



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:30 PM UTC

PDB ID : 7UTI / pdb_00007uti
EMDB ID : EMD-0729
Title : ALTERNATIVE MODELING OF TROPOMYOSIN IN HUMAN CARDIAC
THIN FILAMENT IN THE CALCIUM BOUND STATE
Authors : Rynkiewicz, M.J.; Pavadai, E.; Lehman, W.
Deposited on : 2022-04-27
Resolution : 4.80 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:

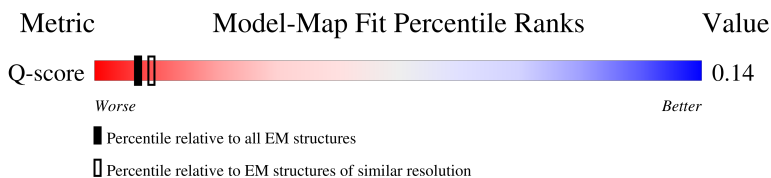
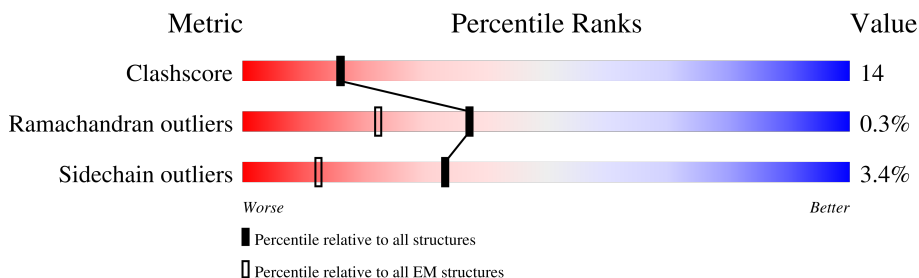
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 4.80 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.




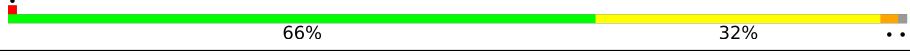

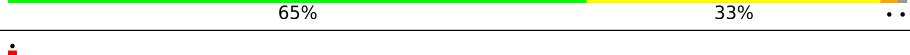
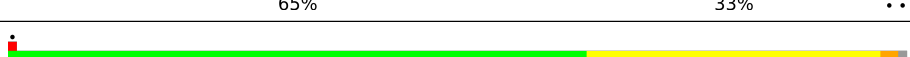
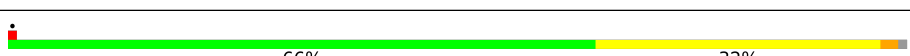













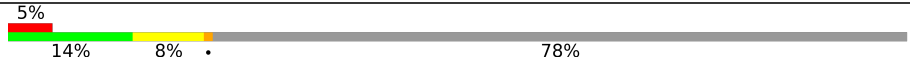

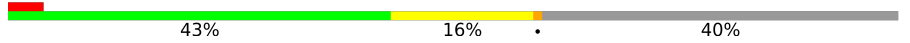



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1575 (4.30 - 5.30)

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	C	377	<p>52% (Poor fit), 63% (0 outliers), 34% (1 outlier), .. (2+ outliers)</p>
1	D	377	<p>66% (0 outliers), 32% (1 outlier), .. (2+ outliers)</p>
1	E	377	<p>62% (0 outliers), 36% (1 outlier), .. (2+ outliers)</p>
1	F	377	<p>65% (0 outliers), 33% (1 outlier), .. (2+ outliers)</p>

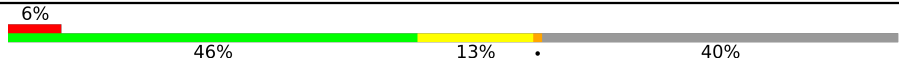


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Mol	Chain	Length	Quality of chain
1	G	377	 64% 33% ..
1	H	377	 66% 32% ..
1	I	377	 66% 32% ..
1	J	377	 65% 33% ..
1	K	377	 65% 33% ..
1	L	377	 65% 33% ..
1	M	377	 66% 32% ..
1	N	377	 66% 32% ..
1	O	377	 65% 32% ..
1	P	377	 64% 34% ..
1	Q	377	 66% 32% ..
1	R	377	 48% 63% 34% ..
2	W	285	 13% 5% 81%
2	b	285	 13% 6% 81%
2	e	285	 76% 16% 6%
2	f	285	 76% 18% 6%
2	g	285	 19% 5% 75%
2	h	285	 20% 5% 75%
2	i	285	 68% 15% 16%
2	j	285	 66% 18% 16%
3	X	288	 6% 14% 8% 78%
3	Y	288	 16% 10% 74%
3	c	288	 5% 14% 8% 78%
3	d	288	 17% 9% 74%
4	V	210	 43% 16% 40%

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Mol	Chain	Length	Quality of chain
4	a	210	
5	U	161	
5	Z	161	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 128171 atoms, of which 63663 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	C	375	5827	1855	2893	493	565	21	0	0
1	D	375	5827	1855	2893	493	565	21	0	0
1	E	375	5827	1855	2893	493	565	21	0	0
1	F	375	5827	1855	2893	493	565	21	0	0
1	G	375	5827	1855	2893	493	565	21	0	0
1	H	375	5827	1855	2893	493	565	21	0	0
1	I	375	5827	1855	2893	493	565	21	0	0
1	J	375	5827	1855	2893	493	565	21	0	0
1	K	375	5827	1855	2893	493	565	21	0	0
1	L	375	5827	1855	2893	493	565	21	0	0
1	M	375	5827	1855	2893	493	565	21	0	0
1	N	375	5827	1855	2893	493	565	21	0	0
1	O	375	5827	1855	2893	493	565	21	0	0
1	P	375	5827	1855	2893	493	565	21	0	0
1	Q	375	5827	1855	2893	493	565	21	0	0
1	R	375	5827	1855	2893	493	565	21	0	0

- Molecule 2 is a protein called Tropomyosin alpha-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	e	267	Total	C	H	N	O	S	0	0
			4284	1310	2136	366	468	4		
2	f	267	Total	C	H	N	O	S	0	0
			4284	1310	2136	366	468	4		
2	W	53	Total	C	H	N	O	S	0	0
			858	255	442	74	84	3		
2	b	53	Total	C	H	N	O	S	0	0
			858	255	442	74	84	3		
2	i	240	Total	C	H	N	O	S	0	0
			3869	1185	1932	328	420	4		
2	j	240	Total	C	H	N	O	S	0	0
			3869	1185	1932	328	420	4		
2	g	72	Total	C	H	N	O	S	0	0
			1160	350	589	97	121	3		
2	h	72	Total	C	H	N	O	S	0	0
			1160	350	589	97	121	3		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	0	ACE	-	acetylation	UNP P09493
f	0	ACE	-	acetylation	UNP P09493
W	0	ACE	-	acetylation	UNP P09493
b	0	ACE	-	acetylation	UNP P09493
i	0	ACE	-	acetylation	UNP P09493
j	0	ACE	-	acetylation	UNP P09493
g	0	ACE	-	acetylation	UNP P09493
h	0	ACE	-	acetylation	UNP P09493

- Molecule 3 is a protein called Isoform 6 of Troponin T, cardiac muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace	
3	X	63	Total	C	H	N	O	S	0	0
			1123	332	564	120	106	1		
3	Y	74	Total	C	H	N	O		0	0
			1306	401	663	123	119			
3	c	63	Total	C	H	N	O	S	0	0
			1123	332	564	120	106	1		
3	d	74	Total	C	H	N	O		0	0
			1306	401	663	123	119			

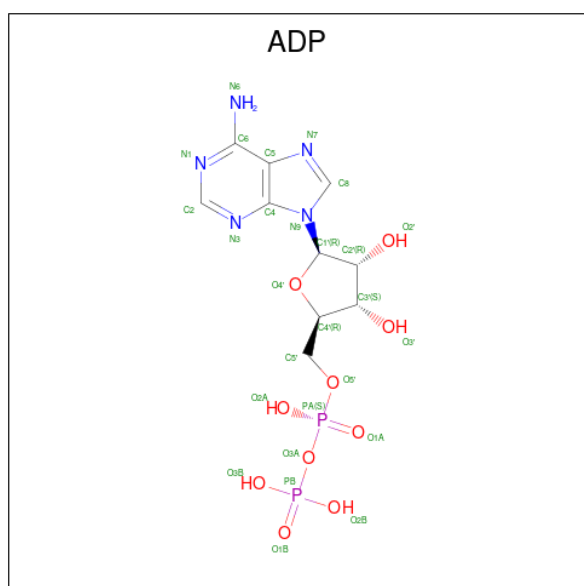
- Molecule 4 is a protein called Troponin I, cardiac muscle.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	V	126	Total	C	H	N	O	S	0	0
			2073	624	1065	193	187	4		
4	a	126	Total	C	H	N	O	S	0	0
			2072	624	1064	193	187	4		

- Molecule 5 is a protein called Troponin C, slow skeletal and cardiac muscles.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	U	160	Total	C	H	N	O	S	0	0
			2474	788	1201	195	278	12		
5	Z	160	Total	C	H	N	O	S	0	0
			2474	788	1201	195	278	12		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
6	C	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
6	D	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
6	E	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
6	F	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
6	G	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
6	H	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	

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Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
6	I	1	39	10	12	5	10	2	0
6	J	1	39	10	12	5	10	2	0
6	K	1	39	10	12	5	10	2	0
6	L	1	39	10	12	5	10	2	0
6	M	1	39	10	12	5	10	2	0
6	N	1	39	10	12	5	10	2	0
6	O	1	39	10	12	5	10	2	0
6	P	1	39	10	12	5	10	2	0
6	Q	1	39	10	12	5	10	2	0
6	R	1	39	10	12	5	10	2	0

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
7	C	1	Total 1	Mg 1	0
7	D	1	Total 1	Mg 1	0
7	E	1	Total 1	Mg 1	0
7	F	1	Total 1	Mg 1	0
7	G	1	Total 1	Mg 1	0
7	H	1	Total 1	Mg 1	0
7	I	1	Total 1	Mg 1	0
7	J	1	Total 1	Mg 1	0
7	K	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
7	L	1	Total 1	Mg 1	0
7	M	1	Total 1	Mg 1	0
7	N	1	Total 1	Mg 1	0
7	O	1	Total 1	Mg 1	0
7	P	1	Total 1	Mg 1	0
7	Q	1	Total 1	Mg 1	0
7	R	1	Total 1	Mg 1	0

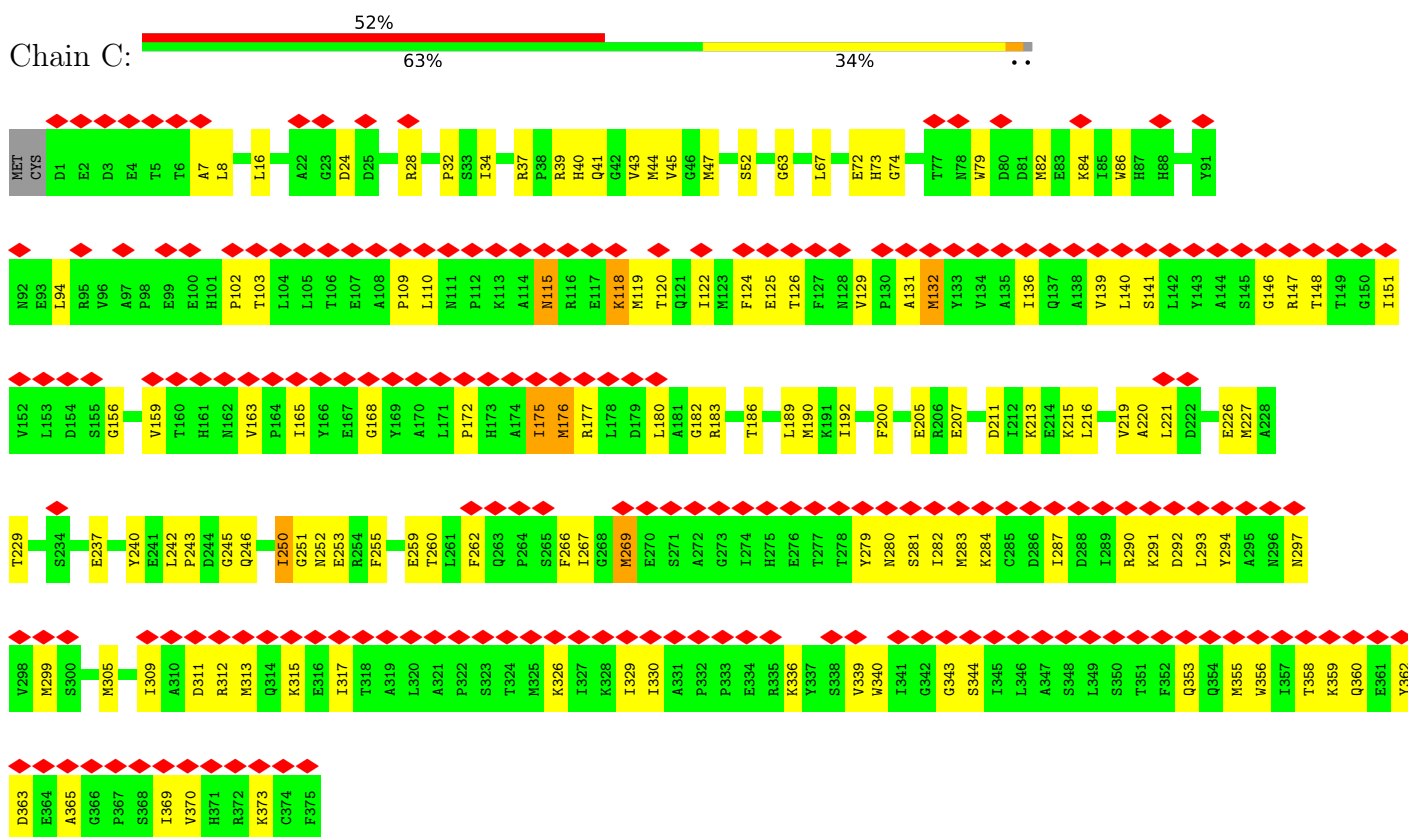
- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
8	U	3	Total 3	Ca 3	0
8	Z	3	Total 3	Ca 3	0

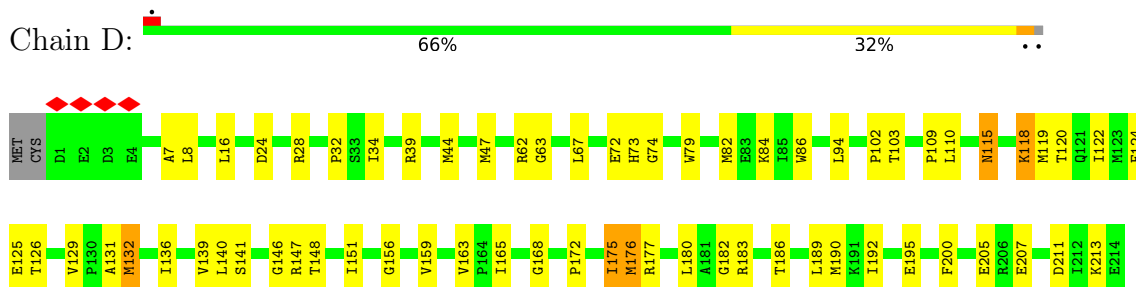
3 Residue-property plots i

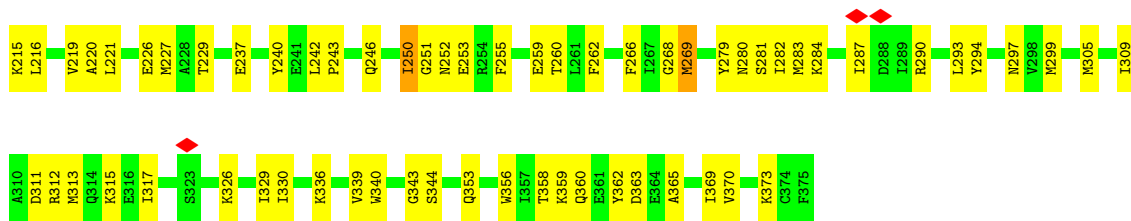
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

