



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:11 AM UTC

PDB ID : 6VEQ / pdb_00006veq
Title : Con-Ins G1 in complex with the human insulin microreceptor in turn in complex with Fv 83-7
Authors : Menting, J.G.; Chou, D.H.-C.; Lawrence, M.C.; Xiong, X.
Deposited on : 2020-01-02
Resolution : 3.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

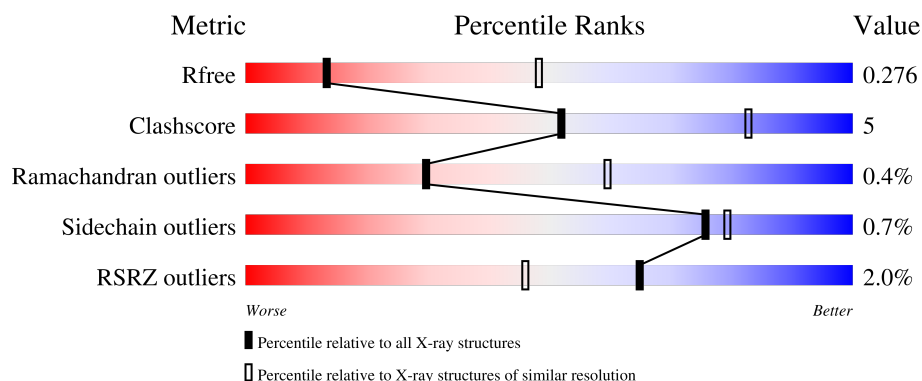
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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}	180053	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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	20	10% 60% 35% 5%
1	G	20	70% 30%
2	B	23	65% 9% 26%
2	H	23	65% 9% 26%
3	E	317	2% 76% 14% 9%

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Mol	Chain	Length	Quality of chain
3	K	317	 2% 76% 15% 9%
4	F	16	 75% 19% 6%
4	L	16	 6% 62% 6% 31%
5	C	138	 2% 72% 13% 14%
5	I	138	 70% 15% 15%
6	D	121	 2% 87% 7% 6%
6	J	121	 2% 88% 1% 8%
7	M	4	 50% 25% 25%
7	O	4	 50% 25% 25%
8	N	4	 100%
8	P	4	 100%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 9267 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 Con-Ins G1a A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	20	Total	C	N	O	S	0	0	0
			162	98	31	29	4			
1	G	20	Total	C	N	O	S	0	0	0
			162	98	31	29	4			

- Molecule 2 is a protein called Con-Ins G1 B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	17	Total	C	N	O	S	0	0	0
			137	81	24	29	3			
2	H	17	Total	C	N	O	S	0	0	0
			137	81	24	29	3			

- Molecule 3 is a protein called Insulin receptor subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	287	Total	C	N	O	S	0	0	0
			2292	1443	395	422	32			
3	K	287	Total	C	N	O	S	0	0	0
			2292	1443	395	422	32			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	144	HIS	TYR	conflict	UNP P06213
E	311	SER	-	expression tag	UNP P06213
E	312	SER	-	expression tag	UNP P06213
E	313	SER	-	expression tag	UNP P06213
E	314	LEU	-	expression tag	UNP P06213
E	315	VAL	-	expression tag	UNP P06213
E	316	PRO	-	expression tag	UNP P06213
E	317	ARG	-	expression tag	UNP P06213

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Chain	Residue	Modelled	Actual	Comment	Reference
K	144	HIS	TYR	conflict	UNP P06213
K	311	SER	-	expression tag	UNP P06213
K	312	SER	-	expression tag	UNP P06213
K	313	SER	-	expression tag	UNP P06213
K	314	LEU	-	expression tag	UNP P06213
K	315	VAL	-	expression tag	UNP P06213
K	316	PRO	-	expression tag	UNP P06213
K	317	ARG	-	expression tag	UNP P06213

- Molecule 4 is a protein called Insulin receptor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	15	Total	C	N	O	0	0	0
			130	86	21	23			
4	L	11	Total	C	N	O	0	0	0
			98	67	14	17			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	718	PRO	LYS	conflict	UNP P06213
F	719	SER	THR	conflict	UNP P06213
L	718	PRO	LYS	conflict	UNP P06213
L	719	SER	THR	conflict	UNP P06213

- Molecule 5 is a protein called Fv 83-7 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	118	Total	C	N	O	S	0	0	0
			904	568	153	178	5			
5	I	117	Total	C	N	O	S	0	0	0
			898	565	152	176	5			

- Molecule 6 is a protein called Fv 83-7 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	114	Total	C	N	O	S	0	0	0
			887	562	146	175	4			
6	J	111	Total	C	N	O	S	0	0	0
			866	550	142	170	4			

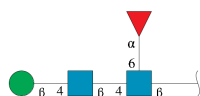
- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranos

e-(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
7	M	4	Total	C	N	O	0	0	0
			50	28	2	20			
7	O	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 8 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.



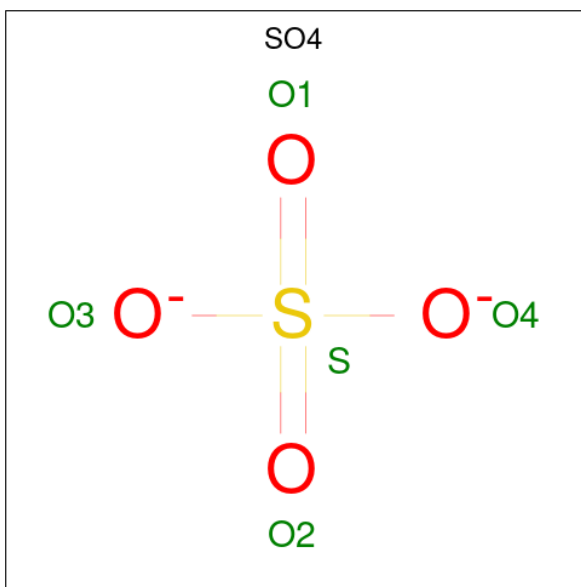
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	N	4	Total	C	N	O	0	0	0
			49	28	2	19			
8	P	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	E	1	Total	C	N	O	0	0
			14	8	1	5		
9	E	1	Total	C	N	O	0	0
			14	8	1	5		
9	E	1	Total	C	N	O	0	0
			14	8	1	5		
9	K	1	Total	C	N	O	0	0
			14	8	1	5		
9	K	1	Total	C	N	O	0	0
			14	8	1	5		
9	K	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

