wwPDB X-ray Structure Validation Summary Report (i)

Aug 9, 2020 – 12:43 AM BST

PDB ID	:	4I9X
Title	:	Crystal structure of human cytomegalovirus glycoprotein UL141 targeting the death receptor TRAIL-R2
Authors	:	Nemcovicova, I.; Zajonc, D.M.
Deposited on	:	2012-12-05
Resolution	:	2.10 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.
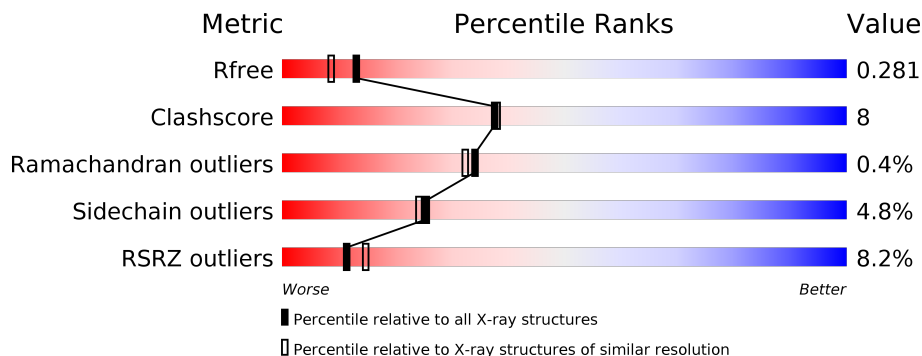
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	215	7% / 70% / 15% / • / 13%
1	B	215	11% / 70% / 14% / • / 13%
2	C	127	2% / 69% / 12% / • / 17%
2	D	127	6% / 70% / 15% / 15%
3	E	2	50% / 50%
3	F	2	100%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4933 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 Protein UL141.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	Se	0	0	0
			1500	959	261	270	4	6			
1	B	188	Total	C	N	O	S	Se	0	0	0
			1506	963	263	270	4	6			

- Molecule 2 is a protein called Tumor necrosis factor receptor superfamily member 10B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	105	Total	C	N	O	S	Se	0	1	0
			801	479	144	162	14	2			
2	D	108	Total	C	N	O	S	Se	0	0	0
			812	486	147	163	14	2			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		
5	A	1	Total	Ca	0	0
			1	1		
5	D	2	Total	Ca	0	0
			2	2		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Na	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	79	Total	O	0	0
			79	79		
7	B	74	Total	O	0	0
			74	74		

