



## wwPDB EM Validation Summary Report ⓘ

Dec 4, 2024 – 06:11 pm GMT

PDB ID : 6EZN  
EMDB ID : EMD-4161  
Title : Cryo-EM structure of the yeast oligosaccharyltransferase (OST) complex  
Authors : Wild, R.; Kowal, J.; Eyring, J.; Ngwa, E.M.; Aebi, M.; Locher, K.P.  
Deposited on : 2017-11-16  
Resolution : 3.30 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

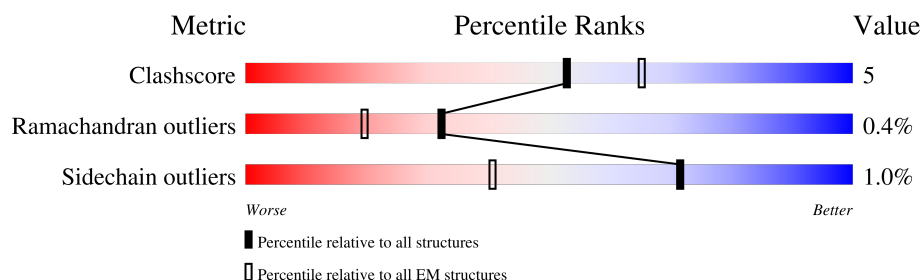
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	<div> <div>11%</div> <div>72%</div> <div>19%</div> <div>8%</div> </div>
2	B	130	<div> <div>14%</div> <div>75%</div> <div>9%</div> <div>15%</div> </div>
3	C	350	<div> <div>5%</div> <div>32%</div> <div>66%</div> </div>
4	D	36	<div> <div>89%</div> <div>6%</div> <div>6%</div> </div>
5	E	86	<div> <div>7%</div> <div>92%</div> <div>7%</div> </div>
6	F	718	<div> <div>7%</div> <div>79%</div> <div>11%</div> <div>9%</div> </div>
7	G	430	<div> <div>7%</div> <div>75%</div> <div>17%</div> <div>8%</div> </div>
8	H	286	<div> <div>36%</div> <div>79%</div> <div>10%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
9	I	3	<div><div></div><div>67%33%</div></div>
10	J	2	<div><div></div><div>50%100%</div></div>
10	L	2	<div><div></div><div>100%100%</div></div>
11	K	8	<div><div></div><div>38%25%75%</div></div>

## 2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 17008 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
1	A	438	Total	C	N	O	S	0	0
			3534	2293	564	670	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	110	Total	C	N	O	S	0	0
			879	594	141	138	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	120	Total	C	N	O	S	0	0
			973	662	147	159	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	34	Total	C	N	O	S	0	0
			258	166	38	50	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	650	Total	C	N	O	S	0	0
			5186	3428	829	906	23		

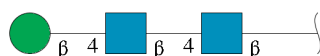
- Molecule 7 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	394	Total	C	N	O	S	0	0
			3179	2042	525	609	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	259	Total	C	N	O	S	0	0
			1880	1229	313	335	3		

- 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		

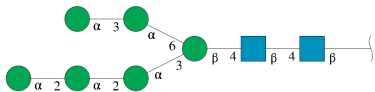
- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

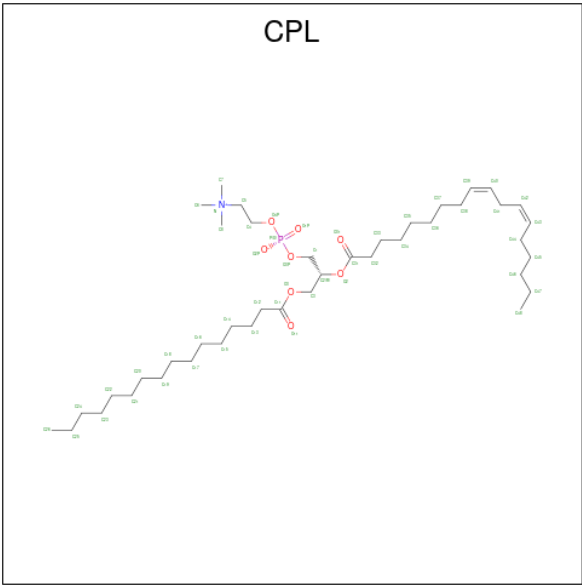
- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyra

nose-(1-2)-alpha-D-mannopyranose-(1-3)-[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.



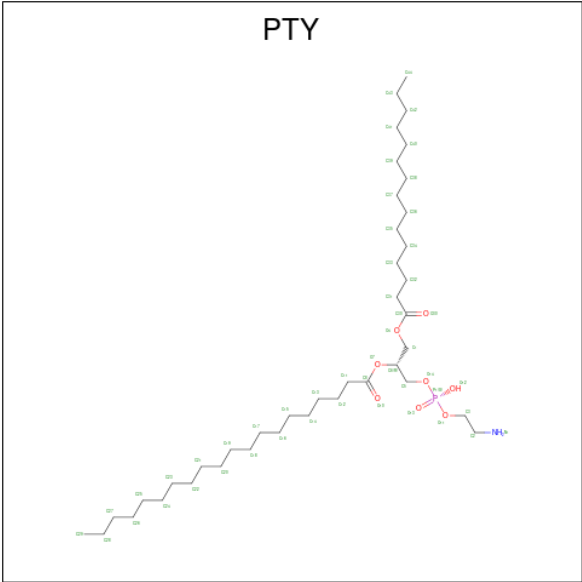
Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	8	Total	C	N	O	0	0
			94	52	2	40		

- Molecule 12 is 1-PALMITOYL-2-LINOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: CPL) (formula: C<sub>42</sub>H<sub>80</sub>NO<sub>8</sub>P).



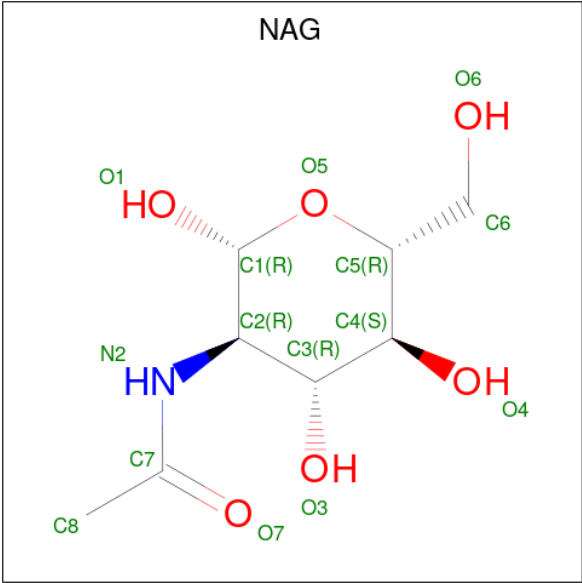
Mol	Chain	Residues	Atoms					AltConf
12	A	1	Total	C	N	O	P	0
			52	42	1	8	1	
12	E	1	Total	C	N	O	P	0
			52	42	1	8	1	
12	F	1	Total	C	N	O	P	0
			52	42	1	8	1	
12	H	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 13 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula: C<sub>40</sub>H<sub>80</sub>NO<sub>8</sub>P).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
13	F	1	42	32	1	8	1	0

- Molecule 14 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).

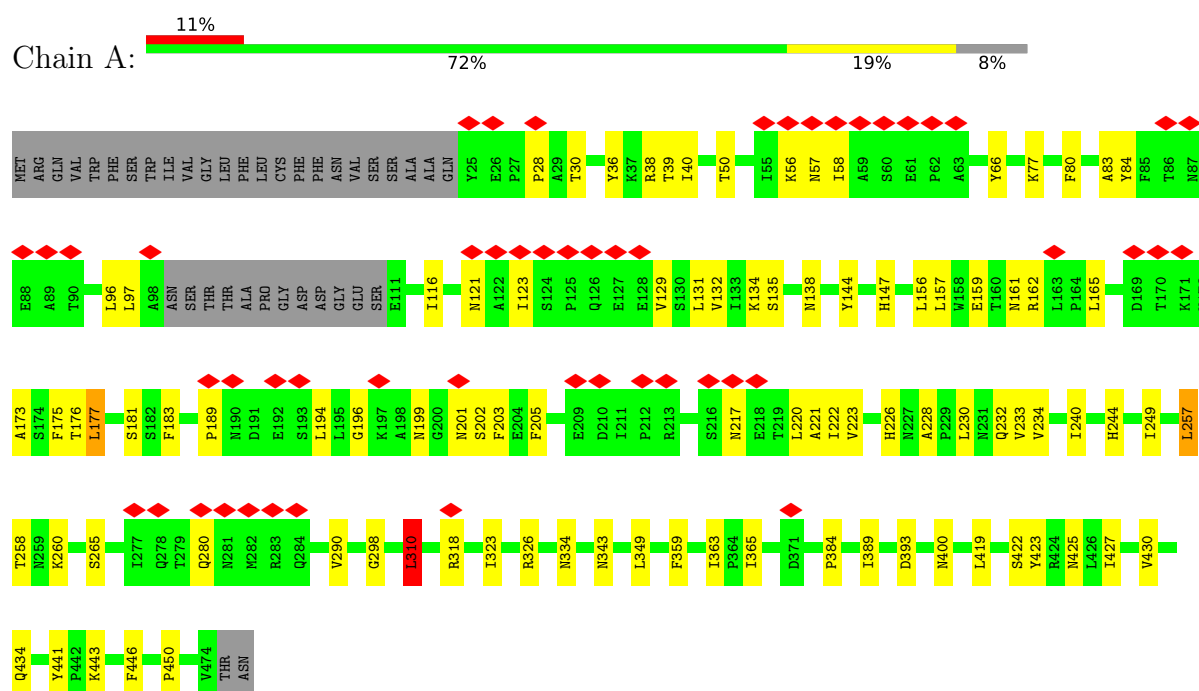


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
14	G	1	14	8	1	5	0

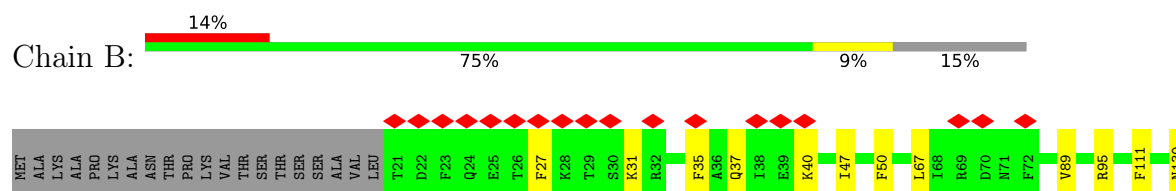
### 3 Residue-property plots

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.