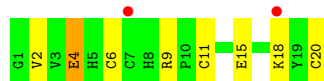


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	E	1	Total	O	S	0	0
			5	4	1		
10	E	1	Total	O	S	0	0
			5	4	1		
10	D	1	Total	O	S	0	0
			5	4	1		
10	K	1	Total	O	S	0	0
			5	4	1		

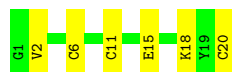
3 Residue-property plots [i](#)

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: Con-Ins G1a A chain



- Molecule 1: Con-Ins G1a A chain



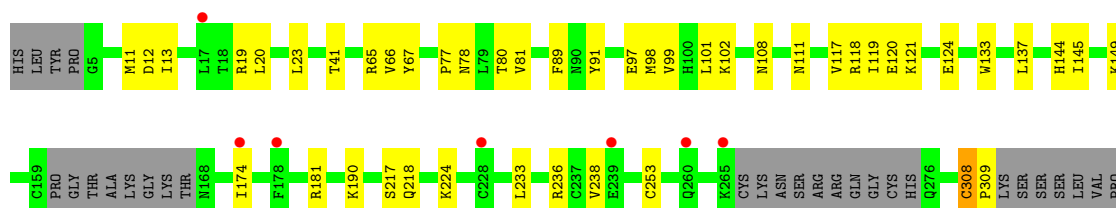
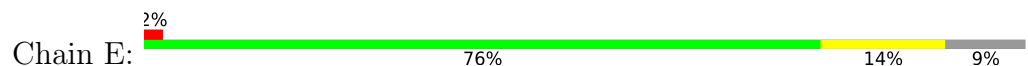
- Molecule 2: Con-Ins G1 B chain



- Molecule 2: Con-Ins G1 B chain

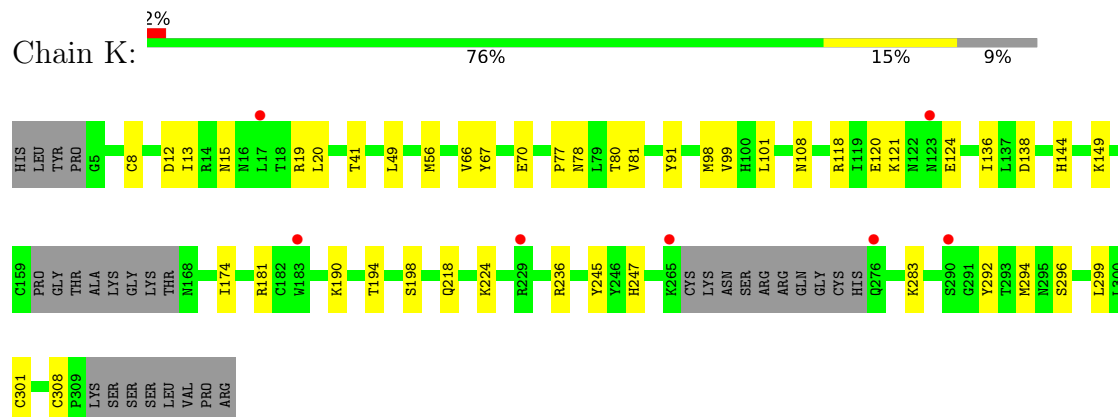


- Molecule 3: Insulin receptor subunit alpha

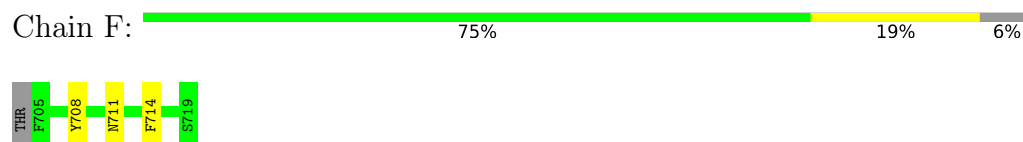


ARG

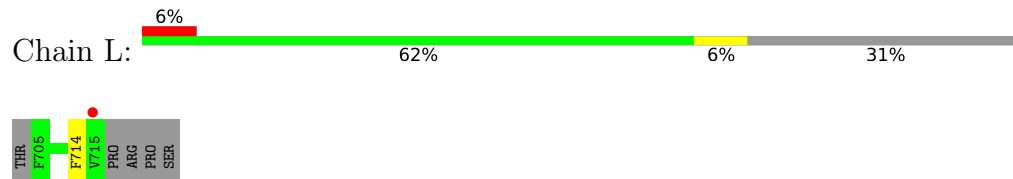
- Molecule 3: Insulin receptor subunit alpha



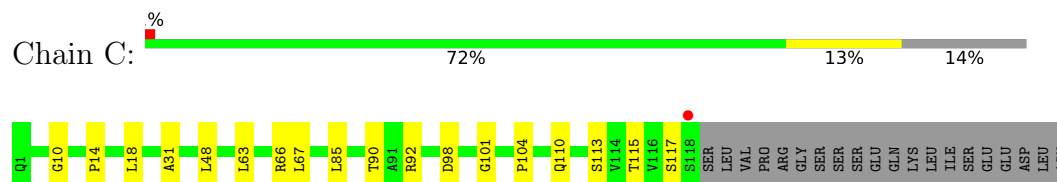
- Molecule 4: Insulin receptor



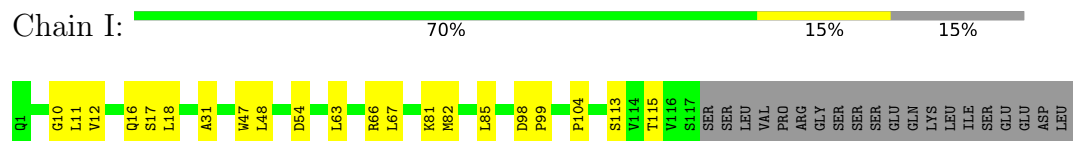
- Molecule 4: Insulin receptor



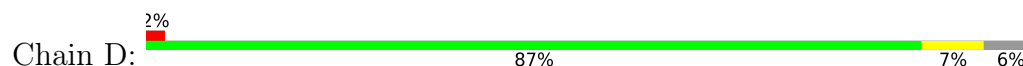
- Molecule 5: Fv 83-7 heavy chain



- Molecule 5: Fv 83-7 heavy chain

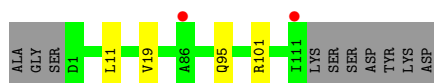
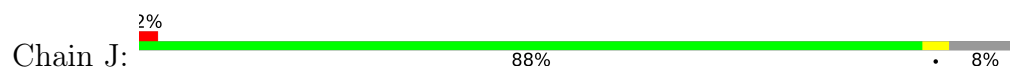


