



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 10:05 AM UTC

PDB ID : 6TER / pdb_00006ter
Title : Crystal structure of a galactokinase from Bifidobacterium infantis in complex with Galactose
Authors : Keenan, T.; Parmeggiani, F.; Fontenelle, C.Q.; Malassis, J.; Vendeville, J.; Offen, W.A.; Both, P.; Huang, K.; Marchesi, A.; Heyam, A.; Young, C.; Charnock, S.; Davies, G.J.; Linclau, B.; Flitsch, S.L.; Fascione, M.A.
Deposited on : 2019-11-12
Resolution : 1.68 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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](#) ①) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

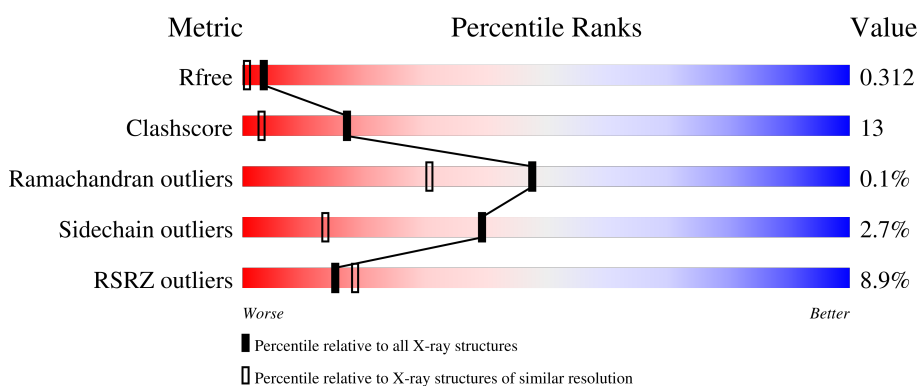
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

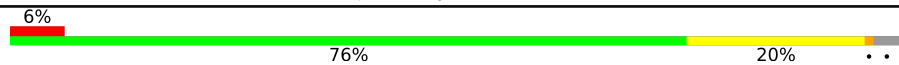
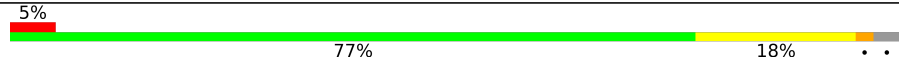


The reported resolution of this entry is 1.68 Å.

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	1054 (1.68-1.68)
Clashscore	190562	1078 (1.68-1.68)
Ramachandran outliers	187476	1068 (1.68-1.68)
Sidechain outliers	187428	1067 (1.68-1.68)
RSRZ outliers	180081	1055 (1.68-1.68)

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	429	
1	B	429	
1	C	429	
1	D	429	

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	GOL	A	911	-	-	X	-
2	GOL	B	701	-	-	X	-
2	GOL	B	706	-	-	X	-
2	GOL	B	710	-	-	X	-
2	GOL	C	606	-	-	X	-
3	PEG	A	903	-	-	X	-
3	PEG	A	904	-	-	X	-
3	PEG	A	907	-	-	X	-
3	PEG	A	912	-	-	X	-
3	PEG	A	918[A]	-	-	X	-
3	PEG	B	702	-	-	X	-
3	PEG	B	704	-	-	X	-
4	PGE	A	919	-	-	X	-
4	PGE	A	921	-	-	X	-
5	PG4	A	922	-	-	X	-

2 Entry composition i

There are 11 unique types of molecules in this entry. The entry contains 14073 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 Galactokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	418	3182	1982	559	629	12	0	11	0
1	B	418	3212	1999	566	633	14	0	12	0
1	C	416	3188	1983	563	629	13	0	12	0
1	D	416	3207	2001	560	634	12	0	15	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	417	LYS	-	expression tag	UNP B7GUI0
A	418	LEU	-	expression tag	UNP B7GUI0
A	419	ALA	-	expression tag	UNP B7GUI0
A	420	ALA	-	expression tag	UNP B7GUI0
A	421	ALA	-	expression tag	UNP B7GUI0
A	422	LEU	-	expression tag	UNP B7GUI0
A	423	GLU	-	expression tag	UNP B7GUI0
A	424	HIS	-	expression tag	UNP B7GUI0
A	425	HIS	-	expression tag	UNP B7GUI0
A	426	HIS	-	expression tag	UNP B7GUI0
A	427	HIS	-	expression tag	UNP B7GUI0
A	428	HIS	-	expression tag	UNP B7GUI0
A	429	HIS	-	expression tag	UNP B7GUI0
B	417	LYS	-	expression tag	UNP B7GUI0
B	418	LEU	-	expression tag	UNP B7GUI0
B	419	ALA	-	expression tag	UNP B7GUI0
B	420	ALA	-	expression tag	UNP B7GUI0
B	421	ALA	-	expression tag	UNP B7GUI0
B	422	LEU	-	expression tag	UNP B7GUI0
B	423	GLU	-	expression tag	UNP B7GUI0
B	424	HIS	-	expression tag	UNP B7GUI0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	425	HIS	-	expression tag	UNP B7GUI0
B	426	HIS	-	expression tag	UNP B7GUI0
B	427	HIS	-	expression tag	UNP B7GUI0
B	428	HIS	-	expression tag	UNP B7GUI0
B	429	HIS	-	expression tag	UNP B7GUI0
C	417	LYS	-	expression tag	UNP B7GUI0
C	418	LEU	-	expression tag	UNP B7GUI0
C	419	ALA	-	expression tag	UNP B7GUI0
C	420	ALA	-	expression tag	UNP B7GUI0
C	421	ALA	-	expression tag	UNP B7GUI0
C	422	LEU	-	expression tag	UNP B7GUI0
C	423	GLU	-	expression tag	UNP B7GUI0
C	424	HIS	-	expression tag	UNP B7GUI0
C	425	HIS	-	expression tag	UNP B7GUI0
C	426	HIS	-	expression tag	UNP B7GUI0
C	427	HIS	-	expression tag	UNP B7GUI0
C	428	HIS	-	expression tag	UNP B7GUI0
C	429	HIS	-	expression tag	UNP B7GUI0
D	417	LYS	-	expression tag	UNP B7GUI0
D	418	LEU	-	expression tag	UNP B7GUI0
D	419	ALA	-	expression tag	UNP B7GUI0
D	420	ALA	-	expression tag	UNP B7GUI0
D	421	ALA	-	expression tag	UNP B7GUI0
D	422	LEU	-	expression tag	UNP B7GUI0
D	423	GLU	-	expression tag	UNP B7GUI0
D	424	HIS	-	expression tag	UNP B7GUI0
D	425	HIS	-	expression tag	UNP B7GUI0
D	426	HIS	-	expression tag	UNP B7GUI0
D	427	HIS	-	expression tag	UNP B7GUI0
D	428	HIS	-	expression tag	UNP B7GUI0
D	429	HIS	-	expression tag	UNP B7GUI0

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



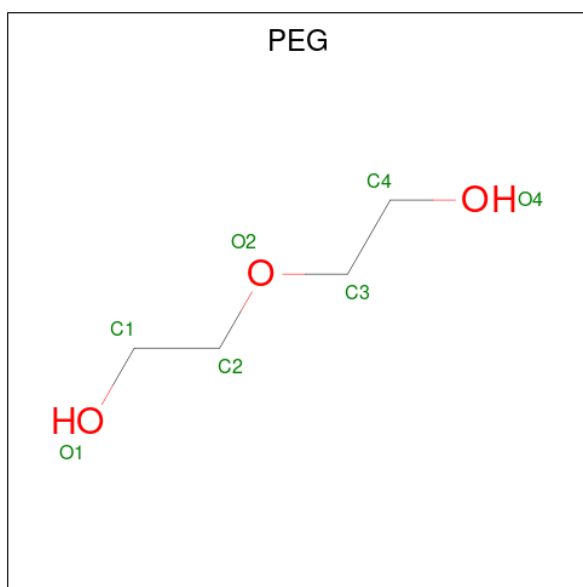
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total 6	C 3	O 3	0	0
2	B	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



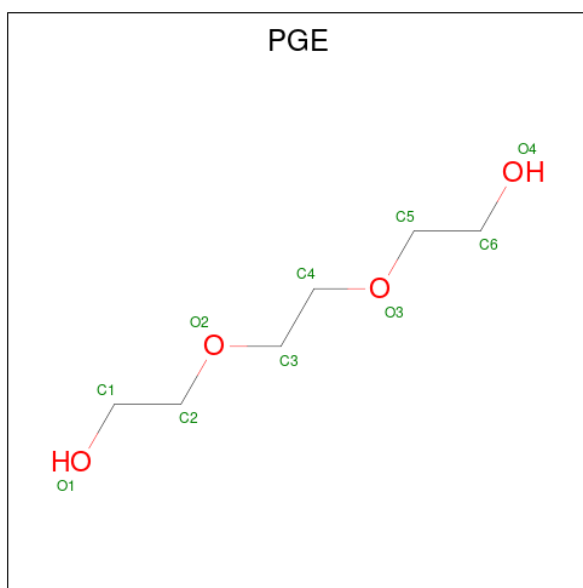
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 14 8 6	0	1
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 14 8 6	0	1
3	A	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0

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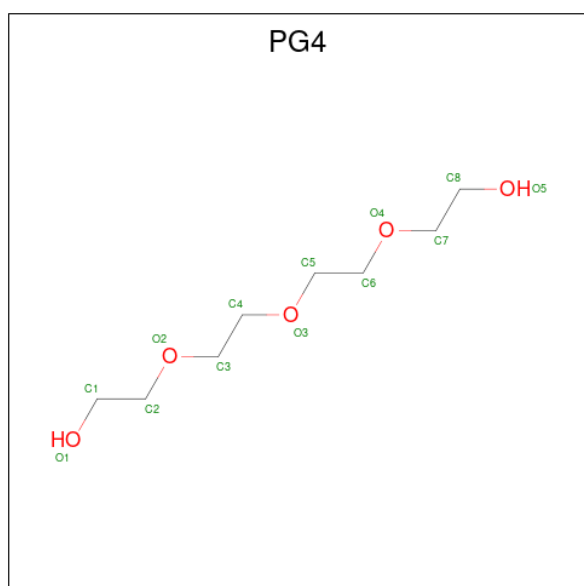
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	B	1	Total C O 7 4 3	0	0
3	C	1	Total C O 14 8 6	0	1
3	C	1	Total C O 7 4 3	0	0
3	C	1	Total C O 7 4 3	0	0
3	D	1	Total C O 7 4 3	0	0
3	D	1	Total C O 7 4 3	0	0

