



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:20 PM UTC

PDB ID : 6EU2 / pdb_00006eu2
EMDB ID : EMD-3957
Title : Apo RNA Polymerase III - open conformation (oPOL3)
Authors : Abascal-Palacios, G.; Ramsay, E.P.; Beuron, F.; Morris, E.; Vannini, A.
Deposited on : 2017-10-27
Resolution : 3.40 Å(reported)

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

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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

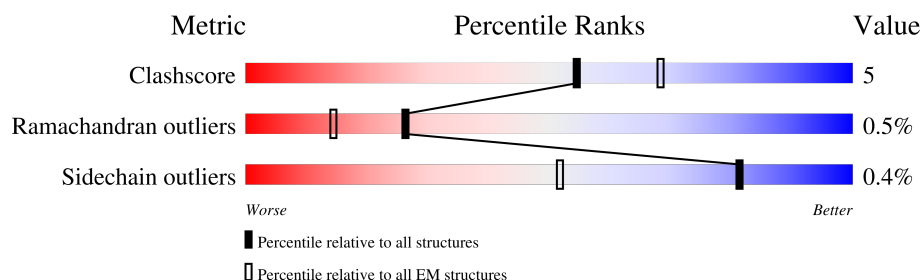
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

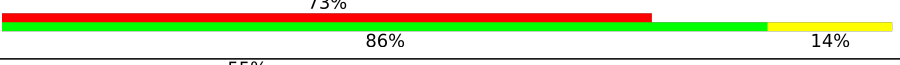
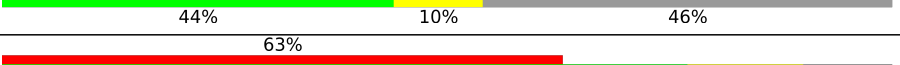
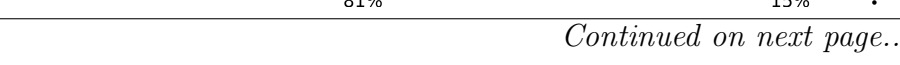
The reported resolution of this entry is 3.40 Å.

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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	1460	
2	B	1149	
3	C	335	
4	D	161	
5	E	215	
6	F	155	
7	G	212	
8	H	146	

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Mol	Chain	Length	Quality of chain
9	I	110	
10	J	70	
11	K	142	
12	L	70	
13	M	282	
14	N	422	
15	O	654	
16	P	317	
17	Q	251	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 38329 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 III subunit RPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1402	Total	C	N	O	S	0	0
			10980	6924	1930	2068	58		

- Molecule 2 is a protein called DNA-directed RNA polymerase III subunit RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1114	Total	C	N	O	S	0	0
			8788	5558	1516	1654	60		

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	335	Total	C	N	O	S	0	0
			2655	1681	454	511	9		

- Molecule 4 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	119	Total	C	N	O	S	0	0
			977	628	156	187	6		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	215	Total	C	N	O	S	0	0
			1759	1116	310	321	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	83	Total	C	N	O	S	0	0
			671	429	114	125	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	191	Total	C	N	O	S	0	0
			1544	1007	250	281	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	140	Total	C	N	O	S	0	0
			1120	703	188	224	5		

- Molecule 9 is a protein called DNA-directed RNA polymerase III subunit RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	42	Total	C	N	O	S	0	0
			321	204	47	64	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	68	Total	C	N	O	S	0	0
			558	356	97	99	6		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	101	Total	C	N	O	S	0	0
			792	496	130	161	5		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			358	221	71	62	4		

- Molecule 13 is a protein called DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	165	Total	C	N	O	S	0	0
			1347	862	229	255	1		

- Molecule 14 is a protein called DNA-directed RNA polymerase III subunit RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	105	Total	C	N	O	S	0	0
			802	508	144	147	3		

- Molecule 15 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	537	Total	C	N	O	S	0	0
			4315	2748	738	810	19		

- Molecule 16 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	123	Total	C	N	O	S	0	0
			1024	667	161	192	4		

- Molecule 17 is a protein called DNA-directed RNA polymerase III subunit RPC7.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	40	Total	C	N	O	0	0
			311	204	50	57		

- Molecule 18 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

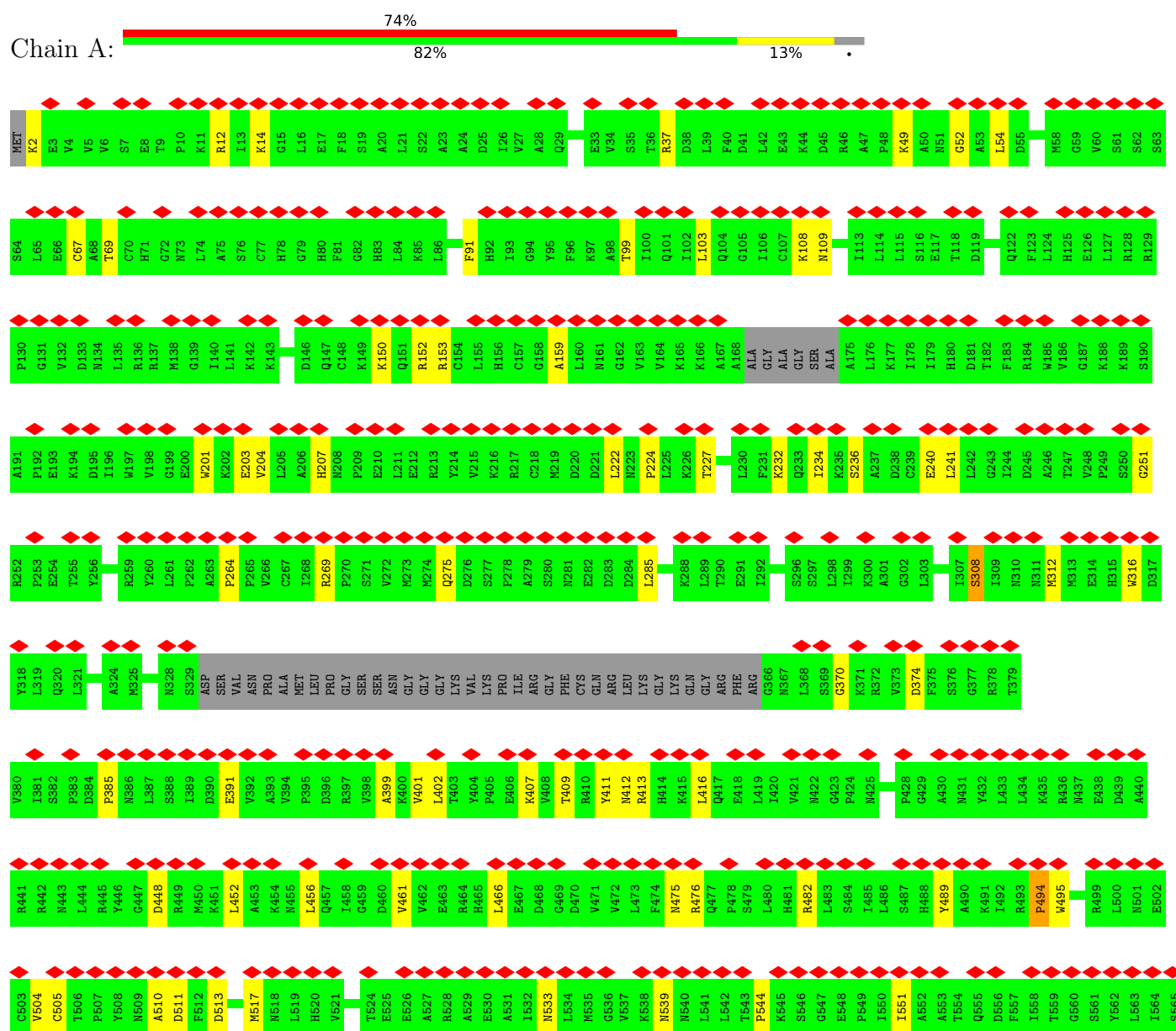
- Molecule 19 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

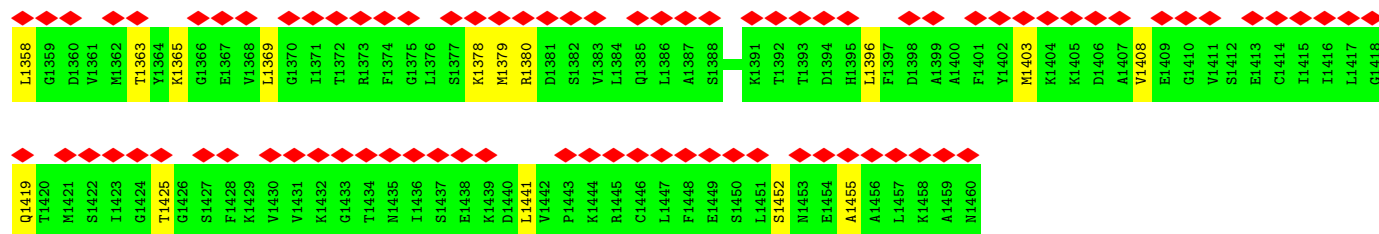
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

