



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 02:23 AM UTC

PDB ID : 9LEG / pdb_00009leg
EMDB ID : EMD-63025
Title : AMO complex
Authors : Li, Z.Q.; Yang, X.Y.
Deposited on : 2025-01-07
Resolution : 2.36 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

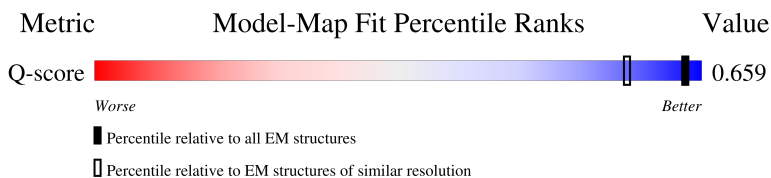
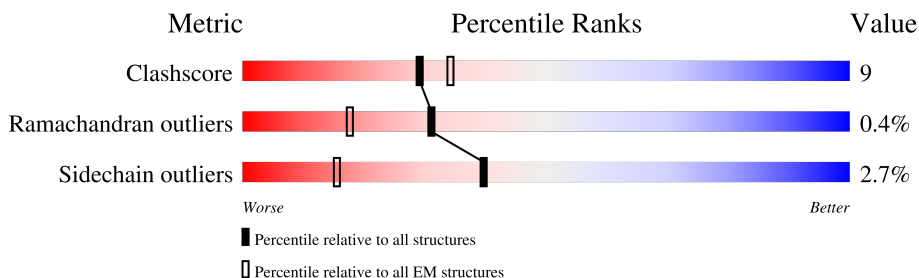
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.36 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.



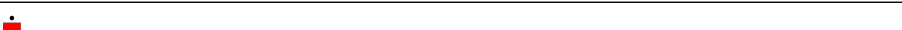
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4686 (1.86 - 2.86)

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	274	 85% 15%
1	L	274	 86% 14%
1	U	274	 84% 15%
2	B	420	 76% 14% • 9%

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Mol	Chain	Length	Quality of chain
2	M	420	
2	V	420	
3	C	271	
3	N	271	
3	W	271	
4	D	67	
4	O	67	
4	X	67	
5	E	45	
5	P	45	
5	Y	45	

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
7	DKA	A	310	-	-	X	-
7	DKA	A	311	-	-	X	-
7	DKA	L	310	-	-	X	-
7	DKA	L	311	-	-	X	-
7	DKA	U	302	-	-	X	-
7	DKA	U	303	-	-	X	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 28749 atoms, of which 2730 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 Ammonia monooxygenase subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	274	Total	C	N	O	S	0	0
			2248	1515	354	363	16		
1	L	274	Total	C	N	O	S	0	0
			2248	1515	354	363	16		
1	U	274	Total	C	N	O	S	0	0
			2248	1515	354	363	16		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	ILE	VAL	conflict	UNP A0A1H3PUN8
A	34	VAL	ILE	conflict	UNP A0A1H3PUN8
A	192	ILE	VAL	conflict	UNP A0A1H3PUN8
A	270	ALA	PRO	conflict	UNP A0A1H3PUN8
L	33	ILE	VAL	conflict	UNP A0A1H3PUN8
L	34	VAL	ILE	conflict	UNP A0A1H3PUN8
L	192	ILE	VAL	conflict	UNP A0A1H3PUN8
L	270	ALA	PRO	conflict	UNP A0A1H3PUN8
U	33	ILE	VAL	conflict	UNP A0A1H3PUN8
U	34	VAL	ILE	conflict	UNP A0A1H3PUN8
U	192	ILE	VAL	conflict	UNP A0A1H3PUN8
U	270	ALA	PRO	conflict	UNP A0A1H3PUN8

- Molecule 2 is a protein called Ammonia monooxygenase subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	383	Total	C	N	O	S	0	0
			3042	1961	529	540	12		
2	M	383	Total	C	N	O	S	0	0
			3042	1961	529	540	12		
2	V	383	Total	C	N	O	S	0	0
			3042	1961	529	540	12		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	73	THR	SER	conflict	UNP A0A1H3PUR7
B	88	ARG	LYS	conflict	UNP A0A1H3PUR7
B	233	LEU	ARG	conflict	UNP A0A1H3PUR7
B	366	VAL	ILE	conflict	UNP A0A1H3PUR7
M	73	THR	SER	conflict	UNP A0A1H3PUR7
M	88	ARG	LYS	conflict	UNP A0A1H3PUR7
M	233	LEU	ARG	conflict	UNP A0A1H3PUR7
M	366	VAL	ILE	conflict	UNP A0A1H3PUR7
V	73	THR	SER	conflict	UNP A0A1H3PUR7
V	88	ARG	LYS	conflict	UNP A0A1H3PUR7
V	233	LEU	ARG	conflict	UNP A0A1H3PUR7
V	366	VAL	ILE	conflict	UNP A0A1H3PUR7

- Molecule 3 is a protein called Ammonia monooxygenase subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	258	Total	C	N	O	S	0	0
			2160	1445	343	357	15		
3	N	258	Total	C	N	O	S	0	0
			2160	1445	343	357	15		
3	W	258	Total	C	N	O	S	0	0
			2160	1445	343	357	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	84	ILE	VAL	conflict	UNP A0A1H3PUB4
N	84	ILE	VAL	conflict	UNP A0A1H3PUB4
W	84	ILE	VAL	conflict	UNP A0A1H3PUB4

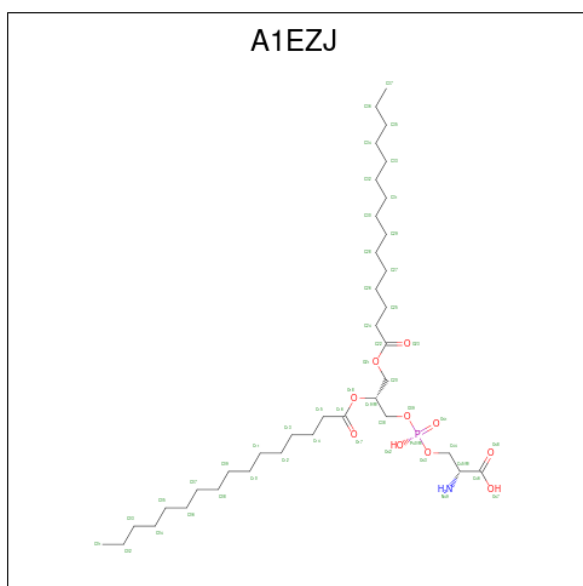
- Molecule 4 is a protein called Lipoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	19	Total	C	N	O	0	0
			151	95	25	31		
4	O	19	Total	C	N	O	0	0
			151	95	25	31		
4	X	19	Total	C	N	O	0	0
			151	95	25	31		

- Molecule 5 is a protein called AmoD.

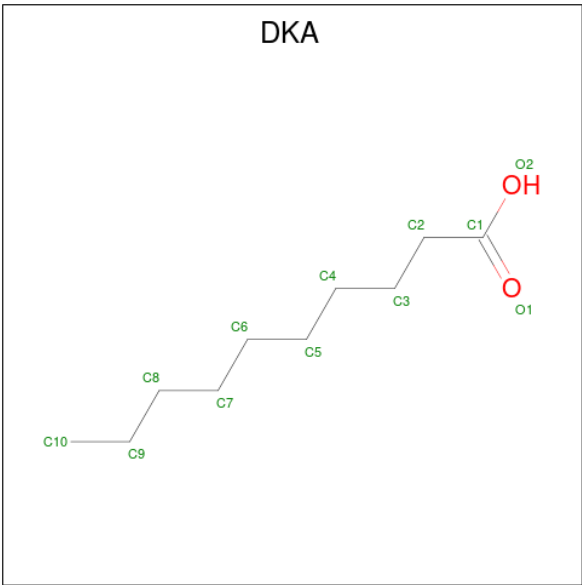
Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	39	Total	C	N	O	0	0
			309	200	50	59		
5	P	39	Total	C	N	O	0	0
			309	200	50	59		
5	Y	39	Total	C	N	O	0	0
			309	200	50	59		

- Molecule 6 is (2 {R})-2-azanyl-3-[[[(2 {R})-2-hexadecanoyloxy-3-pentadecanoyloxy-propoxy]-oxidanyl-phosphoryl]oxy-propanoic acid (CCD ID: A1EZJ) (formula: C₃₇H₇₂NO₁₀P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
6	A	1	Total	C	H	N	O	P	0
			119	37	70	1	10	1	
6	A	1	Total	C	H	N	O	P	0
			119	37	70	1	10	1	
6	C	1	Total	C	H	N	O	P	0
			119	37	70	1	10	1	
6	L	1	Total	C	H	N	O	P	0
			119	37	70	1	10	1	
6	L	1	Total	C	H	N	O	P	0
			119	37	70	1	10	1	
6	U	1	Total	C	H	N	O	P	0
			119	37	70	1	10	1	

- Molecule 7 is DECANOIC ACID (CCD ID: DKA) (formula: C₁₀H₂₀O₂).



Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	A	1	Total	C	H	O	0
			31	10	19	2	
7	B	1	Total	C	H	O	0
			31	10	19	2	
7	B	1	Total	C	H	O	0
			31	10	19	2	
7	B	1	Total	C	H	O	0
			31	10	19	2	
7	B	1	Total	C	H	O	0
			31	10	19	2	
7	C	1	Total	C	H	O	0
			31	10	19	2	

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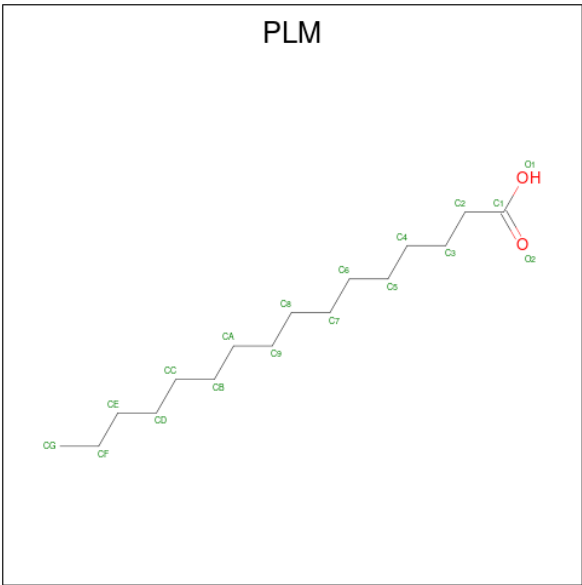
Mol	Chain	Residues	Atoms				AltConf
7	C	1	Total 31	C 10	H 19	O 2	0
7	C	1	Total 31	C 10	H 19	O 2	0
7	C	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	L	1	Total 31	C 10	H 19	O 2	0
7	M	1	Total 31	C 10	H 19	O 2	0
7	M	1	Total 31	C 10	H 19	O 2	0
7	M	1	Total 31	C 10	H 19	O 2	0
7	M	1	Total 31	C 10	H 19	O 2	0
7	N	1	Total 31	C 10	H 19	O 2	0
7	N	1	Total 31	C 10	H 19	O 2	0
7	N	1	Total 31	C 10	H 19	O 2	0
7	N	1	Total 31	C 10	H 19	O 2	0
7	U	1	Total 31	C 10	H 19	O 2	0

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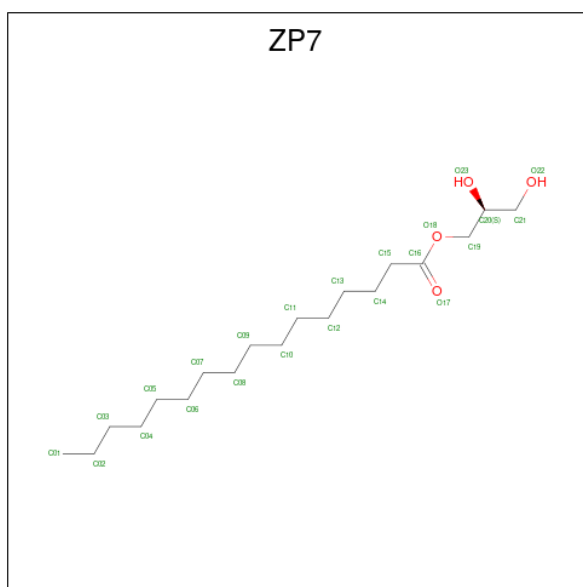
Mol	Chain	Residues	Atoms				AltConf
7	U	1	Total	C	H	O	0
			31	10	19	2	
7	U	1	Total	C	H	O	0
			31	10	19	2	
7	U	1	Total	C	H	O	0
			31	10	19	2	
7	U	1	Total	C	H	O	0
			31	10	19	2	
7	U	1	Total	C	H	O	0
			31	10	19	2	
7	U	1	Total	C	H	O	0
			31	10	19	2	
7	V	1	Total	C	H	O	0
			31	10	19	2	
7	V	1	Total	C	H	O	0
			31	10	19	2	
7	V	1	Total	C	H	O	0
			31	10	19	2	
7	V	1	Total	C	H	O	0
			31	10	19	2	
7	W	1	Total	C	H	O	0
			31	10	19	2	
7	W	1	Total	C	H	O	0
			31	10	19	2	
7	W	1	Total	C	H	O	0
			31	10	19	2	
7	W	1	Total	C	H	O	0
			31	10	19	2	

- Molecule 8 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms				AltConf
8	B	1	Total	C	H	O	0
			49	16	31	2	
8	B	1	Total	C	H	O	0
			49	16	31	2	
8	C	1	Total	C	H	O	0
			49	16	31	2	
8	M	1	Total	C	H	O	0
			49	16	31	2	
8	M	1	Total	C	H	O	0
			49	16	31	2	
8	N	1	Total	C	H	O	0
			49	16	31	2	
8	V	1	Total	C	H	O	0
			49	16	31	2	
8	V	1	Total	C	H	O	0
			49	16	31	2	
8	W	1	Total	C	H	O	0
			49	16	31	2	

- Molecule 9 is (2S)-2,3-dihydroxypropyl hexadecanoate (CCD ID: ZP7) (formula: C₁₉H₃₈O₄).

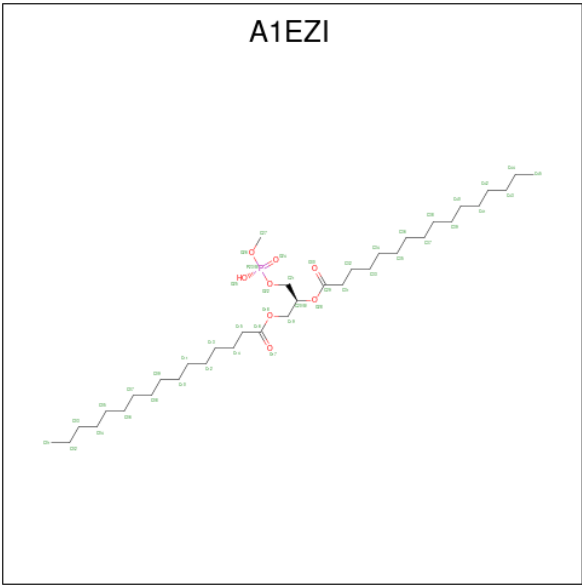


Mol	Chain	Residues	Atoms				AltConf
9	B	1	Total	C	H	O	0
			61	19	38	4	
9	C	1	Total	C	H	O	0
			61	19	38	4	
9	M	1	Total	C	H	O	0
			61	19	38	4	
9	N	1	Total	C	H	O	0
			61	19	38	4	
9	V	1	Total	C	H	O	0
			61	19	38	4	
9	W	1	Total	C	H	O	0
			61	19	38	4	

- Molecule 10 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

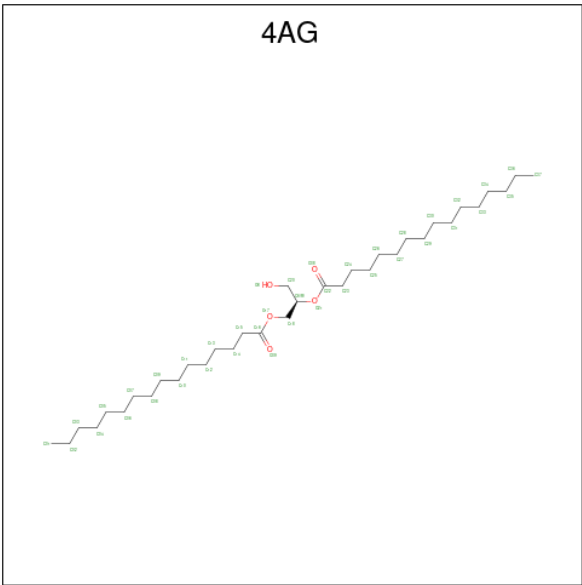
Mol	Chain	Residues	Atoms		AltConf
10	B	1	Total	Cu	0
			1	1	
10	C	2	Total	Cu	0
			2	2	
10	M	1	Total	Cu	0
			1	1	
10	N	2	Total	Cu	0
			2	2	
10	V	1	Total	Cu	0
			1	1	
10	W	2	Total	Cu	0
			2	2	

- Molecule 11 is [(2 {S})-2-hexadecanoyloxy-3-[methoxy(oxidanyl)phosphoryl]oxy-propyl] hexadecanoate (CCD ID: A1EZI) (formula: C₃₆H₇₁O₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
11	C	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	C	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	C	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	N	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	N	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	N	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	W	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	W	1	Total	C	H	O	P	0
			115	36	70	8	1	
11	W	1	Total	C	H	O	P	0
			115	36	70	8	1	

- Molecule 12 is (2R)-3-HYDROXYPROPANE-1,2-DIYL DIHEXADECANOATE (CCD ID: 4AG) (formula: C₃₅H₆₈O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
12	C	1	Total	C	H	O	0
			108	35	68	5	
12	N	1	Total	C	H	O	0
			108	35	68	5	
12	W	1	Total	C	H	O	0
			108	35	68	5	

- Molecule 13 is water.

