



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:40 AM UTC

PDB ID : 4XAJ / pdb_00004xaj
Title : Crystal structure of human NR2E1/TLX
Authors : Zhi, X.; Zhou, E.; Xu, E.
Deposited on : 2014-12-14
Resolution : 3.55 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

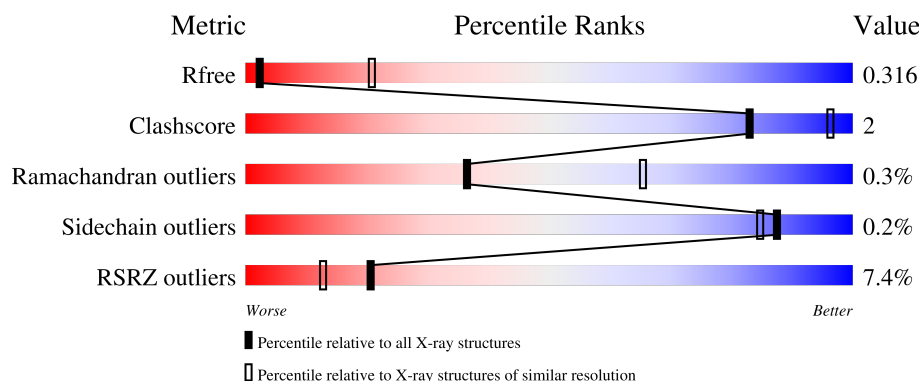
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.55 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.



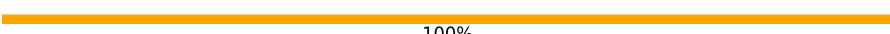
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1410 (3.62-3.50)
Clashscore	190562	1480 (3.62-3.50)
Ramachandran outliers	187476	1440 (3.62-3.50)
Sidechain outliers	187428	1441 (3.62-3.50)
RSRZ outliers	180081	1409 (3.62-3.50)

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	576	6% 90% 8% ..
1	B	576	5% 94% 5% .
1	C	576	4% 90% 8% .
1	D	576	14% 90% 8% ..
2	P	18	17% 94% 6%

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Mol	Chain	Length	Quality of chain
2	Q	18	 83% 17%
3	E	2	 50% 50%
3	F	2	 50% 50%
3	G	2	 50% 50%
3	H	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GLC	H	1	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18097 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 Maltose-binding periplasmic protein,Nuclear receptor subfamily 2 group E member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	568	Total	C	N	O	S	0	0	0
			4424	2847	729	835	13			
1	C	568	Total	C	N	O	S	0	0	0
			4424	2848	729	834	13			
1	B	570	Total	C	N	O	S	0	0	0
			4437	2856	731	836	14			
1	D	568	Total	C	N	O	S	0	0	0
			4424	2848	729	834	13			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEY0
A	369	ASN	-	linker	UNP P0AEY0
A	370	ALA	-	linker	UNP P0AEY0
A	371	ALA	-	linker	UNP P0AEY0
A	372	ALA	-	linker	UNP P0AEY0
A	373	GLU	-	linker	UNP P0AEY0
A	374	PHE	-	linker	UNP P0AEY0
A	1257	ARG	LYS	engineered mutation	UNP Q9Y466
A	1259	THR	ASN	engineered mutation	UNP Q9Y466
A	1260	LEU	LYS	engineered mutation	UNP Q9Y466
A	1338	VAL	CYS	engineered mutation	UNP Q9Y466
B	1	MET	-	initiating methionine	UNP P0AEY0
B	369	ASN	-	linker	UNP P0AEY0
B	370	ALA	-	linker	UNP P0AEY0
B	371	ALA	-	linker	UNP P0AEY0
B	372	ALA	-	linker	UNP P0AEY0
B	373	GLU	-	linker	UNP P0AEY0
B	374	PHE	-	linker	UNP P0AEY0
B	1257	ARG	LYS	engineered mutation	UNP Q9Y466
B	1259	THR	ASN	engineered mutation	UNP Q9Y466

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1260	LEU	LYS	engineered mutation	UNP Q9Y466
B	1338	VAL	CYS	engineered mutation	UNP Q9Y466
C	1	MET	-	initiating methionine	UNP P0AEY0
C	369	ASN	-	linker	UNP P0AEY0
C	370	ALA	-	linker	UNP P0AEY0
C	371	ALA	-	linker	UNP P0AEY0
C	372	ALA	-	linker	UNP P0AEY0
C	373	GLU	-	linker	UNP P0AEY0
C	374	PHE	-	linker	UNP P0AEY0
C	1257	ARG	LYS	engineered mutation	UNP Q9Y466
C	1259	THR	ASN	engineered mutation	UNP Q9Y466
C	1260	LEU	LYS	engineered mutation	UNP Q9Y466
C	1338	VAL	CYS	engineered mutation	UNP Q9Y466
D	1	MET	-	initiating methionine	UNP P0AEY0
D	369	ASN	-	linker	UNP P0AEY0
D	370	ALA	-	linker	UNP P0AEY0
D	371	ALA	-	linker	UNP P0AEY0
D	372	ALA	-	linker	UNP P0AEY0
D	373	GLU	-	linker	UNP P0AEY0
D	374	PHE	-	linker	UNP P0AEY0
D	1257	ARG	LYS	engineered mutation	UNP Q9Y466
D	1259	THR	ASN	engineered mutation	UNP Q9Y466
D	1260	LEU	LYS	engineered mutation	UNP Q9Y466
D	1338	VAL	CYS	engineered mutation	UNP Q9Y466

- Molecule 2 is a protein called Atrophin/grunge.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Q	18	Total	C	N	O	0	0	0
			148	93	27	28			
2	P	18	Total	C	N	O	0	0	0
			148	93	27	28			

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	E	2	Total	C	O	0	0	0
			23	12	11			

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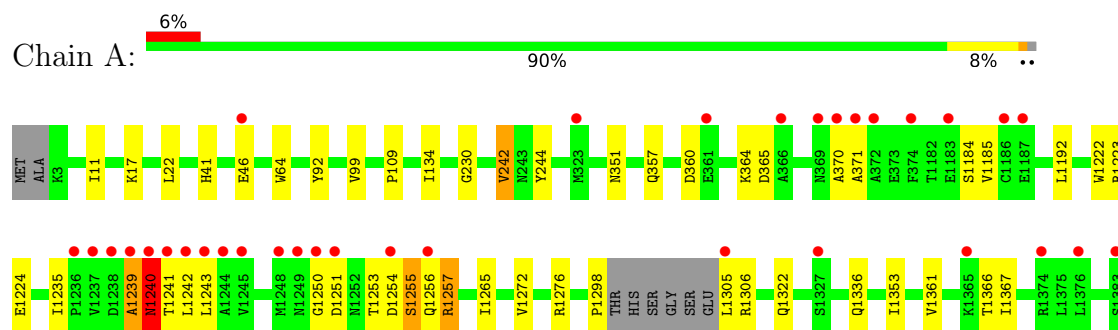
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	F	2	Total	C	O	0	0	0
			23	12	11			
3	G	2	Total	C	O	0	0	0
			23	12	11			
3	H	2	Total	C	O	0	0	0
			23	12	11			

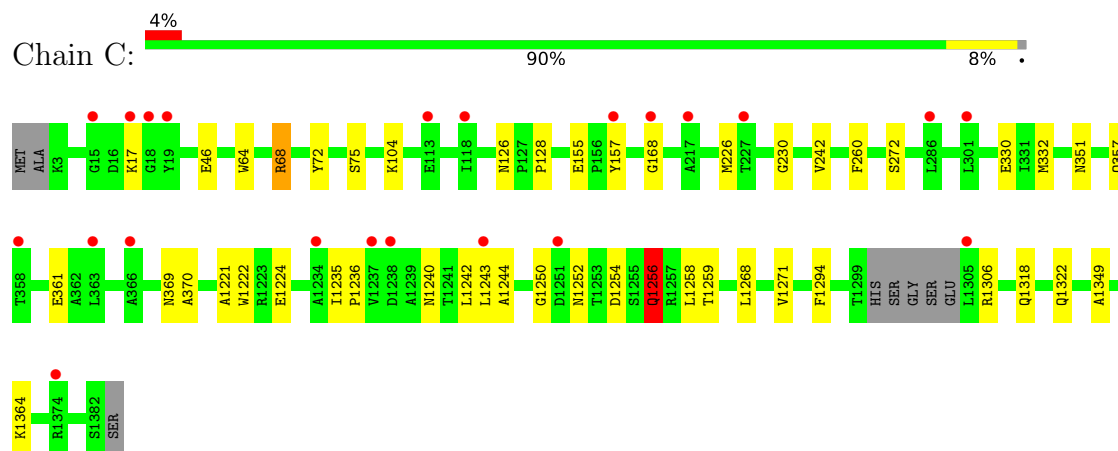
3 Residue-property plots

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.

