wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2020 – 06:45 AM BST

PDB ID	:	2B8O
Title	:	Crystal Structure of Glu-Gly-Arg-Chloromethyl Ketone-Factor VIIa/Soluble Tissue Factor Complex
Authors	:	Bajaj, S.P.; Schmidt, A.E.; Padmanabhan, K.
Deposited on	:	2005-10-08
Resolution	:	2.80 Å(reported)

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

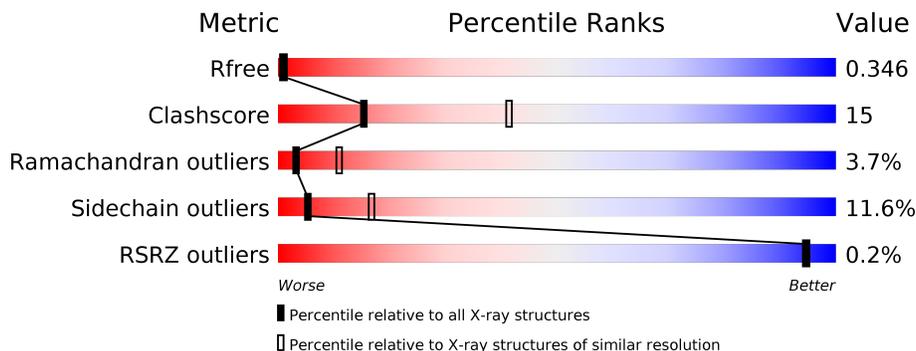|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 2.80 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	Percentile Ranks	Value
Rfree		0.346
Clashscore		15
Ramachandran outliers		3.7%
Sidechain outliers		11.6%
RSRZ outliers		0.2%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	L	142	59% 35% 6%
2	H	254	64% 30% 6%
3	T	205	57% 32% · · 7%

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
11	CL	H	514	-	-	X	-
11	CL	H	515	-	-	X	-
4	GLC	L	501	X	-	-	-
5	FUC	L	502	X	-	-	-
9	NA	H	511	-	-	-	X

2 Entry composition ⓘ

There are 12 unique types of molecules in this entry. The entry contains 4959 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 Coagulation factor VII light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	142	Total	C	N	O	S	0	0	0
			1135	683	189	248	15			

- Molecule 2 is a protein called Coagulation factor VII heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	254	Total	C	N	O	S	0	0	0
			1974	1253	351	357	13			

- Molecule 3 is a protein called Tissue factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	191	Total	C	N	O	S	0	0	0
			1551	987	250	309	5			

- Molecule 4 is alpha-D-glucopyranose (three-letter code: GLC) (formula: $C_6H_{12}O_6$).
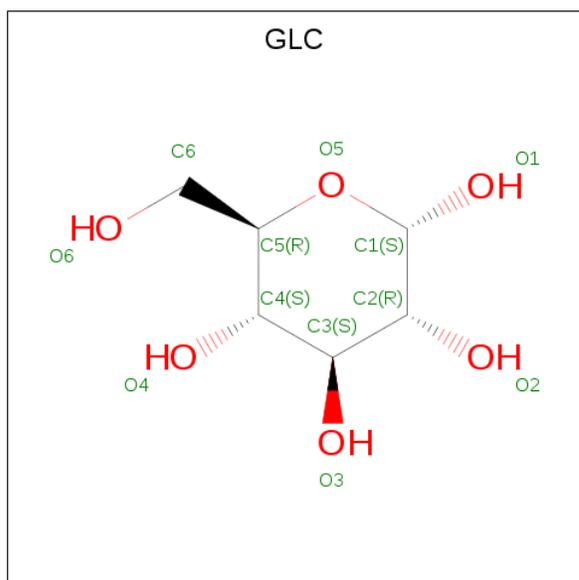
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total 11	C 6	O 5	0	0