Mol	Chain	Residues	Atoms		AltConf
13	A	39	Total	O	0
			39	39	
13	B	125	Total	O	0
			125	125	
13	C	18	Total	O	0
			18	18	
13	D	1	Total	O	0
			1	1	
13	L	39	Total	O	0
			39	39	
13	M	125	Total	O	0
			125	125	
13	N	18	Total	O	0
			18	18	
13	O	1	Total	O	0
			1	1	
13	U	39	Total	O	0
			39	39	

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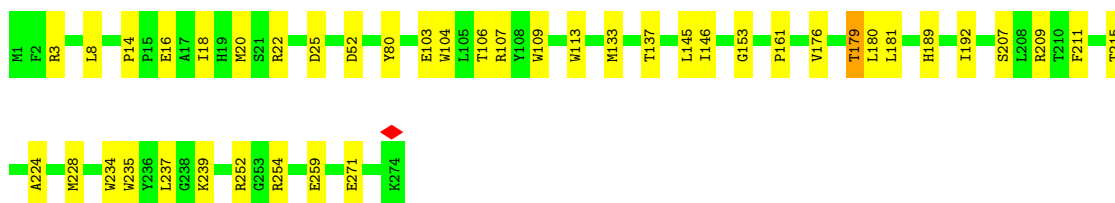
Mol	Chain	Residues	Atoms		AltConf
13	V	125	Total 125	O 125	0
13	W	18	Total 18	O 18	0
13	X	1	Total 1	O 1	0

3 Residue-property plots

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

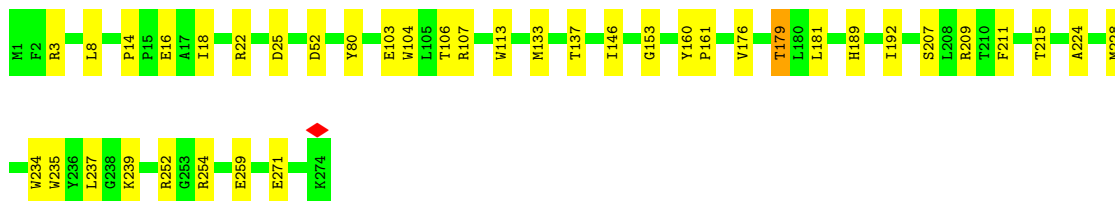
- Molecule 1: Ammonia monooxygenase subunit A

Chain A: 



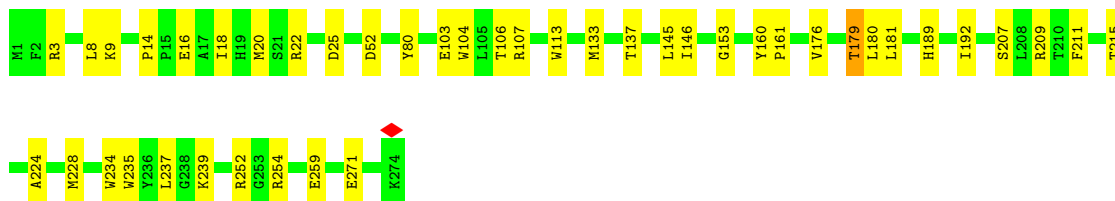
- Molecule 1: Ammonia monooxygenase subunit A

Chain L: 



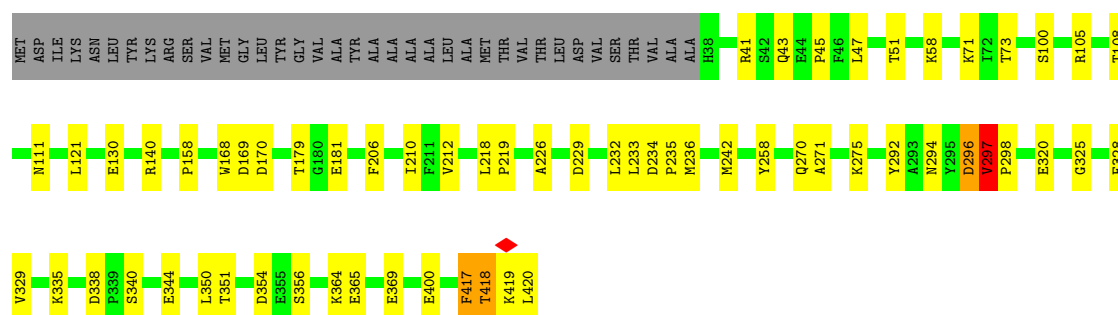
- Molecule 1: Ammonia monooxygenase subunit A

Chain U: 



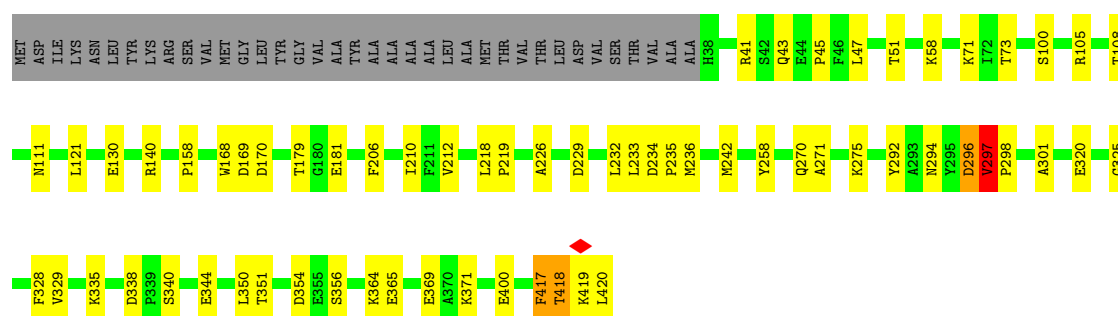
- Molecule 2: Ammonia monooxygenase subunit B

Chain B: 



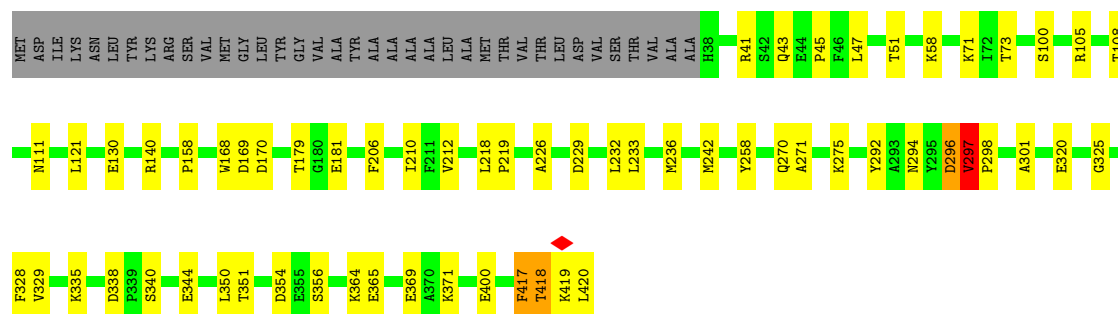
• Molecule 2: Ammonia monooxygenase subunit B

Chain M: 76% 15% 9%



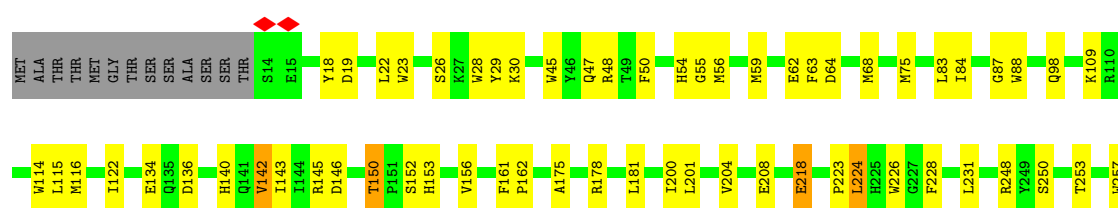
• Molecule 2: Ammonia monooxygenase subunit B

Chain V: 76% 14% 9%



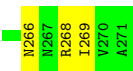
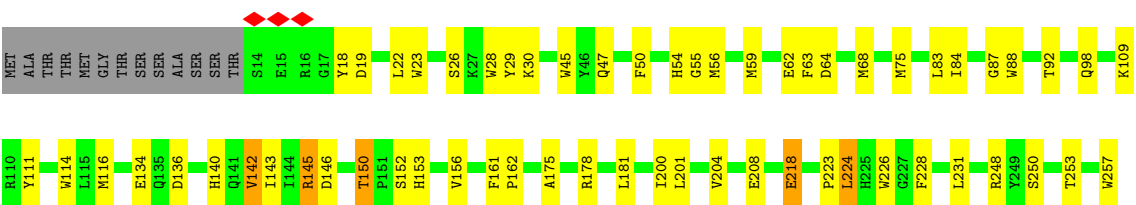
• Molecule 3: Ammonia monooxygenase subunit C

Chain C: 71% 23% 5%

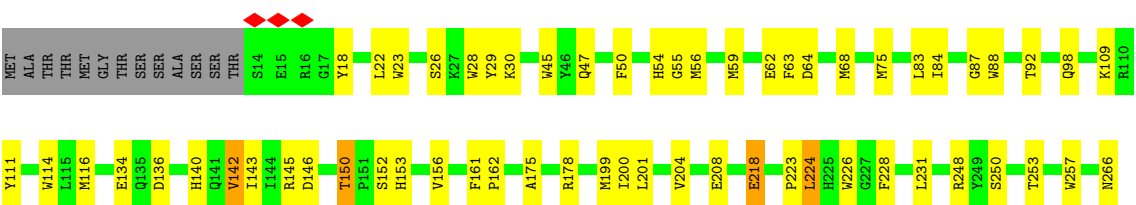




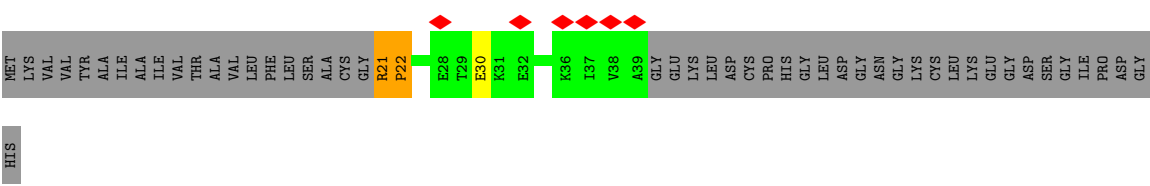
• Molecule 3: Ammonia monooxygenase subunit C



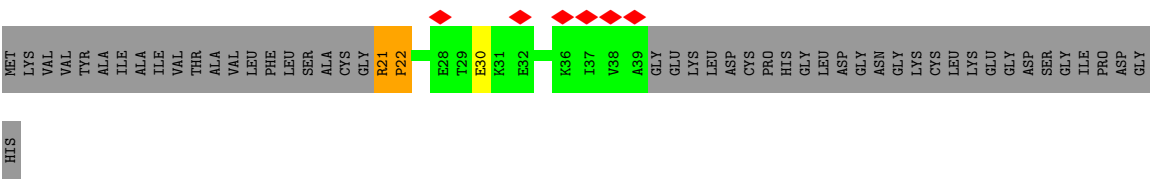
• Molecule 3: Ammonia monooxygenase subunit C



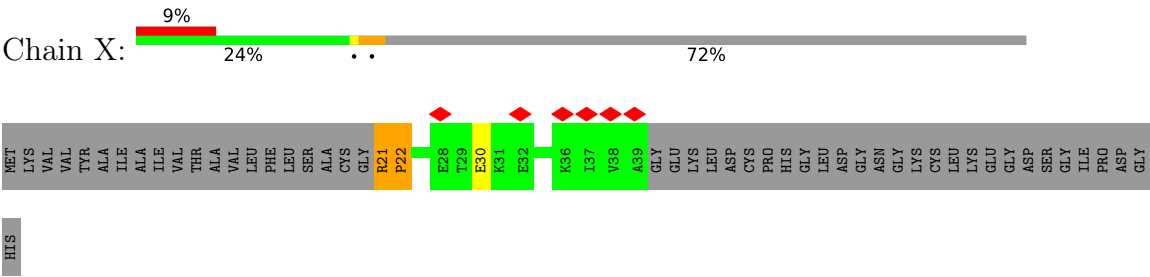
• Molecule 4: Lipoprotein



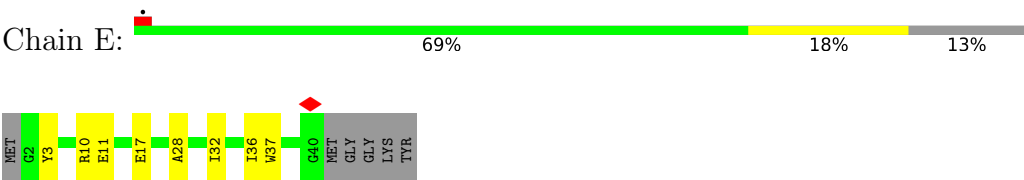
• Molecule 4: Lipoprotein



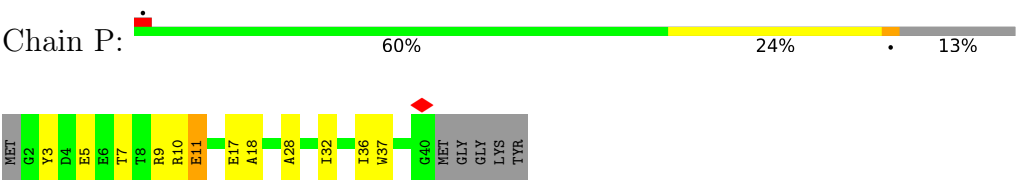
● Molecule 4: Lipoprotein



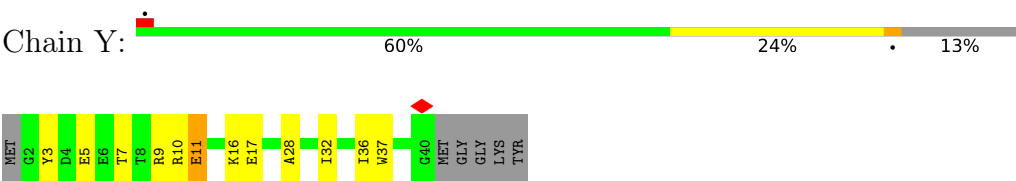
● Molecule 5: AmoD



● Molecule 5: AmoD



● Molecule 5: AmoD



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94482	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.168	Depositor
Minimum map value	-1.135	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	299.26398, 299.26398, 299.26398	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6679999, 0.6679999, 0.6679999	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4AG, ZP7, A1EZI, A1EZJ, PLM, CU, DKA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.27	0/2334	0.43	2/3184 (0.1%)
1	L	0.27	0/2334	0.43	2/3184 (0.1%)
1	U	0.27	0/2334	0.43	2/3184 (0.1%)
2	B	0.27	0/3133	0.41	1/4266 (0.0%)
2	M	0.27	0/3133	0.41	1/4266 (0.0%)
2	V	0.27	0/3133	0.41	1/4266 (0.0%)
3	C	0.27	0/2244	0.45	1/3059 (0.0%)
3	N	0.27	0/2244	0.45	1/3059 (0.0%)
3	W	0.27	0/2244	0.45	1/3059 (0.0%)
4	D	0.29	0/153	0.65	0/206
4	O	0.30	0/153	0.66	0/206
4	X	0.29	0/153	0.66	0/206
5	E	0.27	0/315	0.35	0/425
5	P	0.27	0/315	0.35	0/425
5	Y	0.27	0/315	0.35	0/425
All	All	0.27	0/24537	0.43	12/33420 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	U	192	ILE	N-CA-C	8.10	119.42	109.30
1	A	192	ILE	N-CA-C	8.09	119.41	109.30
1	L	192	ILE	N-CA-C	8.09	119.41	109.30
2	M	417	PHE	N-CA-C	6.09	119.97	112.54
2	B	417	PHE	N-CA-C	6.08	119.95	112.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2248	0	2216	29	0
1	L	2248	0	2216	27	0
1	U	2248	0	2216	29	0
2	B	3042	0	3004	49	0
2	M	3042	0	3004	49	0
2	V	3042	0	3004	49	0
3	C	2160	0	2086	60	0
3	N	2160	0	2086	59	0
3	W	2160	0	2086	55	0
4	D	151	0	151	5	0
4	O	151	0	151	5	0
4	X	151	0	151	5	0
5	E	309	0	303	6	0
5	P	309	0	303	9	0
5	Y	309	0	303	9	0
6	A	98	140	0	1	0
6	C	49	70	0	0	0
6	L	98	140	0	2	0
6	U	49	70	0	2	0
7	A	108	171	171	25	0
7	B	48	76	76	3	0
7	C	48	76	76	3	0
7	L	108	171	171	26	0
7	M	48	76	76	3	0
7	N	48	76	76	3	0
7	U	108	171	171	24	0
7	V	48	76	76	3	0
7	W	48	76	76	4	0
8	B	36	62	62	4	0
8	C	18	31	31	1	0
8	M	36	62	62	4	0
8	N	18	31	31	1	0
8	V	36	62	62	4	0
8	W	18	31	31	1	0
9	B	23	38	0	3	0
9	C	23	38	0	0	0
9	M	23	38	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	N	23	38	0	0	0
9	V	23	38	0	3	0
9	W	23	38	0	0	0
10	B	1	0	0	0	0
10	C	2	0	0	0	0
10	M	1	0	0	0	0
10	N	2	0	0	0	0
10	V	1	0	0	0	0
10	W	2	0	0	0	0
11	C	135	210	0	18	0
11	N	135	210	0	17	0
11	W	135	210	0	17	0
12	C	40	68	68	4	0
12	N	40	68	68	4	0
12	W	40	68	68	4	0
13	A	39	0	0	2	0
13	B	125	0	0	10	0
13	C	18	0	0	1	0
13	D	1	0	0	0	0
13	L	39	0	0	1	0
13	M	125	0	0	10	0
13	N	18	0	0	1	0
13	O	1	0	0	0	0
13	U	39	0	0	2	0
13	V	125	0	0	10	0
13	W	18	0	0	1	0
13	X	1	0	0	0	0
All	All	26019	2730	24732	469	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 9.

