



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 25, 2025 – 04:25 PM JST

PDB ID : 9LGG / pdb_00009lgg
Title : Crystal structure of the human MuSK(Ig3_Fz)/L1 peptide complex
Authors : Matoba, K.; Mizutani, F.; Arimori, T.; Takagi, J.
Deposited on : 2025-01-10
Resolution : 2.69 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:

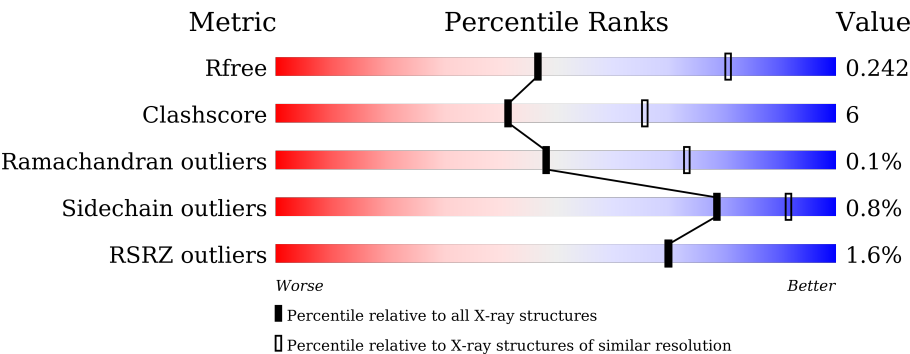
MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 2.69 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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	279	<div><div>%</div><div><div></div><div>79%</div><div>12%</div><div>9%</div></div></div>
1	B	279	<div><div>%</div><div><div></div><div>73%</div><div>18%</div><div>9%</div></div></div>
1	C	279	<div><div>%</div><div><div></div><div>80%</div><div>11%</div><div>9%</div></div></div>
1	D	279	<div><div>2%</div><div><div></div><div>72%</div><div>18%</div><div>10%</div></div></div>
2	E	2	<div><div></div><div>100%</div></div>
2	F	2	<div><div></div><div>50%</div><div>50%</div></div>

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 50%50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8049 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 Muscle, skeletal receptor tyrosine-protein kinase,Ig3-Fz domains of hMuSK:L1 peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			1999	1277	341	366	15			
1	B	254	Total	C	N	O	S	0	0	0
			1990	1271	339	365	15			
1	C	253	Total	C	N	O	S	0	0	0
			1979	1263	337	364	15			
1	D	250	Total	C	N	O	S	0	0	0
			1955	1248	333	359	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	GLY	-	expression tag	UNP O15146
A	206	LYS	-	expression tag	UNP O15146
A	207	ASP	-	expression tag	UNP O15146
A	208	GLY	-	expression tag	UNP O15146
A	209	SER	-	expression tag	UNP O15146
A	454	GLU	-	linker	UNP O15146
A	455	SER	-	linker	UNP O15146
A	456	ARG	-	linker	UNP O15146
B	205	GLY	-	expression tag	UNP O15146
B	206	LYS	-	expression tag	UNP O15146
B	207	ASP	-	expression tag	UNP O15146
B	208	GLY	-	expression tag	UNP O15146
B	209	SER	-	expression tag	UNP O15146
B	454	GLU	-	linker	UNP O15146
B	455	SER	-	linker	UNP O15146
B	456	ARG	-	linker	UNP O15146
C	205	GLY	-	expression tag	UNP O15146
C	206	LYS	-	expression tag	UNP O15146
C	207	ASP	-	expression tag	UNP O15146
C	208	GLY	-	expression tag	UNP O15146

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Chain	Residue	Modelled	Actual	Comment	Reference
C	209	SER	-	expression tag	UNP O15146
C	454	GLU	-	linker	UNP O15146
C	455	SER	-	linker	UNP O15146
C	456	ARG	-	linker	UNP O15146
D	205	GLY	-	expression tag	UNP O15146
D	206	LYS	-	expression tag	UNP O15146
D	207	ASP	-	expression tag	UNP O15146
D	208	GLY	-	expression tag	UNP O15146
D	209	SER	-	expression tag	UNP O15146
D	454	GLU	-	linker	UNP O15146
D	455	SER	-	linker	UNP O15146
D	456	ARG	-	linker	UNP O15146

- Molecule 2 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
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

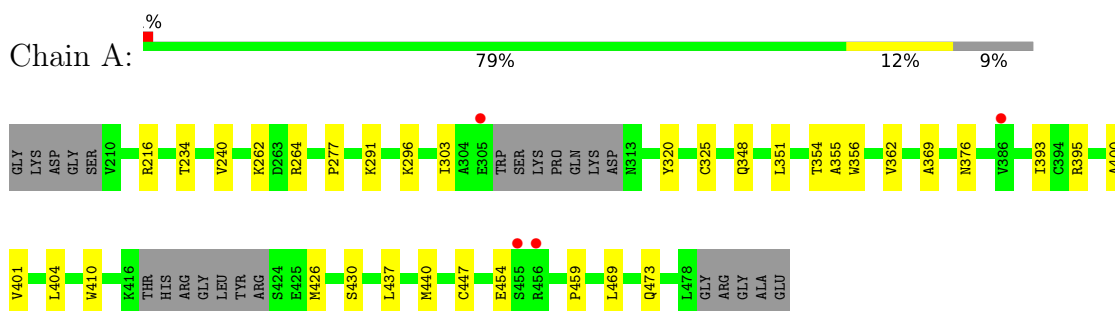


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	D	1	14	8	1	5	0	0

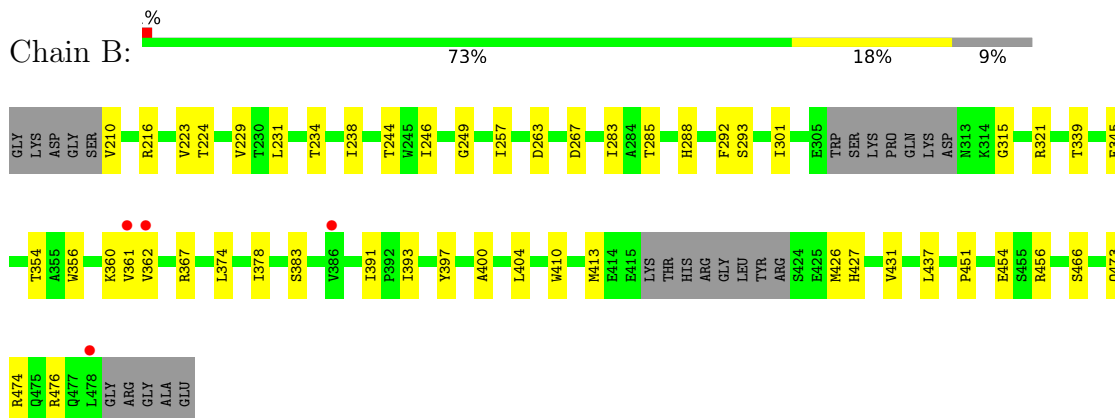
3 Residue-property plots [i](#)

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.

