



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:59 PM UTC

PDB ID : 6J15 / pdb_00006j15
Title : Complex structure of GY-5 Fab and PD-1
Authors : Chen, D.; Tan, S.; Zhang, H.; Wang, H.; Chai, Y.; Qi, J.; Yan, J.; Gao, G.F.
Deposited on : 2018-12-27
Resolution : 2.60 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 : 4-5-2 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

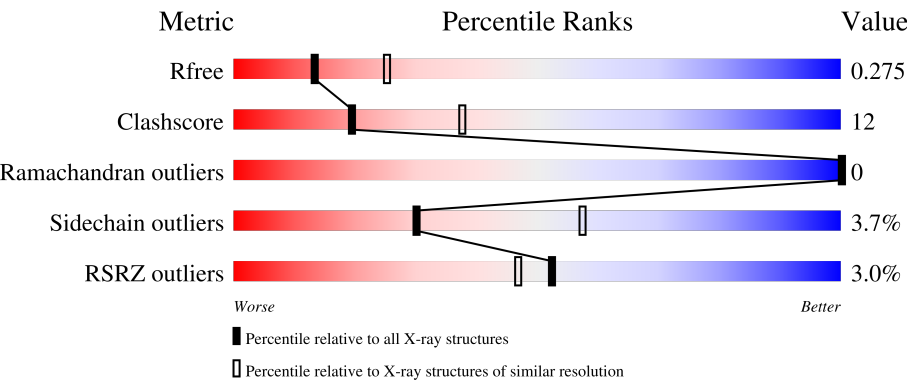
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



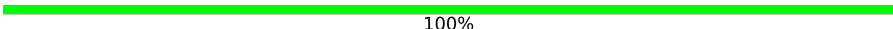
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	C	120	0% 67% 23% 8%
1	D	120	2% 58% 25% 6% 12%
2	A	219	5% 72% 19% 6%
2	H	219	2% 71% 20% 7%
3	B	216	6% 64% 34% •

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Mol	Chain	Length	Quality of chain
3	L	216	 86%14%
4	E	3	 100%
5	F	4	 75%25%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8342 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 Programmed cell death protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	110	Total	C	N	O	S	0	0	0
			872	546	158	163	5			
1	D	106	Total	C	N	O	S	0	0	0
			839	527	152	155	5			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	28	ASP	-	expression tag	UNP Q15116
C	29	GLY	-	expression tag	UNP Q15116
C	30	ILE	-	expression tag	UNP Q15116
C	31	GLN	-	expression tag	UNP Q15116
D	28	ASP	-	expression tag	UNP Q15116
D	29	GLY	-	expression tag	UNP Q15116
D	30	ILE	-	expression tag	UNP Q15116
D	31	GLN	-	expression tag	UNP Q15116

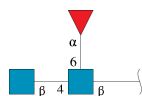
- Molecule 2 is a protein called GY-5 heavy chain Fab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	203	Total	C	N	O	S	0	0	0
			1572	1003	254	309	6			
2	A	205	Total	C	N	O	S	0	0	0
			1590	1016	256	312	6			

- Molecule 3 is a protein called GY-5 light chain Fab.

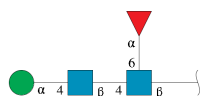
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	216	Total	C	N	O	S	0	0	0
			1677	1052	283	336	6			
3	B	216	Total	C	N	O	S	0	0	0
			1677	1052	283	336	6			

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



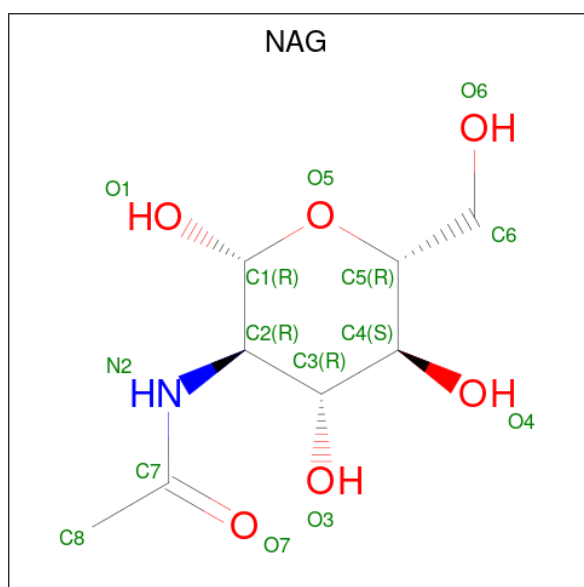
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 is an oligosaccharide called alpha-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
5	F	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

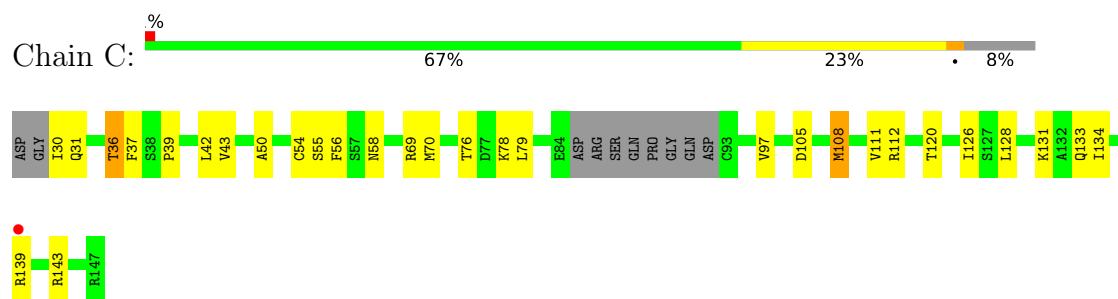


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		

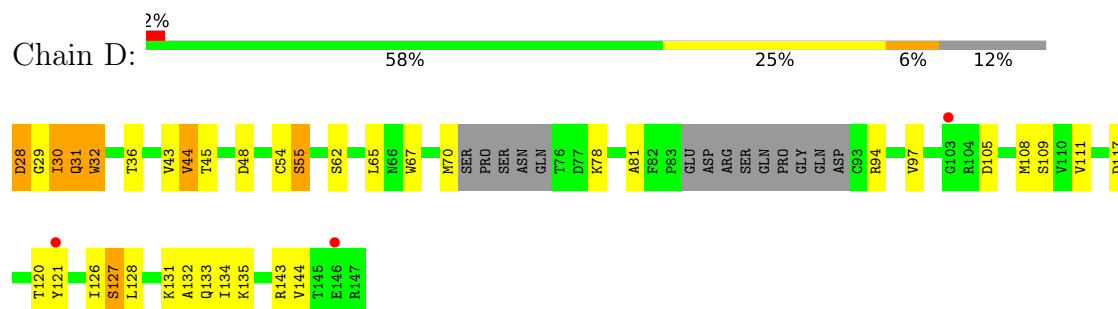
3 Residue-property plots [i](#)

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.

