



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:07 PM UTC

PDB ID : 7OCI / pdb_00007oci
EMDB ID : EMD-12808
Title : Cryo-EM structure of yeast Ost6p containing oligosaccharyltransferase complex
Authors : Wild, R.; Neuhaus, J.D.; Eyring, J.; Irobalieva, R.N.; Kowal, J.; Lin, C.W.; Locher, K.P.; Aebi, M.
Deposited on : 2021-04-27
Resolution : 3.46 Å (reported)
Based on initial model : 6EZN

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

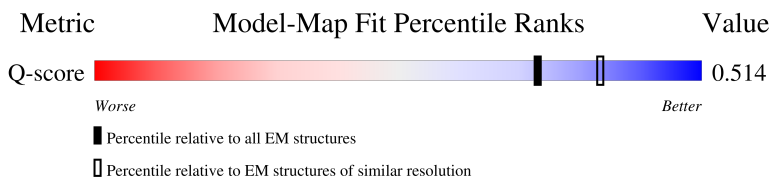
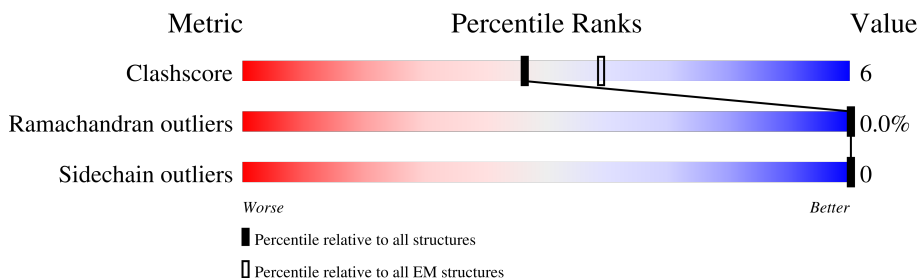
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.46 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.






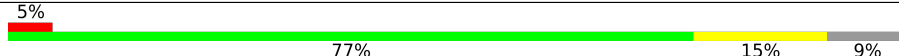
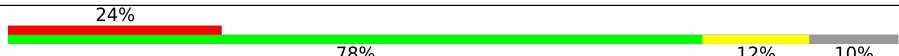

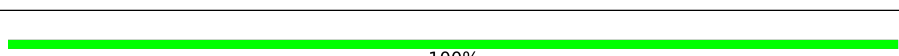
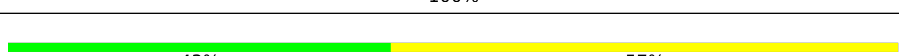
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13788 (2.96 - 3.96)

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	476	<p>7% (red), 75% (green), 16% (yellow), 9% (grey)</p>
2	B	130	<p>7% (red), 68% (green), 15% (yellow), 17% (grey)</p>
3	C	332	<p>33% (green), 64% (grey)</p>

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Mol	Chain	Length	Quality of chain
4	D	36	
5	E	86	
6	F	718	
7	G	430	
8	H	286	
9	I	24	
10	K	2	
11	J	7	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
14	AJP	B	202	X	-	-	-
14	AJP	D	102	X	-	-	-

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 17077 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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	434	3503	2275	558	664	6	0	0

- Molecule 2 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	108	869	588	139	136	6	0	0

- Molecule 3 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	119	933	638	138	148	9	0	0

- Molecule 4 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	35	267	172	40	51	4	0	0

- Molecule 5 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	85	666	448	99	118	1	0	0

- Molecule 6 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	639	5130	3394	817	896	23	0	0

- Molecule 7 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	393	3177	2041	524	609	3	0	0

- Molecule 8 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit SWP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	258	1873	1228	311	331	3	0	0

- Molecule 9 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST6 - TM1.

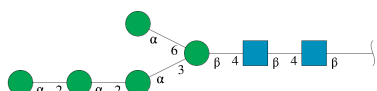
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	I	24	120	72	24	24	0	0

- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



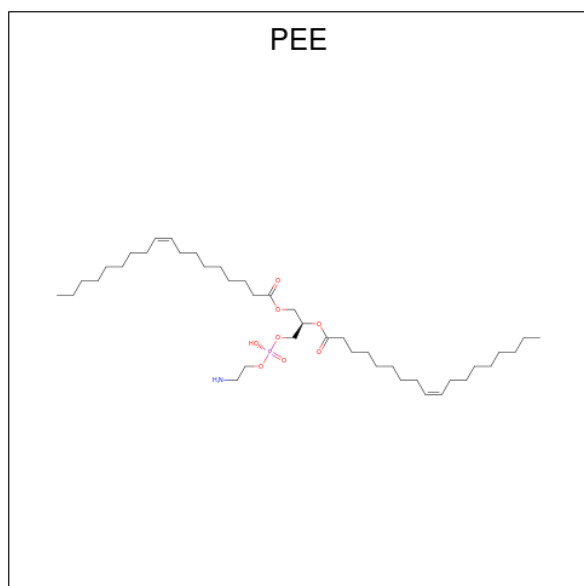
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	K	2	28	16	2	10	0	0

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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
			Total	C	N	O		
11	J	7	83	46	2	35	0	0

- Molecule 12 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



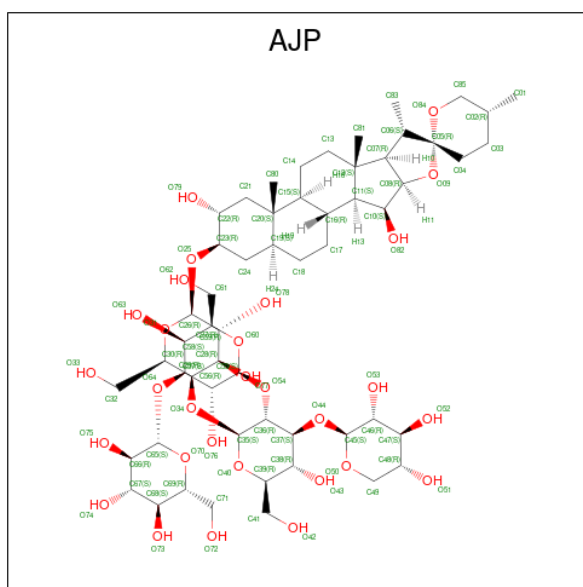
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
12	A	1	35	25	1	8	1	0
12	B	1	33	23	1	8	1	0
12	C	1	36	26	1	8	1	0
12	D	1	38	28	1	8	1	0
12	F	1	42	32	1	8	1	0
12	H	1	44	34	1	8	1	0

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
13	A	1	Total	C	N	O	0
			14	8	1	5	
13	G	1	Total	C	N	O	0
			14	8	1	5	
13	G	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 14 is Digitonin (CCD ID: AJP) (formula: $C_{56}H_{92}O_{29}$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
14	B	1	Total	C	O	0
			54	39	15	

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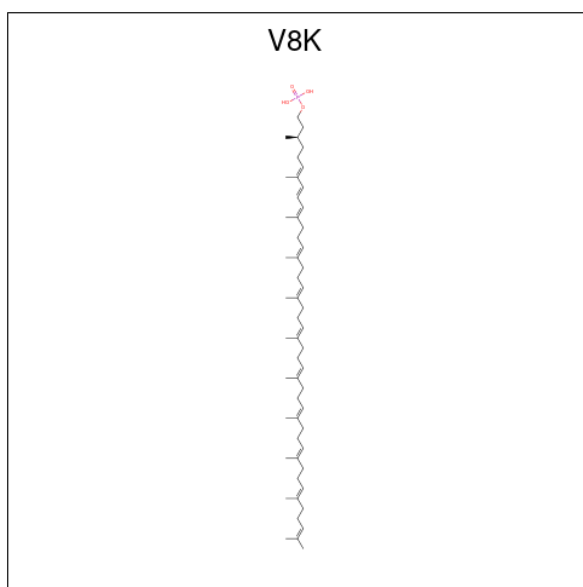
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Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
14	D	1	43	33	10	0

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
15	F	1	1	1	0

- Molecule 16 is Dolichylphosphate (CCD ID: V8K) (formula: C₅₅H₉₁O₄P).

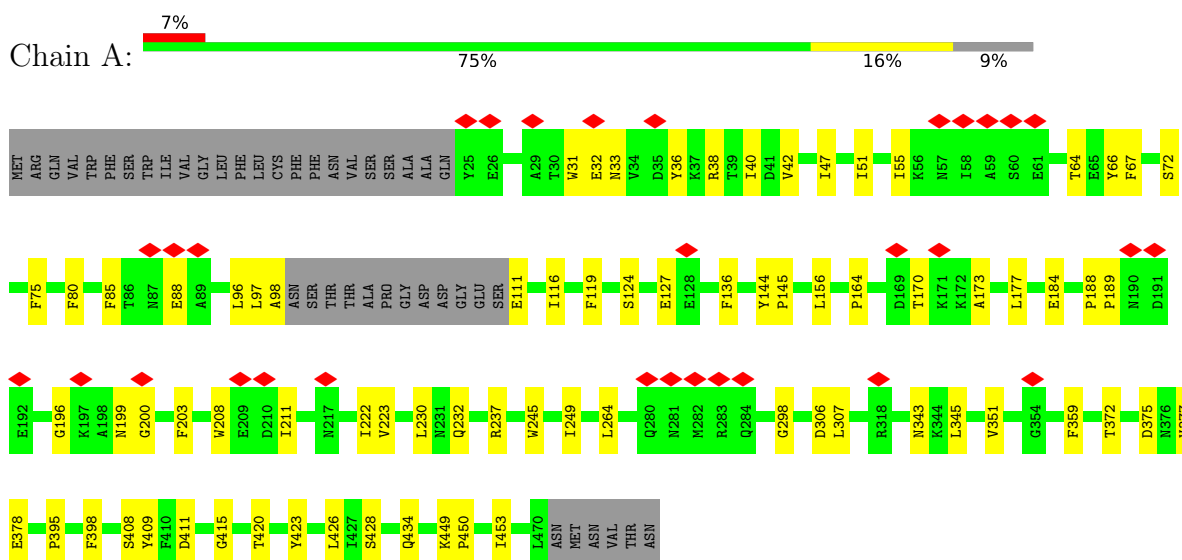


Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
16	F	1	60	55	4	1	0

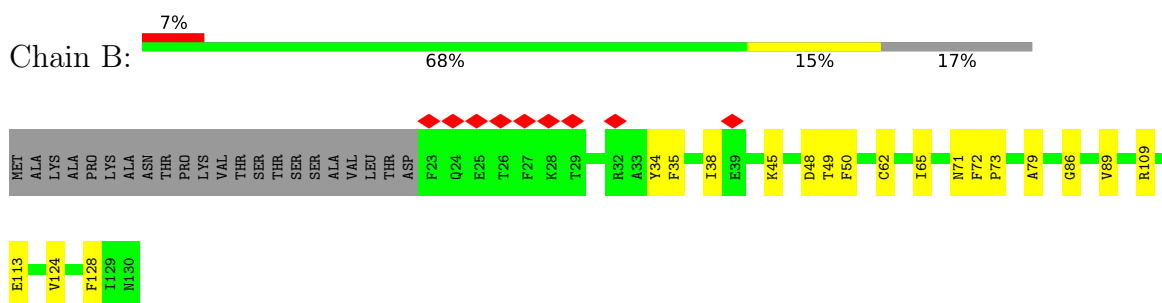
3 Residue-property plots

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.