- Molecule 5 is alpha-L-fucopyranose (three-letter code: FUC) (formula: $C_6H_{12}O_5$).
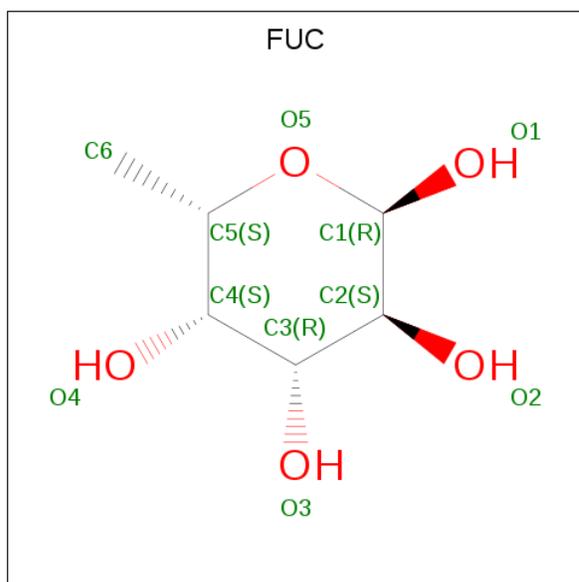
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total 10	C 6	O 4	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	1	Total 1	Ca 1	0	0
6	L	5	Total 5	Ca 5	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	L	2	Total 2	Mg 2	0	0

- Molecule 8 is L-alpha-glutamyl-N-{(1S)-4-{[amino(iminio)methyl]amino}-1-[(1S)-2-chloro-1 -hydroxyethyl]butyl}glycinamide (three-letter code: 0GJ) (formula: $C_{14}H_{28}ClN_6O_5$).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	H	1	Total	C	N	O	0	0
			25	14	6	5		

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	H	1	Total	Na	0	0
			1	1		

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	H	2	Total	Zn	0	0
			2	2		

- Molecule 11 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	H	2	Total	Cl	0	0
			2	2		
11	T	1	Total	Cl	0	0
			1	1		

- Molecule 12 is water.

| Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	L	66	Total O 66 66	0	0
12	H	91	Total O 91 91	0	0
12	T	82	Total O 82 82	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.
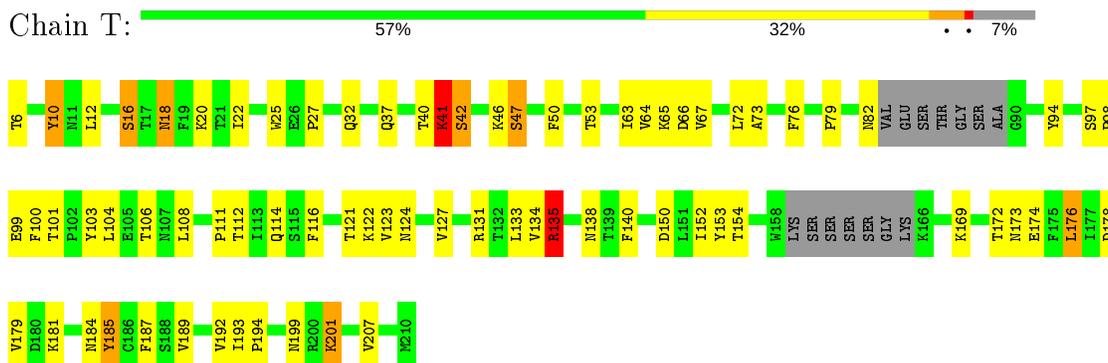
- Molecule 1: Coagulation factor VII light chain
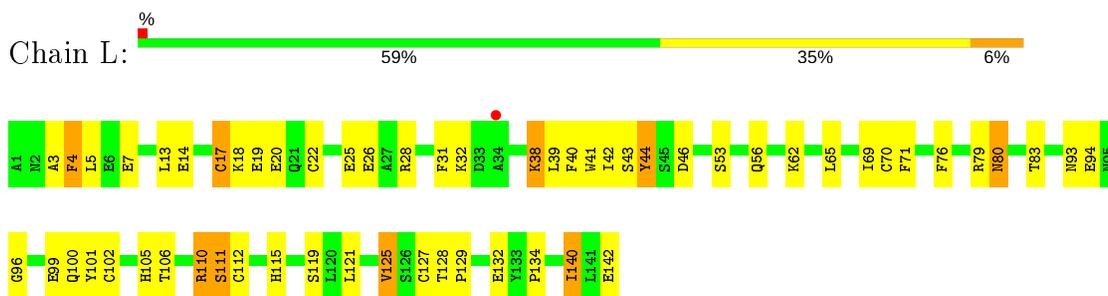
- Molecule 2: Coagulation factor VII heavy chain
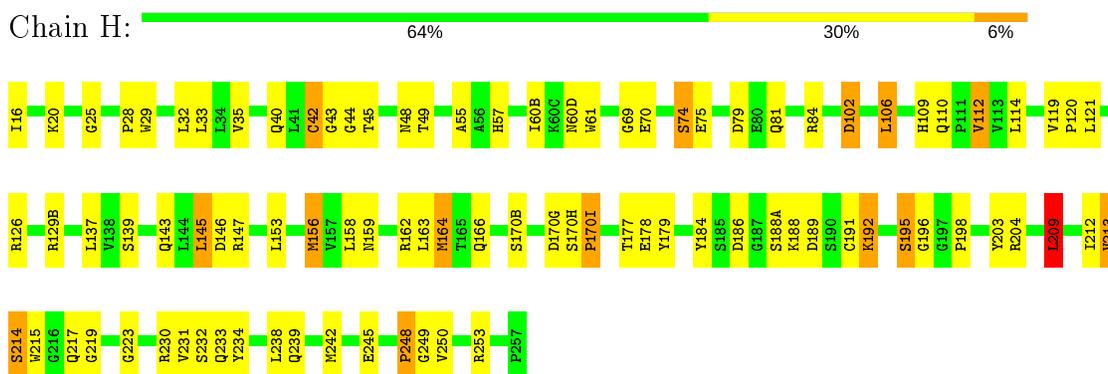
- Molecule 3: Tissue factor

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	70.28Å 81.11Å 126.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.80 40.72 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.80) 54.3 (40.72-2.20)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	5.73 (at 2.20Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.225 , 0.285 0.215 , 0.346	Depositor DCC
R_{free} test set	2013 reflections (9.89%)	wwPDB-VP
Wilson B-factor (Å^2)	24.8	Xtriage
Anisotropy	0.944	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 61.5	EDS
L-test for twinning [2]	$<|L|>=0.50$, $<L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	4959	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% of the height of the origin peak. No significant pseudotranslation is detected.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CL, NA, CA, GLC, 0GJ, MG, FUC, CGU

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	L	0.64	0/1029	0.93	1/1374 (0.1%)
2	H	0.72	0/2024	0.99	1/2755 (0.0%)
3	T	0.72	0/1585	0.99	3/2156 (0.1%)
All	All	0.70	0/4638	0.97	5/6285 (0.1%)

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	L	0	1
3	T	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	T	135	ARG	NE-CZ-NH1	6.15	123.37	120.30
3	T	20	LYS	N-CA-C	-5.21	96.93	111.00
1	L	17	CYS	CA-CB-SG	5.15	123.26	114.00
2	H	209	LEU	CA-CB-CG	5.07	126.96	115.30
3	T	66	ASP	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	44	TYR	Sidechain
3	T	103	TYR	Sidechain

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	L	1135	0	987	38	0
2	H	1974	0	1950	60	0
3	T	1551	0	1501	46	0
4	L	11	0	10	0	0
5	L	10	0	10	3	0
6	H	1	0	0	0	0
6	L	5	0	0	0	0
7	L	2	0	0	0	0
8	H	25	0	25	8	0
9	H	1	0	0	0	0
10	H	2	0	0	0	0
11	H	2	0	0	4	0
11	T	1	0	0	1	0
12	H	91	0	0	1	0
12	L	66	0	0	0	0
12	T	82	0	0	3	0
All	All	4959	0	4483	137	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 15.