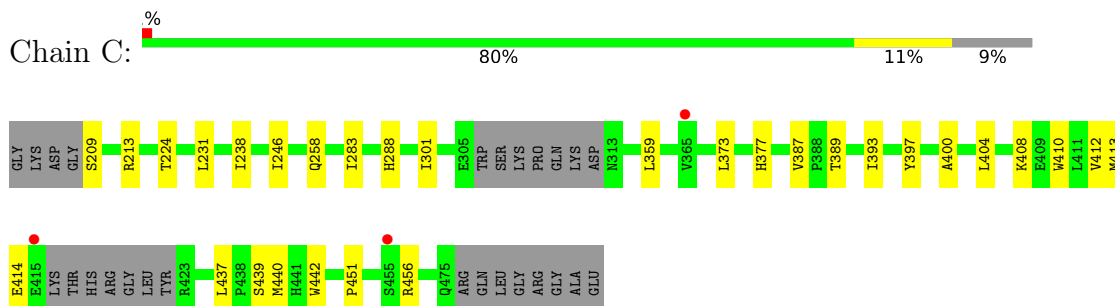
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase,Ig3-Fz domains of hMuSK:L1 peptide



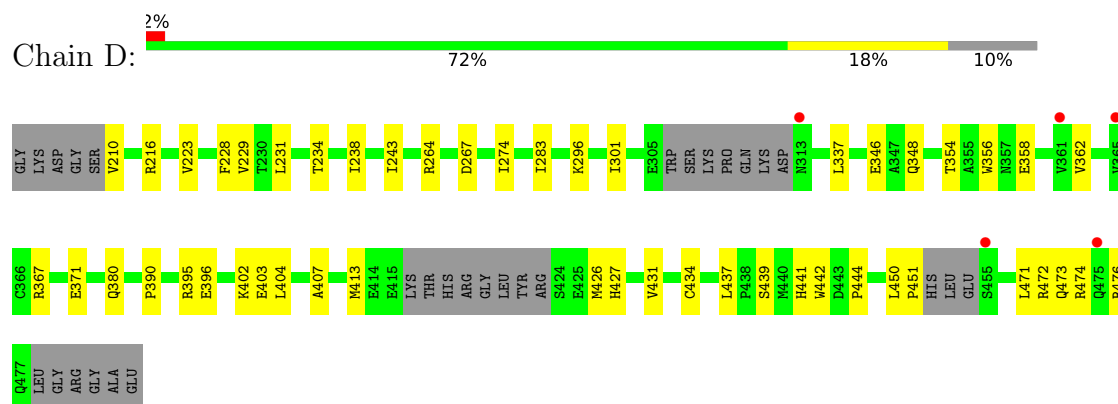
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase,Ig3-Fz domains of hMuSK:L1 peptide



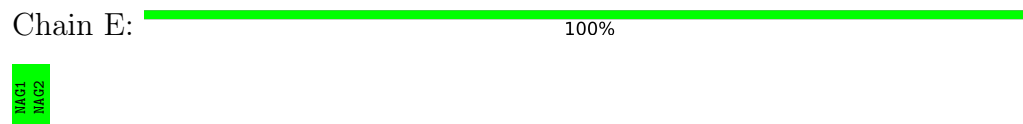
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase,Ig3-Fz domains of hMuSK:L1 peptide



- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase,Ig3-Fz domains of hMuSK:L1 peptide



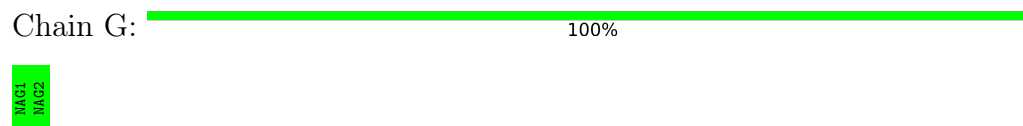
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	103.64Å 103.64Å 305.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.68 – 2.69 38.68 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.3 (38.68-2.69) 99.3 (38.68-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.204 , 0.242 0.202 , 0.242	Depositor DCC
R_{free} test set	2539 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	72.5	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.046 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8049	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.17	0/2048	0.34	0/2787
1	B	0.17	0/2039	0.34	0/2776
1	C	0.15	0/2028	0.33	0/2761
1	D	0.20	0/2002	0.36	0/2724
All	All	0.17	0/8117	0.34	0/11048

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	1999	0	1976	18	0
1	B	1990	0	1963	33	0
1	C	1979	0	1949	20	0
1	D	1955	0	1926	37	1
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
3	D	14	0	13	0	0
All	All	8049	0	7927	101	1

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 6.

