



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:10 PM UTC

PDB ID : 8EA4 / pdb_00008ea4
EMDB ID : EMD-27972
Title : V-K CAST Transpososome from *Scytonema hofmanni*, minor configuration
Authors : Rizo, A.R.; Park, J.-U.; Tsai, A.W.; Kellogg, E.K.
Deposited on : 2022-08-27
Resolution : 3.00 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:

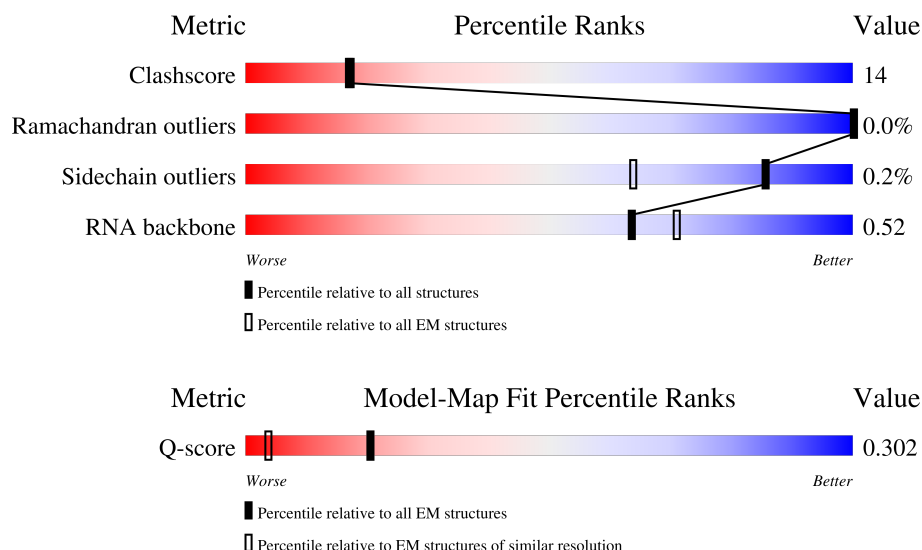
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.00 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.













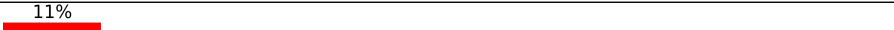

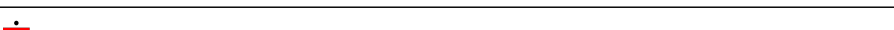
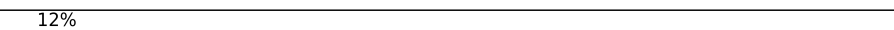


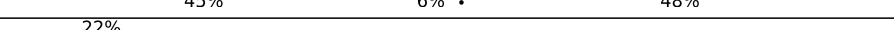
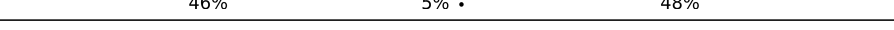
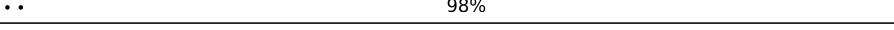
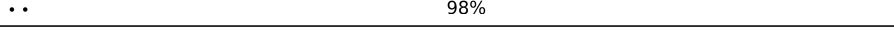
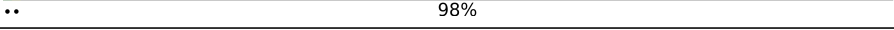
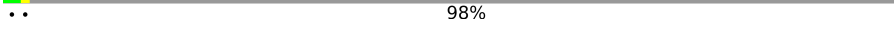
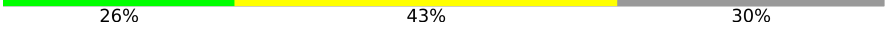

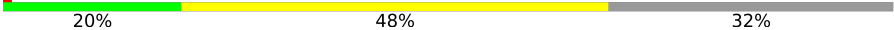
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	276	
1	B	276	
1	C	276	

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Mol	Chain	Length	Quality of chain
1	D	276	
1	E	276	
1	F	276	
1	G	276	
1	H	276	
1	I	276	
1	J	276	
1	K	276	
1	L	276	
1	M	276	
2	O	639	
3	Q	167	
4	S	89	
5	W	584	
5	X	584	
5	Y	584	
5	Z	584	
5	w	584	
5	x	584	
5	y	584	
5	z	584	
6	1	141	
7	2	51	
8	3	71	
9	4	75	

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Mol	Chain	Length	Quality of chain
10	5	50	
11	6	20	
12	7	265	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
14	ATP	I	302	-	-	X	-
14	ATP	M	302	-	-	X	-

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 58049 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 TnsC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	B	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	C	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	D	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	E	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	F	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	G	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	H	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	I	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	J	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	K	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	L	257	Total 2066	C 1306	N 377	O 375	S 8	0	0
1	M	257	Total 2066	C 1306	N 377	O 375	S 8	0	0

- Molecule 2 is a protein called Cas12k.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	601	Total 4865	C 3069	N 881	O 900	S 15	0	0

- Molecule 3 is a protein called TniQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	164	Total	C	N	O	S	0	0
			1306	832	240	220	14		

- Molecule 4 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	87	Total	C	N	O	S	0	0
			702	433	140	128	1		

- Molecule 5 is a protein called TnsB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	514	Total	C	N	O	S	0	0
			4122	2570	760	780	12		
5	X	507	Total	C	N	O	S	0	0
			4068	2537	748	771	12		
5	Y	304	Total	C	N	O	S	0	0
			2453	1537	449	457	10		
5	Z	301	Total	C	N	O	S	0	0
			2426	1522	442	452	10		
5	w	14	Total	C	N	O		0	0
			129	83	19	27			
5	x	14	Total	C	N	O		0	0
			129	83	19	27			
5	y	14	Total	C	N	O		0	0
			129	83	19	27			
5	z	14	Total	C	N	O		0	0
			129	83	19	27			

- Molecule 6 is a DNA chain called Target-LE.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1	98	Total	C	N	O	P	0	0
			2010	961	368	583	98		

- Molecule 7 is a DNA chain called LE_R.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	2	28	Total	C	N	O	P	0	0
			573	275	103	168	27		

- Molecule 8 is a DNA chain called Non-target_R.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	3	48	Total	C	N	O	P	0	0
			980	470	169	293	48		

- Molecule 9 is a DNA chain called RE_F.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	4	48	Total	C	N	O	P	0	0
			982	468	183	283	48		

- Molecule 10 is a DNA chain called RE_R1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	5	28	Total	C	N	O	P	0	0
			573	277	98	171	27		

- Molecule 11 is a DNA chain called RE_R2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	6	15	Total	C	N	O	P	0	0
			301	144	54	89	14		

- Molecule 12 is a RNA chain called sg_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	7	230	Total	C	N	O	P	0	0
			4896	2187	863	1616	230		

- Molecule 13 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

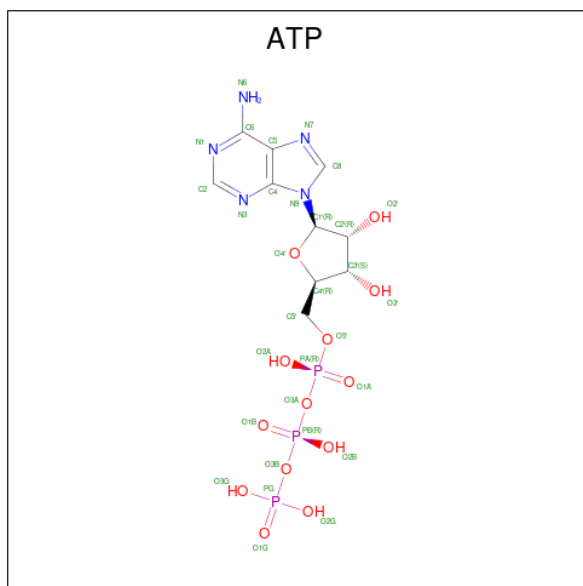
Mol	Chain	Residues	Atoms		AltConf
13	A	1	Total	Mg	0
			1	1	
13	B	1	Total	Mg	0
			1	1	
13	C	1	Total	Mg	0
			1	1	
13	D	1	Total	Mg	0
			1	1	
13	E	1	Total	Mg	0
			1	1	
13	F	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
13	G	1	Total	Mg	0
			1	1	
13	H	1	Total	Mg	0
			1	1	
13	I	1	Total	Mg	0
			1	1	
13	J	1	Total	Mg	0
			1	1	
13	K	1	Total	Mg	0
			1	1	
13	L	1	Total	Mg	0
			1	1	
13	M	1	Total	Mg	0
			1	1	
13	W	1	Total	Mg	0
			1	1	
13	X	1	Total	Mg	0
			1	1	

- Molecule 14 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
14	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
14	B	1	Total	C	N	O	P	0
			31	10	5	13	3	

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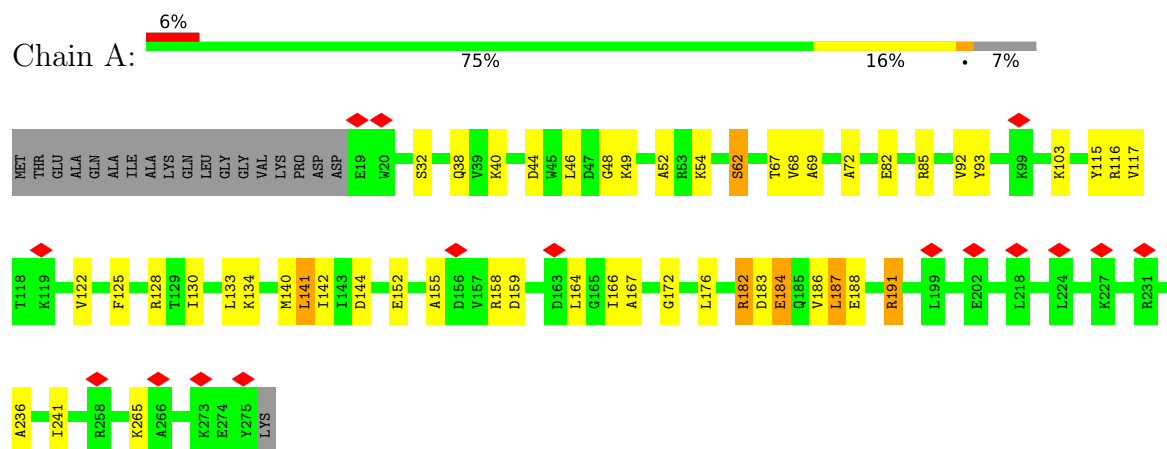
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Mol	Chain	Residues	Atoms					AltConf
14	C	1	Total 31	C 10	N 5	O 13	P 3	0
14	D	1	Total 31	C 10	N 5	O 13	P 3	0
14	E	1	Total 31	C 10	N 5	O 13	P 3	0
14	F	1	Total 31	C 10	N 5	O 13	P 3	0
14	G	1	Total 31	C 10	N 5	O 13	P 3	0
14	H	1	Total 31	C 10	N 5	O 13	P 3	0
14	I	1	Total 31	C 10	N 5	O 13	P 3	0
14	J	1	Total 31	C 10	N 5	O 13	P 3	0
14	K	1	Total 31	C 10	N 5	O 13	P 3	0
14	L	1	Total 31	C 10	N 5	O 13	P 3	0
14	M	1	Total 31	C 10	N 5	O 13	P 3	0

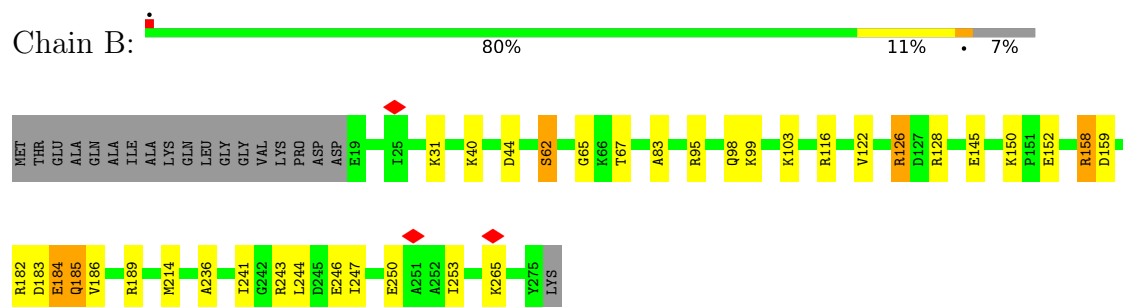
3 Residue-property plots [i](#)

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.

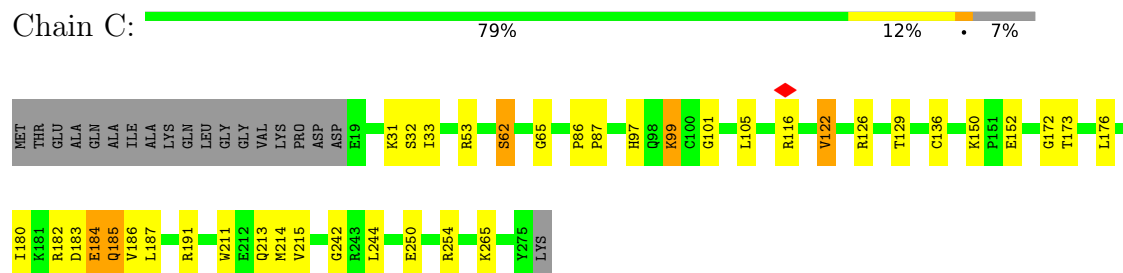
• Molecule 1: TnsC




• Molecule 1: TnsC

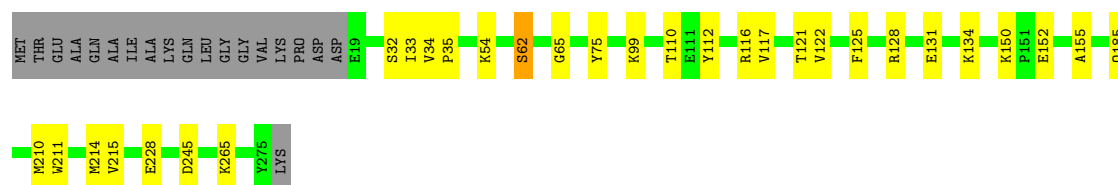


• Molecule 1: TnsC




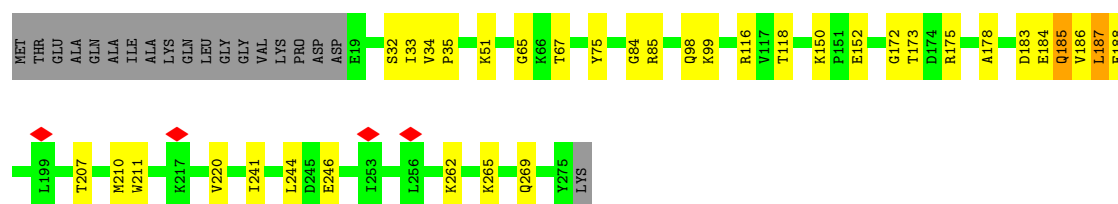
• Molecule 1: TnsC

Chain D: 




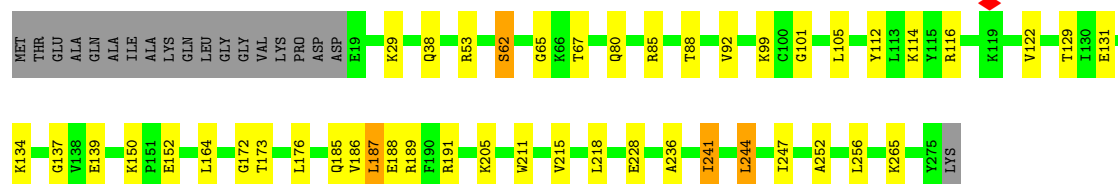
• Molecule 1: TnsC

Chain E: 



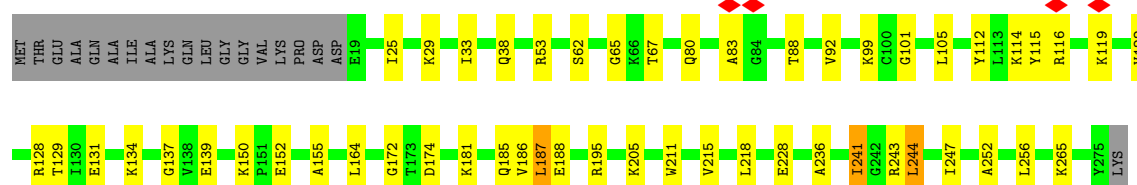
• Molecule 1: TnsC

Chain F: 




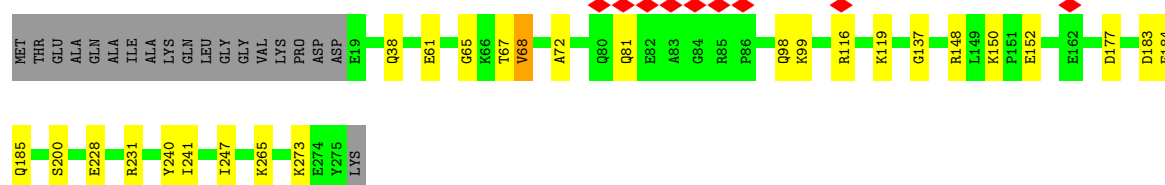
• Molecule 1: TnsC

Chain G: 