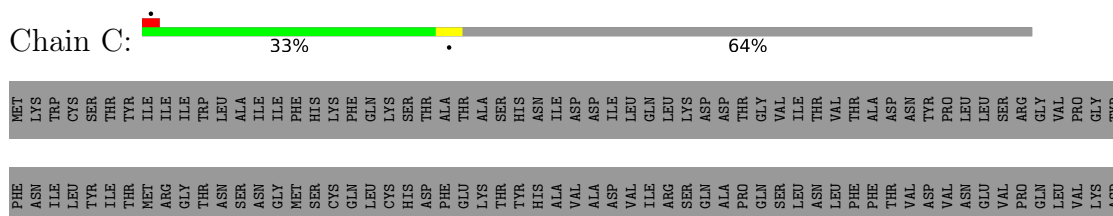
- Molecule 1: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1

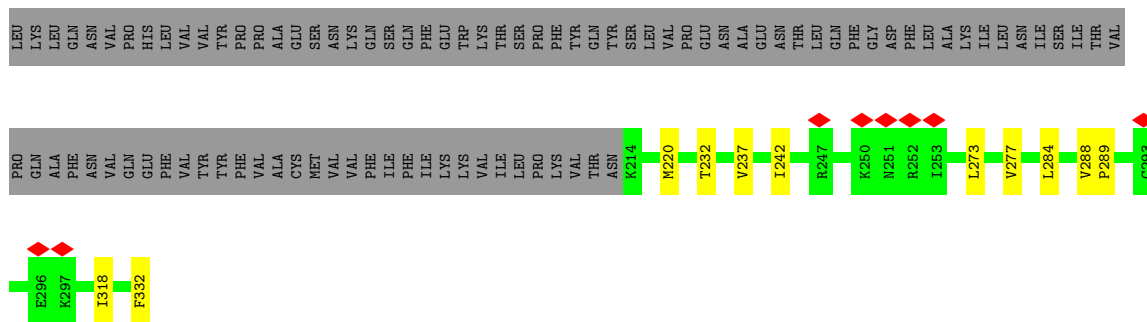


- Molecule 2: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST2

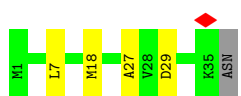
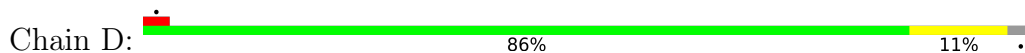


- Molecule 3: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST6

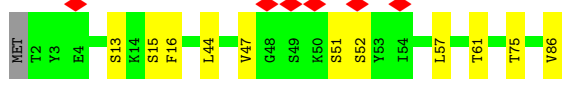
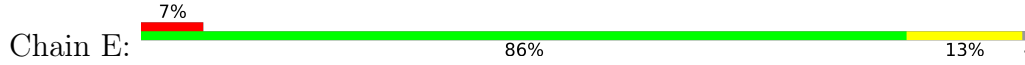




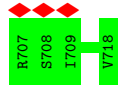
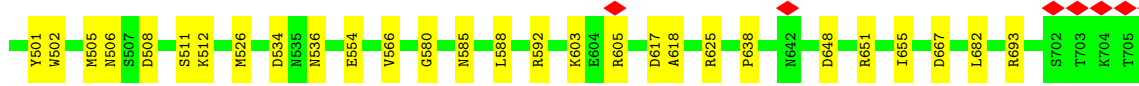
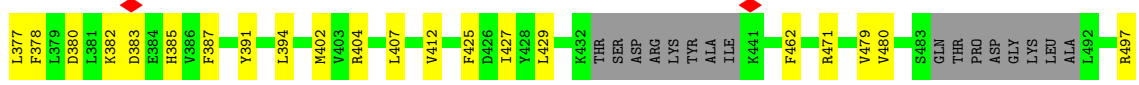
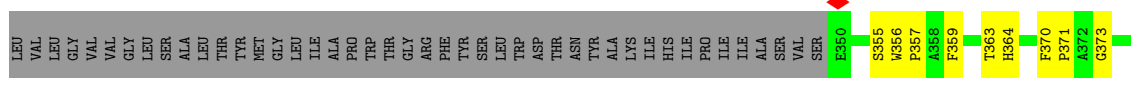
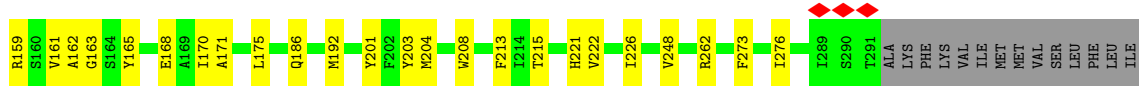
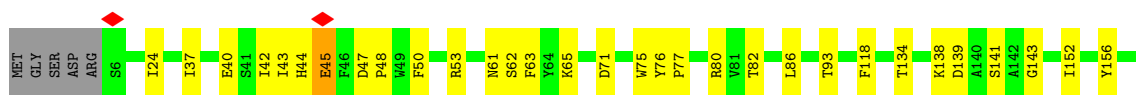
- Molecule 4: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST4



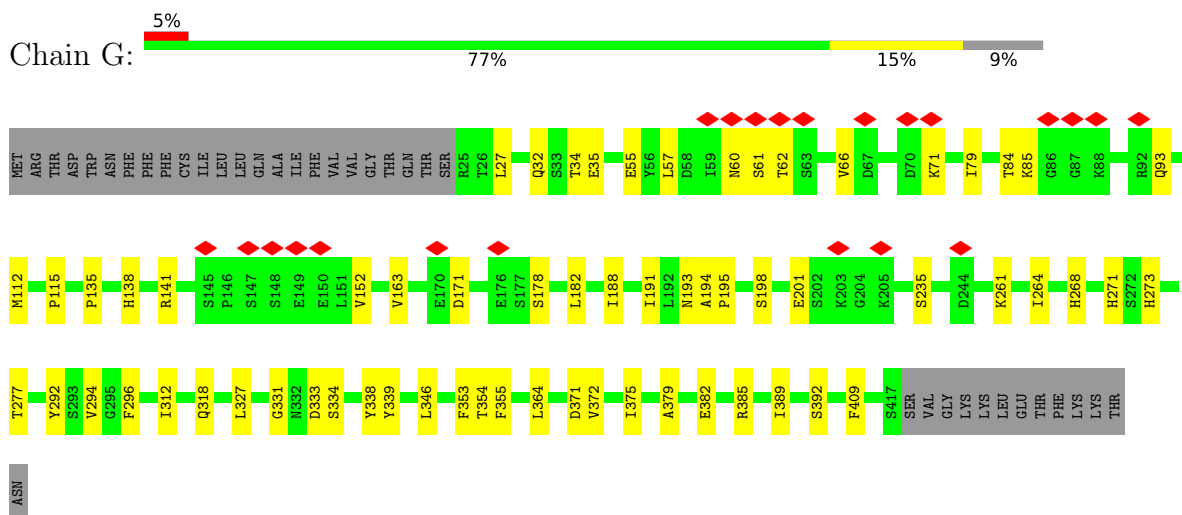
- Molecule 5: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST5



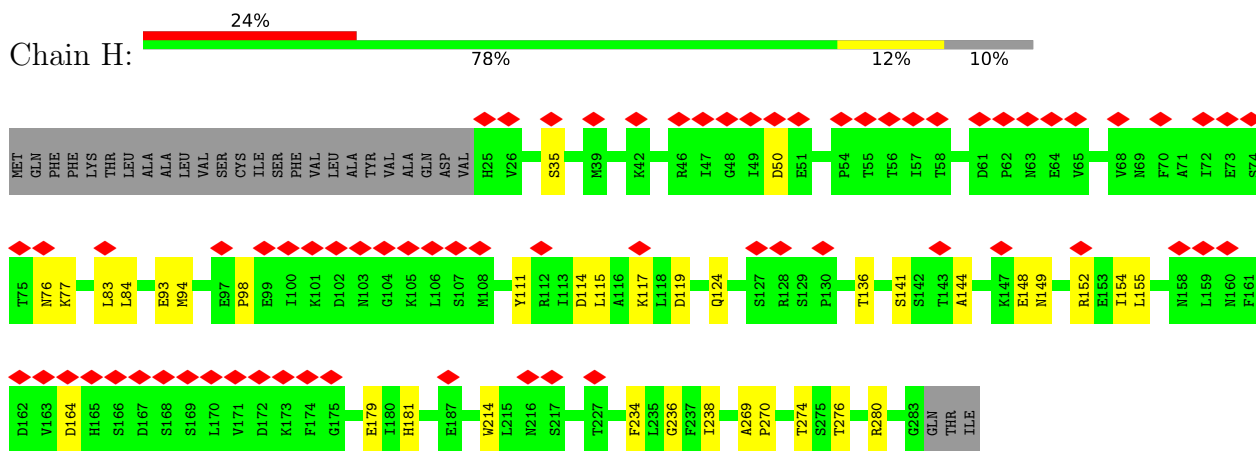
- Molecule 6: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3



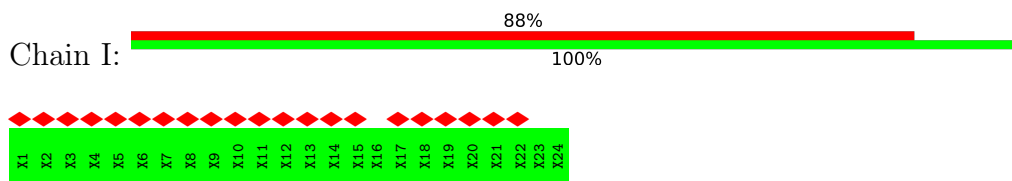
- Molecule 7: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1



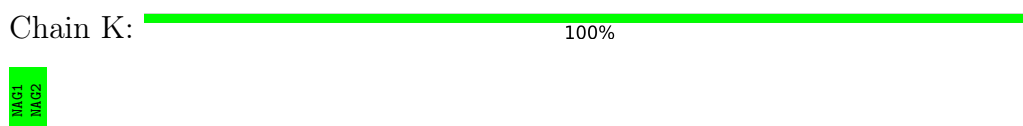
- Molecule 8: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit SWP1



- Molecule 9: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST6-TM1



- Molecule 10: 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-(1-2)-alpha-D-mannopyranose-(1-3)-[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

Chain J:  43% 57%

MAN1
MAN2
MAN3
MAN4
MAN5
MAN6
MAN7

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220536	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 ($e^-/\text{\AA}^2$)	67	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	0.208	Depositor
Minimum map value	-0.159	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.022	Depositor
Map size (\AA)	322.56, 322.56, 322.56	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.84, 0.84, 0.84	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, V8K, PEE, MAN, NAG, AJP, BMA

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	0.13	0/3605	0.34	0/4908
2	B	0.14	0/891	0.31	0/1203
3	C	0.13	0/961	0.27	0/1301
4	D	0.12	0/270	0.22	0/365
5	E	0.12	0/684	0.29	0/926
6	F	0.16	0/5281	0.35	0/7186
7	G	0.12	0/3259	0.32	0/4431
8	H	0.11	0/1912	0.31	0/2606
All	All	0.14	0/16863	0.32	0/22926

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3503	0	3378	47	0
2	B	869	0	899	16	0
3	C	933	0	956	8	0
4	D	267	0	280	4	0
5	E	666	0	677	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	5130	0	5053	77	0
7	G	3177	0	3058	39	0
8	H	1873	0	1787	21	0
9	I	120	0	26	0	0
10	K	28	0	25	0	0
11	J	83	0	70	0	0
12	A	35	0	44	2	0
12	B	33	0	40	0	0
12	C	36	0	46	0	0
12	D	38	0	50	0	0
12	F	42	0	58	1	0
12	H	44	0	62	2	0
13	A	14	0	13	0	0
13	G	28	0	26	1	0
14	B	54	0	0	1	0
14	D	43	0	0	1	0
15	F	1	0	0	0	0
16	F	60	0	0	0	0
All	All	17077	0	16548	205	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 6.