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| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	40	Total 40	O 40	0	0
7	D	46	Total 46	O 46	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.
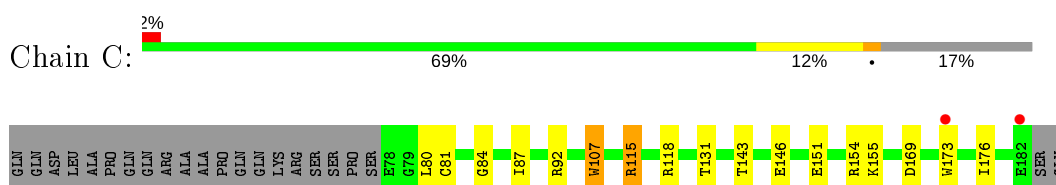
- Molecule 1: Protein UL141
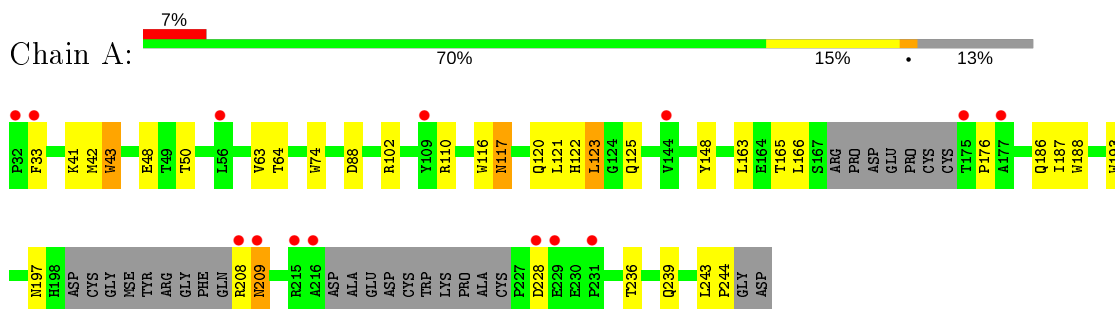
- Molecule 1: Protein UL141
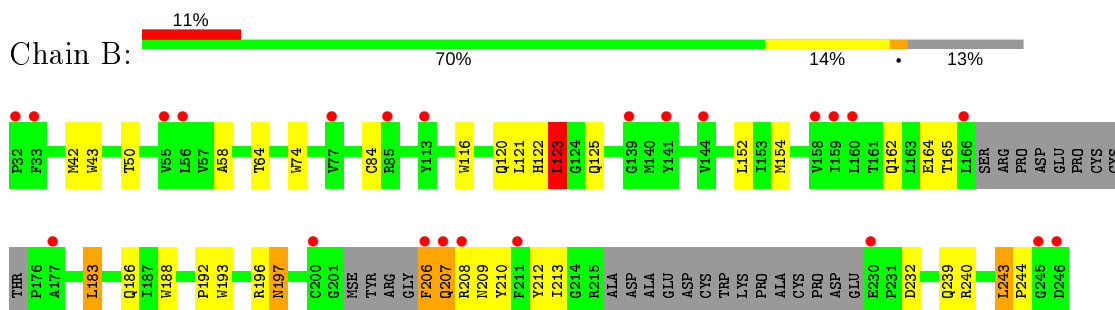
- Molecule 2: Tumor necrosis factor receptor superfamily member 10B

- Molecule 2: Tumor necrosis factor receptor superfamily member 10B
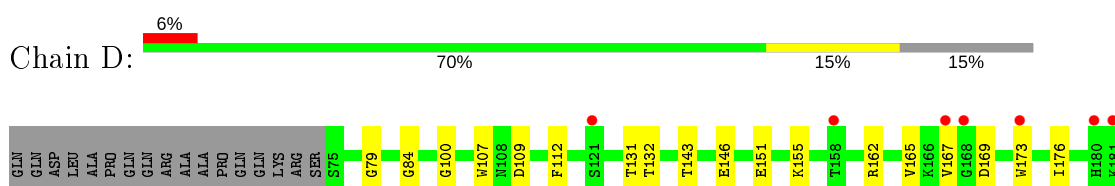
E182
SER
GLY

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

Chain E:

50%   50%

NAG1
NAG2

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

Chain F:

100%

NAG1
NAG2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	67.92Å 97.04Å 141.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.83 – 2.10 19.83 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.83-2.10) 99.6 (19.83-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.42 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.6.0104	Depositor
R, R_{free}	0.223 , 0.274 0.227 , 0.281	Depositor DCC
R_{free} test set	994 reflections (1.80%)	wwPDB-VP
Wilson B-factor (Å²)	41.3	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol}(e/Å³), B_{sol}(Å²)	0.37 , 54.0	EDS
L-test for twinning [2]	$<|L|> = 0.49$, $<L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4933	wwPDB-VP
Average B, all atoms (Å²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ 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: NA, CA, 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	0.78	3/1535 (0.2%)	0.73	1/2080 (0.0%)
1	B	0.82	3/1541 (0.2%)	0.75	1/2086 (0.0%)
2	C	0.70	2/815 (0.2%)	0.65	0/1101
2	D	0.77	2/828 (0.2%)	0.72	0/1121
All	All	0.78	10/4719 (0.2%)	0.72	2/6388 (0.0%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	188	TRP	CD2-CE2	6.60	1.49	1.41
1	B	188	TRP	CD2-CE2	6.22	1.48	1.41
1	A	43	TRP	CD2-CE2	5.96	1.48	1.41
2	D	173	TRP	CD2-CE2	5.88	1.48	1.41
1	B	43	TRP	CD2-CE2	5.43	1.47	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	123	LEU	CA-CB-CG	7.15	131.75	115.30
1	A	123	LEU	CA-CB-CG	6.50	130.24	115.30

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	A	1500	0	1434	23	0
1	B	1506	0	1435	29	0
2	C	801	0	705	13	0
2	D	812	0	710	11	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
4	A	14	0	13	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	D	2	0	0	0	0
6	B	1	0	0	0	0
7	A	79	0	0	2	0
7	B	74	0	0	0	0
7	C	40	0	0	2	0
7	D	46	0	0	3	0
All	All	4933	0	4347	70	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 8.

