



wwPDB EM Validation Summary Report ⓘ

Mar 1, 2026 – 04:55 PM UTC

PDB ID : 6Z9S / pdb_00006z9s
EMDB ID : EMD-11090
Title : Transcription termination intermediate complex 4
Authors : Said, N.; Hilal, T.; Loll, B.; Wahl, M.C.
Deposited on : 2020-06-04
Resolution : 4.40 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

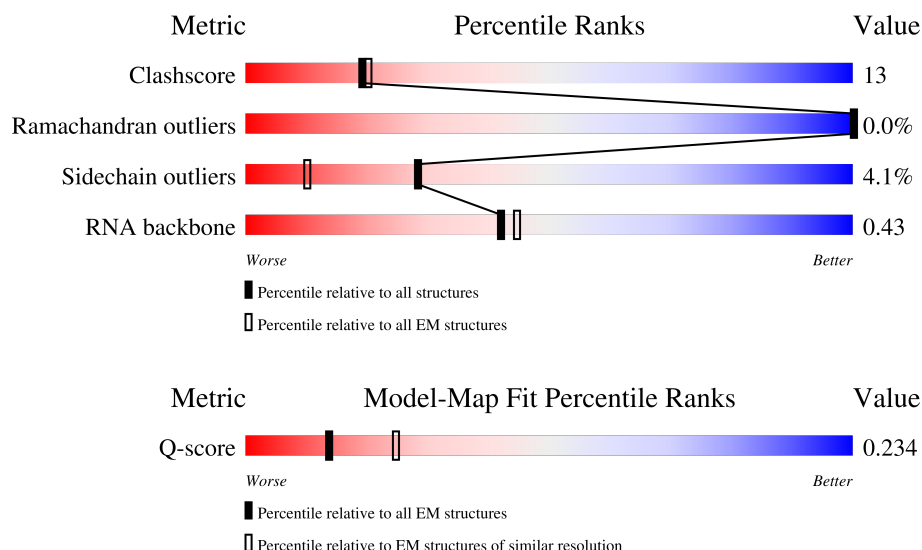
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.40 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.



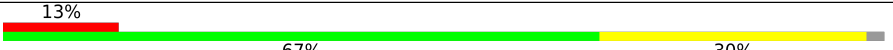
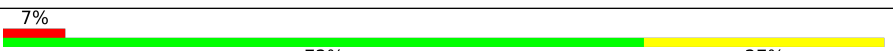
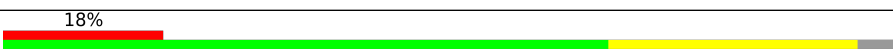
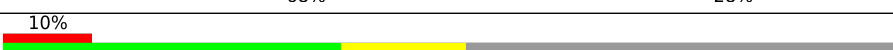
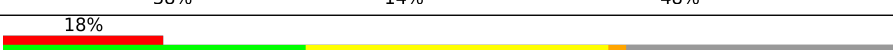
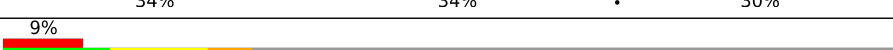
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3132 (3.91 - 4.90)

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	419	7% 66% 28% 5%
1	b	419	64% 30% 5%
1	c	419	65% 29% 5%

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Mol	Chain	Length	Quality of chain
1	d	419	
1	e	419	
1	f	419	
2	A	497	
3	U	329	
3	V	329	
4	W	91	
5	X	1342	
6	Y	1416	
7	K	50	
8	L	50	
9	R	99	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 51608 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	C	N	O	S	0	0
			3280	2065	581	617	17		
1	a	417	Total	C	N	O	S	0	0
			3280	2065	581	617	17		
1	b	417	Total	C	N	O	S	0	0
			3280	2065	581	617	17		
1	c	417	Total	C	N	O	S	0	0
			3280	2065	581	617	17		
1	d	417	Total	C	N	O	S	0	0
			3280	2065	581	617	17		
1	e	417	Total	C	N	O	S	0	0
			3280	2065	581	617	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	495	Total	C	N	O	S	0	0
			3850	2395	669	773	13		

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	C	N	O	S	0	0
			1825	1135	325	359	6		
3	V	321	Total	C	N	O	S	0	0
			2504	1566	441	489	8		

- 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	1358	Total	C	N	O	S	0	0
			10545	6620	1883	1992	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 non template strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	26	Total	C	N	O	P	0	0
			538	254	103	155	26		

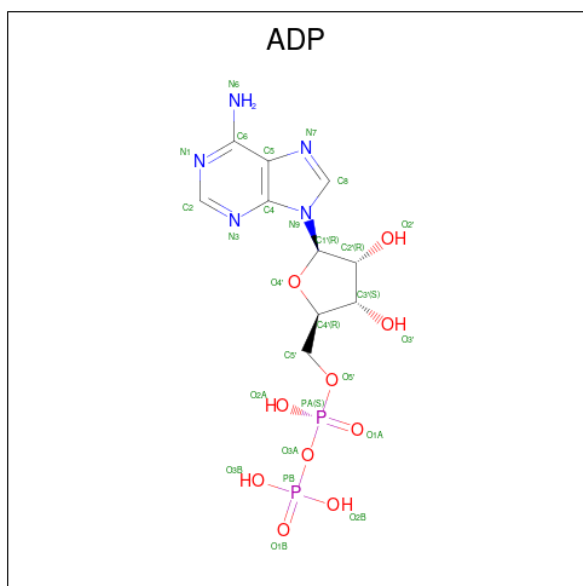
- Molecule 8 is a DNA chain called template strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	35	Total	C	N	O	P	0	0
			704	335	127	208	34		

- Molecule 9 is a RNA chain called rut RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	R	28	Total	C	N	O	P	0	0
			590	264	103	195	28		

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: 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 (CCD ID: MG) (formula: Mg).

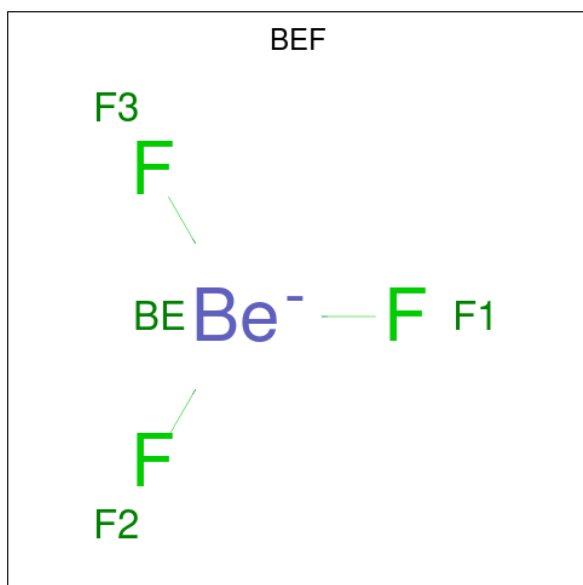
Mol	Chain	Residues	Atoms		AltConf
11	a	1	Total	Mg	0
			1	1	
11	b	1	Total	Mg	0
			1	1	
11	c	1	Total	Mg	0
			1	1	
11	d	1	Total	Mg	0
			1	1	

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

- Molecule 12 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF₃).



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

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

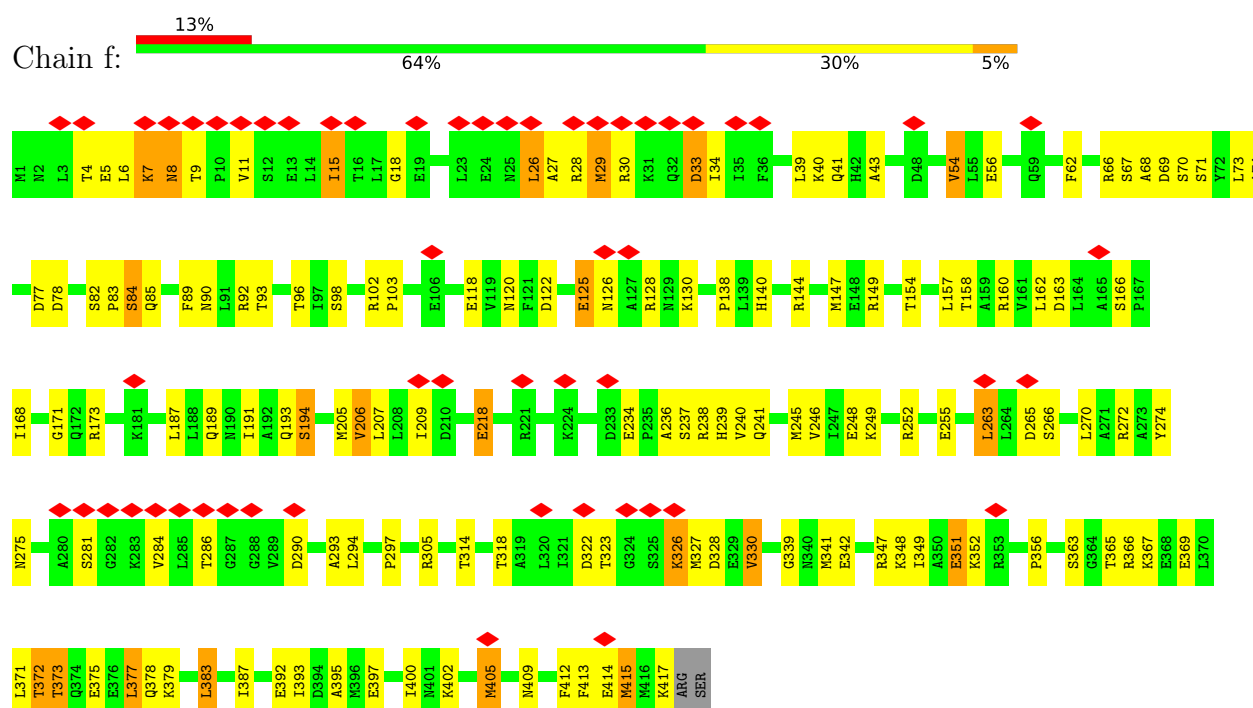
- Molecule 14 is water.