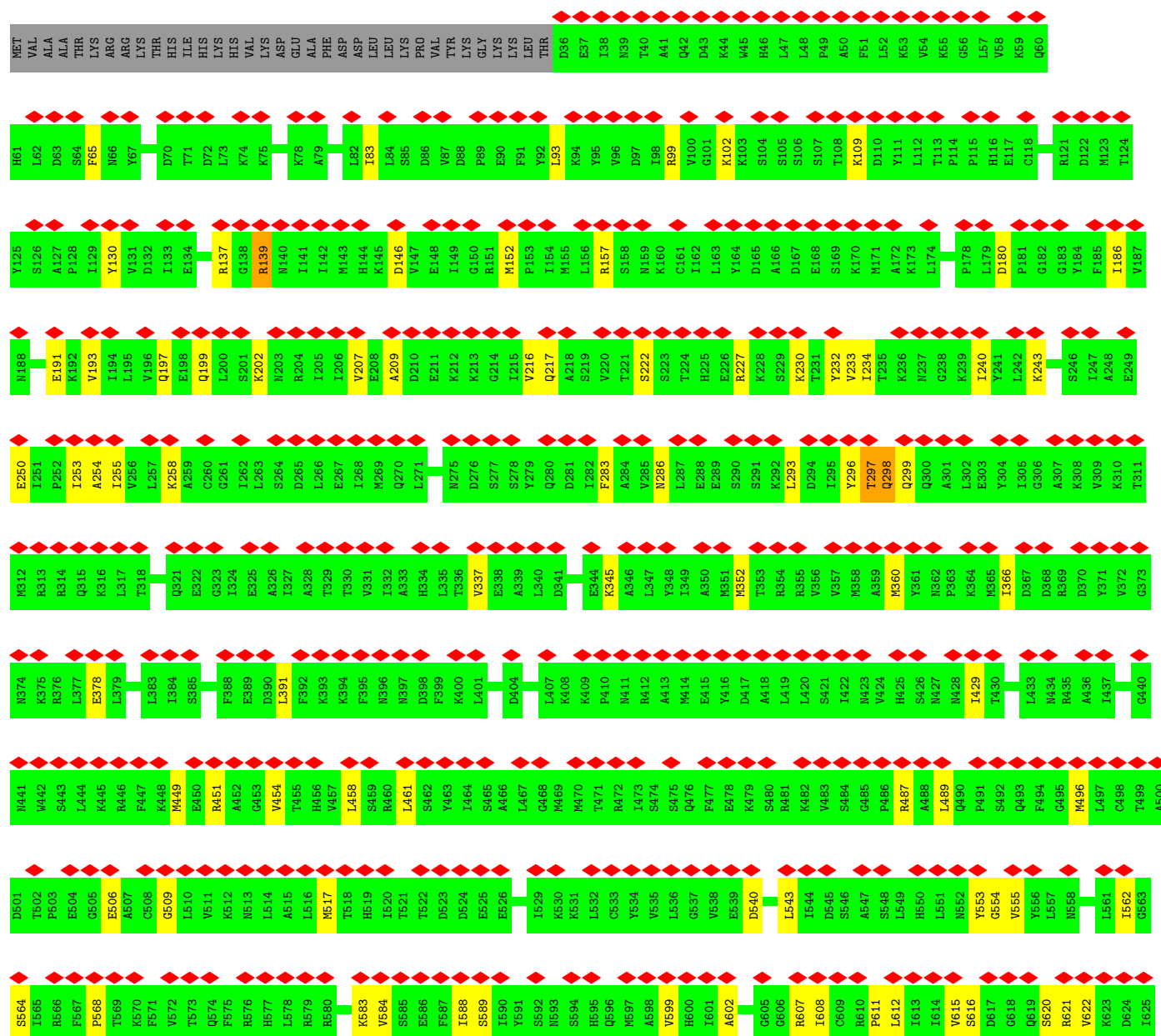
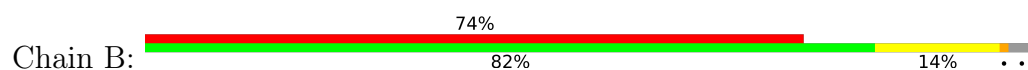
- Molecule 1: DNA-directed RNA polymerase III subunit RPC1

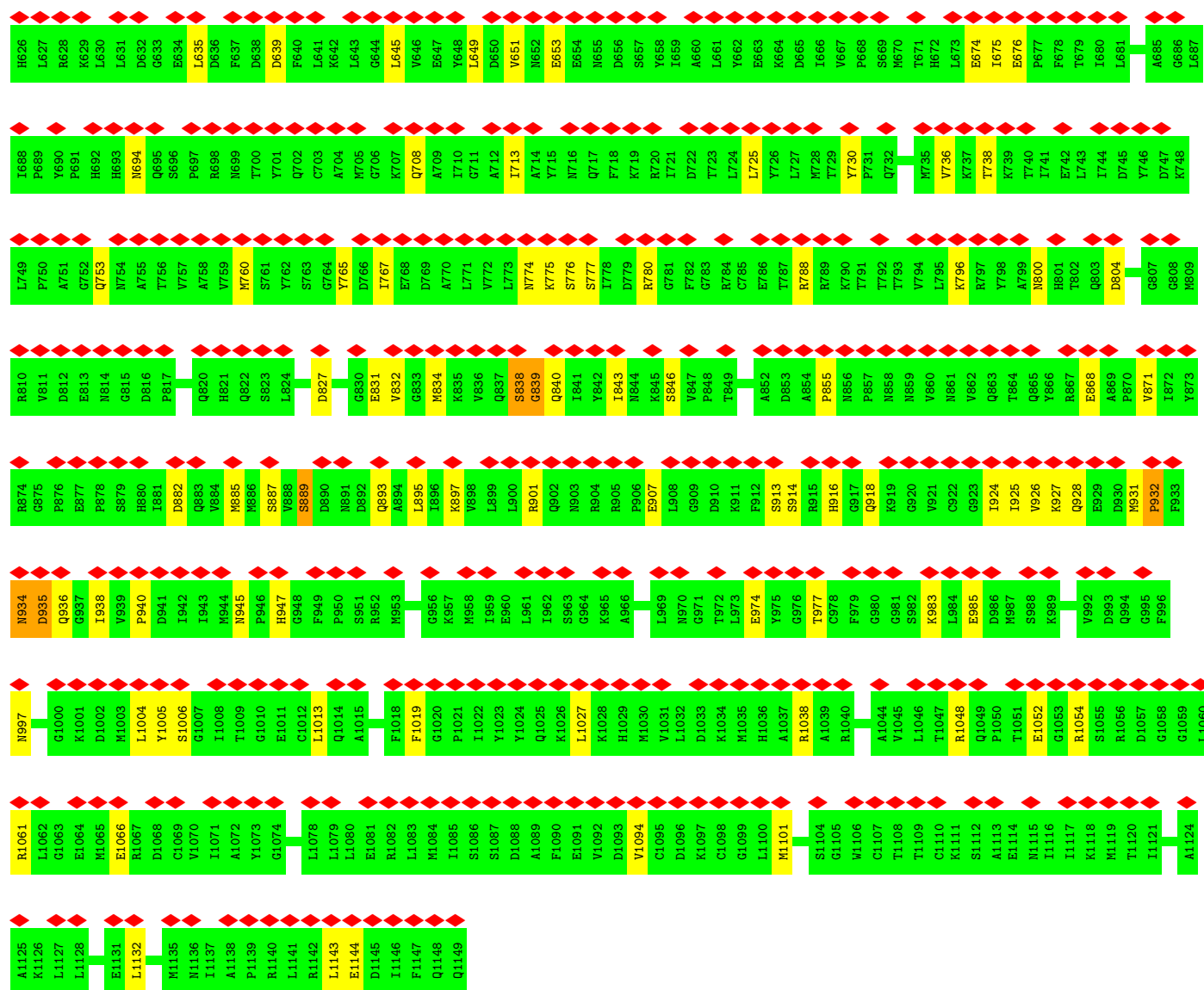




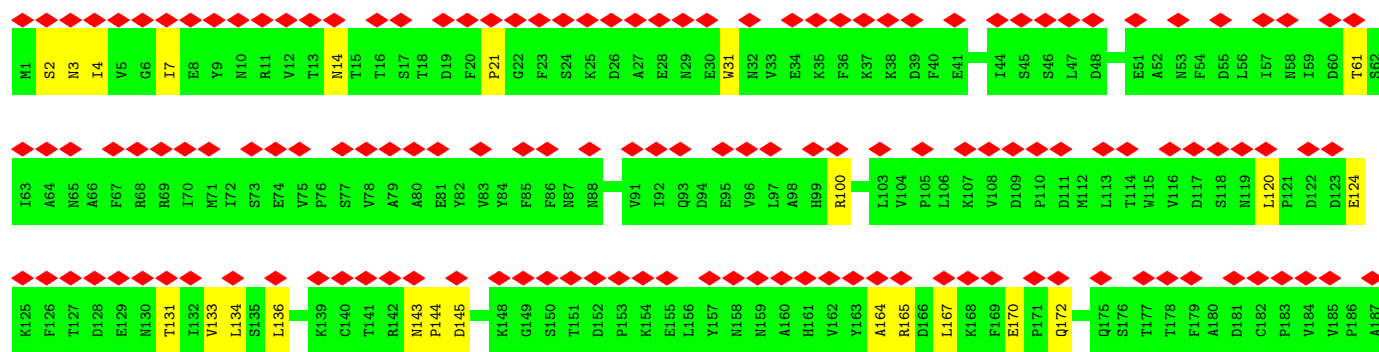
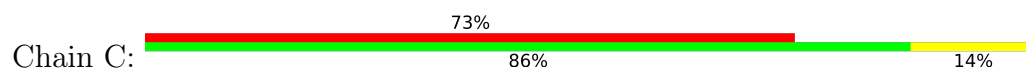


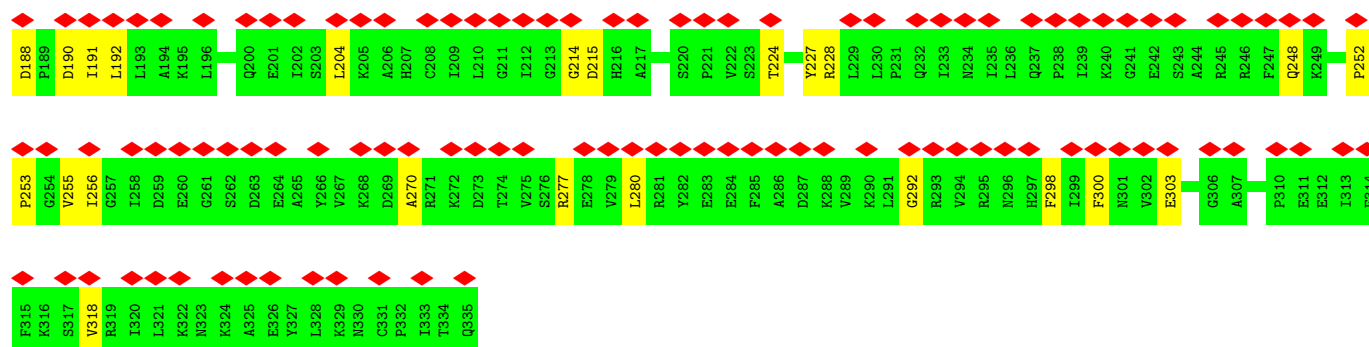
• Molecule 2: DNA-directed RNA polymerase III subunit RPC2