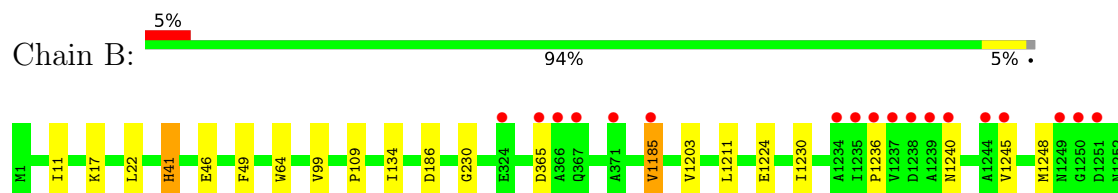
- Molecule 1: Maltose-binding periplasmic protein,Nuclear receptor subfamily 2 group E member 1

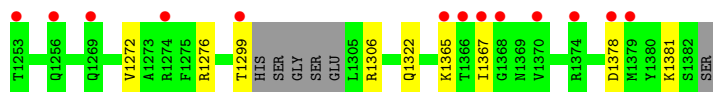


- Molecule 1: Maltose-binding periplasmic protein,Nuclear receptor subfamily 2 group E member 1

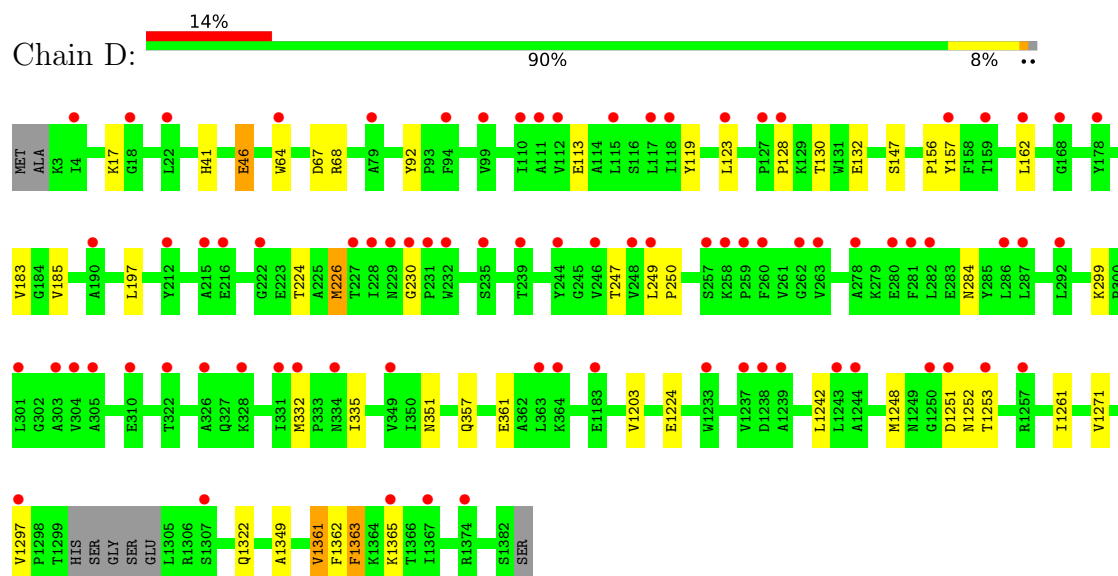


- Molecule 1: Maltose-binding periplasmic protein,Nuclear receptor subfamily 2 group E member 1

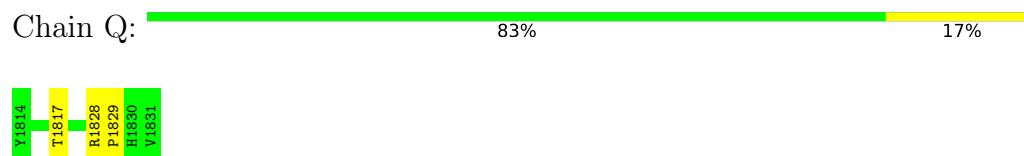




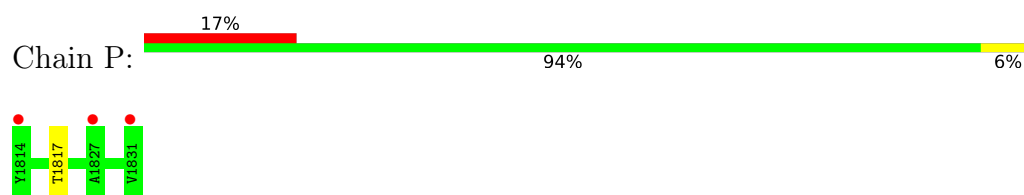
- Molecule 1: Maltose-binding periplasmic protein,Nuclear receptor subfamily 2 group E member 1



- Molecule 2: Atrophin/grunge



- Molecule 2: Atrophin/grunge



- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose





- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain G:  50% 50%



- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain H:  100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.26Å 130.74Å 308.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.90 – 3.55 39.90 – 3.55	Depositor EDS
% Data completeness (in resolution range)	97.8 (39.90-3.55) 97.9 (39.90-3.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 3.57Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.273 , 0.314 0.275 , 0.316	Depositor DCC
R_{free} test set	2532 reflections (6.98%)	wwPDB-VP
Wilson B-factor (Å ²)	58.9	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18097	wwPDB-VP
Average B, all atoms (Å ²)	65.0	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 51.47 % 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 5.5865e-05. 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: GLC

