



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 10:35 PM EDT

PDB ID : 6TEQ
Title : Crystal structure of a galactokinase from Bifidobacterium infantis in complex with 2-deoxy-2-fluoro-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 : 1.44 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	:	4.02b-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

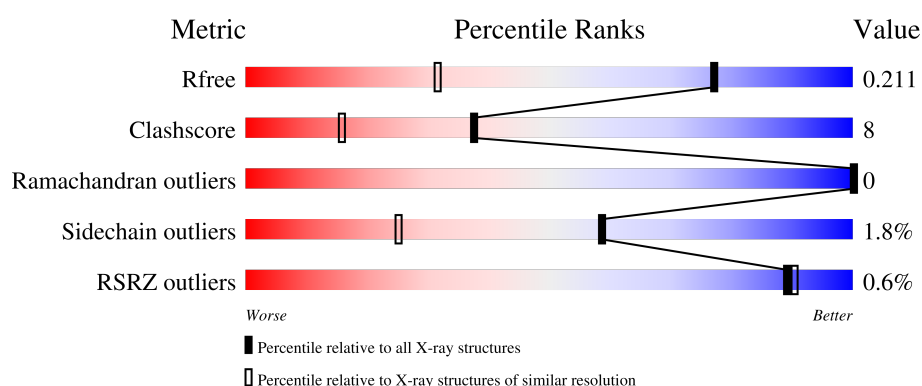
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.44 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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
3	PEG	B	601	-	-	X	-
3	PEG	C	602	-	-	X	-
3	PEG	C	603	-	-	X	-
3	PEG	C	605	-	-	X	-
3	PEG	C	613	-	-	X	-
3	PEG	C	614	-	-	X	-
3	PEG	C	618	-	-	X	-
4	GOL	B	602	-	-	X	-
4	GOL	C	608	-	-	X	-
4	GOL	C	610	-	-	X	-
4	GOL	D	704	-	-	X	-
4	GOL	D	707	-	-	X	-
9	PGE	C	611	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 15169 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
1	A	418	Total	C	N	O	S	0	24	0
			3321	2063	584	660	14			
1	B	418	Total	C	N	O	S	0	30	0
			3338	2067	586	671	14			
1	C	419	Total	C	N	O	S	0	22	1
			3296	2048	578	658	12			
1	D	418	Total	C	N	O	S	0	21	0
			3279	2037	579	649	14			

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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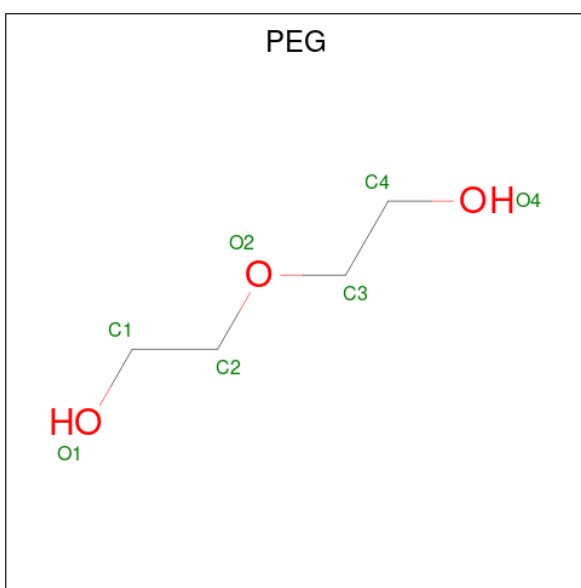
Chain	Residue	Modelled	Actual	Comment	Reference
B	425	HIS	-	expression tag	UNP B7GUI0
B	426	HIS	-	expression tag	UNP B7GUI0
B	427	HIS	-	expression tag	UNP B7GUI0
B	428	HIS	-	expression tag	UNP B7GUI0
B	429	HIS	-	expression tag	UNP B7GUI0
C	417	LYS	-	expression tag	UNP B7GUI0
C	418	LEU	-	expression tag	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 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		

