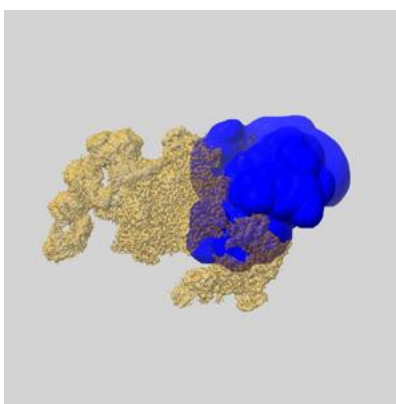


Z

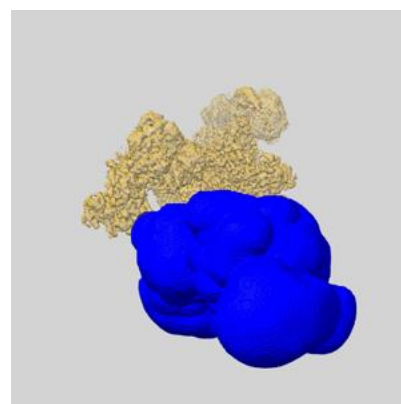
6.6.2 emd_13016_msk_2.map [i](#)



X

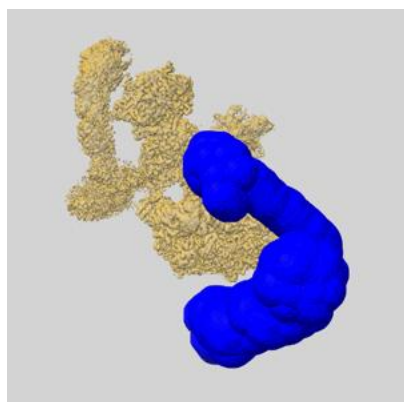


Y

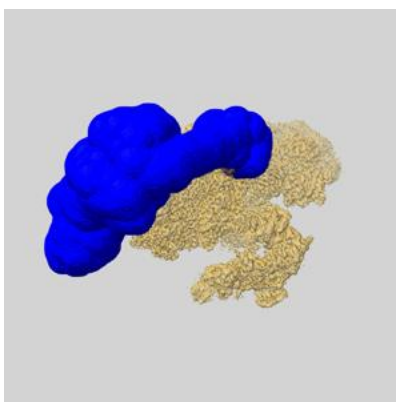


Z

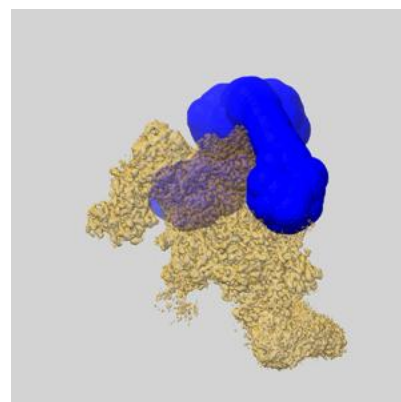
6.6.3 emd_13016_msk_3.map [i](#)



X

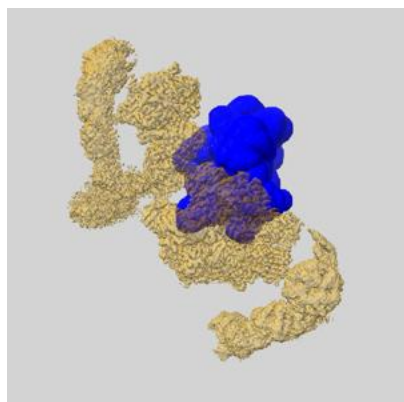


Y

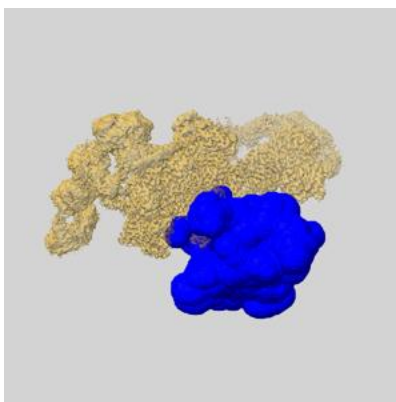


Z

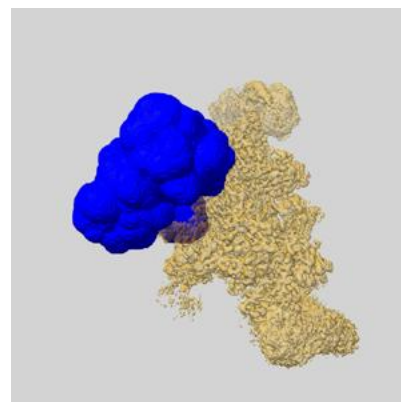
6.6.4 emd_13016_msk_4.map [i](#)



