



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 01:47 PM BST

PDB ID : 3NXQ
Title : Angiotensin Converting Enzyme N domain glycoylation mutant (Ndom389)
in complex with RXP407
Authors : Anthony, C.S.; Corradi, H.R.; Schwager, S.L.U.; Redelinghuys, P.; Georgiadis,
D.; Dive, V.; Acharya, K.R.; Sturrock, E.D.
Deposited on : 2010-07-14
Resolution : 1.99 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 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 : 2.13.1
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) : 2.13.1

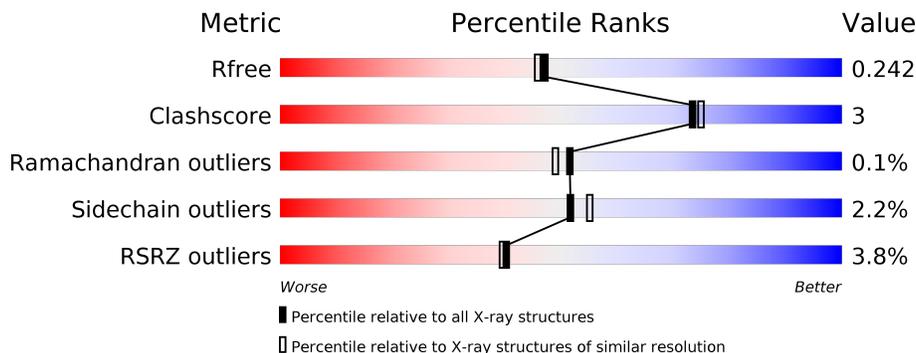
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 on 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	629	 3% 88% 8%
1	B	629	 5% 88% 9%
2	C	2	 100%
2	F	2	 100%
3	D	2	 100%
3	G	2	 100%

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Mol	Chain	Length	Quality of chain
4	E	4	
4	H	4	

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
3	NAG	G	2	-	-	-	X

2 Entry composition i

There are 11 unique types of molecules in this entry. The entry contains 10796 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 Angiotensin-converting enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	607	Total	C	N	O	S	0	6	0
			4955	3189	850	897	19			
1	B	610	Total	C	N	O	S	0	3	0
			4935	3181	841	894	19			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLN	ASN	engineered mutation	UNP P12821
A	25	GLN	ASN	engineered mutation	UNP P12821
A	82	GLN	ASN	engineered mutation	UNP P12821
A	117	GLN	ASN	engineered mutation	UNP P12821
A	131	GLN	ASN	engineered mutation	UNP P12821
A	289	GLN	ASN	engineered mutation	UNP P12821
A	545	ARG	GLN	engineered mutation	UNP P12821
A	576	LEU	PRO	engineered mutation	UNP P12821
A	629	LEU	ARG	engineered mutation	UNP P12821
B	9	GLN	ASN	engineered mutation	UNP P12821
B	25	GLN	ASN	engineered mutation	UNP P12821
B	82	GLN	ASN	engineered mutation	UNP P12821
B	117	GLN	ASN	engineered mutation	UNP P12821
B	131	GLN	ASN	engineered mutation	UNP P12821
B	289	GLN	ASN	engineered mutation	UNP P12821
B	545	ARG	GLN	engineered mutation	UNP P12821
B	576	LEU	PRO	engineered mutation	UNP P12821
B	629	LEU	ARG	engineered mutation	UNP P12821

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



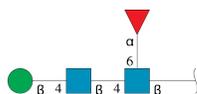
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	F	2	Total	C	N	O	0	0	0
			24	14	1	9			

- 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	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

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

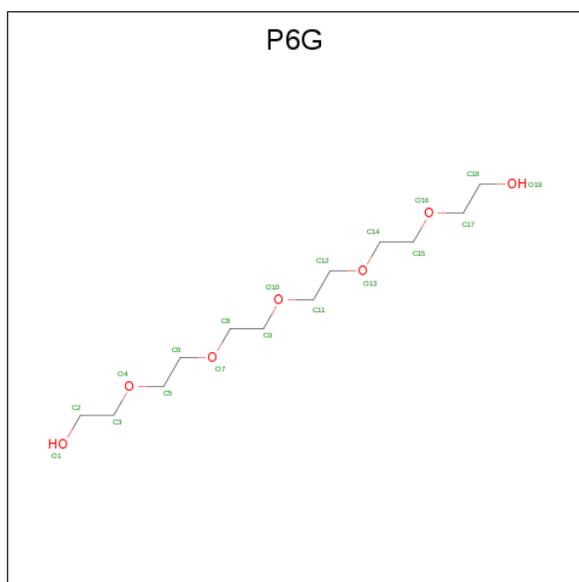


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	4	Total	C	N	O	0	0	0
			49	28	2	19			
4	H	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		

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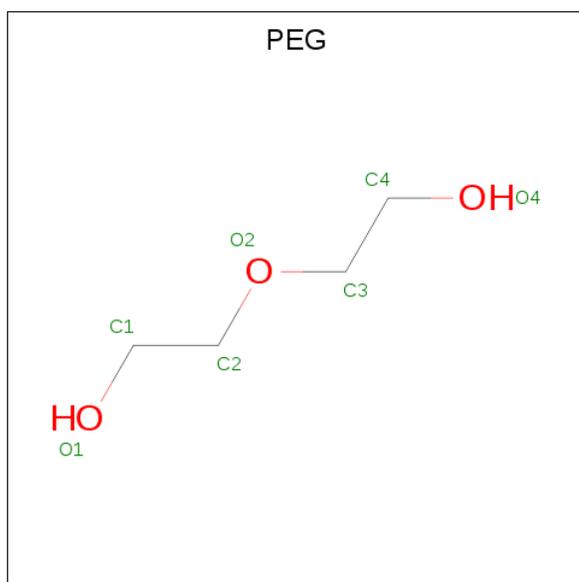


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 13 8 5	0	0
7	B	1	Total C O 19 12 7	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

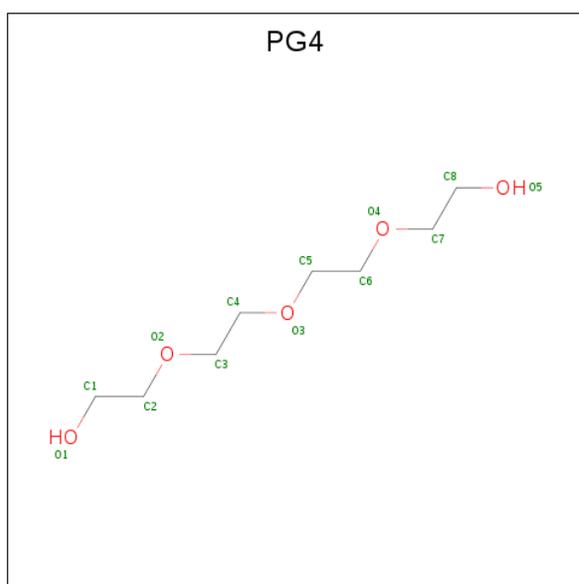
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total Cl 1 1	0	0
8	A	1	Total Cl 1 1	0	0

- Molecule 9 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			7	4	3		
9	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 10 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			10	6	4		
10	B	1	Total	C	O	0	0
			13	8	5		

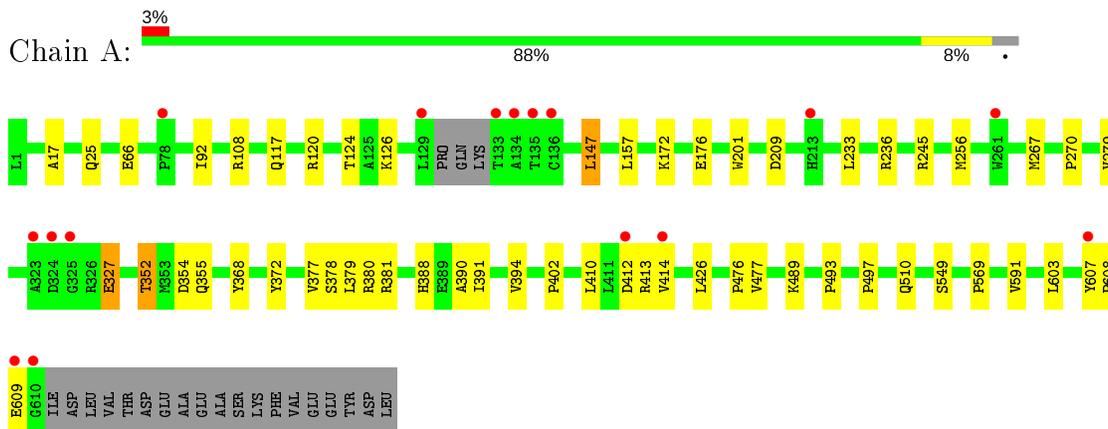
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	303	Total 303	O 303	0	0
11	B	260	Total 260	O 260	0	0

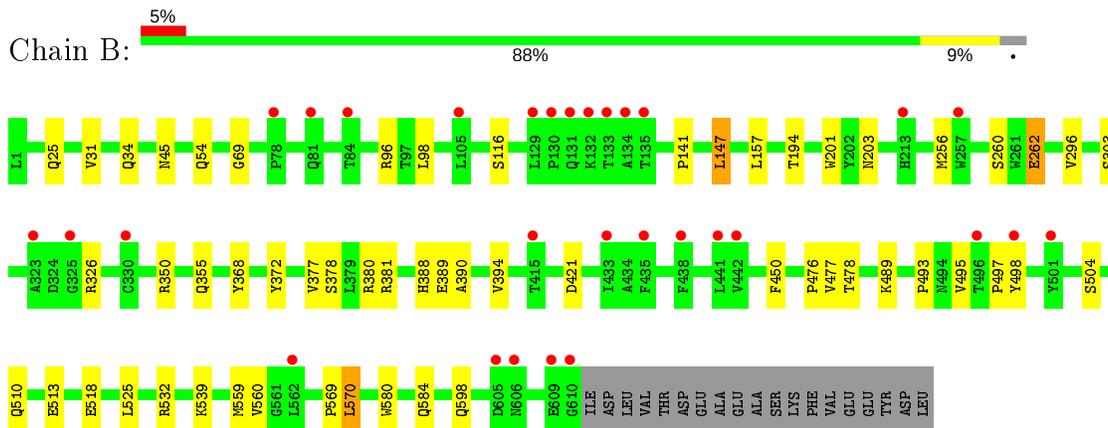
3 Residue-property plots [i](#)

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.