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



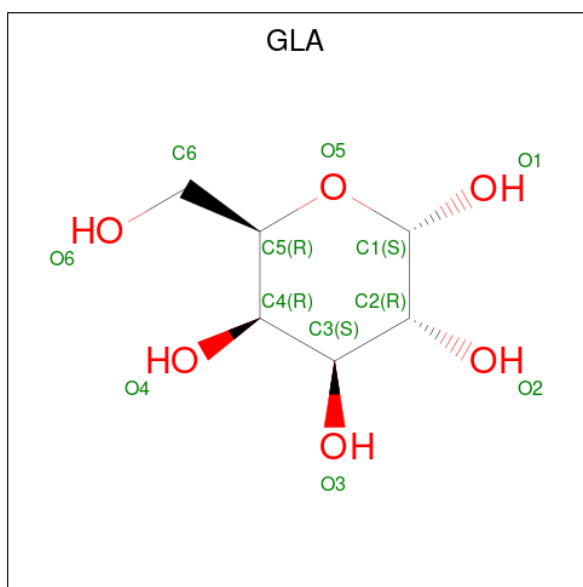
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



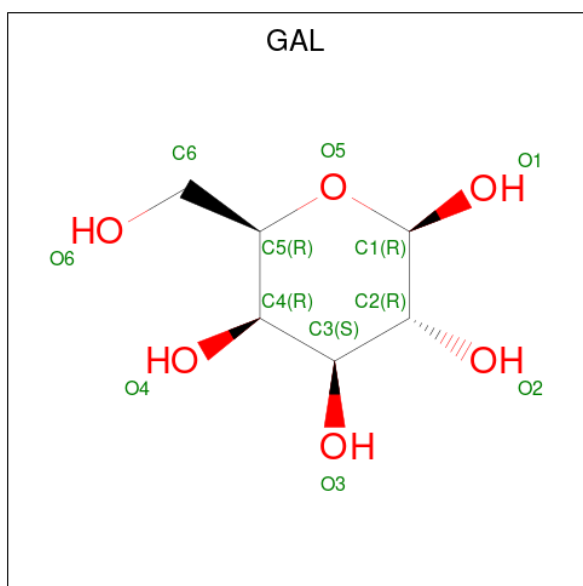
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	8	5		
5	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is alpha-D-galactopyranose (CCD ID: GLA) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	1
			12	6	6		
6	B	1	Total	C	O	0	1
			12	6	6		
6	C	1	Total	C	O	0	0
			12	6	6		
6	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 7 is beta-D-galactopyranose (CCD ID: GAL) (formula: $C_6H_{12}O_6$) (labeled as "Ligand of Interest" by depositor).



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

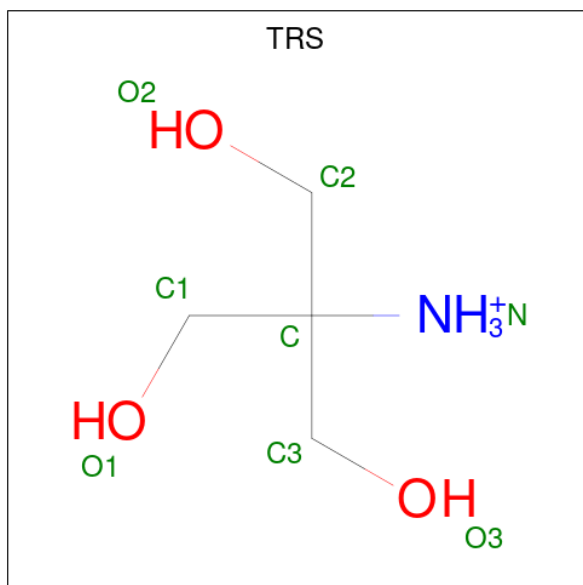
- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0
8	C	2	Total Cl 2 2	0	0

- Molecule 9 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	3	Total Na 3 3	0	0
9	C	1	Total Na 1 1	0	0
9	D	2	Total Na 2 2	0	0

- Molecule 10 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
10	D	1	8	4	1	3	0	0

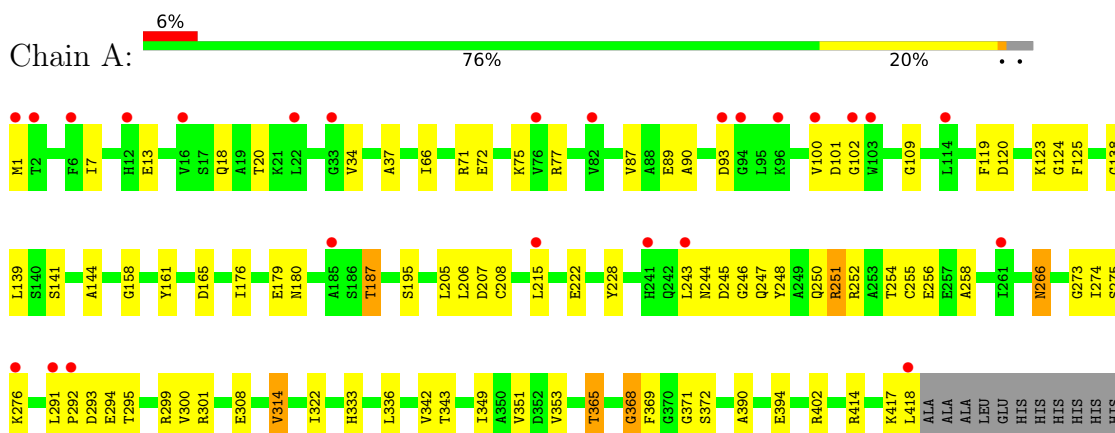
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	214	Total 214	O 214	0	0
11	B	209	Total 209	O 209	0	0
11	C	201	Total 201	O 201	0	0
11	D	140	Total 140	O 140	0	0

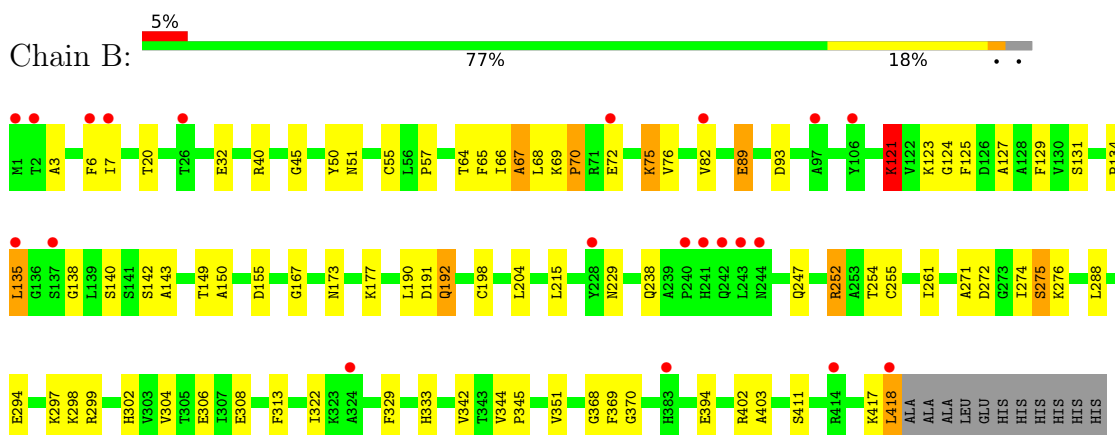
3 Residue-property plots

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.

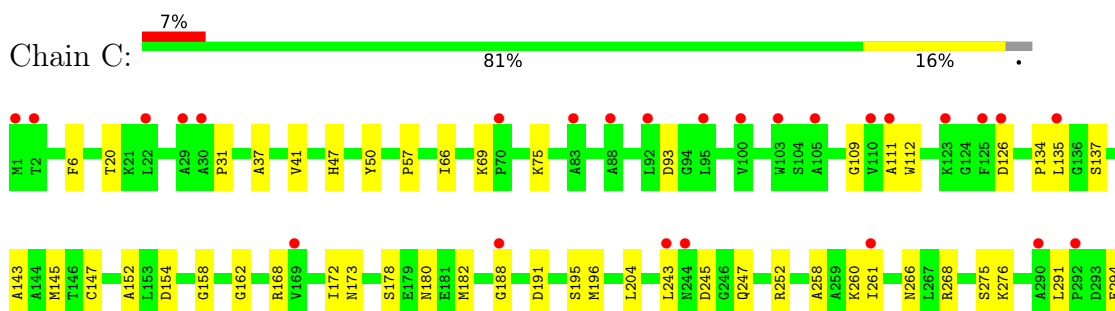
- Molecule 1: Galactokinase



- Molecule 1: Galactokinase

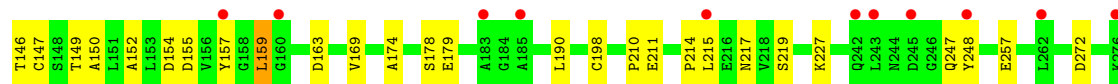
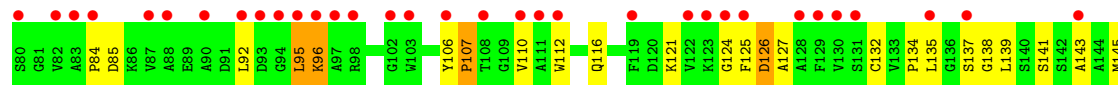
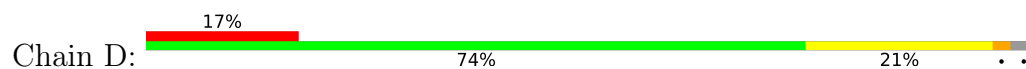


- Molecule 1: Galactokinase





● Molecule 1: Galactokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.32Å 164.93Å 113.63Å 90.00° 94.97° 90.00°	Depositor
Resolution (Å)	82.60 – 1.68 82.60 – 1.68	Depositor EDS
% Data completeness (in resolution range)	94.5 (82.60-1.68) 94.6 (82.60-1.68)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 1.68Å)	Xtrriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.224 , 0.308 0.231 , 0.312	Depositor DCC
R_{free} test set	10249 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtrriage
Anisotropy	0.743	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14073	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PG4, GOL, TRS, PEG, GLA, PGE, GAL, NA, CL

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	1.32	11/3236 (0.3%)	1.55	16/4392 (0.4%)
1	B	1.33	10/3265 (0.3%)	1.54	15/4425 (0.3%)
1	C	1.29	9/3242 (0.3%)	1.53	13/4398 (0.3%)
1	D	1.23	3/3259 (0.1%)	1.58	18/4417 (0.4%)
All	All	1.29	33/13002 (0.3%)	1.55	62/17632 (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
1	D	0	1
All	All	0	2