- Molecule 6: Fv 83-7 light chain





- Molecule 6: Fv 83-7 light chain



- Molecule 7: 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 7: 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 8: 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



- Molecule 8: 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



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	106.16Å 227.12Å 228.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.15 – 3.25 48.15 – 3.25	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.15-3.25) 99.8 (48.15-3.25)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.06 (at 3.25Å)	Xtriage
Refinement program	PHENIX (1.13-2998_1692)	Depositor
R, R_{free}	0.228 , 0.277 0.235 , 0.276	Depositor DCC
R_{free} test set	1743 reflections (3.97%)	wwPDB-VP
Wilson B-factor (Å ²)	107.1	Xtriage
Anisotropy	0.329	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 105.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.024 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9267	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: MAN, BMA, HYP, SO4, NAG, FUC, CGU, CY3

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	0.09	0/146	0.36	0/193
1	G	0.09	0/146	0.32	0/193
2	B	0.09	0/117	0.25	0/153
2	H	0.07	0/117	0.23	0/153
3	E	0.10	0/2346	0.29	0/3181
3	K	0.09	0/2346	0.29	0/3181
4	F	0.10	0/135	0.25	0/183
4	L	0.07	0/101	0.19	0/137
5	C	0.09	0/926	0.26	0/1258
5	I	0.09	0/920	0.27	0/1250
6	D	0.10	0/906	0.28	0/1223
6	J	0.08	0/885	0.26	0/1196
All	All	0.09	0/9091	0.28	0/12301

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	162	0	144	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	162	0	144	3	0
2	B	137	0	122	0	0
2	H	137	0	122	0	0
3	E	2292	0	2188	29	0
3	K	2292	0	2188	31	0
4	F	130	0	119	3	0
4	L	98	0	87	1	0
5	C	904	0	879	11	0
5	I	898	0	874	16	0
6	D	887	0	874	5	0
6	J	866	0	851	4	0
7	M	50	0	43	1	0
7	O	50	0	43	3	0
8	N	49	0	43	0	0
8	P	49	0	43	0	0
9	E	42	0	39	2	0
9	K	42	0	39	1	0
10	D	5	0	0	1	0
10	E	10	0	0	0	0
10	K	5	0	0	0	0
All	All	9267	0	8842	93	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 93 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)
3:K:120:GLU:HG2	3:K:121:LYS:HG3	1.76	0.67
3:E:120:GLU:HG2	3:E:121:LYS:HG3	1.76	0.65
5:C:63:LEU:HD22	5:C:66:ARG:HH21	1.62	0.64
5:I:63:LEU:HD22	5:I:66:ARG:HH21	1.64	0.63
3:E:119:ILE:HB	3:E:145:ILE:HG23	1.81	0.62

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	G	17/20 (85%)	16 (94%)	1 (6%)	0	100	100
2	H	14/23 (61%)	14 (100%)	0	0	100	100
3	K	281/317 (89%)	256 (91%)	24 (8%)	1 (0%)	30	59
4	L	9/16 (56%)	8 (89%)	1 (11%)	0	100	100
5	C	26/138 (19%)	22 (85%)	3 (12%)	1 (4%)	2	15
5	I	115/138 (83%)	109 (95%)	5 (4%)	1 (1%)	14	42
6	D	106/121 (88%)	99 (93%)	7 (7%)	0	100	100
6	J	109/121 (90%)	102 (94%)	7 (6%)	0	100	100
All	All	677/894 (76%)	626 (92%)	48 (7%)	3 (0%)	30	59

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	K	15	ASN
5	C	104	PRO
5	I	104	PRO

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	G	16/16 (100%)	16 (100%)	0	100	100
2	H	14/20 (70%)	14 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	122/293 (42%)	121 (99%)	1 (1%)	73	78
3	K	267/293 (91%)	264 (99%)	3 (1%)	65	75
4	F	15/16 (94%)	15 (100%)	0	100	100
4	L	11/16 (69%)	11 (100%)	0	100	100
5	C	101/120 (84%)	101 (100%)	0	100	100
5	I	100/120 (83%)	100 (100%)	0	100	100
6	D	101/106 (95%)	100 (99%)	1 (1%)	68	75
6	J	98/106 (92%)	97 (99%)	1 (1%)	68	75
All	All	845/1106 (76%)	839 (99%)	6 (1%)	76	79

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	K	194	THR
3	K	308	CYS
6	J	95	GLN
6	D	95	GLN
3	E	308	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
6	J	35	GLN
2	H	5	HIS
3	K	144	HIS
3	K	230	ASN
3	K	263	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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
1	CGU	A	4	1	9,11,12	1.46	1 (11%)	10,14,16	0.95	0
2	HYP	H	3	2	7,8,9	5.04	4 (57%)	5,10,12	1.18	0
2	HYP	B	3	2	7,8,9	5.01	4 (57%)	5,10,12	1.12	0
2	CGU	B	10	2	9,11,12	1.60	2 (22%)	10,14,16	0.88	0
2	CGU	H	10	2	9,11,12	1.52	1 (11%)	10,14,16	0.91	0
1	CY3	G	20	1,2	6,6,6	2.83	3 (50%)	5,7,7	1.39	0
1	CGU	G	4	1	9,11,12	1.29	0	10,14,16	0.88	0
1	CY3	A	20	1,2	6,6,6	2.82	3 (50%)	5,7,7	1.24	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
1	CGU	A	4	1	-	7/13/14/16	-
2	HYP	H	3	2	-	0/0/11/13	0/1/1/1
2	HYP	B	3	2	-	0/0/11/13	0/1/1/1
2	CGU	B	10	2	-	3/13/14/16	-
2	CGU	H	10	2	-	2/13/14/16	-
1	CY3	G	20	1,2	-	1/6/6/6	-
1	CGU	G	4	1	-	8/13/14/16	-
1	CY3	A	20	1,2	-	2/6/6/6	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	3	HYP	CB-CA	-9.07	1.34	1.54
2	B	3	HYP	CB-CA	-9.03	1.34	1.54
2	H	3	HYP	CA-N	7.83	1.62	1.48
2	B	3	HYP	CA-N	7.75	1.62	1.48
1	A	20	CY3	C-N1	5.08	1.44	1.32

There are no bond angle outliers.