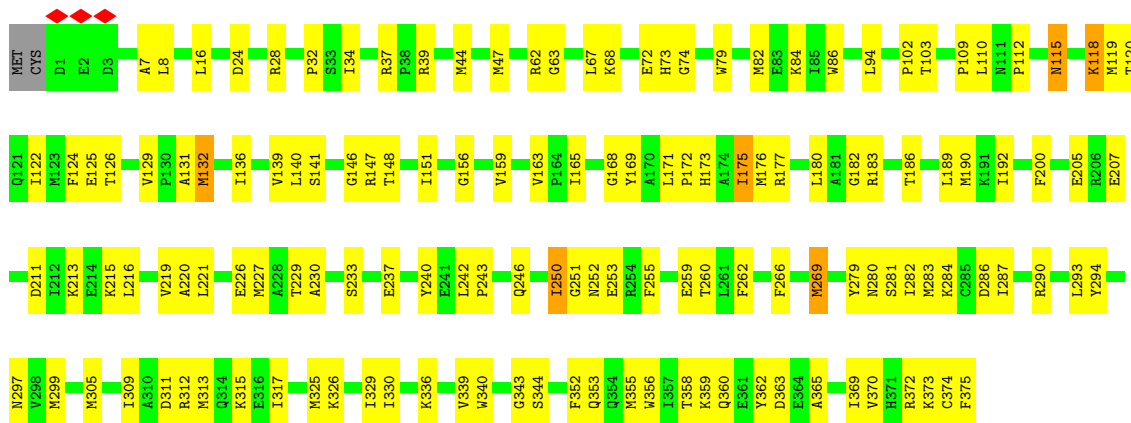


- Molecule 1: Actin, alpha skeletal muscle

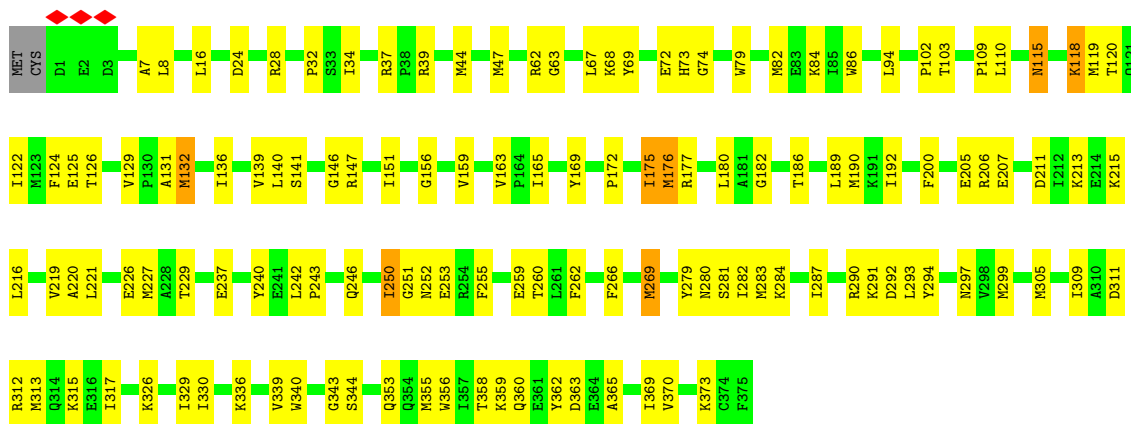




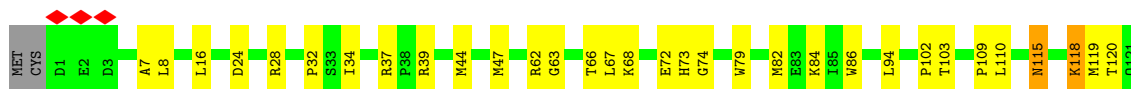
• Molecule 1: Actin, alpha skeletal muscle

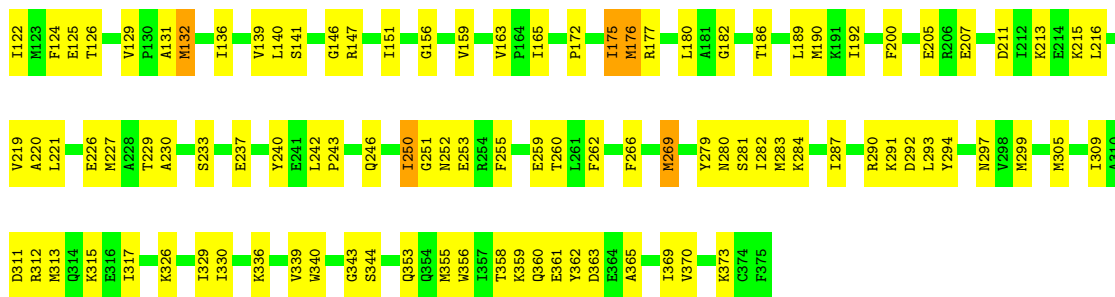


• Molecule 1: Actin, alpha skeletal muscle

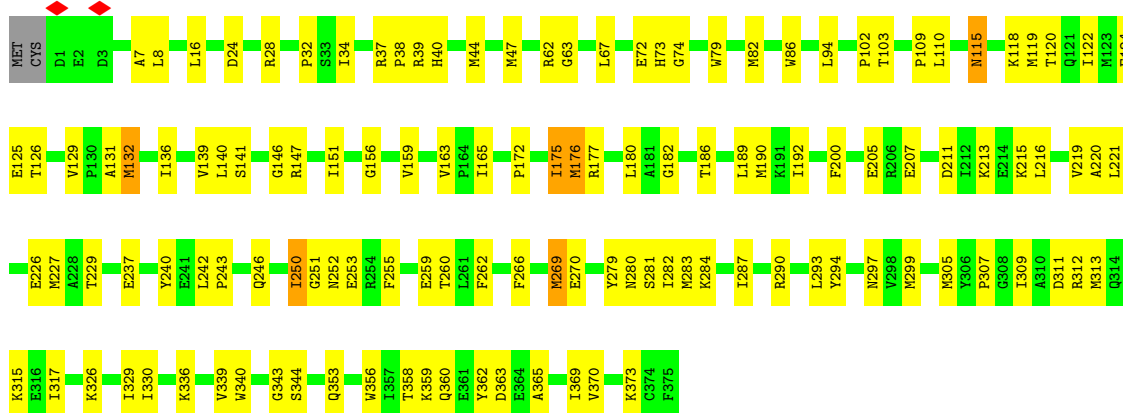


• Molecule 1: Actin, alpha skeletal muscle

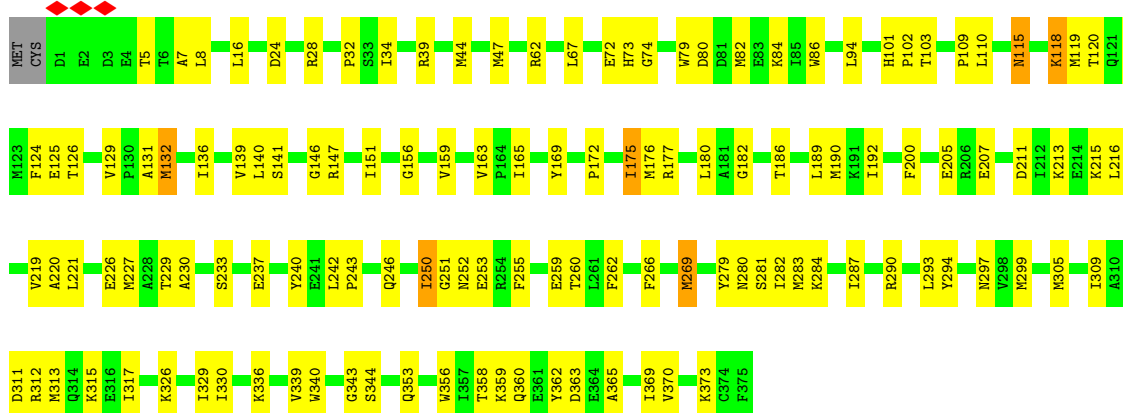




• Molecule 1: Actin, alpha skeletal muscle

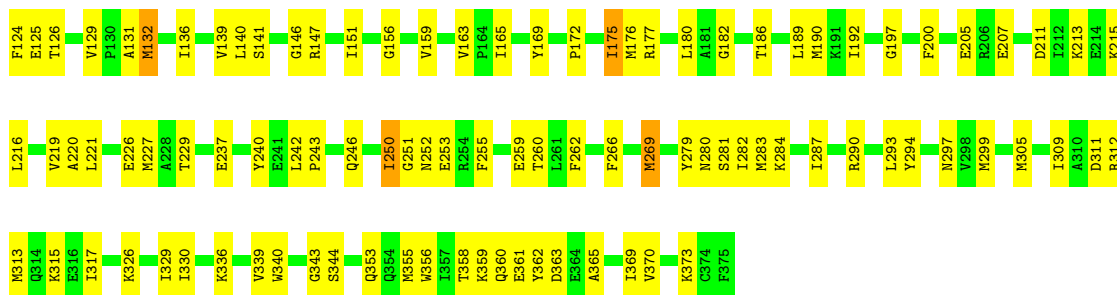


• Molecule 1: Actin, alpha skeletal muscle

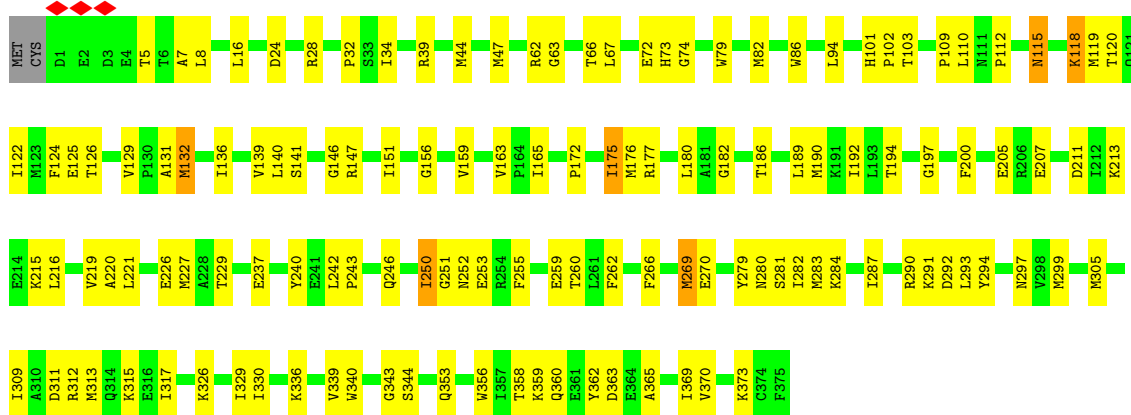


• Molecule 1: Actin, alpha skeletal muscle

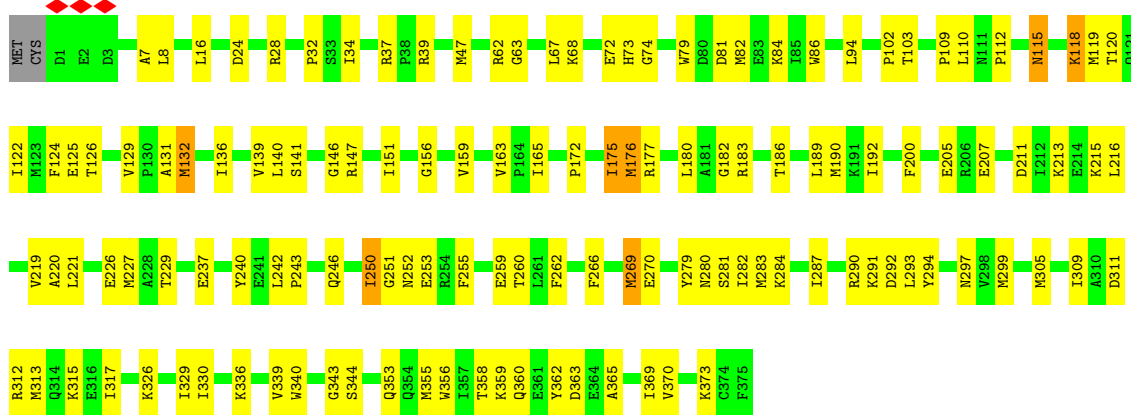




• Molecule 1: Actin, alpha skeletal muscle

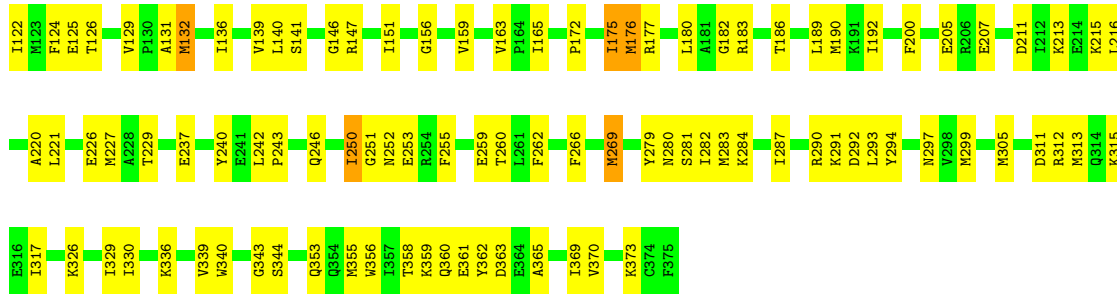


• Molecule 1: Actin, alpha skeletal muscle

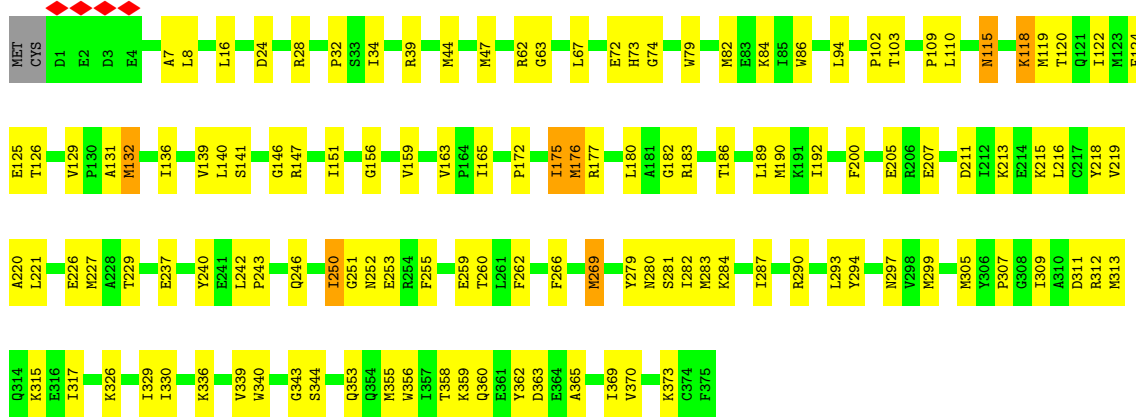


• Molecule 1: Actin, alpha skeletal muscle

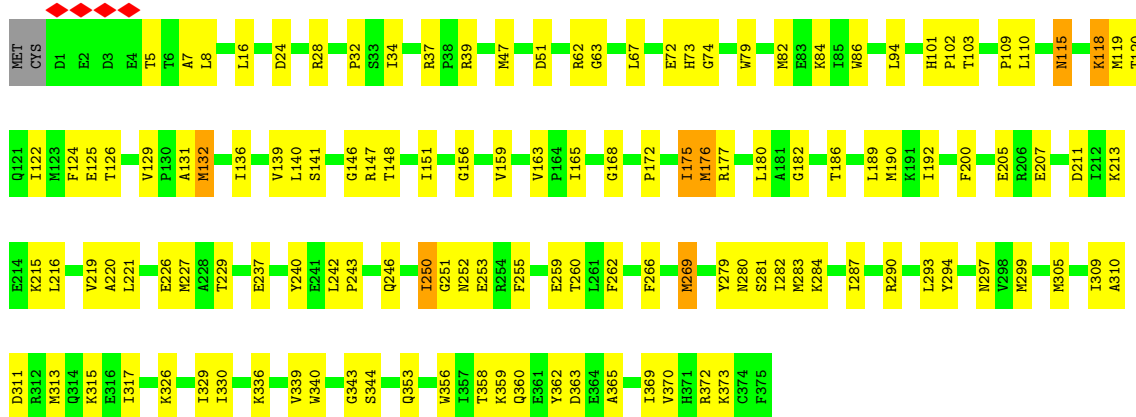




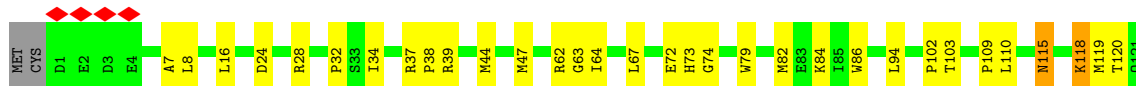
• Molecule 1: Actin, alpha skeletal muscle