All (101) 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:D:413:MET:HE1	1:D:431:VAL:HG11	1.54	0.90
1:A:240:VAL:HG22	1:A:264:ARG:HA	1.66	0.77
1:D:356:TRP:HZ3	1:D:362:VAL:HG11	1.48	0.77
1:B:454:GLU:HG3	1:B:456:ARG:HH12	1.53	0.73
1:B:413:MET:HE1	1:B:431:VAL:HG11	1.73	0.71
1:A:356:TRP:HZ3	1:A:362:VAL:HG11	1.58	0.68
1:C:377:HIS:HB2	1:C:393:ILE:HD13	1.75	0.68
1:D:234:THR:HG22	1:D:267:ASP:HA	1.75	0.68
1:D:395:ARG:NH1	1:D:437:LEU:O	2.27	0.67
1:D:228:PHE:CE1	1:D:346:GLU:HB3	2.30	0.67
1:C:231:LEU:HD21	1:C:301:ILE:HD11	1.78	0.66
1:D:223:VAL:HG11	1:D:229:VAL:HG21	1.80	0.64
1:D:367:ARG:NH1	1:D:371:GLU:OE1	2.26	0.64
1:D:367:ARG:HH12	1:D:371:GLU:CD	2.06	0.63
1:B:231:LEU:HD11	1:B:301:ILE:HD11	1.81	0.63
1:B:216:ARG:HB3	1:B:234:THR:HG23	1.80	0.63
1:D:413:MET:HE3	1:D:427:HIS:NE2	2.14	0.62
1:C:238:ILE:O	1:C:288:HIS:NE2	2.31	0.61
1:B:292:PHE:HD2	1:D:444:PRO:HB2	1.65	0.61
1:B:292:PHE:CD2	1:D:444:PRO:HB2	2.35	0.61
1:B:356:TRP:HH2	1:B:367:ARG:HG3	1.65	0.60
1:D:231:LEU:HD21	1:D:301:ILE:HD11	1.84	0.59
1:D:356:TRP:CZ3	1:D:362:VAL:HG11	2.35	0.59
1:B:383:SER:HA	1:B:391:ILE:HD11	1.85	0.58
1:D:337:LEU:HD23	1:D:348:GLN:HE22	1.69	0.57
1:D:472:ARG:O	1:D:476:ARG:HG3	2.04	0.57
1:B:413:MET:HE3	1:B:427:HIS:NE2	2.21	0.55
1:B:315:GLY:HA2	1:B:339:THR:HG23	1.87	0.55
1:C:410:TRP:O	1:C:414:GLU:HG3	2.07	0.55
1:D:426:MET:HA	1:D:426:MET:HE2	1.88	0.54
1:C:387:VAL:HG12	1:C:389:THR:HG23	1.88	0.54
1:D:450:LEU:HD23	1:D:451:PRO:HD2	1.88	0.54
1:A:369:ALA:HB1	1:A:401:VAL:HG22	1.90	0.52
1:C:456:ARG:HH11	1:C:456:ARG:HG2	1.73	0.52
1:C:209:SER:HA	1:C:213:ARG:HH21	1.76	0.51
1:A:376:ASN:HB3	1:A:393:ILE:HD11	1.94	0.50
1:B:473:GLN:OE1	1:B:476:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ALA:HA	1:A:404:LEU:HD12	1.95	0.49
1:D:396:GLU:OE2	1:D:439:SER:OG	2.27	0.48
1:D:283:ILE:HD12	1:D:296:LYS:HG2	1.95	0.48
1:B:210:VAL:HG12	1:B:288:HIS:NE2	2.29	0.47
1:B:393:ILE:HG13	1:B:437:LEU:HD13	1.97	0.47
1:B:374:LEU:O	1:B:378:ILE:HG13	2.14	0.47
1:B:238:ILE:O	1:B:288:HIS:HE1	1.97	0.47
1:A:348:GLN:HA	1:A:351:LEU:HD12	1.96	0.46
1:D:402:LYS:O	1:D:407:ALA:HA	2.15	0.46
1:C:456:ARG:HG2	1:C:456:ARG:NH1	2.31	0.46
1:B:321:ARG:HH21	1:B:345:GLU:CD	2.23	0.46
1:D:380:GLN:OE1	1:D:390:PRO:HB2	2.16	0.46
1:A:291:LYS:HE3	1:A:291:LYS:HB3	1.73	0.45
1:A:469:LEU:O	1:A:473:GLN:HG3	2.16	0.45
1:C:440:MET:HE3	1:C:440:MET:HB2	1.72	0.45
1:C:400:ALA:O	1:C:404:LEU:HB2	2.16	0.45
1:B:454:GLU:HG3	1:B:456:ARG:NH1	2.27	0.45
1:B:354:THR:HG21	1:B:426:MET:HB3	1.97	0.45
1:D:216:ARG:HB3	1:D:234:THR:OG1	2.17	0.45
1:D:228:PHE:CE1	1:D:346:GLU:CB	2.99	0.45
1:A:296:LYS:HE3	1:C:442:TRP:O	2.17	0.45
1:B:474:ARG:HE	1:B:474:ARG:HB3	1.65	0.44
1:D:337:LEU:HD23	1:D:348:GLN:NE2	2.31	0.44
1:B:234:THR:HG22	1:B:267:ASP:OD1	2.17	0.44
1:B:244:THR:HG21	1:D:441:HIS:HB3	1.99	0.44
1:D:403:GLU:O	1:D:404:LEU:HD23	2.16	0.44
1:D:471:LEU:HD23	1:D:471:LEU:HA	1.76	0.43
1:B:249:GLY:O	1:D:442:TRP:NE1	2.51	0.43
1:C:408:LYS:O	1:C:412:VAL:HG23	2.19	0.43
1:B:360:LYS:O	1:B:362:VAL:HG23	2.18	0.43
1:A:277:PRO:HD3	1:A:303:ILE:HG13	2.01	0.43
1:C:397:TYR:CZ	1:C:451:PRO:HD3	2.54	0.43
1:A:216:ARG:HB3	1:A:234:THR:HB	1.99	0.43
1:C:359:LEU:HD23	1:C:413:MET:HE2	2.01	0.43
1:A:262:LYS:HD3	1:A:262:LYS:HA	1.73	0.43
1:A:355:ALA:HB2	1:A:430:SER:HB2	2.02	0.42
1:B:246:ILE:HD11	1:B:283:ILE:HG13	2.02	0.42
1:A:395:ARG:NH2	1:A:437:LEU:O	2.52	0.42
1:D:473:GLN:HA	1:D:476:ARG:HD2	2.02	0.42
1:C:439:SER:HB3	1:C:442:TRP:CE2	2.55	0.42
1:A:354:THR:HG21	1:A:426:MET:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:393:ILE:HG13	1:C:437:LEU:HD13	2.02	0.42
1:D:434:CYS:HA	1:D:437:LEU:HD12	2.01	0.42
1:C:246:ILE:HD12	1:C:283:ILE:HG13	2.01	0.42
1:C:359:LEU:HD23	1:C:359:LEU:HA	1.90	0.41
1:B:400:ALA:O	1:B:404:LEU:HB2	2.20	0.41
1:B:285:THR:HG21	1:D:444:PRO:HG2	2.02	0.41
1:D:223:VAL:HG11	1:D:229:VAL:CG2	2.46	0.41
1:B:360:LYS:HD3	1:B:360:LYS:HA	1.77	0.41
1:B:397:TYR:CZ	1:B:451:PRO:HD3	2.55	0.41
1:C:373:LEU:HD11	1:C:393:ILE:HD12	2.02	0.41
1:B:360:LYS:HB3	1:B:361:VAL:H	1.79	0.41
1:D:210:VAL:HG21	1:D:238:ILE:HD12	2.03	0.41
1:D:354:THR:O	1:D:358:GLU:HG2	2.21	0.41
1:A:320:TYR:CZ	1:A:325:CYS:HB2	2.56	0.41
1:B:223:VAL:HG11	1:B:229:VAL:HG11	2.02	0.41
1:B:285:THR:HA	1:B:293:SER:O	2.20	0.41
1:A:459:PRO:HD3	1:B:257:ILE:HD12	2.02	0.41
1:D:238:ILE:HD11	1:D:264:ARG:NH2	2.35	0.41
1:D:274:ILE:HG13	1:D:301:ILE:HG21	2.02	0.41
1:A:440:MET:HA	1:A:447:CYS:SG	2.62	0.40
1:B:356:TRP:CH2	1:B:367:ARG:HG3	2.52	0.40
1:C:258:GLN:HE21	1:C:258:GLN:HB2	1.75	0.40
1:D:450:LEU:HA	1:D:451:PRO:HD3	1.85	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:346:GLU:OE2	1:D:474:ARG:NH2[4_455]	1.89	0.31

