wwPDB EM Validation Summary Report

Dec 18, 2022 – 09:23 am GMT

PDB ID	:	7ADE
EMDB ID	:	EMD-11725
Title	:	Transcription termination complex IVa
Authors	:	Said, N.; Hilal, T.; Loll, B.; Wahl, C.M.
Deposited on	:	2020-09-14
Resolution	:	4.20 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:

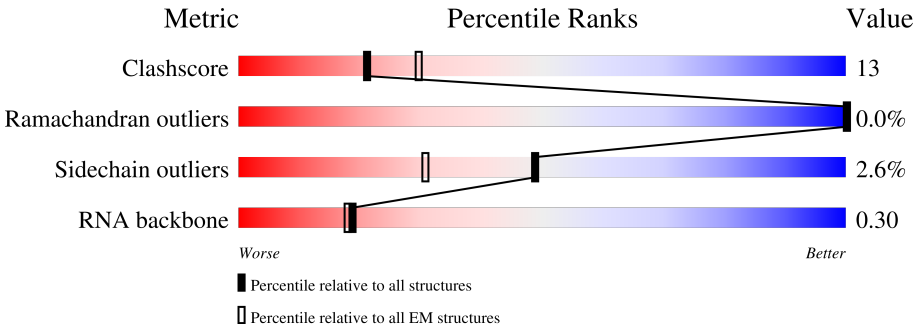
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	419	94% 5%
1	b	419	94% 5%
1	c	419	94% 5%
1	d	419	94% 5%
1	e	419	6% 94% 5%
1	f	419	9% 94% 5%
2	A	497	48% 70% 29%

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Mol	Chain	Length	Quality of chain
3	U	329	47% 24% 29%
3	V	329	10% 72% 26%
4	W	91	78% 63% 24% 13%
5	X	1342	71% 29%
6	Y	1416	13% 67% 27% 5%
7	L	50	14% 16% 56% 26%
8	K	50	6% 10% 34% 54%
9	R	99	6% 11% 15% 6% 68%

2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 51553 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 Transcription termination factor Rho.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	f	417	Total 3280	C 2065	N 581	O 617	S 17	0	0
1	a	417	Total 3280	C 2065	N 581	O 617	S 17	0	0
1	b	417	Total 3280	C 2065	N 581	O 617	S 17	0	0
1	c	417	Total 3280	C 2065	N 581	O 617	S 17	0	0
1	d	417	Total 3280	C 2065	N 581	O 617	S 17	0	0
1	e	417	Total 3280	C 2065	N 581	O 617	S 17	0	0

- Molecule 2 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	495	Total 3852	C 2396	N 669	O 774	S 13	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP C3SSN7
A	0	ALA	-	expression tag	UNP C3SSN7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	U	235	Total 1825	C 1135	N 325	O 359	S 6	0	0
3	V	321	Total 2504	C 1566	N 441	O 489	S 8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	W	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Y	1343	Total	C	N	O	S	0	0
			10431	6553	1854	1974	50		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	1408	LEU	-	expression tag	UNP C3SIA2
Y	1409	GLU	-	expression tag	UNP C3SIA2
Y	1410	VAL	-	expression tag	UNP C3SIA2
Y	1411	HIS	-	expression tag	UNP C3SIA2
Y	1412	HIS	-	expression tag	UNP C3SIA2
Y	1413	HIS	-	expression tag	UNP C3SIA2
Y	1414	HIS	-	expression tag	UNP C3SIA2
Y	1415	HIS	-	expression tag	UNP C3SIA2
Y	1416	HIS	-	expression tag	UNP C3SIA2

- Molecule 7 is a DNA chain called tDNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	37	Total	C	N	O	P	0	0
			741	355	131	218	37		

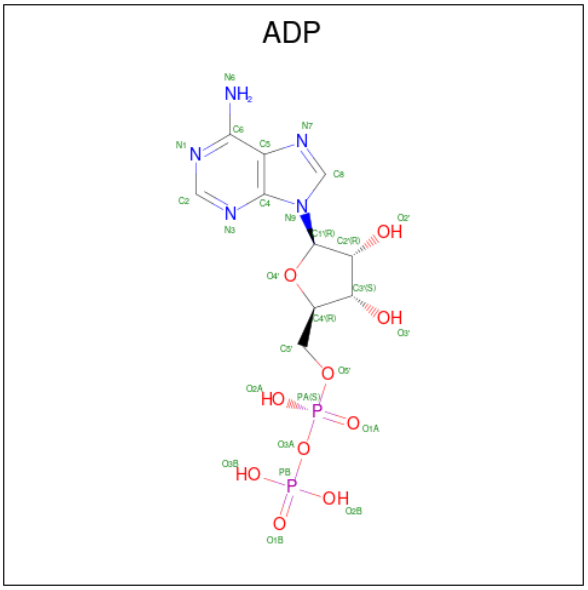
- Molecule 8 is a DNA chain called ntDNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	23	Total	C	N	O	P	0	0
			474	225	96	130	23		

- Molecule 9 is a RNA chain called rut RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	R	32	Total	C	N	O	P	0	0
			674	302	117	223	32		

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
10	a	1	Total	C	N	O	P	0
			27	10	5	10	2	
10	b	1	Total	C	N	O	P	0
			27	10	5	10	2	
10	c	1	Total	C	N	O	P	0
			27	10	5	10	2	
10	d	1	Total	C	N	O	P	0
			27	10	5	10	2	
10	e	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 11 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
11	a	1	Total	Mg	0
			1	1	
11	b	1	Total	Mg	0
			1	1	
11	c	1	Total	Mg	0
			1	1	

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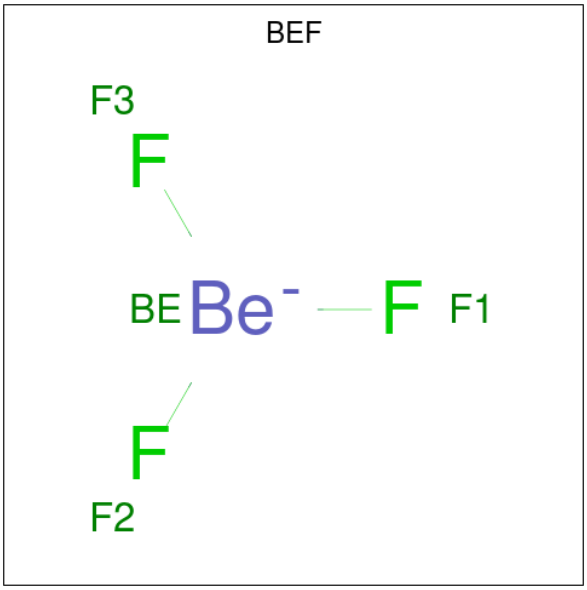
Mol	Chain	Residues	Atoms	AltConf
11	d	1	Total Mg 1 1	0
11	e	1	Total Mg 1 1	0
11	Y	1	Total Mg 1 1	0

- Molecule 12 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF_3).



Mol	Chain	Residues	Atoms	AltConf
12	a	1	Total Be F 4 1 3	0
12	b	1	Total Be F 4 1 3	0
12	c	1	Total Be F 4 1 3	0
12	d	1	Total Be F 4 1 3	0
12	e	1	Total Be F 4 1 3	0

- Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
13	Y	2	Total Zn 2 2	0

- Molecule 14 is water.

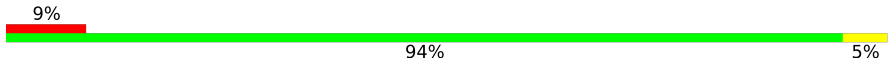
Mol	Chain	Residues	Atoms	AltConf
14	a	3	Total O 3 3	0
14	b	3	Total O 3 3	0
14	c	3	Total O 3 3	0
14	d	3	Total O 3 3	0
14	e	3	Total O 3 3	0

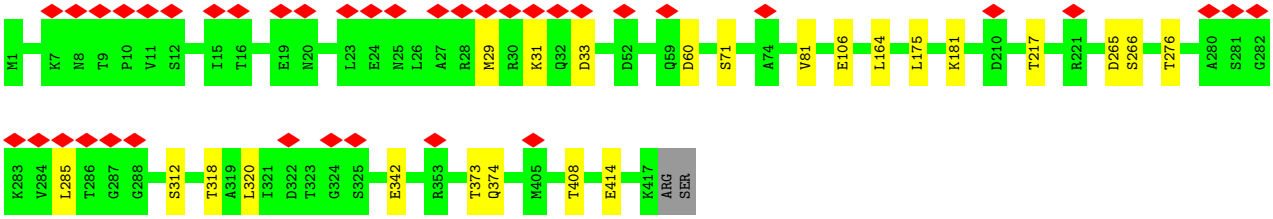
3 Residue-property plots (i)

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

• Molecule 1: Transcription termination factor Rho

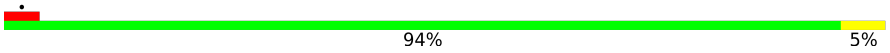
Chain f:

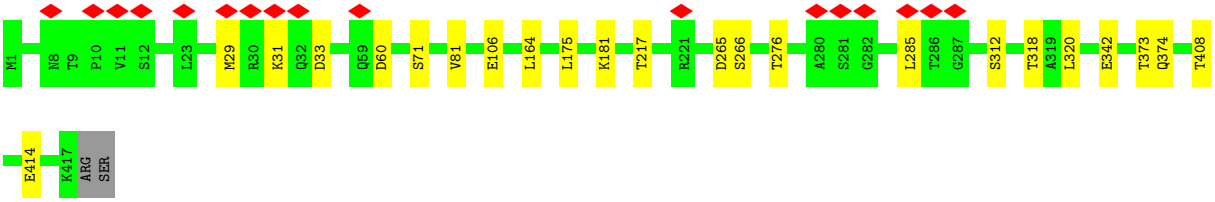




• Molecule 1: Transcription termination factor Rho

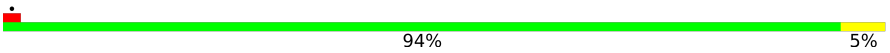
Chain a:

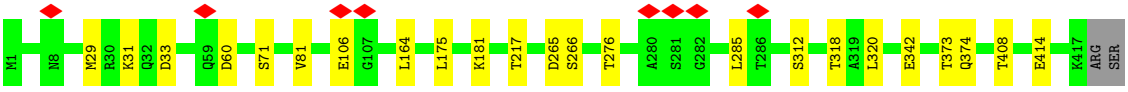




• Molecule 1: Transcription termination factor Rho

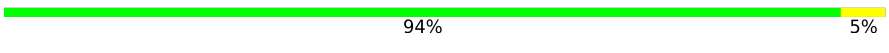
Chain b:

