



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 22, 2024 – 01:22 AM JST

PDB ID : 5YYL
Title : Structure of Major Royal Jelly Protein 1 Oligomer
Authors : Tian, W.; Chen, Z.
Deposited on : 2017-12-10
Resolution : 2.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

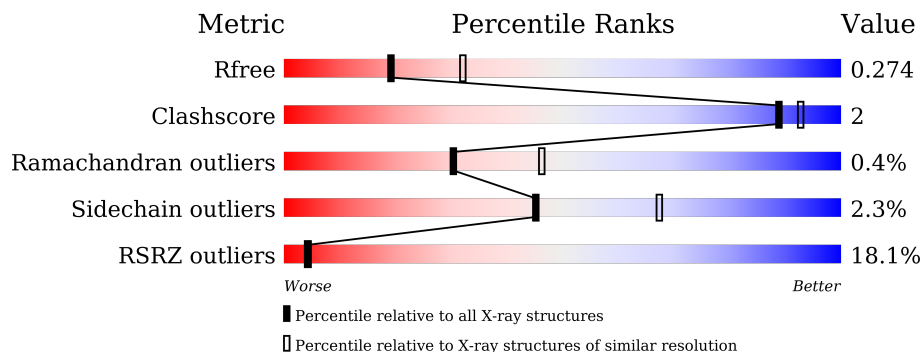
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1003 (2.66-2.66)
Clashscore	180529	1063 (2.66-2.66)
Ramachandran outliers	177936	1052 (2.66-2.66)
Sidechain outliers	177891	1052 (2.66-2.66)
RSRZ outliers	164620	1003 (2.66-2.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	432	<div> <div>8%</div> <div>88%</div> <div>6%</div> <div>6%</div> </div>
1	B	432	<div> <div>28%</div> <div>83%</div> <div>•</div> <div>13%</div> </div>
2	C	78	<div> <div>51%</div> <div>•</div> <div>47%</div> </div>
2	D	78	<div> <div>4%</div> <div>54%</div> <div>•</div> <div>45%</div> </div>
3	E	2	<div> <div>50%</div> <div>50%</div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6562 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Major royal jelly protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3054	1944	508	585	17			
1	B	375	Total	C	N	O	S	0	0	0
			2624	1665	453	492	14			

- Molecule 2 is a protein called Apisimin.

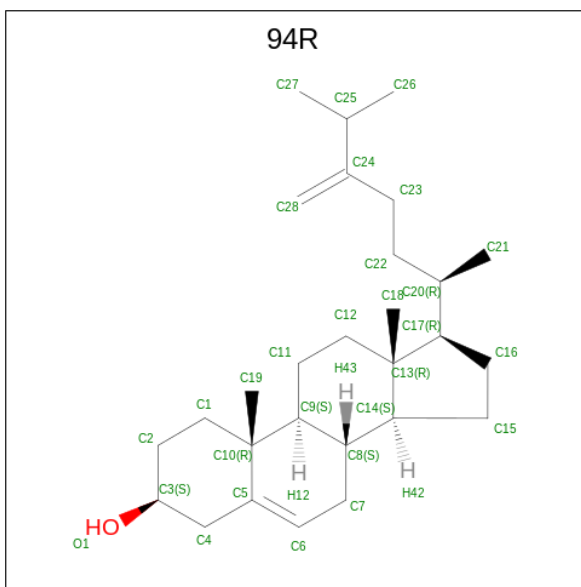
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	41	Total	C	N	O	0	0	0
			296	190	48	58			
2	D	43	Total	C	N	O	0	0	0
			298	191	49	58			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



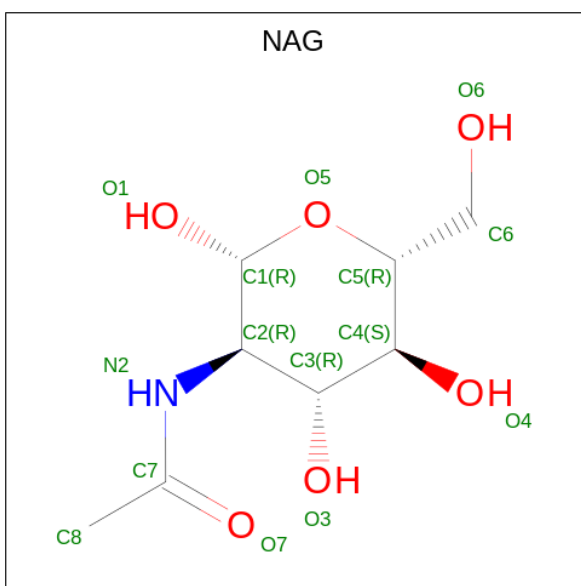
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			21	12	2	7			

- Molecule 4 is (3beta,14beta,17alpha)-ergosta-5,24(28)-dien-3-ol (three-letter code: 94R) (formula: C₂₈H₄₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			29	28	1		
4	B	1	Total	C	O	0	0
			29	28	1		
4	C	1	Total	C	O	0	0
			29	28	1		
4	C	1	Total	C	O	0	0
			29	28	1		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			9	5	1	3		