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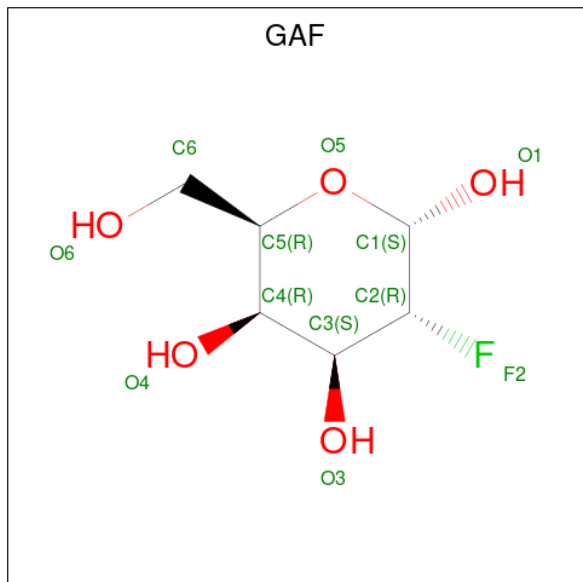
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



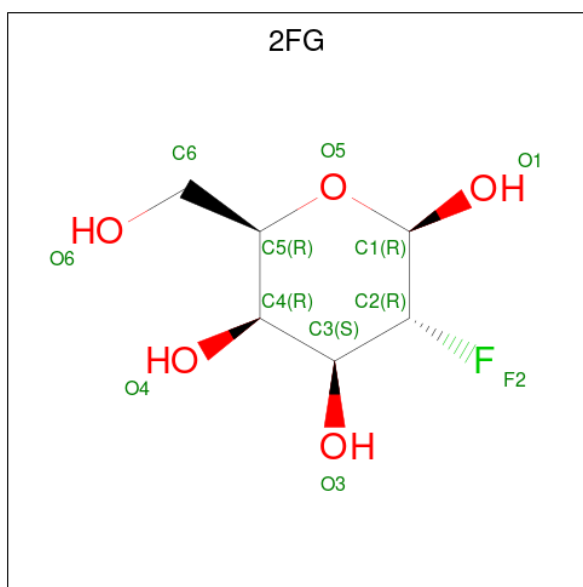
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	1
			12	6	6		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 2-deoxy-2-fluoro- α -D-galactopyranose (three-letter code: GAF) (formula: $C_6H_{11}FO_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	F	O	0	1
			12	6	1	5		
5	B	1	Total	C	F	O	0	1
			12	6	1	5		
5	C	1	Total	C	F	O	0	1
			12	6	1	5		
5	D	1	Total	C	F	O	0	1
			12	6	1	5		

- Molecule 6 is 2-deoxy-2-fluoro- β -D-galactopyranose (three-letter code: 2FG) (formula: $C_6H_{11}FO_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	F	O	0	1
			12	6	1	5		
6	B	1	Total	C	F	O	0	1
			12	6	1	5		
6	C	1	Total	C	F	O	0	1
			12	6	1	5		
6	D	1	Total	C	F	O	0	1
			12	6	1	5		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		
7	B	2	Total	Cl	0	0
			2	2		
7	C	2	Total	Cl	0	0
			2	2		
7	D	2	Total	Cl	0	0
			2	2		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



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

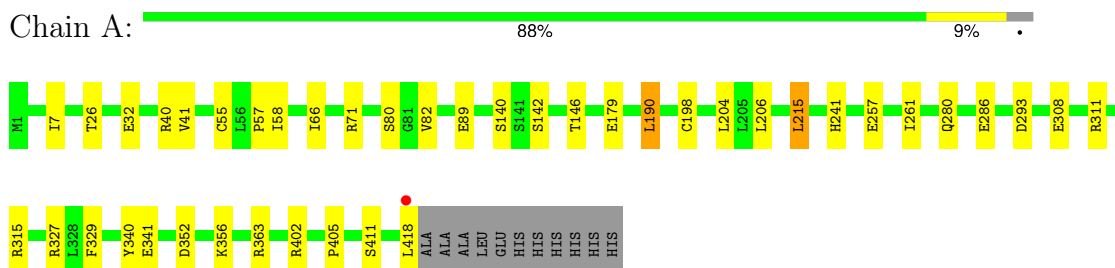
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	468	Total 468	O 468	0	0
10	B	358	Total 358	O 358	0	0
10	C	402	Total 402	O 402	0	0
10	D	343	Total 343	O 343	0	0