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	0.45	0/4521	1.06	19/6137 (0.3%)
1	B	0.45	0/4534	1.07	18/6156 (0.3%)
1	C	0.46	0/4521	1.05	19/6139 (0.3%)
1	D	0.45	0/4521	1.10	33/6139 (0.5%)
2	P	0.47	0/152	1.26	2/206 (1.0%)
2	Q	0.46	0/152	1.14	2/206 (1.0%)
All	All	0.45	0/18401	1.07	93/24983 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1256	GLN	N-CA-C	8.29	121.24	111.71
1	A	1255	SER	N-CA-C	8.13	121.75	109.63
1	D	1365	LYS	N-CA-C	-7.68	103.01	113.30
1	B	1248	MET	N-CA-C	7.64	118.08	108.45
1	C	1236	PRO	N-CA-C	-7.49	99.44	111.19
1	D	1361	VAL	N-CA-C	7.20	117.80	110.82
1	B	134	ILE	CB-CA-C	-7.19	106.73	114.35
1	D	41	HIS	CA-C-N	7.07	127.03	120.03
1	D	41	HIS	C-N-CA	7.07	127.03	120.03
1	A	1224	GLU	N-CA-C	-7.05	103.02	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1381	LYS	N-CA-C	7.00	118.80	111.03
1	D	1252	ASN	N-CA-C	6.95	125.60	110.80
1	C	1235	ILE	CA-C-N	-6.84	112.92	119.76
1	C	1235	ILE	C-N-CA	-6.84	112.92	119.76
1	A	242	VAL	N-CA-C	6.82	118.23	109.30
1	A	230	GLY	CA-C-N	6.79	128.33	119.84
1	A	230	GLY	C-N-CA	6.79	128.33	119.84
2	P	1817	THR	CA-C-N	6.74	127.01	119.32
2	P	1817	THR	C-N-CA	6.74	127.01	119.32
1	D	1251	ASP	N-CA-C	6.71	121.55	113.23
1	A	1242	LEU	N-CA-C	6.70	122.43	111.37
1	B	230	GLY	CA-C-N	6.61	128.10	119.84
1	B	230	GLY	C-N-CA	6.61	128.10	119.84
1	A	134	ILE	CB-CA-C	-6.59	107.36	114.35
1	D	230	GLY	CA-C-N	6.55	128.03	119.84
1	D	230	GLY	C-N-CA	6.55	128.03	119.84
1	A	1367	ILE	N-CA-C	6.43	117.95	110.62
1	D	1297	VAL	CA-C-N	6.37	125.80	118.85
1	D	1297	VAL	C-N-CA	6.37	125.80	118.85
1	C	1224	GLU	N-CA-C	-6.33	103.91	111.69
1	D	1363	PHE	CA-C-N	-6.33	113.48	122.41
1	D	1363	PHE	C-N-CA	-6.33	113.48	122.41
1	C	272	SER	CA-C-N	6.28	126.83	120.04
1	C	272	SER	C-N-CA	6.28	126.83	120.04
1	C	168	GLY	N-CA-C	-6.25	103.63	112.37
1	B	41	HIS	CA-C-N	6.19	126.15	119.78
1	B	41	HIS	C-N-CA	6.19	126.15	119.78
1	A	1240	ASN	CA-C-N	6.14	132.75	121.70
1	A	1240	ASN	C-N-CA	6.14	132.75	121.70
1	B	1245	VAL	N-CA-C	6.09	116.73	110.82
1	C	361	GLU	N-CA-C	-6.03	104.66	112.68
1	D	361	GLU	N-CA-C	-6.00	103.40	112.04
1	B	1224	GLU	N-CA-C	-5.96	104.36	111.69
1	A	1336	GLN	CA-C-N	5.92	125.46	119.19
1	A	1336	GLN	C-N-CA	5.92	125.46	119.19
1	A	1250	GLY	N-CA-C	5.84	127.03	113.18
2	Q	1817	THR	CA-C-N	5.83	125.45	119.56
2	Q	1817	THR	C-N-CA	5.83	125.45	119.56
1	D	1261	ILE	N-CA-C	5.81	116.59	110.72
1	D	1322	GLN	CB-CA-C	-5.81	101.69	110.92
1	B	1240	ASN	N-CA-C	5.78	123.12	110.80
1	C	126	ASN	CA-C-N	5.77	126.32	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	126	ASN	C-N-CA	5.77	126.32	120.38
1	D	1224	GLU	N-CA-C	-5.76	105.09	111.36
1	C	1235	ILE	N-CA-C	-5.75	96.46	108.88
1	D	1203	VAL	N-CA-C	5.73	112.77	107.56
1	C	1322	GLN	CB-CA-C	-5.70	101.86	110.92
1	D	299	LYS	CA-C-N	5.68	125.69	119.90
1	D	299	LYS	C-N-CA	5.68	125.69	119.90
1	C	1252	ASN	N-CA-C	5.62	118.05	108.67
1	A	92	TYR	CA-C-N	5.58	125.11	119.19
1	A	92	TYR	C-N-CA	5.58	125.11	119.19
1	C	1221	ALA	N-CA-C	5.56	120.07	113.28
1	A	1257	ARG	N-CA-C	5.56	119.54	112.87
1	B	1322	GLN	CB-CA-C	-5.53	102.14	110.92
1	B	1185	VAL	N-CA-C	5.49	120.75	109.34
1	A	1322	GLN	CB-CA-C	-5.47	102.22	110.92
1	D	92	TYR	CA-C-N	5.47	125.14	119.56
1	D	92	TYR	C-N-CA	5.47	125.14	119.56
1	B	1306	ARG	N-CA-C	5.34	118.29	109.85
1	C	230	GLY	CA-C-N	5.30	126.46	119.84
1	C	230	GLY	C-N-CA	5.30	126.46	119.84
1	A	1222	TRP	N-CA-C	5.25	117.01	111.28
1	D	1322	GLN	CA-CB-CG	5.25	124.61	114.10
1	D	226	MET	N-CA-C	5.25	116.82	108.79
1	A	1361	VAL	N-CA-C	5.24	115.45	110.53
1	D	332	MET	CA-C-N	5.22	125.16	119.78
1	D	332	MET	C-N-CA	5.22	125.16	119.78
1	D	119	TYR	N-CA-C	5.21	117.30	109.23
1	D	335	ILE	CA-C-N	5.20	125.00	119.28
1	D	335	ILE	C-N-CA	5.20	125.00	119.28
1	C	242	VAL	N-CA-C	5.19	115.94	108.93
1	D	1362	PHE	CA-C-N	-5.19	113.84	122.92
1	D	1362	PHE	C-N-CA	-5.19	113.84	122.92
1	B	1203	VAL	N-CA-C	5.17	112.67	107.55
1	B	186	ASP	N-CA-C	5.17	118.61	112.72
1	D	247	THR	N-CA-C	5.17	114.96	108.45
1	D	284	ASN	N-CA-C	5.14	120.55	113.97
1	B	1378	ASP	N-CA-C	5.09	116.64	111.14
1	C	1222	TRP	N-CA-C	5.05	117.51	111.71
1	D	123	LEU	N-CA-C	-5.04	106.98	113.23
1	B	49	PHE	CA-C-N	-5.02	113.87	119.19
1	B	49	PHE	C-N-CA	-5.02	113.87	119.19

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	370	ALA	Peptide

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	A	4424	0	4442	23	0
1	B	4437	0	4461	11	0
1	C	4424	0	4444	28	0
1	D	4424	0	4444	24	0
2	P	148	0	140	0	0
2	Q	148	0	140	1	0
3	E	23	0	21	1	0
3	F	23	0	21	6	0
3	G	23	0	21	1	0
3	H	23	0	21	10	0
All	All	18097	0	18155	87	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 2.