The worst 5 of 469 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)
7:L:310:DKA:H42	7:L:311:DKA:H31	1.18	1.16
7:A:310:DKA:H42	7:A:311:DKA:H31	1.18	1.15
3:C:178:ARG:NH1	11:C:301:A1EZI:O25	1.81	1.14
3:W:178:ARG:NH1	11:W:301:A1EZI:O25	1.81	1.14
7:A:309:DKA:H82	7:A:311:DKA:O2	1.50	1.12

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	272/274 (99%)	266 (98%)	6 (2%)	0	100	100
1	L	272/274 (99%)	266 (98%)	6 (2%)	0	100	100
1	U	272/274 (99%)	266 (98%)	6 (2%)	0	100	100
2	B	381/420 (91%)	372 (98%)	7 (2%)	2 (0%)	24	27
2	M	381/420 (91%)	372 (98%)	7 (2%)	2 (0%)	24	27
2	V	381/420 (91%)	372 (98%)	7 (2%)	2 (0%)	24	27
3	C	256/271 (94%)	244 (95%)	11 (4%)	1 (0%)	30	34
3	N	256/271 (94%)	244 (95%)	11 (4%)	1 (0%)	30	34
3	W	256/271 (94%)	244 (95%)	11 (4%)	1 (0%)	30	34
4	D	17/67 (25%)	16 (94%)	0	1 (6%)	1	0
4	O	17/67 (25%)	16 (94%)	0	1 (6%)	1	0
4	X	17/67 (25%)	16 (94%)	0	1 (6%)	1	0
5	E	37/45 (82%)	37 (100%)	0	0	100	100
5	P	37/45 (82%)	37 (100%)	0	0	100	100
5	Y	37/45 (82%)	37 (100%)	0	0	100	100
All	All	2889/3231 (89%)	2805 (97%)	72 (2%)	12 (0%)	31	34

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	297	VAL
2	M	297	VAL
2	V	297	VAL
2	B	418	THR
2	V	418	THR

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	229/229 (100%)	223 (97%)	6 (3%)	40	54
1	L	229/229 (100%)	224 (98%)	5 (2%)	45	59
1	U	229/229 (100%)	223 (97%)	6 (3%)	40	54
2	B	321/348 (92%)	314 (98%)	7 (2%)	45	59
2	M	321/348 (92%)	314 (98%)	7 (2%)	45	59
2	V	321/348 (92%)	314 (98%)	7 (2%)	45	59
3	C	223/233 (96%)	217 (97%)	6 (3%)	39	52
3	N	223/233 (96%)	217 (97%)	6 (3%)	39	52
3	W	223/233 (96%)	216 (97%)	7 (3%)	35	47
4	D	16/52 (31%)	15 (94%)	1 (6%)	16	19
4	O	16/52 (31%)	15 (94%)	1 (6%)	16	19
4	X	16/52 (31%)	15 (94%)	1 (6%)	16	19
5	E	30/34 (88%)	28 (93%)	2 (7%)	15	17
5	P	30/34 (88%)	28 (93%)	2 (7%)	15	17
5	Y	30/34 (88%)	28 (93%)	2 (7%)	15	17
All	All	2457/2688 (91%)	2391 (97%)	66 (3%)	40	52

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	W	150	THR
3	W	218	GLU
5	Y	36	ILE
1	L	215	THR
1	L	207	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
3	N	238	GLN
1	U	214	HIS
3	W	258	ASN
3	N	260	GLN
2	V	189	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 93 ligands modelled in this entry, 9 are monoatomic - leaving 84 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
8	PLM	B	501	-	17,17,17	0.54	0	17,17,17	1.36	1 (5%)
7	DKA	V	508	-	11,11,11	0.71	0	11,11,11	0.83	0
12	4AG	W	307	-	39,39,39	0.85	4 (10%)	41,41,41	0.87	2 (4%)
7	DKA	M	504	-	11,11,11	0.65	0	11,11,11	1.48	1 (9%)
7	DKA	U	301	-	11,11,11	0.68	0	11,11,11	0.87	1 (9%)
7	DKA	U	304	-	11,11,11	0.68	0	11,11,11	0.83	0
7	DKA	W	312	-	11,11,11	0.67	0	11,11,11	0.91	0
6	A1EZJ	U	309	-	47,48,48	0.95	2 (4%)	49,55,55	1.11	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	DKA	L	309	-	11,11,11	0.68	0	11,11,11	0.87	1 (9%)
7	DKA	C	307	-	11,11,11	0.64	0	11,11,11	0.97	1 (9%)
6	A1EZJ	L	307	-	47,48,48	0.95	2 (4%)	49,55,55	1.11	4 (8%)
6	A1EZJ	A	307	-	47,48,48	0.95	2 (4%)	49,55,55	1.11	4 (8%)
9	ZP7	C	305	-	22,22,22	0.83	2 (9%)	23,23,23	0.73	1 (4%)
7	DKA	A	309	-	11,11,11	0.68	0	11,11,11	0.87	1 (9%)
7	DKA	U	306	-	11,11,11	0.60	0	11,11,11	0.94	1 (9%)
11	A1EZI	N	302	-	44,44,44	0.92	4 (9%)	47,49,49	0.90	2 (4%)
7	DKA	L	305	-	11,11,11	0.67	0	11,11,11	0.92	1 (9%)
11	A1EZI	C	301	-	44,44,44	0.93	3 (6%)	47,49,49	0.94	2 (4%)
7	DKA	L	310	-	11,11,11	0.66	0	11,11,11	0.91	0
7	DKA	M	506	-	11,11,11	0.66	0	11,11,11	0.92	0
7	DKA	W	311	-	11,11,11	0.66	0	11,11,11	0.93	0
11	A1EZI	C	302	-	44,44,44	0.92	4 (9%)	47,49,49	0.90	2 (4%)
7	DKA	L	303	-	11,11,11	0.66	0	11,11,11	0.92	0
11	A1EZI	N	301	-	44,44,44	0.93	3 (6%)	47,49,49	0.94	2 (4%)
7	DKA	A	303	-	11,11,11	0.65	0	11,11,11	0.92	0
7	DKA	N	309	-	11,11,11	0.68	0	11,11,11	0.88	0
7	DKA	N	308	-	11,11,11	0.64	0	11,11,11	0.97	1 (9%)
8	PLM	M	505	-	17,17,17	0.55	0	17,17,17	0.79	0
7	DKA	C	310	-	11,11,11	0.66	0	11,11,11	0.93	0
7	DKA	L	308	-	11,11,11	0.66	0	11,11,11	0.82	0
7	DKA	U	305	-	11,11,11	0.66	0	11,11,11	0.92	0
7	DKA	V	504	-	11,11,11	0.65	0	11,11,11	1.48	1 (9%)
7	DKA	L	311	-	11,11,11	0.59	0	11,11,11	0.97	1 (9%)
7	DKA	A	311	-	11,11,11	0.59	0	11,11,11	0.97	1 (9%)
12	4AG	N	307	-	39,39,39	0.85	4 (10%)	41,41,41	0.87	2 (4%)
7	DKA	L	304	-	11,11,11	0.60	0	11,11,11	0.94	1 (9%)
9	ZP7	B	502	-	22,22,22	0.81	2 (9%)	23,23,23	0.79	1 (4%)
7	DKA	U	302	-	11,11,11	0.66	0	11,11,11	0.91	0
12	4AG	C	306	-	39,39,39	0.85	4 (10%)	41,41,41	0.87	2 (4%)
7	DKA	U	308	-	11,11,11	0.63	0	11,11,11	0.88	0
9	ZP7	V	503	-	22,22,22	0.81	2 (9%)	23,23,23	0.78	1 (4%)
7	DKA	L	306	-	11,11,11	0.63	0	11,11,11	0.89	0
7	DKA	V	506	-	11,11,11	0.67	0	11,11,11	0.92	0
7	DKA	W	308	-	11,11,11	0.64	0	11,11,11	0.97	1 (9%)
7	DKA	B	506	-	11,11,11	0.66	0	11,11,11	0.91	0
7	DKA	A	305	-	11,11,11	0.68	0	11,11,11	0.92	1 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	DKA	U	307	-	11,11,11	0.68	0	11,11,11	0.92	1 (9%)
9	ZP7	N	306	-	22,22,22	0.83	2 (9%)	23,23,23	0.73	1 (4%)
8	PLM	B	504	-	17,17,17	0.55	0	17,17,17	0.79	0
11	A1EZI	W	302	-	44,44,44	0.92	4 (9%)	47,49,49	0.90	2 (4%)
7	DKA	N	311	-	11,11,11	0.65	0	11,11,11	0.93	0
8	PLM	W	310	-	17,17,17	0.53	0	17,17,17	0.86	1 (5%)
7	DKA	L	302	-	11,11,11	0.68	0	11,11,11	0.83	0
7	DKA	C	311	-	11,11,11	0.67	0	11,11,11	0.91	0
7	DKA	A	306	-	11,11,11	0.63	0	11,11,11	0.89	0
7	DKA	A	308	-	11,11,11	0.66	0	11,11,11	0.82	0
11	A1EZI	N	303	-	44,44,44	0.92	4 (9%)	47,49,49	0.84	2 (4%)
7	DKA	A	304	-	11,11,11	0.61	0	11,11,11	0.95	1 (9%)
7	DKA	U	310	-	11,11,11	0.66	0	11,11,11	0.82	0
6	A1EZJ	C	304	-	47,48,48	0.93	4 (8%)	49,55,55	1.04	3 (6%)
7	DKA	A	302	-	11,11,11	0.68	0	11,11,11	0.83	0
8	PLM	M	502	-	17,17,17	0.54	0	17,17,17	1.36	1 (5%)
8	PLM	V	502	-	17,17,17	0.53	0	17,17,17	1.36	1 (5%)
7	DKA	M	508	-	11,11,11	0.70	0	11,11,11	0.82	0
7	DKA	N	312	-	11,11,11	0.67	0	11,11,11	0.91	0
7	DKA	B	505	-	11,11,11	0.66	0	11,11,11	0.91	0
6	A1EZJ	L	301	-	47,48,48	0.92	4 (8%)	49,55,55	1.04	3 (6%)
7	DKA	V	507	-	11,11,11	0.67	0	11,11,11	0.92	0
7	DKA	C	308	-	11,11,11	0.68	0	11,11,11	0.88	0
11	A1EZI	W	301	-	44,44,44	0.92	3 (6%)	47,49,49	0.94	2 (4%)
11	A1EZI	C	303	-	44,44,44	0.93	4 (9%)	47,49,49	0.84	2 (4%)
6	A1EZJ	A	301	-	47,48,48	0.92	4 (8%)	49,55,55	1.04	3 (6%)
9	ZP7	M	503	-	22,22,22	0.80	2 (9%)	23,23,23	0.79	1 (4%)
7	DKA	B	507	-	11,11,11	0.71	0	11,11,11	0.83	0
8	PLM	N	310	-	17,17,17	0.53	0	17,17,17	0.86	1 (5%)
7	DKA	W	309	-	11,11,11	0.68	0	11,11,11	0.88	0
8	PLM	V	505	-	17,17,17	0.55	0	17,17,17	0.79	0
8	PLM	C	309	-	17,17,17	0.53	0	17,17,17	0.86	1 (5%)
11	A1EZI	W	303	-	44,44,44	0.93	4 (9%)	47,49,49	0.84	2 (4%)
9	ZP7	W	306	-	22,22,22	0.84	2 (9%)	23,23,23	0.73	1 (4%)
7	DKA	M	507	-	11,11,11	0.65	0	11,11,11	0.91	0
7	DKA	B	503	-	11,11,11	0.65	0	11,11,11	1.48	1 (9%)
7	DKA	A	310	-	11,11,11	0.66	0	11,11,11	0.91	0
7	DKA	U	303	-	11,11,11	0.59	0	11,11,11	0.97	1 (9%)

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
8	PLM	B	501	-	-	10/15/15/15	-
7	DKA	V	508	-	-	7/9/9/9	-
12	4AG	W	307	-	-	17/41/41/41	-
7	DKA	M	504	-	-	6/9/9/9	-
7	DKA	U	301	-	-	4/9/9/9	-
7	DKA	U	304	-	-	1/9/9/9	-
7	DKA	W	312	-	-	4/9/9/9	-
6	A1EZJ	U	309	-	-	26/54/54/54	-
7	DKA	L	309	-	-	4/9/9/9	-
7	DKA	C	307	-	-	5/9/9/9	-
6	A1EZJ	L	307	-	-	26/54/54/54	-
6	A1EZJ	A	307	-	-	26/54/54/54	-
9	ZP7	C	305	-	-	8/22/22/22	-
7	DKA	A	309	-	-	4/9/9/9	-
7	DKA	U	306	-	-	3/9/9/9	-
11	A1EZI	N	302	-	-	29/48/48/48	-
7	DKA	L	305	-	-	5/9/9/9	-
11	A1EZI	C	301	-	-	22/48/48/48	-
7	DKA	L	310	-	-	6/9/9/9	-
7	DKA	M	506	-	-	6/9/9/9	-
7	DKA	W	311	-	-	4/9/9/9	-
11	A1EZI	C	302	-	-	29/48/48/48	-
7	DKA	L	303	-	-	6/9/9/9	-
11	A1EZI	N	301	-	-	22/48/48/48	-
7	DKA	A	303	-	-	6/9/9/9	-
7	DKA	N	309	-	-	3/9/9/9	-
7	DKA	N	308	-	-	5/9/9/9	-
8	PLM	M	505	-	-	10/15/15/15	-
7	DKA	C	310	-	-	4/9/9/9	-
7	DKA	L	308	-	-	6/9/9/9	-
7	DKA	U	305	-	-	6/9/9/9	-
7	DKA	V	504	-	-	6/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	DKA	L	311	-	-	6/9/9/9	-
7	DKA	A	311	-	-	6/9/9/9	-
12	4AG	N	307	-	-	17/41/41/41	-
7	DKA	L	304	-	-	3/9/9/9	-
9	ZP7	B	502	-	-	15/22/22/22	-
7	DKA	U	302	-	-	6/9/9/9	-
12	4AG	C	306	-	-	17/41/41/41	-
7	DKA	U	308	-	-	5/9/9/9	-
9	ZP7	V	503	-	-	15/22/22/22	-
7	DKA	L	306	-	-	5/9/9/9	-
7	DKA	V	506	-	-	6/9/9/9	-
7	DKA	W	308	-	-	5/9/9/9	-
7	DKA	B	506	-	-	5/9/9/9	-
7	DKA	A	305	-	-	5/9/9/9	-
7	DKA	U	307	-	-	5/9/9/9	-
9	ZP7	N	306	-	-	8/22/22/22	-
8	PLM	B	504	-	-	10/15/15/15	-
11	A1EZI	W	302	-	-	29/48/48/48	-
7	DKA	N	311	-	-	4/9/9/9	-
8	PLM	W	310	-	-	8/15/15/15	-
7	DKA	L	302	-	-	1/9/9/9	-
7	DKA	C	311	-	-	4/9/9/9	-
7	DKA	A	306	-	-	5/9/9/9	-
7	DKA	A	308	-	-	6/9/9/9	-
11	A1EZI	N	303	-	-	25/48/48/48	-
7	DKA	A	304	-	-	3/9/9/9	-
7	DKA	U	310	-	-	6/9/9/9	-
6	A1EZJ	C	304	-	-	30/54/54/54	-
7	DKA	A	302	-	-	1/9/9/9	-
8	PLM	M	502	-	-	10/15/15/15	-
8	PLM	V	502	-	-	10/15/15/15	-
7	DKA	M	508	-	-	7/9/9/9	-
7	DKA	N	312	-	-	4/9/9/9	-
7	DKA	B	505	-	-	6/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	A1EZJ	L	301	-	-	30/54/54/54	-
7	DKA	V	507	-	-	5/9/9/9	-
7	DKA	C	308	-	-	3/9/9/9	-
11	A1EZI	W	301	-	-	22/48/48/48	-
11	A1EZI	C	303	-	-	25/48/48/48	-
6	A1EZJ	A	301	-	-	30/54/54/54	-
9	ZP7	M	503	-	-	15/22/22/22	-
7	DKA	B	507	-	-	7/9/9/9	-
8	PLM	N	310	-	-	8/15/15/15	-
7	DKA	W	309	-	-	3/9/9/9	-
8	PLM	V	505	-	-	10/15/15/15	-
8	PLM	C	309	-	-	8/15/15/15	-
11	A1EZI	W	303	-	-	25/48/48/48	-
9	ZP7	W	306	-	-	8/22/22/22	-
7	DKA	M	507	-	-	5/9/9/9	-
7	DKA	B	503	-	-	6/9/9/9	-
7	DKA	A	310	-	-	6/9/9/9	-
7	DKA	U	303	-	-	6/9/9/9	-

The worst 5 of 75 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	307	A1EZJ	O18-C19	-3.47	1.38	1.46
6	L	307	A1EZJ	O18-C19	-3.47	1.38	1.46
6	U	309	A1EZJ	O18-C19	-3.47	1.38	1.46
11	W	302	A1EZI	O28-C20	-2.92	1.39	1.46
11	C	302	A1EZI	O28-C20	-2.92	1.39	1.46

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	M	502	PLM	C6-C5-C4	4.52	137.19	114.37
8	B	501	PLM	C6-C5-C4	4.51	137.18	114.37
8	V	502	PLM	C6-C5-C4	4.51	137.15	114.37
7	M	504	DKA	C8-C7-C6	3.87	133.94	114.37
7	B	503	DKA	C8-C7-C6	3.87	133.91	114.37

There are no chirality outliers.

5 of 846 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	301	A1EZJ	C15-C16-O18-C19
6	A	301	A1EZJ	O17-C16-O18-C19
6	A	301	A1EZJ	C44-C45-C46-O47
6	A	301	A1EZJ	C44-C45-C46-O48
6	A	307	A1EZJ	C15-C16-O18-C19

There are no ring outliers.

57 monomers are involved in 172 short contacts:

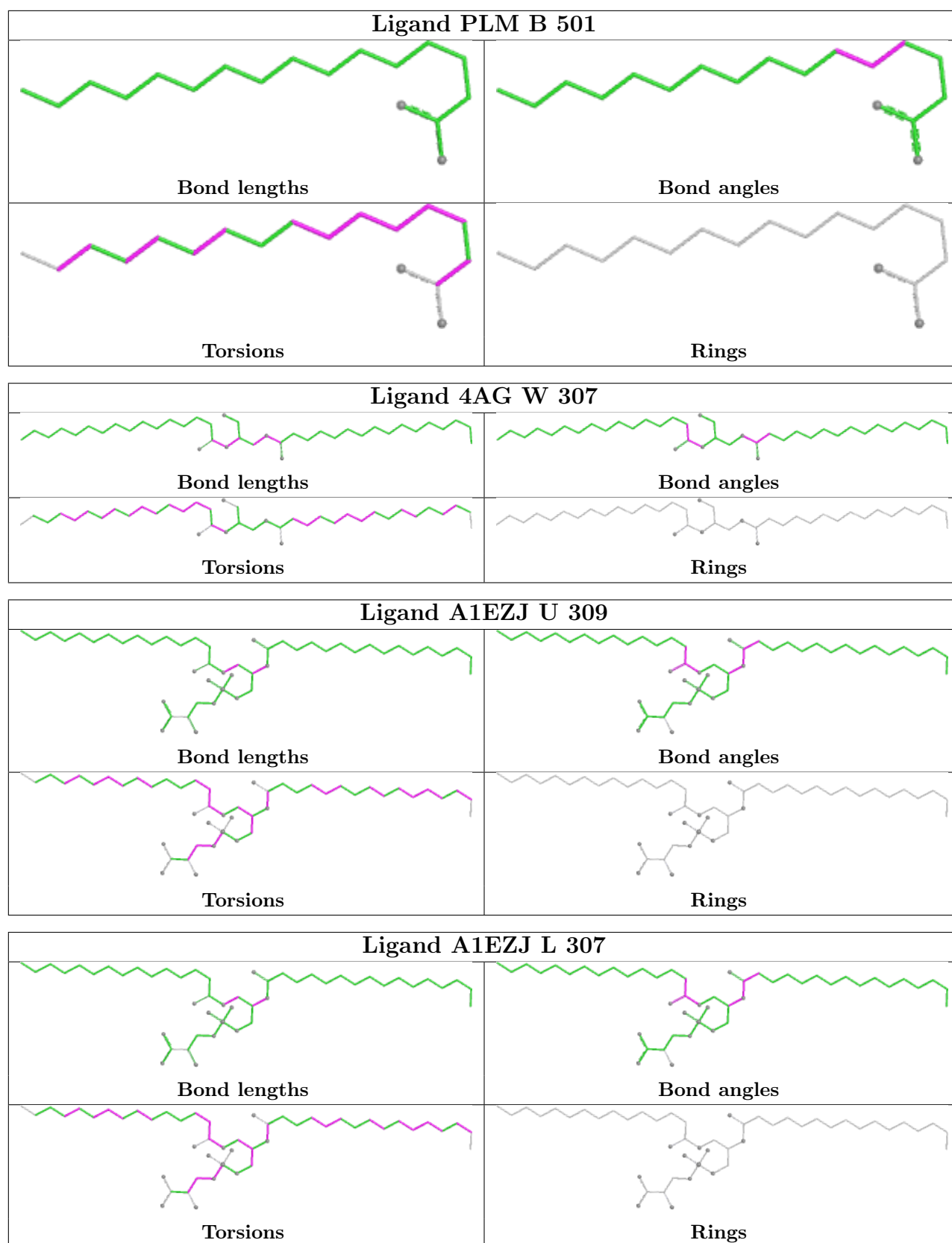
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	501	PLM	3	0
7	V	508	DKA	1	0
12	W	307	4AG	4	0
7	U	301	DKA	5	0
6	U	309	A1EZJ	2	0
7	L	309	DKA	5	0
7	C	307	DKA	2	0
6	L	307	A1EZJ	2	0
6	A	307	A1EZJ	1	0
7	A	309	DKA	5	0
11	N	302	A1EZI	4	0
11	C	301	A1EZI	6	0
7	L	310	DKA	15	0
7	M	506	DKA	1	0
11	C	302	A1EZI	4	0
7	L	303	DKA	3	0
11	N	301	A1EZI	5	0
7	A	303	DKA	3	0
7	N	309	DKA	3	0
7	N	308	DKA	2	0
8	M	505	PLM	1	0
7	L	308	DKA	3	0
7	U	305	DKA	2	0
7	L	311	DKA	19	0
7	A	311	DKA	18	0
12	N	307	4AG	4	0
9	B	502	ZP7	3	0
7	U	302	DKA	14	0
12	C	306	4AG	4	0
9	V	503	ZP7	3	0
7	V	506	DKA	1	0