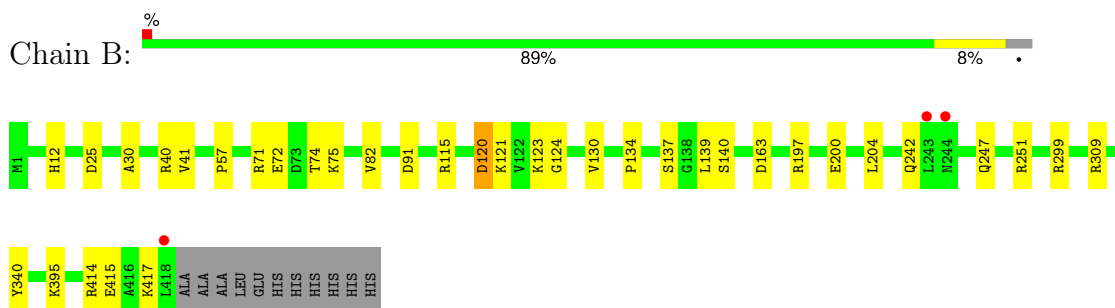
3 Residue-property plots [i](#)

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.

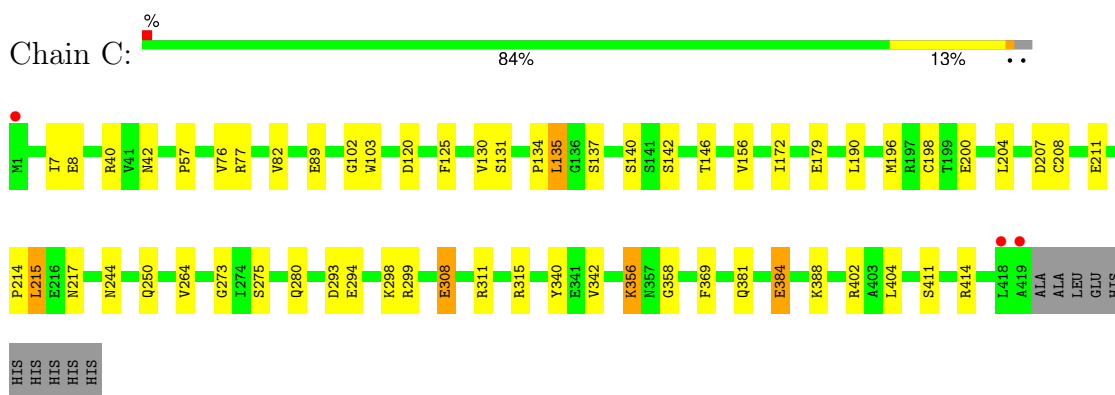
- Molecule 1: Galactokinase



- Molecule 1: Galactokinase

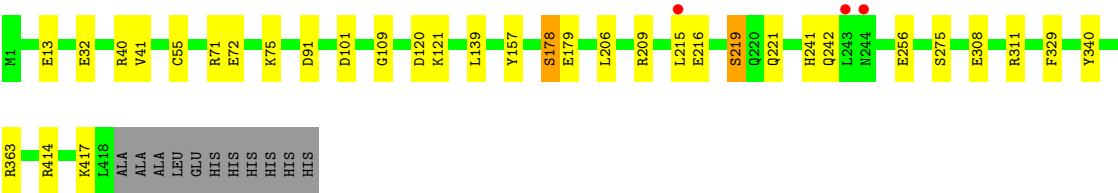


- Molecule 1: Galactokinase



- 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	52.22Å 164.39Å 115.87Å 90.00° 95.94° 90.00°	Depositor
Resolution (Å)	94.55 – 1.44 94.37 – 1.44	Depositor EDS
% Data completeness (in resolution range)	99.9 (94.55-1.44) 99.9 (94.37-1.44)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.44Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.169 , 0.203 0.179 , 0.211	Depositor DCC
R_{free} test set	17586 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	15.5	Xtriage
Anisotropy	0.487	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15169	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.67% 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: GAF, 2FG, PGE, PEG, EDO, MES, GOL, 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	0.90	1/3373 (0.0%)	0.99	5/4571 (0.1%)
1	B	0.92	1/3389 (0.0%)	0.99	5/4588 (0.1%)
1	C	0.90	1/3349 (0.0%)	0.99	4/4541 (0.1%)
1	D	0.92	5/3332 (0.2%)	0.97	5/4513 (0.1%)
All	All	0.91	8/13443 (0.1%)	0.98	19/18213 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	308	GLU	CD-OE1	-6.90	1.18	1.25
1	D	178[A]	SER	CA-CB	-6.67	1.43	1.52
1	D	178[B]	SER	CA-CB	-6.67	1.43	1.52
1	C	308	GLU	CD-OE1	-6.41	1.18	1.25
1	D	216	GLU	CD-OE2	6.37	1.32	1.25