The worst 5 of 70 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:B:120:GLN:HE22	1:B:125:GLN:HE21	1.09	0.99
2:C:115:ARG:HG3	2:C:115:ARG:HH11	1.31	0.93
2:D:162:ARG:HG3	7:D:322:HOH:O	1.69	0.92
1:A:120:GLN:HE22	1:A:125:GLN:HE21	1.15	0.91
2:C:169:ASP:HA	2:C:176:ILE:HG22	1.57	0.86

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	179/215 (83%)	175 (98%)	4 (2%)	0	100	100
1	B	180/215 (84%)	168 (93%)	10 (6%)	2 (1%)	14	9
2	C	104/127 (82%)	100 (96%)	4 (4%)	0	100	100
2	D	106/127 (84%)	100 (94%)	6 (6%)	0	100	100
All	All	569/684 (83%)	543 (95%)	24 (4%)	2 (0%)	34	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	183	LEU
1	B	207	GLN

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	160/181 (88%)	150 (94%)	10 (6%)	18	15
1	B	159/181 (88%)	153 (96%)	6 (4%)	33	34
2	C	91/112 (81%)	89 (98%)	2 (2%)	52	57
2	D	92/112 (82%)	86 (94%)	6 (6%)	17	14
All	All	502/586 (86%)	478 (95%)	24 (5%)	25	24

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	123	LEU
1	B	208	ARG
2	D	176	ILE
1	B	197	ASN
1	B	206	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	ASN
1	B	197	ASN
1	B	108	GLN
1	A	186	GLN
1	A	239	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

4 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	NAG	E	1	1,3	14,14,15	0.54	0	17,19,21	0.94	0
3	NAG	E	2	3	14,14,15	0.71	0	17,19,21	1.42	2 (11%)
3	NAG	F	1	1,3	14,14,15	0.57	0	17,19,21	1.23	2 (11%)
3	NAG	F	2	3	14,14,15	0.66	0	17,19,21	1.22	2 (11%)

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	E	1	1,3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	2	NAG	C4-C3-C2	3.95	116.81	111.02
3	F	2	NAG	C4-C3-C2	3.45	116.08	111.02
3	F	1	NAG	O5-C5-C6	3.11	112.08	107.20
3	F	1	NAG	C2-N2-C7	-2.67	119.10	122.90
3	E	2	NAG	C3-C4-C5	2.56	114.80	110.24

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	F	1	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.

