



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2023 – 05:29 AM EDT

PDB ID : 3ES6
Title : Crystal structure of the novel complex formed between Zinc 2-glycoprotein (ZAG) and Prolactin inducible protein (PIP) from human seminal plasma
Authors : Hassan, M.I.; Bilgrami, S.; Kumar, V.; Singh, N.; Yadav, S.; Kaur, P.; Singh, T.P.
Deposited on : 2008-10-04
Resolution : 3.23 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 : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

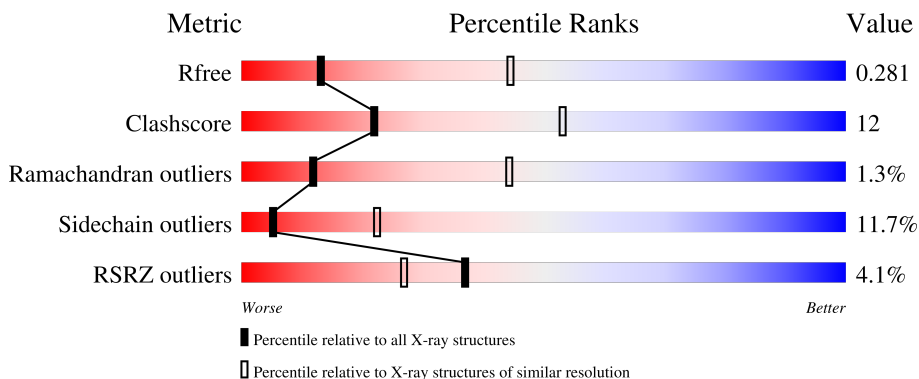
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.23 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}	130704	1619 (3.28-3.20)
Clashscore	141614	1755 (3.28-3.20)
Ramachandran outliers	138981	1728 (3.28-3.20)
Sidechain outliers	138945	1727 (3.28-3.20)
RSRZ outliers	127900	1567 (3.28-3.20)

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	278	 4% 73% 24%
2	B	118	 5% 68% 23% 8%
3	C	5	 40% 60%
4	D	4	 25% 75%

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
1	PCA	A	1	-	-	-	X
4	NAG	D	1	X	-	-	-
4	NAG	D	2	-	-	-	X
4	BMA	D	3	-	-	-	X
4	MAN	D	4	X	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3354 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.

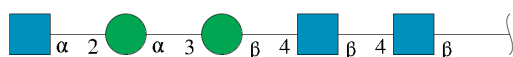
- Molecule 1 is a protein called Zinc-alpha-2-glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	277	2266	1444	385	430	7	0	0	0

- Molecule 2 is a protein called Prolactin-inducible protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	118	951	612	155	179	5	0	0	0

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



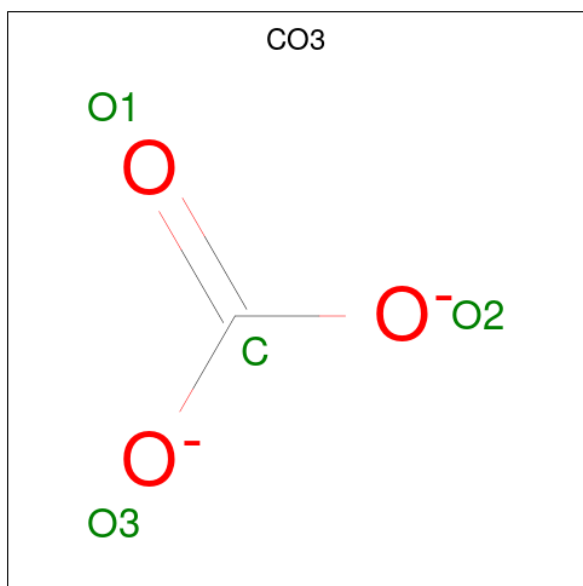
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	5	64	36	3	25	0	0	0

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



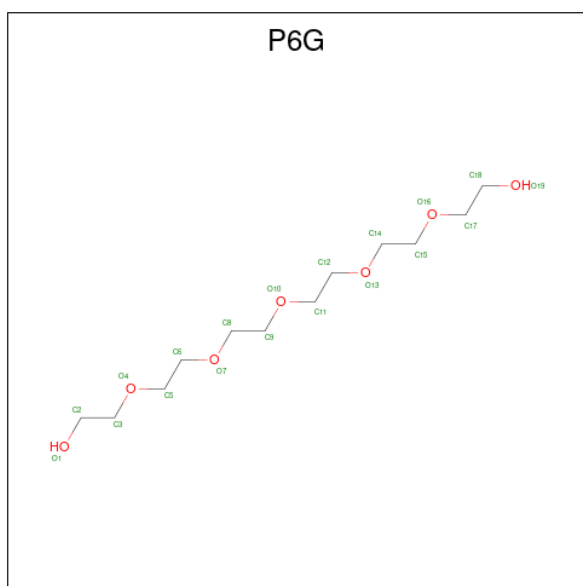
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	D	4	50	28	2	20	0	0	0

- Molecule 5 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	1	3	0	0

- Molecule 6 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: C₁₂H₂₆O₇).

