Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 03:51 AM EDT

PDB ID	:	2C4F
Title	:	crystal structure of factor VII.stf complexed with pd0297121
Authors	:	Kohrt, J.T.; Zhang, E.
Deposited on	:	2005-10-18
Resolution	:	1.72 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 (i) 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 (i)) were used in the production of this report:

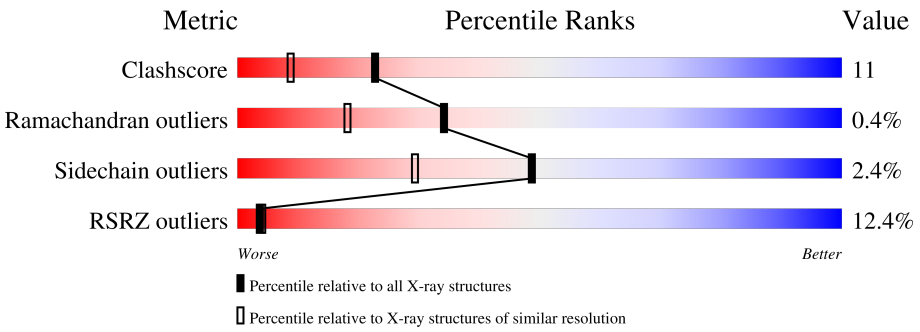
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.72 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))
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629 (1.74-1.70)

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 <=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	H	254	10%, 76%, 22%, •
2	L	142	17%, 70%, 25%, • •
3	T	75	%, 87%, 13%
4	U	116	17%, 75%, 25%

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
2	CGU	L	35	-	-	-	X

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 5058 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 PRECURSOR.

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

- Molecule 2 is a protein called COAGULATION FACTOR VII PRECURSOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	139	1117	673	185	244	15	0	0	0

- Molecule 3 is a protein called TISSUE FACTOR PRECURSOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	T	75	615	397	95	121	2	0	0	0

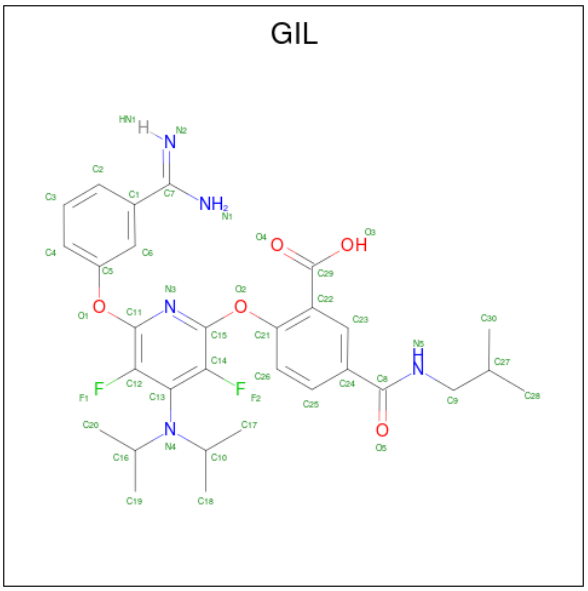
- Molecule 4 is a protein called TISSUE FACTOR PRECURSOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	U	116	940	593	155	189	3	0	0	0

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

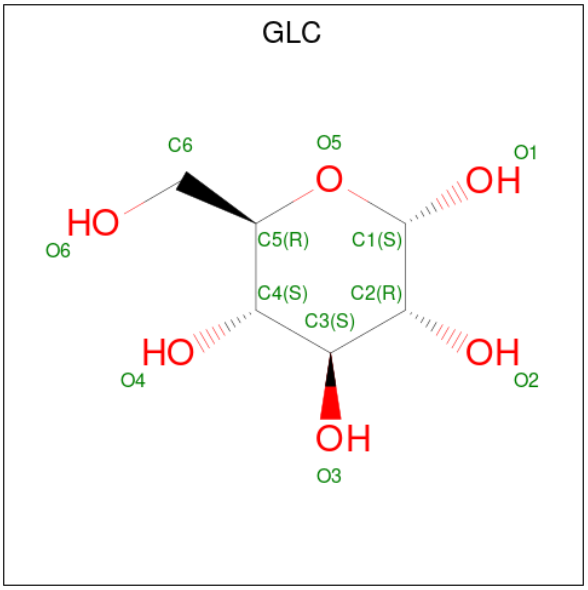
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
5	H	1	1	1	0	0
5	L	4	4	4	0	0

- Molecule 6 is 2-{[6-{3-[AMINO(IMINO)METHYL]PHENOXY}-4-(DIISOPROPYLAMINO)-3,5-DIFLUOROPYRIDIN-2-YL]OXY}-5-[(ISOBUTYLAMINO)CARBONYL]BEN ZOIC ACID (three-letter code: GIL) (formula: $C_{30}H_{35}F_2N_5O_5$).