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	249/279 (89%)	241 (97%)	8 (3%)	0	100	100
1	B	248/279 (89%)	237 (96%)	10 (4%)	1 (0%)	30	55
1	C	247/279 (88%)	241 (98%)	6 (2%)	0	100	100
1	D	242/279 (87%)	233 (96%)	9 (4%)	0	100	100
All	All	986/1116 (88%)	952 (97%)	33 (3%)	1 (0%)	48	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	263	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	222/240 (92%)	220 (99%)	2 (1%)	75	90
1	B	221/240 (92%)	218 (99%)	3 (1%)	62	84
1	C	220/240 (92%)	219 (100%)	1 (0%)	86	95
1	D	217/240 (90%)	216 (100%)	1 (0%)	86	95
All	All	880/960 (92%)	873 (99%)	7 (1%)	79	91

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	410	TRP
1	A	454	GLU
1	B	224	THR
1	B	410	TRP
1	B	466	SER
1	C	224	THR
1	D	243	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	319	GLN
1	B	258	GLN
1	B	288	HIS
1	B	477	GLN
1	C	313	ASN
1	C	376	ASN
1	C	441	HIS
1	D	258	GLN
1	D	376	ASN
1	D	473	GLN

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 ⓘ

8 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	E	1	2,1	14,14,15	0.29	0	17,19,21	0.51	0
2	NAG	E	2	2	14,14,15	0.34	0	17,19,21	0.55	0
2	NAG	F	1	2,1	14,14,15	0.52	0	17,19,21	0.84	1 (5%)
2	NAG	F	2	2	14,14,15	0.40	0	17,19,21	0.54	0
2	NAG	G	1	2,1	14,14,15	0.29	0	17,19,21	0.65	0
2	NAG	G	2	2	14,14,15	0.37	0	17,19,21	0.60	0
2	NAG	H	1	2,1	14,14,15	0.34	0	17,19,21	0.57	0
2	NAG	H	2	2	14,14,15	0.22	0	17,19,21	0.58	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
2	NAG	E	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	3/6/23/26	0/1/1/1
2	NAG	F	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	NAG	G	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	NAG	C1-O5-C5	2.36	115.38	112.19
2	H	2	NAG	C1-O5-C5	2.01	114.92	112.19

There are no chirality outliers.

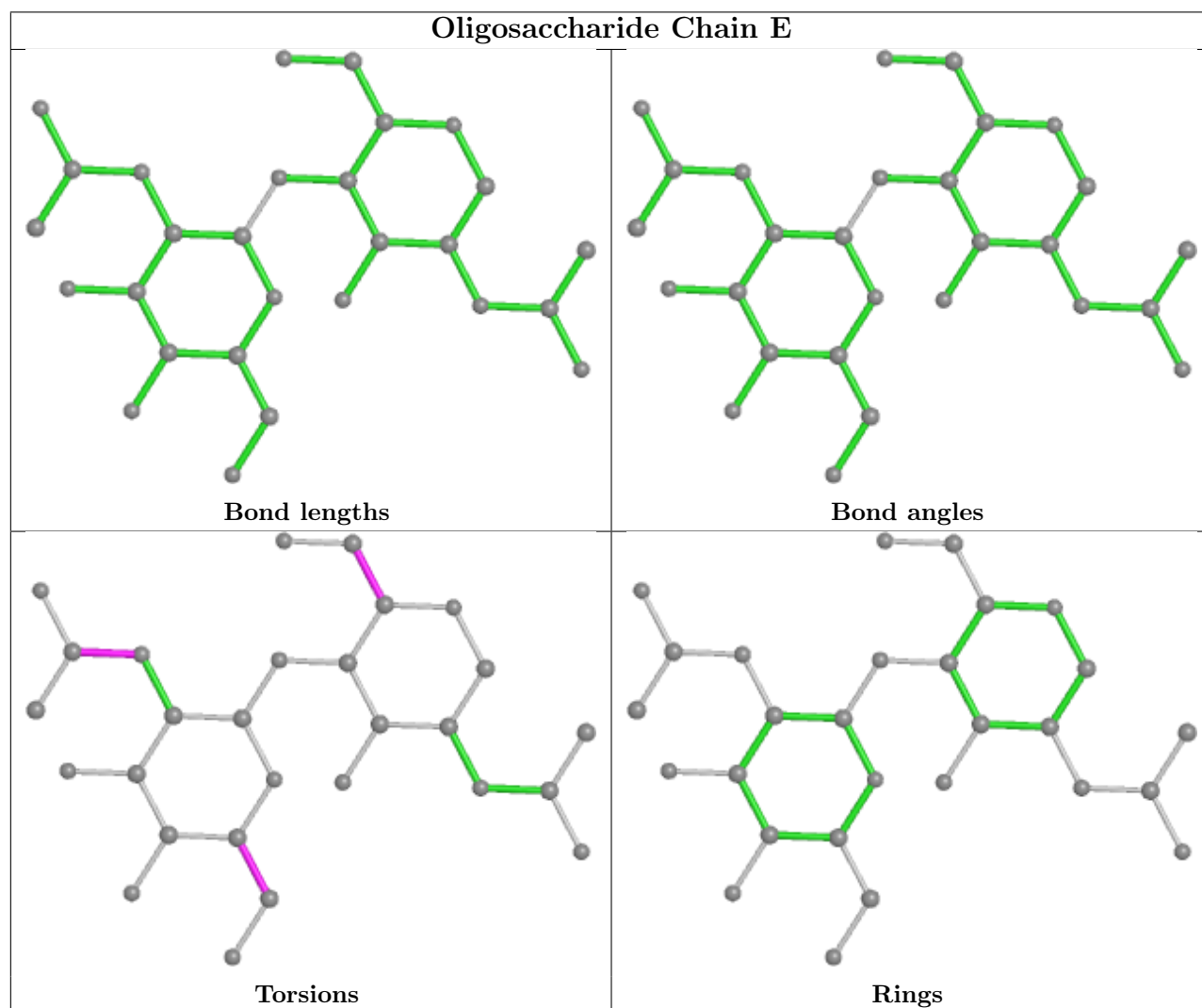
All (13) torsion outliers are listed below:

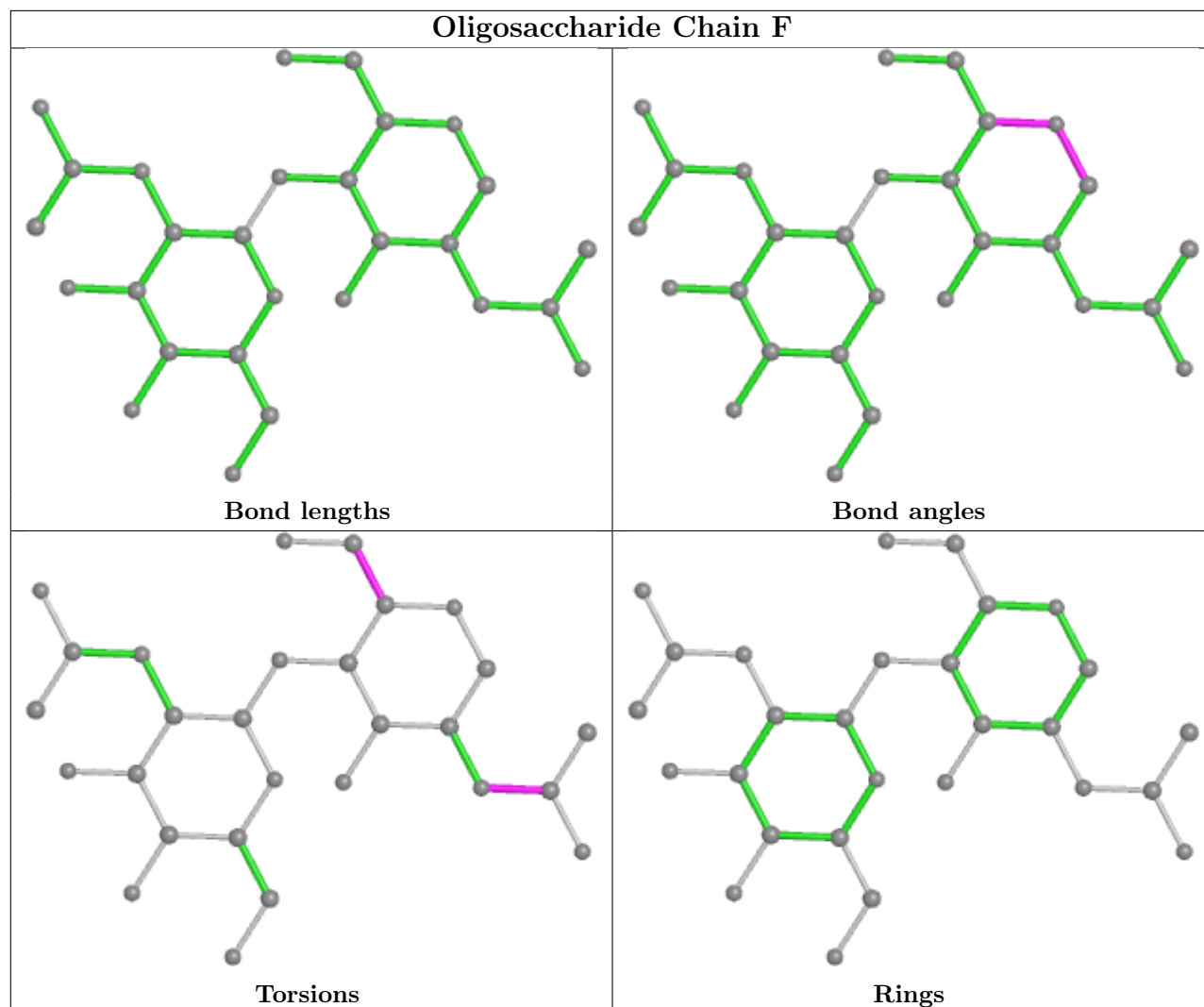
Mol	Chain	Res	Type	Atoms
2	H	2	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
2	H	2	NAG	C4-C5-C6-O6
2	E	2	NAG	C8-C7-N2-C2
2	E	2	NAG	O7-C7-N2-C2
2	F	1	NAG	C8-C7-N2-C2
2	F	1	NAG	O7-C7-N2-C2
2	E	1	NAG	O5-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
2	G	1	NAG	O5-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6