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

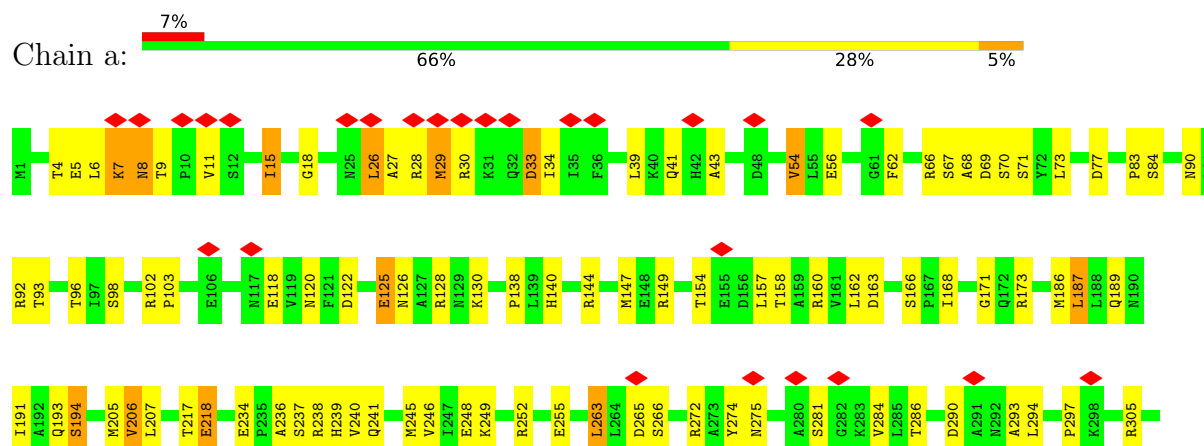
3 Residue-property plots

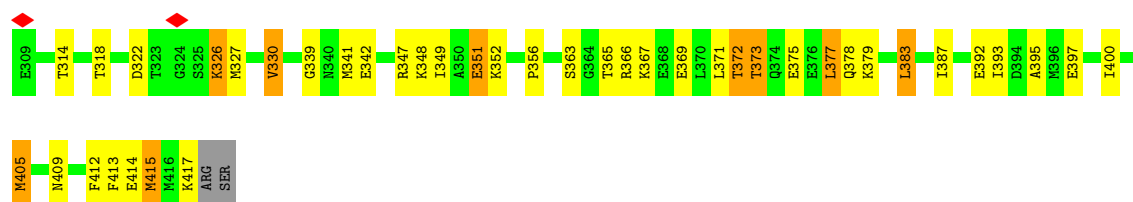
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Transcription termination factor Rho

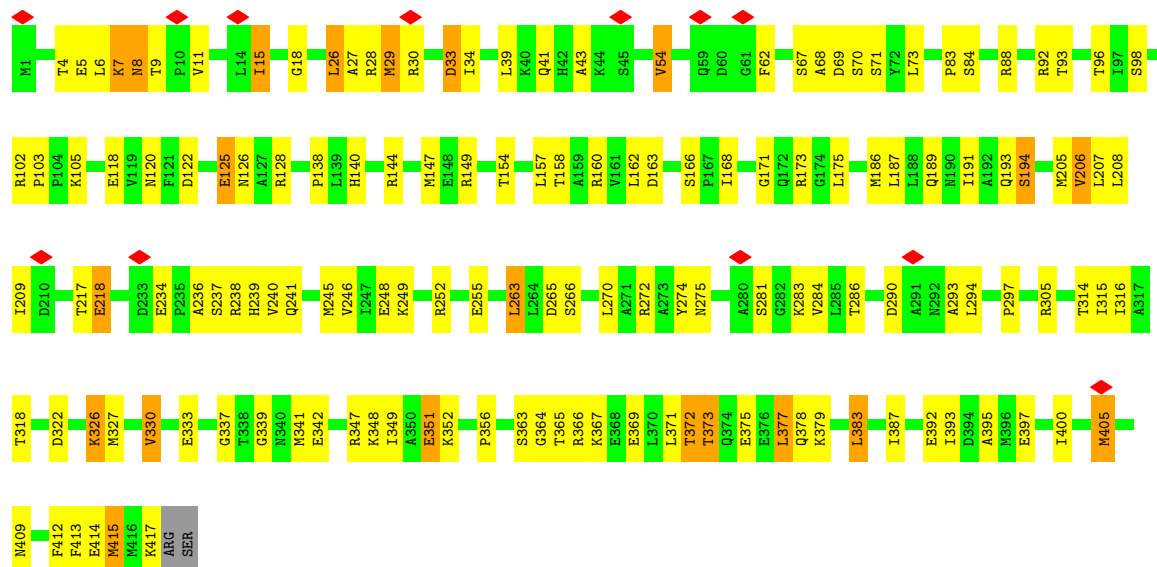


• Molecule 1: Transcription termination factor Rho

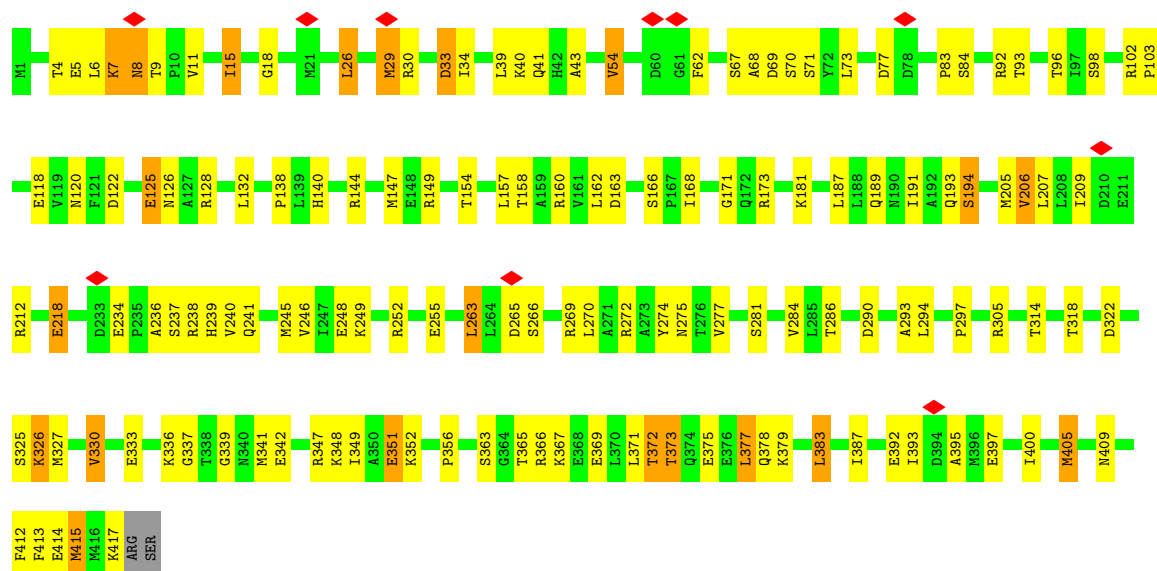




• Molecule 1: Transcription termination factor Rho

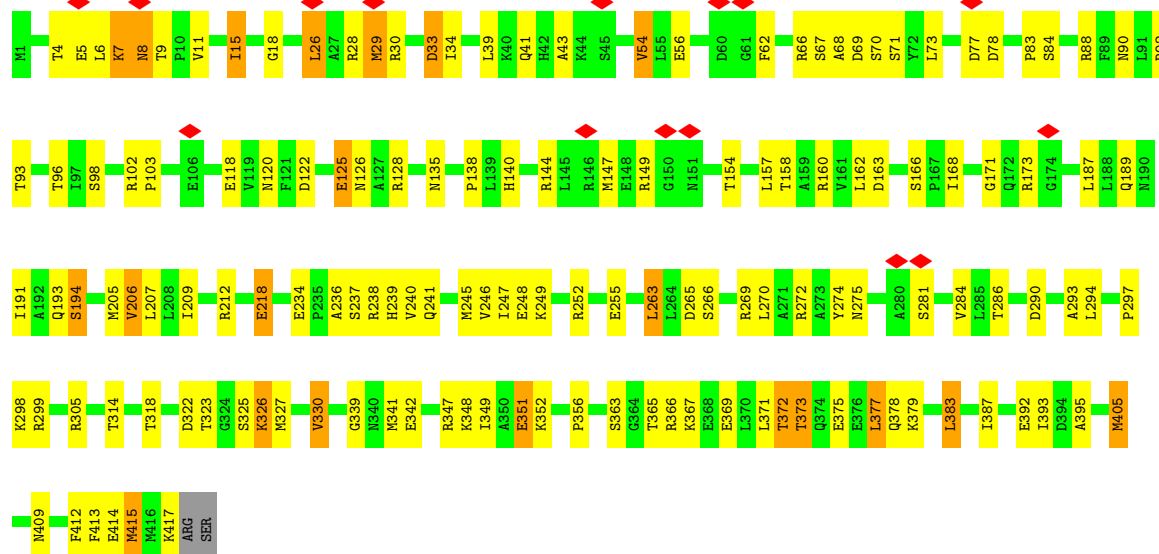


• Molecule 1: Transcription termination factor Rho



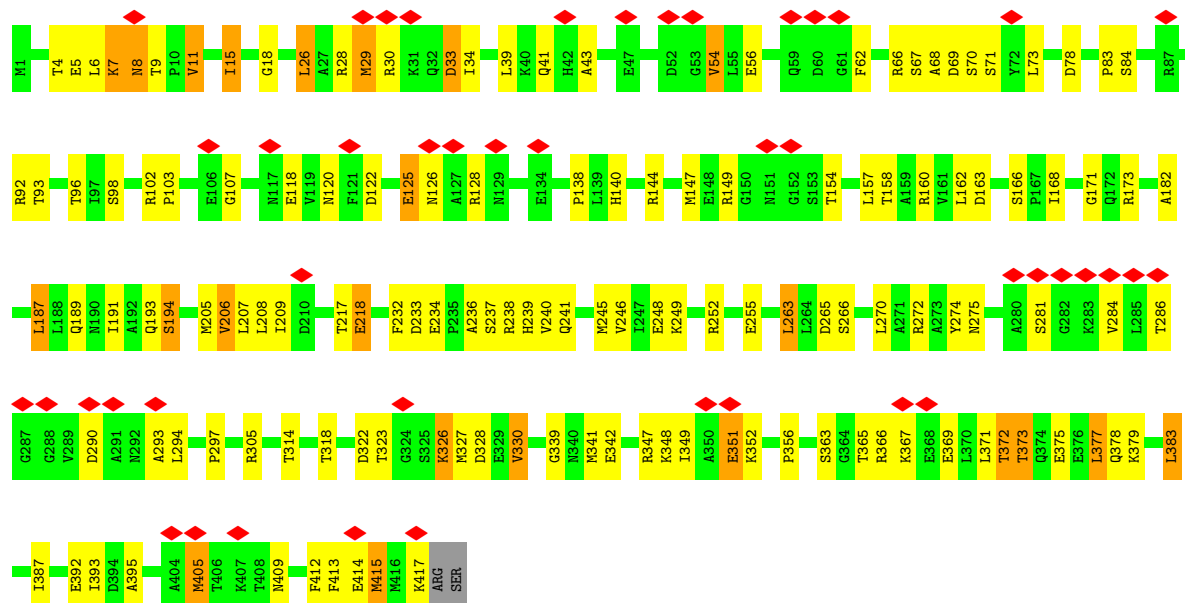
• Molecule 1: Transcription termination factor Rho

Chain d: 