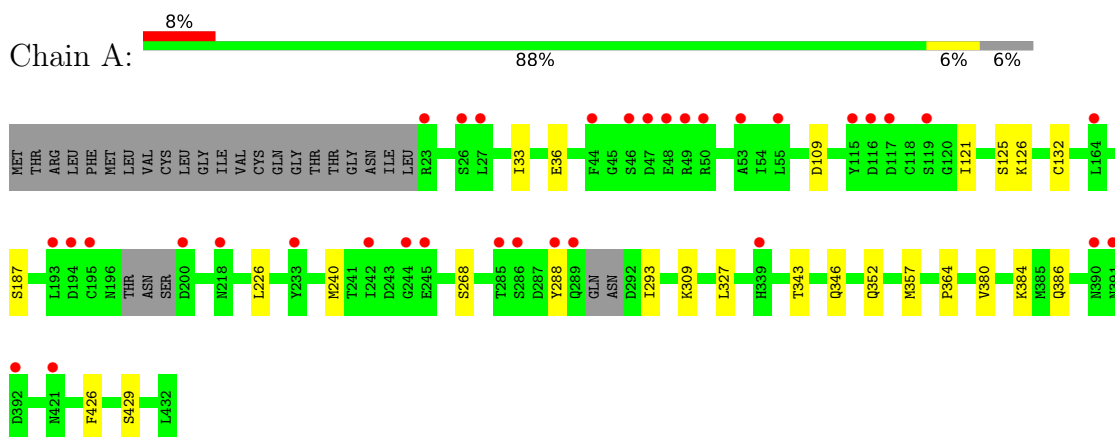
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	74	Total	O	0	0
			74	74		
6	B	46	Total	O	0	0
			46	46		
6	C	11	Total	O	0	0
			11	11		
6	D	13	Total	O	0	0
			13	13		

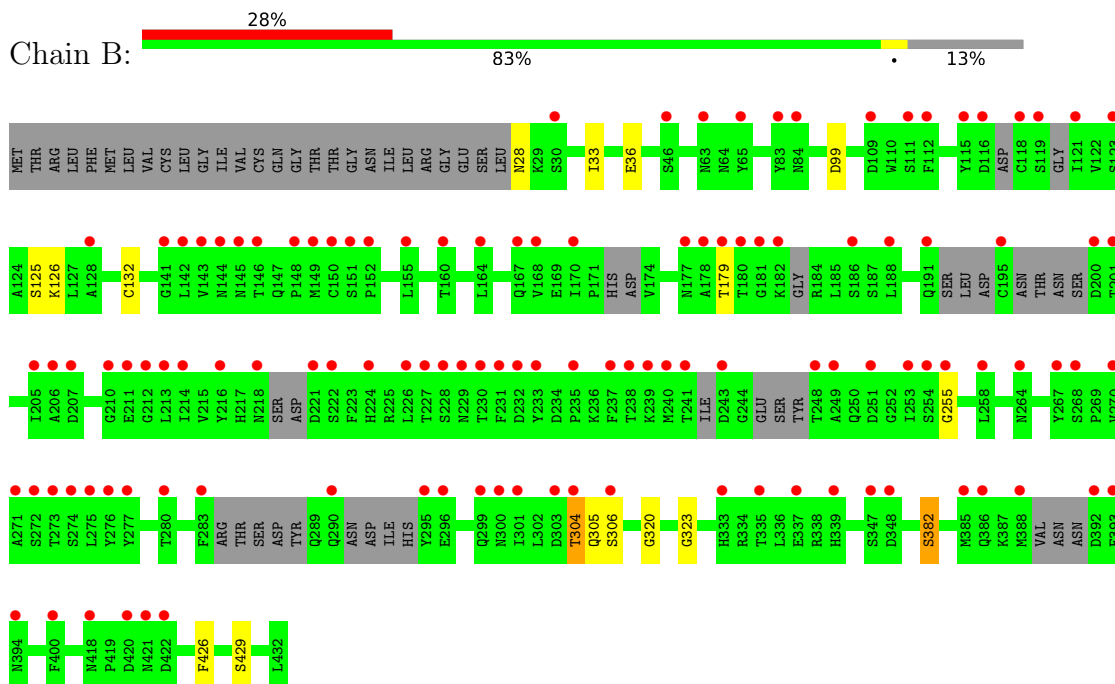
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Major royal jelly protein 1



- Molecule 1: Major royal jelly protein 1



Chain C:

51%

47%



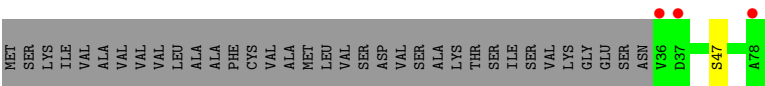
● Molecule 2: Apisimin

Chain D:

4%

54%

45%



● Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

50%

50%



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	211.58Å 211.58Å 149.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.65 50.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	86.3 (50.00-2.65) 86.3 (50.00-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.239 , 0.275 0.241 , 0.274	Depositor DCC
R_{free} test set	1941 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6562	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: NAG, 94R

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	0.50	0/3123	0.69	0/4248
1	B	0.49	0/2670	0.66	0/3609
2	C	0.39	0/296	0.57	0/406
2	D	0.48	0/298	0.62	0/407
All	All	0.49	0/6387	0.67	0/8670

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	3054	0	2784	15	0
1	B	2624	0	2209	9	0
2	C	296	0	314	0	0
2	D	298	0	307	0	0
3	E	21	0	15	0	0
4	A	29	0	0	1	0
4	B	29	0	0	0	0
4	C	58	0	0	0	0
5	B	9	0	5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	74	0	0	0	0
6	B	46	0	0	0	0
6	C	11	0	0	0	0
6	D	13	0	0	0	0
All	All	6562	0	5634	22	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 2.