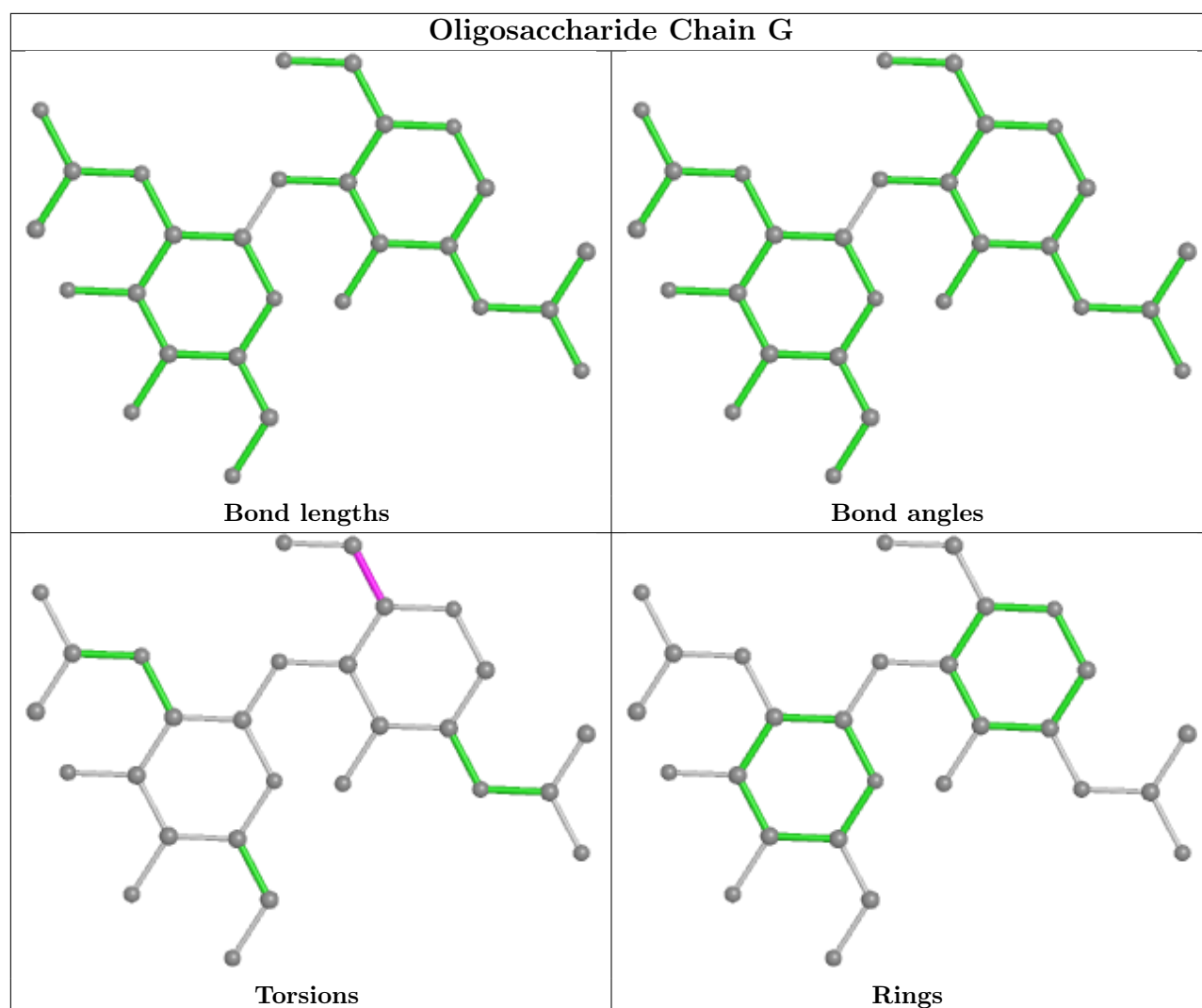
There are no ring outliers.

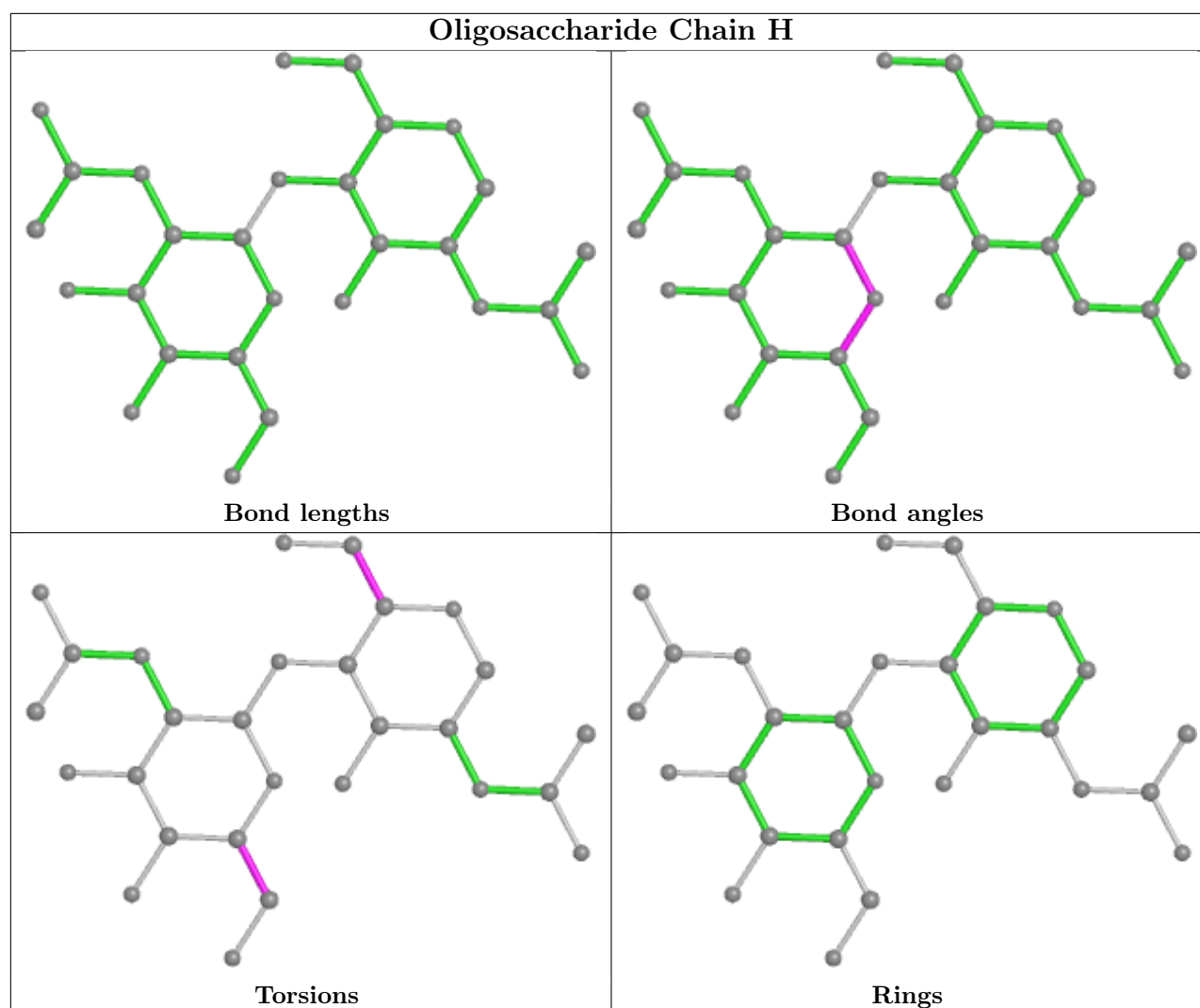
No monomer is involved in short contacts.

