



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:26 PM UTC

PDB ID : 6TPS / pdb\_00006tps  
EMDB ID : EMD-10544  
Title : early intermediate RNA Polymerase I Pre-initiation complex - eiPIC  
Authors : Pilsl, M.; Engel, C.  
Deposited on : 2019-12-14  
Resolution : 3.54 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](mailto: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>.

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

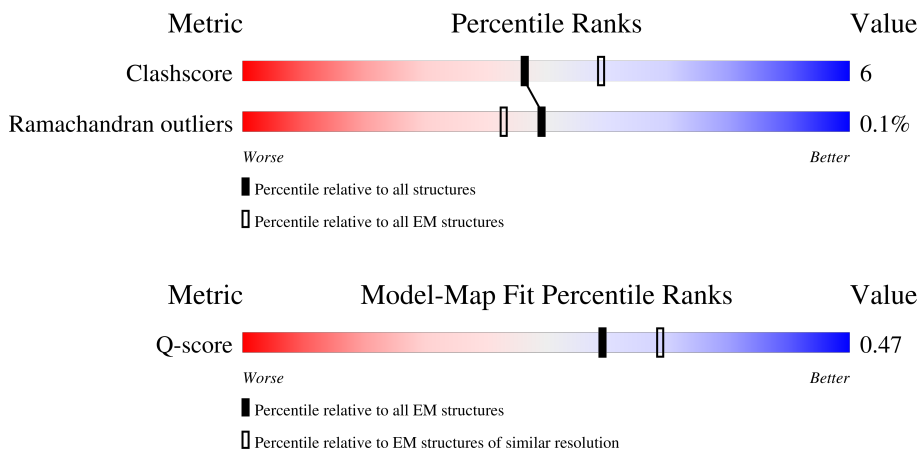
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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



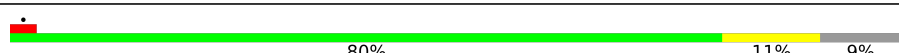
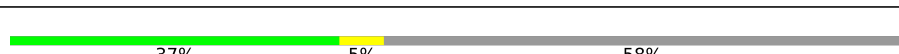

The reported resolution of this entry is 3.54 Å.

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.






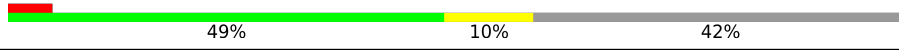




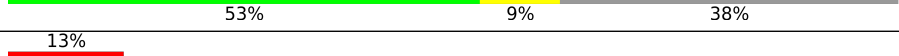
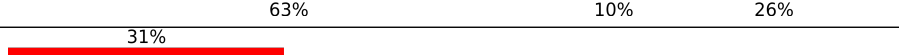
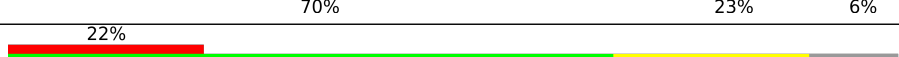



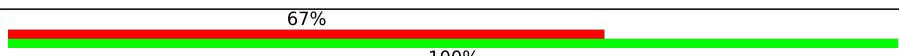


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	12891 ( 3.04 - 4.04 )

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  $\geq 3$ , 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	1664	 78% 11% 11%
2	B	1203	 85% 13% .
3	C	335	 80% 11% 9%
4	D	137	 37% 5% 58%
5	E	215	 84% 14% .

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Mol	Chain	Length	Quality of chain
6	F	155	
7	G	326	
8	H	146	
9	I	125	
10	J	70	
11	K	142	
12	L	70	
13	M	415	
14	N	233	
15	O	627	
16	P	636	
17	Q	514	
18	R	507	
19	S	27	
20	T	27	
21	U	12	
22	V	12	

## 2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 50070 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 I subunit RPA190.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1475	11659	7364	2029	2205	61	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase I subunit RPA135.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1177	9350	5913	1639	1747	51	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	305	2423	1539	416	460	8	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit RPA14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	58	459	289	78	92	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	212	1735	1102	306	316	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	100	823	522	144	154	3	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	193	1520	982	259	274	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	131	1052	664	176	208	4	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	73	542	340	91	107	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	69	569	362	101	100	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	101	793	496	130	162	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	43	340	211	66	59	4	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerase I subunit RPA49.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	M	105	833	528	138	167	0	0

- Molecule 14 is a protein called DNA-directed RNA polymerase I subunit RPA34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	145	1151	735	188	224	4	0	0

- Molecule 15 is a protein called RNA polymerase I-specific transcription initiation factor RRN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	463	3811	2473	623	694	21	0	0

- Molecule 16 is a protein called RNA polymerase I-specific transcription initiation factor RRN6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	595	4840	3080	823	927	10	0	0

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	44	ARG	-	expression tag	UNP P32786
P	45	PRO	-	expression tag	UNP P32786
P	46	VAL	-	expression tag	UNP P32786
P	47	ASP	-	expression tag	UNP P32786
P	48	ASP	-	expression tag	UNP P32786
P	49	THR	-	expression tag	UNP P32786
P	50	LEU	-	expression tag	UNP P32786
P	51	ALA	-	expression tag	UNP P32786
P	52	GLU	-	expression tag	UNP P32786
P	53	ASP	-	expression tag	UNP P32786
P	54	ALA	-	expression tag	UNP P32786
P	55	LEU	-	expression tag	UNP P32786
P	56	ASP	-	expression tag	UNP P32786
P	57	LEU	-	expression tag	UNP P32786
P	58	HIS	-	expression tag	UNP P32786
P	59	ILE	-	expression tag	UNP P32786
P	60	VAL	-	expression tag	UNP P32786
P	61	VAL	-	expression tag	UNP P32786
P	62	LYS	-	expression tag	UNP P32786
P	63	SER	-	expression tag	UNP P32786
P	64	LEU	-	expression tag	UNP P32786
P	65	LEU	-	expression tag	UNP P32786
P	66	CYS	-	expression tag	UNP P32786

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Chain	Residue	Modelled	Actual	Comment	Reference
P	67	ASP	-	expression tag	UNP P32786
P	68	THR	-	expression tag	UNP P32786

- Molecule 17 is a protein called RNA polymerase I-specific transcription initiation factor RRN7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	461	3839	2473	658	688	20	0	0

- Molecule 18 is a protein called RNA polymerase I-specific transcription initiation factor RRN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	325	2725	1763	479	472	11	0	0

- Molecule 19 is a DNA chain called NTS-DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
19	S	27	567	270	135	135	27	0	0

- Molecule 20 is a DNA chain called TS-DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
20	T	27	539	269	55	188	27	0	0

- Molecule 21 is a DNA chain called DNA foreign.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	U	12	264	120	60	72	12	0	0

- Molecule 22 is a DNA chain called DNA foreign.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	V	12	228	108	36	72	12	0	0