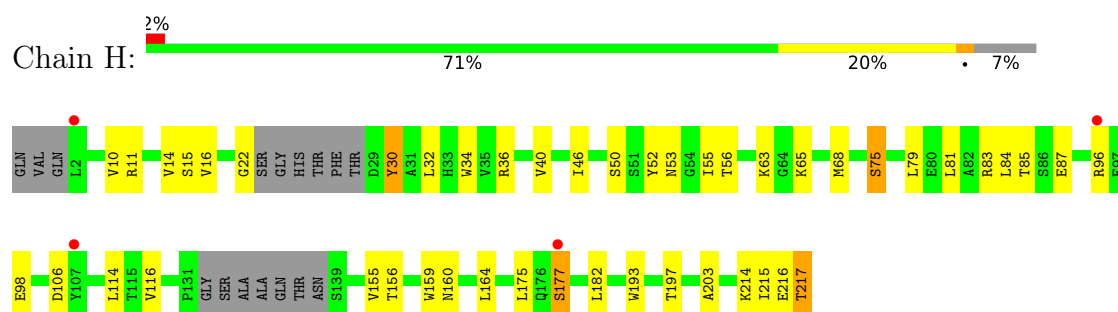
- Molecule 1: Programmed cell death protein 1



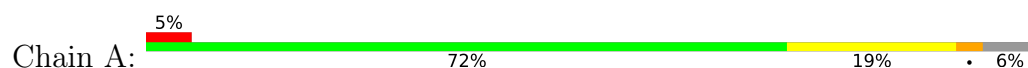
- Molecule 1: Programmed cell death protein 1

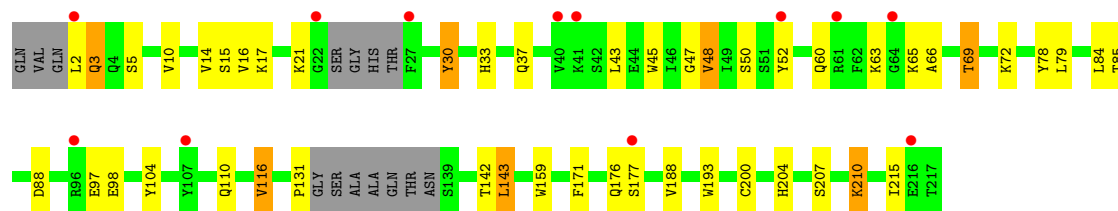


- Molecule 2: GY-5 heavy chain Fab



- Molecule 2: GY-5 heavy chain Fab





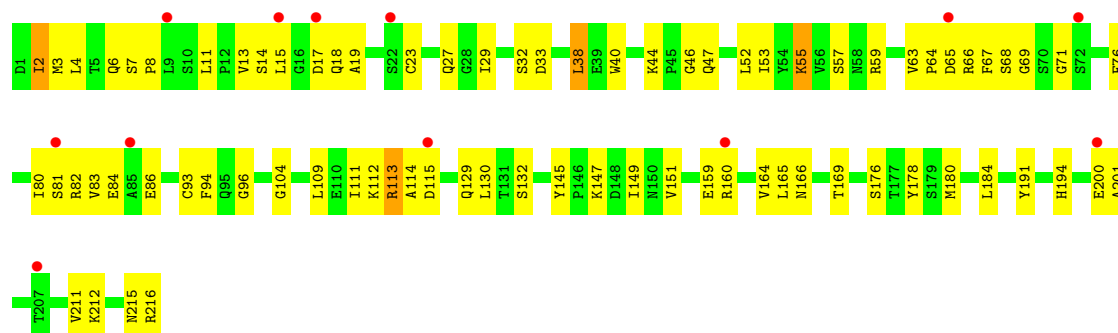
• Molecule 3: GY-5 light chain Fab

Chain L: 86% 14%



• Molecule 3: GY-5 light chain Fab

Chain B: 6% 64% 34%



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

Chain E: 100%



• Molecule 5: alpha-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 F: 75% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.59Å 64.35Å 151.48Å 90.00° 98.04° 90.00°	Depositor
Resolution (Å)	41.62 – 2.60 41.62 – 2.60	Depositor EDS
% Data completeness (in resolution range)	92.2 (41.62-2.60) 92.6 (41.62-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.212 , 0.277 0.212 , 0.275	Depositor DCC
R_{free} test set	1700 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å ²)	41.4	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8342	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 19.84 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.9194e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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

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	C	0.44	0/891	0.63	1/1208 (0.1%)
1	D	0.58	3/856 (0.4%)	0.64	0/1158
2	A	0.55	1/1633 (0.1%)	0.71	1/2231 (0.0%)
2	H	0.61	0/1614	0.68	1/2205 (0.0%)
3	B	0.44	0/1716	0.79	4/2327 (0.2%)
3	L	0.44	0/1716	0.65	2/2327 (0.1%)
All	All	0.51	4/8426 (0.0%)	0.69	9/11456 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	30	ILE	C-O	-6.11	1.17	1.23
2	A	210	LYS	C-O	-5.81	1.17	1.23
1	D	32	TRP	C-O	-5.44	1.17	1.24
1	D	31	GLN	C-O	-5.24	1.18	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	115	ASP	N-CA-C	9.42	122.49	110.24
3	B	114	ALA	N-CA-C	7.86	119.64	108.00
2	A	30	TYR	N-CA-C	6.98	120.03	109.41
3	L	57	SER	N-CA-C	5.90	122.32	114.12
2	H	56	THR	N-CA-C	5.21	117.30	109.23
3	B	38	LEU	CA-C-N	-5.15	114.51	122.59
3	B	38	LEU	C-N-CA	-5.15	114.51	122.59
1	C	31	GLN	N-CA-C	-5.13	98.67	107.23
3	B	14	SER	CB-CA-C	-5.02	101.24	109.53