All (87) 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:64:TRP:HZ2	3:F:2:GLC:H3	1.27	0.96
1:D:67:ASP:OD2	3:H:2:GLC:O3	1.96	0.83
1:C:64:TRP:CZ2	3:F:2:GLC:H3	2.15	0.80
1:A:1255:SER:OG	1:A:1256:GLN:N	2.17	0.76
1:C:17:LYS:NZ	3:F:1:GLC:O2	2.15	0.73
1:C:1306:ARG:HA	1:C:1306:ARG:NE	2.05	0.71
1:D:157:TYR:HB2	3:H:2:GLC:O5	1.95	0.67
1:A:17:LYS:NZ	3:E:1:GLC:O2	2.23	0.65
1:D:46:GLU:HG2	1:D:64:TRP:CH2	2.33	0.64
1:C:68:ARG:HB2	1:C:68:ARG:HH11	1.63	0.64
1:A:364:LYS:HA	1:A:364:LYS:HE2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:GLU:OE2	3:F:2:GLC:O4	2.19	0.60
1:D:157:TYR:CD2	3:H:1:GLC:H61	2.38	0.59
1:C:104:LYS:NZ	1:C:1254:ASP:OD2	2.31	0.58
1:A:41:HIS:ND1	1:A:41:HIS:O	2.41	0.54
1:C:75:SER:HB3	1:C:1244:ALA:HB1	1.90	0.53
1:A:1255:SER:HB3	1:A:1257:ARG:H	1.74	0.53
1:A:1257:ARG:O	1:A:1257:ARG:HG2	2.07	0.53
1:A:1240:ASN:N	1:A:1241:THR:HA	2.24	0.52
1:C:68:ARG:HD3	1:C:72:TYR:CZ	2.45	0.52
1:D:183:VAL:HG22	1:D:185:VAL:H	1.75	0.52
1:D:351:ASN:HB3	1:D:357:GLN:HG2	1.92	0.52
1:D:113:GLU:OE1	3:H:1:GLC:O2	2.24	0.52
1:D:130:THR:OG1	1:D:132:GLU:OE1	2.28	0.51
1:C:260:PHE:HB3	1:C:332:MET:CG	2.40	0.51
1:D:17:LYS:HZ1	3:H:1:GLC:C1	2.24	0.50
1:A:1223:ARG:NH1	1:A:1353:ILE:O	2.45	0.50
1:D:128:PRO:HG3	1:D:226:MET:HE1	1.94	0.50
1:A:1241:THR:HG21	1:A:1265:ILE:HG22	1.93	0.50
1:C:68:ARG:HD3	1:C:72:TYR:CE1	2.46	0.50
1:B:1230:ILE:HG23	1:B:1236:PRO:HD2	1.94	0.49
1:D:1271:VAL:HG22	1:D:1349:ALA:HB1	1.94	0.49
1:A:1272:VAL:O	1:A:1276:ARG:HG2	2.14	0.47
1:C:369:ASN:OD1	1:C:370:ALA:N	2.48	0.47
1:C:1294:PHE:O	1:C:1318:GLN:HB2	2.15	0.46
1:A:1298:PRO:HB2	1:A:1305:LEU:HB2	1.97	0.46
1:C:128:PRO:HG3	1:C:226:MET:HE1	1.97	0.46
1:D:147:SER:HB3	1:D:224:THR:HG22	1.98	0.46
1:C:260:PHE:HB3	1:C:332:MET:HG3	1.98	0.46
1:C:1256:GLN:O	1:C:1259:THR:N	2.45	0.46
1:C:68:ARG:HD3	1:C:72:TYR:OH	2.16	0.46
1:C:1271:VAL:HG22	1:C:1349:ALA:HB1	1.98	0.45
1:D:157:TYR:CE1	3:H:1:GLC:H4	2.51	0.45
1:C:1306:ARG:HA	1:C:1306:ARG:HE	1.81	0.45
1:D:156:PRO:HG2	3:H:2:GLC:H61	1.99	0.45
1:C:155:GLU:HB3	3:F:2:GLC:O6	2.17	0.45
1:D:1242:LEU:HD12	1:D:1242:LEU:HA	1.71	0.45
1:A:1253:THR:OG1	1:A:1254:ASP:N	2.49	0.45
1:C:1256:GLN:C	1:C:1258:LEU:N	2.72	0.45
1:D:162:LEU:HD23	1:D:197:LEU:HG	1.97	0.45
1:B:17:LYS:NZ	3:G:1:GLC:O2	2.25	0.45
1:A:365:ASP:C	1:A:365:ASP:OD1	2.59	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:157:TYR:CD1	3:H:1:GLC:H4	2.51	0.44
1:C:260:PHE:HA	1:C:330:GLU:O	2.18	0.44
1:B:365:ASP:OD1	1:B:365:ASP:C	2.61	0.44
1:A:1239:ALA:HB1	1:A:1243:LEU:HB3	2.00	0.44
1:A:1184:SER:OG	1:A:1185:VAL:N	2.50	0.44
1:B:41:HIS:O	1:B:41:HIS:ND1	2.51	0.44
1:A:242:VAL:HG12	1:A:244:TYR:HB3	2.00	0.43
1:D:17:LYS:NZ	3:H:1:GLC:C1	2.82	0.43
1:D:147:SER:O	1:D:224:THR:HA	2.18	0.43
1:A:99:VAL:HG21	1:A:109:PRO:HD3	1.99	0.43
1:C:157:TYR:HB2	3:F:2:GLC:O5	2.19	0.43
1:C:260:PHE:HB3	1:C:332:MET:HG2	2.00	0.43
1:D:67:ASP:OD1	1:D:68:ARG:N	2.51	0.43
1:B:1211:LEU:HD12	1:B:1211:LEU:HA	1.85	0.42
1:C:1240:ASN:HA	1:C:1243:LEU:HB2	2.01	0.42
1:D:249:LEU:HA	1:D:250:PRO:HD3	1.91	0.42
1:A:351:ASN:HB3	1:A:357:GLN:HG2	2.00	0.42
1:A:1192:LEU:HD11	1:A:1235:ILE:HD12	2.02	0.42
1:B:1299:THR:O	1:B:1299:THR:HG22	2.20	0.42
1:C:1250:GLY:HA2	1:C:1364:LYS:HB3	2.02	0.41
1:D:1242:LEU:HD11	1:D:1361:VAL:HG11	2.01	0.41
1:C:351:ASN:HB3	1:C:357:GLN:HG2	2.02	0.41
1:B:11:ILE:HG21	1:B:22:LEU:HD21	2.03	0.41
1:B:99:VAL:HG21	1:B:109:PRO:HD3	2.03	0.41
1:A:46:GLU:HG2	1:A:64:TRP:CZ2	2.55	0.41
1:B:1272:VAL:O	1:B:1276:ARG:HG2	2.20	0.41
1:D:1248:MET:HE2	1:D:1253:THR:HA	2.02	0.41
1:A:11:ILE:HG21	1:A:22:LEU:HD21	2.03	0.41
1:D:113:GLU:OE1	3:H:1:GLC:C2	2.69	0.40
1:A:360:ASP:O	1:A:364:LYS:HG2	2.22	0.40
2:Q:1828:ARG:HB3	2:Q:1829:PRO:HD3	2.01	0.40
1:B:46:GLU:HG2	1:B:64:TRP:CZ2	2.56	0.40
1:A:1306:ARG:NE	1:A:1306:ARG:HA	2.35	0.40
1:C:1242:LEU:HD21	1:C:1268:LEU:HD23	2.02	0.40
1:B:1365:LYS:C	1:B:1367:ILE:H	2.29	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	A	564/576 (98%)	546 (97%)	13 (2%)	5 (1%)	14	47
1	B	566/576 (98%)	548 (97%)	17 (3%)	1 (0%)	43	73
1	C	564/576 (98%)	545 (97%)	19 (3%)	0	100	100
1	D	564/576 (98%)	544 (96%)	20 (4%)	0	100	100
2	P	16/18 (89%)	16 (100%)	0	0	100	100
2	Q	16/18 (89%)	16 (100%)	0	0	100	100
All	All	2290/2340 (98%)	2215 (97%)	69 (3%)	6 (0%)	36	65

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	371	ALA
1	A	1239	ALA
1	A	1366	THR
1	B	1185	VAL
1	A	1251	ASP
1	A	1240	ASN

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	466/472 (99%)	466 (100%)	0	100	100
1	B	467/472 (99%)	467 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	466/472 (99%)	464 (100%)	2 (0%)	84	80
1	D	466/472 (99%)	464 (100%)	2 (0%)	84	80
2	P	15/15 (100%)	15 (100%)	0	100	100
2	Q	15/15 (100%)	15 (100%)	0	100	100
All	All	1895/1918 (99%)	1891 (100%)	4 (0%)	87	85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	68	ARG
1	C	1256	GLN
1	D	46	GLU
1	D	1363	PHE

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

Mol	Chain	Res	Type
1	A	74	GLN
1	A	126	ASN
1	A	1336	GLN
1	B	74	GLN
1	B	1232	GLN
1	B	1336	GLN
1	D	74	GLN
1	D	1232	GLN
1	D	1318	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	$\# Z > 2$
3	GLC	E	1	3	12,12,12	0.55	0	17,17,17	0.69	0
3	GLC	E	2	3	11,11,12	0.61	0	15,15,17	0.73	0
3	GLC	F	1	3	12,12,12	0.55	0	17,17,17	0.84	0
3	GLC	F	2	3	11,11,12	0.72	0	15,15,17	0.93	1 (6%)
3	GLC	G	1	3	12,12,12	0.55	0	17,17,17	0.57	0
3	GLC	G	2	3	11,11,12	0.64	0	15,15,17	0.60	0
3	GLC	H	1	3	12,12,12	0.72	0	17,17,17	1.45	4 (23%)
3	GLC	H	2	3	11,11,12	0.89	0	15,15,17	1.22	2 (13%)

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	GLC	E	1	3	-	0/2/22/22	0/1/1/1
3	GLC	E	2	3	-	0/2/19/22	0/1/1/1
3	GLC	F	1	3	-	0/2/22/22	0/1/1/1
3	GLC	F	2	3	-	0/2/19/22	0/1/1/1
3	GLC	G	1	3	-	0/2/22/22	0/1/1/1
3	GLC	G	2	3	-	0/2/19/22	0/1/1/1
3	GLC	H	1	3	-	0/2/22/22	0/1/1/1
3	GLC	H	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	1	GLC	C1-O5-C5	-3.55	106.78	113.65
3	H	1	GLC	O2-C2-C3	-2.49	104.51	110.38
3	F	2	GLC	C6-C5-C4	-2.43	107.06	113.02
3	H	2	GLC	C6-C5-C4	-2.33	107.30	113.02
3	H	2	GLC	O5-C5-C6	2.26	112.07	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	1	GLC	C3-C4-C5	2.08	114.01	110.23
3	H	1	GLC	O5-C5-C6	2.07	111.56	106.44

There are no chirality outliers.