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	ARG	NE-CZ-NH1	-7.96	116.32	120.30
1	B	197	ARG	NE-CZ-NH2	-7.55	116.53	120.30
1	C	311	ARG	NE-CZ-NH2	-7.03	116.79	120.30
1	D	363	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	C	299	ARG	NE-CZ-NH2	-6.67	116.97	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3321	0	3219	32	0
1	B	3338	0	3216	43	1
1	C	3296	0	3194	70	0
1	D	3279	0	3183	33	0
2	A	24	0	26	1	0
3	A	21	0	30	3	0
3	B	28	0	38	6	0
3	C	63	0	90	35	0
3	D	7	0	10	3	0
4	A	18	0	24	4	0
4	B	18	0	24	10	0
4	C	24	0	32	12	0
4	D	30	0	40	10	0
5	A	12	0	11	0	0
5	B	12	0	11	0	0
5	C	12	0	11	0	0
5	D	12	0	11	0	0
6	A	12	0	11	0	0
6	B	12	0	11	0	0
6	C	12	0	11	1	0
6	D	12	0	11	0	0
7	A	1	0	0	0	0
7	B	2	0	0	0	0
7	C	2	0	0	0	0
7	D	2	0	0	0	0
8	B	4	0	6	0	0
8	C	4	0	6	0	0
9	C	20	0	28	10	0
10	A	468	0	0	14	1
10	B	358	0	0	10	0
10	C	402	0	0	31	0
10	D	343	0	0	7	0
All	All	15169	0	13254	208	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 208 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:A:241:HIS:CE1	10:A:717:HOH:O	1.76	1.25
1:C:293[A]:ASP:OD1	3:C:613:PEG:H32	1.32	1.22
3:C:602:PEG:H41	10:C:1013:HOH:O	1.43	1.18
1:B:140[A]:SER:OG	10:B:701:HOH:O	1.58	1.15
1:A:140[B]:SER:OG	10:A:702:HOH:O	1.61	1.14

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:395:LYS:NZ	10:A:1004:HOH:O[2_555]	2.04	0.16

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	441/429 (103%)	433 (98%)	8 (2%)	0	100	100
1	B	446/429 (104%)	435 (98%)	11 (2%)	0	100	100
1	C	440/429 (103%)	429 (98%)	11 (2%)	0	100	100
1	D	438/429 (102%)	432 (99%)	6 (1%)	0	100	100
All	All	1765/1716 (103%)	1729 (98%)	36 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	338/326 (104%)	330 (98%)	8 (2%)	49	15
1	B	339/326 (104%)	331 (98%)	8 (2%)	49	15
1	C	337/326 (103%)	327 (97%)	10 (3%)	41	9
1	D	333/326 (102%)	326 (98%)	7 (2%)	53	19
All	All	1347/1304 (103%)	1314 (98%)	33 (2%)	59	15