X

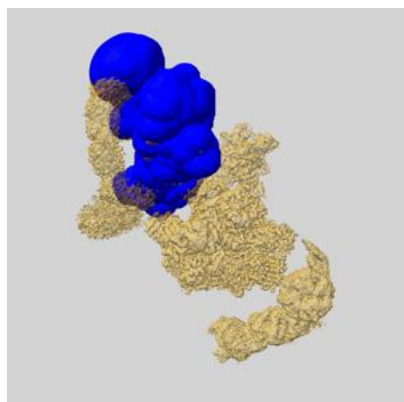


Y

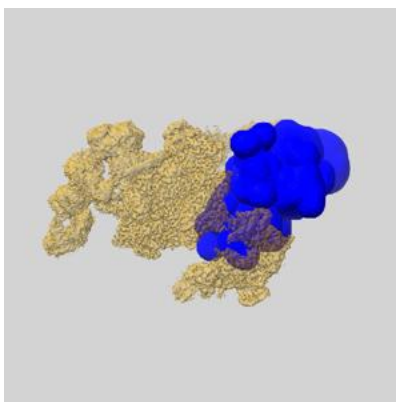


Z

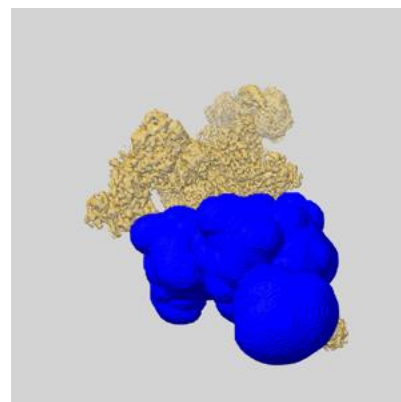
6.6.5 emd_13016_msk_5.map [i](#)



X

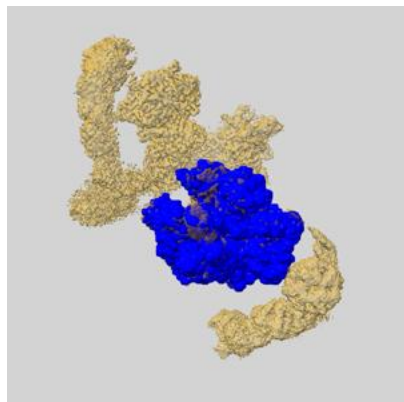


Y

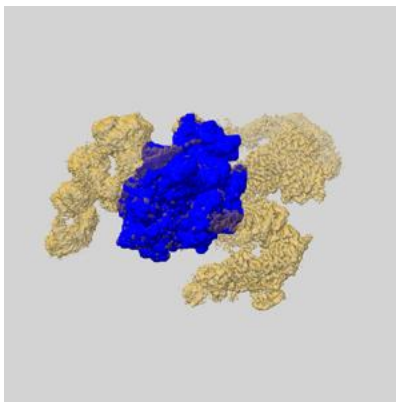


Z

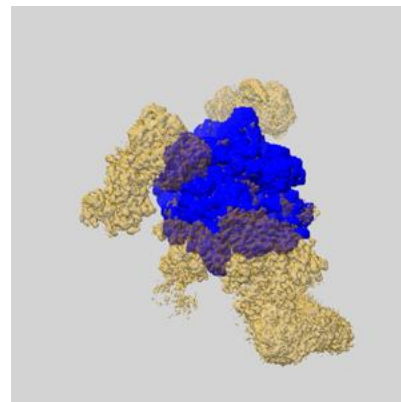
6.6.6 emd_13016_msk_6.map [i](#)



