wwPDB EM Validation Summary Report

Jan 1, 2025 – 09:21 PM EST

PDB ID	:	9BW1
EMDB ID	:	EMD-44944
Title	:	TnsABCD-DNA transpososome
Authors	:	Chang, L.; Wang, S.
Deposited on	:	2024-05-20
Resolution	:	3.65 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:

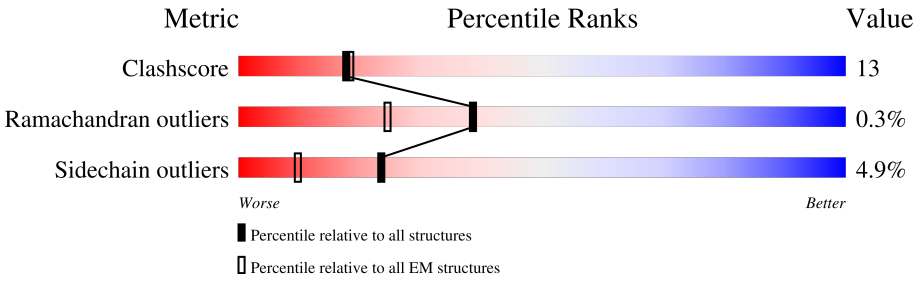
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 3.65 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	2	85	22% 18% 60%
2	4	200	12% 12% 75%
3	5	173	13% 7% 80%
4	6	37	11% 22% 19% 59%
5	H	69	39% 36% 25%
6	I	158	22% 34% 45%
7	J	462	9% 67% 31%
8	M	898	61% 25% 13%

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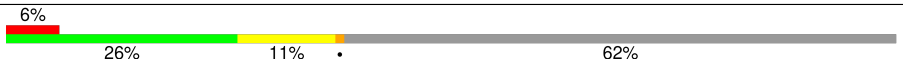
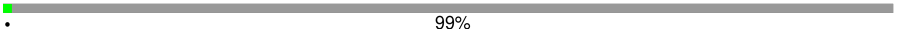
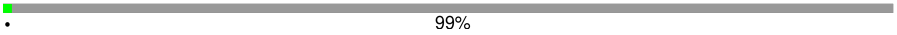
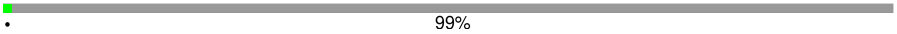
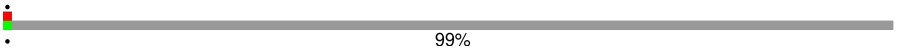
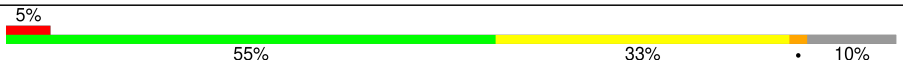
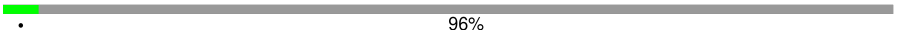
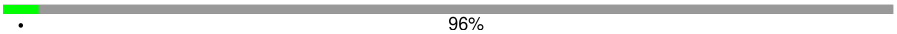
Mol	Chain	Length	Quality of chain
8	N	898	
8	O	898	
8	P	898	
8	a	898	
8	b	898	
8	c	898	
8	d	898	
9	Q	383	
9	R	383	
9	S	383	
9	T	383	
9	U	383	
9	V	383	
9	W	383	
9	x	383	
9	y	383	

2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 47283 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 DNA chain called LE_polyA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	34	692	331	125	202	34	0	0

- Molecule 2 is a DNA chain called RE_target.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	4	50	1030	491	196	294	49	0	0

- Molecule 3 is a DNA chain called RE_polyA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	5	34	690	332	118	206	34	0	0

- Molecule 4 is a DNA chain called Target_downstream.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	6	15	304	146	58	86	14	0	0

- Molecule 5 is a DNA chain called Target_val.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	H	52	1065	510	183	320	52	0	0

- Molecule 6 is a DNA chain called tRNA_LE_LUEGO.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	I	87	1790	852	342	510	86	0	0

- Molecule 7 is a protein called TnsD.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	462	Total	C	N	O	S	0	0
			3707	2365	655	663	24		

- Molecule 8 is a protein called Integrase.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	779	Total	C	N	O	S	0	0
			6349	4024	1130	1177	18		
8	N	779	Total	C	N	O	S	0	0
			6349	4024	1130	1177	18		
8	O	345	Total	C	N	O	S	0	0
			2788	1777	493	508	10		
8	P	345	Total	C	N	O	S	0	0
			2788	1777	493	508	10		
8	a	8	Total	C	N	O		0	0
			70	48	8	14			
8	b	8	Total	C	N	O		0	0
			70	48	8	14			
8	c	8	Total	C	N	O		0	0
			70	48	8	14			
8	d	8	Total	C	N	O		0	0
			70	48	8	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
M	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
N	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
N	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
O	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
O	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
P	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
P	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
a	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
a	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
b	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
b	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
c	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
c	519	ALA	ASP	engineered mutation	UNP A0A235IFR8
d	62	ALA	GLU	engineered mutation	UNP A0A235IFR8
d	519	ALA	ASP	engineered mutation	UNP A0A235IFR8

- Molecule 9 is a protein called TnsC.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	302	Total	C	N	O	S	0	0
			2440	1568	416	448	8		
9	R	343	Total	C	N	O	S	0	0
			2756	1757	483	508	8		
9	S	343	Total	C	N	O	S	0	0
			2756	1757	483	508	8		
9	T	343	Total	C	N	O	S	0	0
			2756	1757	483	508	8		
9	U	343	Total	C	N	O	S	0	0
			2756	1757	483	508	8		
9	V	343	Total	C	N	O	S	0	0
			2756	1757	483	508	8		
9	W	343	Total	C	N	O	S	0	0
			2756	1757	483	508	8		
9	x	15	Total	C	N	O		0	0
			119	75	26	18			
9	y	15	Total	C	N	O		0	0
			119	75	26	18			

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	4	1	Total	Mg	0
			1	1	
10	I	2	Total	Mg	0
			2	2	
10	M	1	Total	Mg	0
			1	1	
10	Q	1	Total	Mg	0
			1	1	
10	R	1	Total	Mg	0
			1	1	
10	S	1	Total	Mg	0
			1	1	
10	T	1	Total	Mg	0
			1	1	
10	U	1	Total	Mg	0
			1	1	
10	V	1	Total	Mg	0
			1	1	

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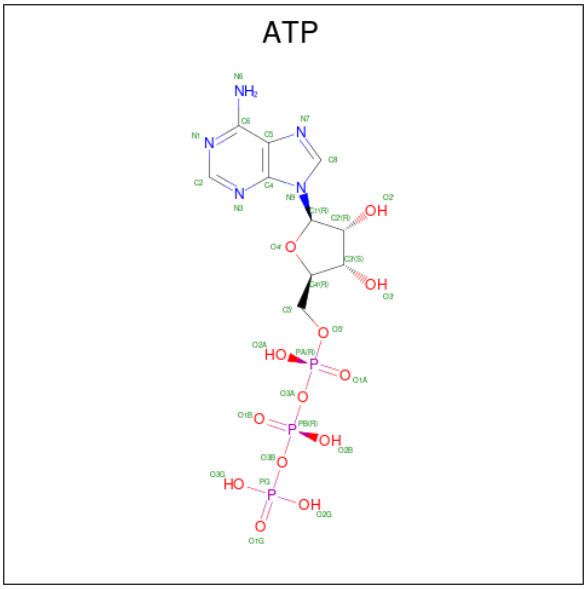
Mol	Chain	Residues	Atoms	AltConf
10	W	1	Total Mg 1 1	0

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
11	J	2	Total Zn 2 2	0

- Molecule 12 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
12	Q	1	Total C N O P 31 10 5 13 3	0
12	R	1	Total C N O P 31 10 5 13 3	0
12	S	1	Total C N O P 31 10 5 13 3	0
12	T	1	Total C N O P 31 10 5 13 3	0
12	U	1	Total C N O P 31 10 5 13 3	0
12	V	1	Total C N O P 31 10 5 13 3	0

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Mol	Chain	Residues	Atoms					AltConf
12	W	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 13 is water.

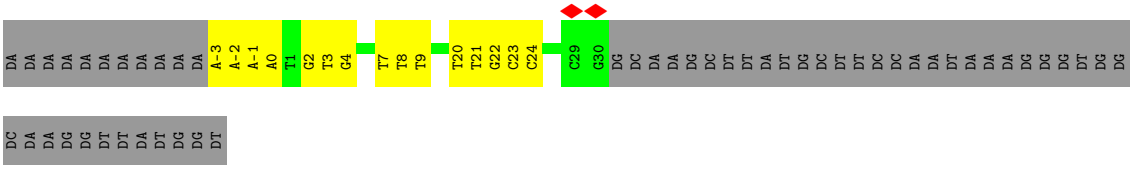
Mol	Chain	Residues	Atoms		AltConf
13	I	1	Total	O	0
			1	1	
13	S	5	Total	O	0
			5	5	
13	T	1	Total	O	0
			1	1	

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: LE_polyA

Chain 2:

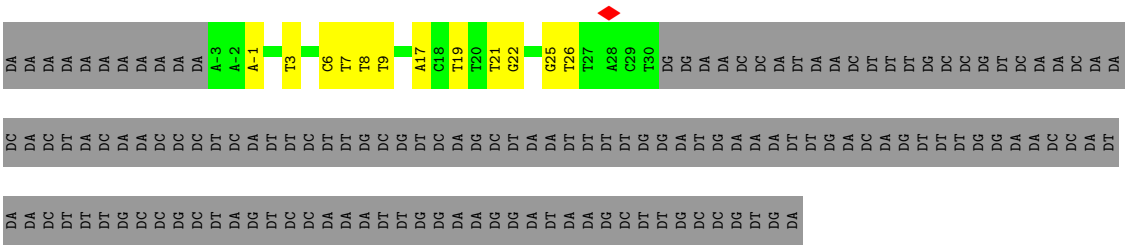


- Molecule 2: RE_target

Chain 4:

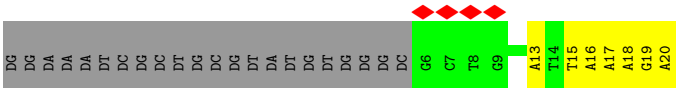
- Molecule 3: RE_polyA

Chain 5:



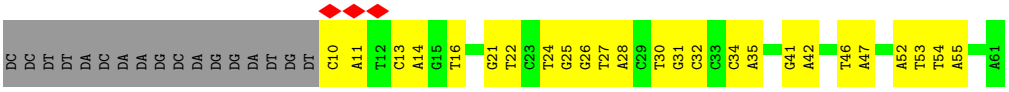
- Molecule 4: Target_downstream

Chain 6:



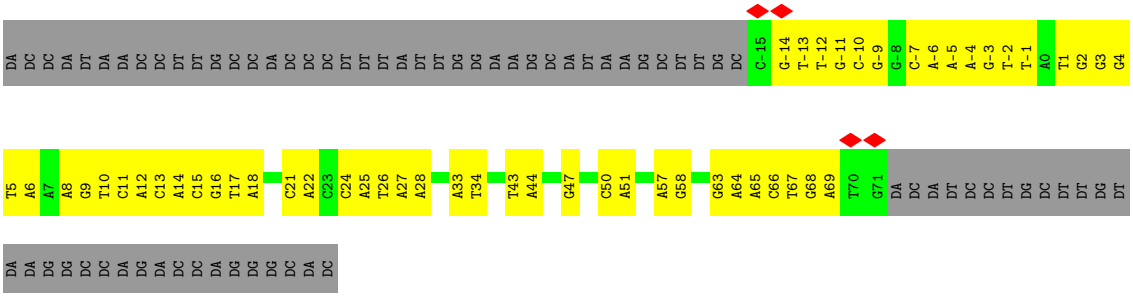
• Molecule 5: Target_val

Chain H:



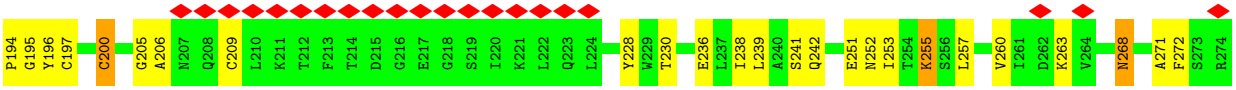
• Molecule 6: tRNA_LE_LUEGO

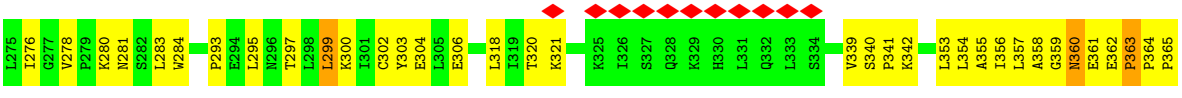
Chain I:

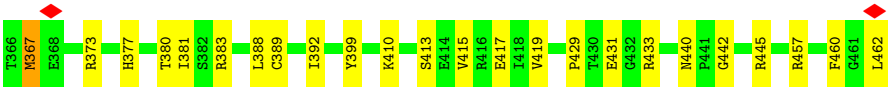


• Molecule 7: TnsD

Chain J:

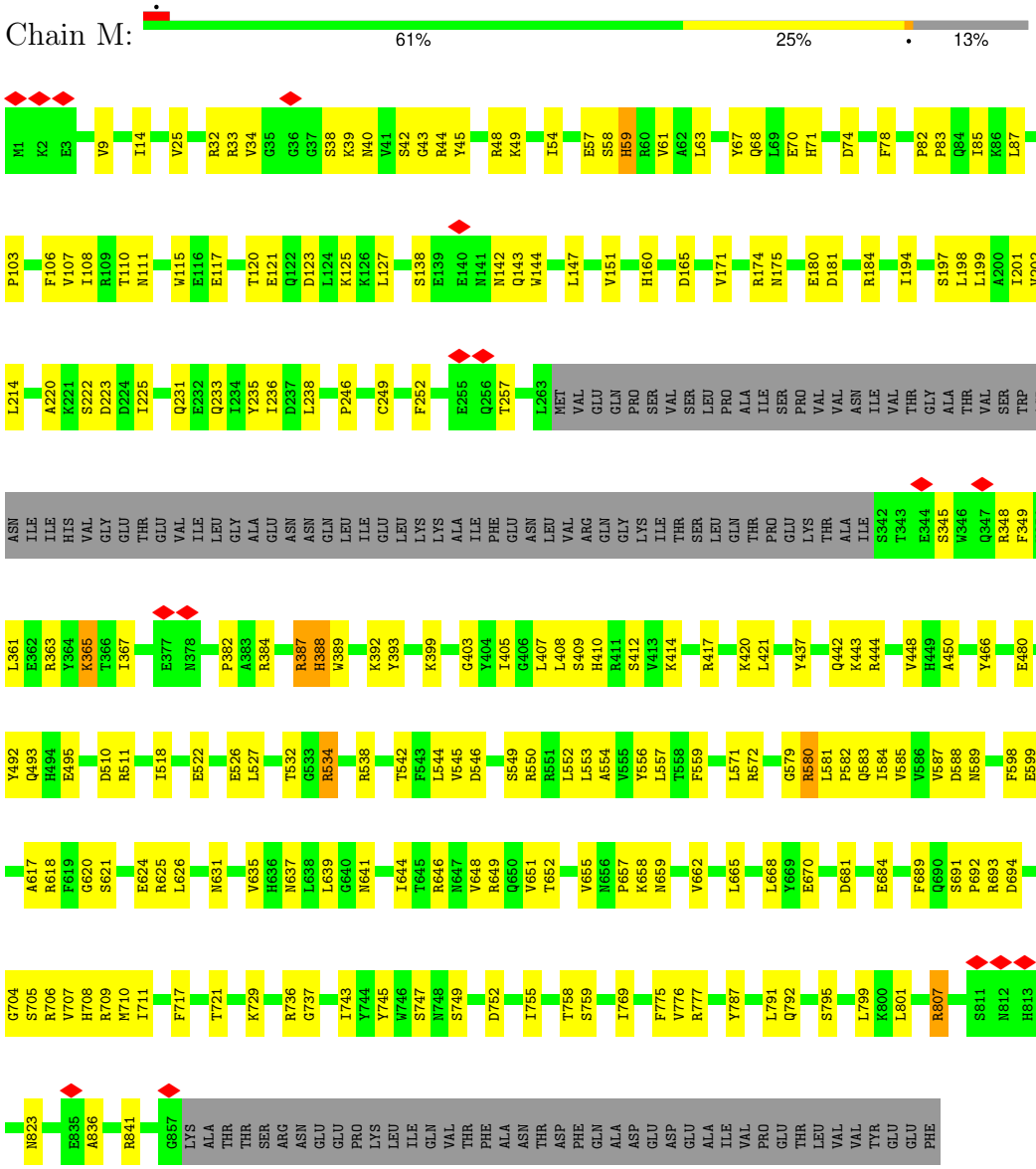






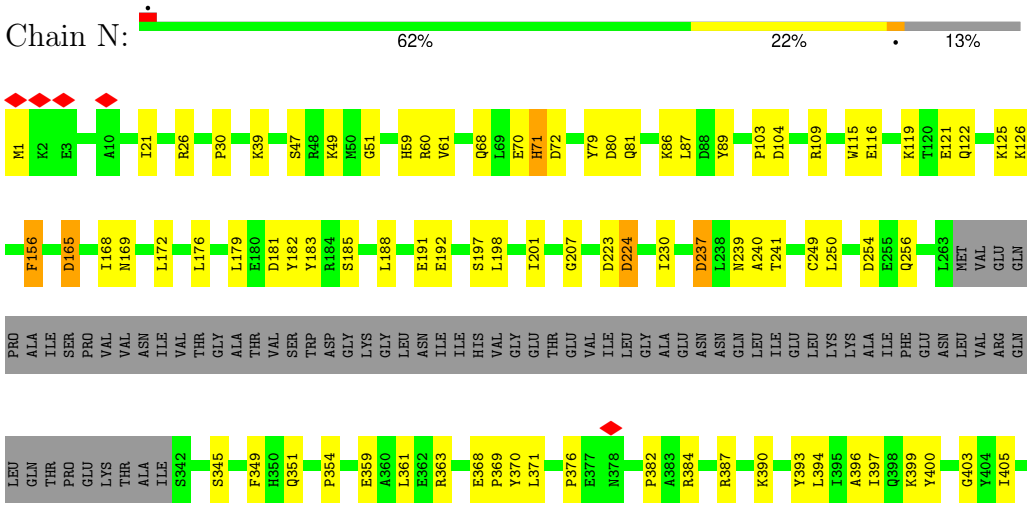
• Molecule 8: Integrase

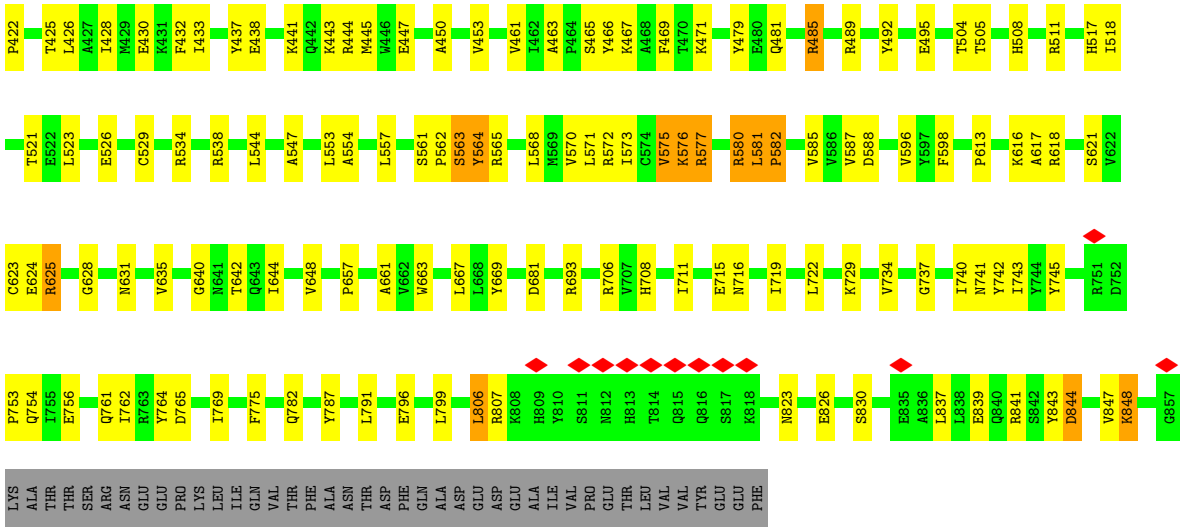
Chain M:



• Molecule 8: Integrase

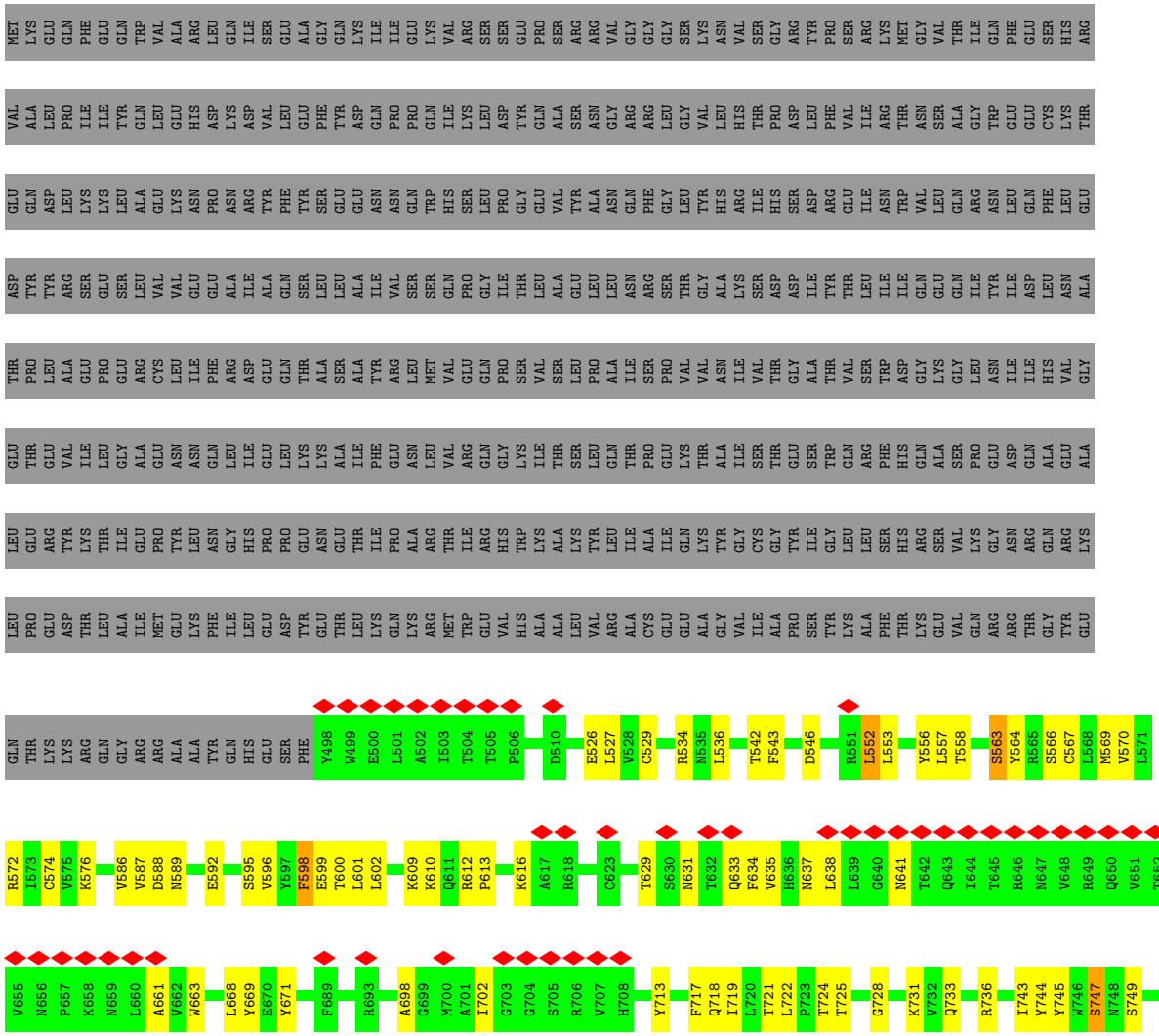
Chain N:

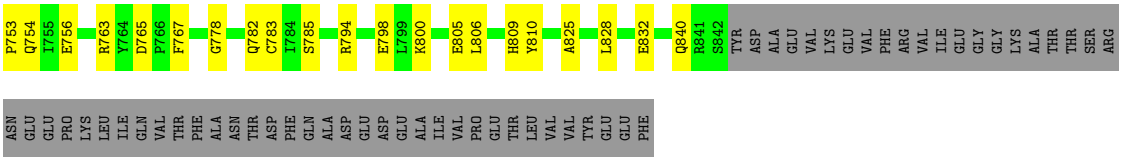




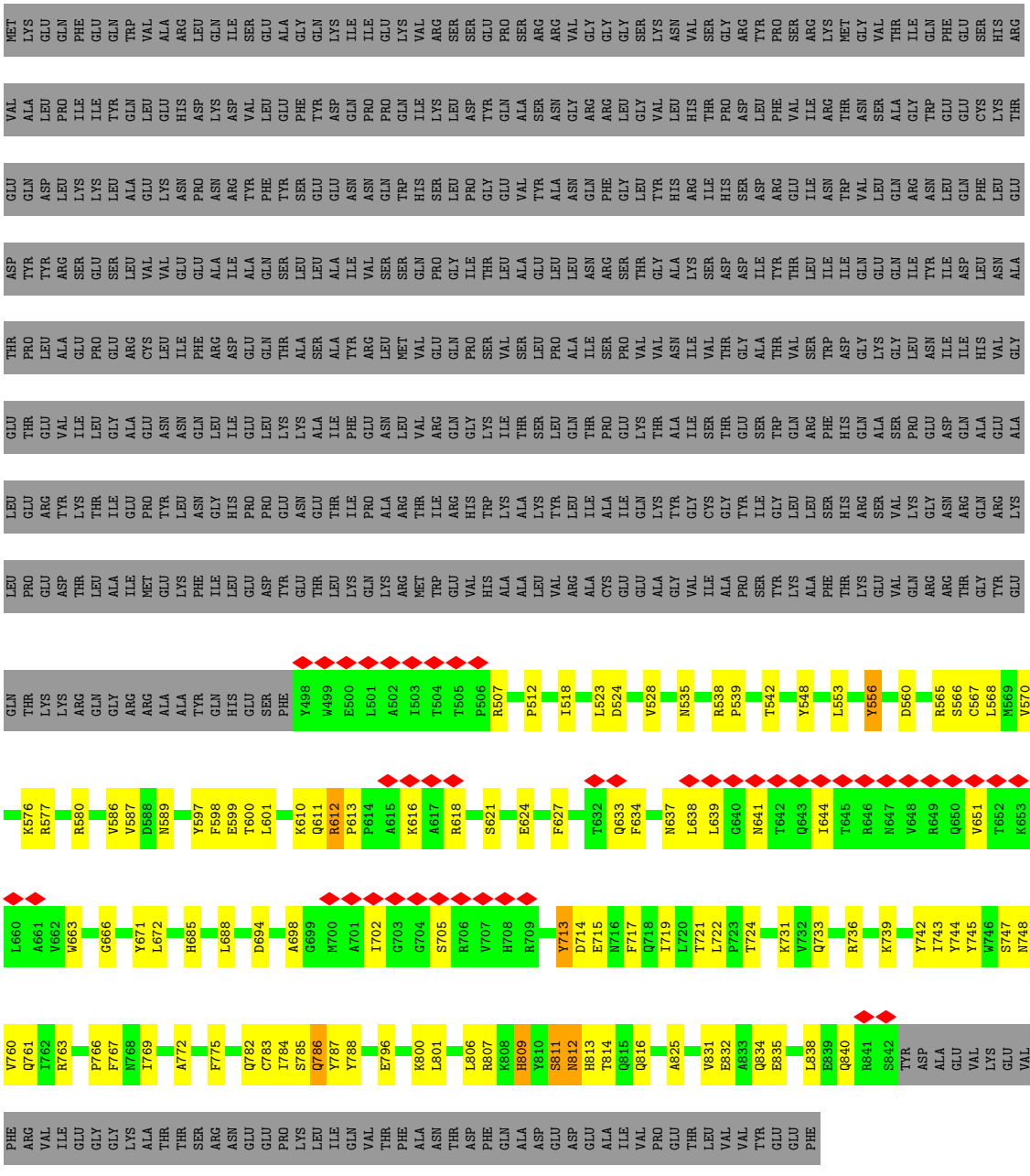
• Molecule 8: Integrase

Chain O:

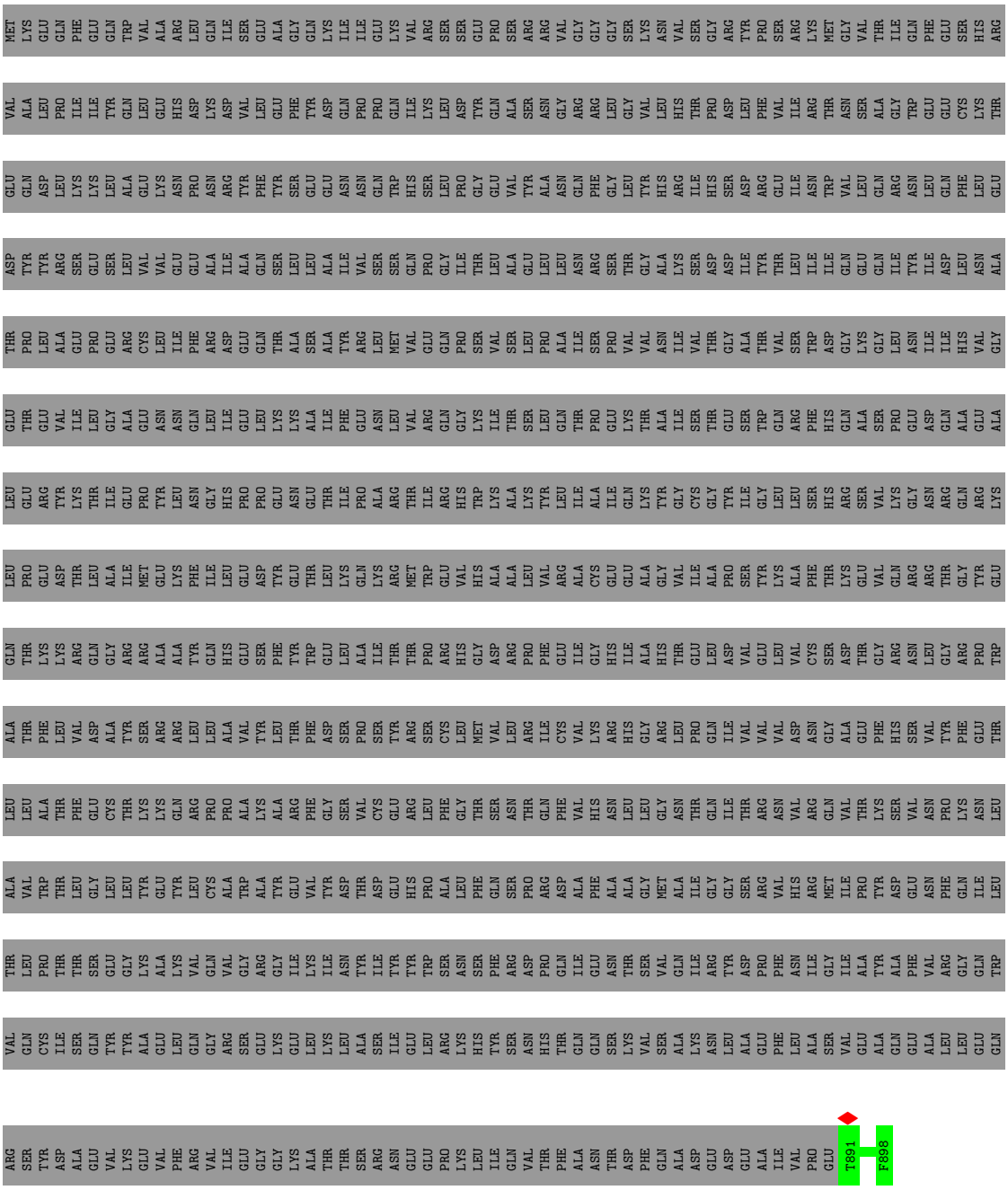




• Molecule 8: Integrase

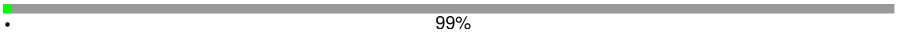


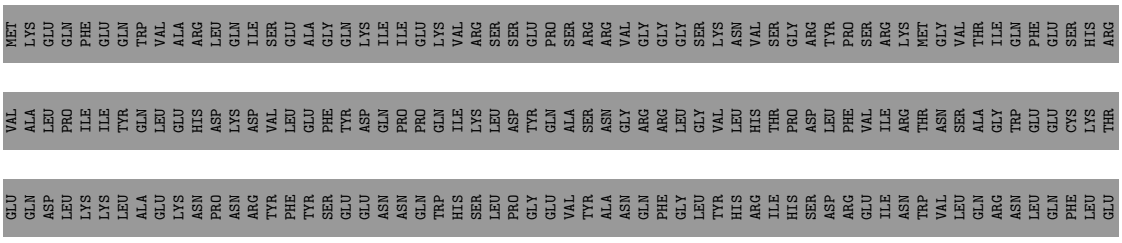
• Molecule 8: Integrase

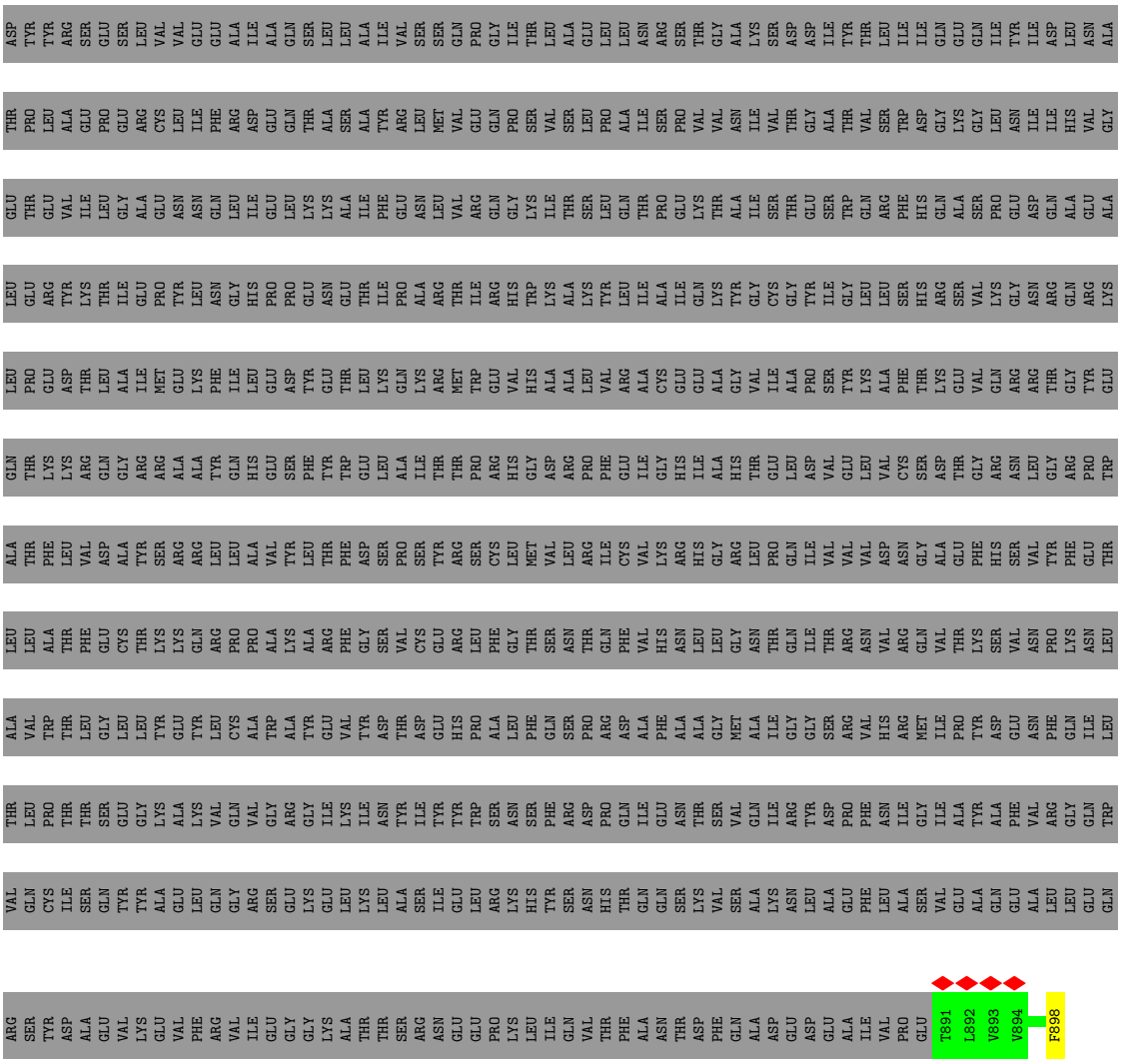


• Molecule 8: Integrase

Chain b:

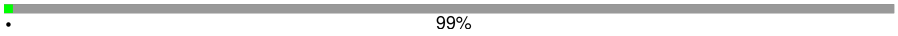


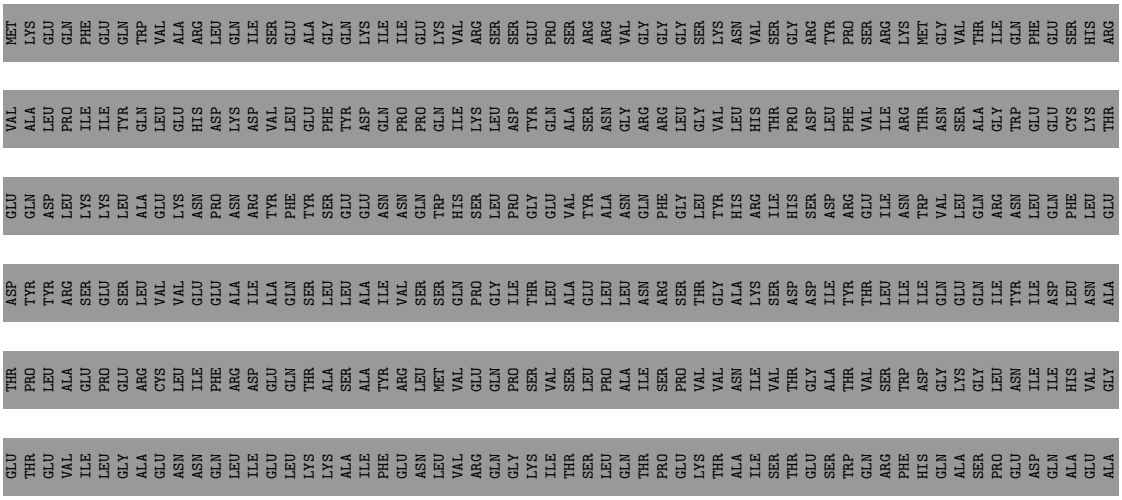


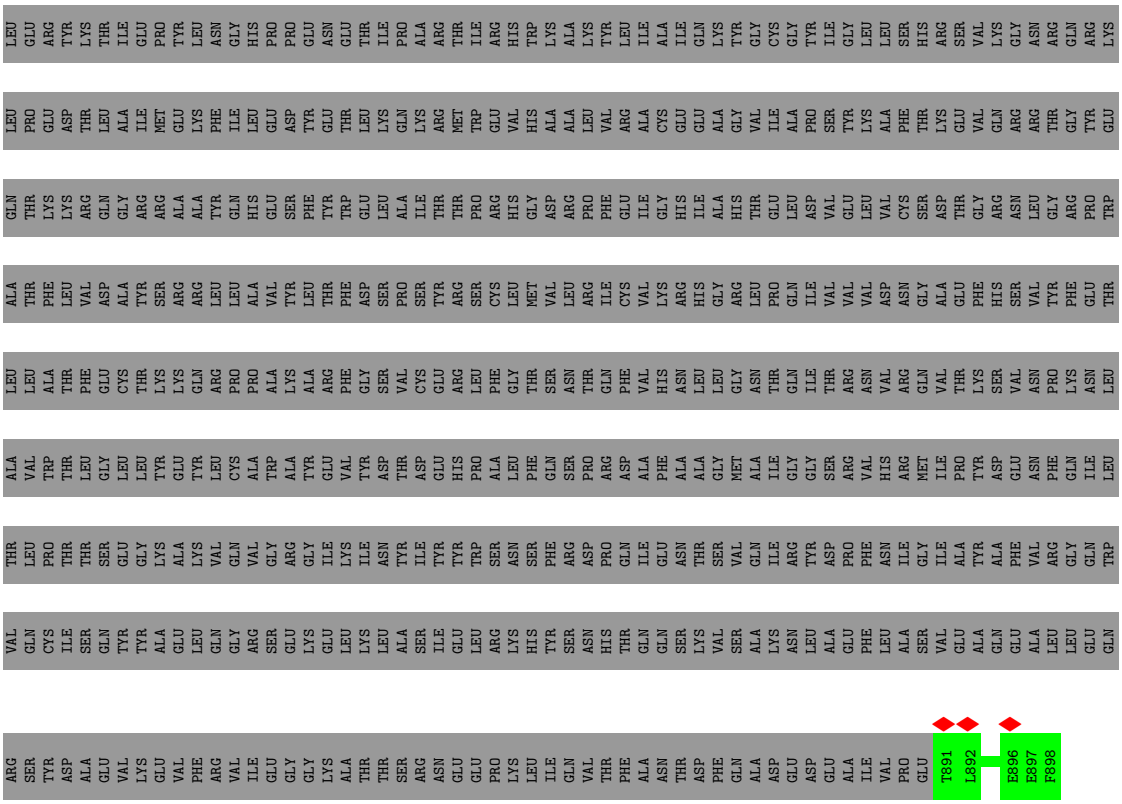


• Molecule 8: Integrase

Chain c:

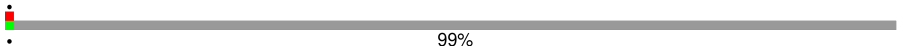


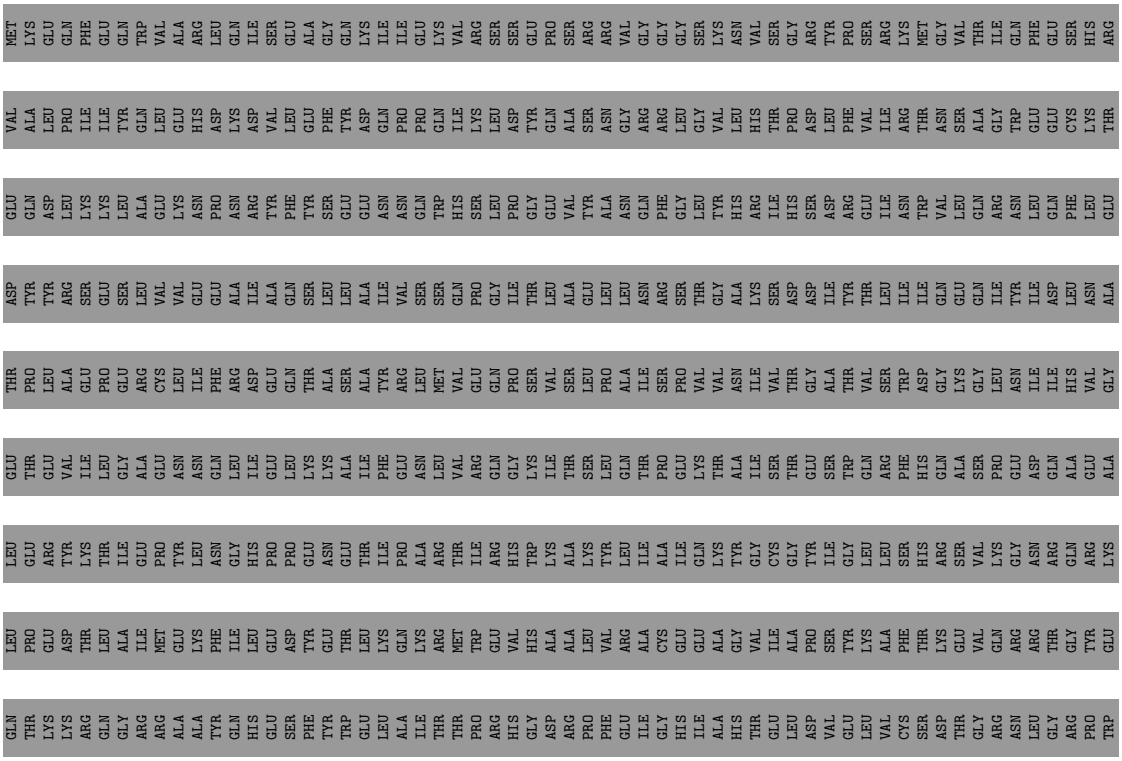




• Molecule 8: Integrase

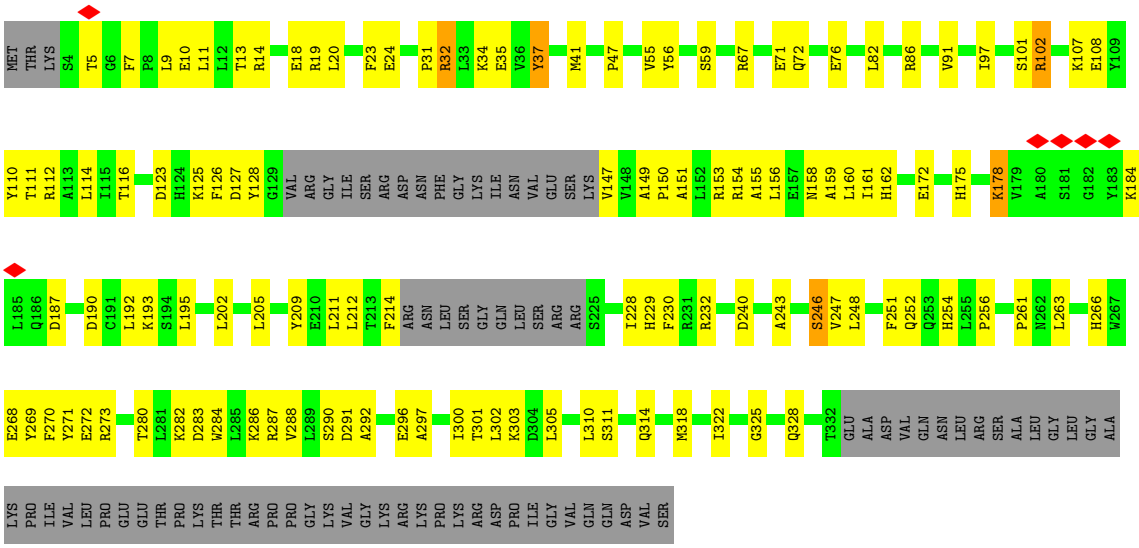
Chain d:





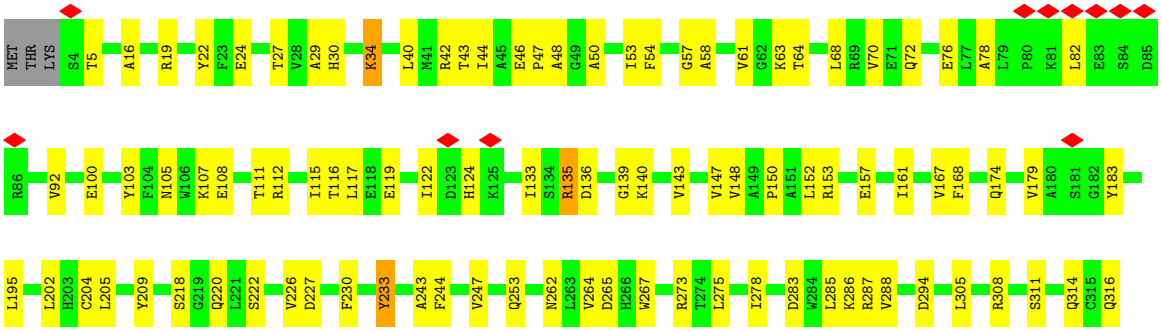
• Molecule 9: TnsC

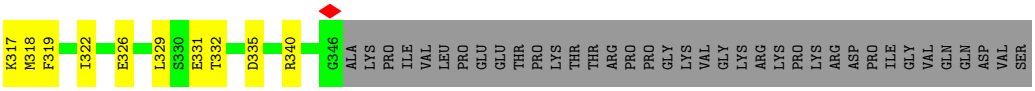
Chain Q:



• Molecule 9: TnsC

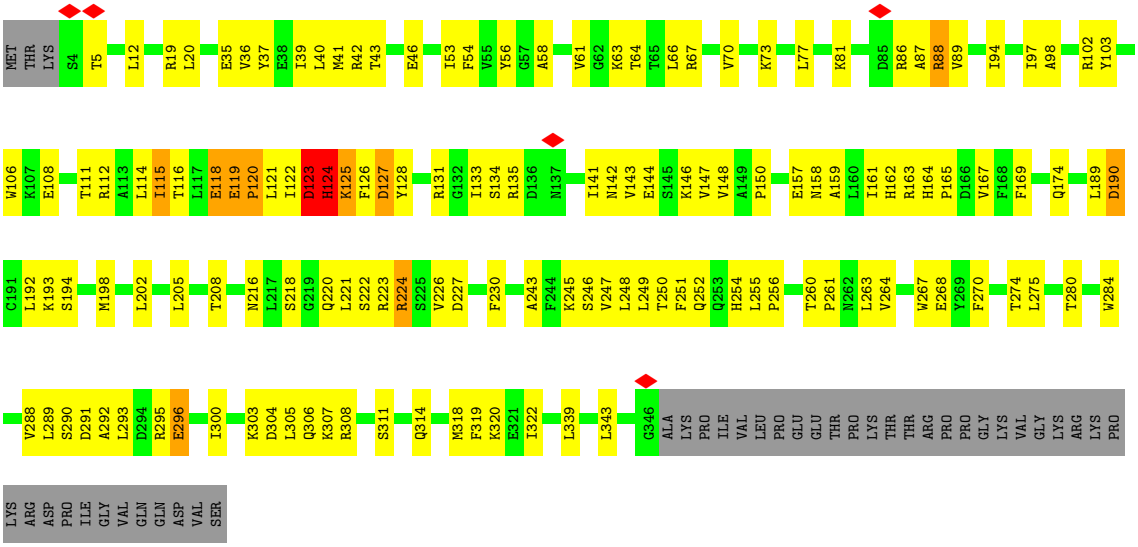
Chain R:





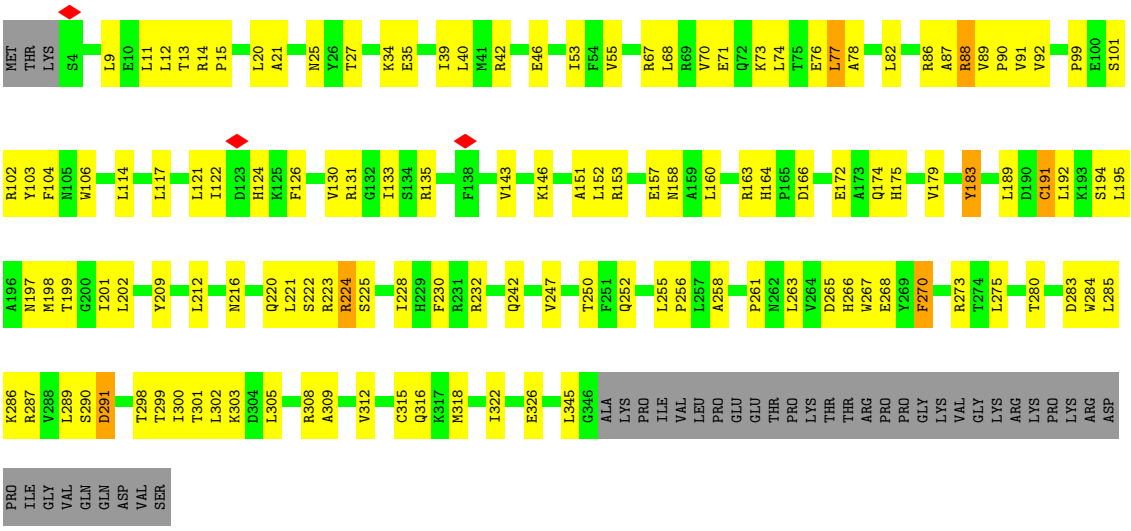
• Molecule 9: TnsC

Chain S:



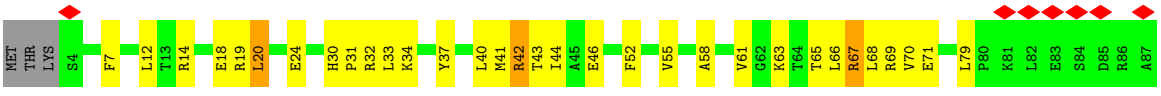
• Molecule 9: TnsC

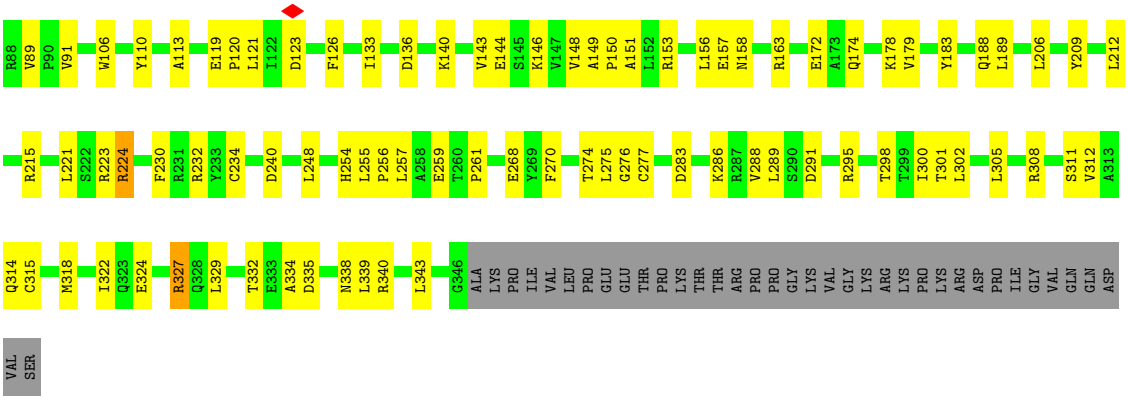
Chain T:



• Molecule 9: TnsC

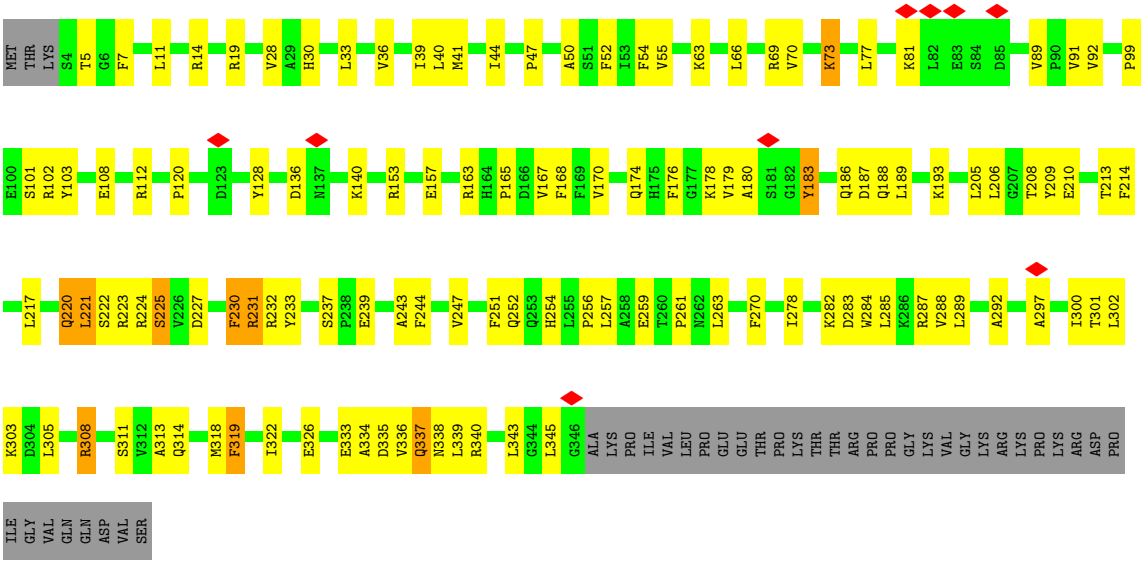
Chain U:





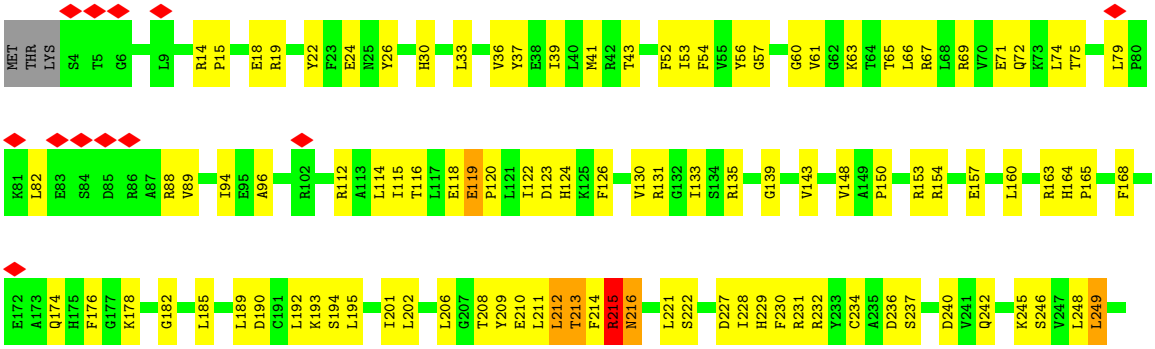
• Molecule 9: TnsC

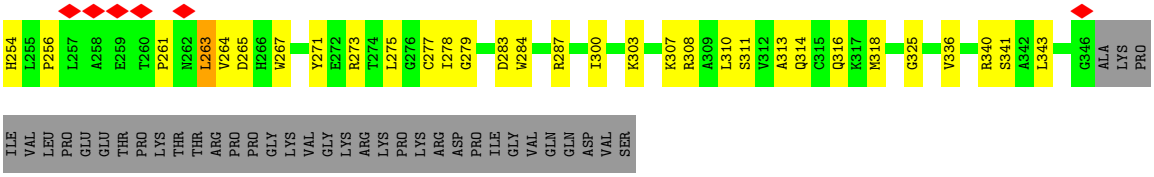
Chain V:



• Molecule 9: TnsC

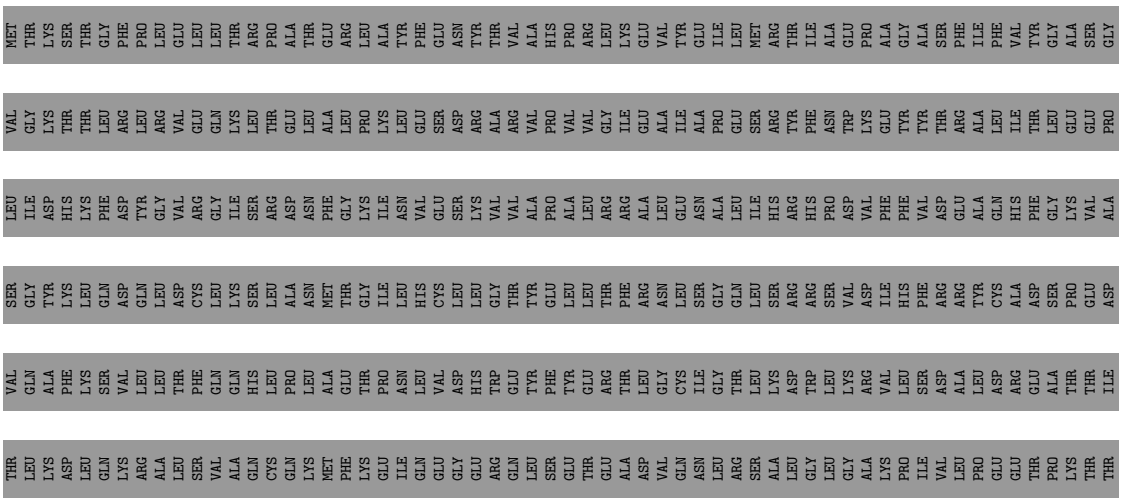
Chain W:

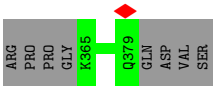




• Molecule 9: TnsC

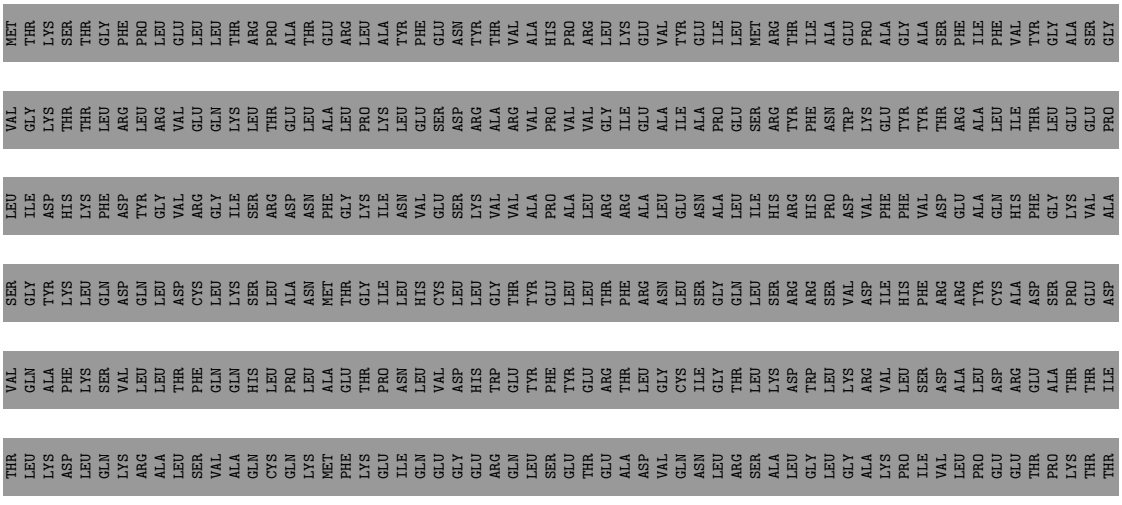
Chain x:

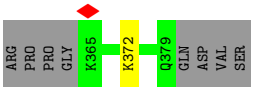




• Molecule 9: TnsC

Chain y:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38326	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	54	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.251	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	394.56, 394.56, 394.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82199997, 0.82199997, 0.82199997	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP, 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	2	0.52	0/775	0.90	0/1192
2	4	0.50	0/1158	0.88	0/1787
3	5	0.50	0/771	0.95	0/1186
4	6	0.48	0/341	0.82	0/524
5	H	0.50	0/1191	0.97	0/1837
6	I	0.52	0/2013	0.89	0/3106
7	J	0.26	0/3792	0.51	0/5142
8	M	0.26	0/6497	0.50	0/8795
8	N	0.32	0/6497	0.54	0/8795
8	O	0.28	0/2857	0.51	0/3878
8	P	0.36	0/2857	0.53	0/3878
8	a	0.27	0/71	0.40	0/96
8	b	0.24	0/71	0.40	0/96
8	c	0.25	0/71	0.38	0/96
8	d	0.25	0/71	0.39	0/96
9	Q	0.29	0/2493	0.52	0/3377
9	R	0.26	0/2812	0.51	0/3805
9	S	0.31	0/2812	0.54	0/3805
9	T	0.31	0/2812	0.54	0/3805
9	U	0.33	0/2812	0.53	0/3805
9	V	0.29	0/2812	0.54	0/3805
9	W	0.29	0/2812	0.56	0/3805
9	x	0.25	0/120	0.54	0/157
9	y	0.26	0/120	0.58	0/157
All	All	0.33	0/48638	0.60	0/67025

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2	692	0	384	17	0
2	4	1030	0	564	24	0
3	5	690	0	387	10	0
4	6	304	0	170	7	0
5	H	1065	0	592	25	0
6	I	1790	0	978	47	0
7	J	3707	0	3761	114	0
8	M	6349	0	6251	148	0
8	N	6349	0	6251	153	0
8	O	2788	0	2745	60	0
8	P	2788	0	2745	66	0
8	a	70	0	65	0	0
8	b	70	0	65	0	0
8	c	70	0	65	0	0
8	d	70	0	65	0	0
9	Q	2440	0	2443	90	0
9	R	2756	0	2772	73	0
9	S	2756	0	2773	114	0
9	T	2756	0	2773	98	0
9	U	2756	0	2772	84	0
9	V	2756	0	2773	93	0
9	W	2756	0	2773	101	0
9	x	119	0	138	0	0
9	y	119	0	138	0	0
10	4	1	0	0	0	0
10	I	2	0	0	0	0
10	M	1	0	0	0	0
10	Q	1	0	0	0	0
10	R	1	0	0	0	0
10	S	1	0	0	0	0
10	T	1	0	0	0	0
10	U	1	0	0	0	0
10	V	1	0	0	0	0
10	W	1	0	0	0	0
11	J	2	0	0	0	0
12	Q	31	0	12	1	0
12	R	31	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	S	31	0	12	1	0
12	T	31	0	12	1	0
12	U	31	0	12	3	0
12	V	31	0	12	0	0
12	W	31	0	12	3	0
13	I	1	0	0	0	0
13	S	5	0	0	0	0
13	T	1	0	0	0	0
All	All	47283	0	44527	1197	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 1197 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)
9:U:209:TYR:O	9:U:212:LEU:HB2	1.61	1.01
7:J:362:GLU:HB2	7:J:363:PRO:HD2	1.40	1.00
9:S:246:SER:HA	9:S:249:LEU:HD12	1.52	0.92
9:Q:150:PRO:HA	9:Q:153:ARG:HE	1.35	0.91
8:N:581:LEU:HD23	8:N:582:PRO:HD2	1.53	0.90

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
7	J	460/462 (100%)	435 (95%)	24 (5%)	1 (0%)	44 72
8	M	775/898 (86%)	758 (98%)	17 (2%)	0	100 100
8	N	775/898 (86%)	740 (96%)	31 (4%)	4 (0%)	25 57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	O	343/898 (38%)	334 (97%)	9 (3%)	0	100	100
8	P	343/898 (38%)	325 (95%)	17 (5%)	1 (0%)	37	67
8	a	6/898 (1%)	6 (100%)	0	0	100	100
8	b	6/898 (1%)	6 (100%)	0	0	100	100
8	c	6/898 (1%)	6 (100%)	0	0	100	100
8	d	6/898 (1%)	6 (100%)	0	0	100	100
9	Q	296/383 (77%)	286 (97%)	10 (3%)	0	100	100
9	R	341/383 (89%)	325 (95%)	16 (5%)	0	100	100
9	S	341/383 (89%)	319 (94%)	19 (6%)	3 (1%)	14	46
9	T	341/383 (89%)	320 (94%)	20 (6%)	1 (0%)	37	67
9	U	341/383 (89%)	324 (95%)	17 (5%)	0	100	100
9	V	341/383 (89%)	326 (96%)	14 (4%)	1 (0%)	37	67
9	W	341/383 (89%)	324 (95%)	15 (4%)	2 (1%)	22	54
9	x	13/383 (3%)	13 (100%)	0	0	100	100
9	y	13/383 (3%)	13 (100%)	0	0	100	100
All	All	5088/11093 (46%)	4866 (96%)	209 (4%)	13 (0%)	38	67