All (22) 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:327:LEU:HD13	1:A:357:MET:HE3	1.64	0.77
1:B:304:THR:HG22	1:B:305:GLN:H	1.65	0.59
1:A:327:LEU:HD13	1:A:357:MET:CE	2.33	0.58
1:A:384:LYS:HB3	1:A:386:GLN:HE22	1.68	0.58
1:A:352:GLN:OE1	1:A:386:GLN:NE2	2.45	0.50
1:A:125:SER:O	1:A:126:LYS:HD2	2.11	0.50
1:A:288:TYR:HB2	1:A:293:ILE:HD11	1.93	0.50
1:B:125:SER:O	1:B:126:LYS:HD2	2.12	0.49
1:A:357:MET:HE2	1:A:380:VAL:HG13	1.97	0.47
1:B:304:THR:HG21	1:B:323:GLY:HA3	1.96	0.47
1:A:268:SER:OG	1:A:309:LYS:NZ	2.47	0.46
1:A:364:PRO:O	4:A:503:94R:O1	2.33	0.46
1:B:382:SER:O	1:B:382:SER:OG	2.34	0.45
1:A:384:LYS:HB3	1:A:386:GLN:NE2	2.30	0.45
1:A:33:ILE:HD13	1:A:36:GLU:OE2	2.17	0.45
1:B:33:ILE:HD13	1:B:36:GLU:OE2	2.17	0.44
1:A:384:LYS:HD2	1:A:386:GLN:HE22	1.83	0.43
1:A:33:ILE:HG21	1:A:36:GLU:HG3	2.01	0.42
1:B:33:ILE:HG21	1:B:36:GLU:HG3	2.03	0.41
1:B:306:SER:HA	1:B:320:GLY:O	2.21	0.40
1:A:426:PHE:HA	1:B:429:SER:O	2.21	0.40
1:A:429:SER:O	1:B:426:PHE:HA	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	399/432 (92%)	376 (94%)	22 (6%)	1 (0%)	37	53
1	B	350/432 (81%)	334 (95%)	14 (4%)	2 (1%)	22	35
2	C	39/78 (50%)	39 (100%)	0	0	100	100
2	D	41/78 (53%)	41 (100%)	0	0	100	100
All	All	829/1020 (81%)	790 (95%)	36 (4%)	3 (0%)	30	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	ILE
1	B	179	THR
1	B	255	GLY

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 X-ray entries followed by that with respect to entries of similar resolution.

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	308/391 (79%)	301 (98%)	7 (2%)	45	67
1	B	222/391 (57%)	217 (98%)	5 (2%)	45	67
2	C	35/66 (53%)	34 (97%)	1 (3%)	37	58
2	D	32/66 (48%)	31 (97%)	1 (3%)	35	55
All	All	597/914 (65%)	583 (98%)	14 (2%)	45	67

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	ASP
1	A	132	CYS
1	A	187	SER
1	A	226	LEU
1	A	240	MET
1	A	343	THR
1	A	346	GLN
1	B	28	ASN
1	B	99	ASP
1	B	132	CYS
1	B	304	THR
1	B	382	SER
2	C	47	SER
2	D	47	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	299	GLN
1	A	386	GLN

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](#)

2 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
3	NAG	E	1	3,1	14,14,15	0.55	0	17,19,21	1.47	3 (17%)
3	NAG	E	2	3	6,6,15	0.60	0	5,5,21	0.35	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
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/4/4/26	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1	NAG	O5-C1-C2	-2.98	106.59	111.29
3	E	1	NAG	C1-O5-C5	2.29	115.30	112.19
3	E	1	NAG	C1-C2-N2	2.11	114.09	110.49

There are no chirality outliers.