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	872	0	848	20	0
1	D	839	0	819	27	0
2	A	1590	0	1543	37	0
2	H	1572	0	1529	39	0
3	B	1677	0	1620	60	0
3	L	1677	0	1620	19	0
4	E	38	0	34	0	0
5	F	49	0	43	0	0
6	C	28	0	26	0	0
All	All	8342	0	8082	191	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 (191) 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:C:39:PRO:HG3	1:D:31:GLN:HG2	1.55	0.88
1:C:131:LYS:NZ	2:A:97:GLU:OE1	2.07	0.87
3:B:6:GLN:NE2	3:B:93:CYS:H	1.73	0.87
2:H:50:SER:HB3	2:H:55:ILE:HG22	1.58	0.86
3:B:215:ASN:O	3:B:216:ARG:O	1.96	0.83
3:B:13:VAL:HG11	3:B:19:ALA:HB2	1.61	0.81
2:A:45:TRP:HZ2	2:A:48:VAL:HG23	1.45	0.81
3:B:6:GLN:HE22	3:B:93:CYS:H	1.32	0.78
2:A:30:TYR:CE1	2:A:98:GLU:HG2	2.20	0.77
3:B:66:ARG:HD2	3:B:82:ARG:O	1.85	0.77
3:B:200:GLU:HG2	3:B:211:VAL:HG22	1.66	0.76
2:A:30:TYR:HE1	2:A:98:GLU:HG2	1.51	0.72
2:H:52:TYR:CZ	2:H:53:ASN:ND2	2.58	0.72
1:D:55:SER:OG	1:D:105:ASP:OD1	2.05	0.72
2:H:160:ASN:HB2	2:H:164:LEU:HD13	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:66:ARG:NH1	3:L:87:ASP:OD2	2.26	0.69
3:B:11:LEU:HB3	3:B:109:LEU:HD12	1.75	0.68
1:C:36:THR:HB	1:C:55:SER:HB2	1.76	0.68
1:C:55:SER:OG	1:C:105:ASP:OD1	2.12	0.68
1:C:120:THR:HG21	1:C:139:ARG:HD2	1.74	0.68
1:D:128:LEU:HD22	2:H:55:ILE:HG23	1.75	0.67
2:A:143:LEU:HG	2:A:215:ILE:HG21	1.77	0.67
3:B:113:ARG:CG	3:B:113:ARG:HH11	2.08	0.65
2:A:17:LYS:HB3	2:A:17:LYS:NZ	2.11	0.65
2:A:69:THR:HG22	2:A:78:TYR:HB2	1.76	0.65
3:L:194:HIS:O	3:L:216:ARG:NH1	2.30	0.65
1:D:30:ILE:C	1:D:30:ILE:HD12	2.22	0.64
2:H:177:SER:O	2:H:177:SER:OG	2.14	0.63
1:D:97:VAL:HG22	1:D:108:MET:HG3	1.79	0.63
3:B:215:ASN:C	3:B:216:ARG:O	2.42	0.63
3:B:59:ARG:NE	3:B:67:PHE:O	2.32	0.62
3:B:115:ASP:OD1	3:B:115:ASP:O	2.19	0.61
2:H:30:TYR:HE1	2:H:98:GLU:CD	2.09	0.61
2:A:16:VAL:HG12	2:A:84:LEU:HD11	1.82	0.61
1:D:126:ILE:HG12	1:D:134:ILE:HG12	1.82	0.60
2:H:16:VAL:HG12	2:H:84:LEU:HD11	1.82	0.60
3:B:200:GLU:CG	3:B:211:VAL:HG22	2.30	0.60
1:D:28:ASP:N	1:D:28:ASP:OD1	2.34	0.60
3:B:38:LEU:O	3:B:55:LYS:O	2.20	0.60
3:L:66:ARG:HH12	3:L:87:ASP:CG	2.10	0.59
2:A:14:VAL:HG22	2:A:15:SER:H	1.66	0.59
1:D:32:TRP:HZ2	1:D:135:LYS:HD2	1.67	0.59
3:L:16:GLY:O	3:L:82:ARG:HG2	2.03	0.59
1:C:69:ARG:HB2	1:C:79:LEU:HD11	1.86	0.58
2:H:10:VAL:HG21	2:H:84:LEU:HD13	1.87	0.56
3:B:17:ASP:CG	3:B:18:GLN:H	2.13	0.56
3:B:4:LEU:HD12	3:B:23:CYS:SG	2.46	0.56
2:H:160:ASN:HD22	2:H:164:LEU:CD1	2.18	0.55
2:H:159:TRP:CH2	2:H:215:ILE:HD11	2.41	0.55
3:B:13:VAL:CG1	3:B:19:ALA:HB2	2.32	0.55
2:H:159:TRP:CZ3	2:H:215:ILE:HD11	2.42	0.55
1:D:44:VAL:HG13	1:D:48:ASP:HB2	1.90	0.54
3:B:194:HIS:O	3:B:216:ARG:NH1	2.41	0.54
1:D:45:THR:HG22	1:D:48:ASP:OD2	2.07	0.53
1:D:43:VAL:HG22	1:D:143:ARG:HB2	1.91	0.53
1:D:128:LEU:HD13	2:H:50:SER:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:78:LYS:HE3	1:D:81:ALA:HB2	1.91	0.53
3:B:66:ARG:CD	3:B:82:ARG:O	2.55	0.53
3:B:112:LYS:HA	3:B:145:TYR:OH	2.09	0.53
2:A:142:THR:C	2:A:143:LEU:HD13	2.34	0.53
3:B:159:GLU:HG3	3:B:160:ARG:N	2.23	0.53
2:H:36:ARG:HB2	2:H:46:ILE:HD11	1.90	0.53
3:B:3:MET:O	3:B:3:MET:HG3	2.08	0.53