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	4	CGU	CA-CB-CG-CD1
1	A	4	CGU	CA-CB-CG-CD2
2	B	10	CGU	O-C-CA-CB
2	B	10	CGU	C-CA-CB-CG
2	H	10	CGU	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	4	CGU	2	0

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	$\# Z > 2$
7	NAG	M	1	7,3	14,14,15	0.44	0	17,19,21	0.83	1 (5%)
7	NAG	M	2	7	14,14,15	0.23	0	17,19,21	0.53	0
7	BMA	M	3	7	11,11,12	0.75	0	15,15,17	0.77	0
7	MAN	M	4	7	11,11,12	0.83	1 (9%)	15,15,17	1.32	2 (13%)
8	NAG	N	1	8,3	14,14,15	0.20	0	17,19,21	0.44	0
8	NAG	N	2	8	14,14,15	0.30	0	17,19,21	0.43	0
8	BMA	N	3	8	11,11,12	0.63	0	15,15,17	0.78	0
8	FUC	N	4	8	10,10,11	0.72	0	14,14,16	0.76	0
7	NAG	O	1	7,3	14,14,15	0.43	0	17,19,21	0.86	1 (5%)
7	NAG	O	2	7	14,14,15	0.27	0	17,19,21	0.56	0
7	BMA	O	3	7	11,11,12	0.64	0	15,15,17	0.68	0
7	MAN	O	4	7	11,11,12	0.73	0	15,15,17	1.01	2 (13%)
8	NAG	P	1	8,3	14,14,15	0.30	0	17,19,21	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	P	2	8	14,14,15	0.23	0	17,19,21	0.41	0
8	BMA	P	3	8	11,11,12	0.63	0	15,15,17	0.76	0
8	FUC	P	4	8	10,10,11	0.73	0	14,14,16	0.69	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	NAG	M	1	7,3	-	4/6/23/26	0/1/1/1
7	NAG	M	2	7	-	0/6/23/26	0/1/1/1
7	BMA	M	3	7	-	0/2/19/22	0/1/1/1
7	MAN	M	4	7	-	0/2/19/22	0/1/1/1
8	NAG	N	1	8,3	-	0/6/23/26	0/1/1/1
8	NAG	N	2	8	-	2/6/23/26	0/1/1/1
8	BMA	N	3	8	-	0/2/19/22	0/1/1/1
8	FUC	N	4	8	-	-	0/1/1/1
7	NAG	O	1	7,3	-	1/6/23/26	0/1/1/1
7	NAG	O	2	7	-	0/6/23/26	0/1/1/1
7	BMA	O	3	7	-	0/2/19/22	0/1/1/1
7	MAN	O	4	7	-	0/2/19/22	0/1/1/1
8	NAG	P	1	8,3	-	0/6/23/26	0/1/1/1
8	NAG	P	2	8	-	2/6/23/26	0/1/1/1
8	BMA	P	3	8	-	0/2/19/22	0/1/1/1
8	FUC	P	4	8	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	4	MAN	C1-C2	2.25	1.57	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	4	MAN	C1-O5-C5	4.09	117.67	112.19
7	O	1	NAG	C1-O5-C5	2.88	116.04	112.19
7	O	4	MAN	C1-O5-C5	2.56	115.61	112.19
7	M	1	NAG	C1-O5-C5	2.48	115.50	112.19
7	O	4	MAN	O2-C2-C3	-2.07	105.87	110.15

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

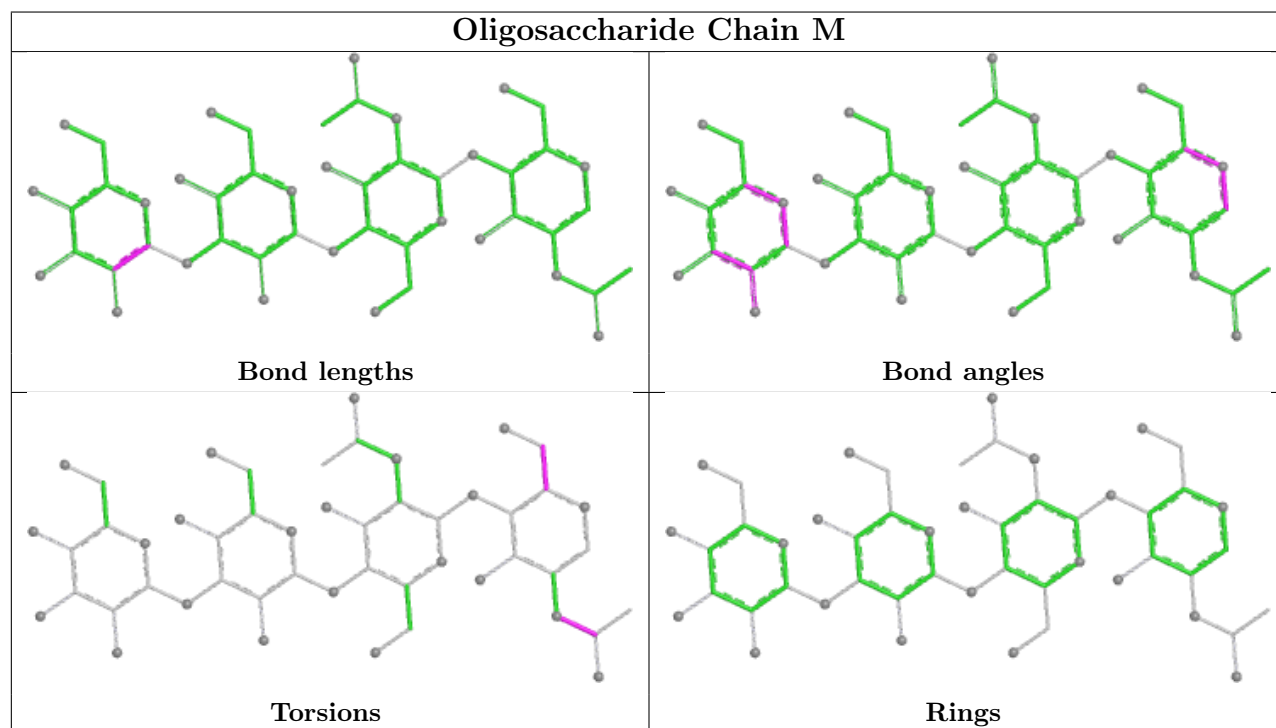
Mol	Chain	Res	Type	Atoms
8	P	2	NAG	O5-C5-C6-O6
8	N	2	NAG	O5-C5-C6-O6
7	M	1	NAG	C4-C5-C6-O6
8	P	2	NAG	C4-C5-C6-O6
8	N	2	NAG	C4-C5-C6-O6