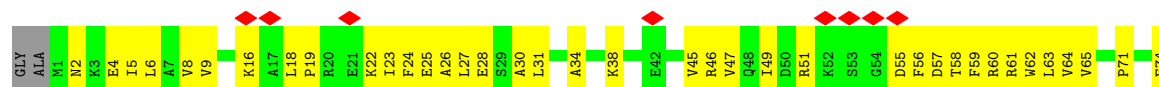
• Molecule 1: Transcription termination factor Rho

Chain e: 



• Molecule 2: Transcription termination/antitermination protein NusA

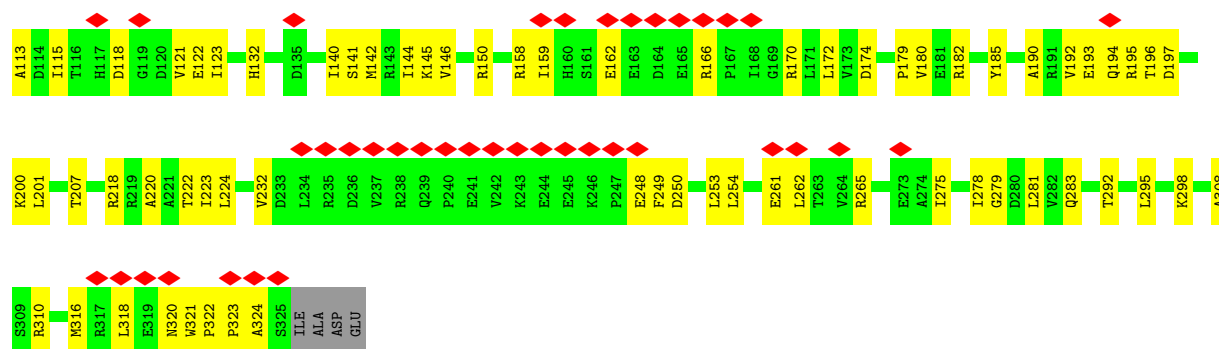
Chain A: 



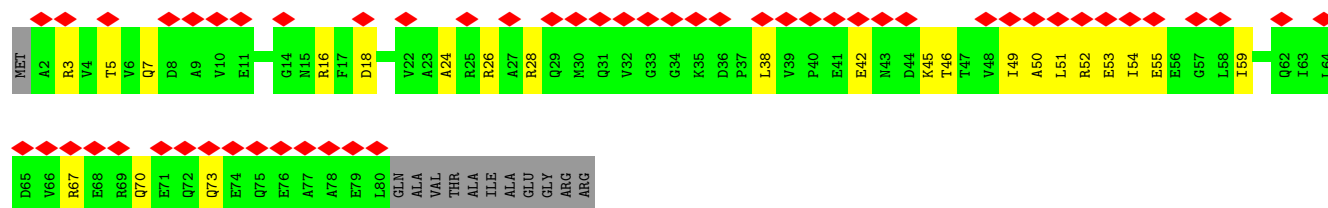


- Molecule 3: DNA-directed RNA polymerase subunit alpha

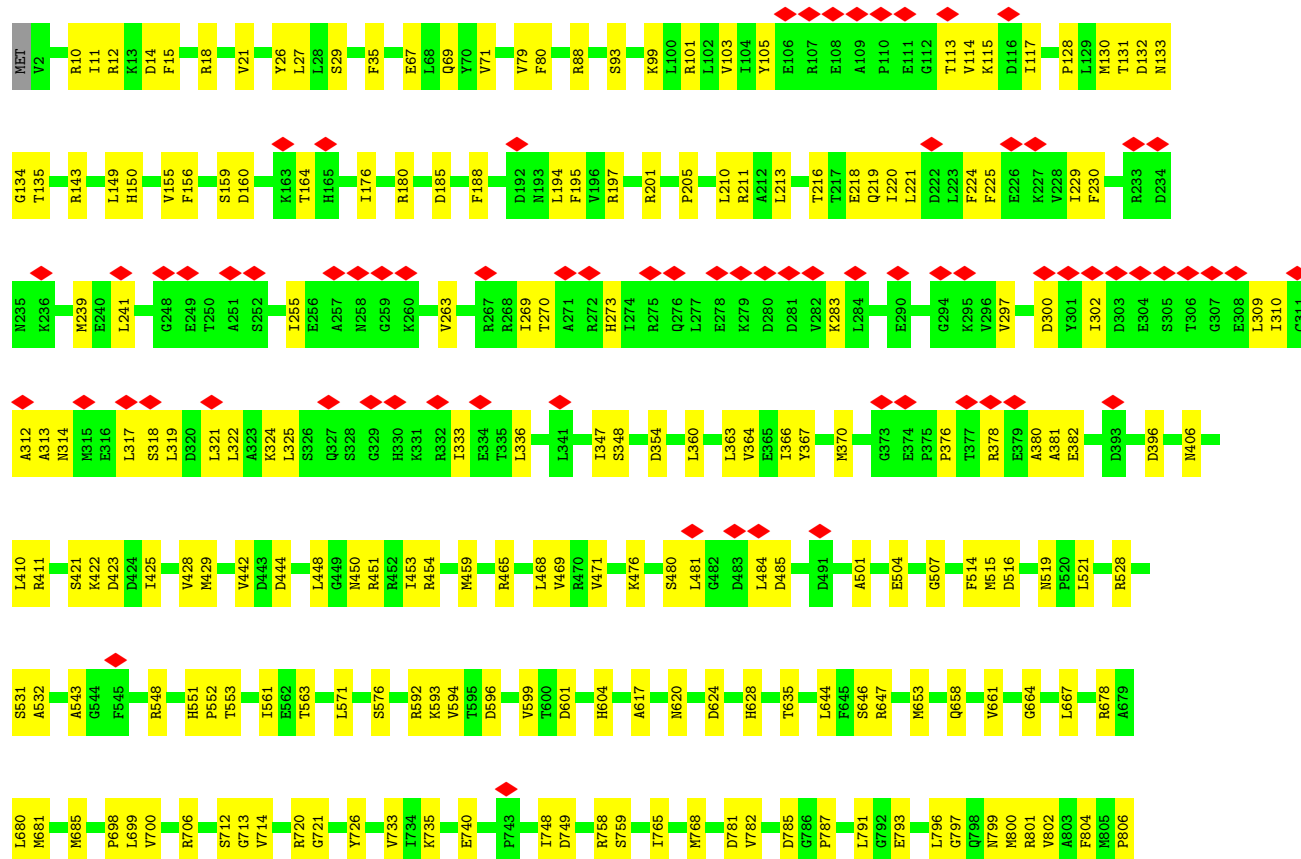
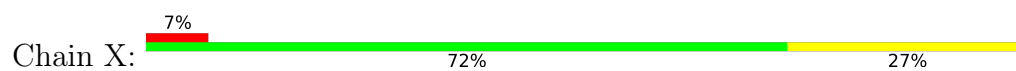
MET
GLN
GLY
SER
V5
T6
E7
D15
I16
V26
T27
L28
E29
P30
H37
T38
I46
L47
L48
S49
S50
M51
V56
T57
E58
I61
D62
G63
K71
L82
L83
N84
L85
K86
R91
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T101
L102
N103
K104
S105
G106
I107
G108
P109
V110
T111
L112