2:A:3:GLN:OE1	2:A:110:GLN:NE2	2.43	0.52
2:A:17:LYS:NZ	2:A:78:TYR:HB3	2.24	0.52
3:B:200:GLU:CD	3:B:211:VAL:HG22	2.34	0.52
2:H:16:VAL:HG11	2:H:114:LEU:HD11	1.92	0.52
3:L:29:ILE:HD11	3:L:76:PHE:CZ	2.44	0.52
3:B:17:ASP:CG	3:B:18:GLN:N	2.67	0.52
2:A:45:TRP:CZ2	2:A:48:VAL:HG23	2.36	0.52
3:B:191:TYR:CE2	3:B:216:ARG:HD2	2.44	0.52
1:C:133:GLN:NE2	3:B:33:ASP:OD2	2.39	0.51
2:A:52:TYR:HA	2:A:72:LYS:HD3	1.92	0.51
3:B:29:ILE:HD11	3:B:76:PHE:CZ	2.45	0.51
3:B:113:ARG:CG	3:B:113:ARG:NH1	2.73	0.51
2:H:14:VAL:HG22	2:H:15:SER:H	1.75	0.51
3:B:2:ILE:HD13	3:B:27:GLN:HG2	1.92	0.51
3:B:38:LEU:HD22	3:B:94:PHE:O	2.11	0.51
1:C:70:MET:HG2	1:C:120:THR:HB	1.92	0.50
2:H:50:SER:CB	2:H:55:ILE:HG22	2.36	0.50
2:A:37:GLN:HB2	2:A:43:LEU:HD23	1.94	0.50
3:B:44:LYS:NZ	3:B:86:GLU:O	2.27	0.50
3:B:64:PRO:HG2	3:B:67:PHE:CD2	2.46	0.50
2:H:87:GLU:N	2:H:87:GLU:OE1	2.45	0.50
3:L:2:ILE:H	3:L:2:ILE:HD12	1.76	0.50
3:L:52:LEU:HA	3:L:63:VAL:HG21	1.94	0.49
1:D:65:LEU:HD23	1:D:108:MET:HE1	1.94	0.49
2:H:197:THR:HB	2:H:214:LYS:HE3	1.95	0.49
3:B:149:ILE:HD11	3:B:201:ALA:HB1	1.93	0.49
3:B:23:CYS:HB2	3:B:40:TRP:CH2	2.48	0.49
3:B:113:ARG:HD2	3:B:176:SER:HB2	1.94	0.49
1:C:36:THR:O	1:C:54:CYS:HA	2.13	0.48
2:H:156:THR:OG1	2:H:203:ALA:HB3	2.13	0.48
2:A:17:LYS:HB3	2:A:17:LYS:HZ2	1.76	0.48
1:D:94:ARG:HH22	1:D:117:ASP:CG	2.22	0.48
2:A:84:LEU:HB3	2:A:116:VAL:HG11	1.96	0.48
3:B:29:ILE:HD11	3:B:76:PHE:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:104:TYR:CE2	3:B:96:GLY:HA3	2.48	0.48
1:D:44:VAL:O	1:D:144:VAL:HA	2.14	0.48
1:C:43:VAL:HG22	1:C:143:ARG:HB3	1.96	0.47
2:A:176:GLN:HB3	3:B:165:LEU:HD11	1.95	0.47
3:B:164:VAL:HG22	3:B:184:LEU:HD13	1.95	0.47
3:L:115:ASP:OD2	3:L:204:LYS:HE2	2.14	0.47
2:H:114:LEU:CD2	2:H:116:VAL:HG23	2.45	0.47
2:H:160:ASN:HD22	2:H:164:LEU:HD11	1.79	0.47
1:D:131:LYS:HA	1:D:131:LYS:HD2	1.69	0.47
2:A:2:LEU:N	2:A:21:LYS:O	2.48	0.47
2:A:143:LEU:HD21	2:A:193:TRP:CD2	2.50	0.47
2:H:175:LEU:HD12	2:H:175:LEU:HA	1.71	0.47
2:H:30:TYR:CE1	2:H:98:GLU:OE2	2.67	0.47
2:H:85:THR:HG22	2:H:87:GLU:H	1.80	0.46
2:H:22:GLY:HA3	2:H:96:ARG:NH2	2.30	0.46
1:C:111:VAL:HG12	1:C:112:ARG:HG3	1.96	0.46
2:A:60:GLN:OE1	2:A:63:LYS:HE3	2.15	0.46
1:C:30:ILE:HA	1:D:43:VAL:HB	1.97	0.46
3:B:82:ARG:HB3	3:B:84:GLU:OE1	2.16	0.46
2:H:81:LEU:HB3	2:H:84:LEU:HD21	1.97	0.46
1:C:97:VAL:HG13	1:C:108:MET:HE2	1.97	0.46
3:B:13:VAL:HG21	3:B:83:VAL:HG11	1.98	0.45
3:B:147:LYS:HG2	3:B:178:TYR:CZ	2.52	0.45
2:H:65:LYS:NZ	2:H:83:ARG:HH11	2.15	0.45
1:D:36:THR:HB	1:D:55:SER:HB2	1.97	0.45
3:L:120:VAL:O	3:L:212:LYS:HE2	2.16	0.45
2:H:155:VAL:HG12	2:H:182:LEU:HD21	1.98	0.45
3:L:191:TYR:CE2	3:L:216:ARG:HD2	2.51	0.45
1:C:56:PHE:CE2	1:C:58:ASN:HB3	2.52	0.44
3:L:24:ARG:NE	3:L:75:ASP:OD1	2.50	0.44
3:B:4:LEU:O	3:B:104:GLY:HA2	2.17	0.44
3:B:53:ILE:HG21	3:B:69:GLY:HA3	1.99	0.44
1:C:37:PHE:HE1	1:C:108:MET:HG3	1.82	0.44
2:H:34:TRP:CE2	2:H:79:LEU:HB2	2.52	0.44
2:A:10:VAL:O	2:A:116:VAL:HA	2.16	0.44
2:A:66:ALA:HB1	2:A:79:LEU:HD11	2.00	0.44
3:B:113:ARG:HH11	3:B:113:ARG:HG3	1.79	0.44
2:H:106:ASP:OD1	2:H:106:ASP:N	2.39	0.44
2:A:159:TRP:CZ3	2:A:200:CYS:HB3	2.53	0.44