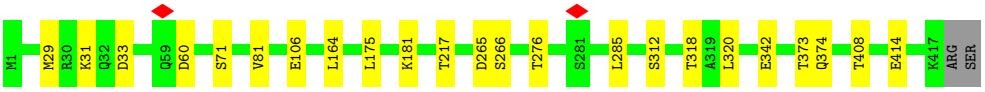




• Molecule 1: Transcription termination factor Rho

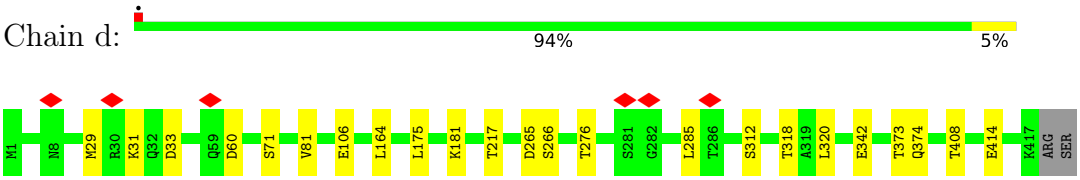
Chain c:





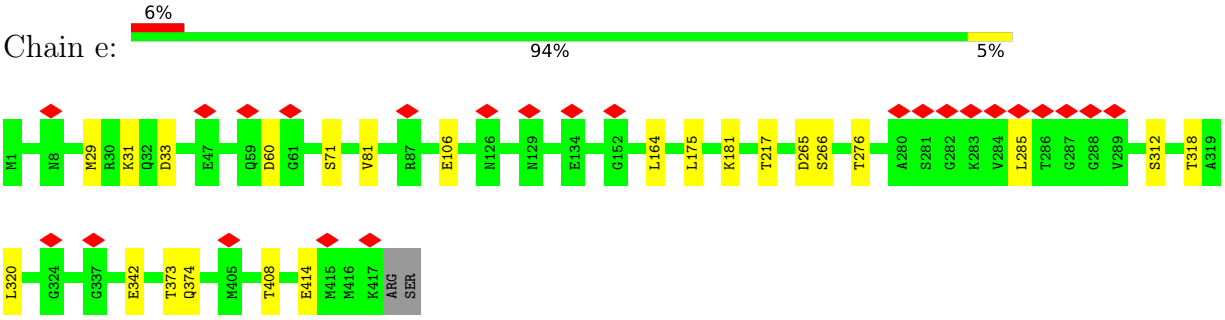
• Molecule 1: Transcription termination factor Rho

Chain d:



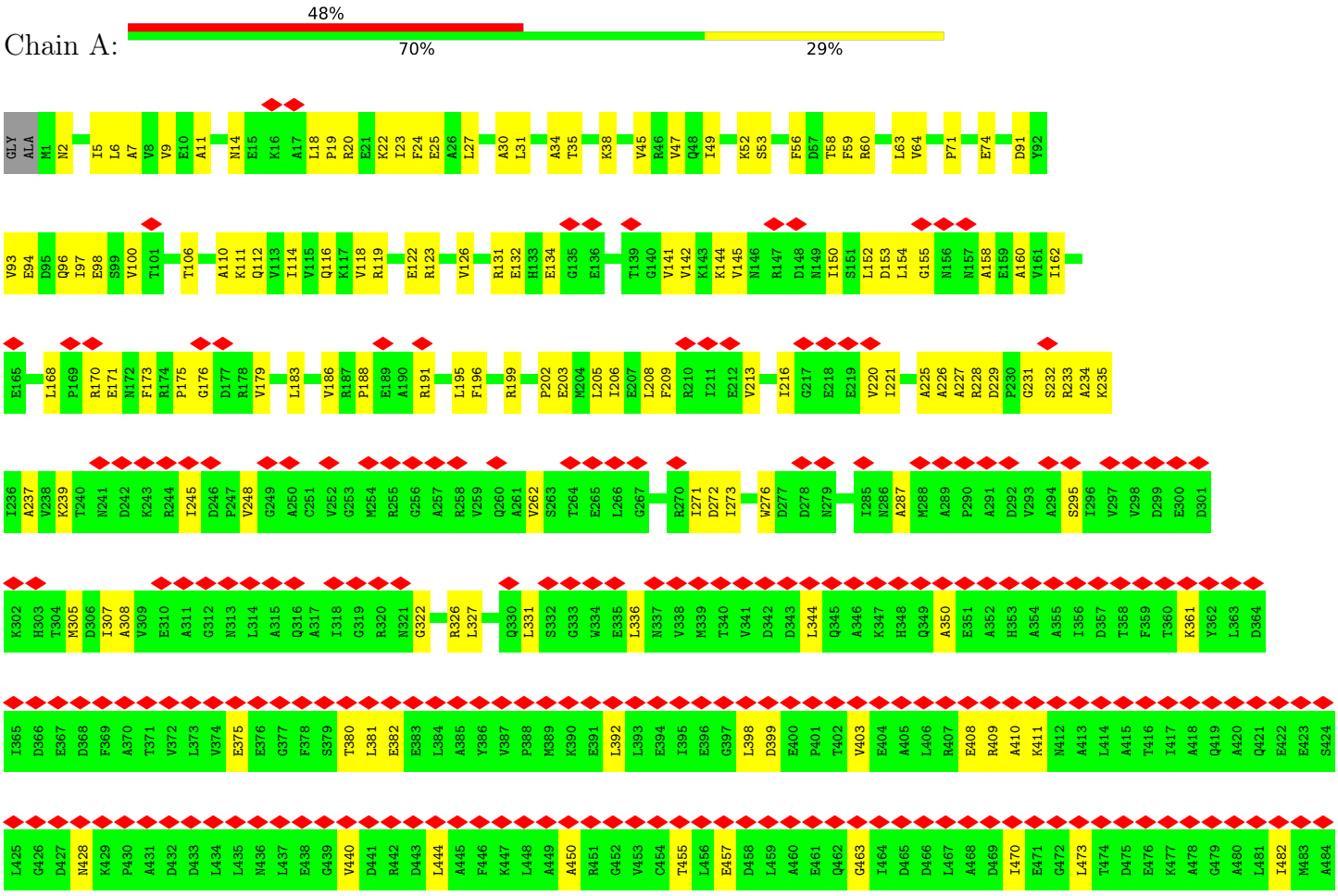
• Molecule 1: Transcription termination factor Rho

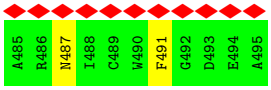
Chain e:



• Molecule 2: Transcription termination/antitermination protein NusA

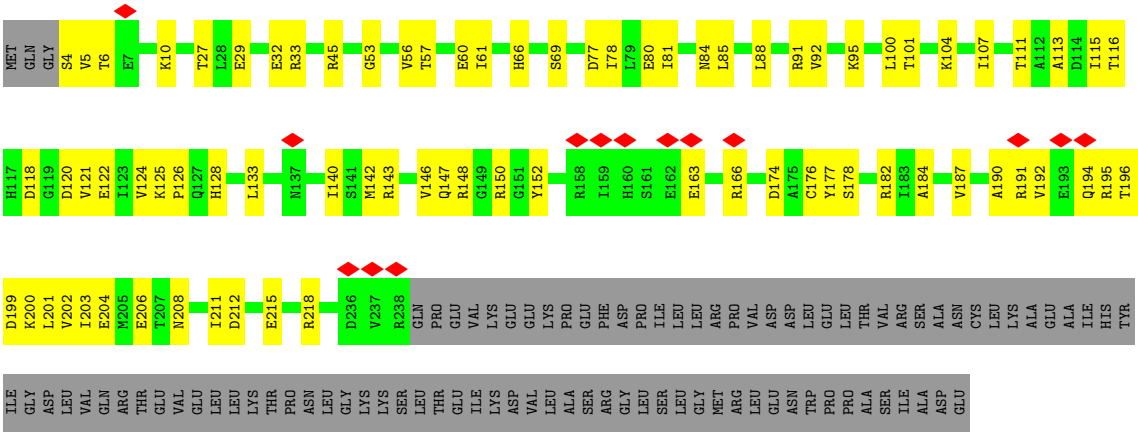
Chain A:





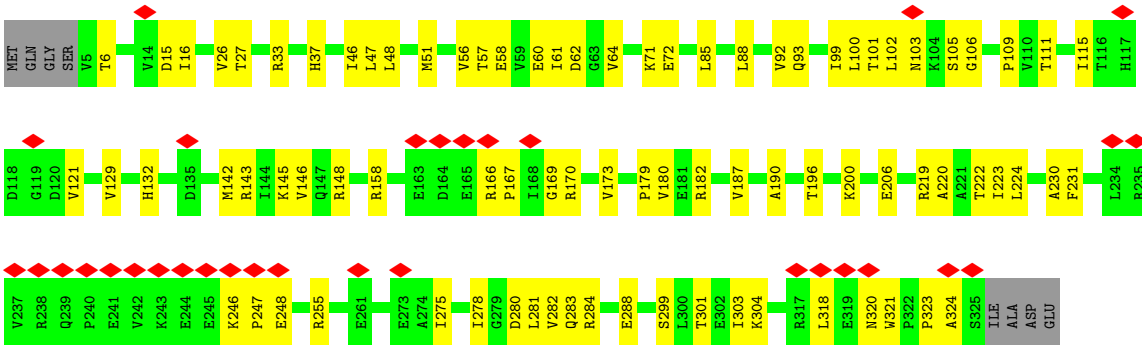
• Molecule 3: DNA-directed RNA polymerase subunit alpha

Chain U:



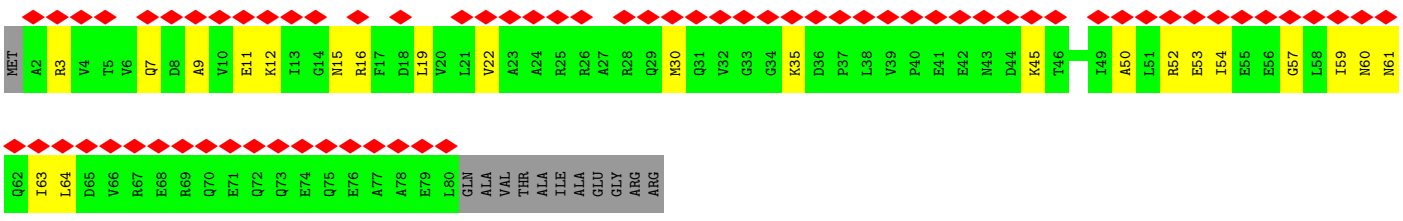
• Molecule 3: DNA-directed RNA polymerase subunit alpha