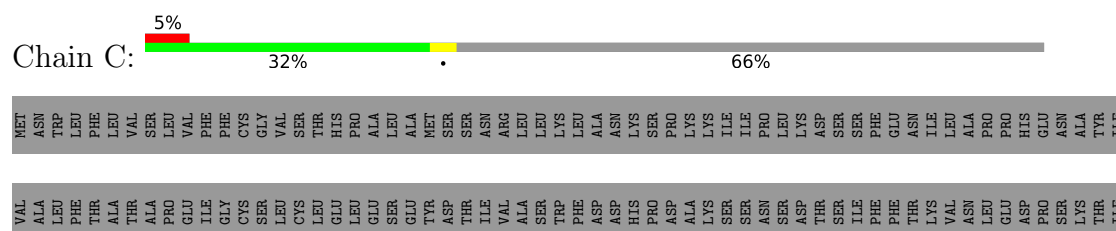
- Molecule 1: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1



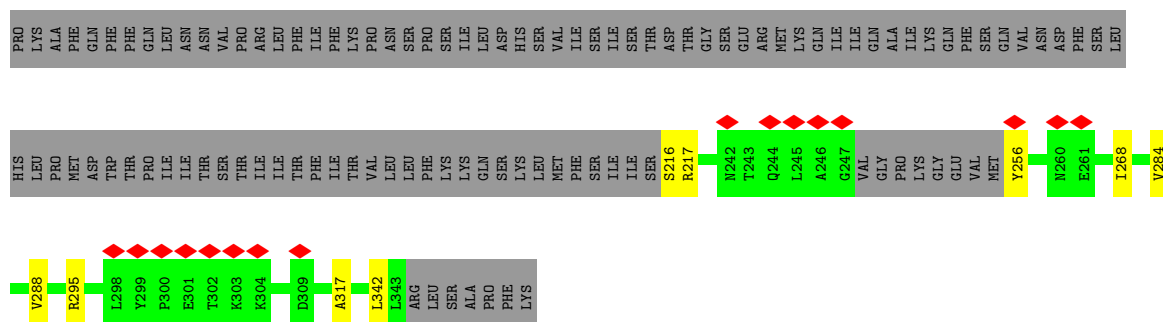
- Molecule 2: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST2



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







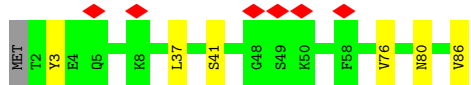
- Molecule 4: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST4

Chain D: 89% 6% 6%



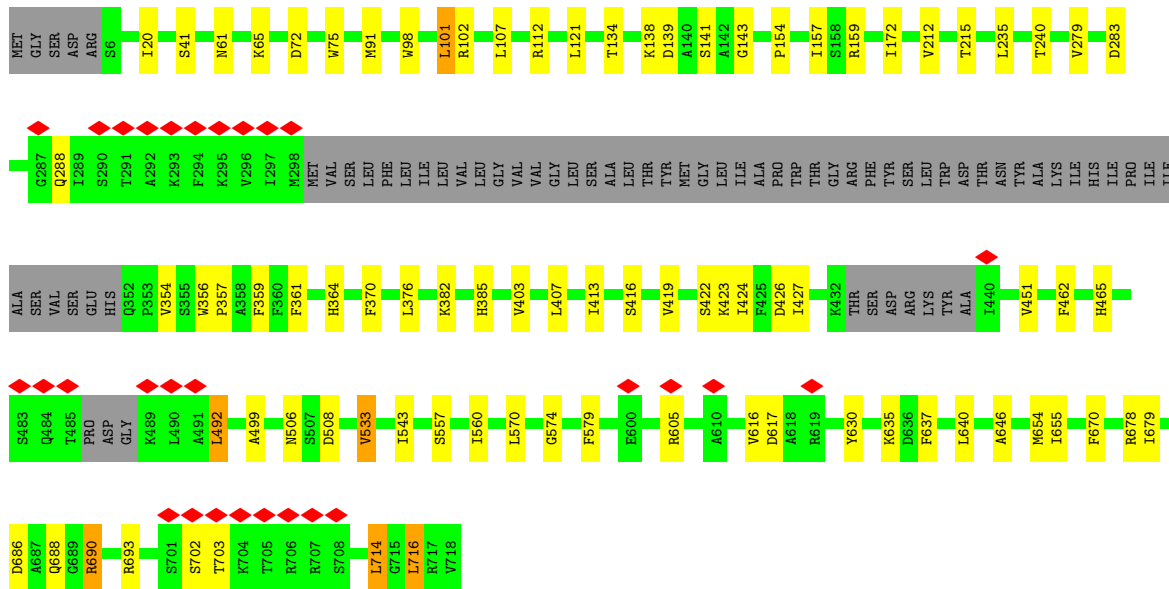
- Molecule 5: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit OST5

Chain E: 7% 92% 7%



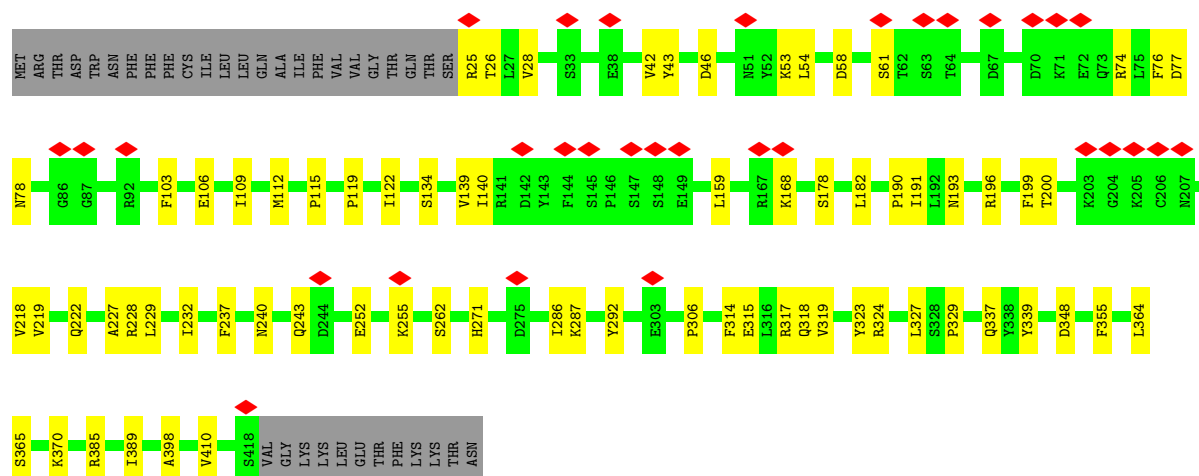
- Molecule 6: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3

Chain F: 79% 11% 9%

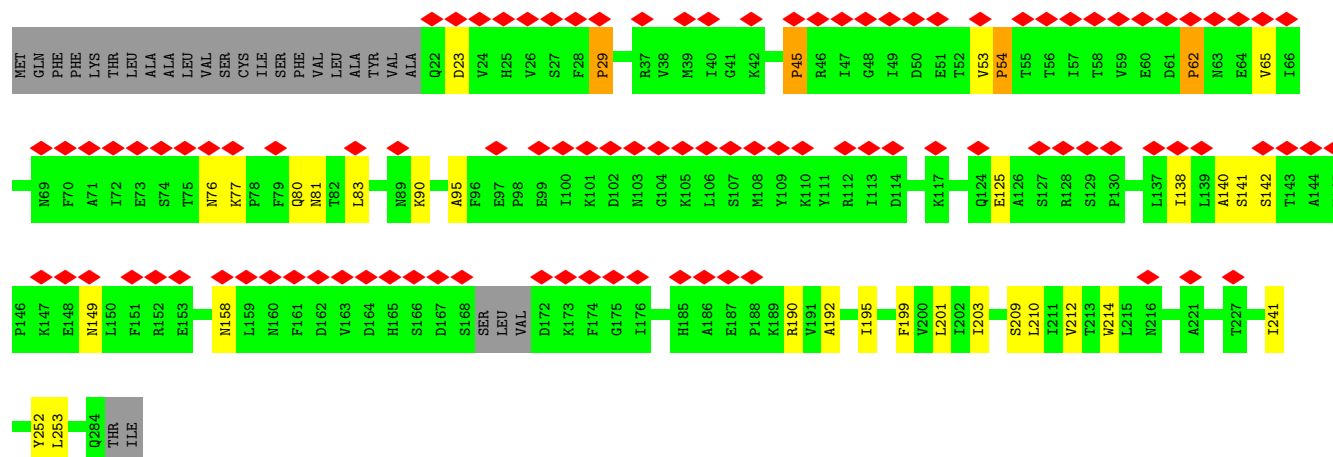
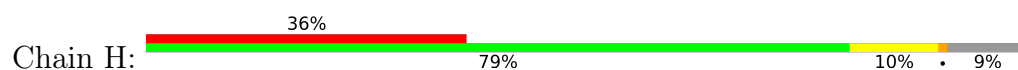


- Molecule 7: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1

Chain G: 7% 75% 17% 8%



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



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



- 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-(1-3)-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



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	110091	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 ( $e^-/\text{\AA}^2$ )	2	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	0.293	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.037	Depositor
Map size (Å)	319.50003, 319.50003, 319.50003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, MAN, PTY, CPL

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	0.36	0/3636	0.66	5/4950 (0.1%)
2	B	0.37	0/901	0.61	0/1217
3	C	0.34	0/1001	0.57	1/1362 (0.1%)
4	D	0.31	0/261	0.51	0/354
5	E	0.34	0/684	0.60	0/926
6	F	0.39	0/5336	0.67	8/7262 (0.1%)
7	G	0.34	0/3261	0.60	1/4434 (0.0%)
8	H	0.31	0/1917	0.64	5/2611 (0.2%)
All	All	0.36	0/16997	0.64	20/23116 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
6	F	0	3
All	All	0	5

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	310	LEU	CA-CB-CG	8.70	135.32	115.30
6	F	492	LEU	CA-CB-CG	8.01	133.73	115.30
6	F	716	LEU	CA-CB-CG	7.50	132.55	115.30
6	F	101	LEU	CA-CB-CG	7.41	132.33	115.30
1	A	257	LEU	CA-CB-CG	6.97	131.32	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	144	TYR	Peptide
1	A	280	GLN	Peptide
6	F	533	VAL	Peptide
6	F	605	ARG	Peptide
6	F	75	TRP	Peptide

## 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	3534	0	3408	53	0
2	B	879	0	903	11	0
3	C	973	0	998	5	0
4	D	258	0	267	2	0
5	E	666	0	677	5	0
6	F	5186	0	5095	48	0
7	G	3179	0	3059	43	0
8	H	1880	0	1791	16	0
9	I	39	0	34	1	0
10	J	28	0	25	0	0
10	L	28	0	25	0	0
11	K	94	0	79	0	0
12	A	52	0	80	1	0
12	E	52	0	80	0	0
12	F	52	0	80	4	0
12	H	52	0	80	2	0
13	F	42	0	60	2	0
14	G	14	0	13	0	0
All	All	17008	0	16754	171	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 5.

The worst 5 of 171 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)
6:F:422:SER:O	6:F:426:ASP:HB2	1.74	0.88
7:G:315:GLU:HA	7:G:323:TYR:O	1.76	0.85
1:A:156:LEU:O	1:A:223:VAL:HA	1.84	0.77
6:F:357:PRO:O	6:F:361:PHE:HB2	1.88	0.73
7:G:222:GLN:HE22	7:G:365:SER:HA	1.55	0.71

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	434/476 (91%)	389 (90%)	44 (10%)	1 (0%)	44	71
2	B	108/130 (83%)	102 (94%)	6 (6%)	0	100	100
3	C	116/350 (33%)	109 (94%)	7 (6%)	0	100	100
4	D	32/36 (89%)	30 (94%)	2 (6%)	0	100	100
5	E	83/86 (96%)	78 (94%)	5 (6%)	0	100	100
6	F	642/718 (89%)	592 (92%)	50 (8%)	0	100	100
7	G	392/430 (91%)	361 (92%)	30 (8%)	1 (0%)	37	66
8	H	255/286 (89%)	217 (85%)	32 (12%)	6 (2%)	5	25
All	All	2062/2512 (82%)	1878 (91%)	176 (8%)	8 (0%)	32	61

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	45	PRO
8	H	54	PRO
8	H	62	PRO
8	H	65	VAL
8	H	29	PRO

### 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	393/426 (92%)	387 (98%)	6 (2%)	60	77
2	B	94/115 (82%)	94 (100%)	0	100	100
3	C	104/316 (33%)	103 (99%)	1 (1%)	73	84
4	D	31/33 (94%)	31 (100%)	0	100	100
5	E	74/75 (99%)	74 (100%)	0	100	100
6	F	539/613 (88%)	532 (99%)	7 (1%)	65	79
7	G	351/392 (90%)	349 (99%)	2 (1%)	84	90
8	H	175/249 (70%)	173 (99%)	2 (1%)	70	82
All	All	1761/2219 (79%)	1743 (99%)	18 (1%)	71	84

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	168	LYS
8	H	201	LEU
8	H	158	ASN
6	F	288	GLN
6	F	716	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
7	G	271	HIS
8	H	158	ASN
5	E	80	ASN
6	F	385	HIS
6	F	506	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 ⓘ