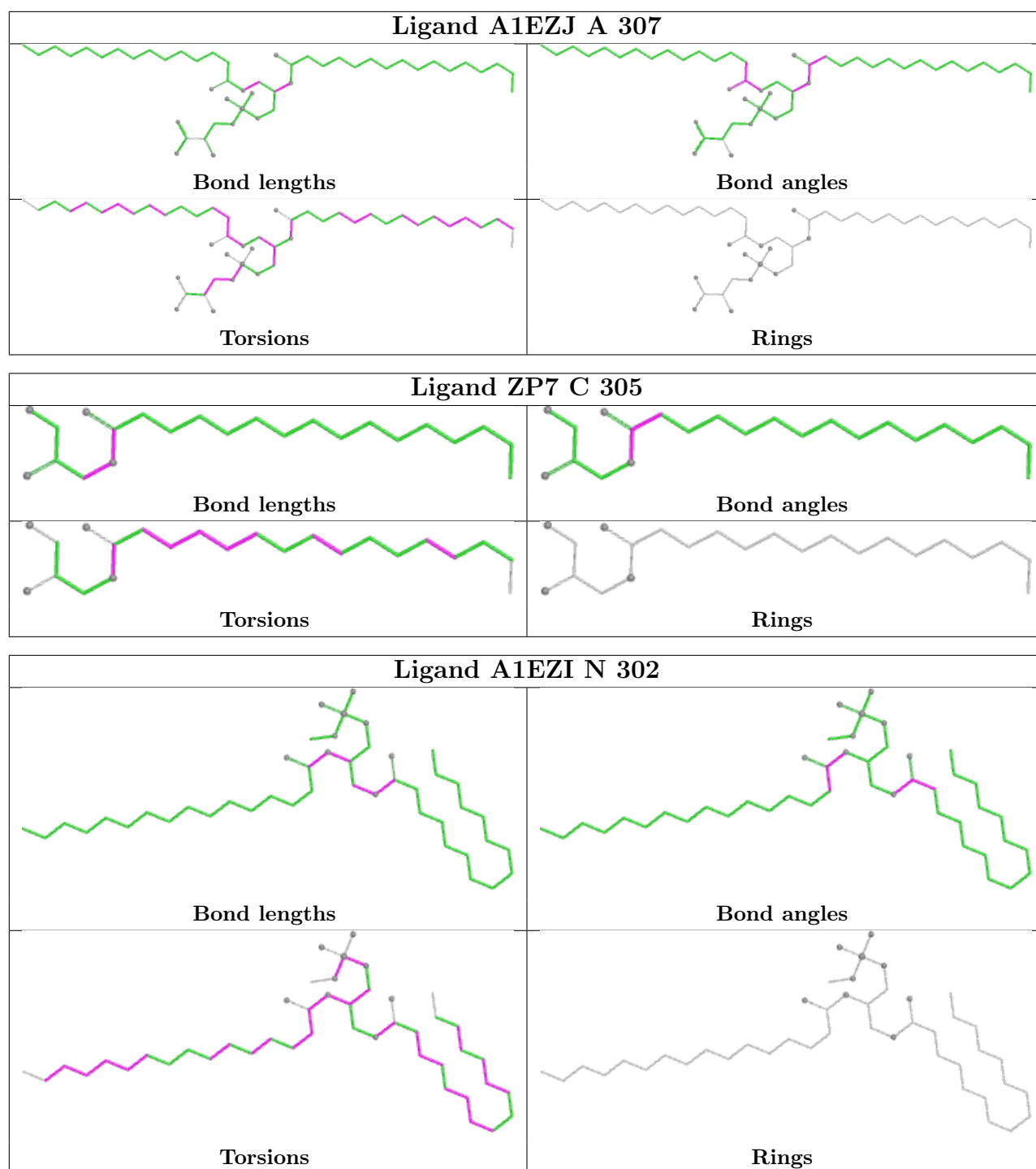
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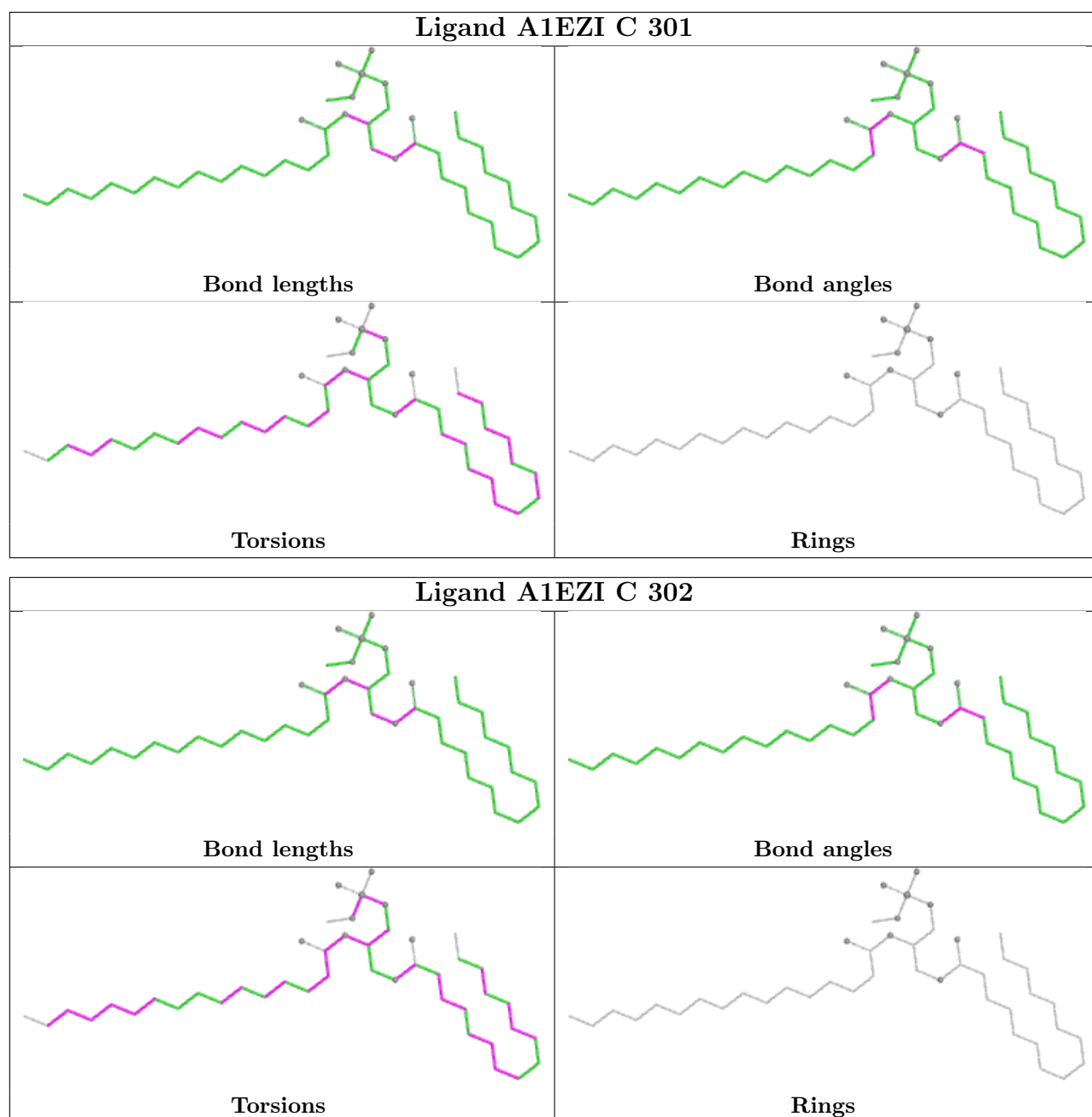
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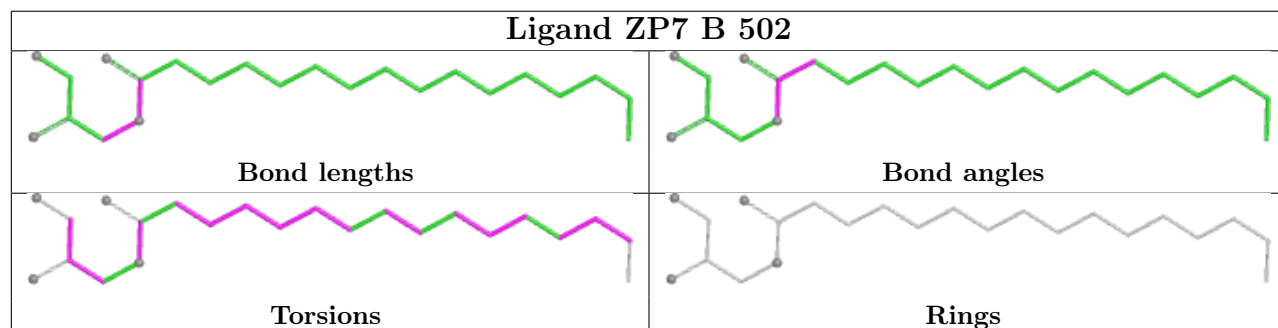
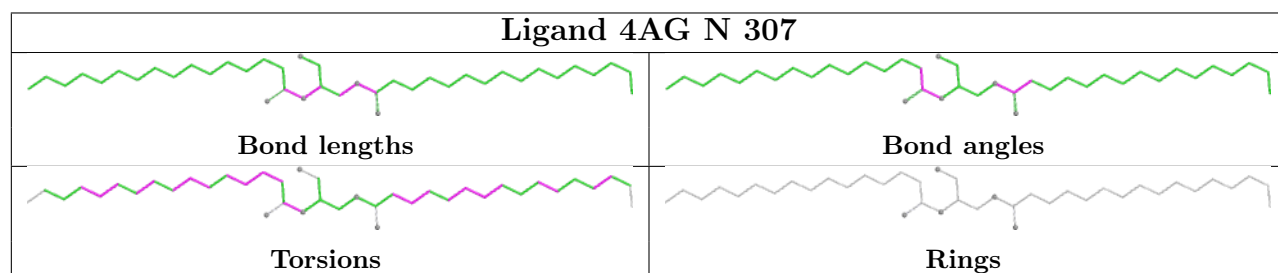
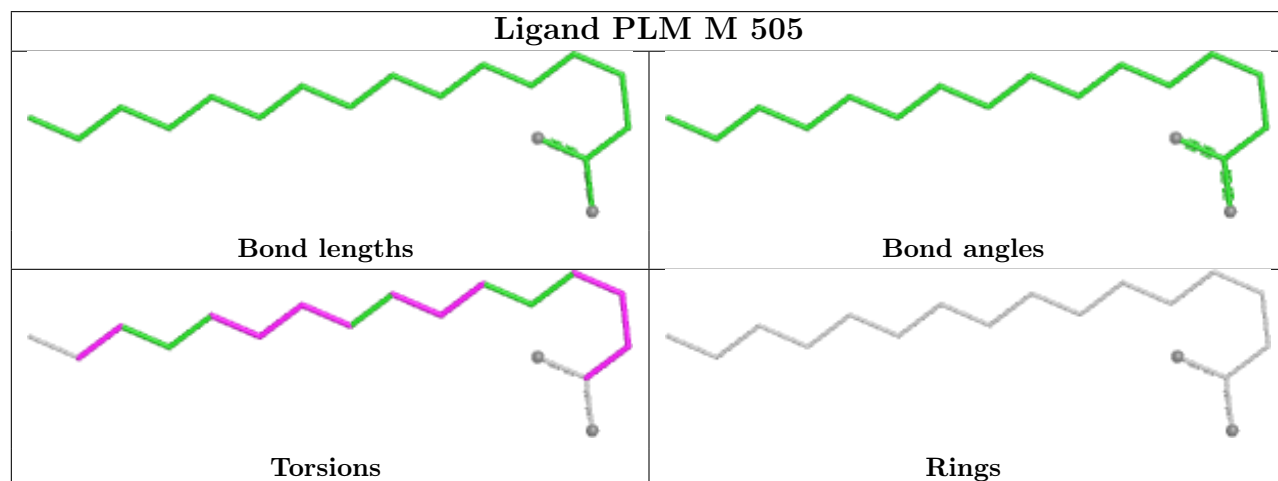
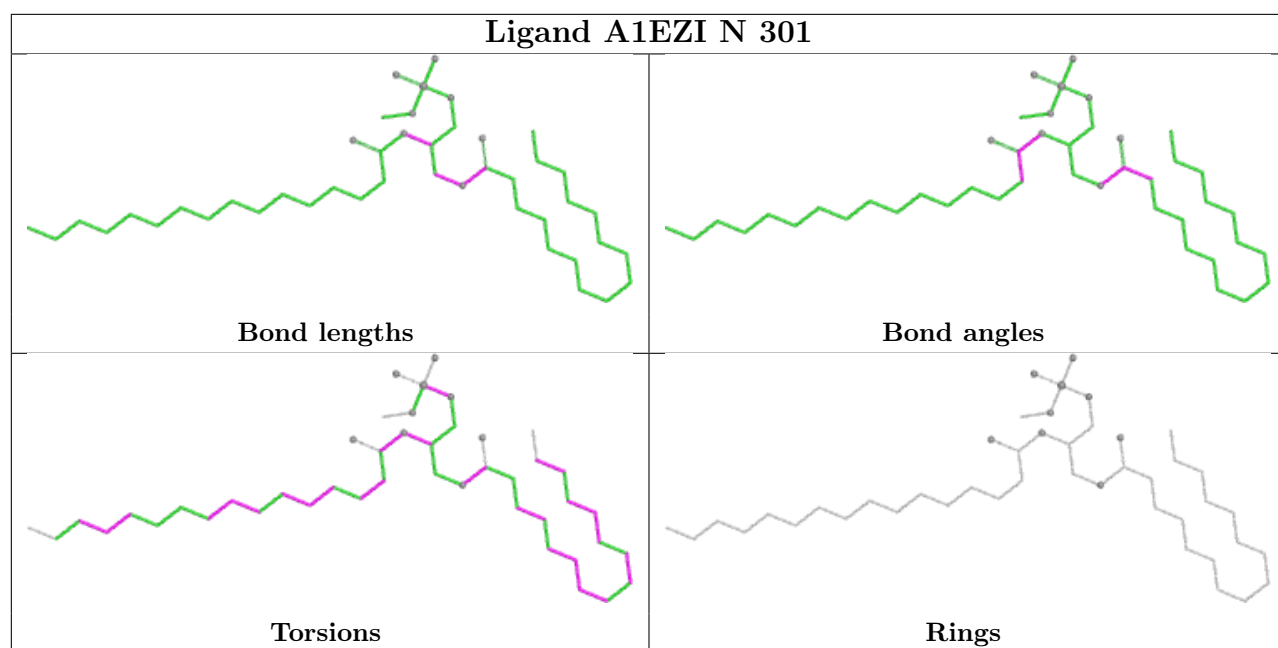
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	W	308	DKA	3	0
7	B	506	DKA	1	0
8	B	504	PLM	1	0
11	W	302	A1EZI	4	0
8	W	310	PLM	1	0
7	A	308	DKA	3	0
11	N	303	A1EZI	8	0
7	U	310	DKA	3	0
8	M	502	PLM	3	0
8	V	502	PLM	3	0
7	M	508	DKA	1	0
7	B	505	DKA	1	0
7	V	507	DKA	1	0
7	C	308	DKA	3	0
11	W	301	A1EZI	5	0
11	C	303	A1EZI	8	0
9	M	503	ZP7	3	0
7	B	507	DKA	1	0
8	N	310	PLM	1	0
7	W	309	DKA	4	0
8	V	505	PLM	1	0
8	C	309	PLM	1	0
11	W	303	A1EZI	8	0
7	M	507	DKA	1	0
7	A	310	DKA	14	0
7	U	303	DKA	18	0

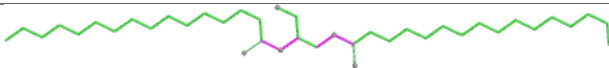
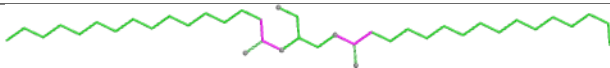
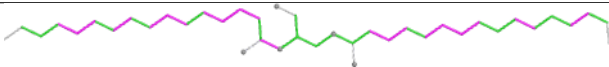
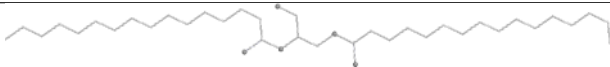
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

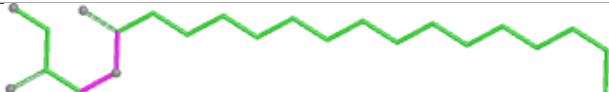
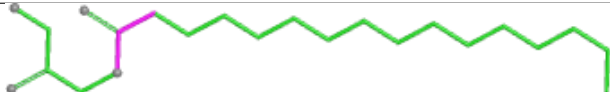
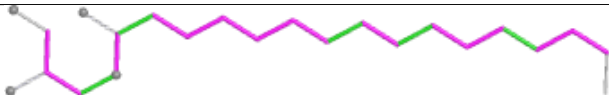
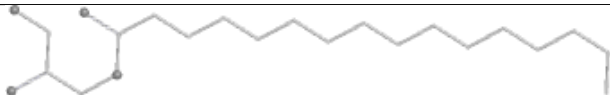