Chain V:



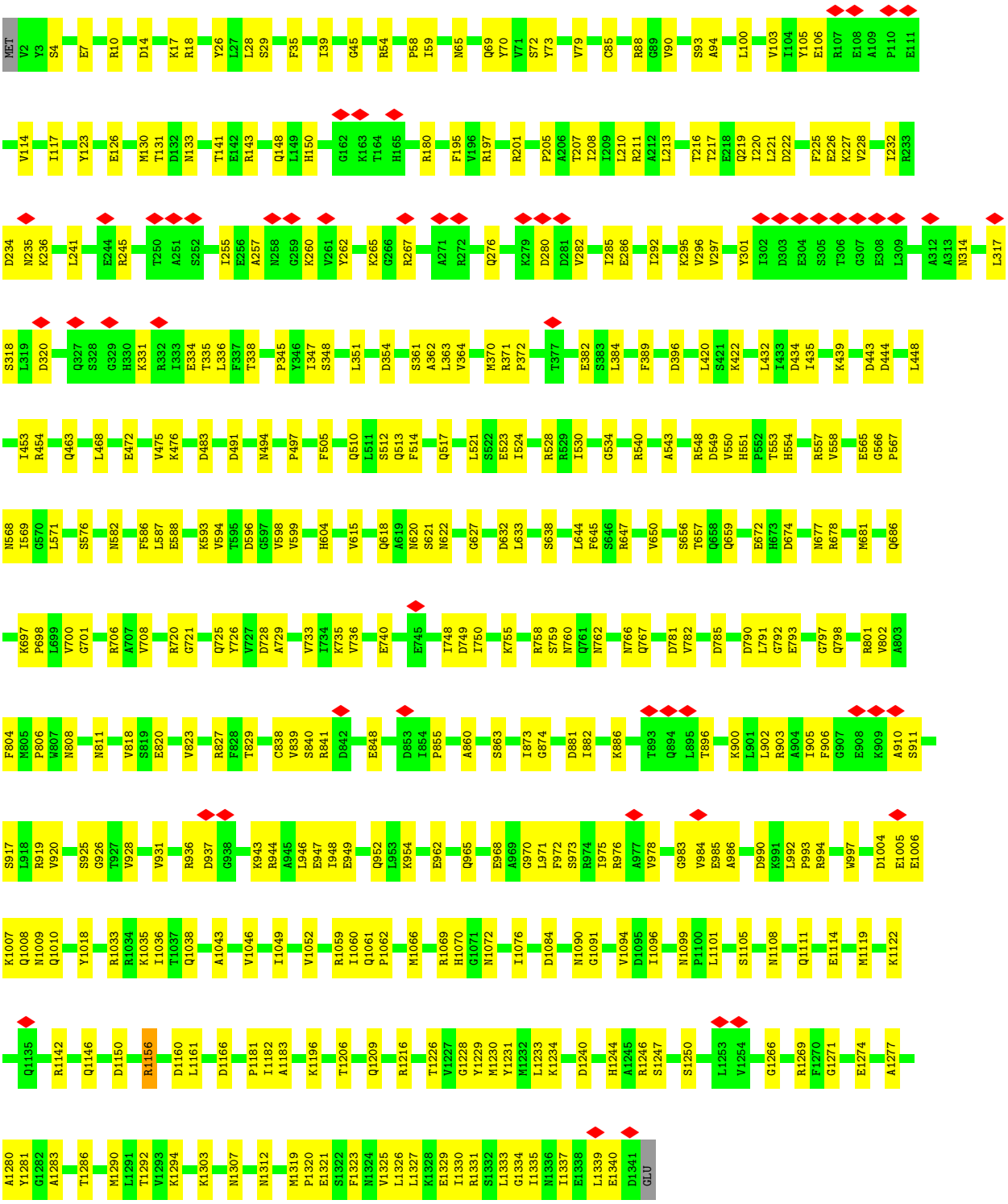
• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain W:

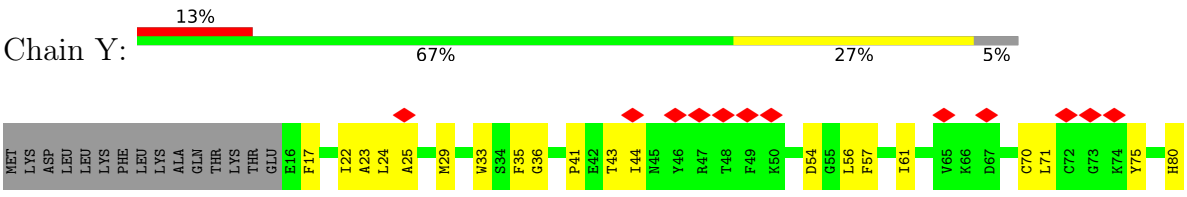


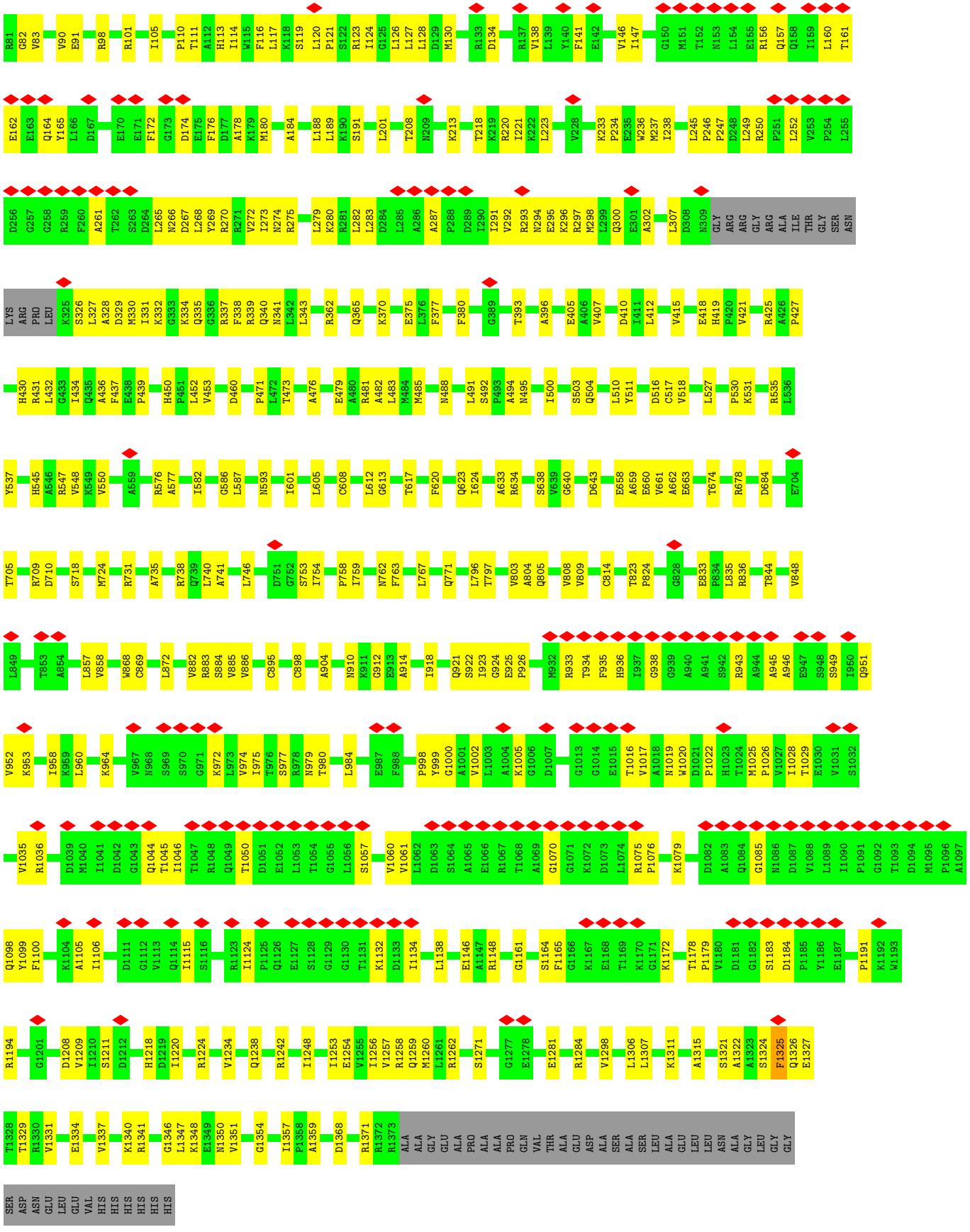
• Molecule 5: DNA-directed RNA polymerase subunit beta

Chain X:

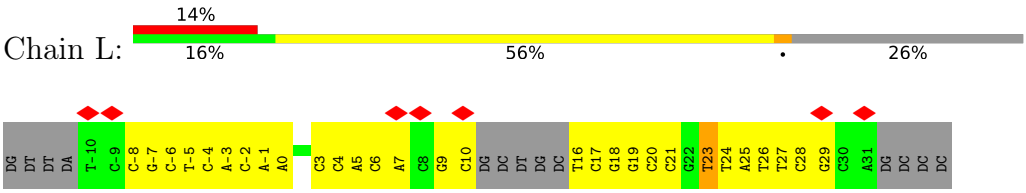


• Molecule 6: DNA-directed RNA polymerase subunit beta'