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	219[A]	SER
1	D	219[B]	SER
1	D	340	TYR
1	B	242[B]	GLN
1	B	242[A]	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 53 ligands modelled in this entry, 7 are monoatomic - leaving 46 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
6	2FG	B	609[A]	-	12,12,12	0.91	1 (8%)	16,17,17	2.34	1 (6%)
4	GOL	C	610	-	5,5,5	0.16	0	5,5,5	0.51	0
3	PEG	C	601	-	6,6,6	0.23	0	5,5,5	0.22	0
9	PGE	C	611	-	9,9,9	0.45	0	8,8,8	0.36	0
2	MES	A	601	-	12,12,12	0.75	0	15,16,16	1.16	2 (13%)
4	GOL	D	707	-	5,5,5	0.20	0	5,5,5	0.65	0
4	GOL	C	608	-	5,5,5	0.27	0	5,5,5	0.68	0
4	GOL	B	602	-	5,5,5	0.21	0	5,5,5	0.51	0
4	GOL	A	603	-	5,5,5	0.19	0	5,5,5	0.34	0
3	PEG	B	608	-	6,6,6	0.51	0	5,5,5	0.45	0
6	2FG	A	610[B]	-	12,12,12	0.77	0	16,17,17	1.36	1 (6%)
2	MES	A	606	-	12,12,12	0.76	0	15,16,16	1.02	2 (13%)
3	PEG	C	617	-	6,6,6	0.27	0	5,5,5	0.13	0
5	GAF	B	610[B]	-	12,12,12	1.03	1 (8%)	16,17,17	1.67	2 (12%)
4	GOL	C	612	-	5,5,5	0.25	0	5,5,5	0.71	0
9	PGE	C	609	-	9,9,9	0.23	0	8,8,8	0.36	0
5	GAF	A	609[A]	-	12,12,12	1.15	1 (8%)	16,17,17	0.84	0
3	PEG	C	605	-	6,6,6	0.23	0	5,5,5	0.24	0
4	GOL	D	702[B]	-	5,5,5	0.09	0	5,5,5	0.36	0
3	PEG	B	604	-	6,6,6	0.60	0	5,5,5	0.36	0
3	PEG	A	604	-	6,6,6	0.72	0	5,5,5	0.23	0
3	PEG	C	618	-	6,6,6	0.30	0	5,5,5	0.18	0
5	GAF	C	615[A]	-	12,12,12	0.99	0	16,17,17	1.29	2 (12%)
5	GAF	D	706[B]	-	12,12,12	1.09	1 (8%)	16,17,17	1.26	1 (6%)
3	PEG	C	603	-	6,6,6	0.87	0	5,5,5	0.51	0
4	GOL	A	608	-	5,5,5	0.14	0	5,5,5	0.64	0
4	GOL	D	702[A]	-	5,5,5	0.14	0	5,5,5	0.36	0
3	PEG	B	606	-	6,6,6	0.65	0	5,5,5	0.28	0
3	PEG	C	614	-	6,6,6	0.46	0	5,5,5	0.41	0
8	EDO	C	607	-	3,3,3	0.41	0	2,2,2	0.58	0
4	GOL	A	605	-	5,5,5	0.14	0	5,5,5	0.23	0
3	PEG	C	602	-	6,6,6	0.32	0	5,5,5	0.16	0
4	GOL	C	604	-	5,5,5	0.15	0	5,5,5	0.34	0
3	PEG	C	613	-	6,6,6	0.45	0	5,5,5	0.18	0
4	GOL	D	704	-	5,5,5	0.19	0	5,5,5	0.46	0
4	GOL	B	603	-	5,5,5	0.20	0	5,5,5	0.55	0
4	GOL	D	703	-	5,5,5	0.19	0	5,5,5	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	B	605	-	5,5,5	0.21	0	5,5,5	0.55	0
6	2FG	D	705[A]	-	12,12,12	1.02	1 (8%)	16,17,17	1.89	1 (6%)
3	PEG	B	601	-	6,6,6	0.71	0	5,5,5	0.28	0
3	PEG	C	606	-	6,6,6	0.34	0	5,5,5	0.30	0