15 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	1,9	14,14,15	0.25	0	17,19,21	0.51	0
9	NAG	I	2	9	14,14,15	0.21	0	17,19,21	0.73	1 (5%)
9	BMA	I	3	9	11,11,12	0.75	0	15,15,17	0.86	0
10	NAG	J	1	10,1	14,14,15	0.34	0	17,19,21	0.54	0
10	NAG	J	2	10	14,14,15	0.37	0	17,19,21	0.43	0
11	NAG	K	1	11,6	14,14,15	0.49	0	17,19,21	0.63	0
11	NAG	K	2	11	14,14,15	0.25	0	17,19,21	0.54	0
11	BMA	K	3	11	11,11,12	0.65	0	15,15,17	0.86	1 (6%)
11	MAN	K	4	11	11,11,12	0.81	0	15,15,17	1.66	2 (13%)
11	MAN	K	5	11	11,11,12	0.70	0	15,15,17	1.25	2 (13%)
11	MAN	K	6	11	11,11,12	0.92	1 (9%)	15,15,17	0.98	1 (6%)
11	MAN	K	7	11	11,11,12	1.26	1 (9%)	15,15,17	1.28	2 (13%)
11	MAN	K	8	11	11,11,12	0.70	0	15,15,17	1.05	2 (13%)
10	NAG	L	1	10,7	14,14,15	0.42	0	17,19,21	0.56	0
10	NAG	L	2	10	14,14,15	0.34	0	17,19,21	0.49	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
9	NAG	I	1	1,9	-	0/6/23/26	0/1/1/1
9	NAG	I	2	9	-	2/6/23/26	0/1/1/1
9	BMA	I	3	9	-	0/2/19/22	0/1/1/1

*Continued on next page...*

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	J	1	10,1	-	2/6/23/26	0/1/1/1
10	NAG	J	2	10	-	2/6/23/26	0/1/1/1
11	NAG	K	1	11,6	-	2/6/23/26	0/1/1/1
11	NAG	K	2	11	-	1/6/23/26	0/1/1/1
11	BMA	K	3	11	-	2/2/19/22	0/1/1/1
11	MAN	K	4	11	-	0/2/19/22	0/1/1/1
11	MAN	K	5	11	-	1/2/19/22	0/1/1/1
11	MAN	K	6	11	-	0/2/19/22	0/1/1/1
11	MAN	K	7	11	-	0/2/19/22	0/1/1/1
11	MAN	K	8	11	-	2/2/19/22	0/1/1/1
10	NAG	L	1	10,7	-	1/6/23/26	0/1/1/1
10	NAG	L	2	10	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	K	7	MAN	C2-C3	2.53	1.56	1.52
11	K	6	MAN	O5-C1	-2.11	1.40	1.43

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	4	MAN	C1-O5-C5	4.40	118.15	112.19
11	K	4	MAN	O2-C2-C3	-3.79	102.55	110.14
11	K	7	MAN	C1-O5-C5	3.15	116.47	112.19
11	K	5	MAN	O2-C2-C3	-3.07	103.98	110.14
11	K	5	MAN	C1-O5-C5	3.00	116.25	112.19

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

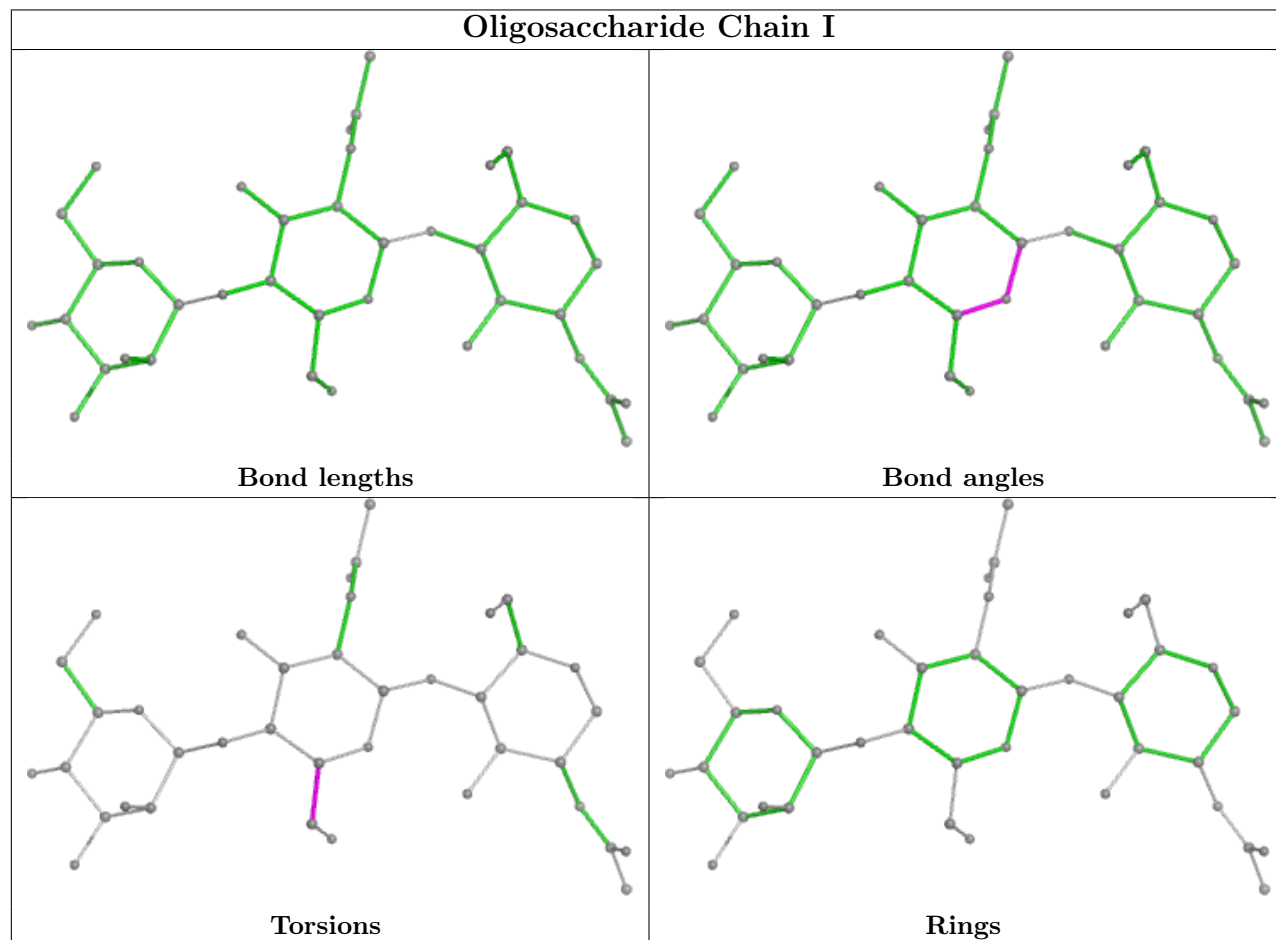
Mol	Chain	Res	Type	Atoms
10	J	2	NAG	O5-C5-C6-O6
10	J	2	NAG	C4-C5-C6-O6
11	K	3	BMA	C4-C5-C6-O6
10	J	1	NAG	O5-C5-C6-O6
11	K	3	BMA	O5-C5-C6-O6

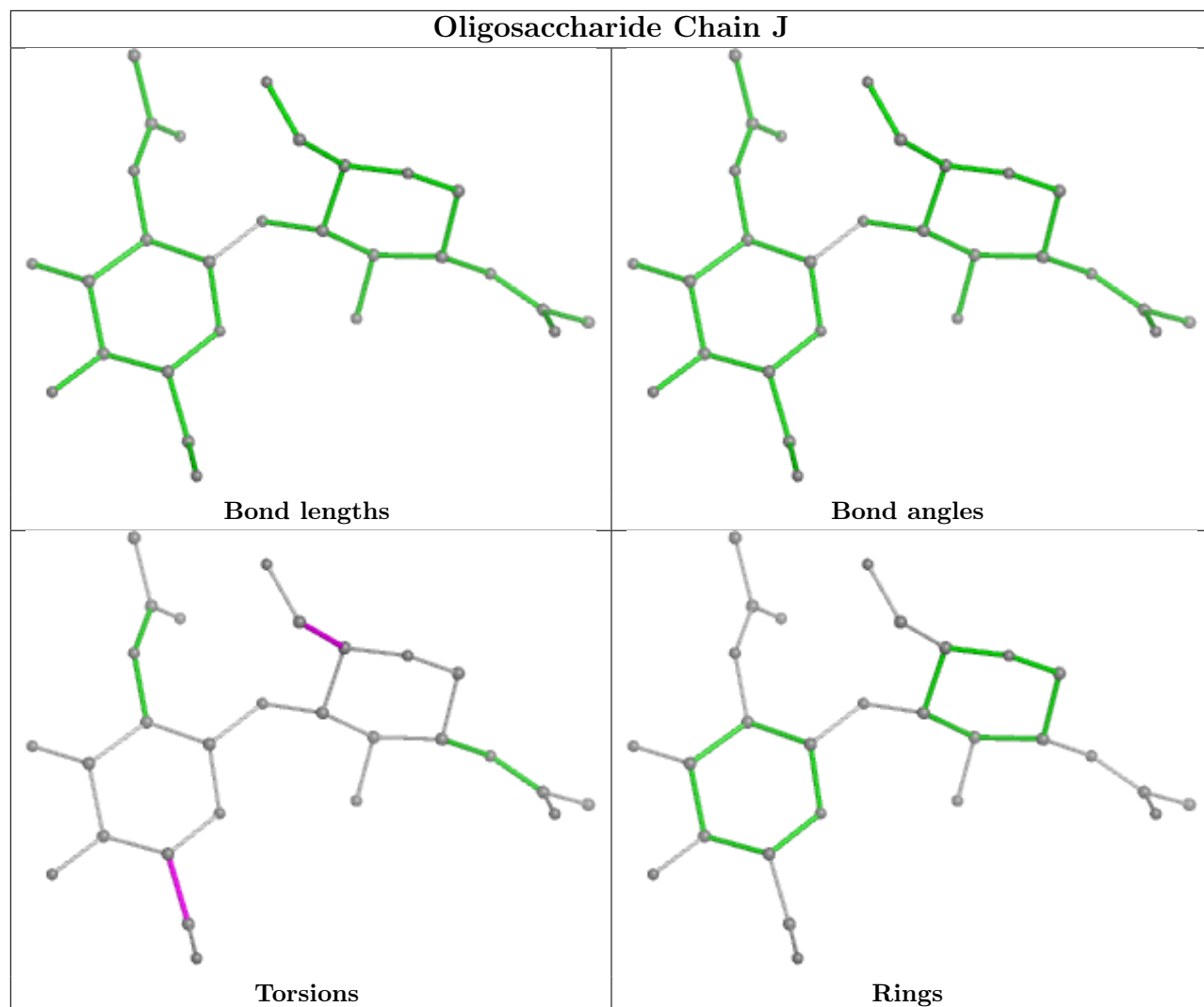
There are no ring outliers.