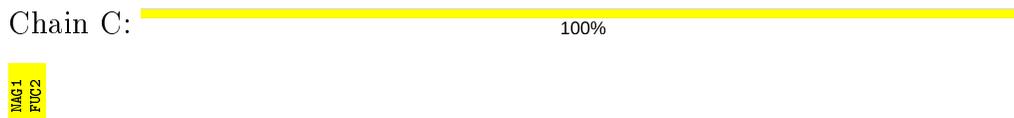
- Molecule 1: Angiotensin-converting enzyme



- Molecule 1: Angiotensin-converting enzyme



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
FUC2

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

Chain D:  100%MAG1
MAG2

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

Chain G:  100%MAG1
MAG2

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

Chain E:  75% 25%MAG1
MAG2
BMA3
FUC4

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

Chain H:  50% 50%MAG1
MAG2
BMA3
FUC4

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	72.88Å 76.69Å 82.65Å 88.63° 64.17° 75.70°	Depositor
Resolution (Å)	40.81 – 1.99 40.81 – 1.99	Depositor EDS
% Data completeness (in resolution range)	95.6 (40.81-1.99) 95.6 (40.81-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.194 , 0.237 0.202 , 0.242	Depositor DCC
R_{free} test set	1025 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtrriage
Anisotropy	0.045	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10796	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.29% 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: ZN, BMA, NAG, CL, PG4, FUC, P6G, PEG, RX4

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	0.39	0/5129	0.51	0/6989
1	B	0.39	0/5101	0.51	1/6959 (0.0%)
All	All	0.39	0/10230	0.51	1/13948 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	570	LEU	CB-CG-CD1	5.66	120.62	111.00

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	4955	0	4715	34	0
1	B	4935	0	4677	30	0
2	C	24	0	22	0	0
2	F	24	0	22	2	0
3	D	28	0	25	0	0
3	G	28	0	25	0	0
4	E	49	0	43	0	0
4	H	49	0	43	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	34	0	29	3	0
6	B	34	0	29	3	0
7	A	13	0	17	0	0
7	B	19	0	26	1	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	7	0	10	0	0
9	B	7	0	10	0	0
10	B	23	0	31	0	0
11	A	303	0	0	0	0
11	B	260	0	0	3	0
All	All	10796	0	9724	66	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 3.

All (66) 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:352:THR:HG22	1:A:355:GLN:H	1.37	0.89
1:B:69:GLY:HA3	1:B:98[B]:LEU:HD21	1.57	0.86
1:B:518:GLU:HG3	1:B:539:LYS:HD2	1.69	0.74
1:B:350:ARG:H	1:B:355:GLN:HE21	1.36	0.73
1:A:236:ARG:HD2	1:A:267:MET:HE3	1.73	0.70
1:B:489:LYS:HZ1	6:B:700:RX4:HAD2	1.44	0.66
1:B:380:ARG:O	1:B:381:ARG:HD2	1.96	0.65
1:A:391:ILE:O	1:A:394[B]:VAL:HG12	1.99	0.63
1:A:157:LEU:HD11	1:A:477:VAL:HG13	1.81	0.62
1:A:25:GLN:HE21	1:A:378:SER:H	1.45	0.61
1:A:17:ALA:HB1	1:A:92:ILE:CD1	2.30	0.61
1:B:303:SER:HB2	1:B:532:ARG:HG2	1.83	0.59
1:B:201:TRP:HZ3	1:B:497:PRO:HG2	1.68	0.59
1:B:489:LYS:NZ	6:B:700:RX4:HAD2	2.00	0.59
1:B:25:GLN:HE21	1:B:378:SER:H	1.50	0.59
1:B:157:LEU:HD11	1:B:477:VAL:HG13	1.85	0.58
1:A:279:VAL:HG11	1:A:410:LEU:HD13	1.87	0.56
1:A:402:PRO:HB2	1:A:414:VAL:HG11	1.86	0.56
1:B:260:SER:OG	1:B:262:GLU:OE1	2.22	0.56
1:A:201:TRP:HZ3	1:A:497:PRO:HG2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:GLN:HG2	1:A:120[A]:ARG:HH22	1.71	0.56
1:A:489:LYS:HZ1	6:A:700:RX4:HAD2	1.54	0.54
1:A:201:TRP:CZ3	1:A:497:PRO:HG2	2.42	0.54
1:A:66:GLU:CD	1:A:108:ARG:HH22	2.11	0.54
1:A:412:ASP:O	1:A:413:ARG:C	2.46	0.54
1:B:539:LYS:HE3	1:B:559:MET:O	2.09	0.53
1:A:147:LEU:HD22	1:A:256:MET:HA	1.90	0.53
1:A:17:ALA:HB1	1:A:92:ILE:HD11	1.90	0.52
1:A:510:GLN:HG2	1:A:569:PRO:HG2	1.92	0.52
1:A:270:PRO:HD3	1:A:426:LEU:HD22	1.90	0.52
1:B:495:VAL:HG12	1:B:495:VAL:O	2.09	0.52
1:A:489:LYS:O	1:A:493:PRO:HD2	2.10	0.52
1:A:380:ARG:O	1:A:381:ARG:HD2	2.10	0.51
1:A:352:THR:CG2	1:A:354:ASP:OD2	2.60	0.50
1:A:477:VAL:HG12	1:A:603:LEU:HD21	1.94	0.50
1:B:296:VAL:HG22	7:B:709:P6G:H152	1.93	0.50
1:A:489:LYS:NZ	6:A:700:RX4:HAD2	2.10	0.49
1:B:478:THR:HB	2:F:2:FUC:H4	1.93	0.49
1:B:147:LEU:HD22	1:B:256:MET:HA	1.95	0.49
1:B:201:TRP:CZ3	1:B:497:PRO:HG2	2.48	0.48
1:A:402:PRO:CB	1:A:414:VAL:HG11	2.44	0.48
1:A:233:LEU:HD23	1:A:267:MET:HE2	1.96	0.48
1:B:513:GLU:HA	1:B:525:LEU:HD11	1.95	0.48
1:A:172:LYS:O	1:A:176:GLU:HG3	2.14	0.47
1:A:352:THR:HG21	1:A:354:ASP:OD2	2.14	0.47
1:A:126:LYS:NZ	1:A:327:GLU:OE2	2.45	0.46
1:B:31:VAL:O	1:B:34:GLN:HG3	2.16	0.46
1:A:390:ALA:O	1:A:394[A]:VAL:HG23	2.16	0.45
1:B:510:GLN:HG2	1:B:569:PRO:HG2	1.98	0.45
1:B:54:GLN:NE2	11:B:829:HOH:O	2.24	0.45
1:B:141:PRO:HB3	1:B:350:ARG:HD3	2.00	0.44
1:A:245:ARG:HG2	1:A:591:VAL:HG11	2.00	0.44
1:B:390:ALA:O	1:B:394:VAL:HG23	2.18	0.43
11:B:706:HOH:O	2:F:2:FUC:H5	2.19	0.43
1:B:194:THR:HB	1:B:450:PHE:CD2	2.54	0.43
1:B:389:GLU:HB2	1:B:504:SER:HB2	2.00	0.42
1:A:124:THR:HG22	1:A:327:GLU:HG2	2.00	0.42
1:B:498:TYR:OH	6:B:700:RX4:NAD	2.52	0.42
1:A:607:TYR:HA	1:A:608:PRO:HA	1.83	0.42
1:B:598:GLN:NE2	11:B:779:HOH:O	2.52	0.42
1:B:489:LYS:O	1:B:493:PRO:HD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:LEU:HD22	1:A:549:SER:HA	2.01	0.41
1:B:157:LEU:HD13	1:B:476:PRO:HB2	2.03	0.41
1:B:580:TRP:O	1:B:584:GLN:HG2	2.20	0.41
6:A:700:RX4:HBF	6:A:700:RX4:HAA1	1.75	0.41
1:A:157:LEU:HD13	1:A:476:PRO:HB2	2.02	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	609/629 (97%)	598 (98%)	11 (2%)	0	100	100
1	B	611/629 (97%)	596 (98%)	14 (2%)	1 (0%)	47	44
All	All	1220/1258 (97%)	1194 (98%)	25 (2%)	1 (0%)	51	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	45	ASN

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	515/541 (95%)	506 (98%)	9 (2%)	60	65
1	B	508/541 (94%)	495 (97%)	13 (3%)	46	48
All	All	1023/1082 (94%)	1001 (98%)	22 (2%)	52	55

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147	LEU
1	A	209	ASP
1	A	327	GLU
1	A	352	THR
1	A	368	TYR
1	A	372	TYR
1	A	377	VAL
1	A	388	HIS
1	A	609	GLU
1	B	96	ARG
1	B	116	SER
1	B	147	LEU
1	B	203	ASN
1	B	262	GLU
1	B	326	ARG
1	B	368	TYR
1	B	372	TYR
1	B	377	VAL
1	B	388	HIS
1	B	421	ASP
1	B	560	VAL
1	B	570	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	285	GLN
1	A	371	GLN
1	A	491	HIS
1	A	598	GLN

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Mol	Chain	Res	Type
1	B	25	GLN
1	B	355	GLN
1	B	406	HIS
1	B	491	HIS
1	B	579	GLN
1	B	598	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](#)