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	167	GLY	C-O	7.88	1.33	1.23
1	C	145	MET	C-O	7.35	1.32	1.24
1	B	275	SER	C-O	7.29	1.32	1.24
1	D	33	GLY	C-O	6.83	1.30	1.23
1	A	390	ALA	C-O	6.55	1.31	1.24

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	49	ASP	CA-CB-CG	7.46	120.06	112.60
1	B	121	LYS	CB-CA-C	-7.10	98.78	110.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	GLU	N-CA-C	-7.08	103.64	111.36
1	A	301	ARG	CA-C-O	-6.90	113.18	120.63
1	C	333	HIS	CA-CB-CG	-6.76	107.04	113.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	244	ASN	Peptide
1	D	38	PRO	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3182	0	3065	99	0
1	B	3212	0	3131	85	0
1	C	3188	0	3093	37	0
1	D	3207	0	3119	77	0
2	A	54	0	72	20	0
2	B	42	0	56	18	0
2	C	42	0	56	7	0
2	D	24	0	32	3	0
3	A	98	0	140	40	0
3	B	63	0	90	24	0
3	C	28	0	40	7	0
3	D	14	0	20	0	0
4	A	30	0	42	27	0
4	B	10	0	14	0	0
5	A	26	0	36	8	0
6	A	12	0	12	0	0
6	B	12	0	12	0	0
6	C	12	0	12	0	0
6	D	12	0	12	0	0
7	A	12	0	12	2	0
7	B	12	0	12	0	0
8	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	2	0	0	0	0
9	B	3	0	0	0	0
9	C	1	0	0	0	0
9	D	2	0	0	0	0
10	D	8	0	12	3	0
11	A	214	0	0	14	0
11	B	209	0	0	12	0
11	C	201	0	0	4	0
11	D	140	0	0	6	0
All	All	14073	0	13090	334	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 13.

The worst 5 of 334 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)
3:A:918[A]:PEG:O4	3:A:918[A]:PEG:H22	1.58	1.04
1:D:159[B]:LEU:N	1:D:159[B]:LEU:HD22	1.76	0.99
1:D:71:ARG:HD2	1:D:126:ASP:OD1	1.65	0.96
1:B:125:PHE:CE1	11:B:1002:HOH:O	2.18	0.96
4:A:921:PGE:H4	11:A:1005:HOH:O	1.63	0.95

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	A	427/429 (100%)	413 (97%)	14 (3%)	0	100 100
1	B	428/429 (100%)	413 (96%)	15 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	426/429 (99%)	410 (96%)	15 (4%)	1 (0%)	43	27
1	D	427/429 (100%)	403 (94%)	24 (6%)	0	100	100
All	All	1708/1716 (100%)	1639 (96%)	68 (4%)	1 (0%)	48	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	158	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	A	317/326 (97%)	313 (99%)	4 (1%)	61	39
1	B	325/326 (100%)	318 (98%)	7 (2%)	45	19
1	C	322/326 (99%)	311 (97%)	11 (3%)	32	8
1	D	323/326 (99%)	304 (94%)	19 (6%)	18	2
All	All	1287/1304 (99%)	1246 (97%)	41 (3%)	39	9

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	96[B]	LYS
1	D	219	SER
1	D	126	ASP
1	D	137[B]	SER
1	D	247[A]	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	250	GLN

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Mol	Chain	Res	Type
1	D	381	GLN
1	C	266	ASN
1	C	383	HIS
1	D	116	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 78 ligands modelled in this entry, 9 are monoatomic - leaving 69 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	$\# Z > 2$
2	GOL	A	909	-	5,5,5	0.08	0	5,5,5	0.30	0
3	PEG	B	708	-	6,6,6	0.38	0	5,5,5	0.27	0
2	GOL	A	923	-	5,5,5	0.14	0	5,5,5	0.30	0
2	GOL	B	710	-	5,5,5	0.21	0	5,5,5	0.54	0
3	PEG	A	903	-	6,6,6	0.29	0	5,5,5	0.29	0
2	GOL	B	701	-	5,5,5	0.21	0	5,5,5	0.41	0
2	GOL	C	605	-	5,5,5	0.14	0	5,5,5	0.43	0
2	GOL	B	709	-	5,5,5	0.09	0	5,5,5	0.28	0
2	GOL	D	604	-	5,5,5	0.14	0	5,5,5	0.26	0
3	PEG	B	704	-	6,6,6	0.34	0	5,5,5	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	901	-	5,5,5	0.08	0	5,5,5	0.27	0
3	PEG	B	711	-	6,6,6	0.25	0	5,5,5	0.19	0
7	GAL	A	928[B]	-	12,12,12	0.48	0	17,17,17	0.91	0
3	PEG	A	908[B]	-	6,6,6	0.12	0	5,5,5	0.21	0
4	PGE	A	919	-	9,9,9	0.23	0	8,8,8	0.15	0
3	PEG	A	915	-	6,6,6	0.38	0	5,5,5	0.39	0
10	TRS	D	601	-	7,7,7	0.17	0	9,9,9	0.56	0
5	PG4	A	924	-	12,12,12	0.21	0	11,11,11	0.26	0
3	PEG	B	703	-	6,6,6	0.43	0	5,5,5	0.30	0
2	GOL	A	925	-	5,5,5	0.10	0	5,5,5	0.40	0
3	PEG	A	917	-	6,6,6	0.26	0	5,5,5	0.44	0
3	PEG	A	926	-	6,6,6	0.28	0	5,5,5	0.23	0
2	GOL	C	603	-	5,5,5	0.13	0	5,5,5	0.32	0
3	PEG	A	907	-	6,6,6	0.28	0	5,5,5	0.29	0
2	GOL	D	606	-	5,5,5	0.16	0	5,5,5	0.43	0
2	GOL	B	707	-	5,5,5	0.14	0	5,5,5	0.37	0
3	PEG	A	918[B]	-	6,6,6	0.29	0	5,5,5	0.10	0
4	PGE	B	714	-	9,9,9	0.29	0	8,8,8	0.22	0
3	PEG	A	908[A]	-	6,6,6	0.20	0	5,5,5	0.21	0
3	PEG	A	910	-	6,6,6	0.17	0	5,5,5	0.18	0
3	PEG	C	610	-	6,6,6	0.24	0	5,5,5	0.33	0
3	PEG	B	713	-	6,6,6	0.27	0	5,5,5	0.43	0
2	GOL	B	712	-	5,5,5	0.15	0	5,5,5	0.40	0
5	PG4	A	922	-	12,12,12	0.29	0	11,11,11	0.15	0
3	PEG	C	607[B]	-	6,6,6	0.23	0	5,5,5	0.17	0
6	GLA	A	927[A]	-	12,12,12	1.23	1 (8%)	17,17,17	1.36	3 (17%)
2	GOL	A	913	-	5,5,5	0.16	0	5,5,5	0.40	0
2	GOL	C	606	-	5,5,5	0.17	0	5,5,5	0.41	0
2	GOL	D	603	-	5,5,5	0.20	0	5,5,5	0.38	0
3	PEG	A	918[A]	-	6,6,6	0.24	0	5,5,5	0.14	0
2	GOL	C	609	-	5,5,5	0.15	0	5,5,5	0.29	0
3	PEG	C	608	-	6,6,6	0.45	0	5,5,5	0.54	0
4	PGE	A	920	-	9,9,9	0.30	0	8,8,8	0.34	0
3	PEG	A	912	-	6,6,6	0.39	0	5,5,5	0.27	0
6	GLA	B	718[A]	-	12,12,12	0.90	0	17,17,17	1.00	0
2	GOL	C	604	-	5,5,5	0.11	0	5,5,5	0.27	0
3	PEG	A	906	-	6,6,6	0.27	0	5,5,5	0.19	0
2	GOL	C	602	-	5,5,5	0.18	0	5,5,5	0.39	0
3	PEG	B	702	-	6,6,6	0.45	0	5,5,5	0.38	0
3	PEG	B	716	-	6,6,6	0.36	0	5,5,5	0.24	0
3	PEG	C	607[A]	-	6,6,6	0.42	0	5,5,5	0.37	0
6	GLA	D	608	-	12,12,12	0.90	0	17,17,17	1.28	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	C	601	-	5,5,5	0.17	0	5,5,5	0.47	0
2	GOL	A	905	-	5,5,5	0.16	0	5,5,5	0.45	0
2	GOL	B	706	-	5,5,5	0.11	0	5,5,5	0.31	0
3	PEG	D	605	-	6,6,6	0.34	0	5,5,5	0.30	0
7	GAL	B	719[B]	-	12,12,12	0.45	0	17,17,17	0.69	0
3	PEG	B	715	-	6,6,6	0.39	0	5,5,5	0.24	0
3	PEG	B	705	-	6,6,6	0.40	0	5,5,5	0.25	0
3	PEG	A	904	-	6,6,6	0.31	0	5,5,5	0.24	0
2	GOL	B	717	-	5,5,5	0.12	0	5,5,5	0.36	0
2	GOL	D	607	-	5,5,5	0.16	0	5,5,5	0.44	0
2	GOL	A	902	-	5,5,5	0.24	0	5,5,5	0.55	0
4	PGE	A	921	-	9,9,9	0.32	0	8,8,8	0.18	0
6	GLA	C	611	-	12,12,12	1.13	0	17,17,17	1.44	3 (17%)
2	GOL	A	911	-	5,5,5	0.16	0	5,5,5	0.55	0
3	PEG	A	914	-	6,6,6	0.46	0	5,5,5	0.25	0
3	PEG	D	602	-	6,6,6	0.31	0	5,5,5	0.30	0
2	GOL	A	916	-	5,5,5	0.09	0	5,5,5	0.30	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
2	GOL	A	909	-	-	4/4/4/4	-
3	PEG	B	708	-	-	3/4/4/4	-
2	GOL	A	923	-	-	4/4/4/4	-
2	GOL	B	710	-	-	4/4/4/4	-
3	PEG	A	903	-	-	4/4/4/4	-
2	GOL	B	701	-	-	0/4/4/4	-
2	GOL	C	605	-	-	2/4/4/4	-
2	GOL	B	709	-	-	3/4/4/4	-
2	GOL	D	604	-	-	0/4/4/4	-
3	PEG	B	704	-	-	3/4/4/4	-
2	GOL	A	901	-	-	2/4/4/4	-
3	PEG	B	711	-	-	1/4/4/4	-
7	GAL	A	928[B]	-	-	2/2/22/22	0/1/1/1
3	PEG	A	908[B]	-	-	3/4/4/4	-
4	PGE	A	919	-	-	4/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	A	915	-	-	2/4/4/4	-
10	TRS	D	601	-	-	2/9/9/9	-
5	PG4	A	924	-	-	7/10/10/10	-
3	PEG	B	703	-	-	2/4/4/4	-
2	GOL	A	925	-	-	2/4/4/4	-
3	PEG	A	917	-	-	3/4/4/4	-
3	PEG	A	926	-	-	3/4/4/4	-
2	GOL	C	603	-	-	3/4/4/4	-
3	PEG	A	907	-	-	3/4/4/4	-
2	GOL	D	606	-	-	4/4/4/4	-
2	GOL	B	707	-	-	4/4/4/4	-
3	PEG	A	918[B]	-	-	3/4/4/4	-
4	PGE	B	714	-	-	4/7/7/7	-
3	PEG	A	908[A]	-	-	3/4/4/4	-
3	PEG	A	910	-	-	2/4/4/4	-
3	PEG	C	610	-	-	3/4/4/4	-
3	PEG	B	713	-	-	4/4/4/4	-
2	GOL	B	712	-	-	3/4/4/4	-
5	PG4	A	922	-	-	5/10/10/10	-
3	PEG	C	607[B]	-	-	3/4/4/4	-
6	GLA	A	927[A]	-	-	1/2/22/22	0/1/1/1
2	GOL	A	913	-	-	0/4/4/4	-
2	GOL	C	606	-	-	4/4/4/4	-
2	GOL	D	603	-	-	2/4/4/4	-
3	PEG	A	918[A]	-	-	2/4/4/4	-
2	GOL	C	609	-	-	2/4/4/4	-
3	PEG	C	608	-	-	4/4/4/4	-
4	PGE	A	920	-	-	4/7/7/7	-
3	PEG	A	912	-	-	3/4/4/4	-
6	GLA	B	718[A]	-	-	1/2/22/22	0/1/1/1
2	GOL	C	604	-	-	4/4/4/4	-
3	PEG	A	906	-	-	3/4/4/4	-
2	GOL	C	602	-	-	1/4/4/4	-
3	PEG	B	702	-	-	3/4/4/4	-
3	PEG	B	716	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	C	607[A]	-	-	3/4/4/4	-
6	GLA	D	608	-	-	2/2/22/22	0/1/1/1
2	GOL	C	601	-	-	2/4/4/4	-
2	GOL	A	905	-	-	0/4/4/4	-
2	GOL	B	706	-	-	0/4/4/4	-
3	PEG	D	605	-	-	2/4/4/4	-
7	GAL	B	719[B]	-	-	1/2/22/22	0/1/1/1
3	PEG	B	715	-	-	4/4/4/4	-
3	PEG	B	705	-	-	3/4/4/4	-
3	PEG	A	904	-	-	2/4/4/4	-
2	GOL	B	717	-	-	4/4/4/4	-
2	GOL	D	607	-	-	2/4/4/4	-
2	GOL	A	902	-	-	3/4/4/4	-
4	PGE	A	921	-	-	4/7/7/7	-
6	GLA	C	611	-	-	1/2/22/22	0/1/1/1
2	GOL	A	911	-	-	4/4/4/4	-
3	PEG	A	914	-	-	3/4/4/4	-
3	PEG	D	602	-	-	4/4/4/4	-
2	GOL	A	916	-	-	3/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	927[A]	GLA	C4-C3	2.11	1.57	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	608	GLA	O3-C3-C4	3.11	117.70	110.38
6	C	611	GLA	O2-C2-C3	3.02	117.50	110.38
6	C	611	GLA	C1-O5-C5	2.92	119.30	113.65
6	A	927[A]	GLA	O5-C5-C6	2.82	113.42	106.44
6	A	927[A]	GLA	C1-O5-C5	2.55	118.58	113.65