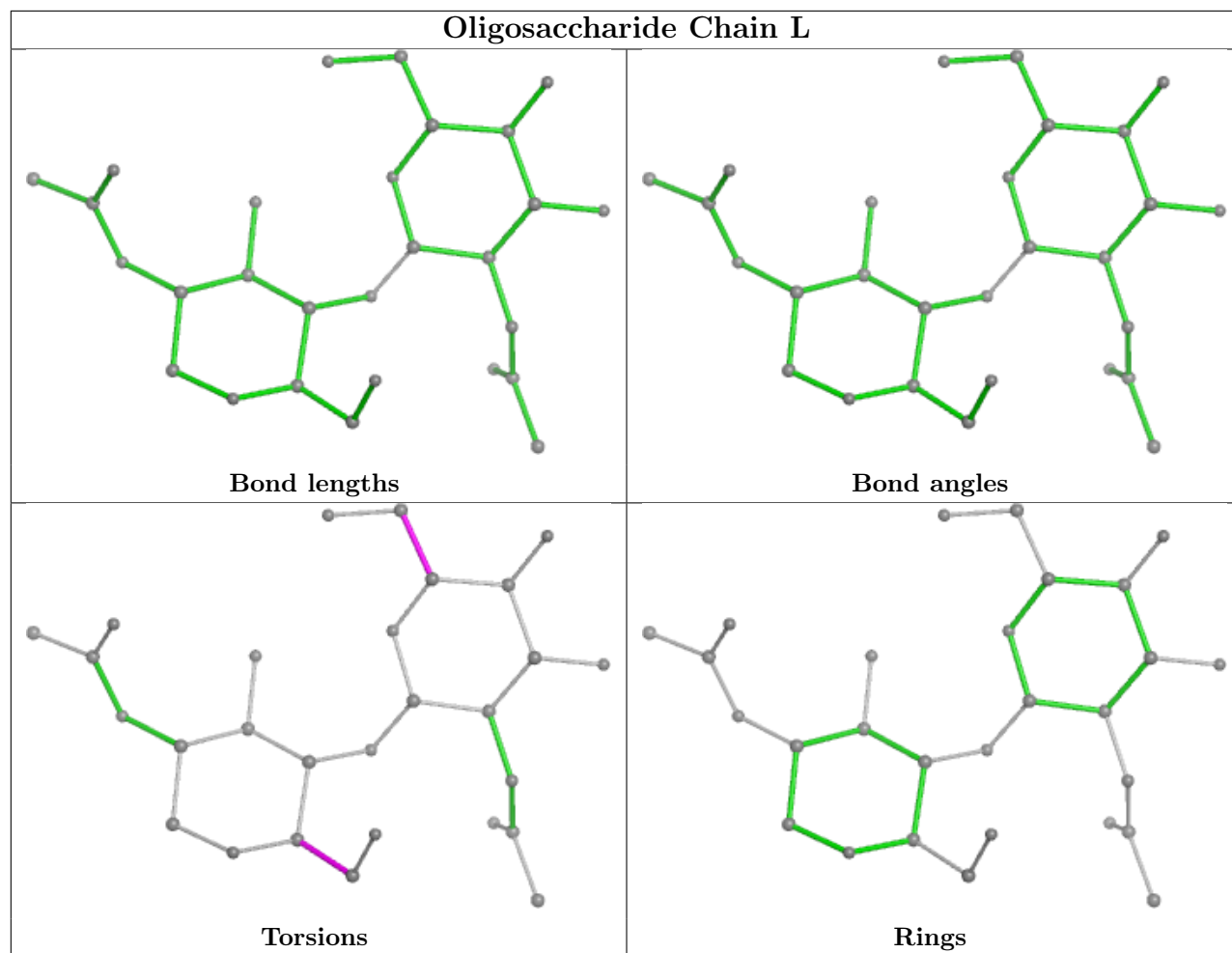
1 monomer is involved in 1 short contact:

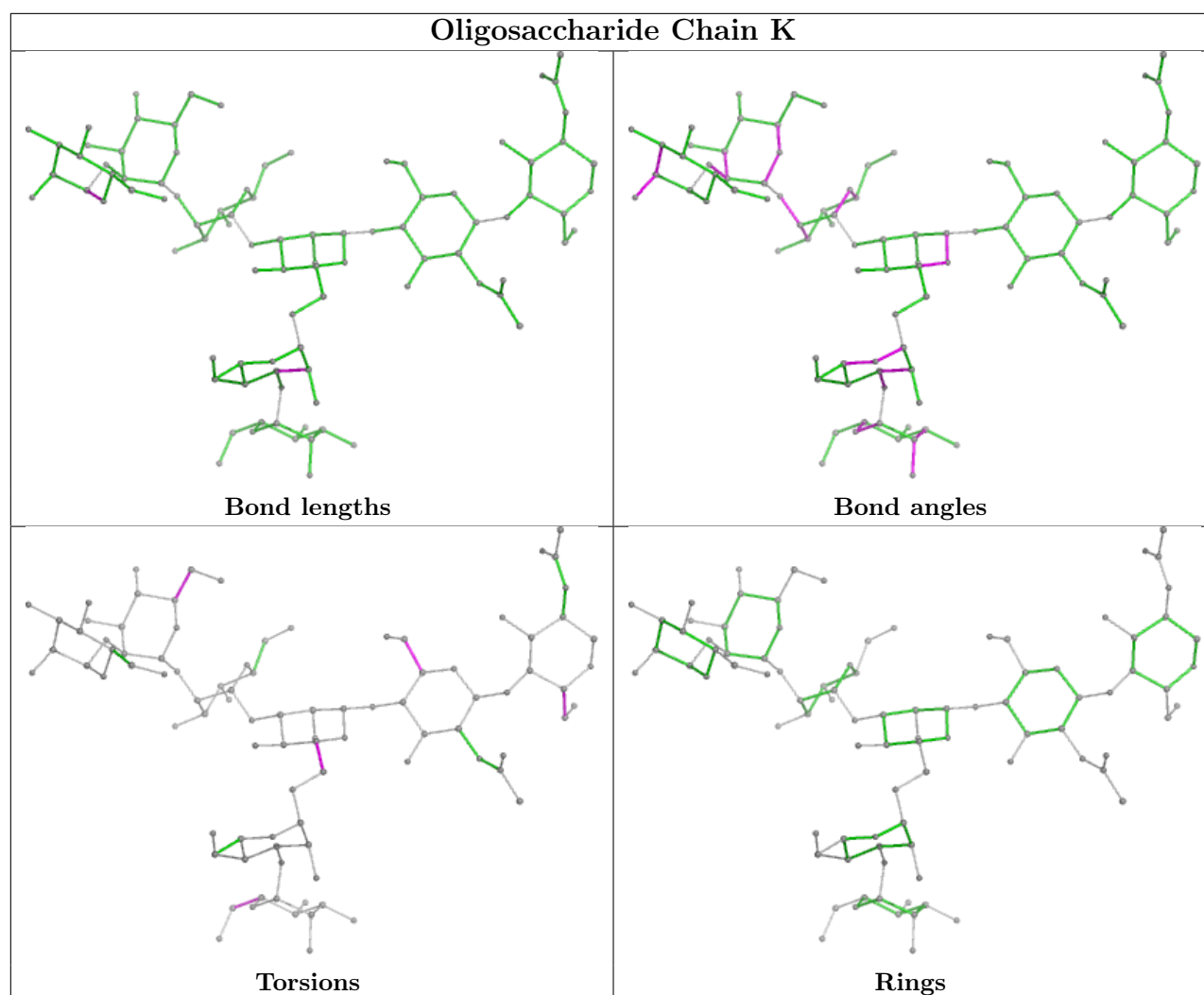
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	I	2	NAG	1	0

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](#)

6 ligands 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	$\# Z  > 2$
12	CPL	A	506	-	51,51,51	1.09	3 (5%)	57,59,59	0.95	3 (5%)
12	CPL	F	809	-	51,51,51	1.09	3 (5%)	57,59,59	0.90	3 (5%)
13	PTY	F	810	-	41,41,49	1.01	2 (4%)	44,46,54	1.16	3 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
14	NAG	G	503	7	14,14,15	0.59	0	17,19,21	0.65	1 (5%)
12	CPL	E	101	-	51,51,51	1.12	3 (5%)	57,59,59	0.90	3 (5%)
12	CPL	H	301	-	51,51,51	1.11	3 (5%)	57,59,59	0.95	3 (5%)

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	CPL	A	506	-	-	25/55/55/55	-
12	CPL	F	809	-	-	27/55/55/55	-
13	PTY	F	810	-	-	21/45/45/53	-
14	NAG	G	503	7	-	1/6/23/26	0/1/1/1
12	CPL	E	101	-	-	29/55/55/55	-
12	CPL	H	301	-	-	25/55/55/55	-

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	F	810	PTY	O7-C8	4.19	1.46	1.34
13	F	810	PTY	O4-C30	4.12	1.45	1.33
12	E	101	CPL	O3-C11	3.14	1.42	1.33
12	E	101	CPL	O2-C31	2.97	1.42	1.34
12	F	809	CPL	O2-C31	2.94	1.42	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	F	810	PTY	O7-C8-C11	5.01	122.30	111.50
12	A	506	CPL	O2-C31-C32	3.95	120.01	111.50
12	H	301	CPL	O2-C31-C32	3.93	119.97	111.50
12	E	101	CPL	O2-C31-C32	3.79	119.68	111.50
12	F	809	CPL	O2-C31-C32	3.37	118.77	111.50

There are no chirality outliers.

5 of 128 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	506	CPL	C32-C31-O2-C2

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Mol	Chain	Res	Type	Atoms
12	A	506	CPL	C1-O3P-P-O1P
12	A	506	CPL	C1-O3P-P-O2P
12	A	506	CPL	C1-O3P-P-O4P
12	A	506	CPL	C4-O4P-P-O1P