16 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
2	NAG	C	1	1,2	14,14,15	0.53	0	17,19,21	1.14	1 (5%)
2	FUC	C	2	2	10,10,11	0.63	0	14,14,16	1.49	2 (14%)
3	NAG	D	1	1,3	14,14,15	0.55	0	17,19,21	0.93	1 (5%)
3	NAG	D	2	3	14,14,15	0.47	0	17,19,21	0.93	1 (5%)
4	NAG	E	1	1,4	14,14,15	0.62	0	17,19,21	0.79	0
4	NAG	E	2	4	14,14,15	0.53	0	17,19,21	0.79	0
4	BMA	E	3	4	11,11,12	0.36	0	15,15,17	0.96	1 (6%)
4	FUC	E	4	4	10,10,11	0.59	0	14,14,16	0.54	0
2	NAG	F	1	1,2	14,14,15	0.51	0	17,19,21	1.31	2 (11%)
2	FUC	F	2	2	10,10,11	0.60	0	14,14,16	0.95	0
3	NAG	G	1	1,3	14,14,15	0.60	0	17,19,21	0.89	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	2	3	14,14,15	0.43	0	17,19,21	1.10	1 (5%)
4	NAG	H	1	1,4	14,14,15	0.57	0	17,19,21	0.86	1 (5%)
4	NAG	H	2	4	14,14,15	0.53	0	17,19,21	0.75	0
4	BMA	H	3	4	11,11,12	0.46	0	15,15,17	1.33	2 (13%)
4	FUC	H	4	4	10,10,11	0.44	0	14,14,16	0.54	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	FUC	C	2	2	-	-	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
4	NAG	E	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	1/6/23/26	0/1/1/1
4	BMA	E	3	4	-	0/2/19/22	0/1/1/1
4	FUC	E	4	4	-	-	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	FUC	F	2	2	-	-	0/1/1/1
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	1/6/23/26	0/1/1/1
4	NAG	H	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	1/2/19/22	0/1/1/1
4	FUC	H	4	4	-	-	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	FUC	C1-C2-C3	4.09	114.69	109.67
3	G	2	NAG	C1-O5-C5	3.89	117.46	112.19
2	C	1	NAG	O5-C5-C6	3.58	112.81	107.20
4	H	3	BMA	C1-C2-C3	3.42	113.87	109.67
2	F	1	NAG	C4-C3-C2	3.14	115.62	111.02
4	H	3	BMA	C1-O5-C5	2.72	115.88	112.19
2	C	2	FUC	O5-C1-C2	2.59	114.77	110.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	NAG	C1-O5-C5	2.46	115.53	112.19
4	E	3	BMA	C1-C2-C3	2.41	112.63	109.67
2	F	1	NAG	O5-C5-C6	2.18	110.63	107.20
3	D	1	NAG	C1-O5-C5	2.16	115.12	112.19
3	G	1	NAG	C4-C3-C2	2.12	114.13	111.02
4	H	1	NAG	C1-O5-C5	2.11	115.06	112.19

There are no chirality outliers.

All (13) torsion outliers are listed below:

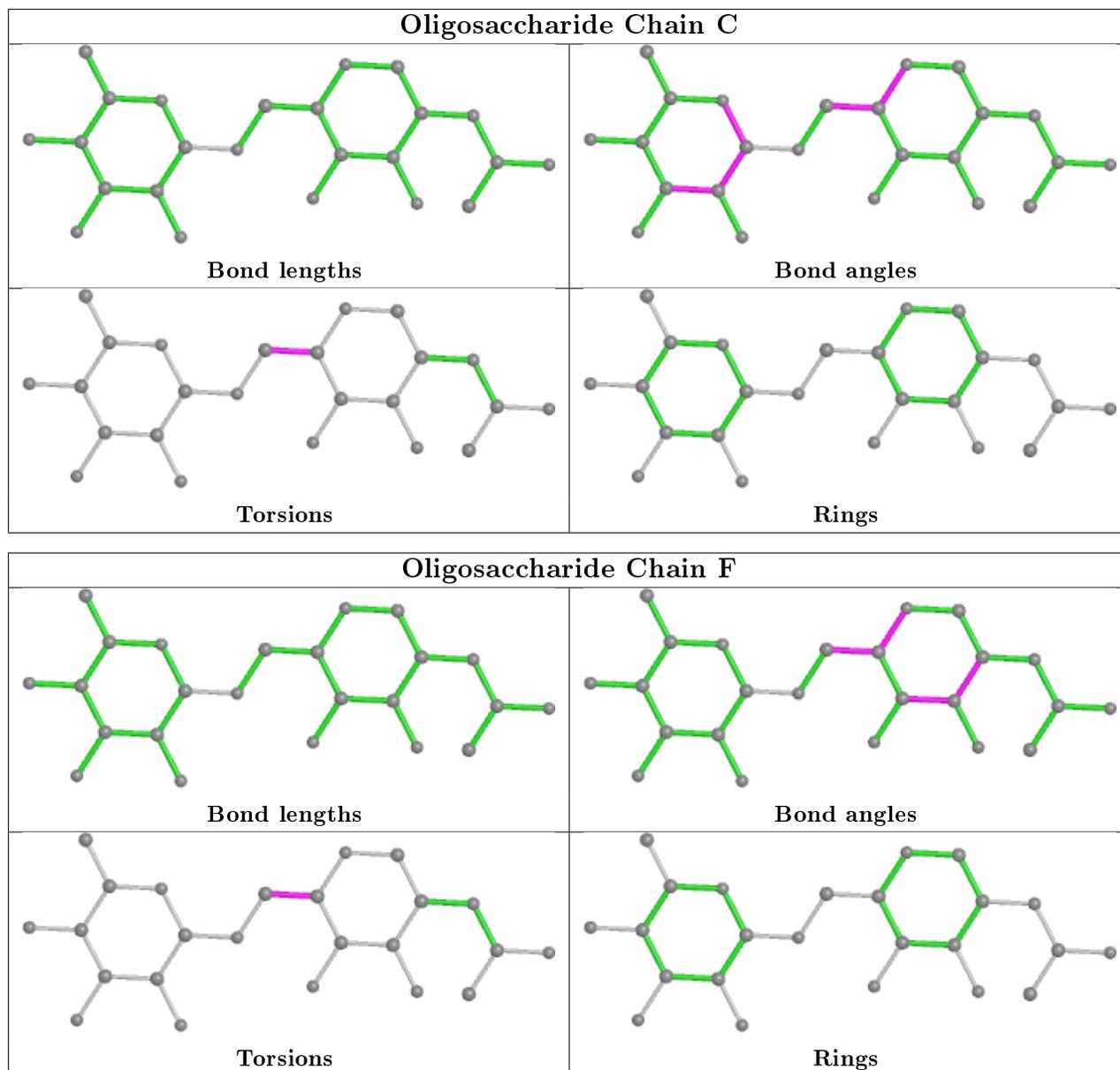
Mol	Chain	Res	Type	Atoms
2	F	1	NAG	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
4	H	1	NAG	O5-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
4	H	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
4	H	3	BMA	C4-C5-C6-O6

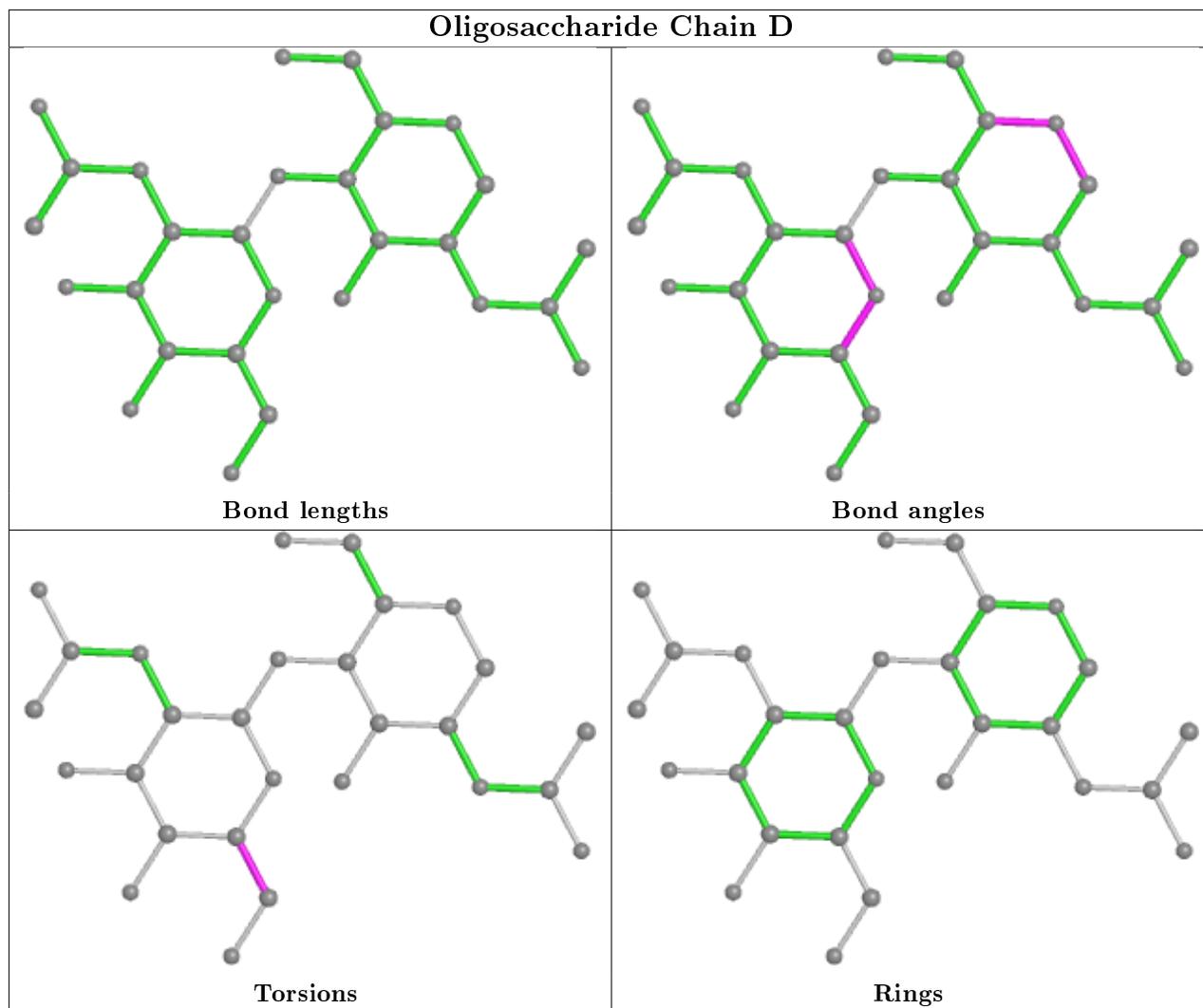
There are no ring outliers.