There are no chirality outliers.

5 of 189 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	GOL	O1-C1-C2-O2
2	A	901	GOL	O1-C1-C2-C3
2	A	902	GOL	O1-C1-C2-C3
2	A	909	GOL	O1-C1-C2-O2
2	A	909	GOL	O1-C1-C2-C3

There are no ring outliers.

47 monomers are involved in 152 short contacts:

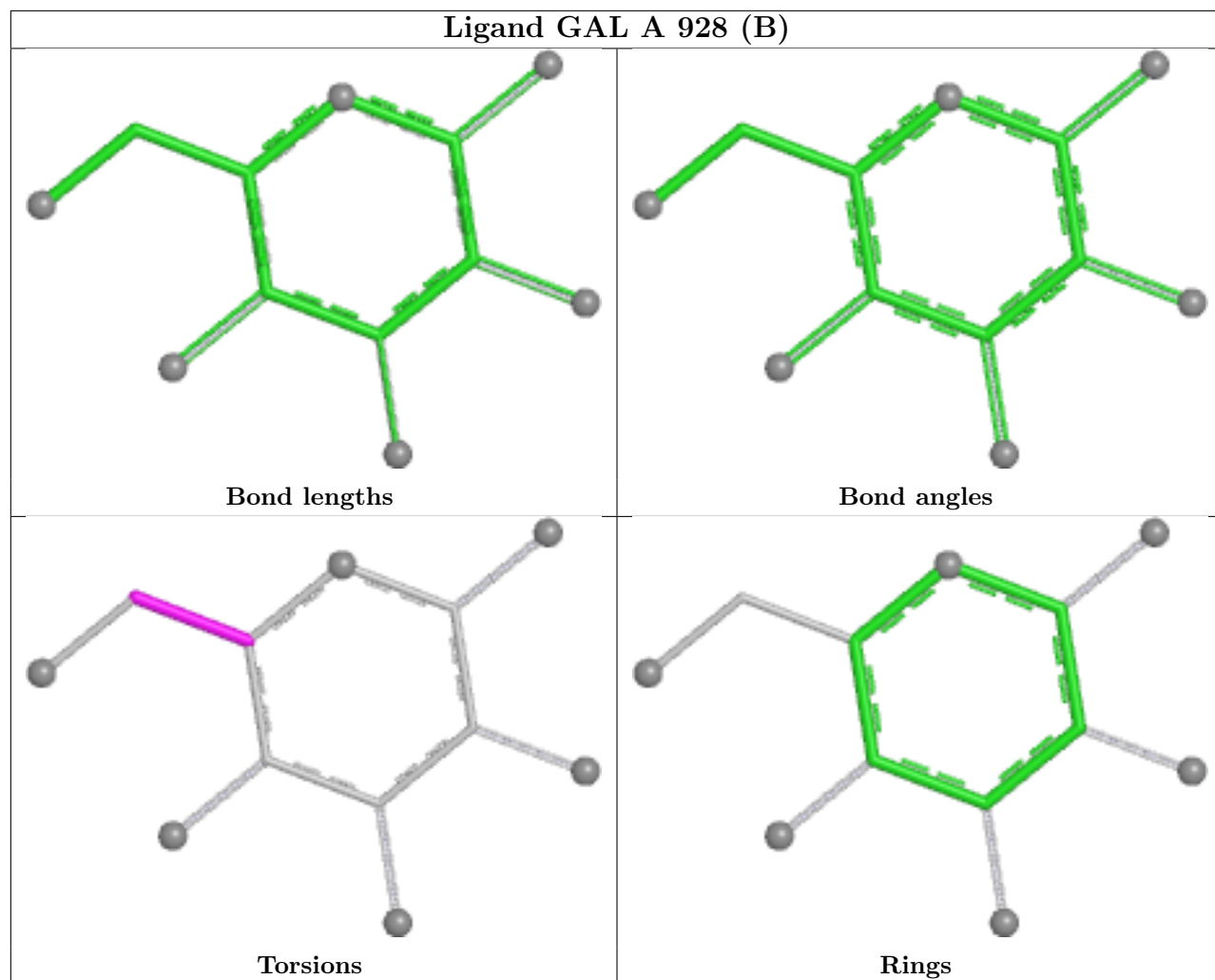
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	909	GOL	2	0
2	A	923	GOL	3	0
2	B	710	GOL	6	0
3	A	903	PEG	4	0
2	B	701	GOL	7	0
3	B	704	PEG	12	0
2	A	901	GOL	1	0
3	B	711	PEG	1	0
7	A	928[B]	GAL	2	0
3	A	908[B]	PEG	1	0
4	A	919	PGE	8	0
3	A	915	PEG	2	0
10	D	601	TRS	3	0
5	A	924	PG4	1	0
3	B	703	PEG	3	0
2	A	925	GOL	3	0
3	A	917	PEG	1	0
3	A	926	PEG	3	0
2	C	603	GOL	1	0
3	A	907	PEG	4	0
2	D	606	GOL	1	0
3	A	908[A]	PEG	2	0
3	C	610	PEG	1	0
3	B	713	PEG	1	0
5	A	922	PG4	7	0
3	C	607[B]	PEG	1	0
2	A	913	GOL	2	0
2	C	606	GOL	5	0
2	D	603	GOL	2	0
3	A	918[A]	PEG	8	0
2	C	609	GOL	1	0
3	C	608	PEG	3	0
4	A	920	PGE	5	0