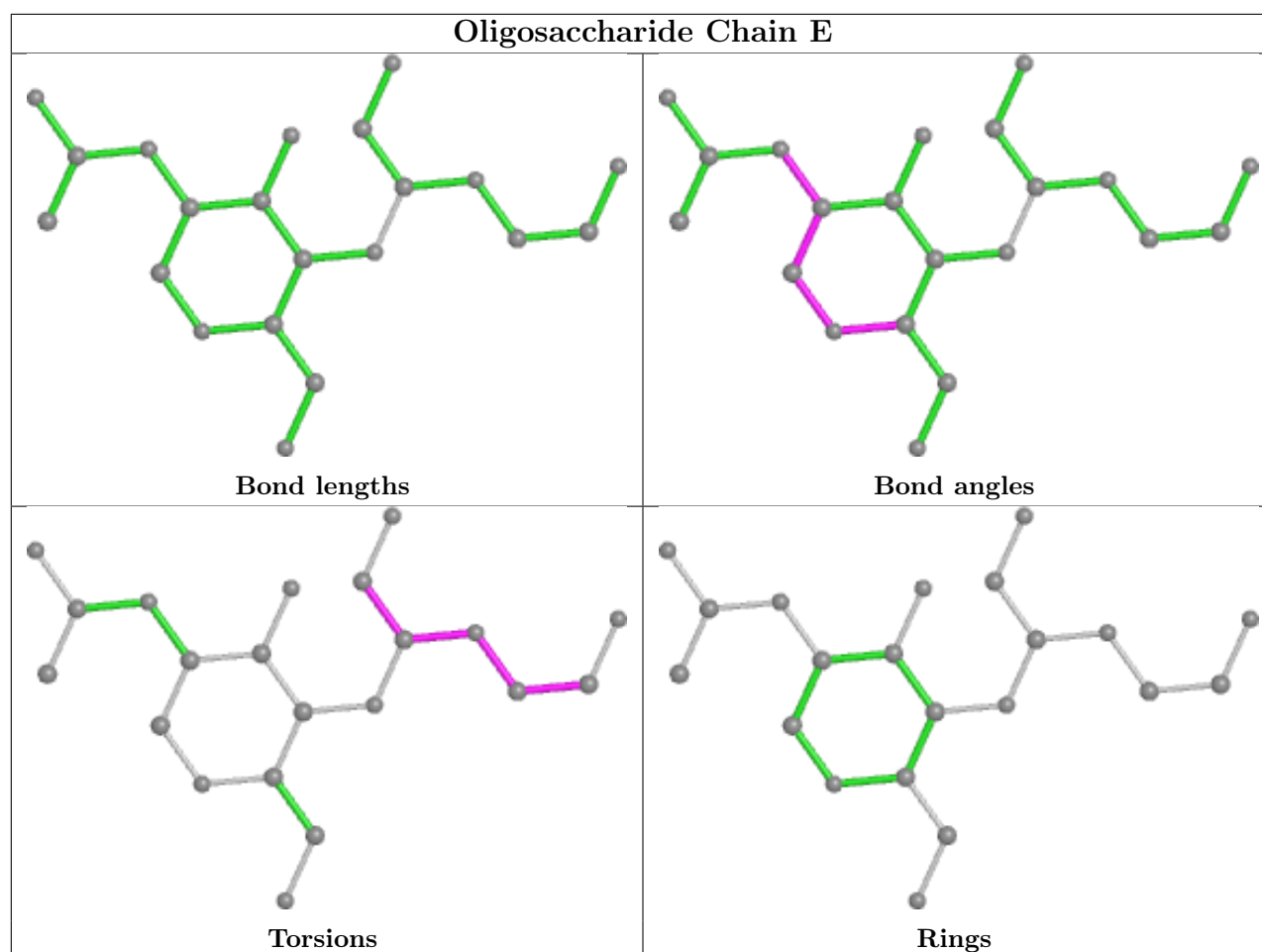
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O5-C1-C2-N2
3	E	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C2-C1-O5-C5
3	E	2	NAG	C6-C5-O5-C1

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](#)

5 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	$\# Z > 2$
4	94R	C	101	-	32,32,32	0.57	0	49,50,50	1.09	4 (8%)
4	94R	C	102	-	32,32,32	0.52	0	49,50,50	1.18	7 (14%)
4	94R	A	503	-	32,32,32	0.64	0	49,50,50	1.05	2 (4%)
5	NAG	B	501	1	9,9,15	0.66	0	8,12,21	1.33	1 (12%)
4	94R	B	502	-	32,32,32	0.64	0	49,50,50	1.15	3 (6%)

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
4	94R	C	101	-	-	0/13/71/71	0/4/4/4
4	94R	C	102	-	-	0/13/71/71	0/4/4/4
4	94R	A	503	-	-	0/13/71/71	0/4/4/4
5	NAG	B	501	1	-	-	0/1/1/1
4	94R	B	502	-	-	4/13/71/71	0/4/4/4

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	502	94R	C4-C5-C10	3.84	121.52	116.42
4	B	502	94R	C23-C22-C20	-3.71	107.74	114.52
4	A	503	94R	C4-C5-C10	3.31	120.82	116.42
5	B	501	NAG	C5-O5-C1	3.28	116.56	111.52
4	A	503	94R	C4-C5-C6	-3.27	115.90	120.61
4	C	101	94R	C12-C11-C9	3.01	118.33	113.11
4	B	502	94R	C4-C5-C6	-3.00	116.29	120.61
4	C	102	94R	C12-C11-C9	2.62	117.66	113.11
4	C	102	94R	C7-C8-C9	-2.51	106.67	109.71
4	C	101	94R	C4-C5-C10	2.29	119.47	116.42
4	C	101	94R	C21-C20-C17	-2.29	109.41	112.92
4	C	101	94R	C19-C10-C5	-2.17	104.83	108.34
4	C	102	94R	C21-C20-C17	-2.16	109.61	112.92
4	C	102	94R	C12-C13-C14	-2.13	103.96	107.27
4	C	102	94R	C10-C9-C8	-2.13	109.54	112.73
4	C	102	94R	C11-C9-C8	2.08	114.75	111.75
4	C	102	94R	C22-C23-C24	-2.04	109.18	115.36

There are no chirality outliers.

