



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 05:08 AM UTC

PDB ID : 6S7O / pdb_00006s7o
EMDB ID : EMD-10110
Title : Cryo-EM structure of human oligosaccharyltransferase complex OST-A
Authors : Ramirez, A.S.; Kowal, J.; Locher, K.P.
Deposited on : 2019-07-05
Resolution : 3.50 Å(reported)

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

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

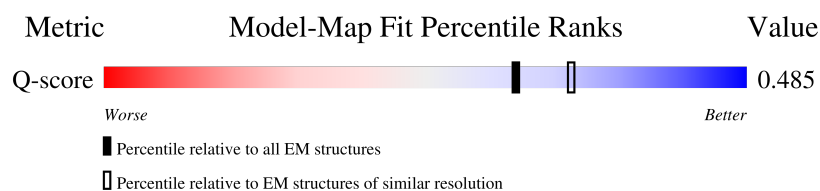
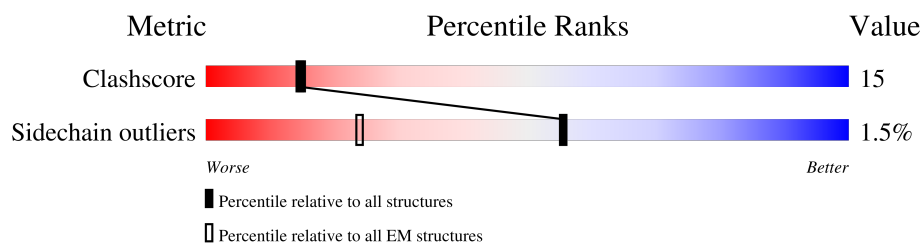
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



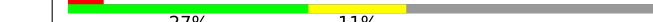
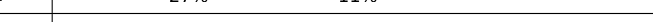
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	705	
2	B	37	
3	C	79	
4	D	113	
5	E	607	

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Mol	Chain	Length	Quality of chain
6	F	631	
7	G	456	
8	H	149	
9	I	3	
10	J	8	
11	K	8	

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 18118 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	656	Total	C	N	O	S	0	0
			5313	3484	856	937	36		

- Molecule 2 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	33	Total	C	N	O	S	0	0
			258	174	39	43	2		

- Molecule 3 is a protein called Transmembrane protein 258.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	78	Total	C	N	O	S	0	0
			634	435	91	105	3		

- Molecule 4 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	110	Total	C	N	O	S	0	0
			862	573	135	150	4		

- Molecule 5 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	560	Total	C	N	O	S	0	0
			4179	2671	712	789	7		

- Molecule 6 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	241	Total	C	N	O	S	0	0
			1919	1257	316	342	4		

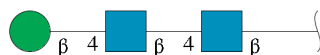
- Molecule 7 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	411	Total	C	N	O	S	0	0
			3238	2088	534	611	5		

- Molecule 8 is a protein called Oligosaccharyltransferase complex subunit OSTC.

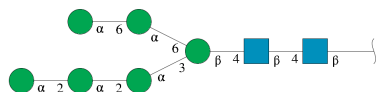
Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	108	Total	C	N	O	S	0	0
			845	570	130	138	7		

- Molecule 9 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	3	Total	C	N	O		0	0
			39	22	2	15			

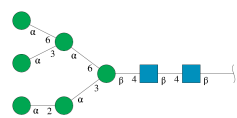
- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	8	Total	C	N	O		0	0
			94	52	2	40			

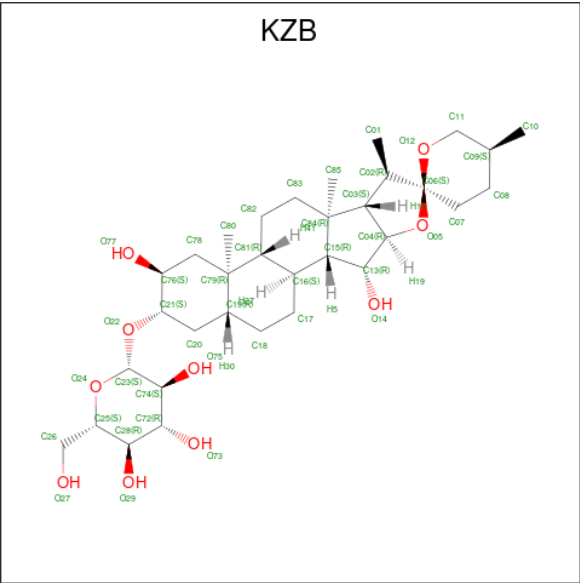
- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

ranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	8	Total	C	N	O	0	0
			94	52	2	40		

- Molecule 12 is (2 {S},3 {R},4 {R},5 {S},6 {S})-2-(hydroxymethyl)-6-[(1 {S},2 {R},3 {R},4 {R},5' {S},6 {S},7 {R},8 {S},9 {R},12 {R},13 {R},15 {S},16 {S},18 {R})-5',7,9,13-tetramethyl-3,15-bis(oxidanyl)spiro[5-oxapentacyclo[10.8.0.0^{2,9}.0^{4,8}.0^{13,18}]icosane-6,2'-oxane]-16-yl]oxy-oxane-3,4,5-triol (CCD ID: KZB) (formula: C₃₃H₅₄O₁₀).



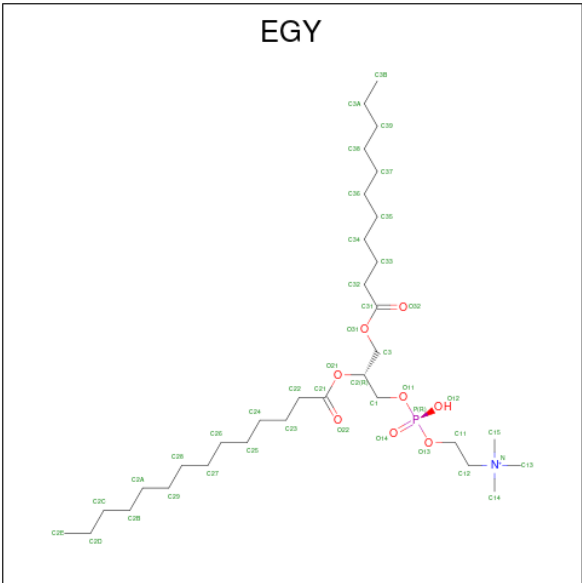
Mol	Chain	Residues	Atoms			AltConf
12	A	1	Total	C	O	0
			43	33	10	
12	A	1	Total	C	O	0
			43	33	10	
12	A	1	Total	C	O	0
			32	27	5	
12	E	1	Total	C	O	0
			32	27	5	
12	E	1	Total	C	O	0
			32	27	5	
12	F	1	Total	C	O	0
			32	27	5	

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Mol	Chain	Residues	Atoms			AltConf
12	F	1	Total	C	O	0
			32	27	5	
12	F	1	Total	C	O	0
			32	27	5	
12	G	1	Total	C	O	0
			32	27	5	

- Molecule 13 is (4R,7R)-4-hydroxy-N,N,N-trimethyl-4,9-dioxo-7-[(undecanoyloxy)methyl]-3,5,8-trioxa-4lambda 5 -phosphadocosan-1-aminium (CCD ID: EGY) (formula: C₃₃H₆₇NO₈P).

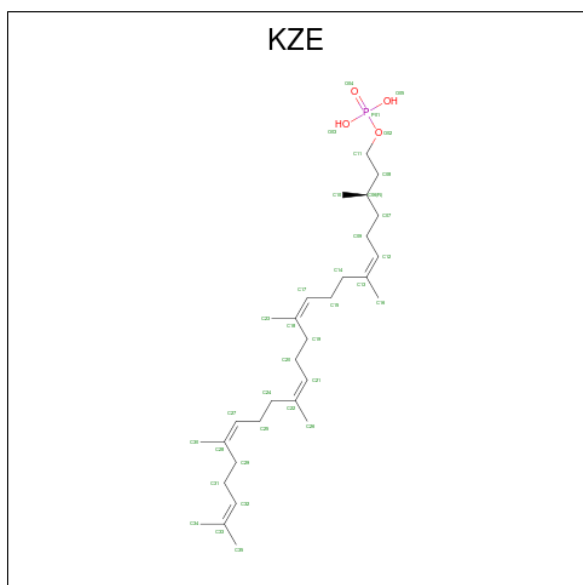


Mol	Chain	Residues	Atoms					AltConf
13	A	1	Total	C	N	O	P	0
			43	33	1	8	1	
13	A	1	Total	C	N	O	P	0
			43	33	1	8	1	
13	C	1	Total	C	N	O	P	0
			43	33	1	8	1	
13	C	1	Total	C	N	O	P	0
			43	33	1	8	1	
13	D	1	Total	C	N	O	P	0
			43	33	1	8	1	
13	E	1	Total	C	N	O	P	0
			43	33	1	8	1	
13	F	1	Total	C	N	O	P	0
			43	33	1	8	1	

- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
14	A	1	Total	Mg	0
			1	1	
14	E	1	Total	Mg	0
			1	1	

- Molecule 15 is [(3 {R},6 {Z},10 {Z},14 {Z},18 {Z})-3,7,11,15,19,23-hexamethyltetracos-6,10,14,18,22-pentaenyl] dihydrogen phosphate (CCD ID: KZE) (formula: C₃₀H₅₃O₄P).

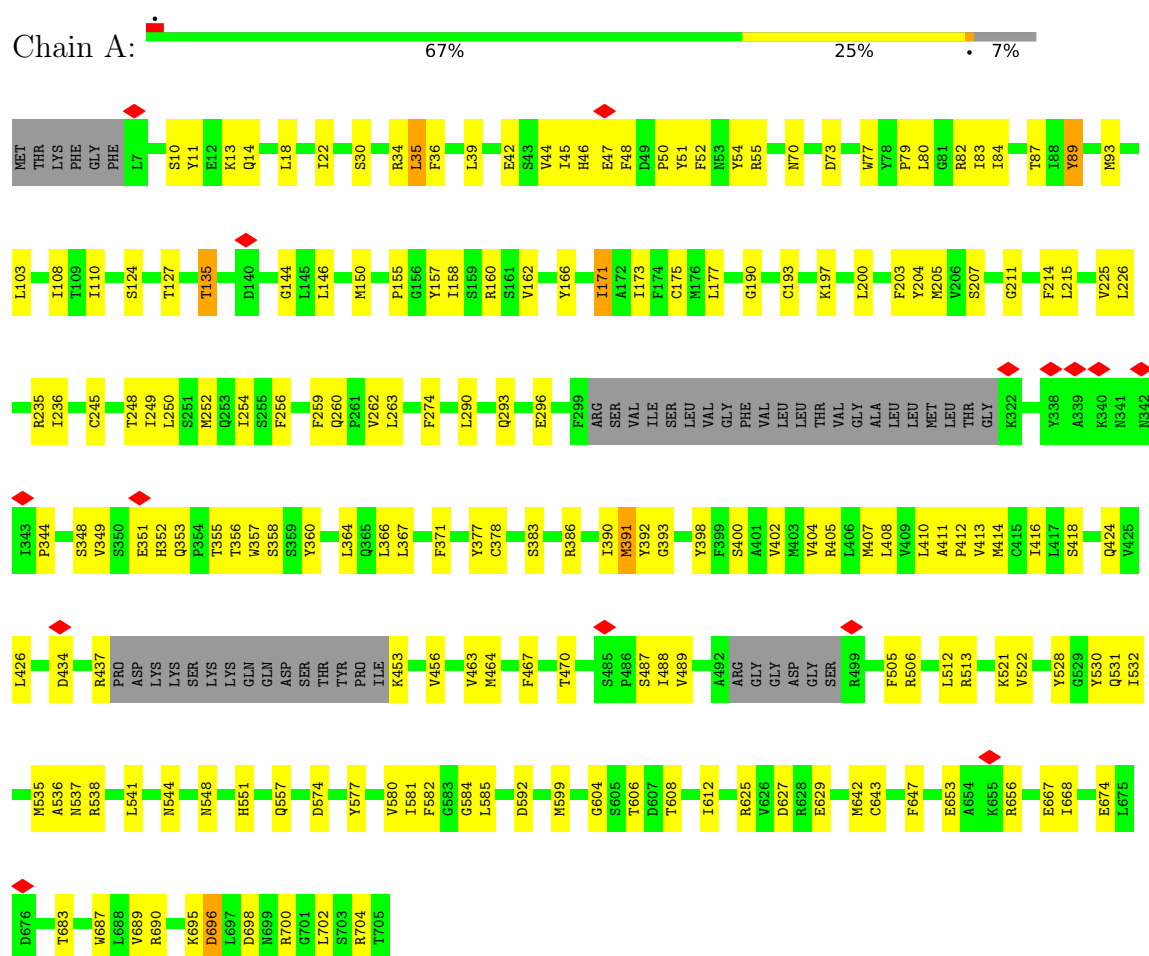


Mol	Chain	Residues	Atoms				AltConf
15	A	1	Total	C	O	P	0
			30	25	4	1	

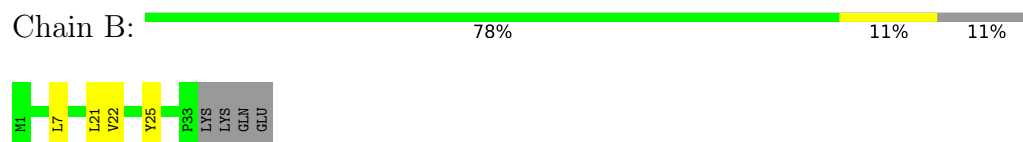
3 Residue-property plots

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.