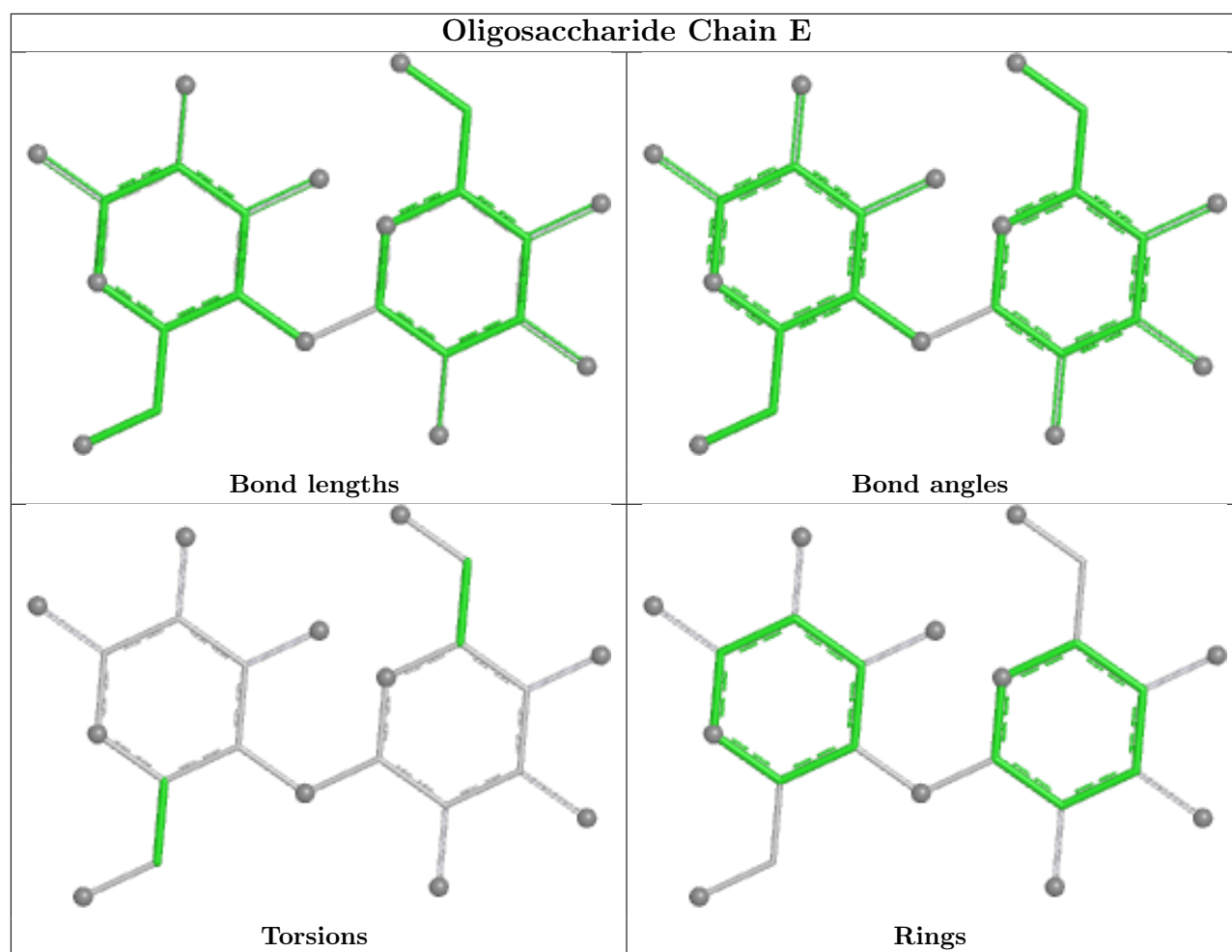
There are no torsion outliers.

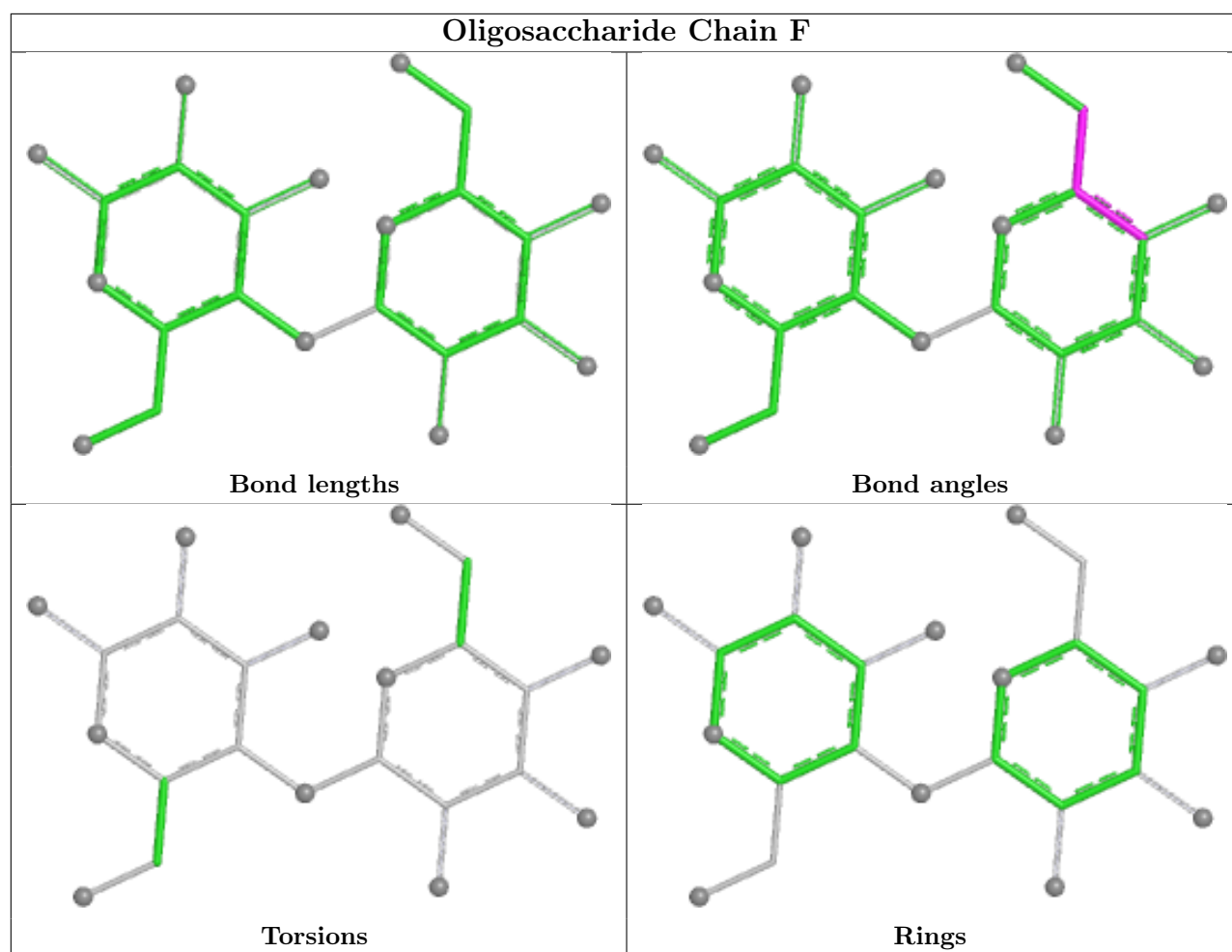
There are no ring outliers.

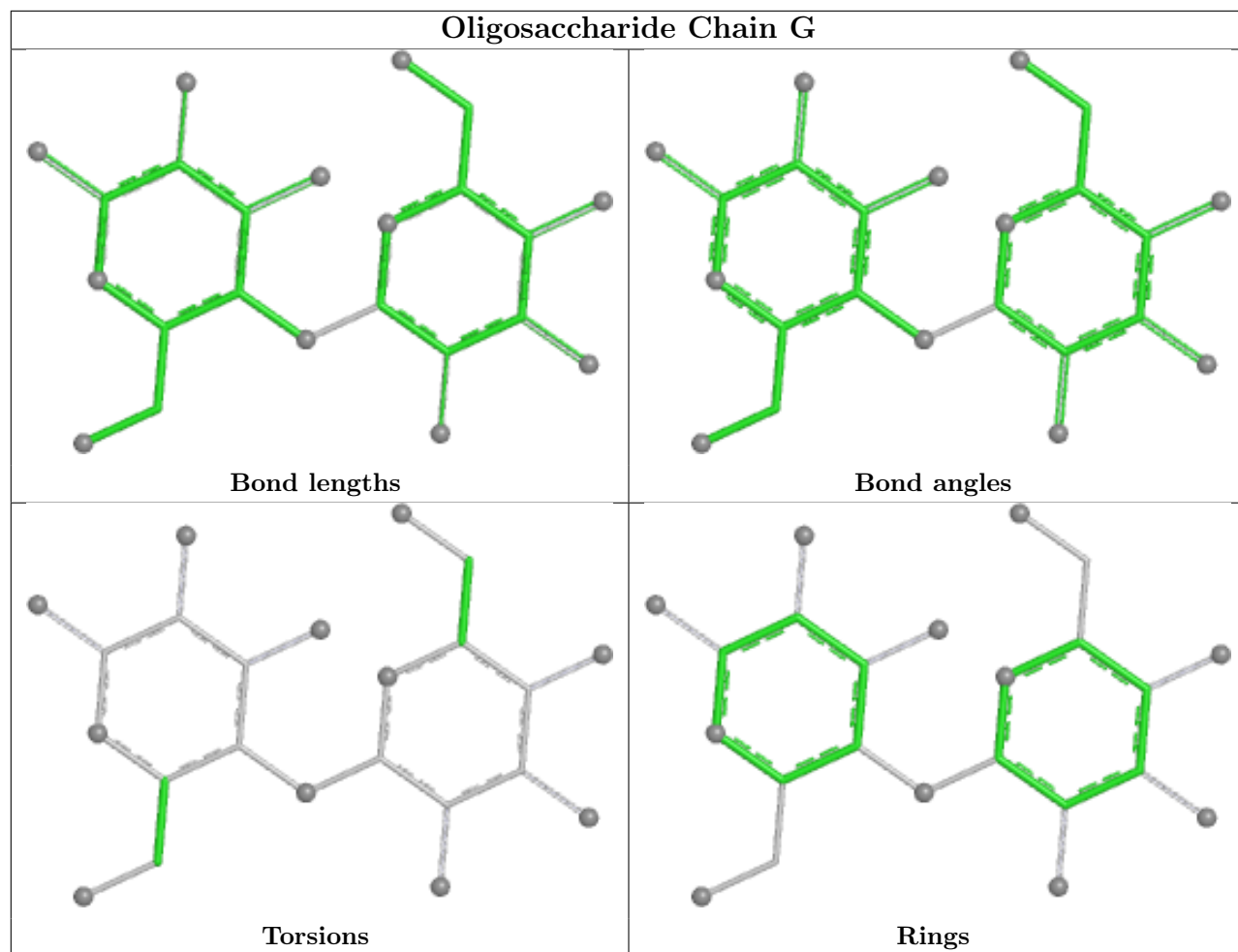
6 monomers are involved in 18 short contacts:

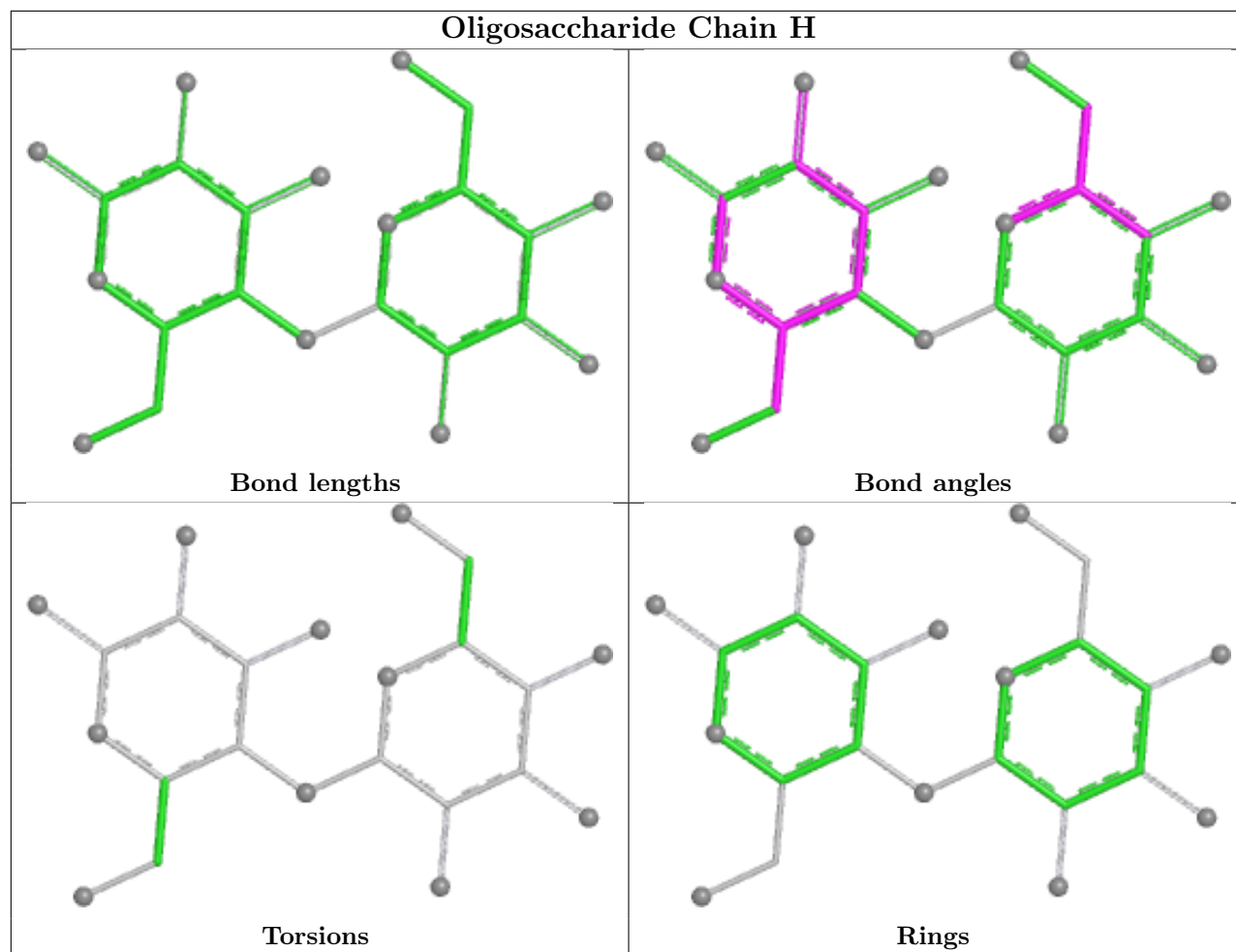
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	2	GLC	5	0
3	E	1	GLC	1	0
3	G	1	GLC	1	0
3	H	1	GLC	7	0
3	H	2	GLC	3	0
3	F	1	GLC	1	0

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	568/576 (98%)	0.40	34 (5%) 27 16	17, 35, 74, 96	0
1	B	570/576 (98%)	0.38	31 (5%) 31 18	15, 35, 76, 107	0
1	C	568/576 (98%)	0.70	22 (3%) 43 23	17, 88, 122, 150	0
1	D	568/576 (98%)	1.10	81 (14%) 6 5	18, 116, 185, 210	0
2	P	18/18 (100%)	0.76	3 (16%) 4 4	57, 71, 83, 91	0
2	Q	18/18 (100%)	0.44	0 100 100	50, 63, 90, 91	0
All	All	2310/2340 (98%)	0.64	171 (7%) 20 13	15, 47, 155, 210	0