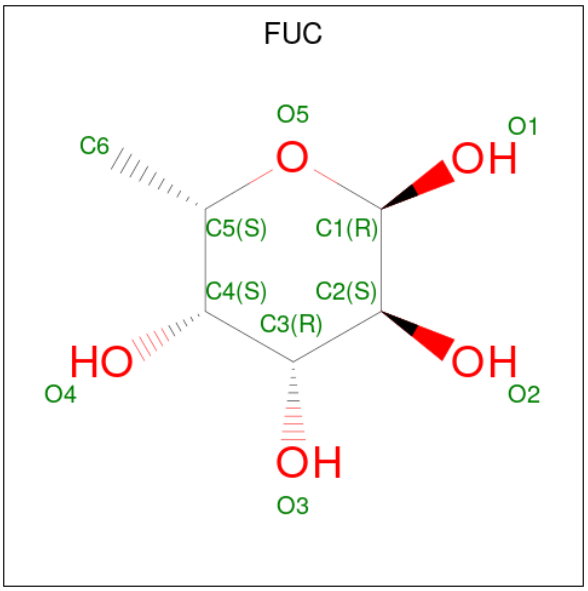
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
6	H	1	42	30	2	5	5	0	0

- Molecule 7 is alpha-D-glucopyranose (three-letter code: GLC) (formula: $C_6H_{12}O_6$).



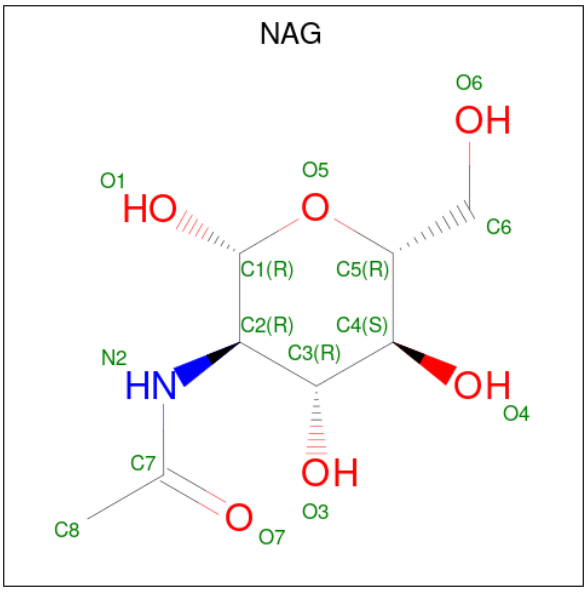
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	L	1	12	6	6	0	0

- Molecule 8 is alpha-L-fucopyranose (three-letter code: FUC) (formula: $C_6H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	L	1	11	6	5	0	0

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 10 is water.

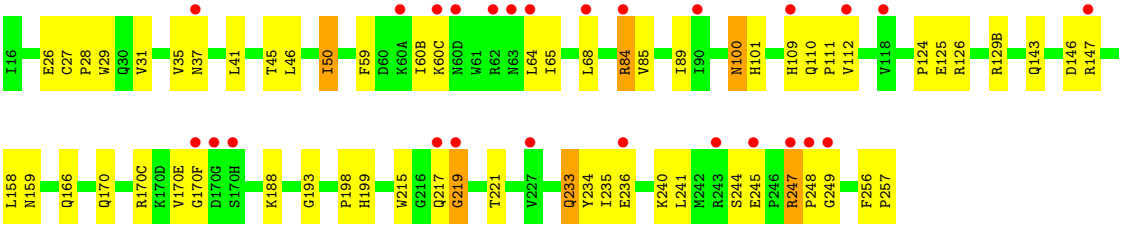
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	H	154	154	154	0	0
			Total	O		
10	L	63	63	63	0	0
			Total	O		
10	T	58	58	58	0	0
			Total	O		
10	U	53	53	53	0	0

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 PRECURSOR

Chain H:

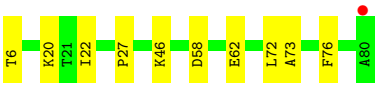


• Molecule 2: COAGULATION FACTOR VII PRECURSOR

Chain L:

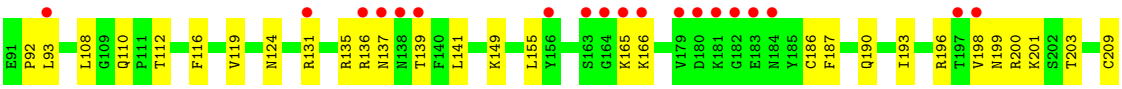
• Molecule 3: TISSUE FACTOR PRECURSOR

Chain T:



• Molecule 4: TISSUE FACTOR PRECURSOR

Chain U:



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4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	70.99Å 81.30Å 125.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.72 19.54 – 1.73	Depositor EDS
% Data completeness (in resolution range)	88.8 (50.00-1.72) 92.0 (19.54-1.73)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	-0.06 (at 1.72Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.229 , (Not available) 0.231 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	18.6	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 51.5	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	0.93	EDS
Total number of atoms	5058	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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: NAG, GIL, FUC, CA, CGU, 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	H	0.27	0/2024	0.65	1/2755 (0.0%)
2	L	0.26	0/1011	0.53	0/1349
3	T	0.29	0/631	0.68	1/860 (0.1%)
4	U	0.27	0/958	0.63	0/1299
All	All	0.27	0/4624	0.63	2/6263 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	199	HIS	N-CA-C	-6.55	93.30	111.00
3	T	20	LYS	N-CA-C	-5.07	97.31	111.00