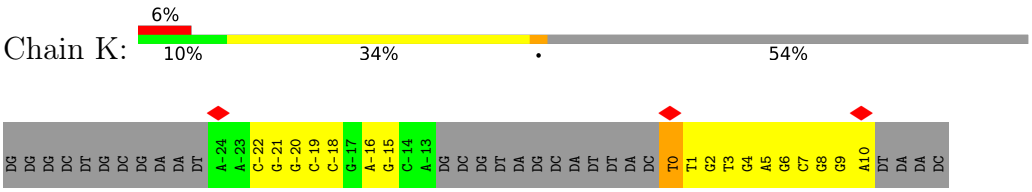




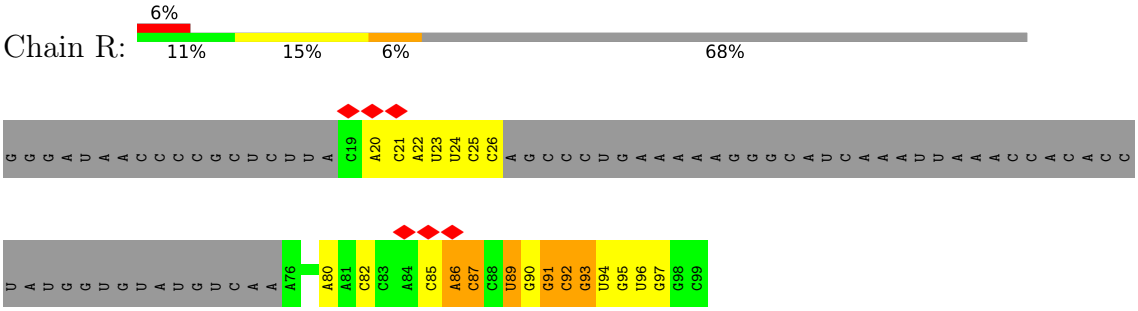
• Molecule 7: tDNA



• Molecule 8: ntDNA



• Molecule 9: rut RNA



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42083	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	8000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.323	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	372.0, 372.0, 372.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.24, 1.24, 1.24	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	a	0.25	0/3329	0.43	0/4483
1	b	0.25	0/3329	0.43	0/4483
1	c	0.25	0/3329	0.43	0/4483
1	d	0.25	0/3329	0.43	0/4483
1	e	0.25	0/3329	0.43	0/4483
1	f	0.25	0/3329	0.43	0/4483
2	A	0.23	0/3897	0.45	0/5273
3	U	0.23	0/1847	0.43	0/2503
3	V	0.23	0/2538	0.44	0/3441
4	W	0.23	0/629	0.43	0/847
5	X	0.25	0/10736	0.42	0/14487
6	Y	0.24	0/10590	0.44	0/14301
7	L	0.65	0/827	1.03	1/1262 (0.1%)
8	K	0.63	0/533	0.94	1/812 (0.1%)
9	R	0.25	0/750	1.07	7/1162 (0.6%)
All	All	0.26	0/52321	0.47	9/70986 (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
6	Y	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	R	85	C	N1-C2-O2	8.80	124.18	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	R	85	C	C2-N1-C1'	8.74	128.42	118.80
9	R	85	C	N3-C2-O2	-7.04	116.97	121.90
9	R	89	U	N1-C2-O2	6.51	127.36	122.80
9	R	85	C	C6-N1-C1'	-6.00	113.59	120.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	Y	120	LEU	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	3280	0	3358	0	0
1	b	3280	0	3358	0	0
1	c	3280	0	3358	0	0
1	d	3280	0	3358	0	0
1	e	3280	0	3358	0	0
1	f	3280	0	3359	0	0
2	A	3852	0	3835	101	0
3	U	1825	0	1853	57	0
3	V	2504	0	2558	55	0
4	W	627	0	634	17	0
5	X	10567	0	10585	288	0
6	Y	10431	0	10636	284	0
7	L	741	0	417	37	0
8	K	474	0	258	19	0
9	R	674	0	347	13	0
10	a	27	0	12	0	0
10	b	27	0	12	0	0
10	c	27	0	12	0	0
10	d	27	0	12	0	0
10	e	27	0	12	0	0
11	Y	1	0	0	0	0
11	a	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	b	1	0	0	0	0
11	c	1	0	0	0	0
11	d	1	0	0	0	0
11	e	1	0	0	0	0
12	a	4	0	0	0	0
12	b	4	0	0	0	0
12	c	4	0	0	0	0
12	d	4	0	0	0	0
12	e	4	0	0	0	0
13	Y	2	0	0	0	0
14	a	3	0	0	0	0
14	b	3	0	0	0	0
14	c	3	0	0	0	0
14	d	3	0	0	0	0
14	e	3	0	0	0	0
All	All	51553	0	51332	818	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 13.

The worst 5 of 818 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)
3:V:167:PRO:HD2	3:V:170:ARG:HG2	1.58	0.85
5:X:1327:LEU:HB3	5:X:1337:ILE:HG21	1.58	0.85
6:Y:287:ALA:HB1	6:Y:291:ILE:HG21	1.57	0.84
2:A:142:VAL:HG12	2:A:152:LEU:HG	1.60	0.83
3:U:107:ILE:HA	3:U:133:LEU:O	1.78	0.82

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	415/419 (99%)	406 (98%)	9 (2%)	0	100	100
1	b	415/419 (99%)	405 (98%)	10 (2%)	0	100	100
1	c	415/419 (99%)	406 (98%)	9 (2%)	0	100	100
1	d	415/419 (99%)	406 (98%)	9 (2%)	0	100	100
1	e	415/419 (99%)	406 (98%)	9 (2%)	0	100	100
1	f	415/419 (99%)	406 (98%)	9 (2%)	0	100	100
2	A	493/497 (99%)	450 (91%)	43 (9%)	0	100	100
3	U	233/329 (71%)	227 (97%)	6 (3%)	0	100	100
3	V	319/329 (97%)	292 (92%)	27 (8%)	0	100	100
4	W	77/91 (85%)	74 (96%)	3 (4%)	0	100	100
5	X	1338/1342 (100%)	1252 (94%)	86 (6%)	0	100	100
6	Y	1339/1416 (95%)	1266 (94%)	72 (5%)	1 (0%)	51	85
All	All	6289/6518 (96%)	5996 (95%)	292 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	Y	1325	PHE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	357/359 (99%)	334 (94%)	23 (6%)	17	45
1	b	357/359 (99%)	334 (94%)	23 (6%)	17	45
1	c	357/359 (99%)	334 (94%)	23 (6%)	17	45
1	d	357/359 (99%)	334 (94%)	23 (6%)	17	45
1	e	357/359 (99%)	334 (94%)	23 (6%)	17	45
1	f	357/359 (99%)	334 (94%)	23 (6%)	17	45
2	A	409/409 (100%)	409 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	U	203/286 (71%)	203 (100%)	0	100 100
3	V	280/286 (98%)	279 (100%)	1 (0%)	91 94
4	W	67/75 (89%)	67 (100%)	0	100 100
5	X	1155/1157 (100%)	1154 (100%)	1 (0%)	93 97
6	Y	1123/1177 (95%)	1123 (100%)	0	100 100
All	All	5379/5544 (97%)	5239 (97%)	140 (3%)	49 67

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	e	29	MET
1	e	71	SER
1	e	312	SER
1	b	33	ASP
1	b	31	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
5	X	41	GLN
6	Y	1244	GLN
5	X	659	GLN
6	Y	897	HIS
6	Y	365	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	R	30/99 (30%)	12 (40%)	1 (3%)

5 of 12 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	R	23	U
9	R	24	U
9	R	25	C
9	R	26	C
9	R	80	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	R	23	U

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
10	ADP	e	1000	11	24,29,29	0.97	1 (4%)	29,45,45	1.44	4 (13%)
12	BEF	c	1002	-	0,3,3	-	-	-		
12	BEF	a	1002	-	0,3,3	-	-	-		
12	BEF	b	1002	-	0,3,3	-	-	-		
10	ADP	d	1000	11	24,29,29	0.95	1 (4%)	29,45,45	1.42	4 (13%)
10	ADP	c	1000	11	24,29,29	0.95	1 (4%)	29,45,45	1.47	4 (13%)
12	BEF	e	1002	-	0,3,3	-	-	-		
12	BEF	d	1002	-	0,3,3	-	-	-		
10	ADP	a	1000	11	24,29,29	0.96	1 (4%)	29,45,45	1.45	4 (13%)
10	ADP	b	1000	11	24,29,29	0.96	1 (4%)	29,45,45	1.44	4 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	ADP	e	1000	11	-	3/12/32/32	0/3/3/3
10	ADP	d	1000	11	-	2/12/32/32	0/3/3/3
10	ADP	c	1000	11	-	4/12/32/32	0/3/3/3
10	ADP	a	1000	11	-	3/12/32/32	0/3/3/3
10	ADP	b	1000	11	-	3/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	a	1000	ADP	C5-C4	2.52	1.47	1.40
10	d	1000	ADP	C5-C4	2.50	1.47	1.40
10	b	1000	ADP	C5-C4	2.48	1.47	1.40
10	c	1000	ADP	C5-C4	2.48	1.47	1.40
10	e	1000	ADP	C5-C4	2.47	1.47	1.40

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	d	1000	ADP	C3'-C2'-C1'	3.54	106.31	100.98
10	c	1000	ADP	C3'-C2'-C1'	3.52	106.28	100.98
10	b	1000	ADP	C3'-C2'-C1'	3.48	106.21	100.98
10	a	1000	ADP	C3'-C2'-C1'	3.46	106.18	100.98
10	e	1000	ADP	C3'-C2'-C1'	3.43	106.15	100.98

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	b	1000	ADP	C5'-O5'-PA-O3A
10	c	1000	ADP	C5'-O5'-PA-O1A
10	c	1000	ADP	C5'-O5'-PA-O3A
10	e	1000	ADP	C5'-O5'-PA-O1A
10	a	1000	ADP	C5'-O5'-PA-O3A

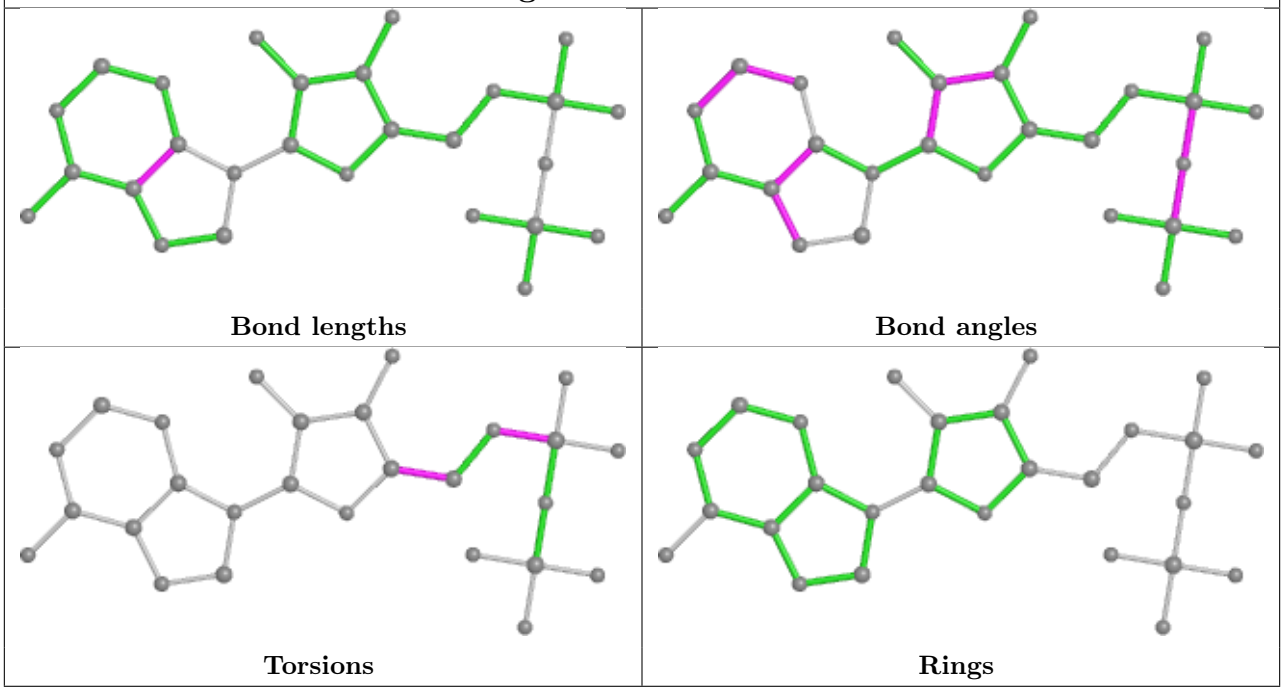
There are no ring outliers.