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 ⓘ

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	D	501	1	14,14,15	0.41	0	17,19,21	0.69	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
3	NAG	D	501	1	-	3/6/23/26	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(°)
3	D	501	NAG	C1-O5-C5	2.23	115.21	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	501	NAG	C8-C7-N2-C2
3	D	501	NAG	O7-C7-N2-C2
3	D	501	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 [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	255/279 (91%)	-0.22	4 (1%) 70 70	42, 70, 113, 134	0
1	B	254/279 (91%)	-0.05	4 (1%) 70 70	47, 78, 120, 140	0
1	C	253/279 (90%)	-0.39	3 (1%) 76 76	43, 62, 94, 137	0
1	D	250/279 (89%)	-0.04	5 (2%) 64 64	55, 79, 120, 141	0
All	All	1012/1116 (90%)	-0.17	16 (1%) 70 70	42, 73, 116, 141	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	478	LEU	5.3
1	A	386	VAL	3.5
1	B	361	VAL	3.1
1	D	455	SER	3.0
1	A	456	ARG	2.8
1	D	365	VAL	2.7
1	B	362	VAL	2.6
1	A	455	SER	2.5
1	D	313	ASN	2.5
1	D	361	VAL	2.3
1	D	475	GLN	2.3
1	A	305	GLU	2.2
1	B	386	VAL	2.1
1	C	415	GLU	2.1
1	C	365	VAL	2.0
1	C	455	SER	2.0

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

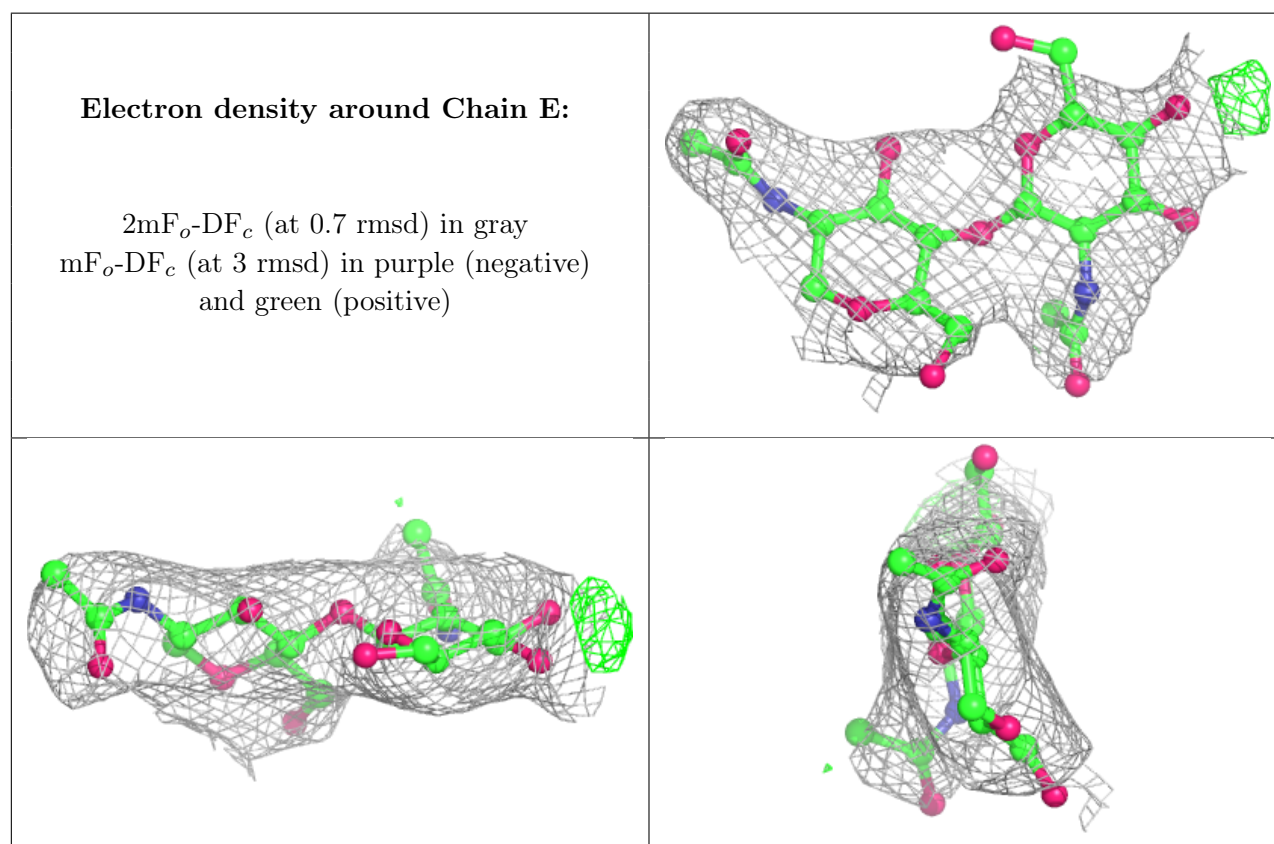
There are no non-standard protein/DNA/RNA residues in this entry.

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.