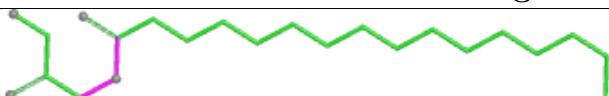
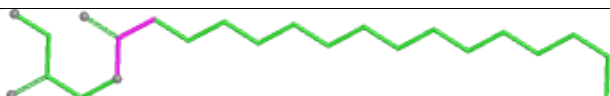
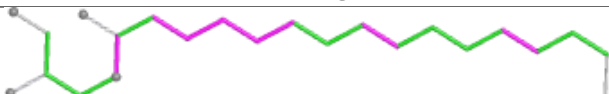
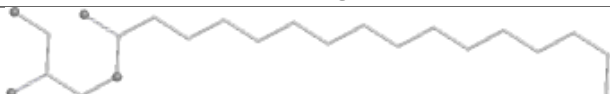


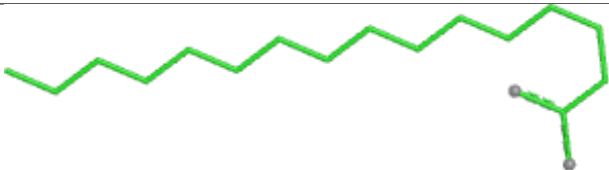
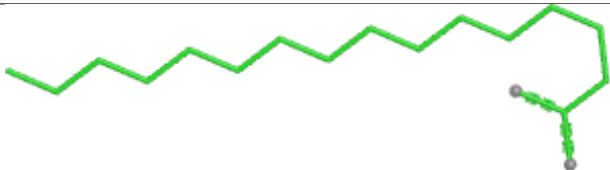
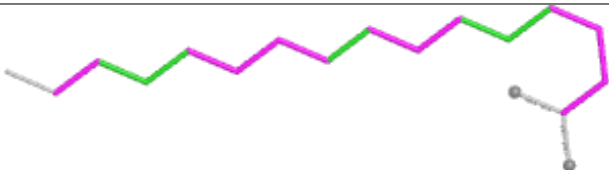
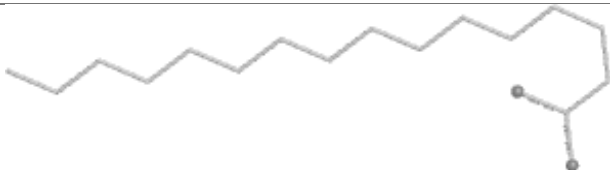


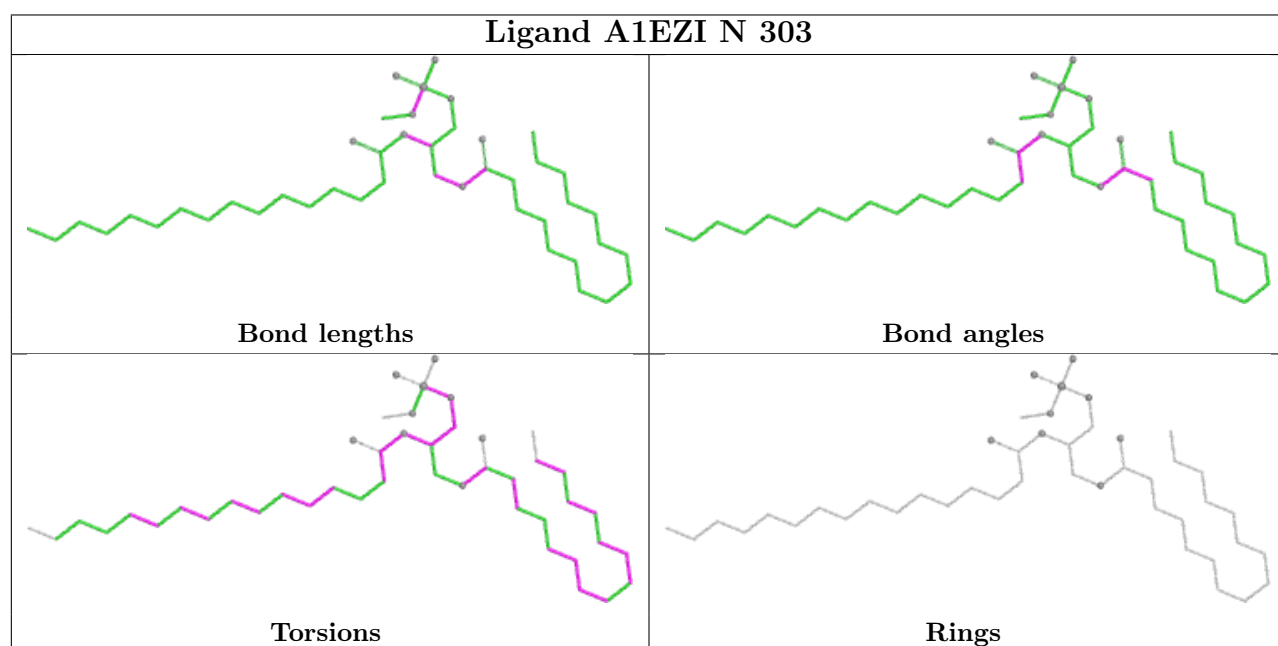
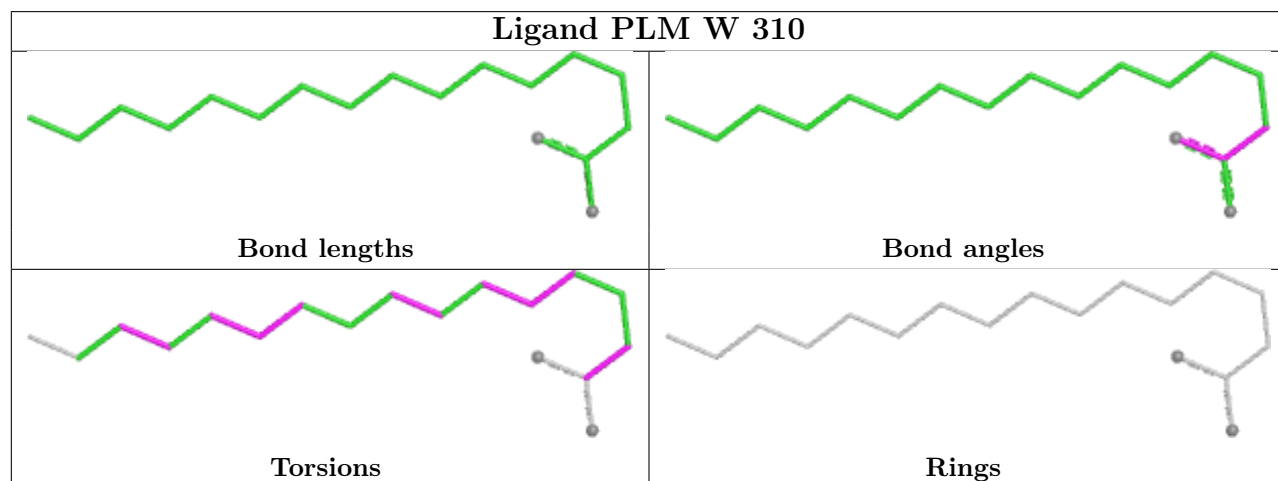
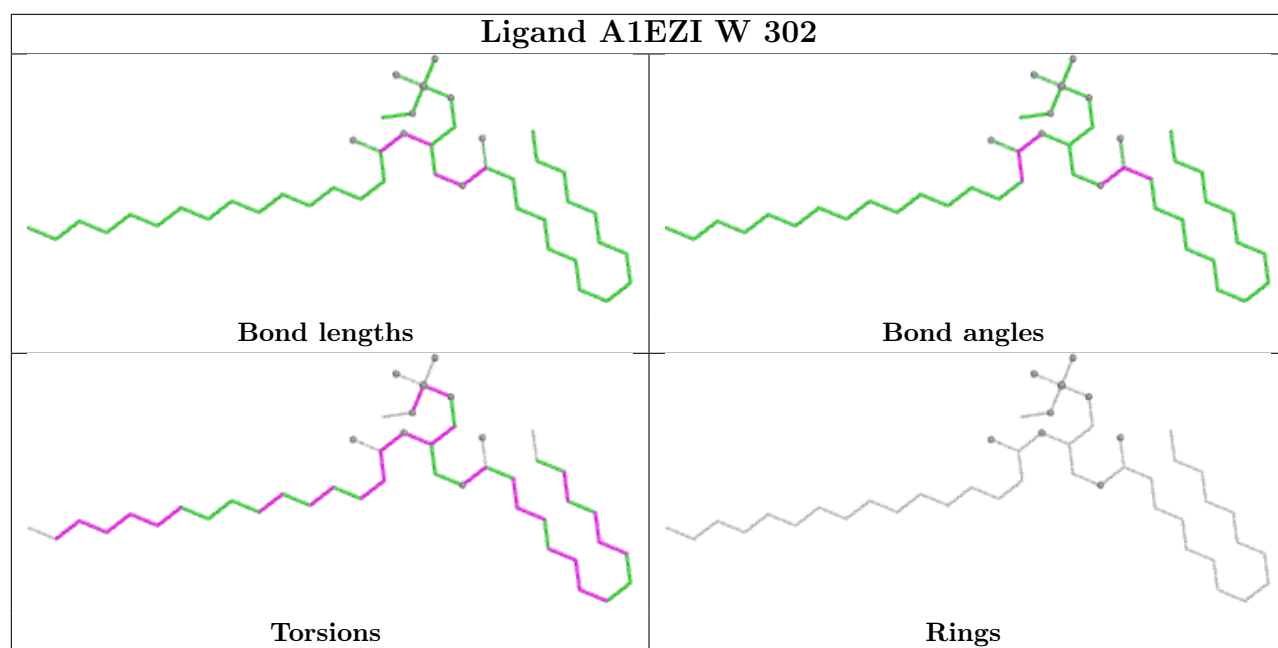


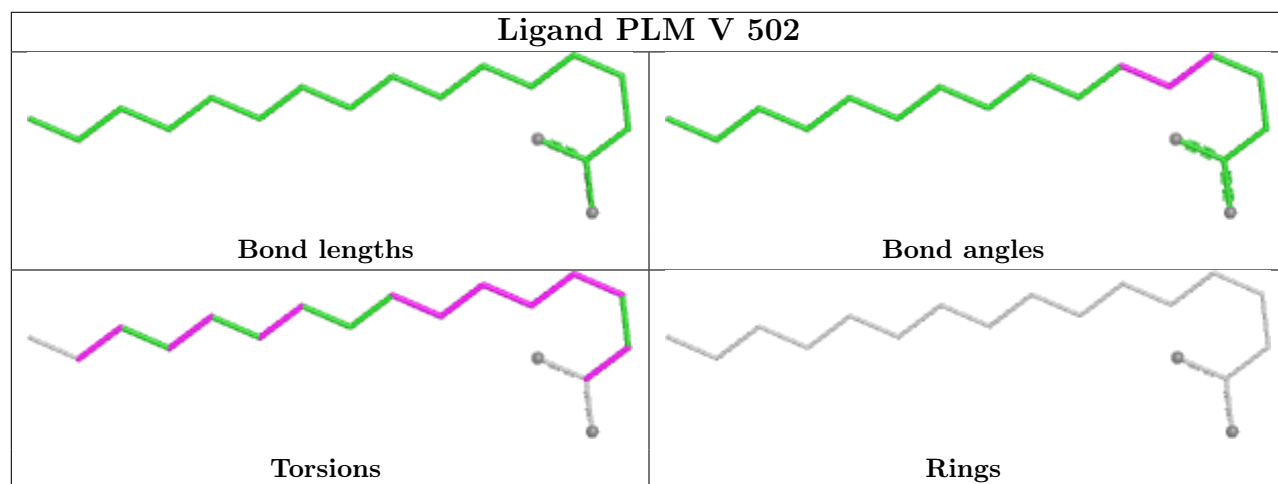
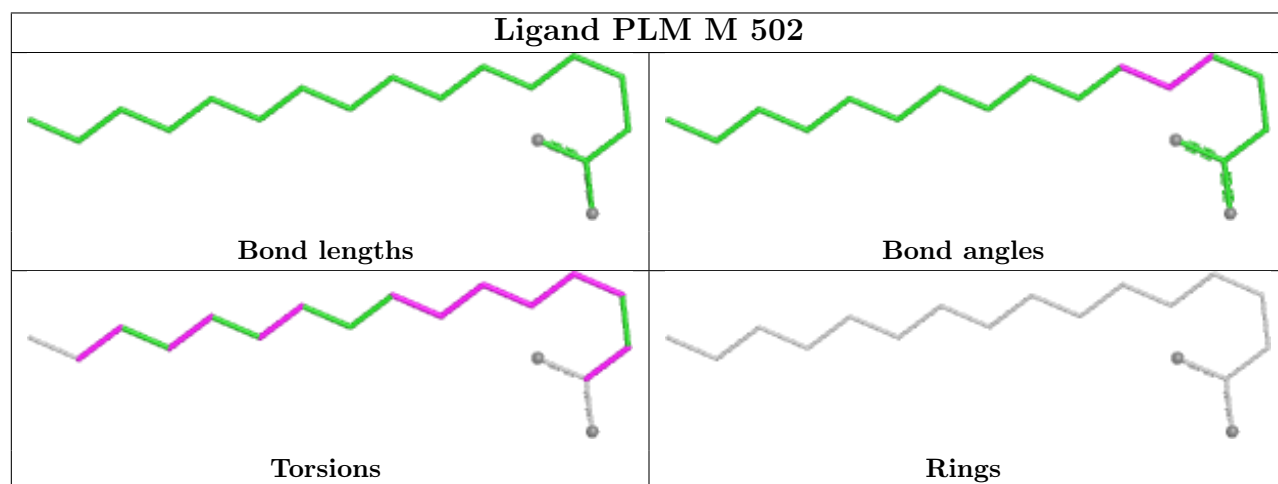
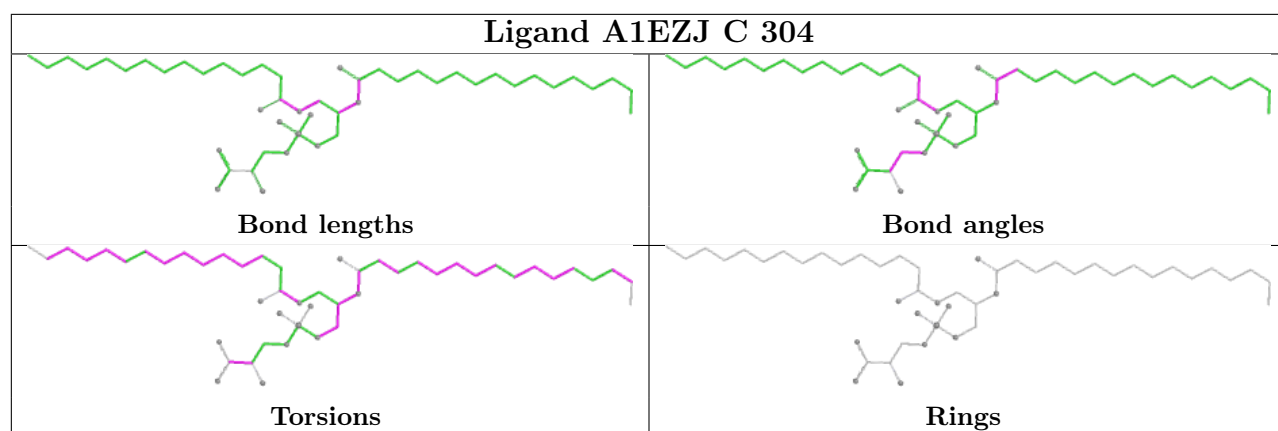
Ligand 4AG C 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