All (4) torsion outliers are listed below:

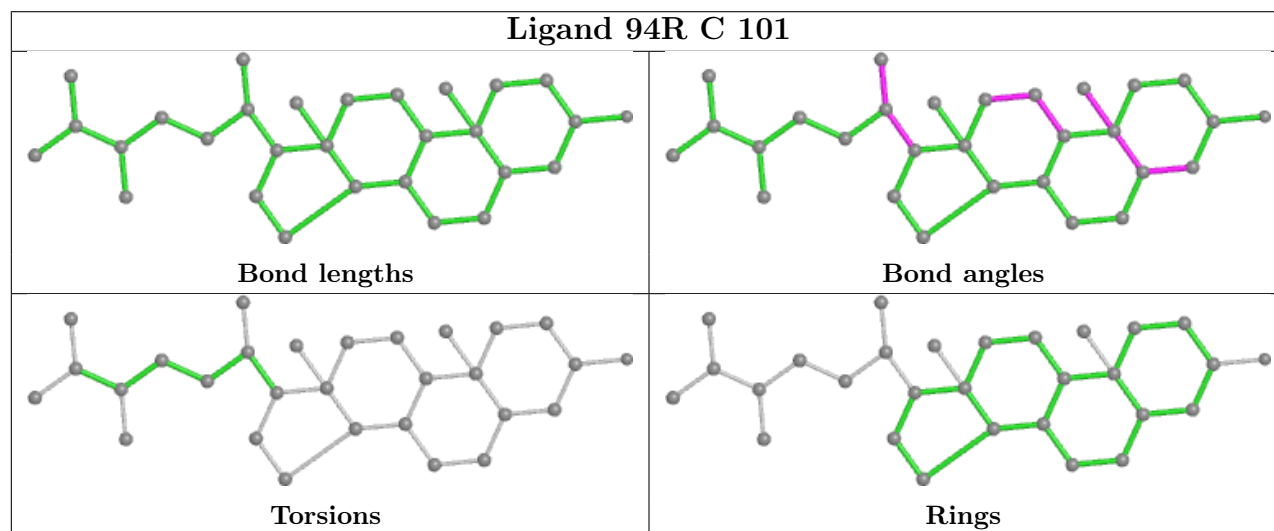
Mol	Chain	Res	Type	Atoms
4	B	502	94R	C17-C20-C22-C23
4	B	502	94R	C21-C20-C22-C23
4	B	502	94R	C22-C23-C24-C28
4	B	502	94R	C22-C23-C24-C25

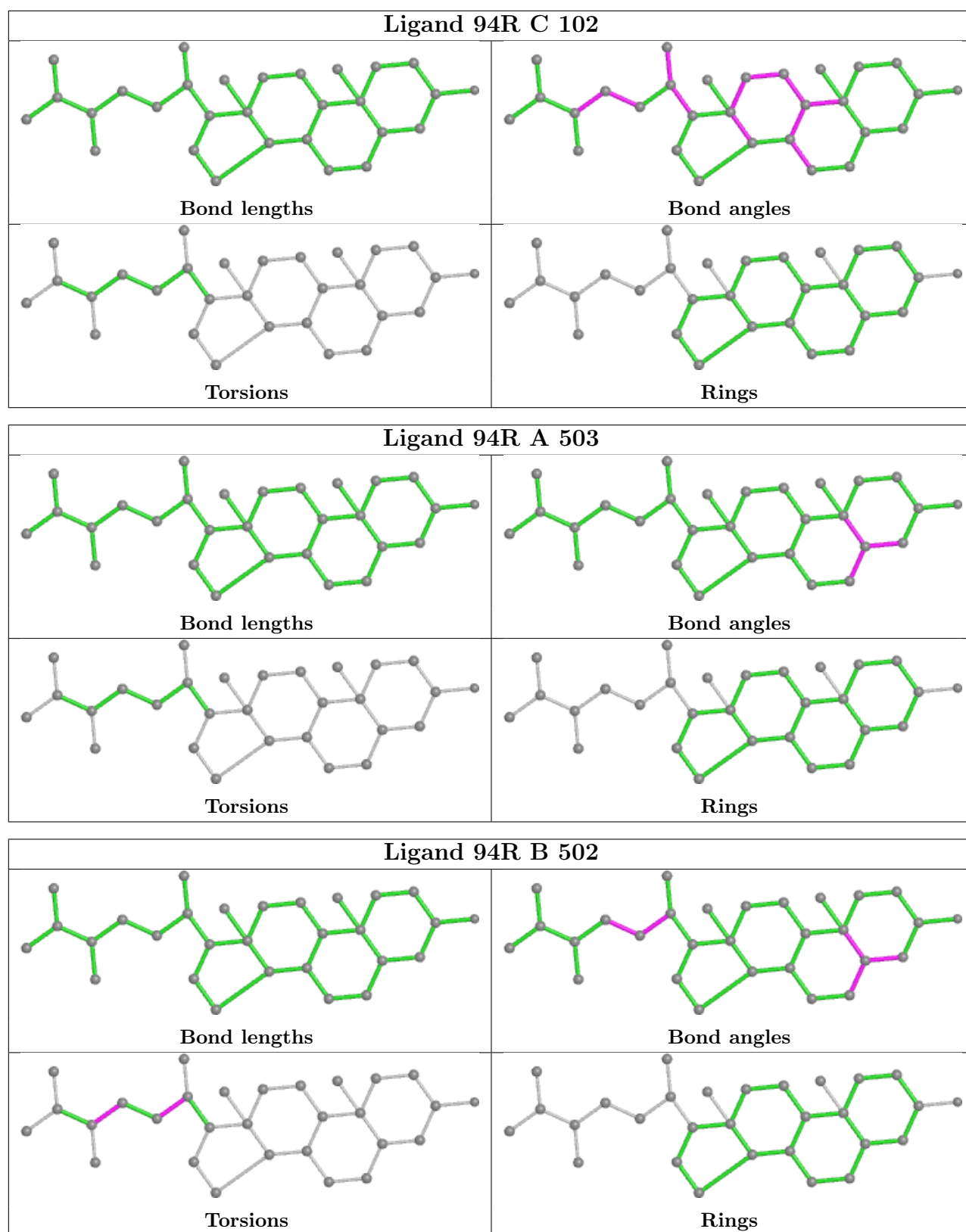
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	94R	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	405/432 (93%)	0.29	34 (8%) 18 17	18, 42, 83, 99	0
1	B	375/432 (86%)	1.47	119 (31%) 1 1	24, 61, 90, 120	2 (0%)
2	C	41/78 (52%)	-0.27	0 100 100	24, 30, 40, 58	0
2	D	43/78 (55%)	0.02	3 (6%) 24 22	26, 32, 52, 77	0
All	All	864/1020 (84%)	0.76	156 (18%) 4 4	18, 48, 88, 120	2 (0%)