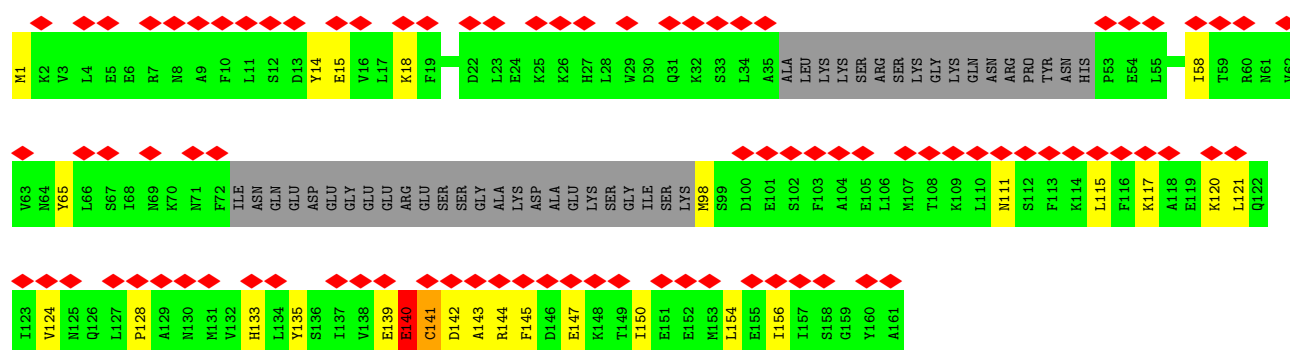


• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

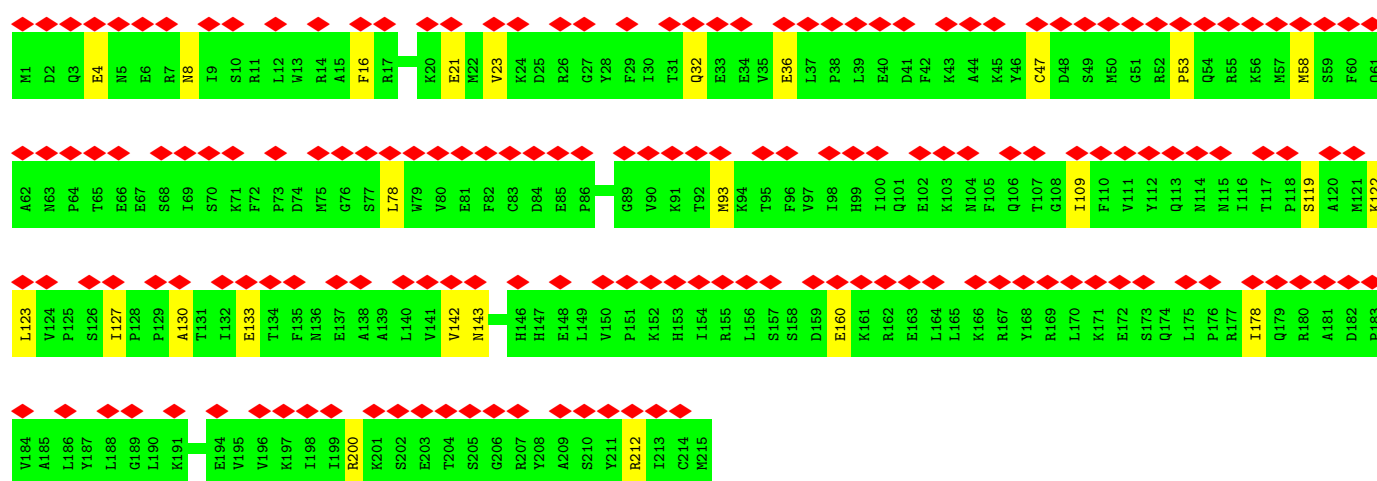
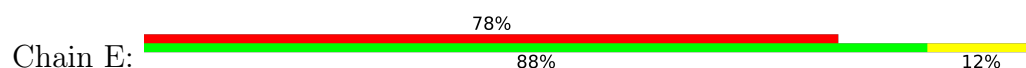




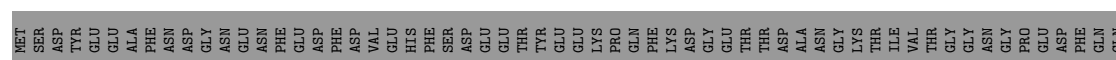
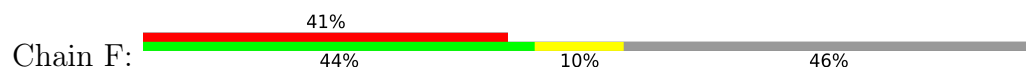
• Molecule 4: DNA-directed RNA polymerase III subunit RPC9

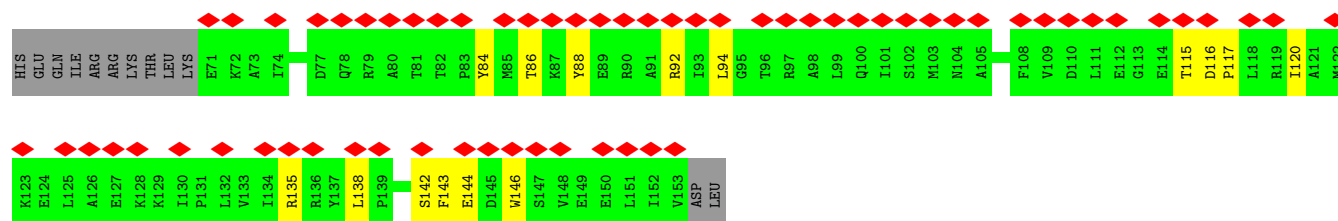


• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

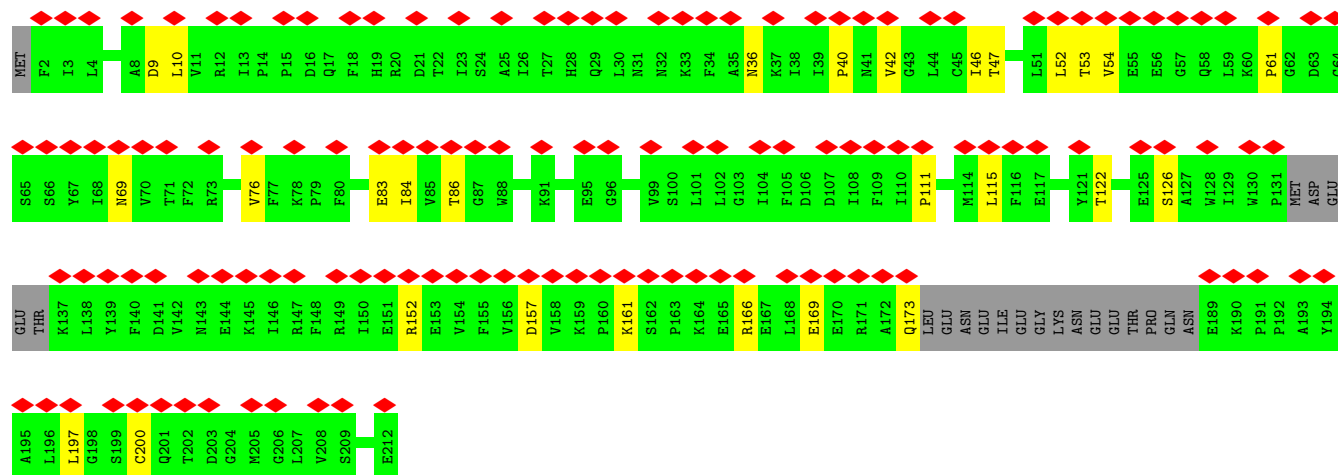
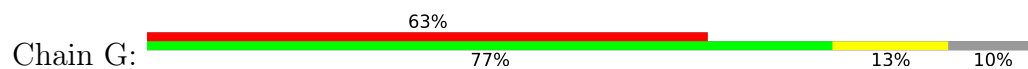


• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

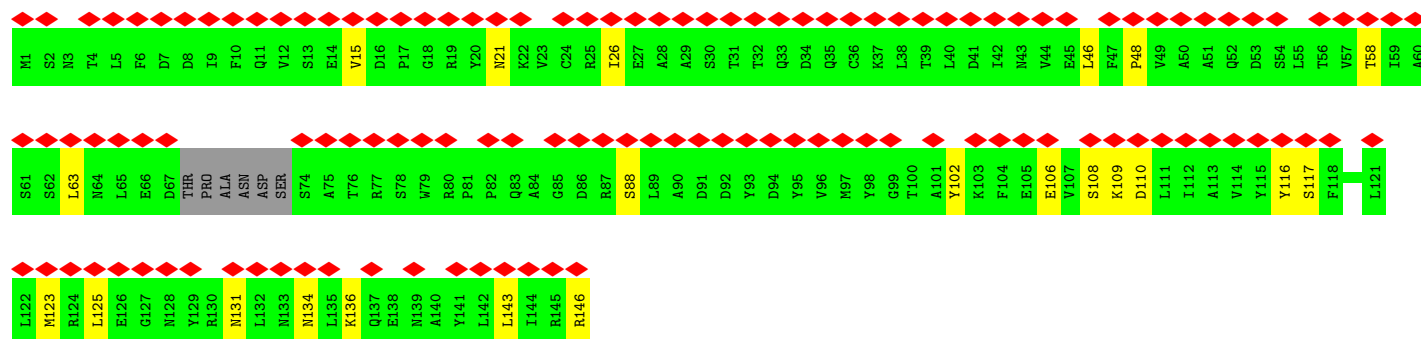
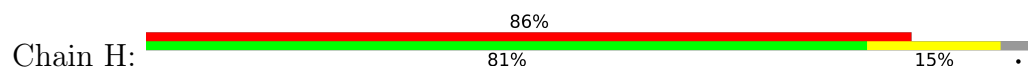




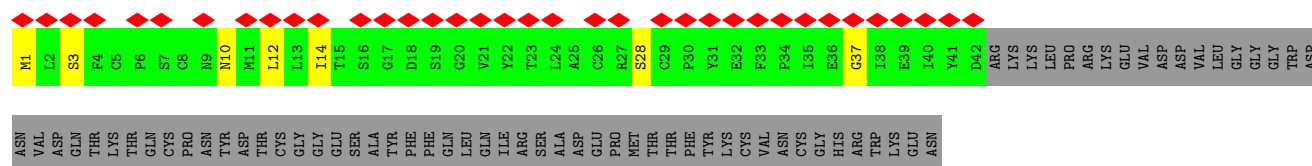
• Molecule 7: DNA-directed RNA polymerase III subunit RPC8