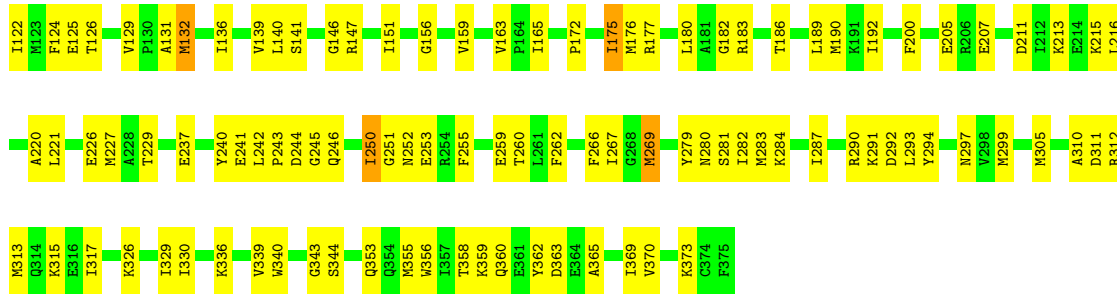


• Molecule 1: Actin, alpha skeletal muscle

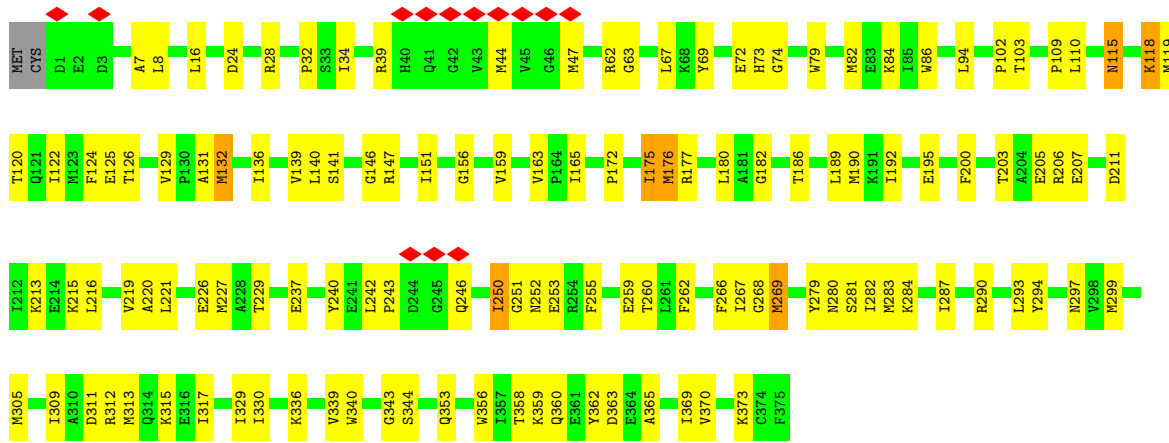


• Molecule 1: Actin, alpha skeletal muscle

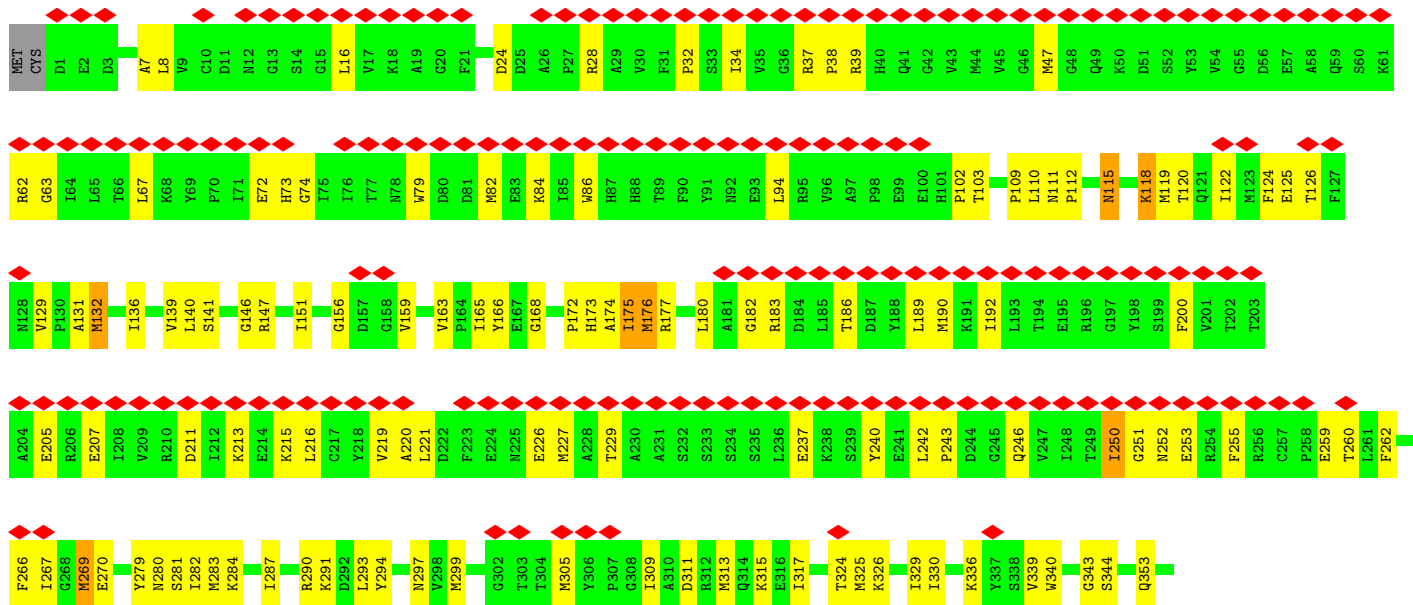


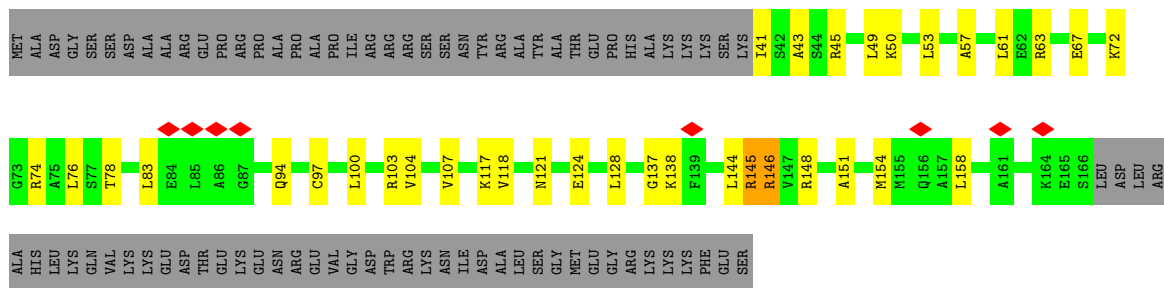


• Molecule 1: Actin, alpha skeletal muscle

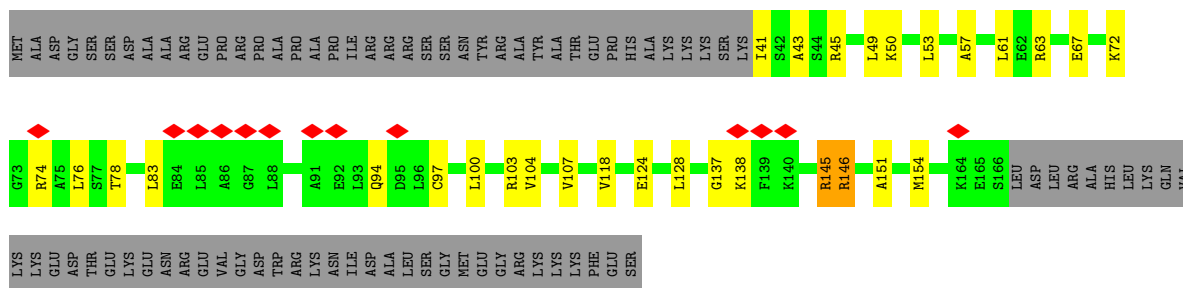


• Molecule 1: Actin, alpha skeletal muscle

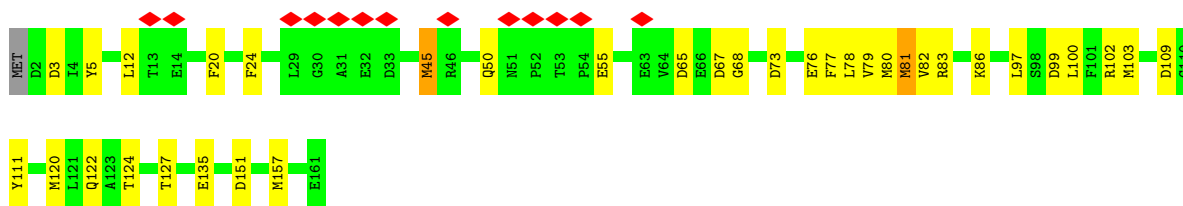
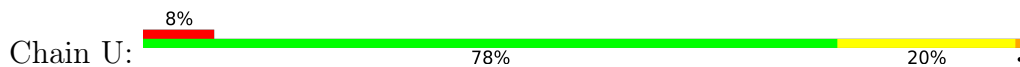




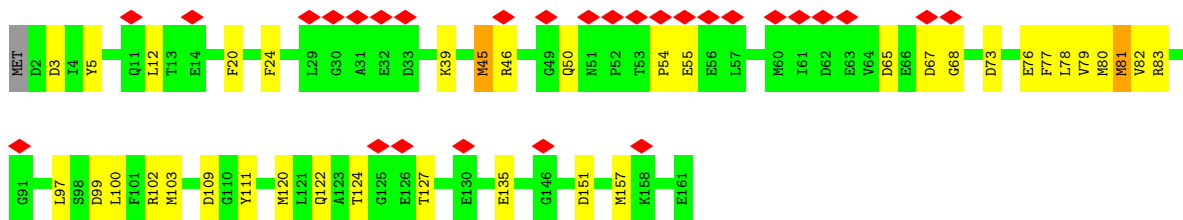
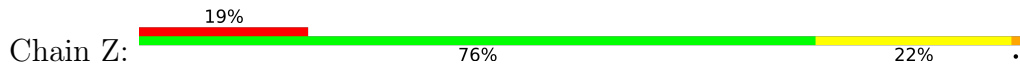
• Molecule 4: Troponin I, cardiac muscle



• Molecule 5: Troponin C, slow skeletal and cardiac muscles



• Molecule 5: Troponin C, slow skeletal and cardiac muscles



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23374	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 200	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	65	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.259	Depositor
Minimum map value	-0.078	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0456	Depositor
Map size (Å)	444.0, 444.0, 444.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.22, 2.22, 2.22	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ACE, ADP, CA, HIC

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	C	0.19	0/2984	0.48	0/4040
1	D	0.17	0/2984	0.47	0/4040
1	E	0.19	0/2984	0.48	0/4040
1	F	0.18	0/2984	0.48	0/4040
1	G	0.18	0/2984	0.48	0/4040
1	H	0.18	0/2984	0.47	0/4040
1	I	0.18	0/2984	0.47	0/4040
1	J	0.19	0/2984	0.47	0/4040
1	K	0.17	0/2984	0.47	0/4040
1	L	0.18	0/2984	0.47	0/4040
1	M	0.17	0/2984	0.47	0/4040
1	N	0.17	0/2984	0.47	0/4040
1	O	0.17	0/2984	0.47	0/4040
1	P	0.19	0/2984	0.47	0/4040
1	Q	0.17	0/2984	0.47	0/4040
1	R	0.18	0/2984	0.49	0/4040
2	W	0.22	0/413	0.56	0/543
2	b	0.16	0/413	0.43	0/543
2	e	0.17	0/2156	0.39	0/2876
2	f	0.22	0/2156	0.38	0/2876
2	g	0.19	0/569	0.49	0/752
2	h	0.15	0/569	0.39	0/752
2	i	0.18	0/1945	0.40	0/2594
2	j	0.20	0/1945	0.38	0/2594
3	X	0.18	0/561	0.47	0/739
3	Y	0.33	1/649 (0.2%)	0.66	0/861
3	c	0.18	0/561	0.47	0/739
3	d	0.34	1/649 (0.2%)	0.68	0/861
4	V	0.19	0/1014	0.47	0/1352
4	a	0.19	0/1014	0.45	0/1352
5	U	0.18	0/1286	0.43	0/1719
5	Z	0.18	0/1286	0.43	0/1719

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.19	2/64930 (0.0%)	0.47	0/87512

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	d	203	THR	C-O	-5.05	1.17	1.24
3	Y	203	THR	C-O	-5.03	1.17	1.24

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	C	2934	2893	2895	107	0
1	D	2934	2893	2895	95	0
1	E	2934	2893	2895	106	0
1	F	2934	2893	2895	90	0
1	G	2934	2893	2895	92	0
1	H	2934	2893	2895	94	0
1	I	2934	2893	2895	90	0
1	J	2934	2893	2895	92	0
1	K	2934	2893	2895	97	0
1	L	2934	2893	2895	95	0
1	M	2934	2893	2895	91	0
1	N	2934	2893	2895	92	0
1	O	2934	2893	2895	95	0
1	P	2934	2893	2895	103	0
1	Q	2934	2893	2895	94	0
1	R	2934	2893	2895	101	0
2	W	416	442	442	20	0
2	b	416	442	442	21	0
2	e	2148	2136	2136	55	0
2	f	2148	2136	2136	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	g	571	589	589	20	0
2	h	571	589	589	12	0
2	i	1937	1932	1932	60	0
2	j	1937	1932	1932	51	0
3	X	559	564	563	18	0
3	Y	643	663	663	24	0
3	c	559	564	563	16	0
3	d	643	663	663	22	0
4	V	1008	1065	1064	29	0
4	a	1008	1064	1064	23	0
5	U	1273	1201	1200	26	0
5	Z	1273	1201	1200	32	0
6	C	27	12	12	1	0
6	D	27	12	12	1	0
6	E	27	12	12	1	0
6	F	27	12	12	1	0
6	G	27	12	12	1	0
6	H	27	12	12	1	0
6	I	27	12	12	1	0
6	J	27	12	12	1	0
6	K	27	12	12	1	0
6	L	27	12	12	1	0
6	M	27	12	12	1	0
6	N	27	12	12	1	0
6	O	27	12	12	1	0
6	P	27	12	12	1	0
6	Q	27	12	12	1	0
6	R	27	12	12	1	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	1	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
7	H	1	0	0	0	0
7	I	1	0	0	0	0
7	J	1	0	0	0	0
7	K	1	0	0	0	0
7	L	1	0	0	0	0
7	M	1	0	0	0	0
7	N	1	0	0	0	0
7	O	1	0	0	0	0
7	P	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Q	1	0	0	0	0
7	R	1	0	0	0	0
8	U	3	0	0	0	0
8	Z	3	0	0	0	0
All	All	64508	63663	63690	1831	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 1831 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:P:245:GLY:HA3	1:R:325:MET:HE3	1.42	0.99
1:C:245:GLY:HA3	1:E:325:MET:HE3	1.45	0.98
2:W:45:SER:HA	2:W:48:LYS:HE2	1.52	0.92
1:C:245:GLY:HA3	1:E:325:MET:CE	2.02	0.90
2:i:141:MET:HB3	2:j:141:MET:HE1	1.54	0.89

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36 71
1	D	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36 71
1	E	372/377 (99%)	351 (94%)	20 (5%)	1 (0%)	36 71
1	F	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36 71
1	G	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36 71
1	H	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36 71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	372/377 (99%)	351 (94%)	20 (5%)	1 (0%)	36	71
1	J	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	K	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	L	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	M	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	N	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	O	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	P	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	Q	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
1	R	372/377 (99%)	352 (95%)	19 (5%)	1 (0%)	36	71
2	W	51/285 (18%)	50 (98%)	0	1 (2%)	6	31
2	b	51/285 (18%)	51 (100%)	0	0	100	100
2	e	265/285 (93%)	265 (100%)	0	0	100	100
2	f	265/285 (93%)	265 (100%)	0	0	100	100
2	g	70/285 (25%)	69 (99%)	0	1 (1%)	9	39
2	h	70/285 (25%)	70 (100%)	0	0	100	100
2	i	238/285 (84%)	238 (100%)	0	0	100	100
2	j	238/285 (84%)	238 (100%)	0	0	100	100
3	X	61/288 (21%)	61 (100%)	0	0	100	100
3	Y	72/288 (25%)	70 (97%)	2 (3%)	0	100	100
3	c	61/288 (21%)	61 (100%)	0	0	100	100
3	d	72/288 (25%)	70 (97%)	2 (3%)	0	100	100
4	V	124/210 (59%)	117 (94%)	5 (4%)	2 (2%)	7	37
4	a	124/210 (59%)	117 (94%)	5 (4%)	2 (2%)	7	37
5	U	158/161 (98%)	140 (89%)	18 (11%)	0	100	100
5	Z	158/161 (98%)	140 (89%)	18 (11%)	0	100	100
All	All	8030/10206 (79%)	7652 (95%)	356 (4%)	22 (0%)	37	71

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	182	GLY
1	D	182	GLY

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Mol	Chain	Res	Type
1	E	182	GLY
1	F	182	GLY
1	G	182	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	317/319 (99%)	304 (96%)	13 (4%)	27	49
1	D	317/319 (99%)	307 (97%)	10 (3%)	34	55
1	E	317/319 (99%)	306 (96%)	11 (4%)	32	53
1	F	317/319 (99%)	305 (96%)	12 (4%)	29	51
1	G	317/319 (99%)	305 (96%)	12 (4%)	29	51
1	H	317/319 (99%)	307 (97%)	10 (3%)	34	55
1	I	317/319 (99%)	305 (96%)	12 (4%)	29	51
1	J	317/319 (99%)	305 (96%)	12 (4%)	29	51
1	K	317/319 (99%)	307 (97%)	10 (3%)	34	55
1	L	317/319 (99%)	306 (96%)	11 (4%)	32	53
1	M	317/319 (99%)	305 (96%)	12 (4%)	29	51
1	N	317/319 (99%)	306 (96%)	11 (4%)	32	53
1	O	317/319 (99%)	307 (97%)	10 (3%)	34	55
1	P	317/319 (99%)	306 (96%)	11 (4%)	32	53
1	Q	317/319 (99%)	307 (97%)	10 (3%)	34	55
1	R	317/319 (99%)	307 (97%)	10 (3%)	34	55
2	W	44/245 (18%)	40 (91%)	4 (9%)	9	28
2	b	44/245 (18%)	42 (96%)	2 (4%)	24	46
2	e	229/245 (94%)	224 (98%)	5 (2%)	45	64
2	f	229/245 (94%)	226 (99%)	3 (1%)	61	72
2	g	61/245 (25%)	57 (93%)	4 (7%)	15	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	h	61/245 (25%)	59 (97%)	2 (3%)	33	55
2	i	208/245 (85%)	203 (98%)	5 (2%)	43	63
2	j	208/245 (85%)	205 (99%)	3 (1%)	59	71
3	X	59/256 (23%)	56 (95%)	3 (5%)	21	43
3	Y	69/256 (27%)	62 (90%)	7 (10%)	7	23
3	c	59/256 (23%)	56 (95%)	3 (5%)	21	43
3	d	69/256 (27%)	63 (91%)	6 (9%)	9	29
4	V	106/176 (60%)	104 (98%)	2 (2%)	50	66
4	a	106/176 (60%)	104 (98%)	2 (2%)	50	66
5	U	141/142 (99%)	138 (98%)	3 (2%)	47	65
5	Z	141/142 (99%)	138 (98%)	3 (2%)	47	65
All	All	6906/8724 (79%)	6672 (97%)	234 (3%)	33	54