Oligosaccharide Chain E

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain F
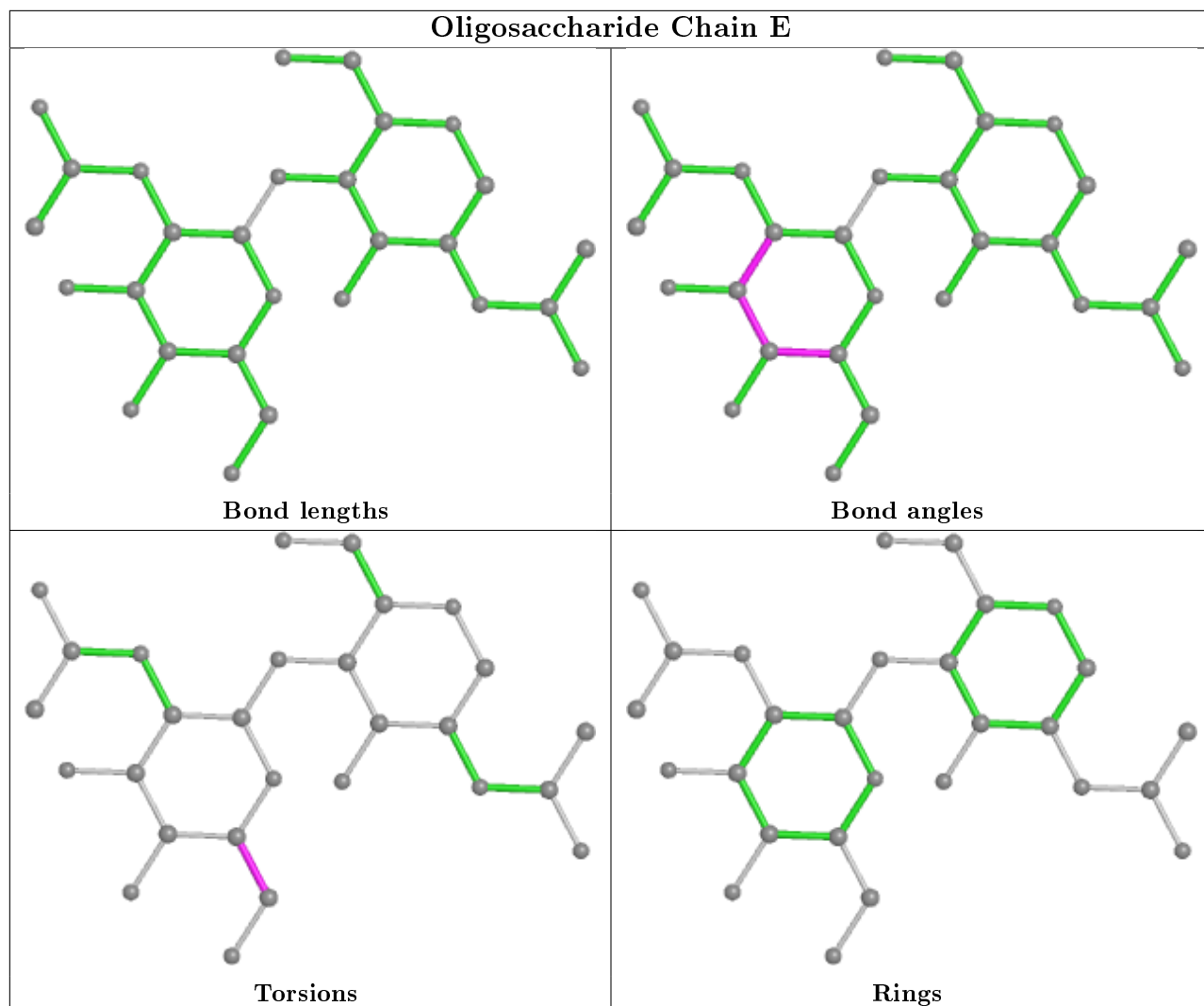