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



• Molecule 9: DNA-directed RNA polymerase III subunit RPC10



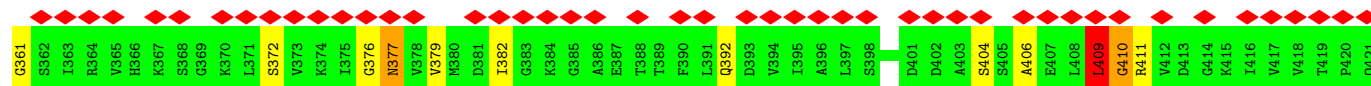
- Chain J:
-
- 63%
- 86%
- 11%
- M1 I2 V3 P4 V5 R6 S9 C10 G11 K12 V13 V14 G15 D16 K17 W18 E19 S20 Y21 N22 N23 L24 L25 Q26 E27 D28 E29 L30 L31 D32 G33 T34 A35 L36 S37 R38 L39 G40 L41 K42 R43 Y44 C45 C46 R47 R48 M49 I50 D55 L56 I57 E58 K59 F60 L61 N64
- L66 E67 K68 ARG ASP

- Chain K:
-
- | Color | Percentage |
|--------|------------|
| Red | 54% |
| Green | 61% |
| Yellow | 11% |
| Grey | 29% |
- Sequence: MET THR GLU ASP ILE GLU GLN LYS LYS THR THR ALA THR THR GLU VAL THR PRO GLN GLU PRO LYS HIS ILE GLN GLU GLU GLU GLU GLU GLU GLU GLU GLU P42 D43 R44 E45 E46 I47 K48 L49 L50 T51 Q52 A53 T54 S55 E56 D57 G58 T59 S60
- Sequence: A61 S62 F63 Q64 I65 V66 E67 H70 T71 L72 G73 N74 A75 L76 R77 Y78 V79 I80 N81 K82 N83 P84 D85 V86 E87 F88 C89 G90 Y91 S92 I93 P94 H95 P96 S97 E98 N99 L100 L101 M102 I103 L104 I105 Q106 T107 Y108 G109 E110 A113 V114 D115 A116 K119 G120 L121 K122 D123
- Sequence: L124 M125 D126 F127 C128 D129 V130 V131 E132 S133 K134 F135 T136 E137 K138 I139 K140 S141 M142

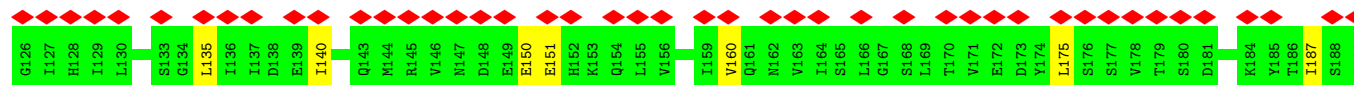
- Chain L:
-
- 50%
- 51%
- 11%
- 36%
- MET SER ARG GLU GLY PHE GLN ILE PRO THR ASN LEU ASP ALA ALA ALA GLY THR SER GLN ALA ARG THR T26 L27 K28 Y29 I30 C31 A32 E33 C34 S35 S36 K37 L38 S39 L40 S41 R42 T43 D44 A45 V46 R47 C48 K49 D50 C51 G52 H53 R54 I55 L56 L57 K58 A59 D60

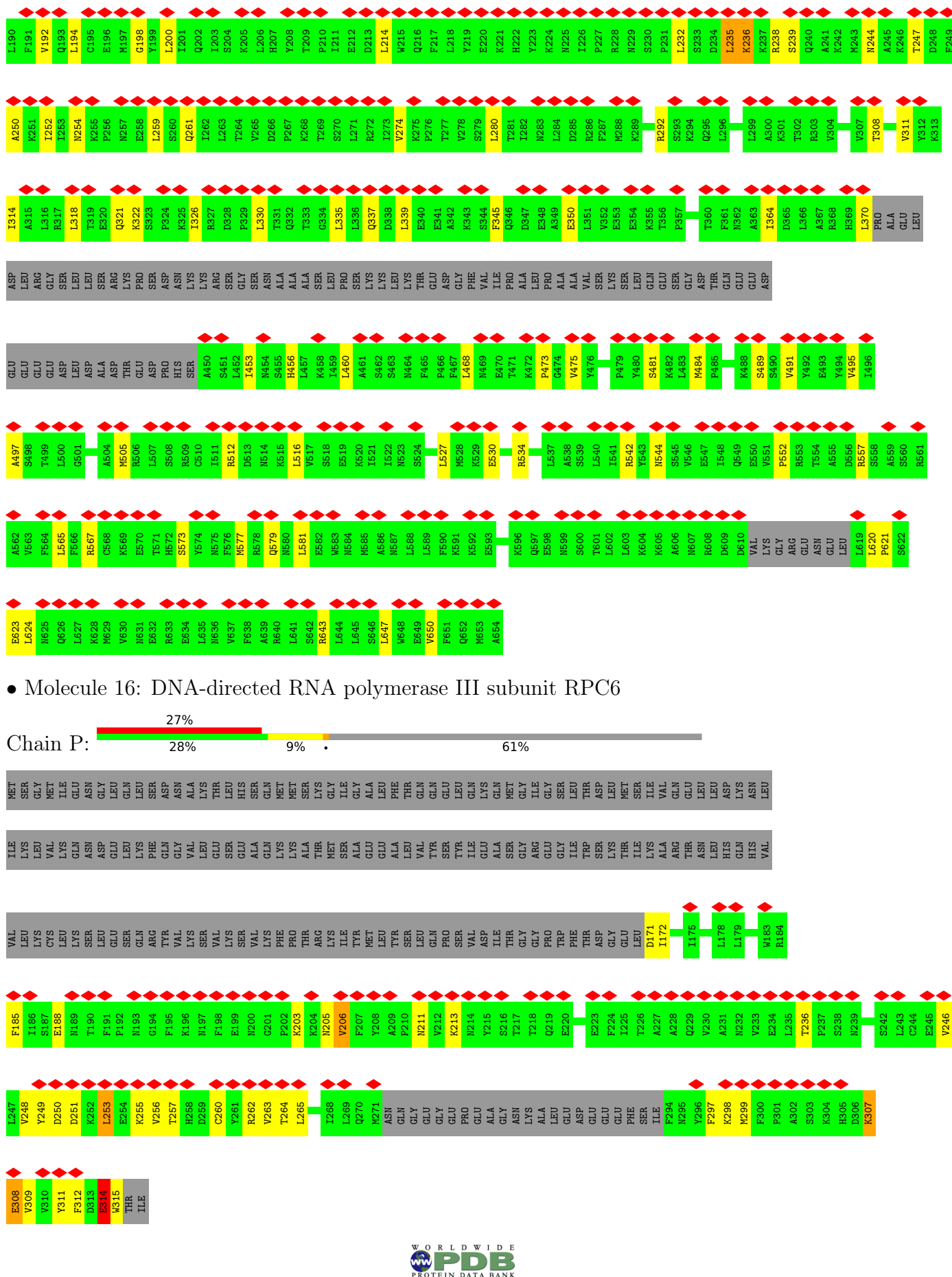
- Chain M:
-
- Sequence logo for Chain M showing amino acid frequencies at each position. The y-axis represents frequency from 0% to 42%. The x-axis shows positions from 1 to 198. The sequence is: MET, SER, ILE, ASP, ASN, LYS, LEU, PHE, VAL, THR, GLU, GLU, ASP, GLU, ASP, ARG, THR, GLN, ASP, ARG, ALA, ASP, VAL, GLU, ASP, GLU, SER, ASN, ASP, ILE, ASP, MET, ILE, ALA, ASP, GLU, ASN, GLY, THR, ASN, SER, ILE, ALA, ASN, GLU, GLN, GLU, LYS, SER, GLU, VAL, LYS, ALA, GLU, ASP, ASP.