All (156) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	145	ASN	6.7
1	A	46	SER	5.6
1	A	116	ASP	5.3
1	B	385	MET	5.2
1	A	117	ASP	4.8
1	B	218	ASN	4.7
1	B	239	LYS	4.6
1	A	47	ASP	4.4
1	B	254	SER	4.4
1	B	119	SER	4.4
1	B	152	PRO	4.4
1	B	178	ALA	4.3
1	B	233	TYR	4.2
1	A	194	ASP	4.2
1	B	232	ASP	4.2
1	B	295	TYR	4.2
1	B	272	SER	4.1
1	B	207	ASP	4.1
1	A	200	ASP	4.1
1	B	155	LEU	4.1
1	B	264	ASN	4.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	177	ASN	3.9
1	B	393	PHE	3.8
1	B	83	TYR	3.8
1	B	420	ASP	3.7
1	B	386	GLN	3.7
1	B	271	ALA	3.7
1	A	286	SER	3.7
1	B	339	HIS	3.7
1	B	116	ASP	3.7
1	B	230	THR	3.7
1	A	49	ARG	3.7
1	B	237	PHE	3.6
1	B	418	ASN	3.6
1	B	268	SER	3.5
1	A	193	LEU	3.5
1	B	274	SER	3.5
1	B	231	PHE	3.5
1	B	118	CYS	3.4
1	B	180	THR	3.4
1	A	23	ARG	3.4
1	B	150	CYS	3.4
1	B	277	TYR	3.4
1	A	50	ARG	3.4
1	B	142	LEU	3.4
1	A	245	GLU	3.4
2	D	36	VAL	3.3
1	B	141	GLY	3.3
1	A	421	ASN	3.3
1	A	119	SER	3.3
1	B	275	LEU	3.2
1	B	212	GLY	3.2
1	B	283	PHE	3.2
1	B	46	SER	3.2
1	B	30	SER	3.1
1	B	240	MET	3.1
2	D	37	ASP	3.1
1	B	84	ASN	3.1
1	B	149	MET	3.1
1	B	181	GLY	3.1
1	A	195	CYS	3.0
1	A	392	ASP	3.0
1	B	251	ASP	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	392	ASP	3.0
1	B	421	ASN	3.0
1	B	296	GLU	3.0
1	B	109	ASP	3.0
1	B	290	GLN	3.0
1	B	300	ASN	3.0
1	B	186	SER	3.0
1	A	53	ALA	2.9
1	B	112	PHE	2.9
1	B	227	THR	2.9
1	B	394	ASN	2.9
1	B	226	LEU	2.9
1	A	48	GLU	2.9
1	B	205	ILE	2.8
1	B	179	THR	2.8
1	B	238	THR	2.8
1	B	241	THR	2.8
1	B	388	MET	2.8
1	B	333	HIS	2.8
1	B	195	CYS	2.7
1	B	148	PRO	2.7
1	A	339	HIS	2.7
1	B	221	ASP	2.7
1	B	270	VAL	2.7
1	B	299	GLN	2.7
1	B	273	THR	2.7
1	A	285	THR	2.7
1	B	348	ASP	2.7
1	B	228	SER	2.7
1	B	200	ASP	2.6
1	B	248	THR	2.6
1	B	243	ASP	2.6
1	B	144	ASN	2.6
1	B	253	ILE	2.6
1	B	216	TYR	2.5
1	B	276	TYR	2.5
1	B	258	LEU	2.5
1	B	111	SER	2.5
1	B	222	SER	2.5
1	A	288	TYR	2.5
1	B	63	ASN	2.5
1	B	211	GLU	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	65	TYR	2.5
1	B	115	TYR	2.5
1	B	146	THR	2.5
1	B	335	THR	2.5
1	B	213	LEU	2.5
1	B	206	ALA	2.5
1	A	244	GLY	2.5
1	B	143	VAL	2.4
1	B	235	PRO	2.4
1	B	229	ASN	2.4
1	B	400	PHE	2.4
1	B	121	ILE	2.4
2	D	78	ALA	2.4
1	A	218	ASN	2.4
1	B	201	THR	2.3
1	B	151	SER	2.3
1	B	347	SER	2.3
1	A	289	GLN	2.3
1	A	164	LEU	2.3
1	B	267	TYR	2.3
1	B	280	THR	2.3
1	B	224	HIS	2.3
1	B	249	ALA	2.3
1	A	391	ASN	2.3
1	B	422	ASP	2.3
1	A	233	TYR	2.2
1	B	188	LEU	2.2
1	B	160	THR	2.2
1	B	214	ILE	2.2
1	B	304	THR	2.2
1	A	55	LEU	2.2
1	B	191	GLN	2.2
1	B	182	LYS	2.2
1	A	27	LEU	2.2
1	B	337	GLU	2.1
1	A	242	ILE	2.1
1	B	168	VAL	2.1
1	B	255	GLY	2.1
1	A	44	PHE	2.1
1	A	390	ASN	2.1
1	B	167	GLN	2.1
1	B	164	LEU	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	210	GLY	2.1
1	B	170	ILE	2.0
1	B	301	ILE	2.0
1	B	306	SER	2.0
1	B	128	ALA	2.0
1	A	26	SER	2.0
1	B	123	SER	2.0
1	A	115	TYR	2.0
1	B	303	ASP	2.0