X



Y

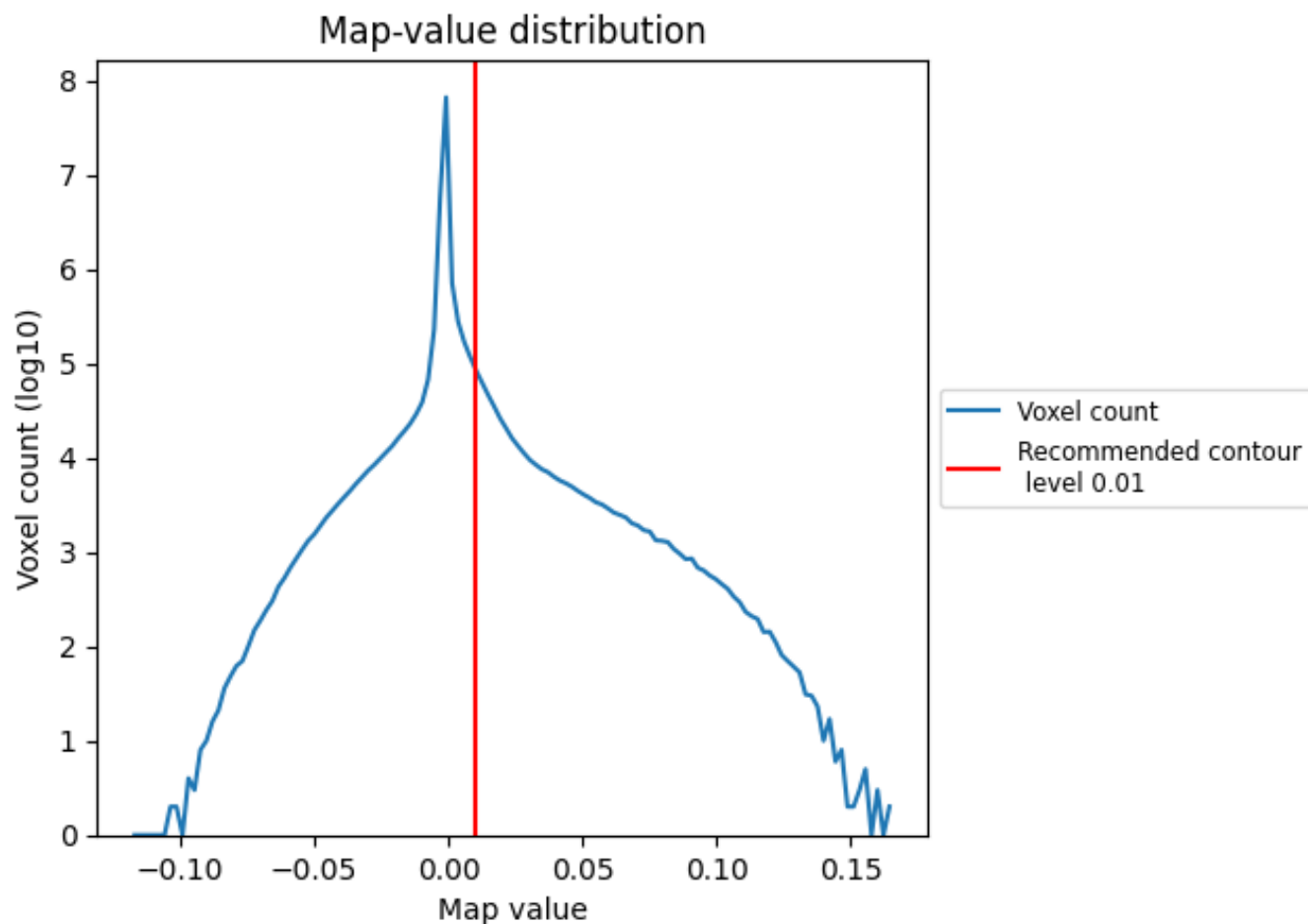


Z

7 Map analysis [i](#)

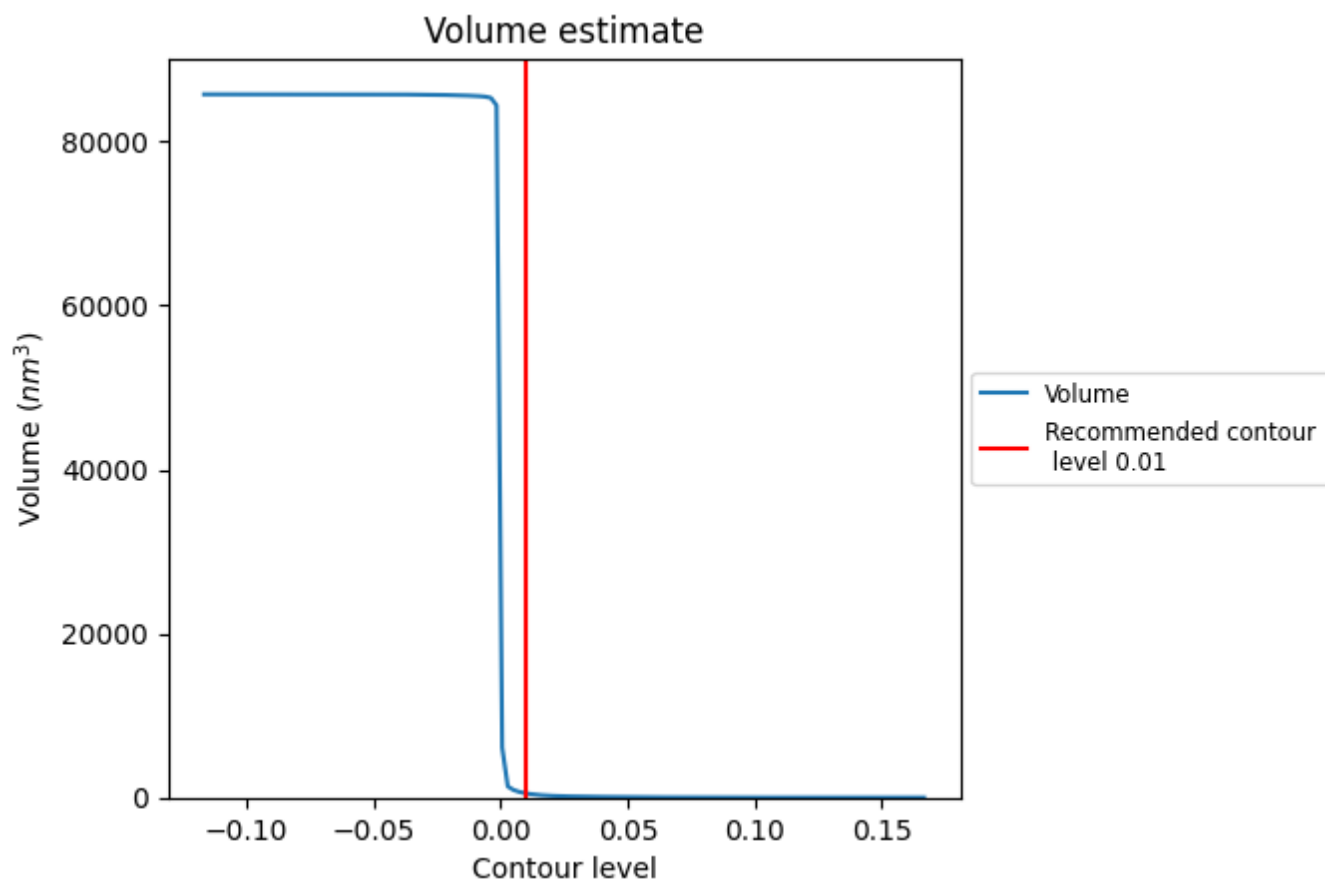
This section contains the results of statistical analysis of the map.

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.