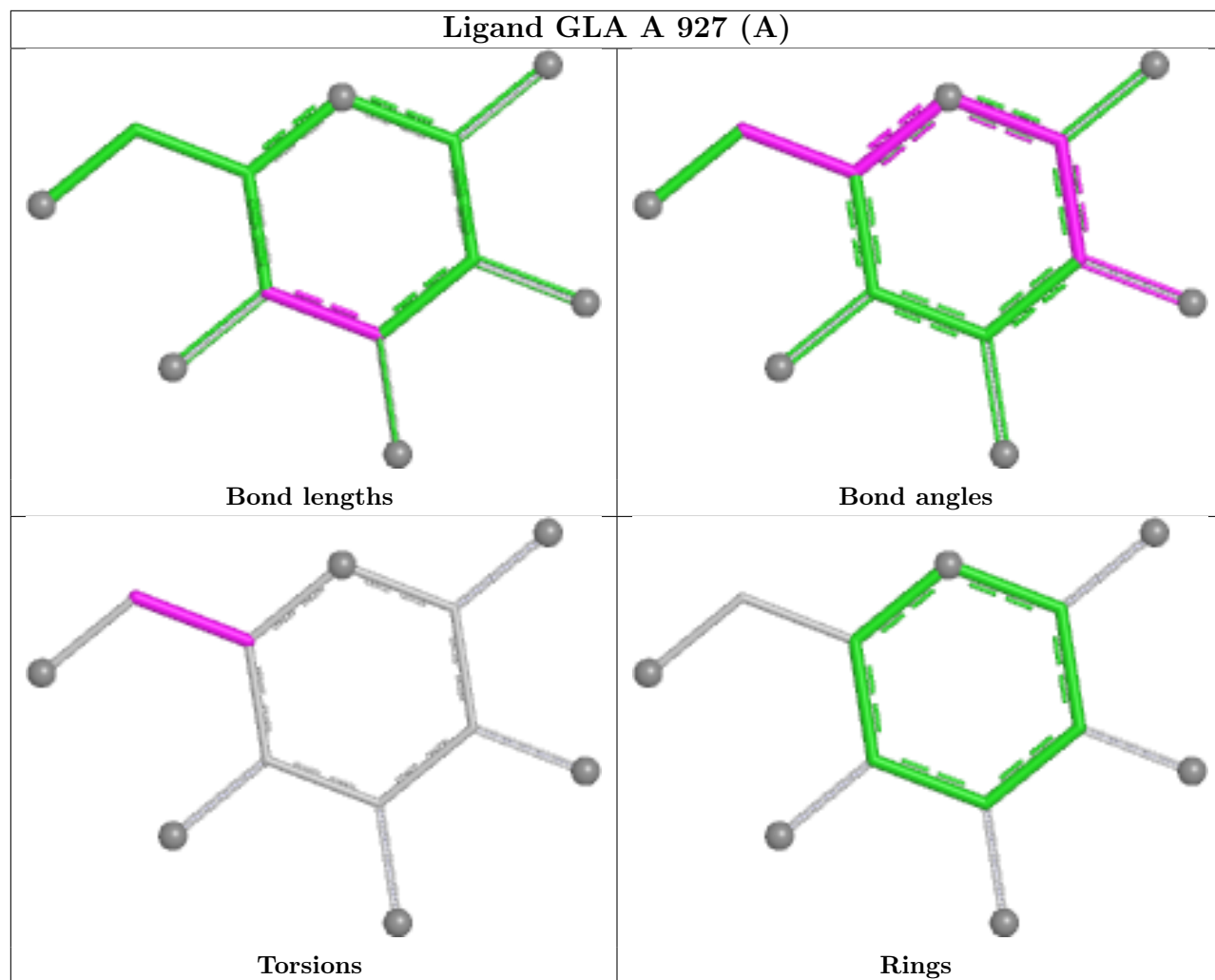
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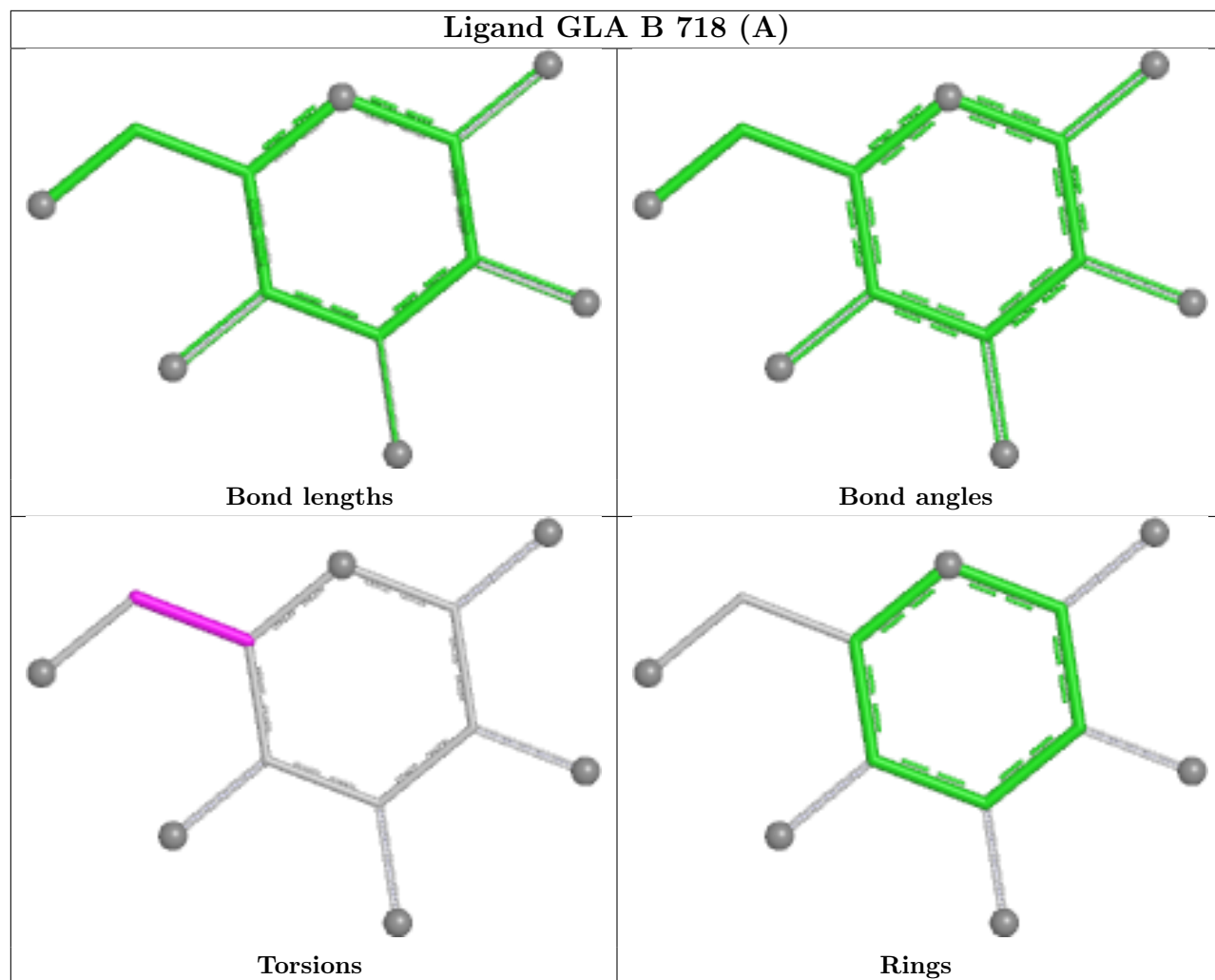
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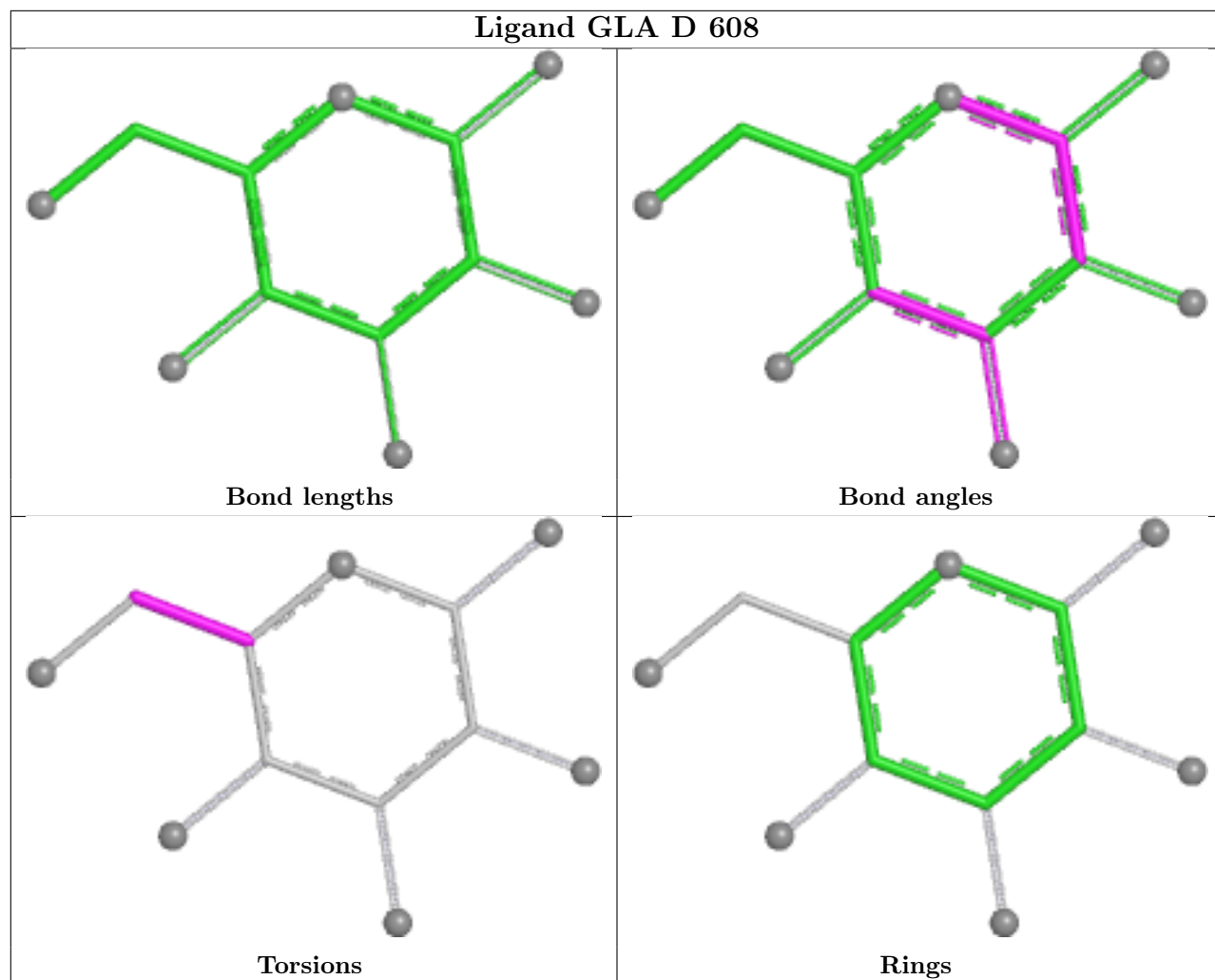
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	912	PEG	6	0
3	A	906	PEG	1	0
3	B	702	PEG	4	0
3	B	716	PEG	1	0
3	C	607[A]	PEG	2	0
2	A	905	GOL	1	0
2	B	706	GOL	4	0
3	B	705	PEG	2	0
3	A	904	PEG	5	0
2	B	717	GOL	1	0
4	A	921	PGE	14	0
2	A	911	GOL	7	0
3	A	914	PEG	3	0
2	A	916	GOL	1	0