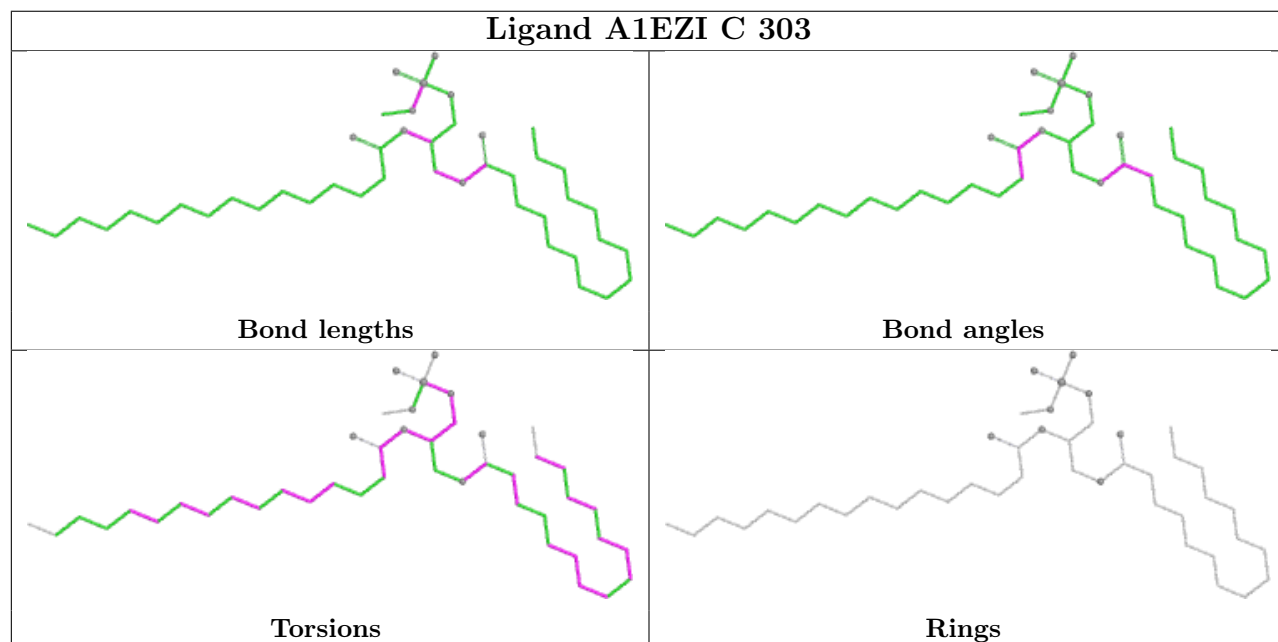
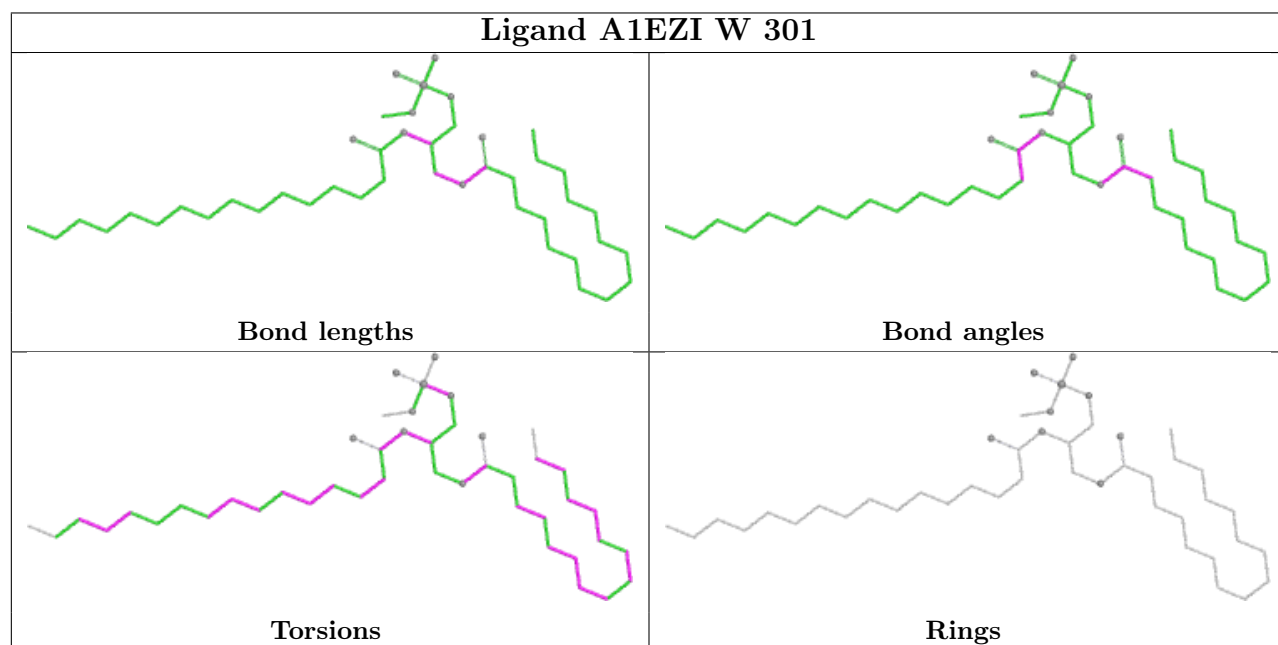
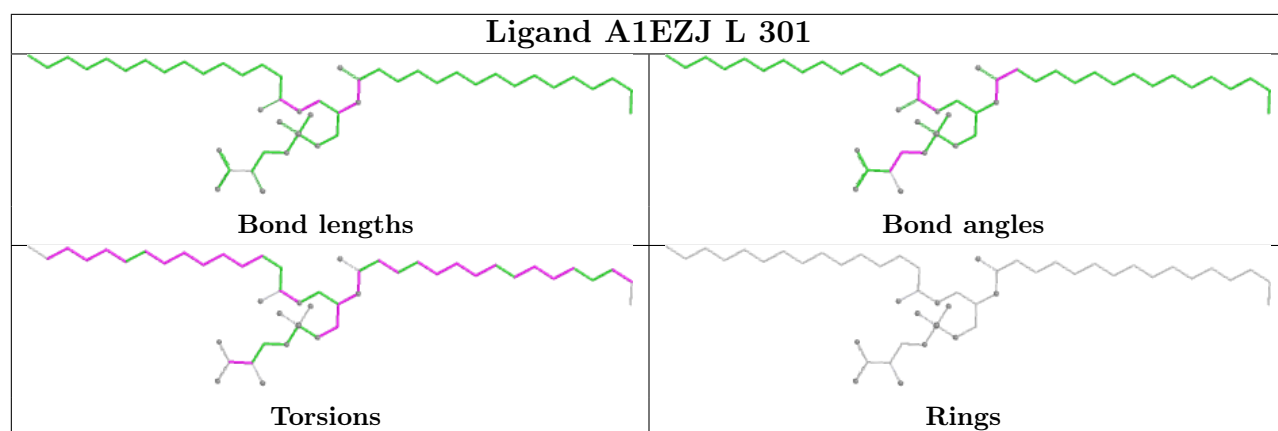
Ligand ZP7 V 503	
 Bond lengths	 Bond angles
 Torsions	 Rings

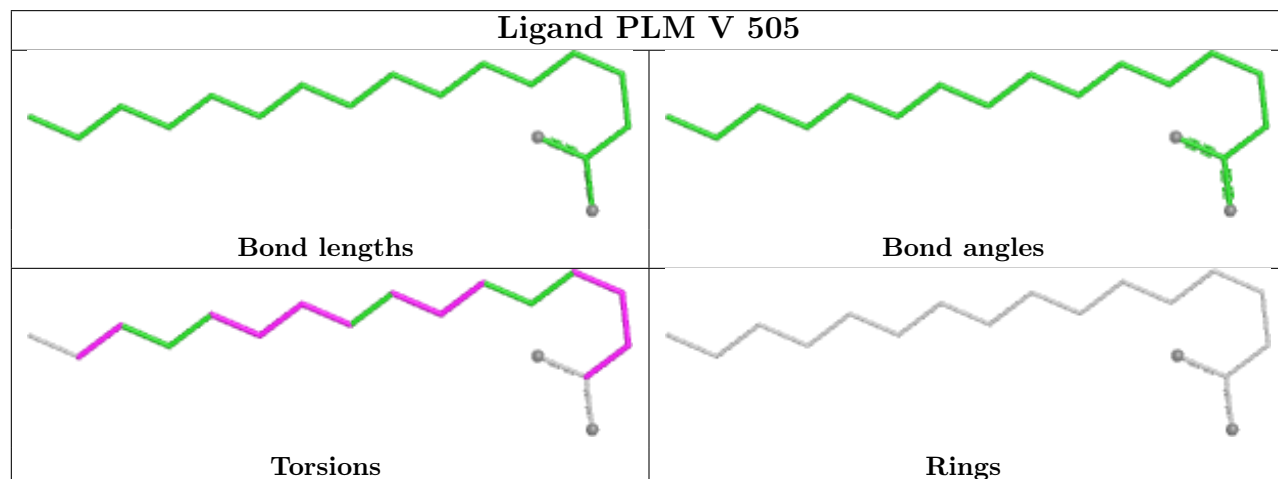
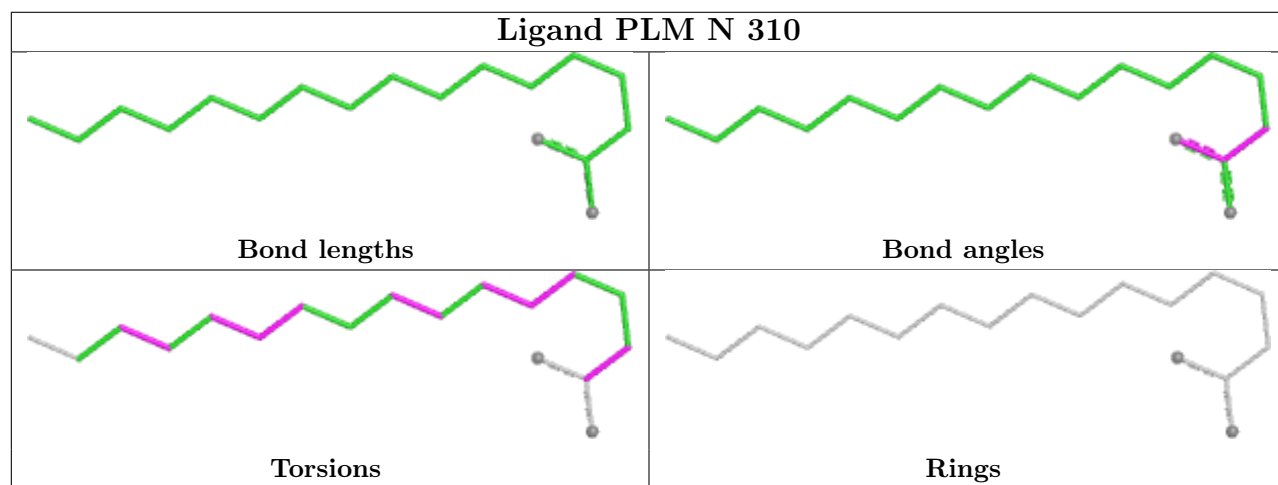
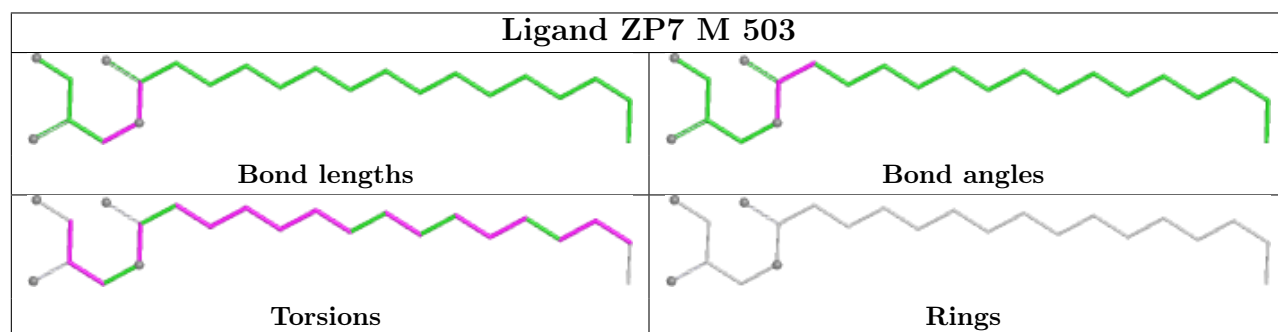
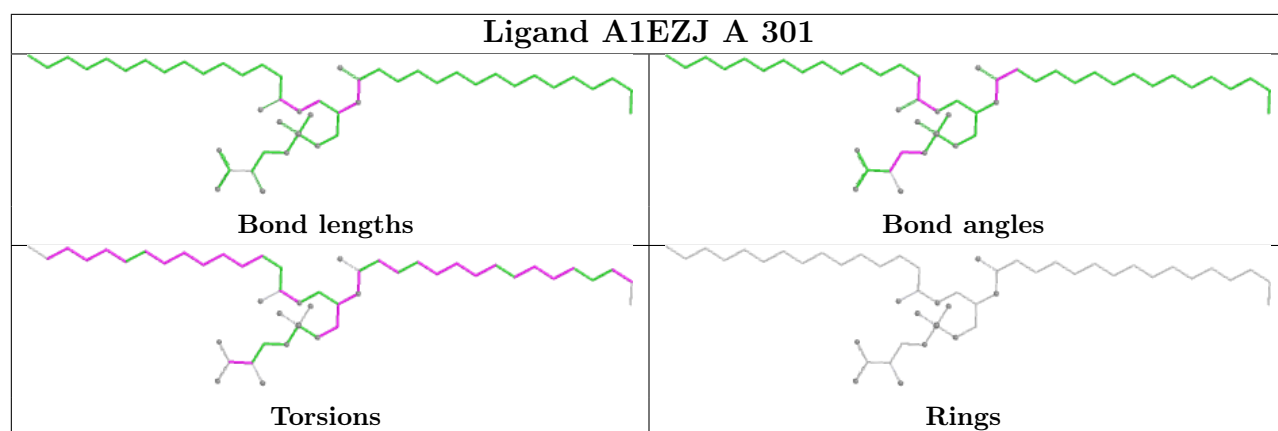
Ligand ZP7 N 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

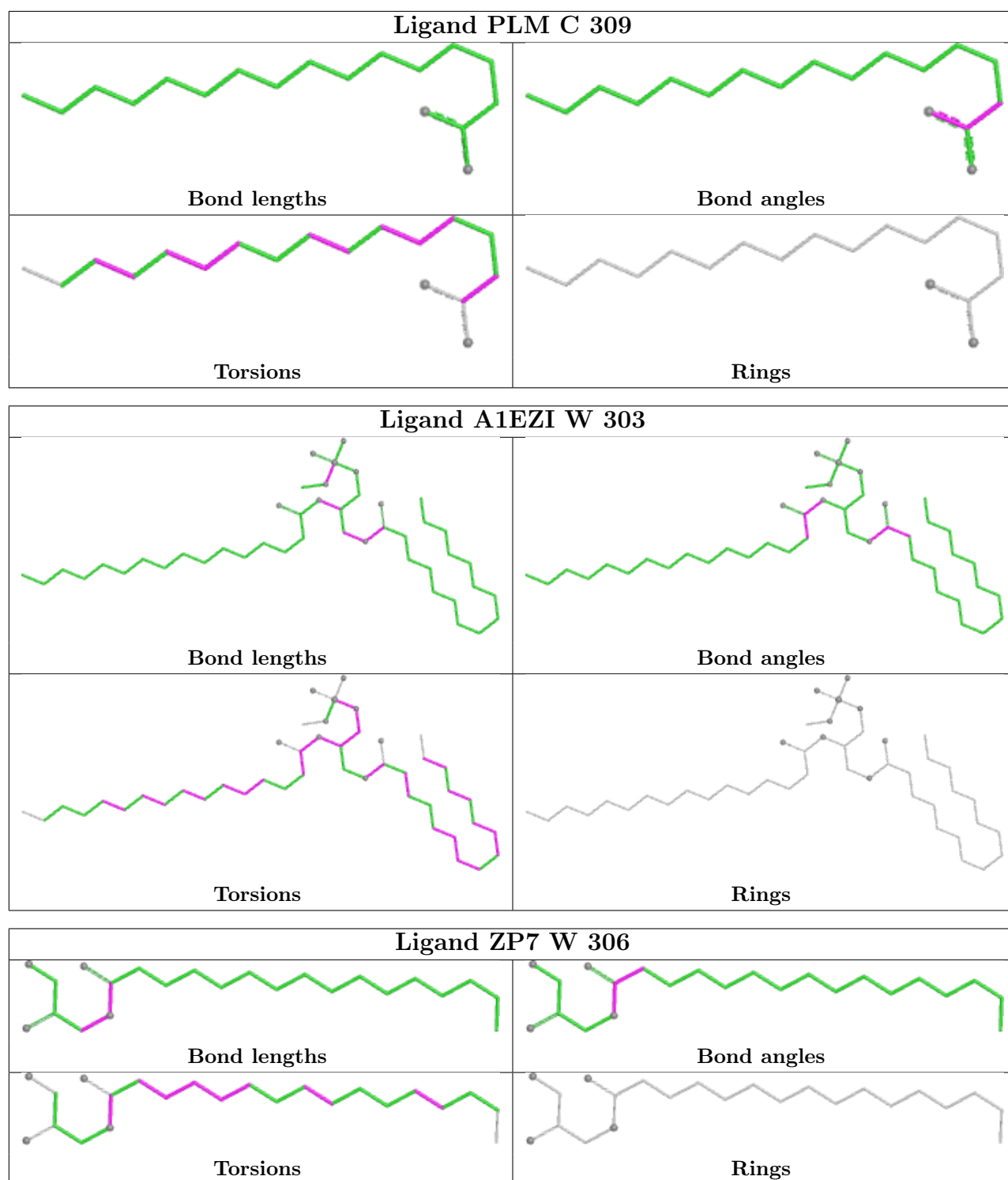
Ligand PLM B 504	
 Bond lengths	 Bond angles
 Torsions	 Rings











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.

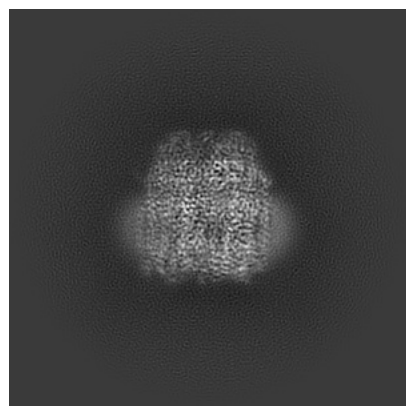
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63025. These allow visual inspection of the internal detail of the map and identification of artifacts.

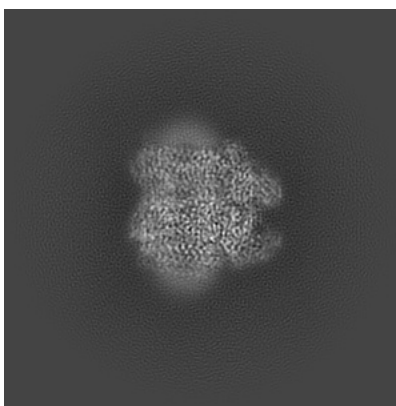
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

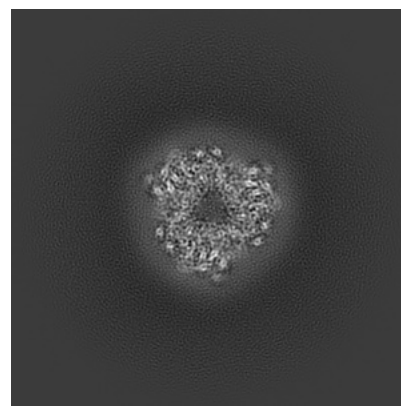
6.1.1 Primary map



X

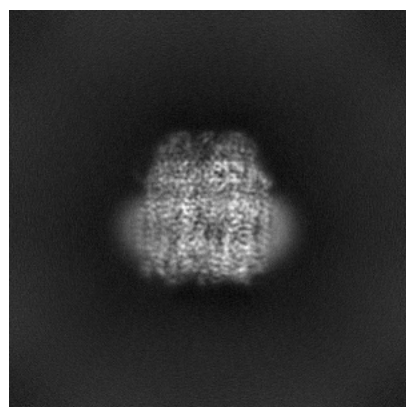


Y

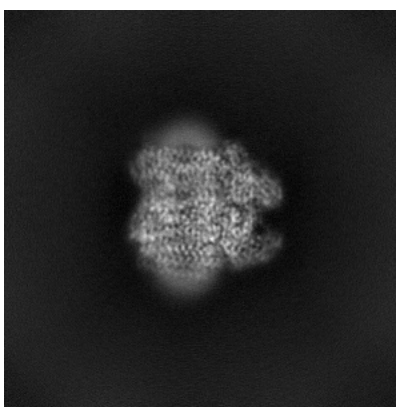


Z

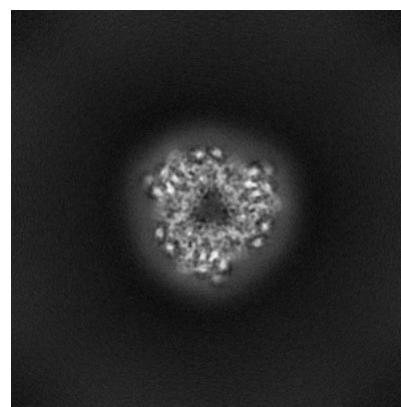
6.1.2 Raw map



X



Y

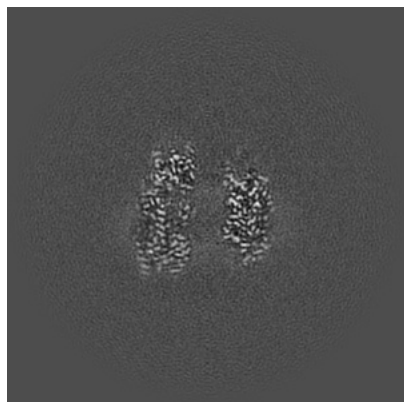


Z

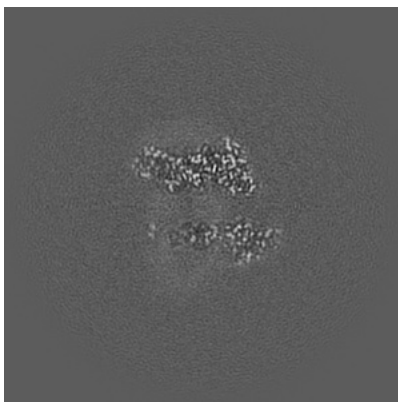
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