No monomer is involved in short contacts.

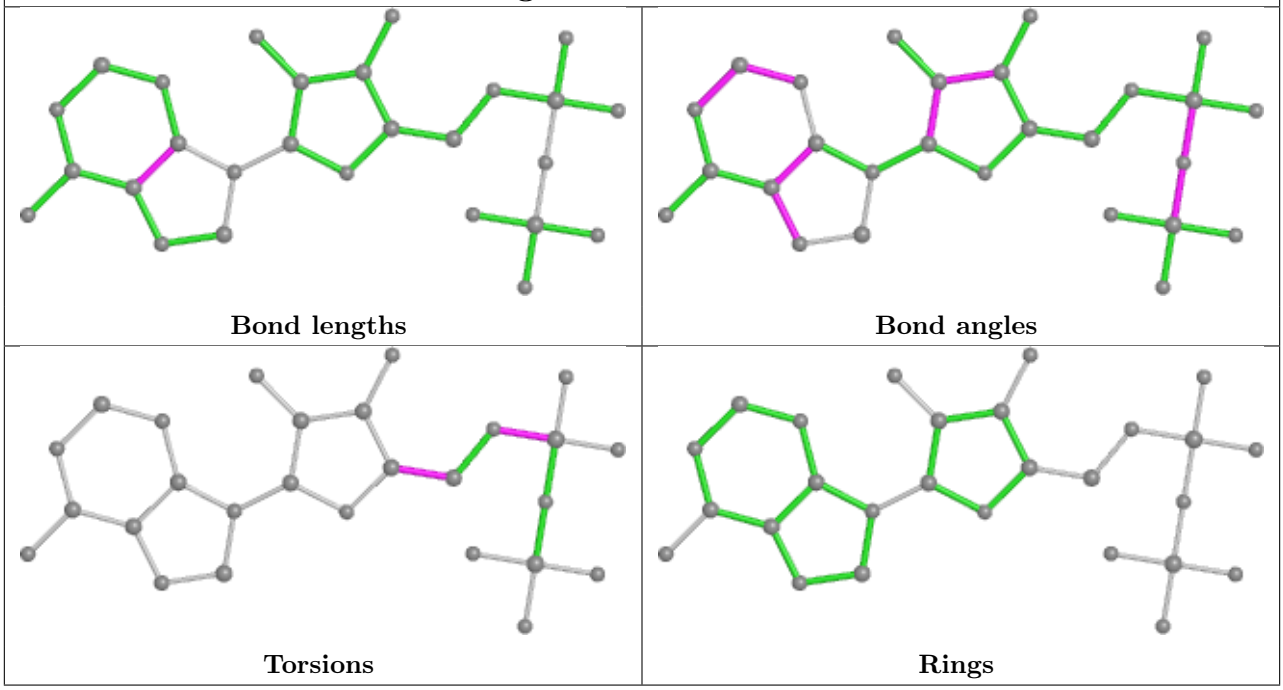
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

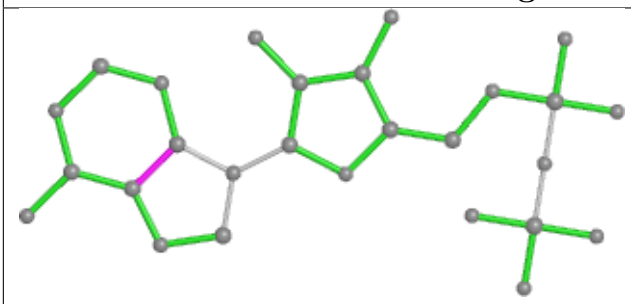
Ligand ADP e 1000



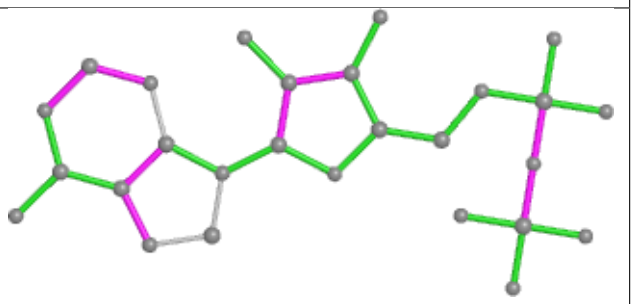
Ligand ADP d 1000



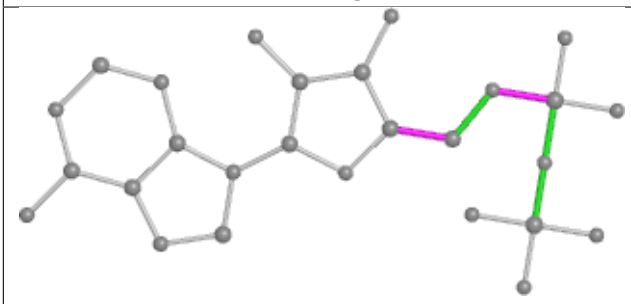
Ligand ADP c 1000



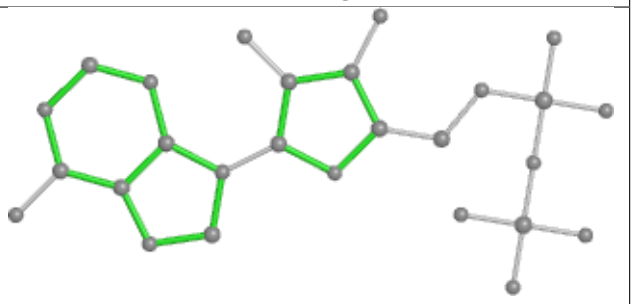
Bond lengths



Bond angles

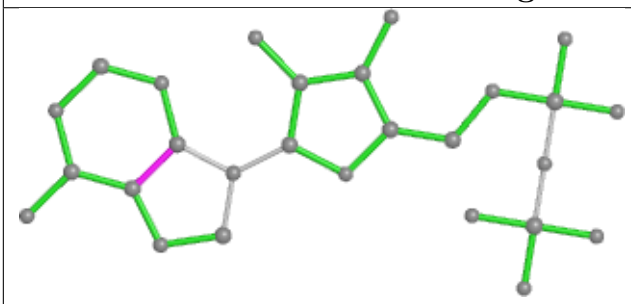


Torsions

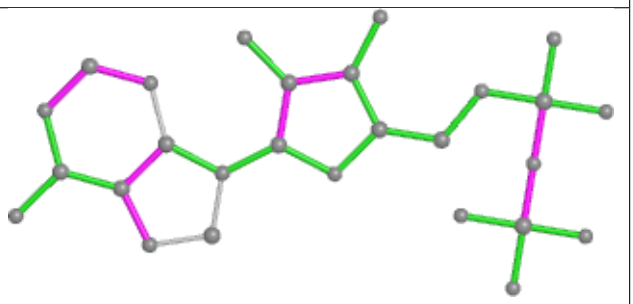


Rings

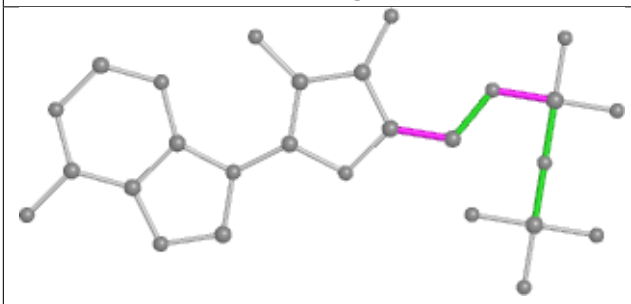
Ligand ADP a 1000



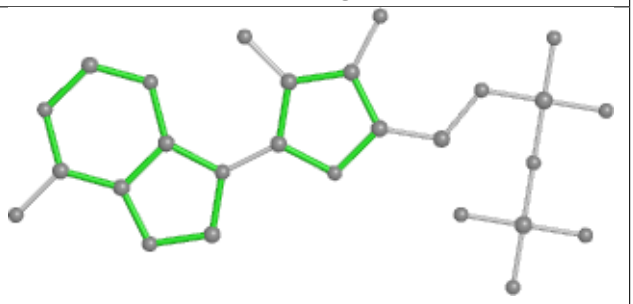
Bond lengths



Bond angles

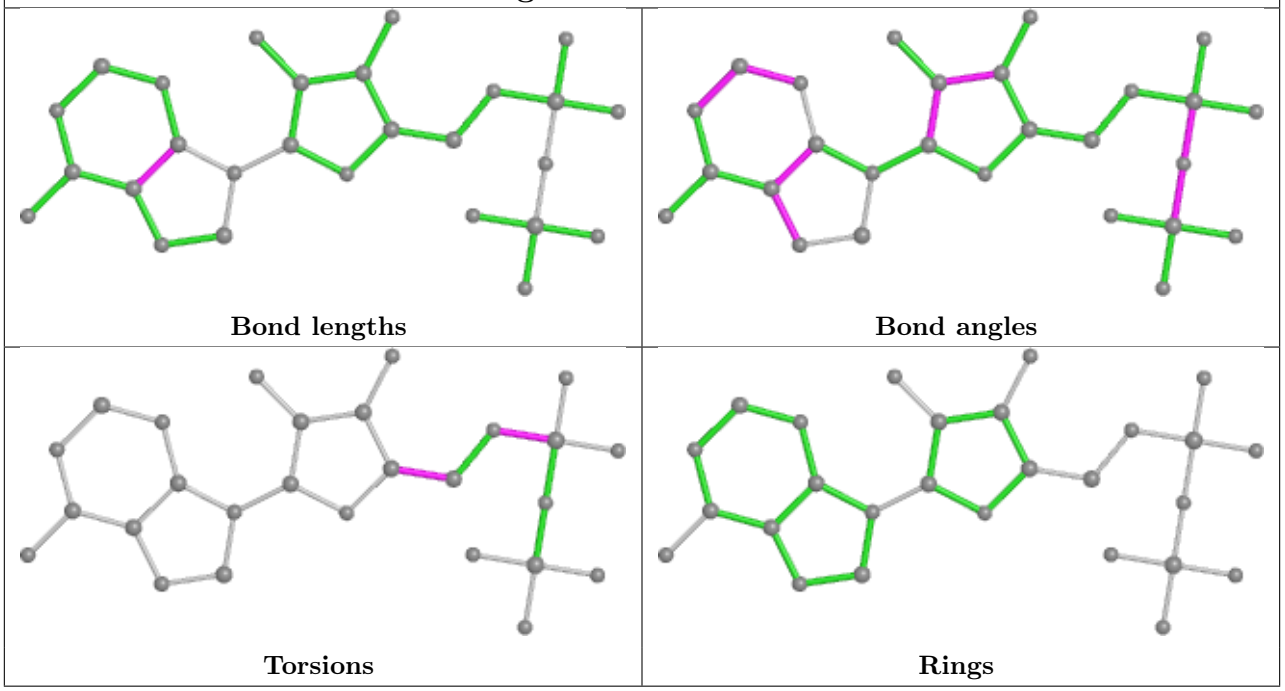


Torsions



Rings

Ligand ADP b 1000



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.