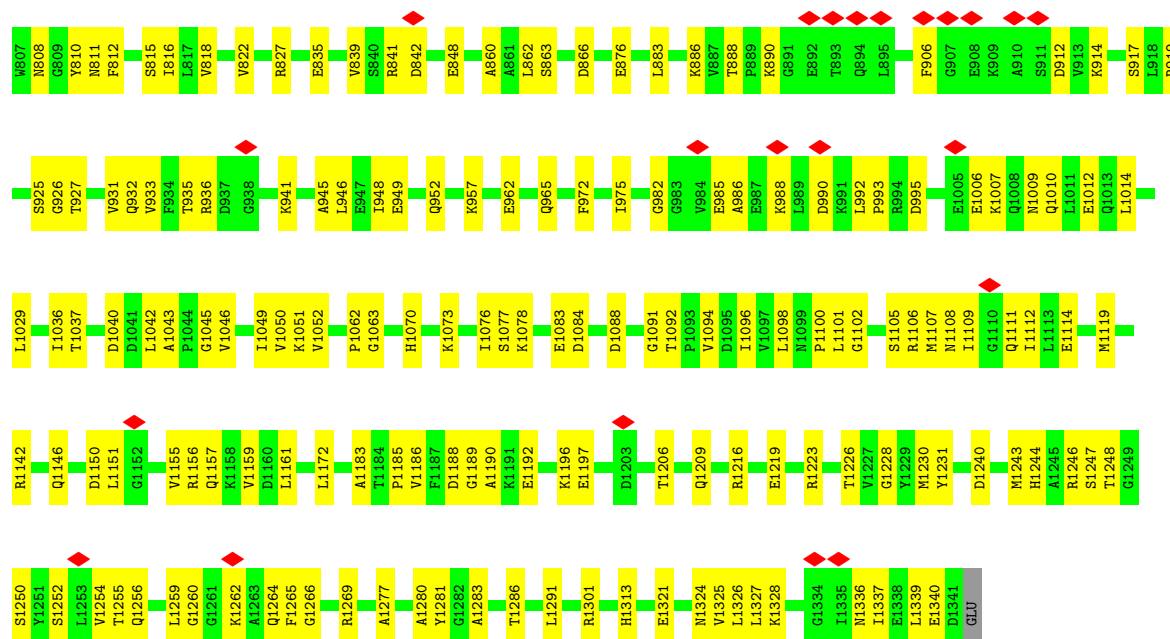


• Molecule 4: DNA-directed RNA polymerase subunit omega

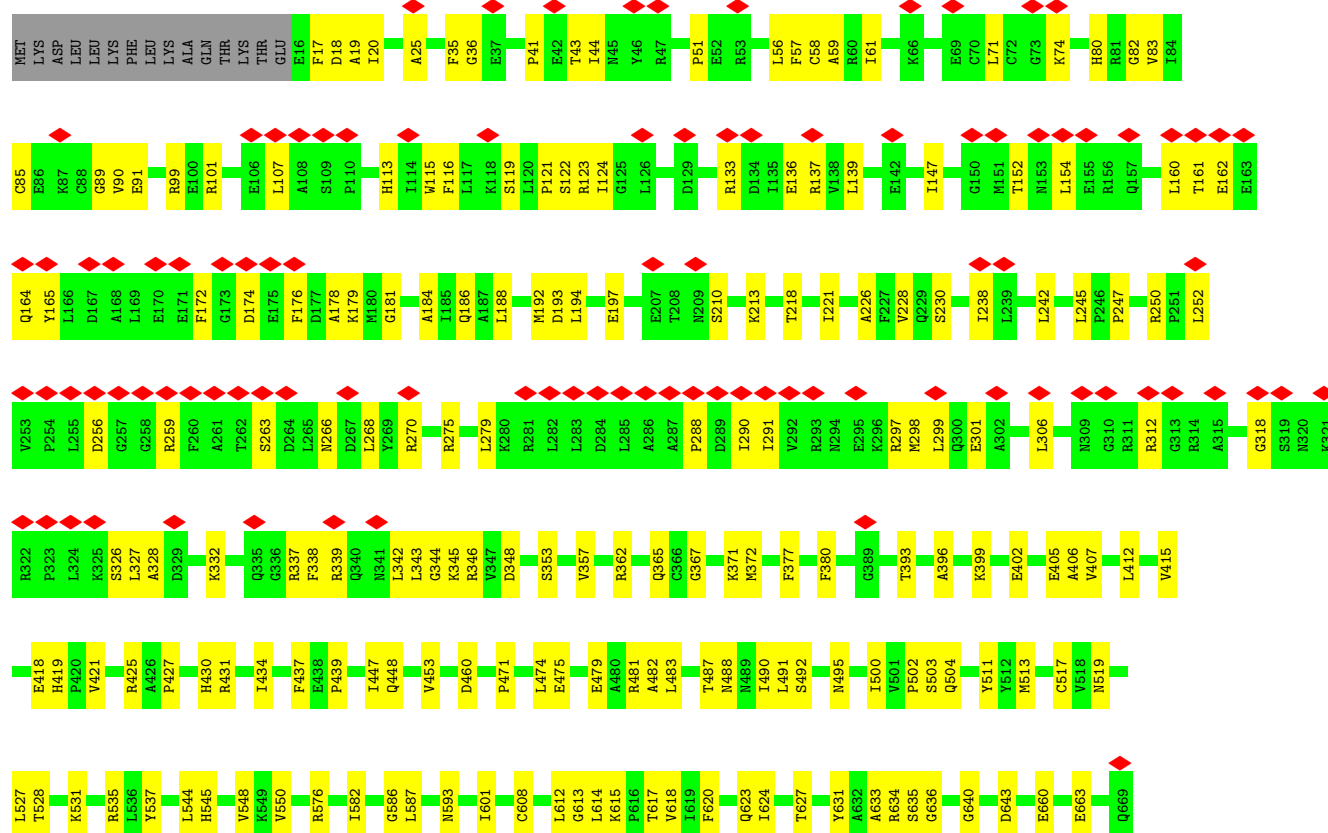


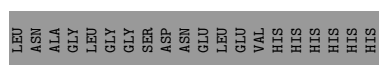
• Molecule 5: DNA-directed RNA polymerase subunit beta

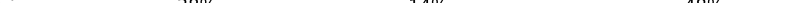




• Molecule 6: DNA-directed RNA polymerase subunit beta'

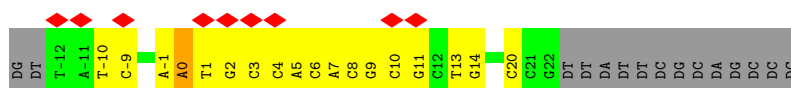




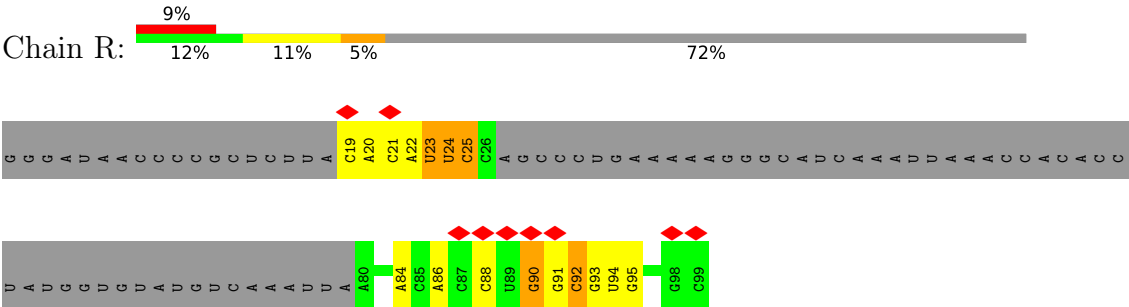
- Chain K: 



- Chain L: 18% 34% 34% 30%



- 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24950	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 ($e^-/\text{\AA}^2$)	50	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	2.108	Depositor
Minimum map value	-0.958	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.35	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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.13	0/3329	0.37	0/4483
1	b	0.13	0/3329	0.37	0/4483
1	c	0.13	0/3329	0.37	0/4483
1	d	0.13	0/3329	0.37	0/4483
1	e	0.13	0/3329	0.37	0/4483
1	f	0.13	0/3329	0.37	0/4483
2	A	0.12	0/3895	0.34	0/5270
3	U	0.11	0/1847	0.29	0/2503
3	V	0.10	0/2538	0.32	0/3441
4	W	0.10	0/629	0.29	0/847
5	X	0.10	0/10736	0.29	0/14487
6	Y	0.10	0/10706	0.29	0/14456
7	K	0.25	0/603	0.38	0/927
8	L	0.18	0/787	0.63	4/1210 (0.3%)
9	R	0.09	0/656	0.22	0/1016
All	All	0.12	0/52371	0.34	4/71055 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	L	0	DA	OP2-P-O3'	-8.81	81.56	108.00
8	L	20	DC	OP2-P-O3'	-8.54	82.37	108.00
8	L	20	DC	OP1-P-O3'	-7.77	84.69	108.00
8	L	0	DA	OP1-P-O3'	-6.94	87.18	108.00

There are no chirality outliers.

There are no planarity outliers.

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	3280	0	3358	92	0
1	b	3280	0	3357	97	0
1	c	3280	0	3358	90	0
1	d	3280	0	3357	101	0
1	e	3280	0	3358	91	0
1	f	3280	0	3359	107	0
2	A	3850	0	3830	139	0
3	U	1825	0	1853	50	0
3	V	2504	0	2558	72	0
4	W	627	0	634	19	0
5	X	10567	0	10585	258	0
6	Y	10545	0	10761	269	0
7	K	538	0	293	5	0
8	L	704	0	393	16	0
9	R	590	0	304	15	0
10	a	27	0	12	1	0
10	b	27	0	12	3	0
10	c	27	0	12	0	0
10	d	27	0	12	0	0
10	e	27	0	12	2	0
11	Y	1	0	0	0	0
11	a	1	0	0	0	0
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	1	0
12	c	4	0	0	0	0
12	d	4	0	0	0	0
12	e	4	0	0	1	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	51608	0	51418	1309	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 1309 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)
8:L:10:DC:H42	9:R:91:G:H1	1.25	0.84
1:f:27:ALA:HB3	2:A:172:ASN:HB2	1.63	0.80
6:Y:362:ARG:H	6:Y:365:GLN:HE21	1.25	0.80
1:d:92:ARG:HG3	1:e:28:ARG:HH12	1.48	0.79
4:W:3:ARG:HH12	4:W:55:GLU:HG3	1.48	0.78

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%)	402 (97%)	13 (3%)	0	100	100
1	b	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	c	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
1	d	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
1	e	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	f	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
2	A	493/497 (99%)	449 (91%)	42 (8%)	2 (0%)	30	66
3	U	233/329 (71%)	222 (95%)	11 (5%)	0	100	100
3	V	319/329 (97%)	293 (92%)	26 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	W	77/91 (85%)	74 (96%)	3 (4%)	0	100	100
5	X	1338/1342 (100%)	1269 (95%)	69 (5%)	0	100	100
6	Y	1356/1416 (96%)	1295 (96%)	61 (4%)	0	100	100
All	All	6306/6518 (97%)	6011 (95%)	293 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	131	ARG
2	A	200	SER

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	357/359 (99%)	320 (90%)	37 (10%)	7	22
1	b	357/359 (99%)	320 (90%)	37 (10%)	7	22
1	c	357/359 (99%)	320 (90%)	37 (10%)	7	22
1	d	357/359 (99%)	320 (90%)	37 (10%)	7	22
1	e	357/359 (99%)	320 (90%)	37 (10%)	7	22
1	f	357/359 (99%)	320 (90%)	37 (10%)	7	22
2	A	408/409 (100%)	408 (100%)	0	100	100
3	U	203/286 (71%)	203 (100%)	0	100	100
3	V	280/286 (98%)	280 (100%)	0	100	100
4	W	67/75 (89%)	67 (100%)	0	100	100
5	X	1155/1157 (100%)	1155 (100%)	0	100	100
6	Y	1134/1177 (96%)	1134 (100%)	0	100	100
All	All	5389/5544 (97%)	5167 (96%)	222 (4%)	28	48

5 of 222 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	c	15	ILE
1	e	415	MET
1	c	378	GLN
1	e	405	MET
1	e	125	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
5	X	1237	HIS
6	Y	1023	HIS
6	Y	196	GLN
6	Y	702	GLN
6	Y	1268	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	R	26/99 (26%)	8 (30%)	0

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	R	23	U
9	R	24	U
9	R	25	C
9	R	84	A
9	R	86	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	b	1000	11	28,29,29	1.41	4 (14%)	43,45,45	1.83	9 (20%)
10	ADP	e	1000	11	28,29,29	1.43	5 (17%)	43,45,45	1.82	9 (20%)
10	ADP	d	1000	11	28,29,29	1.42	4 (14%)	43,45,45	1.84	9 (20%)
12	BEF	d	1002	-	0,3,3	-	-	-	-	-
12	BEF	a	1002	-	0,3,3	-	-	-	-	-
10	ADP	a	1000	11	28,29,29	1.41	4 (14%)	43,45,45	1.85	8 (18%)
12	BEF	b	1002	-	0,3,3	-	-	-	-	-
12	BEF	c	1002	-	0,3,3	-	-	-	-	-
10	ADP	c	1000	11	28,29,29	1.41	4 (14%)	43,45,45	1.84	9 (20%)
12	BEF	e	1002	-	0,3,3	-	-	-	-	-

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	b	1000	11	-	2/16/32/32	0/3/3/3
10	ADP	e	1000	11	-	2/16/32/32	0/3/3/3
10	ADP	d	1000	11	-	2/16/32/32	0/3/3/3
10	ADP	a	1000	11	-	0/16/32/32	0/3/3/3
10	ADP	c	1000	11	-	3/16/32/32	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	a	1000	ADP	C5-C4	4.75	1.47	1.39
10	e	1000	ADP	C5-C4	4.72	1.47	1.39
10	d	1000	ADP	C5-C4	4.72	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	b	1000	ADP	C5-C4	4.69	1.47	1.39
10	c	1000	ADP	C5-C4	4.67	1.47	1.39

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	a	1000	ADP	C5-C4-N3	-6.03	118.41	126.72
10	b	1000	ADP	C5-C4-N3	-5.80	118.72	126.72
10	d	1000	ADP	C5-C4-N3	-5.80	118.73	126.72
10	c	1000	ADP	C5-C4-N3	-5.76	118.78	126.72
10	e	1000	ADP	C5-C4-N3	-5.74	118.82	126.72