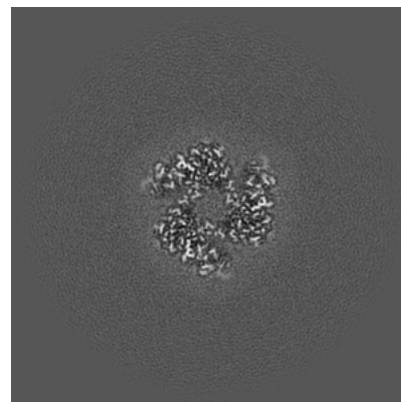
6.2.1 Primary map



X Index: 224

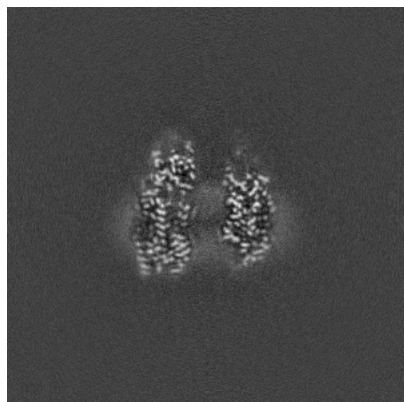


Y Index: 224

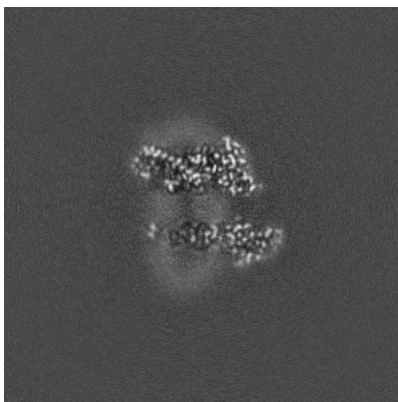


Z Index: 224

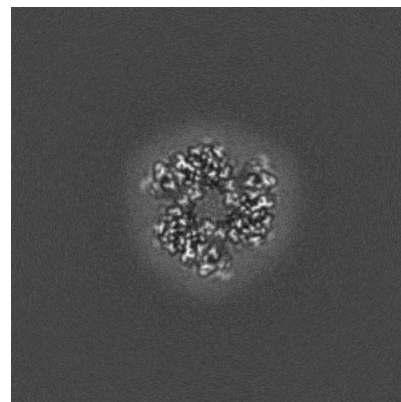
6.2.2 Raw map



X Index: 224



Y Index: 224

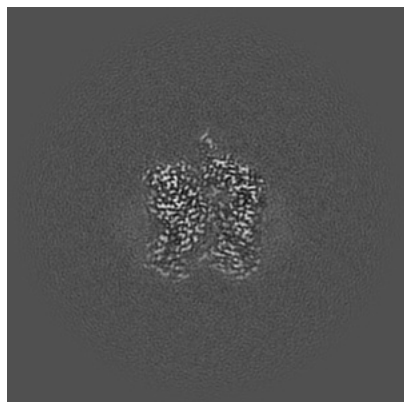


Z Index: 224

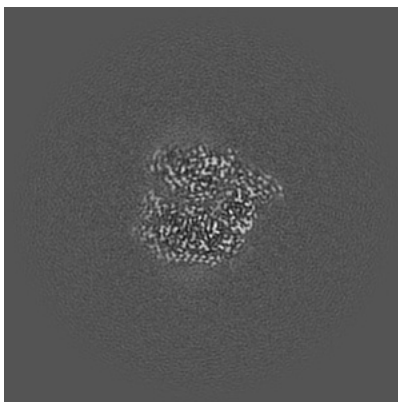
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

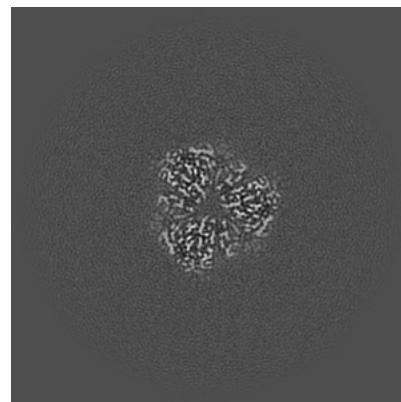
6.3.1 Primary map



X Index: 198

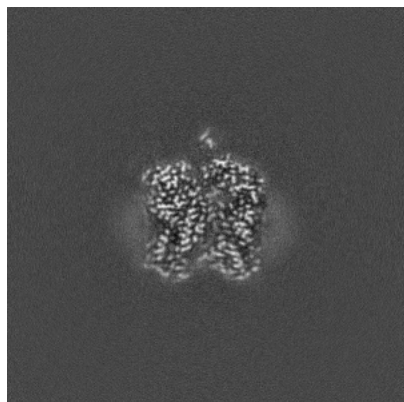


Y Index: 197

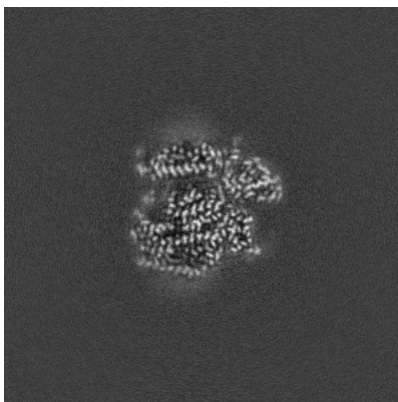


Z Index: 256

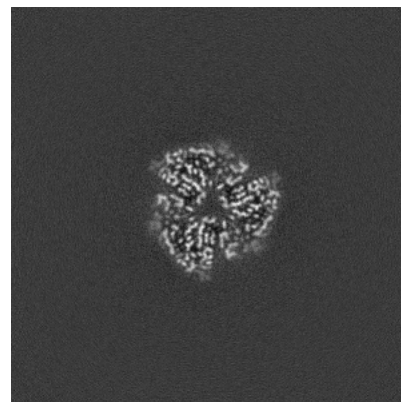
6.3.2 Raw map



X Index: 198



Y Index: 254

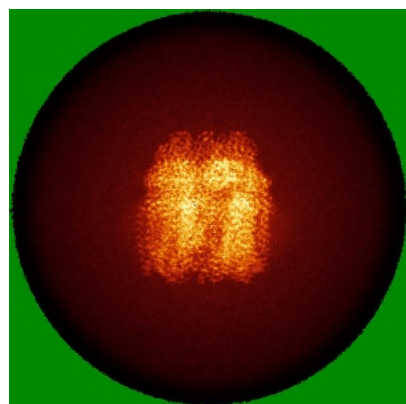


Z Index: 257

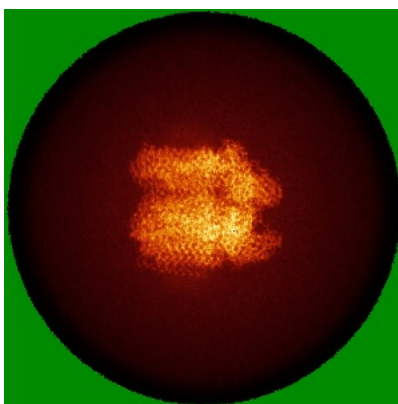
The images above show the largest variance slices of the map in three orthogonal directions.

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

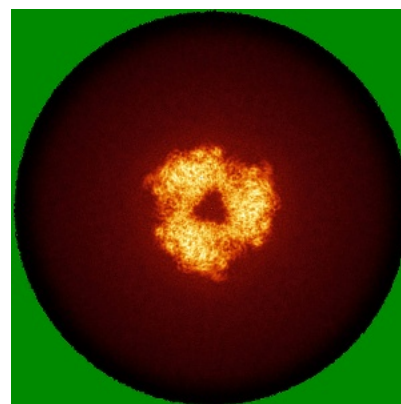
6.4.1 Primary map



X

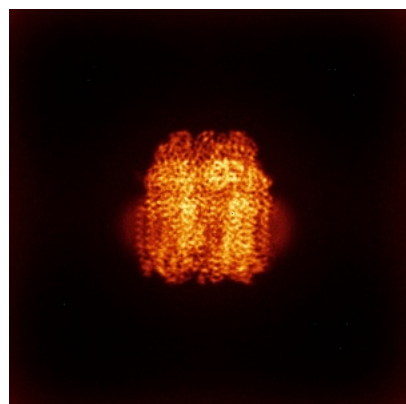


Y

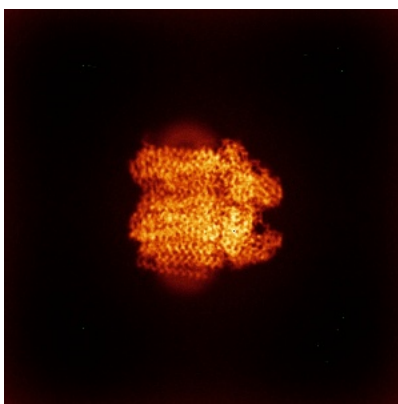


Z

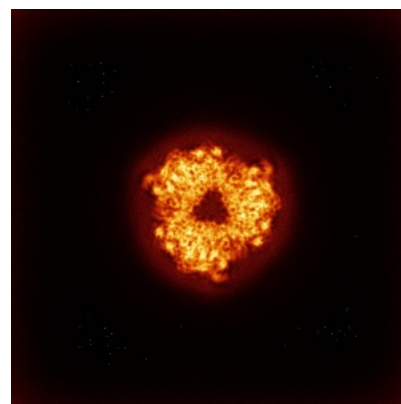
6.4.2 Raw map



X



Y

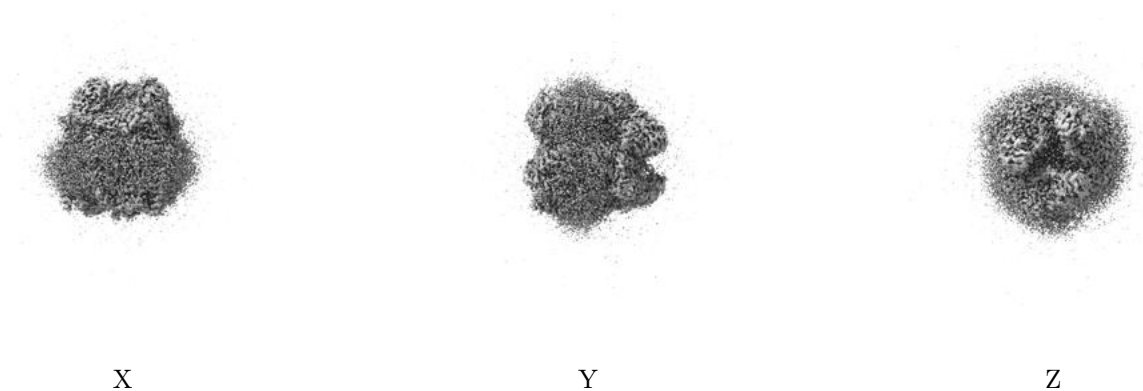


Z

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.

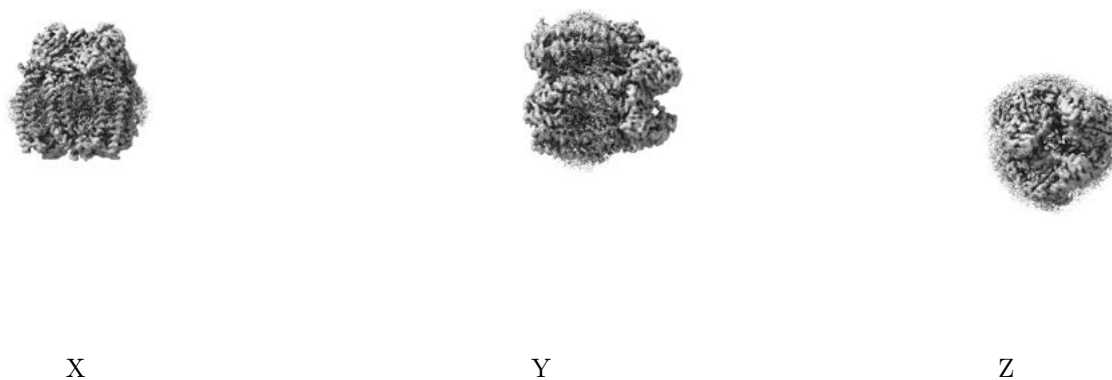
6.5 Orthogonal surface views [i](#)

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.

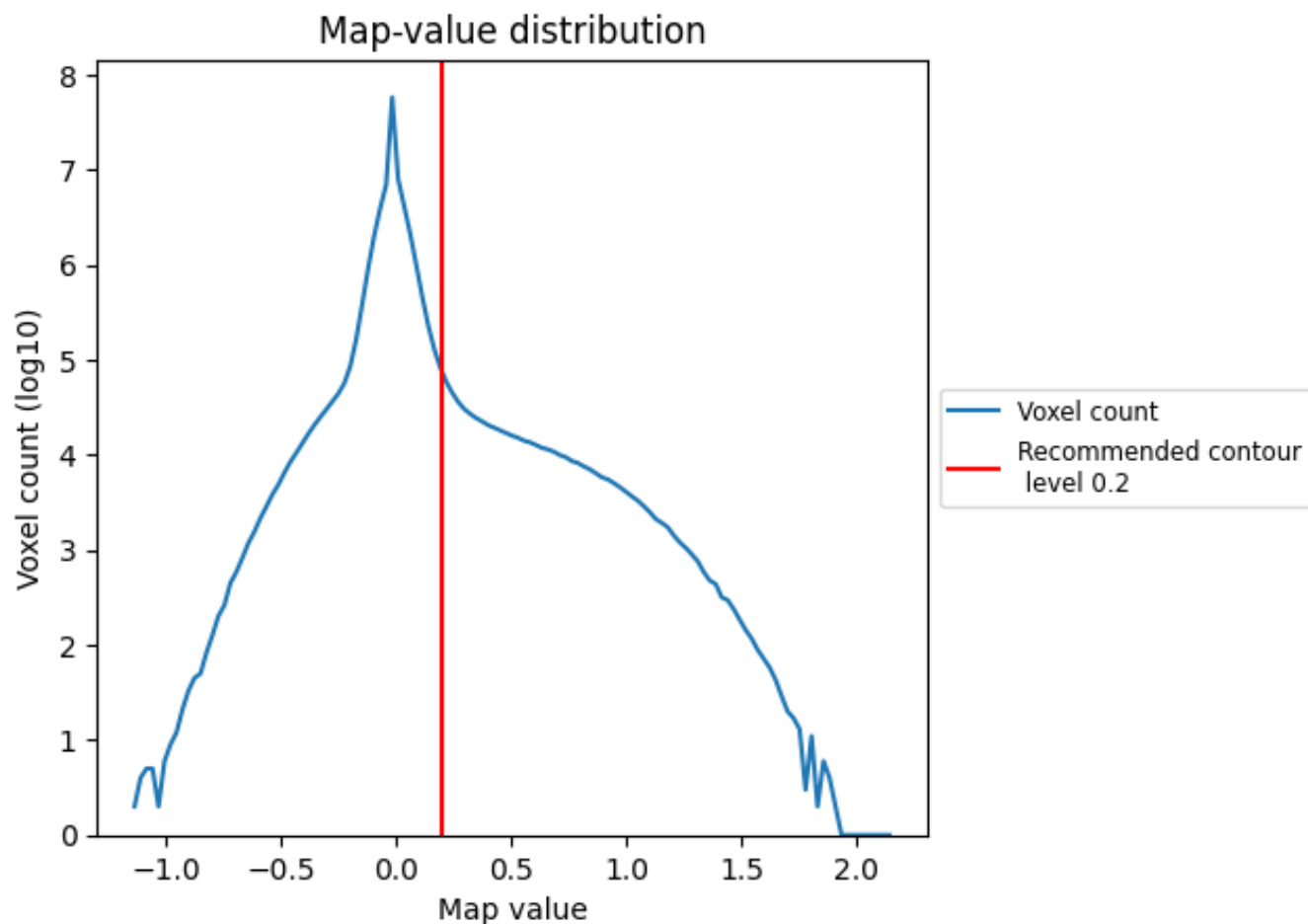
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

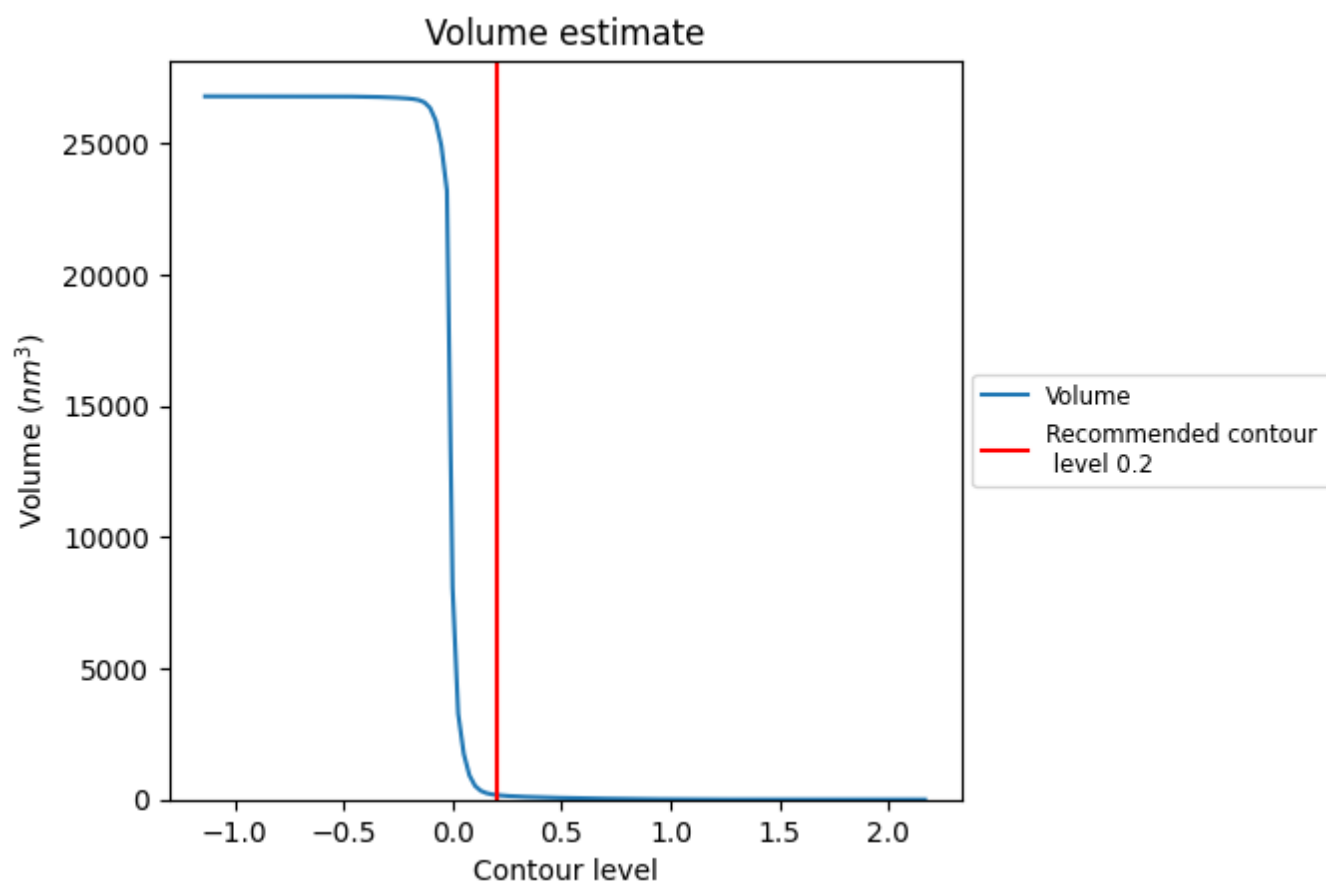
This section contains the results of statistical analysis of the map.