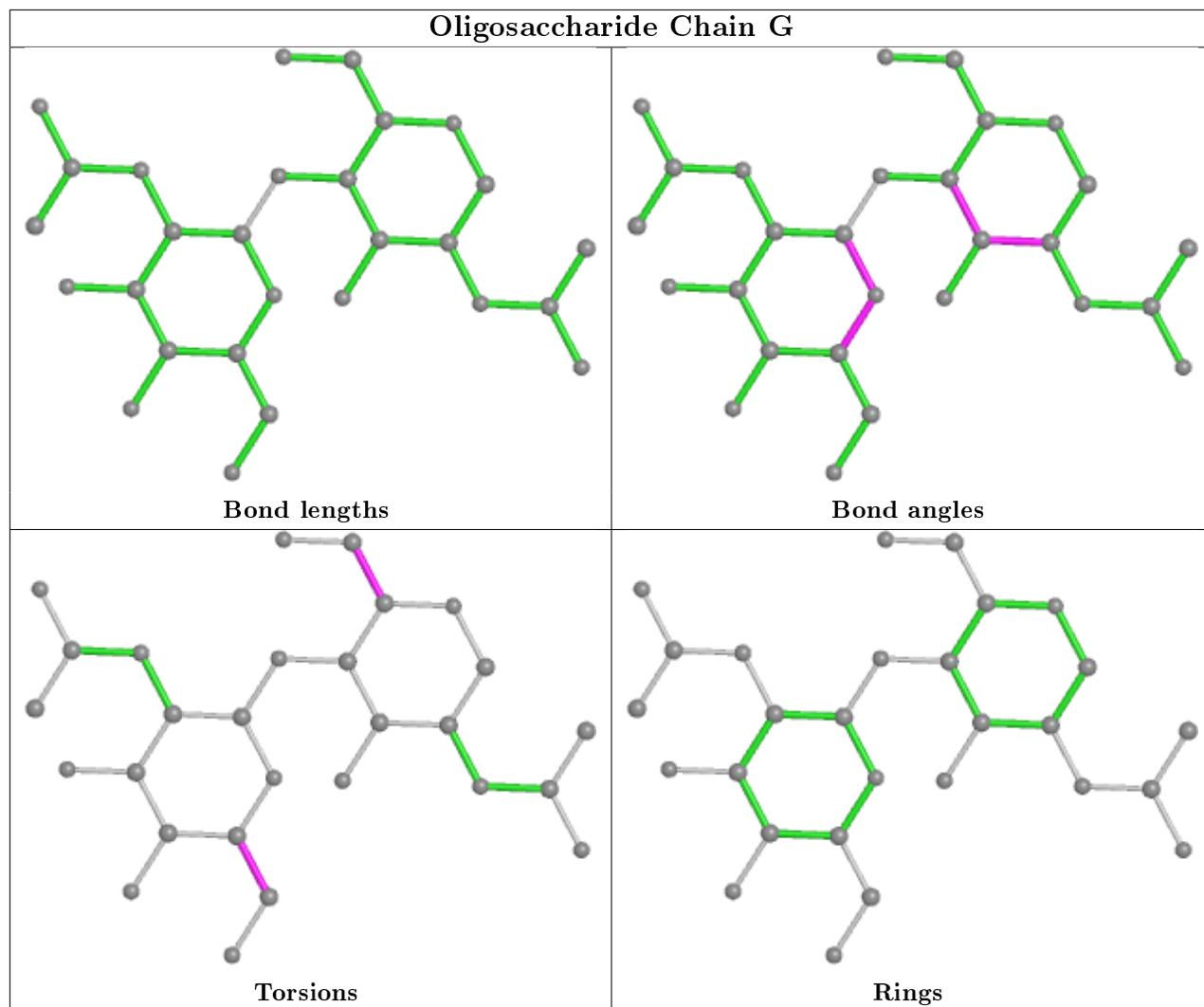
1 monomer is involved in 2 short contacts:

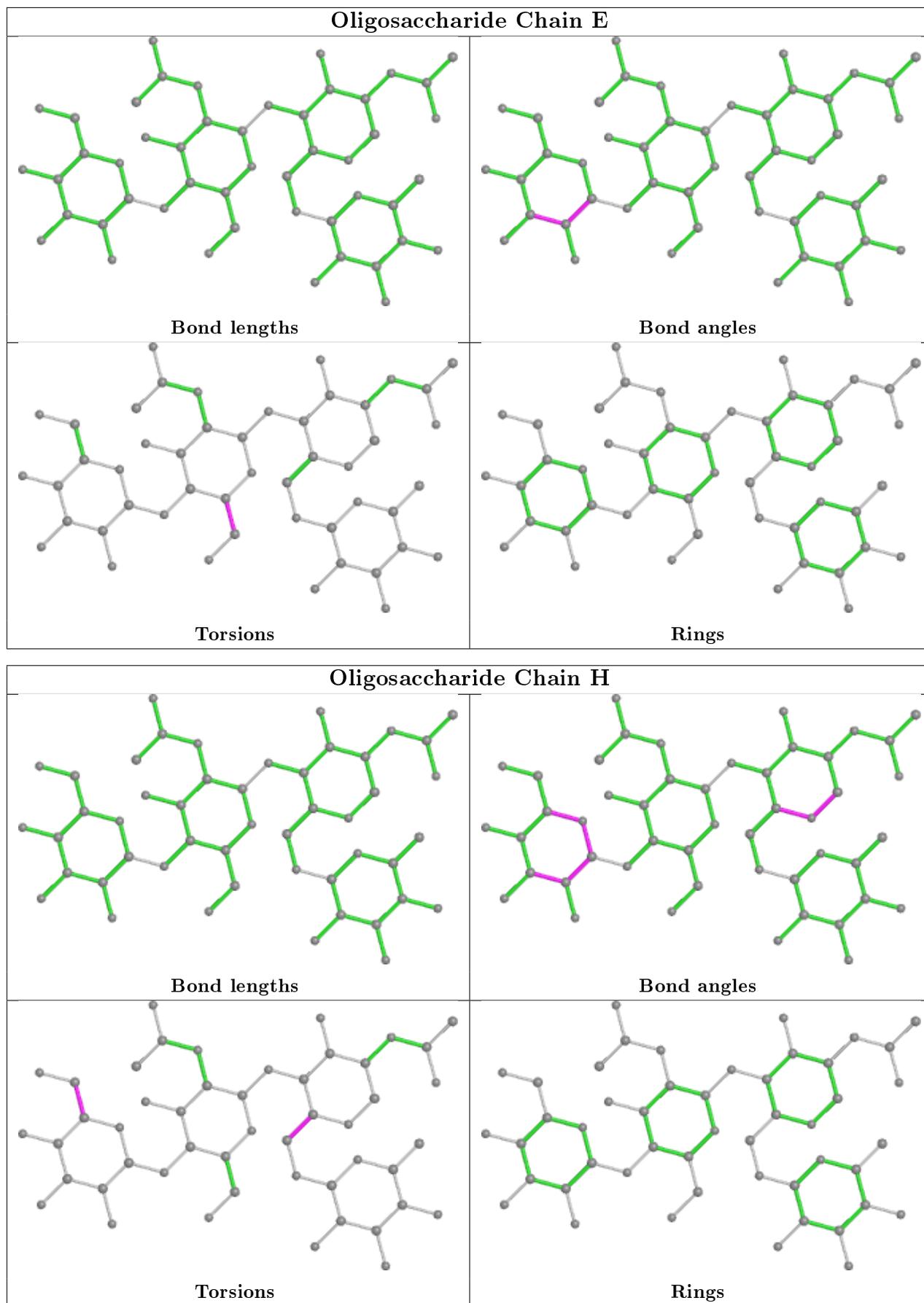
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	FUC	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









5.6 Ligand geometry i

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	P6G	B	709	-	18,18,18	0.50	0	17,17,17	0.29	0
10	PG4	B	704	-	9,9,12	0.41	0	8,8,11	0.39	0
7	P6G	A	708	-	12,12,18	0.46	0	11,11,17	0.34	0
6	RX4	A	700	5	28,34,34	0.59	0	34,47,47	1.11	2 (5%)
6	RX4	B	700	5	28,34,34	0.63	1 (3%)	34,47,47	1.21	3 (8%)
9	PEG	A	706	-	6,6,6	0.42	0	5,5,5	0.33	0
9	PEG	B	710	-	6,6,6	0.41	0	5,5,5	0.35	0
10	PG4	B	705	-	12,12,12	0.44	0	11,11,11	0.30	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
7	P6G	B	709	-	-	10/16/16/16	-
10	PG4	B	704	-	-	5/7/7/10	-
7	P6G	A	708	-	-	3/10/10/16	-
6	RX4	A	700	5	-	5/36/43/43	0/1/1/1
6	RX4	B	700	5	-	2/36/43/43	0/1/1/1
9	PEG	A	706	-	-	2/4/4/4	-
9	PEG	B	710	-	-	2/4/4/4	-
10	PG4	B	705	-	-	3/10/10/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	700	RX4	P1-CAT	2.05	1.81	1.79

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	700	RX4	CAS-CBG-NAW	-5.42	105.00	111.39
6	A	700	RX4	CAS-CBG-NAW	-4.27	106.36	111.39
6	A	700	RX4	CAR-CBF-NAU	-2.70	105.10	110.79
6	B	700	RX4	CAR-CBF-NAU	-2.38	105.78	110.79
6	B	700	RX4	CBC-CAS-CBG	-2.05	108.86	113.38