The worst 5 of 137 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)
8:H:1:0GJ:HB3	11:H:514:CL:CL	2.03	0.94
2:H:196:GLY:HA2	2:H:212:ILE:HG23	1.57	0.84
2:H:81:GLN:OE1	2:H:112:VAL:HG12	1.77	0.83
3:T:10:TYR:HD1	3:T:10:TYR:H	1.31	0.79
2:H:44:GLY:HA2	2:H:196:GLY:O	1.86	0.75

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	L	130/142 (92%)	108 (83%)	18 (14%)	4 (3%)	4	14
2	H	252/254 (99%)	220 (87%)	23 (9%)	9 (4%)	3	11
3	T	185/205 (90%)	160 (86%)	17 (9%)	8 (4%)	2	8
All	All	567/601 (94%)	488 (86%)	58 (10%)	21 (4%)	3	11

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	48	ASN
2	H	195	SER
2	H	248	PRO
3	T	41	LYS
3	T	42	SER

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	L	114/114 (100%)	99 (87%)	15 (13%)	4	12
2	H	216/216 (100%)	192 (89%)	24 (11%)	6	19
3	T	178/189 (94%)	158 (89%)	20 (11%)	6	18
All	All	508/519 (98%)	449 (88%)	59 (12%)	5	17

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	139	SER
2	H	192	LYS
3	T	176	LEU
2	H	145	LEU
2	H	159	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	63	ASN
2	H	109	HIS
2	H	143	GLN
2	H	40	GLN
2	H	117	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

10 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
1	CGU	L	25	1,6	3,11,12	0.48	0	1,14,16	1.34	0
1	CGU	L	6	1,6	3,11,12	0.83	0	1,14,16	0.31	0
1	CGU	L	35	1	3,11,12	0.64	0	1,14,16	0.82	0
1	CGU	L	14	1,7	3,11,12	0.96	0	1,14,16	0.54	0
1	CGU	L	26	1,7	3,11,12	0.67	0	1,14,16	0.82	0
1	CGU	L	19	1,7	3,11,12	0.75	0	1,14,16	0.28	0
1	CGU	L	16	1,7,6	3,11,12	1.15	0	1,14,16	0.30	0
1	CGU	L	20	1	3,11,12	0.94	0	1,14,16	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
1	CGU	L	7	1,6	3,11,12	0.96	0	1,14,16	0.46	0
1	CGU	L	29	1,6	3,11,12	1.03	0	1,14,16	0.40	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CGU	L	25	1,6	-	0/5/14/16	-
1	CGU	L	6	1,6	-	2/5/14/16	-
1	CGU	L	35	1	-	3/5/14/16	-
1	CGU	L	14	1,7	-	2/5/14/16	-
1	CGU	L	26	1,7	-	2/5/14/16	-
1	CGU	L	19	1,7	-	5/5/14/16	-
1	CGU	L	16	1,7,6	-	0/5/14/16	-
1	CGU	L	20	1	-	2/5/14/16	-
1	CGU	L	7	1,6	-	1/5/14/16	-
1	CGU	L	29	1,6	-	0/5/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	L	35	CGU	O-C-CA-CB
1	L	35	CGU	CA-CB-CG-CD1
1	L	35	CGU	CA-CB-CG-CD2
1	L	14	CGU	CA-CB-CG-CD1
1	L	14	CGU	CA-CB-CG-CD2