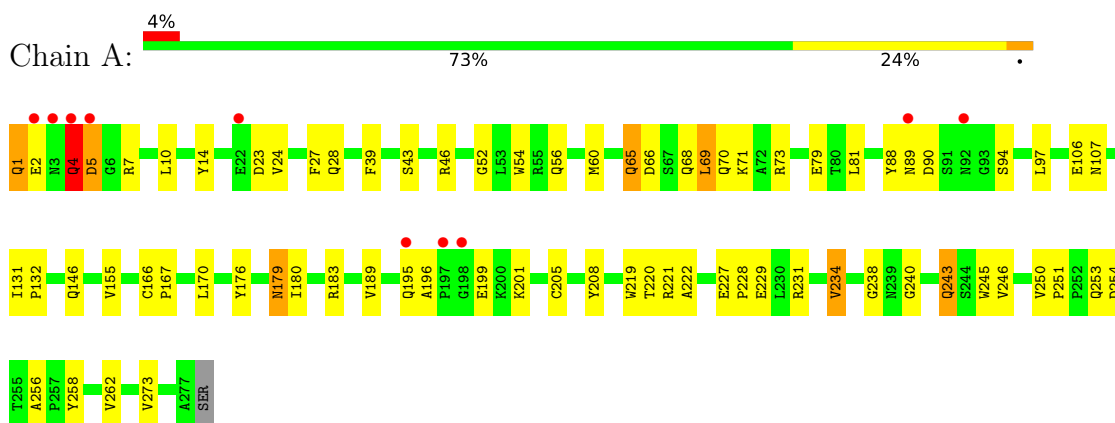


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	19	12	7	0	0

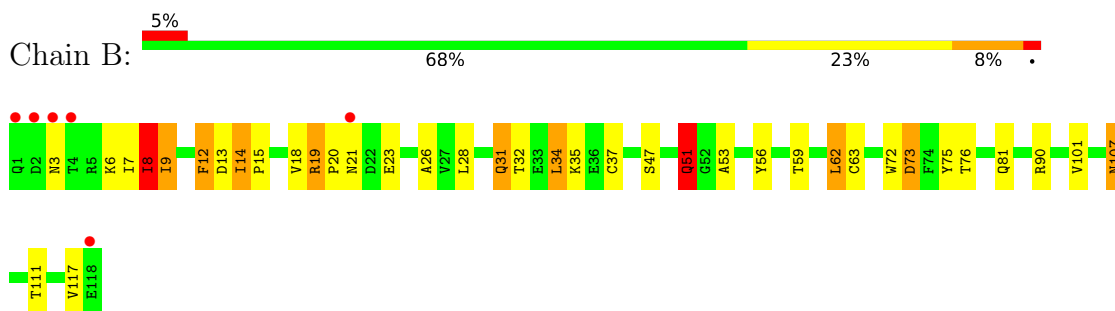
3 Residue-property plots [i](#)

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: Zinc-alpha-2-glycoprotein



- Molecule 2: Prolactin-inducible protein



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



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



MAC1
MAC2
BMA3
MAY4

4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.30Å 132.30Å 73.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 3.23 24.91 – 3.23	Depositor EDS
% Data completeness (in resolution range)	98.8 (25.00-3.23) 98.8 (24.91-3.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 3.23Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.196 , 0.240 0.226 , 0.281	Depositor DCC
R_{free} test set	515 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	49.9	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	3354	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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: NDG, MAN, NAG, P6G, PCA, BMA, CO3

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	0.42	3/2325 (0.1%)	0.57	3/3160 (0.1%)
2	B	0.51	1/969 (0.1%)	0.94	8/1318 (0.6%)
All	All	0.45	4/3294 (0.1%)	0.70	11/4478 (0.2%)

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	1
2	B	0	2
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	231	ARG	CZ-NH2	6.26	1.41	1.33
1	A	2	GLU	C-N	5.49	1.46	1.34
1	A	1	PCA	C-N	5.45	1.46	1.34
2	B	8	ILE	C-N	5.22	1.46	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	9	ILE	N-CA-C	12.78	145.49	111.00
2	B	73	ASP	CA-CB-CG	11.01	137.62	113.40
2	B	23	GLU	CA-CB-CG	9.35	133.96	113.40
1	A	2	GLU	O-C-N	-8.08	109.77	122.70
2	B	9	ILE	N-CA-CB	-6.87	95.01	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	75	TYR	CA-CB-CG	6.80	126.32	113.40
2	B	12	PHE	CA-CB-CG	6.77	130.15	113.90
1	A	69	LEU	CA-CB-CG	6.72	130.76	115.30
2	B	35	LYS	CD-CE-NZ	6.28	126.14	111.70
2	B	51	GLN	CB-CG-CD	5.89	126.90	111.60
1	A	2	GLU	CA-C-N	5.25	128.75	117.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	PCA	Peptide
2	B	8	ILE	Peptide,Mainchain

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	2266	0	2153	46	0
2	B	951	0	963	30	0
3	C	64	0	54	8	0
4	D	50	0	41	4	0
5	A	4	0	0	0	0
6	A	19	0	26	3	0
All	All	3354	0	3237	78	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 12.