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

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

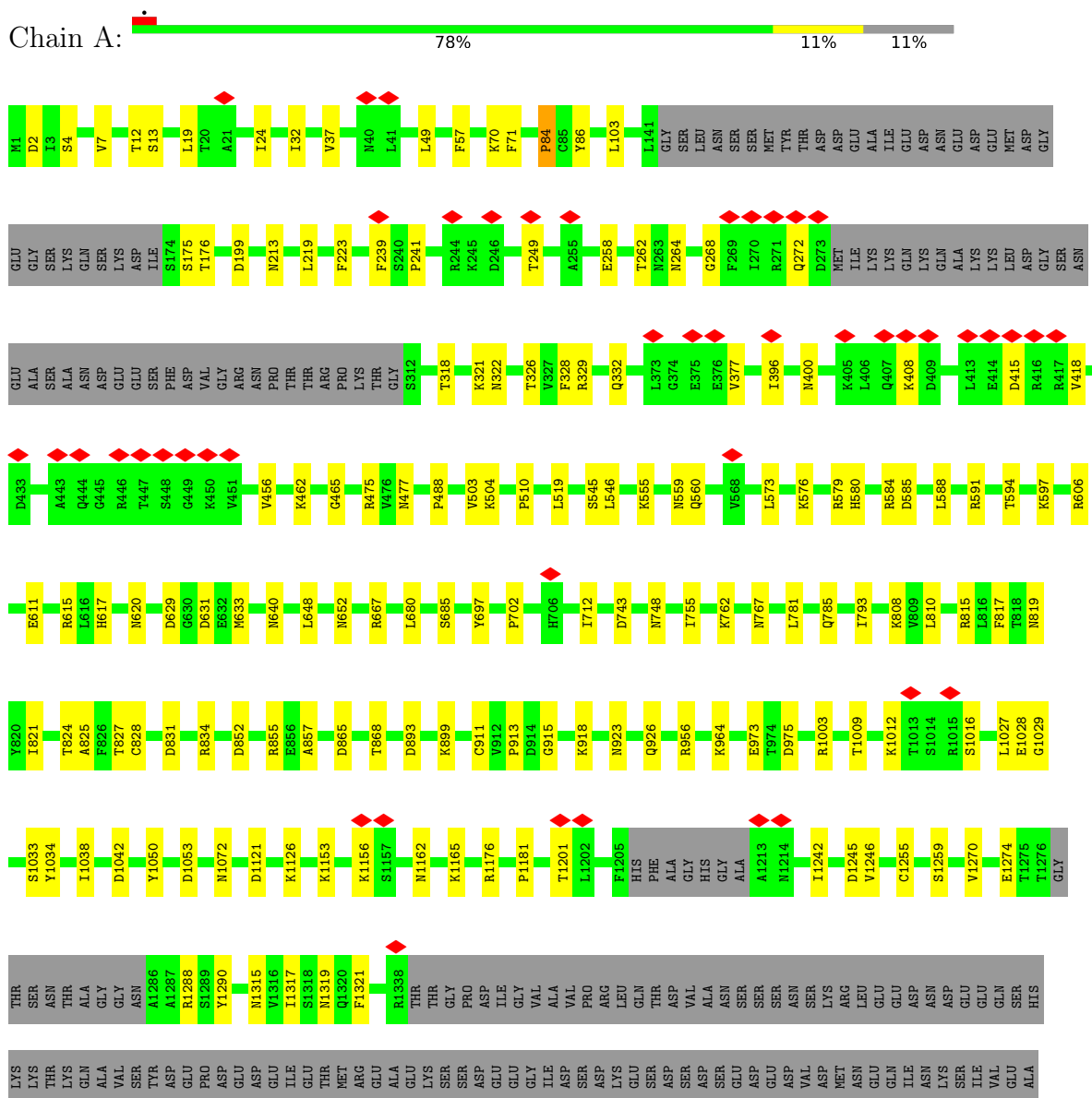
- Molecule 24 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

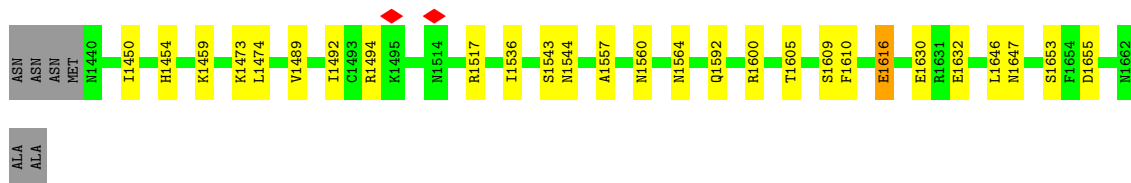
Mol	Chain	Residues	Atoms		AltConf
24	A	1	Total 1	Mg 1	0

### 3 Residue-property plots

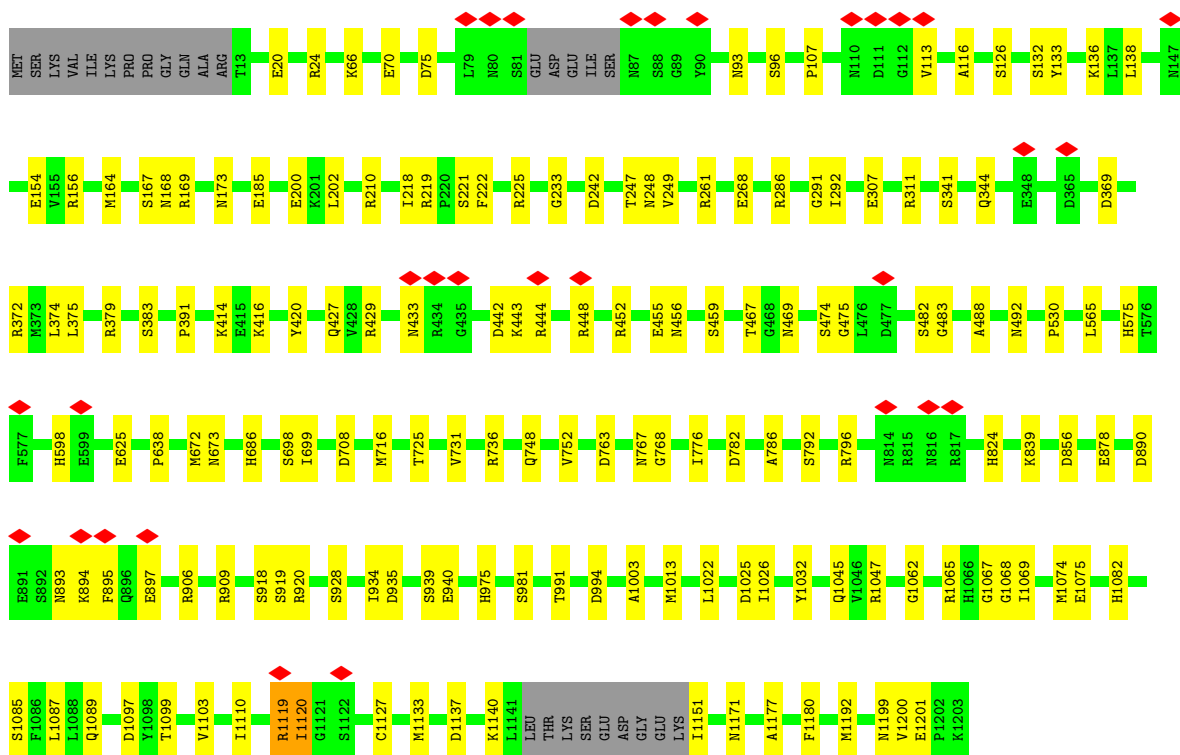
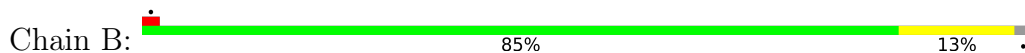
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: DNA-directed RNA polymerase I subunit RPA190