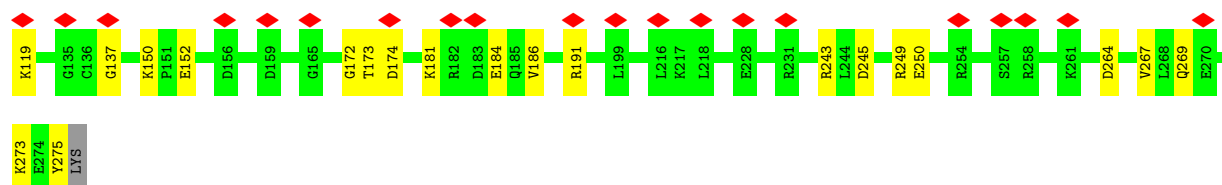


• Molecule 1: TnsC

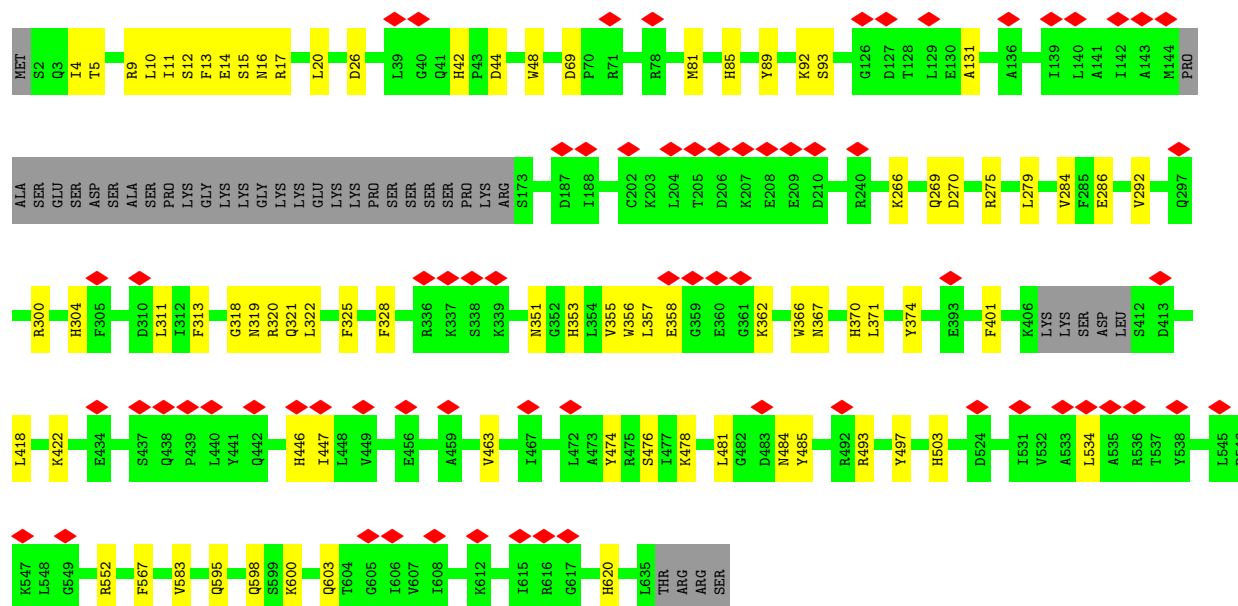
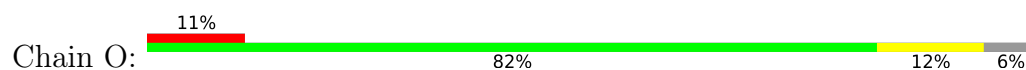
Chain H: 



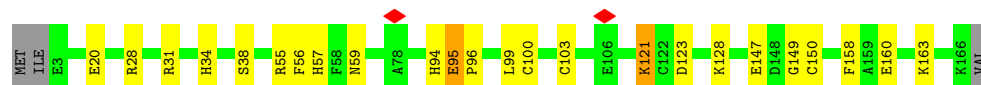
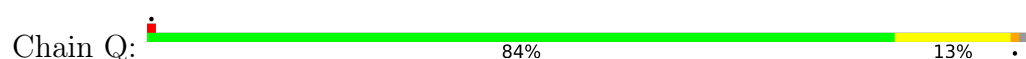
Residue	Score	Color
NET	1.00	Grey
THR	0.99	Grey
GLU	0.98	Grey
GLN	0.97	Grey
ALA	0.96	Grey
ILE	0.95	Grey
ALA	0.94	Grey
LYS	0.93	Grey
GLN	0.92	Grey
LEU	0.91	Grey
GLY	0.90	Grey
GLY	0.89	Grey
VAL	0.88	Grey
LYS	0.87	Grey
PRO	0.86	Grey
ASP	0.85	Grey
ASP	0.84	Grey
E19	0.83	Red
W20	0.82	Yellow
L21	0.81	Yellow
Q22	0.80	Yellow
A23	0.79	Green
K31	0.78	Green
T41	0.77	Yellow
D47	0.76	Orange
G48	0.75	Orange
K49	0.74	Orange
R50	0.73	Orange
K51	0.72	Orange
A52	0.71	Orange
R53	0.70	Green
K54	0.69	Green
S62	0.68	Orange
R63	0.67	Orange
T64	0.66	Green
G65	0.65	Green
V68	0.64	Orange
A69	0.63	Orange
K78	0.62	Red
Q81	0.61	Red
E82	0.60	Red
A83	0.59	Red
G84	0.58	Red
R85	0.57	Green
K99	0.56	Yellow
D104	0.55	Red
R116	0.54	Yellow
V117	0.53	Red



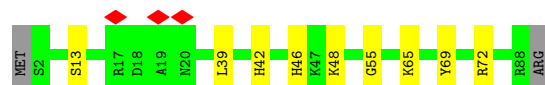
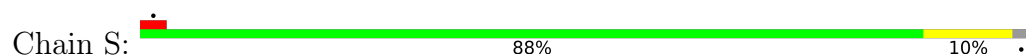
• Molecule 2: Cas12k



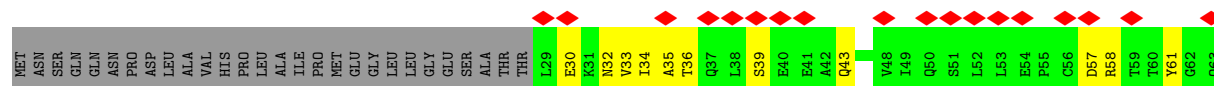
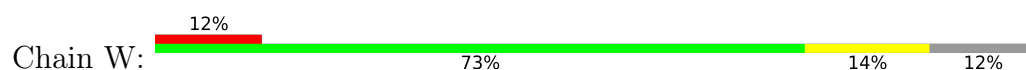
• Molecule 3: TniQ

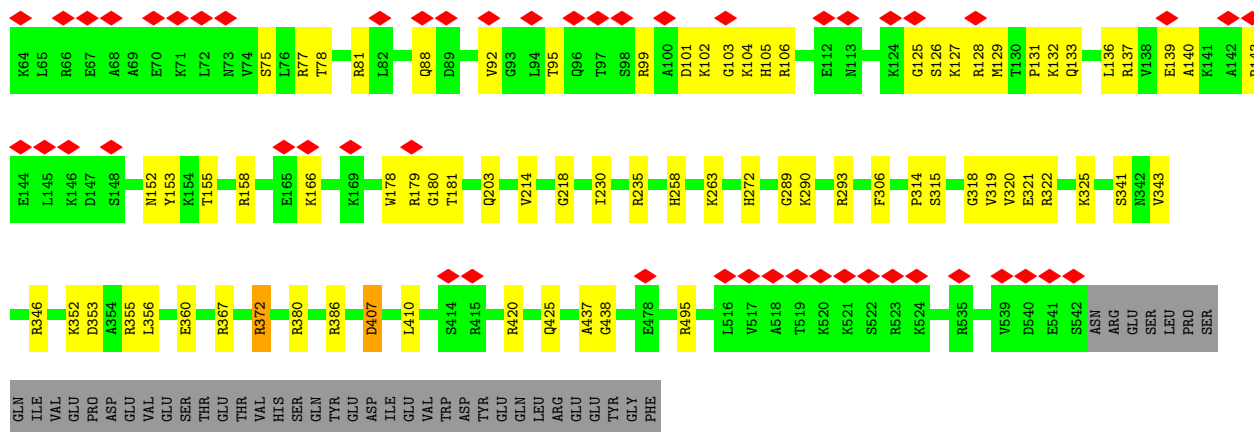


• Molecule 4: 30S ribosomal protein S15

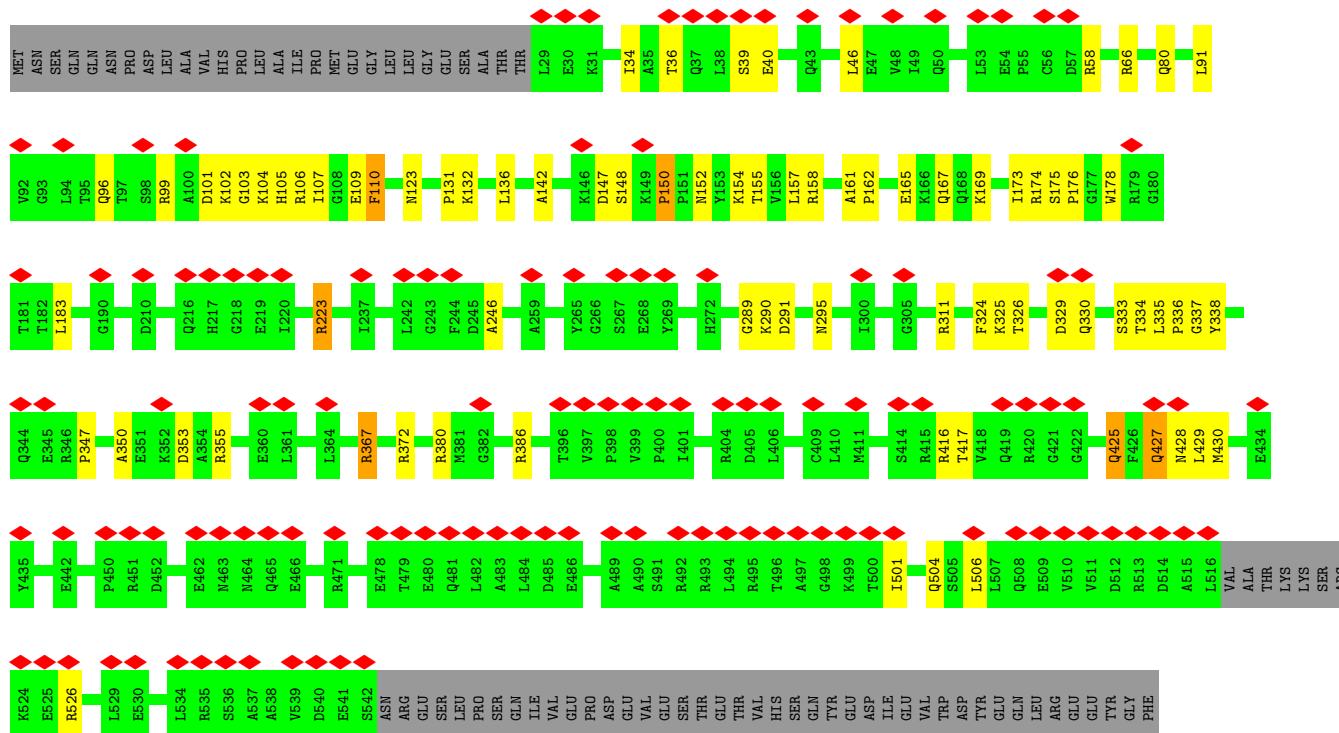
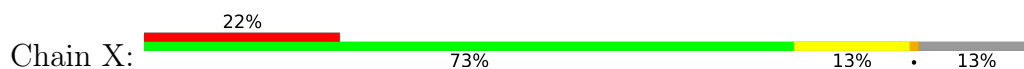


• Molecule 5: TnsB

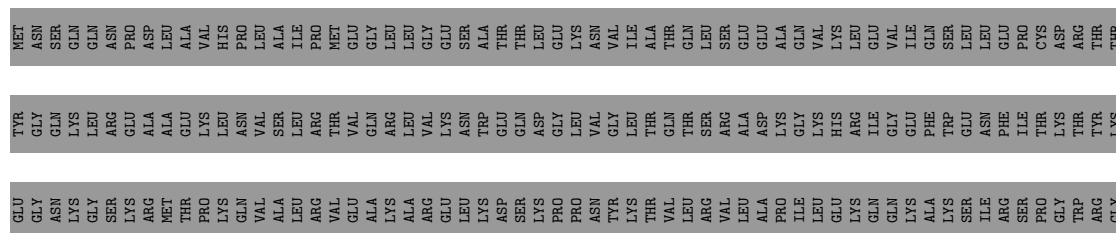


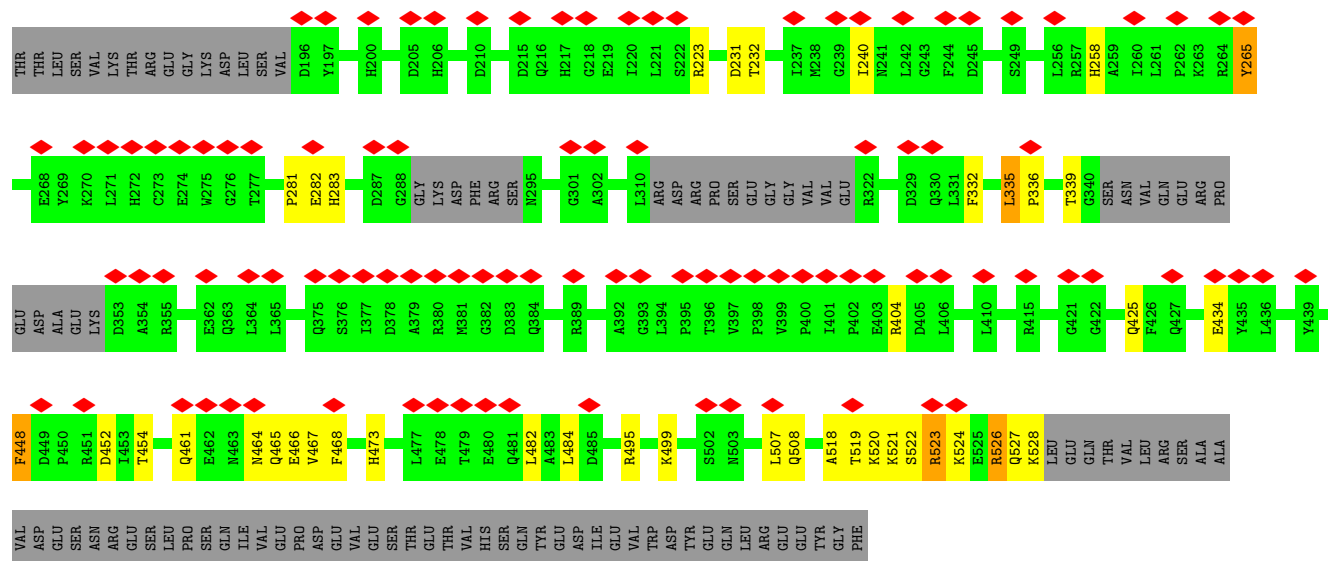


• Molecule 5: TnsB

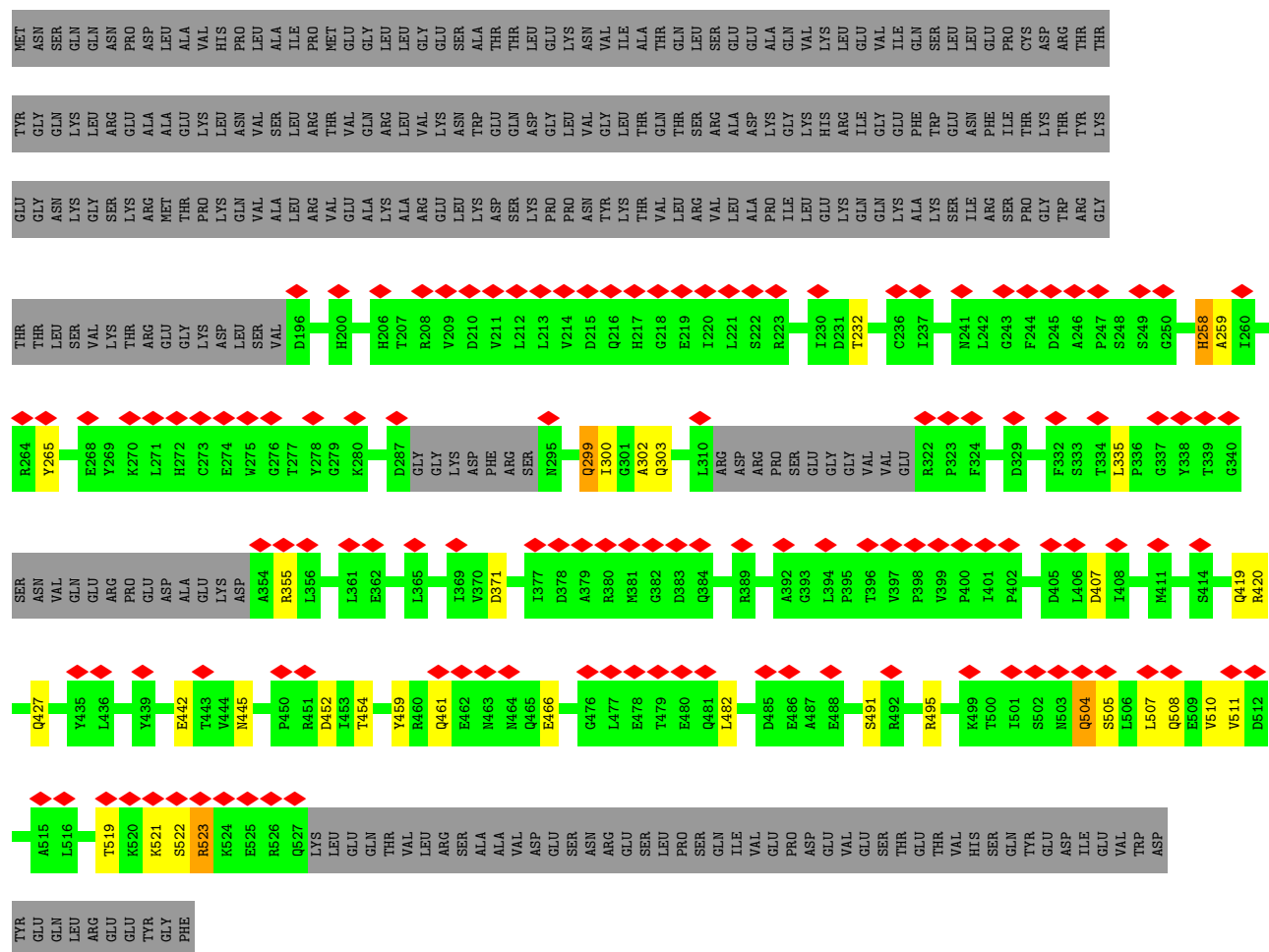


• Molecule 5: TnsB





• Molecule 5: TnsB



• Molecule 5: TnsB

98%

98%



- Molecule 5: TnsB

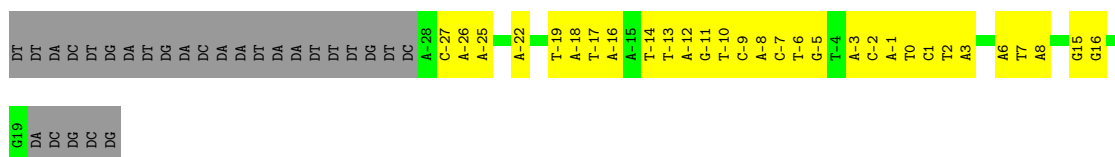
Chain v:

[illegible]

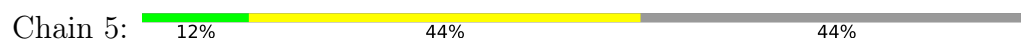
- Molecule 5: TnsB

Chain z: 98%

[illegible]



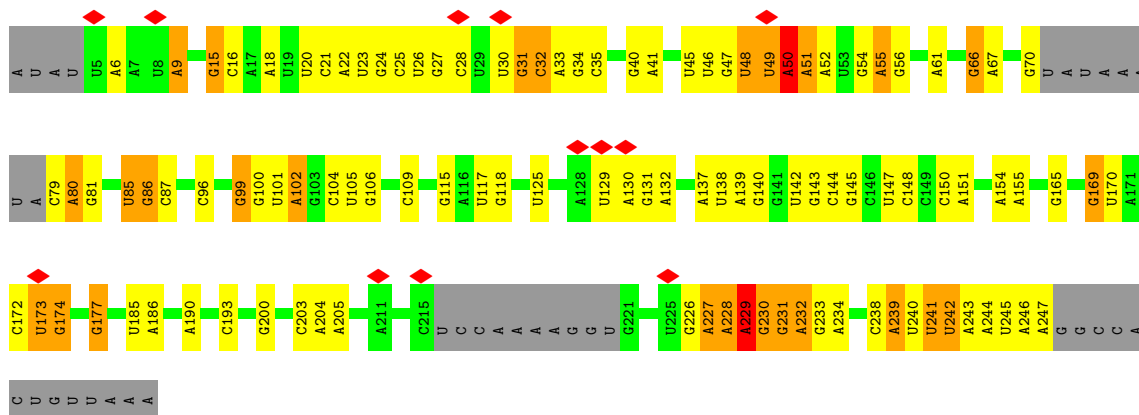
• Molecule 10: RE_R1



• Molecule 11: RE_R2



• Molecule 12: sg_rNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67096	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.885	Depositor
Minimum map value	-0.359	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.2	Depositor
Map size (\AA)	576.18, 576.18, 576.18	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.067, 1.067, 1.067	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

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	1.16	12/2097 (0.6%)	1.30	13/2817 (0.5%)
1	B	1.08	10/2097 (0.5%)	1.30	9/2817 (0.3%)
1	C	1.13	9/2097 (0.4%)	1.30	9/2817 (0.3%)
1	D	0.92	0/2097	1.29	4/2817 (0.1%)
1	E	1.00	6/2097 (0.3%)	1.25	2/2817 (0.1%)
1	F	1.16	11/2097 (0.5%)	1.31	12/2817 (0.4%)
1	G	1.16	11/2097 (0.5%)	1.31	12/2817 (0.4%)
1	H	0.97	2/2097 (0.1%)	1.32	7/2817 (0.2%)
1	I	1.03	8/2097 (0.4%)	1.26	6/2817 (0.2%)
1	J	1.01	6/2097 (0.3%)	1.27	7/2817 (0.2%)
1	K	1.10	7/2097 (0.3%)	1.35	7/2817 (0.2%)
1	L	1.13	11/2097 (0.5%)	1.37	15/2817 (0.5%)
1	M	1.09	7/2097 (0.3%)	1.31	10/2817 (0.4%)
2	O	0.76	0/4952	1.22	5/6677 (0.1%)
3	Q	0.81	0/1345	1.23	3/1819 (0.2%)
4	S	0.83	0/710	1.27	1/950 (0.1%)
5	W	0.85	0/4192	1.18	2/5659 (0.0%)
5	X	0.88	1/4137 (0.0%)	1.33	20/5585 (0.4%)
5	Y	0.85	0/2499	1.25	10/3379 (0.3%)
5	Z	0.80	0/2472	1.30	11/3345 (0.3%)
5	w	0.76	0/132	1.22	0/178
5	x	0.99	0/132	1.10	0/178
5	y	0.90	0/132	1.23	0/178
5	z	0.77	0/132	1.26	0/178
6	1	0.29	0/2256	0.56	0/3479
7	2	0.32	0/642	0.69	1/990 (0.1%)
8	3	0.25	0/1095	0.55	0/1685
9	4	0.21	0/1102	0.39	0/1697
10	5	0.16	0/641	0.38	0/989
11	6	0.23	0/336	0.54	1/516 (0.2%)
12	7	0.28	0/5470	0.50	9/8517 (0.1%)
All	All	0.88	101/59638 (0.2%)	1.16	176/82620 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	2
1	D	0	1
1	H	0	1
1	I	0	2
1	L	0	1
4	S	0	1
5	W	0	3
5	X	0	4
5	Y	0	3
5	Z	0	1
6	1	0	3
7	2	0	1
8	3	0	2
9	4	0	1
12	7	0	4
All	All	0	31

The worst 5 of 101 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	186	VAL	C-O	-7.47	1.15	1.24
1	B	184	GLU	C-O	-7.22	1.15	1.24
1	F	38	GLN	C-O	-7.21	1.15	1.24
1	A	38	GLN	C-O	-7.11	1.15	1.24
1	G	38	GLN	C-O	-7.11	1.15	1.24

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	X	425	GLN	CB-CA-C	14.30	135.54	109.37
5	Y	223	ARG	CA-C-N	9.48	130.19	120.14
5	Y	223	ARG	C-N-CA	9.48	130.19	120.14
12	7	230	G	P-O3'-C3'	-8.74	107.09	120.20
1	L	208	VAL	N-CA-C	-8.26	102.49	110.42

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	182	ARG	Sidechain
1	C	191	ARG	Sidechain
1	C	53	ARG	Sidechain
1	D	128	ARG	Sidechain
1	H	240	TYR	Sidechain

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	2066	0	2157	59	0
1	B	2066	0	2157	70	0
1	C	2066	0	2157	71	0
1	D	2066	0	2157	67	0
1	E	2066	0	2156	68	0
1	F	2066	0	2156	50	0
1	G	2066	0	2158	74	0
1	H	2066	0	2157	39	0
1	I	2066	0	2157	39	0
1	J	2066	0	2157	55	0
1	K	2066	0	2156	70	0
1	L	2066	0	2152	54	0
1	M	2066	0	2155	77	0
2	O	4865	0	4924	220	0
3	Q	1306	0	1290	44	0
4	S	702	0	721	15	0
5	W	4122	0	4147	341	0
5	X	4068	0	4081	151	0
5	Y	2453	0	2421	110	0
5	Z	2426	0	2390	99	0
5	w	129	0	110	21	0
5	x	129	0	110	23	0
5	y	129	0	110	35	0
5	z	129	0	110	19	0
6	1	2010	0	1107	149	0
7	2	573	0	319	56	0
8	3	980	0	547	45	0
9	4	982	0	540	101	0
10	5	573	0	322	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	6	301	0	169	11	0
12	7	4896	0	2469	145	0
13	A	1	0	0	0	0
13	B	1	0	0	0	0
13	C	1	0	0	0	0
13	D	1	0	0	0	0
13	E	1	0	0	0	0
13	F	1	0	0	1	0
13	G	1	0	0	1	0
13	H	1	0	0	0	0
13	I	1	0	0	0	0
13	J	1	0	0	0	0
13	K	1	0	0	0	0
13	L	1	0	0	0	0
13	M	1	0	0	0	0
13	W	1	0	0	0	0
13	X	1	0	0	0	0
14	A	31	0	12	4	0
14	B	31	0	12	3	0
14	C	31	0	12	3	0
14	D	31	0	12	4	0
14	E	31	0	12	2	0
14	F	31	0	12	1	0
14	G	31	0	12	6	0
14	H	31	0	12	7	0
14	I	31	0	12	13	0
14	J	31	0	12	4	0
14	K	31	0	12	4	0
14	L	31	0	12	6	0
14	M	31	0	12	12	0
All	All	58049	0	54075	1542	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 14.

The worst 5 of 1542 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:53:ARG:CG	1:L:29:LYS:NZ	1.71	1.51
5:W:143:ARG:HH22	5:Z:504:GLN:CD	1.09	1.50
1:G:218:LEU:CD2	1:G:256:LEU:HD11	1.43	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:155:THR:CG2	9:4:-12:DA:H2'	1.40	1.48
1:F:218:LEU:CD2	1:F:256:LEU:HD11	1.43	1.45

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	255/276 (92%)	250 (98%)	5 (2%)	0	100	100
1	B	255/276 (92%)	254 (100%)	1 (0%)	0	100	100
1	C	255/276 (92%)	250 (98%)	5 (2%)	0	100	100
1	D	255/276 (92%)	248 (97%)	7 (3%)	0	100	100
1	E	255/276 (92%)	252 (99%)	3 (1%)	0	100	100
1	F	255/276 (92%)	251 (98%)	4 (2%)	0	100	100
1	G	255/276 (92%)	251 (98%)	4 (2%)	0	100	100
1	H	255/276 (92%)	250 (98%)	5 (2%)	0	100	100
1	I	255/276 (92%)	252 (99%)	3 (1%)	0	100	100
1	J	255/276 (92%)	253 (99%)	2 (1%)	0	100	100
1	K	255/276 (92%)	251 (98%)	4 (2%)	0	100	100
1	L	255/276 (92%)	252 (99%)	3 (1%)	0	100	100
1	M	255/276 (92%)	250 (98%)	5 (2%)	0	100	100
2	O	595/639 (93%)	585 (98%)	10 (2%)	0	100	100
3	Q	162/167 (97%)	152 (94%)	9 (6%)	1 (1%)	21	56
4	S	85/89 (96%)	83 (98%)	2 (2%)	0	100	100
5	W	512/584 (88%)	492 (96%)	20 (4%)	0	100	100
5	X	503/584 (86%)	485 (96%)	17 (3%)	1 (0%)	43	76

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Y	296/584 (51%)	284 (96%)	12 (4%)	0	100	100
5	Z	293/584 (50%)	280 (96%)	13 (4%)	0	100	100
5	w	12/584 (2%)	12 (100%)	0	0	100	100
5	x	12/584 (2%)	12 (100%)	0	0	100	100
5	y	12/584 (2%)	12 (100%)	0	0	100	100
5	z	12/584 (2%)	12 (100%)	0	0	100	100
All	All	5809/9155 (64%)	5673 (98%)	134 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	X	176	PRO
3	Q	95	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	224/238 (94%)	222 (99%)	2 (1%)	70	85
1	B	224/238 (94%)	224 (100%)	0	100	100
1	C	224/238 (94%)	224 (100%)	0	100	100
1	D	224/238 (94%)	224 (100%)	0	100	100
1	E	224/238 (94%)	224 (100%)	0	100	100
1	F	224/238 (94%)	223 (100%)	1 (0%)	84	90
1	G	224/238 (94%)	223 (100%)	1 (0%)	84	90
1	H	224/238 (94%)	224 (100%)	0	100	100
1	I	224/238 (94%)	224 (100%)	0	100	100
1	J	224/238 (94%)	221 (99%)	3 (1%)	61	81
1	K	224/238 (94%)	224 (100%)	0	100	100
1	L	224/238 (94%)	224 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	224/238 (94%)	224 (100%)	0	100	100
2	O	529/564 (94%)	528 (100%)	1 (0%)	87	92
3	Q	136/139 (98%)	136 (100%)	0	100	100
4	S	75/77 (97%)	75 (100%)	0	100	100
5	W	448/512 (88%)	448 (100%)	0	100	100
5	X	442/512 (86%)	441 (100%)	1 (0%)	87	92
5	Y	264/512 (52%)	264 (100%)	0	100	100
5	Z	261/512 (51%)	261 (100%)	0	100	100
5	w	13/512 (2%)	13 (100%)	0	100	100
5	x	13/512 (2%)	12 (92%)	1 (8%)	12	40
5	y	13/512 (2%)	12 (92%)	1 (8%)	12	40
5	z	13/512 (2%)	13 (100%)	0	100	100
All	All	5119/7970 (64%)	5108 (100%)	11 (0%)	85	92

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	418	LEU
5	X	380	ARG
5	y	575	TYR
5	x	575	TYR
1	J	78	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
5	Y	303	GLN
5	Z	203	GLN
5	Y	384	GLN
5	Y	461	GLN
5	Z	296	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	7	227/265 (85%)	54 (23%)	5 (2%)

5 of 54 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	7	9	A
12	7	15	G
12	7	18	A
12	7	22	A
12	7	24	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	7	48	U
12	7	49	U
12	7	50	A
12	7	130	A
12	7	173	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 15 are monoatomic - leaving 13 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	$\# Z > 2$
14	ATP	E	302	13	32,33,33	0.55	0	48,52,52	0.54	0
14	ATP	L	302	13	32,33,33	0.56	0	48,52,52	0.55	0
14	ATP	H	302	13	32,33,33	0.56	0	48,52,52	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
14	ATP	F	302	13	32,33,33	0.55	0	48,52,52	0.54	0
14	ATP	J	302	13	32,33,33	0.56	0	48,52,52	0.54	0
14	ATP	G	302	13	32,33,33	0.55	0	48,52,52	0.54	0
14	ATP	M	302	13	32,33,33	0.56	0	48,52,52	0.54	0
14	ATP	I	302	13	32,33,33	0.55	0	48,52,52	0.55	0
14	ATP	C	302	13	32,33,33	0.56	0	48,52,52	0.54	0
14	ATP	D	302	13	32,33,33	0.56	0	48,52,52	0.54	0
14	ATP	B	302	13	32,33,33	0.55	0	48,52,52	0.54	0
14	ATP	K	302	13	32,33,33	0.55	0	48,52,52	0.53	0
14	ATP	A	302	13	32,33,33	0.55	0	48,52,52	0.54	0

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
14	ATP	E	302	13	-	3/22/38/38	0/3/3/3
14	ATP	L	302	13	-	4/22/38/38	0/3/3/3
14	ATP	H	302	13	-	9/22/38/38	0/3/3/3
14	ATP	F	302	13	-	1/22/38/38	0/3/3/3
14	ATP	J	302	13	-	4/22/38/38	0/3/3/3
14	ATP	G	302	13	-	8/22/38/38	0/3/3/3
14	ATP	M	302	13	-	2/22/38/38	0/3/3/3
14	ATP	I	302	13	-	9/22/38/38	0/3/3/3
14	ATP	C	302	13	-	4/22/38/38	0/3/3/3
14	ATP	D	302	13	-	2/22/38/38	0/3/3/3
14	ATP	B	302	13	-	6/22/38/38	0/3/3/3
14	ATP	K	302	13	-	1/22/38/38	0/3/3/3
14	ATP	A	302	13	-	7/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
14	A	302	ATP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
14	A	302	ATP	C5'-O5'-PA-O3A
14	B	302	ATP	PB-O3B-PG-O2G
14	B	302	ATP	O4'-C4'-C5'-O5'
14	G	302	ATP	PB-O3B-PG-O2G

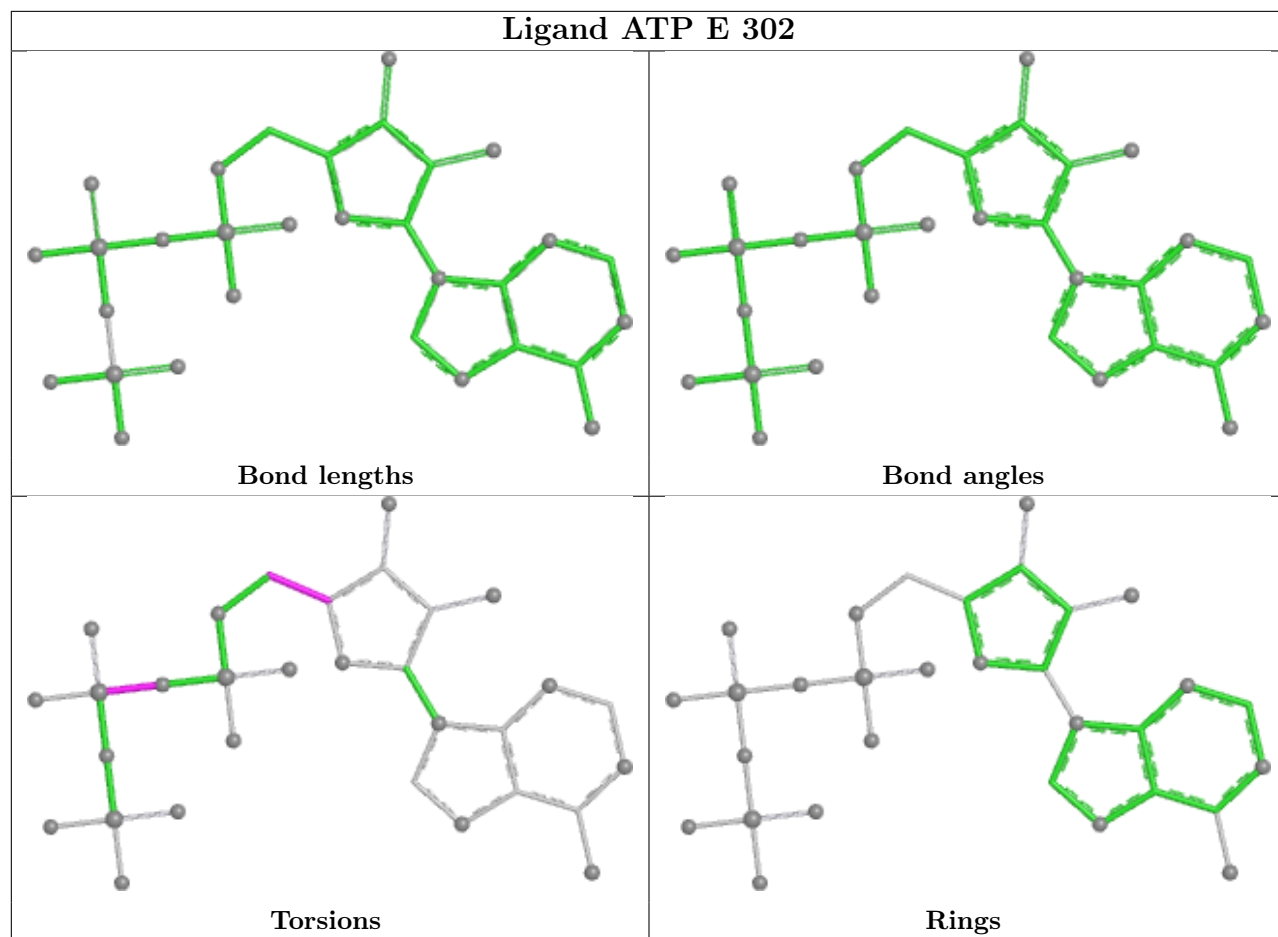
There are no ring outliers.