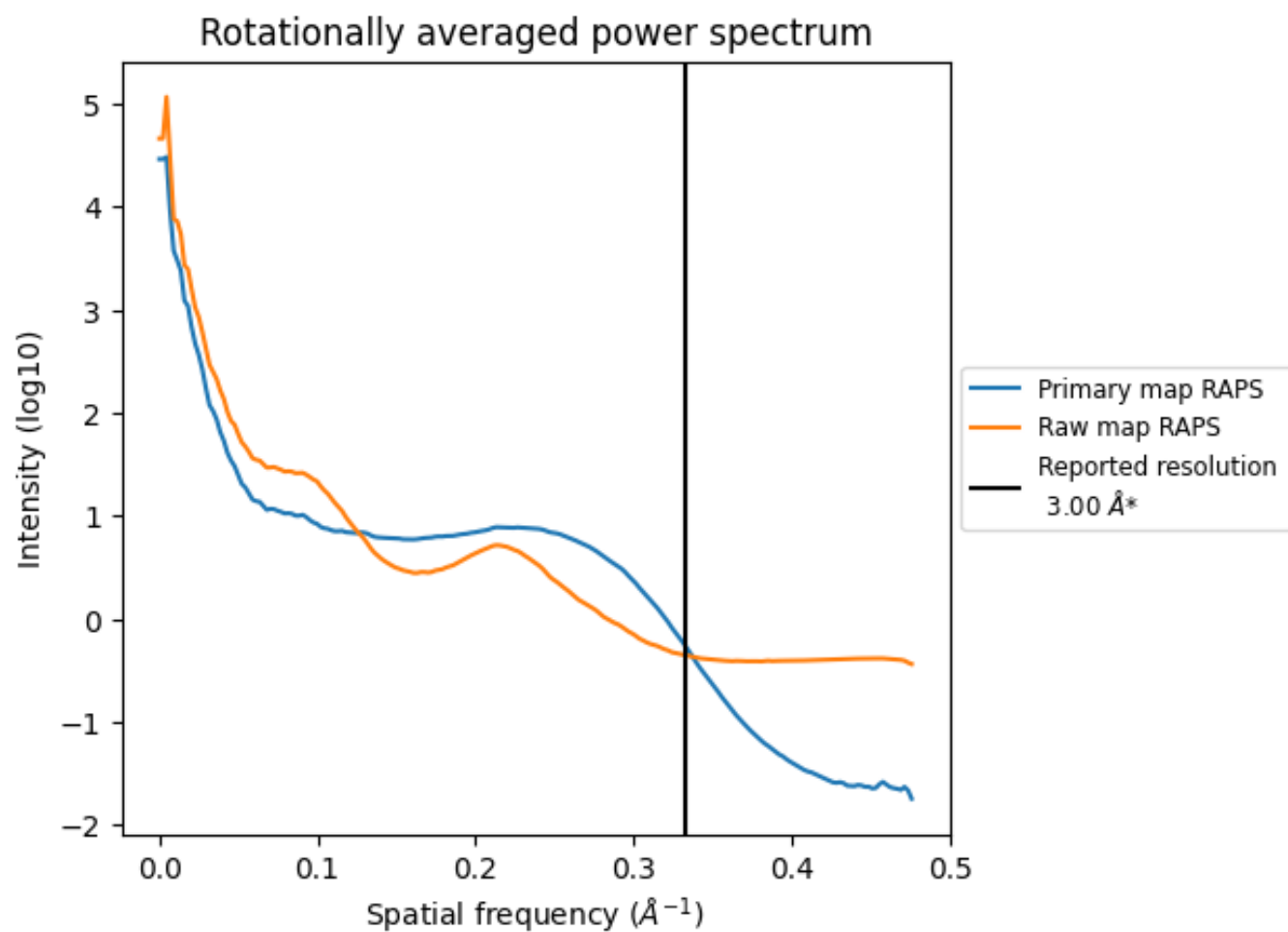
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 512 nm³; this corresponds to an approximate mass of 463 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 ⓘ