All (78) 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)
4:D:4:MAN:C3	4:D:4:MAN:O3	1.78	1.30
2:B:18:VAL:HG12	2:B:19:ARG:H	1.13	1.08
3:C:2:NAG:O3	3:C:3:BMA:H2	1.55	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:ILE:HB	2:B:15:PRO:HD2	1.37	1.00
1:A:196:ALA:HB3	1:A:199:GLU:HB3	1.44	0.98
3:C:2:NAG:H4	3:C:3:BMA:O2	1.74	0.88
2:B:18:VAL:HG12	2:B:19:ARG:N	1.93	0.83
1:A:189:VAL:HG11	1:A:262:VAL:HG21	1.63	0.80
2:B:18:VAL:CG1	2:B:19:ARG:H	1.95	0.78
2:B:14:ILE:HB	2:B:15:PRO:CD	2.15	0.75
1:A:251:PRO:HG2	1:A:254:ASP:HB2	1.69	0.75
3:C:4:MAN:O3	3:C:5:NDG:C1	2.36	0.74
1:A:245:TRP:HH2	2:B:56:TYR:CD1	2.06	0.74
1:A:24:VAL:HG21	2:B:81:GLN:HG3	1.68	0.73
1:A:60:MET:HE2	1:A:176:TYR:HB2	1.75	0.69
1:A:180:ILE:O	1:A:183:ARG:HG3	1.93	0.68
2:B:32:THR:OG1	2:B:34:LEU:HB2	1.93	0.68
3:C:1:NAG:O3	3:C:2:NAG:O5	2.12	0.67
1:A:52:GLY:HA2	1:A:238:GLY:HA2	1.76	0.66
2:B:14:ILE:HG21	2:B:26:ALA:HA	1.78	0.65
1:A:73:ARG:NH1	6:A:701:P6G:H61	2.13	0.64
1:A:196:ALA:HB3	1:A:199:GLU:CB	2.26	0.61
4:D:3:BMA:O2	4:D:4:MAN:O2	2.18	0.61
2:B:8:ILE:HG22	2:B:9:ILE:H	1.64	0.61
2:B:26:ALA:HB3	2:B:72:TRP:HB2	1.83	0.60
1:A:73:ARG:HH11	6:A:701:P6G:H61	1.67	0.60
1:A:183:ARG:NH2	1:A:240:GLY:O	2.37	0.58
1:A:245:TRP:CH2	2:B:56:TYR:CE1	2.91	0.58
2:B:14:ILE:CG2	2:B:26:ALA:HA	2.35	0.57
1:A:245:TRP:CH2	2:B:56:TYR:CD1	2.92	0.56
3:C:4:MAN:HO3	3:C:5:NDG:C1	2.16	0.56
2:B:14:ILE:CB	2:B:15:PRO:HD2	2.24	0.56
3:C:1:NAG:O3	3:C:2:NAG:C1	2.54	0.55
1:A:166:CYS:HB3	1:A:167:PRO:HD3	1.90	0.54
2:B:8:ILE:O	2:B:32:THR:HA	2.09	0.53
1:A:73:ARG:HH11	6:A:701:P6G:C6	2.22	0.51
1:A:179:ASN:H	1:A:179:ASN:HD22	1.59	0.51
1:A:222:ALA:HB2	1:A:256:ALA:HB1	1.94	0.50
1:A:228:PRO:HB3	1:A:246:VAL:HG13	1.93	0.49
1:A:27:PHE:HB3	1:A:43:SER:HB3	1.94	0.49
1:A:7:ARG:HB3	1:A:106:GLU:HG3	1.95	0.49
4:D:3:BMA:O2	4:D:4:MAN:C2	2.60	0.49
1:A:4:GLN:HB2	1:A:107:ASN:HD21	1.78	0.48
2:B:31:GLN:HA	2:B:62:LEU:HD21	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:VAL:HG23	1:A:273:VAL:HG21	1.95	0.47
1:A:201:LYS:HB3	1:A:250:VAL:HG13	1.97	0.47
2:B:53:ALA:HB3	2:B:73:ASP:O	2.13	0.47
2:B:107:ASN:HD22	2:B:107:ASN:H	1.63	0.47
1:A:54:TRP:CD1	1:A:60:MET:HE1	2.50	0.46
4:D:2:NAG:H61	4:D:3:BMA:H2	1.96	0.46
1:A:81:LEU:HD13	1:A:97:LEU:HB2	1.98	0.46
1:A:28:GLN:NE2	2:B:47:SER:O	2.44	0.45
1:A:179:ASN:HD22	1:A:179:ASN:N	2.14	0.45
1:A:234:VAL:HG21	2:B:56:TYR:CE1	2.52	0.45
1:A:245:TRP:HH2	2:B:56:TYR:CE1	2.29	0.45
1:A:208:TYR:CE2	3:C:2:NAG:H61	2.52	0.44
1:A:234:VAL:HG21	2:B:56:TYR:HE1	1.82	0.44
1:A:65:GLN:O	1:A:68:GLN:HB2	2.18	0.44
2:B:107:ASN:HD22	2:B:107:ASN:N	2.14	0.44
2:B:8:ILE:HG22	2:B:9:ILE:HG13	2.00	0.43
1:A:131:ILE:HB	1:A:132:PRO:C	2.37	0.43
1:A:14:TYR:HD2	1:A:27:PHE:CZ	2.37	0.43
1:A:88:TYR:C	1:A:90:ASP:H	2.22	0.43
1:A:65:GLN:HE21	1:A:65:GLN:HB2	1.59	0.43
2:B:20:PRO:HD3	2:B:117:VAL:HG12	2.00	0.43
3:C:2:NAG:HO3	3:C:3:BMA:H2	1.75	0.43
1:A:208:TYR:CB	1:A:243:GLN:HG3	2.50	0.42
1:A:10:LEU:HB2	1:A:170:LEU:HD13	2.01	0.42
1:A:189:VAL:CG2	1:A:273:VAL:HG21	2.50	0.42
1:A:60:MET:HE2	1:A:176:TYR:CB	2.47	0.41
2:B:51:GLN:H	2:B:51:GLN:HG3	1.19	0.41
1:A:54:TRP:NE1	1:A:60:MET:HE1	2.36	0.41
1:A:205:CYS:HB2	1:A:219:TRP:CZ2	2.56	0.40
2:B:14:ILE:CB	2:B:15:PRO:CD	2.86	0.40
1:A:221:ARG:HG3	1:A:258:TYR:CZ	2.56	0.40
1:A:234:VAL:CG2	2:B:56:TYR:CE1	3.05	0.40
2:B:31:GLN:HE21	2:B:31:GLN:HB3	1.65	0.40
1:A:66:ASP:O	1:A:70:GLN:HG2	2.22	0.40