5 of 234 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	118	LYS
3	c	97	LYS
1	O	250	ILE
2	h	9	GLN
3	Y	227	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	Q	12	ASN
3	Y	257	GLN
1	Q	59	GLN
2	e	47	GLN
2	i	144	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

16 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	HIC	G	73	1	10,11,12	1.52	1 (10%)	9,14,16	1.21	1 (11%)
1	HIC	F	73	1	10,11,12	1.54	1 (10%)	9,14,16	1.24	1 (11%)
1	HIC	I	73	1	10,11,12	1.53	2 (20%)	9,14,16	1.22	1 (11%)
1	HIC	Q	73	1	10,11,12	1.53	1 (10%)	9,14,16	1.23	1 (11%)
1	HIC	R	73	1	10,11,12	1.53	1 (10%)	9,14,16	1.22	1 (11%)
1	HIC	E	73	1	10,11,12	1.51	1 (10%)	9,14,16	1.26	1 (11%)
1	HIC	L	73	1	10,11,12	1.52	1 (10%)	9,14,16	1.22	1 (11%)
1	HIC	C	73	1	10,11,12	1.54	1 (10%)	9,14,16	1.23	1 (11%)
1	HIC	N	73	1	10,11,12	1.51	1 (10%)	9,14,16	1.27	1 (11%)
1	HIC	P	73	1	10,11,12	1.53	1 (10%)	9,14,16	1.27	1 (11%)
1	HIC	D	73	1	10,11,12	1.52	1 (10%)	9,14,16	1.24	1 (11%)
1	HIC	H	73	1	10,11,12	1.52	1 (10%)	9,14,16	1.19	1 (11%)
1	HIC	J	73	1	10,11,12	1.52	1 (10%)	9,14,16	1.19	1 (11%)
1	HIC	M	73	1	10,11,12	1.53	1 (10%)	9,14,16	1.23	1 (11%)
1	HIC	O	73	1	10,11,12	1.51	1 (10%)	9,14,16	1.22	1 (11%)
1	HIC	K	73	1	10,11,12	1.51	1 (10%)	9,14,16	1.20	1 (11%)

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
1	HIC	G	73	1	-	2/5/6/8	0/1/1/1
1	HIC	F	73	1	-	2/5/6/8	0/1/1/1
1	HIC	I	73	1	-	2/5/6/8	0/1/1/1
1	HIC	Q	73	1	-	2/5/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HIC	R	73	1	-	2/5/6/8	0/1/1/1
1	HIC	E	73	1	-	2/5/6/8	0/1/1/1
1	HIC	L	73	1	-	2/5/6/8	0/1/1/1
1	HIC	C	73	1	-	2/5/6/8	0/1/1/1
1	HIC	N	73	1	-	2/5/6/8	0/1/1/1
1	HIC	P	73	1	-	2/5/6/8	0/1/1/1
1	HIC	D	73	1	-	2/5/6/8	0/1/1/1
1	HIC	H	73	1	-	2/5/6/8	0/1/1/1
1	HIC	J	73	1	-	2/5/6/8	0/1/1/1
1	HIC	M	73	1	-	2/5/6/8	0/1/1/1
1	HIC	O	73	1	-	2/5/6/8	0/1/1/1
1	HIC	K	73	1	-	2/5/6/8	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	73	HIC	CD2-CG	3.13	1.41	1.36
1	M	73	HIC	CD2-CG	3.13	1.41	1.36
1	C	73	HIC	CD2-CG	3.12	1.41	1.36
1	F	73	HIC	CD2-CG	3.11	1.41	1.36
1	Q	73	HIC	CD2-CG	3.11	1.41	1.36

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	73	HIC	NE2-CE1-ND1	-3.13	111.46	112.66
1	P	73	HIC	NE2-CE1-ND1	-3.12	111.47	112.66
1	E	73	HIC	NE2-CE1-ND1	-3.08	111.49	112.66
1	D	73	HIC	NE2-CE1-ND1	-3.03	111.50	112.66
1	F	73	HIC	NE2-CE1-ND1	-3.00	111.52	112.66

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	73	HIC	CA-CB-CG-CD2
1	D	73	HIC	CA-CB-CG-CD2
1	E	73	HIC	CA-CB-CG-CD2
1	F	73	HIC	CA-CB-CG-CD2

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Mol	Chain	Res	Type	Atoms
1	G	73	HIC	CA-CB-CG-CD2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 38 ligands modelled in this entry, 22 are monoatomic - leaving 16 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
6	ADP	R	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.82	8 (18%)
6	ADP	J	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.82	8 (18%)
6	ADP	I	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	M	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	O	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	Q	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.82	8 (18%)
6	ADP	F	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	G	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	L	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	D	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	E	401	7	28,29,29	1.41	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	C	401	7	28,29,29	1.41	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	H	401	7	28,29,29	1.41	4 (14%)	43,45,45	1.81	8 (18%)
6	ADP	K	401	7	28,29,29	1.42	4 (14%)	43,45,45	1.82	9 (20%)
6	ADP	N	401	7	28,29,29	1.41	4 (14%)	43,45,45	1.81	8 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	ADP	P	401	7	28,29,29	1.43	4 (14%)	43,45,45	1.82	8 (18%)

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
6	ADP	R	401	7	-	0/16/32/32	0/3/3/3
6	ADP	J	401	7	-	0/16/32/32	0/3/3/3
6	ADP	I	401	7	-	0/16/32/32	0/3/3/3
6	ADP	M	401	7	-	0/16/32/32	0/3/3/3
6	ADP	O	401	7	-	0/16/32/32	0/3/3/3
6	ADP	Q	401	7	-	0/16/32/32	0/3/3/3
6	ADP	F	401	7	-	0/16/32/32	0/3/3/3
6	ADP	G	401	7	-	0/16/32/32	0/3/3/3
6	ADP	L	401	7	-	0/16/32/32	0/3/3/3
6	ADP	D	401	7	-	0/16/32/32	0/3/3/3
6	ADP	E	401	7	-	0/16/32/32	0/3/3/3
6	ADP	C	401	7	-	0/16/32/32	0/3/3/3
6	ADP	H	401	7	-	0/16/32/32	0/3/3/3
6	ADP	K	401	7	-	0/16/32/32	0/3/3/3
6	ADP	N	401	7	-	0/16/32/32	0/3/3/3
6	ADP	P	401	7	-	0/16/32/32	0/3/3/3

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	401	ADP	C5-C4	4.78	1.47	1.39
6	O	401	ADP	C5-C4	4.77	1.47	1.39
6	K	401	ADP	C5-C4	4.77	1.47	1.39
6	P	401	ADP	C5-C4	4.76	1.47	1.39
6	D	401	ADP	C5-C4	4.76	1.47	1.39

The worst 5 of 129 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Q	401	ADP	C5-C4-N3	-5.85	118.66	126.72
6	P	401	ADP	C5-C4-N3	-5.84	118.68	126.72
6	E	401	ADP	C5-C4-N3	-5.84	118.68	126.72
6	N	401	ADP	C5-C4-N3	-5.84	118.68	126.72
6	J	401	ADP	C5-C4-N3	-5.83	118.68	126.72

There are no chirality outliers.

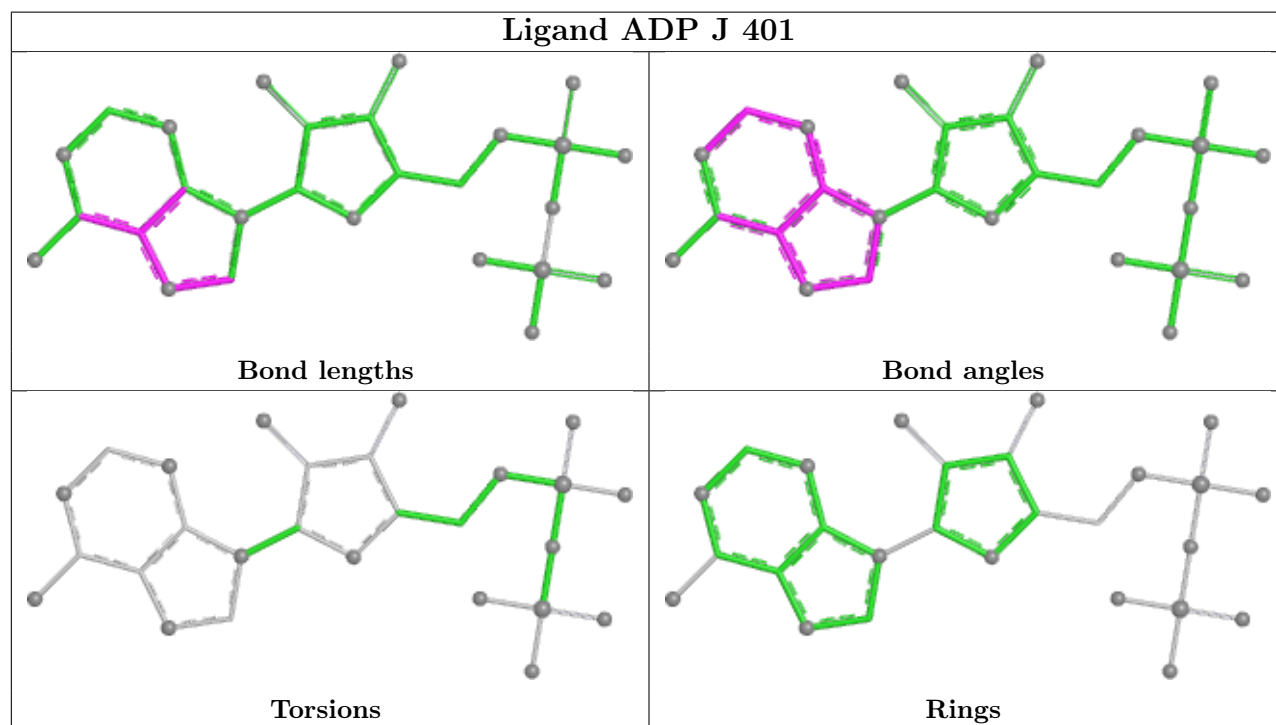
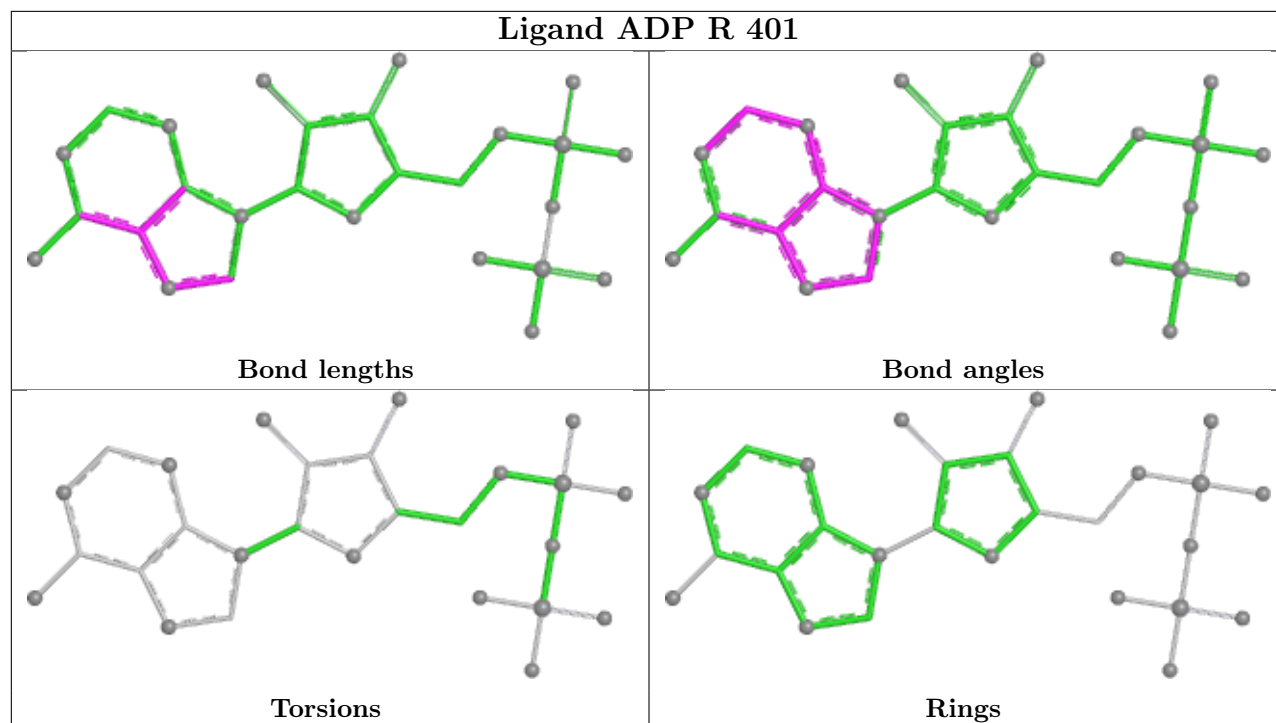
There are no torsion outliers.

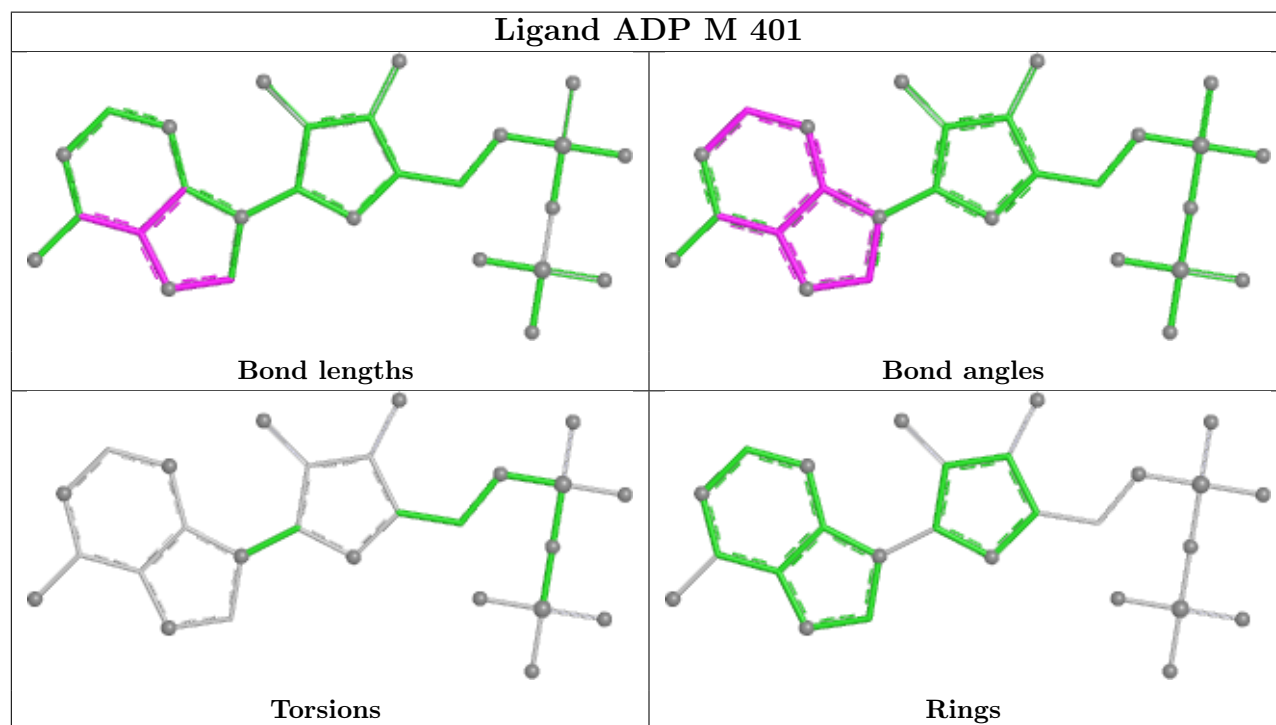
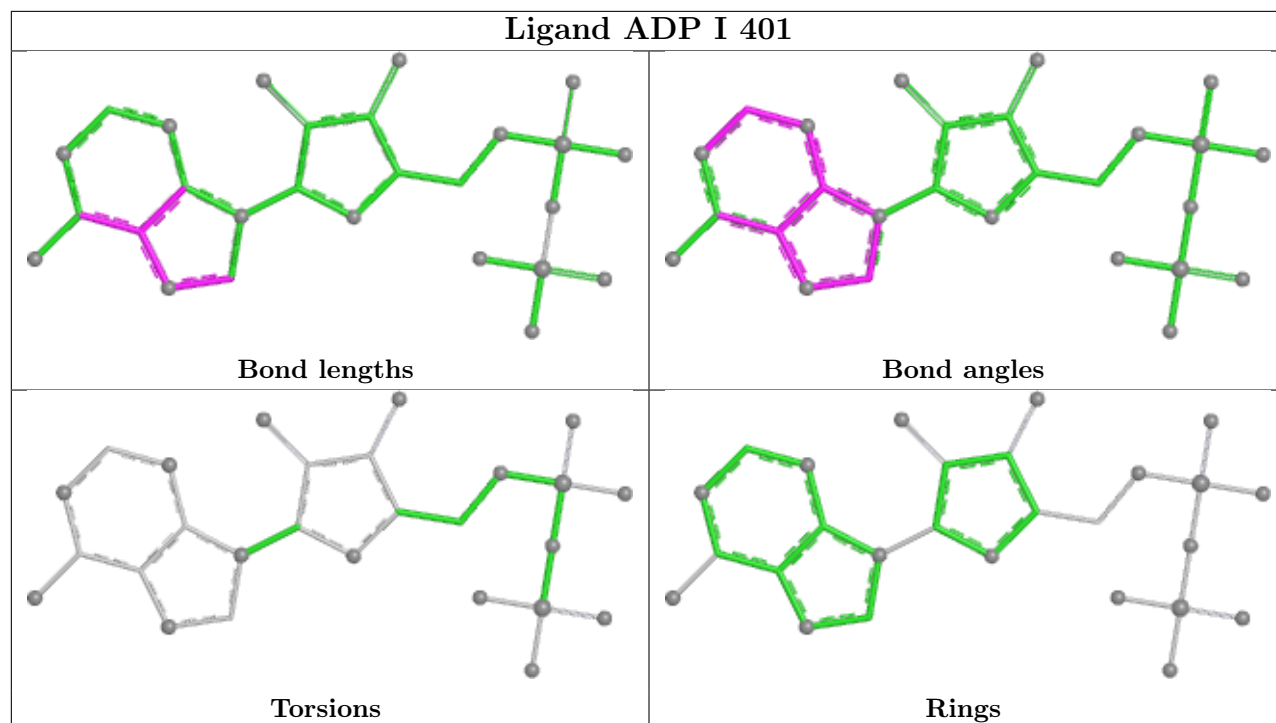
There are no ring outliers.