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	709	P6G	O4-C5-C6-O7
7	B	709	P6G	O10-C11-C12-O13
6	A	700	RX4	CAA-CAX-NAU-CBF
6	A	700	RX4	OAE-CAX-NAU-CBF
10	B	704	PG4	O2-C3-C4-O3
9	A	706	PEG	O1-C1-C2-O2
9	B	710	PEG	O1-C1-C2-O2
9	B	710	PEG	O2-C3-C4-O4
7	B	709	P6G	O7-C8-C9-O10
10	B	704	PG4	O4-C7-C8-O5
10	B	705	PG4	O1-C1-C2-O2
7	B	709	P6G	C5-C6-O7-C8
7	A	708	P6G	C8-C9-O10-C11
10	B	704	PG4	C6-C5-O3-C4
6	A	700	RX4	OAH-CBA-CBD-CAT
6	A	700	RX4	N-CBA-CBD-CAT
6	B	700	RX4	OAH-CBA-CBD-CAT
7	B	709	P6G	C11-C12-O13-C14
7	A	708	P6G	O16-C17-C18-O19
6	A	700	RX4	P1-CAT-CBD-CBA
7	B	709	P6G	C2-C3-O4-C5
7	B	709	P6G	O16-C17-C18-O19
9	A	706	PEG	C4-C3-O2-C2
7	B	709	P6G	C12-C11-O10-C9
10	B	705	PG4	C8-C7-O4-C6
10	B	705	PG4	C4-C3-O2-C2
10	B	704	PG4	C5-C6-O4-C7
10	B	704	PG4	O3-C5-C6-O4
6	B	700	RX4	N-CBA-CBD-CAT
7	A	708	P6G	C12-C11-O10-C9
7	B	709	P6G	O13-C14-C15-O16

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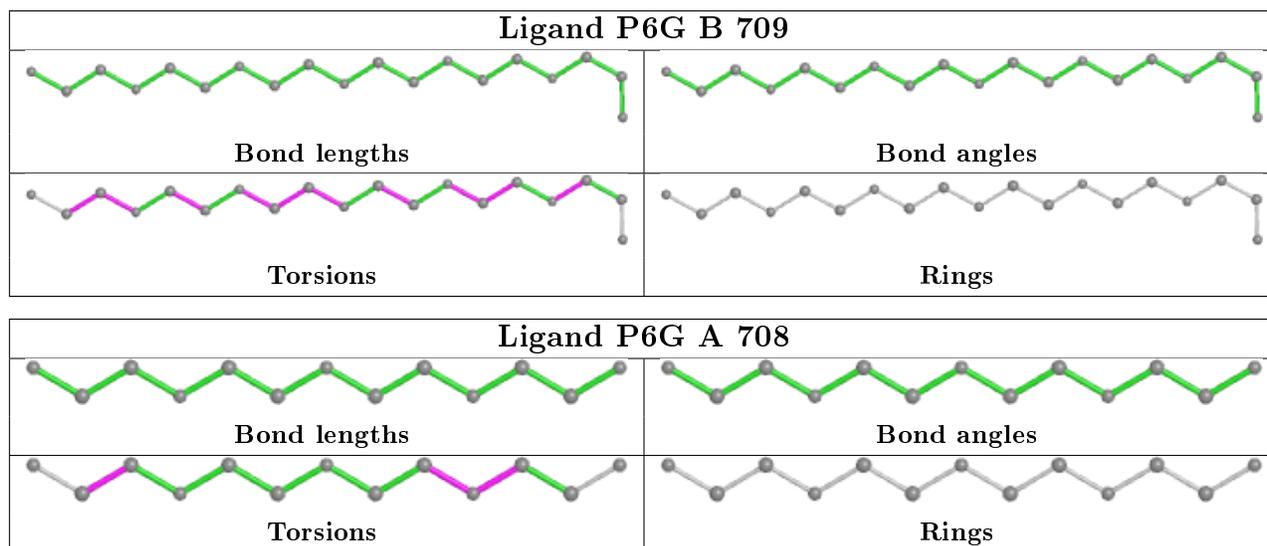
Mol	Chain	Res	Type	Atoms
7	B	709	P6G	C18-C17-O16-C15

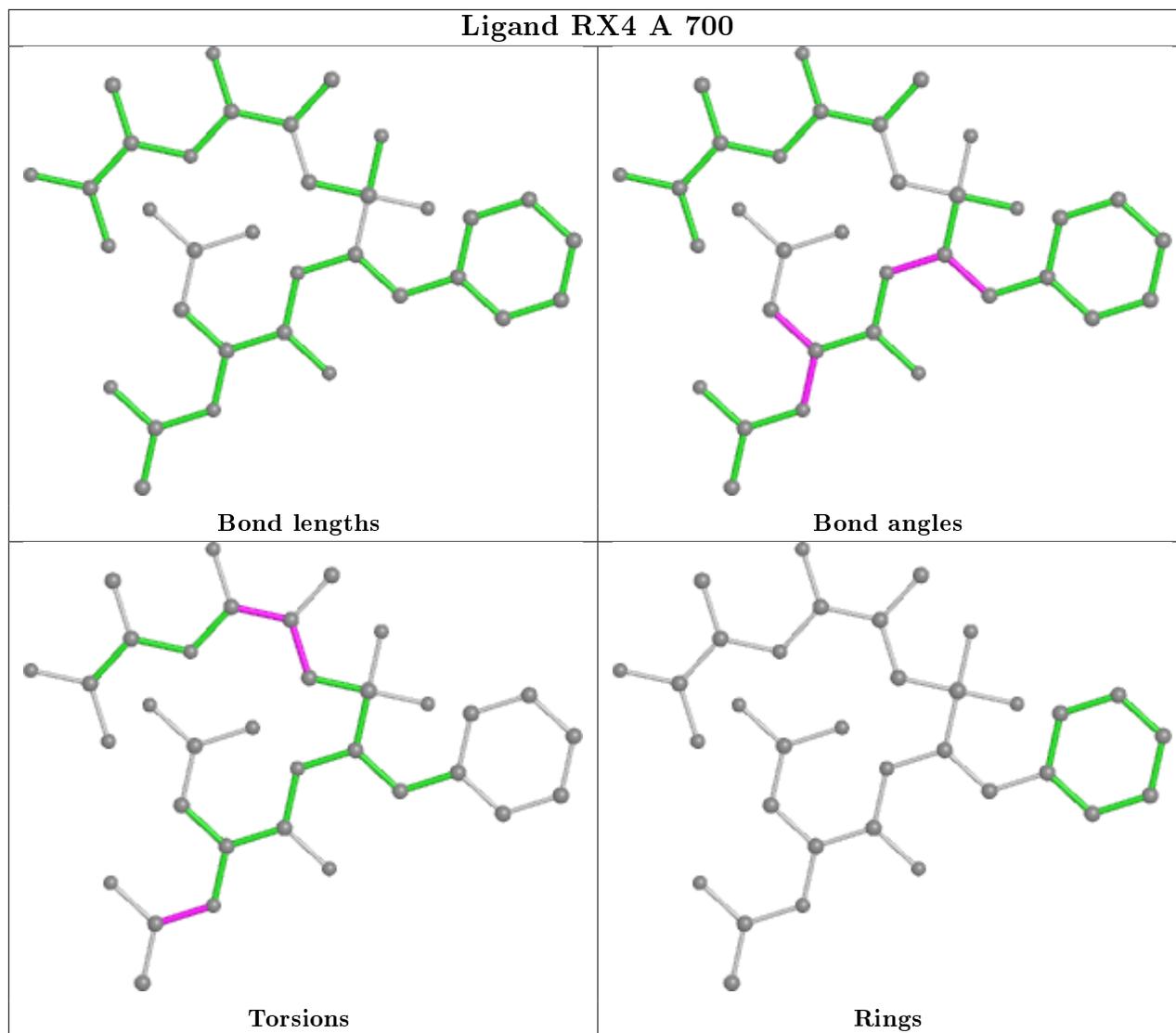
There are no ring outliers.

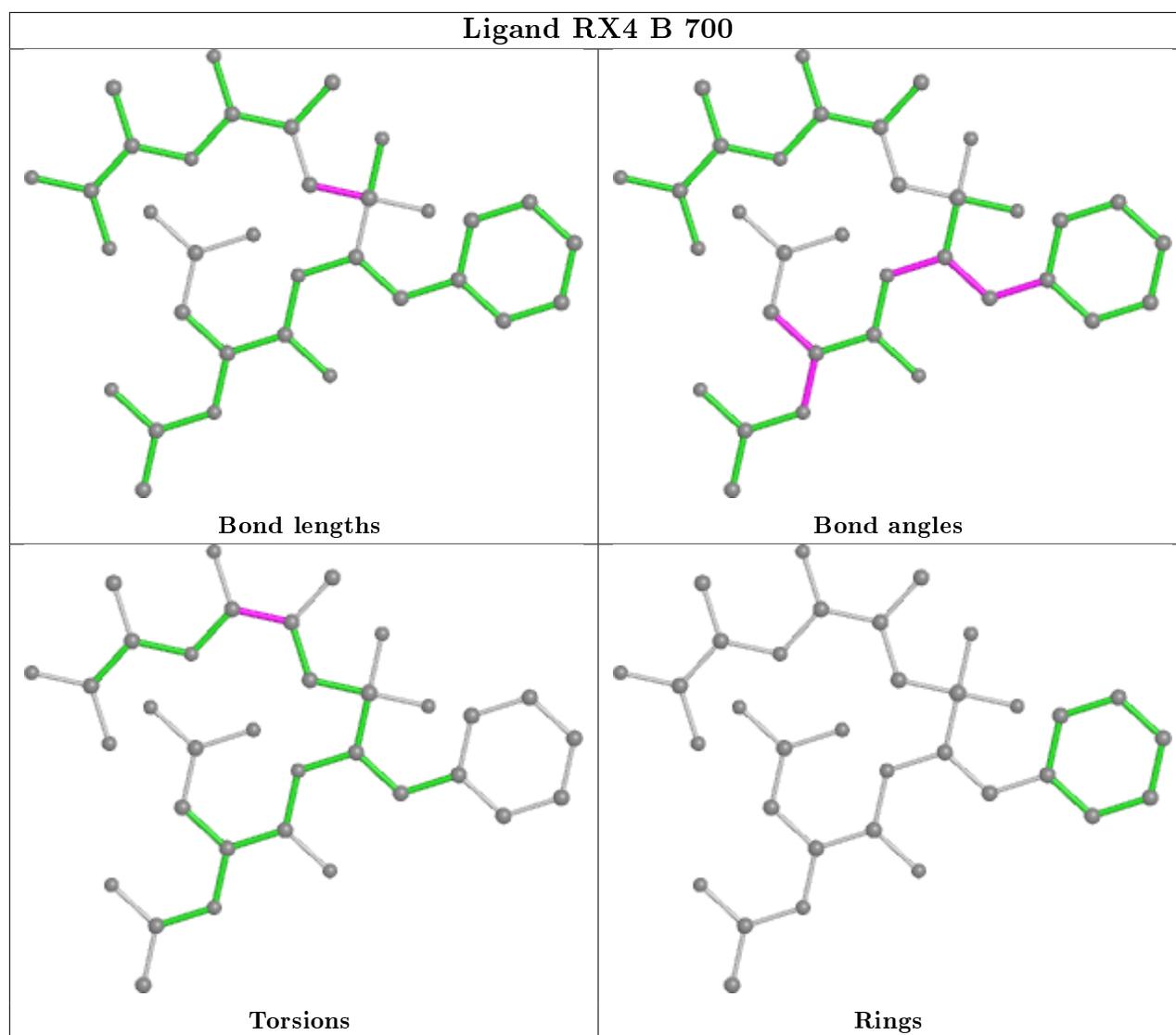
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	709	P6G	1	0
6	A	700	RX4	3	0
6	B	700	RX4	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