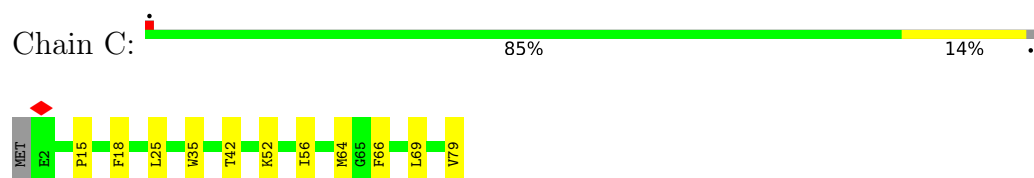
- Molecule 1: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A



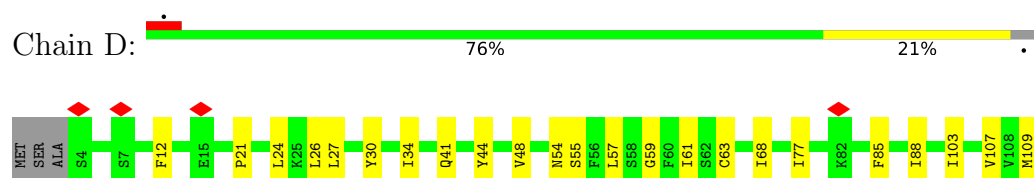
- Molecule 2: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4



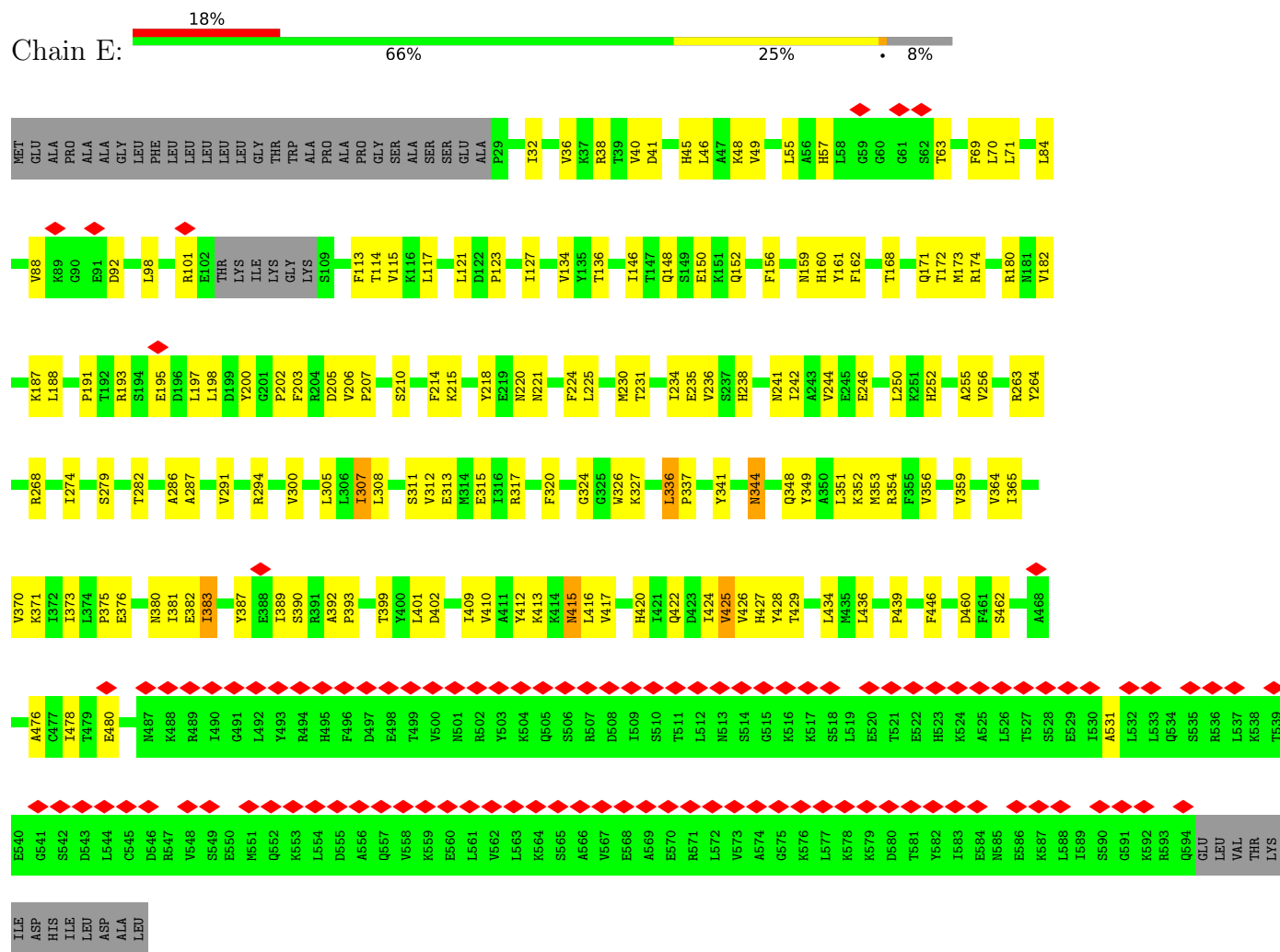
- Molecule 3: Transmembrane protein 258



- Molecule 4: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1

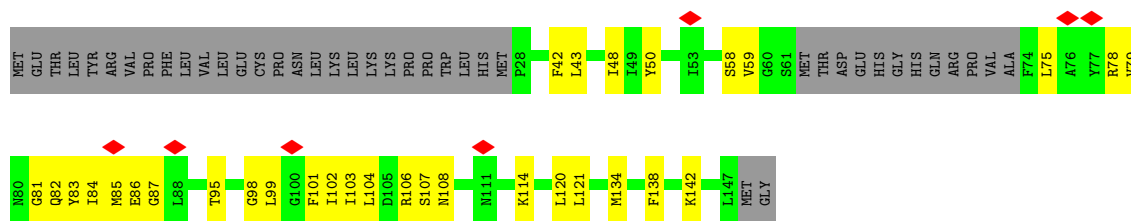


- Molecule 5: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1



- Molecule 6: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2





- Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 11: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	156950	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	68	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0106	Depositor
Map size (Å)	322.56, 322.56, 322.56	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KZE, MG, KZB, NAG, BMA, MAN, EGY

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	0.45	2/5461 (0.0%)	0.60	5/7416 (0.1%)
2	B	0.46	0/263	0.67	0/360
3	C	0.18	0/654	0.35	0/893
4	D	0.29	0/882	0.44	0/1197
5	E	0.35	0/4268	0.48	0/5827
6	F	0.28	0/1963	0.45	0/2668
7	G	0.21	0/3320	0.40	0/4509
8	H	0.30	0/866	0.49	0/1171
All	All	0.35	2/17677 (0.0%)	0.50	5/24041 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	89	TYR	C-N	19.56	1.50	1.33
1	A	260	GLN	C-N	13.01	1.51	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	TYR	CA-C-N	16.45	137.61	120.83
1	A	89	TYR	C-N-CA	16.45	137.61	120.83
1	A	260	GLN	CA-C-N	10.44	130.64	119.05
1	A	260	GLN	C-N-CA	10.44	130.64	119.05
1	A	259	PHE	O-C-N	6.75	130.36	122.19

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	5313	0	5255	206	0
2	B	258	0	272	14	0
3	C	634	0	647	8	0
4	D	862	0	880	30	0
5	E	4179	0	3875	142	0
6	F	1919	0	1962	63	0
7	G	3238	0	3179	96	0
8	H	845	0	880	34	0
9	I	39	0	34	1	0
10	J	94	0	79	0	0
11	K	94	0	79	4	0
12	A	118	0	0	1	0
12	E	64	0	0	0	0
12	F	96	0	0	0	0
12	G	32	0	0	0	0
13	A	86	0	0	0	0
13	C	86	0	0	0	0
13	D	43	0	0	1	0
13	E	43	0	0	2	0
13	F	43	0	0	0	0
14	A	1	0	0	0	0
14	E	1	0	0	0	0
15	A	30	0	0	2	0
All	All	18118	0	17142	533	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 15.

The worst 5 of 533 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:G:158:ASP:OD1	7:G:220:THR:HG22	1.46	1.15
1:A:39:LEU:HD12	2:B:7:LEU:HD22	1.31	1.12
1:A:39:LEU:HD11	2:B:7:LEU:HD13	1.18	1.11
5:E:88:VAL:HG12	5:E:92:ASP:HB3	1.33	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:TYR:CE2	1:A:413:VAL:HG22	1.91	1.06

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	A	574/615 (93%)	567 (99%)	7 (1%)	63	73
2	B	29/33 (88%)	29 (100%)	0	100	100
3	C	69/70 (99%)	69 (100%)	0	100	100
4	D	96/98 (98%)	95 (99%)	1 (1%)	68	75
5	E	407/537 (76%)	397 (98%)	10 (2%)	42	63
6	F	211/541 (39%)	210 (100%)	1 (0%)	81	80
7	G	357/390 (92%)	352 (99%)	5 (1%)	59	71
8	H	92/130 (71%)	89 (97%)	3 (3%)	33	58
All	All	1835/2414 (76%)	1808 (98%)	27 (2%)	55	71

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	415	ASN
5	E	434	LEU
8	H	59	VAL
5	E	426	VAL
6	F	401	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
7	G	415	HIS
8	H	108	ASN
5	E	45	HIS
4	D	81	ASN
8	H	111	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

19 monosaccharides 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	$\# Z > 2$
9	NAG	I	1	9	14,14,15	0.74	1 (7%)	17,19,21	0.54	0
9	NAG	I	2	9	14,14,15	0.33	0	17,19,21	0.38	0
9	BMA	I	3	9	11,11,12	0.54	0	15,15,17	0.72	0
10	NAG	J	1	1,10	14,14,15	0.24	0	17,19,21	0.41	0
10	NAG	J	2	10	14,14,15	0.25	0	17,19,21	0.43	0
10	BMA	J	3	10	11,11,12	0.76	1 (9%)	15,15,17	0.69	0
10	MAN	J	4	10	11,11,12	0.67	0	15,15,17	1.03	2 (13%)
10	MAN	J	5	10	11,11,12	0.69	1 (9%)	15,15,17	0.96	2 (13%)
10	MAN	J	6	10	11,11,12	0.65	0	15,15,17	0.96	2 (13%)
10	MAN	J	7	10	11,11,12	0.73	0	15,15,17	1.25	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	MAN	J	8	10	11,11,12	0.74	0	15,15,17	1.15	2 (13%)
11	NAG	K	1	11,5	14,14,15	0.25	0	17,19,21	0.47	0
11	NAG	K	2	11	14,14,15	0.28	0	17,19,21	0.43	0
11	BMA	K	3	11	11,11,12	0.51	0	15,15,17	0.77	0
11	MAN	K	4	11	11,11,12	0.68	0	15,15,17	0.96	2 (13%)
11	MAN	K	5	11	11,11,12	0.68	0	15,15,17	0.94	2 (13%)
11	MAN	K	6	11	11,11,12	0.74	1 (9%)	15,15,17	1.07	2 (13%)
11	MAN	K	7	11	11,11,12	0.64	0	15,15,17	0.99	2 (13%)
11	MAN	K	8	11	11,11,12	0.62	0	15,15,17	0.98	2 (13%)

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
9	NAG	I	1	9	-	2/6/23/26	0/1/1/1
9	NAG	I	2	9	-	0/6/23/26	0/1/1/1
9	BMA	I	3	9	-	2/2/19/22	0/1/1/1
10	NAG	J	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	J	2	10	-	0/6/23/26	0/1/1/1
10	BMA	J	3	10	-	0/2/19/22	0/1/1/1
10	MAN	J	4	10	-	2/2/19/22	0/1/1/1
10	MAN	J	5	10	-	2/2/19/22	0/1/1/1
10	MAN	J	6	10	-	0/2/19/22	0/1/1/1
10	MAN	J	7	10	-	2/2/19/22	1/1/1/1
10	MAN	J	8	10	-	1/2/19/22	1/1/1/1
11	NAG	K	1	11,5	-	2/6/23/26	0/1/1/1
11	NAG	K	2	11	-	2/6/23/26	0/1/1/1
11	BMA	K	3	11	-	1/2/19/22	0/1/1/1
11	MAN	K	4	11	-	0/2/19/22	0/1/1/1
11	MAN	K	5	11	-	0/2/19/22	0/1/1/1
11	MAN	K	6	11	-	2/2/19/22	0/1/1/1
11	MAN	K	7	11	-	2/2/19/22	0/1/1/1
11	MAN	K	8	11	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	1	NAG	O5-C1	-2.45	1.39	1.43
10	J	3	BMA	O5-C1	-2.13	1.40	1.43
11	K	6	MAN	O5-C1	-2.13	1.40	1.43
10	J	5	MAN	O5-C1	-2.03	1.40	1.43

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	7	MAN	C1-O5-C5	3.63	117.05	112.19
10	J	8	MAN	C1-O5-C5	3.38	116.71	112.19
11	K	6	MAN	C1-O5-C5	2.79	115.93	112.19
10	J	4	MAN	C1-O5-C5	2.58	115.65	112.19
11	K	6	MAN	O2-C2-C3	-2.56	104.84	110.15

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	J	5	MAN	O5-C5-C6-O6
11	K	2	NAG	O5-C5-C6-O6
11	K	6	MAN	O5-C5-C6-O6
10	J	7	MAN	C4-C5-C6-O6
10	J	5	MAN	C4-C5-C6-O6