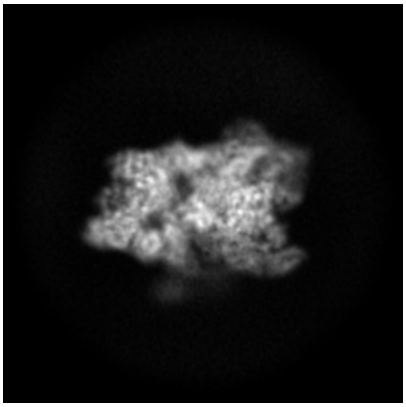
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11725. These allow visual inspection of the internal detail of the map and identification of artifacts.

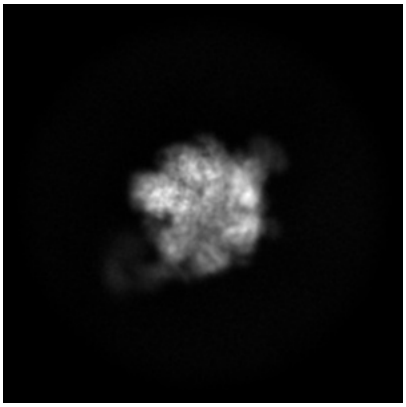
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

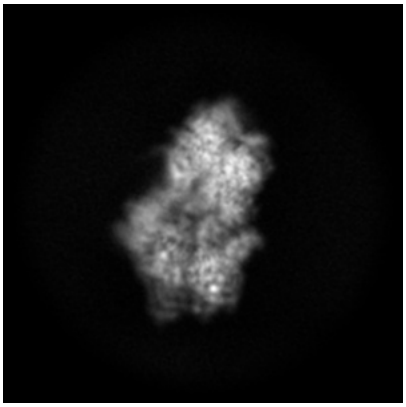
6.1.1 Primary map



X



Y

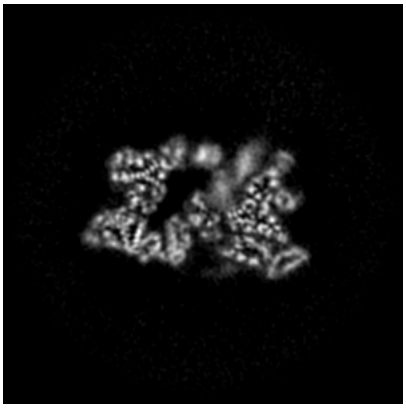


Z

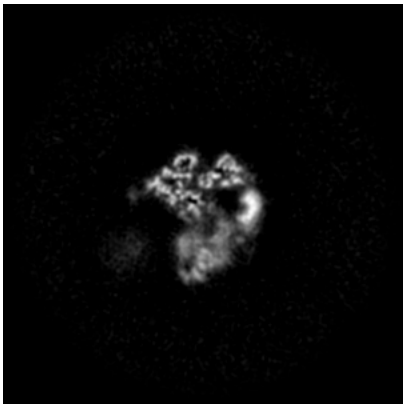
The images above show the map projected in three orthogonal directions.

6.2 Central slices

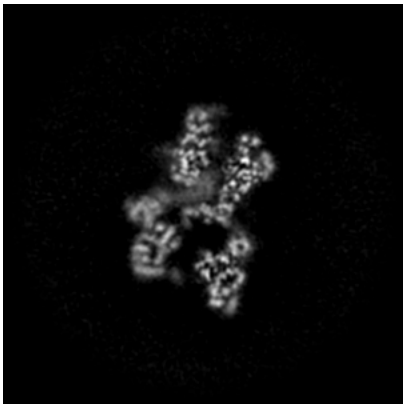
6.2.1 Primary map



X Index: 150



Y Index: 150

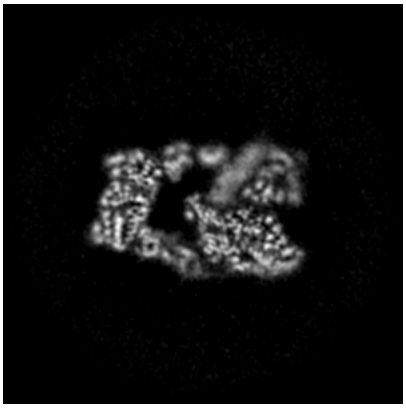


Z Index: 150

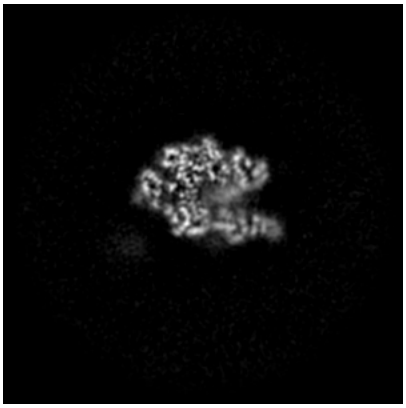
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

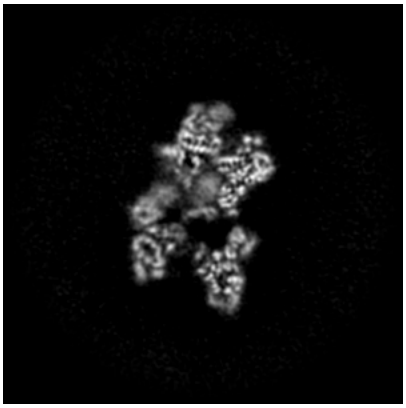
6.3.1 Primary map



X Index: 157



Y Index: 171

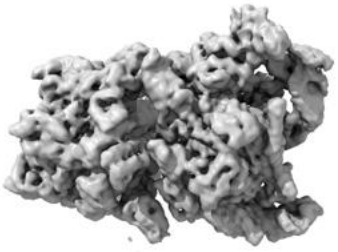


Z Index: 155

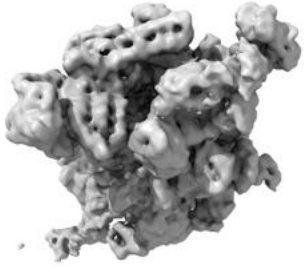
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

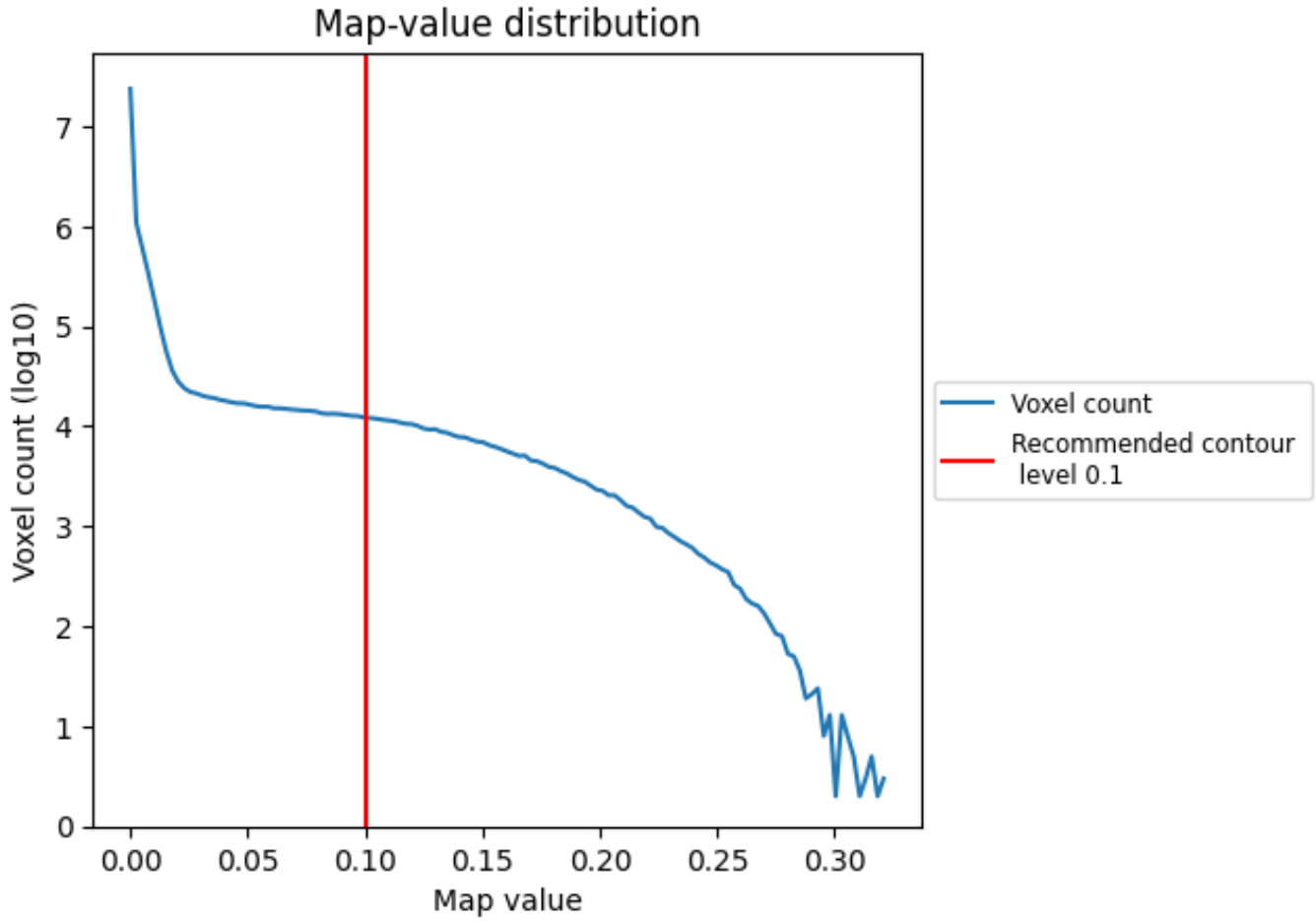
6.5 Mask visualisation (i)