2:H:160:ASN:HD22	2:H:164:LEU:HD13	1.81	0.44
1:D:70:MET:HE3	1:D:70:MET:HB3	1.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:LEU:HD13	2:A:50:SER:HB2	1.99	0.44
2:H:75:SER:O	2:H:75:SER:OG	2.28	0.44
3:B:130:LEU:HD23	3:B:130:LEU:HA	1.79	0.44
2:A:204:HIS:ND1	2:A:207:SER:OG	2.44	0.43
3:B:52:LEU:HA	3:B:63:VAL:HG21	1.99	0.43
3:B:129:GLN:O	3:B:132:SER:OG	2.31	0.43
1:D:127:SER:O	1:D:132:ALA:HA	2.19	0.43
3:B:71:GLY:HA3	3:B:76:PHE:HA	2.00	0.43
2:A:45:TRP:CZ2	2:A:47:GLY:HA2	2.54	0.43
3:B:46:GLY:C	3:B:47:GLN:HG3	2.43	0.43
3:B:59:ARG:NH2	3:B:65:ASP:O	2.52	0.43
3:L:153:TRP:HA	3:L:198:THR:O	2.18	0.43
2:A:14:VAL:HG22	2:A:15:SER:N	2.33	0.43
2:A:33:HIS:NE2	2:A:97:GLU:HB3	2.33	0.43
1:C:42:LEU:HD21	1:C:50:ALA:HB1	2.00	0.43
2:H:11:ARG:O	2:H:14:VAL:HG12	2.19	0.42
2:H:83:ARG:O	2:H:83:ARG:HD3	2.18	0.42
3:L:165:LEU:HD23	3:L:165:LEU:HA	1.79	0.42
3:L:29:ILE:HD11	3:L:76:PHE:CE1	2.55	0.42
2:A:65:LYS:NZ	2:A:88:ASP:OD1	2.50	0.42
2:H:159:TRP:HZ3	2:H:215:ILE:CD1	2.33	0.42
3:B:7:SER:HA	3:B:8:PRO:HA	1.86	0.42
1:D:67:TRP:HE1	1:D:121:TYR:HD2	1.67	0.42
3:B:67:PHE:CD1	3:B:80:ILE:HG12	2.55	0.42
1:D:28:ASP:HB2	1:D:29:GLY:H	1.64	0.42
3:L:4:LEU:O	3:L:104:GLY:HA2	2.20	0.41
1:D:70:MET:HB2	1:D:120:THR:HB	2.02	0.41
1:D:94:ARG:O	1:D:111:VAL:HG22	2.21	0.41
2:A:3:GLN:CD	2:A:110:GLN:HE22	2.27	0.41
3:L:4:LEU:HD23	3:L:102:THR:OG1	2.20	0.41
3:B:66:ARG:HB2	3:B:81:SER:OG	2.20	0.41
3:B:67:PHE:CE1	3:B:80:ILE:HG12	2.56	0.41
3:L:44:LYS:HE3	3:L:86:GLU:O	2.19	0.41
3:L:195:ASN:OD1	3:L:215:ASN:HB3	2.20	0.41
1:C:54:CYS:HB3	1:C:108:MET:HE3	2.03	0.41
2:A:131:PRO:HD3	2:A:143:LEU:CD1	2.51	0.41
2:H:40:VAL:O	2:H:40:VAL:HG12	2.21	0.41
2:H:159:TRP:CZ3	2:H:215:ILE:CD1	3.03	0.41
2:A:85:THR:O	2:A:116:VAL:HG21	2.21	0.41
3:B:151:VAL:HA	3:B:200:GLU:O	2.21	0.41
3:L:191:TYR:CZ	3:L:216:ARG:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:212:LYS:HA	3:B:212:LYS:HD2	1.91	0.41
1:C:126:ILE:HG12	1:C:134:ILE:HG12	2.03	0.40
1:D:36:THR:O	1:D:54:CYS:HA	2.21	0.40
2:A:176:GLN:O	2:A:177:SER:OG	2.35	0.40
3:B:165:LEU:HD23	3:B:165:LEU:HA	1.87	0.40
1:C:43:VAL:HB	1:D:30:ILE:HG13	2.03	0.40
2:H:193:TRP:CH2	2:H:217:THR:HG23	2.57	0.40
2:A:131:PRO:HD3	2:A:143:LEU:HD12	2.04	0.40
3:B:15:LEU:HD11	3:B:111:ILE:HD11	2.03	0.40
3:B:166:ASN:HB3	3:B:180:MET:HE3	2.03	0.40
2:H:85:THR:HG22	2:H:87:GLU:OE1	2.21	0.40
2:A:171:PHE:CE2	3:B:169:THR:HG23	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	106/120 (88%)	102 (96%)	4 (4%)	0	100	100
1	D	100/120 (83%)	92 (92%)	8 (8%)	0	100	100
2	A	199/219 (91%)	190 (96%)	9 (4%)	0	100	100
2	H	197/219 (90%)	189 (96%)	8 (4%)	0	100	100
3	B	214/216 (99%)	206 (96%)	8 (4%)	0	100	100
3	L	214/216 (99%)	208 (97%)	6 (3%)	0	100	100
All	All	1030/1110 (93%)	987 (96%)	43 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	C	97/105 (92%)	93 (96%)	4 (4%)	27	54
1	D	92/105 (88%)	85 (92%)	7 (8%)	12	27
2	A	183/193 (95%)	175 (96%)	8 (4%)	25	50
2	H	181/193 (94%)	173 (96%)	8 (4%)	25	50
3	B	192/192 (100%)	186 (97%)	6 (3%)	35	63
3	L	192/192 (100%)	190 (99%)	2 (1%)	68	86
All	All	937/980 (96%)	902 (96%)	35 (4%)	30	57