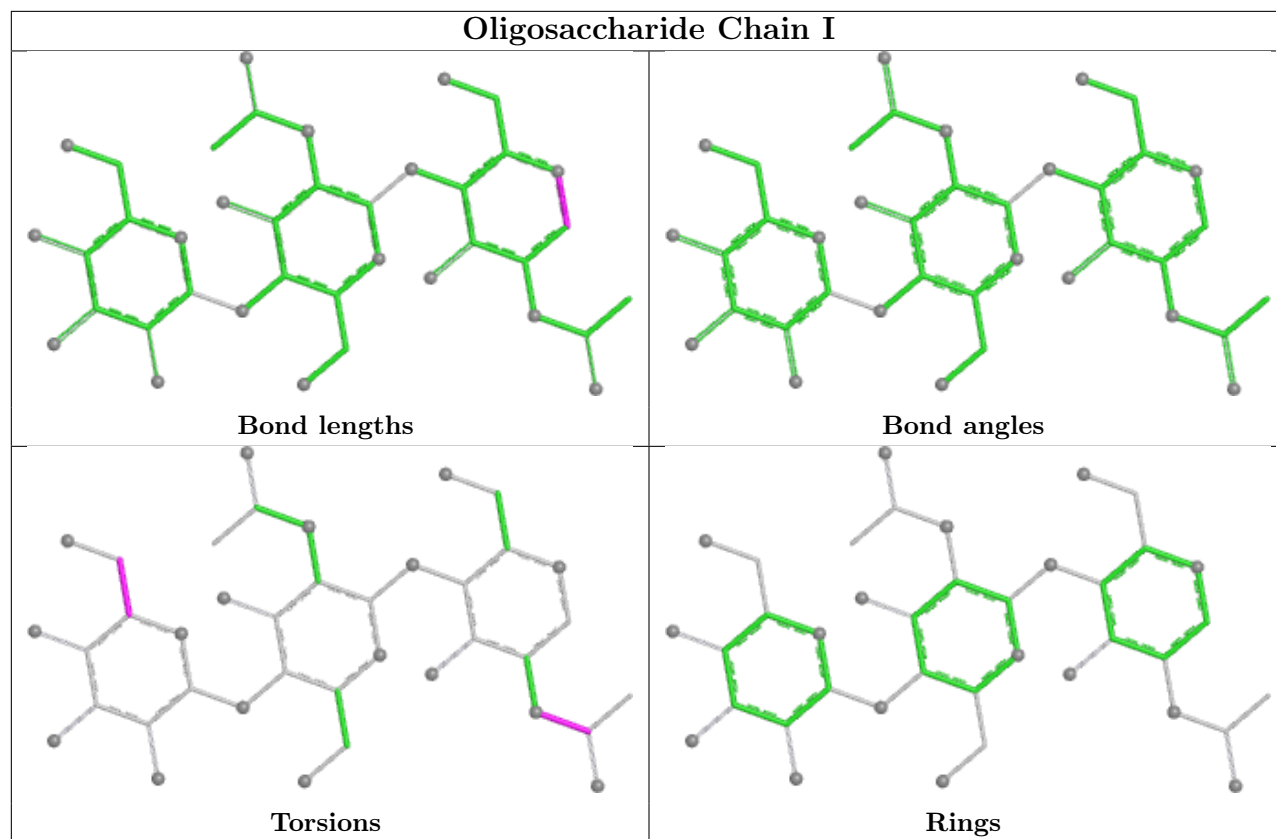
All (2) ring outliers are listed below:

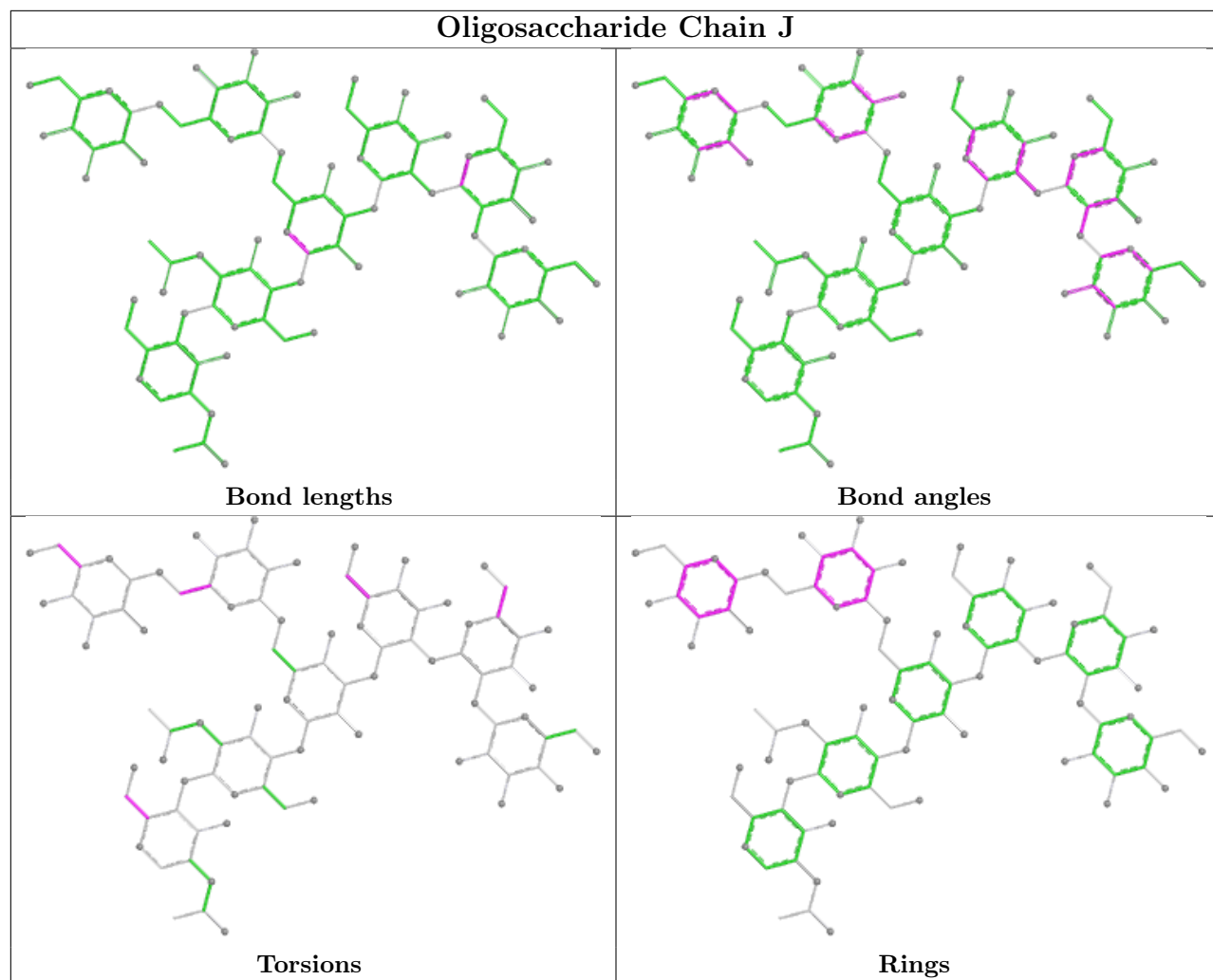
Mol	Chain	Res	Type	Atoms
10	J	8	MAN	C1-C2-C3-C4-C5-O5
10	J	7	MAN	C1-C2-C3-C4-C5-O5

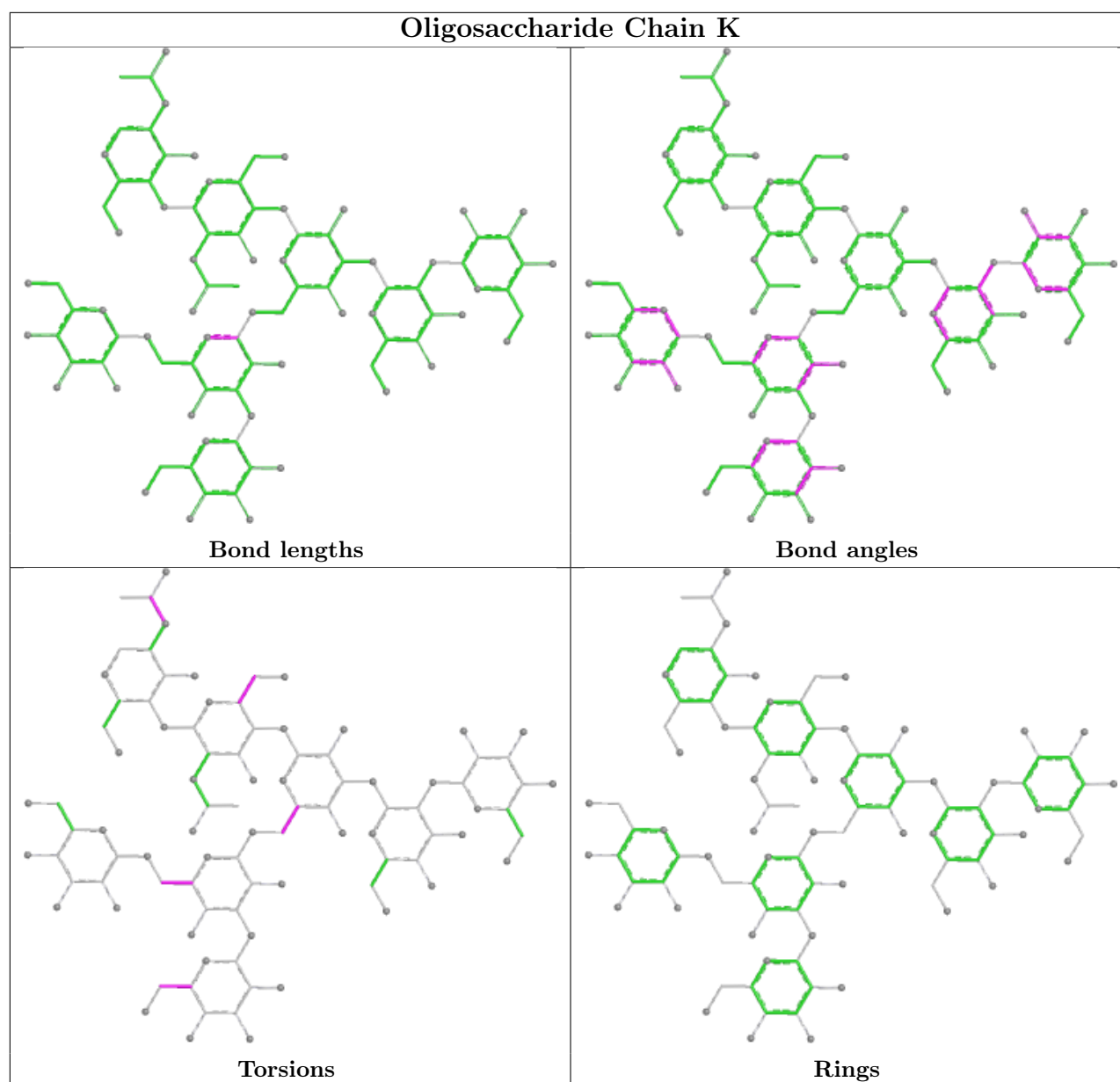
4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	K	1	NAG	1	0
11	K	2	NAG	2	0
9	I	1	NAG	1	0
11	K	7	MAN	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 oligosaccharide.







5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	KZB	E	709	-	37,37,49	0.73	1 (2%)	58,62,80	1.97	14 (24%)
12	KZB	A	813	-	49,49,49	0.63	1 (2%)	75,80,80	1.76	12 (16%)
12	KZB	F	703	-	37,37,49	0.73	1 (2%)	58,62,80	1.94	12 (20%)
13	EGY	C	101	13	42,42,42	1.38	6 (14%)	48,50,50	1.13	2 (4%)
12	KZB	A	812	-	49,49,49	0.72	1 (2%)	75,80,80	1.96	15 (20%)
13	EGY	F	704	-	42,42,42	1.39	7 (16%)	48,50,50	1.19	2 (4%)
15	KZE	A	818	-	29,29,34	1.60	5 (17%)	34,36,42	1.52	8 (23%)
12	KZB	G	501	-	37,37,49	0.72	1 (2%)	58,62,80	1.90	11 (18%)
12	KZB	A	814	-	37,37,49	0.76	1 (2%)	58,62,80	2.03	13 (22%)
12	KZB	F	702	-	37,37,49	0.64	0	58,62,80	1.85	12 (20%)
13	EGY	A	815	13	42,42,42	1.37	6 (14%)	48,50,50	1.11	2 (4%)
13	EGY	C	102	-	42,42,42	1.38	6 (14%)	48,50,50	1.09	2 (4%)
13	EGY	D	701	-	42,42,42	1.38	5 (11%)	48,50,50	1.33	4 (8%)
13	EGY	E	711	-	42,42,42	1.36	6 (14%)	48,50,50	1.10	2 (4%)
13	EGY	A	816	-	42,42,42	1.37	6 (14%)	48,50,50	1.11	2 (4%)
12	KZB	F	701	-	37,37,49	0.71	1 (2%)	58,62,80	1.95	14 (24%)
12	KZB	E	710	-	37,37,49	0.80	1 (2%)	58,62,80	2.14	16 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	KZB	E	709	-	-	-	0/6/6/7
12	KZB	A	813	-	-	3/6/121/121	0/7/7/7
13	EGY	C	101	13	-	24/46/46/46	-
13	EGY	F	704	-	-	20/46/46/46	-
12	KZB	A	812	-	-	5/6/121/121	0/7/7/7
12	KZB	F	701	-	-	-	0/6/6/7
15	KZE	A	818	-	-	10/31/31/37	-
12	KZB	F	703	-	-	-	0/6/6/7
12	KZB	A	814	-	-	-	0/6/6/7
12	KZB	G	501	-	-	-	0/6/6/7
12	KZB	F	702	-	-	-	0/6/6/7
13	EGY	A	815	13	-	22/46/46/46	-
13	EGY	D	701	-	-	16/46/46/46	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	EGY	E	711	-	-	17/46/46/46	-
13	EGY	A	816	-	-	18/46/46/46	-
12	KZB	E	710	-	-	-	0/6/6/7
13	EGY	C	102	-	-	25/46/46/46	-

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	A	818	KZE	P01-O04	4.67	1.65	1.50
13	F	704	EGY	O21-C21	3.57	1.44	1.34
13	C	102	EGY	O21-C21	3.56	1.44	1.34
13	E	711	EGY	O21-C21	3.51	1.44	1.34
13	A	815	EGY	O21-C21	3.48	1.44	1.34

The worst 5 of 143 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	813	KZB	O05-C04-C13	9.14	128.71	110.20
12	F	701	KZB	O05-C04-C13	8.74	127.90	110.20
12	A	812	KZB	O05-C04-C13	8.72	127.86	110.20
12	E	710	KZB	O05-C04-C13	8.70	127.81	110.20
12	E	709	KZB	O05-C04-C13	8.68	127.76	110.20

There are no chirality outliers.