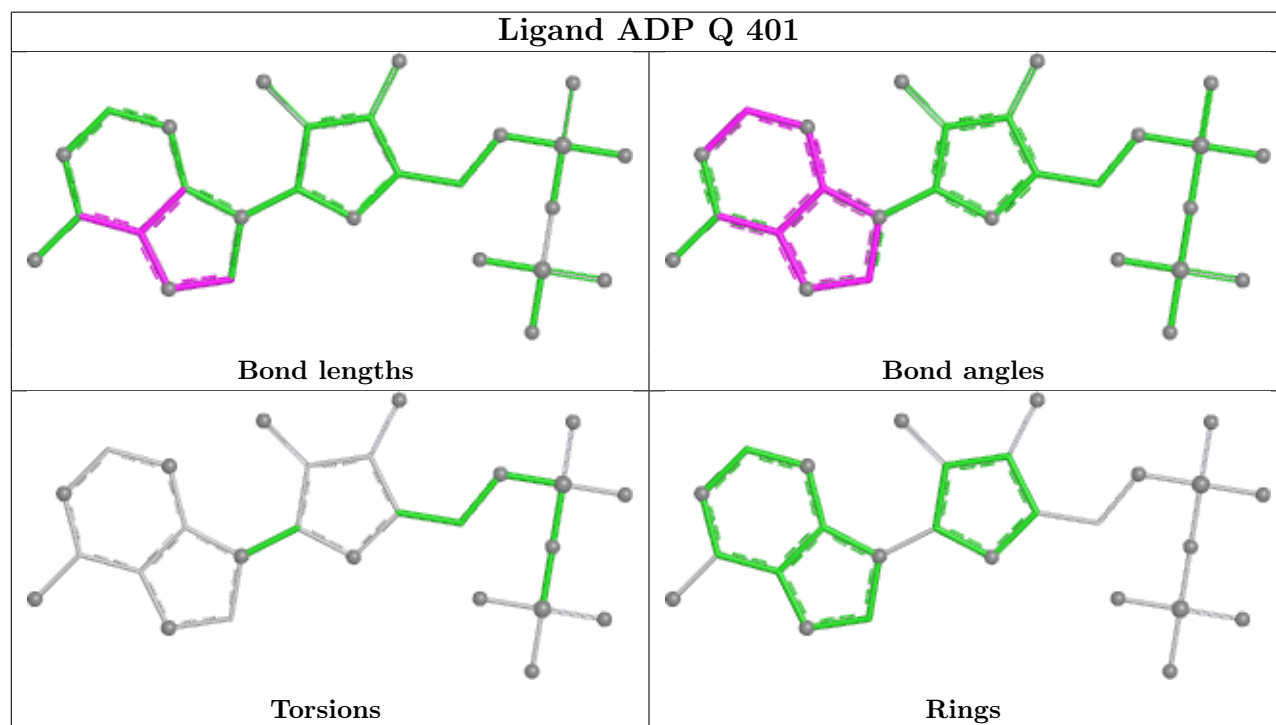
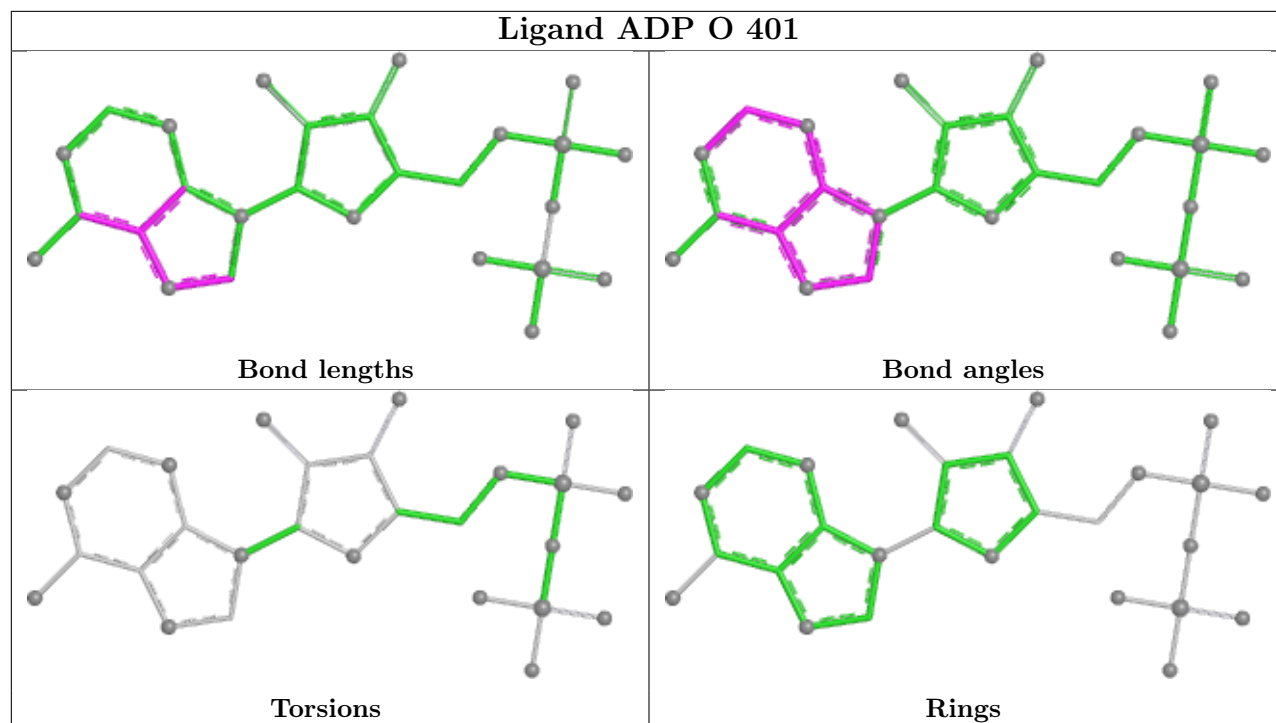
16 monomers are involved in 16 short contacts:

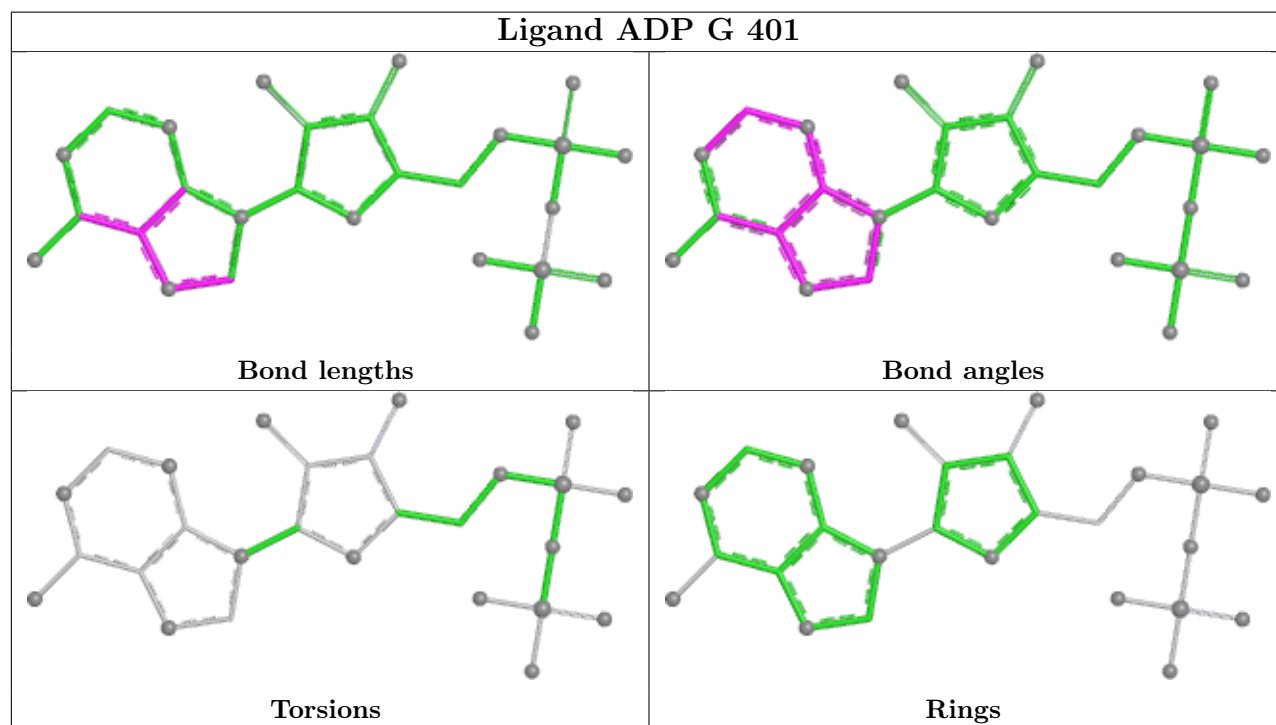
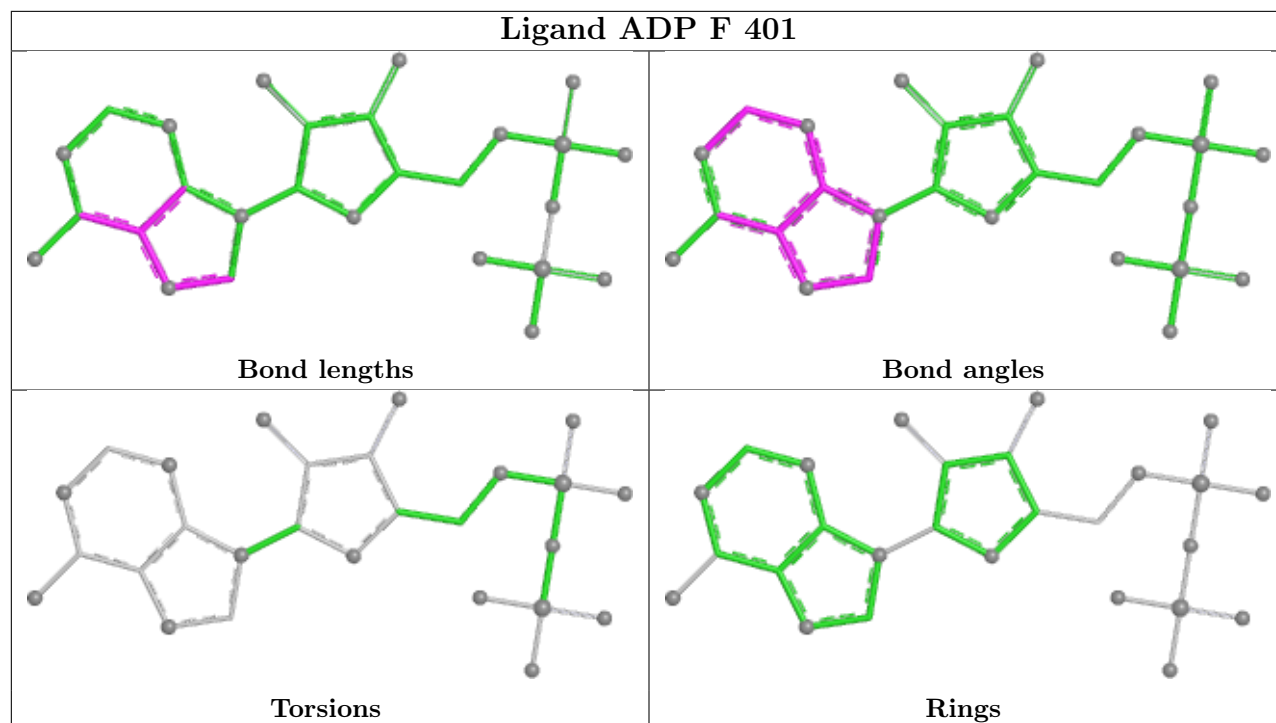
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	R	401	ADP	1	0
6	J	401	ADP	1	0
6	I	401	ADP	1	0
6	M	401	ADP	1	0
6	O	401	ADP	1	0
6	Q	401	ADP	1	0
6	F	401	ADP	1	0
6	G	401	ADP	1	0
6	L	401	ADP	1	0
6	D	401	ADP	1	0
6	E	401	ADP	1	0
6	C	401	ADP	1	0
6	H	401	ADP	1	0
6	K	401	ADP	1	0
6	N	401	ADP	1	0
6	P	401	ADP	1	0