All (171) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1244	ALA	7.3
1	D	111	ALA	7.2
1	A	1240	ASN	6.4
1	D	1238	ASP	6.4
1	A	1236	PRO	6.3
1	D	1243	LEU	5.1
1	A	1243	LEU	4.9
1	B	1374	ARG	4.6
1	A	1238	ASP	4.6
1	D	110	ILE	4.5
1	D	1251	ASP	4.4
1	B	1244	ALA	4.3
1	C	1238	ASP	4.2
1	D	112	VAL	4.2
1	A	1242	LEU	4.2
1	A	1251	ASP	4.2
1	D	303	ALA	4.2
1	B	1250	GLY	4.1
2	P	1831	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	1239	ALA	4.1
1	C	1234	ALA	4.1
1	A	1237	VAL	4.0
1	B	371	ALA	3.9
1	D	262	GLY	3.9
1	D	281	PHE	3.7
1	D	326	ALA	3.7
1	D	115	LEU	3.6
1	B	1234	ALA	3.6
1	B	1299	THR	3.5
1	B	324	GLU	3.5
1	A	1383	SER	3.5
1	B	1366	THR	3.5
1	B	1239	ALA	3.4
1	D	287	LEU	3.4
1	D	228	ILE	3.4
1	B	1249	ASN	3.4
1	D	286	LEU	3.4
1	B	1379	MET	3.4
1	C	1374	ARG	3.3
1	D	331	ILE	3.3
1	B	1240	ASN	3.3
1	A	1183	GLU	3.3
1	A	1241	THR	3.3
1	C	118	ILE	3.2
1	A	372	ALA	3.2
1	B	366	ALA	3.2
1	D	304	VAL	3.2
1	D	230	GLY	3.2
1	B	1245	VAL	3.2
1	D	235	SER	3.2
1	B	1237	VAL	3.1
1	D	1374	ARG	3.1
1	D	322	THR	3.1
1	C	168	GLY	3.1
1	C	1237	VAL	3.0
1	A	1249	ASN	3.0
1	A	1245	VAL	3.0
1	D	1297	VAL	3.0
1	D	1307	SER	3.0
1	B	1235	ILE	3.0
1	D	263	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	282	LEU	2.9
1	D	1237	VAL	2.8
1	D	301	LEU	2.8
1	D	280	GLU	2.8
1	D	159	THR	2.8
1	D	260	PHE	2.8
1	D	18	GLY	2.8
1	B	1238	ASP	2.8
1	B	1274	ARG	2.8
1	A	366	ALA	2.8
1	B	1251	ASP	2.7
1	D	332	MET	2.7
1	A	1365	LYS	2.7
1	D	248	VAL	2.7
1	D	231	PRO	2.7
1	A	1254	ASP	2.6
1	D	249	LEU	2.6
1	B	1365	LYS	2.6
1	D	157	TYR	2.6
1	B	1368	GLY	2.6
1	A	1374	ARG	2.6
1	B	1236	PRO	2.6
1	B	1253	THR	2.5
1	C	157	TYR	2.5
1	B	1269	GLN	2.5
1	D	278	ALA	2.5
1	D	229	ASN	2.5
1	B	1378	ASP	2.5
1	D	257	SER	2.5
1	A	1376	LEU	2.5
1	D	292	LEU	2.5
1	D	310	GLU	2.4
1	D	64	TRP	2.4
1	D	232	TRP	2.4
1	C	301	LEU	2.4
1	C	366	ALA	2.4
1	D	305	ALA	2.4
1	C	1243	LEU	2.4
1	D	363	LEU	2.4
1	A	1256	GLN	2.4
1	A	1327	SER	2.4
1	B	365	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	1248	MET	2.4
1	A	369	ASN	2.3
1	D	22	LEU	2.3
1	A	361	GLU	2.3
1	D	117	LEU	2.3
1	D	162	LEU	2.3
1	D	1253	THR	2.3
1	C	217	ALA	2.3
1	D	1239	ALA	2.3
1	B	1367	ILE	2.3
1	C	227	THR	2.3
1	D	328	LYS	2.3
1	D	4	ILE	2.3
1	D	94	PHE	2.3
1	D	1257	ARG	2.3
1	D	1367	ILE	2.3
1	A	371	ALA	2.3
1	B	367	GLN	2.3
1	C	113	GLU	2.3
1	D	349	VAL	2.3
1	C	358	THR	2.2
1	D	227	THR	2.2
1	A	1305	LEU	2.2
1	A	370	ALA	2.2
1	D	1183	GLU	2.2
1	C	1305	LEU	2.2
1	D	123	LEU	2.2
1	A	46	GLU	2.2
1	C	15	GLY	2.2
1	A	374	PHE	2.2
1	D	212	TYR	2.2
1	D	99	VAL	2.2
1	A	1187	GLU	2.2
1	D	222	GLY	2.2
1	C	17	LYS	2.2
1	D	1233	TRP	2.2
1	D	118	ILE	2.2
1	C	363	LEU	2.2
1	D	1244	ALA	2.1
1	D	244	TYR	2.1
1	D	127	PRO	2.1
1	D	216	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	334	ASN	2.1
1	A	1186	CYS	2.1
1	D	246	VAL	2.1
1	D	364	LYS	2.1
1	C	19	TYR	2.1
1	A	1250	GLY	2.1
1	D	215	ALA	2.1
2	P	1827	ALA	2.1
1	C	18	GLY	2.1
1	D	1250	GLY	2.1
1	D	79	ALA	2.1
1	B	1256	GLN	2.1
1	A	323	MET	2.1
1	D	259	PRO	2.1
1	D	190	ALA	2.1
1	C	286	LEU	2.1
1	D	168	GLY	2.0
1	D	1365	LYS	2.0
1	D	178	TYR	2.0
1	D	239	THR	2.0
1	C	1251	ASP	2.0
1	B	1370	VAL	2.0
1	D	258	LYS	2.0
1	D	128	PRO	2.0
2	P	1814	TYR	2.0
1	B	1185	VAL	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.

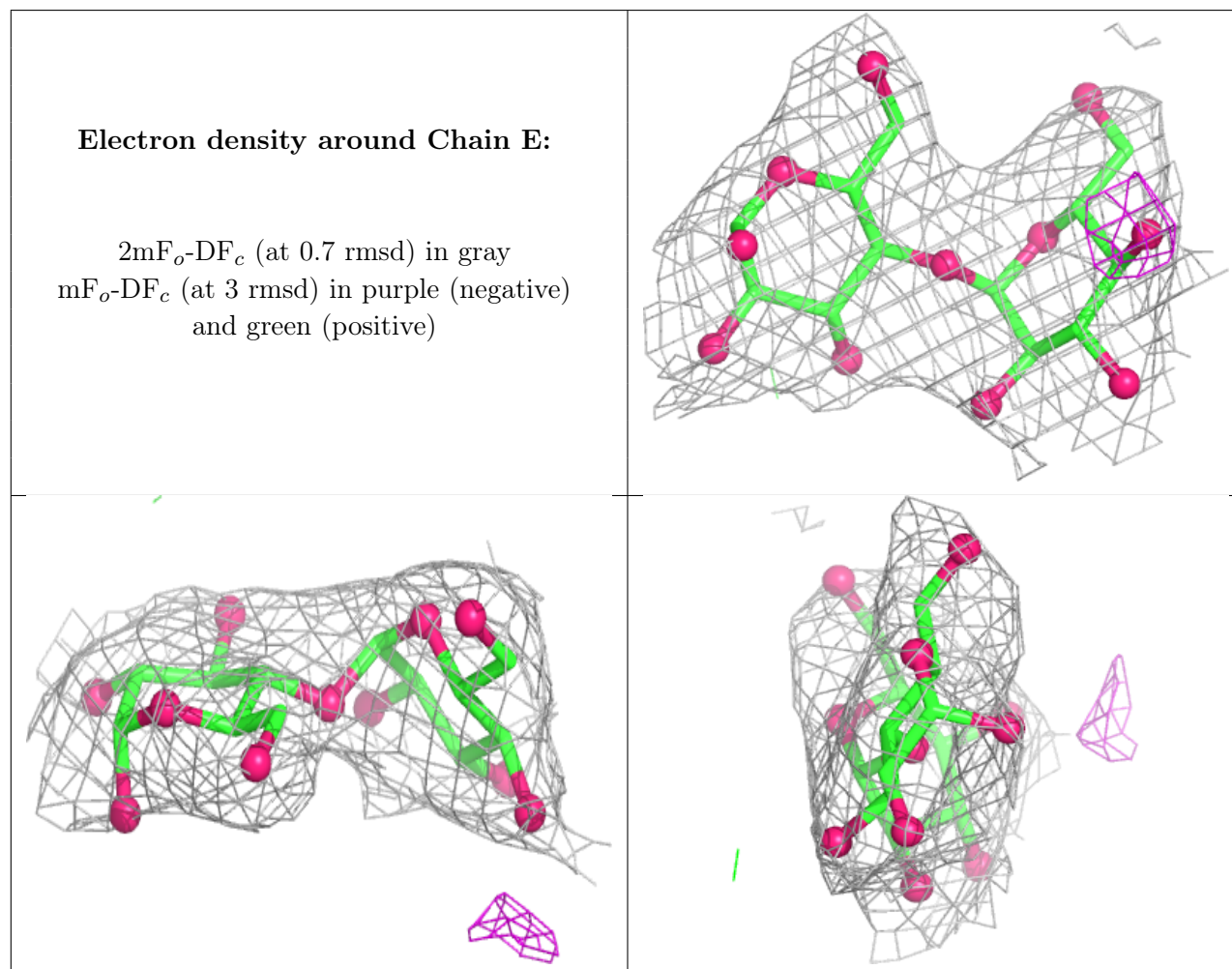
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GLC	E	1	12/12	-	-	14,15,16,17	0
3	GLC	E	2	11/12	-	-	14,15,16,16	0