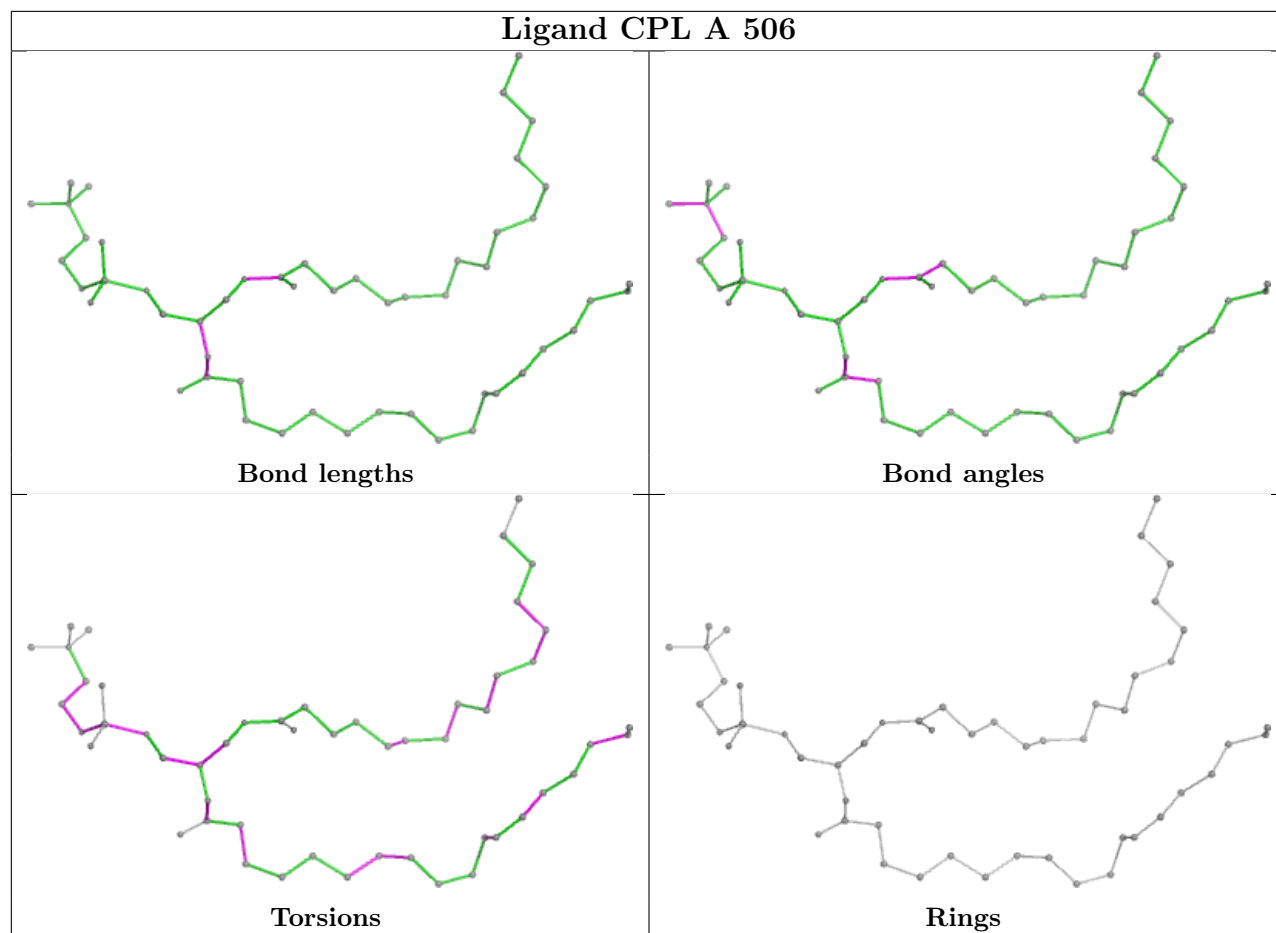
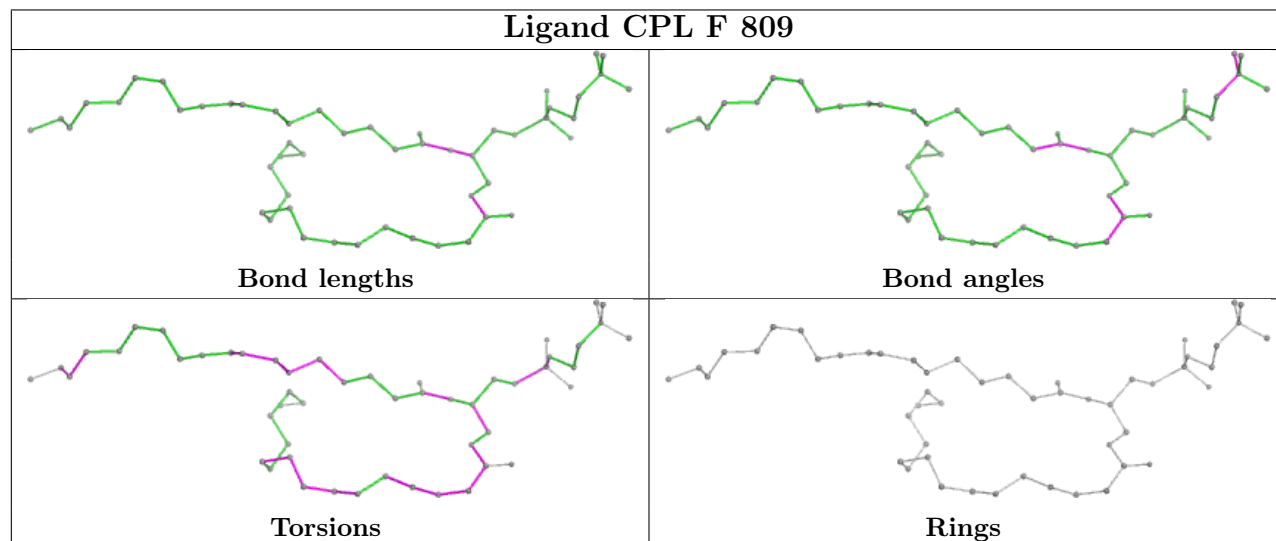
There are no ring outliers.

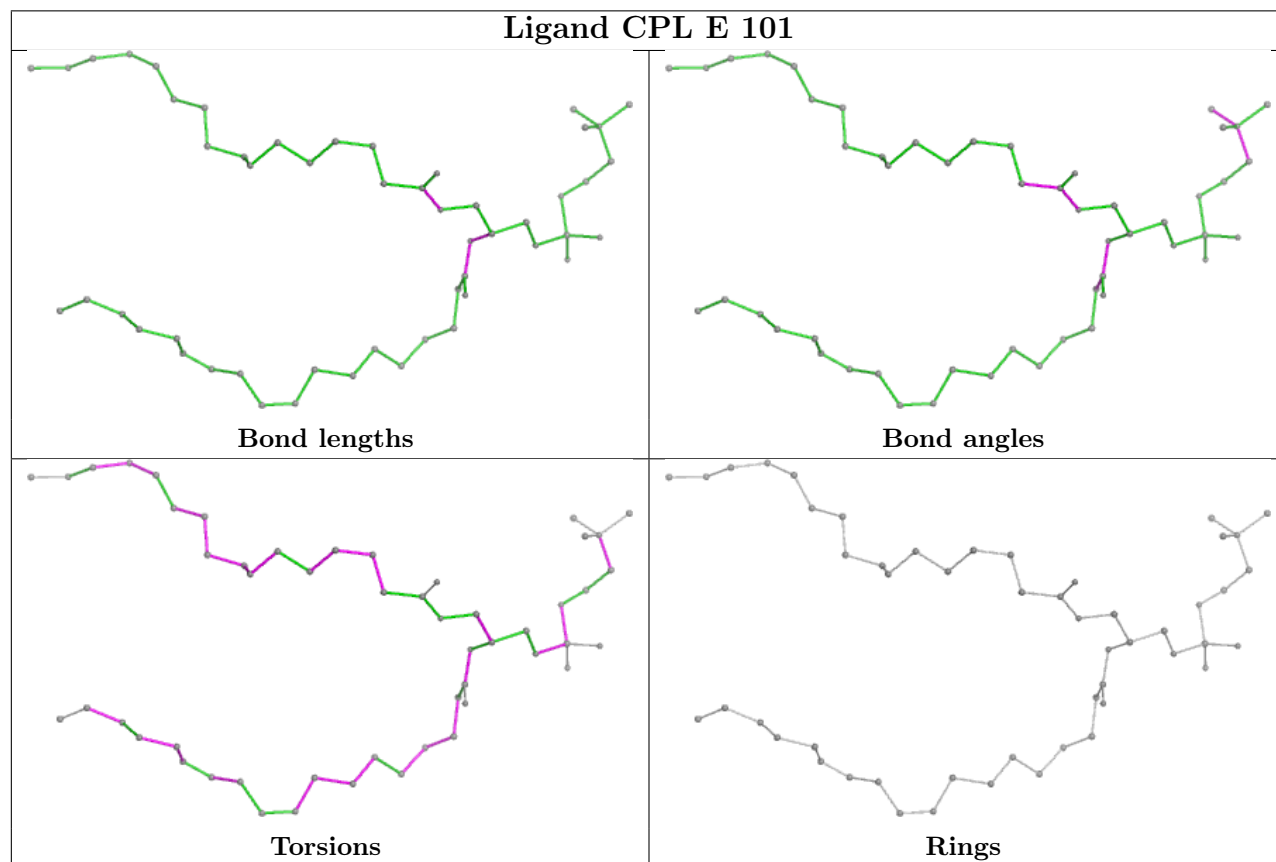
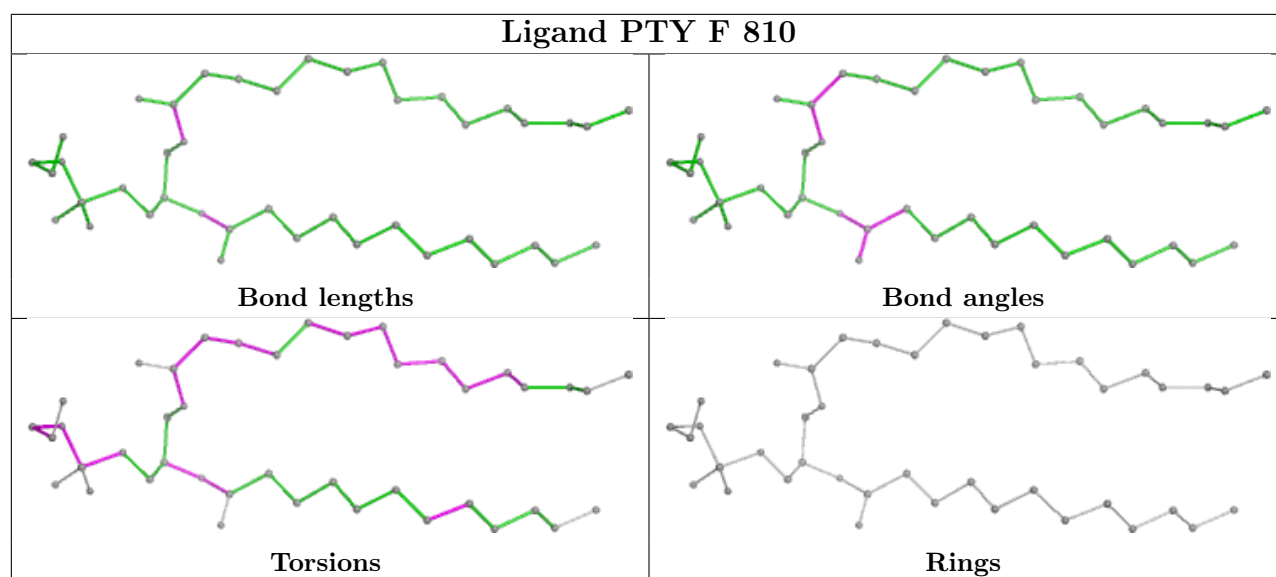
4 monomers are involved in 8 short contacts:

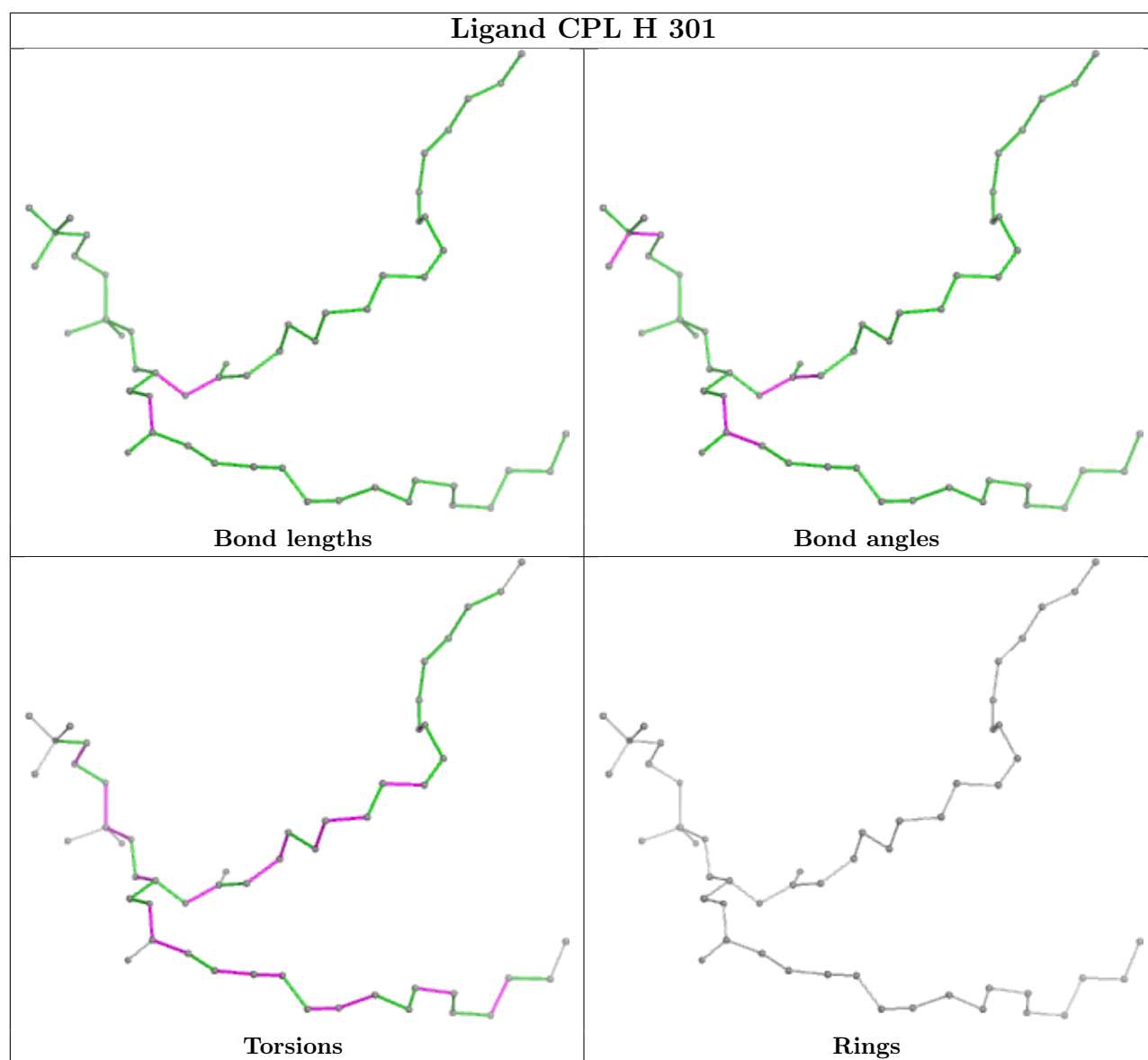
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	506	CPL	1	0
12	F	809	CPL	4	0
13	F	810	PTY	2	0
12	H	301	CPL	2	0