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	H	1974	0	1950	48	0
2	L	1117	0	970	34	0
3	T	615	0	598	9	0
4	U	940	0	911	25	0
5	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	4	0	0	0	0
6	H	42	0	33	3	0
7	L	12	0	12	2	0
8	L	11	0	12	4	0
9	U	14	0	13	1	0
10	H	154	0	0	3	0
10	L	63	0	0	3	0
10	T	58	0	0	2	0
10	U	53	0	0	4	0
All	All	5058	0	4499	106	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 11.

All (106) 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:H:68:LEU:HD12	1:H:112:VAL:HG11	1.37	1.04
2:L:60:SER:HB3	8:L:203:FUC:O1	1.59	1.01
2:L:74:PRO:HA	4:U:135:ARG:HH12	1.38	0.87
2:L:31:PHE:HB2	2:L:37:THR:HG22	1.61	0.81
2:L:60:SER:HB3	8:L:203:FUC:C1	2.10	0.81
2:L:60:SER:OG	2:L:71:PHE:HB2	1.83	0.78
2:L:52:SER:OG	7:L:202:GLC:H1	1.83	0.78
1:H:129(B):ARG:HD3	10:L:305:HOH:O	1.82	0.77
1:H:126:ARG:HA	1:H:235:ILE:HD12	1.66	0.77
1:H:50:ILE:HG22	1:H:111:PRO:HB3	1.68	0.76
4:U:136:ARG:O	4:U:139:THR:HG22	1.87	0.74
3:T:6:THR:HG22	4:U:93:LEU:HD22	1.71	0.73
1:H:143:GLN:NE2	1:H:146:ASP:O	2.22	0.72
2:L:71:PHE:CZ	4:U:131:ARG:HG3	2.27	0.70
2:L:52:SER:OG	7:L:202:GLC:C1	2.40	0.69
4:U:112:THR:HG23	10:U:418:HOH:O	1.92	0.69
2:L:38:LYS:O	2:L:42:ILE:HG13	1.93	0.68
2:L:62:LYS:HE3	10:L:308:HOH:O	1.92	0.68
2:L:74:PRO:HA	4:U:135:ARG:NH1	2.10	0.67
1:H:35:VAL:HG13	1:H:41:LEU:HD22	1.75	0.66
2:L:33:ASP:O	2:L:37:THR:HG23	1.96	0.66
1:H:126:ARG:CA	1:H:235:ILE:HD12	2.26	0.66
1:H:217:GLN:O	1:H:219:GLY:O	2.12	0.66
1:H:219:GLY:O	1:H:221:THR:HG23	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:149:LYS:HD2	10:U:450:HOH:O	1.96	0.64
1:H:125:GLU:HG3	2:L:101:TYR:CZ	2.34	0.63
1:H:35:VAL:CG1	1:H:41:LEU:HD22	2.29	0.62
1:H:124:PRO:O	1:H:235:ILE:HD13	1.98	0.62
1:H:46:LEU:HD13	1:H:68:LEU:HD11	1.82	0.61
3:T:46:LYS:HD2	10:T:124:HOH:O	2.02	0.60
1:H:147:ARG:O	1:H:147:ARG:HG2	2.01	0.60
2:L:18:LYS:HE3	10:U:408:HOH:O	2.03	0.58
1:H:64:LEU:HB3	1:H:85:VAL:HB	1.85	0.58
2:L:31:PHE:HB2	2:L:37:THR:CG2	2.31	0.58
2:L:34:ALA:O	2:L:38:LYS:HG2	2.04	0.58
1:H:26:GLU:HG3	2:L:140:ILE:HD11	1.87	0.57
1:H:45:THR:OG1	1:H:198:PRO:HB3	2.04	0.57
1:H:166:GLN:O	1:H:170:GLN:HG3	2.05	0.57
2:L:28:ARG:HA	2:L:37:THR:HG21	1.88	0.56
4:U:119:VAL:HG23	4:U:119:VAL:O	2.05	0.56
3:T:46:LYS:HD3	3:T:62:GLU:CD	2.28	0.55
1:H:170(E):VAL:HG21	1:H:217:GLN:OE1	2.07	0.54
1:H:240:LYS:HD2	10:H:504:HOH:O	2.08	0.53
4:U:198:VAL:HG22	10:U:404:HOH:O	2.09	0.52
1:H:64:LEU:HD23	1:H:85:VAL:HG11	1.91	0.52
1:H:126:ARG:NH2	1:H:233:GLN:NE2	2.58	0.51
1:H:60(C):LYS:HG2	10:H:534:HOH:O	2.10	0.51
2:L:28:ARG:HA	2:L:37:THR:CG2	2.40	0.51
1:H:84:ARG:N	1:H:84:ARG:HD2	2.25	0.51
3:T:76:PHE:CD1	4:U:92:PRO:HG2	2.46	0.50
3:T:72:LEU:HD13	3:T:73:ALA:N	2.27	0.50