The worst 5 of 205 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:ASP:HB3	1:A:415:GLY:HA2	1.70	0.72
6:F:42:ILE:HG13	6:F:43:ILE:H	1.57	0.69
6:F:77:PRO:O	7:G:318:GLN:NE2	2.27	0.67
6:F:588:LEU:O	6:F:592:ARG:HG2	1.96	0.65
6:F:580:GLY:O	6:F:585:ASN:ND2	2.23	0.65

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	430/476 (90%)	414 (96%)	16 (4%)	0	100	100
2	B	106/130 (82%)	103 (97%)	3 (3%)	0	100	100
3	C	117/332 (35%)	116 (99%)	1 (1%)	0	100	100
4	D	33/36 (92%)	32 (97%)	1 (3%)	0	100	100
5	E	83/86 (96%)	81 (98%)	2 (2%)	0	100	100
6	F	631/718 (88%)	618 (98%)	12 (2%)	1 (0%)	43	74
7	G	391/430 (91%)	381 (97%)	10 (3%)	0	100	100
8	H	256/286 (90%)	244 (95%)	12 (5%)	0	100	100
All	All	2047/2494 (82%)	1989 (97%)	57 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	45	GLU

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	389/426 (91%)	389 (100%)	0	100	100
2	B	94/115 (82%)	94 (100%)	0	100	100
3	C	100/301 (33%)	100 (100%)	0	100	100
4	D	32/33 (97%)	32 (100%)	0	100	100
5	E	74/75 (99%)	74 (100%)	0	100	100
6	F	538/613 (88%)	538 (100%)	0	100	100
7	G	351/392 (90%)	351 (100%)	0	100	100
8	H	174/249 (70%)	174 (100%)	0	100	100
All	All	1752/2204 (80%)	1752 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	536	ASN
6	F	681	GLN
7	G	307	HIS
7	G	242	ASN
7	G	268	HIS

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](#)

9 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	$\# Z > 2$
11	NAG	J	1	6,11	14,14,15	0.32	0	17,19,21	0.50	0
11	NAG	J	2	11	14,14,15	0.21	0	17,19,21	0.52	0
11	BMA	J	3	11	11,11,12	0.45	0	15,15,17	0.83	0
11	MAN	J	4	11	11,11,12	0.62	0	15,15,17	1.16	1 (6%)
11	MAN	J	5	11	11,11,12	0.68	0	15,15,17	0.97	1 (6%)
11	MAN	J	6	11	11,11,12	0.61	0	15,15,17	0.89	1 (6%)
11	MAN	J	7	11	11,11,12	0.66	0	15,15,17	0.93	1 (6%)
10	NAG	K	1	10,1	14,14,15	0.34	0	17,19,21	0.68	0
10	NAG	K	2	10	14,14,15	0.23	0	17,19,21	0.54	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	J	1	6,11	-	2/6/23/26	0/1/1/1
11	NAG	J	2	11	-	2/6/23/26	0/1/1/1
11	BMA	J	3	11	-	1/2/19/22	0/1/1/1
11	MAN	J	4	11	-	0/2/19/22	0/1/1/1
11	MAN	J	5	11	-	1/2/19/22	0/1/1/1
11	MAN	J	6	11	-	0/2/19/22	0/1/1/1
11	MAN	J	7	11	-	0/2/19/22	0/1/1/1
10	NAG	K	1	10,1	-	4/6/23/26	0/1/1/1
10	NAG	K	2	10	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	J	4	MAN	O2-C2-C3	-3.11	103.72	110.15
11	J	5	MAN	O2-C2-C3	-2.66	104.64	110.15
11	J	7	MAN	O2-C2-C3	-2.17	105.66	110.15
11	J	6	MAN	O2-C2-C3	-2.13	105.74	110.15

There are no chirality outliers.

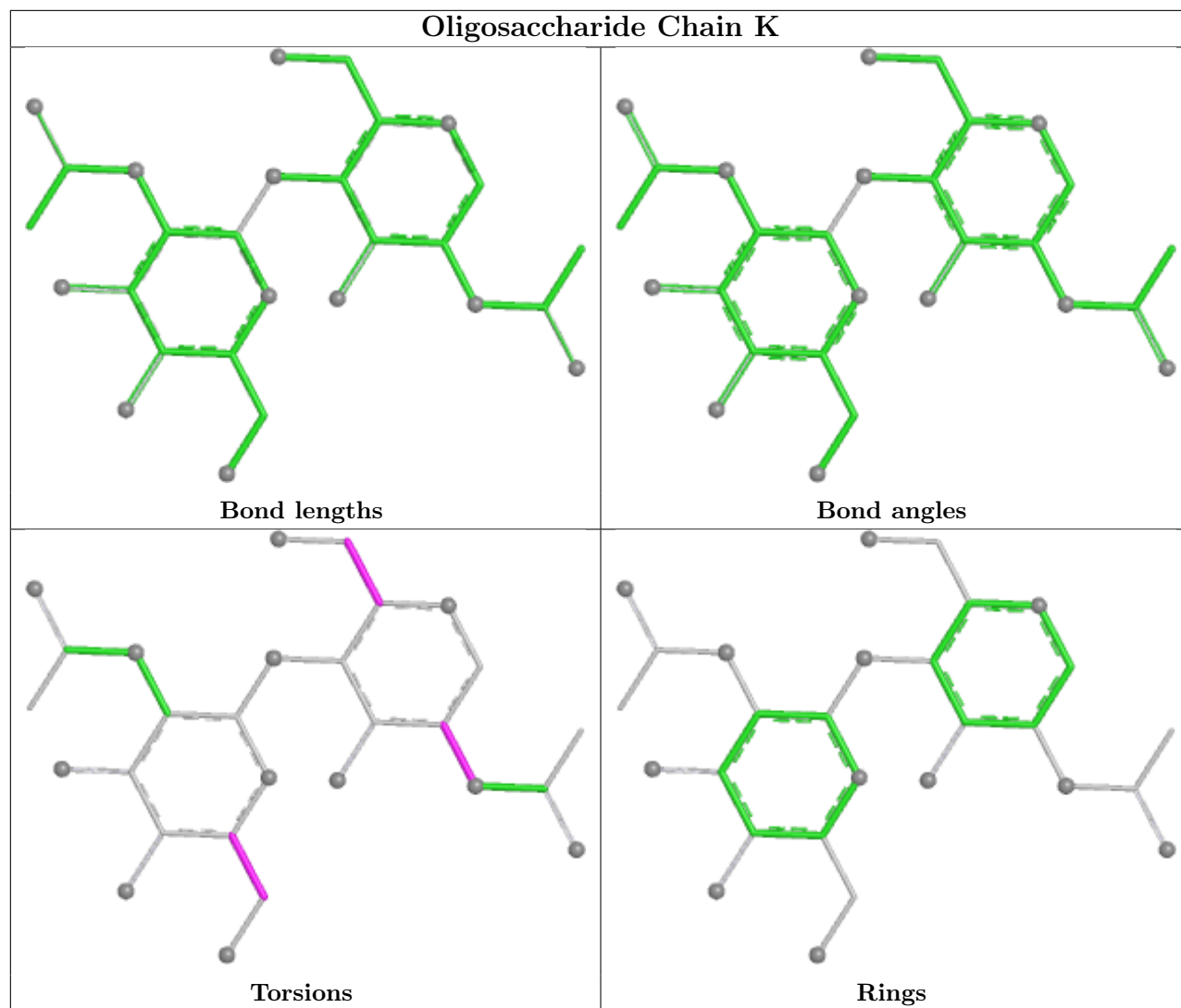
5 of 12 torsion outliers are listed below:

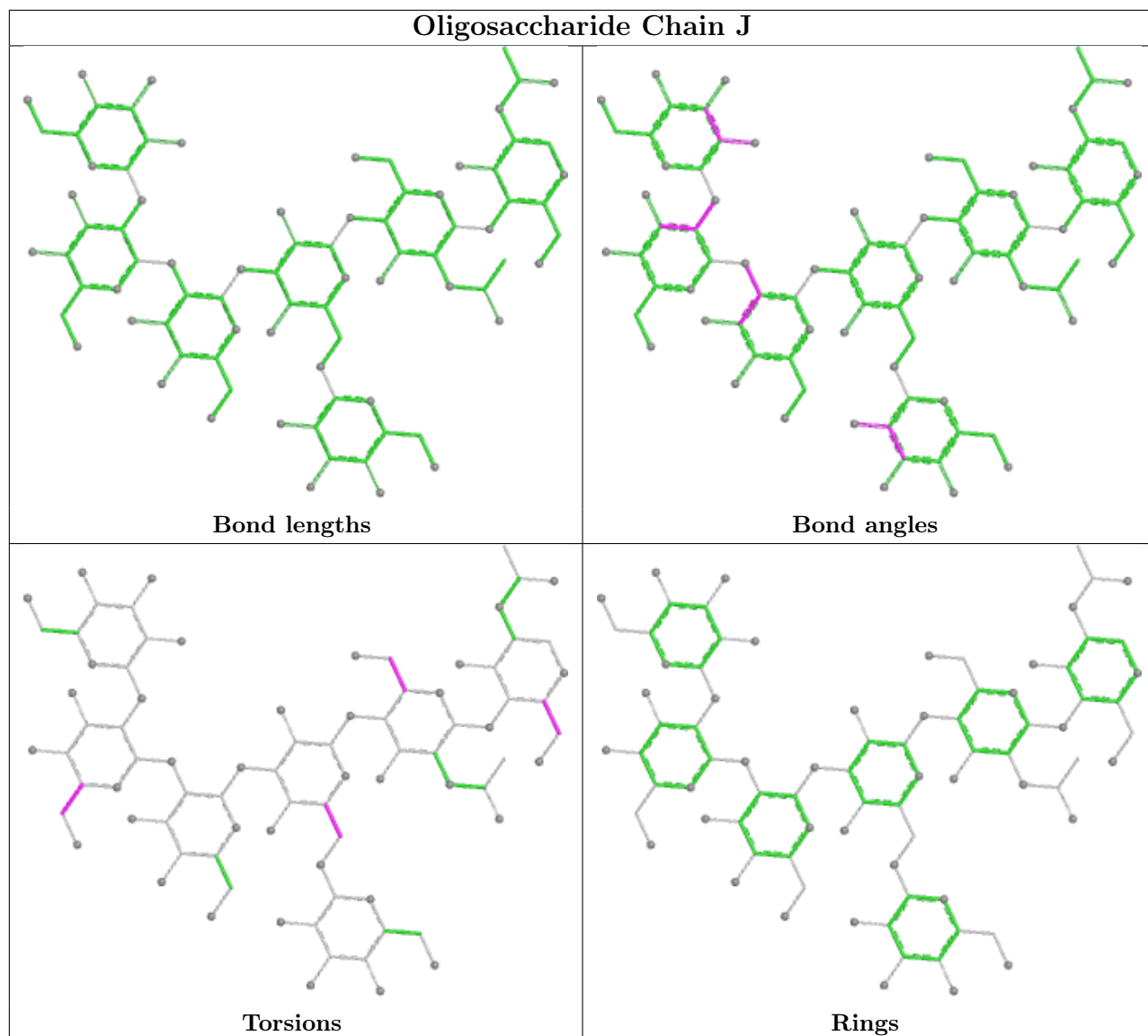
Mol	Chain	Res	Type	Atoms
10	K	2	NAG	O5-C5-C6-O6
11	J	3	BMA	O5-C5-C6-O6
10	K	2	NAG	C4-C5-C6-O6
11	J	5	MAN	O5-C5-C6-O6
11	J	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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	PEE	A	1301	-	34,34,50	1.70	5 (14%)	37,39,55	1.29	4 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	PEE	B	201	-	32,32,50	1.58	4 (12%)	35,37,55	1.13	4 (11%)
12	PEE	H	1101	-	43,43,50	1.55	5 (11%)	46,48,55	1.24	6 (13%)
12	PEE	D	101	-	37,37,50	1.49	4 (10%)	40,42,55	1.18	4 (10%)
13	NAG	G	501	7	14,14,15	0.24	0	17,19,21	0.38	0
14	AJP	B	202	-	61,61,95	0.45	0	93,98,149	1.22	9 (9%)
13	NAG	A	1302	1	14,14,15	0.25	0	17,19,21	0.47	0
12	PEE	F	902	-	41,41,50	1.61	5 (12%)	44,46,55	1.29	6 (13%)
12	PEE	C	1801	-	35,35,50	1.67	5 (14%)	38,40,55	1.28	5 (13%)
13	NAG	G	502	7	14,14,15	0.53	0	17,19,21	0.46	0
16	V8K	F	903	15	59,59,59	1.87	8 (13%)	70,72,72	1.60	16 (22%)
14	AJP	D	102	-	49,49,95	0.55	1 (2%)	75,80,149	1.29	9 (12%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	PEE	A	1301	-	-	19/38/38/54	-
12	PEE	B	201	-	-	12/36/36/54	-
12	PEE	H	1101	-	-	24/47/47/54	-
12	PEE	D	101	-	-	19/41/41/54	-
14	AJP	B	202	-	21/21/24/38	3/12/147/220	0/8/8/11
13	NAG	G	501	7	-	1/6/23/26	0/1/1/1
13	NAG	A	1302	1	-	3/6/23/26	0/1/1/1
12	PEE	F	902	-	-	24/45/45/54	-
12	PEE	C	1801	-	-	15/39/39/54	-
13	NAG	G	502	7	-	3/6/23/26	0/1/1/1
16	V8K	F	903	15	-	27/67/67/67	-
14	AJP	D	102	-	16/16/19/38	3/6/121/220	0/7/7/11

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	F	903	V8K	P57-O56	7.99	1.85	1.60
16	F	903	V8K	C45-C46	7.66	1.54	1.34
12	F	902	PEE	C39-C38	4.45	1.57	1.31
12	H	1101	PEE	C39-C38	4.44	1.56	1.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A	1301	PEE	C39-C38	4.33	1.57	1.29

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	F	903	V8K	C46-C47-C49	4.54	124.82	118.49
14	B	202	AJP	C06-C07-C08	-4.32	97.34	104.28
12	A	1301	PEE	O2-C10-C11	4.09	120.33	111.48
12	C	1801	PEE	O2-C10-C11	3.95	120.02	111.48
12	H	1101	PEE	O2-C10-C11	3.94	120.01	111.48

5 of 37 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
14	B	202	AJP	C38
14	B	202	AJP	C10
14	B	202	AJP	C39
14	B	202	AJP	C02
14	B	202	AJP	C15

5 of 153 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	1301	PEE	C1-O3P-P-O2P
12	A	1301	PEE	C1-O3P-P-O1P
12	A	1301	PEE	C1-O3P-P-O4P
12	A	1301	PEE	O4P-C4-C5-N
12	C	1801	PEE	C17-C18-C19-C20

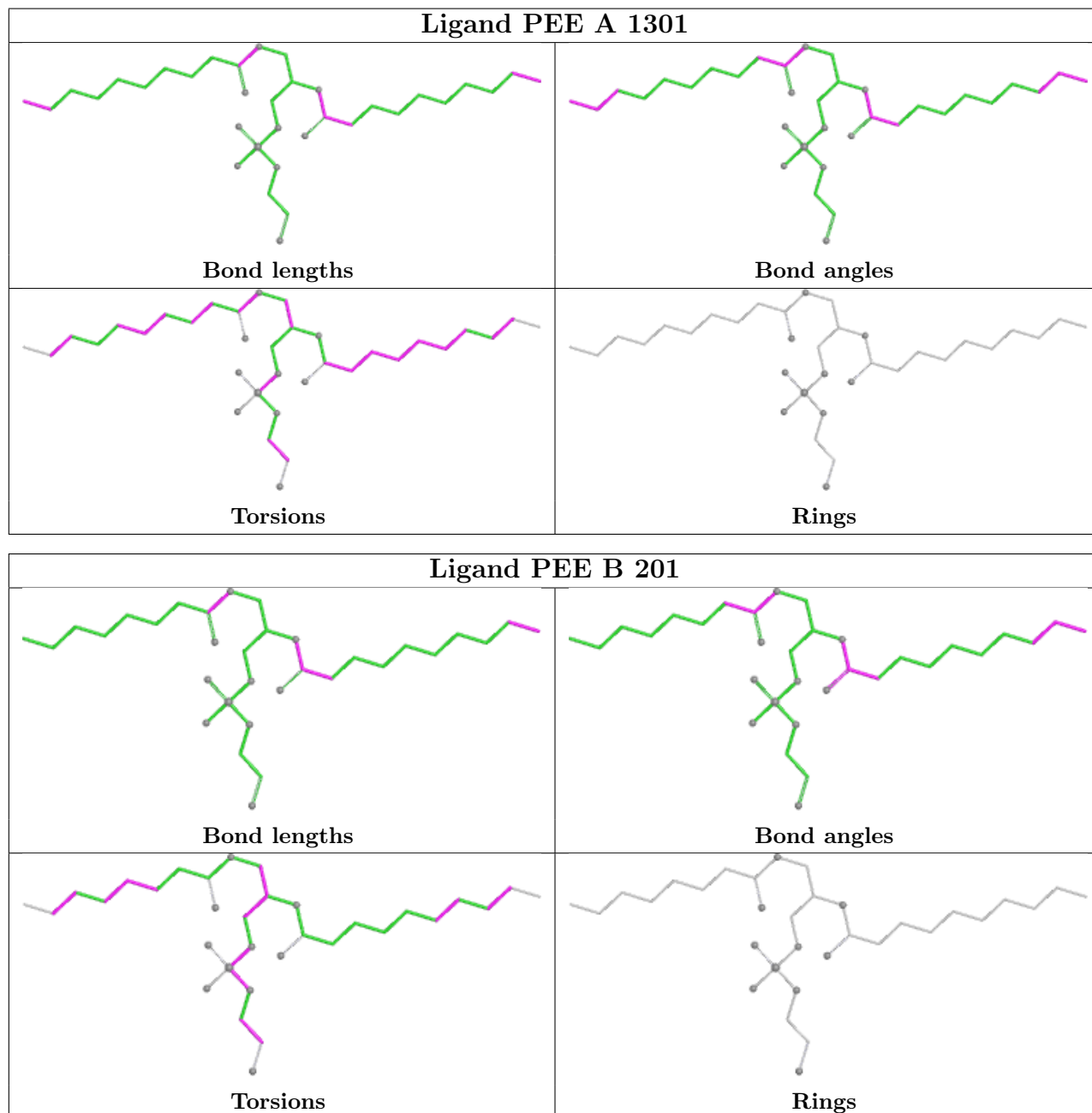
There are no ring outliers.