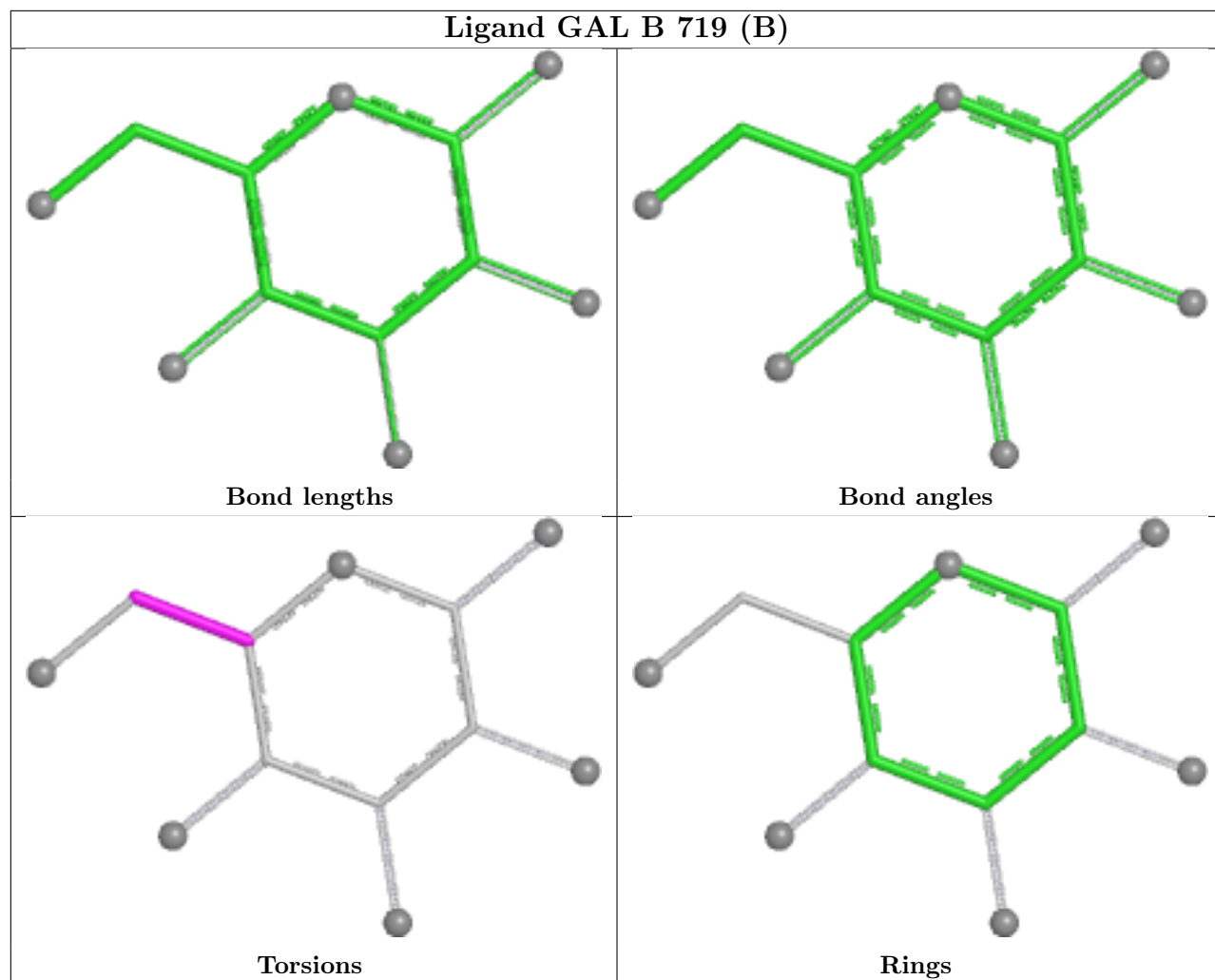
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 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.

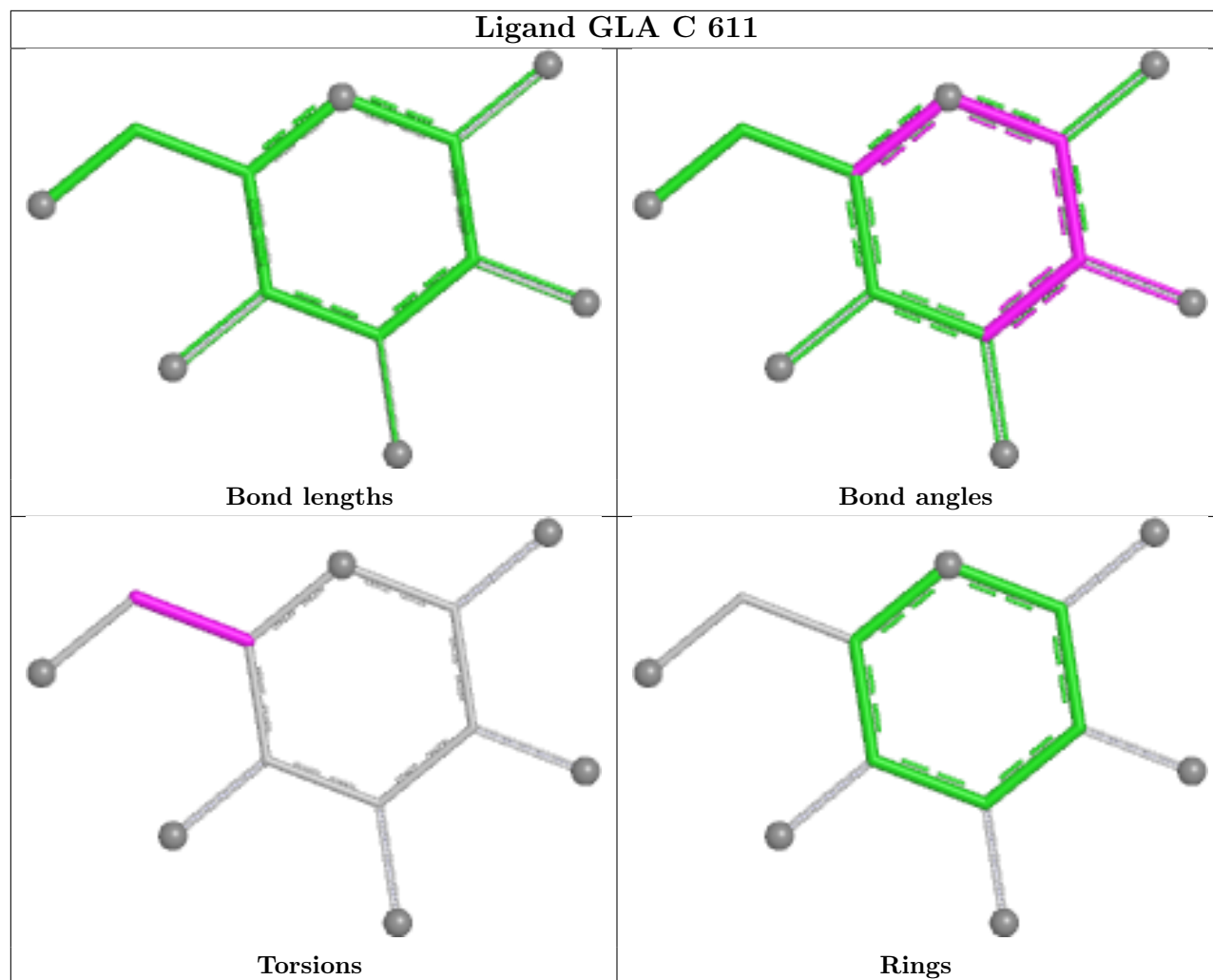












5.7 Other polymers [\(i\)](#)

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	A	418/429 (97%)	0.55	25 (5%) 27 36	8, 22, 36, 66	17 (4%)
1	B	418/429 (97%)	0.56	21 (5%) 34 42	7, 21, 35, 65	17 (4%)
1	C	416/429 (96%)	0.68	28 (6%) 24 30	7, 24, 36, 71	18 (4%)
1	D	416/429 (96%)	1.14	74 (17%) 4 4	9, 30, 48, 69	18 (4%)
All	All	1668/1716 (97%)	0.73	148 (8%) 15 18	7, 24, 41, 71	70 (4%)

The worst 5 of 148 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	398	PHE	5.6
1	D	82	VAL	5.3
1	D	92	LEU	4.9
1	D	94	GLY	4.5
1	D	122	VAL	4.5

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](#)

There are no oligosaccharides 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(\AA^2)	Q<0.9
3	PEG	A	908[A]	7/7	0.73	0.20	14,19,23,28	7
3	PEG	A	908[B]	7/7	0.73	0.20	23,24,27,27	7
2	GOL	C	602	6/6	0.75	0.24	27,30,32,35	6
3	PEG	A	910	7/7	0.75	0.17	40,47,55,55	0
3	PEG	A	915	7/7	0.76	0.20	34,40,51,79	0
10	TRS	D	601	8/8	0.76	0.16	32,39,43,58	0
2	GOL	C	603	6/6	0.77	0.18	45,49,58,58	0
5	PG4	A	924	13/13	0.79	0.17	34,39,47,51	0
7	GAL	A	928[B]	12/12	0.79	0.11	5,6,6,6	12
3	PEG	B	704	7/7	0.79	0.17	29,35,42,43	0
3	PEG	C	608	7/7	0.80	0.15	40,41,46,49	0
4	PGE	A	921	10/10	0.81	0.14	31,43,50,50	0
2	GOL	B	701	6/6	0.81	0.18	17,18,21,29	6
2	GOL	A	923	6/6	0.82	0.13	35,38,48,55	0
3	PEG	C	610	7/7	0.82	0.20	29,32,40,43	4
9	NA	B	720	1/1	0.82	0.15	50,50,50,50	0
9	NA	D	610	1/1	0.82	0.15	51,51,51,51	0
3	PEG	B	705	7/7	0.82	0.18	28,39,47,47	0
3	PEG	A	926	7/7	0.83	0.13	32,37,41,45	0
2	GOL	B	712	6/6	0.83	0.12	49,49,51,61	0
2	GOL	A	911	6/6	0.83	0.18	18,22,24,29	6
7	GAL	B	719[B]	12/12	0.83	0.09	10,11,12,12	12
2	GOL	A	916	6/6	0.83	0.14	41,46,48,49	0
2	GOL	C	604	6/6	0.83	0.25	25,30,33,38	6
3	PEG	D	605	7/7	0.83	0.16	45,50,55,67	0
2	GOL	D	603	6/6	0.84	0.13	31,35,36,39	0
2	GOL	A	902	6/6	0.85	0.13	36,41,44,47	0
3	PEG	B	716	7/7	0.85	0.15	39,42,47,48	0
3	PEG	A	917	7/7	0.85	0.13	34,37,41,41	0
4	PGE	A	919	10/10	0.86	0.14	28,40,45,47	0
2	GOL	B	707	6/6	0.86	0.15	37,45,51,53	0
2	GOL	A	913	6/6	0.86	0.12	30,36,47,51	0
3	PEG	B	711	7/7	0.86	0.14	35,41,46,55	0
2	GOL	A	905	6/6	0.86	0.13	43,45,49,51	0
3	PEG	A	918[A]	7/7	0.86	0.15	21,23,26,27	7
3	PEG	A	918[B]	7/7	0.86	0.15	26,29,42,45	7
2	GOL	B	706	6/6	0.86	0.18	35,49,61,73	0
4	PGE	B	714	10/10	0.87	0.14	36,46,52,60	0
5	PG4	A	922	13/13	0.87	0.15	34,44,52,53	0
3	PEG	A	906	7/7	0.87	0.12	28,34,44,49	0
3	PEG	B	703	7/7	0.87	0.13	31,35,41,43	0
3	PEG	A	904	7/7	0.87	0.14	35,37,45,47	0
3	PEG	A	912	7/7	0.87	0.14	31,37,48,50	0