1:H:126:ARG:HH22	1:H:233:GLN:NE2	2.11	0.49
4:U:166:LYS:HD2	4:U:166:LYS:N	2.28	0.49
1:H:193:GLY:HA3	6:H:302:GIL:H282	1.95	0.48
4:U:155:LEU:HD11	4:U:187:PHE:HB3	1.95	0.48
1:H:236:GLU:HG3	10:H:489:HOH:O	2.14	0.48
4:U:165:LYS:C	4:U:166:LYS:HD2	2.35	0.48
1:H:215:TRP:HB3	6:H:302:GIL:C18	2.44	0.47
1:H:215:TRP:HB3	6:H:302:GIL:H182	1.96	0.47
2:L:137:LYS:O	2:L:139:PRO:HD3	2.15	0.47
2:L:73:LEU:HD21	8:L:203:FUC:H4	1.97	0.46
3:T:22:ILE:HD13	3:T:58:ASP:HA	1.96	0.46
4:U:136:ARG:HE	4:U:141:LEU:HD21	1.79	0.46
4:U:196:ARG:O	4:U:200:ARG:NH1	2.48	0.46
1:H:158:LEU:HD11	1:H:188:LYS:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:170(C):ARG:HG2	1:H:170(C):ARG:HH11	1.79	0.46
4:U:190:GLN:OE1	4:U:201:LYS:HE2	2.16	0.46
1:H:89:ILE:HG21	1:H:241:LEU:HD13	1.98	0.46
2:L:33:ASP:CG	2:L:36:ARG:HD3	2.36	0.46
4:U:136:ARG:HH11	4:U:136:ARG:HG2	1.81	0.46
1:H:35:VAL:O	1:H:35:VAL:HG23	2.16	0.46
1:H:219:GLY:C	1:H:221:THR:HG23	2.37	0.45
3:T:76:PHE:HD1	4:U:92:PRO:HG2	1.80	0.45
3:T:46:LYS:HD3	3:T:62:GLU:OE2	2.16	0.45
4:U:136:ARG:O	4:U:137:ASN:HB2	2.15	0.45
2:L:60:SER:CB	8:L:203:FUC:O1	2.47	0.45
1:H:256:PHE:HA	1:H:257:PRO:C	2.37	0.45
2:L:71:PHE:CE2	4:U:131:ARG:HG3	2.51	0.45
1:H:35:VAL:HG12	1:H:64:LEU:CD1	2.47	0.43
4:U:110:GLN:HB2	4:U:203:THR:CG2	2.48	0.43
2:L:84:HIS:HE1	10:L:345:HOH:O	2.00	0.43
1:H:125:GLU:HG3	2:L:101:TYR:CE2	2.53	0.43
2:L:110:ARG:HD2	2:L:110:ARG:C	2.39	0.43
4:U:186:CYS:HA	4:U:209:CYS:HA	2.01	0.43
3:T:46:LYS:NZ	10:T:104:HOH:O	2.53	0.42
1:H:247:ARG:HB3	1:H:248:PRO:HD2	2.01	0.42
2:L:108:THR:OG1	2:L:109:LYS:N	2.52	0.42
1:H:27:CYS:N	1:H:28:PRO:CD	2.82	0.42
1:H:241:LEU:HA	1:H:244:SER:OG	2.19	0.42
2:L:33:ASP:HB3	2:L:36:ARG:CG	2.50	0.42
4:U:124:ASN:CG	9:U:301:NAG:H82	2.39	0.42
2:L:9:ARG:CZ	2:L:15:ARG:HD3	2.50	0.42
1:H:65:ILE:HD11	1:H:84:ARG:HH12	1.84	0.42
2:L:120:LEU:HD12	2:L:126:SER:O	2.20	0.42
4:U:108:LEU:HD11	4:U:193:ILE:HG13	2.01	0.41
1:H:59:PHE:HA	1:H:60(B):ILE:HG12	2.02	0.41
1:H:101:HIS:HA	1:H:234:TYR:OH	2.20	0.41
2:L:108:THR:HG23	2:L:109:LYS:N	2.35	0.41
1:H:245:GLU:O	1:H:247:ARG:NE	2.53	0.41
2:L:35:CGU:O	2:L:38:LYS:HG2	2.20	0.41
1:H:31:VAL:HG22	1:H:68:LEU:HD21	2.03	0.41
1:H:248:PRO:HG2	1:H:249:GLY:H	1.86	0.41
4:U:116:PHE:HA	4:U:124:ASN:O	2.21	0.41
2:L:54:PRO:O	2:L:80:ASN:HB3	2.21	0.40
1:H:100:ASN:HD22	1:H:100:ASN:HA	1.61	0.40
1:H:109:HIS:ND1	1:H:110:GLN:HG2	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	H	252/254 (99%)	238 (94%)	12 (5%)	2 (1%)	19 6
2	L	127/142 (89%)	122 (96%)	5 (4%)	0	100 100
3	T	73/75 (97%)	72 (99%)	1 (1%)	0	100 100
4	U	112/116 (97%)	107 (96%)	5 (4%)	0	100 100
All	All	564/587 (96%)	539 (96%)	23 (4%)	2 (0%)	34 18