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 CPL A 506****Ligand CPL F 809**





## 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.

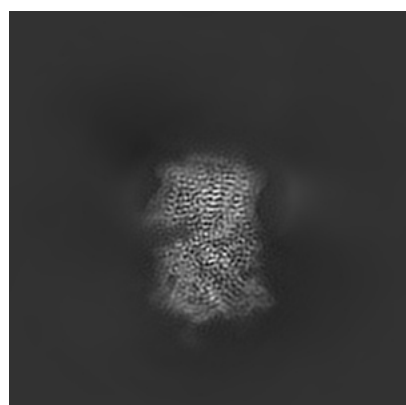
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4161. These allow visual inspection of the internal detail of the map and identification of artifacts.

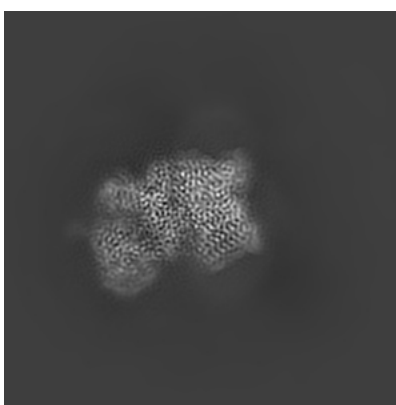
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

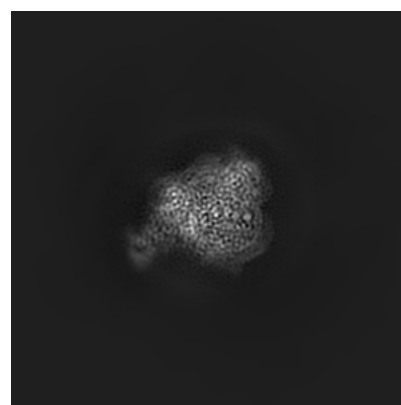
#### 6.1.1 Primary map



X



Y

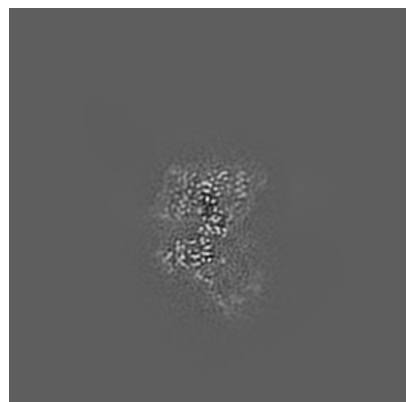


Z

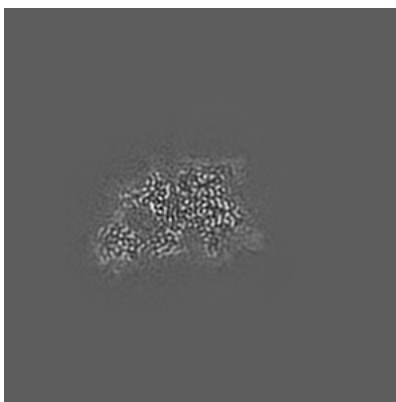
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

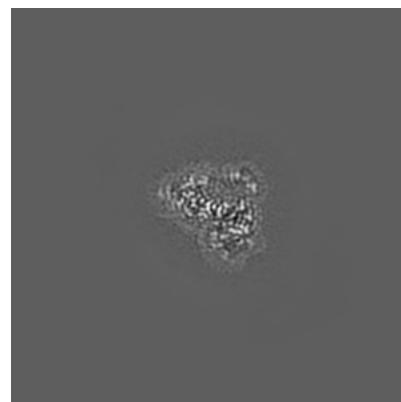
#### 6.2.1 Primary map



X Index: 150



Y Index: 150

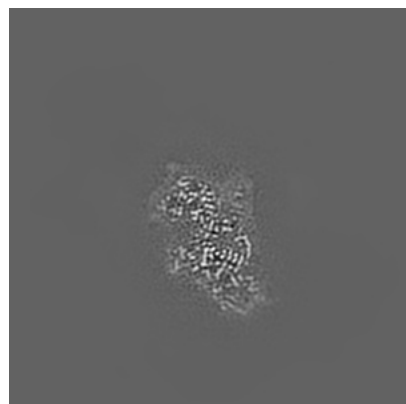


Z Index: 150

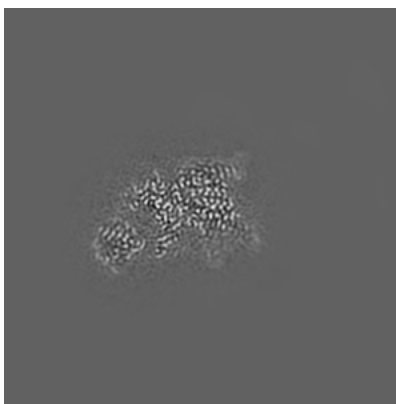
The images above show central slices of the map in three orthogonal directions.

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

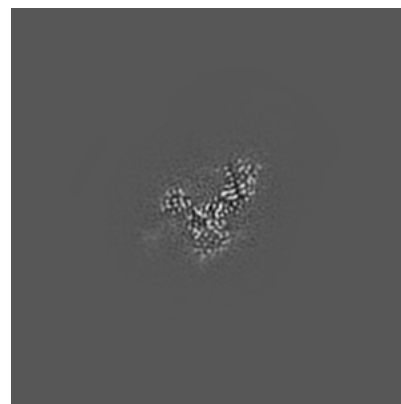
### 6.3.1 Primary map



X Index: 161



Y Index: 148

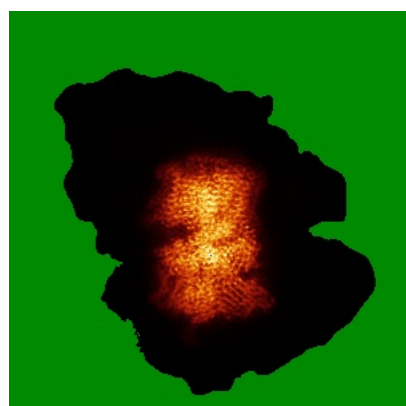


Z Index: 117

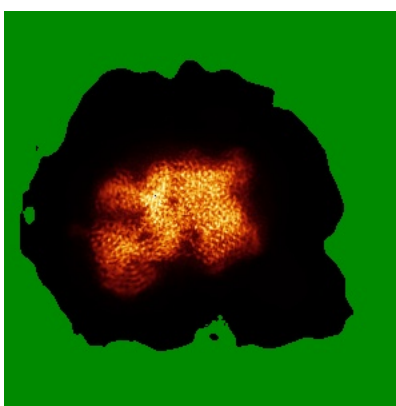
The images above show the largest variance slices of the map in three orthogonal directions.

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

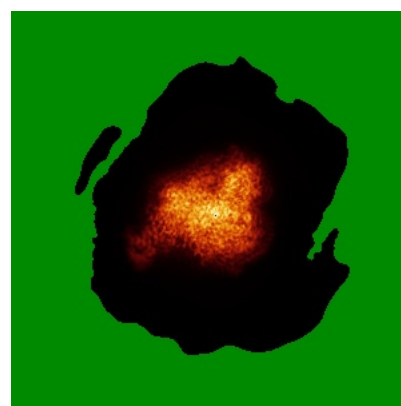
### 6.4.1 Primary map



X



Y

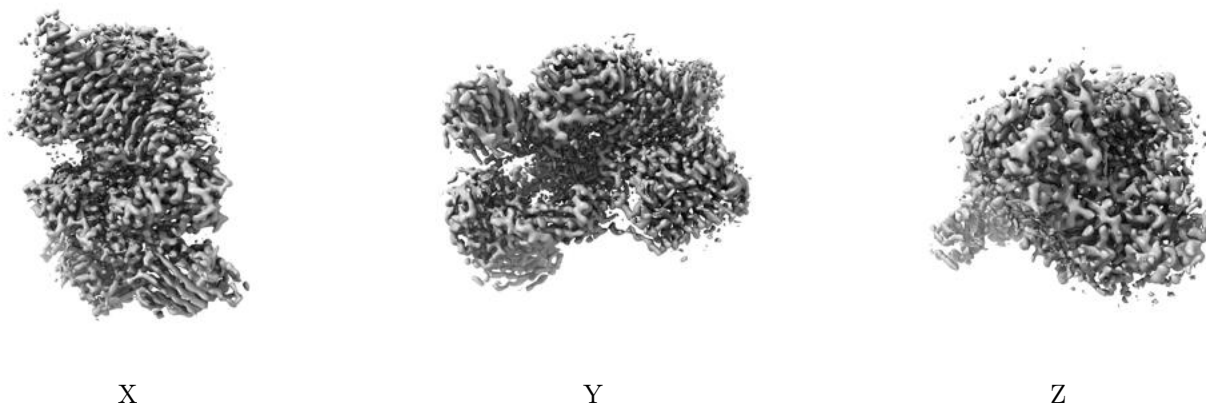


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.037. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