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	J	363	PRO
8	N	564	TYR
9	S	120	PRO
9	W	215	ARG
9	T	224	ARG

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	
7	J	412/412 (100%)	391 (95%)	21 (5%)	20	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
8	M	678/782 (87%)	654 (96%)	24 (4%)	31 55
8	N	678/782 (87%)	644 (95%)	34 (5%)	20 46
8	O	299/782 (38%)	290 (97%)	9 (3%)	36 58
8	P	299/782 (38%)	281 (94%)	18 (6%)	16 42
8	a	8/782 (1%)	8 (100%)	0	100 100
8	b	8/782 (1%)	7 (88%)	1 (12%)	3 18
8	c	8/782 (1%)	8 (100%)	0	100 100
8	d	8/782 (1%)	8 (100%)	0	100 100
9	Q	262/332 (79%)	246 (94%)	16 (6%)	15 42
9	R	296/332 (89%)	285 (96%)	11 (4%)	29 53
9	S	296/332 (89%)	274 (93%)	22 (7%)	11 35
9	T	296/332 (89%)	283 (96%)	13 (4%)	24 49
9	U	296/332 (89%)	282 (95%)	14 (5%)	22 47
9	V	296/332 (89%)	283 (96%)	13 (4%)	24 49
9	W	296/332 (89%)	275 (93%)	21 (7%)	12 37
9	x	13/332 (4%)	13 (100%)	0	100 100
9	y	13/332 (4%)	12 (92%)	1 (8%)	10 35
All	All	4462/9656 (46%)	4244 (95%)	218 (5%)	23 46

5 of 218 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	Q	160	LEU
9	S	124	HIS
9	W	126	PHE
9	Q	246	SER
9	R	233	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
9	V	220	GLN
9	W	72	GLN
9	Q	175	HIS
9	R	174	GLN

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Mol	Chain	Res	Type
9	R	314	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 13 are monoatomic - leaving 7 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	$\#\|Z\| > 2$
12	ATP	U	600	10	28,33,33	0.65	0	34,52,52	0.85	2 (5%)
12	ATP	S	600	10	28,33,33	0.64	0	34,52,52	0.66	1 (2%)
12	ATP	R	600	10	28,33,33	0.62	0	34,52,52	0.72	2 (5%)
12	ATP	V	600	10	28,33,33	0.62	0	34,52,52	0.70	2 (5%)
12	ATP	T	600	10	28,33,33	0.64	0	34,52,52	0.61	1 (2%)
12	ATP	Q	600	10	28,33,33	0.67	0	34,52,52	0.59	1 (2%)
12	ATP	W	600	10	28,33,33	0.62	0	34,52,52	0.62	1 (2%)

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
12	ATP	U	600	10	-	9/18/38/38	0/3/3/3
12	ATP	S	600	10	-	2/18/38/38	0/3/3/3
12	ATP	R	600	10	-	9/18/38/38	0/3/3/3
12	ATP	V	600	10	-	9/18/38/38	0/3/3/3
12	ATP	T	600	10	-	2/18/38/38	0/3/3/3
12	ATP	Q	600	10	-	4/18/38/38	0/3/3/3
12	ATP	W	600	10	-	4/18/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	U	600	ATP	C4'-O4'-C1'	-3.39	106.82	109.92
12	T	600	ATP	C5-C6-N6	2.35	123.89	120.31
12	Q	600	ATP	C5-C6-N6	2.34	123.88	120.31
12	S	600	ATP	C5-C6-N6	2.33	123.86	120.31
12	W	600	ATP	C5-C6-N6	2.33	123.86	120.31

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	Q	600	ATP	C5'-O5'-PA-O1A
12	R	600	ATP	PB-O3B-PG-O2G
12	R	600	ATP	C5'-O5'-PA-O3A
12	U	600	ATP	C5'-O5'-PA-O1A
12	U	600	ATP	C5'-O5'-PA-O2A

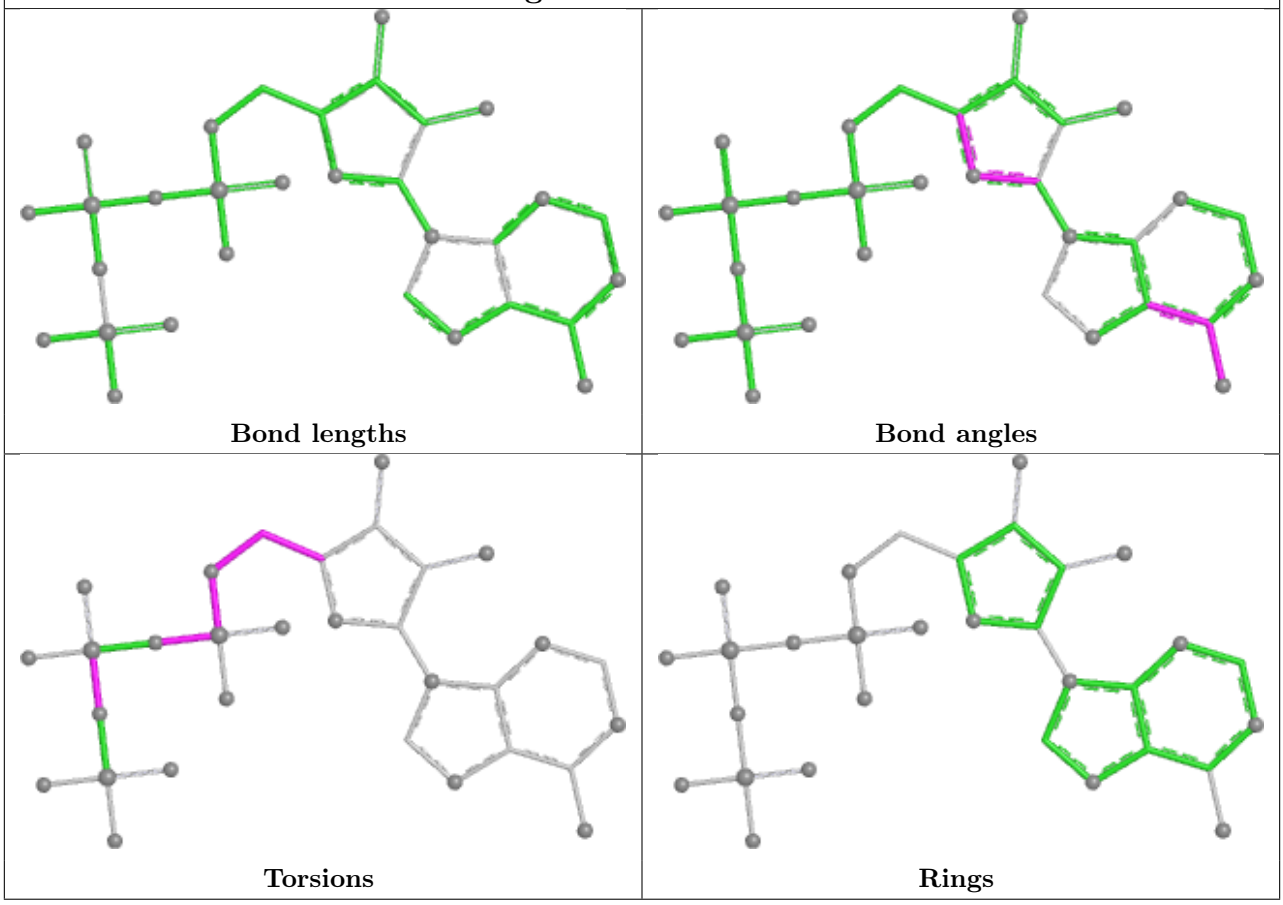
There are no ring outliers.

6 monomers are involved in 12 short contacts:

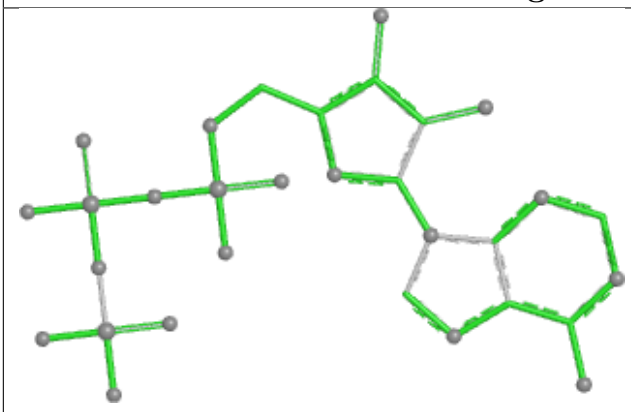
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	U	600	ATP	3	0
12	S	600	ATP	1	0
12	R	600	ATP	3	0
12	T	600	ATP	1	0
12	Q	600	ATP	1	0
12	W	600	ATP	3	0

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 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.