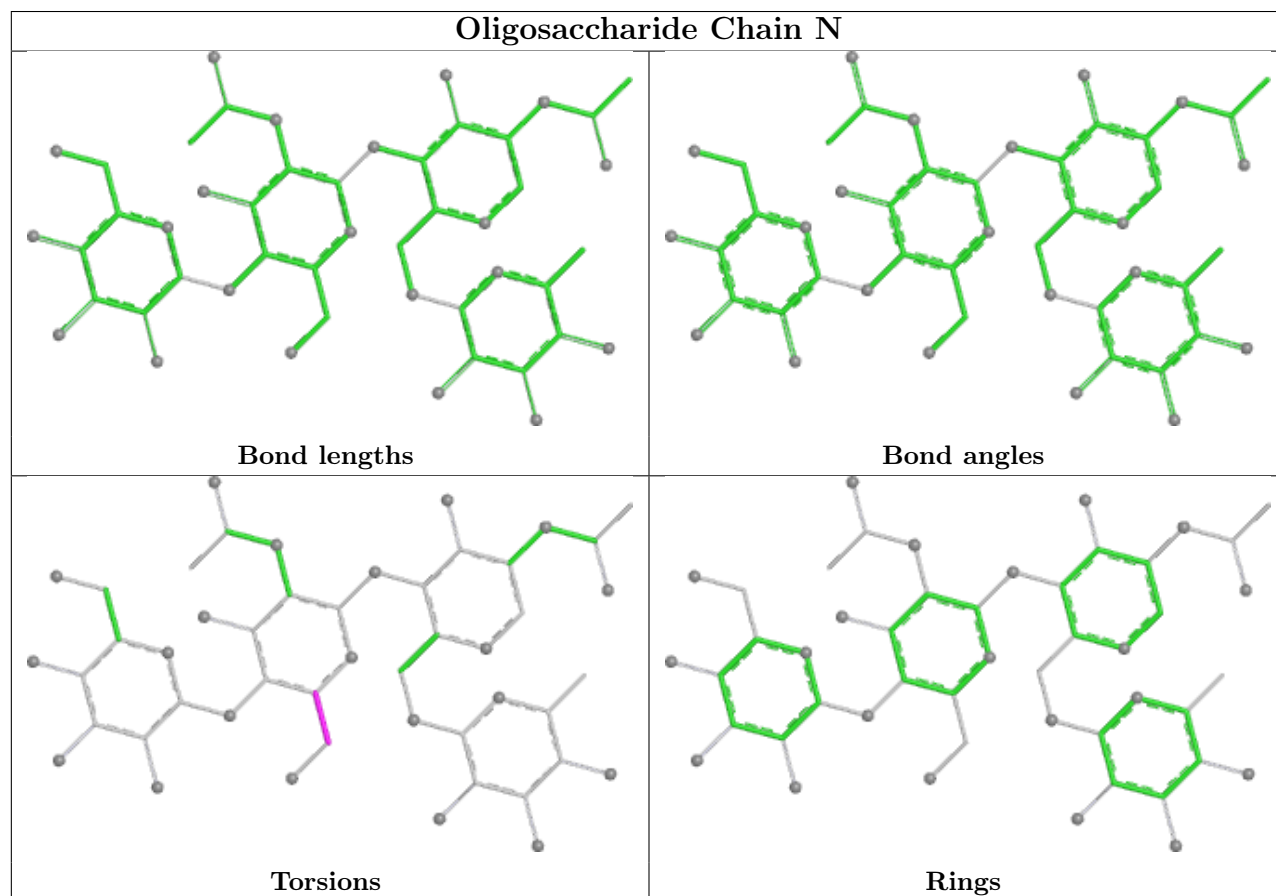
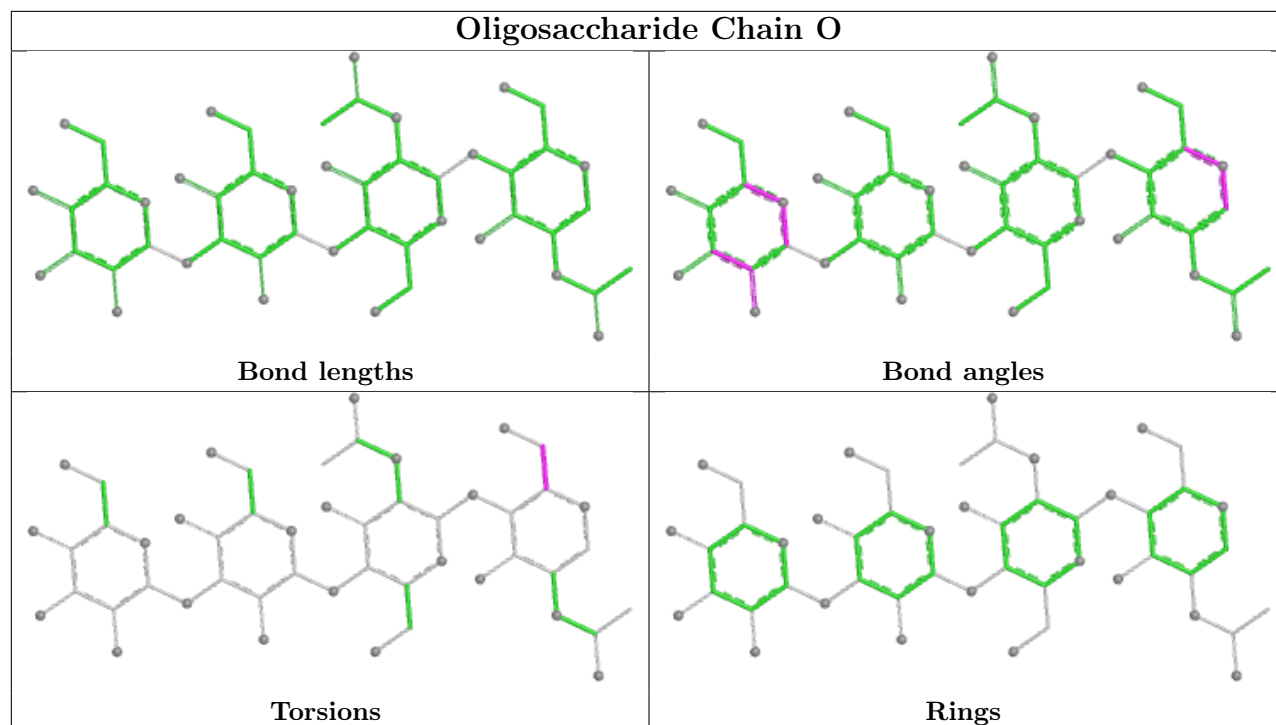
There are no ring outliers.