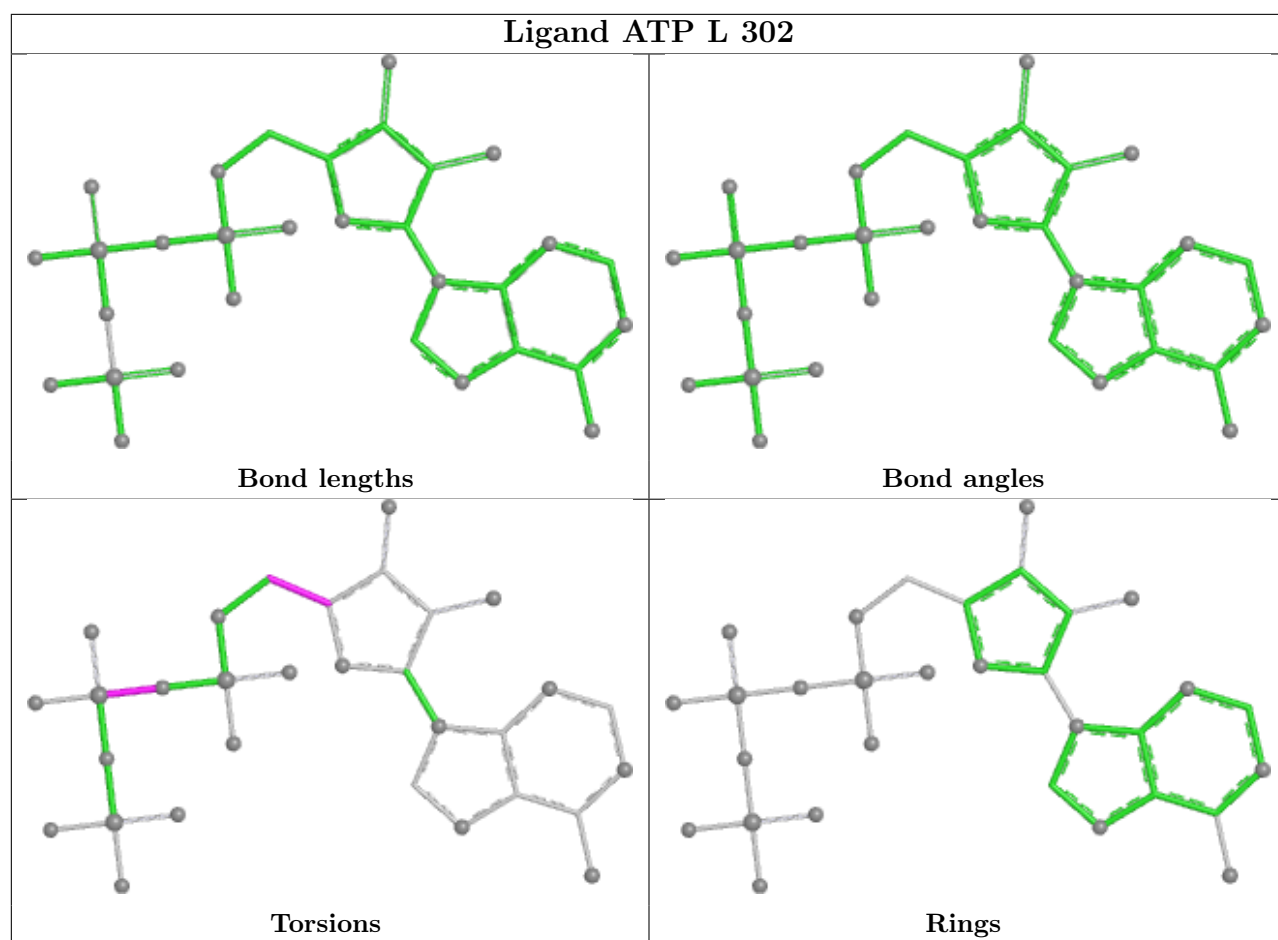
13 monomers are involved in 69 short contacts:

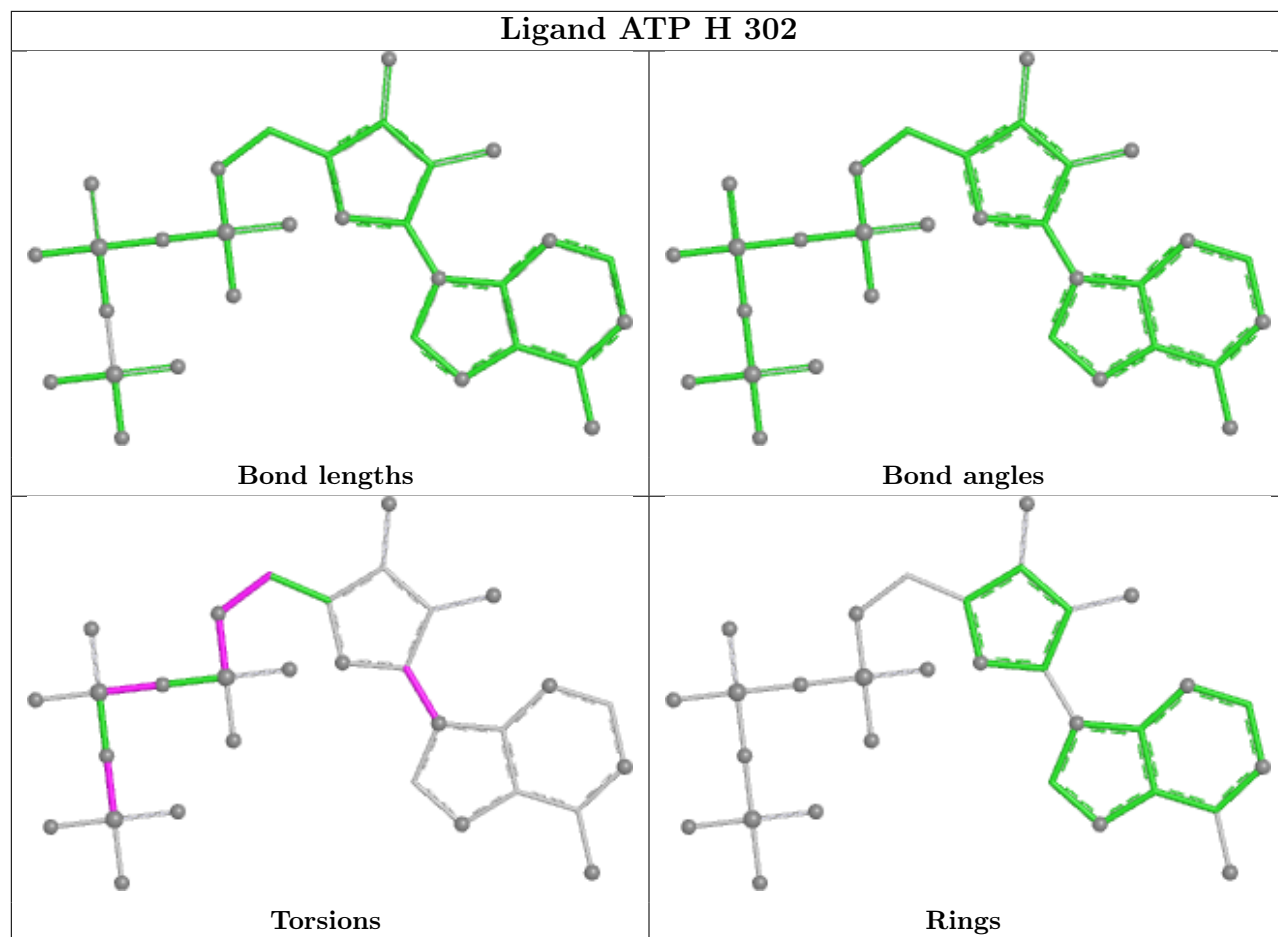
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	E	302	ATP	2	0
14	L	302	ATP	6	0
14	H	302	ATP	7	0
14	F	302	ATP	1	0
14	J	302	ATP	4	0
14	G	302	ATP	6	0
14	M	302	ATP	12	0
14	I	302	ATP	13	0
14	C	302	ATP	3	0
14	D	302	ATP	4	0
14	B	302	ATP	3	0
14	K	302	ATP	4	0
14	A	302	ATP	4	0

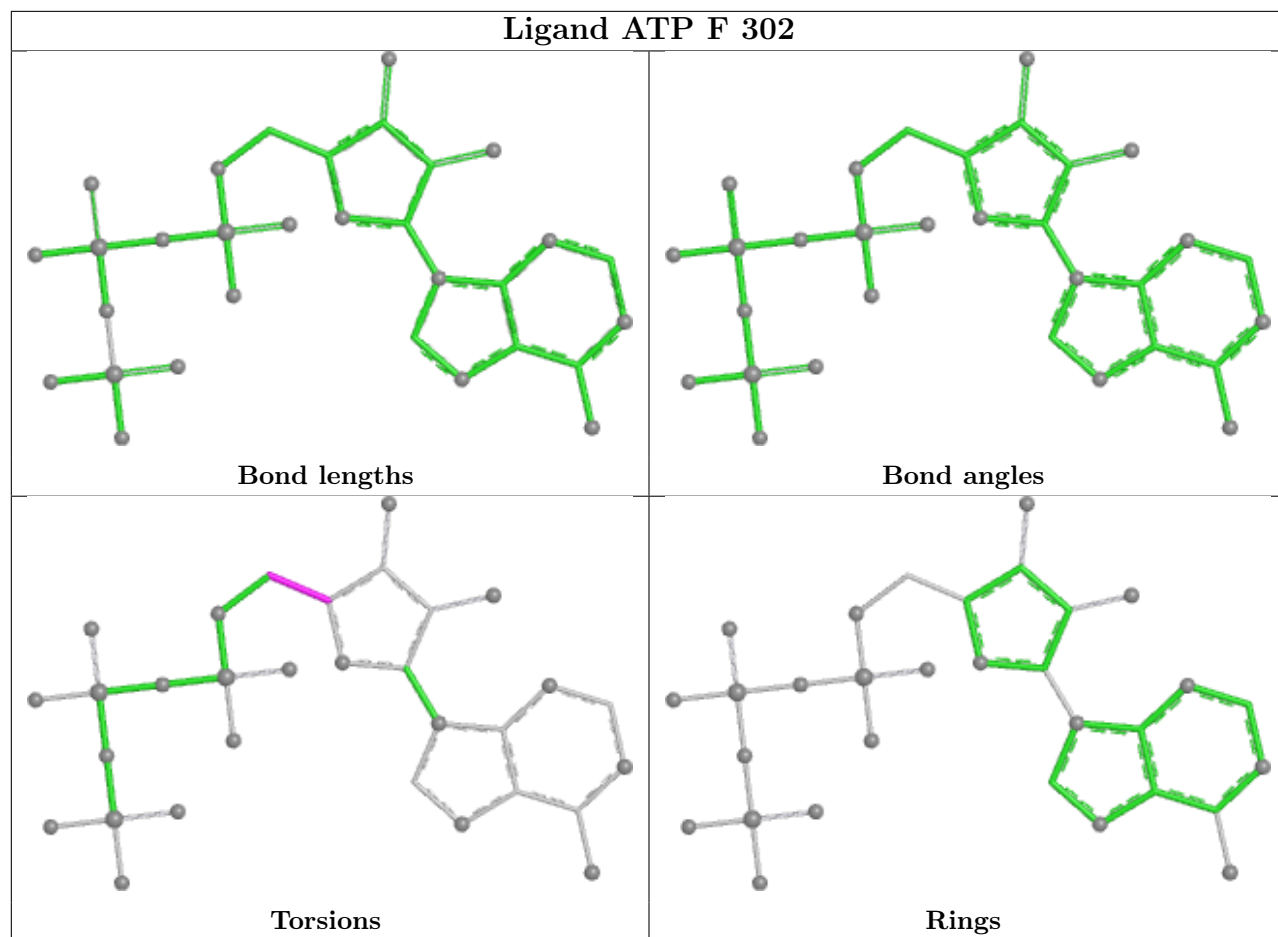
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand ATP E 302