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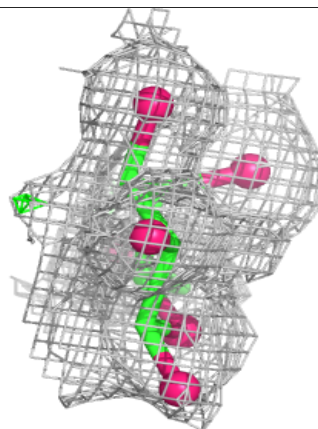
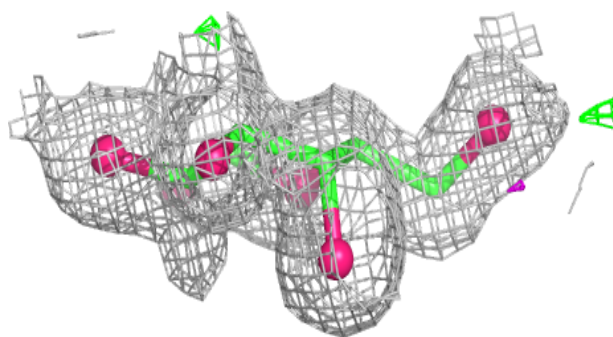
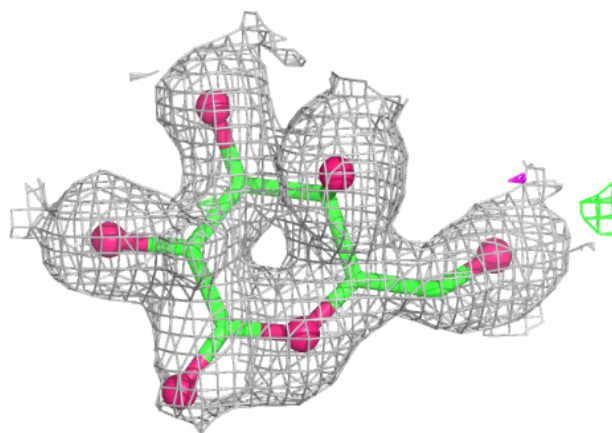
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PEG	B	708	7/7	0.87	0.12	37,44,50,50	0
3	PEG	A	914	7/7	0.87	0.12	40,45,51,59	0
2	GOL	C	601	6/6	0.88	0.13	35,43,47,49	0
2	GOL	B	709	6/6	0.88	0.10	42,54,56,61	0
2	GOL	C	609	6/6	0.89	0.16	34,35,41,43	0
3	PEG	B	713	7/7	0.89	0.10	29,38,41,46	0
2	GOL	B	710	6/6	0.89	0.14	31,35,42,53	0
2	GOL	D	606	6/6	0.89	0.12	47,51,54,55	0
2	GOL	D	607	6/6	0.89	0.12	28,35,38,48	0
3	PEG	A	903	7/7	0.89	0.13	37,44,51,52	0
9	NA	C	612	1/1	0.89	0.14	48,48,48,48	0
2	GOL	B	717	6/6	0.89	0.12	38,39,43,44	0
2	GOL	C	605	6/6	0.89	0.12	38,40,45,55	0
3	PEG	B	715	7/7	0.90	0.13	36,37,50,52	0
2	GOL	C	606	6/6	0.90	0.11	39,40,41,44	0
3	PEG	A	907	7/7	0.90	0.14	34,36,44,55	0
3	PEG	B	702	7/7	0.90	0.14	20,23,31,32	0
3	PEG	C	607[B]	7/7	0.91	0.09	22,24,25,28	7
4	PGE	A	920	10/10	0.91	0.14	19,44,53,57	0
3	PEG	C	607[A]	7/7	0.91	0.09	13,14,17,17	7
2	GOL	A	909	6/6	0.92	0.10	31,33,36,40	0
3	PEG	D	602	7/7	0.92	0.11	28,35,43,44	0
2	GOL	D	604	6/6	0.92	0.09	40,41,42,45	0
6	GLA	A	927[A]	12/12	0.93	0.08	16,19,21,22	0
2	GOL	A	925	6/6	0.93	0.13	23,23,26,31	4
2	GOL	A	901	6/6	0.93	0.13	23,27,31,35	6
8	CL	A	929	1/1	0.93	0.13	49,49,49,49	0
6	GLA	D	608	12/12	0.94	0.07	18,23,25,26	0
6	GLA	C	611	12/12	0.95	0.07	16,19,23,29	0
8	CL	C	613	1/1	0.95	0.11	61,61,61,61	0
6	GLA	B	718[A]	12/12	0.95	0.08	16,21,23,23	0
9	NA	B	721	1/1	0.96	0.12	37,37,37,37	0
9	NA	B	722	1/1	0.97	0.06	40,40,40,40	0
9	NA	D	609	1/1	0.97	0.07	42,42,42,42	0
8	CL	C	614	1/1	0.99	0.04	23,23,23,23	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.

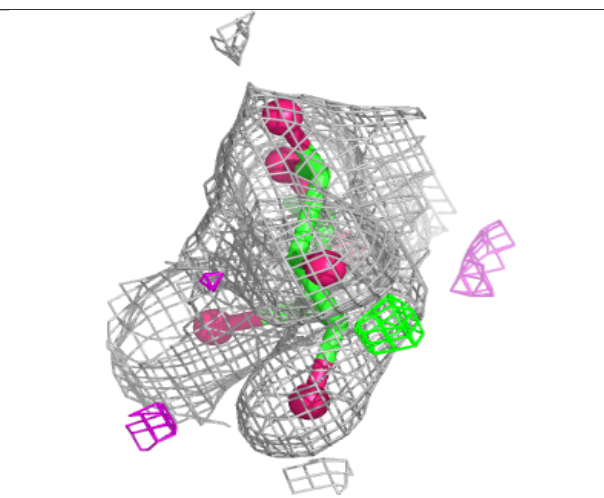
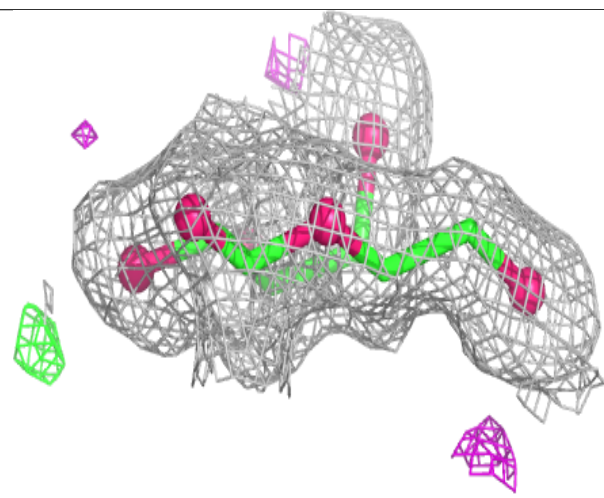
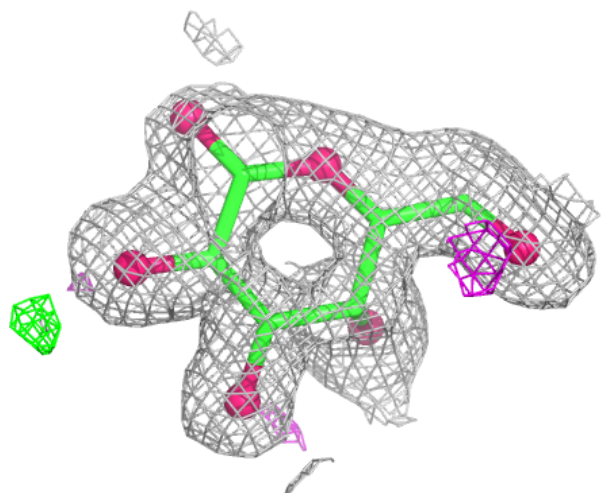
Electron density around GAL A 928 (B):

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



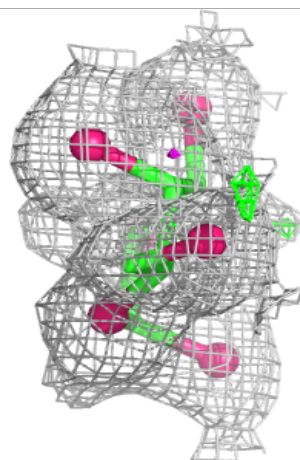
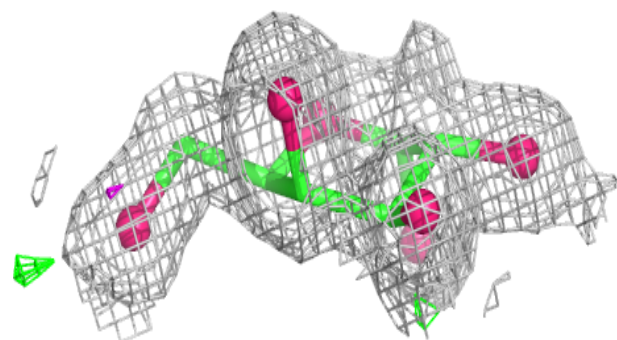
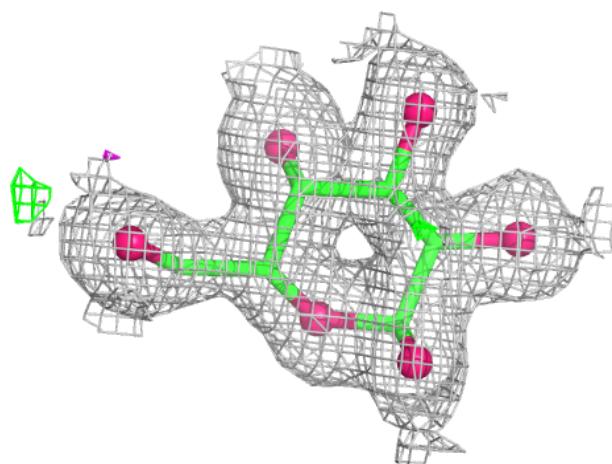
Electron density around GAL B 719 (B):