5 of 160 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	A	816	EGY	O13-C11-C12-N
13	C	101	EGY	C11-O13-P-O12
13	C	101	EGY	C11-O13-P-O11
13	C	101	EGY	C1-O11-P-O12
13	C	101	EGY	C1-O11-P-O14

There are no ring outliers.

4 monomers are involved in 6 short contacts:

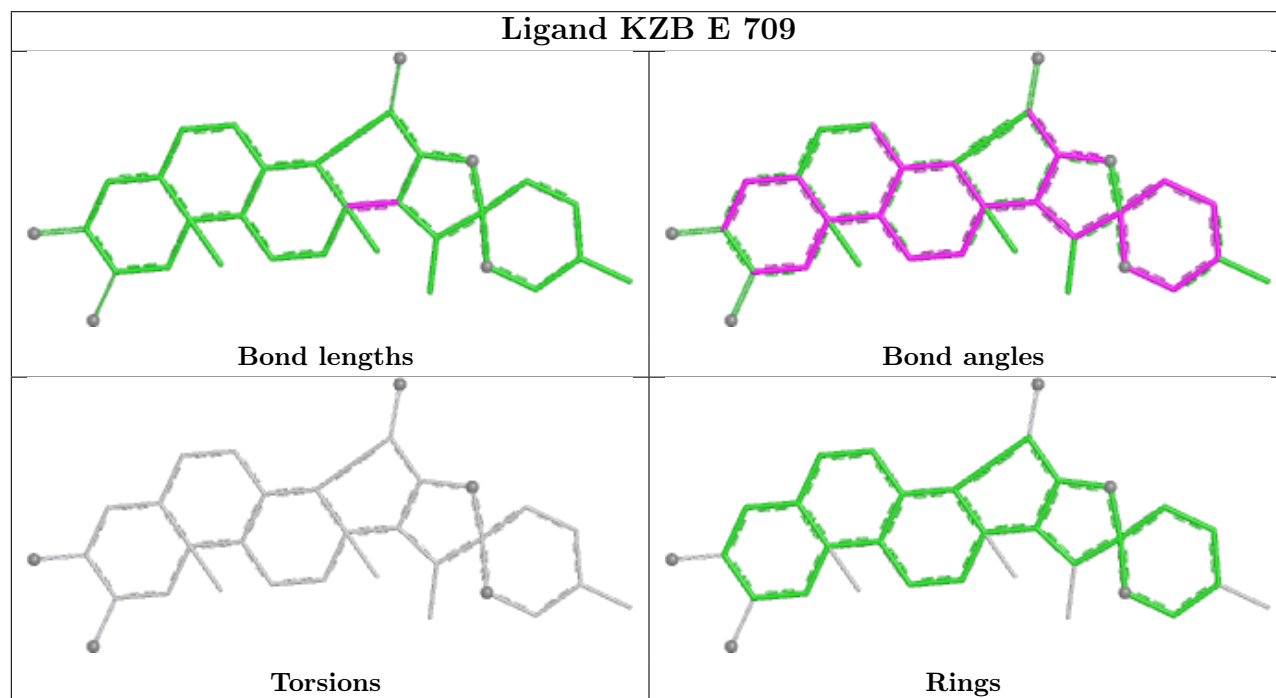
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	812	KZB	1	0
15	A	818	KZE	2	0
13	D	701	EGY	1	0

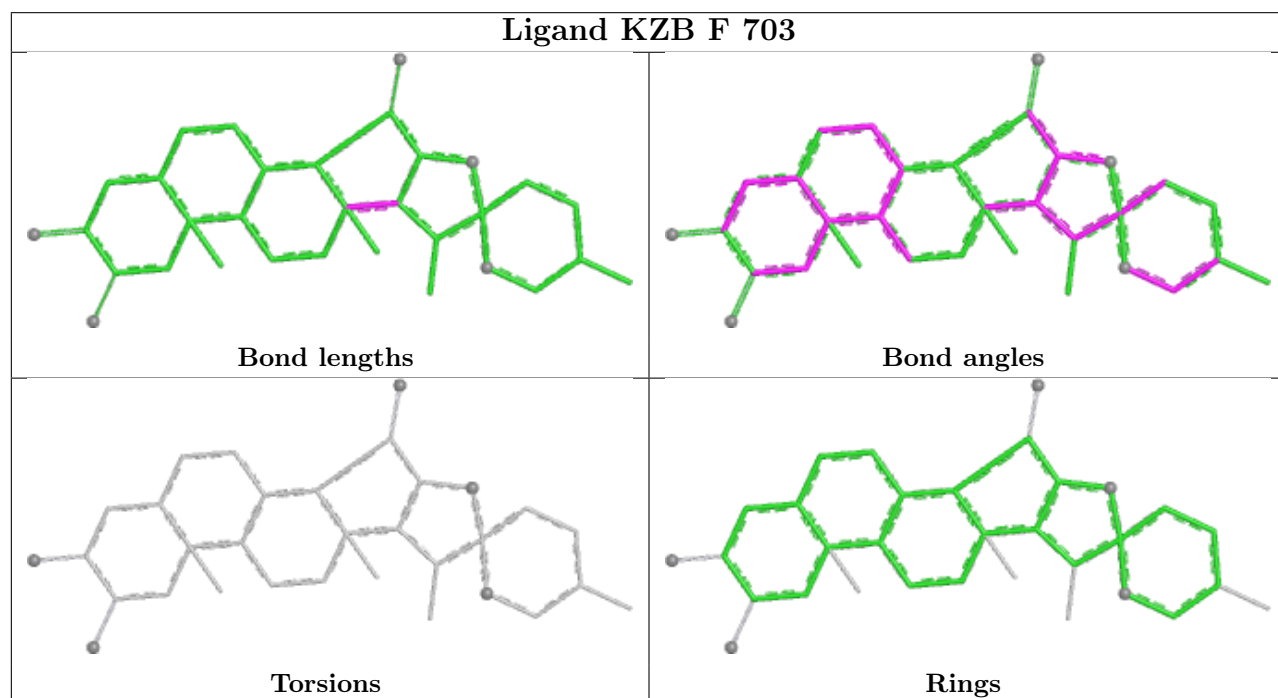