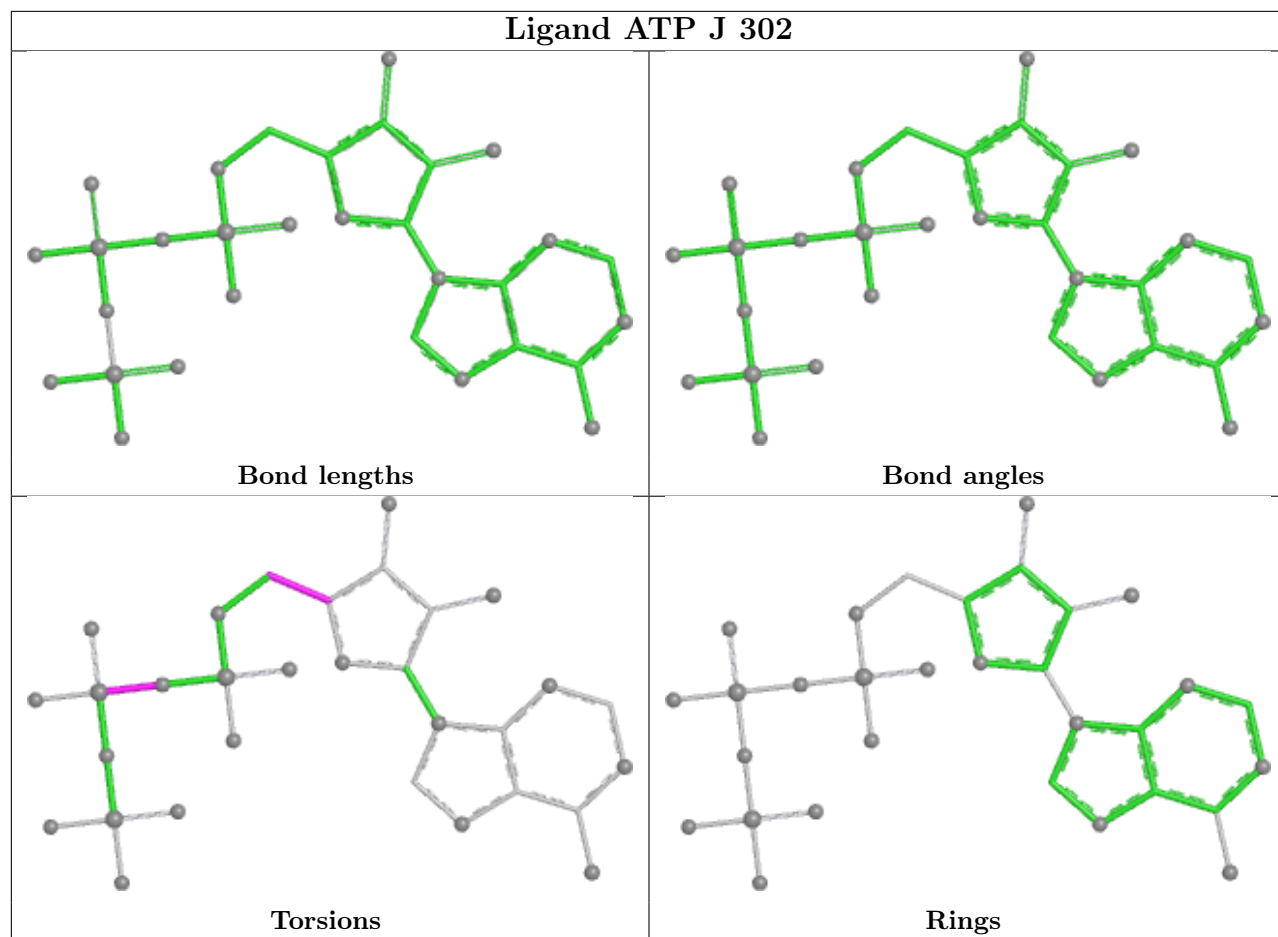


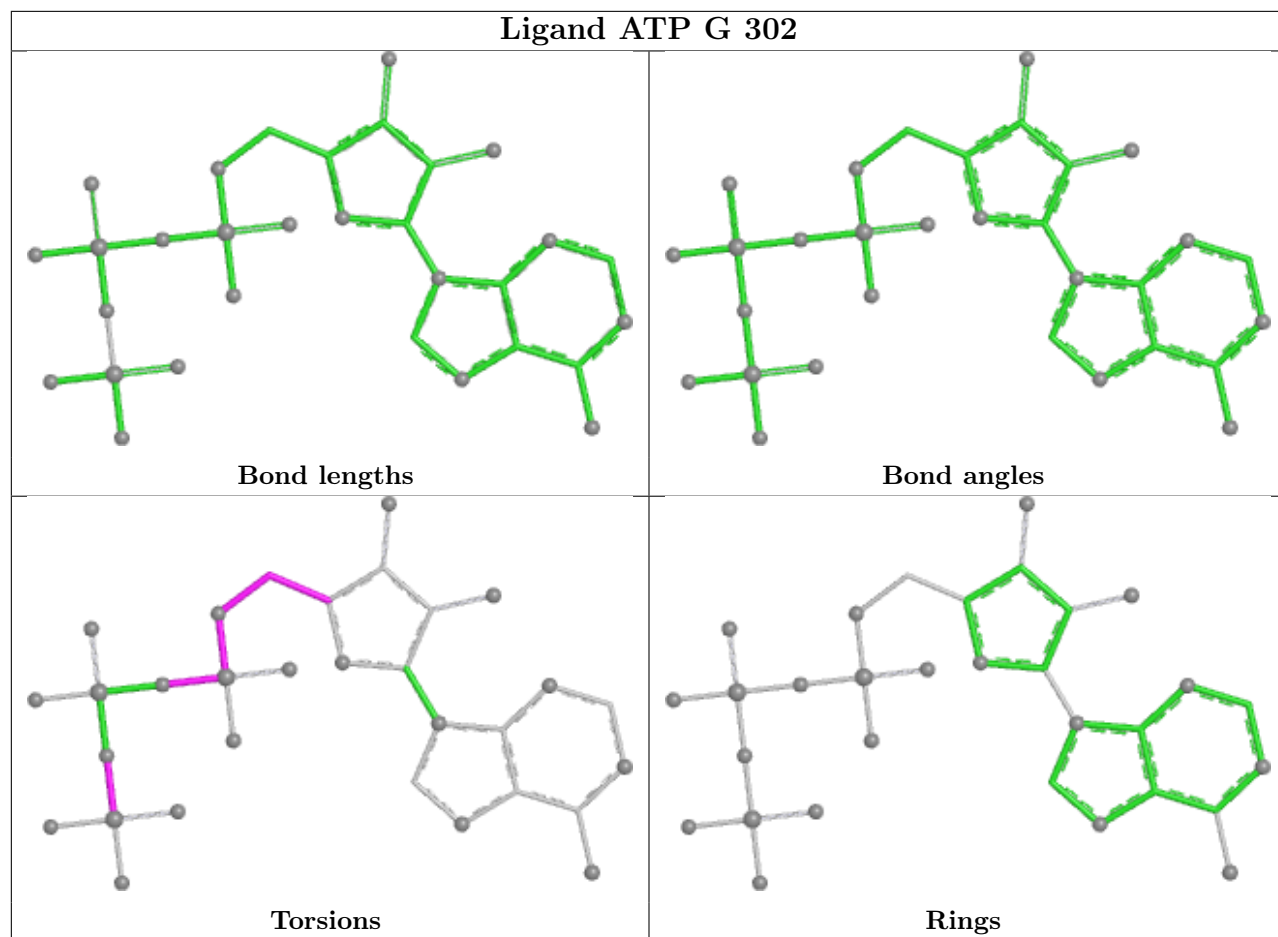


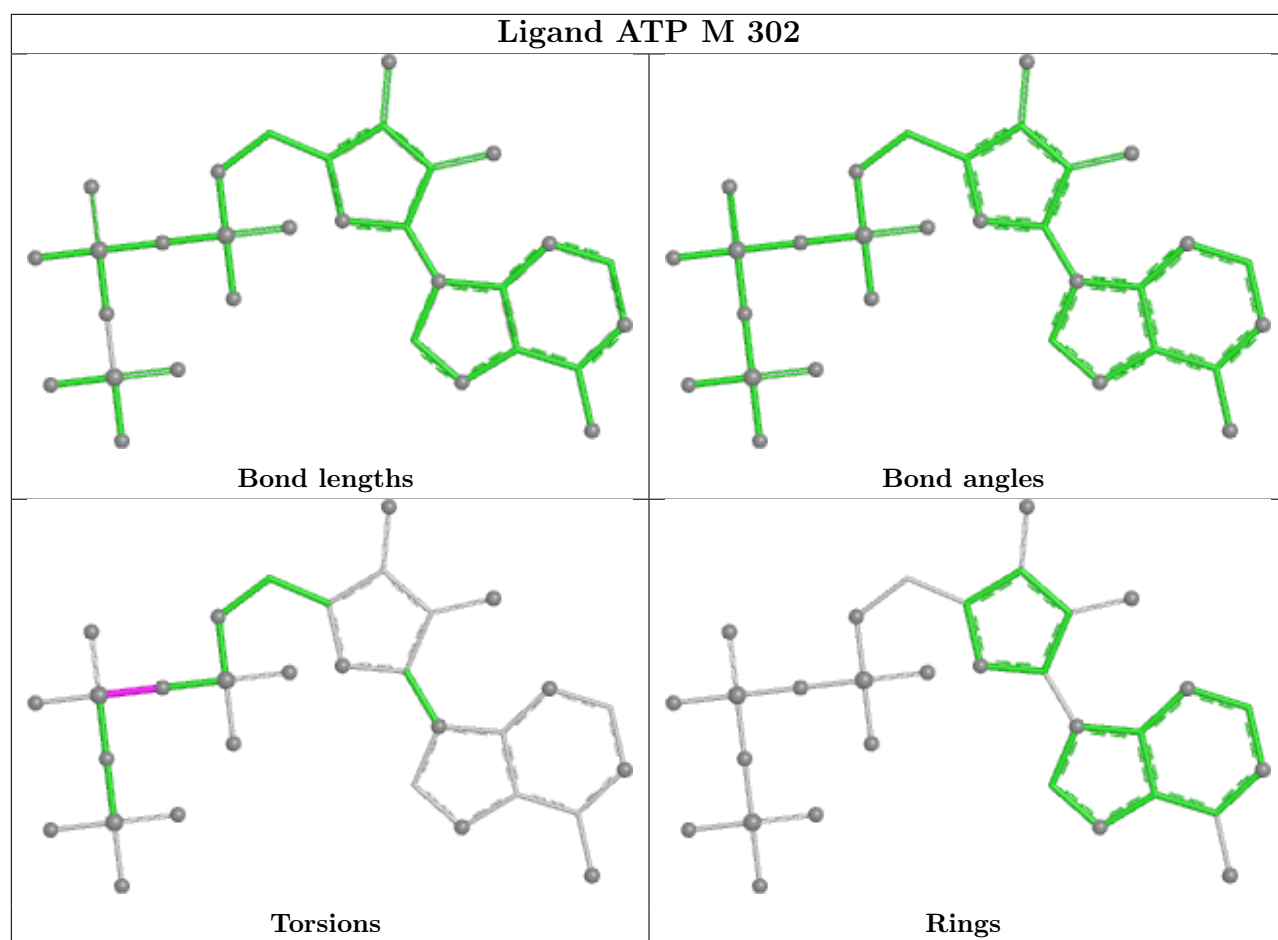


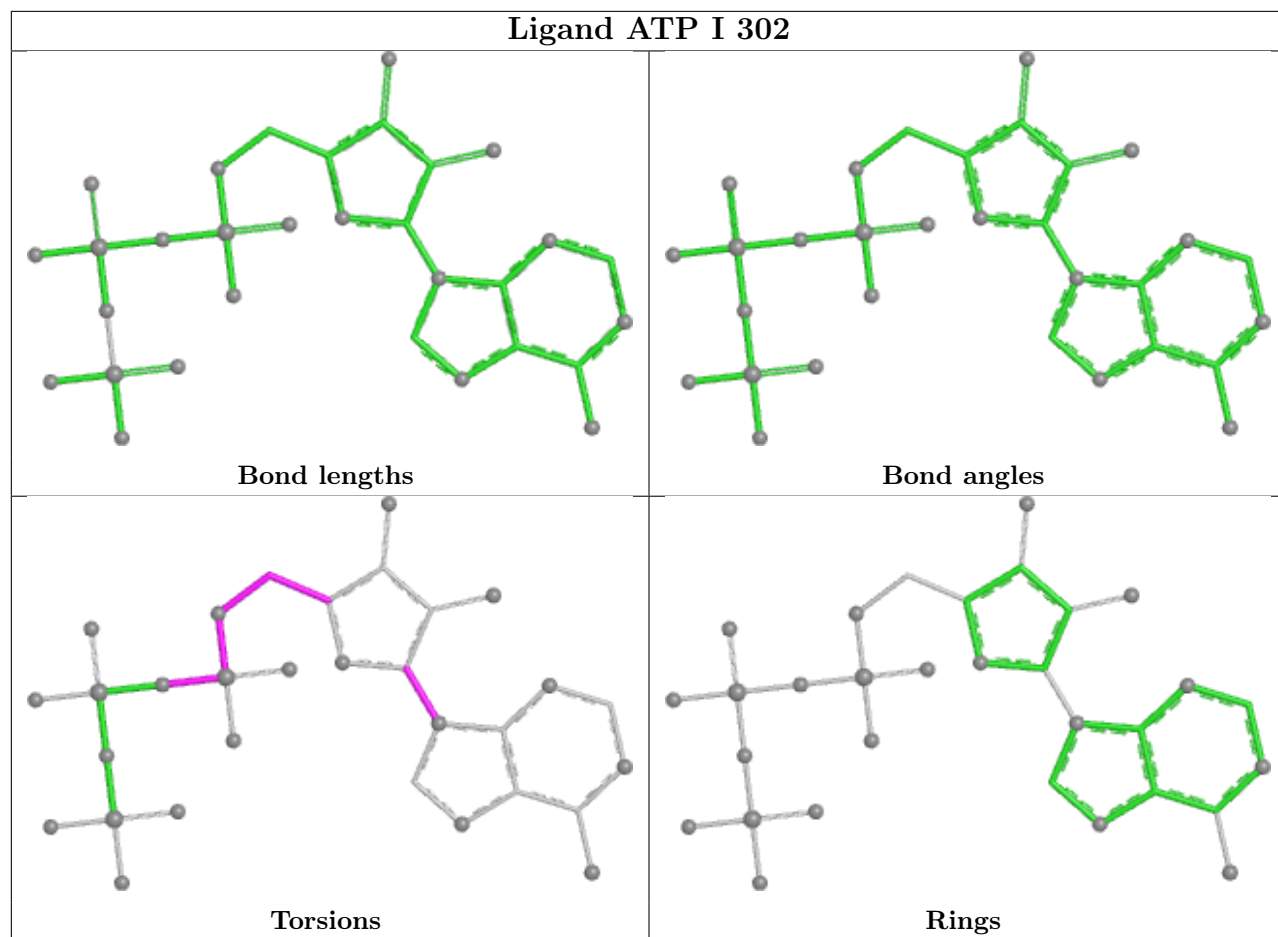


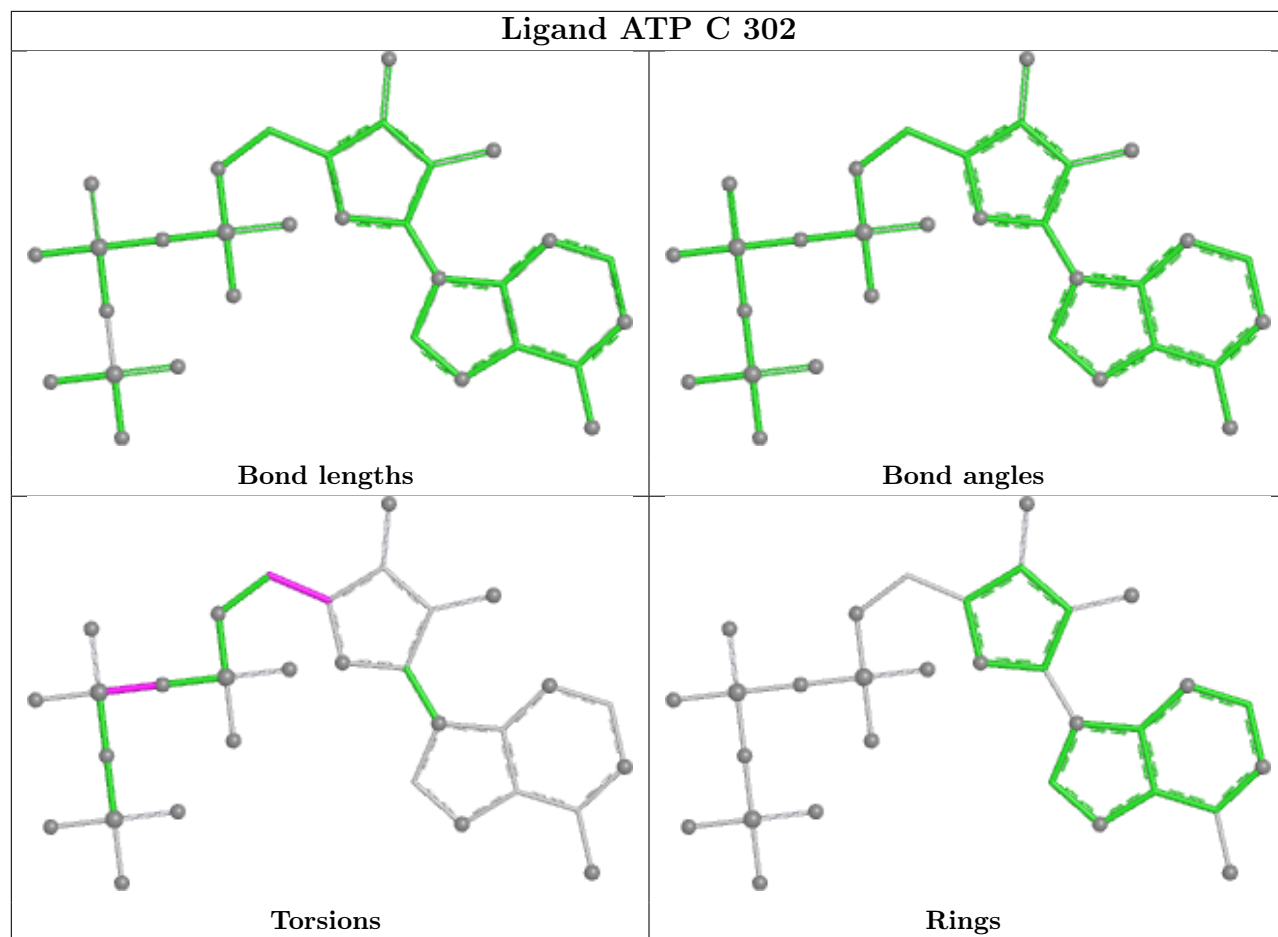
Ligand ATP J 302

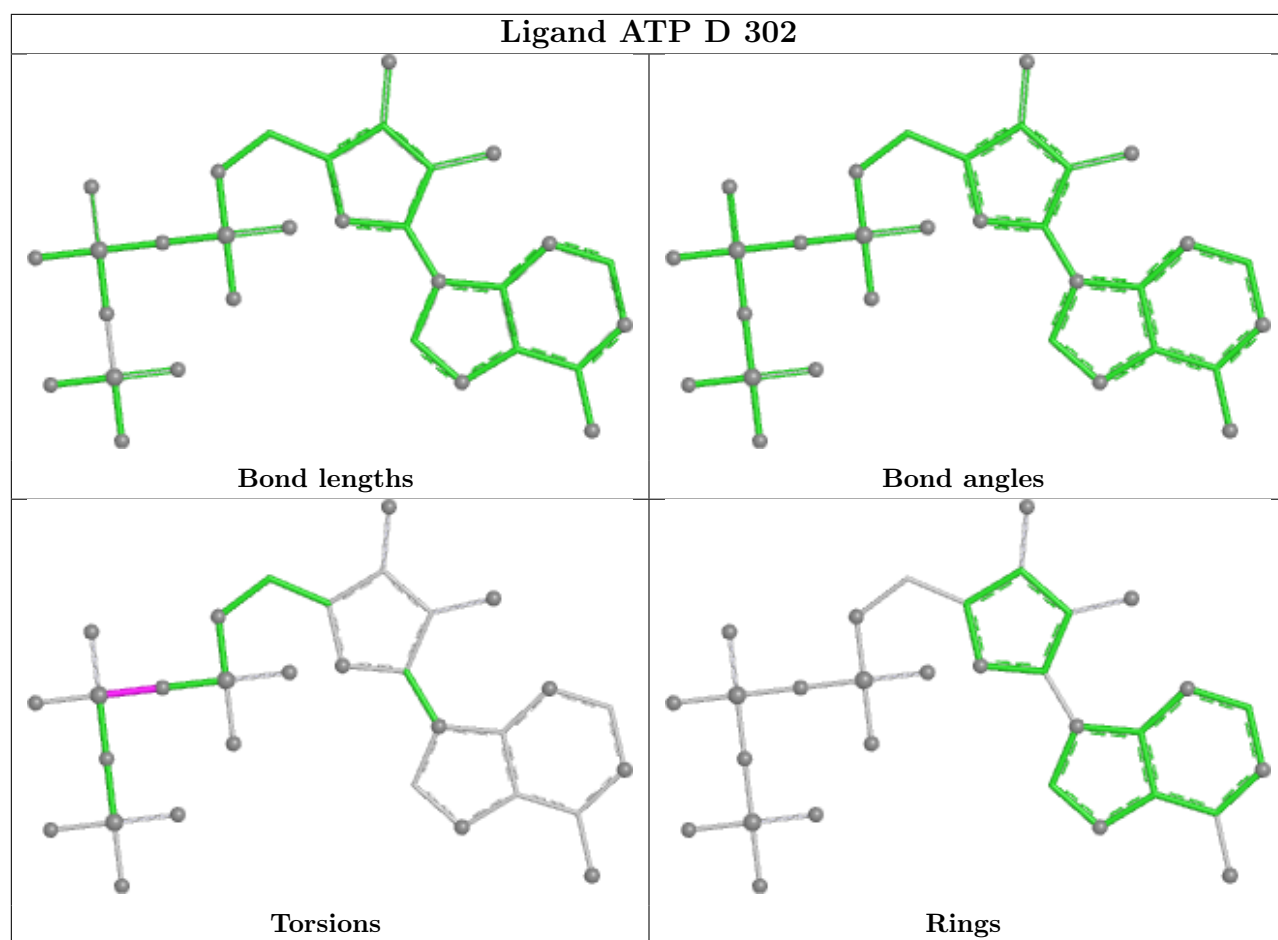


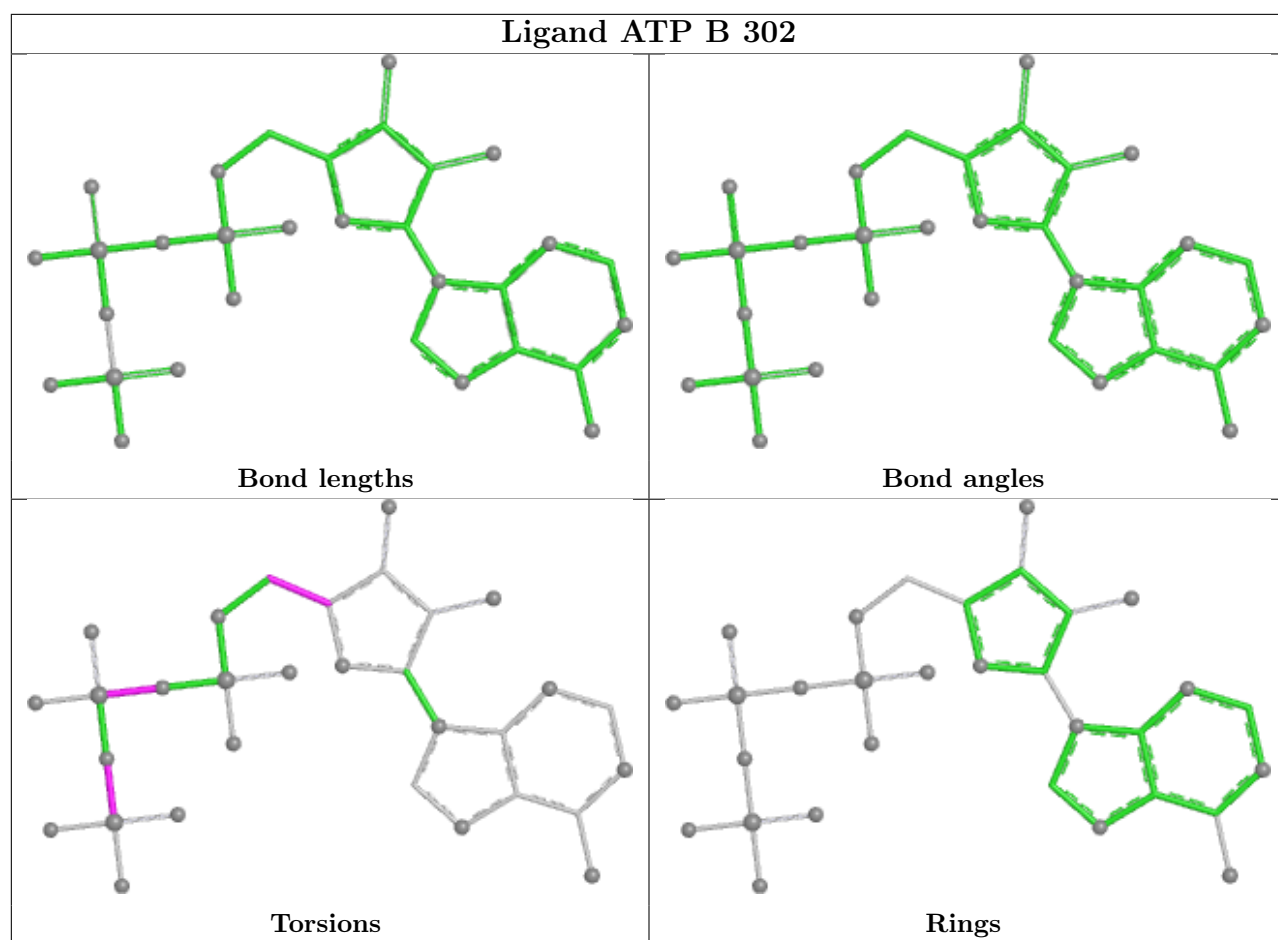


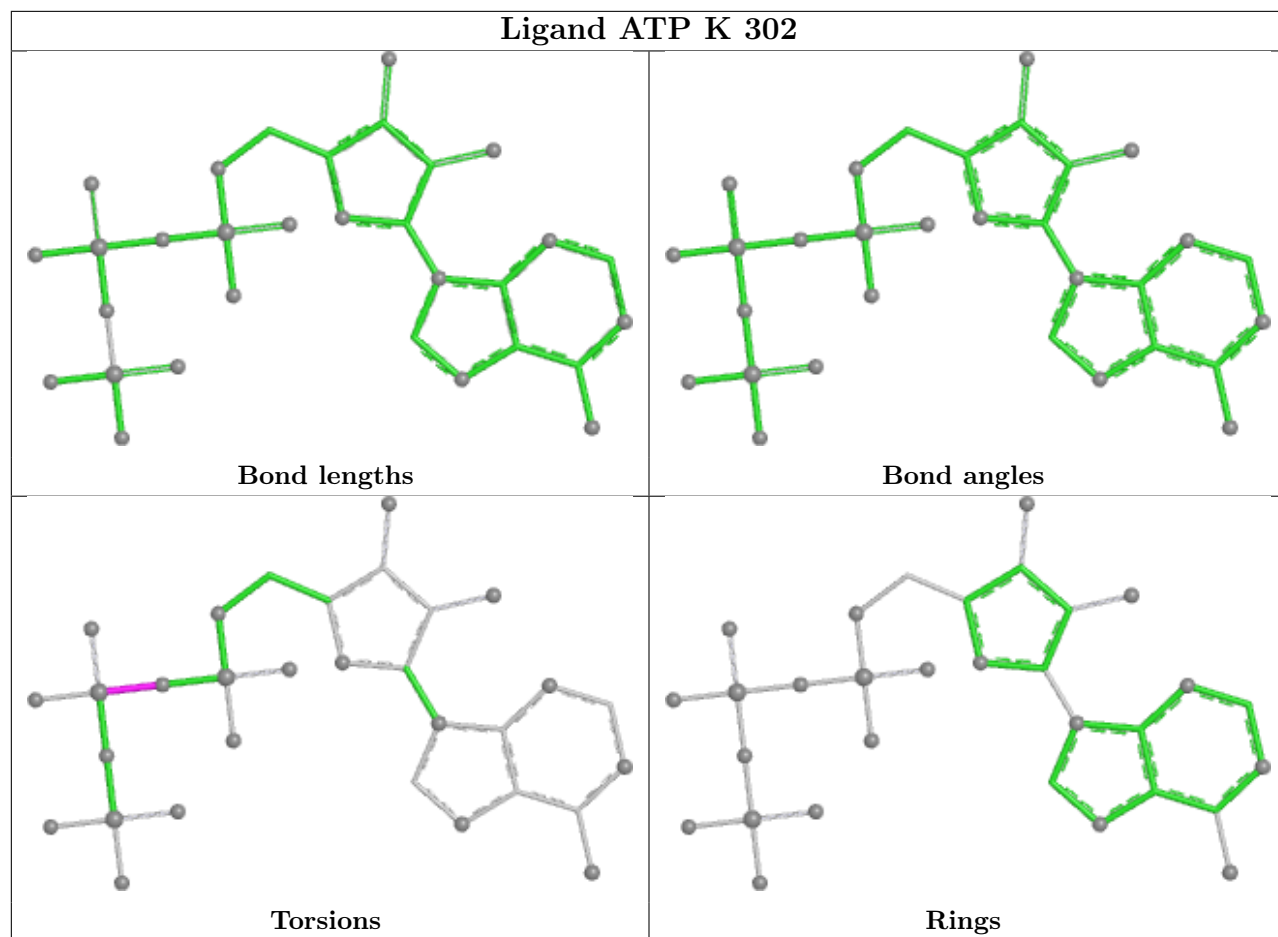


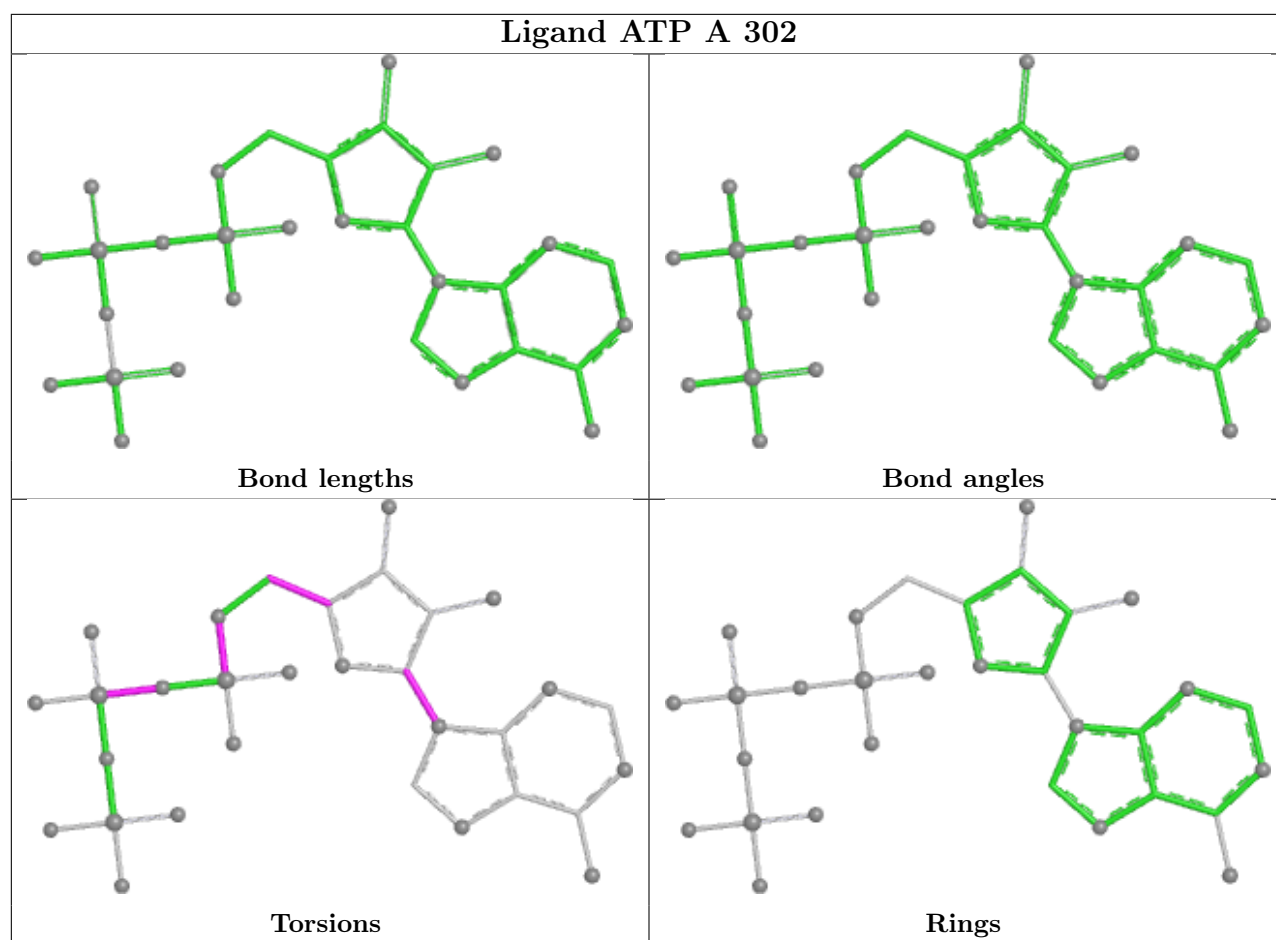












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

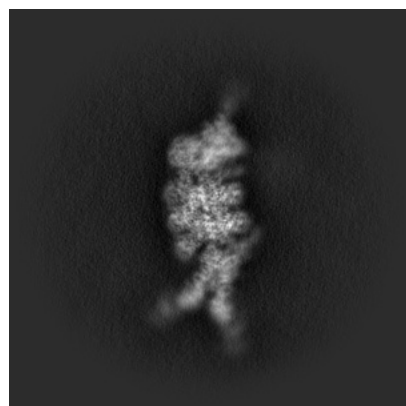
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27972. These allow visual inspection of the internal detail of the map and identification of artifacts.

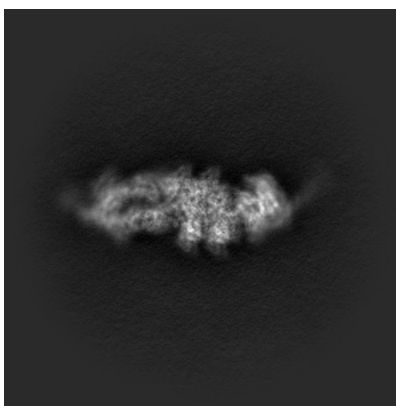
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