3	PEG	A	602	-	6,6,6	0.46	0	5,5,5	0.29	0
3	PEG	D	701	-	6,6,6	0.19	0	5,5,5	0.36	0
3	PEG	A	607	-	6,6,6	0.29	0	5,5,5	0.12	0
6	2FG	C	616[B]	-	12,12,12	0.84	0	16,17,17	1.16	1 (6%)
8	EDO	B	607	-	3,3,3	0.47	0	2,2,2	0.22	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
6	2FG	B	609[A]	-	-	1/2/22/22	0/1/1/1
4	GOL	C	610	-	-	4/4/4/4	-
3	PEG	C	601	-	-	2/4/4/4	-
9	PGE	C	611	-	-	4/7/7/7	-
2	MES	A	601	-	-	0/6/14/14	0/1/1/1
4	GOL	D	707	-	-	0/4/4/4	-
4	GOL	C	608	-	-	3/4/4/4	-
4	GOL	B	602	-	-	2/4/4/4	-
4	GOL	A	603	-	-	3/4/4/4	-
3	PEG	B	608	-	-	3/4/4/4	-
6	2FG	A	610[B]	-	-	1/2/22/22	0/1/1/1
2	MES	A	606	-	-	2/6/14/14	0/1/1/1
3	PEG	C	617	-	-	3/4/4/4	-
5	GAF	B	610[B]	-	-	1/2/22/22	0/1/1/1
4	GOL	C	612	-	-	2/4/4/4	-
9	PGE	C	609	-	-	4/7/7/7	-
5	GAF	A	609[A]	-	-	1/2/22/22	0/1/1/1
3	PEG	C	605	-	-	3/4/4/4	-
4	GOL	D	702[B]	-	-	0/4/4/4	-
3	PEG	B	604	-	-	2/4/4/4	-
3	PEG	A	604	-	-	3/4/4/4	-
3	PEG	C	618	-	-	3/4/4/4	-
5	GAF	C	615[A]	-	-	1/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GAF	D	706[B]	-	-	1/2/22/22	0/1/1/1
3	PEG	C	603	-	-	1/4/4/4	-
4	GOL	A	608	-	-	2/4/4/4	-
4	GOL	D	702[A]	-	-	2/4/4/4	-
3	PEG	B	606	-	-	4/4/4/4	-
3	PEG	C	614	-	-	2/4/4/4	-
8	EDO	C	607	-	-	0/1/1/1	-
4	GOL	A	605	-	-	4/4/4/4	-
3	PEG	C	602	-	-	3/4/4/4	-
4	GOL	C	604	-	-	1/4/4/4	-
3	PEG	C	613	-	-	3/4/4/4	-
4	GOL	D	704	-	-	2/4/4/4	-
4	GOL	B	603	-	-	3/4/4/4	-
4	GOL	D	703	-	-	4/4/4/4	-
4	GOL	B	605	-	-	2/4/4/4	-
6	2FG	D	705[A]	-	-	1/2/22/22	0/1/1/1
3	PEG	B	601	-	-	2/4/4/4	-
3	PEG	C	606	-	-	2/4/4/4	-
3	PEG	A	602	-	-	2/4/4/4	-
3	PEG	D	701	-	-	3/4/4/4	-
3	PEG	A	607	-	-	3/4/4/4	-
6	2FG	C	616[B]	-	-	1/2/22/22	0/1/1/1
8	EDO	B	607	-	-	1/1/1/1	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	706[B]	GAF	F2-C2	-2.66	1.35	1.40
6	D	705[A]	2FG	F2-C2	-2.64	1.35	1.40
5	B	610[B]	GAF	C2-C3	2.48	1.55	1.52
5	A	609[A]	GAF	F2-C2	-2.25	1.36	1.40
6	B	609[A]	2FG	C2-C3	2.14	1.54	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	609[A]	2FG	F2-C2-C3	8.50	116.17	108.81
6	D	705[A]	2FG	F2-C2-C3	6.93	114.81	108.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	610[B]	GAF	F2-C2-C3	5.21	113.33	108.81
6	A	610[B]	2FG	F2-C2-C3	4.69	112.88	108.81
5	D	706[B]	GAF	F2-C2-C3	4.35	112.58	108.81