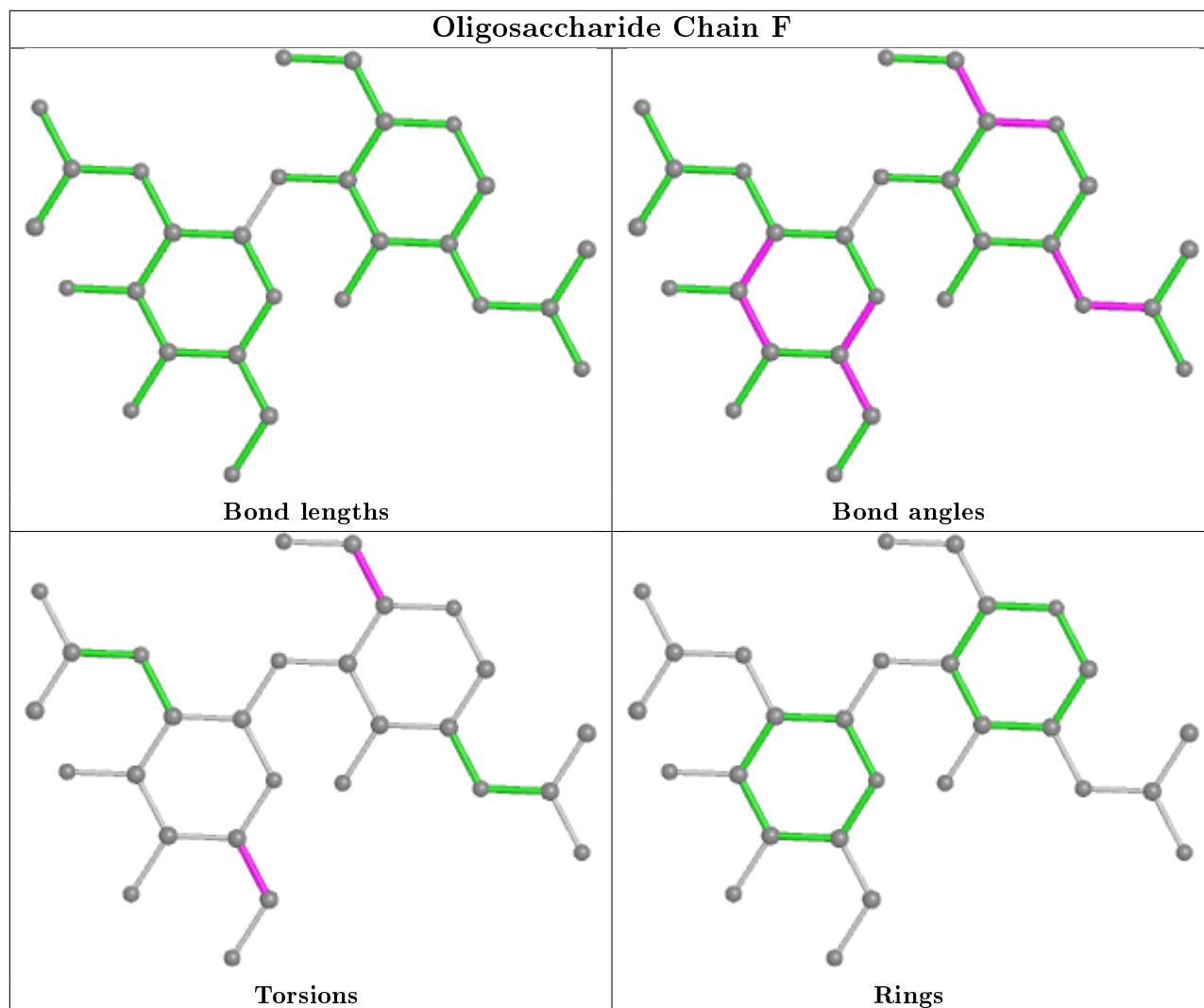
5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
4	NAG	A	303	1	14,14,15	0.61	0	17,19,21	1.66	2 (11%)