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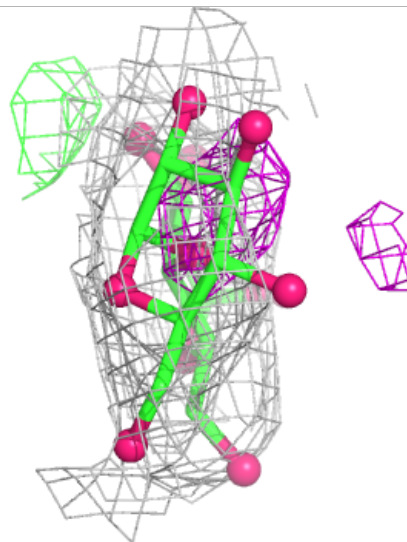
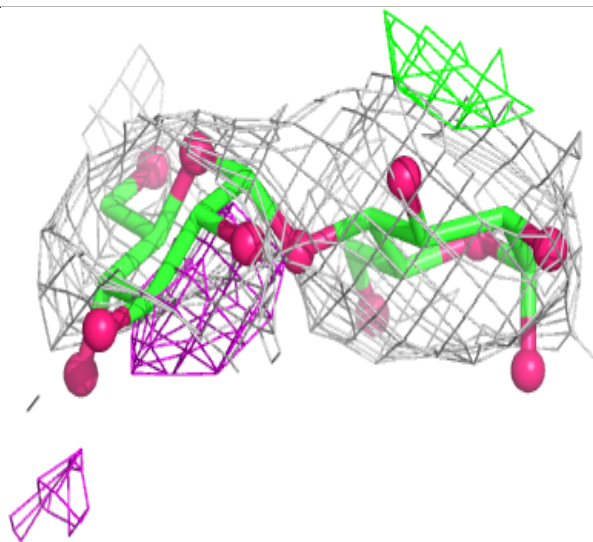
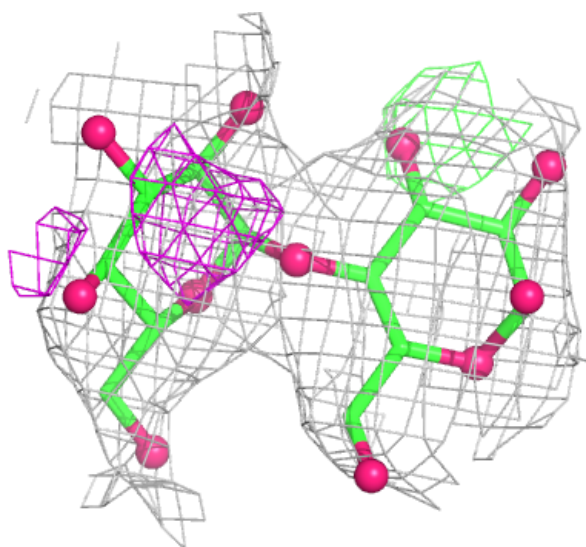
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GLC	F	1	12/12	-	-	63,66,69,69	0
3	GLC	F	2	11/12	-	-	57,60,62,62	0
3	GLC	H	2	11/12	0.50	0.15	84,90,94,94	0
3	GLC	H	1	12/12	0.54	0.18	95,100,104,104	0
3	GLC	G	1	12/12	0.95	0.10	14,16,17,17	0
3	GLC	G	2	11/12	0.95	0.10	14,15,15,16	0

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.



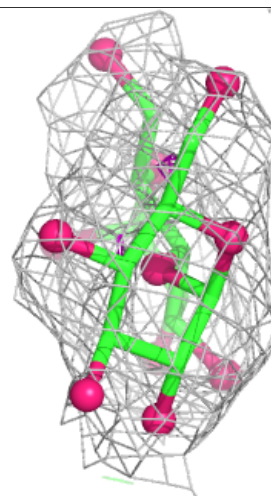
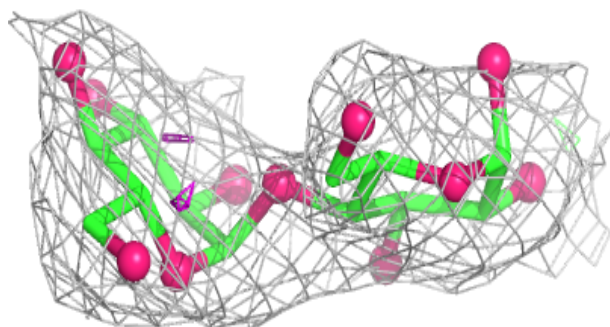
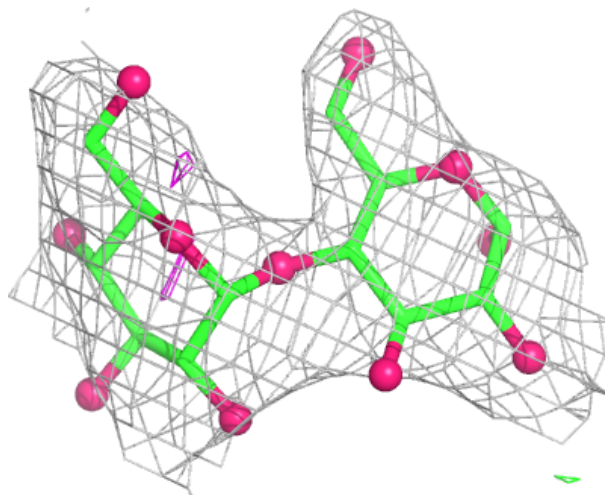
Electron density around Chain F:

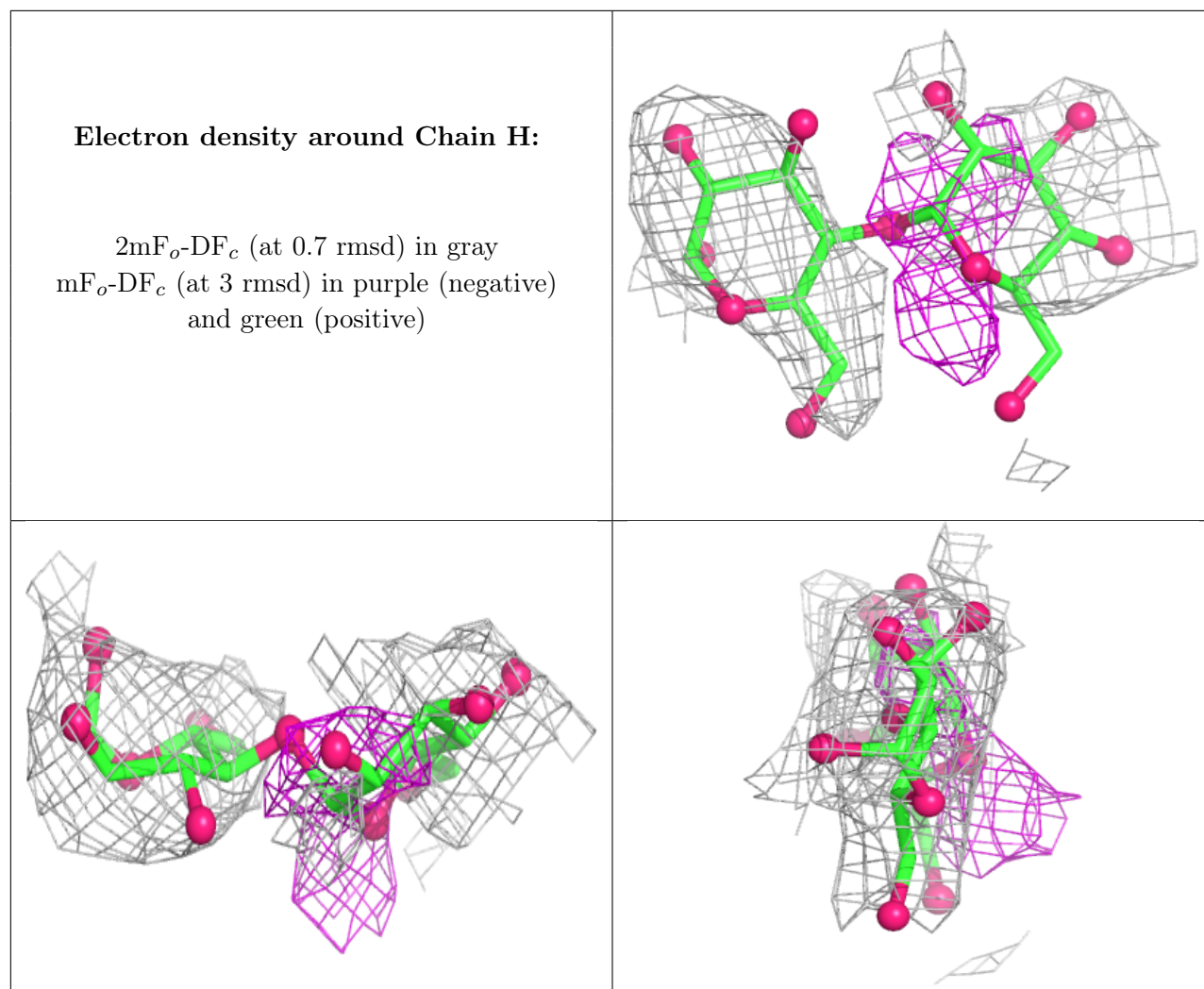
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.