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

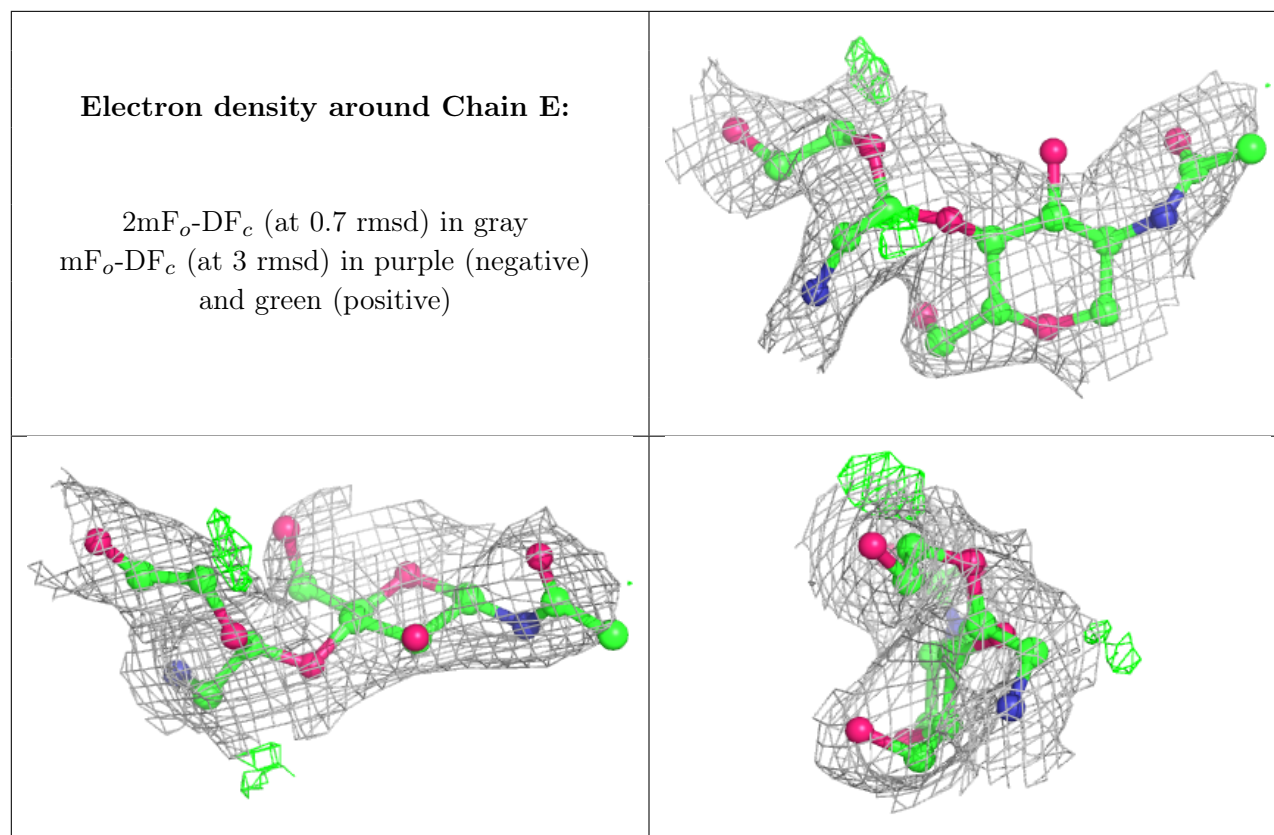
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	E	2	7/15	0.47	0.24	74,77,80,83	2
3	NAG	E	1	14/15	0.83	0.14	80,84,88,89	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands [i](#)