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 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	275/278 (99%)	261 (95%)	11 (4%)	3 (1%)	14	48
2	B	116/118 (98%)	102 (88%)	12 (10%)	2 (2%)	9	39
All	All	391/396 (99%)	363 (93%)	23 (6%)	5 (1%)	12	44

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASP
2	B	8	ILE
1	A	89	ASN
1	A	4	GLN
2	B	6	LYS

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 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	242/243 (100%)	221 (91%)	21 (9%)	10	35
2	B	108/108 (100%)	88 (82%)	20 (18%)	1	7
All	All	350/351 (100%)	309 (88%)	41 (12%)	5	22

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLN

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Mol	Chain	Res	Type
1	A	5	ASP
1	A	23	ASP
1	A	39	PHE
1	A	46	ARG
1	A	56	GLN
1	A	65	GLN
1	A	69	LEU
1	A	71	LYS
1	A	79	GLU
1	A	94	SER
1	A	146	GLN
1	A	155	VAL
1	A	179	ASN
1	A	195	GLN
1	A	220	THR
1	A	227	GLU
1	A	229	GLU
1	A	234	VAL
1	A	243	GLN
1	A	253	GLN
2	B	3	ASN
2	B	7	ILE
2	B	12	PHE
2	B	13	ASP
2	B	14	ILE
2	B	19	ARG
2	B	21	ASN
2	B	28	LEU
2	B	31	GLN
2	B	34	LEU
2	B	37	CYS
2	B	51	GLN
2	B	59	THR
2	B	62	LEU
2	B	63	CYS
2	B	76	THR
2	B	90	ARG
2	B	101	VAL
2	B	107	ASN
2	B	111	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	107	ASN
1	A	179	ASN
1	A	184	GLN
1	A	253	GLN
1	A	263	GLN
2	B	31	GLN
2	B	66	ASN
2	B	107	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
1	PCA	A	1	1	7,8,9	4.59	5 (71%)	9,10,12	3.53	6 (66%)

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
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CD-N	7.34	1.54	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CA-N	6.63	1.54	1.46
1	A	1	PCA	O-C	4.81	1.39	1.19
1	A	1	PCA	OE-CD	4.04	1.31	1.23
1	A	1	PCA	CB-CG	2.77	1.59	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	PCA	CB-CA-C	-6.21	104.16	112.70
1	A	1	PCA	OE-CD-CG	-5.16	117.77	126.76
1	A	1	PCA	CA-N-CD	-4.35	98.69	113.58
1	A	1	PCA	O-C-CA	-3.49	115.63	124.78
1	A	1	PCA	CG-CD-N	2.84	115.76	108.39
1	A	1	PCA	CB-CA-N	2.50	110.49	103.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
3	NAG	C	1	3,1	14,14,15	0.56	0	17,19,21	0.75	0
3	NAG	C	2	3	14,14,15	0.54	0	17,19,21	0.77	0
3	BMA	C	3	3	11,11,12	0.44	0	15,15,17	1.23	1 (6%)
3	MAN	C	4	3	11,11,12	1.35	2 (18%)	15,15,17	2.46	4 (26%)
3	NDG	C	5	3	14,14,15	1.34	1 (7%)	17,19,21	1.05	1 (5%)
4	NAG	D	1	2,4	14,14,15	0.69	0	17,19,21	1.08	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	D	2	4	14,14,15	0.69	0	17,19,21	1.17	1 (5%)
4	BMA	D	3	4	11,11,12	1.98	2 (18%)	15,15,17	1.63	3 (20%)
4	MAN	D	4	4	11,11,12	5.15	3 (27%)	15,15,17	4.16	7 (46%)

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	C	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	2/2/19/22	0/1/1/1
3	NDG	C	5	3	-	4/6/23/26	0/1/1/1
4	NAG	D	1	2,4	1/1/5/7	3/6/23/26	0/1/1/1
4	NAG	D	2	4	-	1/6/23/26	0/1/1/1
4	BMA	D	3	4	-	2/2/19/22	0/1/1/1
4	MAN	D	4	4	1/1/4/5	0/2/19/22	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	4	MAN	O3-C3	15.18	1.78	1.43
4	D	4	MAN	O2-C2	-6.49	1.29	1.43
4	D	3	BMA	O3-C3	4.69	1.54	1.43
3	C	5	NDG	C8-C7	4.04	1.58	1.50
4	D	3	BMA	O4-C4	-3.73	1.34	1.43
4	D	4	MAN	O6-C6	2.92	1.54	1.42
3	C	4	MAN	C2-C3	2.68	1.56	1.52
3	C	4	MAN	O3-C3	-2.60	1.36	1.43