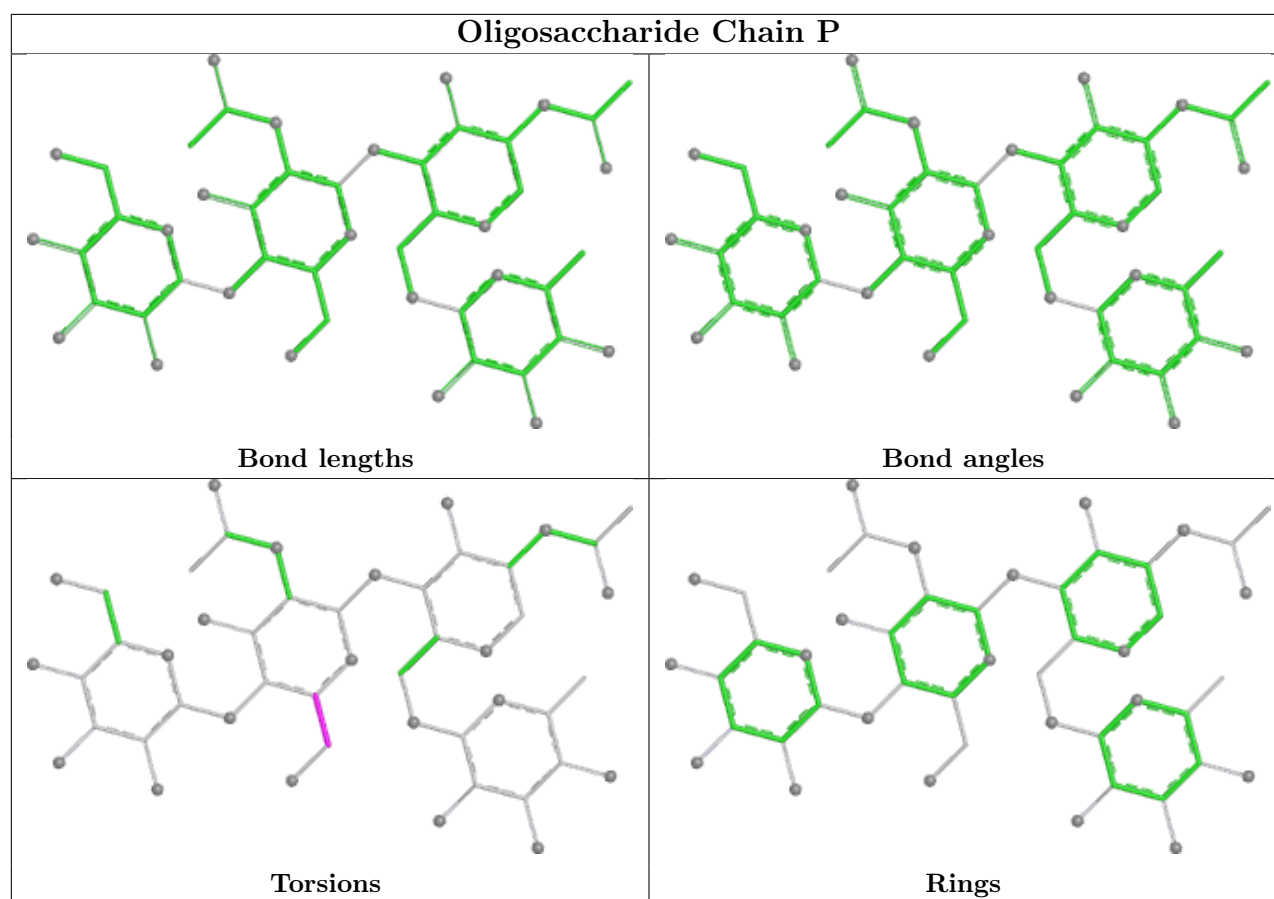
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	O	1	NAG	3	0
7	M	1	NAG	1	0

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







5.6 Ligand geometry [i](#)

10 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	$\# Z > 2$
10	SO4	E	512	-	4,4,4	0.24	0	6,6,6	0.06	0
10	SO4	K	512	-	4,4,4	0.24	0	6,6,6	0.08	0
9	NAG	K	501	3	14,14,15	0.24	0	17,19,21	0.45	0
9	NAG	E	501	3	14,14,15	0.31	0	17,19,21	0.52	0
10	SO4	D	201	-	4,4,4	0.24	0	6,6,6	0.08	0
10	SO4	E	513	-	4,4,4	0.23	0	6,6,6	0.05	0
9	NAG	E	502	3	14,14,15	0.32	0	17,19,21	0.45	0
9	NAG	K	507	3	14,14,15	0.30	0	17,19,21	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	E	507	3	14,14,15	0.30	0	17,19,21	0.60	0
9	NAG	K	502	3	14,14,15	0.24	0	17,19,21	0.49	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	K	501	3	-	1/6/23/26	0/1/1/1
9	NAG	E	501	3	-	0/6/23/26	0/1/1/1
9	NAG	E	502	3	-	1/6/23/26	0/1/1/1
9	NAG	K	507	3	-	4/6/23/26	0/1/1/1
9	NAG	E	507	3	-	2/6/23/26	0/1/1/1
9	NAG	K	502	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	K	502	NAG	C4-C5-C6-O6
9	K	502	NAG	O5-C5-C6-O6
9	K	507	NAG	O5-C5-C6-O6
9	K	507	NAG	C4-C5-C6-O6
9	E	502	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	D	201	SO4	1	0
9	K	507	NAG	1	0
9	E	507	NAG	2	0