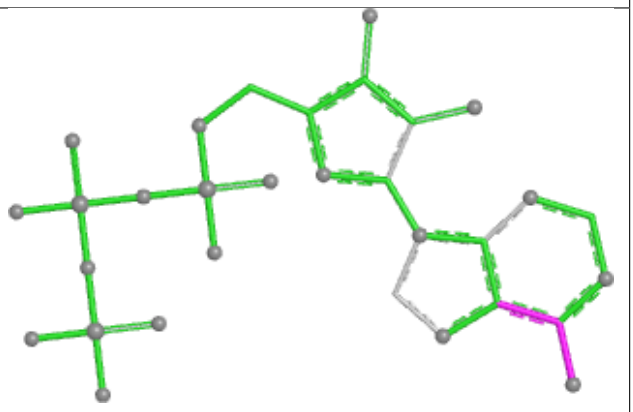
Ligand ATP U 600



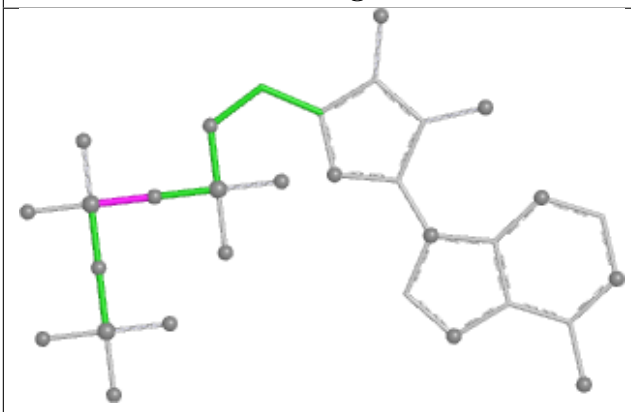
Ligand ATP S 600



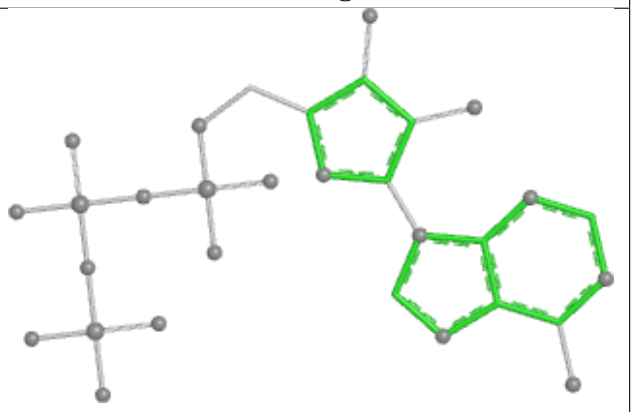
Bond lengths



Bond angles

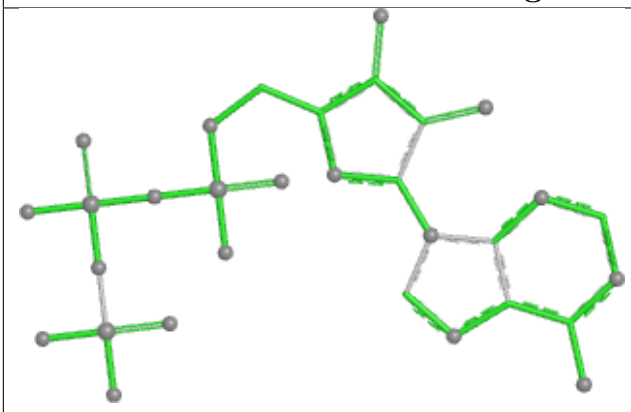


Torsions

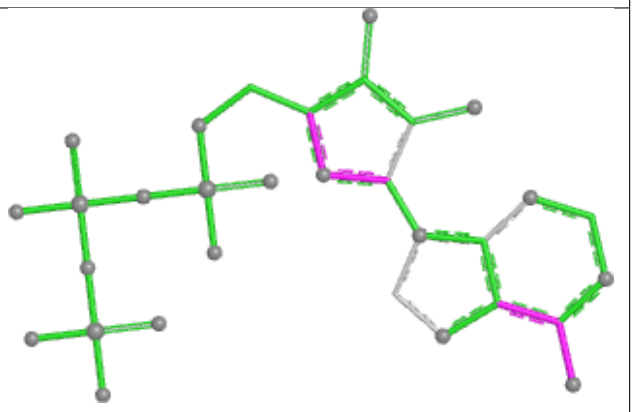


Rings

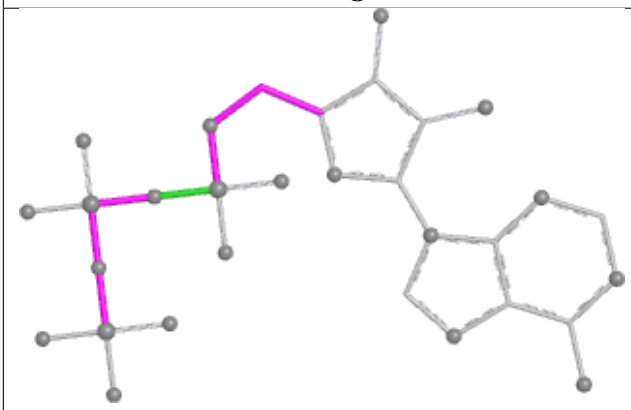
Ligand ATP R 600



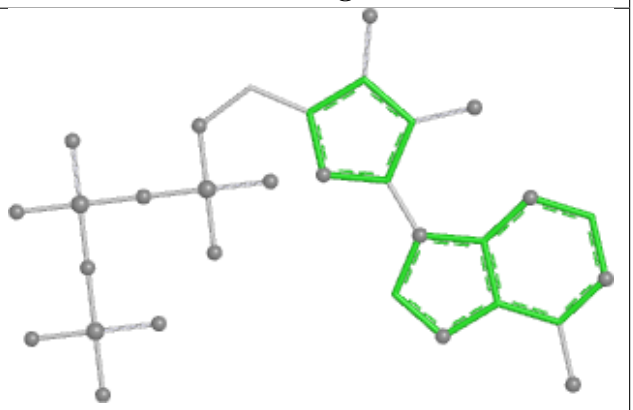
Bond lengths



Bond angles

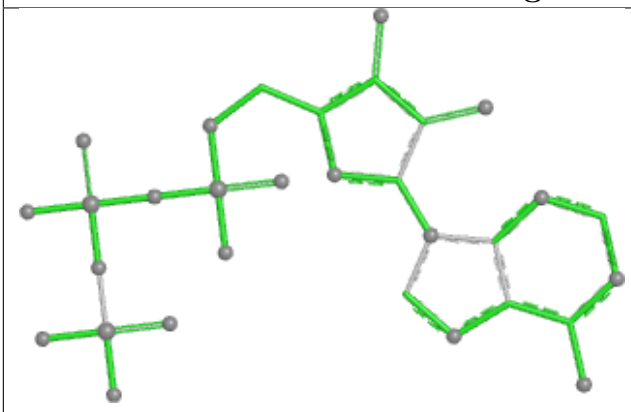


Torsions

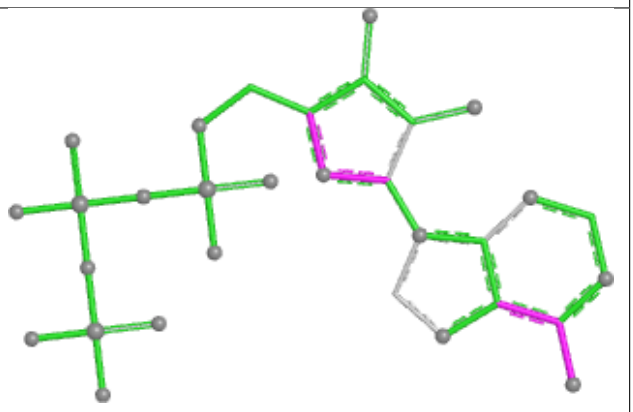


Rings

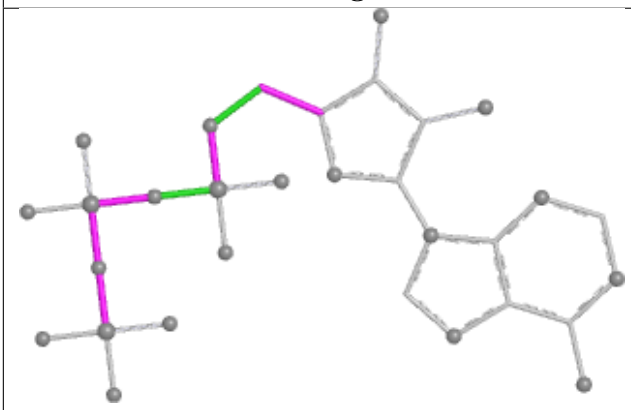
Ligand ATP V 600



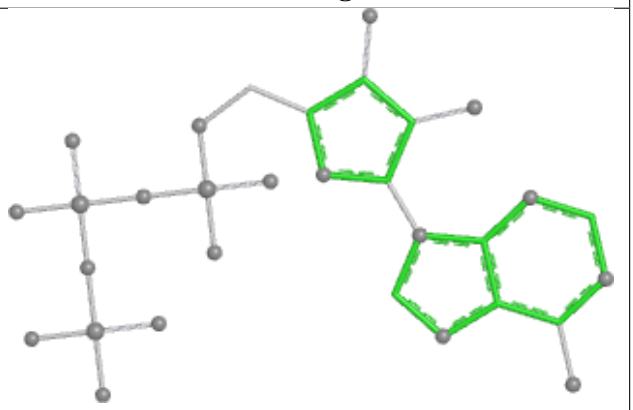
Bond lengths



Bond angles

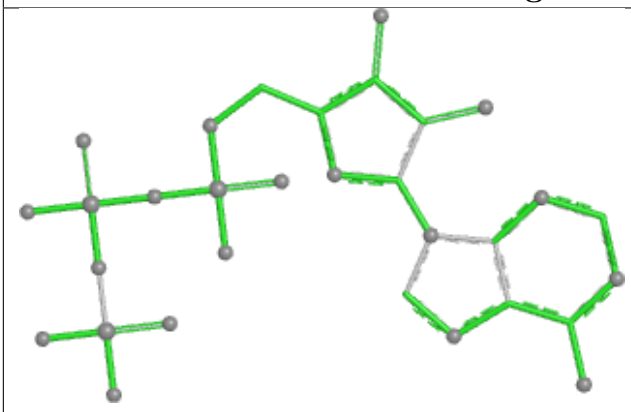


Torsions

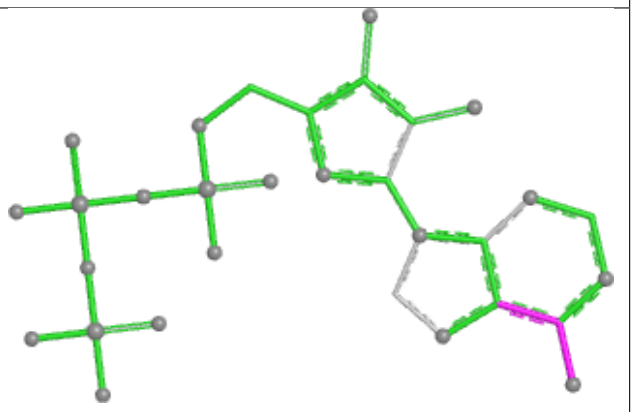


Rings

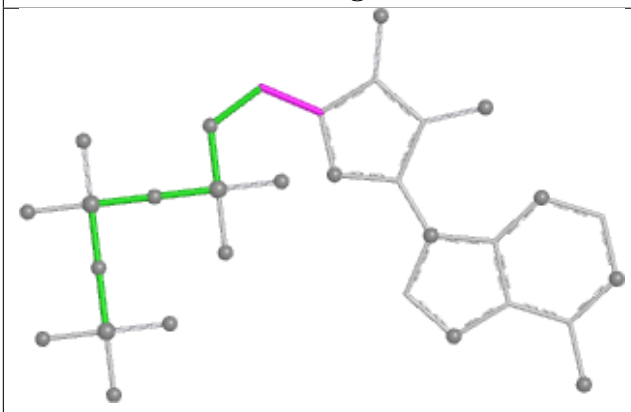
Ligand ATP T 600



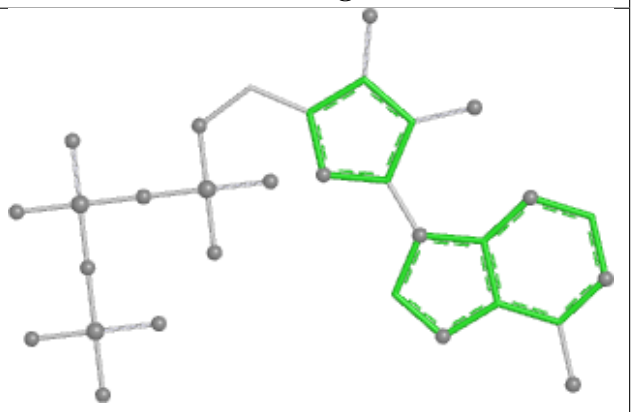
Bond lengths



Bond angles

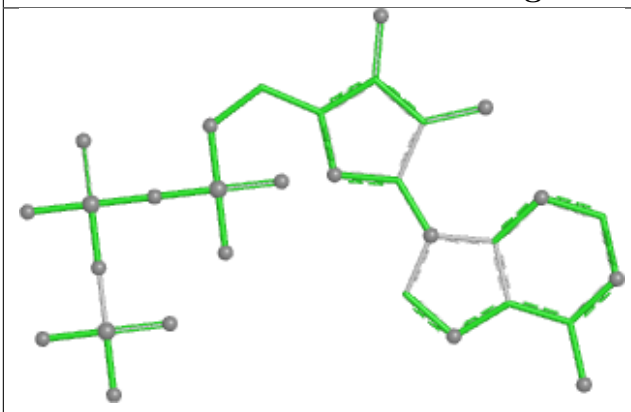


Torsions

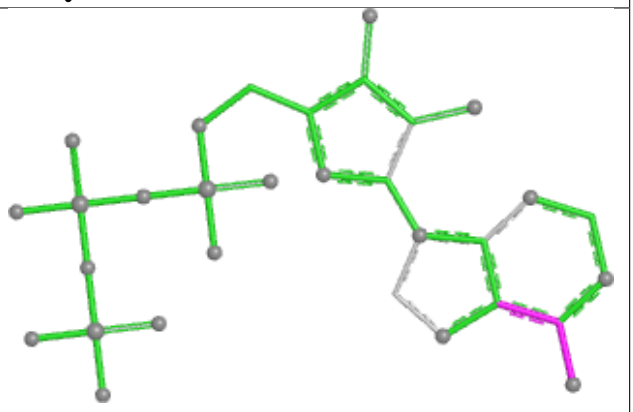


Rings

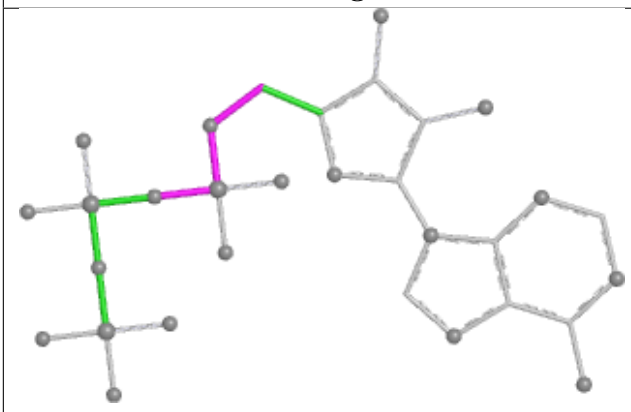
Ligand ATP Q 600



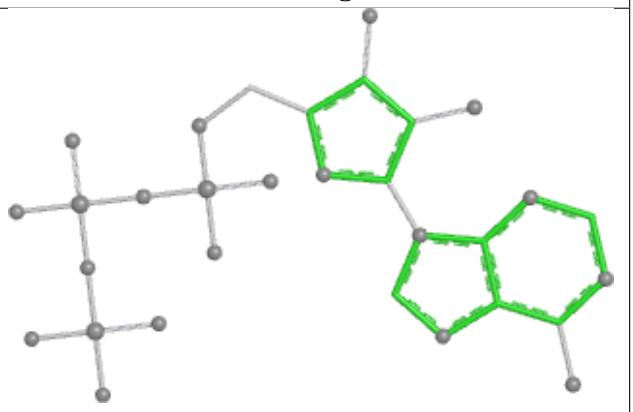
Bond lengths



Bond angles

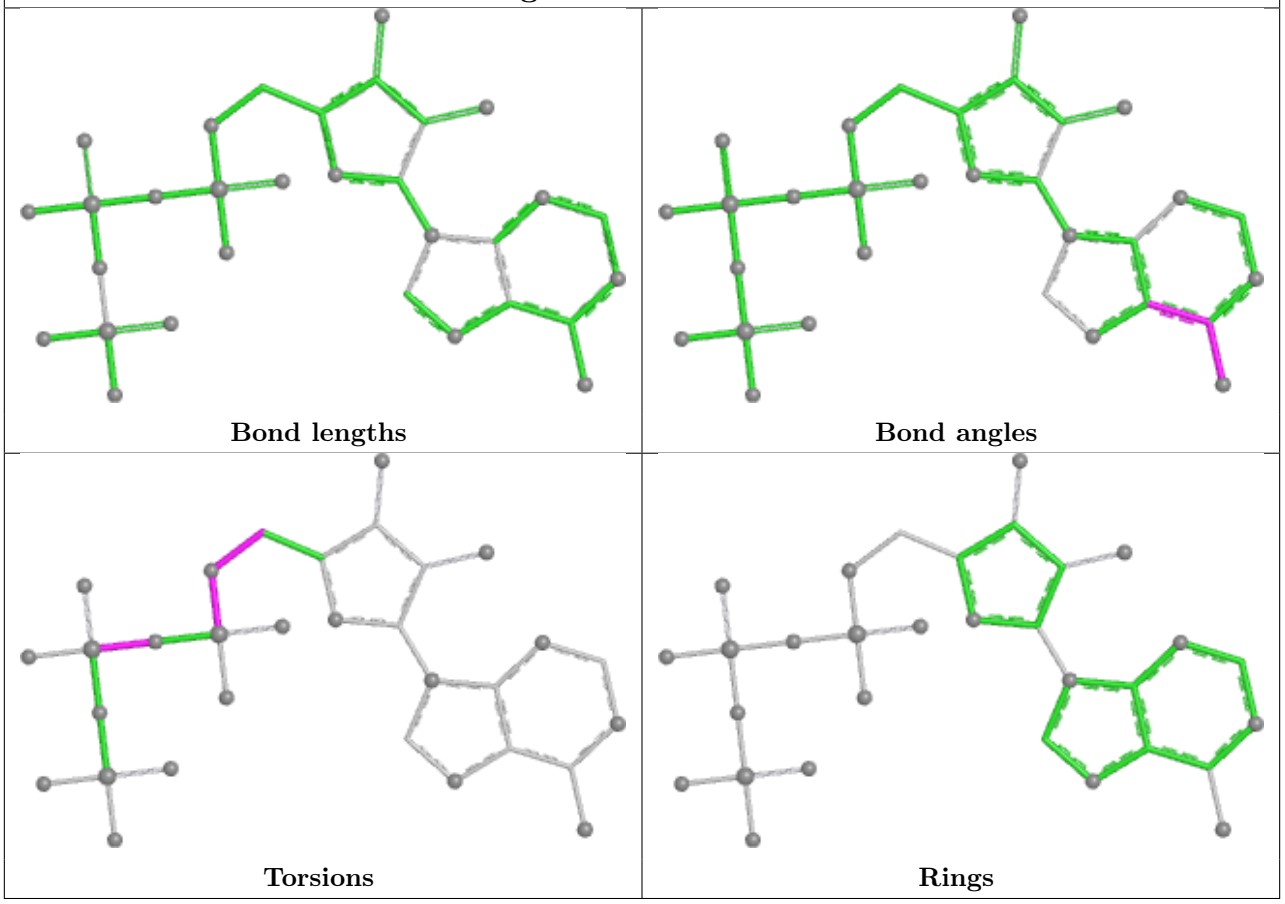


Torsions



Rings

Ligand ATP W 600



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.

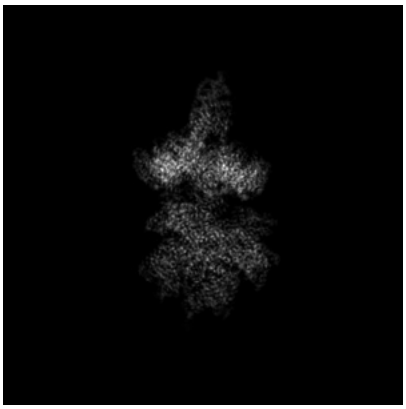
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44944. These allow visual inspection of the internal detail of the map and identification of artifacts.

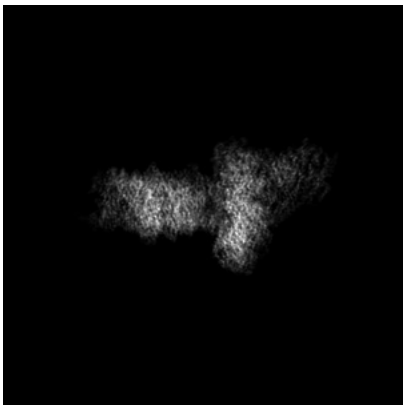
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

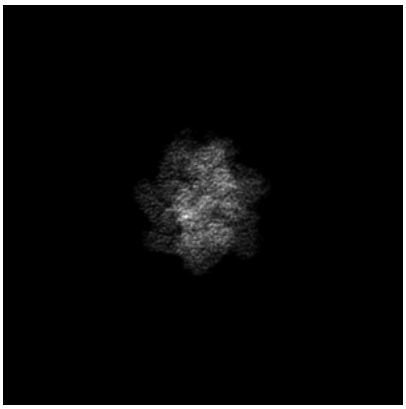
6.1.1 Primary map



X

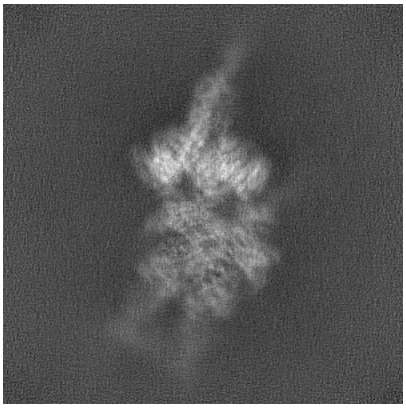


Y

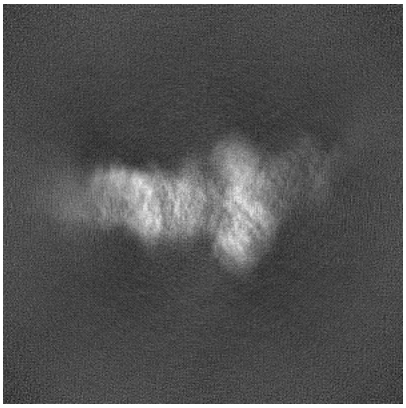


Z

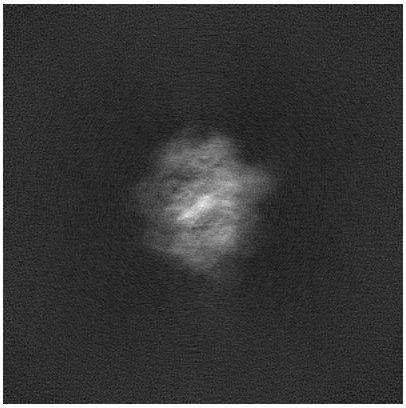
6.1.2 Raw map



X



Y



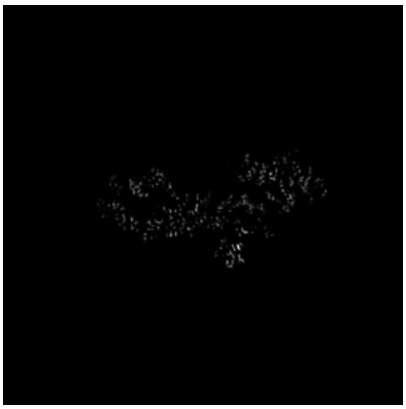
Z

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

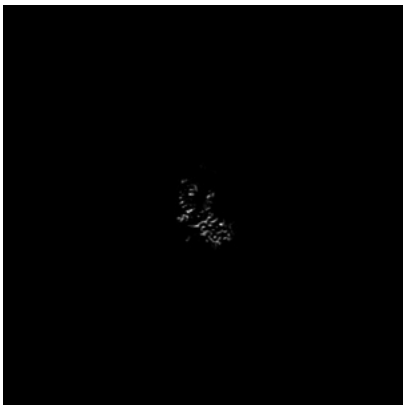
6.2 Central slices (i)