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	219	GLY
1	H	170(F)	GLY

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	H	216/216 (100%)	208 (96%)	8 (4%)	34 14
2	L	113/114 (99%)	111 (98%)	2 (2%)	59 41
3	T	70/70 (100%)	69 (99%)	1 (1%)	67 52
4	U	109/109 (100%)	108 (99%)	1 (1%)	78 69
All	All	508/509 (100%)	496 (98%)	12 (2%)	49 29

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	29	TRP
1	H	37	ASN
1	H	50	ILE
1	H	84	ARG
1	H	100	ASN
1	H	159	ASN
1	H	233	GLN
1	H	247	ARG
2	L	36	ARG
2	L	110	ARG
3	T	27	PRO
4	U	199	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	37	ASN
1	H	63	ASN
1	H	100	ASN
1	H	110	GLN
1	H	143	GLN
1	H	159	ASN
1	H	202	HIS
1	H	233	GLN
1	H	239	GLN
2	L	80	ASN
2	L	84	HIS
3	T	31	ASN
4	U	171	ASN
4	U	199	ASN

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	$\#\|Z\| > 2$
2	CGU	L	14	5,2	9,11,12	1.19	1 (11%)	10,14,16	1.45	1 (10%)
2	CGU	L	29	5,2	9,11,12	1.25	1 (11%)	10,14,16	1.41	1 (10%)
2	CGU	L	20	2	9,11,12	1.21	1 (11%)	10,14,16	1.41	1 (10%)
2	CGU	L	26	5,2	9,11,12	1.25	1 (11%)	10,14,16	1.70	2 (20%)
2	CGU	L	35	2	9,11,12	1.17	1 (11%)	10,14,16	1.45	1 (10%)
2	CGU	L	6	2	9,11,12	1.20	1 (11%)	10,14,16	1.34	1 (10%)
2	CGU	L	7	2	9,11,12	1.17	1 (11%)	10,14,16	1.49	1 (10%)
2	CGU	L	16	5,2	9,11,12	1.25	1 (11%)	10,14,16	1.48	1 (10%)
2	CGU	L	19	5,2	9,11,12	1.20	1 (11%)	10,14,16	1.39	1 (10%)
2	CGU	L	25	5,2	9,11,12	1.24	1 (11%)	10,14,16	1.45	1 (10%)

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	CGU	L	14	5,2	-	2/13/14/16	-
2	CGU	L	29	5,2	-	0/13/14/16	-
2	CGU	L	20	2	-	1/13/14/16	-
2	CGU	L	26	5,2	-	7/13/14/16	-
2	CGU	L	35	2	-	3/13/14/16	-
2	CGU	L	6	2	-	4/13/14/16	-
2	CGU	L	7	2	-	1/13/14/16	-
2	CGU	L	16	5,2	-	6/13/14/16	-
2	CGU	L	19	5,2	-	2/13/14/16	-
2	CGU	L	25	5,2	-	0/13/14/16	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	25	CGU	OE22-CD2	-2.48	1.22	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	20	CGU	OE22-CD2	-2.44	1.22	1.30
2	L	6	CGU	OE22-CD2	-2.44	1.22	1.30
2	L	19	CGU	OE22-CD2	-2.43	1.22	1.30
2	L	14	CGU	OE22-CD2	-2.42	1.22	1.30
2	L	16	CGU	OE22-CD2	-2.37	1.23	1.30
2	L	7	CGU	OE22-CD2	-2.33	1.23	1.30
2	L	35	CGU	OE22-CD2	-2.33	1.23	1.30
2	L	29	CGU	OE22-CD2	-2.32	1.23	1.30
2	L	26	CGU	OE22-CD2	-2.22	1.23	1.30

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	L	26	CGU	CB-CG-CD2	-3.96	105.07	113.11
2	L	16	CGU	CB-CG-CD2	-3.62	105.76	113.11
2	L	7	CGU	CB-CG-CD2	-3.47	106.06	113.11
2	L	35	CGU	CB-CG-CD2	-3.35	106.32	113.11
2	L	14	CGU	CB-CG-CD2	-3.31	106.39	113.11
2	L	29	CGU	CB-CG-CD2	-3.29	106.42	113.11
2	L	25	CGU	CB-CG-CD2	-3.26	106.49	113.11
2	L	19	CGU	CB-CG-CD2	-3.24	106.54	113.11
2	L	20	CGU	CB-CG-CD2	-3.22	106.56	113.11
2	L	6	CGU	CB-CG-CD2	-3.07	106.88	113.11
2	L	26	CGU	CB-CA-C	-2.45	107.22	110.99