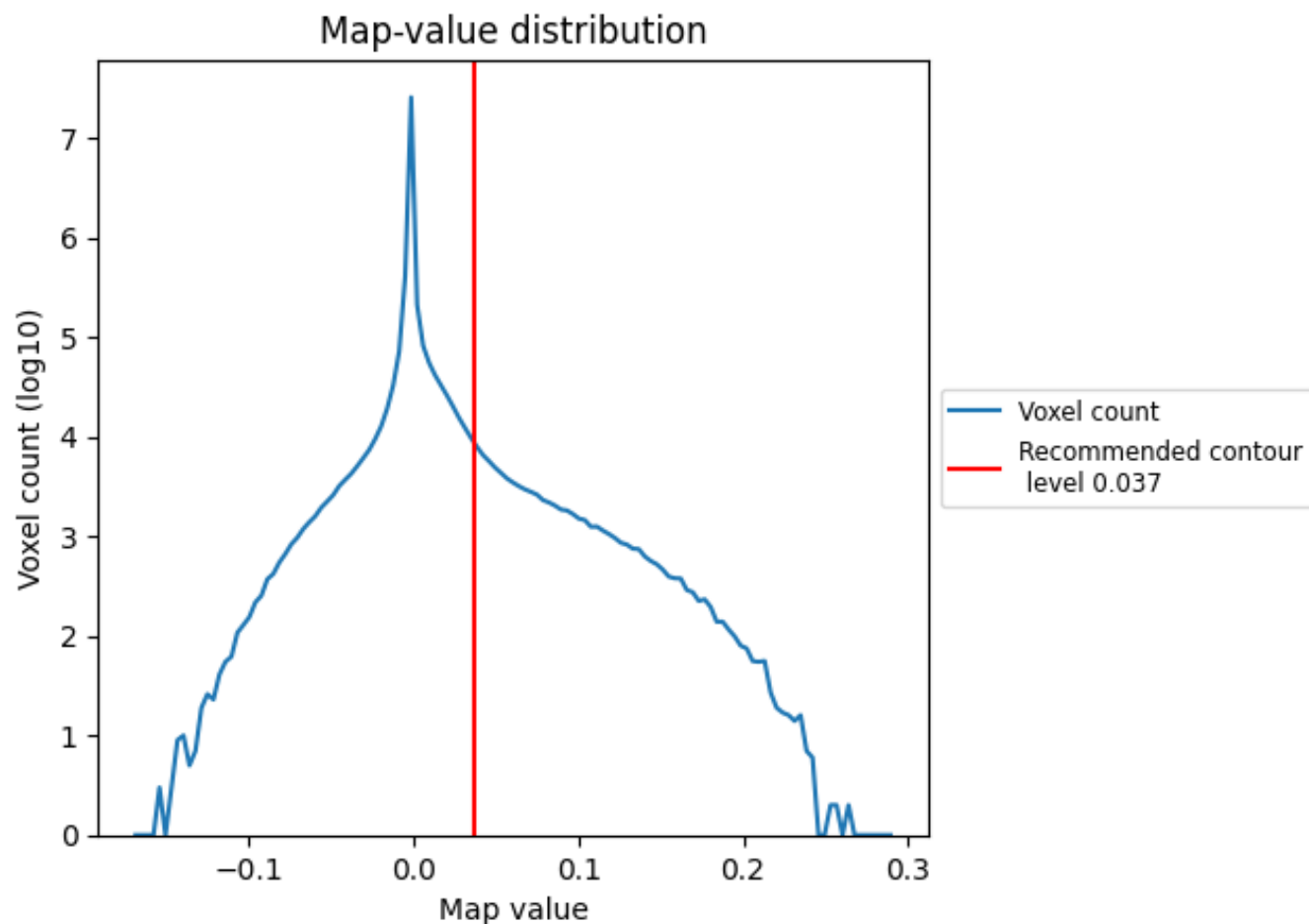
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

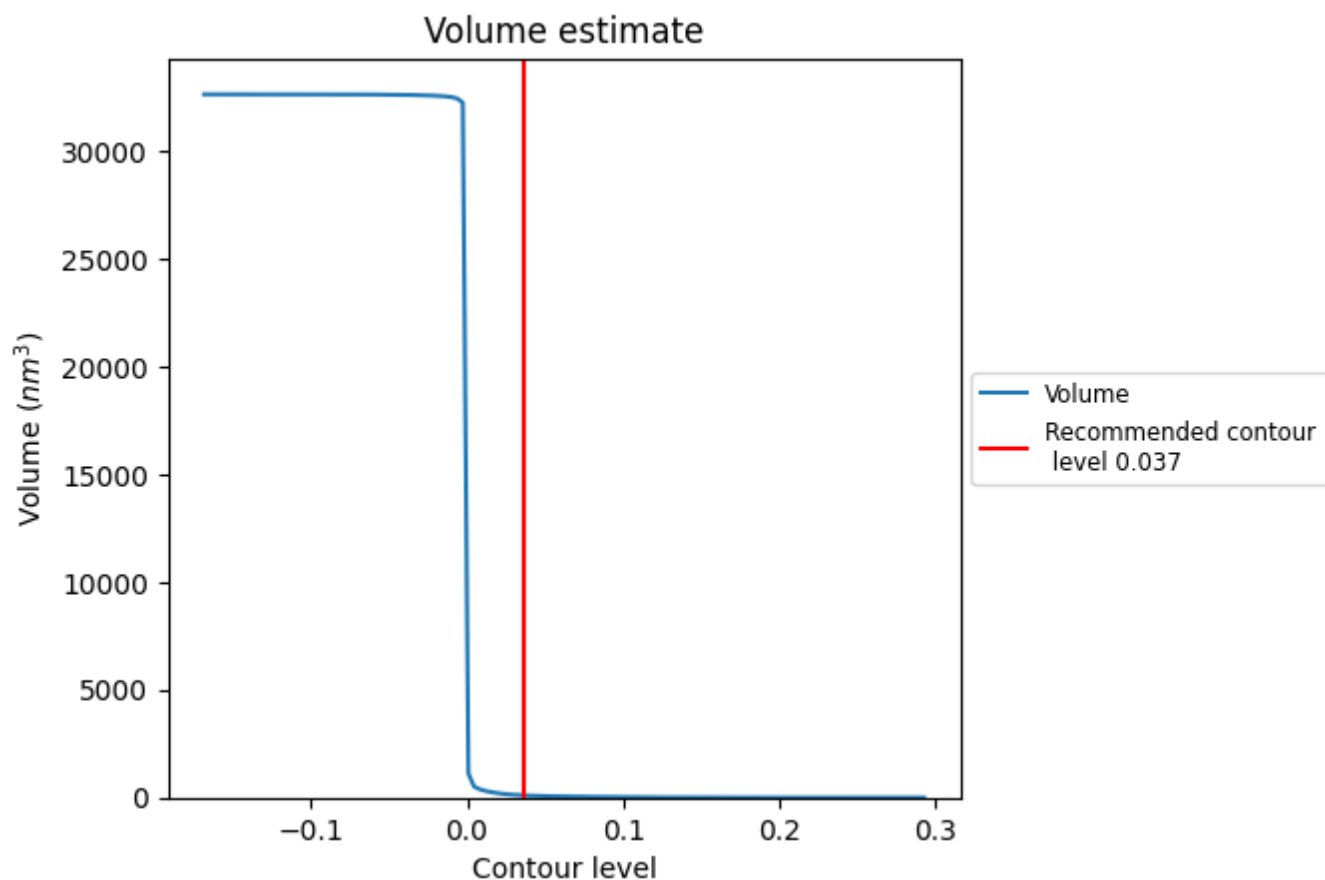
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

## 7.2 Volume estimate [i](#)

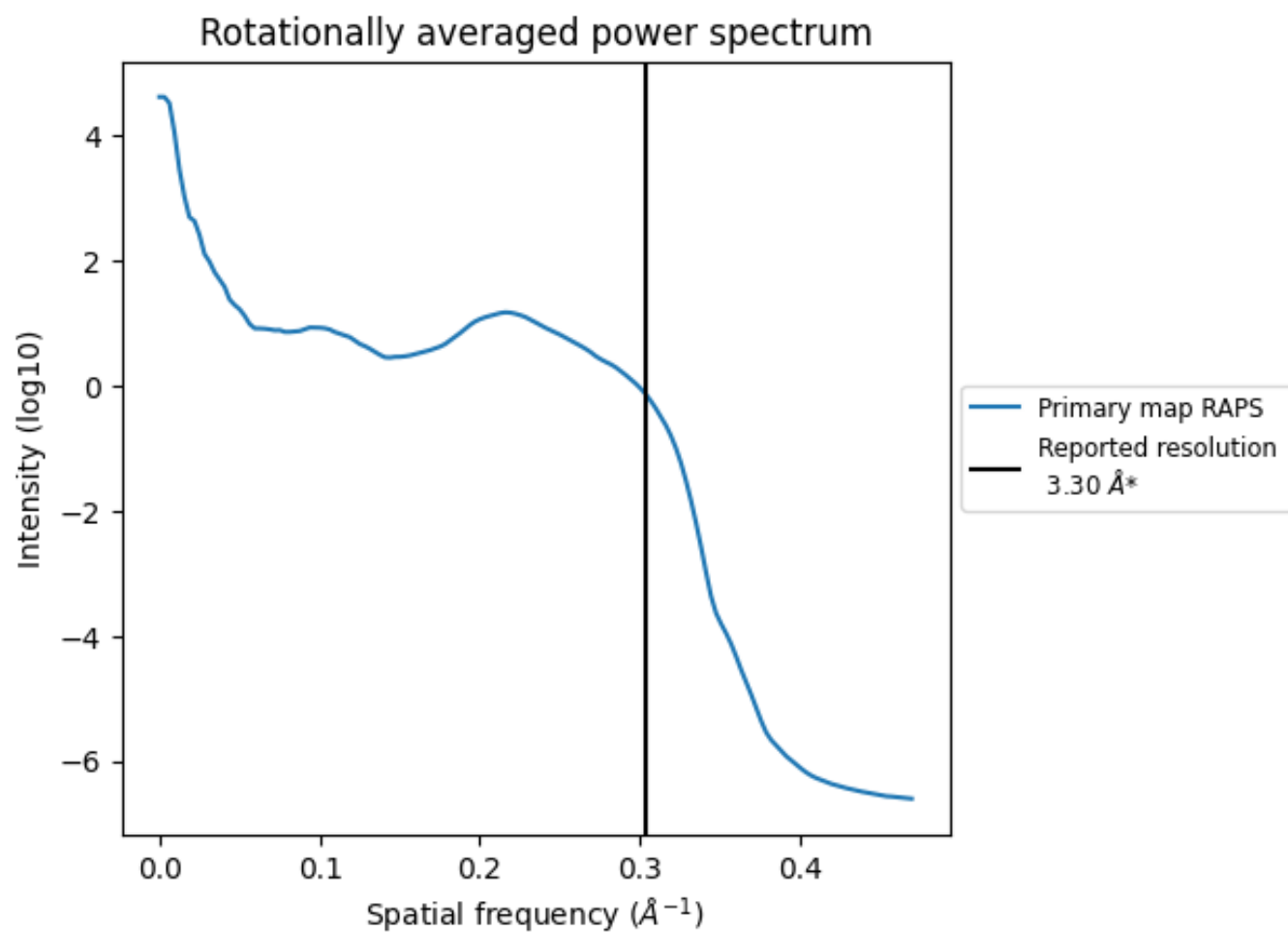


The volume at the recommended contour level is 99  $\text{nm}^3$ ; this corresponds to an approximate mass of 89 kDa.