6.1 Protein, DNA and RNA chains

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	607/629 (96%)	0.04	16 (2%) 56 54	19, 31, 43, 66	0
1	B	610/629 (96%)	0.23	30 (4%) 29 28	21, 33, 51, 66	0
All	All	1217/1258 (96%)	0.13	46 (3%) 40 39	19, 31, 48, 66	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	130	PRO	8.4
1	B	135	THR	6.8
1	B	134	ALA	5.3
1	A	610	GLY	5.1
1	A	323	ALA	4.9
1	B	325	GLY	4.7
1	B	131	GLN	4.7
1	A	134	ALA	4.7
1	B	129	LEU	4.6
1	A	325	GLY	4.4
1	B	133	THR	4.2
1	B	323	ALA	3.9
1	B	609	GLU	3.9
1	A	135	THR	3.8
1	B	415	THR	3.7
1	B	438	PHE	3.6
1	B	78	PRO	3.5
1	B	132	LYS	3.4
1	A	133	THR	3.3
1	B	84	THR	3.3
1	A	607	TYR	3.0
1	B	605	ASP	3.0
1	A	136	CYS	2.7
1	A	324	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	442	VAL	2.6
1	B	435	PHE	2.5
1	B	498	TYR	2.5
1	B	501	TYR	2.5
1	B	257	TRP	2.4
1	A	129	LEU	2.3
1	B	330	CYS	2.3
1	A	78	PRO	2.3
1	A	609	GLU	2.3
1	B	441	LEU	2.3
1	B	81	GLN	2.2
1	B	213	HIS	2.2
1	B	433	ILE	2.2
1	B	610	GLY	2.2
1	B	606	ASN	2.2
1	A	412	ASP	2.2
1	A	213[A]	HIS	2.1
1	B	105	LEU	2.1
1	B	496	THR	2.1
1	A	261	TRP	2.1
1	A	414	VAL	2.1
1	B	562	LEU	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.

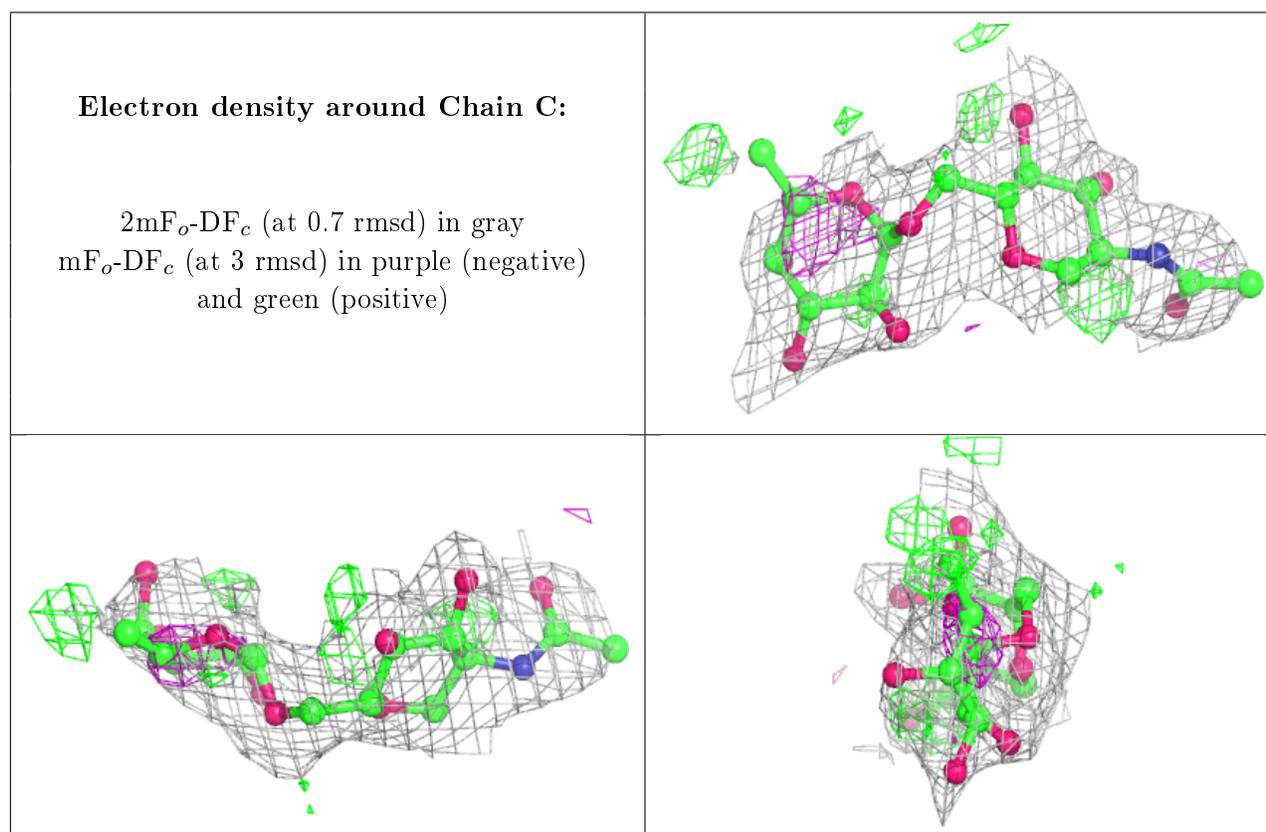
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FUC	C	2	10/11	0.74	0.32	56,58,59,59	0
2	FUC	F	2	10/11	0.76	0.37	58,60,60,60	0
4	BMA	E	3	11/12	0.78	0.23	61,62,63,63	0
4	FUC	E	4	10/11	0.79	0.17	53,55,55,56	0
3	NAG	G	2	14/15	0.79	0.40	55,58,59,60	0
4	BMA	H	3	11/12	0.81	0.32	66,67,67,67	0

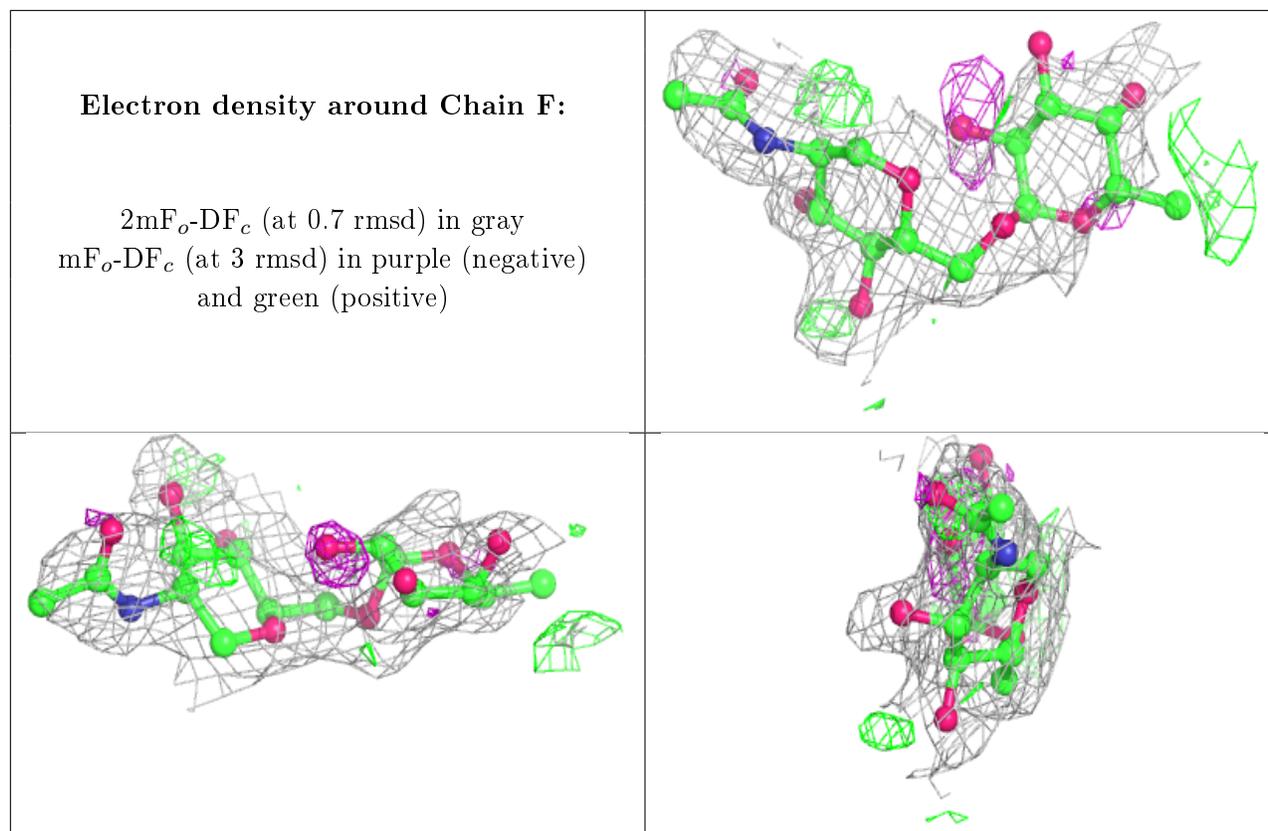
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	F	1	14/15	0.83	0.13	40,46,49,54	0
3	NAG	D	2	14/15	0.85	0.28	51,53,56,56	0
3	NAG	G	1	14/15	0.87	0.23	38,44,47,51	0
2	NAG	C	1	14/15	0.88	0.13	38,45,48,52	0
4	NAG	H	1	14/15	0.89	0.19	52,56,59,62	0
4	NAG	E	2	14/15	0.89	0.17	54,56,57,60	0
4	NAG	H	2	14/15	0.90	0.26	62,64,65,65	0
4	FUC	H	4	10/11	0.91	0.28	63,63,64,64	0
3	NAG	D	1	14/15	0.91	0.14	39,43,45,48	0
4	NAG	E	1	14/15	0.92	0.11	43,47,51,51	0