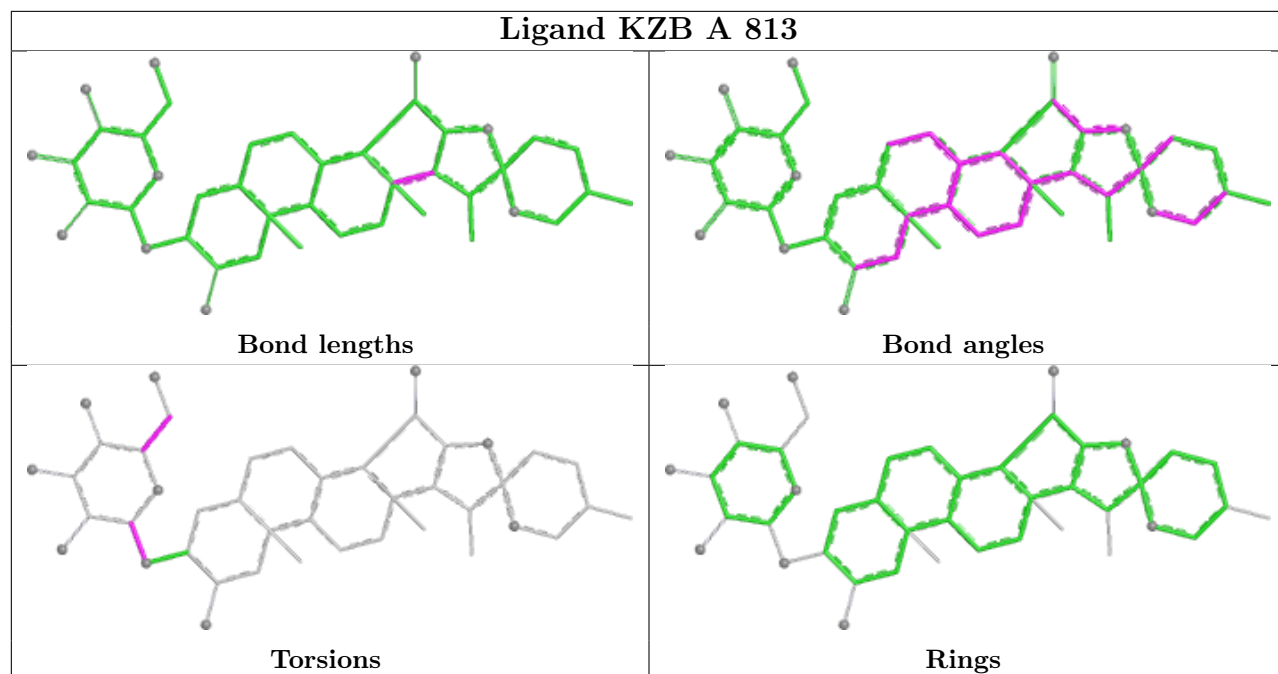
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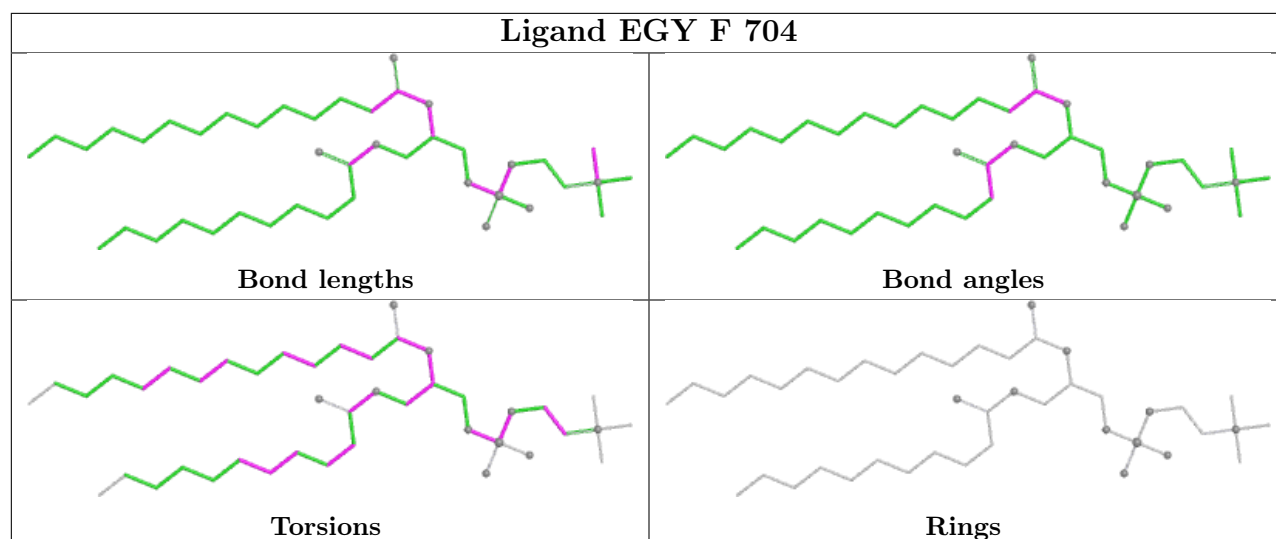
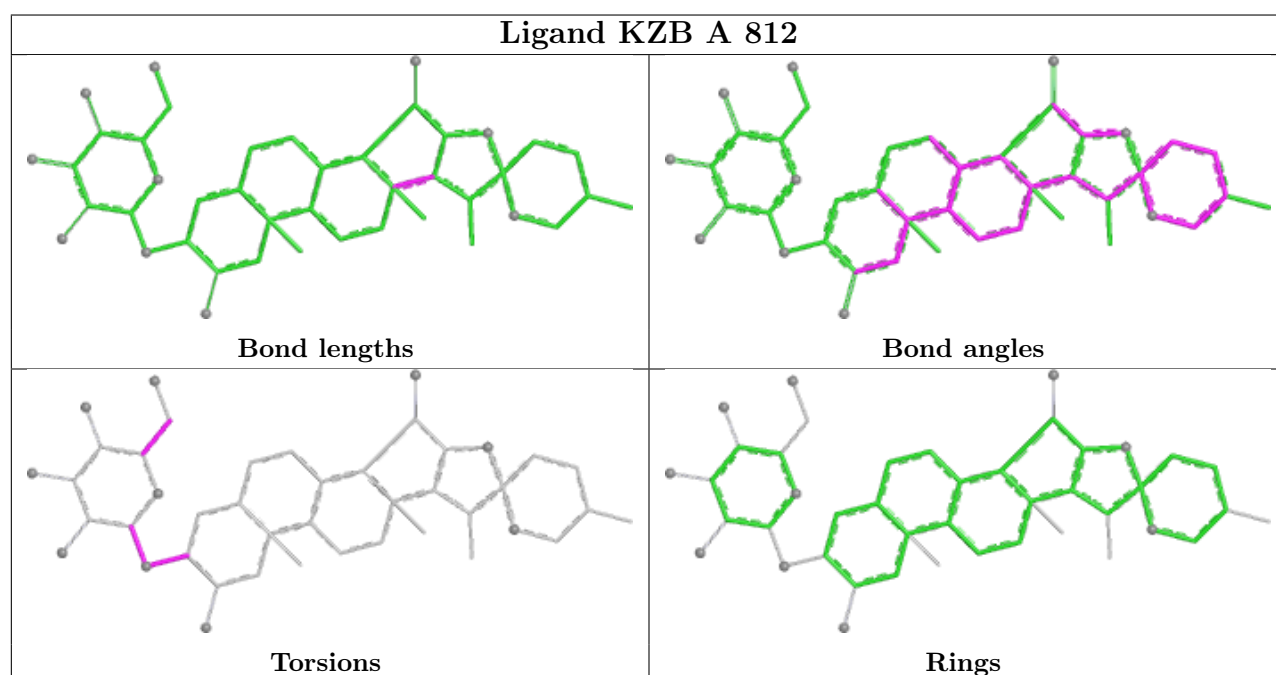
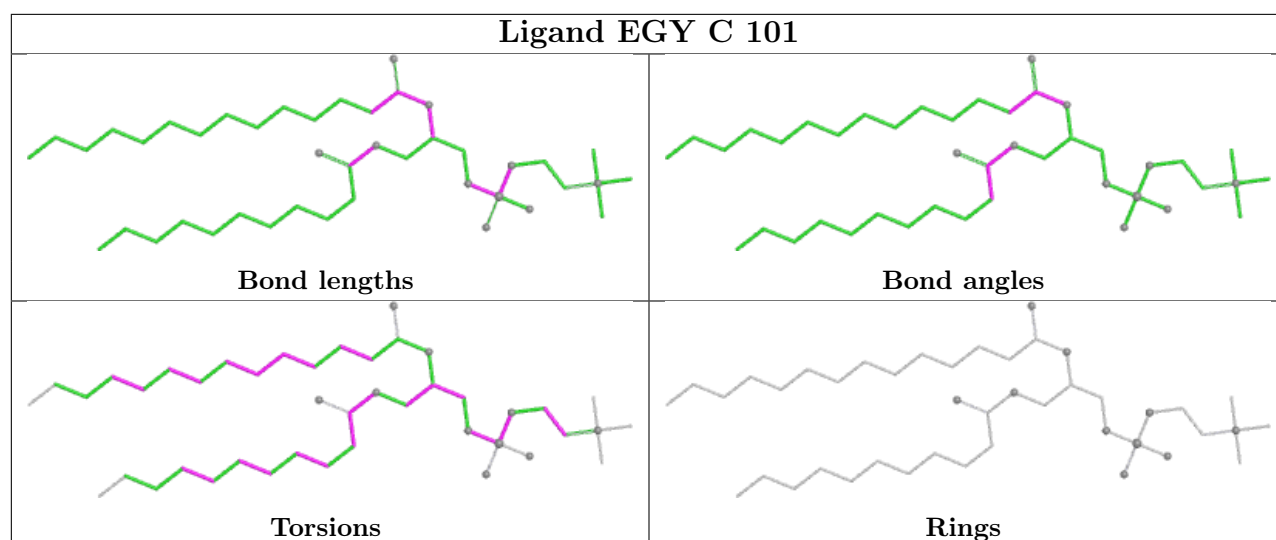
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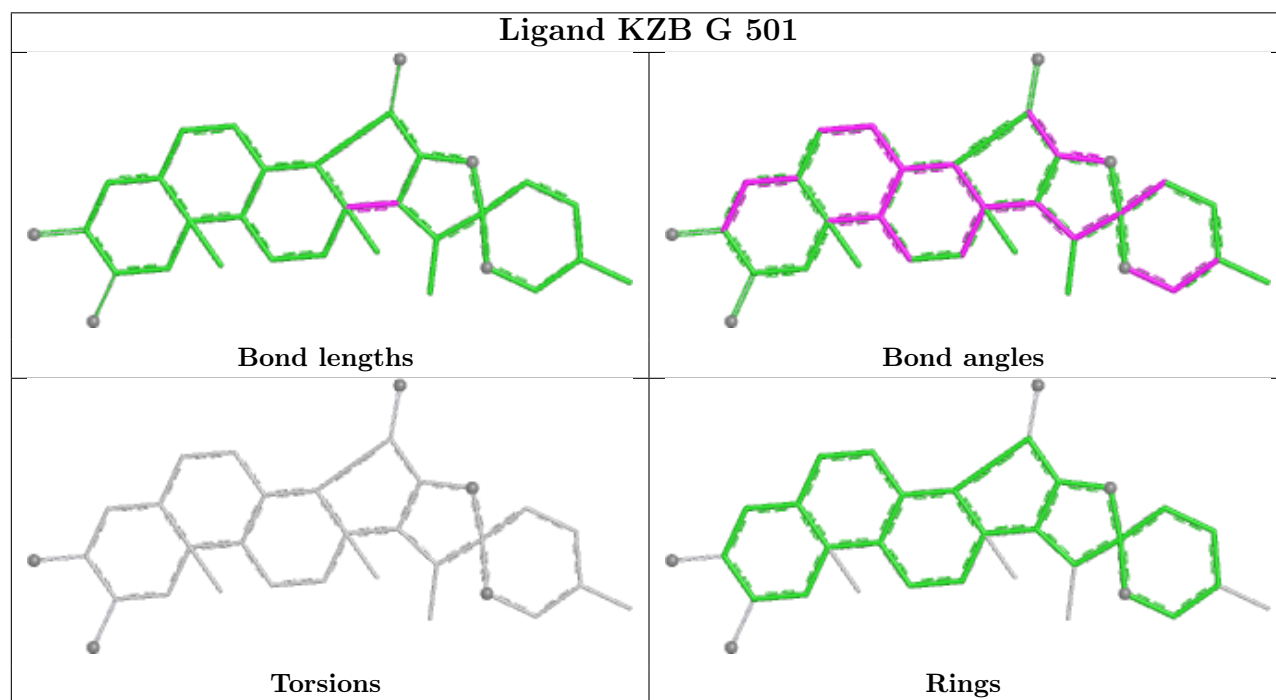
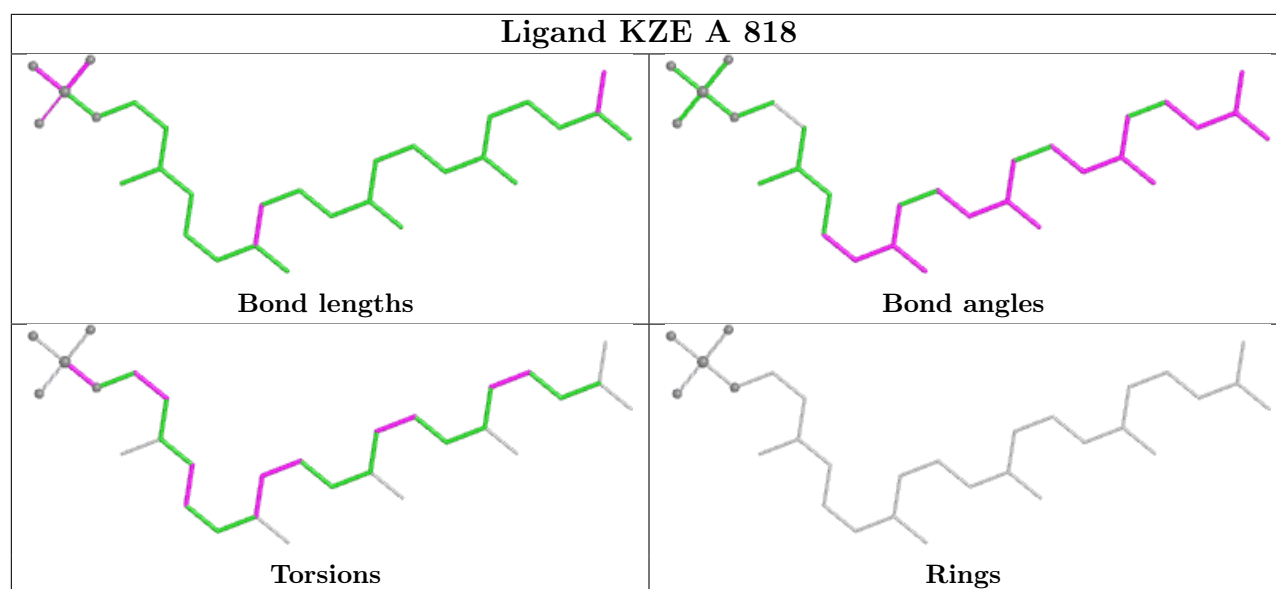
Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	E	711	EGY	2	0