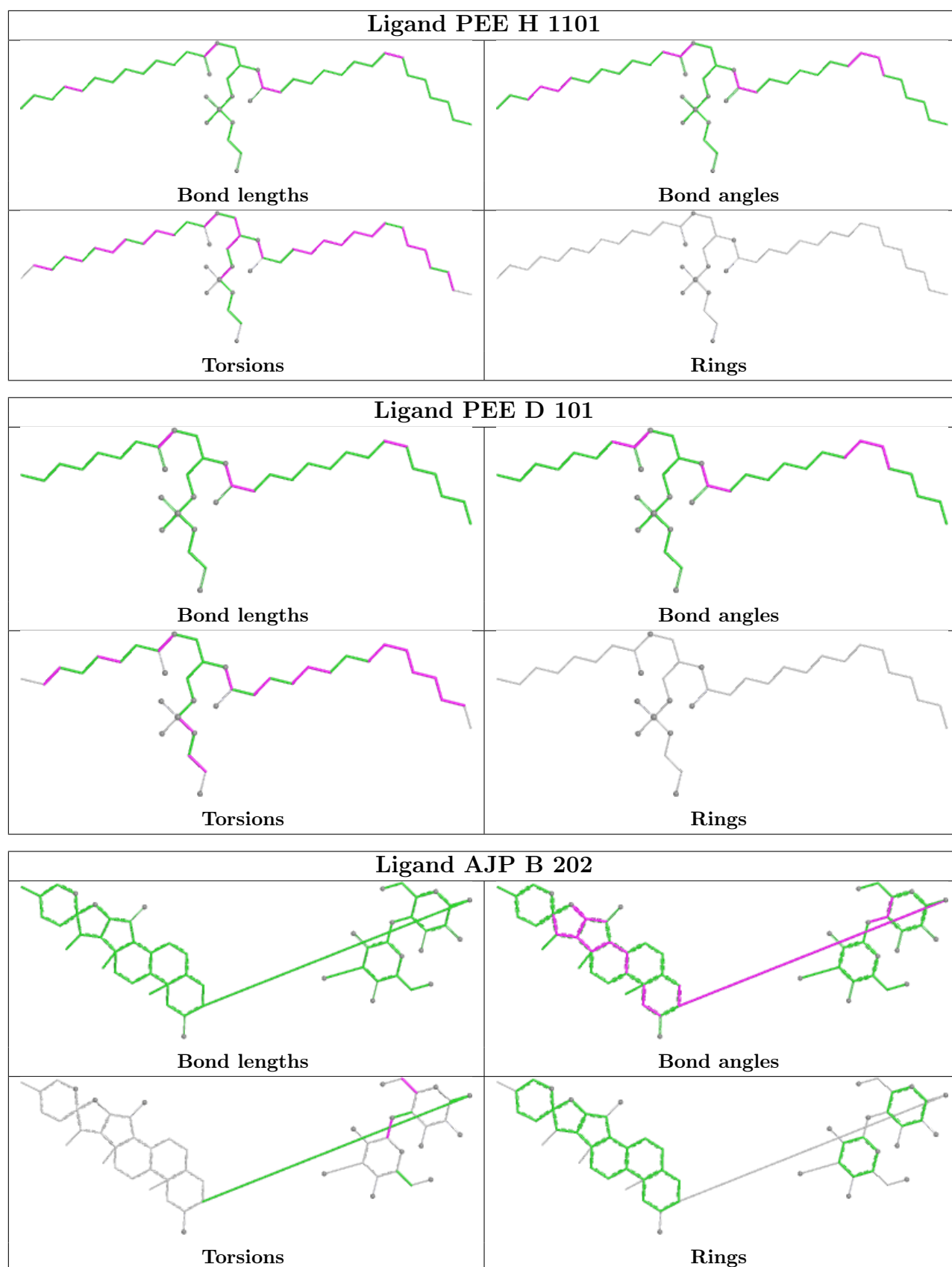
6 monomers are involved in 7 short contacts:

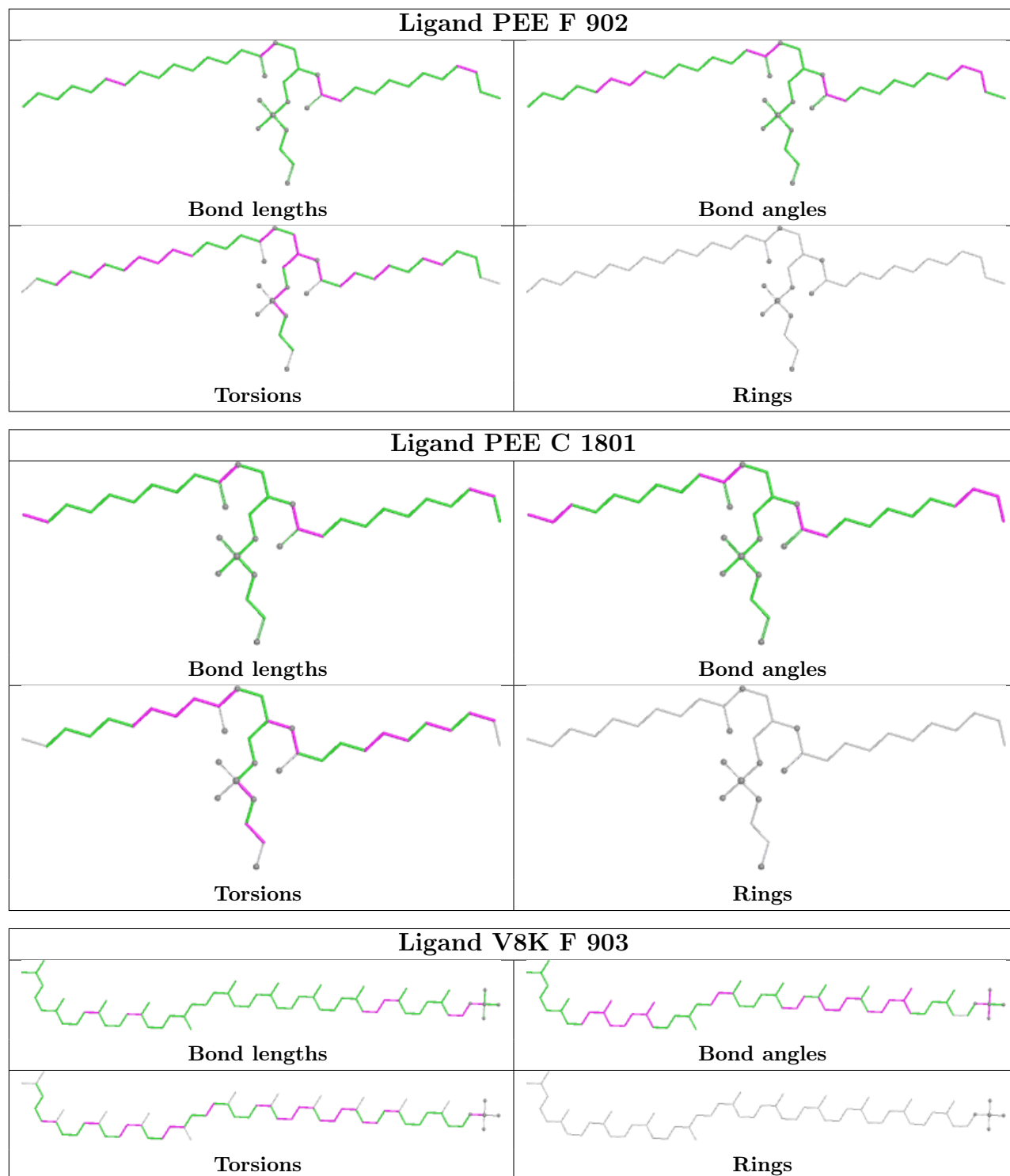
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	1301	PEE	2	0
12	H	1101	PEE	2	0
14	B	202	AJP	1	0
12	F	902	PEE	1	0
13	G	502	NAG	1	0
14	D	102	AJP	1	0

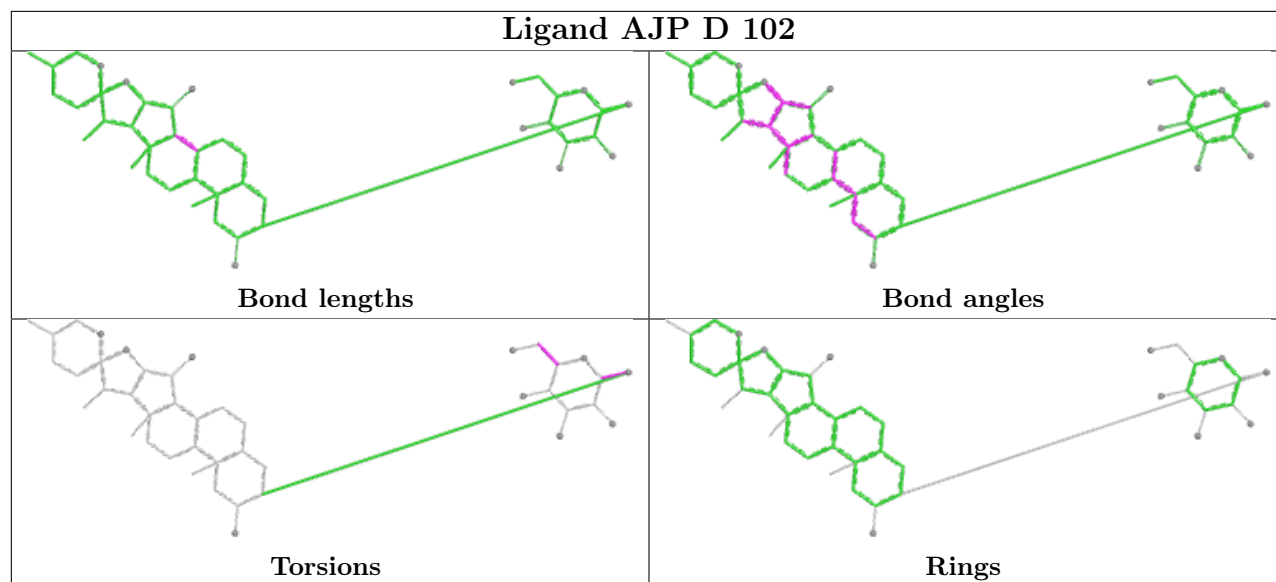
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

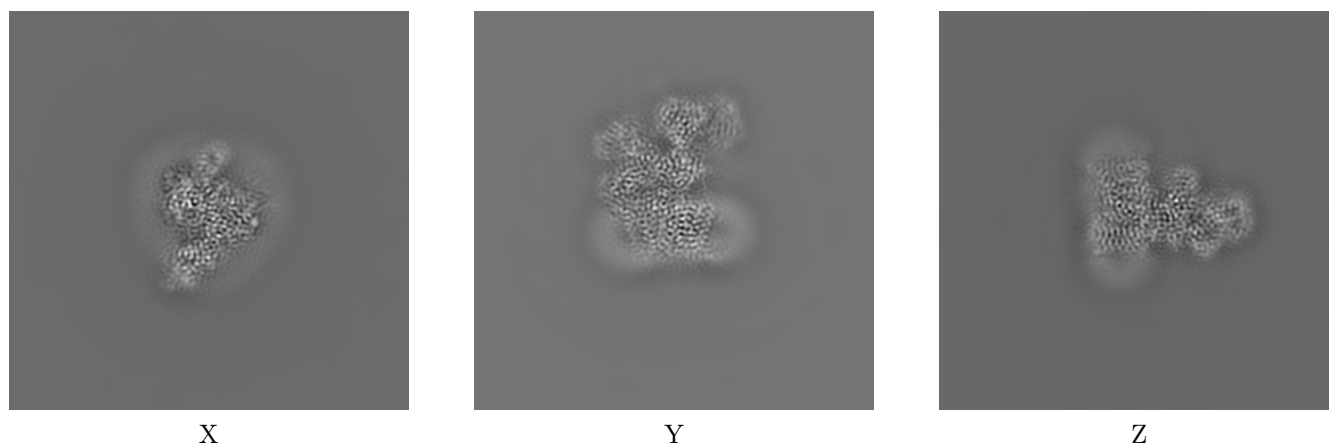
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12808. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