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	18/20 (90%)	0.77	2 (11%) 10 9	136, 172, 192, 208	0
1	G	18/20 (90%)	0.60	0 100 100	147, 174, 201, 210	0
2	B	15/23 (65%)	-0.03	0 100 100	118, 130, 169, 173	0
2	H	15/23 (65%)	0.55	0 100 100	147, 174, 190, 215	0
3	E	287/317 (90%)	0.13	7 (2%) 59 40	74, 111, 166, 237	0
3	K	287/317 (90%)	0.22	7 (2%) 59 40	94, 128, 180, 230	0
4	F	15/16 (93%)	0.64	0 100 100	108, 129, 170, 174	0
4	L	11/16 (68%)	0.66	1 (9%) 15 11	125, 136, 169, 169	0
5	C	118/138 (85%)	-0.06	1 (0%) 82 68	77, 102, 131, 152	0
5	I	117/138 (84%)	0.17	0 100 100	85, 116, 157, 191	0
6	D	114/121 (94%)	-0.07	2 (1%) 67 48	61, 96, 127, 139	0
6	J	111/121 (91%)	0.18	2 (1%) 67 48	97, 131, 163, 209	0
All	All	1126/1270 (88%)	0.16	22 (1%) 65 46	61, 118, 175, 237	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
6	D	114	SER	3.9
3	E	265	LYS	3.7
5	C	118	SER	3.6
3	K	17	LEU	3.5
6	J	111	ILE	3.1

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(Å ²)	Q<0.9
2	CGU	H	10	12/13	0.64	0.12	160,177,189,189	0
2	HYP	H	3	8/9	0.67	0.15	118,134,143,145	0
1	CY3	A	20	7/7	0.68	0.20	158,171,194,195	0
2	HYP	B	3	8/9	0.71	0.15	110,123,131,135	0
1	CGU	G	4	12/13	0.73	0.14	153,164,170,173	0
1	CY3	G	20	7/7	0.76	0.16	202,207,236,240	0
2	CGU	B	10	12/13	0.78	0.11	127,154,165,168	0
1	CGU	A	4	12/13	0.80	0.11	128,147,171,171	0

6.3 Carbohydrates [i](#)

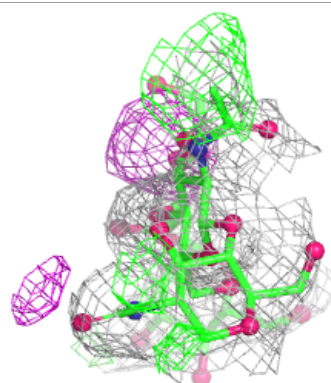
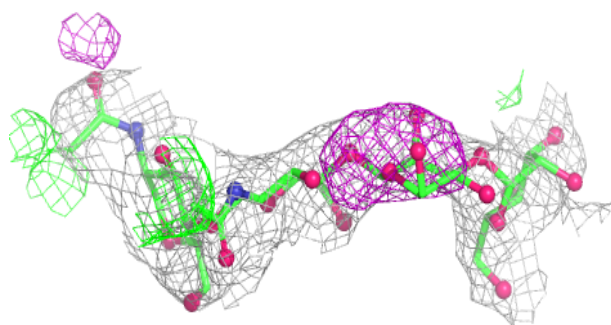
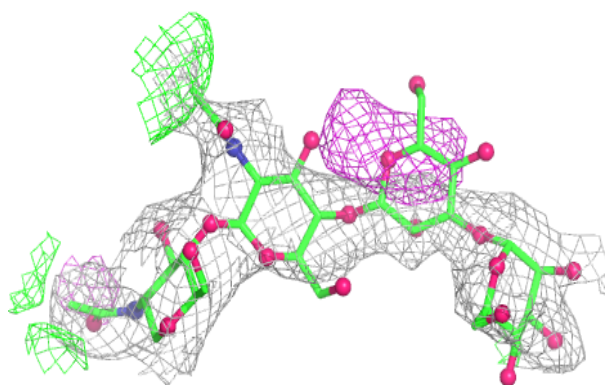
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	BMA	O	3	11/12	0.13	0.13	179,192,202,206	0
7	BMA	M	3	11/12	0.15	0.16	191,194,204,206	0
7	NAG	M	2	14/15	0.35	0.19	159,171,183,185	0
8	BMA	P	3	11/12	0.37	0.14	168,181,186,192	0
8	BMA	N	3	11/12	0.42	0.14	165,188,195,195	0
7	MAN	O	4	11/12	0.57	0.13	207,211,215,215	0
7	MAN	M	4	11/12	0.59	0.14	172,196,201,201	0
7	NAG	O	2	14/15	0.78	0.12	143,166,179,185	0
8	FUC	P	4	10/11	0.82	0.18	125,150,162,177	0
8	NAG	P	2	14/15	0.83	0.10	122,139,154,171	0
8	NAG	N	2	14/15	0.84	0.12	119,157,183,189	0
7	NAG	M	1	14/15	0.88	0.11	76,95,110,136	0
8	NAG	N	1	14/15	0.91	0.10	93,123,146,147	0
8	FUC	N	4	10/11	0.92	0.15	141,159,165,170	0
7	NAG	O	1	14/15	0.94	0.08	74,117,130,141	0
8	NAG	P	1	14/15	0.96	0.08	68,101,118,121	0