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	A	303	1	-	0/6/23/26	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(^{o})	Ideal(^{o})
4	A	303	NAG	C4-C3-C2	5.04	118.40	111.02
4	A	303	NAG	O5-C1-C2	-2.34	107.60	111.29

There are no chirality outliers.

There are no torsion outliers.

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	181/215 (84%)	0.33	14 (7%)	13	17	30, 45, 83, 99	0
1	B	182/215 (84%)	0.42	23 (12%)	3	5	28, 46, 84, 103	0
2	C	103/127 (81%)	0.26	2 (1%)	66	71	32, 53, 80, 101	0
2	D	106/127 (83%)	0.41	8 (7%)	14	18	33, 51, 85, 109	1 (0%)
All	All	572/684 (83%)	0.36	47 (8%)	11	15	28, 48, 85, 109	1 (0%)

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	200	CYS	5.9
1	A	216	ALA	5.6
1	A	33	PHE	5.5
1	B	245	GLY	5.2
1	A	109	TYR	4.9

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.
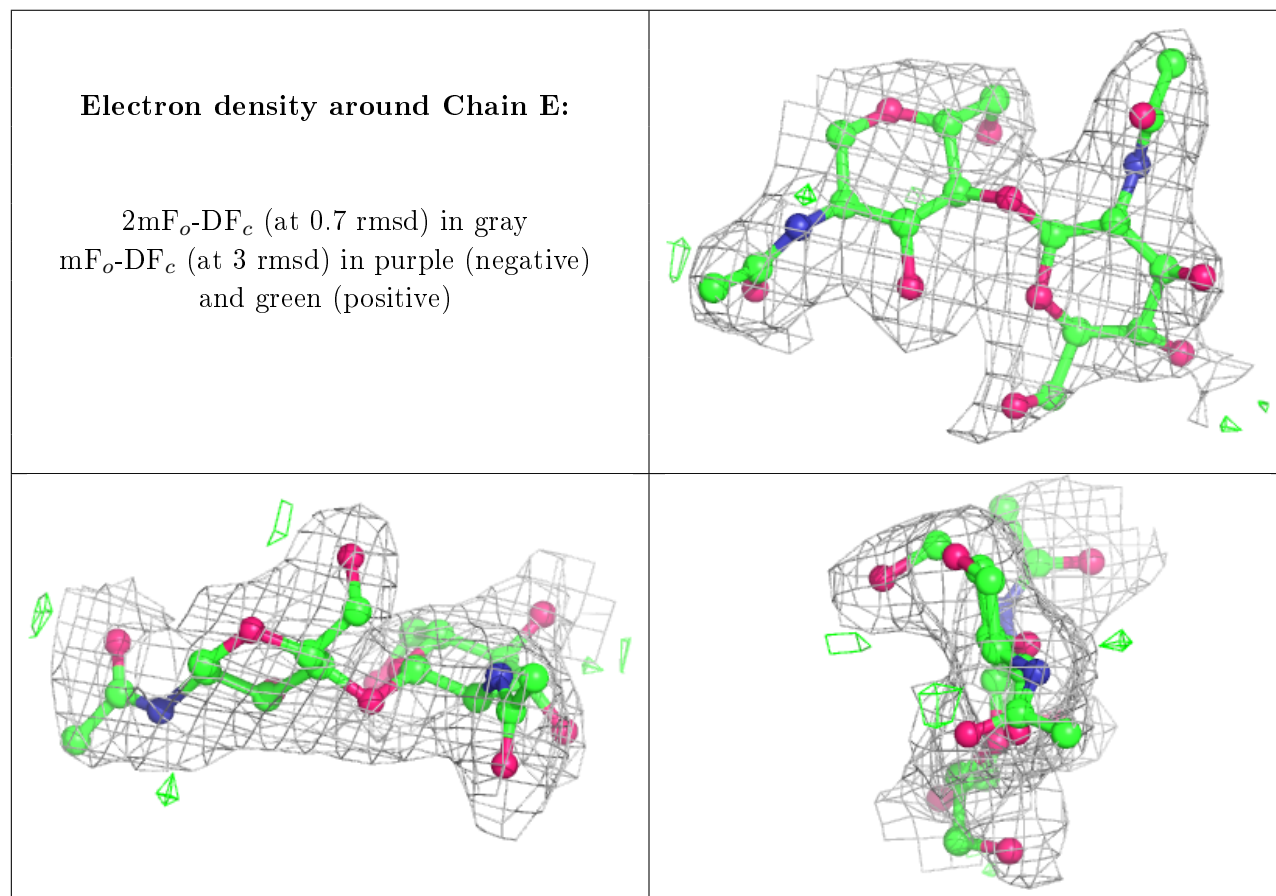
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	F	2	14/15	0.80	0.33	54,70,85,88	0
3	NAG	E	2	14/15	0.85	0.29	50,75,84,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å²)	Q<0.9
3	NAG	F	1	14/15	0.94	0.10	42,52,59,62	0
3	NAG	E	1	14/15	0.96	0.10	46,52,58,60	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:

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

Electron density around Chain F:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
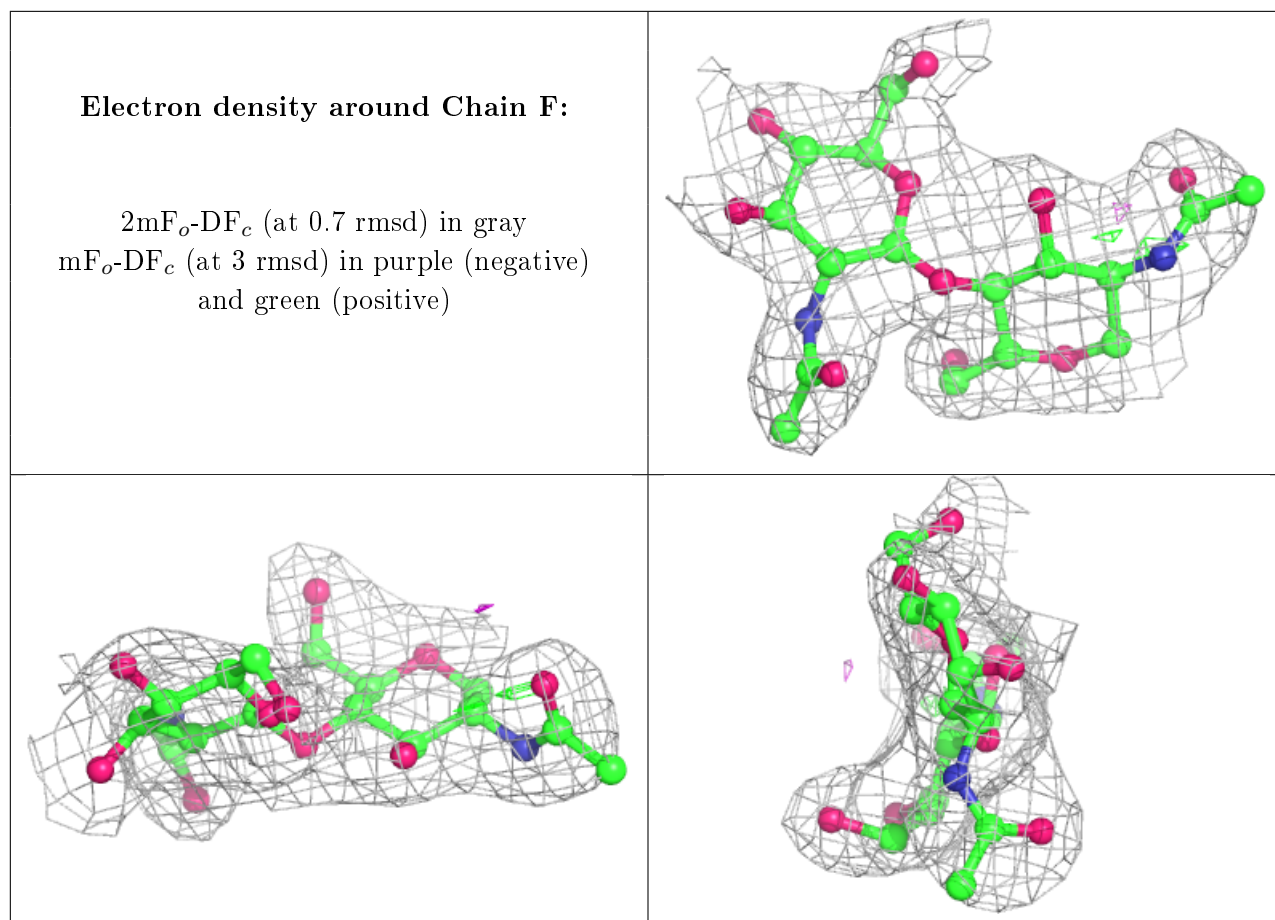
6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	A	303	14/15	0.77	0.23	87,96,103,105	0
6	NA	B	304	1/1	0.79	0.16	64,64,64,64	0
5	CA	D	201	1/1	0.81	0.21	74,74,74,74	0
5	CA	D	202	1/1	0.93	0.25	92,92,92,92	0
5	CA	B	303	1/1	0.94	0.23	65,65,65,65	0
5	CA	A	304	1/1	0.97	0.59	93,93,93,93	0

6.5 Other polymers (i)

There are no such residues in this entry.