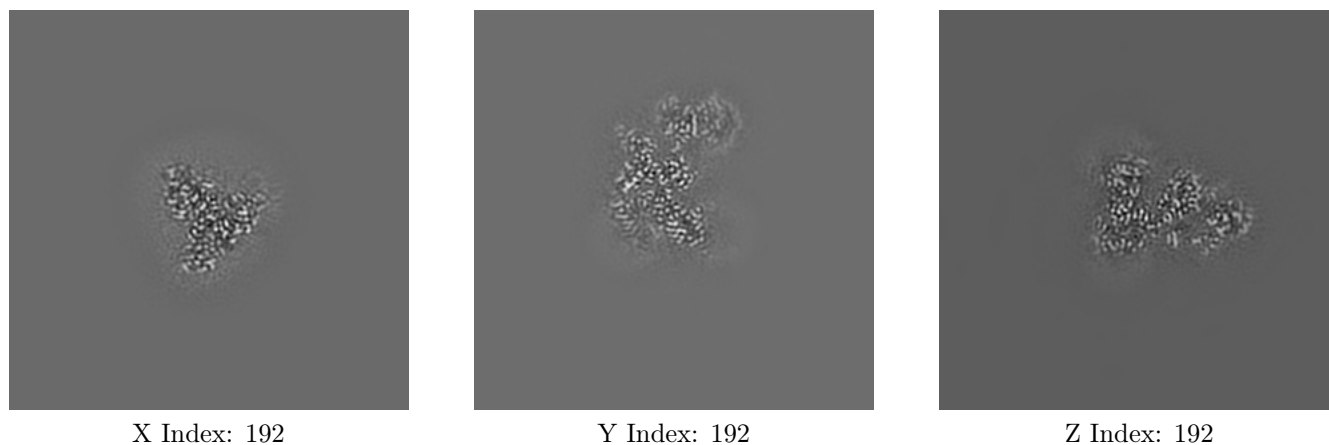
6.1.1 Primary map



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

6.2 Central slices [i](#)

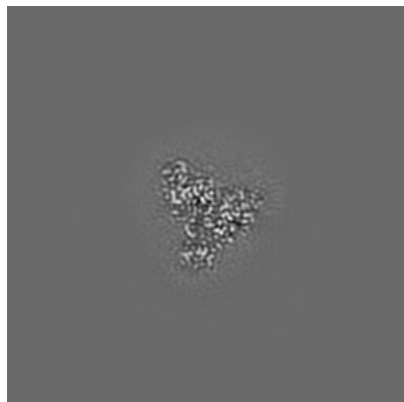
6.2.1 Primary map



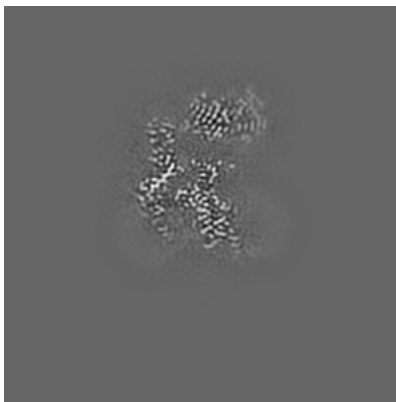
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

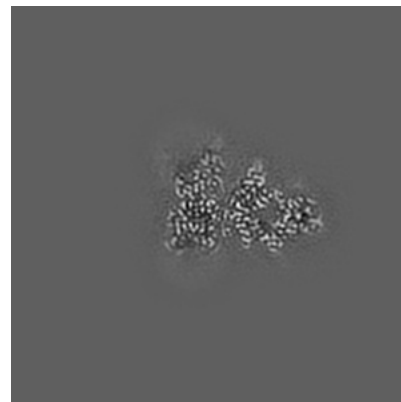
6.3.1 Primary map



X Index: 190



Y Index: 185

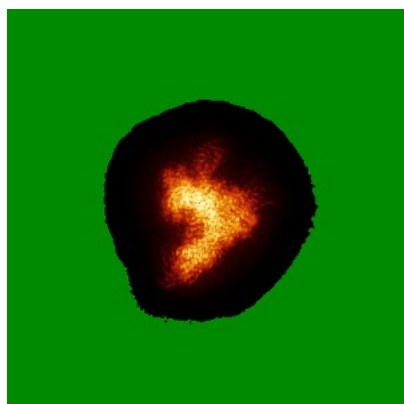


Z Index: 199

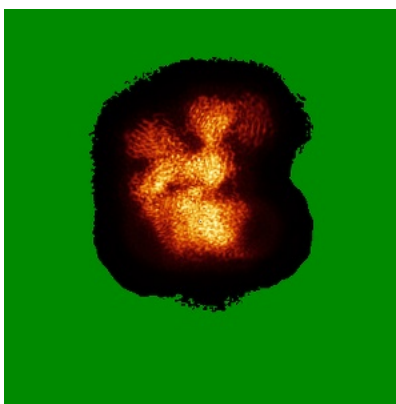
The images above show the largest variance slices of the map in three orthogonal directions.

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

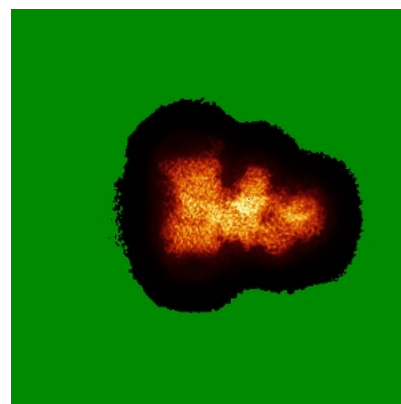
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

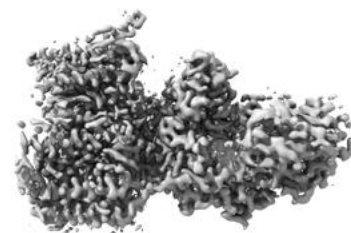
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

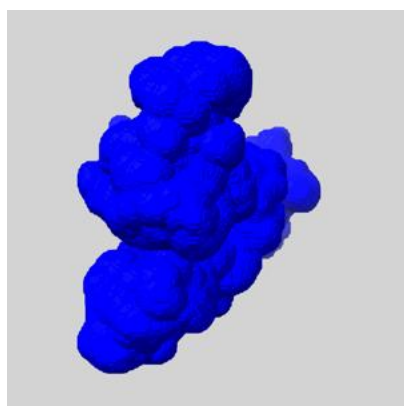
6.6 Mask visualisation [i](#)

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

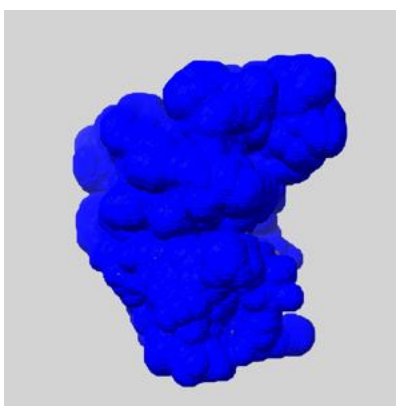
A mask typically either:

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

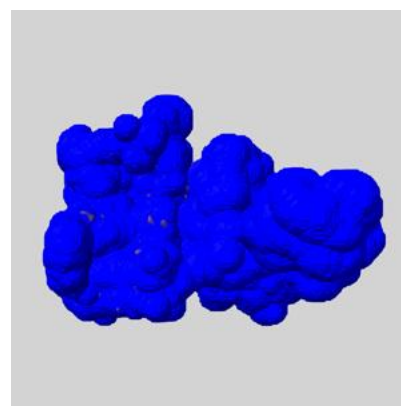
6.6.1 emd_12808_msk_1.map [i](#)