6.2.1 Primary map

X Index: 240

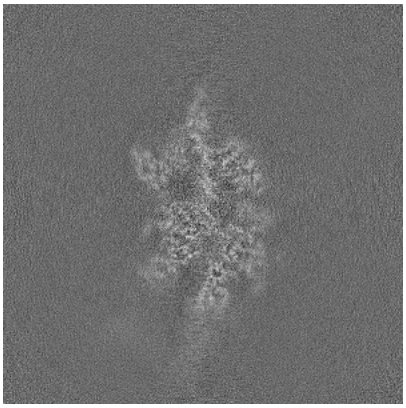


Y Index: 240

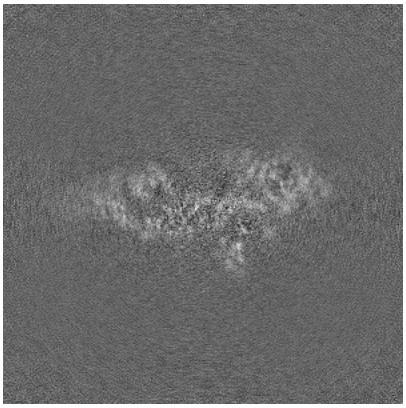


Z Index: 240

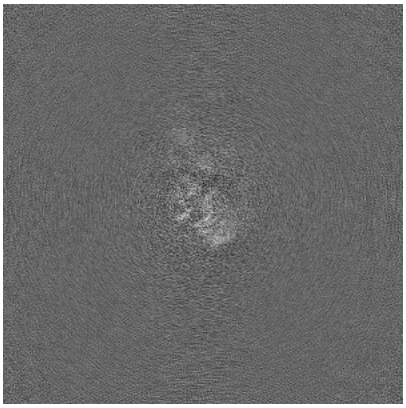
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

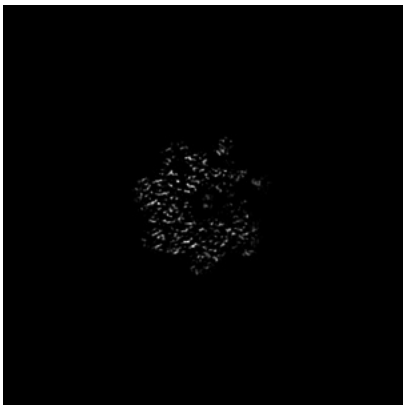
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

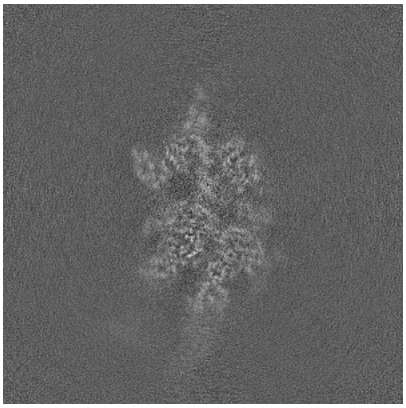
X Index: 237

Y Index: 263

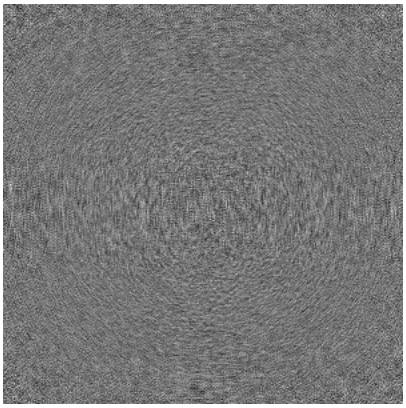


Z Index: 284

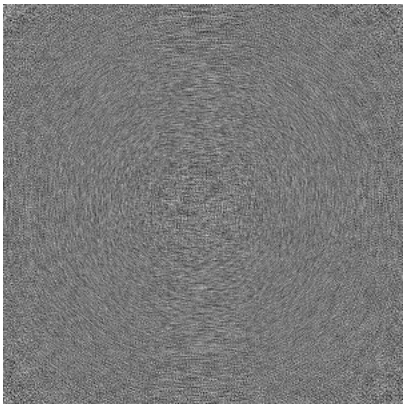
6.3.2 Raw map



X Index: 237



Y Index: 0

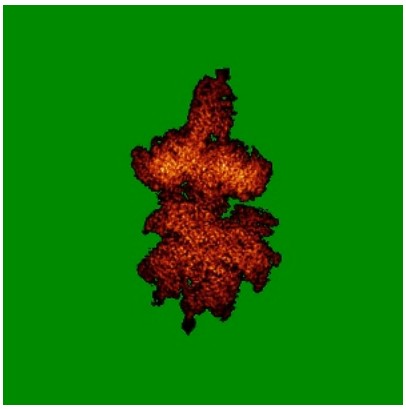


Z Index: 0

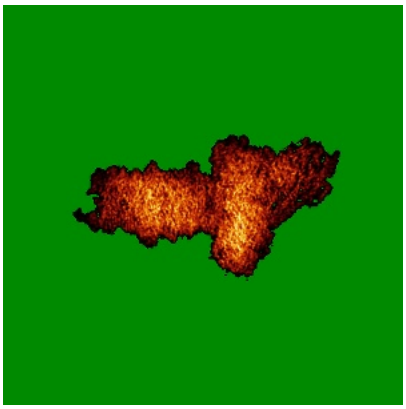
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

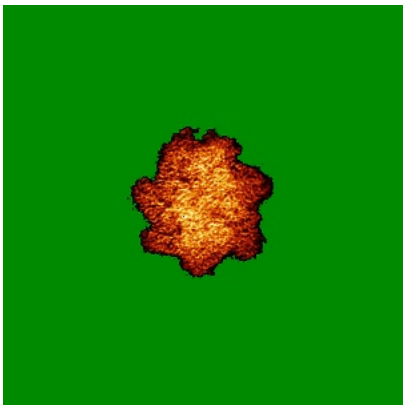
6.4.1 Primary map



X

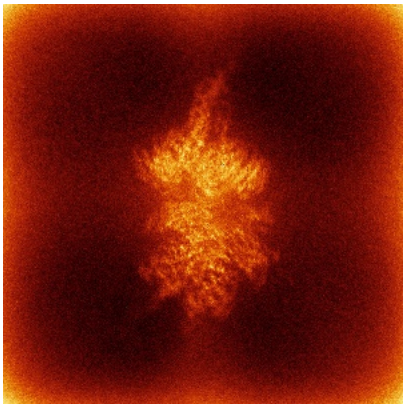


Y

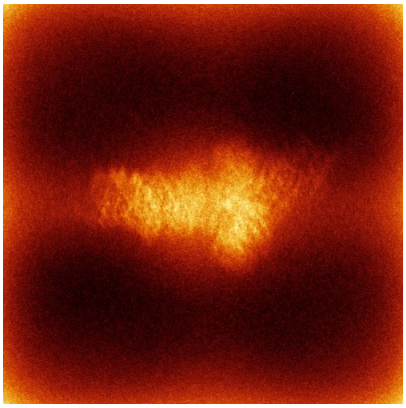


Z

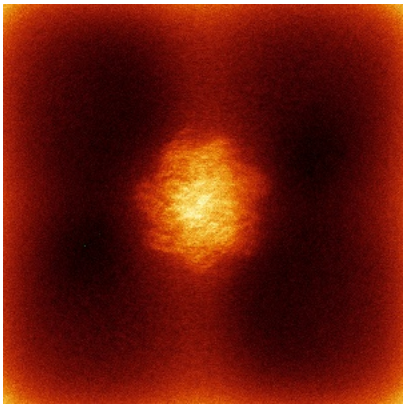
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

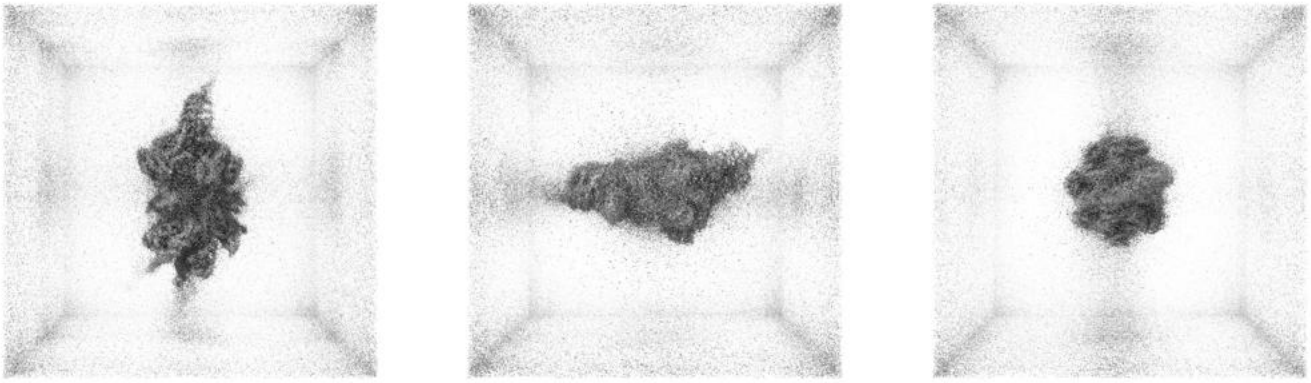
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

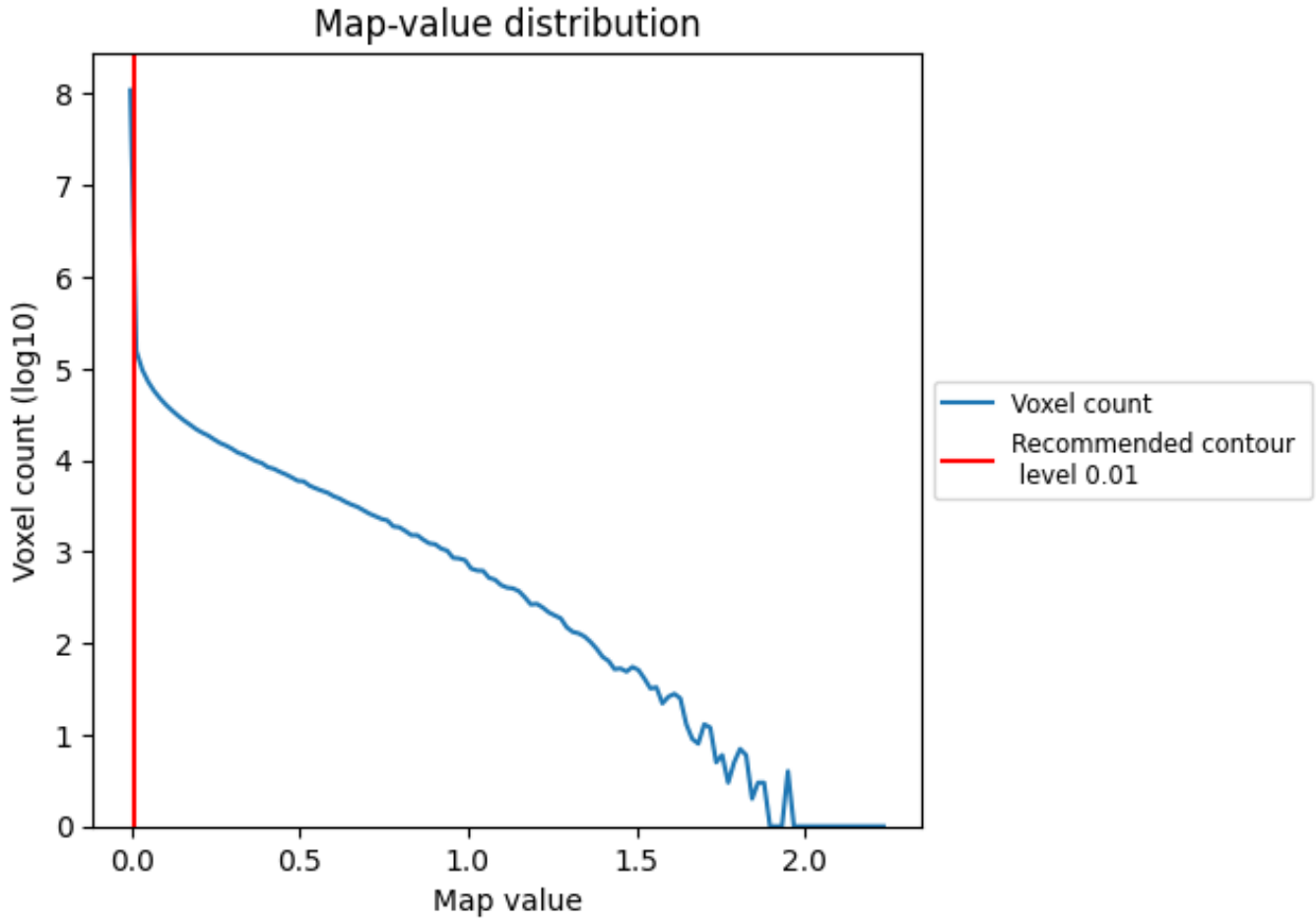
6.6 Mask visualisation (i)

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

7 Map analysis

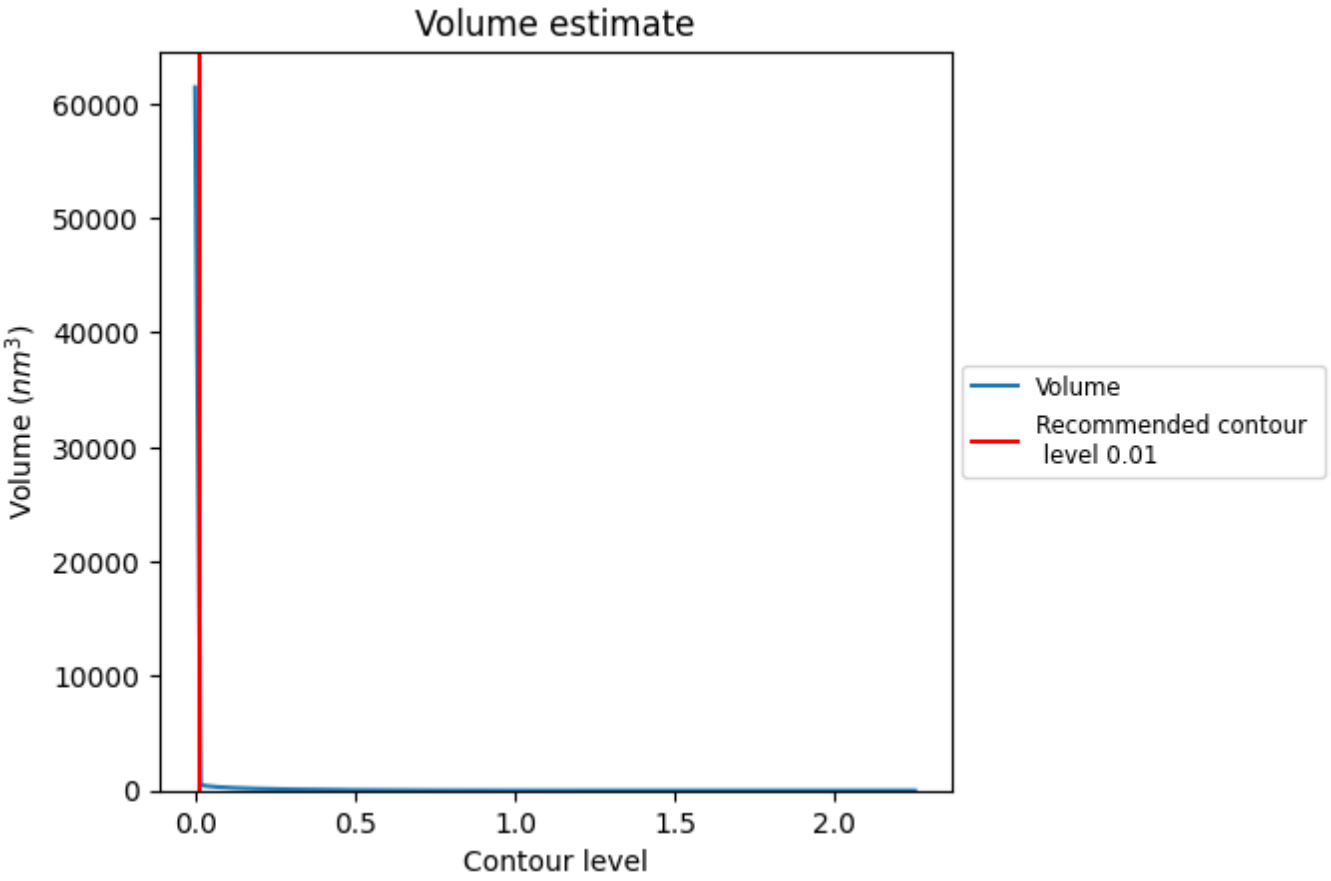
This section contains the results of statistical analysis of the map.

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.