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	7	CGU	O-C-CA-CB
2	L	20	CGU	N-CA-CB-CG
2	L	26	CGU	CA-CB-CG-CD1
2	L	35	CGU	N-CA-CB-CG
2	L	35	CGU	OE12-CD1-CG-CD2
2	L	6	CGU	OE21-CD2-CG-CB
2	L	16	CGU	OE11-CD1-CG-CB
2	L	16	CGU	OE12-CD1-CG-CB
2	L	16	CGU	OE21-CD2-CG-CB
2	L	16	CGU	OE22-CD2-CG-CB
2	L	19	CGU	OE11-CD1-CG-CB
2	L	26	CGU	OE11-CD1-CG-CB
2	L	26	CGU	OE12-CD1-CG-CB

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Mol	Chain	Res	Type	Atoms
2	L	26	CGU	OE21-CD2-CG-CB
2	L	26	CGU	OE22-CD2-CG-CB
2	L	16	CGU	OE21-CD2-CG-CD1
2	L	16	CGU	OE22-CD2-CG-CD1
2	L	26	CGU	OE11-CD1-CG-CD2
2	L	26	CGU	OE12-CD1-CG-CD2
2	L	35	CGU	OE11-CD1-CG-CD2
2	L	6	CGU	OE22-CD2-CG-CB
2	L	14	CGU	OE11-CD1-CG-CB
2	L	14	CGU	OE12-CD1-CG-CB
2	L	19	CGU	OE12-CD1-CG-CB
2	L	6	CGU	OE21-CD2-CG-CD1
2	L	6	CGU	OE22-CD2-CG-CD1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	35	CGU	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
7	GLC	L	202	-	12,12,12	0.28	0	17,17,17	0.33	0
9	NAG	U	301	4	14,14,15	0.55	0	17,19,21	0.66	0
6	GIL	H	302	-	44,44,44	1.67	11 (25%)	58,63,63	1.40	7 (12%)
8	FUC	L	203	-	11,11,11	0.32	0	16,16,16	0.48	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
7	GLC	L	202	-	-	0/2/22/22	0/1/1/1
9	NAG	U	301	4	-	3/6/23/26	0/1/1/1
6	GIL	H	302	-	-	16/37/37/37	0/3/3/3
8	FUC	L	203	-	-	-	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	302	GIL	C12-C11	3.85	1.43	1.38
6	H	302	GIL	C15-N3	3.20	1.36	1.32
6	H	302	GIL	C23-C24	2.89	1.43	1.39
6	H	302	GIL	C13-C12	2.88	1.44	1.39
6	H	302	GIL	C11-N3	2.62	1.36	1.32
6	H	302	GIL	C10-N4	2.55	1.53	1.48
6	H	302	GIL	C2-C1	2.41	1.43	1.39
6	H	302	GIL	C22-C21	2.35	1.45	1.40
6	H	302	GIL	C13-C14	2.26	1.43	1.39
6	H	302	GIL	C25-C24	2.06	1.42	1.39
6	H	302	GIL	C6-C1	2.04	1.42	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	H	302	GIL	C16-N4-C10	5.21	127.64	116.87
6	H	302	GIL	O1-C11-C12	3.87	122.52	117.67
6	H	302	GIL	C17-C10-N4	2.73	117.10	112.09
6	H	302	GIL	O2-C15-C14	-2.67	114.32	117.67
6	H	302	GIL	O1-C11-N3	-2.50	115.42	119.61
6	H	302	GIL	C21-O2-C15	2.47	121.44	117.86
6	H	302	GIL	O2-C21-C22	2.19	123.95	118.96

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	H	302	GIL	C12-C11-O1-C5
6	H	302	GIL	O5-C8-N5-C9

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Mol	Chain	Res	Type	Atoms
6	H	302	GIL	C30-C27-C9-N5
9	U	301	NAG	C8-C7-N2-C2
9	U	301	NAG	O7-C7-N2-C2
6	H	302	GIL	C24-C8-N5-C9
6	H	302	GIL	C17-C10-N4-C16
6	H	302	GIL	C28-C27-C9-N5
6	H	302	GIL	C21-C22-C29-O3
6	H	302	GIL	C12-C13-N4-C10
6	H	302	GIL	C12-C13-N4-C16
6	H	302	GIL	C14-C13-N4-C16
6	H	302	GIL	C21-C22-C29-O4
6	H	302	GIL	N3-C11-O1-C5
6	H	302	GIL	C2-C1-C7-N1
6	H	302	GIL	C6-C1-C7-N1
9	U	301	NAG	C4-C5-C6-O6
6	H	302	GIL	C2-C1-C7-N2
6	H	302	GIL	C6-C1-C7-N2