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.

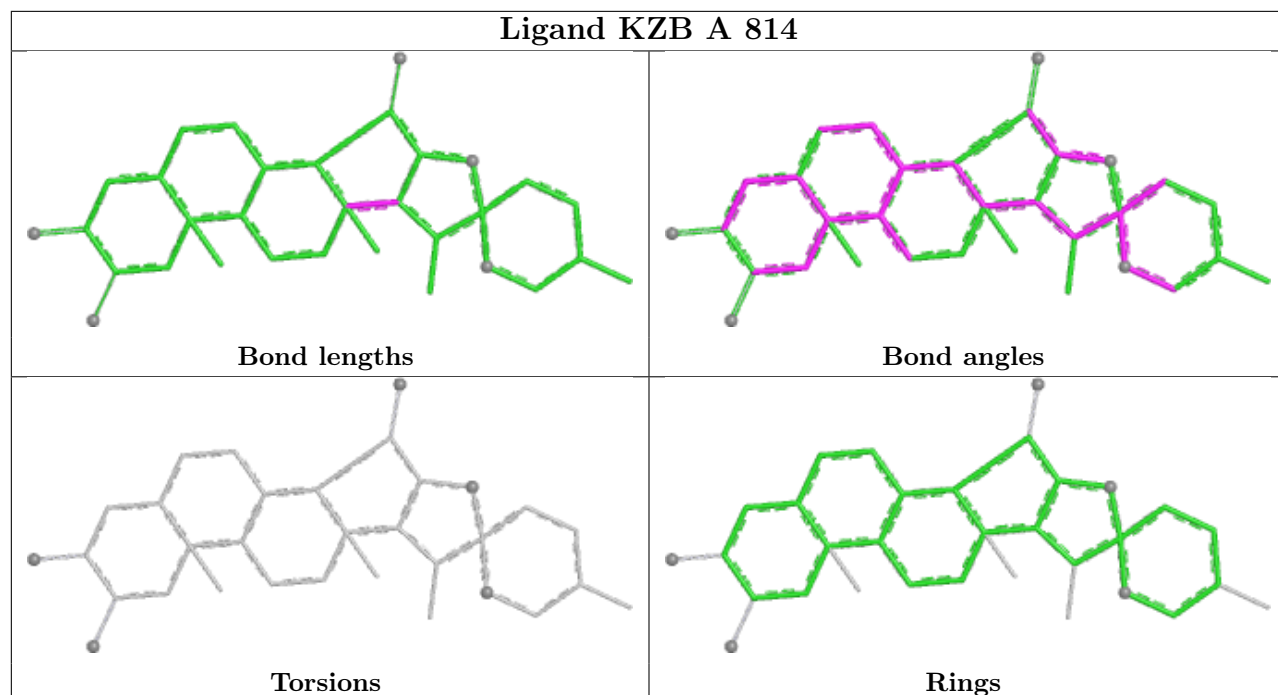




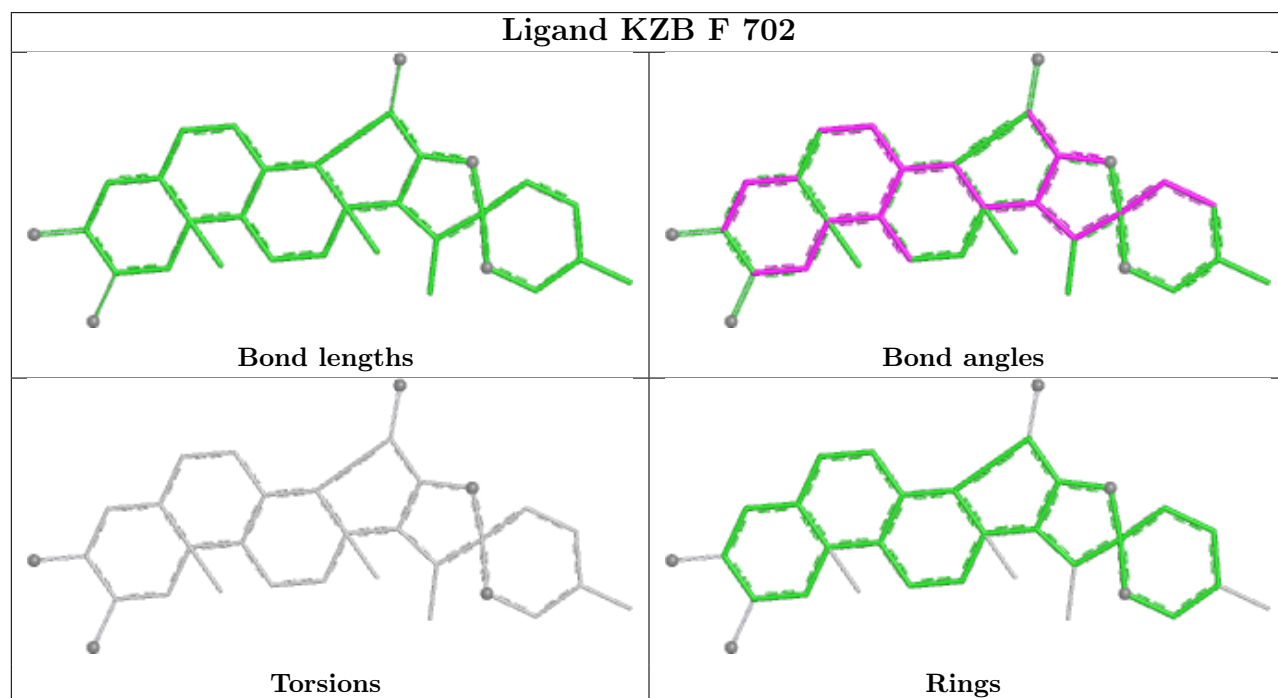


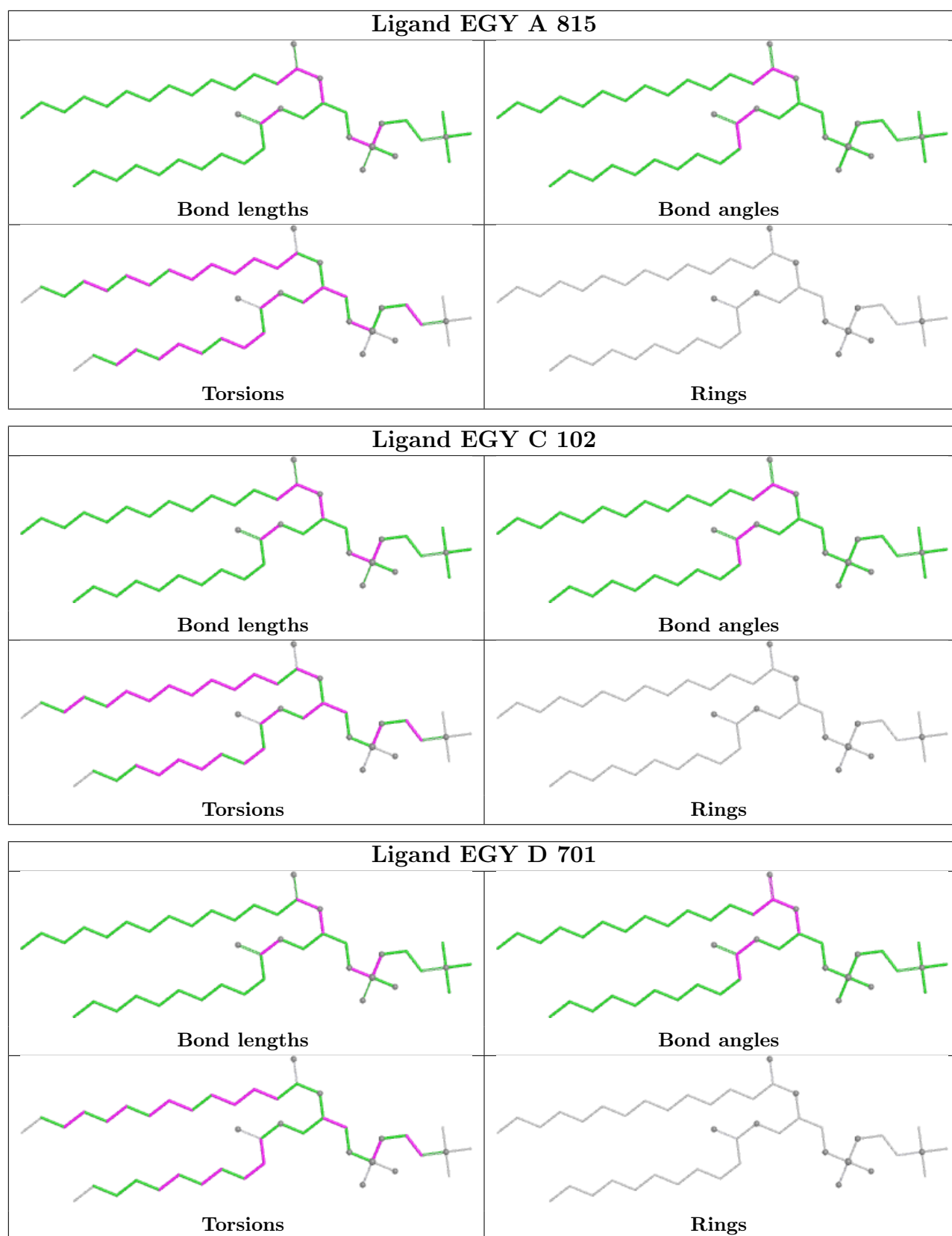


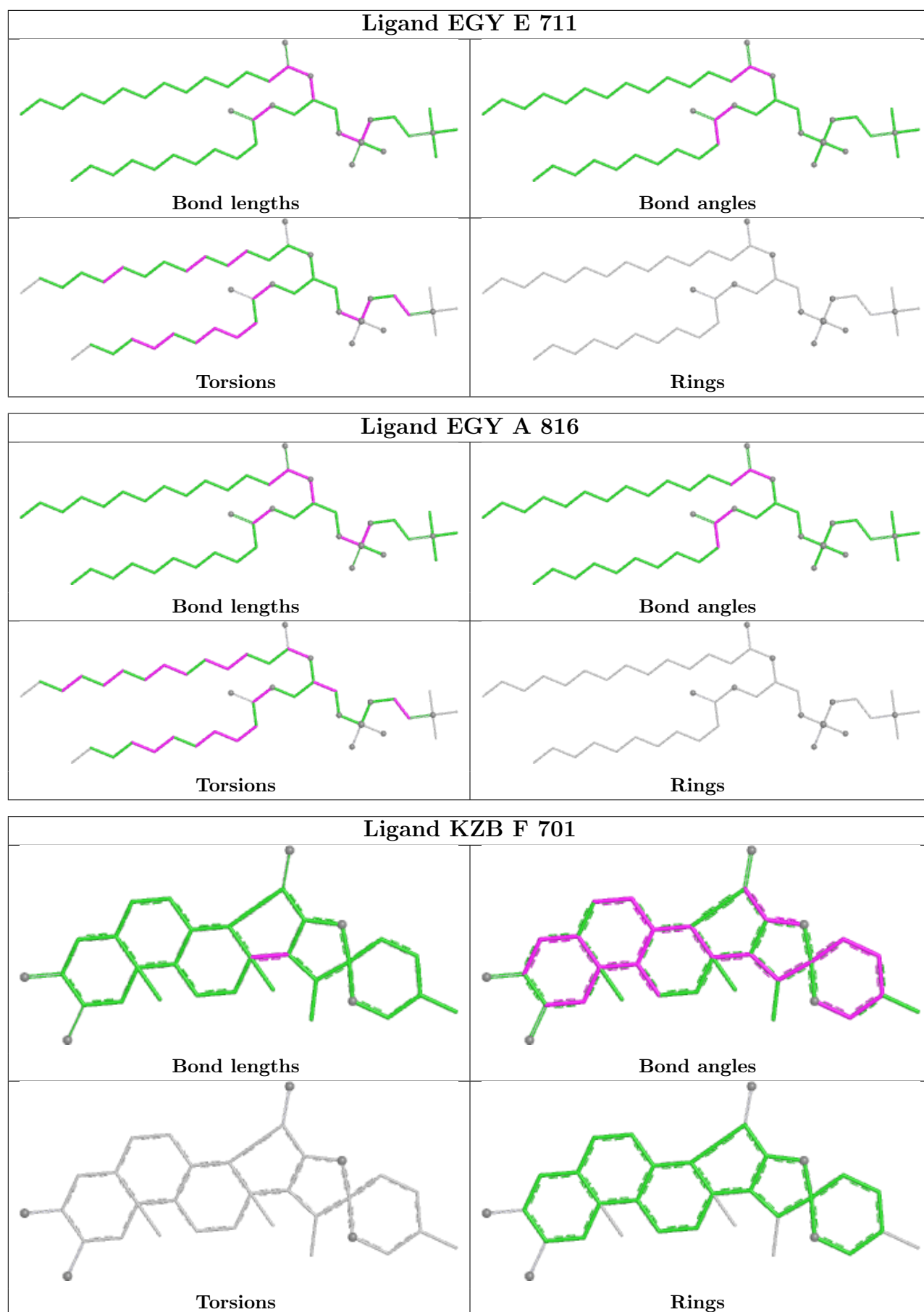
Ligand KZB A 814

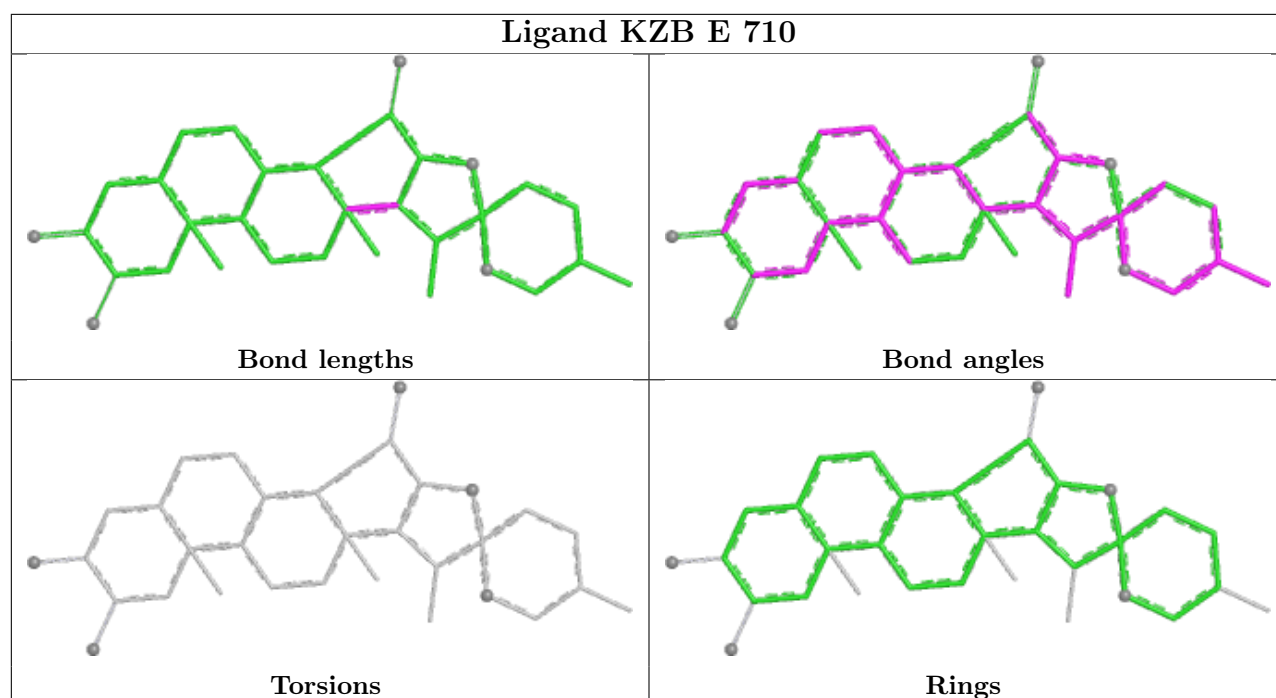


Ligand KZB F 702









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

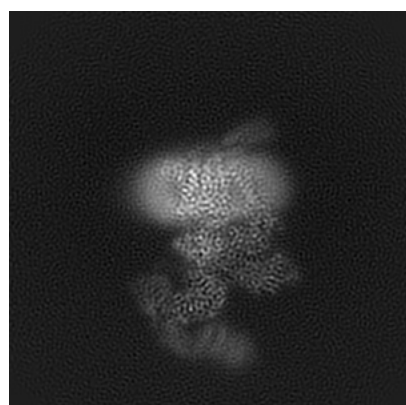
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10110. These allow visual inspection of the internal detail of the map and identification of artifacts.

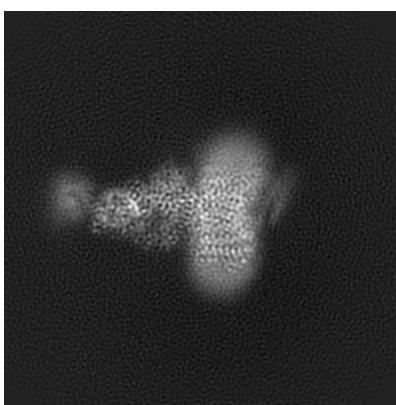
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

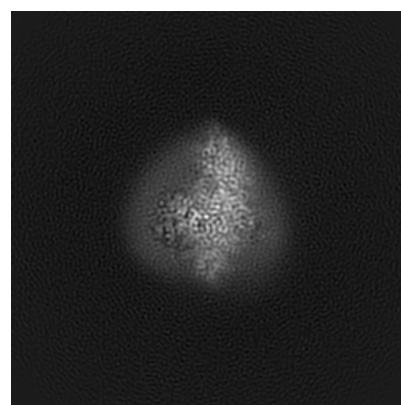
6.1.1 Primary map



X



Y

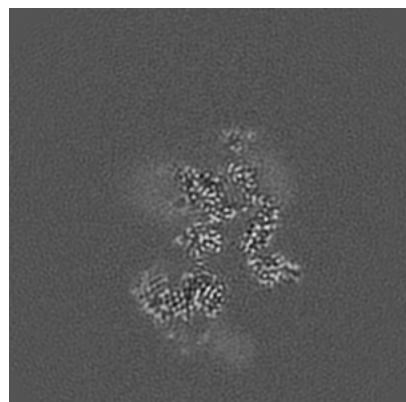


Z

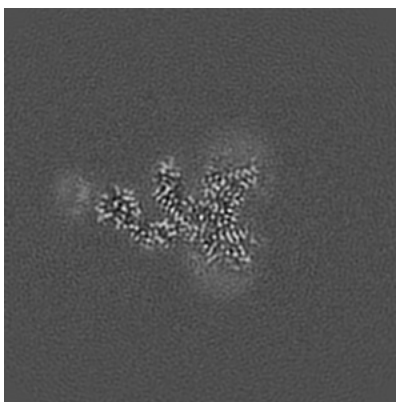
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

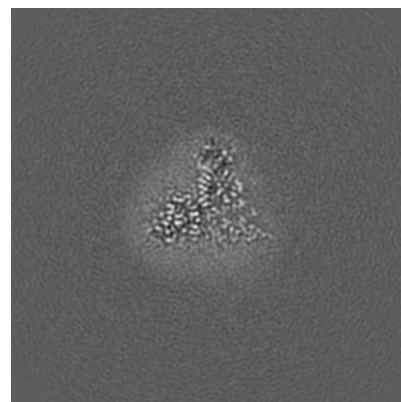
6.2.1 Primary map



X Index: 192



Y Index: 192

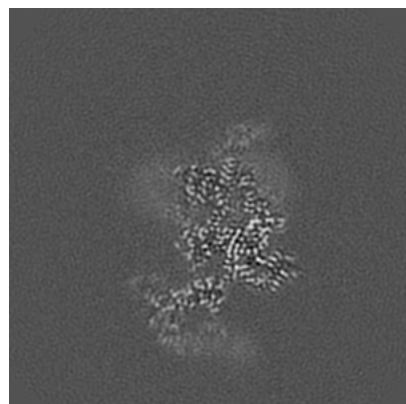


Z Index: 192

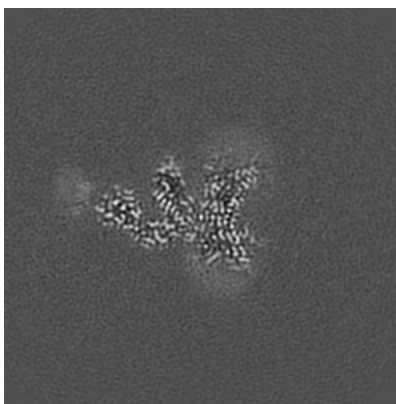
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