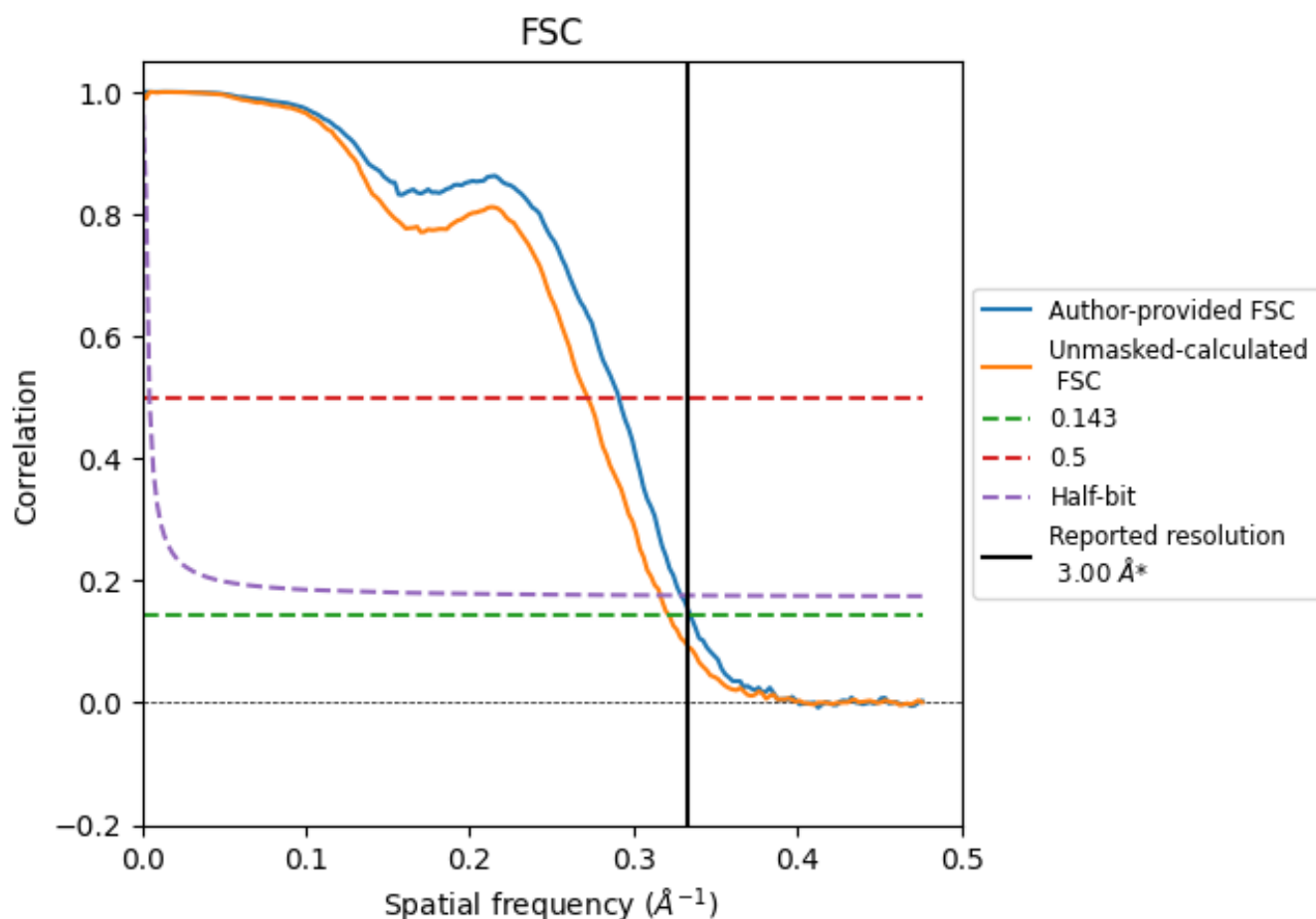


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

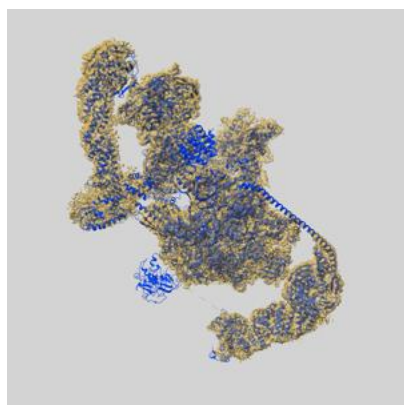
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.99	3.44	3.04
Unmasked-calculated*	3.11	3.68	3.16

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

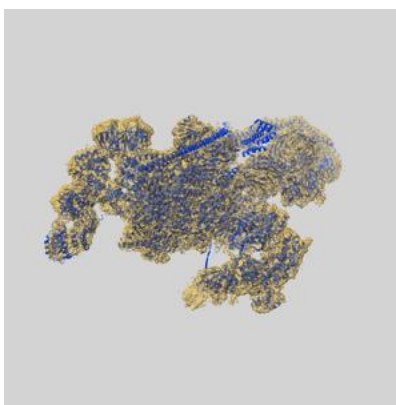
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13016 and PDB model 7OPD. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

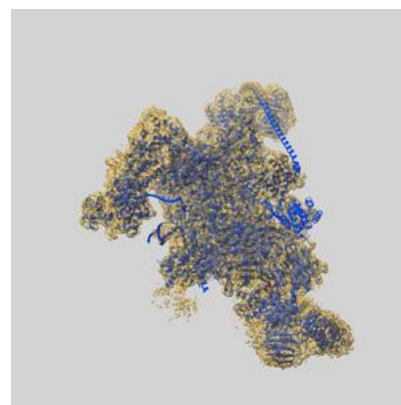
9.1 Map-model overlay [i](#)