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

7 Map analysis

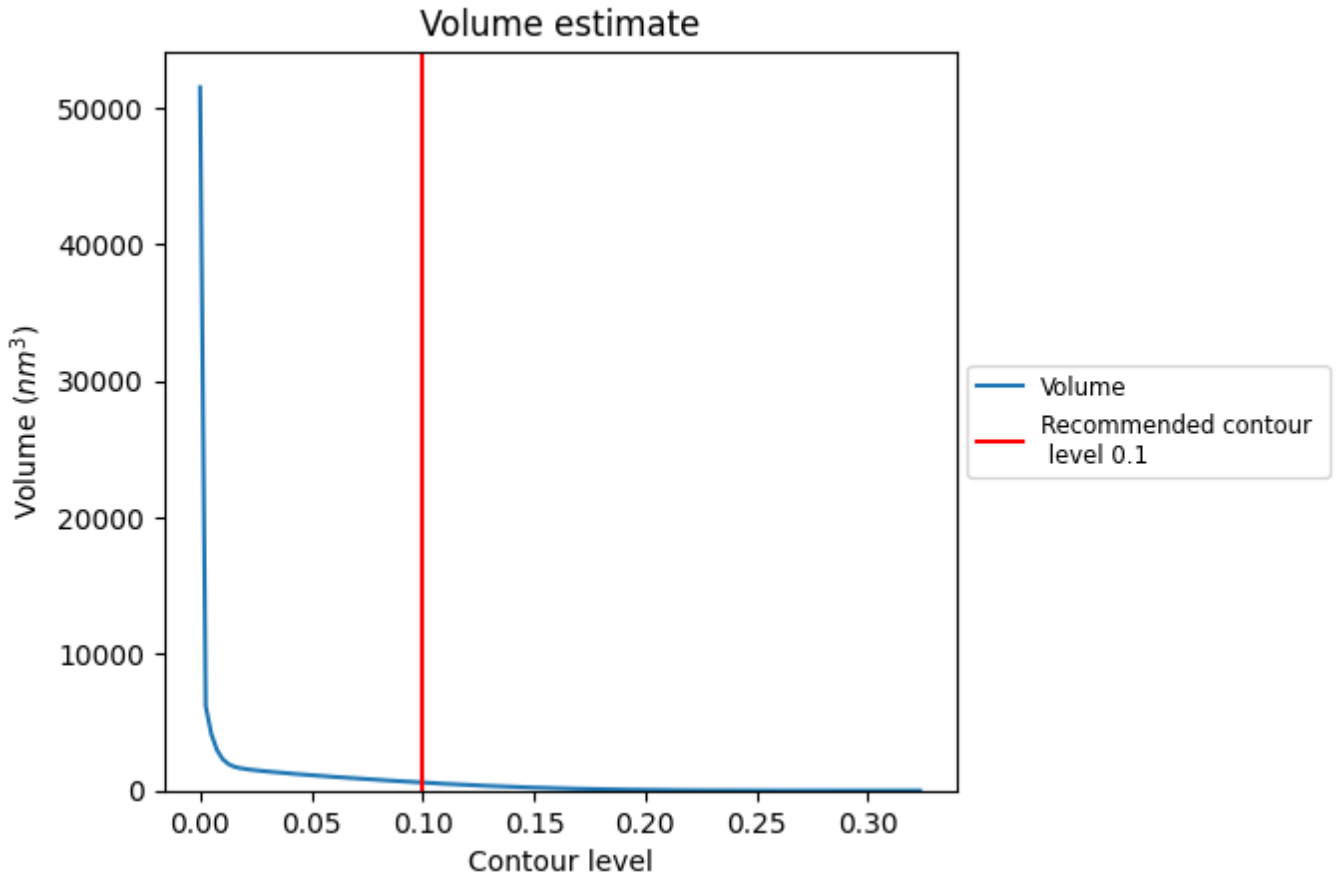
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

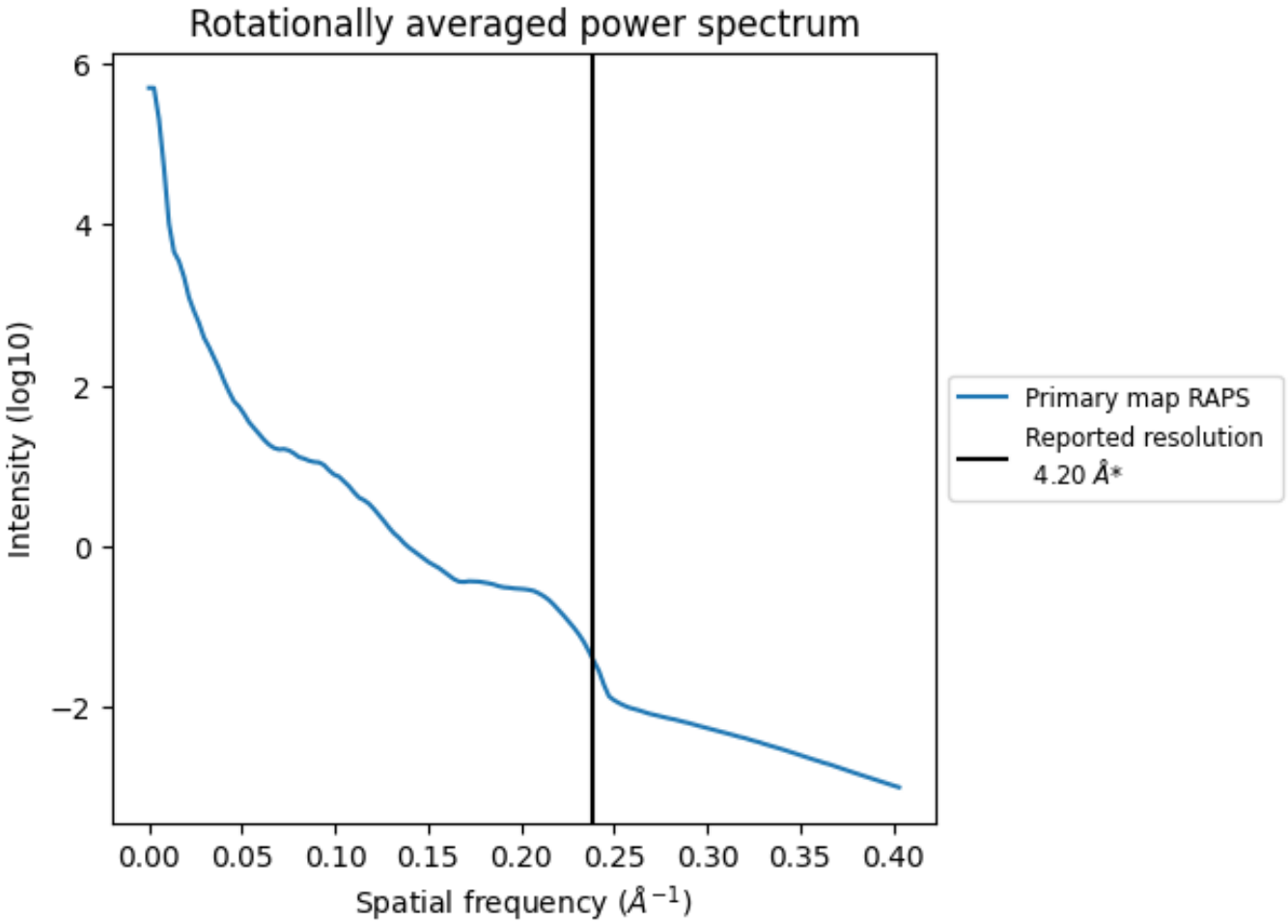
7.2 Volume estimate (i)



The volume at the recommended contour level is 585 nm^3; this corresponds to an approximate mass of 529 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)