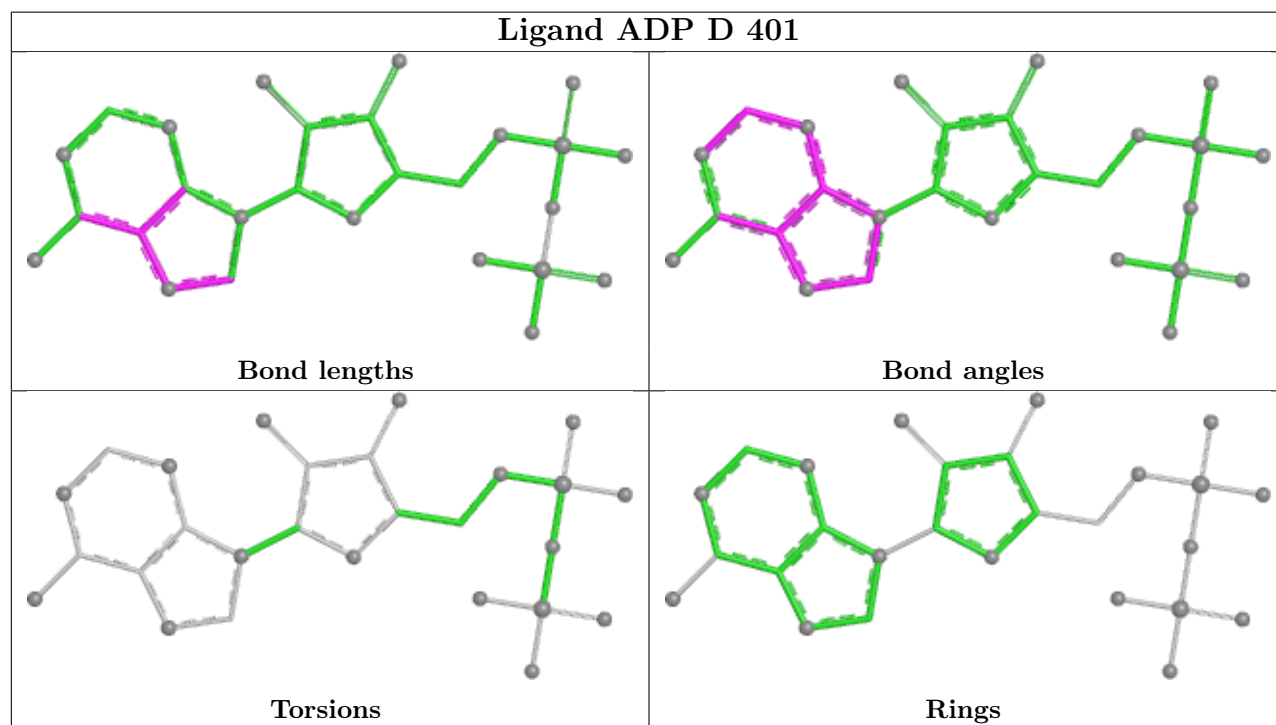
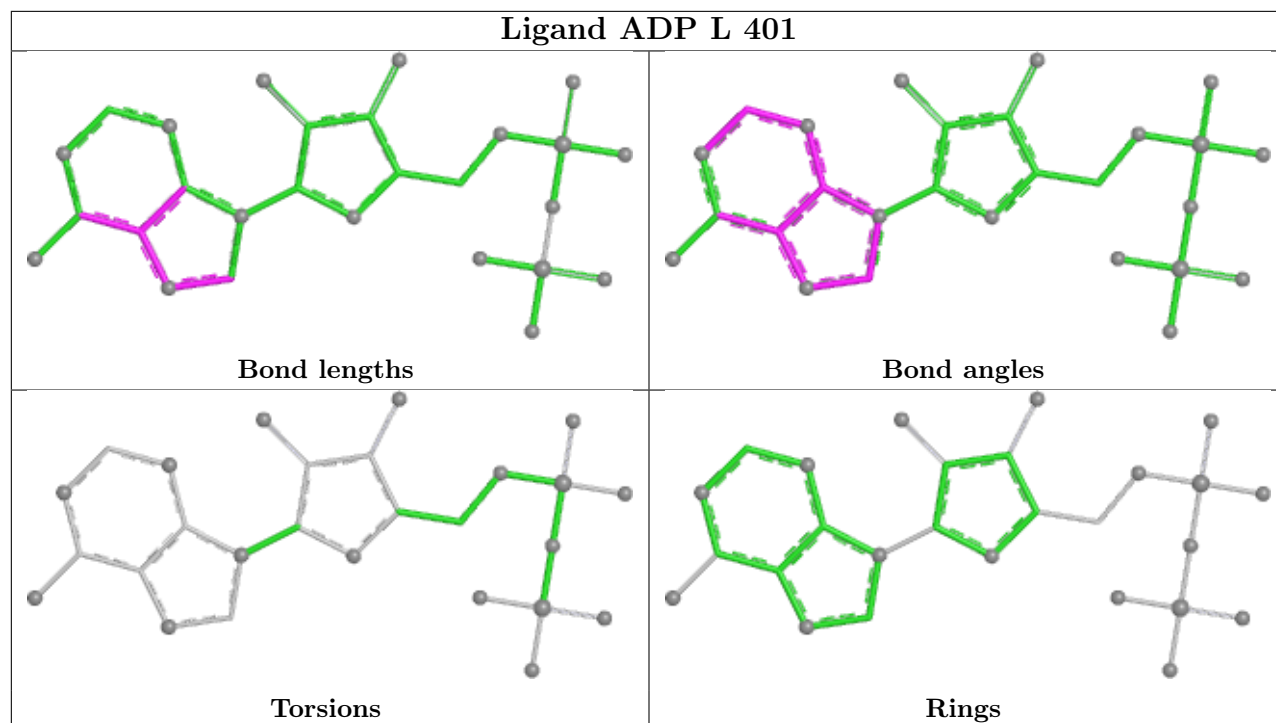
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

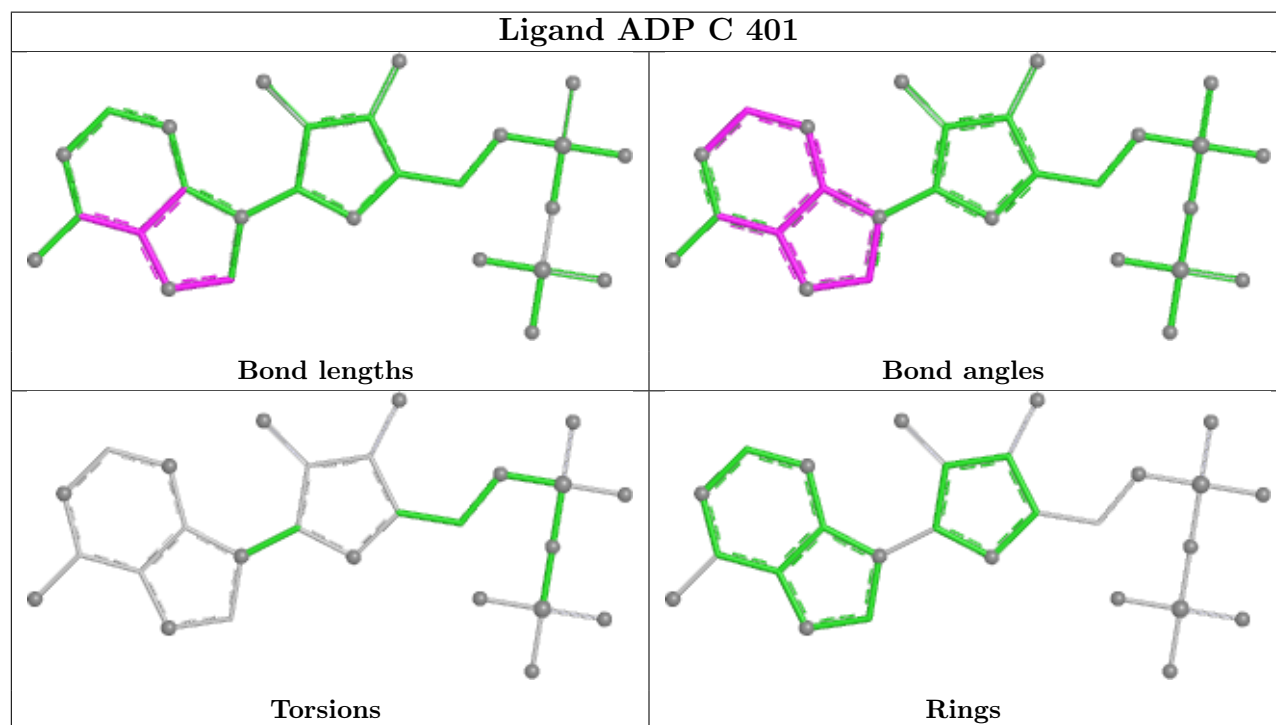
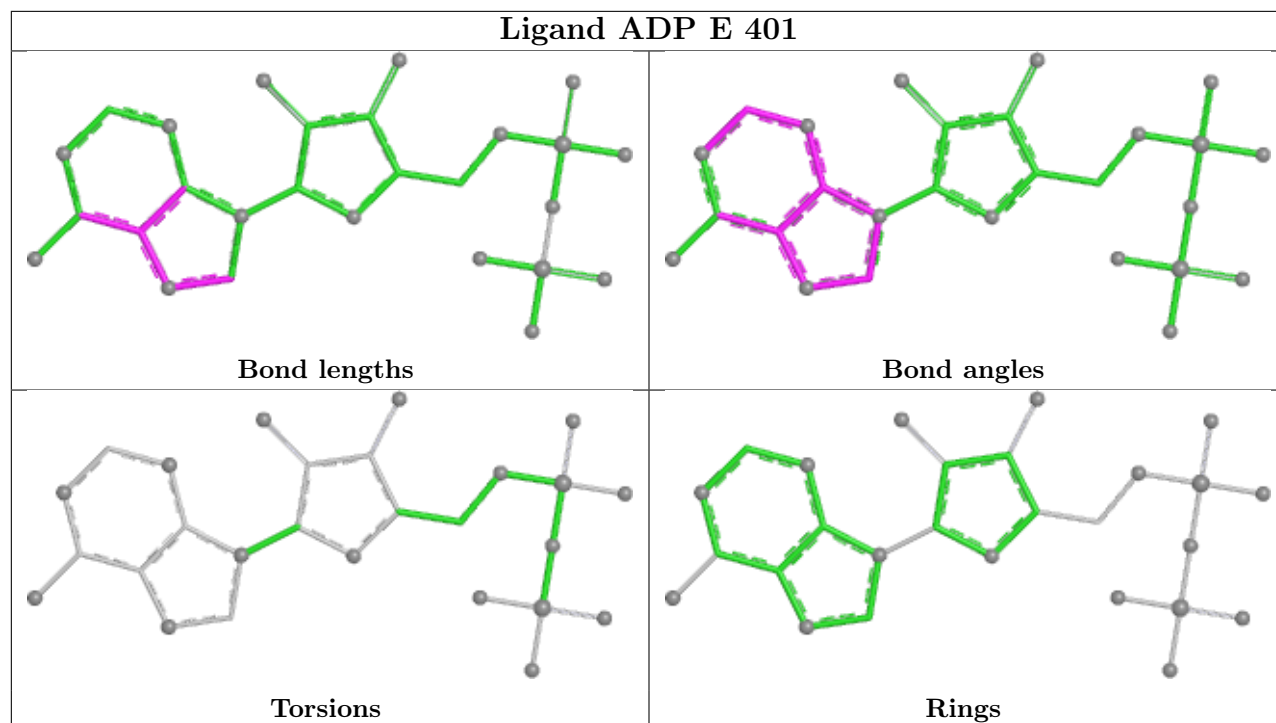


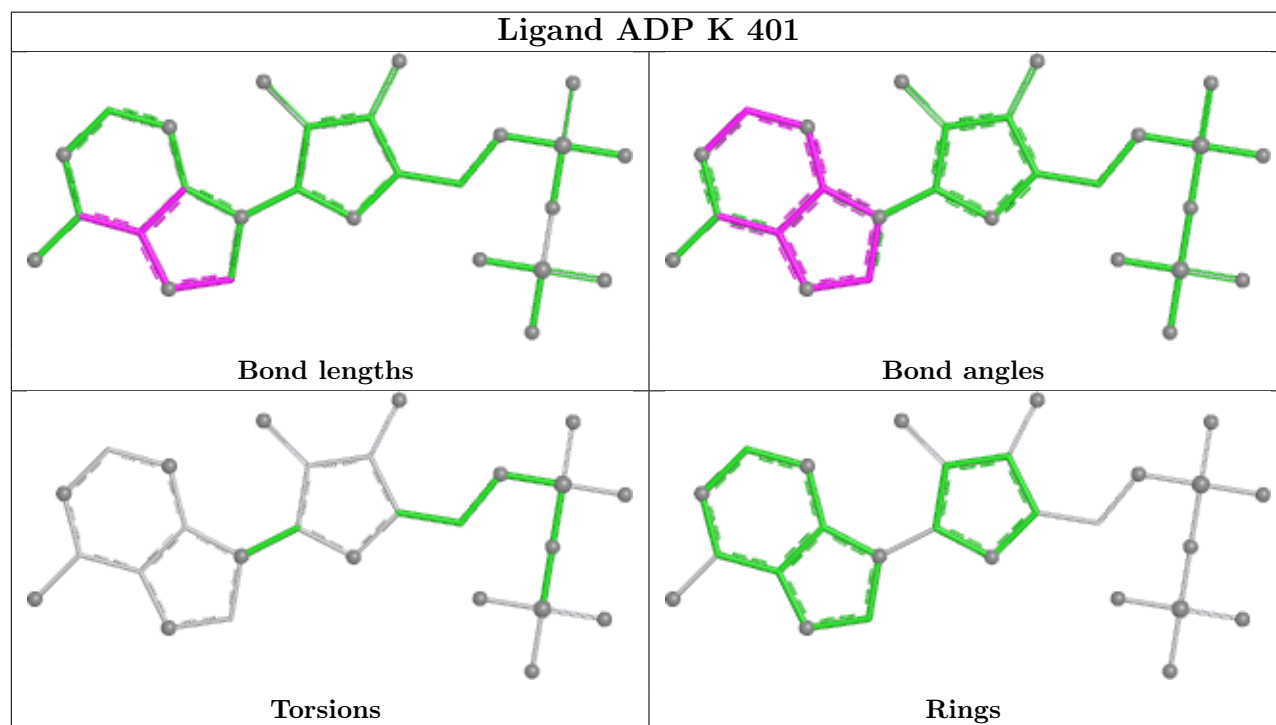
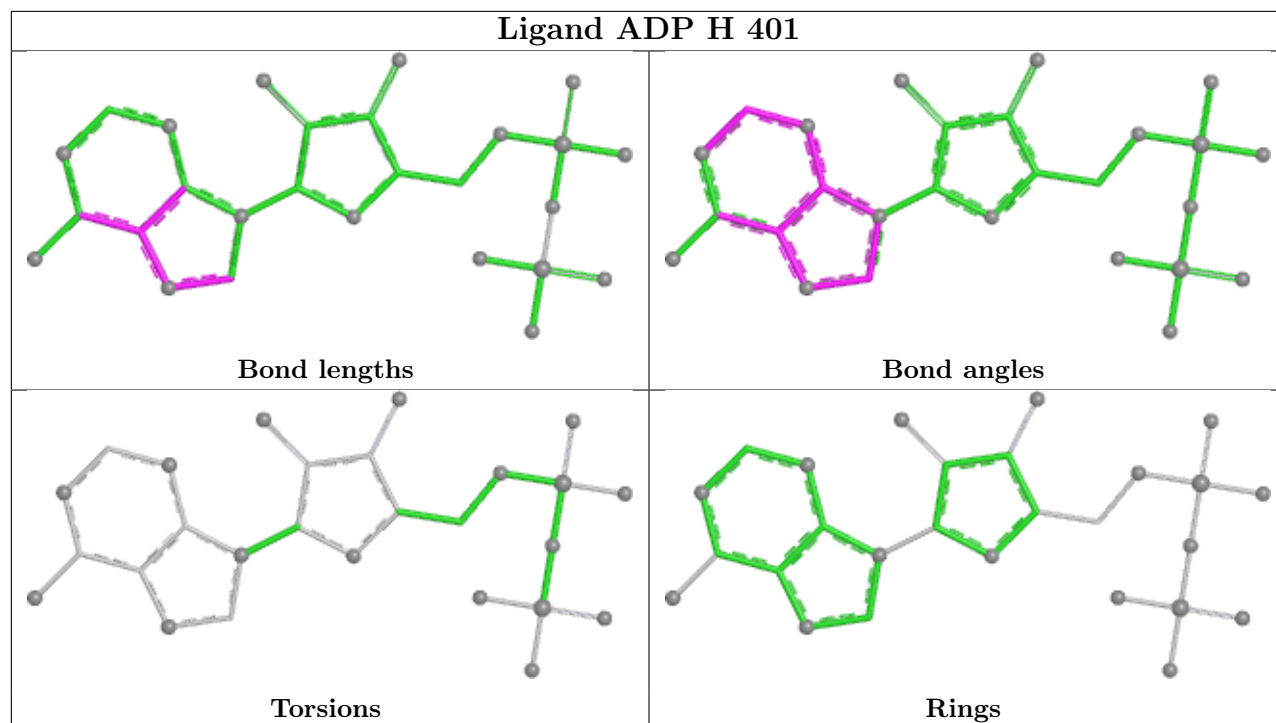