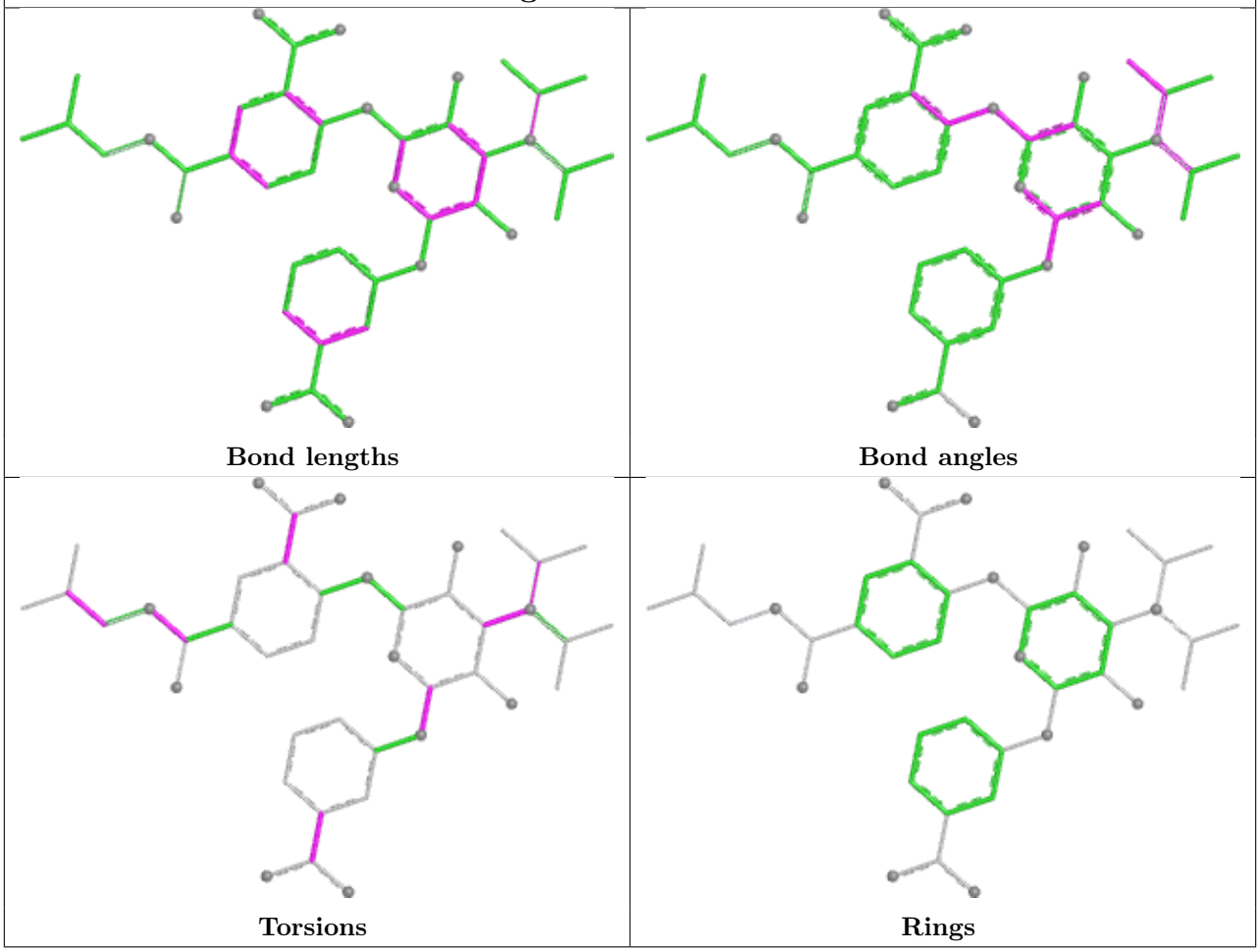
There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	202	GLC	2	0
9	U	301	NAG	1	0
6	H	302	GIL	3	0
8	L	203	FUC	4	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.

Ligand GIL H 302



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	U	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U	158:TRP	C	163:SER	N	9.35