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	36	THR
1	C	76	THR
1	C	78	LYS
1	C	108	MET
1	D	28	ASP
1	D	44	VAL
1	D	55	SER
1	D	62	SER
1	D	109	SER
1	D	127	SER
1	D	133	GLN
2	H	30	TYR
2	H	32	LEU
2	H	63	LYS
2	H	68	MET
2	H	75	SER
2	H	177	SER
2	H	216	GLU
2	H	217	THR
3	L	20	SER
3	L	128	GLU
2	A	3	GLN

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Mol	Chain	Res	Type
2	A	5	SER
2	A	48	VAL
2	A	69	THR
2	A	116	VAL
2	A	143	LEU
2	A	188	VAL
2	A	210	LYS
3	B	2	ILE
3	B	32	SER
3	B	55	LYS
3	B	57	SER
3	B	68	SER
3	B	113	ARG

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

Mol	Chain	Res	Type
2	H	53	ASN
2	H	57	ASN
2	H	160	ASN
3	L	98	HIS
3	L	150	ASN
2	A	39	HIS
2	A	57	ASN
3	B	195	ASN
3	B	215	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

7 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	$\# Z > 2$
4	NAG	E	1	4,1	14,14,15	0.25	0	17,19,21	0.52	0
4	NAG	E	2	4	14,14,15	0.29	0	17,19,21	0.55	0
4	FUC	E	3	4	10,10,11	0.30	0	14,14,16	0.58	0
5	NAG	F	1	5,1	14,14,15	0.27	0	17,19,21	0.67	0
5	NAG	F	2	5	14,14,15	0.45	0	17,19,21	0.76	1 (5%)
5	MAN	F	3	5	11,11,12	0.27	0	15,15,17	0.64	0
5	FUC	F	4	5	10,10,11	0.60	0	14,14,16	0.74	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
4	NAG	E	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	FUC	E	3	4	-	-	0/1/1/1
5	NAG	F	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	F	2	5	-	2/6/23/26	0/1/1/1
5	MAN	F	3	5	-	2/2/19/22	0/1/1/1
5	FUC	F	4	5	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	2	NAG	C1-O5-C5	2.42	115.43	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	3	MAN	O5-C5-C6-O6

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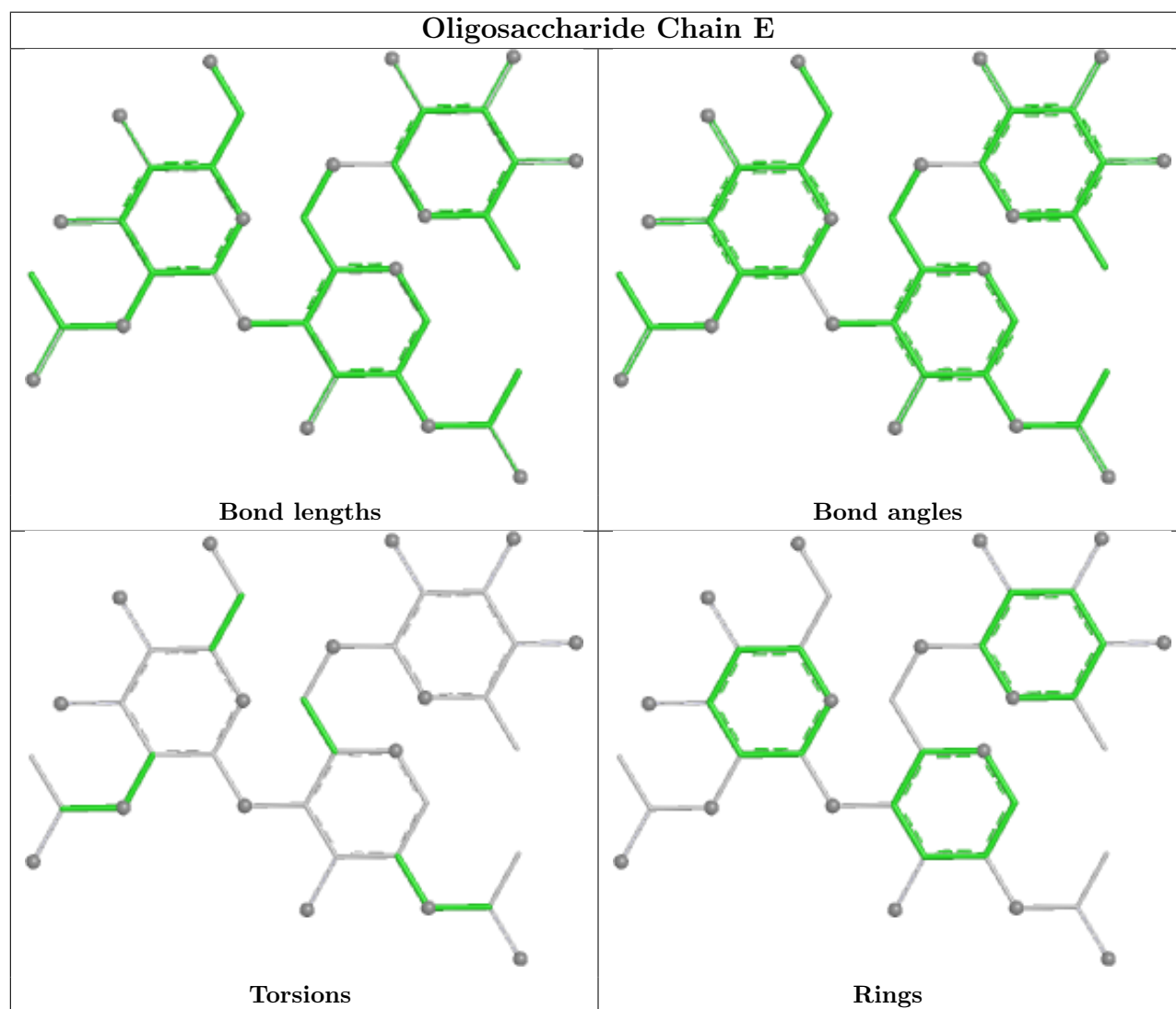
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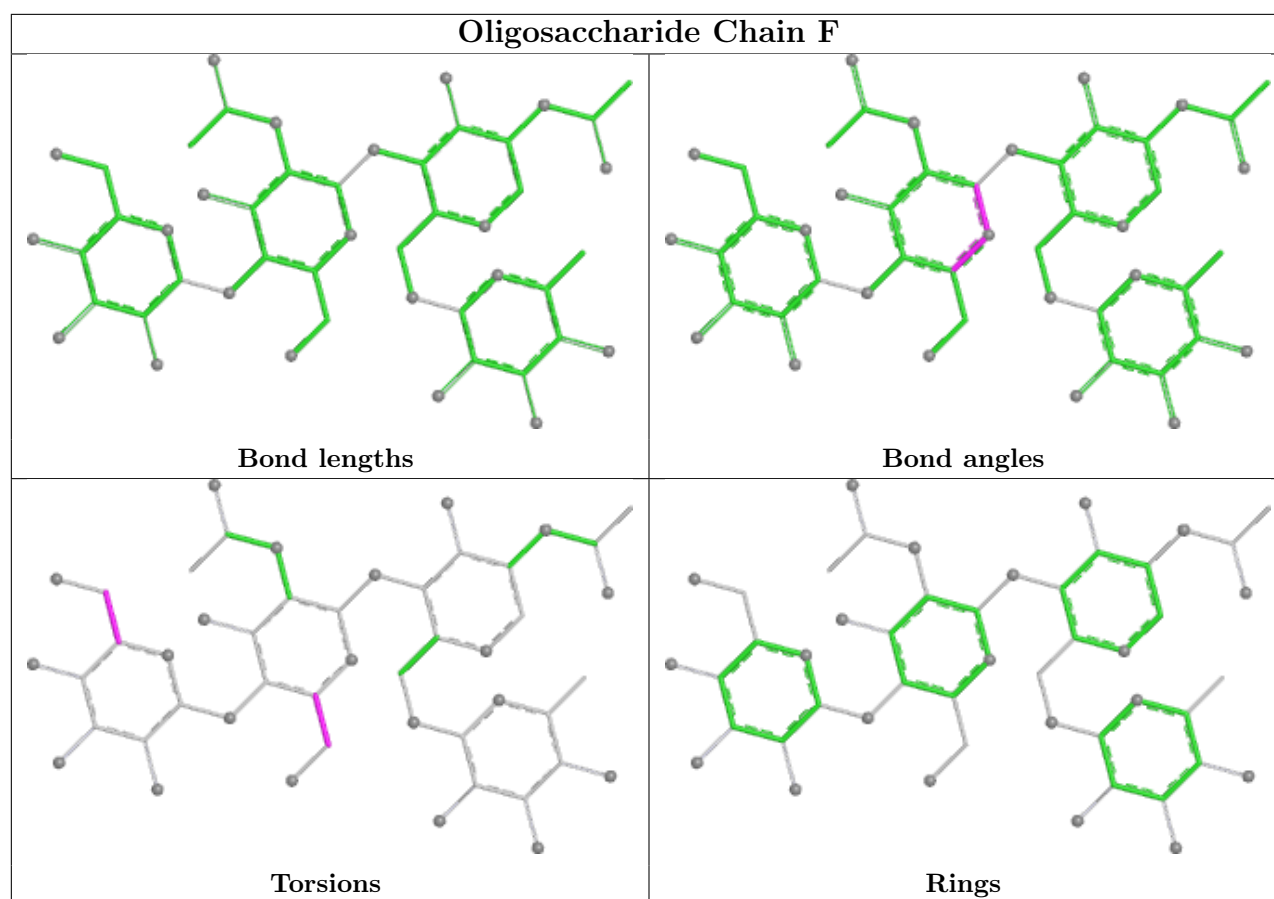
Mol	Chain	Res	Type	Atoms
5	F	2	NAG	O5-C5-C6-O6
5	F	3	MAN	C4-C5-C6-O6
5	F	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