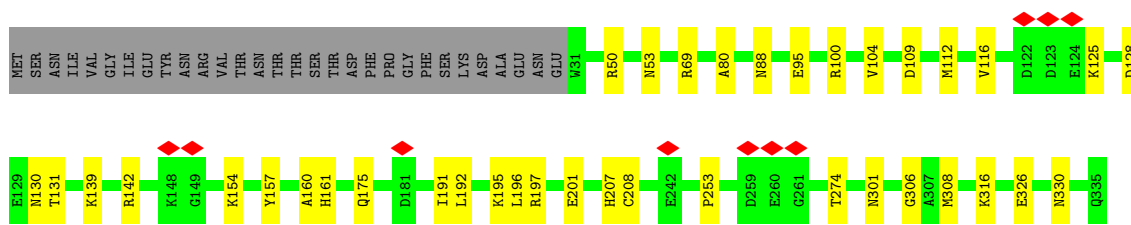
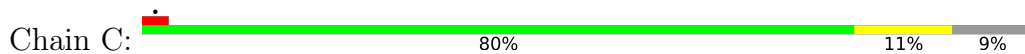




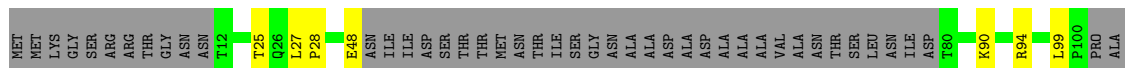
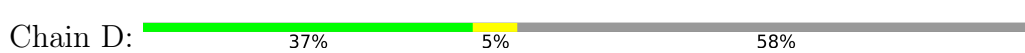
• Molecule 2: DNA-directed RNA polymerase I subunit RPA135



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

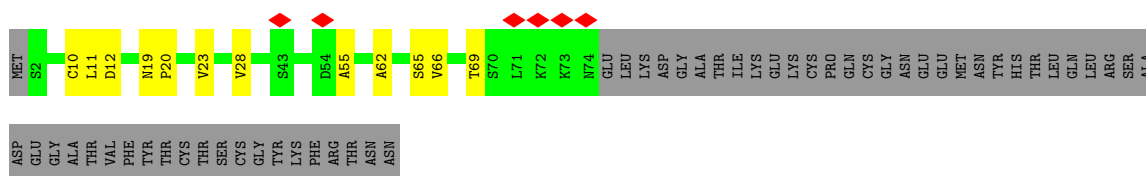


• Molecule 4: DNA-directed RNA polymerase I subunit RPA14

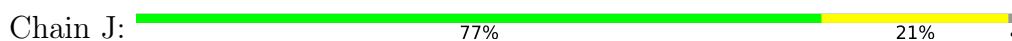




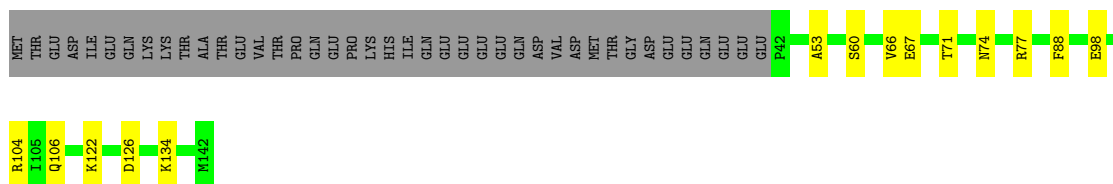
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



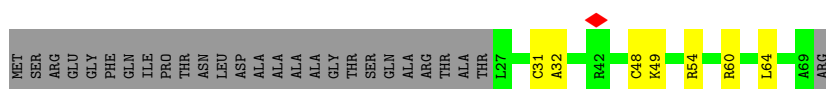
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



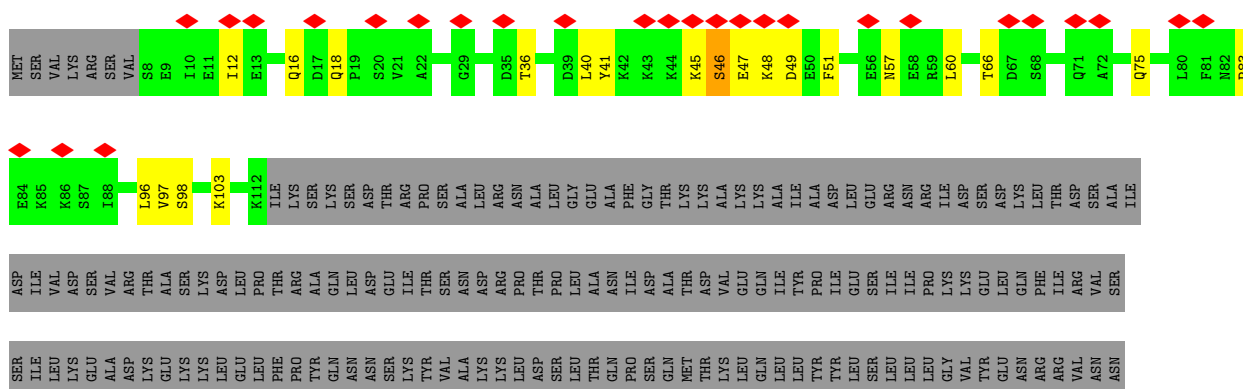
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2



- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

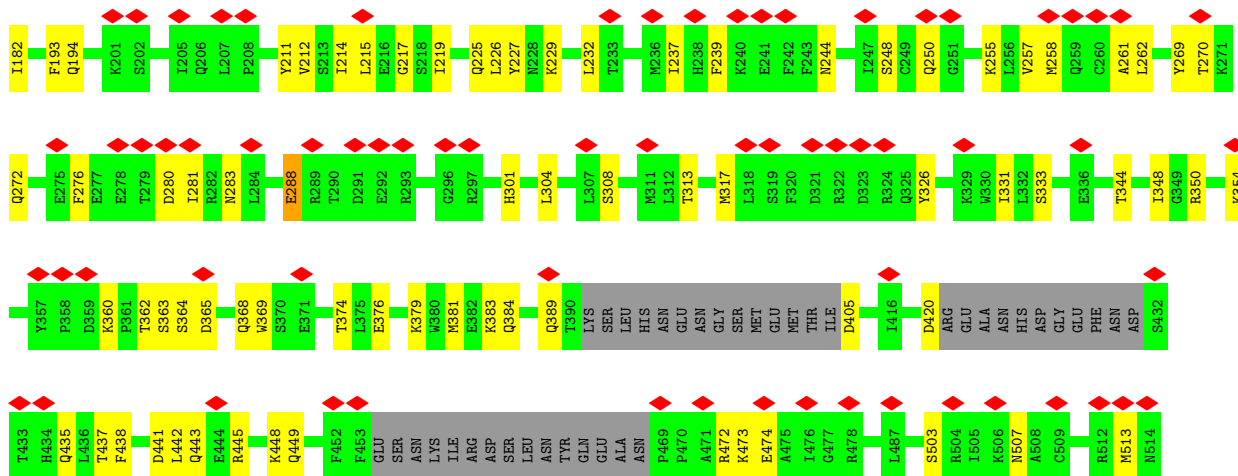


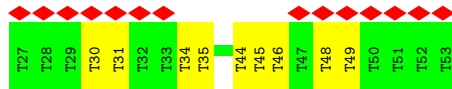
- Molecule 13: DNA-directed RNA polymerase I subunit RPA49