X



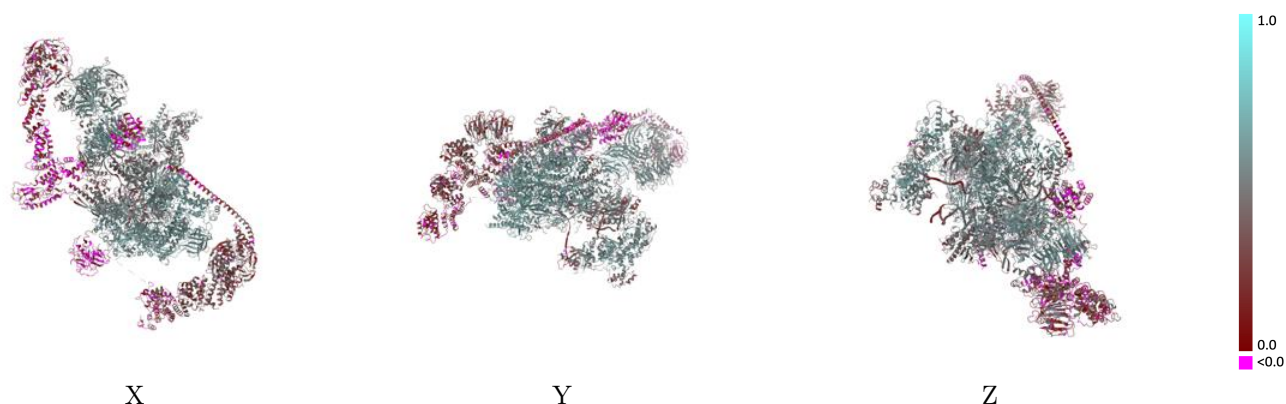
Y



Z

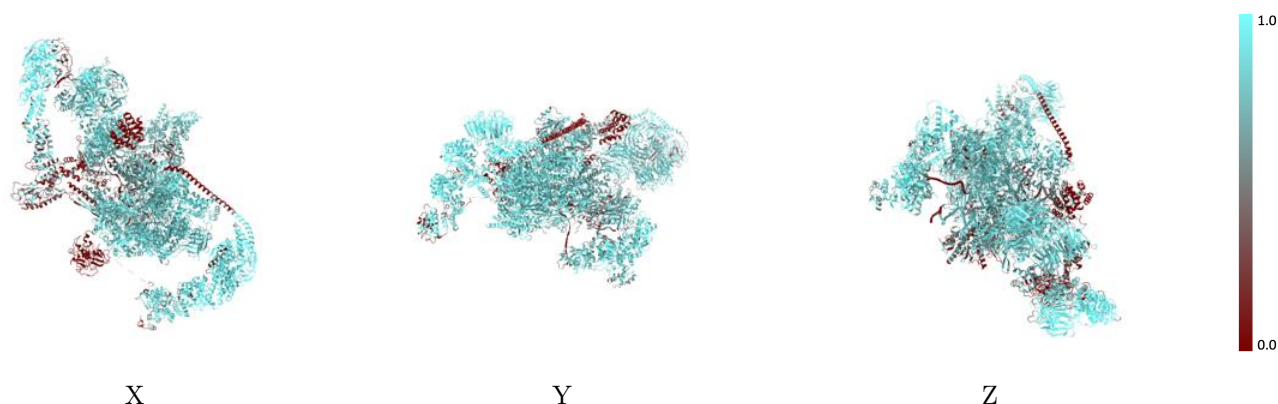
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