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



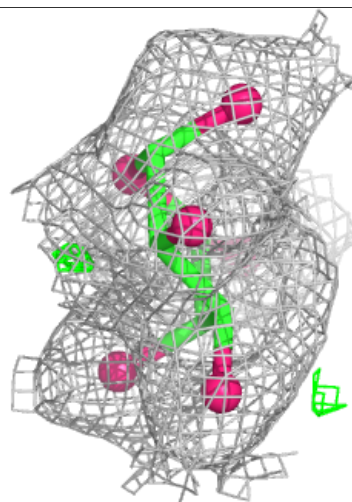
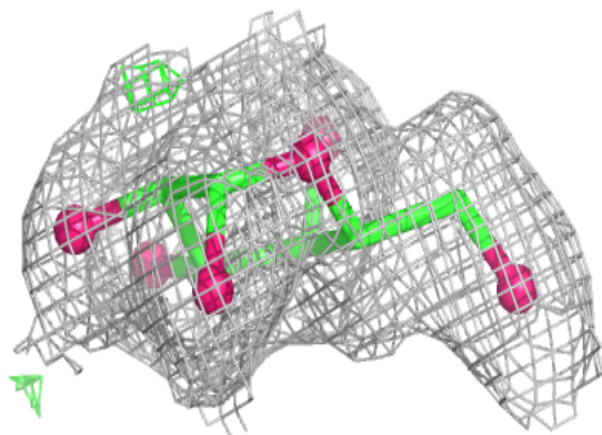
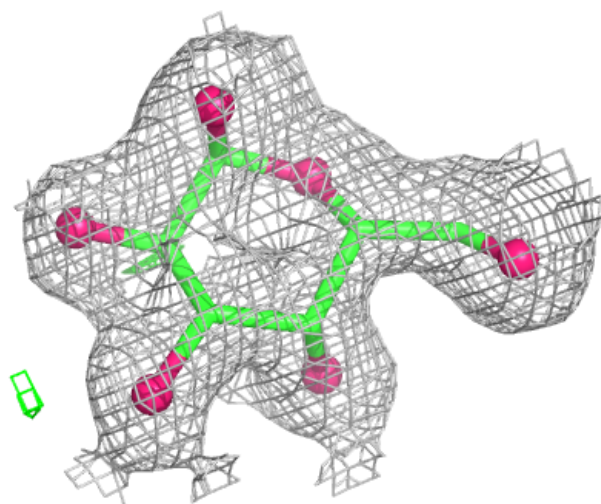
Electron density around GLA A 927 (A):

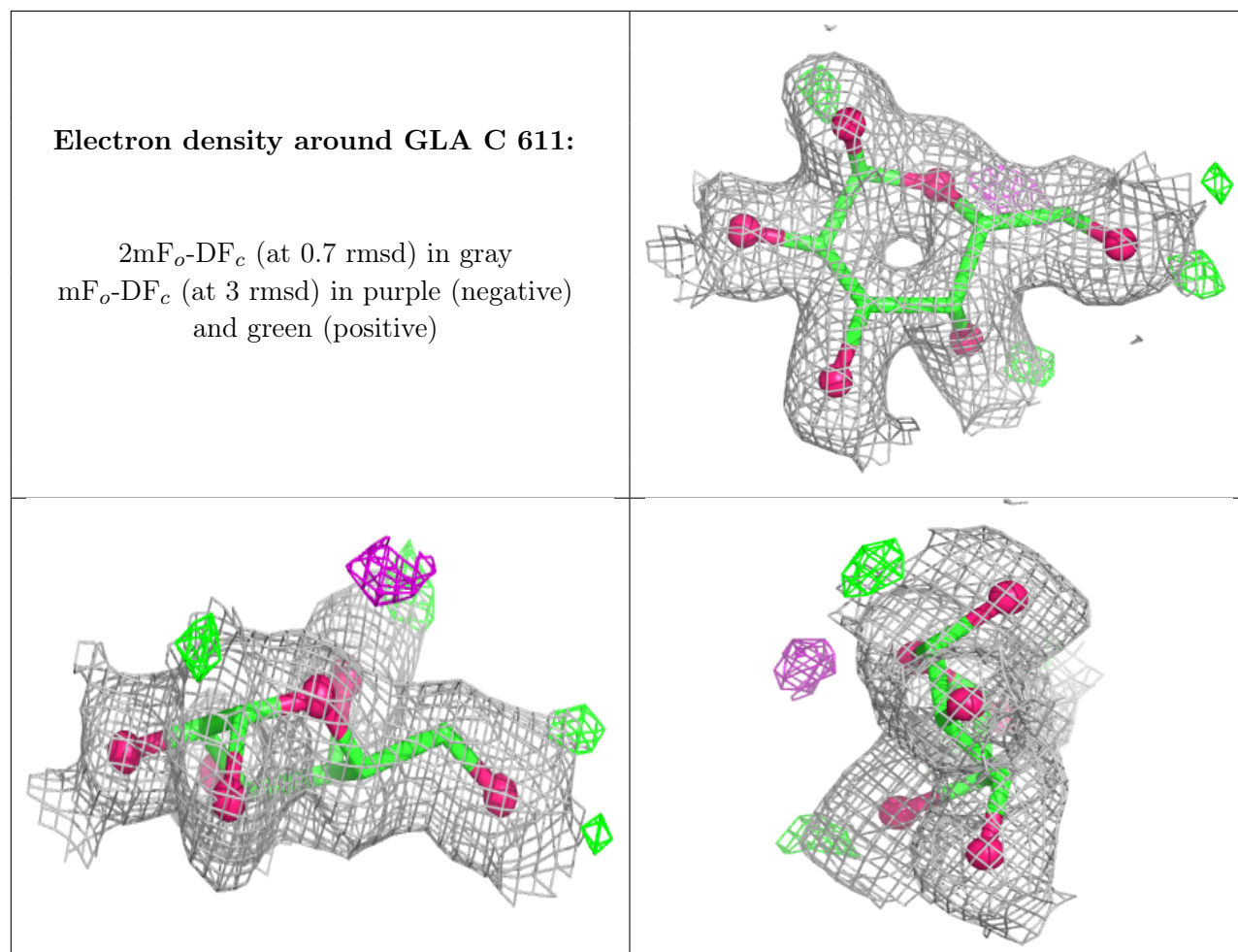
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

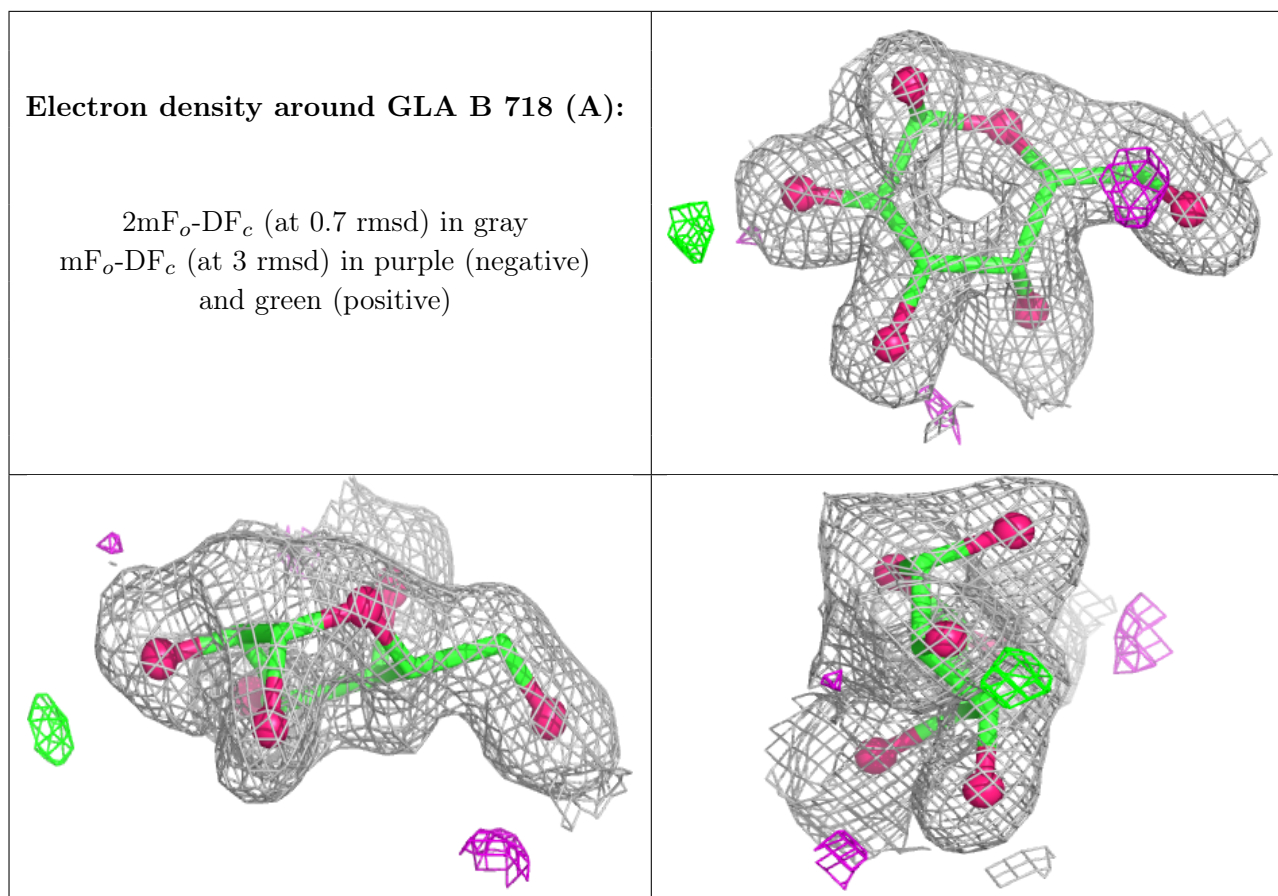


Electron density around GLA D 608:

$2mF_o-DF_c$ (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.