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	b	1000	ADP	C5'-O5'-PA-O3A
10	d	1000	ADP	O4'-C4'-C5'-O5'
10	d	1000	ADP	C3'-C4'-C5'-O5'
10	c	1000	ADP	O4'-C4'-C5'-O5'
10	b	1000	ADP	C5'-O5'-PA-O1A

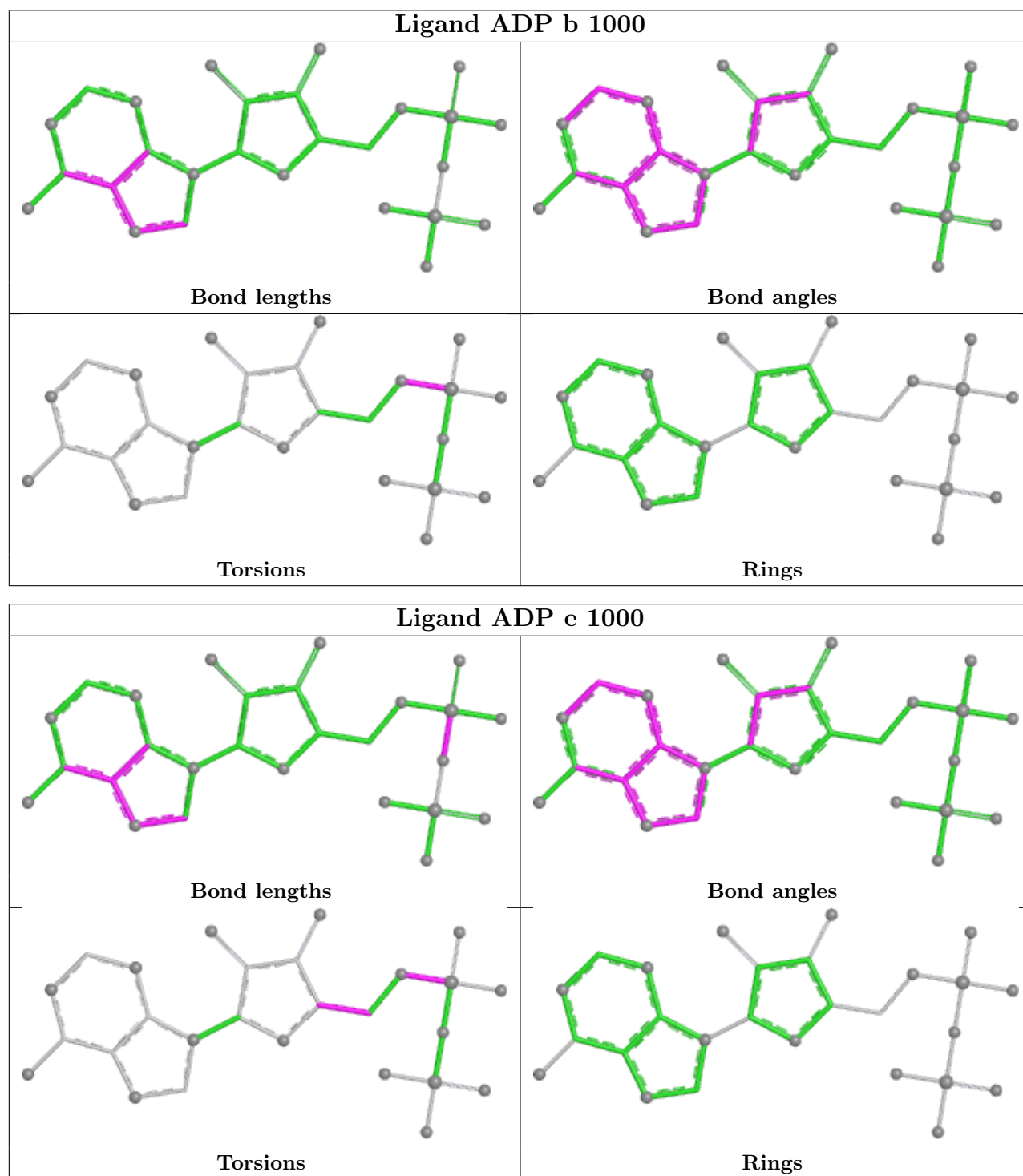
There are no ring outliers.

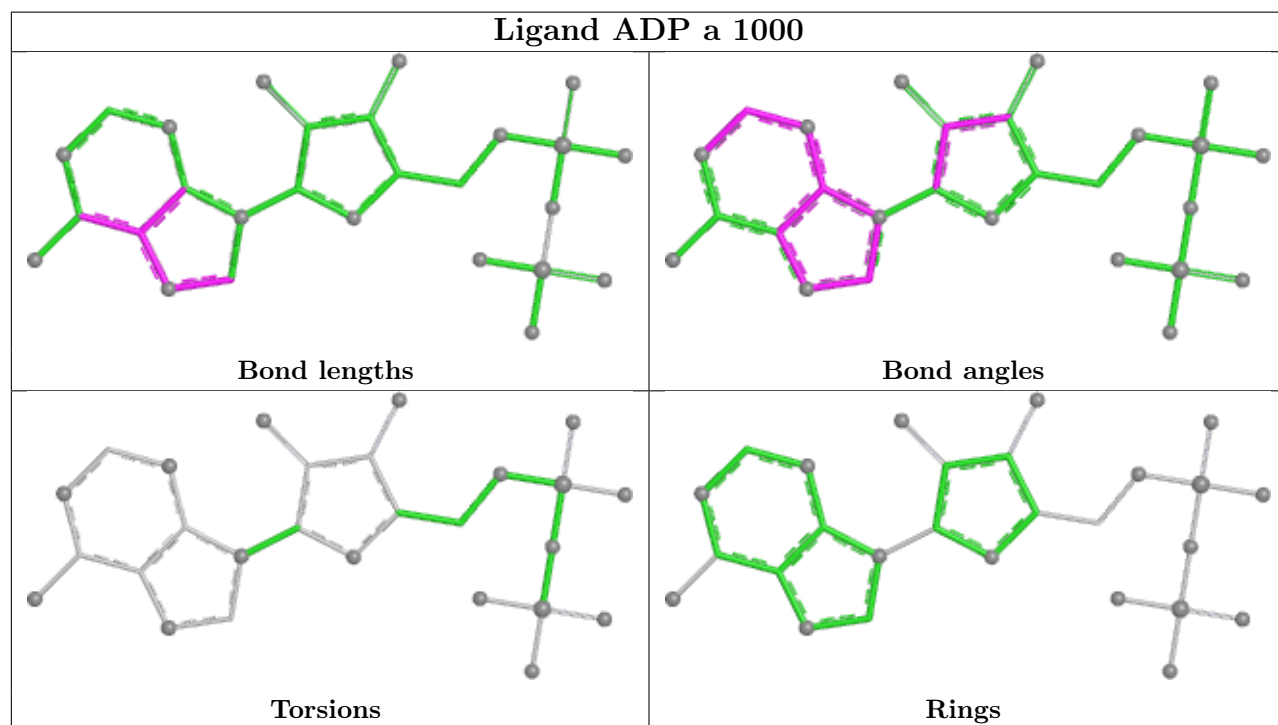
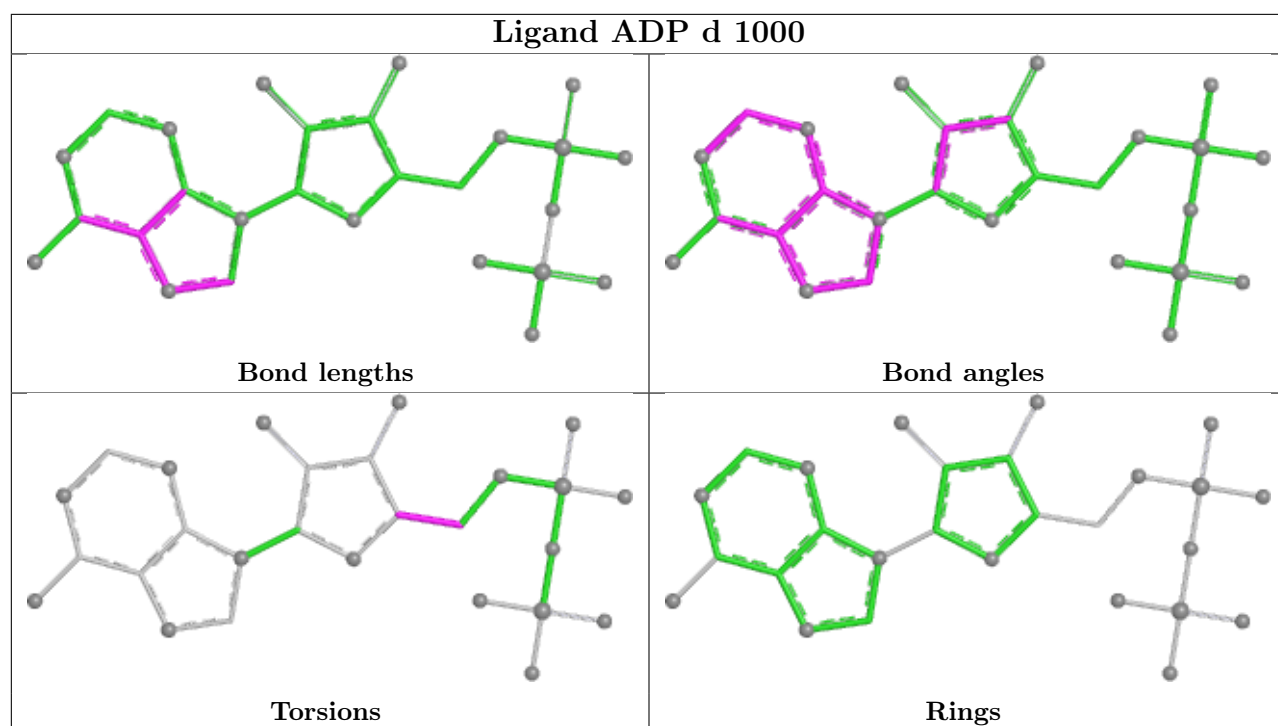
5 monomers are involved in 6 short contacts:

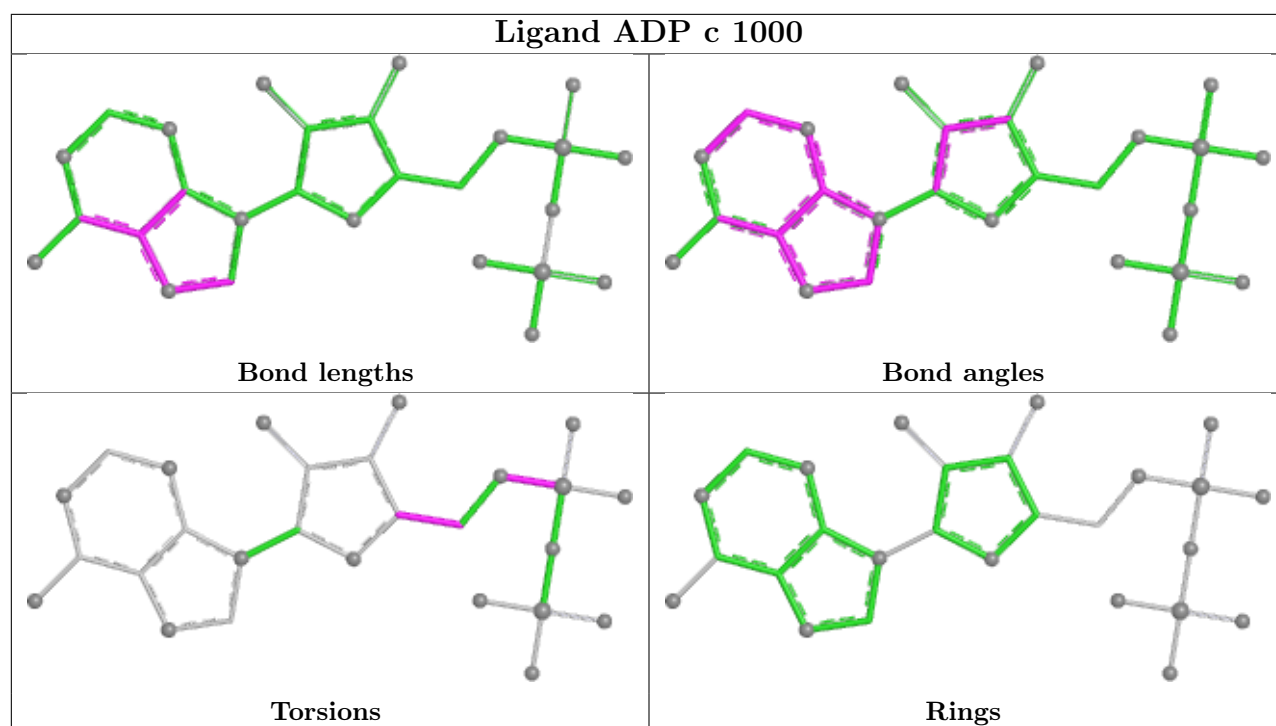
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	b	1000	ADP	3	0
10	e	1000	ADP	2	0
10	a	1000	ADP	1	0
12	b	1002	BEF	1	0
12	e	1002	BEF	1	0

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 than 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.







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.

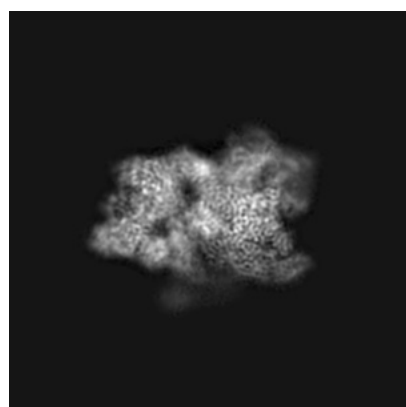
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11090. These allow visual inspection of the internal detail of the map and identification of artifacts.

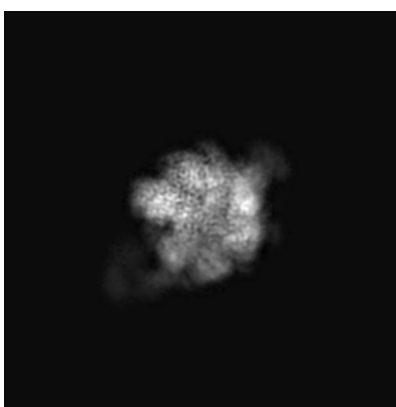
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

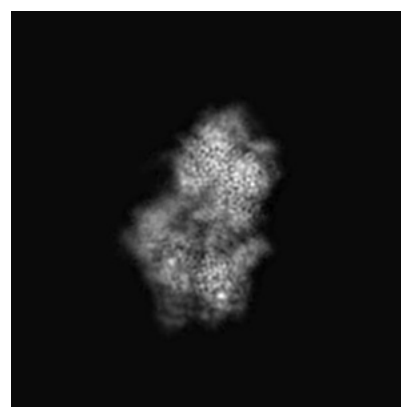
6.1.1 Primary map



X



Y

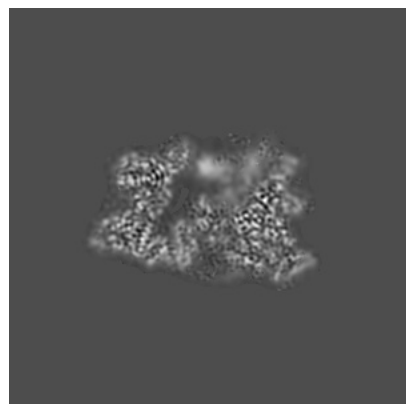


Z

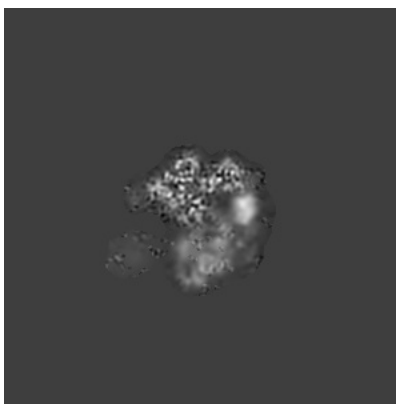
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150



Y Index: 150

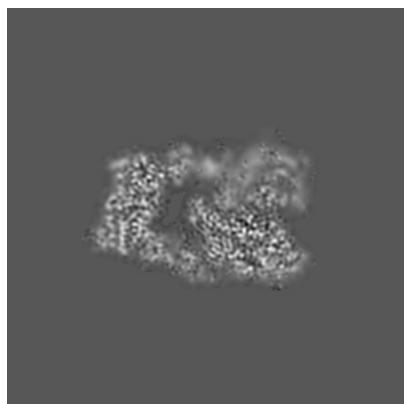


Z Index: 150

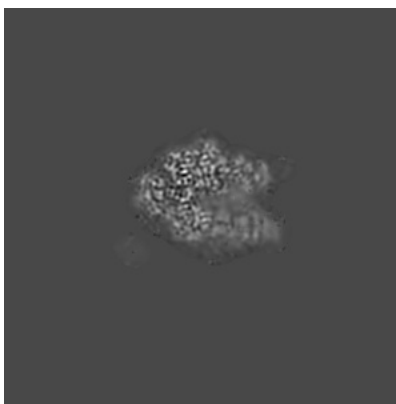
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

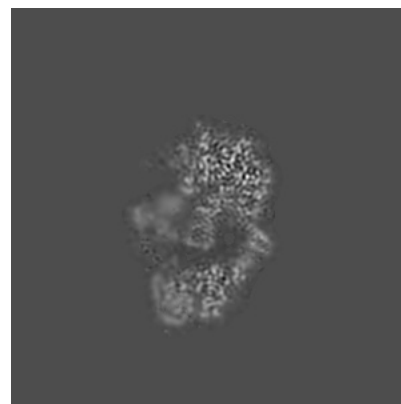
6.3.1 Primary map



X Index: 157



Y Index: 173

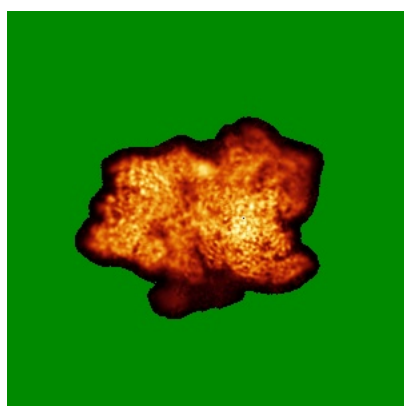


Z Index: 135

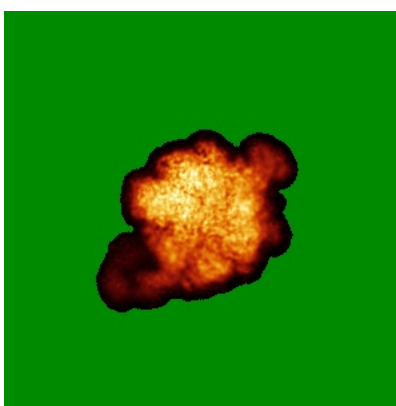
The images above show the largest variance slices of the map in three orthogonal directions.