5.6 Ligand geometry [i](#)

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	NAG	C	305	1	14,14,15	0.41	0	17,19,21	0.41	0
6	NAG	C	301	1	14,14,15	0.45	0	17,19,21	0.66	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	C	305	1	-	0/6/23/26	0/1/1/1
6	NAG	C	301	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	301	NAG	C1-O5-C5	2.01	114.89	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	301	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	C	110/120 (91%)	-0.09	1 (0%) 81 78	23, 36, 70, 88	0
1	D	106/120 (88%)	0.21	3 (2%) 55 49	22, 49, 84, 99	0
2	A	205/219 (93%)	0.26	12 (5%) 28 23	20, 44, 83, 112	0
2	H	203/219 (92%)	-0.08	4 (1%) 65 60	22, 38, 70, 88	0
3	B	216/216 (100%)	0.48	12 (5%) 30 24	25, 54, 88, 102	0
3	L	216/216 (100%)	-0.22	0 100 100	15, 37, 56, 81	0
All	All	1056/1110 (95%)	0.10	32 (3%) 52 47	15, 43, 82, 112	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	96	ARG	5.1
3	B	81	SER	3.8
2	A	52	TYR	3.6
2	H	2	LEU	3.3
2	A	216	GLU	3.2
3	B	160	ARG	3.1
3	B	85	ALA	3.1
2	A	40	VAL	3.1
2	A	61	ARG	3.1
2	A	2	LEU	3.0
2	A	41	LYS	3.0
2	A	107	TYR	3.0
2	A	64	GLY	2.9
3	B	200	GLU	2.8
3	B	65	ASP	2.7
2	H	177	SER	2.7
2	A	27	PHE	2.6
2	A	177	SER	2.6
2	A	22	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
2	A	96	ARG	2.4
3	B	115	ASP	2.4
1	D	121	TYR	2.4
3	B	72	SER	2.4
1	D	103	GLY	2.4
3	B	22	SER	2.3
3	B	17	ASP	2.2
1	C	139	ARG	2.2
3	B	15	LEU	2.1
3	B	9	LEU	2.1
3	B	207	THR	2.0
2	H	107	TYR	2.0
1	D	146	GLU	2.0