X



Y

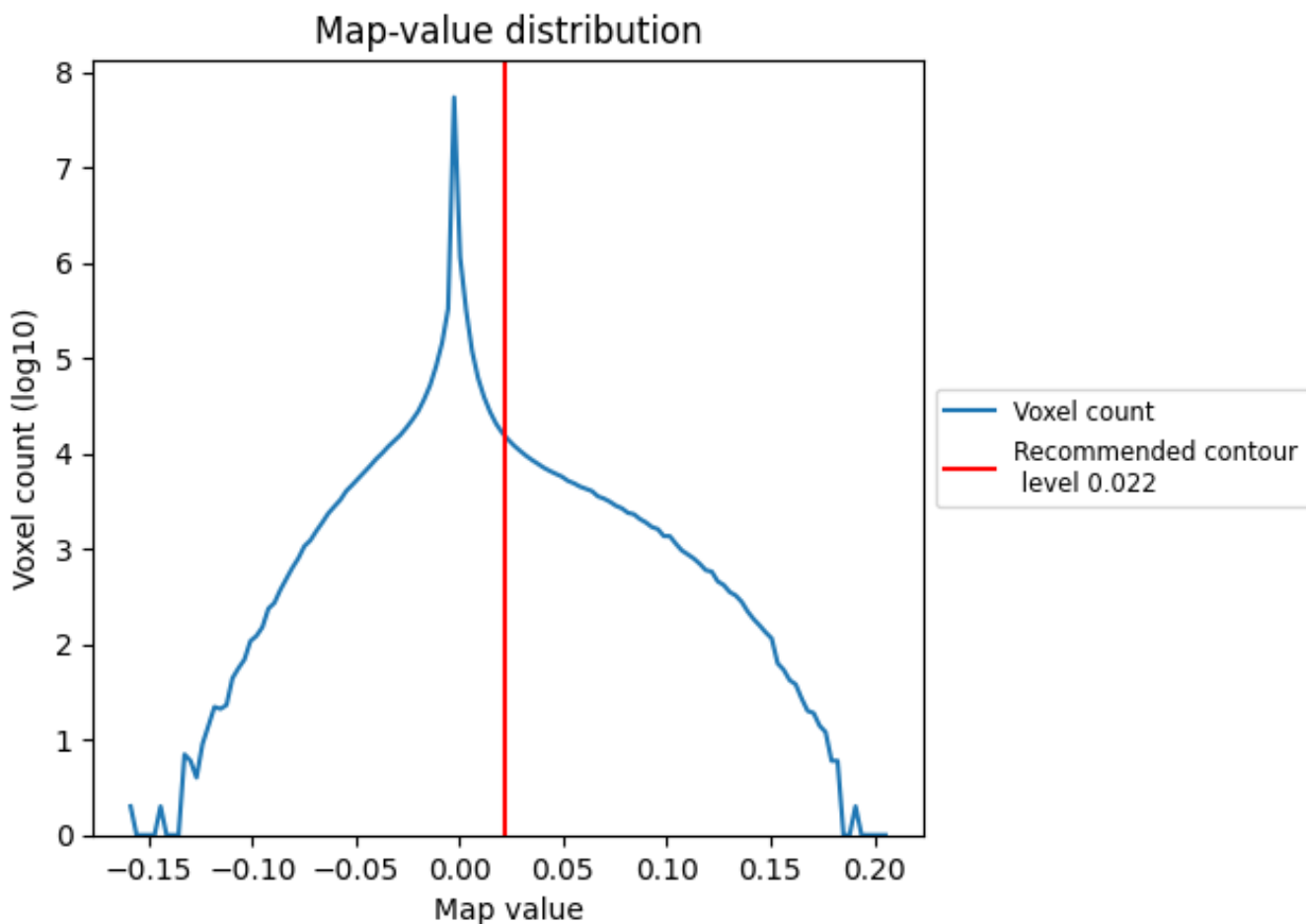


Z

7 Map analysis [i](#)

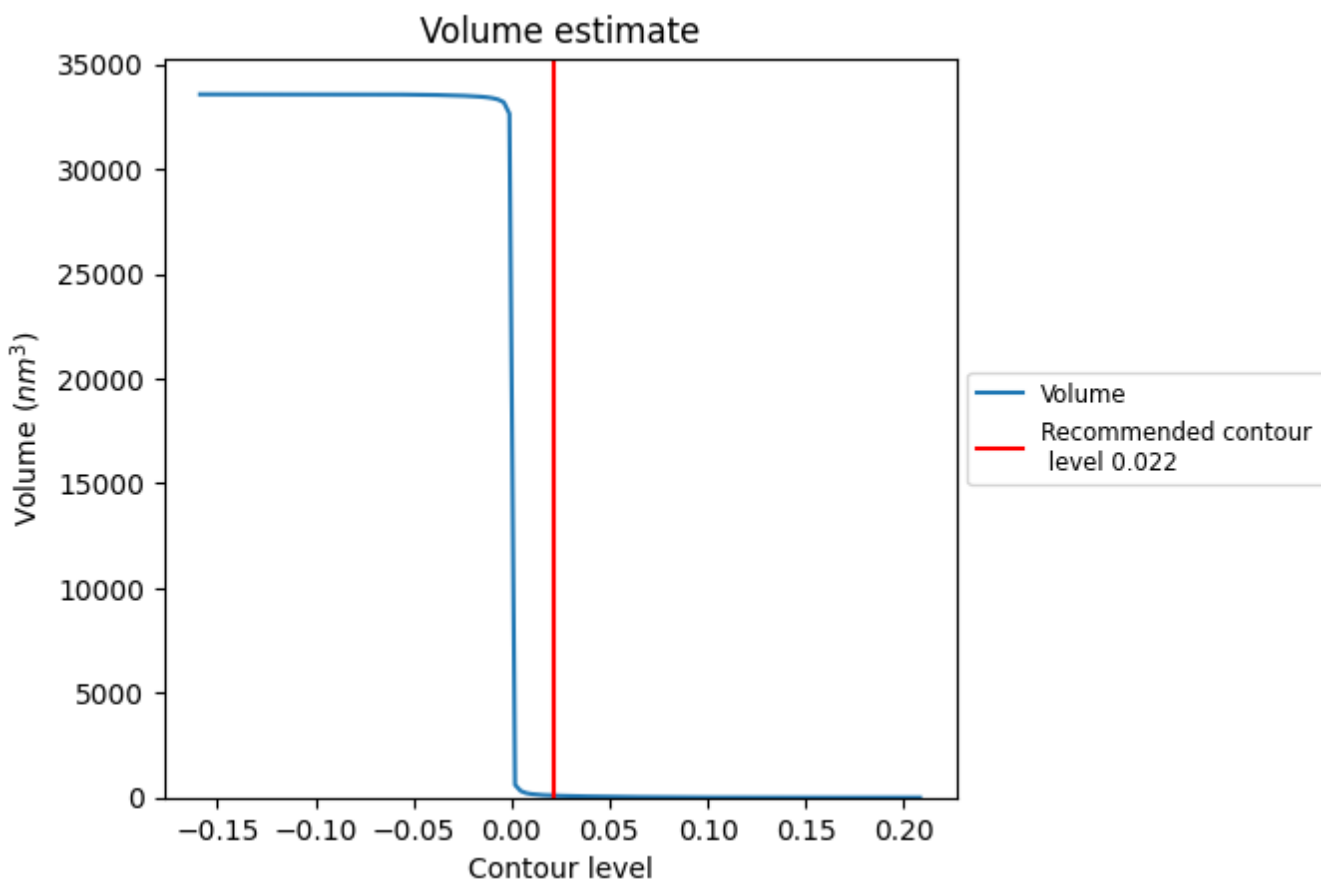
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

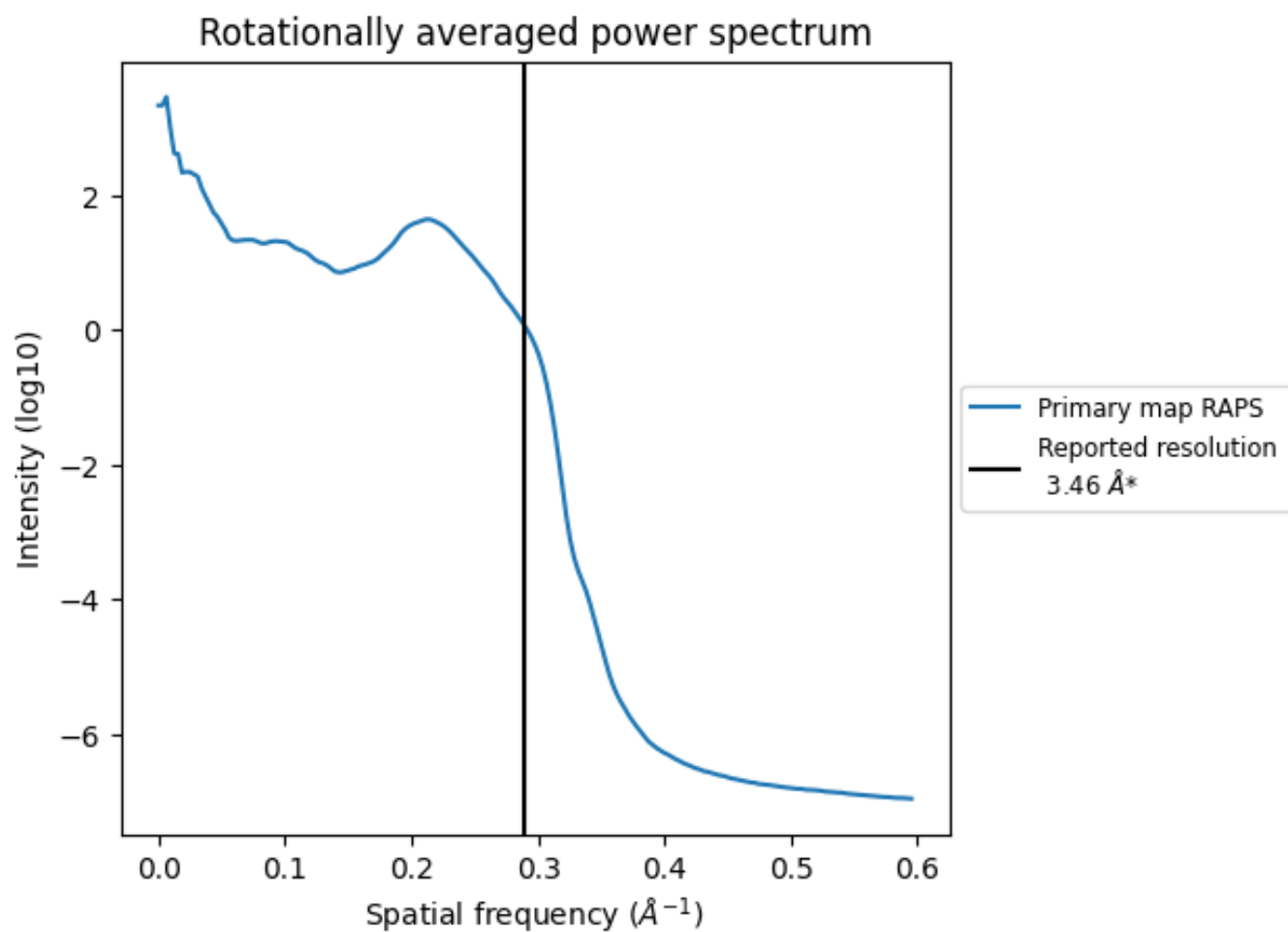
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 93 nm³; this corresponds to an approximate mass of 84 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

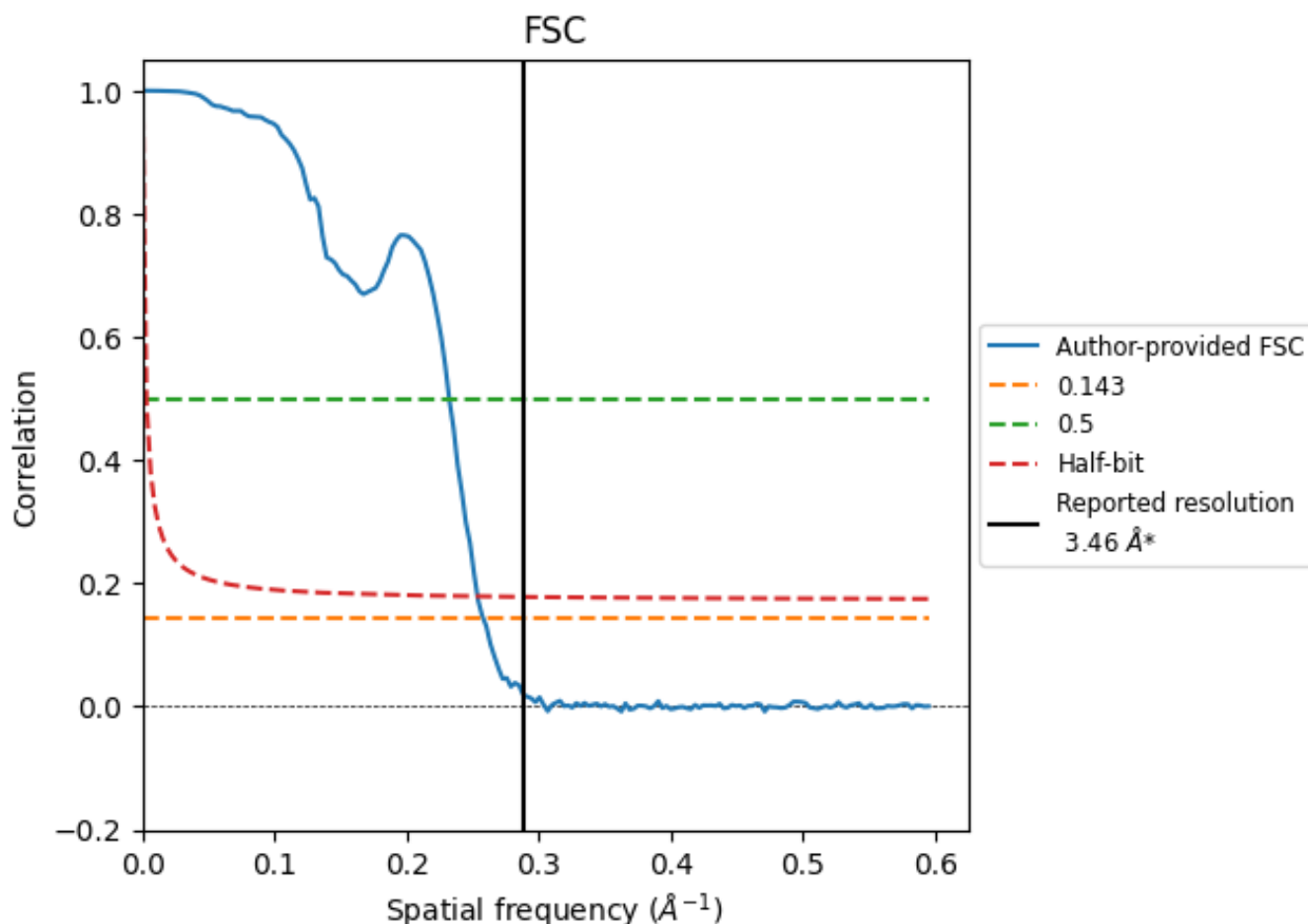


*Reported resolution corresponds to spatial frequency of 0.289\AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