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	4	MAN	O2-C2-C3	-10.36	89.38	110.14
4	D	4	MAN	O2-C2-C1	7.55	124.59	109.15
3	C	4	MAN	O3-C3-C2	7.33	124.04	109.99
4	D	4	MAN	O3-C3-C2	7.22	123.81	109.99
4	D	3	BMA	O4-C4-C5	4.74	121.06	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4	MAN	O3-C3-C4	-4.47	100.02	110.35
4	D	4	MAN	C1-O5-C5	-3.77	107.09	112.19
4	D	2	NAG	C4-C3-C2	3.36	115.94	111.02
4	D	4	MAN	O5-C1-C2	3.03	115.45	110.77
3	C	3	BMA	C3-C4-C5	2.99	115.57	110.24
4	D	1	NAG	C4-C3-C2	2.94	115.32	111.02
4	D	4	MAN	O5-C5-C6	2.78	111.56	107.20
3	C	4	MAN	O5-C5-C6	2.65	111.36	107.20
4	D	3	BMA	O4-C4-C3	2.56	116.27	110.35
4	D	3	BMA	O5-C5-C6	2.19	110.64	107.20
3	C	4	MAN	C1-C2-C3	2.15	112.31	109.67
4	D	4	MAN	C1-C2-C3	-2.10	107.08	109.67
3	C	5	NDG	C1-O5-C5	2.09	115.03	112.19

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	D	1	NAG	C1
4	D	4	MAN	C1

All (16) torsion outliers are listed below:

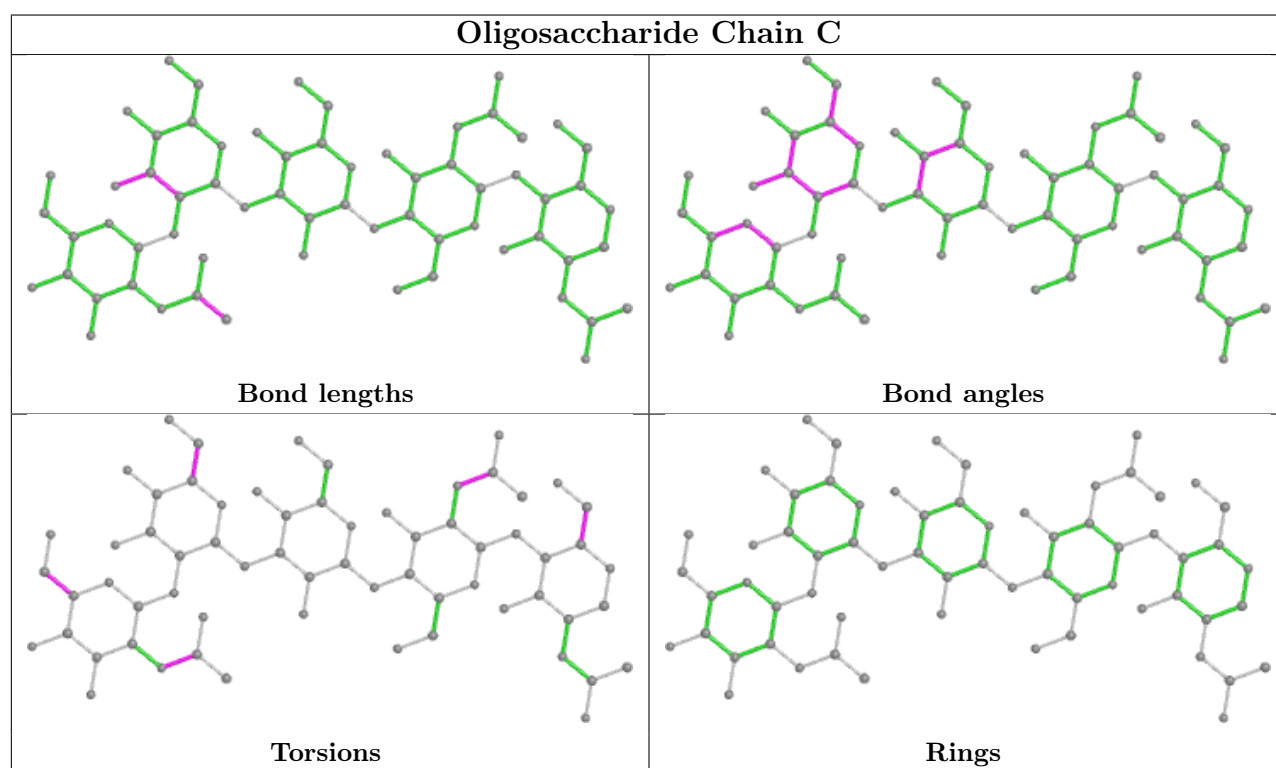
Mol	Chain	Res	Type	Atoms
3	C	5	NDG	C8-C7-N2-C2
3	C	5	NDG	O7-C7-N2-C2
4	D	1	NAG	C3-C2-N2-C7
4	D	1	NAG	C8-C7-N2-C2
4	D	1	NAG	O7-C7-N2-C2
3	C	4	MAN	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
3	C	4	MAN	C4-C5-C6-O6
4	D	3	BMA	O5-C5-C6-O6
4	D	3	BMA	C4-C5-C6-O6
3	C	5	NDG	C4-C5-C6-O6
3	C	5	NDG	O5-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
4	D	2	NAG	C4-C5-C6-O6