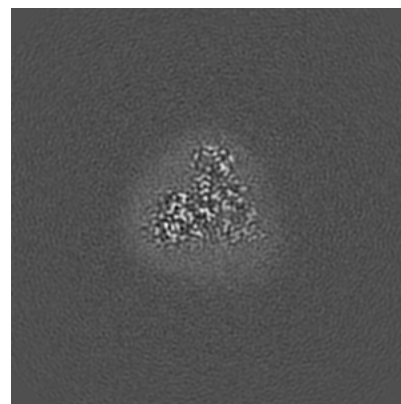
6.3.1 Primary map



X Index: 201



Y Index: 191

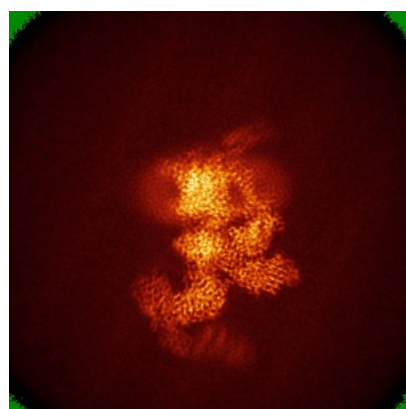


Z Index: 194

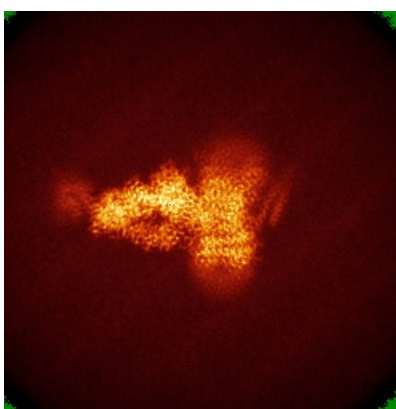
The images above show the largest variance slices of the map in three orthogonal directions.

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

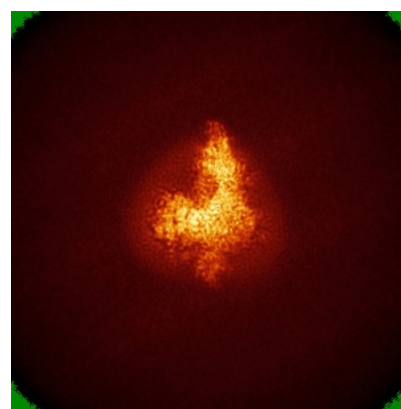
6.4.1 Primary map



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

This section was not generated.

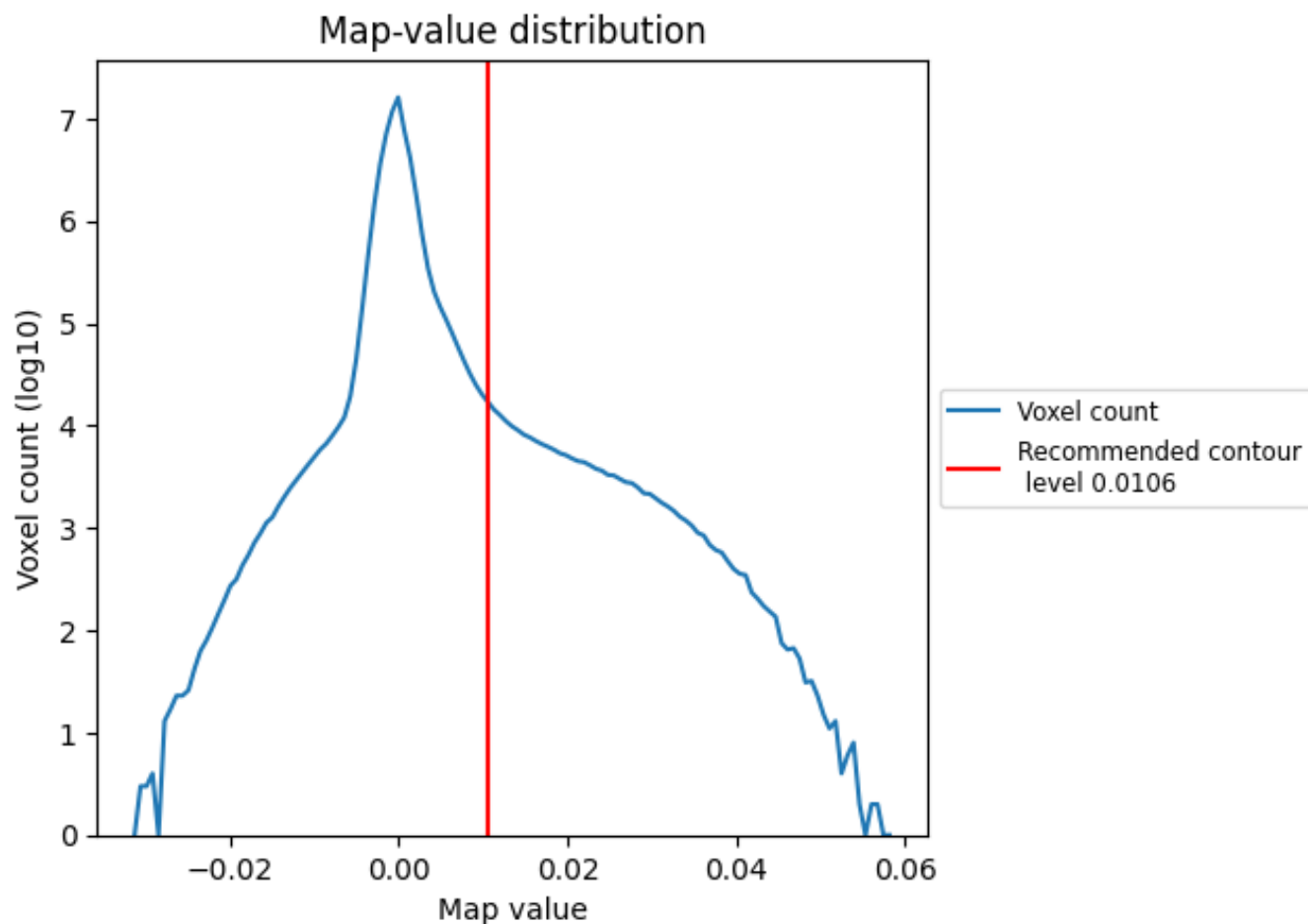
6.6 Mask visualisation

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

7 Map analysis [i](#)

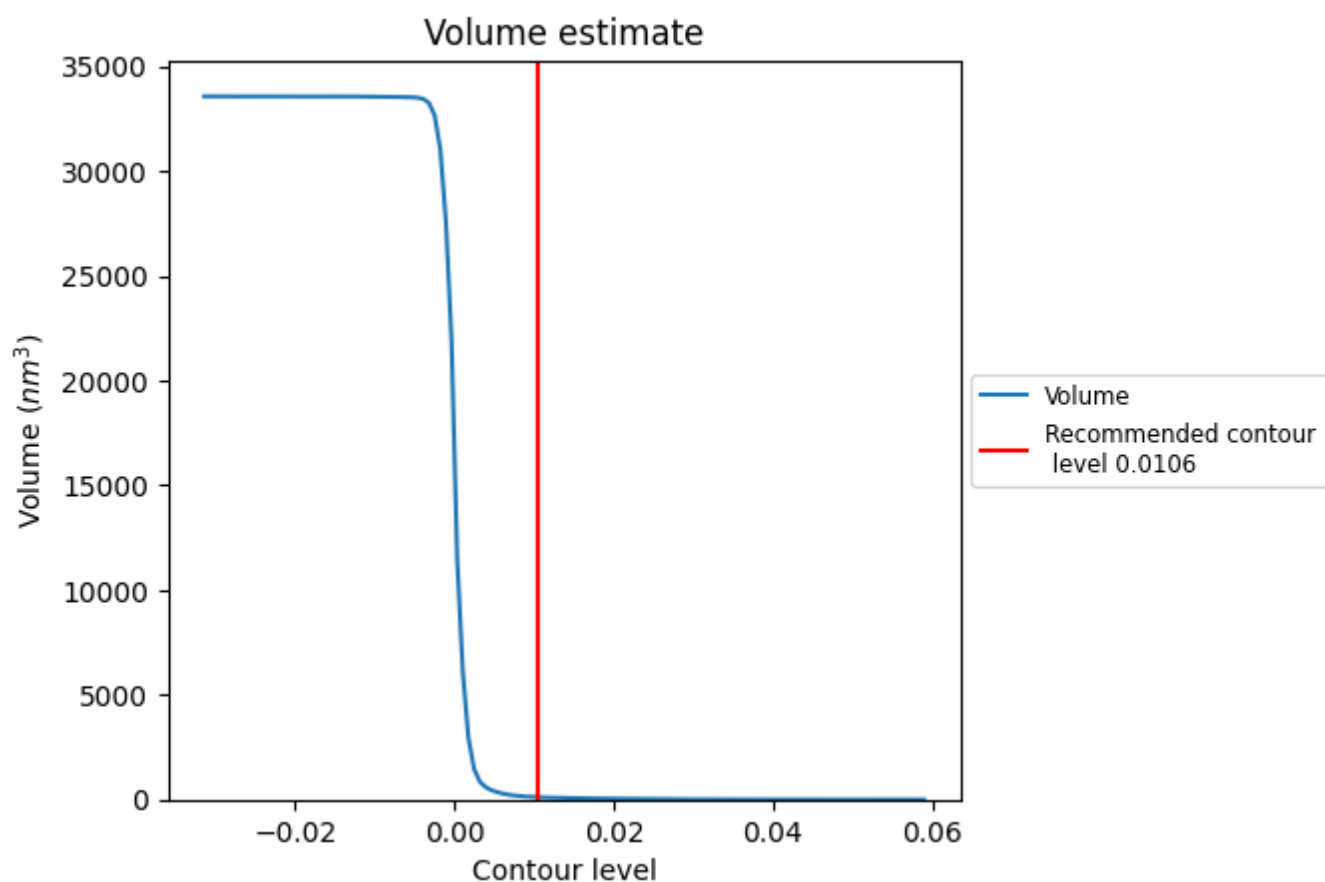
This section contains the results of statistical analysis of the map.

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.

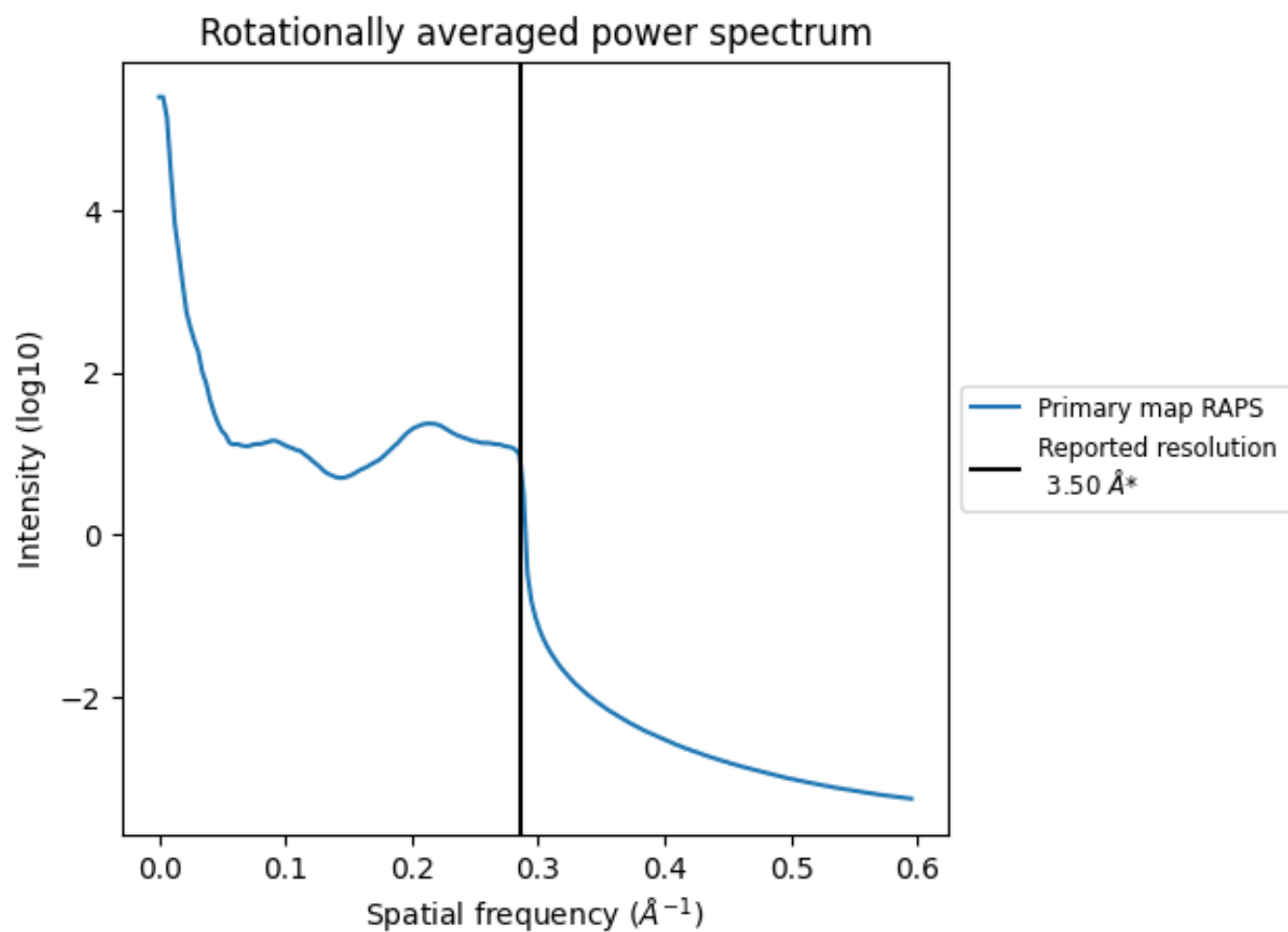
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 113 nm^3 ; this corresponds to an approximate mass of 102 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 ⓘ