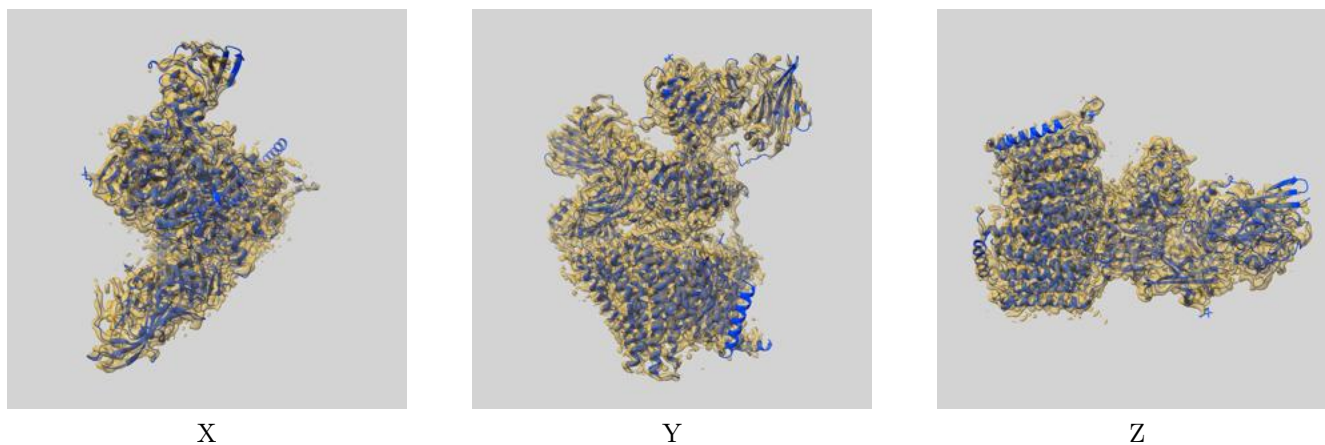
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.88	4.30	3.94
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.88 differs from the reported value 3.46 by more than 10 %

9 Map-model fit [i](#)

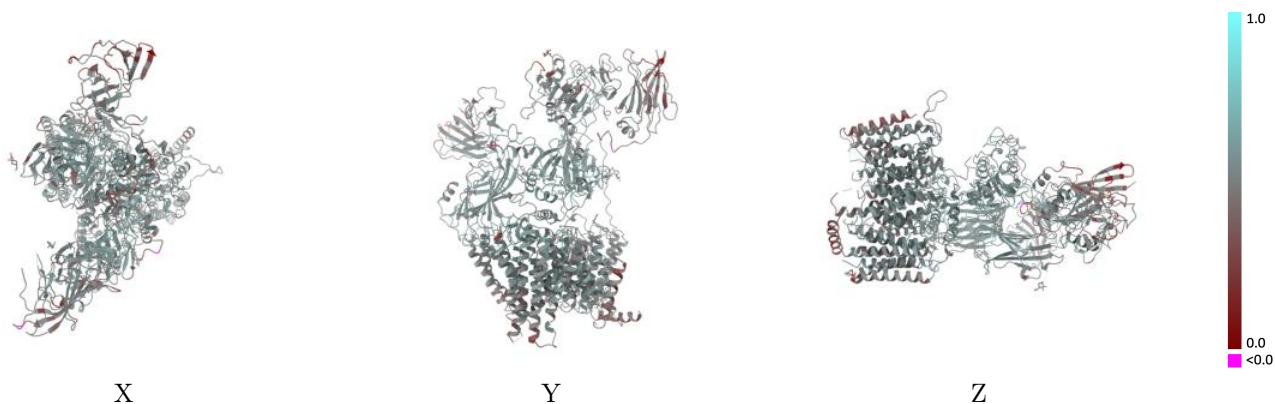
This section contains information regarding the fit between EMDB map EMD-12808 and PDB model 7OCI. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



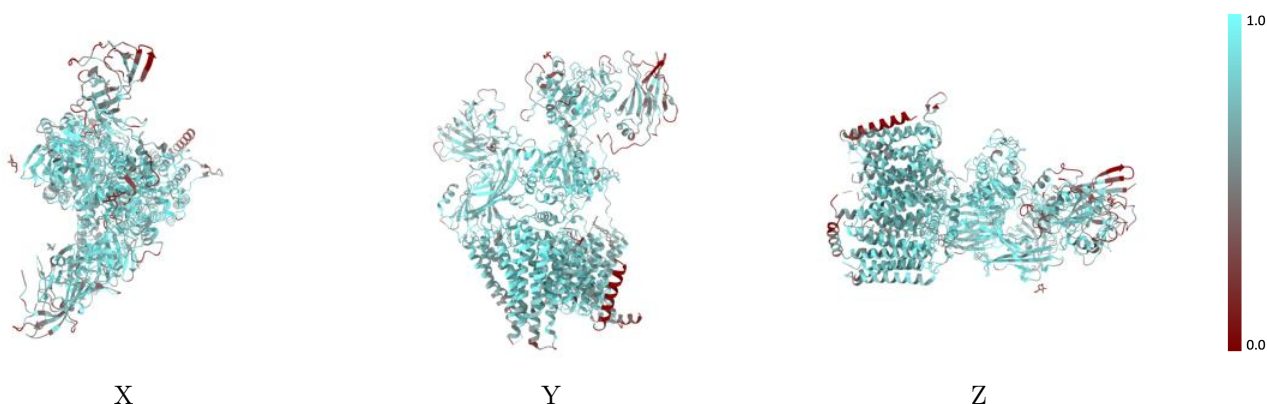
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



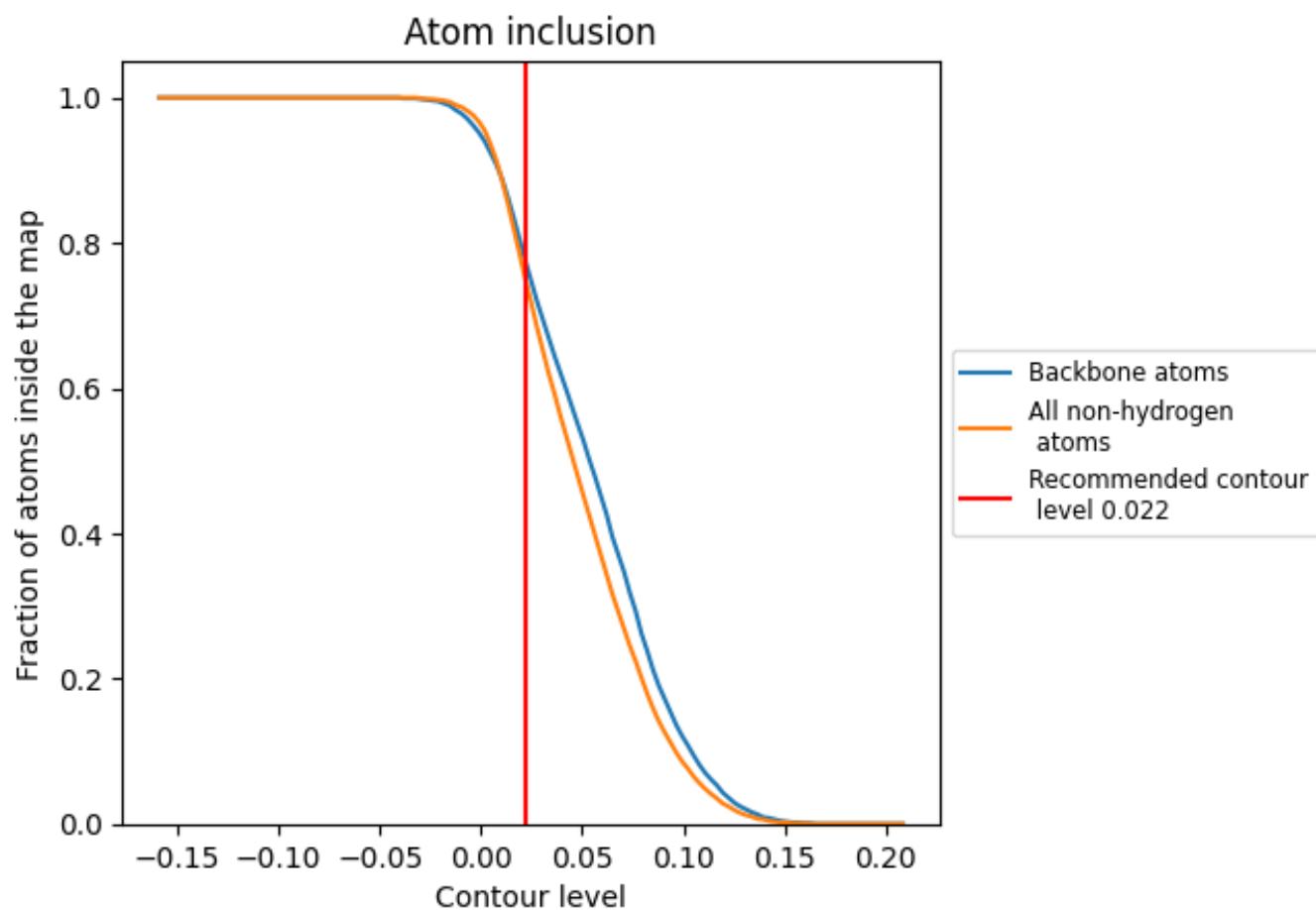
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).

























9.4 Atom inclusion [i](#)



At the recommended contour level, 78% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7490	 0.5140
A	 0.7400	 0.5150
B	 0.7390	 0.4990
C	 0.7190	 0.4960
D	 0.7550	 0.5210
E	 0.6930	 0.4830
F	 0.8280	 0.5410
G	 0.7690	 0.5230
H	 0.5970	 0.4590
I	 0.1250	 0.3940
J	 0.8430	 0.5380
K	 0.7500	 0.5020