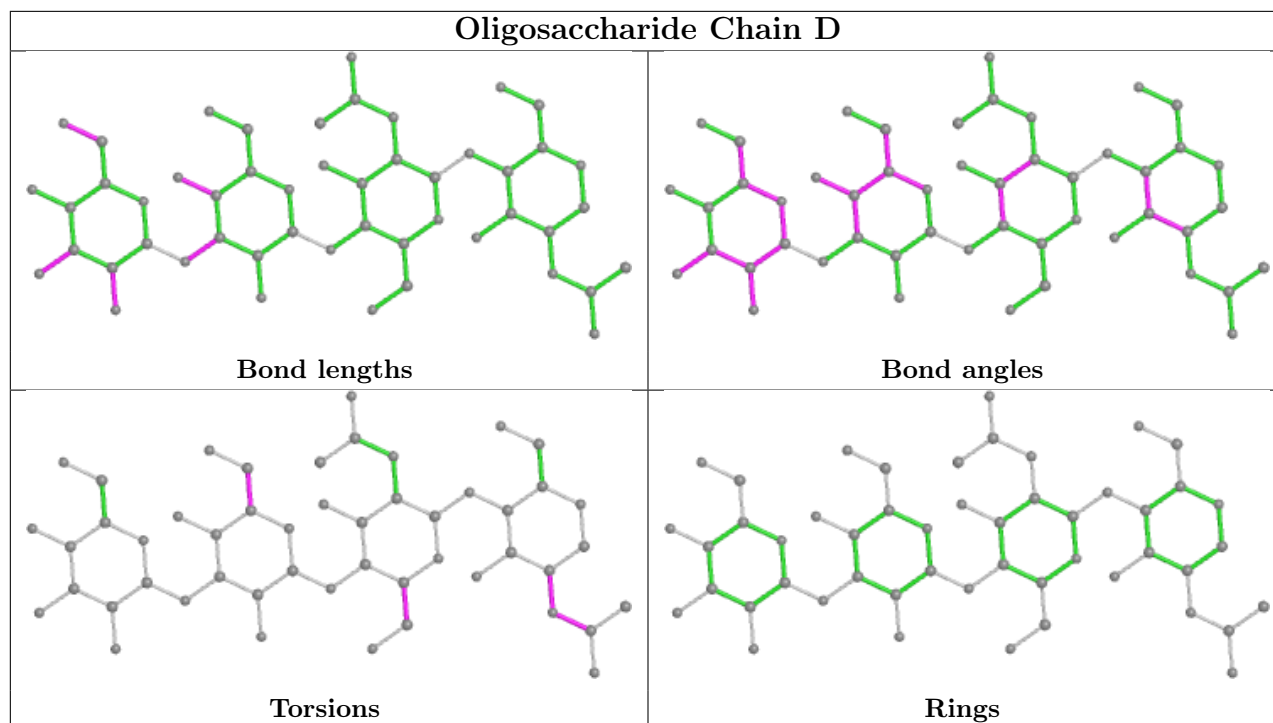
There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	3	BMA	3	0
3	C	1	NAG	2	0
3	C	4	MAN	2	0
4	D	4	MAN	3	0
3	C	5	NDG	2	0
4	D	2	NAG	1	0
3	C	3	BMA	3	0
3	C	2	NAG	6	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](#)

2 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$
6	P6G	A	701	-	18,18,18	1.30	3 (16%)	17,17,17	0.58	0
5	CO3	A	688	-	2,3,3	0.30	0	2,3,3	0.13	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
6	P6G	A	701	-	-	6/16/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	701	P6G	C9-C8	3.55	1.67	1.49
6	A	701	P6G	C3-C2	2.56	1.63	1.49
6	A	701	P6G	O4-C3	2.10	1.51	1.42

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

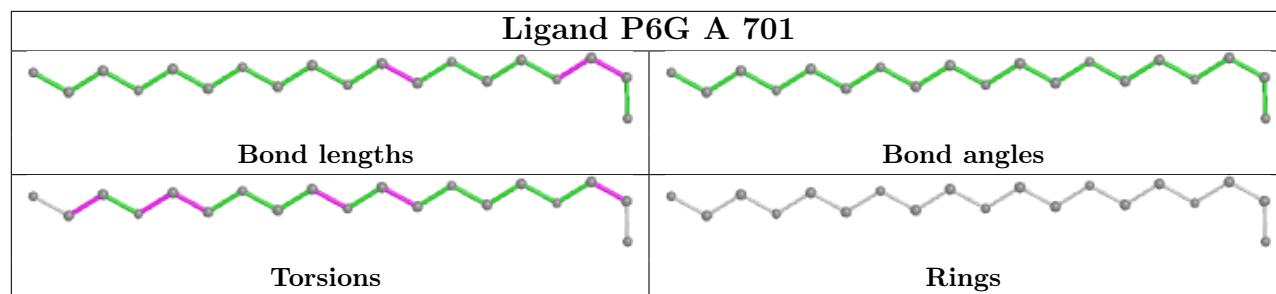
Mol	Chain	Res	Type	Atoms
6	A	701	P6G	O13-C14-C15-O16
6	A	701	P6G	O1-C2-C3-O4
6	A	701	P6G	O16-C17-C18-O19
6	A	701	P6G	O7-C8-C9-O10
6	A	701	P6G	C12-C11-O10-C9
6	A	701	P6G	C14-C15-O16-C17

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	701	P6G	3	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 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	276/278 (99%)	-0.16	10 (3%) 42 31	19, 30, 49, 61	0
2	B	118/118 (100%)	0.01	6 (5%) 28 18	20, 33, 58, 74	0
All	All	394/396 (99%)	-0.11	16 (4%) 37 27	19, 31, 52, 74	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	GLU	5.8
2	B	2	ASP	5.2
2	B	1	GLN	5.2
2	B	3	ASN	4.8
1	A	3	ASN	4.5
1	A	4	GLN	4.4
2	B	118	GLU	3.1
1	A	198	GLY	3.0
1	A	92	ASN	3.0
1	A	197	PRO	2.8
1	A	5	ASP	2.6
1	A	195	GLN	2.6
1	A	89	ASN	2.3
2	B	4	THR	2.2
2	B	21	ASN	2.2
1	A	22	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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(\AA^2)	Q<0.9
1	PCA	A	1	8/9	0.64	0.80	61,61,62,62	0