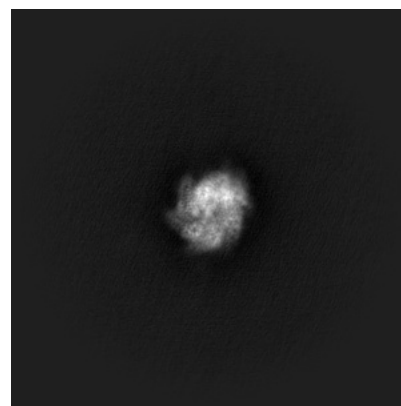
6.1.1 Primary map



X

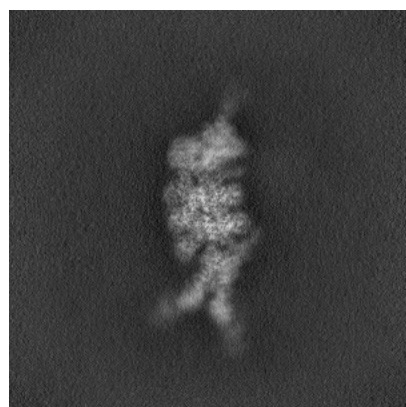


Y

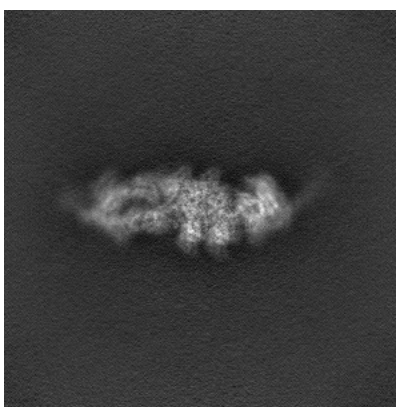


Z

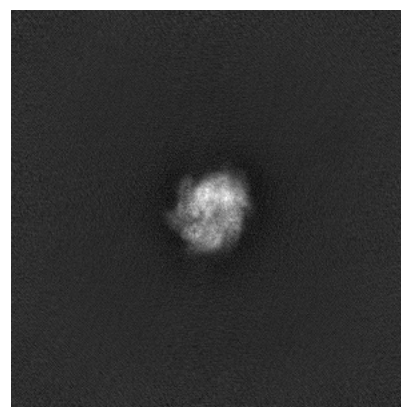
6.1.2 Raw map



X



Y

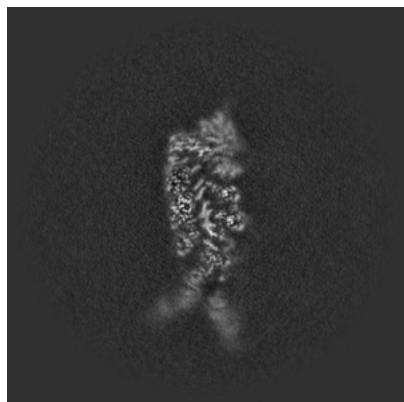


Z

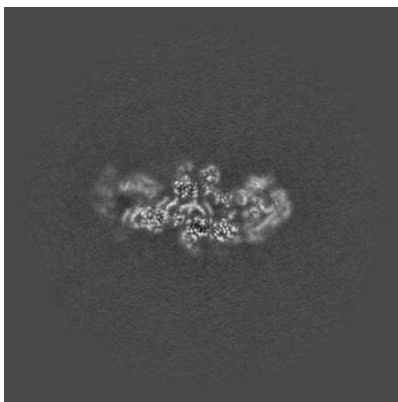
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

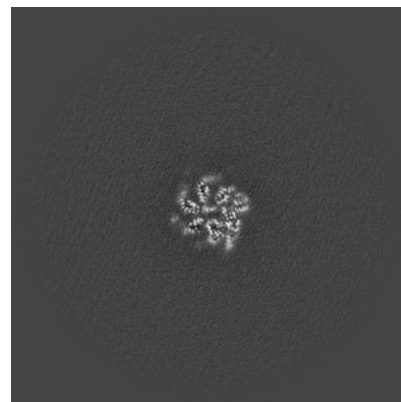
6.2.1 Primary map



X Index: 270

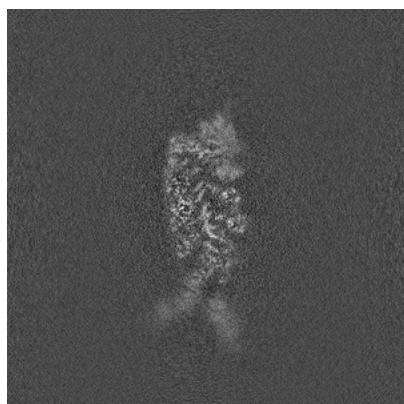


Y Index: 270

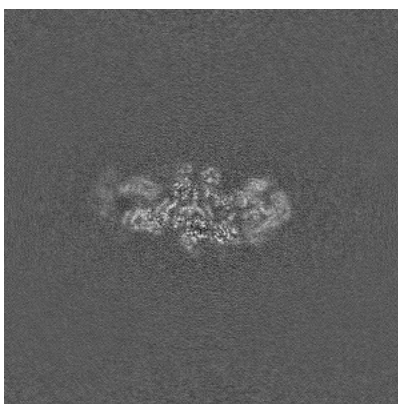


Z Index: 270

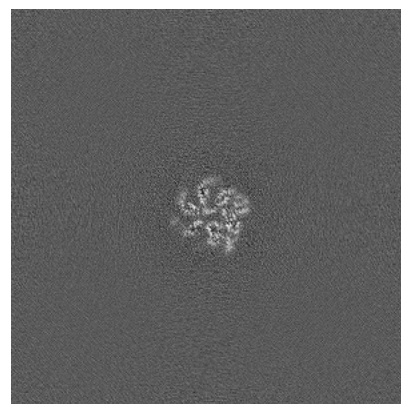
6.2.2 Raw map



X Index: 270



Y Index: 270

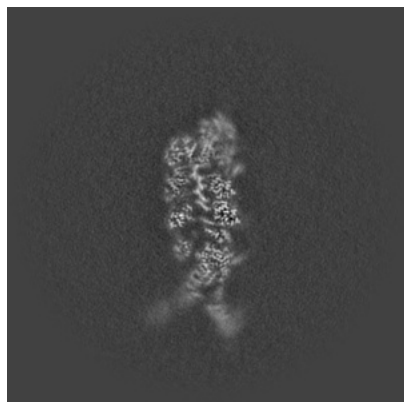


Z Index: 270

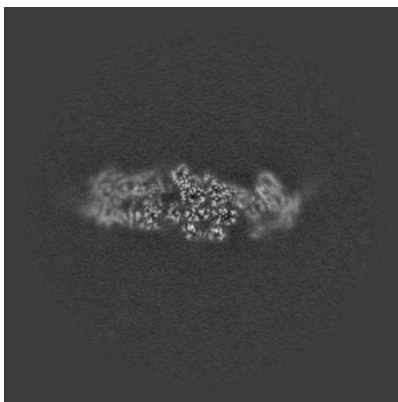
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