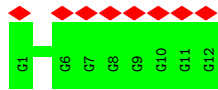




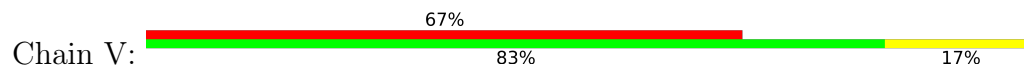




- Molecule 21: DNA foreign



- Molecule 22: DNA foreign



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	122099	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.4	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size ( $\text{\AA}$ )	457.80002, 457.80002, 457.80002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.09, 1.09, 1.09	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	0.46	0/11873	0.59	2/16035 (0.0%)
2	B	0.49	0/9557	0.60	2/12918 (0.0%)
3	C	0.44	0/2475	0.54	0/3354
4	D	0.31	0/465	0.56	0/630
5	E	0.37	0/1771	0.53	2/2383 (0.1%)
6	F	0.45	0/838	0.52	0/1129
7	G	0.34	0/1558	0.49	0/2120
8	H	0.41	0/1070	0.50	0/1449
9	I	0.29	0/548	0.52	0/740
10	J	0.53	0/578	0.54	0/775
11	K	0.45	0/804	0.52	0/1083
12	L	0.42	0/342	0.58	0/454
13	M	0.25	0/849	0.49	0/1140
14	N	0.27	0/1172	0.52	0/1580
15	O	0.28	0/3897	0.55	0/5268
16	P	0.27	0/4939	0.60	0/6689
17	Q	0.28	0/3928	0.67	3/5302 (0.1%)
18	R	0.32	0/2789	0.62	0/3755
19	S	0.26	0/647	0.46	0/995
20	T	0.31	0/592	0.63	0/912
21	U	0.32	0/299	0.50	0/464
22	V	0.27	0/251	0.42	0/380
All	All	0.40	0/51242	0.58	9/69555 (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	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3
3	C	0	1
13	M	0	1
16	P	0	6
17	Q	0	7
18	R	0	4
All	All	0	25

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	15	CYS	C-N-CD	-11.98	94.24	120.60
17	Q	15	CYS	CA-C-N	10.88	153.10	127.00
17	Q	15	CYS	C-N-CA	10.88	153.10	127.00
2	B	1062	GLY	CA-C-N	6.28	133.54	121.54
2	B	1062	GLY	C-N-CA	6.28	133.54	121.54

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1616	GLU	Peptide
1	A	57	PHE	Peptide
1	A	84	PRO	Peptide
2	B	116	ALA	Peptide
2	B	893	ASN	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11659	0	11753	127	0
2	B	9350	0	9242	112	0
3	C	2423	0	2412	28	0
4	D	459	0	462	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1735	0	1764	17	0
6	F	823	0	841	8	0
7	G	1520	0	1529	21	0
8	H	1052	0	1021	14	0
9	I	542	0	557	8	0
10	J	569	0	586	11	0
11	K	793	0	790	9	0
12	L	340	0	362	5	0
13	M	833	0	826	16	0
14	N	1151	0	1169	19	0
15	O	3811	0	3804	40	0
16	P	4840	0	4773	103	0
17	Q	3839	0	3861	74	0
18	R	2725	0	2798	44	0
19	S	567	0	298	4	0
20	T	539	0	324	7	0
21	U	264	0	133	0	0
22	V	228	0	133	1	0
23	A	2	0	0	0	0
23	B	1	0	0	0	0
23	I	1	0	0	0	0
23	J	1	0	0	0	0
23	L	1	0	0	0	0
23	Q	1	0	0	0	0
24	A	1	0	0	0	0
All	All	50070	0	49438	598	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 6.

The worst 5 of 598 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)
1:A:239:PHE:H	1:A:264:ASN:HD21	1.45	0.65
16:P:584:ARG:HH12	16:P:588:SER:HB3	1.60	0.65
2:B:467:THR:HG23	2:B:469:ASN:H	1.61	0.65
16:P:228:ASN:ND2	16:P:232:ASN:OD1	2.30	0.64
18:R:427:PRO:HD2	18:R:430:LEU:HB2	1.79	0.64

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	1063/1664 (64%)	977 (92%)	85 (8%)	1 (0%)	48	79
2	B	1171/1203 (97%)	1083 (92%)	85 (7%)	3 (0%)	36	66
3	C	303/335 (90%)	281 (93%)	22 (7%)	0	100	100
4	D	54/137 (39%)	52 (96%)	2 (4%)	0	100	100
5	E	210/215 (98%)	193 (92%)	17 (8%)	0	100	100
6	F	98/155 (63%)	93 (95%)	5 (5%)	0	100	100
7	G	189/326 (58%)	172 (91%)	17 (9%)	0	100	100
8	H	127/146 (87%)	115 (91%)	12 (9%)	0	100	100
9	I	71/125 (57%)	63 (89%)	8 (11%)	0	100	100
10	J	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
11	K	99/142 (70%)	92 (93%)	7 (7%)	0	100	100
12	L	41/70 (59%)	35 (85%)	6 (15%)	0	100	100
13	M	103/415 (25%)	89 (86%)	14 (14%)	0	100	100
14	N	139/233 (60%)	121 (87%)	18 (13%)	0	100	100
15	O	457/627 (73%)	431 (94%)	26 (6%)	0	100	100
16	P	583/636 (92%)	515 (88%)	68 (12%)	0	100	100
17	Q	451/514 (88%)	402 (89%)	47 (10%)	2 (0%)	30	61
18	R	317/507 (62%)	273 (86%)	44 (14%)	0	100	100
All	All	5543/7520 (74%)	5052 (91%)	485 (9%)	6 (0%)	49	79

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1028	GLU
2	B	1119	ARG
2	B	894	LYS
2	B	1120	ILE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
17	Q	16	PRO

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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 8 ligands modelled in this entry, 8 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
16	P	1
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	P	68:THR	C	169:GLN	N	23.31
1	B	121:VAL	C	122:TYR	N	1.20

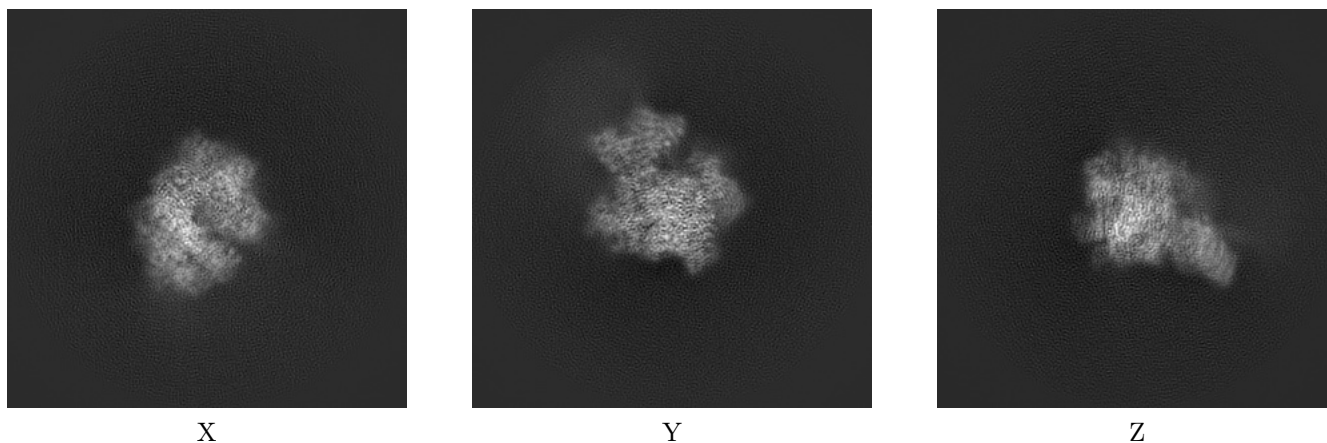
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10544. 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](#)