6.3 Carbohydrates [i](#)

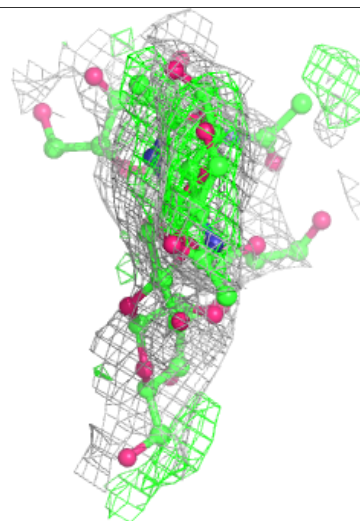
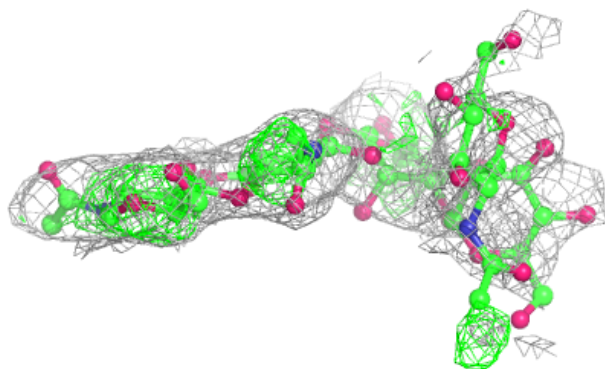
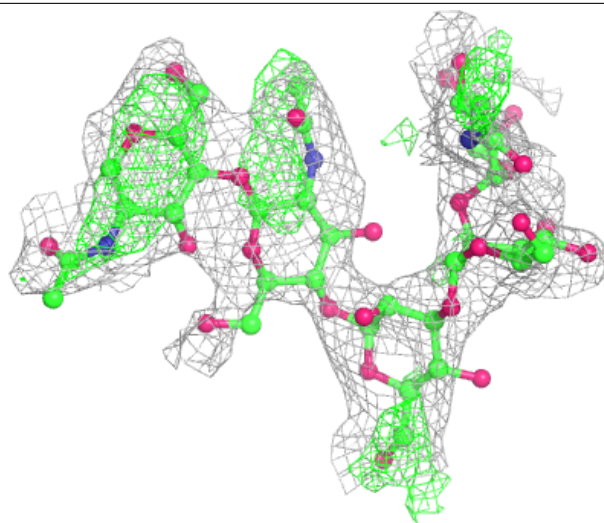
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

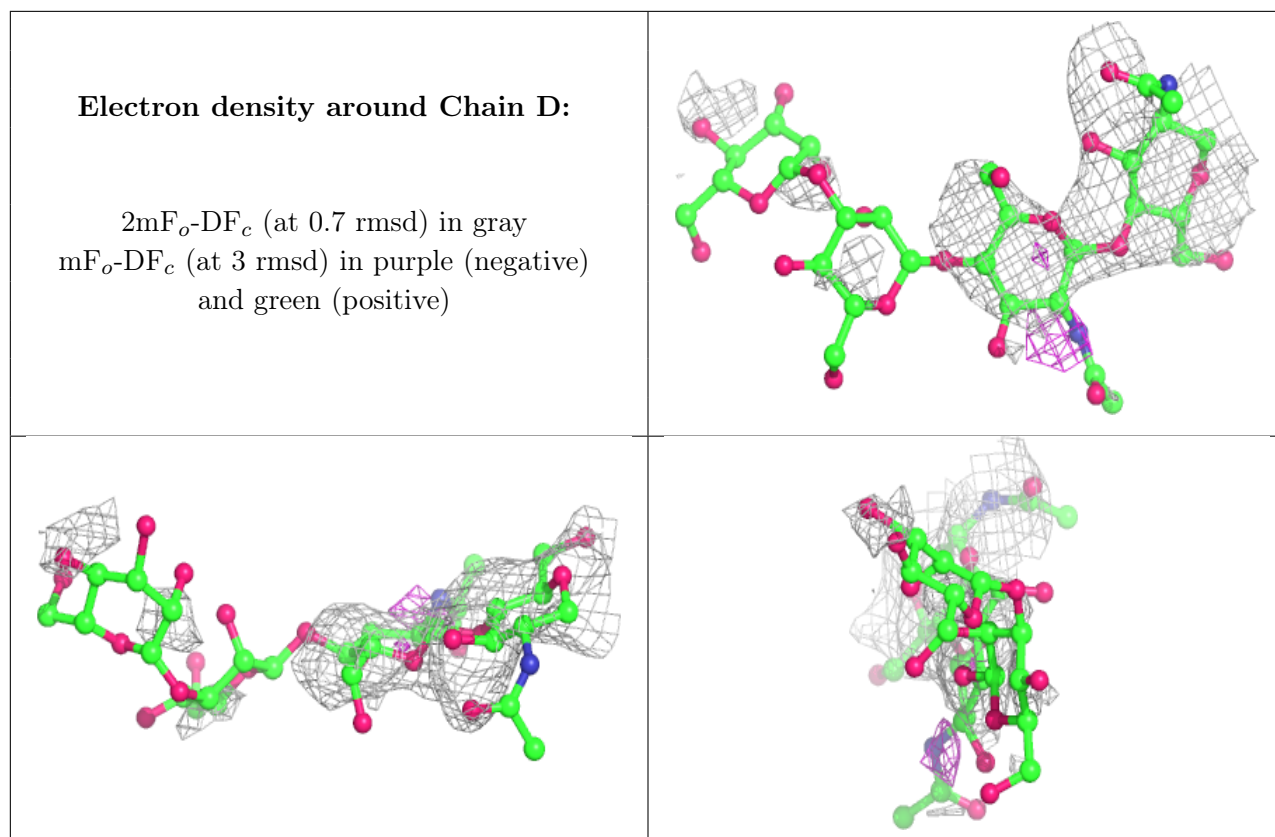
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MAN	D	4	11/12	0.32	0.69	70,70,70,70	11
4	BMA	D	3	11/12	0.54	0.71	70,70,70,70	11
3	NDG	C	5	14/15	0.65	0.37	33,35,35,35	14
4	NAG	D	2	14/15	0.66	0.67	68,70,73,74	0
4	NAG	D	1	14/15	0.73	0.30	56,58,61,64	14
3	NAG	C	2	14/15	0.81	0.30	22,23,25,27	14
3	BMA	C	3	11/12	0.82	0.22	29,30,31,32	11
3	MAN	C	4	11/12	0.85	0.24	33,34,34,35	11
3	NAG	C	1	14/15	0.87	0.31	18,20,22,22	14