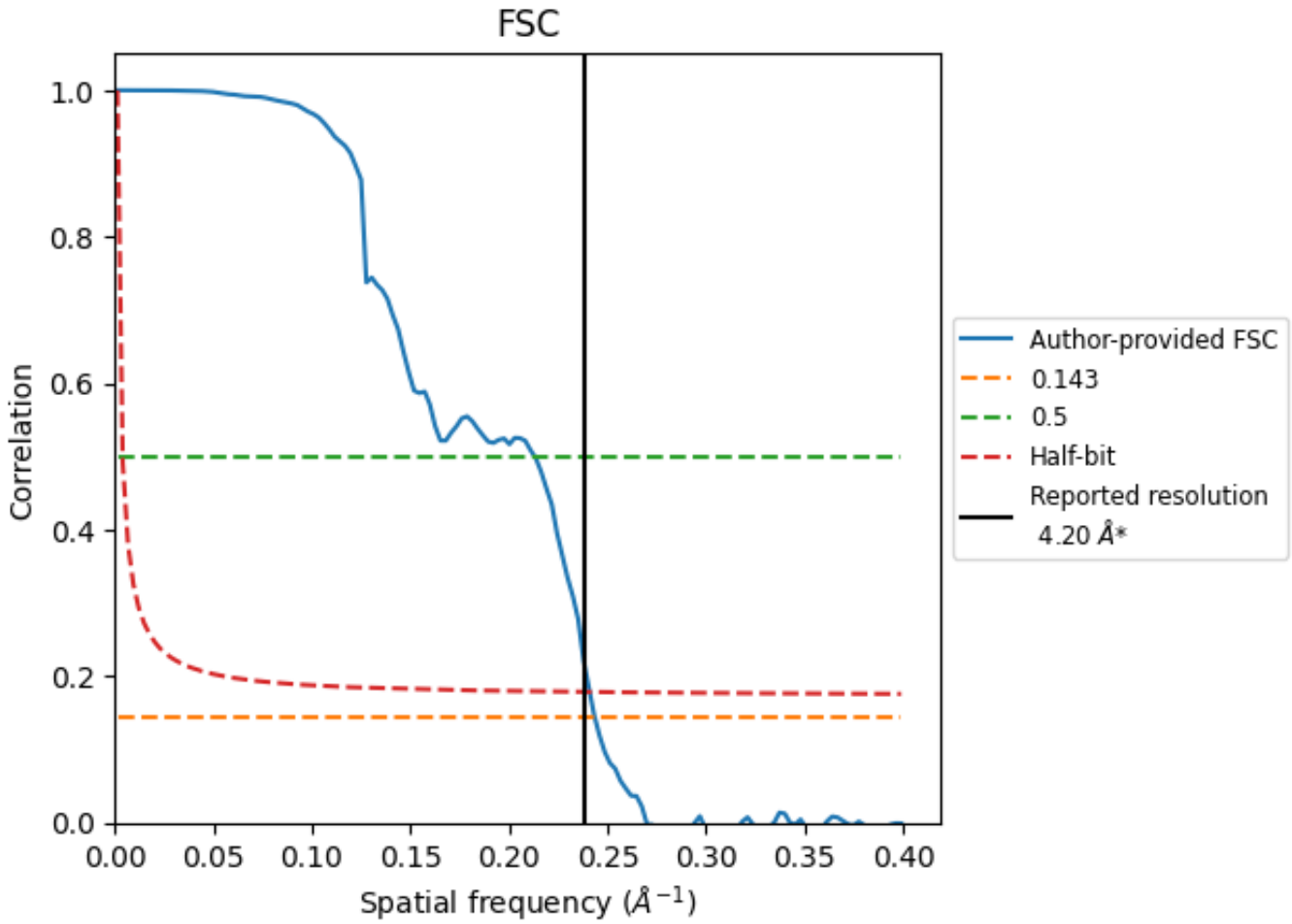


*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

8.2 Resolution estimates (i)

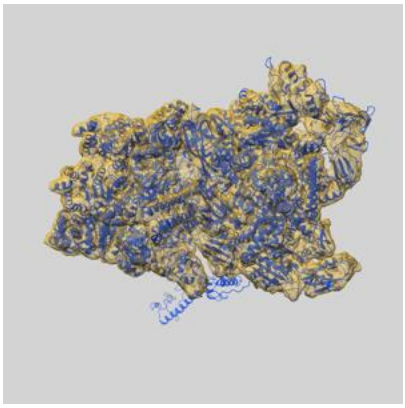
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.11	4.69	4.15
Unmasked-calculated*	-	-	-

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

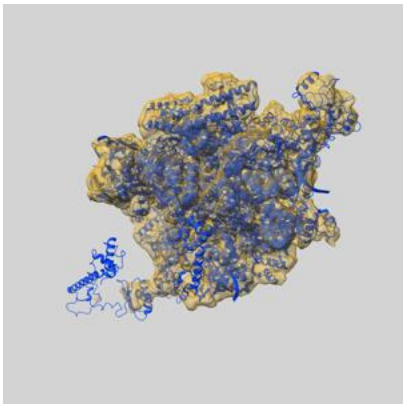
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-11725 and PDB model 7ADE. Per-residue inclusion information can be found in section 3 on page 9.

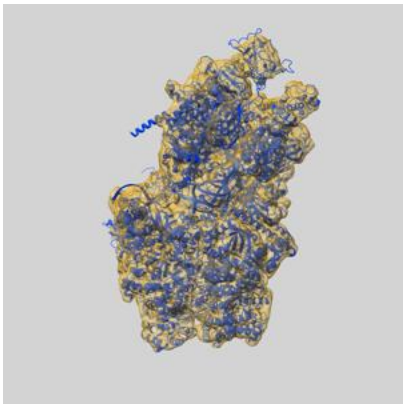
9.1 Map-model overlay



X



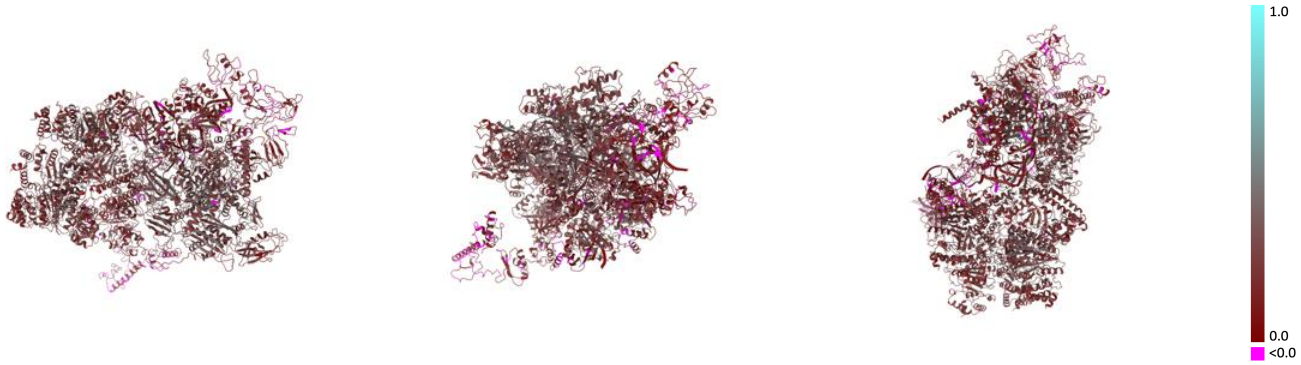
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

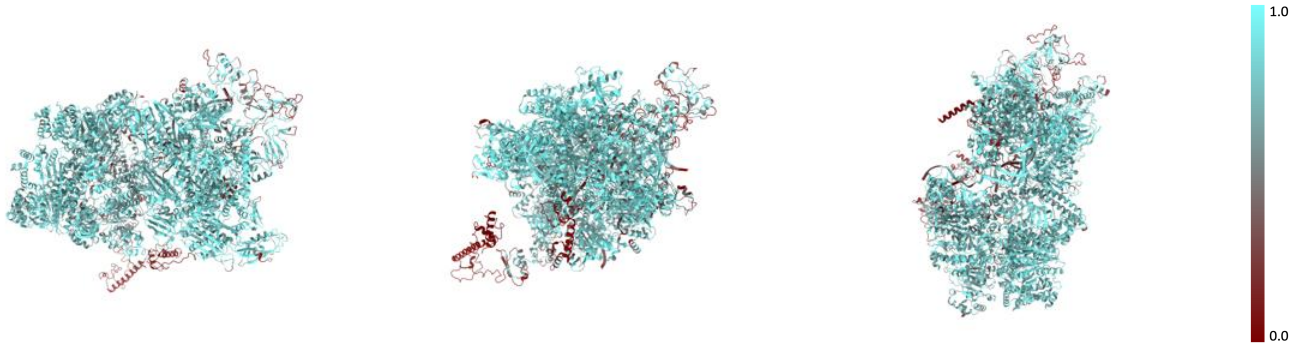
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

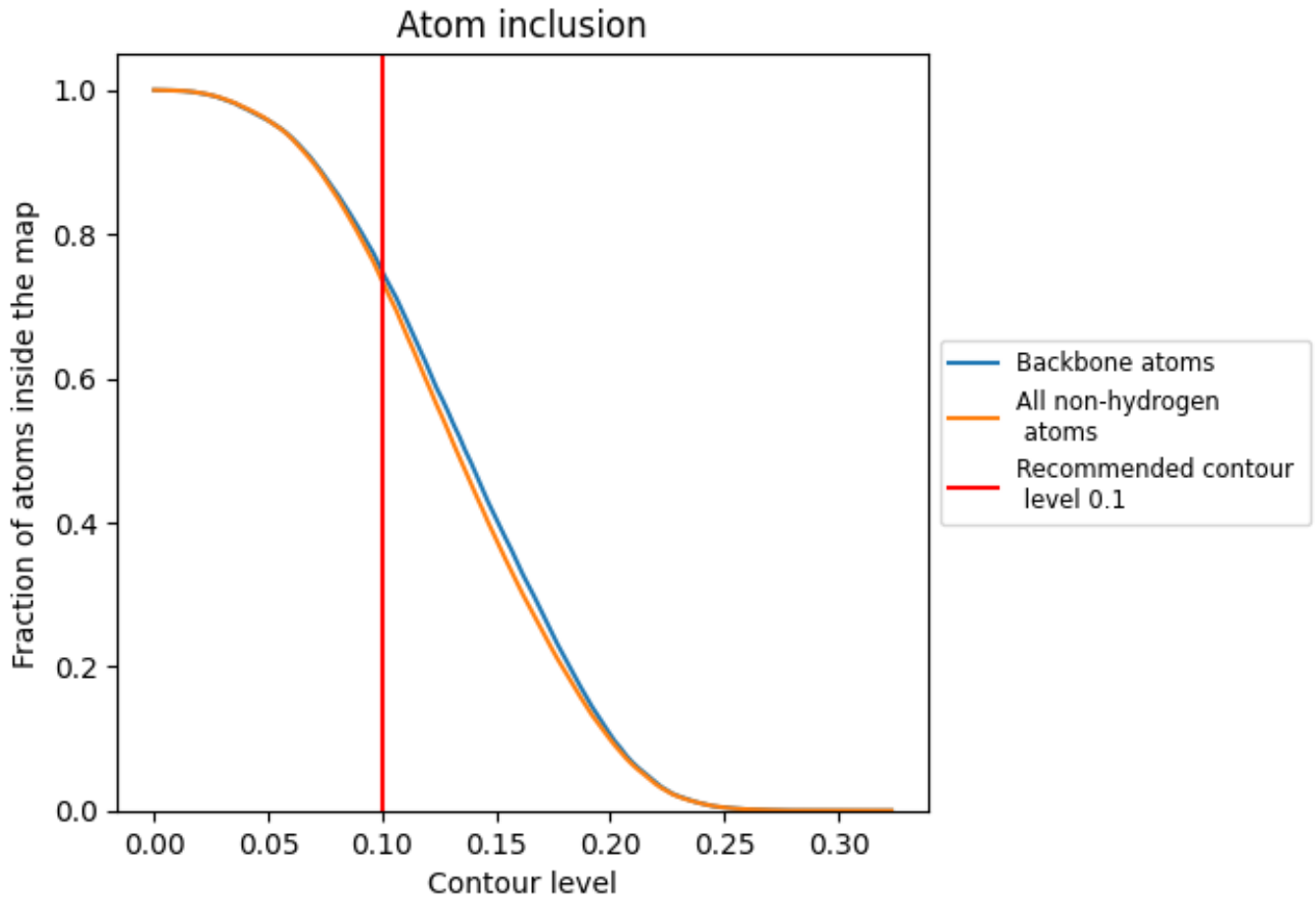
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 75% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7349	0.2350
A	0.4219	0.1450
K	0.7806	0.1130
L	0.7139	0.0770
R	0.7507	0.1610
U	0.8022	0.3050
V	0.7541	0.2480
W	0.1391	0.2090
X	0.8063	0.2790
Y	0.7279	0.2230
a	0.7924	0.2420
b	0.8262	0.2670
c	0.8226	0.2620
d	0.8096	0.2550
e	0.7523	0.2120
f	0.7355	0.2000