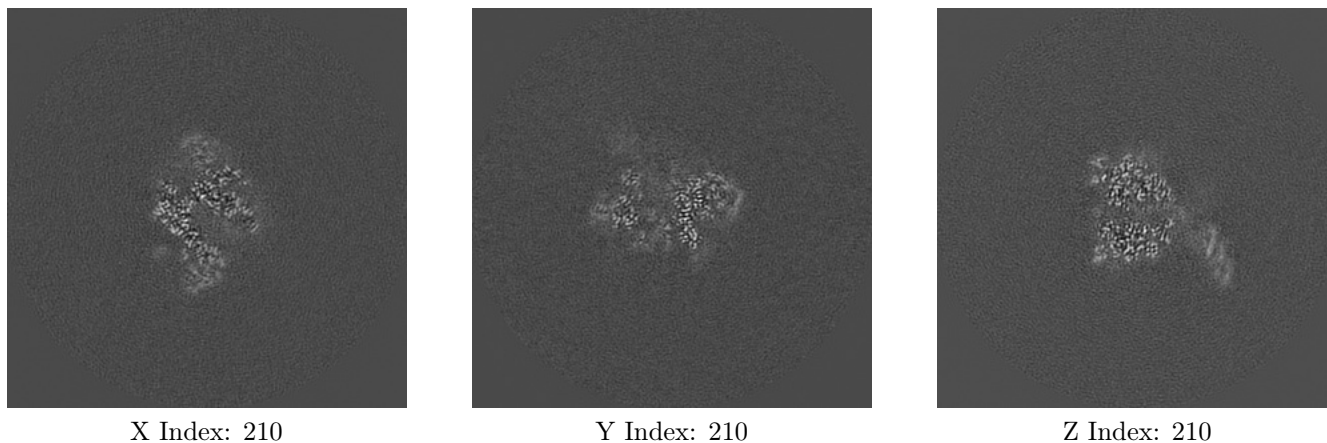
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

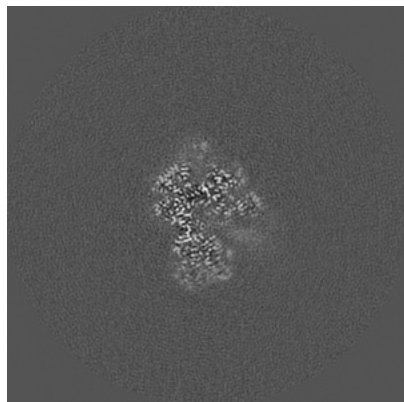
#### 6.2.1 Primary map



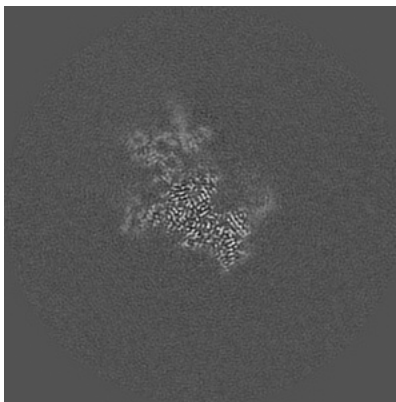
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

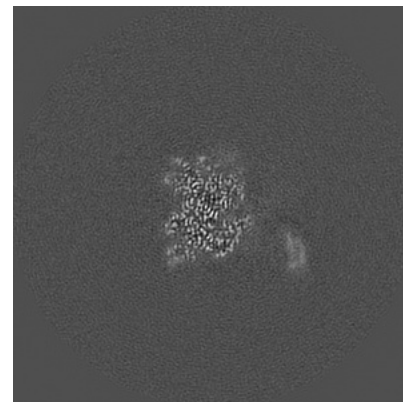
### 6.3.1 Primary map



X Index: 199



Y Index: 186

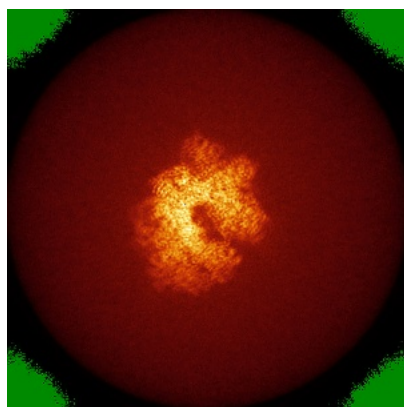


Z Index: 219

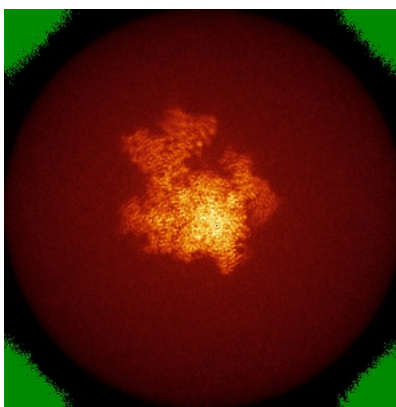
The images above show the largest variance slices of the map in three orthogonal directions.

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

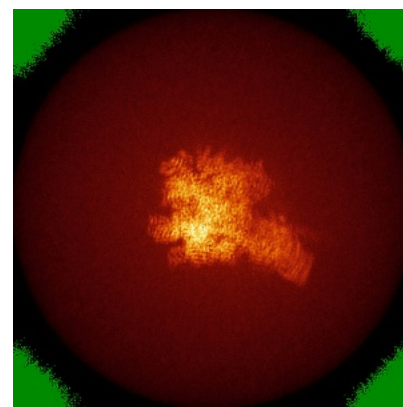
### 6.4.1 Primary map



X



Y

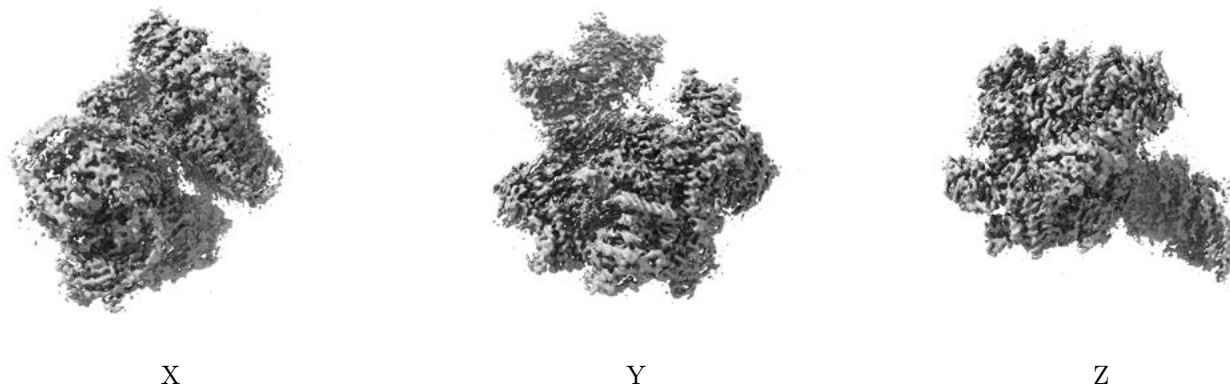


Z

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 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