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L	25	CGU	2	0
1	L	14	CGU	2	0
1	L	26	CGU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L	19	CGU	1	0
1	L	20	CGU	1	0
1	L	7	CGU	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 17 ligands modelled in this entry, 14 are monoatomic - leaving 3 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	GLC	L	501	1	11,11,12	1.70	3 (27%)	15,15,17	1.35	1 (6%)
8	0GJ	H	1	-	20,24,25	1.68	7 (35%)	23,30,31	1.34	3 (13%)
5	FUC	L	502	1	10,10,11	1.29	2 (20%)	14,14,16	0.68	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	GLC	L	501	1	1/1/4/5	2/2/19/22	0/1/1/1
8	0GJ	H	1	-	-	9/27/29/31	-
5	FUC	L	502	1	1/1/4/5	-	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	501	GLC	C2-C3	3.54	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	1	0GJ	CA1-C1	-3.24	1.42	1.52
8	H	1	0GJ	CB-CA	2.58	1.58	1.53
8	H	1	0GJ	CA2-N2	2.51	1.50	1.46
4	L	501	GLC	C1-C2	2.44	1.57	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	L	501	GLC	C1-O5-C5	4.05	117.67	112.19
8	H	1	0GJ	CB-CA-N	2.94	117.88	110.17
8	H	1	0GJ	CB1-CA2-C2	2.43	116.74	112.51
8	H	1	0GJ	CB1-CA2-N2	-2.15	107.51	110.33

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	502	FUC	C1
4	L	501	GLC	C1

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	H	1	0GJ	C1-CA1-N1-C
8	H	1	0GJ	O2-C2-CA2-CB1
8	H	1	0GJ	O-C-N1-CA1
8	H	1	0GJ	CA-C-N1-CA1
4	L	501	GLC	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	H	1	0GJ	8	0
5	L	502	FUC	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.
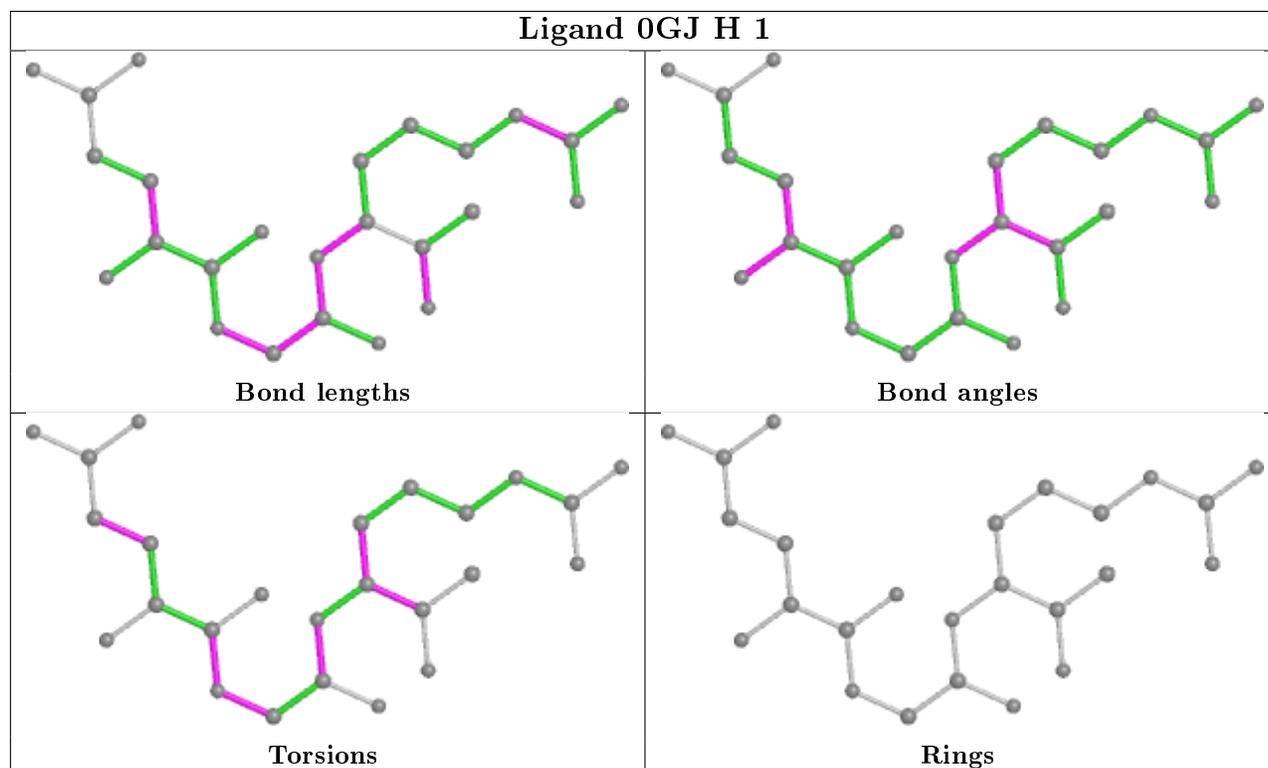
5.7 Other polymers (i)