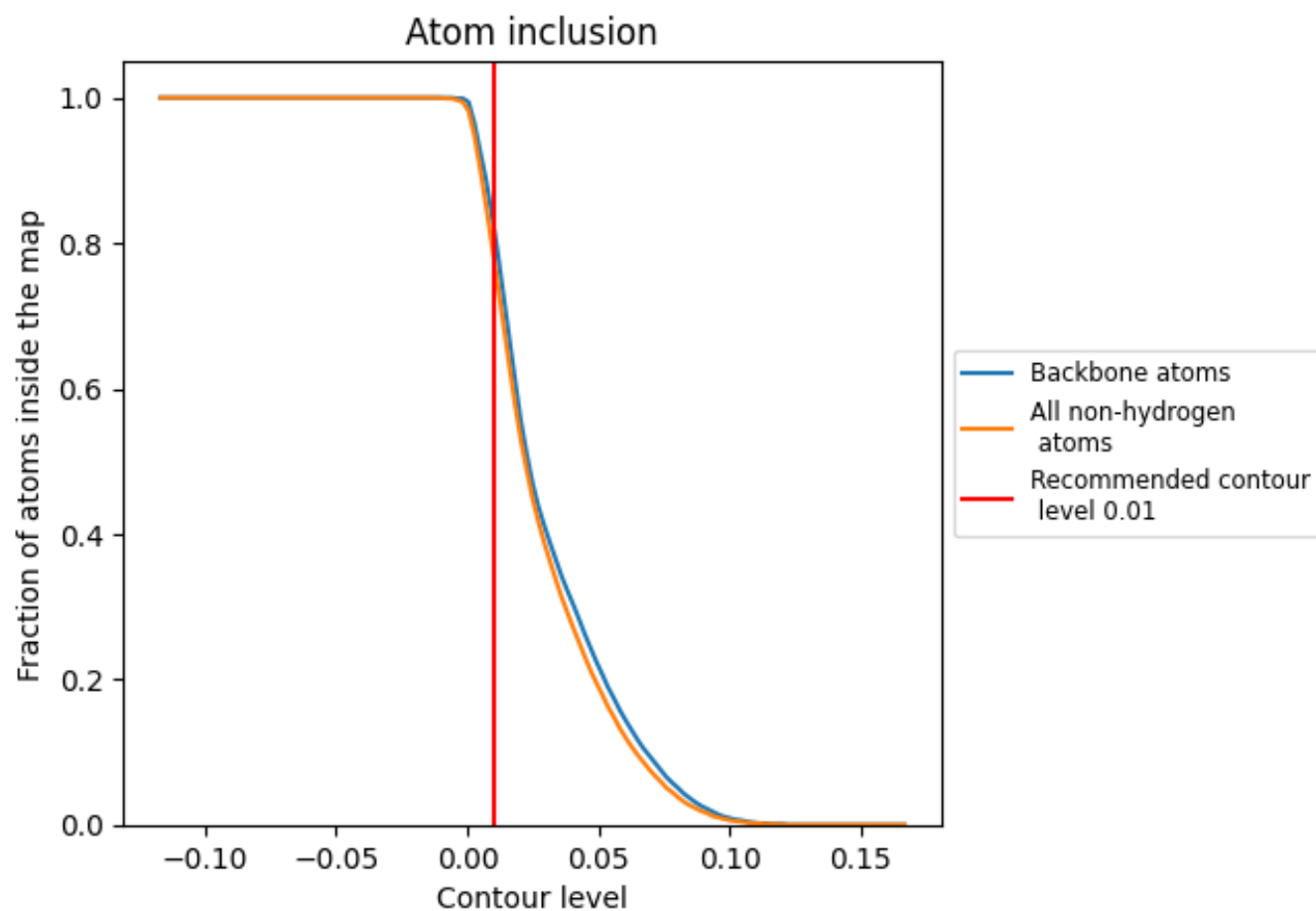
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7850	 0.4720
A	 0.8420	 0.5530
B	 0.8510	 0.5600
C	 0.9120	 0.5890
D	 0.6760	 0.4030
E	 0.8620	 0.5410
F	 0.8720	 0.5720
G	 0.7160	 0.4960
H	 0.8900	 0.5830
I	 0.7500	 0.4910
J	 0.9330	 0.6180
K	 0.9200	 0.5950
L	 0.8090	 0.5080
M	 0.8370	 0.5000
N	 0.6600	 0.4260
P	 0.5020	 0.3840
R	 0.2000	 0.3300
S	 0.7810	 0.2280
T	 0.6830	 0.4590
U	 0.0000	 0.0120
V	 0.2500	 0.0820
Y	 0.9600	 0.3240
Z	 0.8550	 0.3060
a	 0.9070	 0.5870
b	 0.6660	 0.4790
c	 0.0050	 0.0250
d	 0.8000	 0.4670
e	 0.5960	 0.1270
f	 0.2380	 0.1570