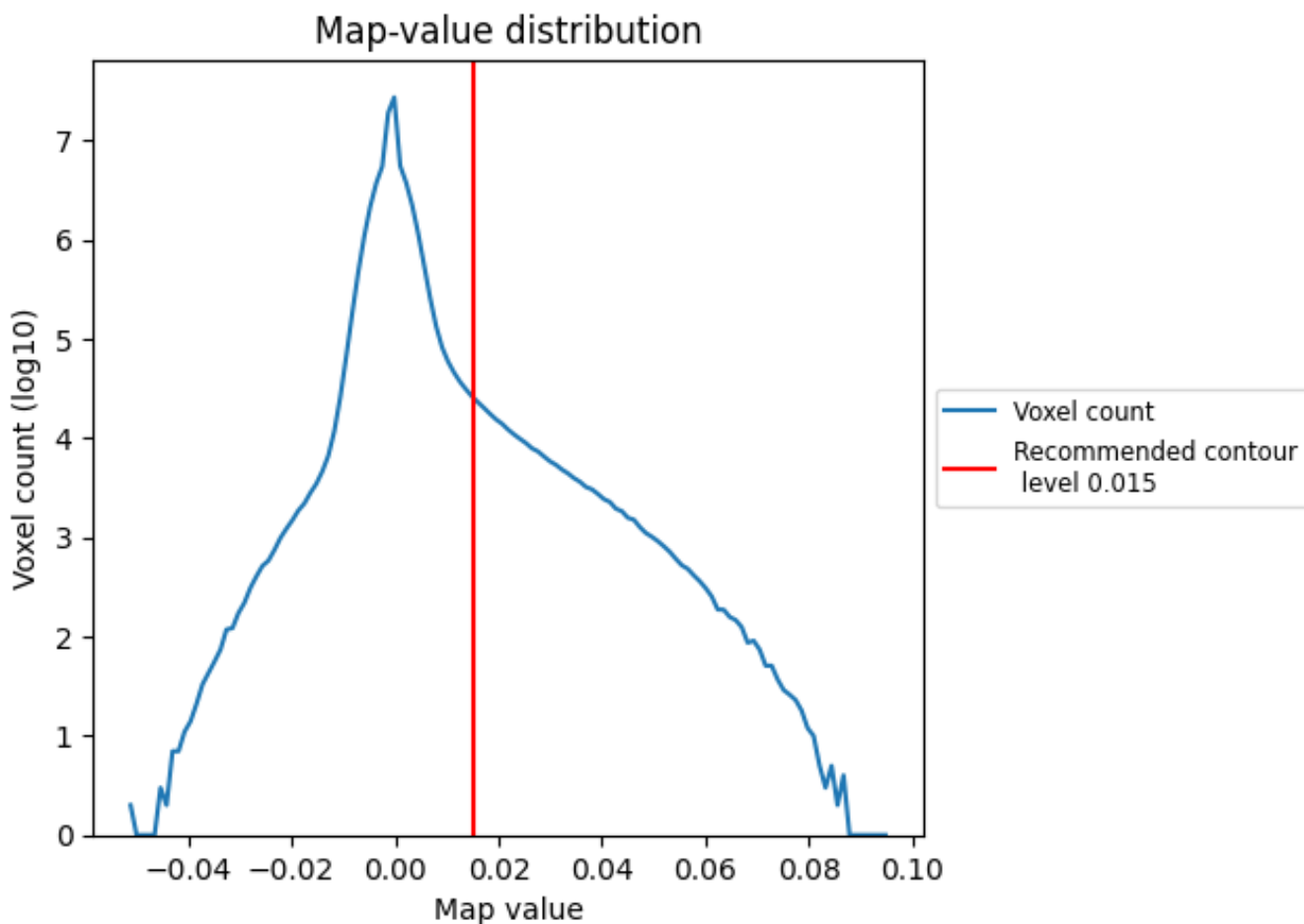
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

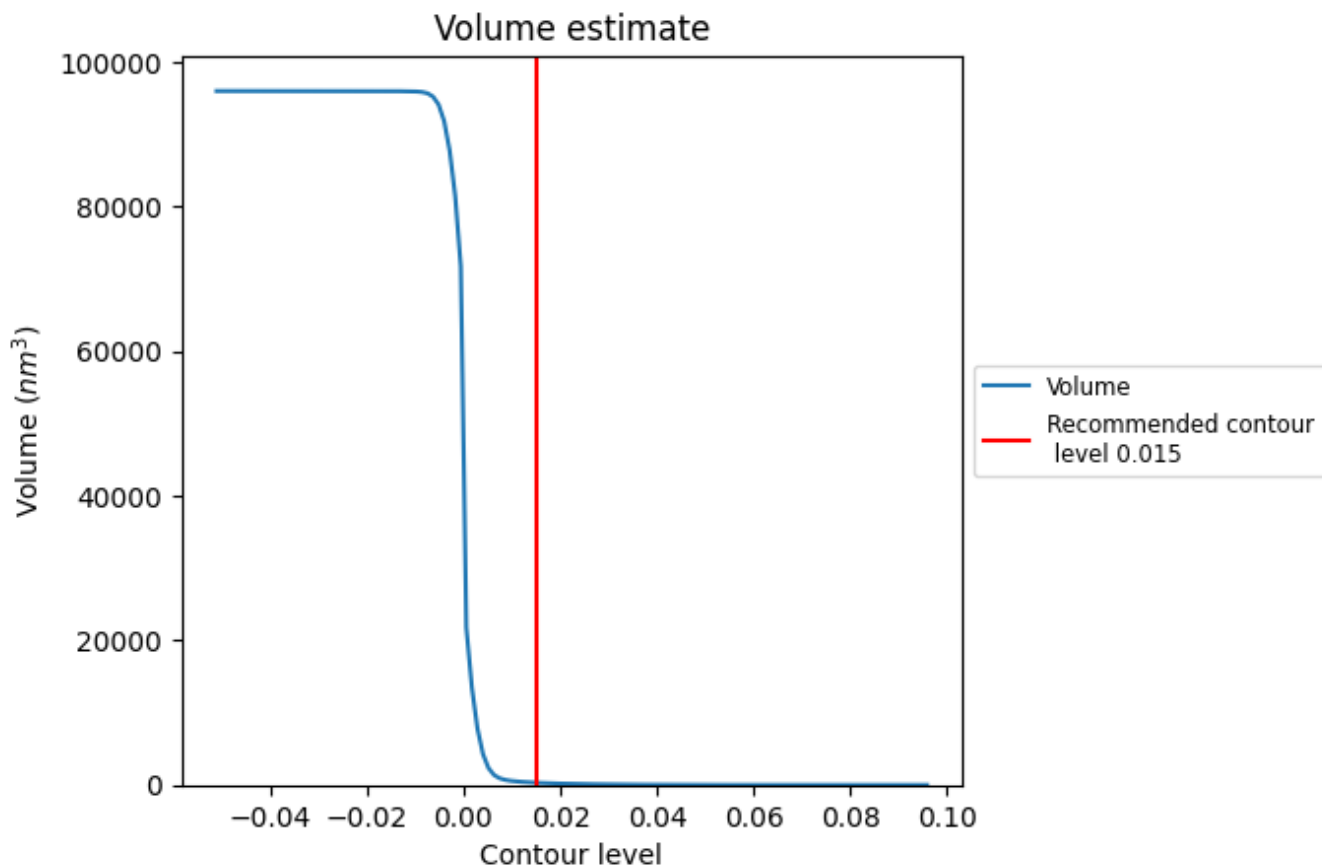
This section contains the results of statistical analysis of the map.