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	L	132/142 (92%)	-0.75	1 (0%)	86	81	3, 20, 38, 40	0
2	H	254/254 (100%)	-0.74	0	100	100	2, 12, 28, 47	0
3	T	191/205 (93%)	-0.90	0	100	100	3, 17, 34, 40	0
All	All	577/601 (96%)	-0.80	1 (0%)	95	94	2, 15, 33, 47	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	34	ALA	2.0

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

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

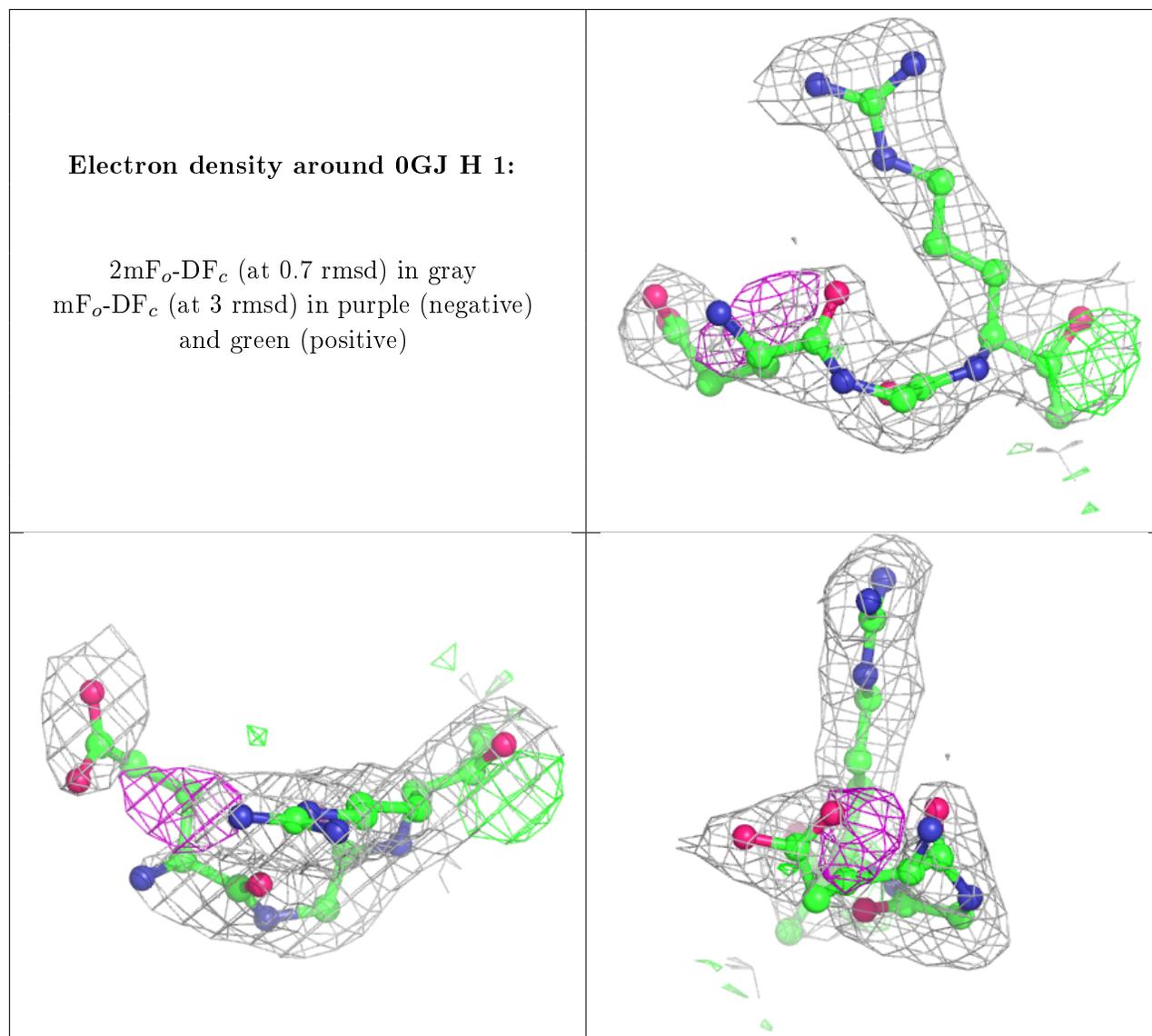| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CGU	L	35	12/13	0.68	0.22	40,46,50,51	0
1	CGU	L	6	12/13	0.71	0.22	27,32,39,40	0
1	CGU	L	20	12/13	0.78	0.15	30,37,45,45	0
1	CGU	L	25	12/13	0.79	0.18	20,33,37,42	0
1	CGU	L	14	12/13	0.81	0.14	26,41,43,43	0
1	CGU	L	29	12/13	0.82	0.12	18,22,26,26	0
1	CGU	L	19	12/13	0.84	0.14	29,38,46,47	0
1	CGU	L	16	12/13	0.85	0.10	9,12,26,28	0
1	CGU	L	7	12/13	0.86	0.15	21,27,29,30	0
1	CGU	L	26	12/13	0.87	0.12	22,27,36,37	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