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.

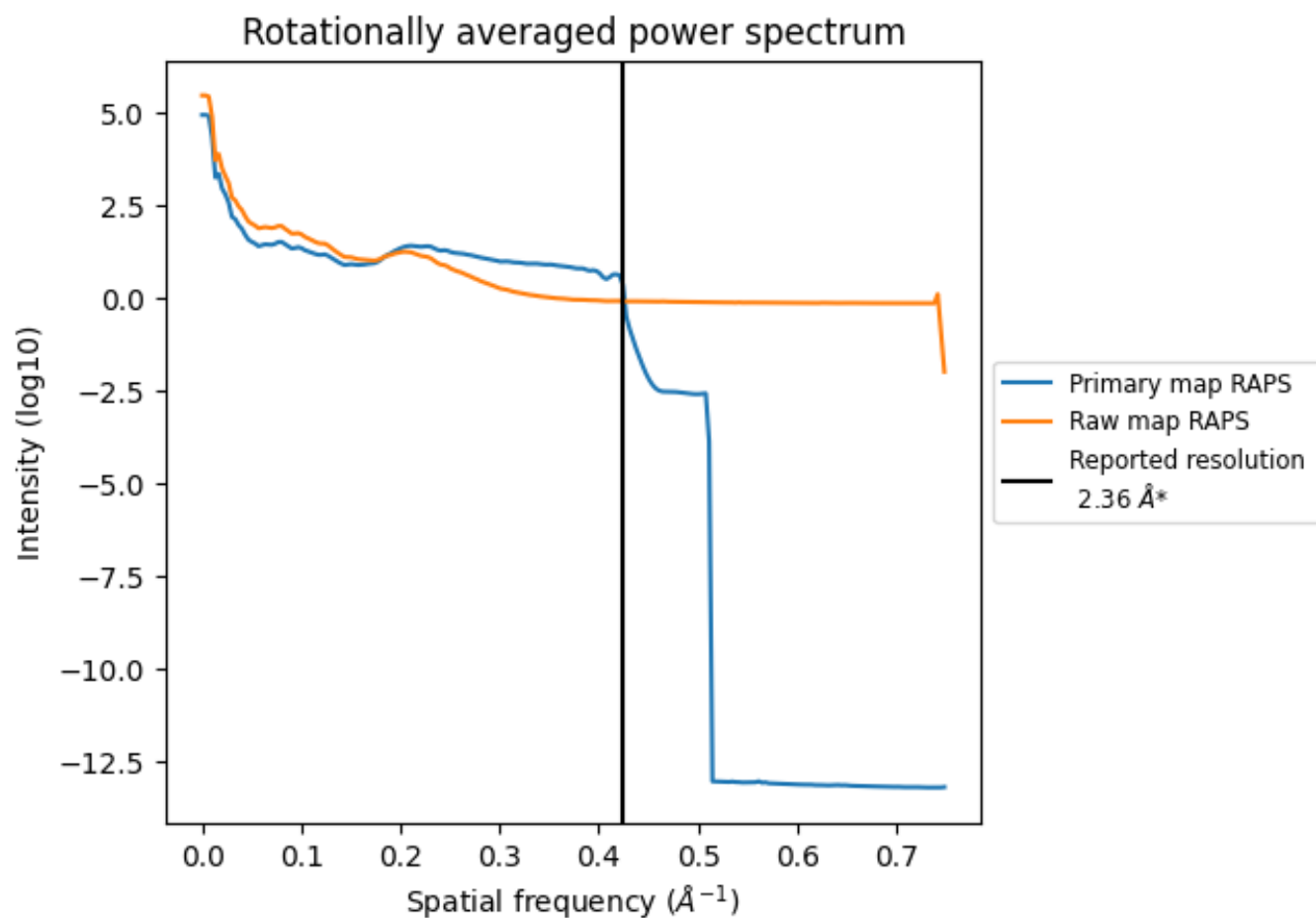
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 177 nm^3 ; this corresponds to an approximate mass of 160 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 ⓘ

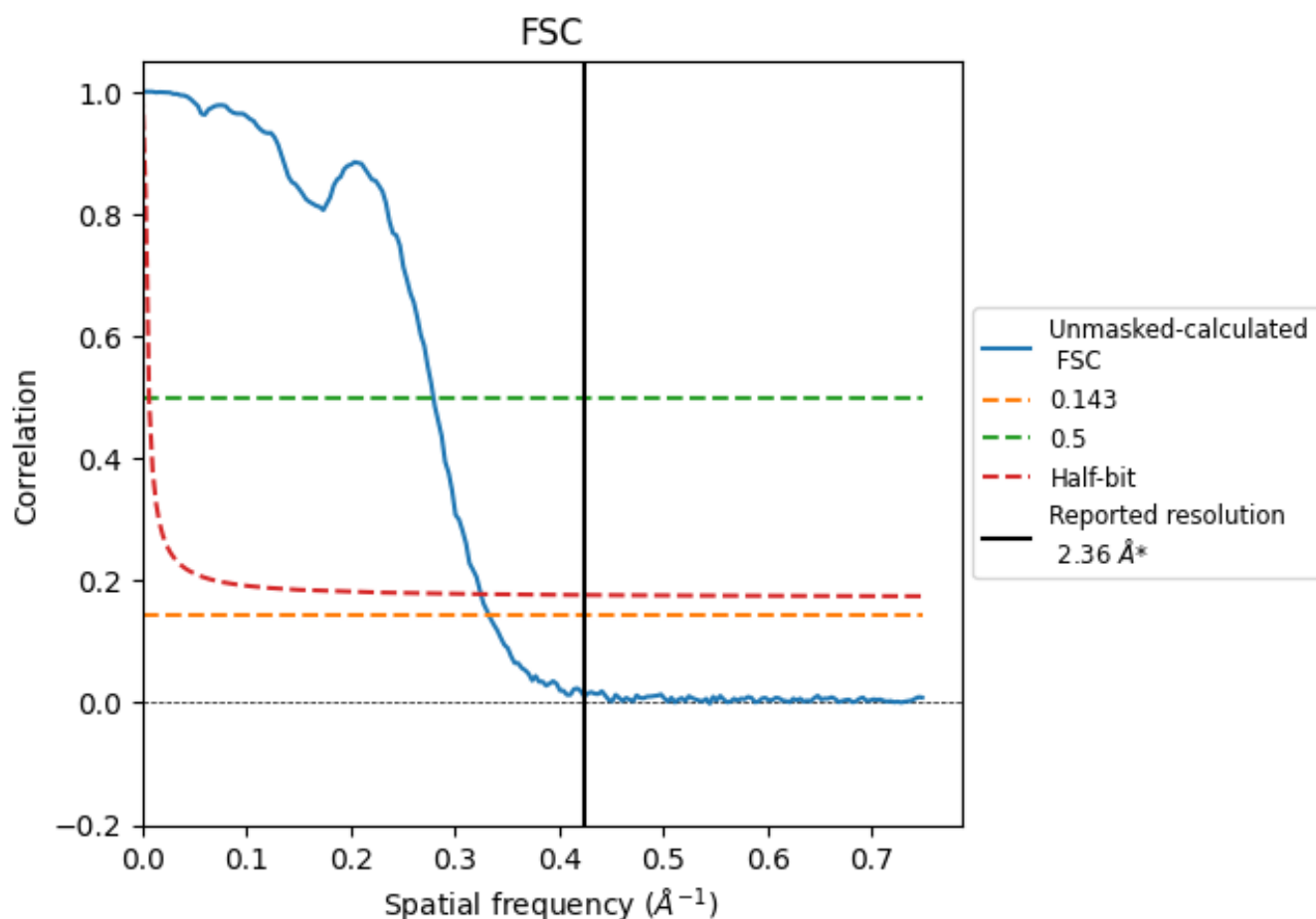


*Reported resolution corresponds to spatial frequency of 0.424 Å⁻¹

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 $0.424 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

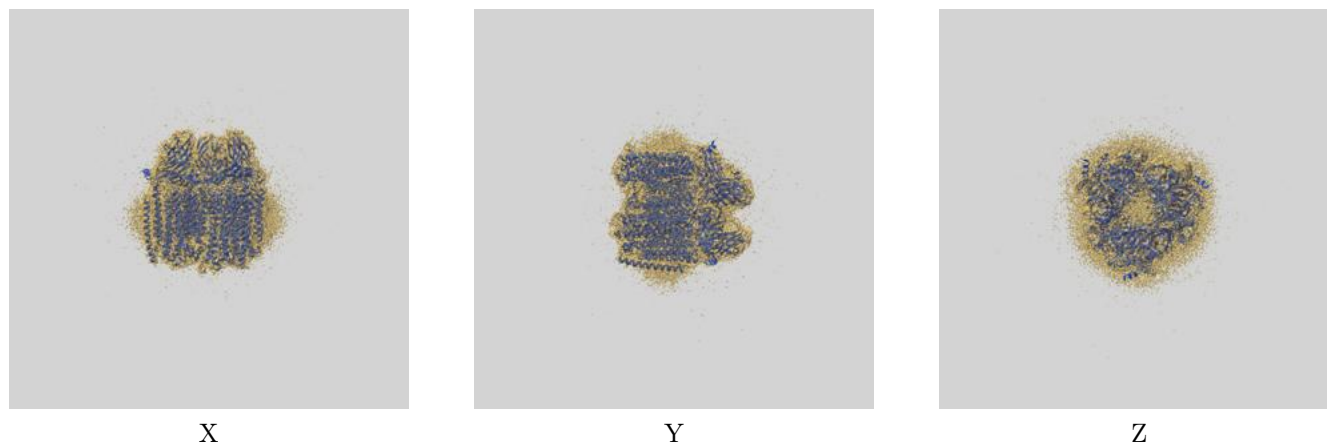
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.36	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.00	3.58	3.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.00 differs from the reported value 2.36 by more than 10 %

9 Map-model fit [i](#)

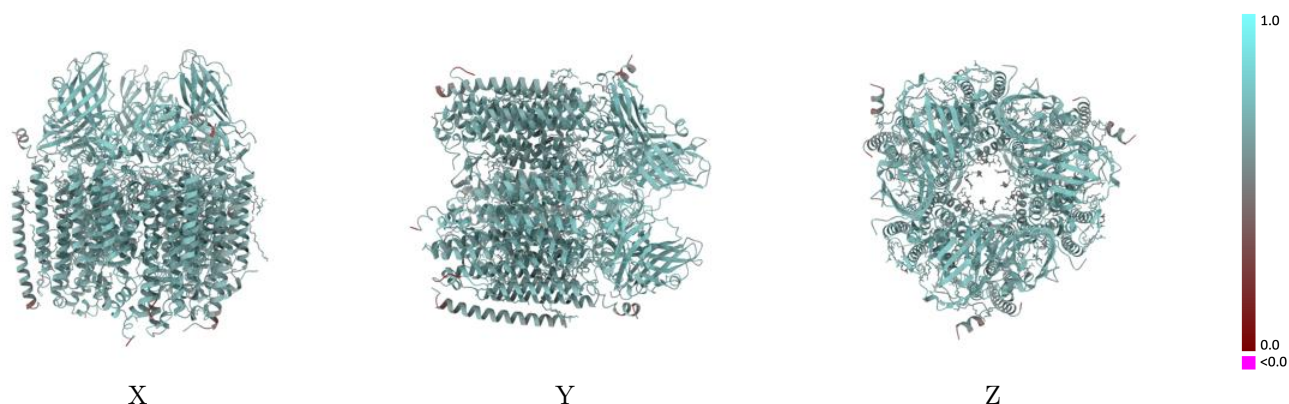
This section contains information regarding the fit between EMDB map EMD-63025 and PDB model 9LEG. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



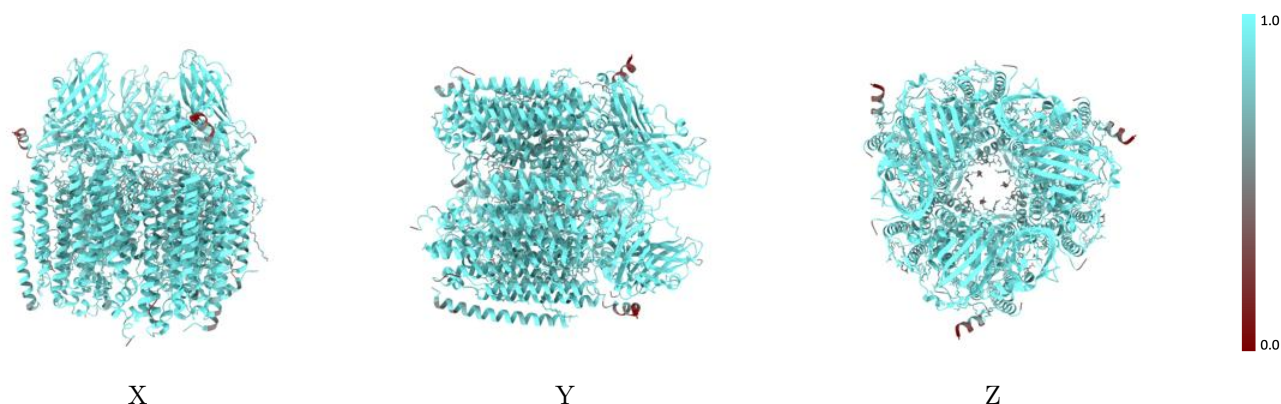
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



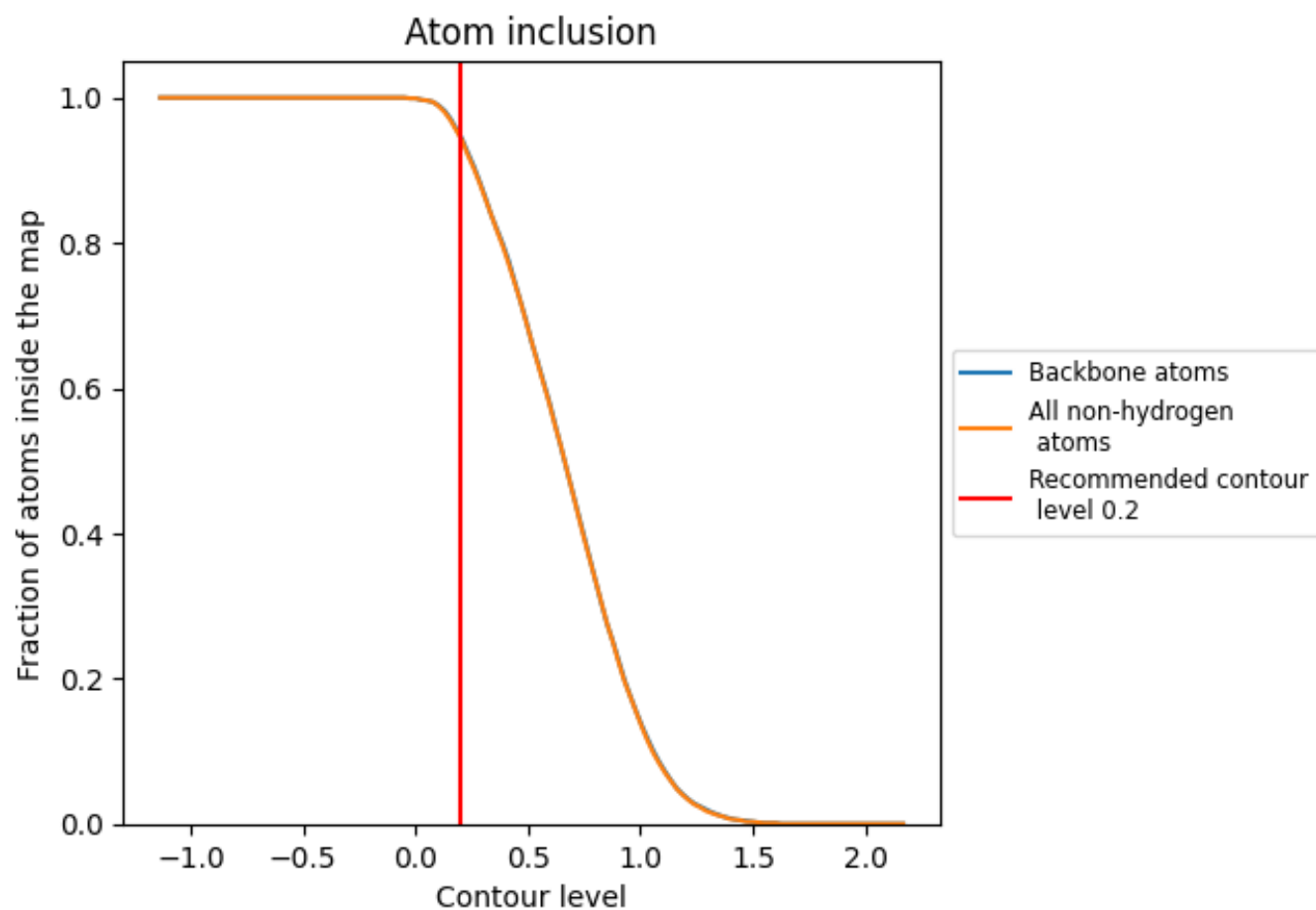
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 95% of all backbone atoms, 94% 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	0.9450	0.6590
A	0.9540	0.6760
B	0.9680	0.6710
C	0.9390	0.6440
D	0.5680	0.5350
E	0.8480	0.5530
L	0.9540	0.6750
M	0.9680	0.6710
N	0.9440	0.6470
O	0.5740	0.5350
P	0.8410	0.5520
U	0.9600	0.6790
V	0.9690	0.6710
W	0.9450	0.6480
X	0.5680	0.5410
Y	0.8410	0.5560