### 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.

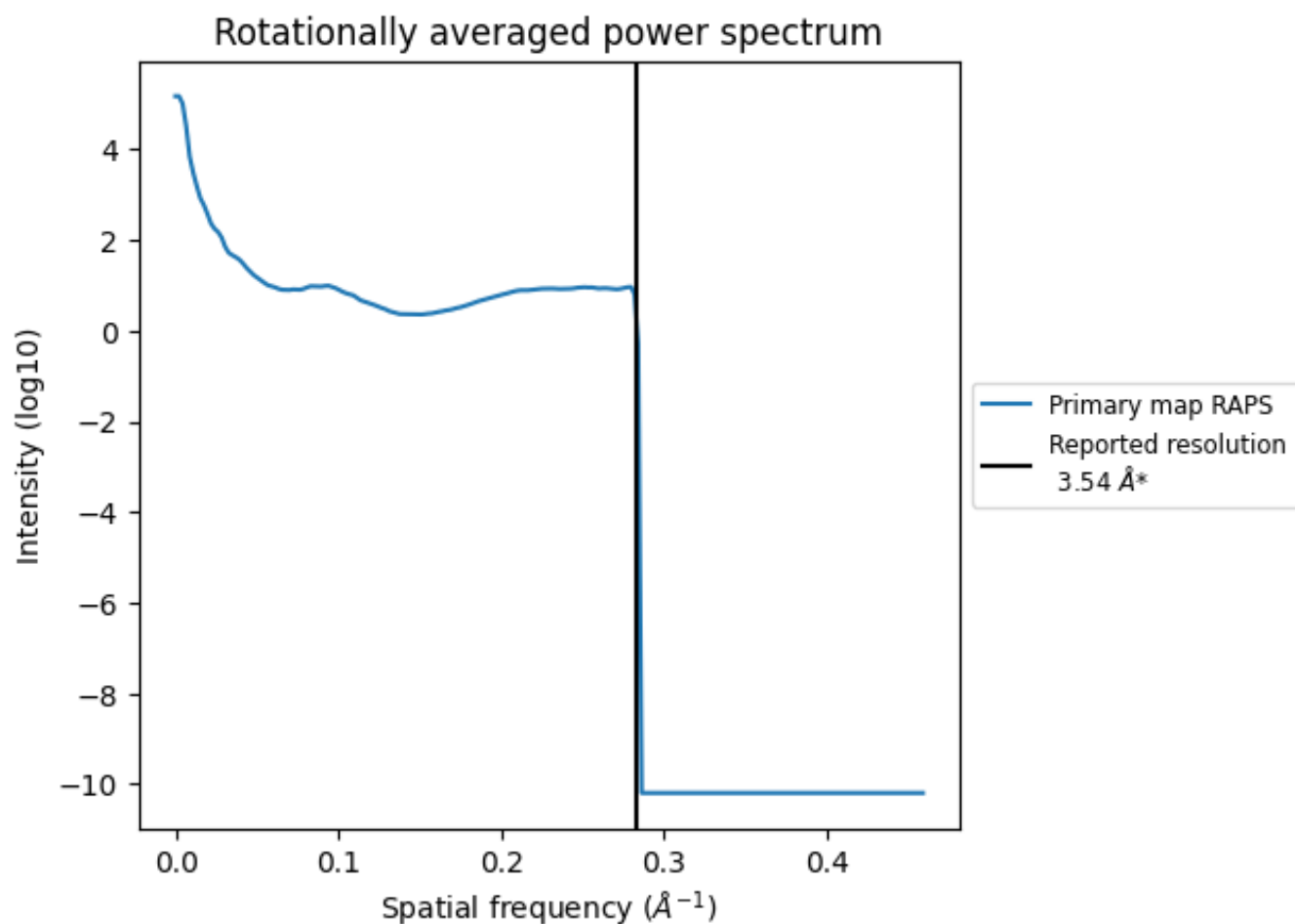
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 308  $\text{nm}^3$ ; this corresponds to an approximate mass of 278 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of  $0.282 \text{\AA}^{-1}$

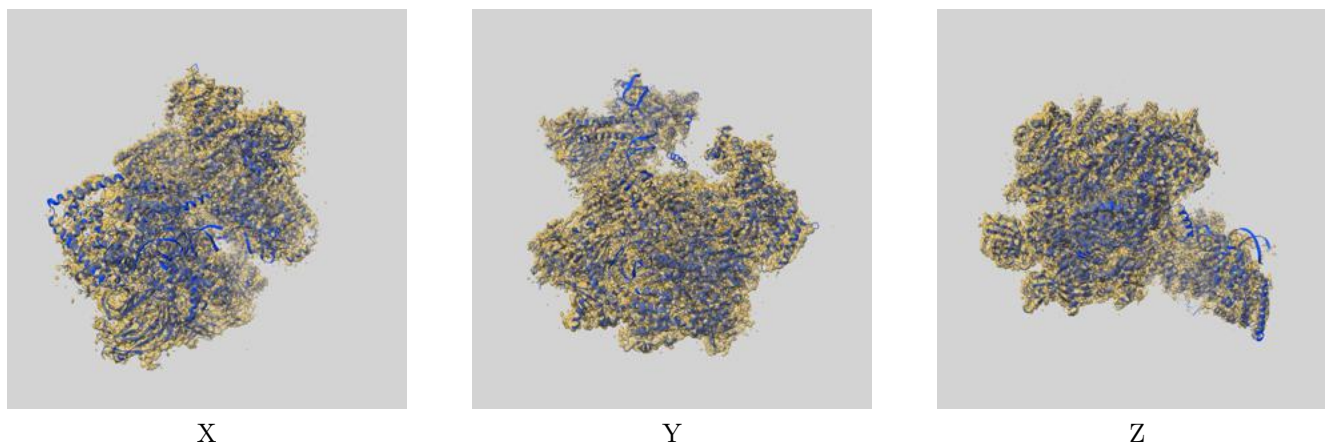
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

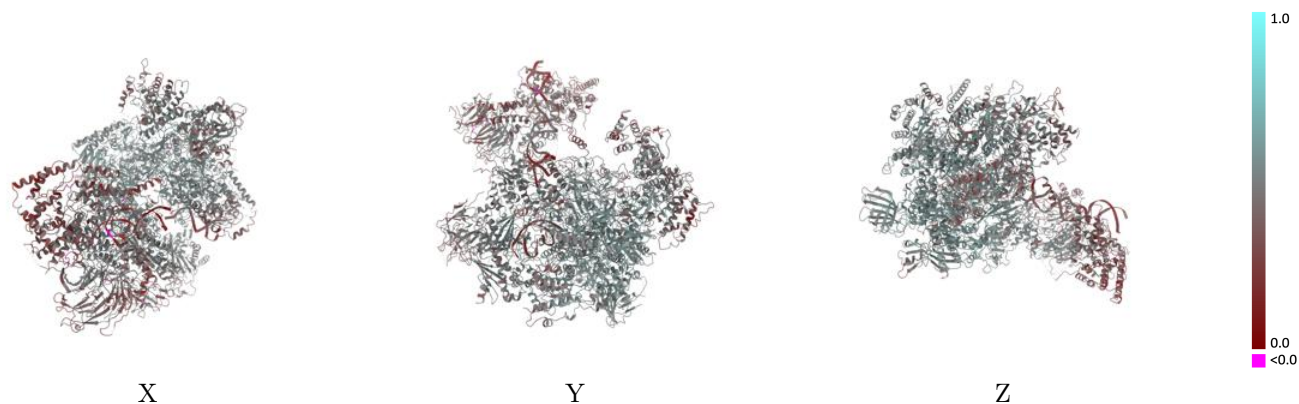
This section contains information regarding the fit between EMDB map EMD-10544 and PDB model 6TPS. Per-residue inclusion information can be found in section 3 on page 9.