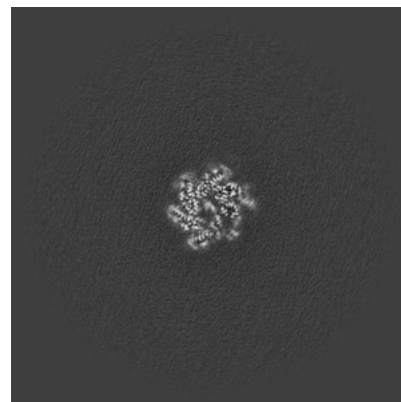
6.3.1 Primary map



X Index: 264

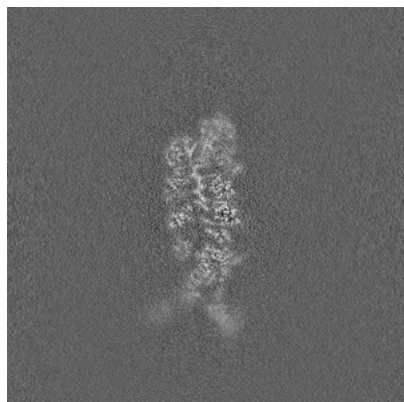


Y Index: 286

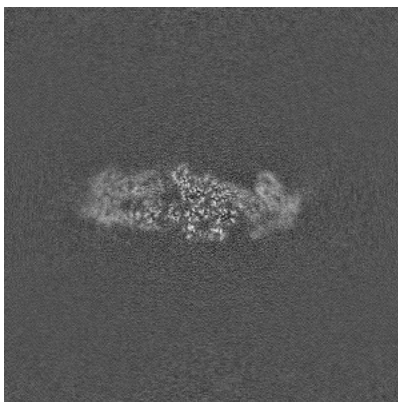


Z Index: 249

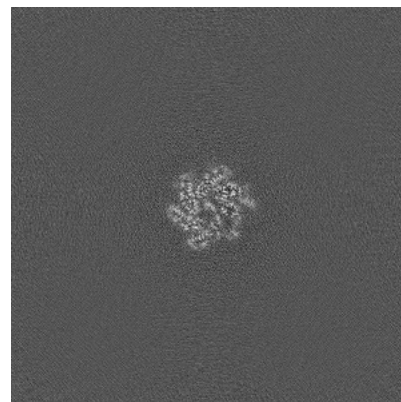
6.3.2 Raw map



X Index: 264



Y Index: 286

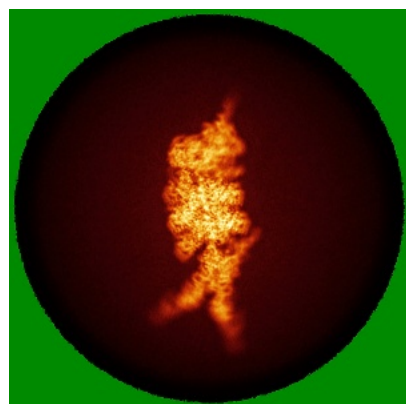


Z Index: 249

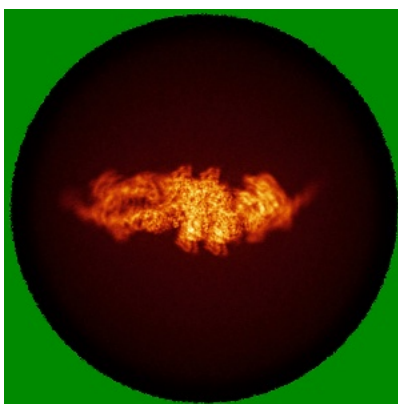
The images above show the largest variance slices of the map in three orthogonal directions.

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

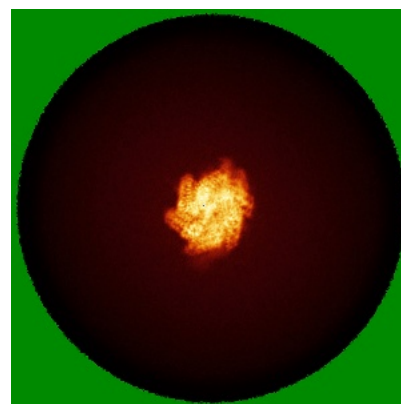
6.4.1 Primary map



X

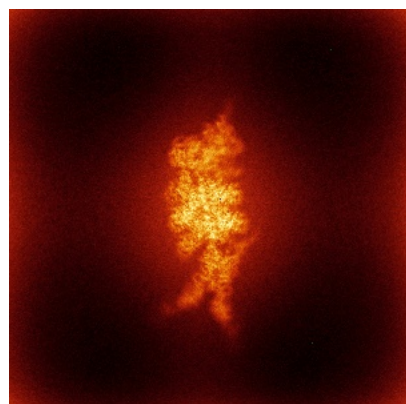


Y

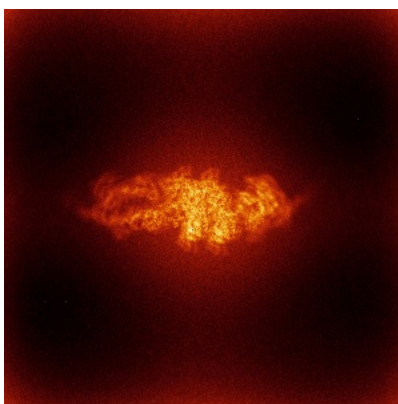


Z

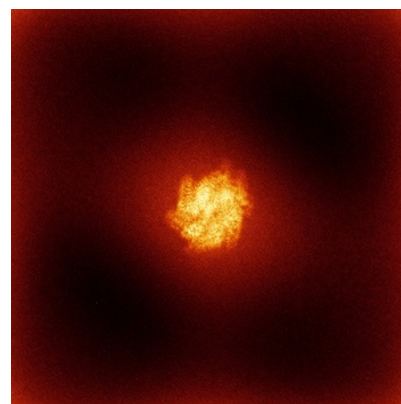
6.4.2 Raw map



X



Y

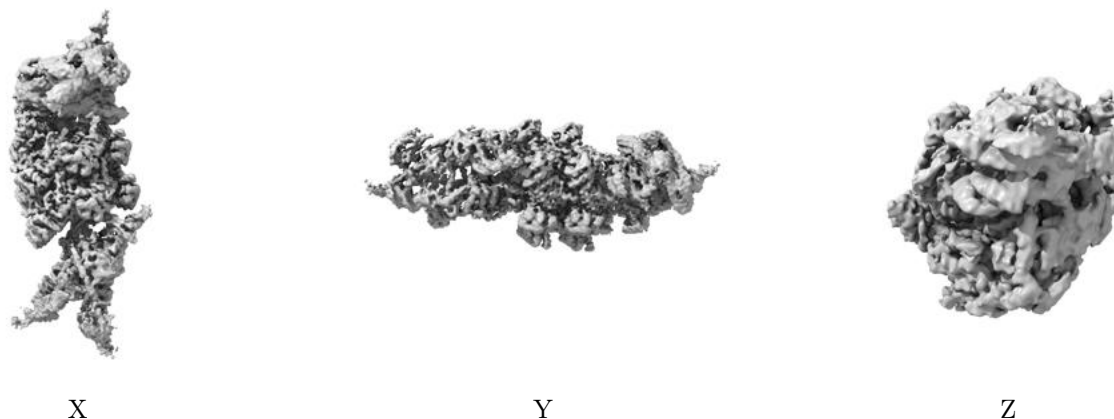


Z

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.

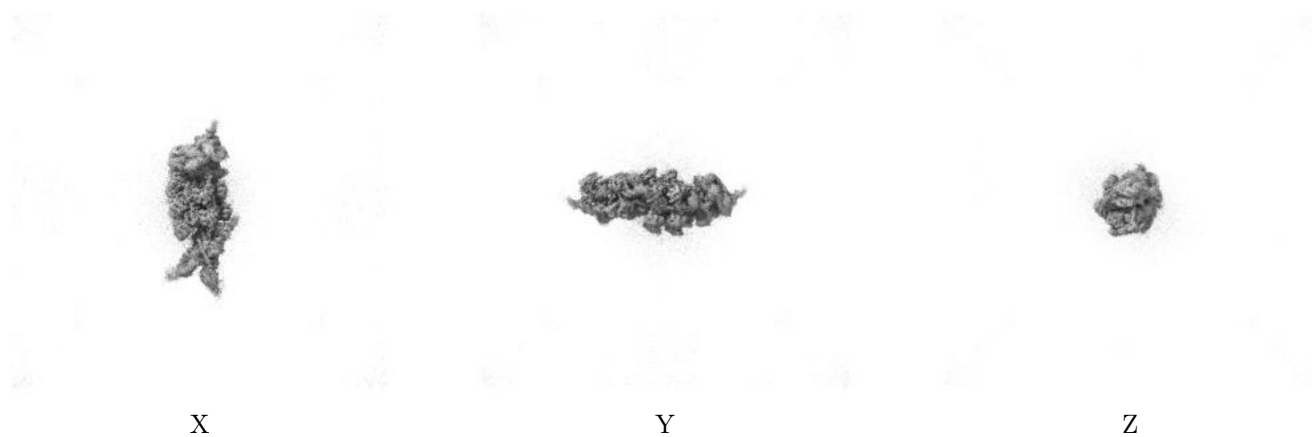
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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



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.

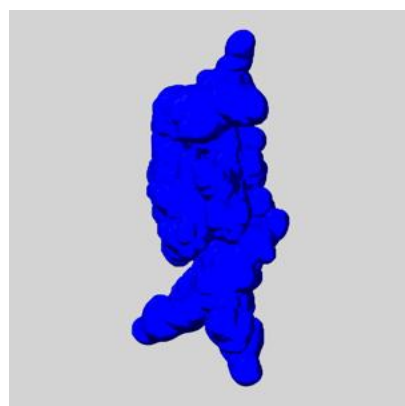
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

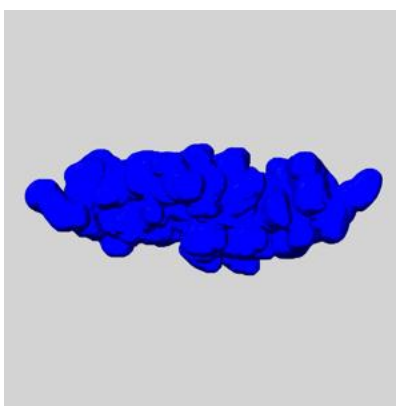
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

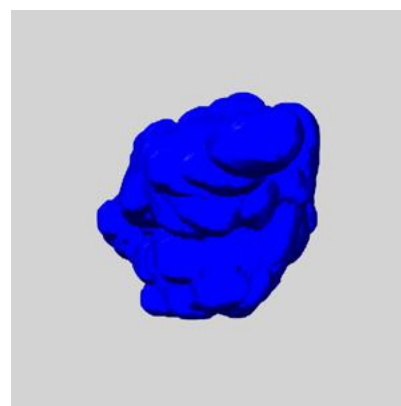
6.6.1 emd_27972_msk_1.map [i](#)



X



Y

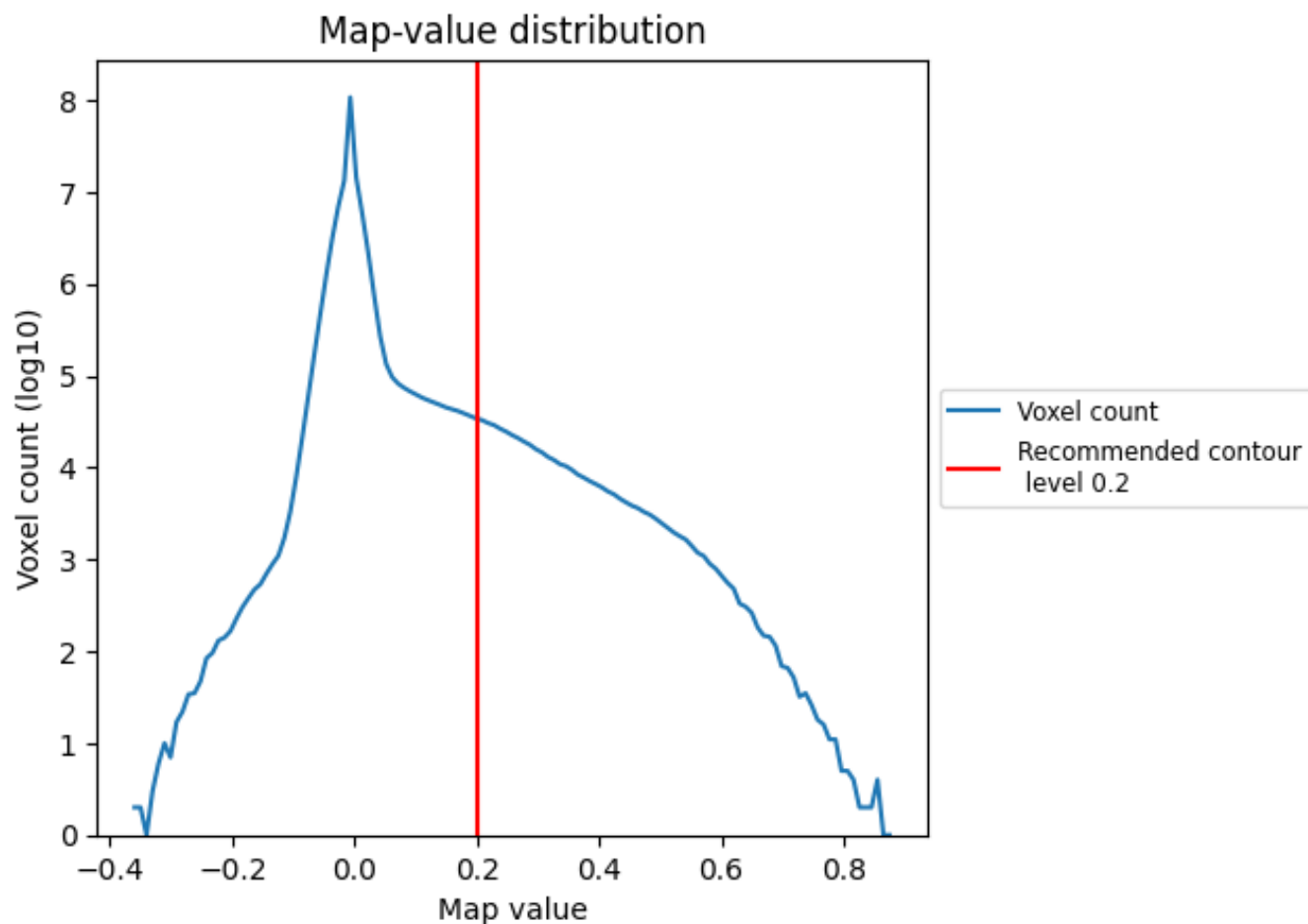


Z

7 Map analysis [i](#)

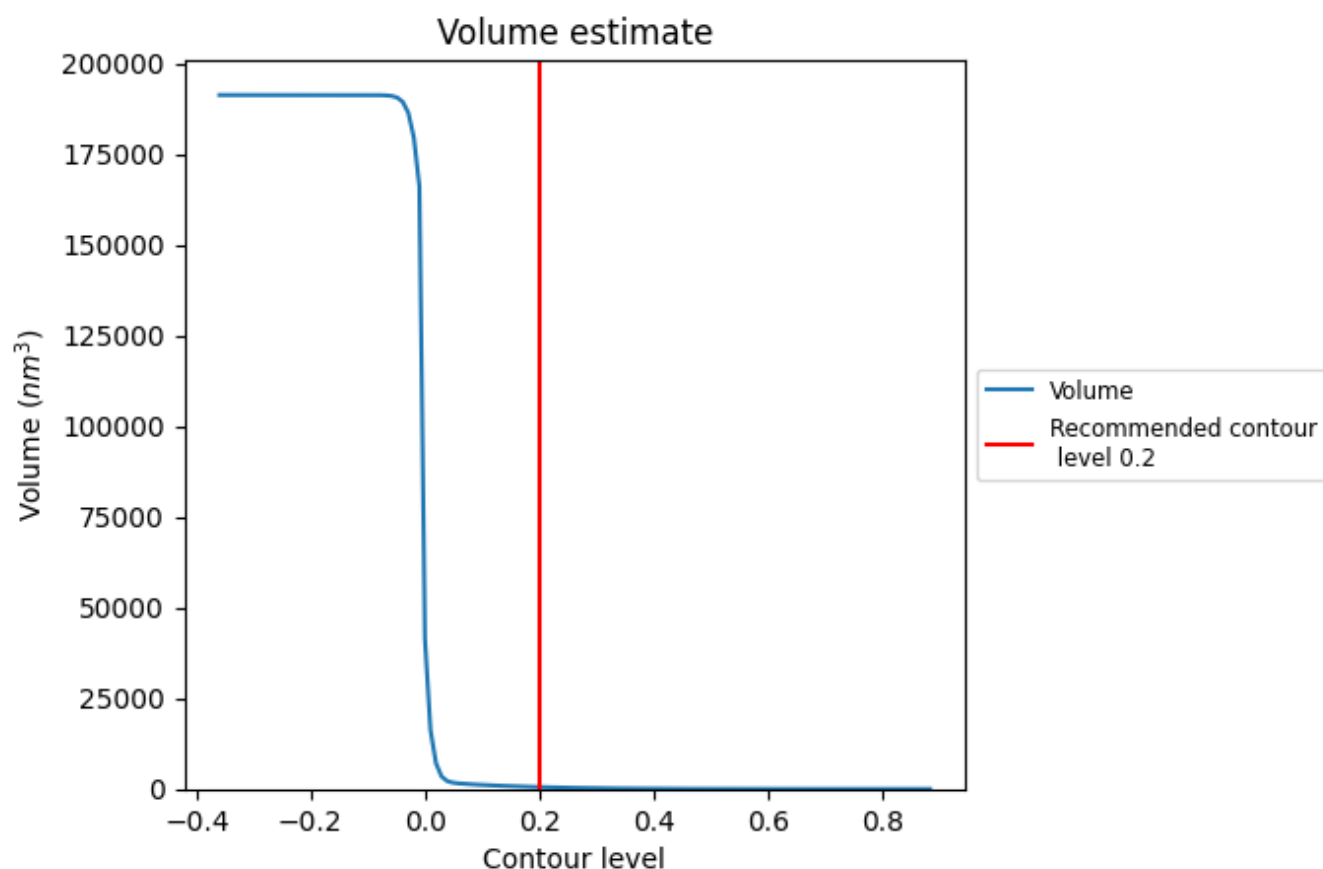
This section contains the results of statistical analysis of the map.