- Molecule 14: DNA-directed RNA polymerase III subunit RPC4

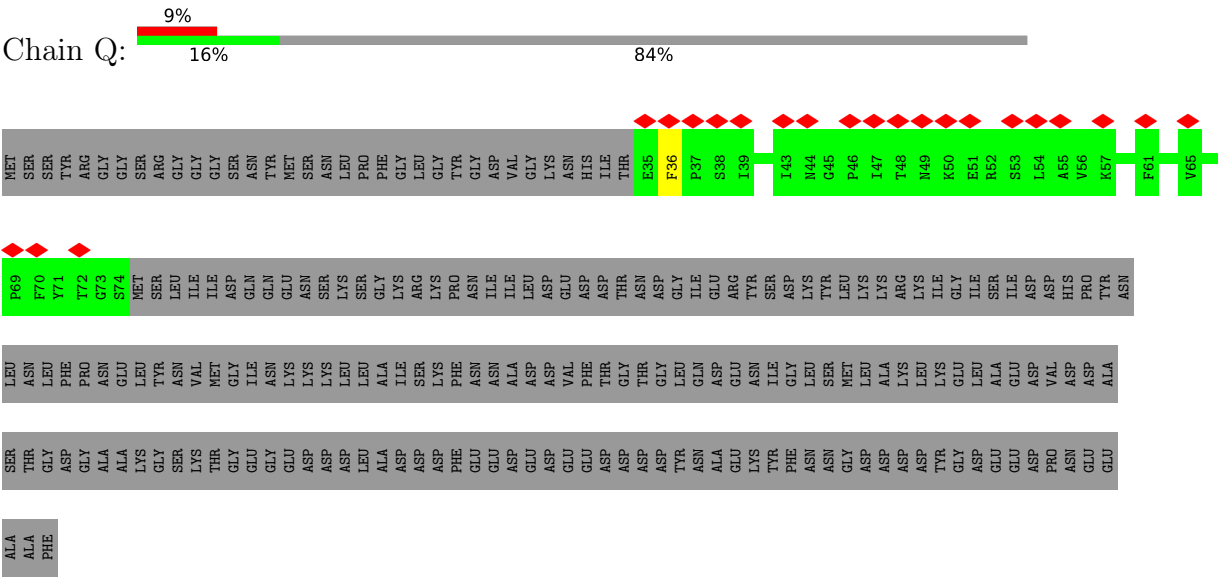


- Molecule 15: DNA-directed RNA polymerase III subunit RPC3





● Molecule 17: DNA-directed RNA polymerase III subunit RPC7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54213	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	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.356	Depositor
Minimum map value	-0.168	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	323.4, 323.4, 323.4	wwPDB
Map dimensions	308, 308, 308	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: 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	0.21	0/11176	0.56	2/15104 (0.0%)
2	B	0.20	0/8943	0.58	7/12068 (0.1%)
3	C	0.20	0/2711	0.55	0/3676
4	D	0.21	0/991	0.58	0/1328
5	E	0.20	0/1795	0.49	0/2416
6	F	0.21	0/683	0.60	0/923
7	G	0.20	0/1583	0.56	2/2146 (0.1%)
8	H	0.21	0/1138	0.60	2/1540 (0.1%)
9	I	0.17	0/328	0.53	0/445
10	J	0.20	0/567	0.66	0/761
11	K	0.20	0/803	0.62	2/1083 (0.2%)
12	L	0.20	0/360	0.61	0/478
13	M	0.22	0/1378	0.67	2/1863 (0.1%)
14	N	0.26	0/810	0.79	3/1088 (0.3%)
15	O	0.21	0/4379	0.59	2/5906 (0.0%)
16	P	0.33	0/1050	0.95	3/1424 (0.2%)
17	Q	0.37	0/320	0.73	0/434
All	All	0.21	0/39015	0.60	25/52683 (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	7
2	B	0	7
3	C	0	1
8	H	0	1
12	L	0	1
13	M	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
14	N	0	3
15	O	0	1
16	P	0	6
All	All	0	28

There are no bond length outliers.

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	409	LEU	N-CA-C	-9.46	90.66	110.80
15	O	198	GLY	CA-C-N	5.81	129.53	120.82
15	O	198	GLY	C-N-CA	5.81	129.53	120.82
2	B	889	SER	CA-C-N	5.74	129.43	120.82
2	B	889	SER	C-N-CA	5.74	129.43	120.82

There are no chirality outliers.

5 of 28 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	275	GLN	Peptide
1	A	308	SER	Peptide
1	A	494	PRO	Peptide
1	A	511	ASP	Peptide
1	A	631	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	10980	0	11097	117	0
2	B	8788	0	8903	101	0
3	C	2655	0	2628	26	0
4	D	977	0	983	28	0
5	E	1759	0	1788	15	0
6	F	671	0	692	11	0
7	G	1544	0	1540	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1120	0	1089	14	0
9	I	321	0	305	4	0
10	J	558	0	573	5	0
11	K	792	0	790	10	0
12	L	358	0	382	7	0
13	M	1347	0	1315	14	0
14	N	802	0	851	12	0
15	O	4315	0	4484	49	0
16	P	1024	0	992	21	0
17	Q	311	0	315	2	0
18	A	2	0	0	0	0
18	B	1	0	0	0	0
18	I	1	0	0	0	0
18	J	1	0	0	0	0
18	L	1	0	0	0	0
19	A	1	0	0	0	0
All	All	38329	0	38727	392	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 392 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)
4:D:135:TYR:CE1	4:D:142:ASP:HA	1.58	1.37
4:D:135:TYR:CZ	4:D:142:ASP:HB3	1.68	1.27
4:D:135:TYR:HE1	4:D:142:ASP:CA	1.52	1.22
4:D:135:TYR:CE1	4:D:142:ASP:CA	2.23	1.19
4:D:143:ALA:O	4:D:145:PHE:N	1.79	1.15

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	1394/1460 (96%)	1219 (87%)	167 (12%)	8 (1%)	21	50
2	B	1112/1149 (97%)	980 (88%)	127 (11%)	5 (0%)	30	59
3	C	333/335 (99%)	299 (90%)	33 (10%)	1 (0%)	36	65
4	D	113/161 (70%)	97 (86%)	13 (12%)	3 (3%)	4	20
5	E	213/215 (99%)	195 (92%)	18 (8%)	0	100	100
6	F	81/155 (52%)	68 (84%)	13 (16%)	0	100	100
7	G	185/212 (87%)	159 (86%)	26 (14%)	0	100	100
8	H	136/146 (93%)	117 (86%)	19 (14%)	0	100	100
9	I	40/110 (36%)	34 (85%)	6 (15%)	0	100	100
10	J	66/70 (94%)	58 (88%)	8 (12%)	0	100	100
11	K	99/142 (70%)	88 (89%)	11 (11%)	0	100	100
12	L	43/70 (61%)	36 (84%)	7 (16%)	0	100	100
13	M	161/282 (57%)	120 (74%)	39 (24%)	2 (1%)	10	35
14	N	101/422 (24%)	80 (79%)	21 (21%)	0	100	100
15	O	531/654 (81%)	468 (88%)	62 (12%)	1 (0%)	43	71
16	P	119/317 (38%)	72 (60%)	42 (35%)	5 (4%)	2	14
17	Q	38/251 (15%)	32 (84%)	6 (16%)	0	100	100
All	All	4765/6151 (78%)	4122 (86%)	618 (13%)	25 (0%)	26	54

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	839	GLY
2	B	935	ASP
4	D	140	GLU
4	D	144	ARG
16	P	308	GLU

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	1215/1257 (97%)	1211 (100%)	4 (0%)	86	84
2	B	975/1006 (97%)	973 (100%)	2 (0%)	87	85
3	C	296/296 (100%)	296 (100%)	0	100	100
4	D	110/145 (76%)	108 (98%)	2 (2%)	51	67
5	E	197/197 (100%)	197 (100%)	0	100	100
6	F	73/137 (53%)	73 (100%)	0	100	100
7	G	170/190 (90%)	170 (100%)	0	100	100
8	H	123/128 (96%)	123 (100%)	0	100	100
9	I	38/98 (39%)	37 (97%)	1 (3%)	40	61
10	J	63/65 (97%)	63 (100%)	0	100	100
11	K	91/130 (70%)	91 (100%)	0	100	100
12	L	40/57 (70%)	39 (98%)	1 (2%)	42	62
13	M	143/249 (57%)	143 (100%)	0	100	100
14	N	88/360 (24%)	87 (99%)	1 (1%)	65	74
15	O	492/593 (83%)	489 (99%)	3 (1%)	78	80
16	P	116/285 (41%)	113 (97%)	3 (3%)	40	61
17	Q	35/212 (16%)	35 (100%)	0	100	100
All	All	4265/5405 (79%)	4248 (100%)	17 (0%)	81	83

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

Mol	Chain	Res	Type
16	P	263	VAL
16	P	314	GLU
4	D	156	ILE
9	I	10	ASN
12	L	27	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
13	M	190	ASN
15	O	631	ASN
14	N	284	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	O	202	GLN
2	B	197	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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.

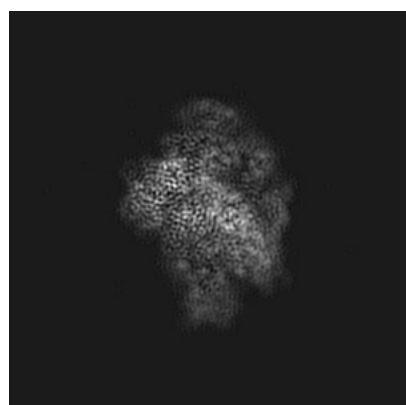
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3957. These allow visual inspection of the internal detail of the map and identification of artifacts.

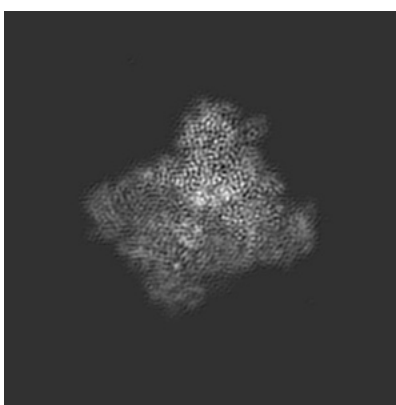
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

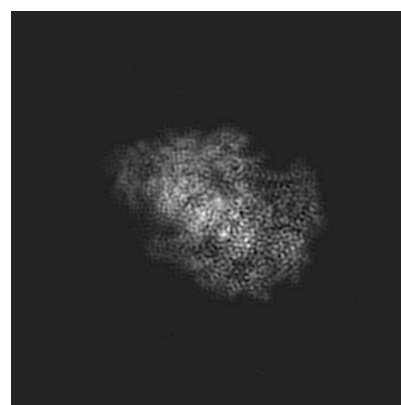
6.1.1 Primary map



X



Y

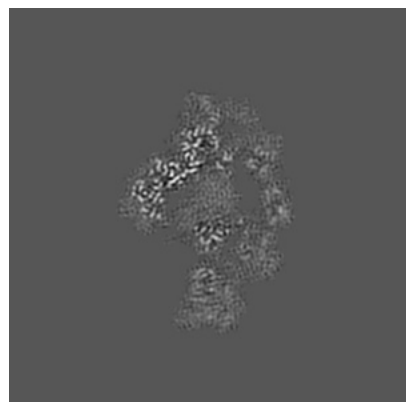


Z

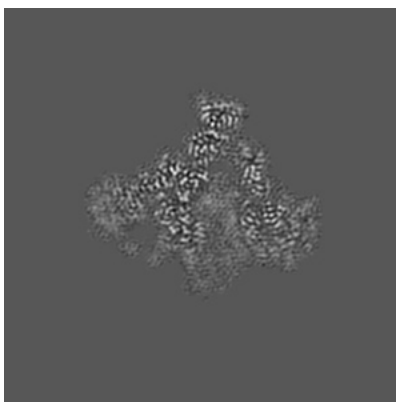
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