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

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

6.3 Carbohydrates ⓘ

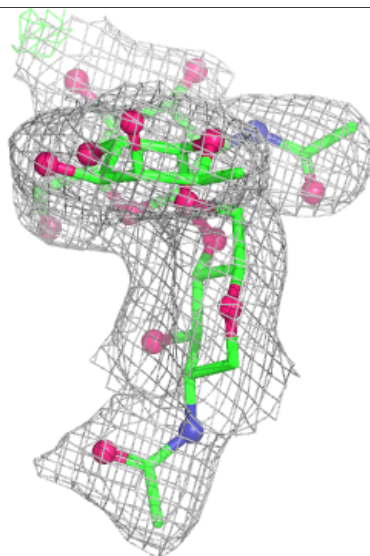
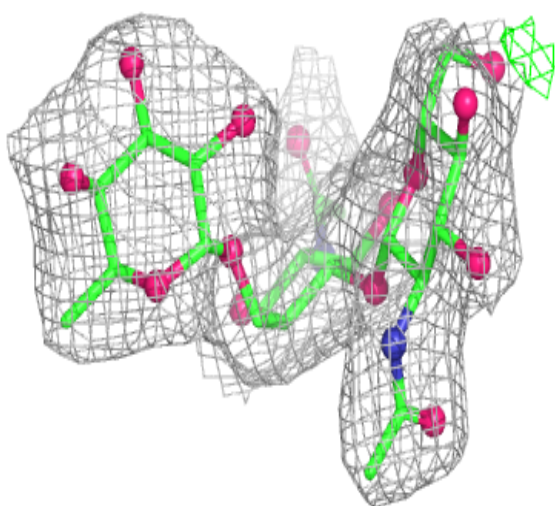
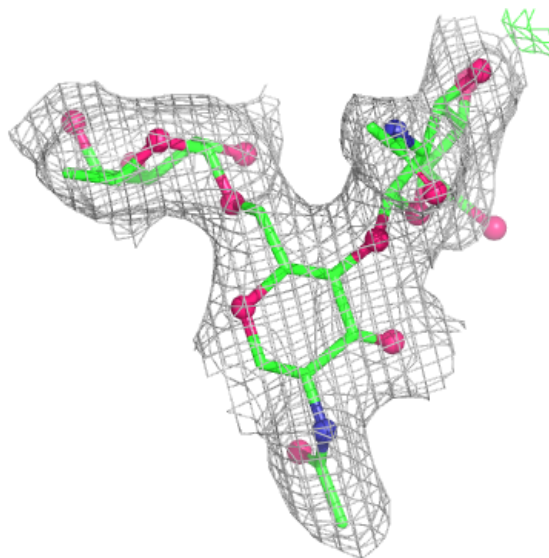
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

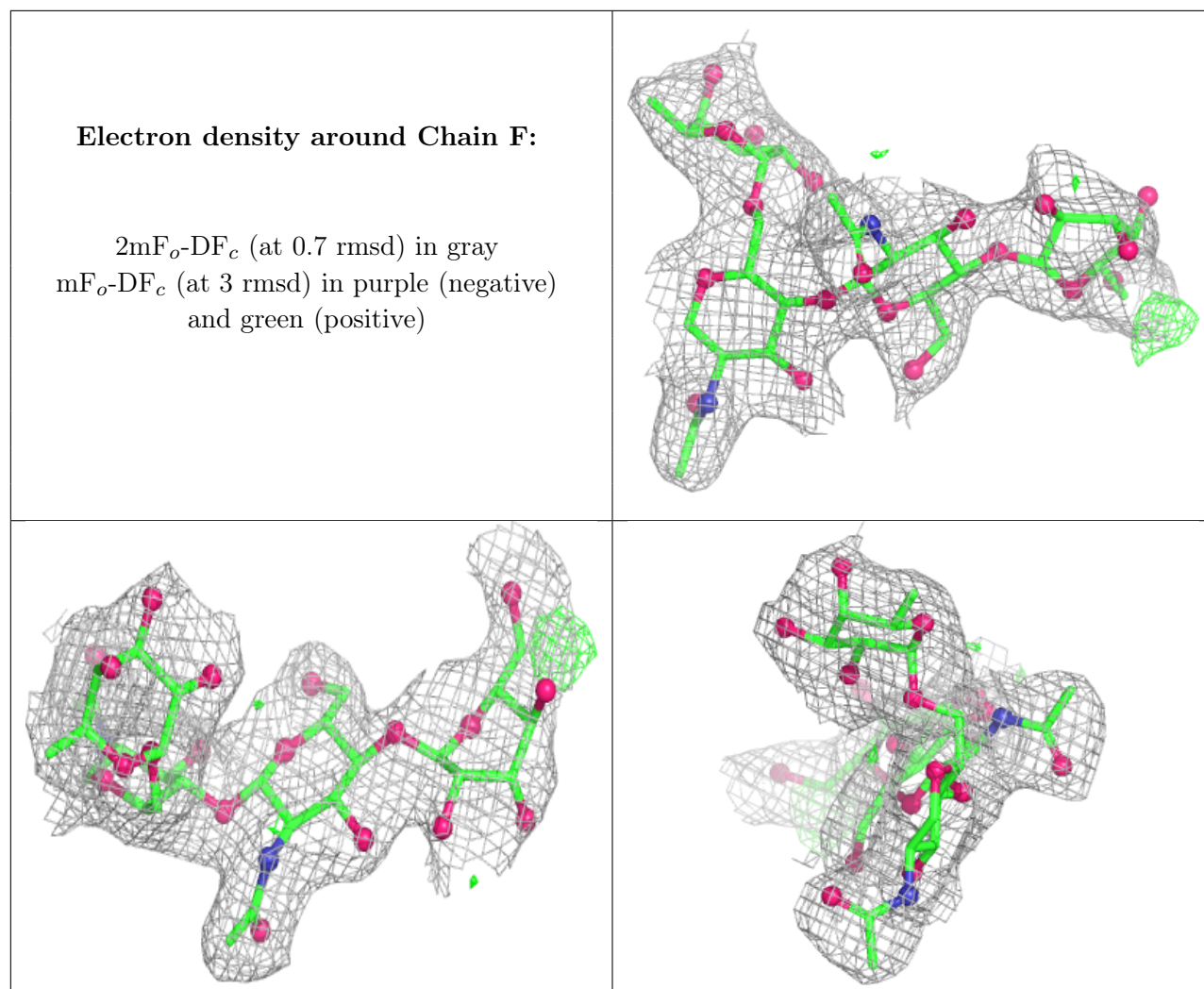
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	E	1	14/15	-	-	13,30,33,45	0
4	NAG	E	2	14/15	-	-	38,55,65,78	0
4	FUC	E	3	10/11	-	-	21,34,39,48	0
5	NAG	F	1	14/15	-	-	28,37,45,49	0
5	NAG	F	2	14/15	-	-	36,51,60,61	0
5	MAN	F	3	11/12	-	-	55,66,76,84	0
5	FUC	F	4	10/11	-	-	29,40,50,53	0

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 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($\text{\AA}^2$)	Q<0.9
6	NAG	C	305	14/15	0.73	0.12	67,81,90,92	0
6	NAG	C	301	14/15	0.76	0.13	45,59,67,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.