### 9.1 Map-model overlay [i](#)



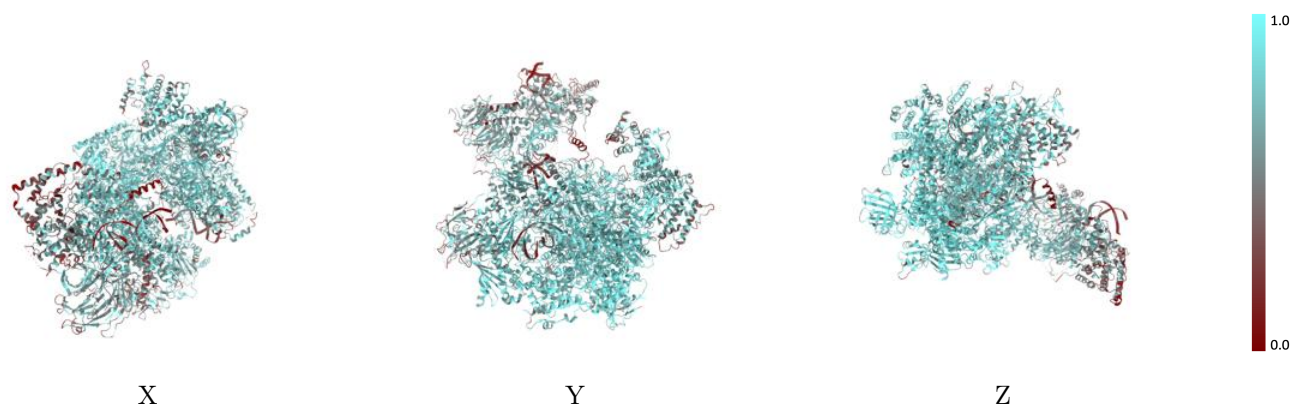
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



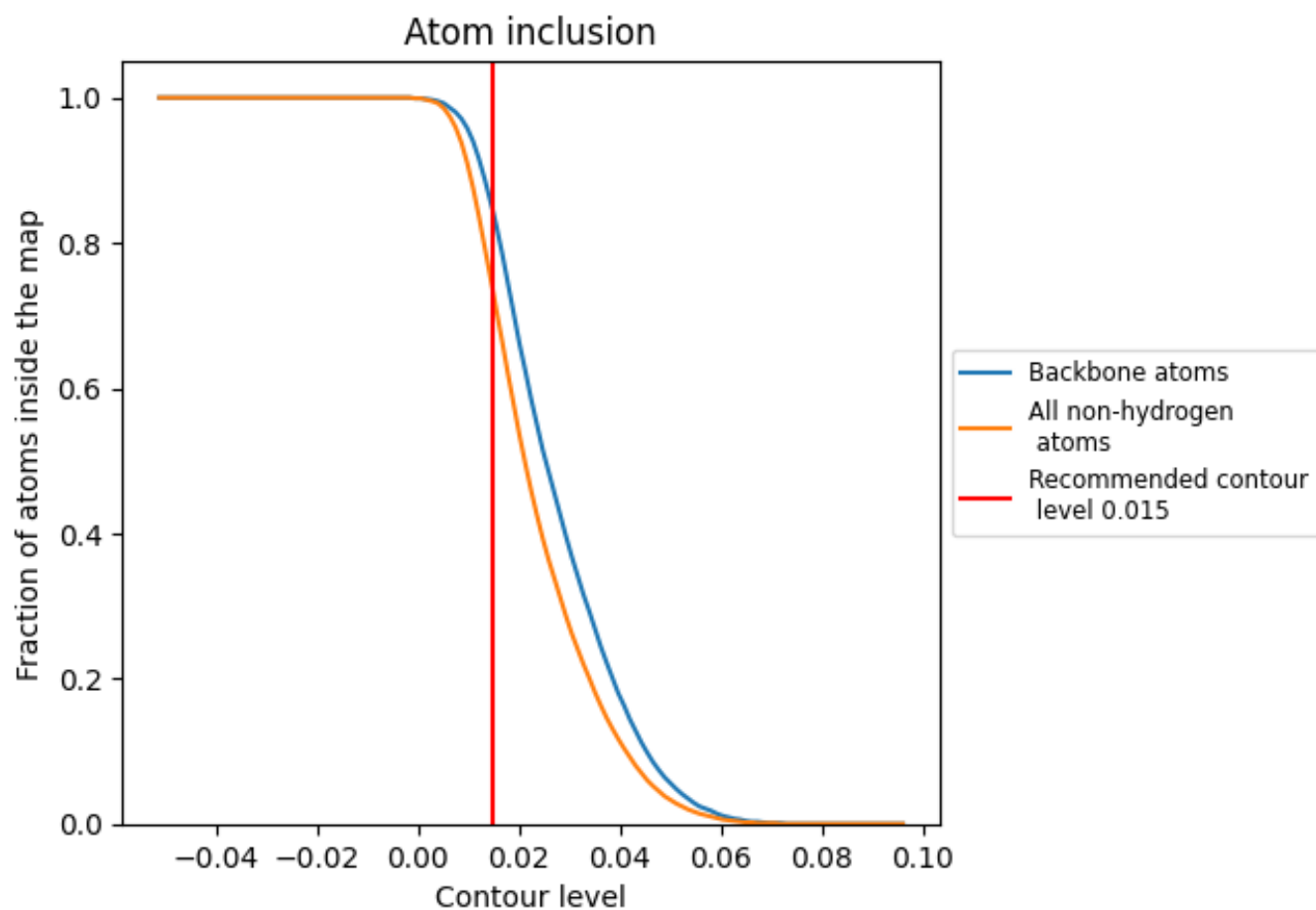
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).















































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 73% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.4700
A	 0.8240	 0.5190
B	 0.8370	 0.5300
C	 0.8380	 0.5240
D	 0.7820	 0.4860
E	 0.8080	 0.4930
F	 0.8340	 0.5350
G	 0.7690	 0.4810
H	 0.8340	 0.5230
I	 0.7190	 0.4400
J	 0.8970	 0.5470
K	 0.8610	 0.5260
L	 0.8670	 0.5250
M	 0.5600	 0.4260
N	 0.5080	 0.4250
O	 0.6510	 0.4250
P	 0.5200	 0.3670
Q	 0.5630	 0.3860
R	 0.6710	 0.4270
S	 0.4390	 0.2710
T	 0.4270	 0.2650
U	 0.3070	 0.2440
V	 0.3250	 0.2830