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.

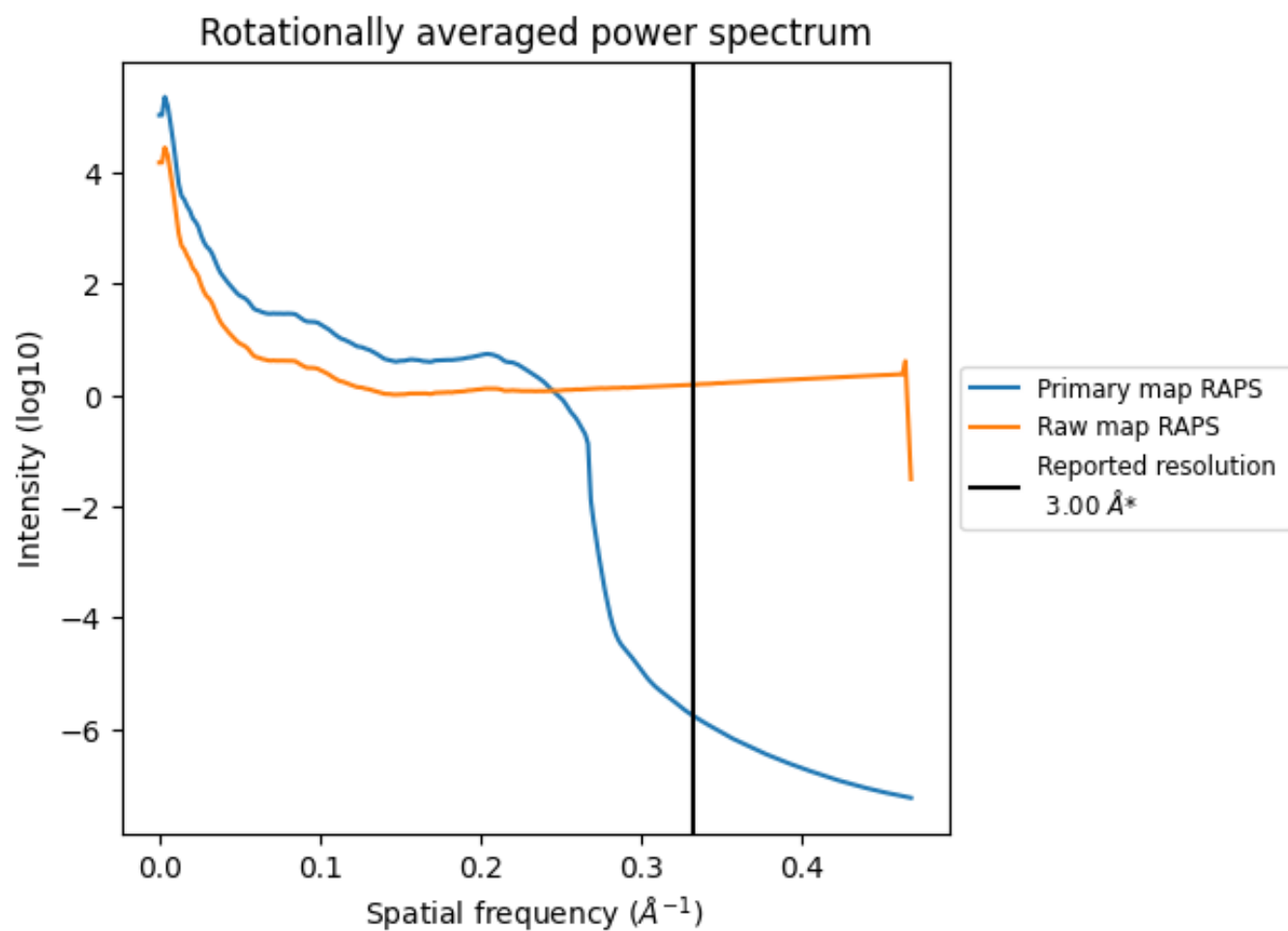
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 525 nm^3 ; this corresponds to an approximate mass of 475 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 ⓘ

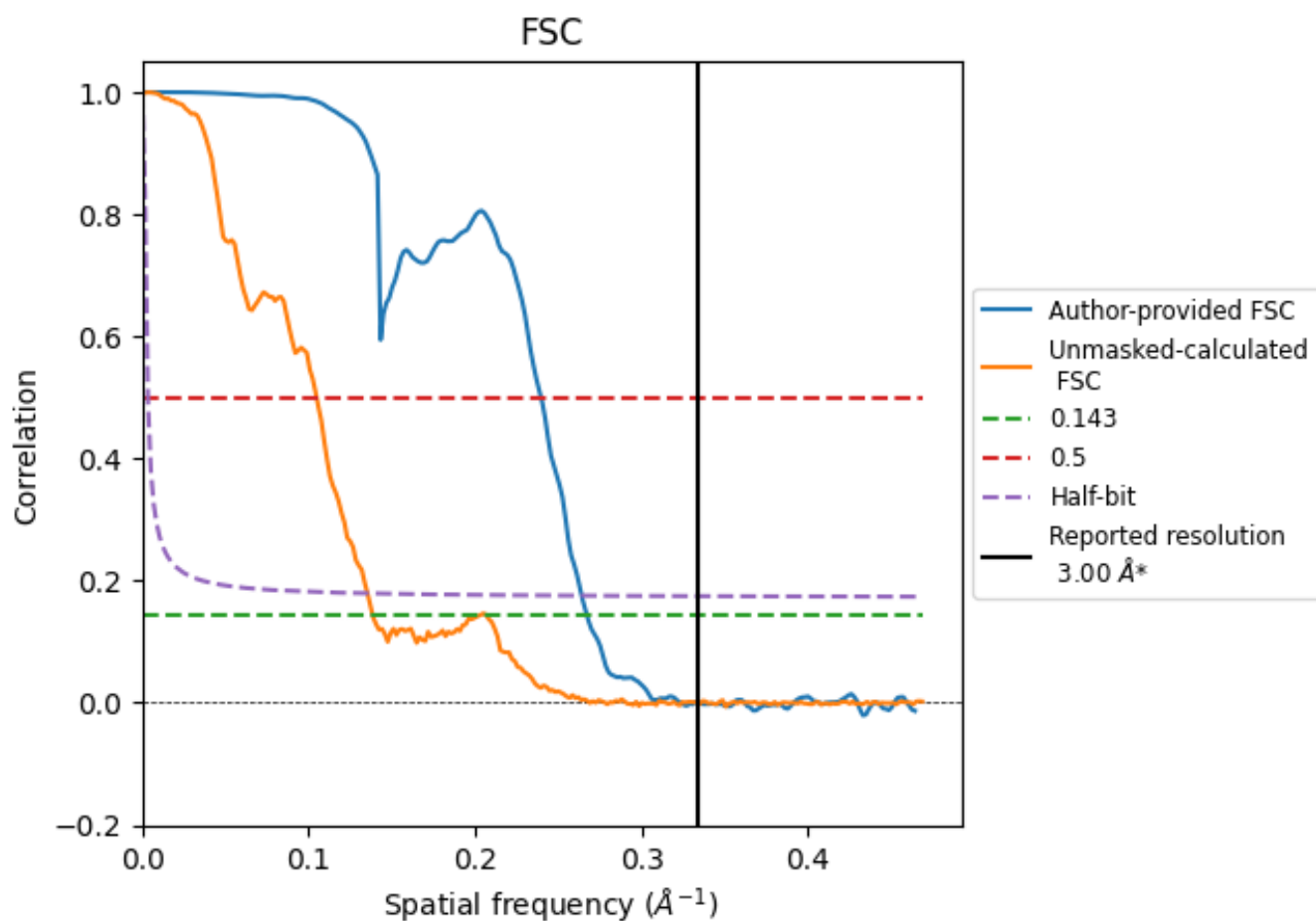


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

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 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.74	4.17	3.79
Unmasked-calculated*	7.22	9.54	7.39

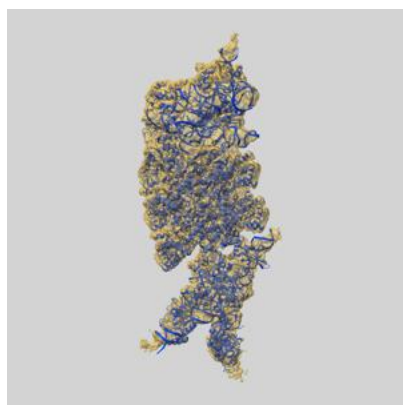
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 3.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.22 differs from the reported value 3.0 by more than 10 %

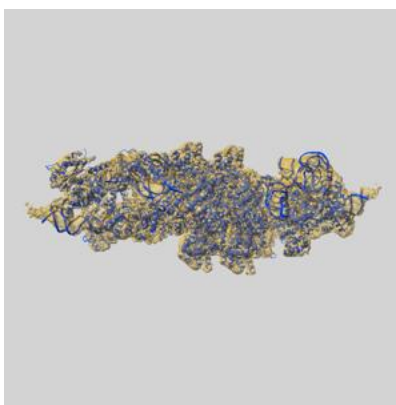
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27972 and PDB model 8EA4. Per-residue inclusion information can be found in section [3](#) on page [10](#).

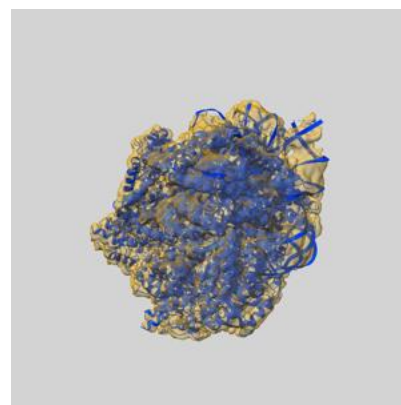
9.1 Map-model overlay [i](#)



X



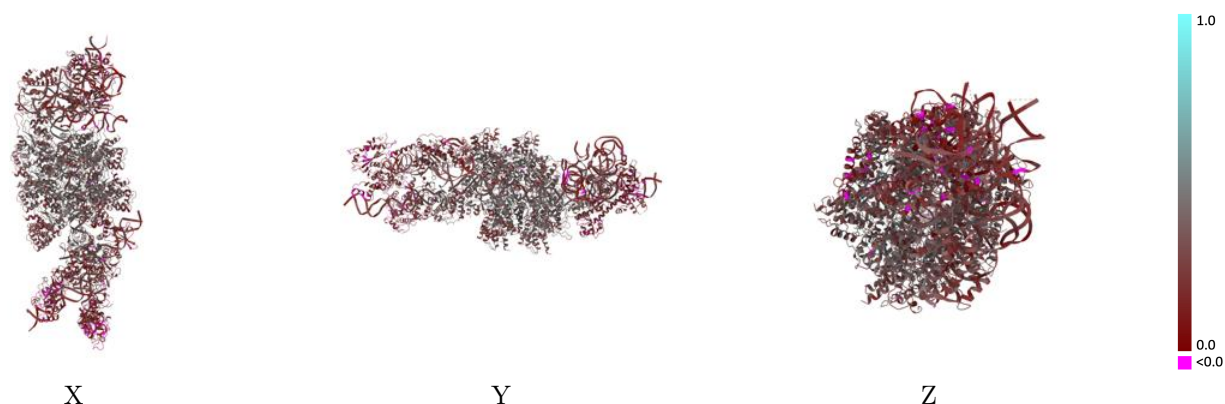
Y



Z

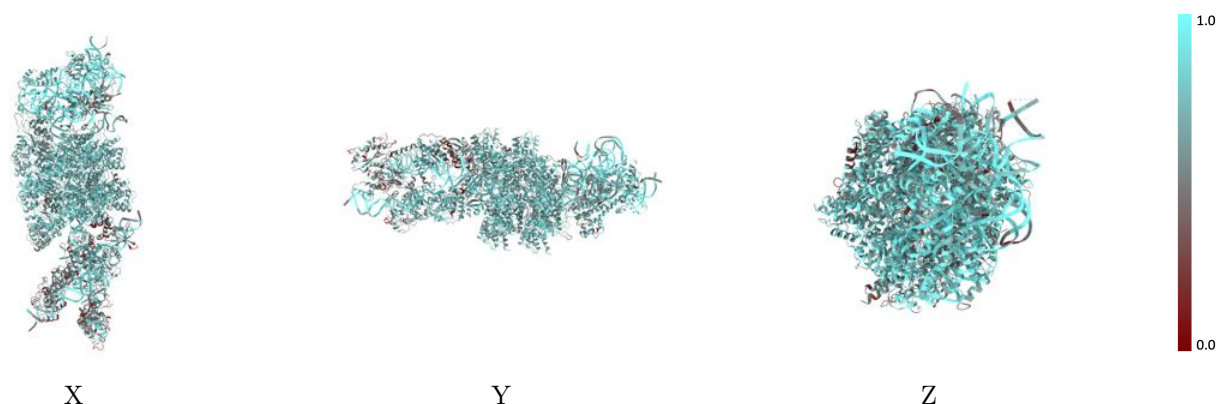
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



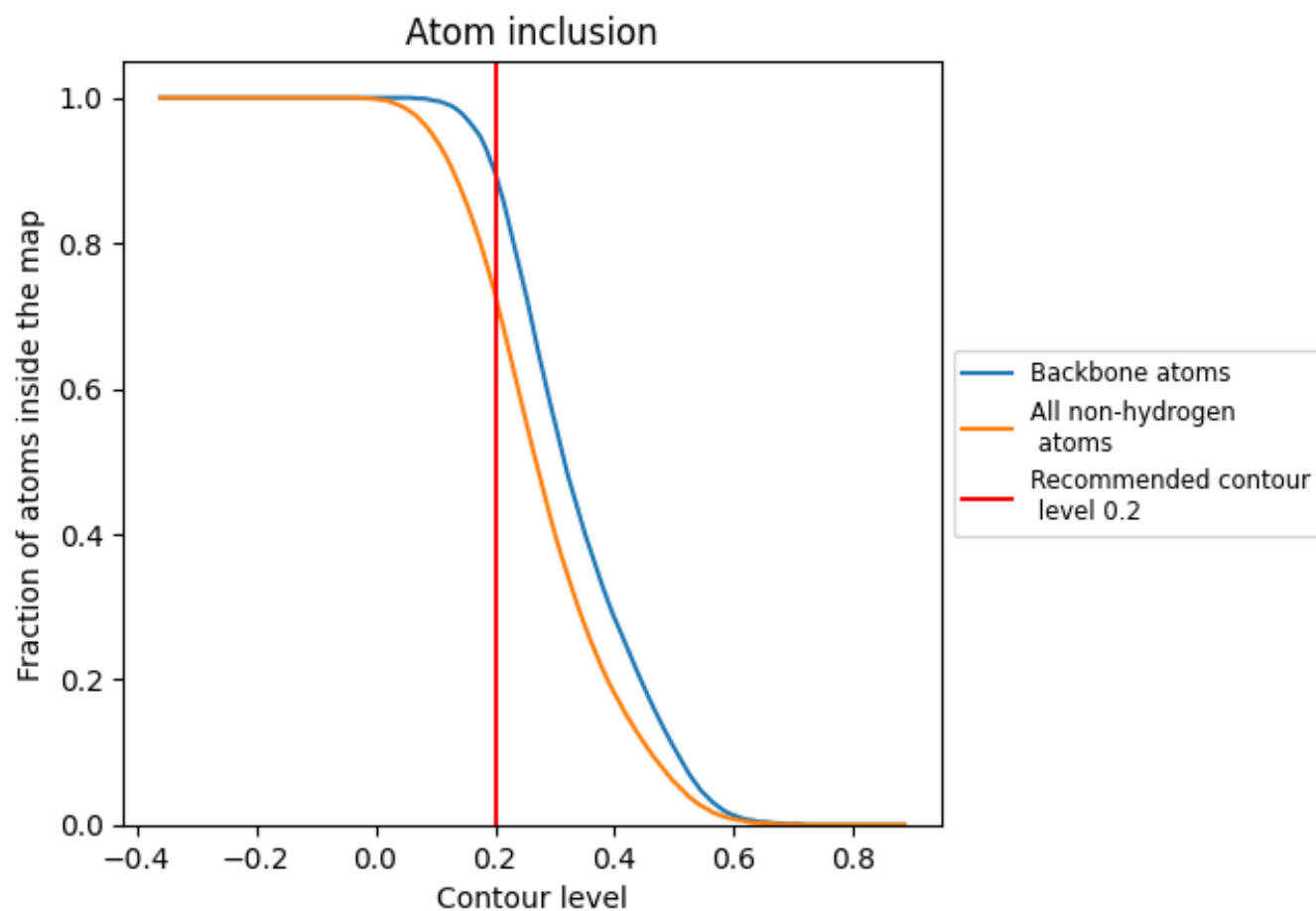
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

































































9.4 Atom inclusion ⓘ



At the recommended contour level, 90% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7300	 0.3020
1	 0.9000	 0.3110
2	 0.7800	 0.2550
3	 0.9050	 0.3400
4	 0.8600	 0.2740
5	 0.8870	 0.2830
6	 0.8170	 0.2510
7	 0.8410	 0.2300
A	 0.6780	 0.3330
B	 0.7560	 0.3630
C	 0.7810	 0.3660
D	 0.7850	 0.3790
E	 0.7670	 0.3550
F	 0.7940	 0.3800
G	 0.7880	 0.3810
H	 0.7810	 0.3770
I	 0.7670	 0.3690
J	 0.7670	 0.3770
K	 0.7650	 0.3740
L	 0.7960	 0.3810
M	 0.6250	 0.3470
O	 0.6950	 0.2160
Q	 0.8080	 0.3450
S	 0.7710	 0.2620
W	 0.6810	 0.3130
X	 0.5820	 0.2280
Y	 0.5190	 0.1420
Z	 0.4670	 0.1690
w	 0.4920	 0.2160
x	 0.4680	 0.2820
y	 0.4440	 0.1870
z	 0.3710	 0.2010