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	H	254/254 (100%)	0.64	26 (10%)	6	7	10, 19, 39, 61	1 (0%)
2	L	129/142 (90%)	1.04	24 (18%)	1	1	16, 27, 44, 51	0
3	T	75/75 (100%)	0.37	1 (1%)	77	81	12, 18, 25, 30	0
4	U	116/116 (100%)	1.16	20 (17%)	1	1	15, 23, 50, 55	1 (0%)
All	All	574/587 (97%)	0.80	71 (12%)	4	4	10, 22, 41, 61	2 (0%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	U	137	ASN	8.5
4	U	181	LYS	7.8
1	H	248	PRO	7.6
4	U	182	GLY	7.2
2	L	9	ARG	6.6
4	U	138	ASN	6.5
1	H	170(G)	ASP	6.3
4	U	156	TYR	5.7
2	L	122	ALA	5.2
1	H	247	ARG	5.2
1	H	62	ARG	5.0
1	H	147	ARG	5.0
4	U	197	THR	5.0
2	L	106	THR	4.9
1	H	219	GLY	4.7
4	U	164	GLY	4.5
1	H	37	ASN	4.4
3	T	80	ALA	4.3
2	L	107	GLY	4.3
4	U	163	SER	4.3
4	U	136	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
2	L	15	ARG	4.1
4	U	139	THR	3.8
1	H	249	GLY	3.7
4	U	180	ASP	3.7
2	L	21	GLN	3.6
2	L	108	THR	3.5
4	U	198	VAL	3.5
4	U	165	LYS	3.4
2	L	42	ILE	3.4
1	H	109	HIS	3.1
1	H	84	ARG	3.0
4	U	183	GLU	3.0
2	L	66	GLN	3.0
1	H	64	LEU	3.0
4	U	184	ASN	2.9
1	H	170(F)	GLY	2.9
2	L	10	PRO	2.9
2	L	18	LYS	2.9
1	H	245	GLU	2.9
1	H	60(C)	LYS	2.8
2	L	32	LYS	2.8
2	L	69	ILE	2.7
2	L	140	ILE	2.7
4	U	131	ARG	2.7
1	H	60(D)	ASN	2.7
2	L	11	GLY	2.6
1	H	68	LEU	2.6
1	H	243	ARG	2.5
2	L	51	ALA	2.5
1	H	90	ILE	2.5
4	U	166	LYS	2.5
1	H	236	GLU	2.5
2	L	37	THR	2.4
1	H	217	GLN	2.4
4	U	179	VAL	2.3
4	U	93	LEU	2.3
2	L	70	CYS	2.3
2	L	34	ALA	2.3
1	H	118	VAL	2.3
2	L	121	LEU	2.2
4	U	210	MET	2.2
2	L	60	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	63	ASN	2.2
2	L	38	LYS	2.2
2	L	48	ASP	2.1
1	H	112	VAL	2.1
1	H	227	VAL	2.1
1	H	60(A)	LYS	2.1
1	H	170(H)	SER	2.1
2	L	142	GLU	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
2	CGU	L	35	12/13	0.42	0.47	39,51,53,54	0
2	CGU	L	14	12/13	0.71	0.29	37,46,48,49	0
2	CGU	L	20	12/13	0.72	0.34	44,50,52,53	0
2	CGU	L	19	12/13	0.75	0.33	46,51,54,54	0
2	CGU	L	6	12/13	0.81	0.23	26,34,37,38	0
2	CGU	L	7	12/13	0.81	0.20	30,33,36,38	0
2	CGU	L	26	12/13	0.85	0.20	23,29,33,35	0
2	CGU	L	16	12/13	0.86	0.17	34,35,37,37	0
2	CGU	L	25	12/13	0.87	0.20	25,26,28,29	0
2	CGU	L	29	12/13	0.90	0.13	25,27,30,30	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

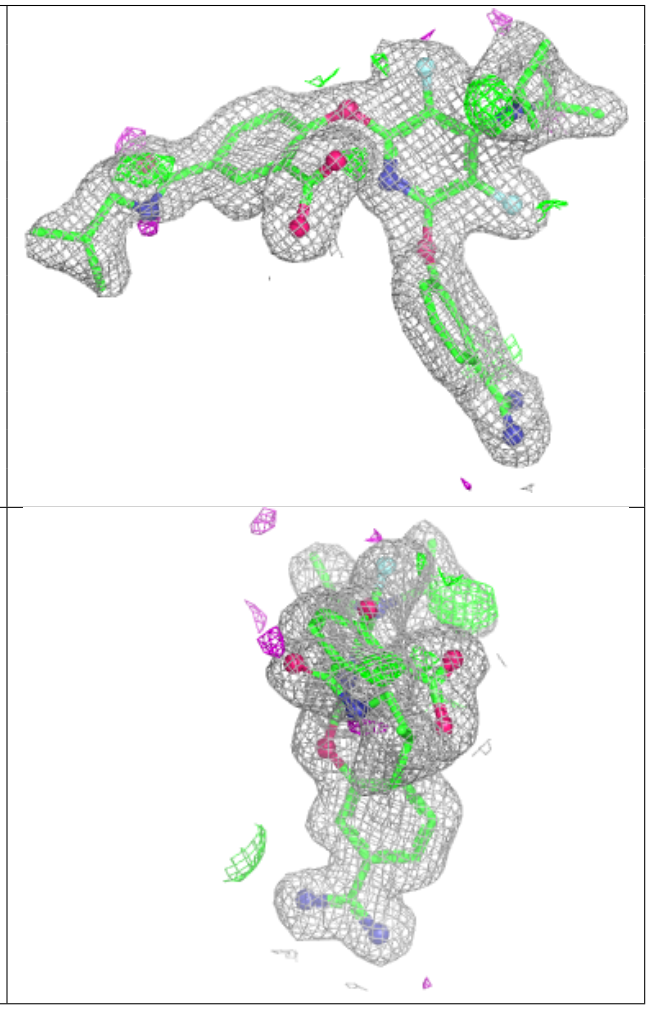
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	FUC	L	203	11/11	0.67	0.19	35,36,39,42	0
7	GLC	L	202	12/12	0.70	0.19	50,52,52,52	0
9	NAG	U	301	14/15	0.81	0.21	24,31,41,41	0
5	CA	L	205	1/1	0.86	0.14	85,85,85,85	0
6	GIL	H	302	42/42	0.88	0.14	14,25,34,36	0
5	CA	L	206	1/1	0.95	0.14	45,45,45,45	0
5	CA	L	204	1/1	0.96	0.15	46,46,46,46	0
5	CA	L	201	1/1	0.97	0.05	28,28,28,28	0
5	CA	H	301	1/1	0.98	0.13	29,29,29,29	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 GIL H 302:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.