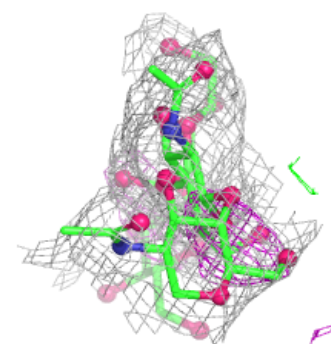
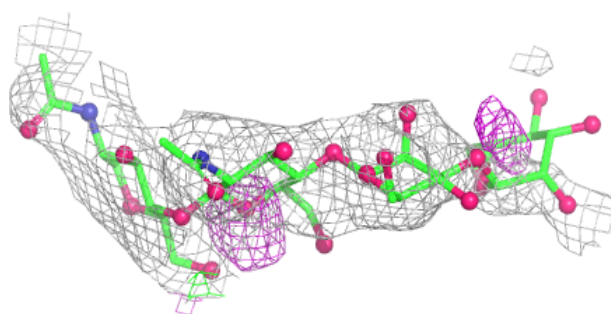
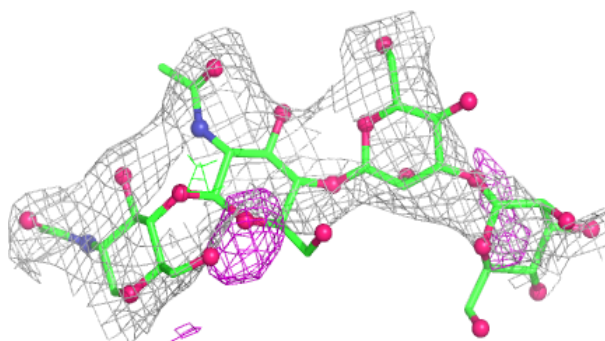
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain M:

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

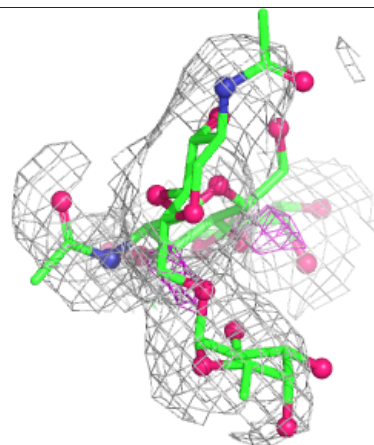
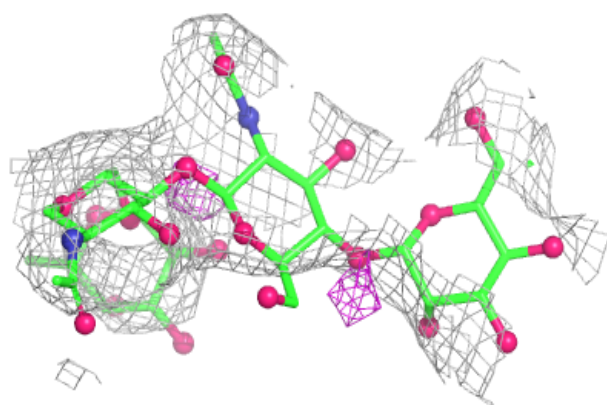
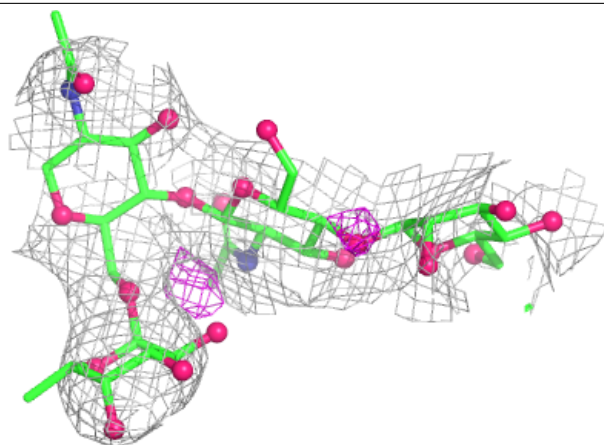
**Electron density around Chain O:**

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

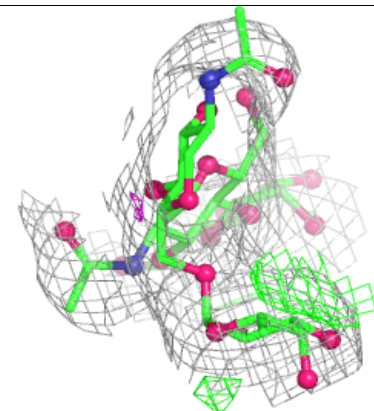
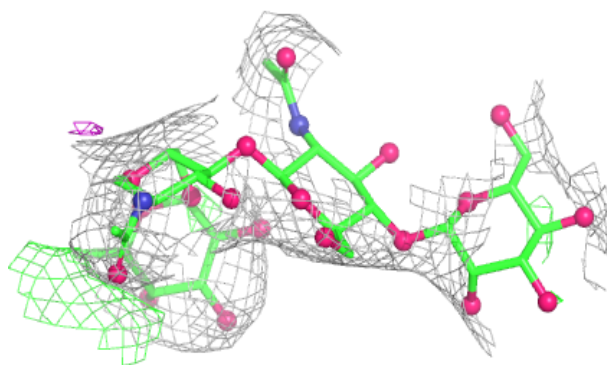
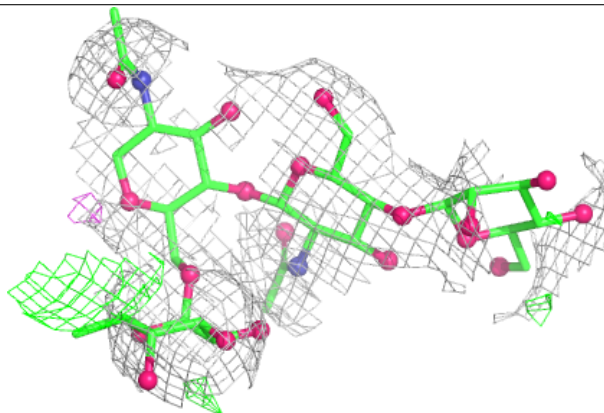


Electron density around Chain N:

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

**Electron density around Chain P:**

$2mF_o - DF_c$ (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
9	NAG	K	501	14/15	0.29	0.15	155,178,188,190	0
9	NAG	E	501	14/15	0.42	0.16	152,167,181,190	0
9	NAG	K	502	14/15	0.62	0.12	128,159,176,181	0
9	NAG	E	502	14/15	0.63	0.12	136,159,171,173	0
10	SO4	D	201	5/5	0.87	0.10	120,129,130,132	0
10	SO4	E	513	5/5	0.88	0.10	122,128,131,138	0
10	SO4	E	512	5/5	0.88	0.12	111,112,115,120	0
10	SO4	K	512	5/5	0.88	0.11	121,129,140,141	0
9	NAG	E	507	14/15	0.89	0.11	121,147,156,157	0
9	NAG	K	507	14/15	0.90	0.09	102,131,137,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.