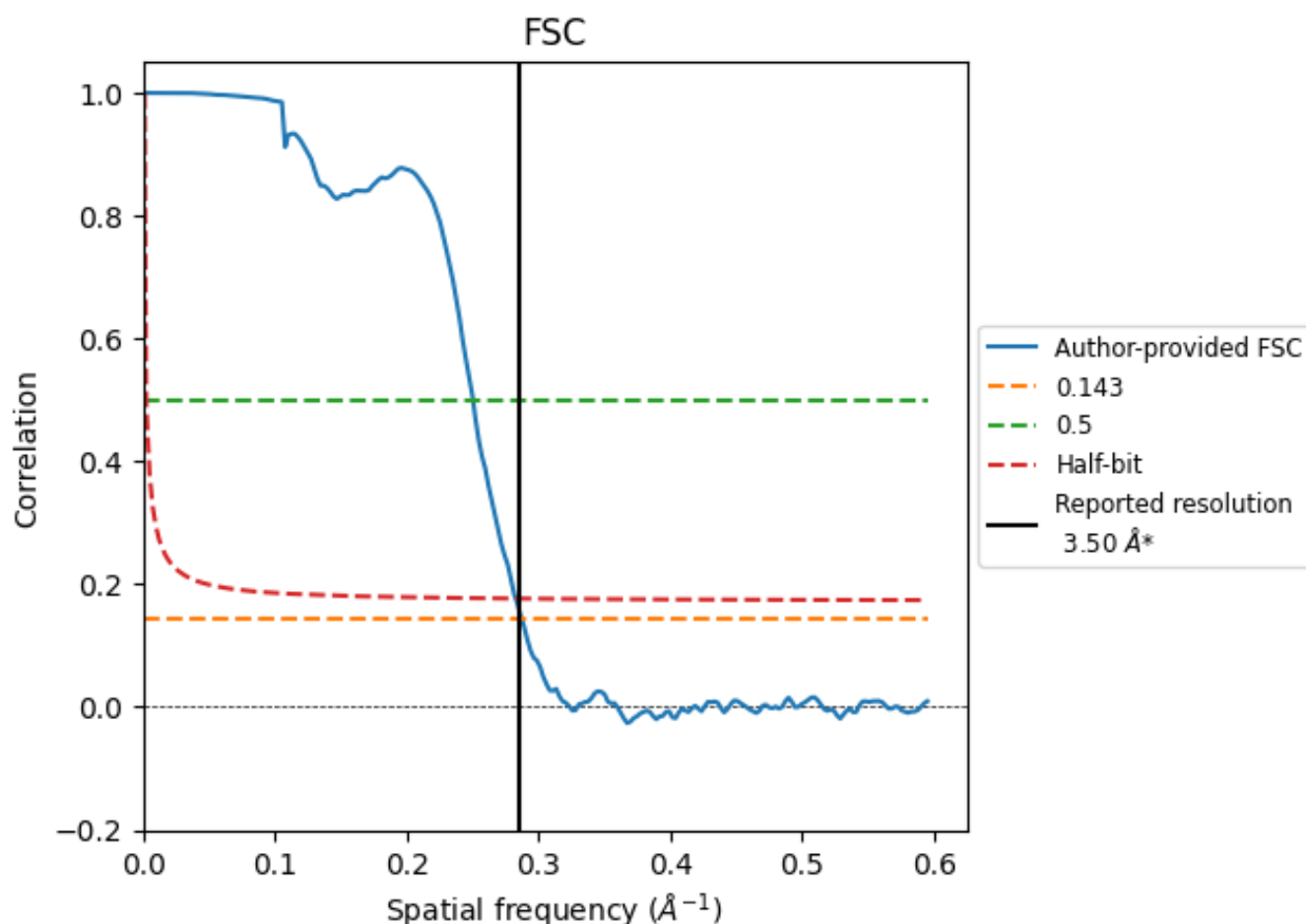


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

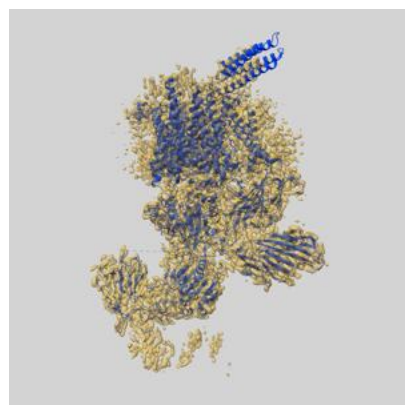
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.48	4.00	3.54
Unmasked-calculated*	-	-	-

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

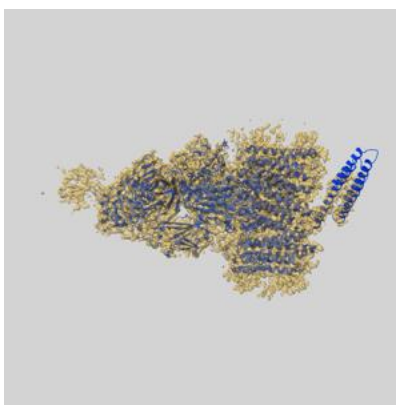
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10110 and PDB model 6S7O. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

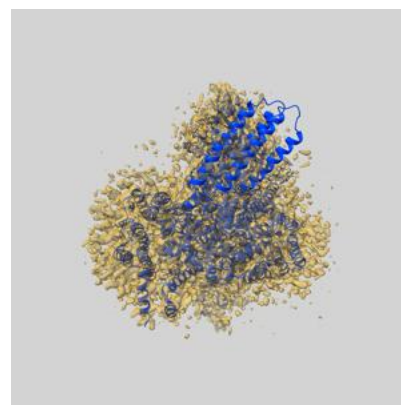
9.1 Map-model overlay [i](#)



X



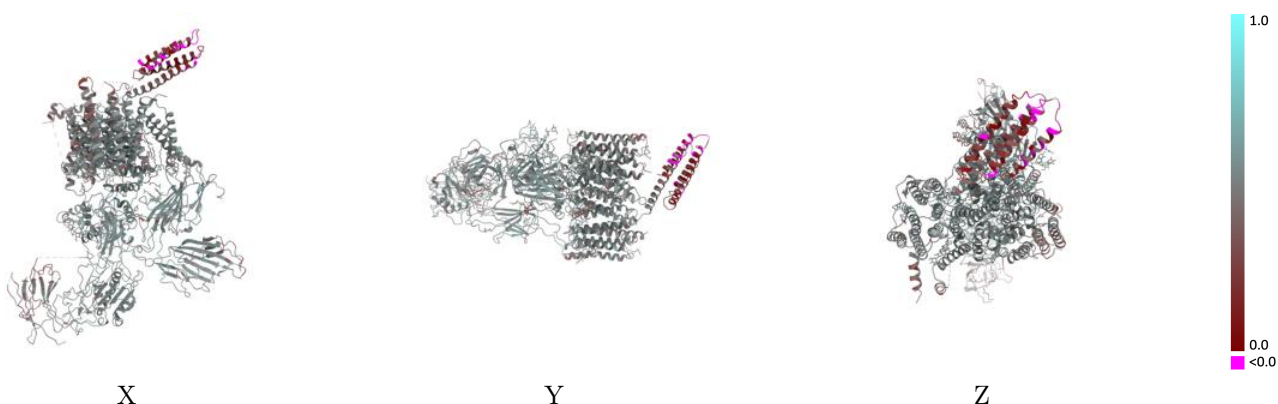
Y



Z

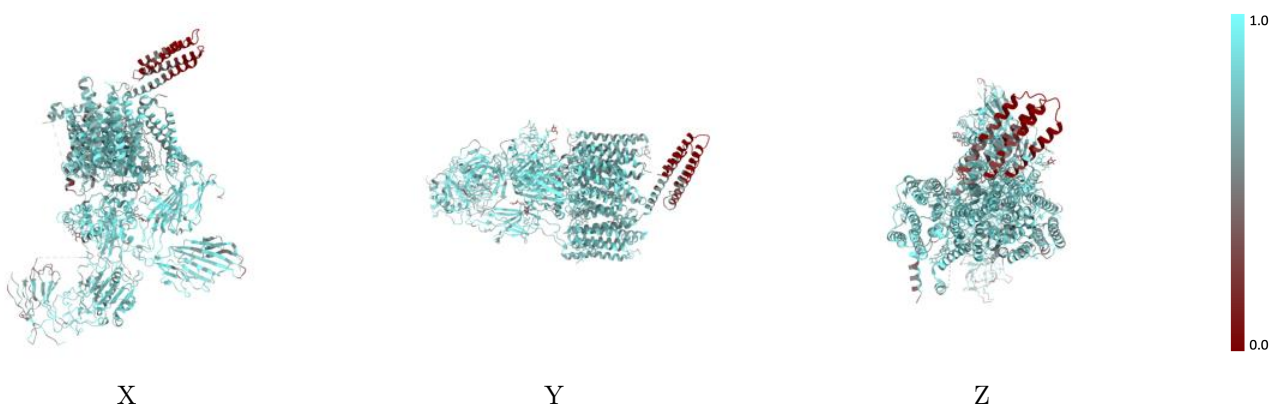
The images above show the 3D surface view of the map at the recommended contour level 0.0106 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



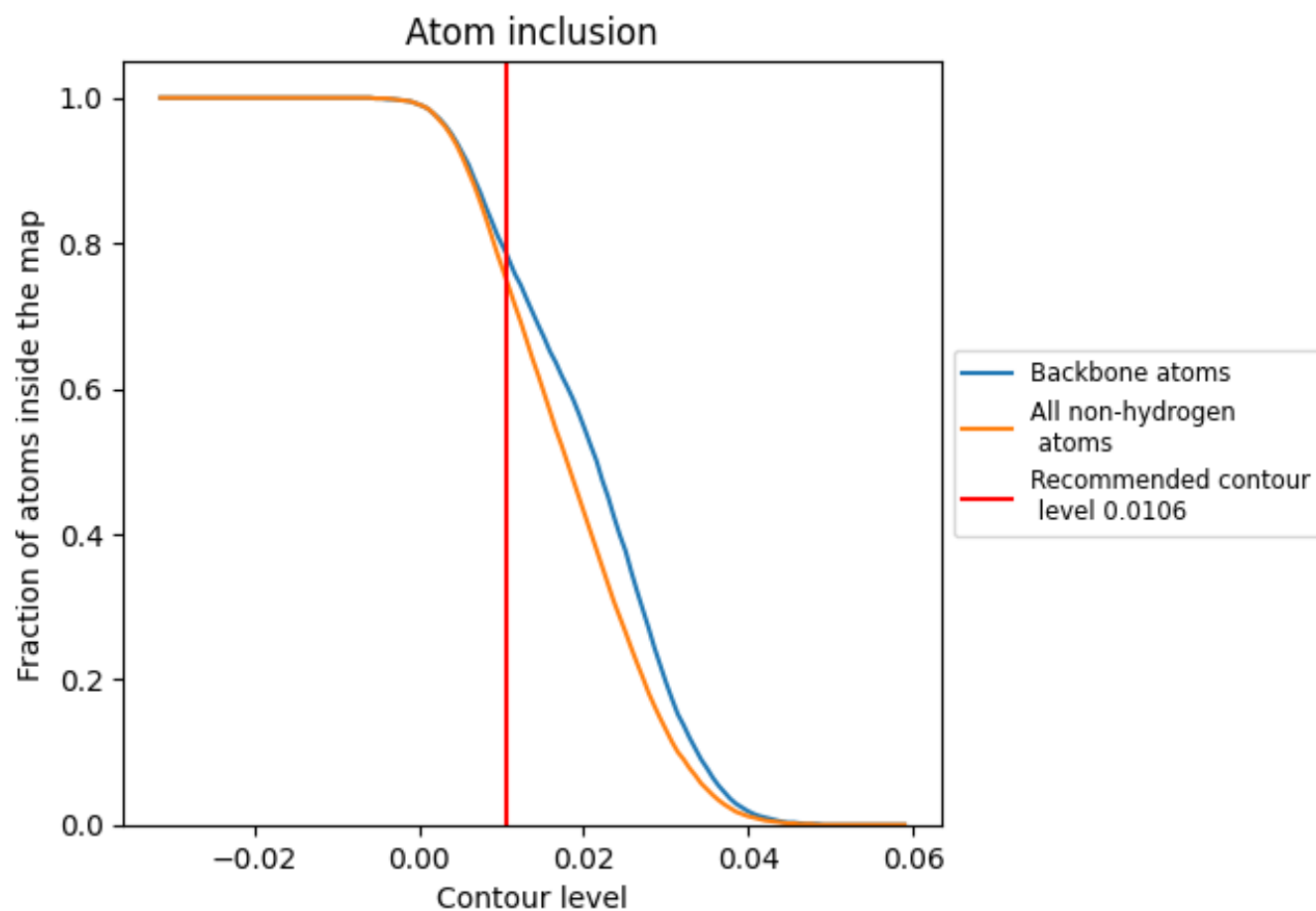
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0106).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (0.0106) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7500	0.4850
A	0.7930	0.5100
B	0.7580	0.4730
C	0.7530	0.5020
D	0.7770	0.4890
E	0.6960	0.4580
F	0.6940	0.4500
G	0.7970	0.5100
H	0.6910	0.4390
I	0.4100	0.2920
J	0.7020	0.5050
K	0.7230	0.5310

1.0

0.0

<0.0