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

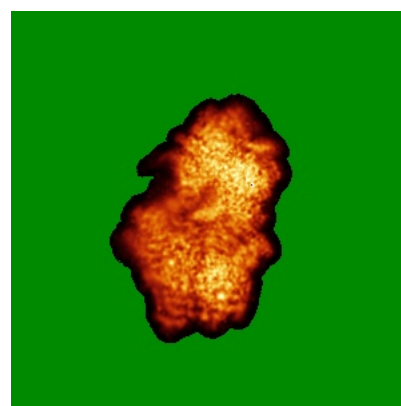
6.4.1 Primary map



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

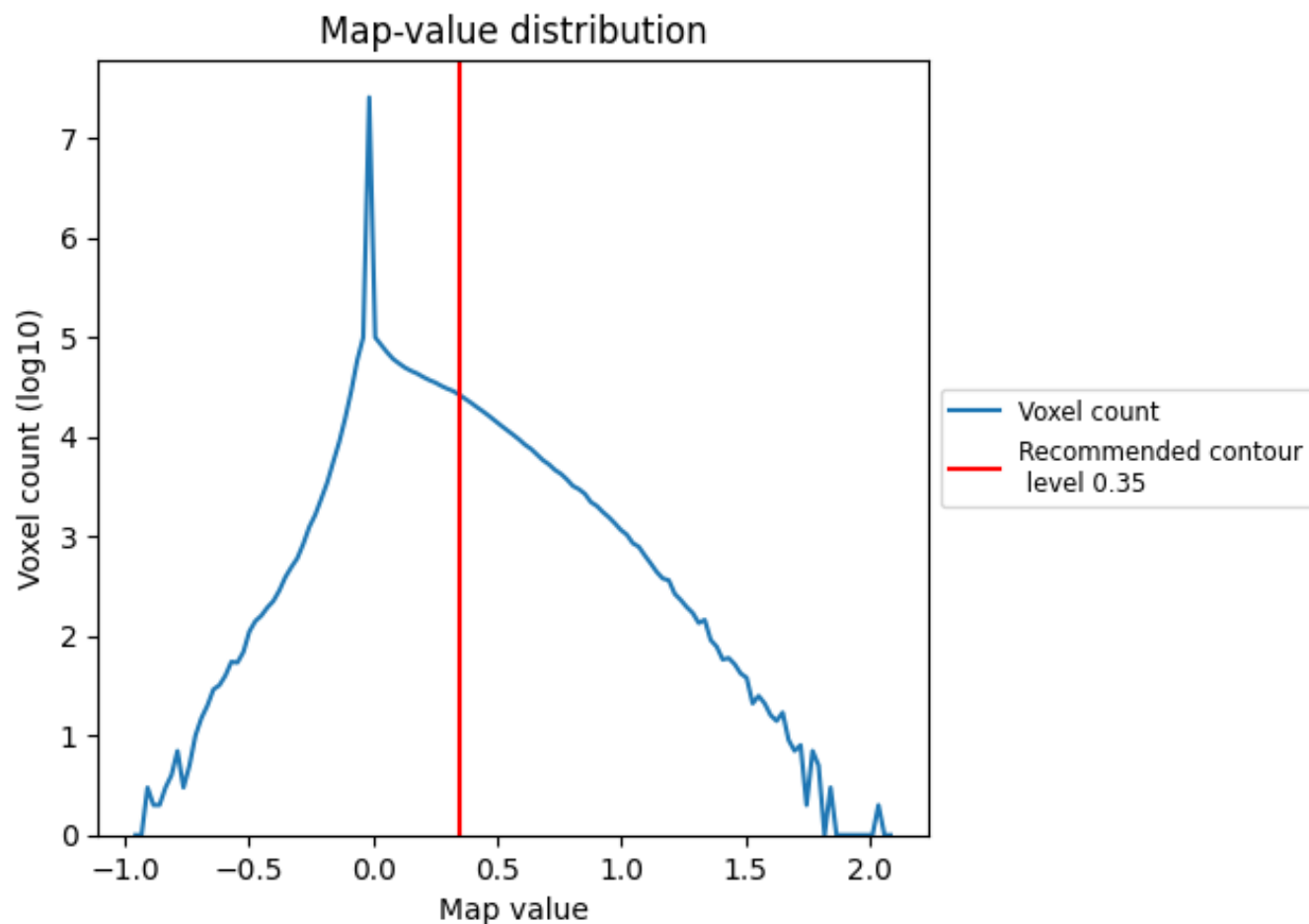
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

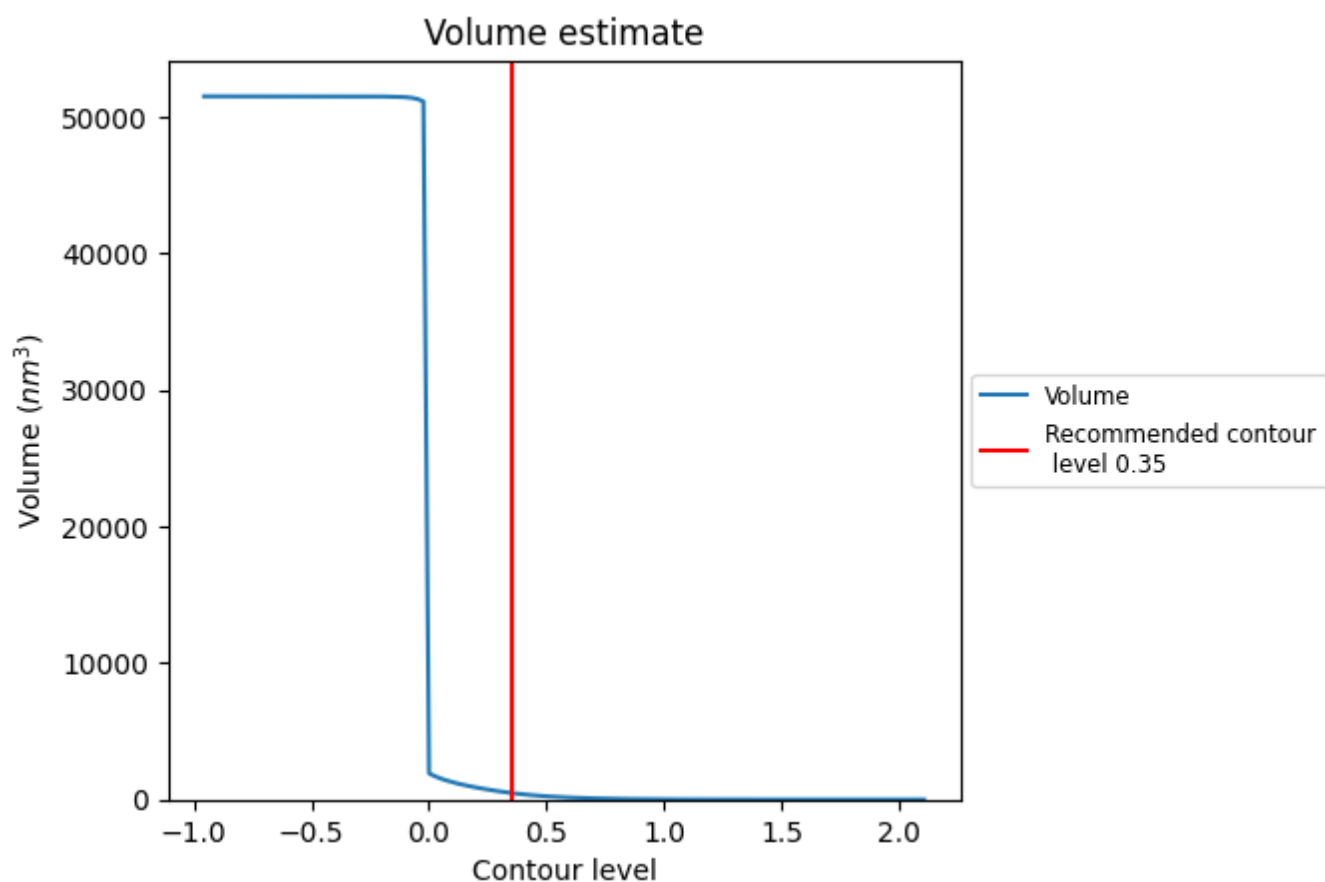
This section contains the results of statistical analysis of the map.

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.

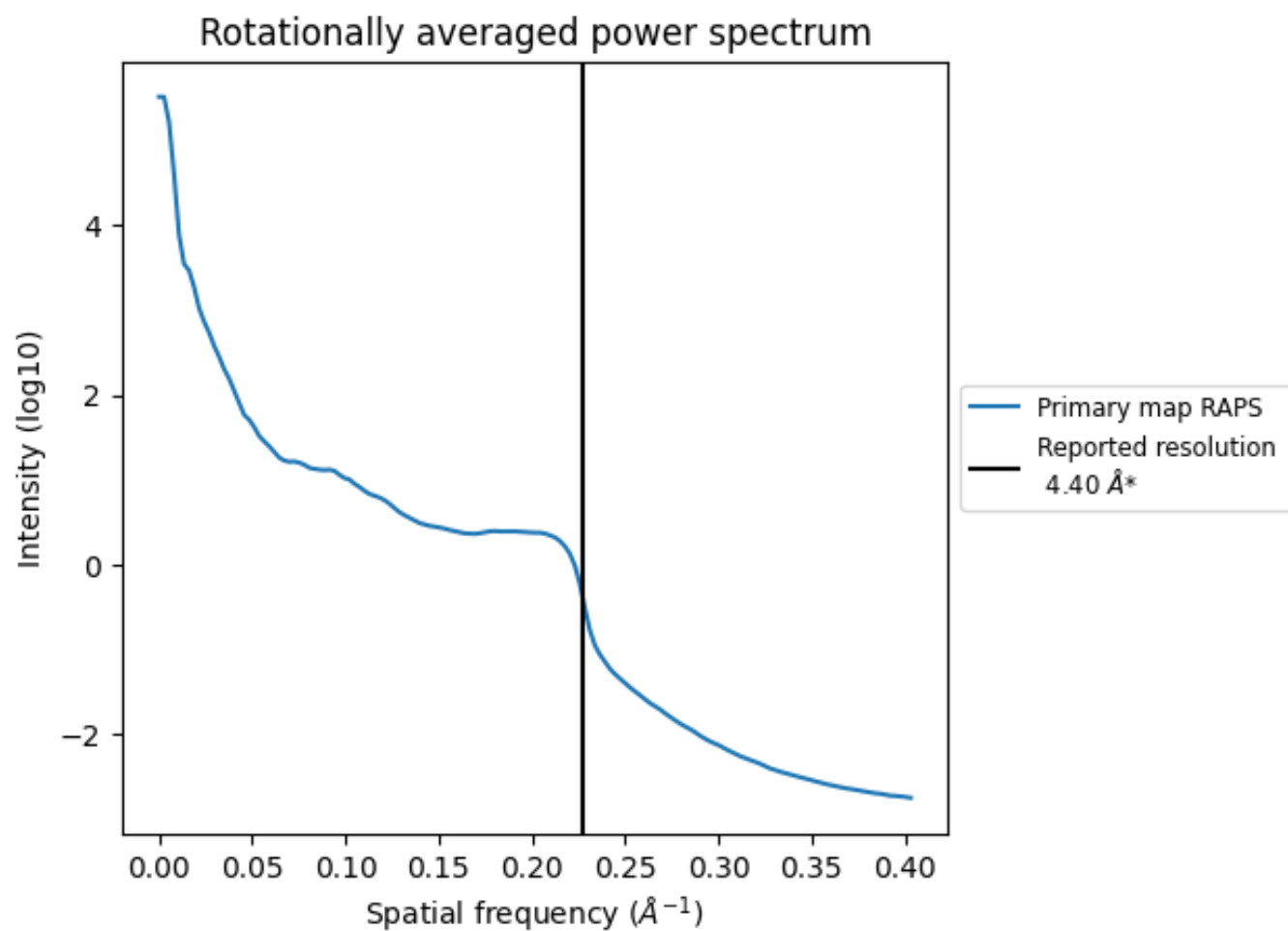
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 483 nm³; this corresponds to an approximate mass of 437 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 ⓘ