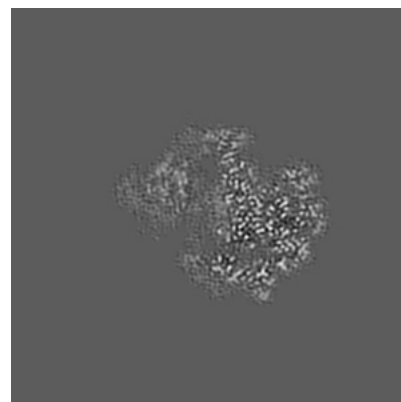
6.2.1 Primary map



X Index: 154



Y Index: 154

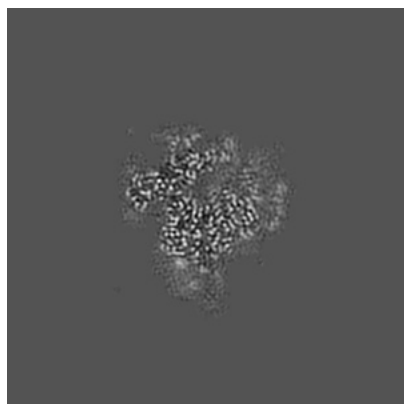


Z Index: 154

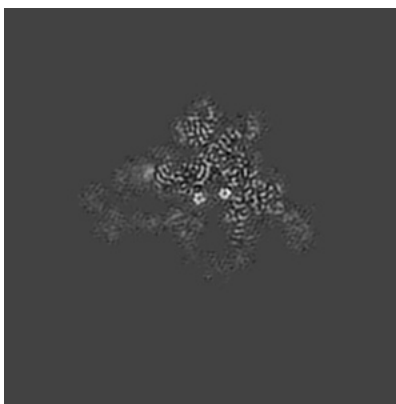
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

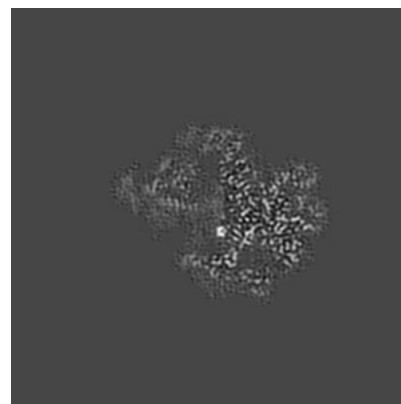
6.3.1 Primary map



X Index: 177



Y Index: 135

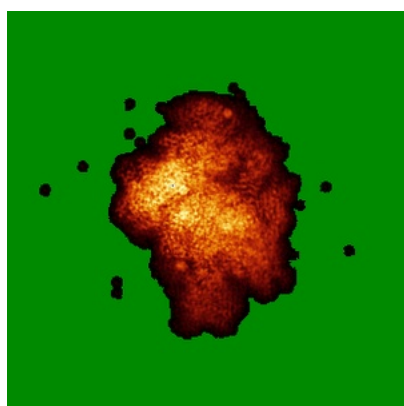


Z Index: 152

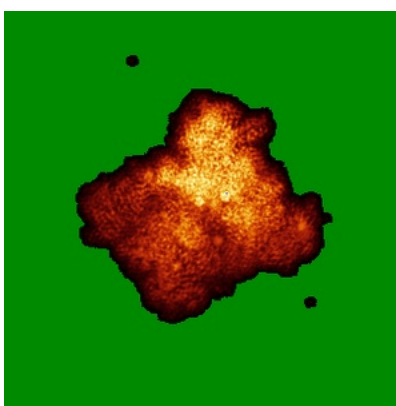
The images above show the largest variance slices of the map in three orthogonal directions.

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

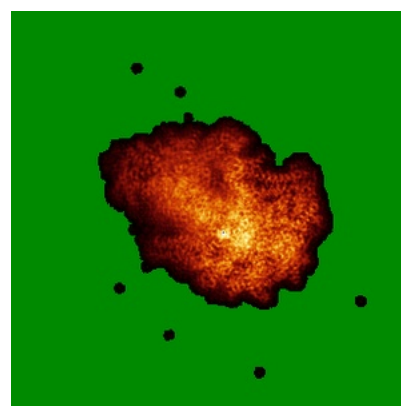
6.4.1 Primary map



X



Y

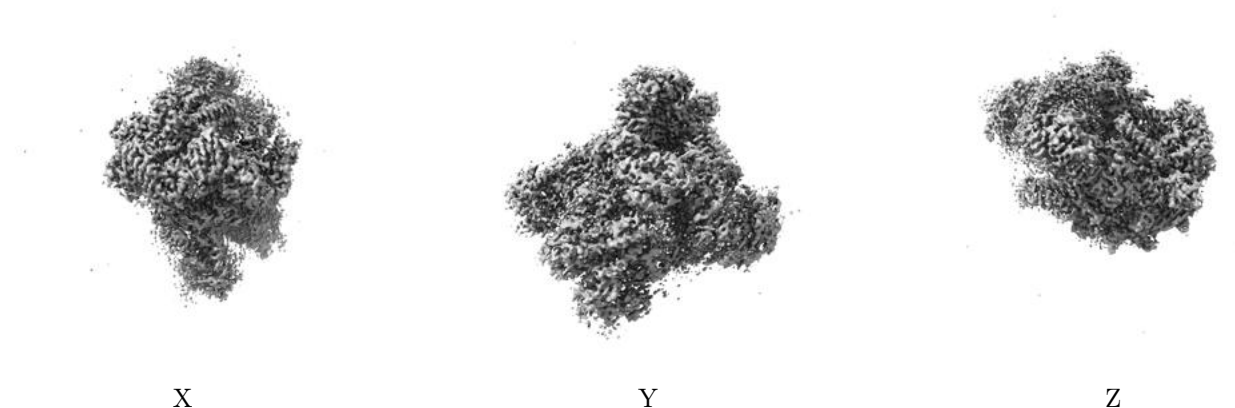


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

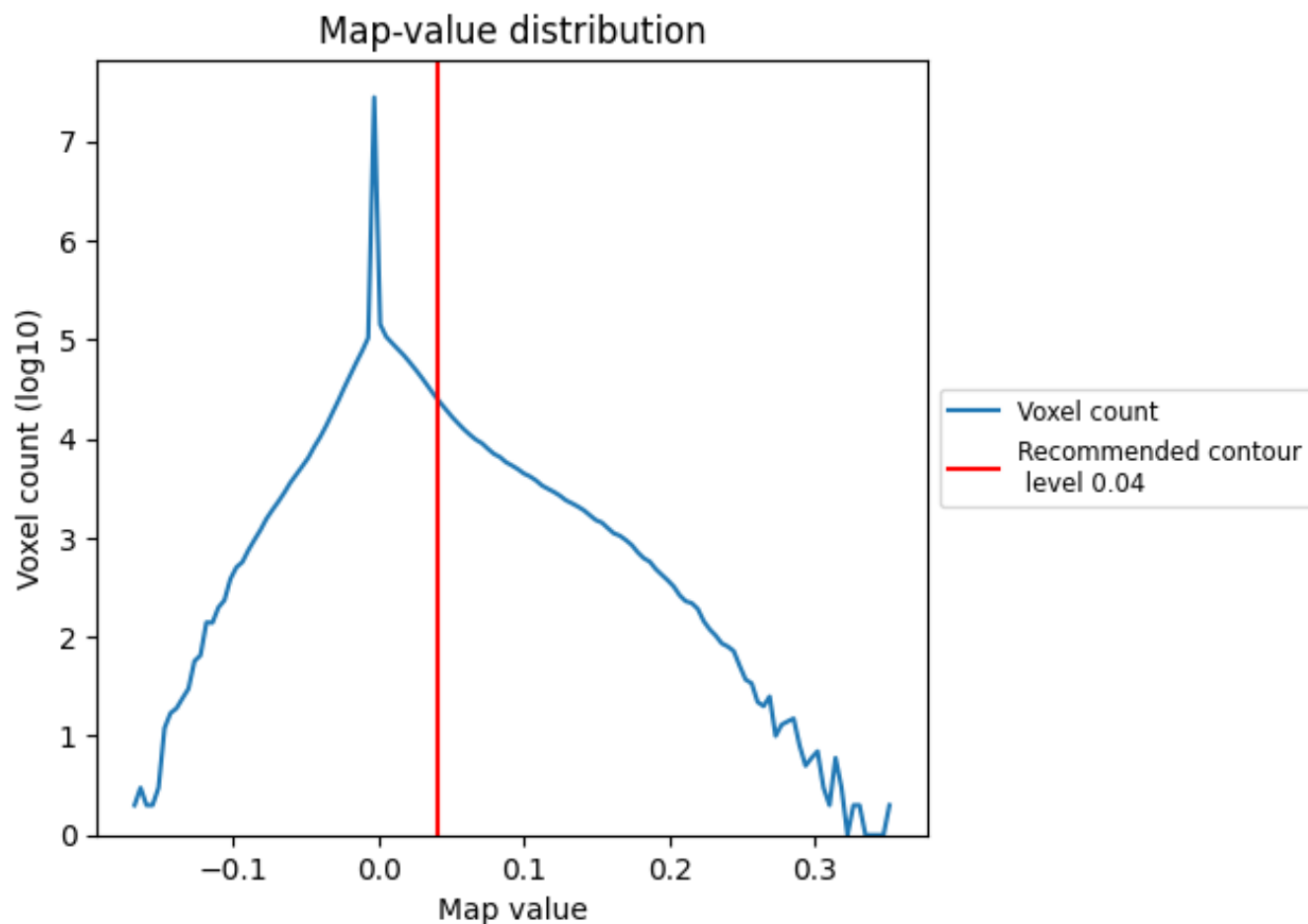
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