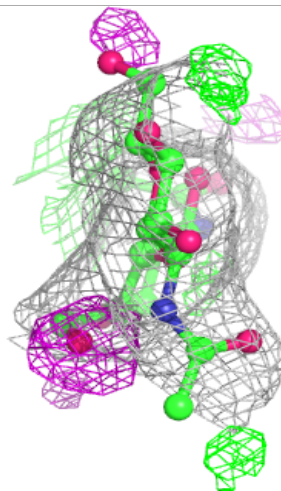
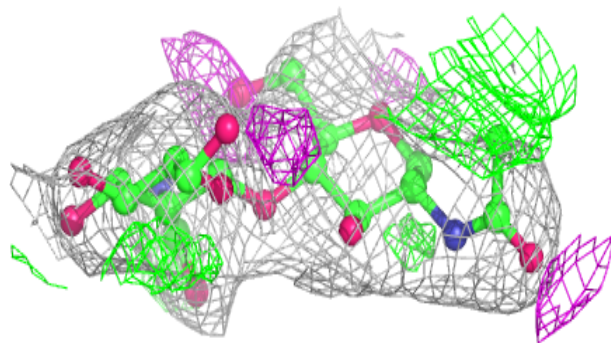
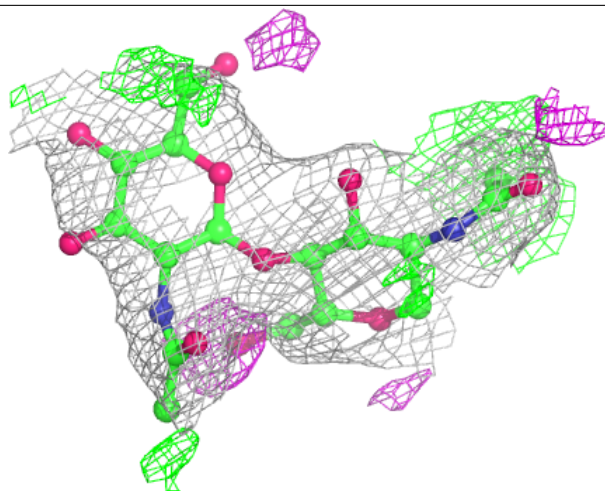
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	F	2	14/15	0.66	0.14	93,110,120,120	0
2	NAG	F	1	14/15	0.74	0.16	70,84,93,108	0
2	NAG	E	2	14/15	0.77	0.13	87,105,114,119	0
2	NAG	H	2	14/15	0.77	0.12	87,104,111,115	0
2	NAG	G	2	14/15	0.84	0.14	77,97,114,119	0
2	NAG	H	1	14/15	0.92	0.09	69,78,89,90	0
2	NAG	G	1	14/15	0.93	0.09	57,69,84,91	0
2	NAG	E	1	14/15	0.94	0.08	65,79,92,99	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.



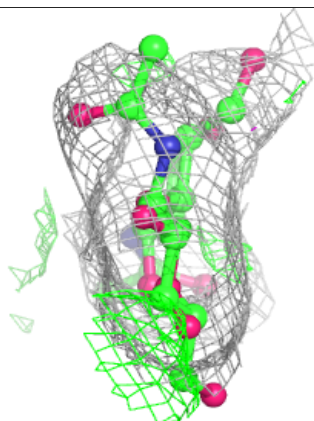
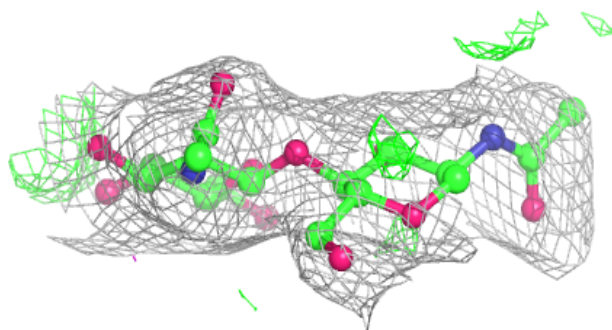
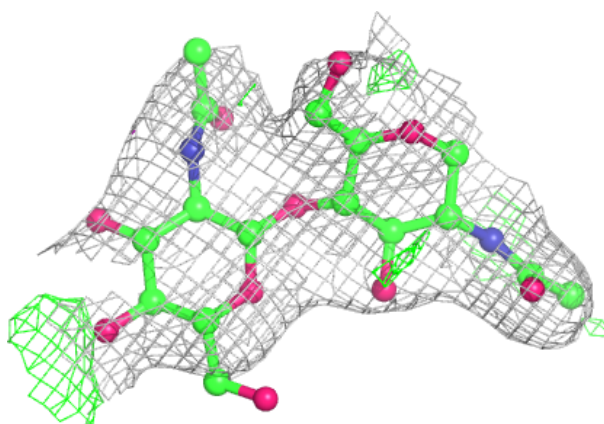
Electron density around Chain F:

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

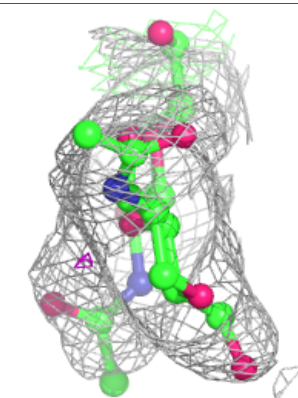
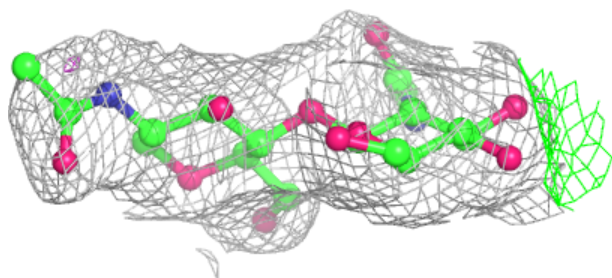
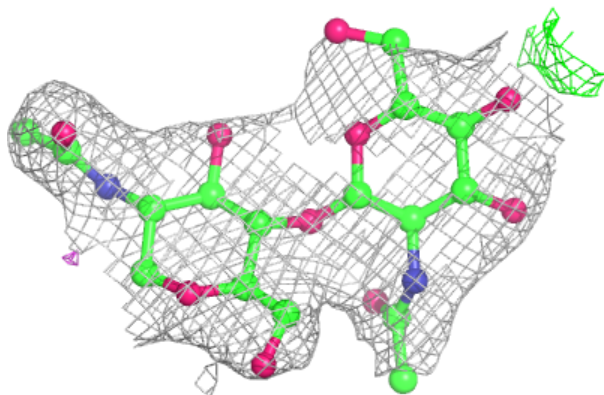


Electron density around Chain G:

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

**Electron density around Chain H:**

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



6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	D	501	14/15	0.60	0.15	88,107,122,124	0

6.5 Other polymers

There are no such residues in this entry.