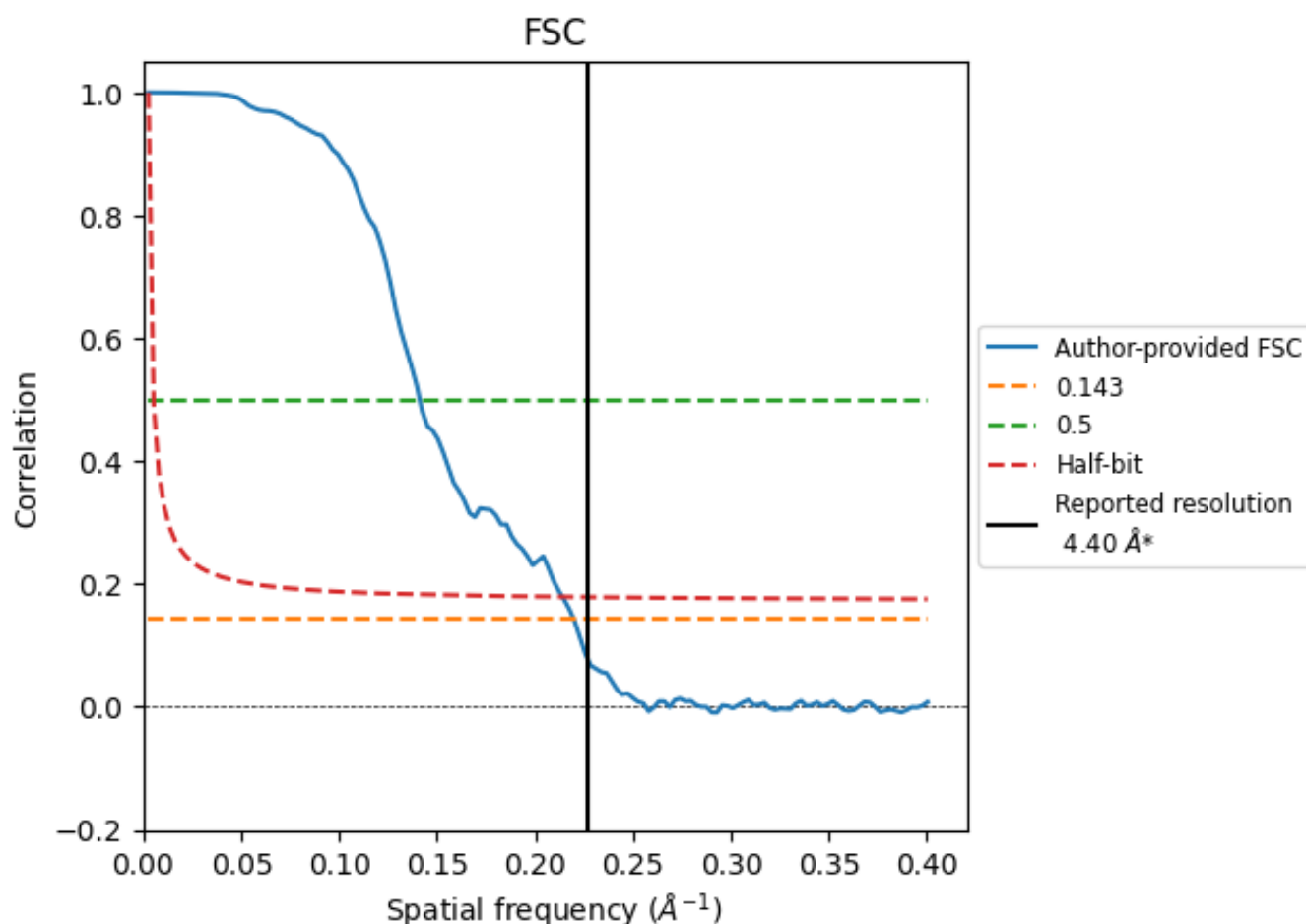


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.55	7.08	4.67
Unmasked-calculated*	-	-	-

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

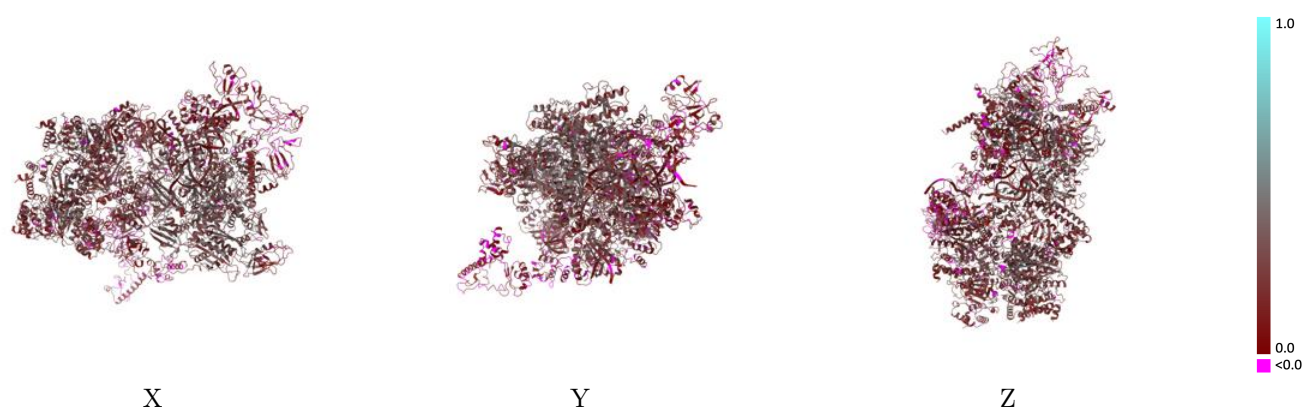
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11090 and PDB model 6Z9S. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

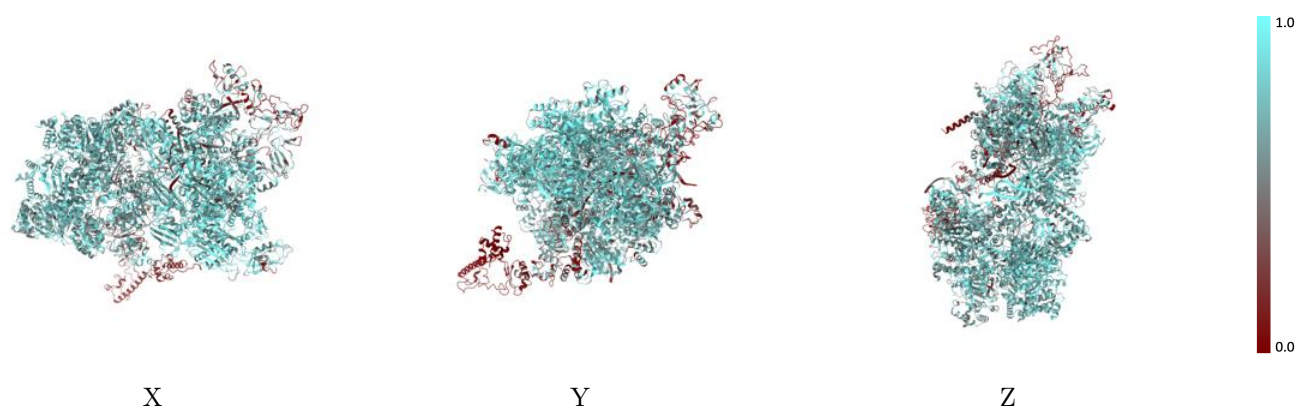
This section was not generated.

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



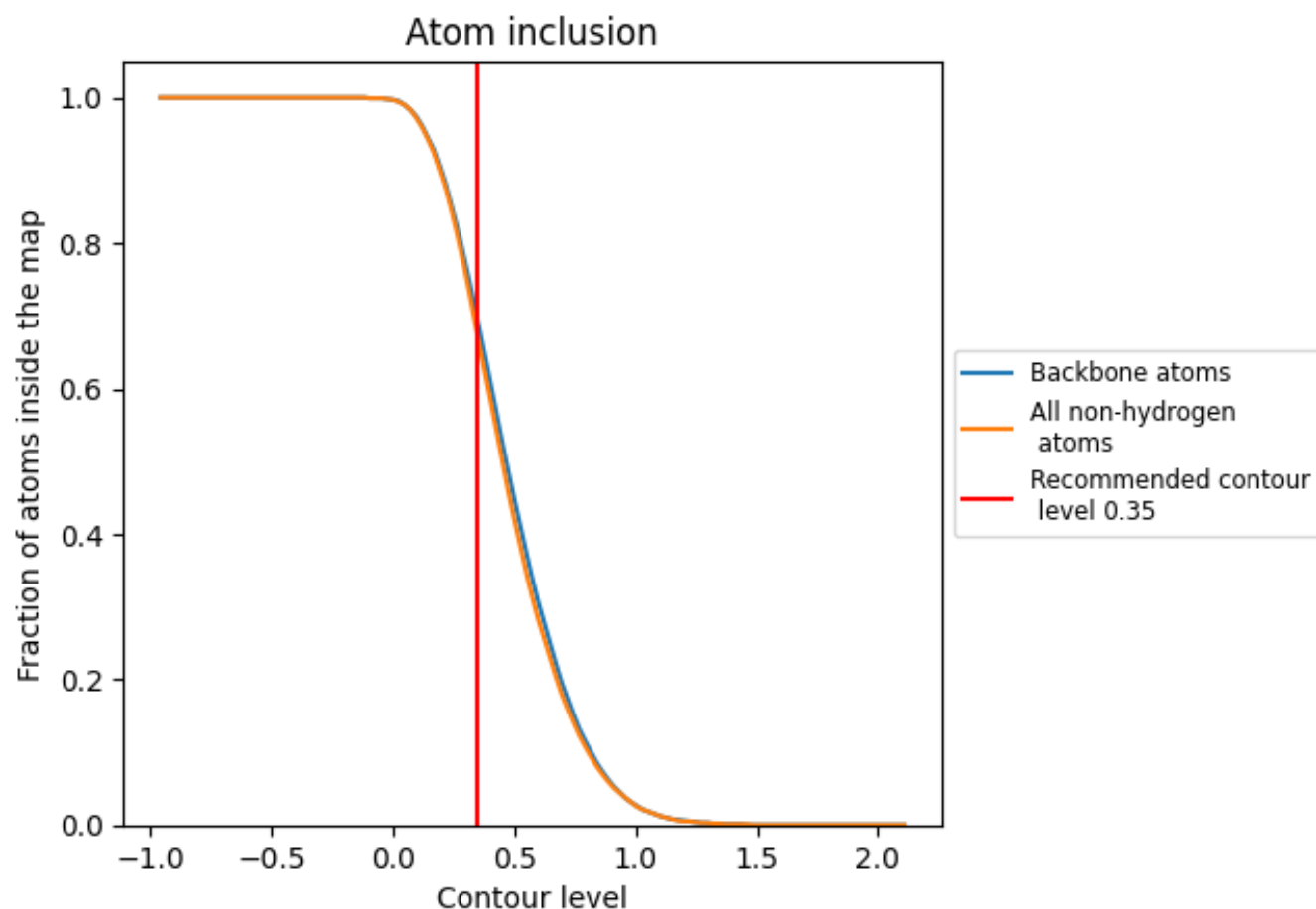
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 67% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6730	0.2340
A	0.3290	0.1140
K	0.7290	0.1730
L	0.6320	0.1510
R	0.5970	0.1600
U	0.7880	0.3150
V	0.6680	0.2400
W	0.2860	0.2240
X	0.7520	0.2840
Y	0.6610	0.2260
a	0.7360	0.2350
b	0.7620	0.2600
c	0.7800	0.2710
d	0.7490	0.2530
e	0.6640	0.1920
f	0.6700	0.1860

1.0

0.0

<0.0