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	GLC	L	501	11/12	0.54	0.36	44,48,51,51	0
9	NA	H	511	1/1	0.59	0.43	49,49,49,49	0
6	CA	L	504	1/1	0.67	0.16	60,60,60,60	0
6	CA	L	503	1/1	0.74	0.13	50,50,50,50	0
8	0GJ	H	1	25/26	0.76	0.26	20,27,34,34	0
6	CA	L	507	1/1	0.81	0.18	66,66,66,66	0
5	FUC	L	502	10/11	0.86	0.20	34,36,38,39	0
11	CL	H	514	1/1	0.87	0.33	49,49,49,49	0
7	MG	L	508	1/1	0.88	0.06	38,38,38,38	0
7	MG	L	505	1/1	0.89	0.14	25,25,25,25	0
6	CA	L	506	1/1	0.90	0.04	55,55,55,55	0
6	CA	L	509	1/1	0.93	0.05	29,29,29,29	0
10	ZN	H	513	1/1	0.93	0.46	57,57,57,57	0
11	CL	T	516	1/1	0.94	0.11	23,23,23,23	0
10	ZN	H	512	1/1	0.96	0.21	44,44,44,44	0
6	CA	H	510	1/1	0.96	0.14	35,35,35,35	0
11	CL	H	515	1/1	0.98	0.04	27,27,27,27	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 0GJ H 1:

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

6.5 Other polymers (i)

There are no such residues in this entry.