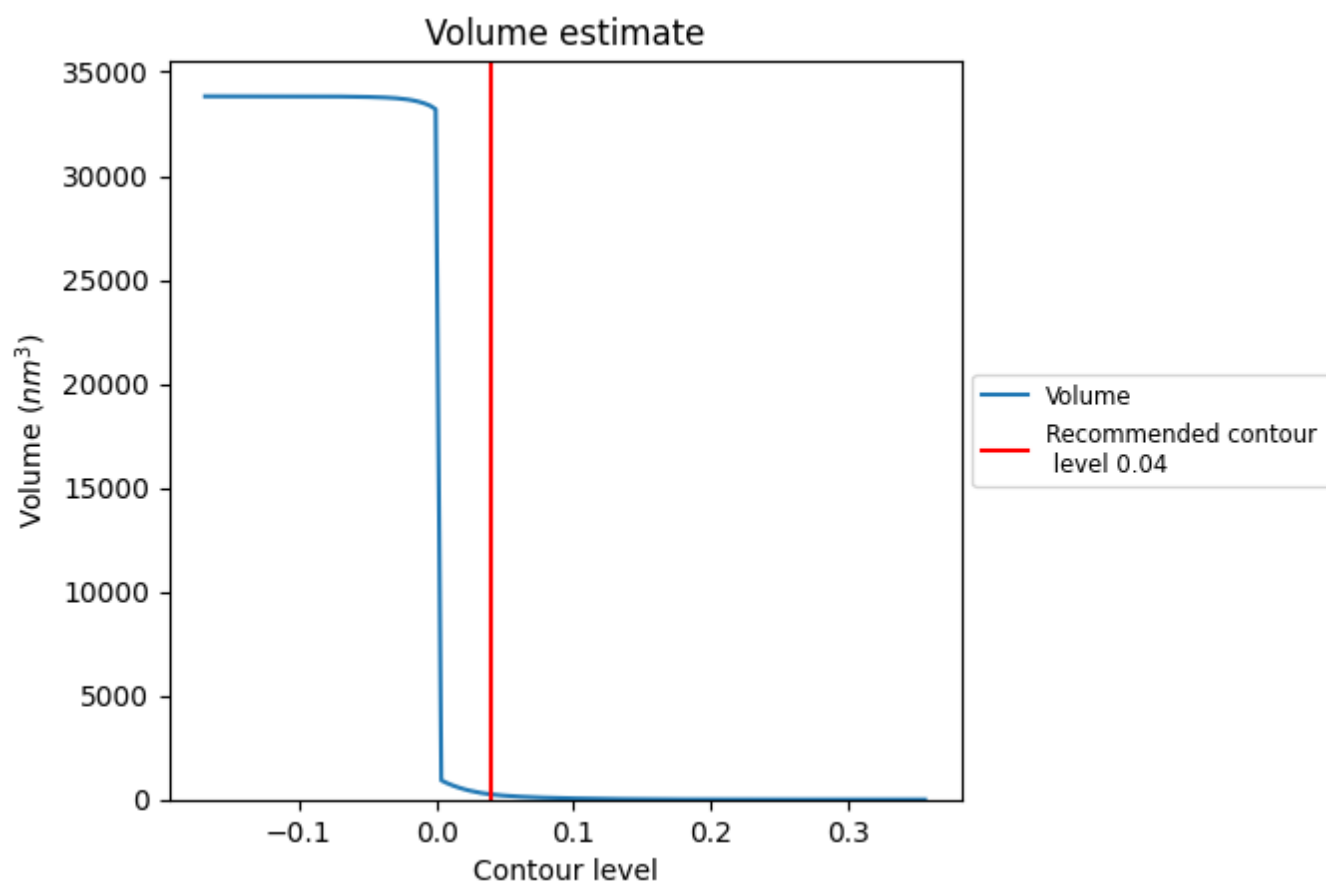
This section contains the results of statistical analysis of the map.

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.

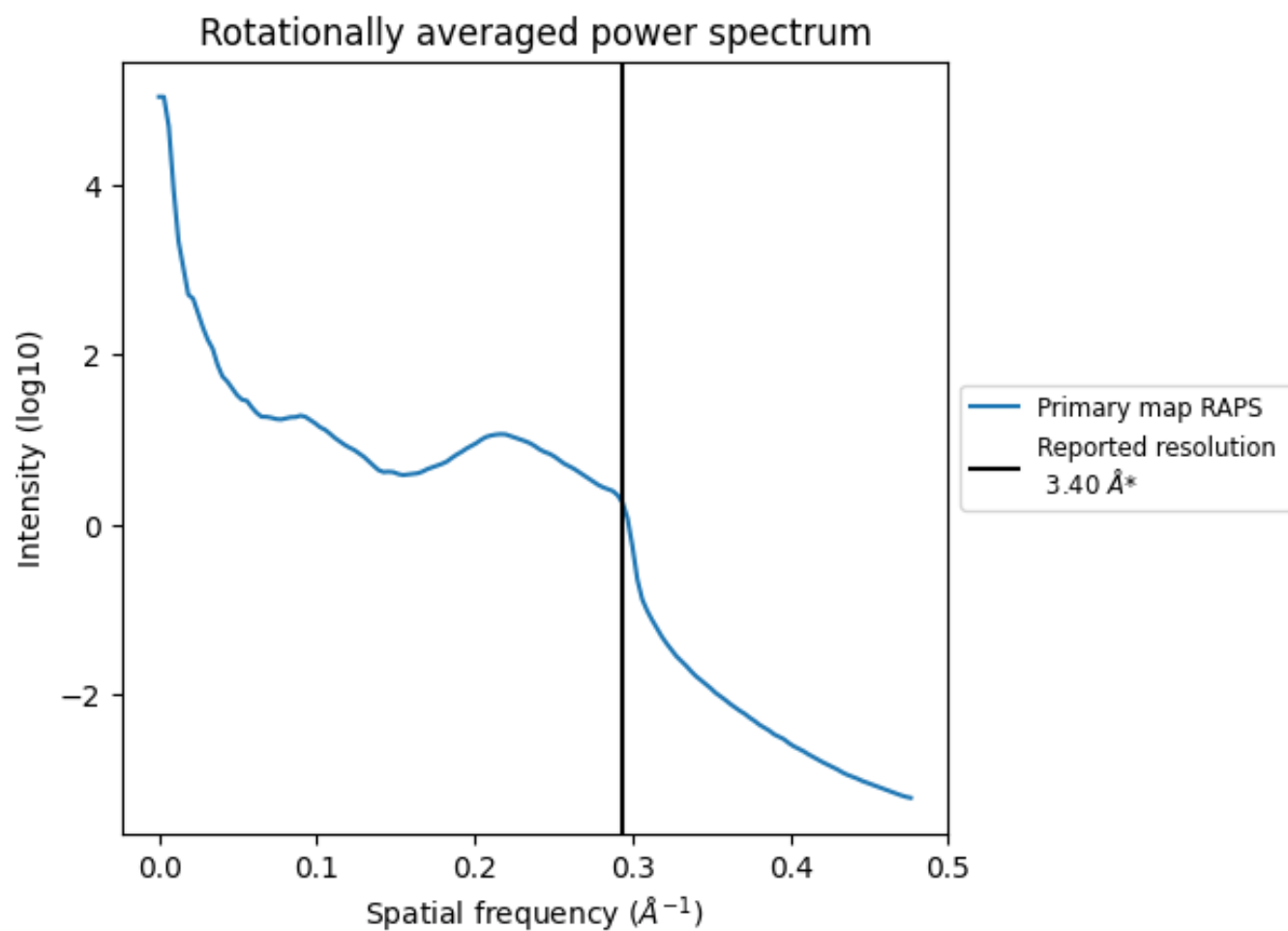
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 250 nm³; this corresponds to an approximate mass of 226 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 ⓘ