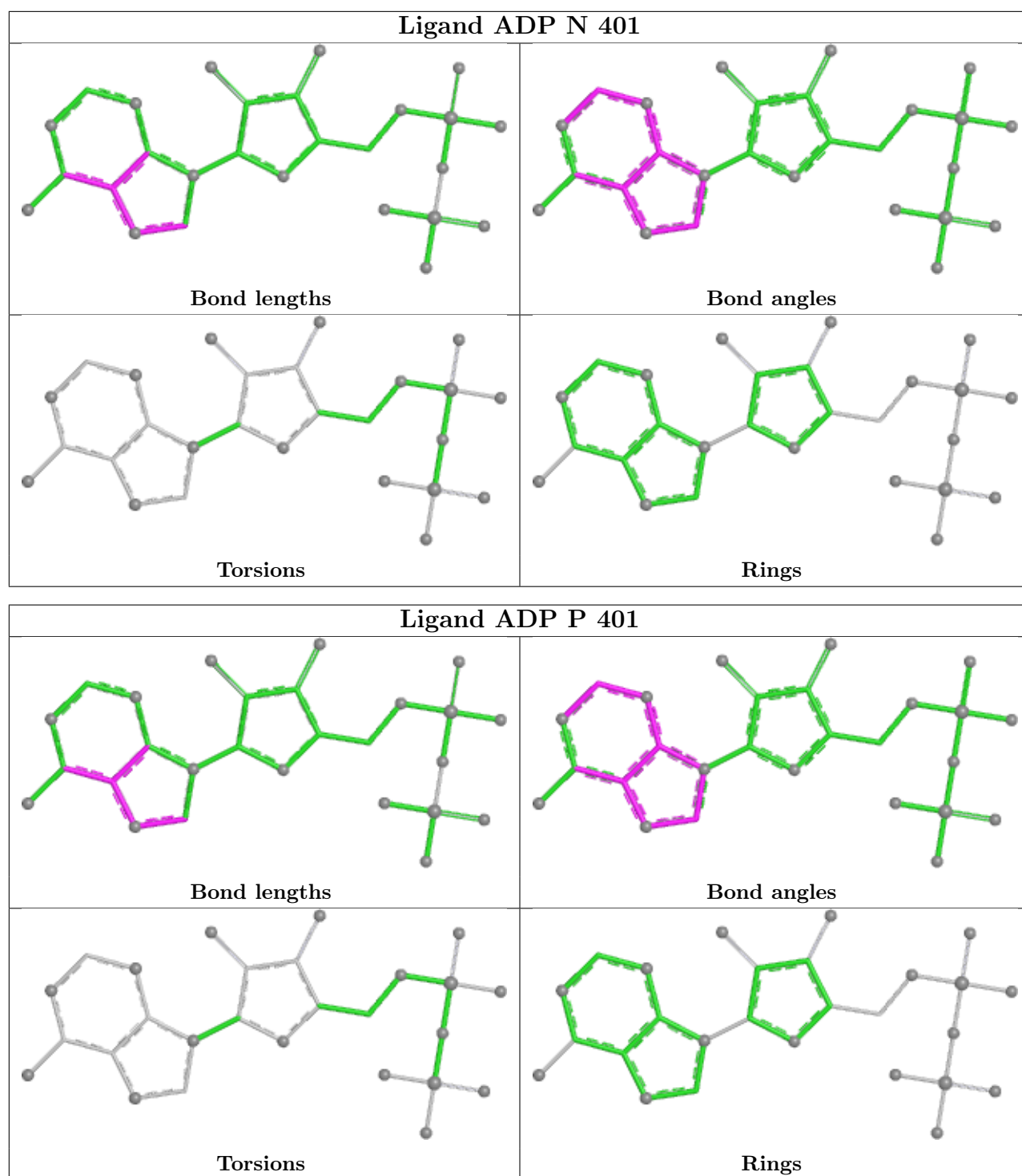












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

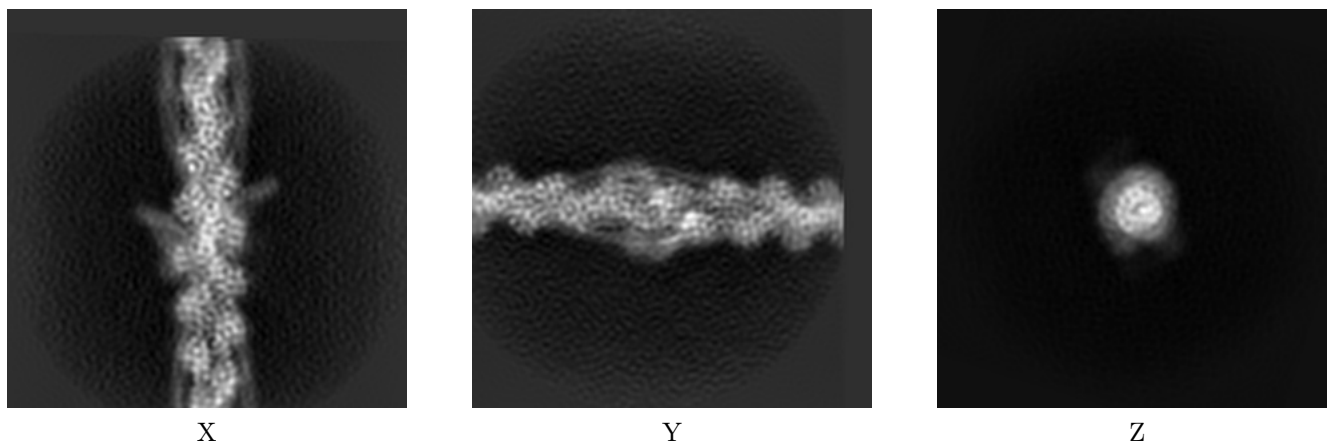
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0729. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

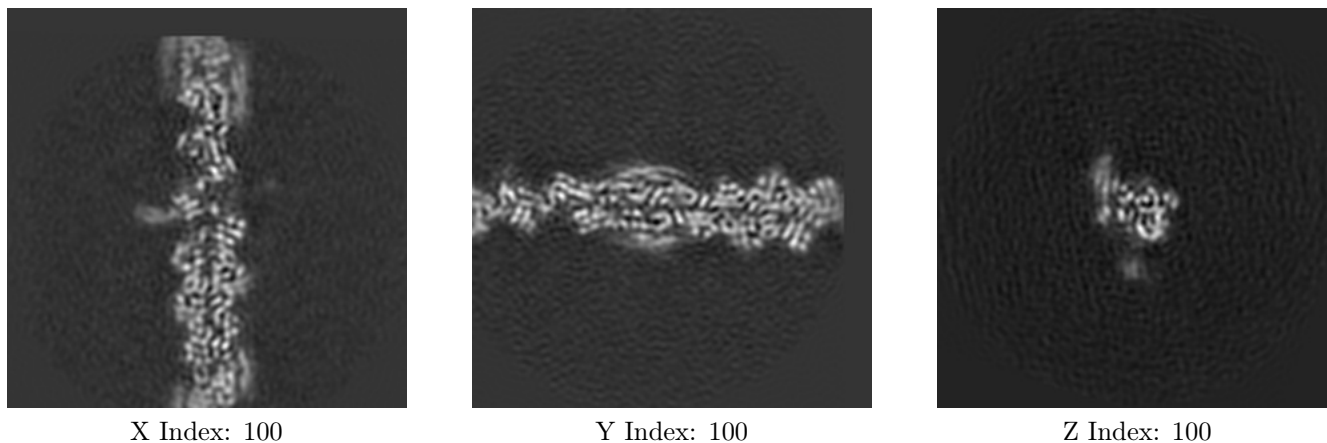
6.1.1 Primary map



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

6.2 Central slices [i](#)

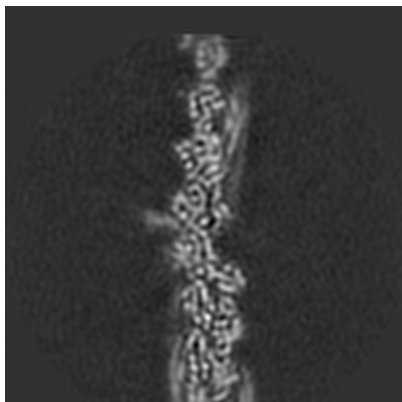
6.2.1 Primary map



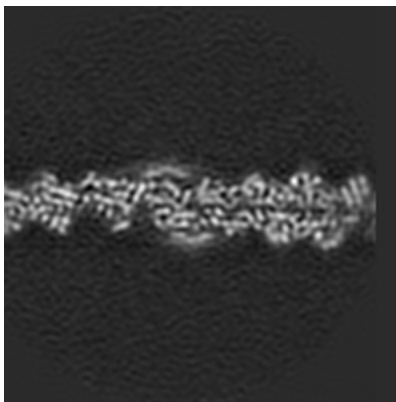
The images above show central slices of the map in three orthogonal directions.

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

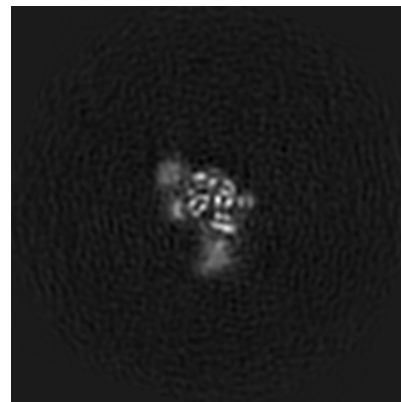
6.3.1 Primary map



X Index: 106



Y Index: 98

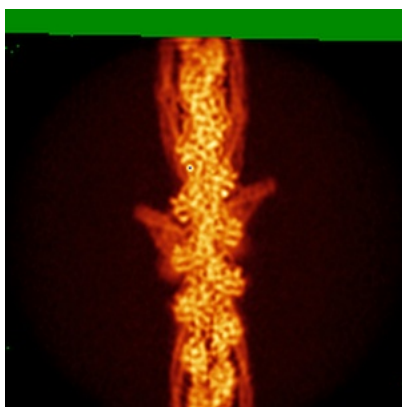


Z Index: 94

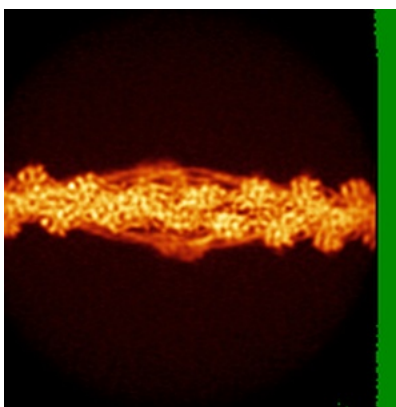
The images above show the largest variance slices of the map in three orthogonal directions.

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

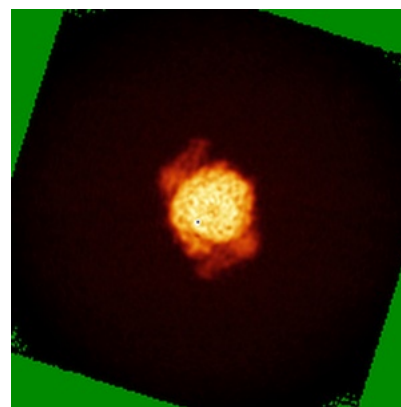
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0456. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

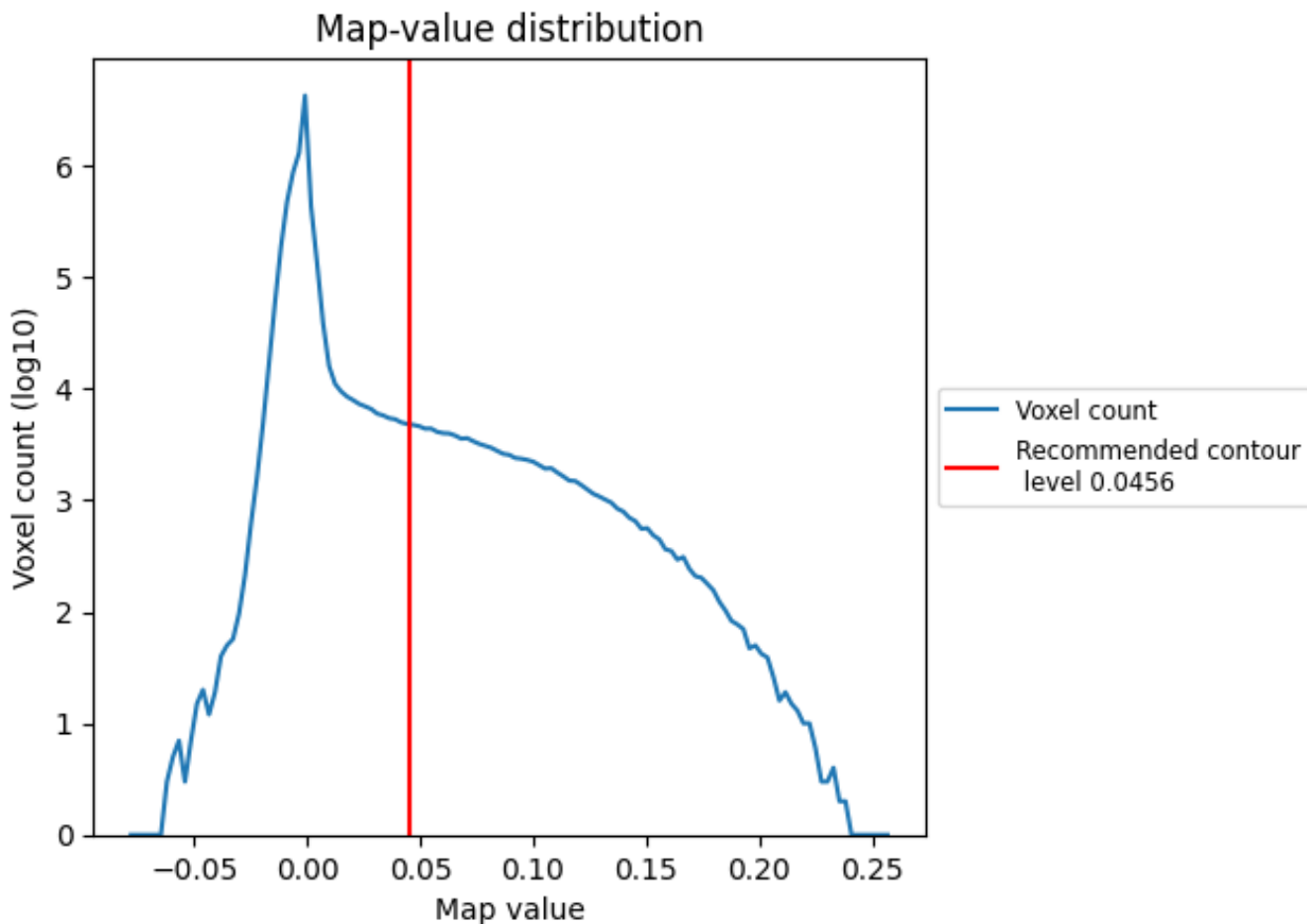
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

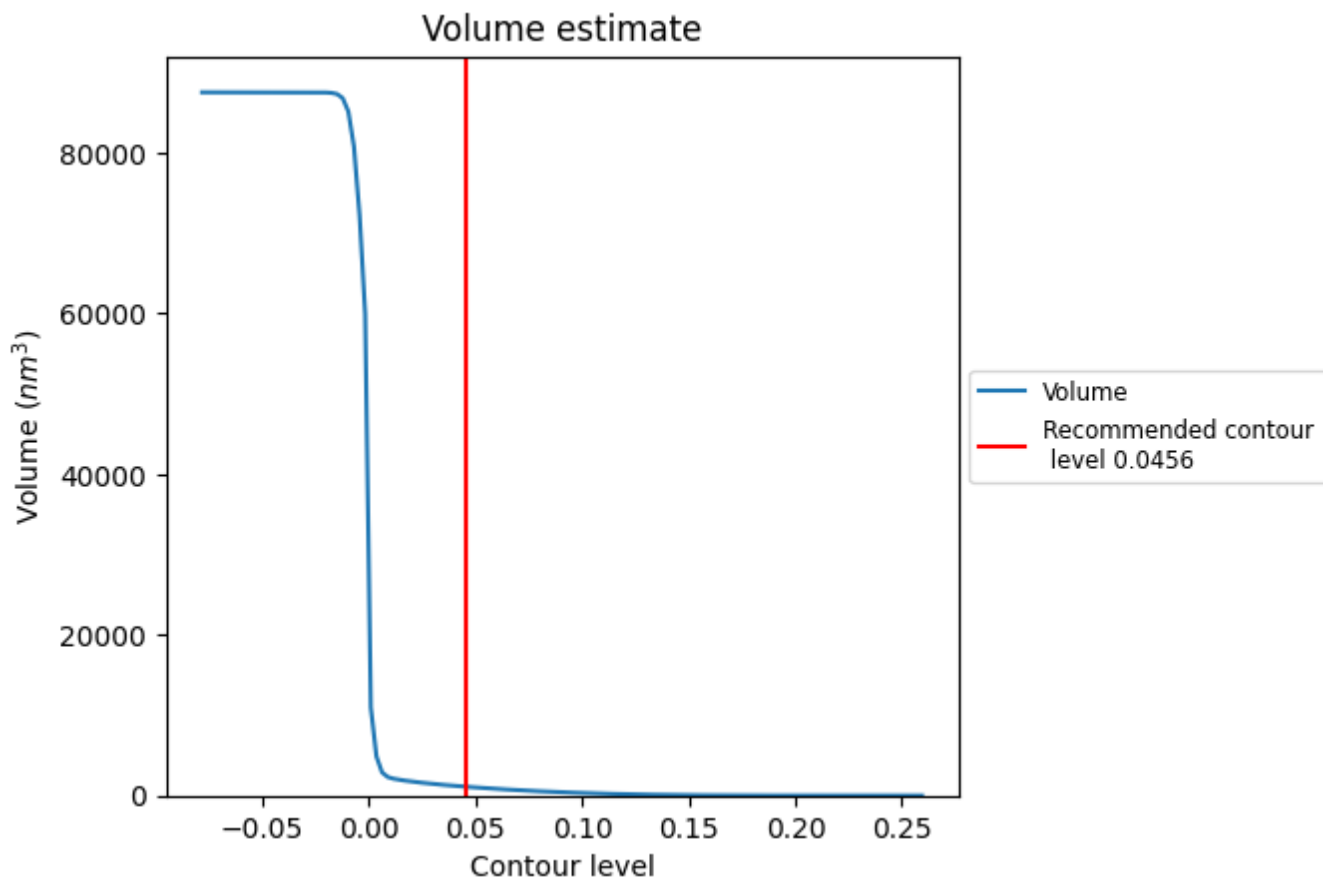
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