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.

Electron density around Chain C:

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



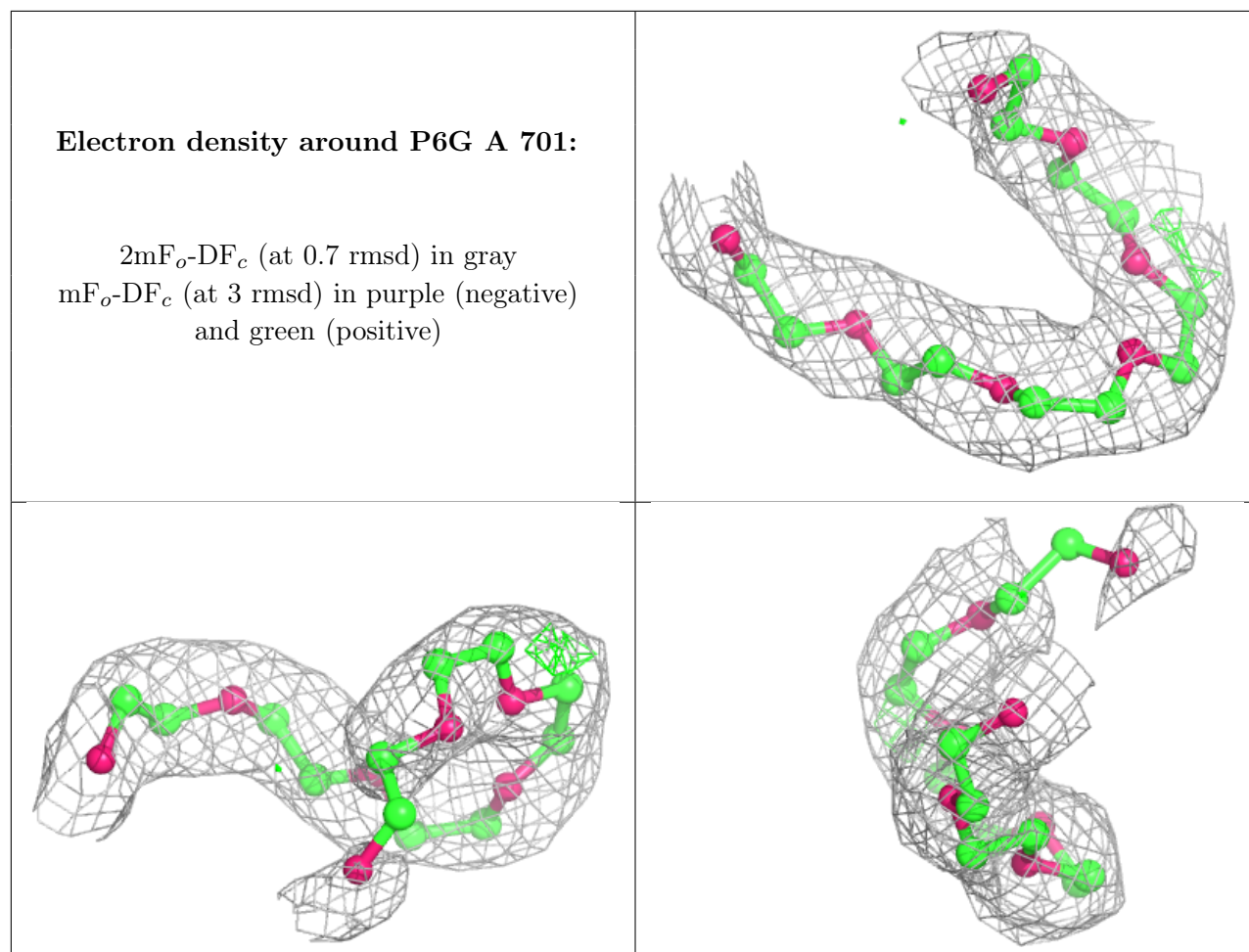


6.4 Ligands [i](#)

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	CO3	A	688	4/4	0.83	0.31	56,56,56,56	0
6	P6G	A	701	19/19	0.88	0.28	43,45,49,49	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.