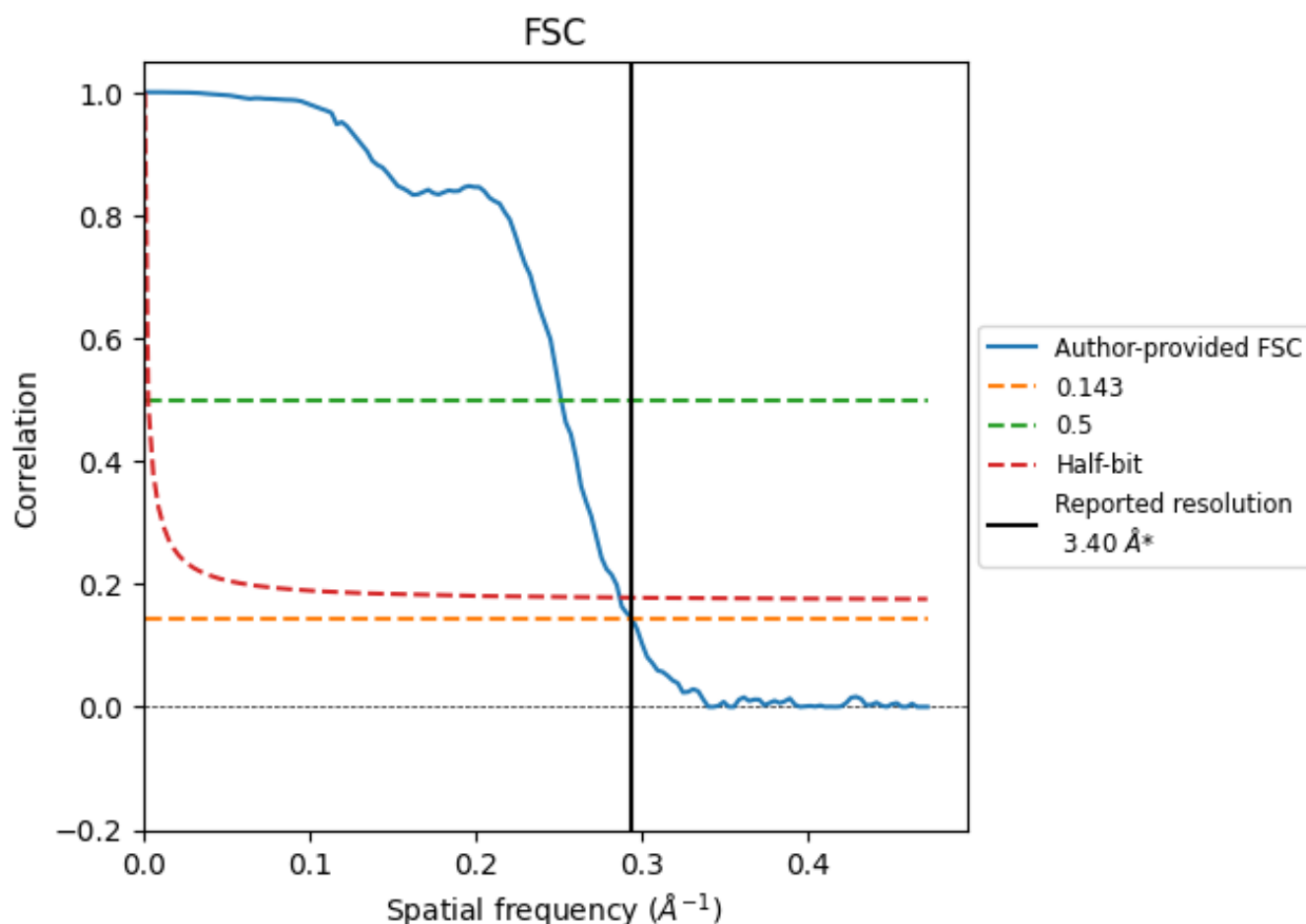


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

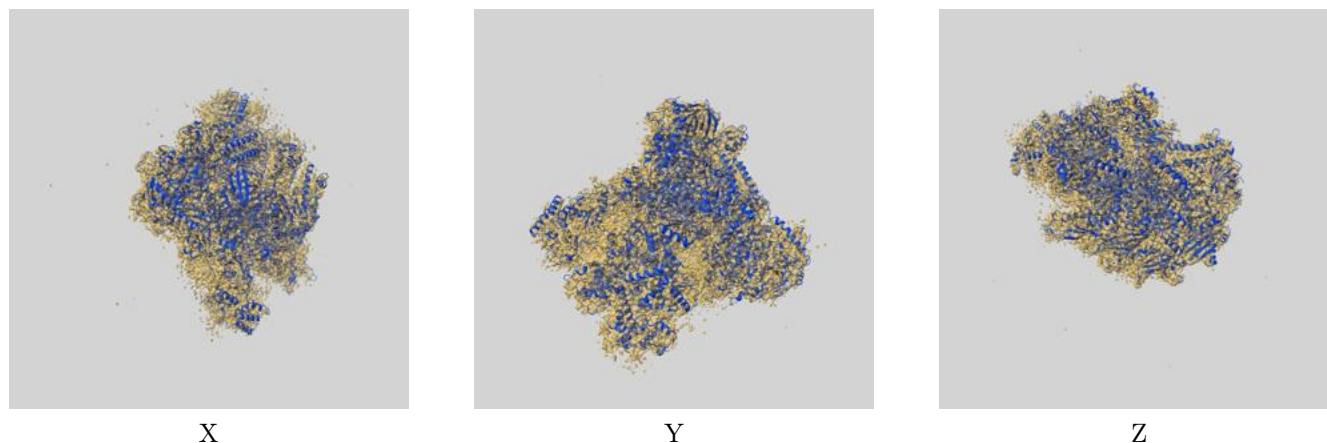
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	3.98	3.49
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

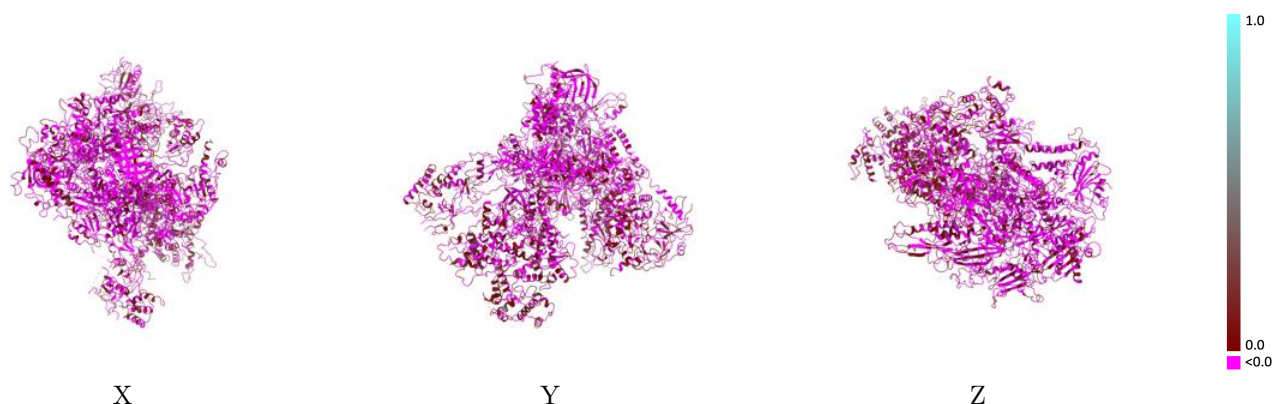
This section contains information regarding the fit between EMDB map EMD-3957 and PDB model 6EU2. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



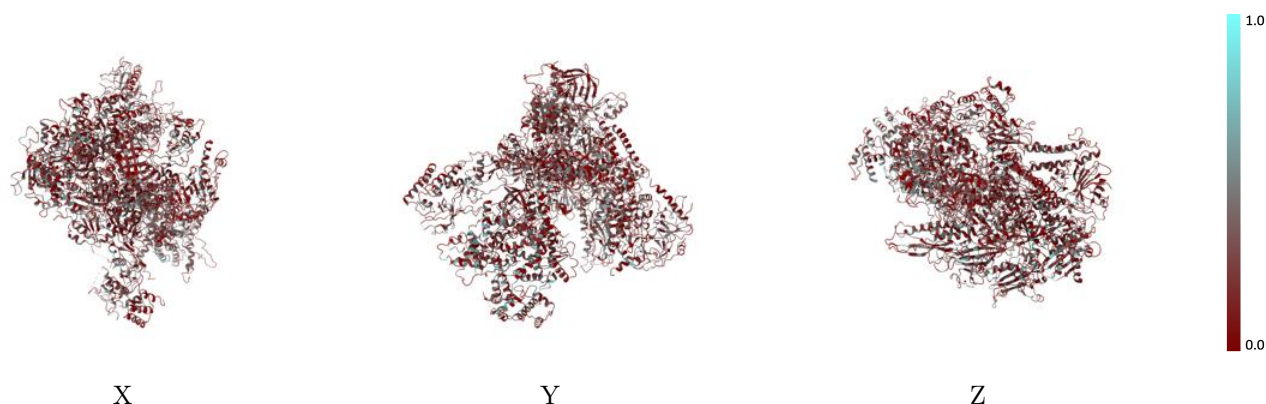
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



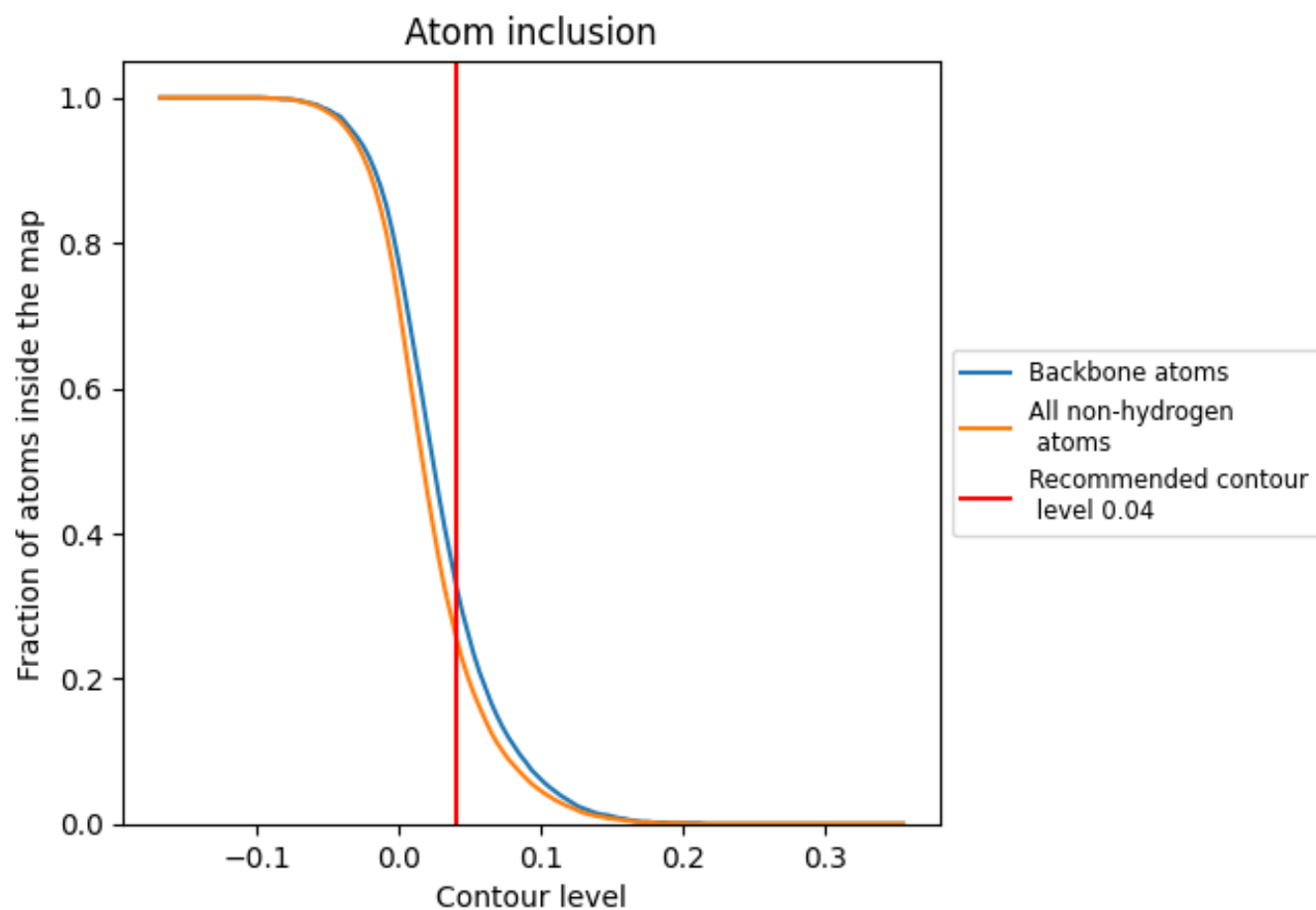
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 33% of all backbone atoms, 26% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2610	 -0.0350
A	 0.2500	 -0.0460
B	 0.2580	 -0.0620
C	 0.2730	 -0.0670
D	 0.2720	 0.0430
E	 0.2340	 -0.0410
F	 0.2670	 -0.0560
G	 0.2780	 -0.0060
H	 0.1960	 -0.0960
I	 0.1640	 -0.0440
J	 0.2930	 -0.0540
K	 0.2640	 -0.0740
L	 0.3060	 -0.0190
M	 0.2670	 0.0540
N	 0.2310	 -0.0310
O	 0.2920	 0.0130
P	 0.2990	 0.0370
Q	 0.3710	 0.1120