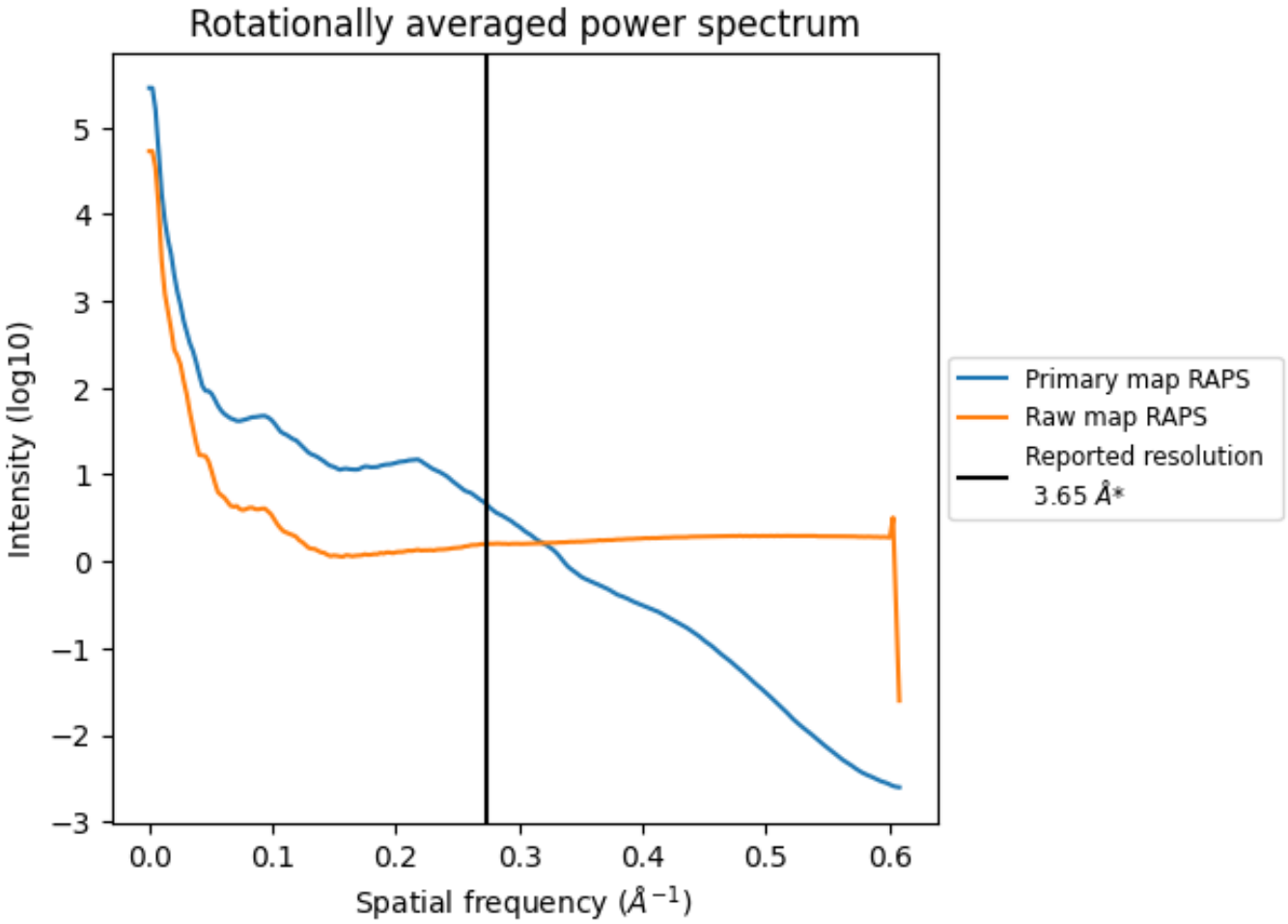
7.2 Volume estimate



The volume at the recommended contour level is 18457 nm^3; this corresponds to an approximate mass of 16673 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)

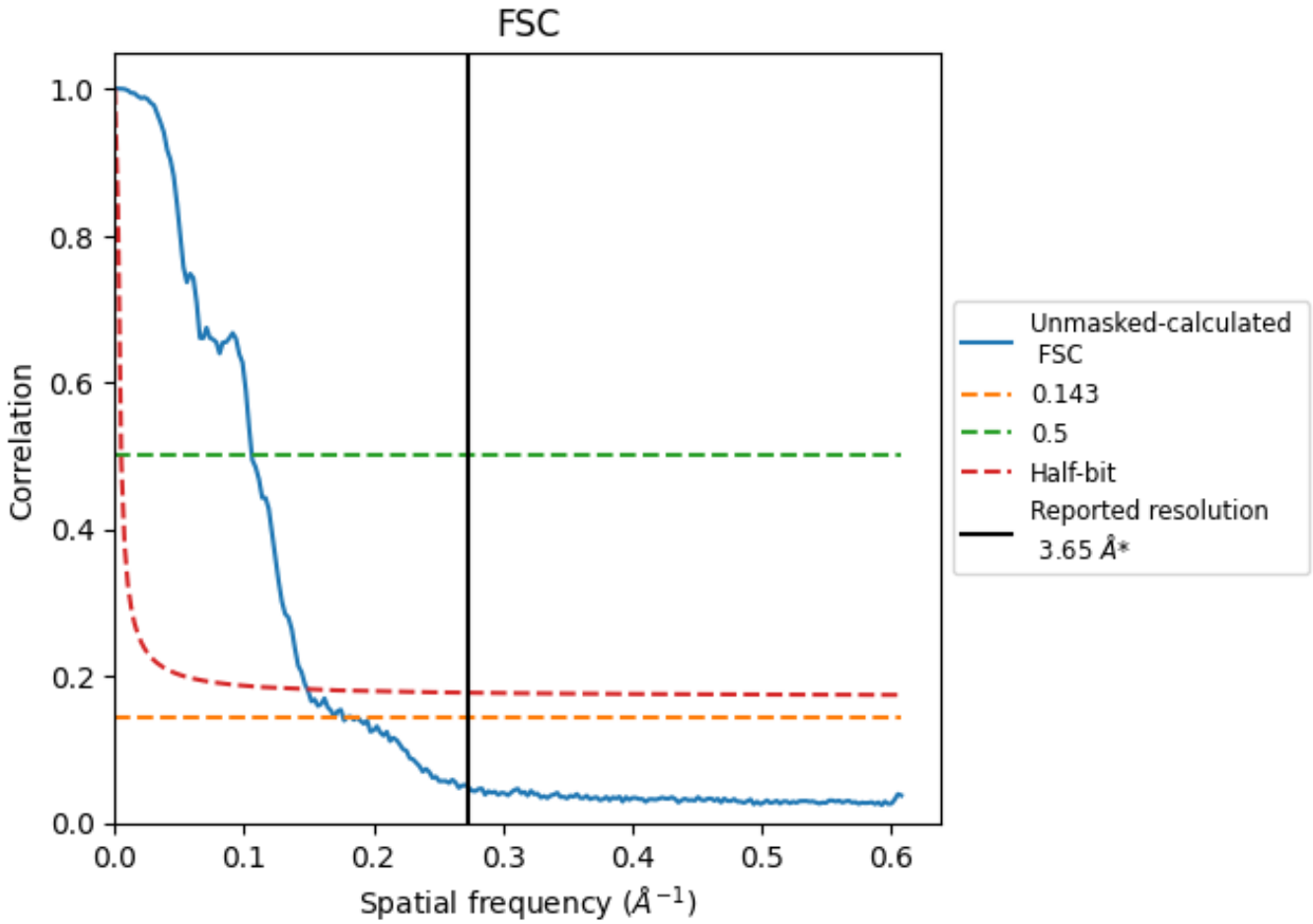


*Reported resolution corresponds to spatial frequency of 0.274 Å^{-1}

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 0.274 Å^{-1}

8.2 Resolution estimates (i)

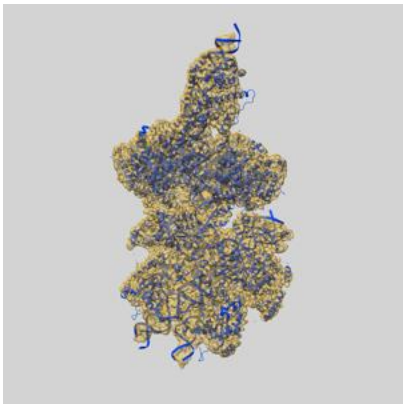
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.65	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.66	9.43	6.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.66 differs from the reported value 3.65 by more than 10 %

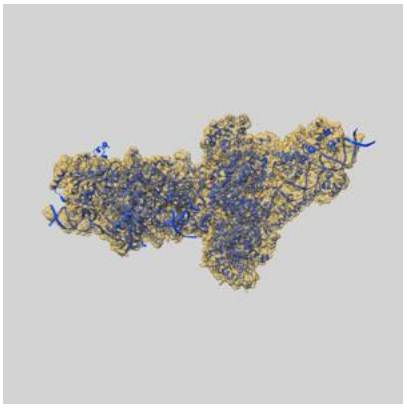
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-44944 and PDB model 9BW1. Per-residue inclusion information can be found in section 3 on page 9.

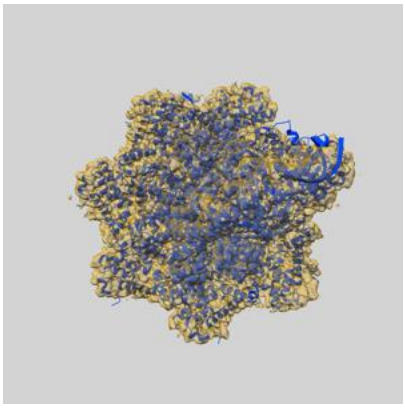
9.1 Map-model overlay



X



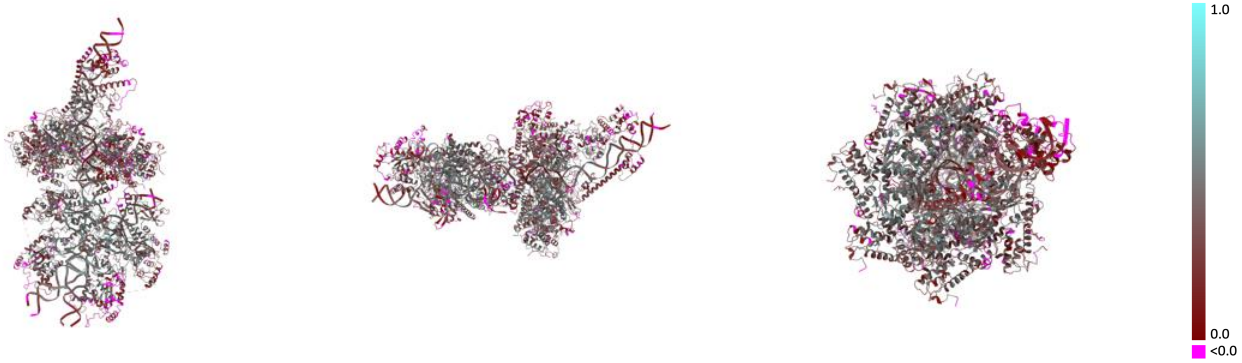
Y



Z

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

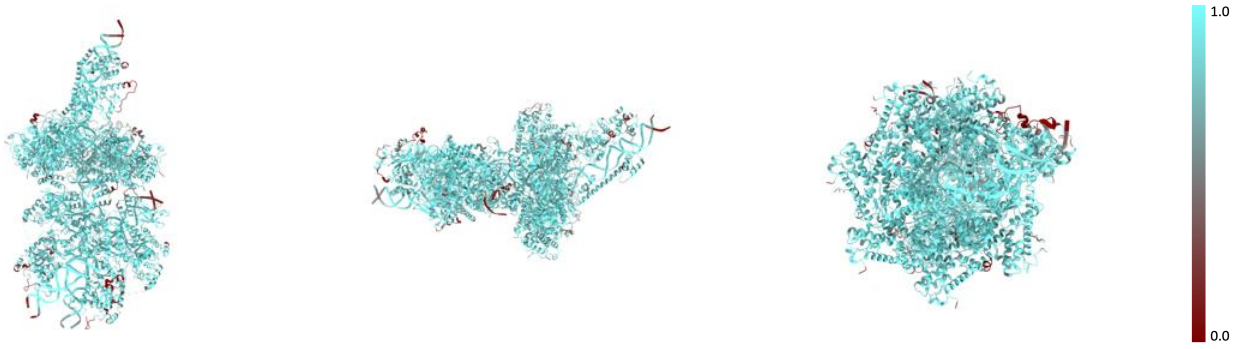
9.2 Q-score mapped to coordinate model



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.

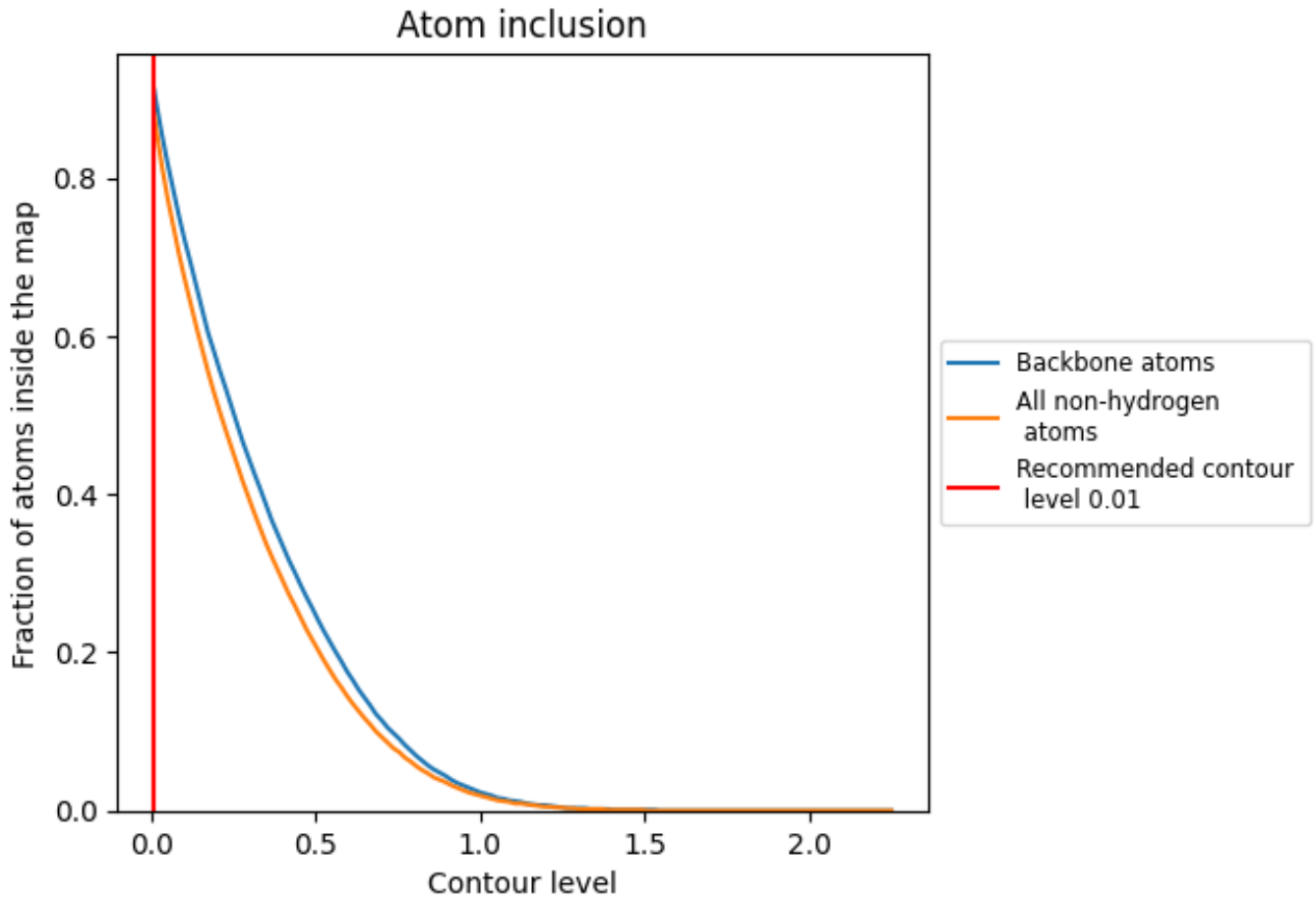
9.3 Atom inclusion mapped to coordinate model



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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8800	0.3490
2	0.9350	0.4270
4	0.8610	0.3790
5	0.9350	0.3860
6	0.6910	0.2760
H	0.8880	0.3210
I	0.9080	0.3470
J	0.8070	0.2560
M	0.9090	0.3680
N	0.9200	0.3830
O	0.7920	0.2910
P	0.8020	0.3110
Q	0.9080	0.3280
R	0.9170	0.3660
S	0.9270	0.3870
T	0.9320	0.4280
U	0.9190	0.4020
V	0.9050	0.3630
W	0.8440	0.2660
a	0.6670	0.2120
b	0.3910	0.0970
c	0.5360	0.1390
d	0.3040	-0.0330
x	0.8350	0.3840
y	0.8610	0.4000