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 ⓘ

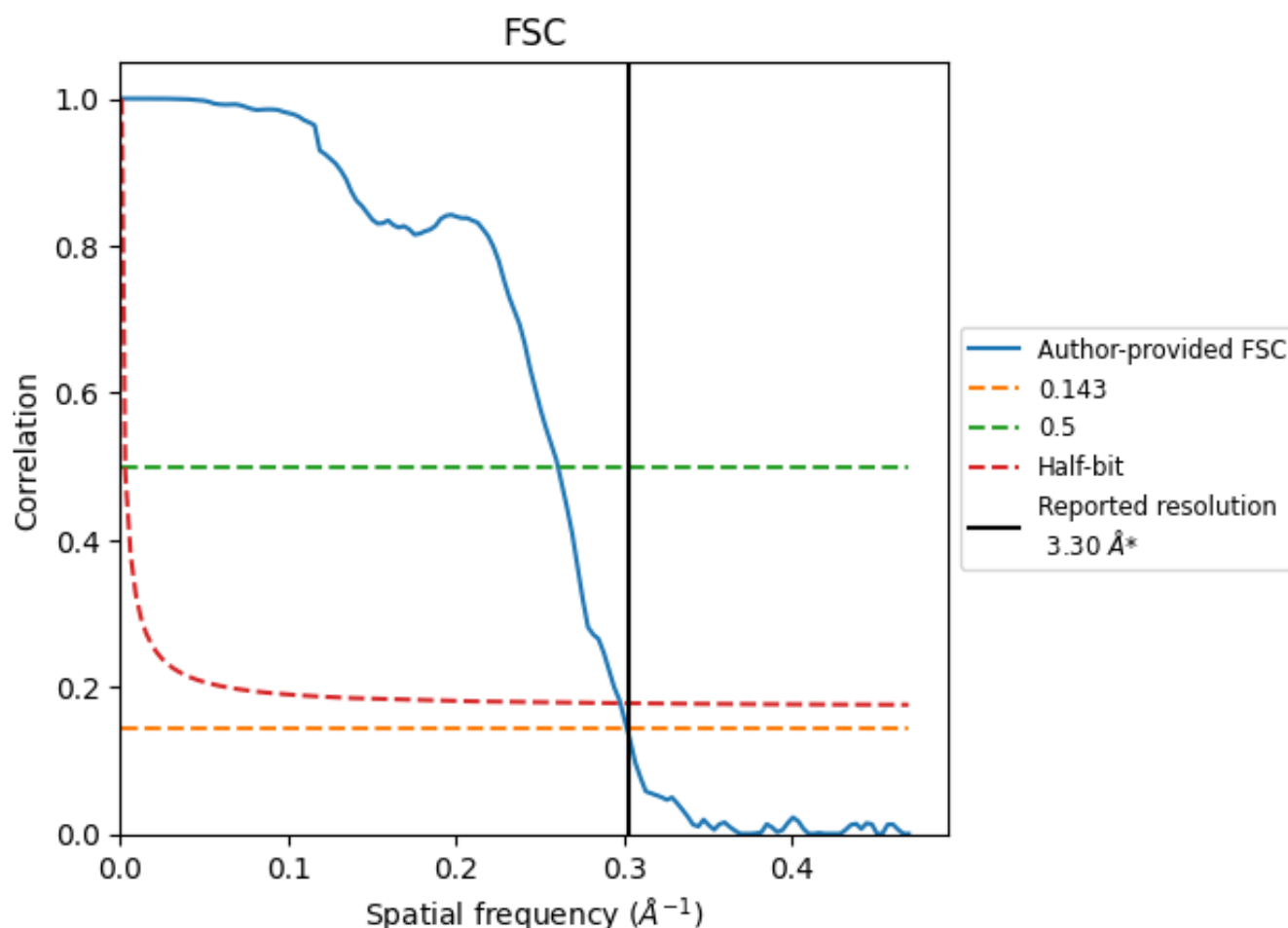


\*Reported resolution corresponds to spatial frequency of 0.303  $\text{\AA}^{-1}$

## 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 0.303  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

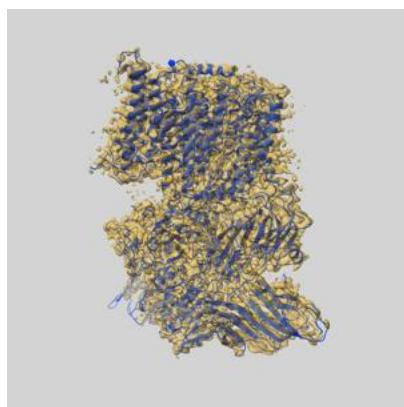
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.31	3.84	3.36
Unmasked-calculated*	-	-	-

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

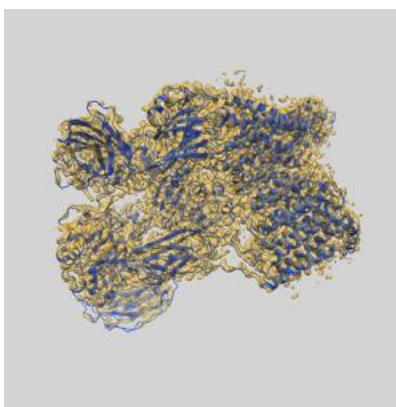
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4161 and PDB model 6EZN. Per-residue inclusion information can be found in section 3 on page 8.

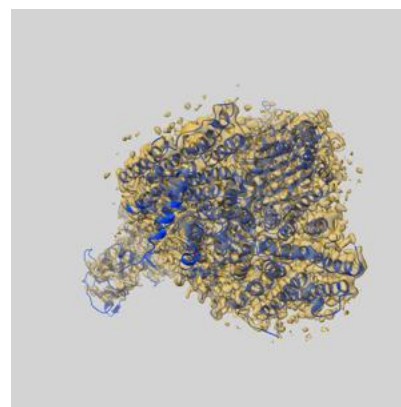
### 9.1 Map-model overlay [i](#)



X



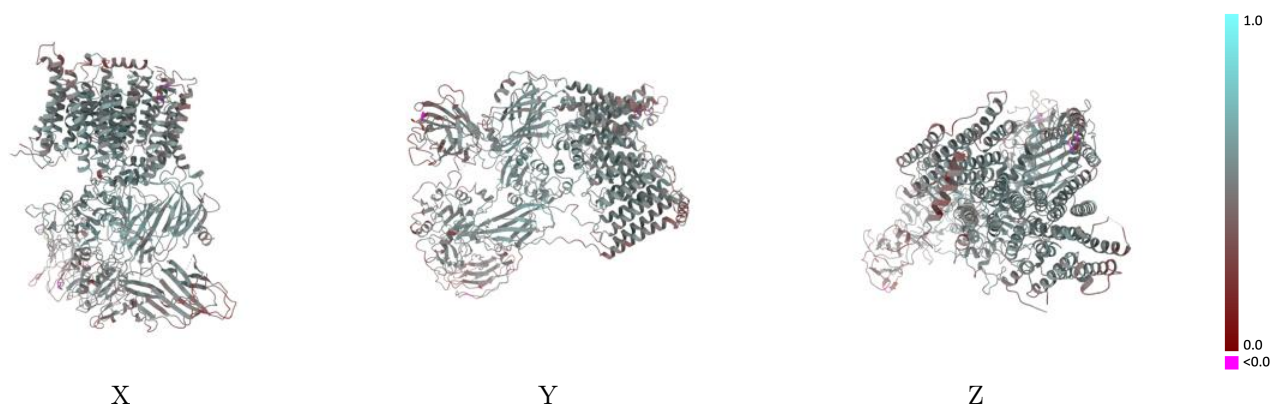
Y



Z

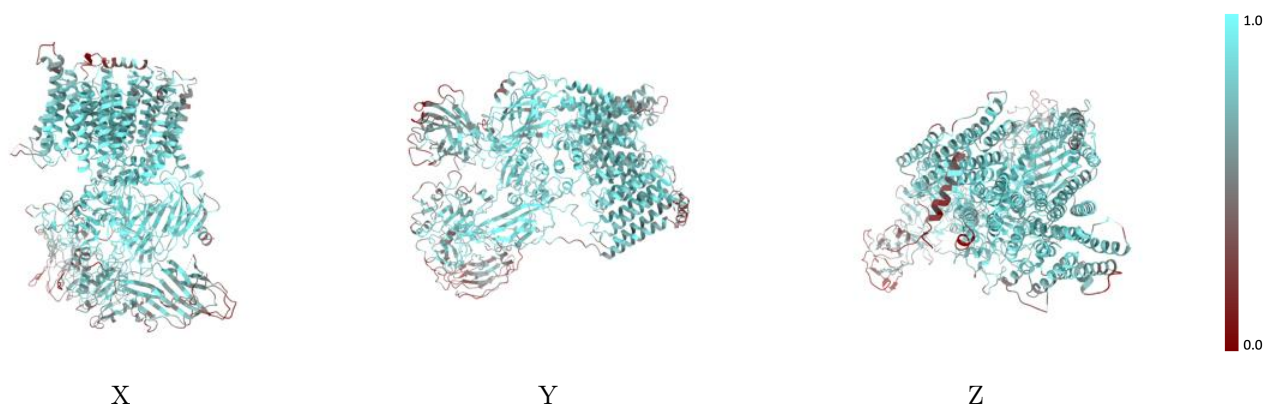
The images above show the 3D surface view of the map at the recommended contour level 0.037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



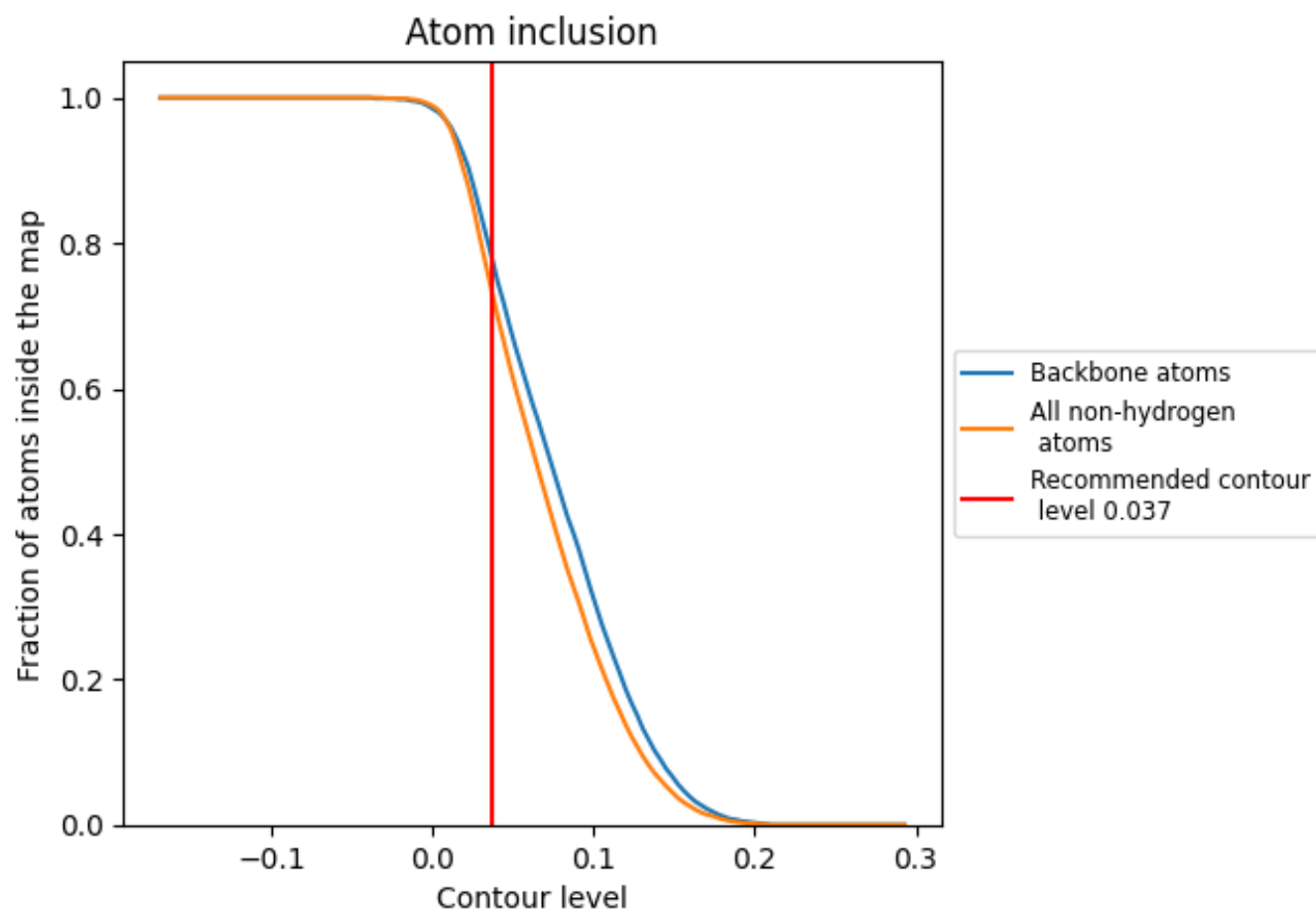
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.037).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 73% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.037) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7330	<div></div> 0.4940
A	<div></div> 0.7150	<div></div> 0.4870
B	<div></div> 0.7260	<div></div> 0.4800
C	<div></div> 0.6820	<div></div> 0.4760
D	<div></div> 0.8170	<div></div> 0.5100
E	<div></div> 0.7430	<div></div> 0.4800
F	<div></div> 0.8360	<div></div> 0.5350
G	<div></div> 0.7400	<div></div> 0.4930
H	<div></div> 0.5100	<div></div> 0.4180
I	<div></div> 0.7690	<div></div> 0.4980
J	<div></div> 0.3930	<div></div> 0.3780
K	<div></div> 0.6700	<div></div> 0.5160
L	<div></div> 0.0000	<div></div> 0.2240

1.0

0.0

<0.0