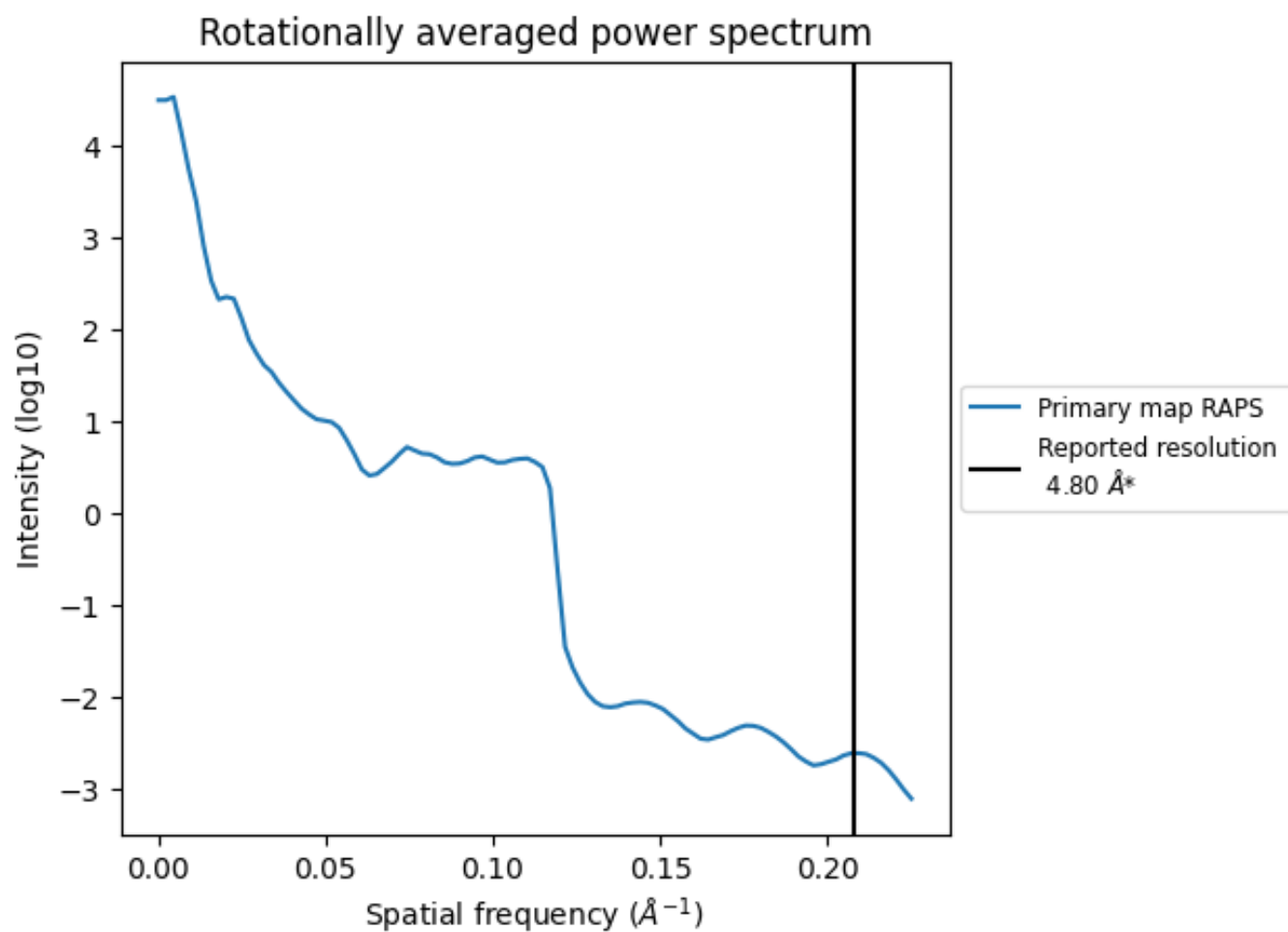
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1101 nm^3 ; this corresponds to an approximate mass of 995 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

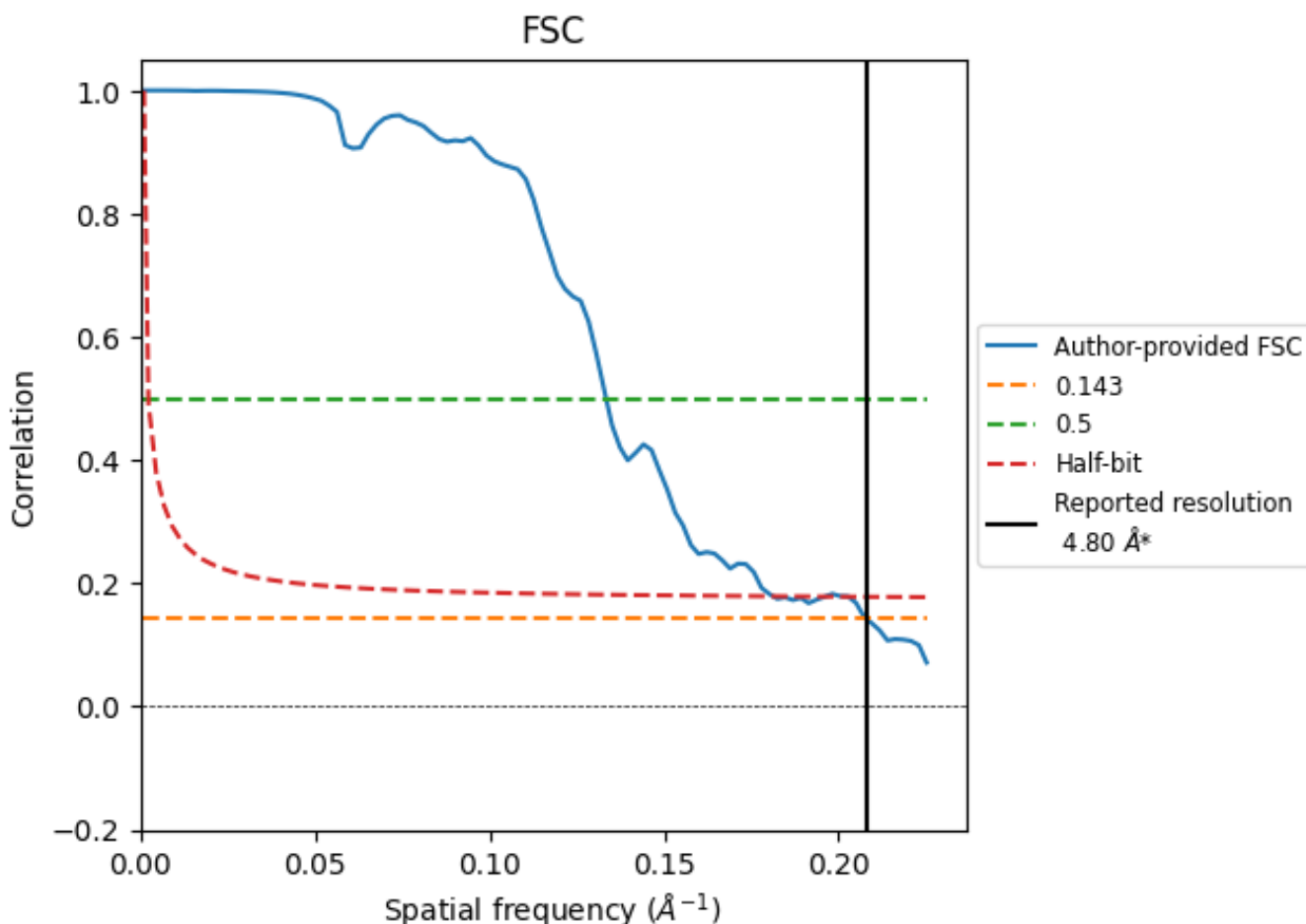


*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

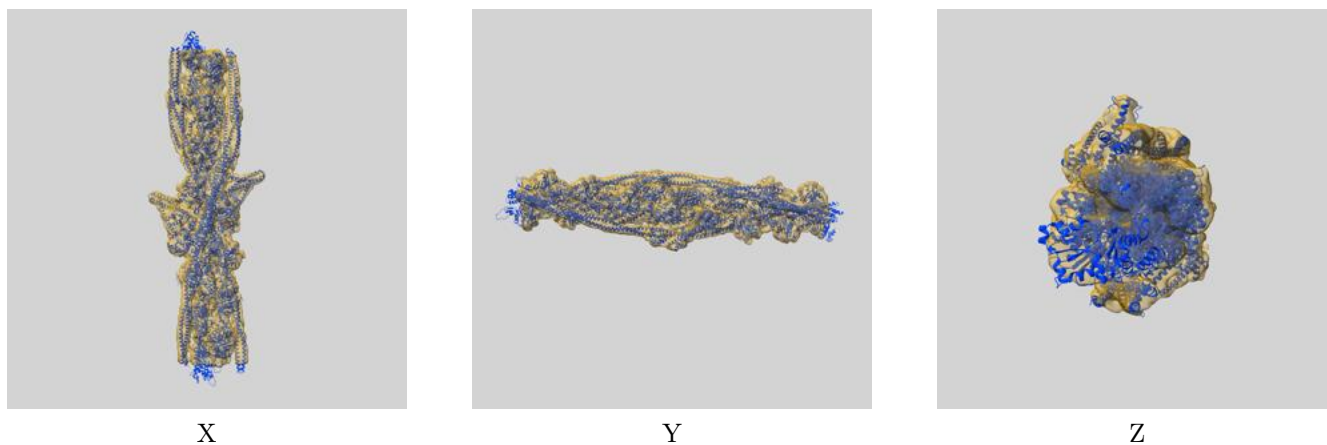
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	4.81	7.50	5.52
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

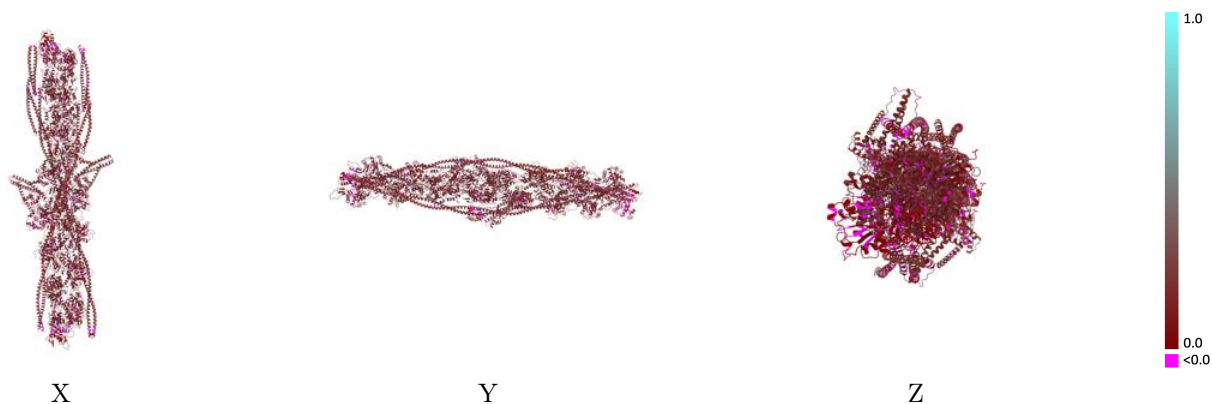
This section contains information regarding the fit between EMDB map EMD-0729 and PDB model 7UTI. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



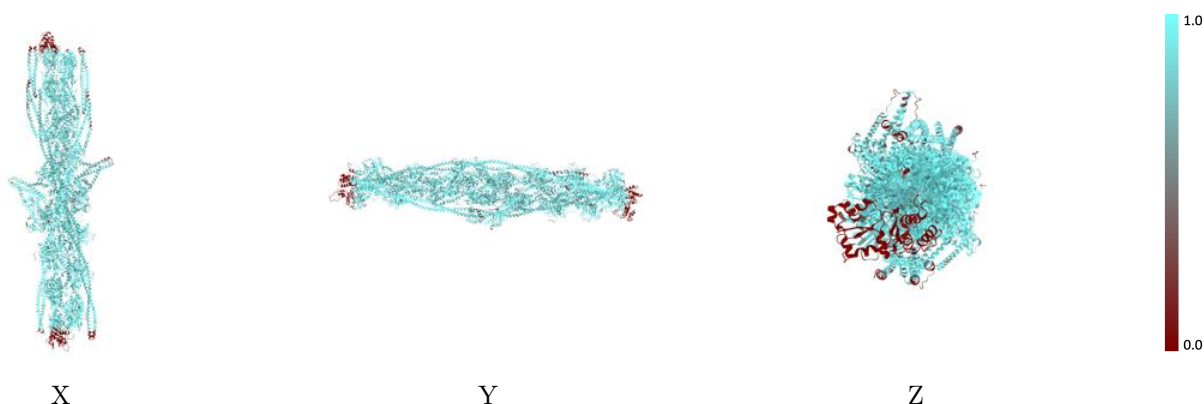
The images above show the 3D surface view of the map at the recommended contour level 0.0456 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



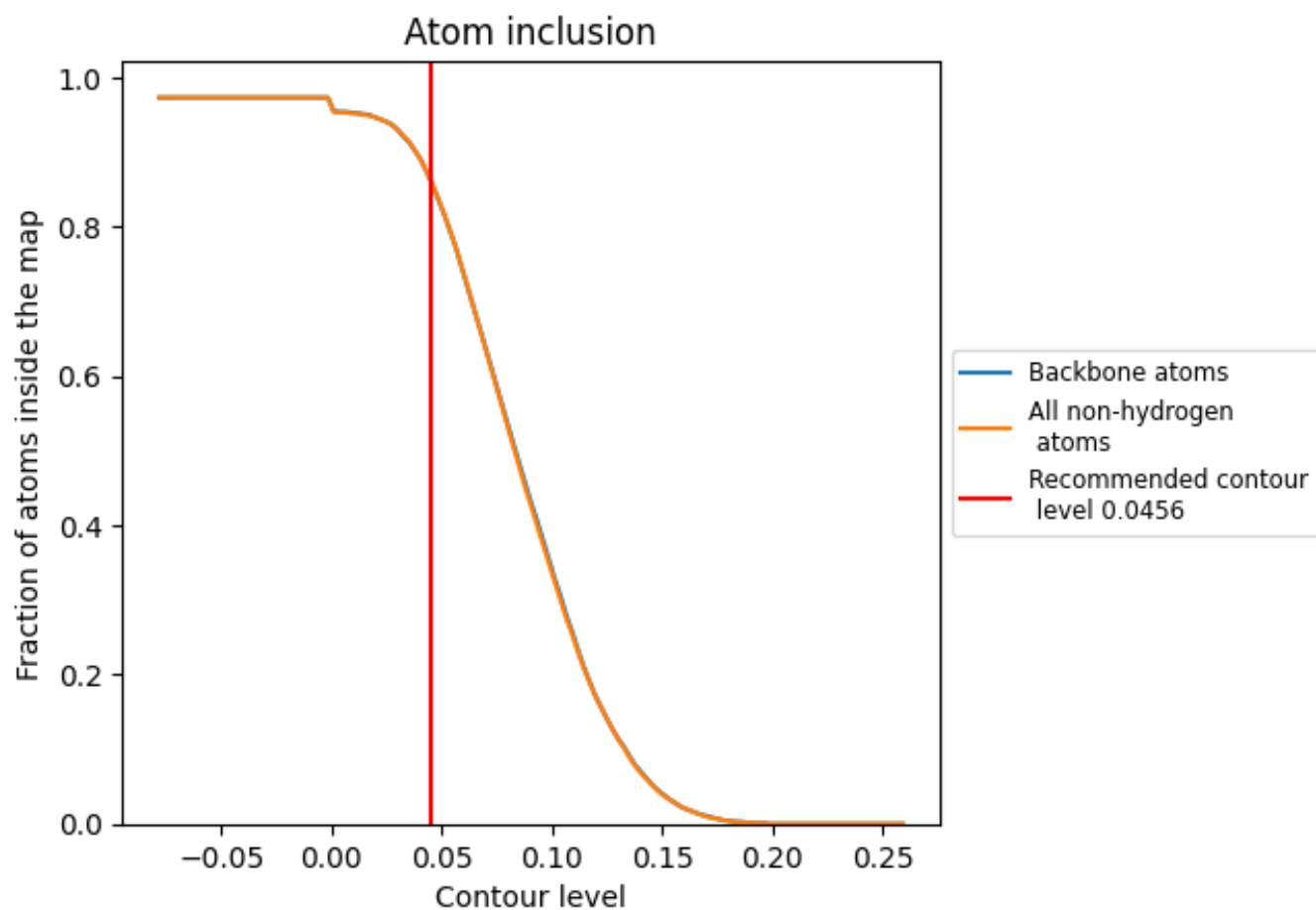
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0456).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.0456) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8600	 0.1400
C	 0.4500	 0.0520
D	 0.9510	 0.1420
E	 0.9470	 0.1470
F	 0.9410	 0.1480
G	 0.9270	 0.1490
H	 0.9240	 0.1460
I	 0.9340	 0.1540
J	 0.9190	 0.1490
K	 0.9180	 0.1490
L	 0.9200	 0.1460
M	 0.9320	 0.1450
N	 0.9340	 0.1470
O	 0.9240	 0.1480
P	 0.9370	 0.1500
Q	 0.9180	 0.1450
R	 0.4710	 0.0600
U	 0.8550	 0.1290
V	 0.8450	 0.1420
W	 0.8660	 0.1570
X	 0.6680	 0.1270
Y	 0.8950	 0.1790
Z	 0.7540	 0.1070
a	 0.7750	 0.1380
b	 0.7010	 0.1390
c	 0.6680	 0.1370
d	 0.8200	 0.1660
e	 0.8720	 0.1660
f	 0.8830	 0.1610
g	 0.8430	 0.1470
h	 0.8050	 0.1220
i	 0.8730	 0.1590
j	 0.8940	 0.1630