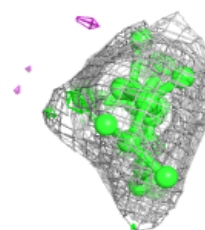
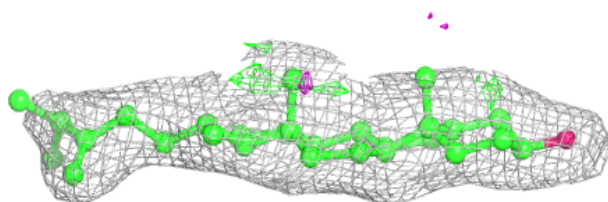
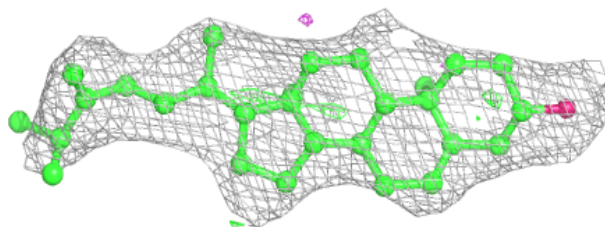
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	B	501	9/15	0.72	0.14	82,90,94,96	1
4	94R	C	102	29/29	0.89	0.17	53,59,64,67	0
4	94R	C	101	29/29	0.92	0.12	44,47,52,55	0
4	94R	B	502	29/29	0.93	0.11	29,31,34,41	0
4	94R	A	503	29/29	0.95	0.10	29,31,35,39	0

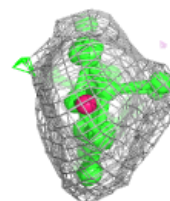
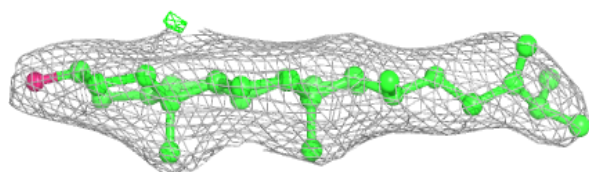
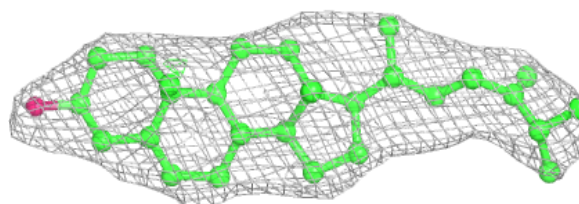
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 94R C 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

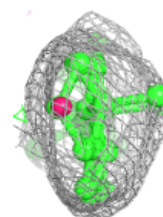
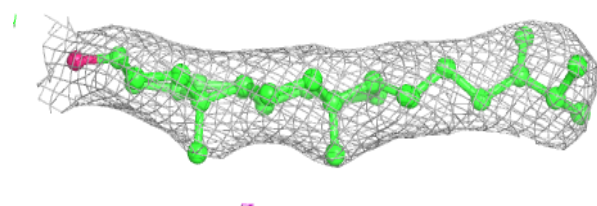
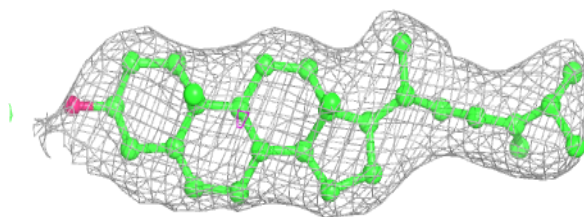
**Electron density around 94R C 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

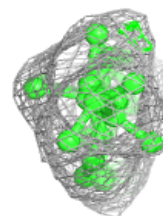
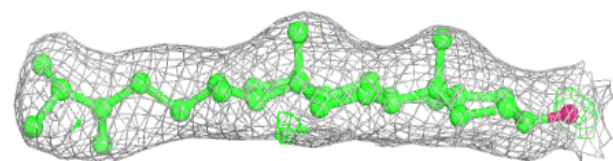
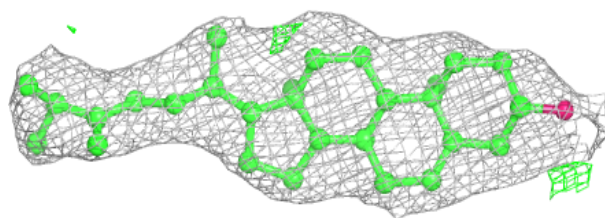


Electron density around 94R B 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around 94R A 503:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.