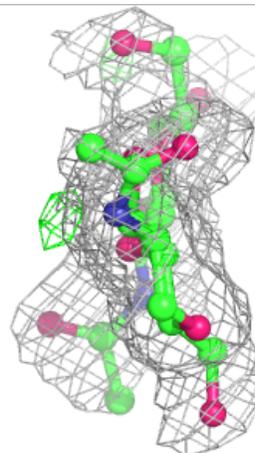
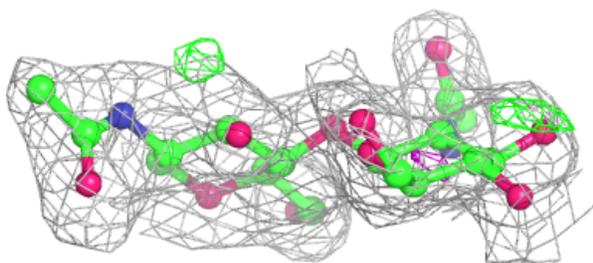
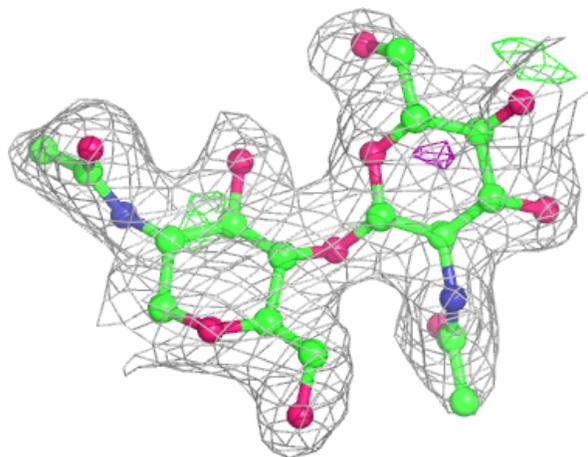
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





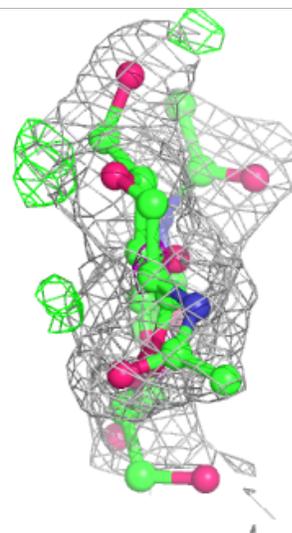
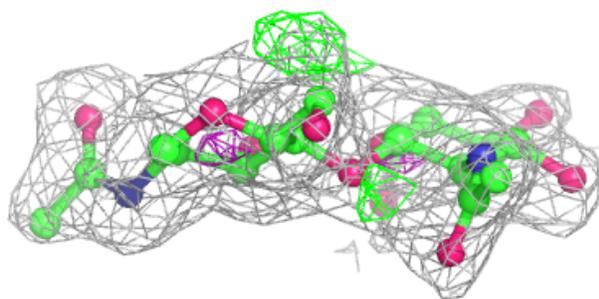
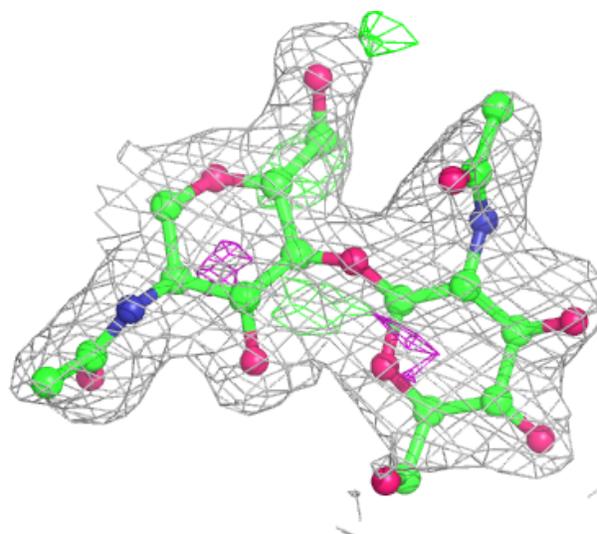
Electron density around Chain D:

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



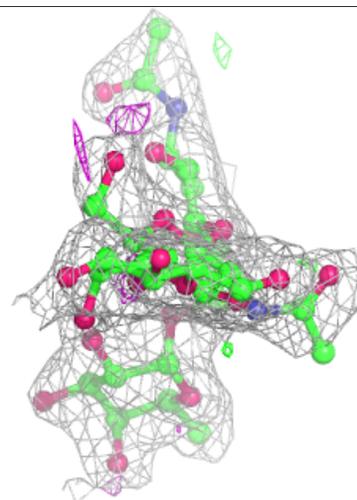
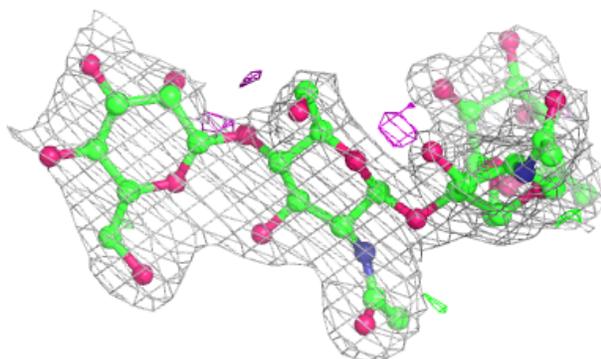
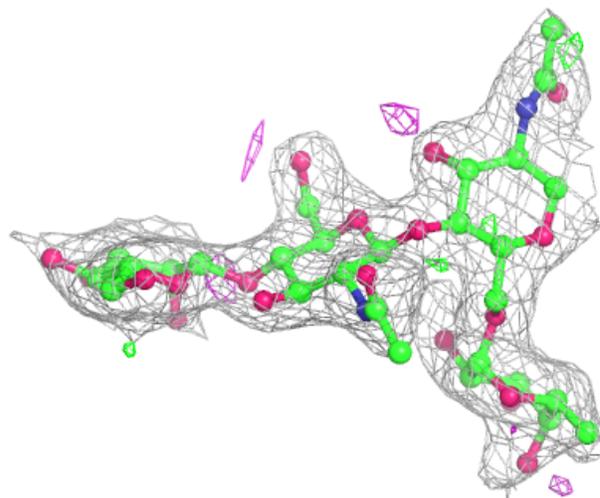
Electron density around Chain G:

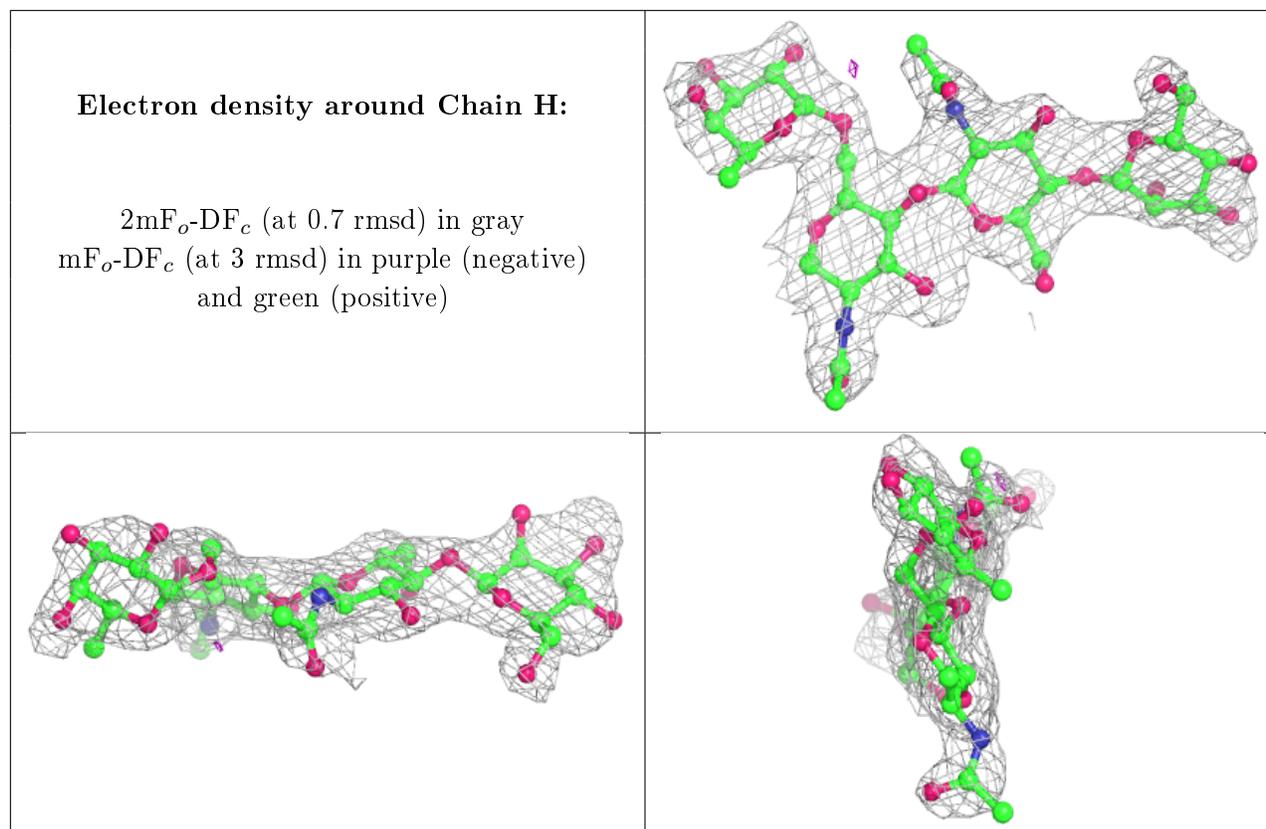
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain E:

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





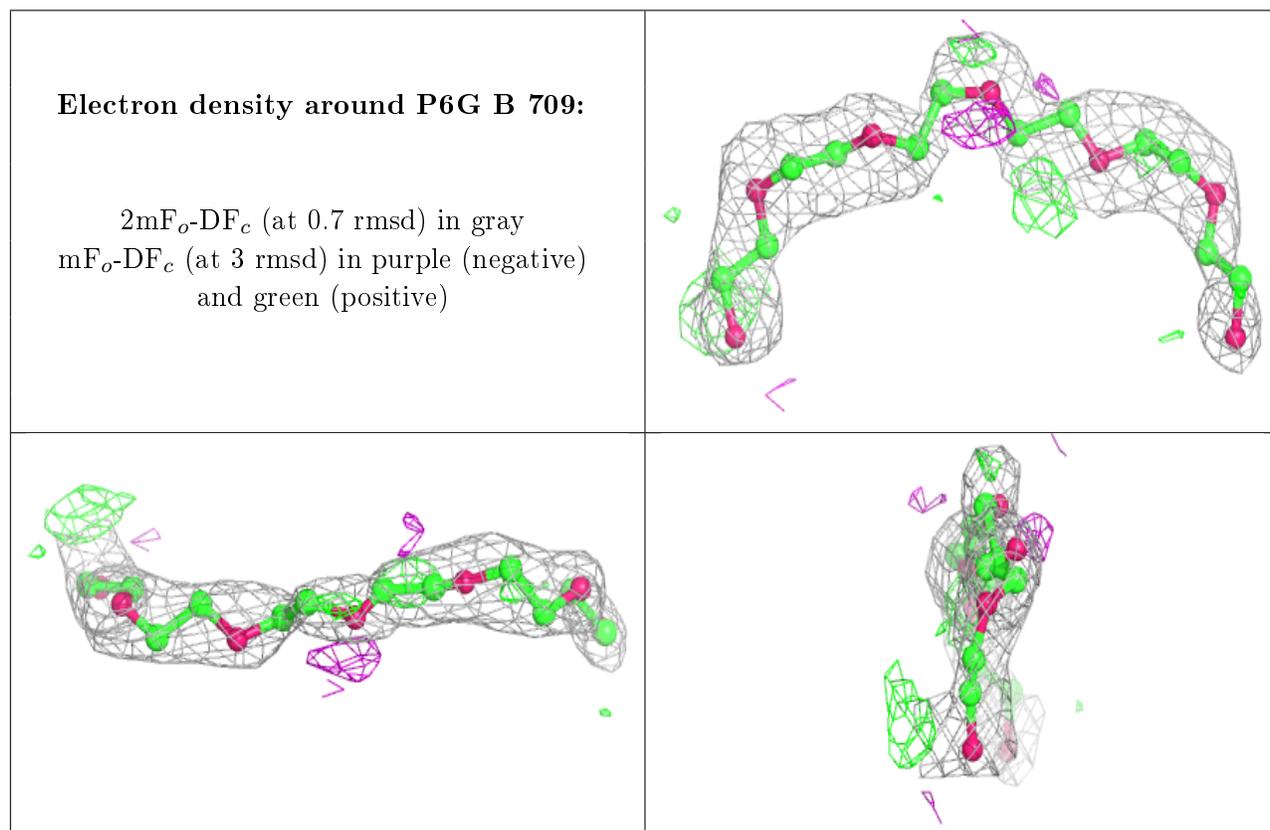
6.4 Ligands [i](#)

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
7	P6G	B	709	19/19	0.73	0.20	60,60,61,61	0
7	P6G	A	708	13/19	0.83	0.17	46,47,49,49	0
9	PEG	B	710	7/7	0.83	0.24	66,67,67,67	0
10	PG4	B	704	10/13	0.87	0.15	52,52,52,53	0
10	PG4	B	705	13/13	0.89	0.10	52,53,54,55	0
9	PEG	A	706	7/7	0.93	0.13	51,52,52,52	0
6	RX4	A	700	34/34	0.94	0.14	20,26,35,39	0
6	RX4	B	700	34/34	0.96	0.17	19,23,37,38	0
8	CL	A	900	1/1	0.99	0.07	23,23,23,23	0
5	ZN	A	650	1/1	1.00	0.11	23,23,23,23	0
5	ZN	B	650	1/1	1.00	0.10	21,21,21,21	0
8	CL	B	900	1/1	1.00	0.09	28,28,28,28	0

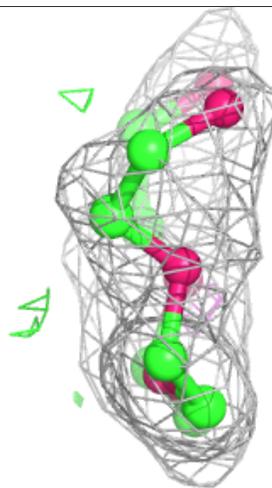
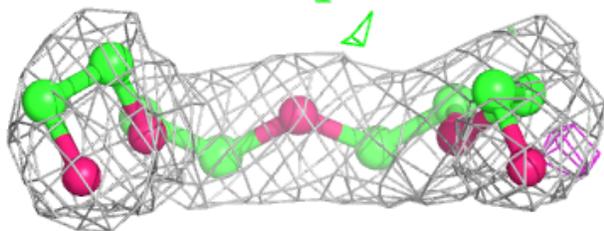
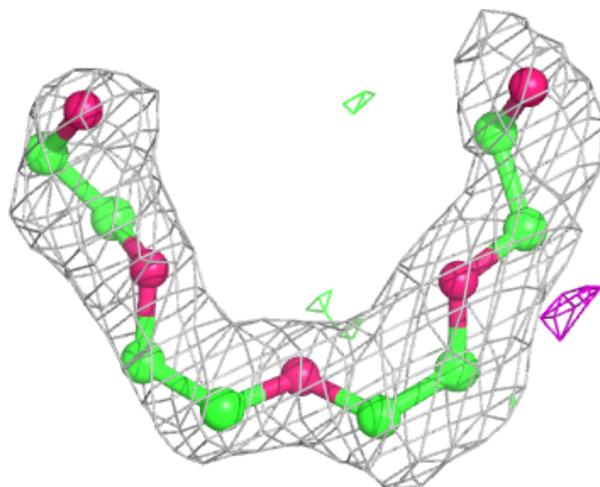
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



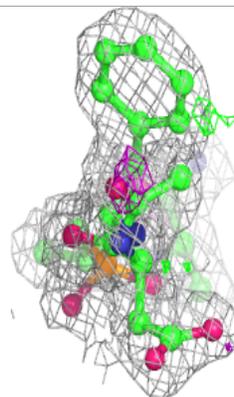
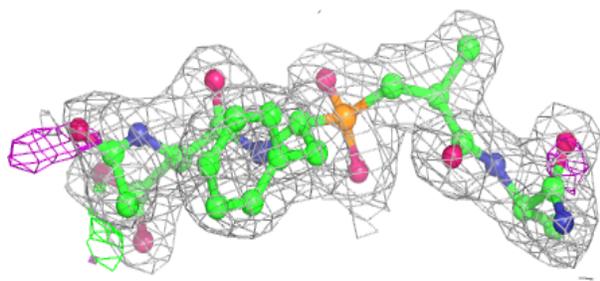
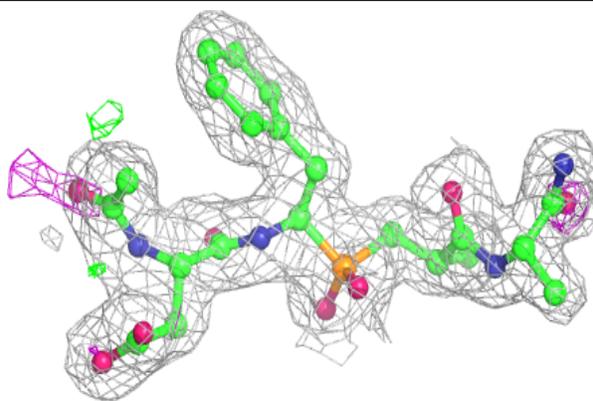
Electron density around P6G A 708:

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

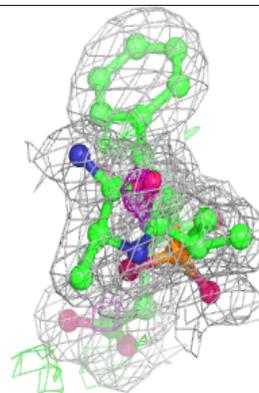
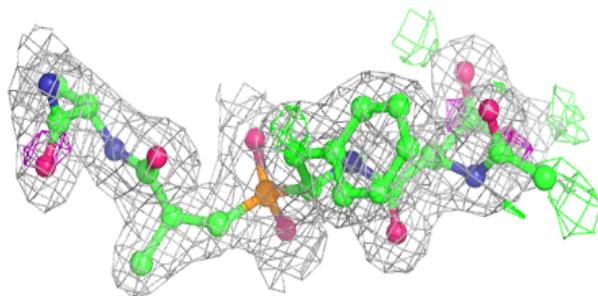
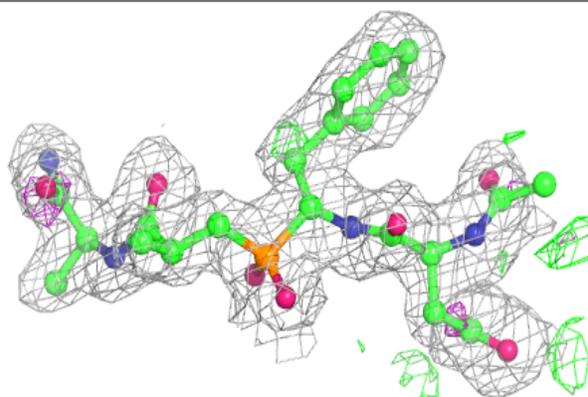


Electron density around RX4 A 700:

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

**Electron density around RX4 B 700:**

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



6.5 Other polymers

There are no such residues in this entry.