There are no chirality outliers.

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	606	MES	C8-C7-N4-C5
2	A	606	MES	N4-C7-C8-S
4	A	603	GOL	O1-C1-C2-C3
4	A	605	GOL	O1-C1-C2-C3
4	A	605	GOL	C1-C2-C3-O3

There are no ring outliers.

32 monomers are involved in 91 short contacts:

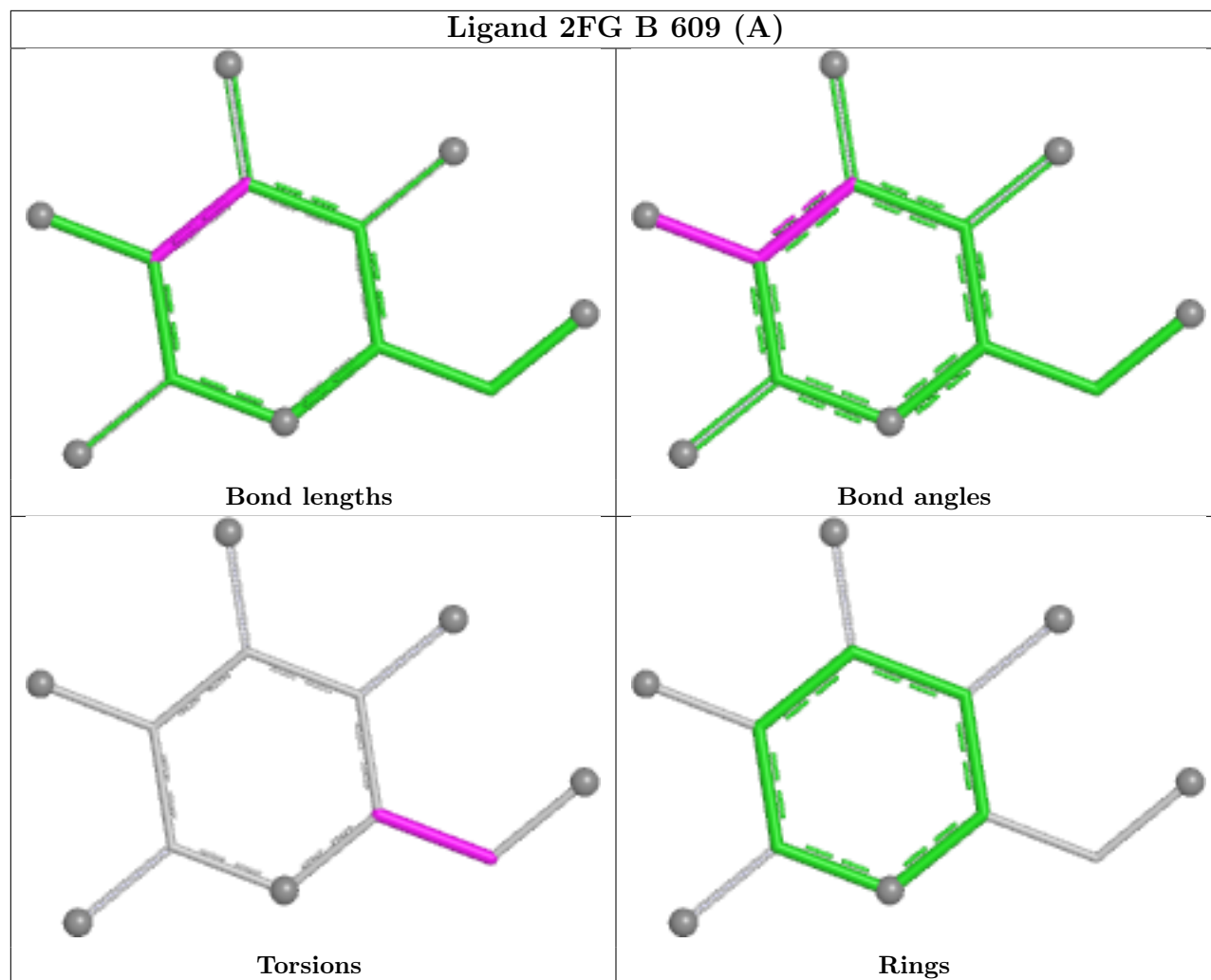
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	610	GOL	4	0
9	C	611	PGE	7	0
4	D	707	GOL	4	0
4	C	608	GOL	4	0
4	B	602	GOL	7	0
4	A	603	GOL	2	0
3	B	608	PEG	1	0
2	A	606	MES	1	0
3	C	617	PEG	3	0
4	C	612	GOL	3	0
9	C	609	PGE	3	0
3	C	605	PEG	4	0
4	D	702[B]	GOL	1	0
3	B	604	PEG	1	0
3	A	604	PEG	1	0
3	C	618	PEG	5	0
3	C	603	PEG	6	0
4	A	608	GOL	1	0
3	C	614	PEG	4	0
4	A	605	GOL	1	0
3	C	602	PEG	4	0
4	C	604	GOL	1	0
3	C	613	PEG	7	0

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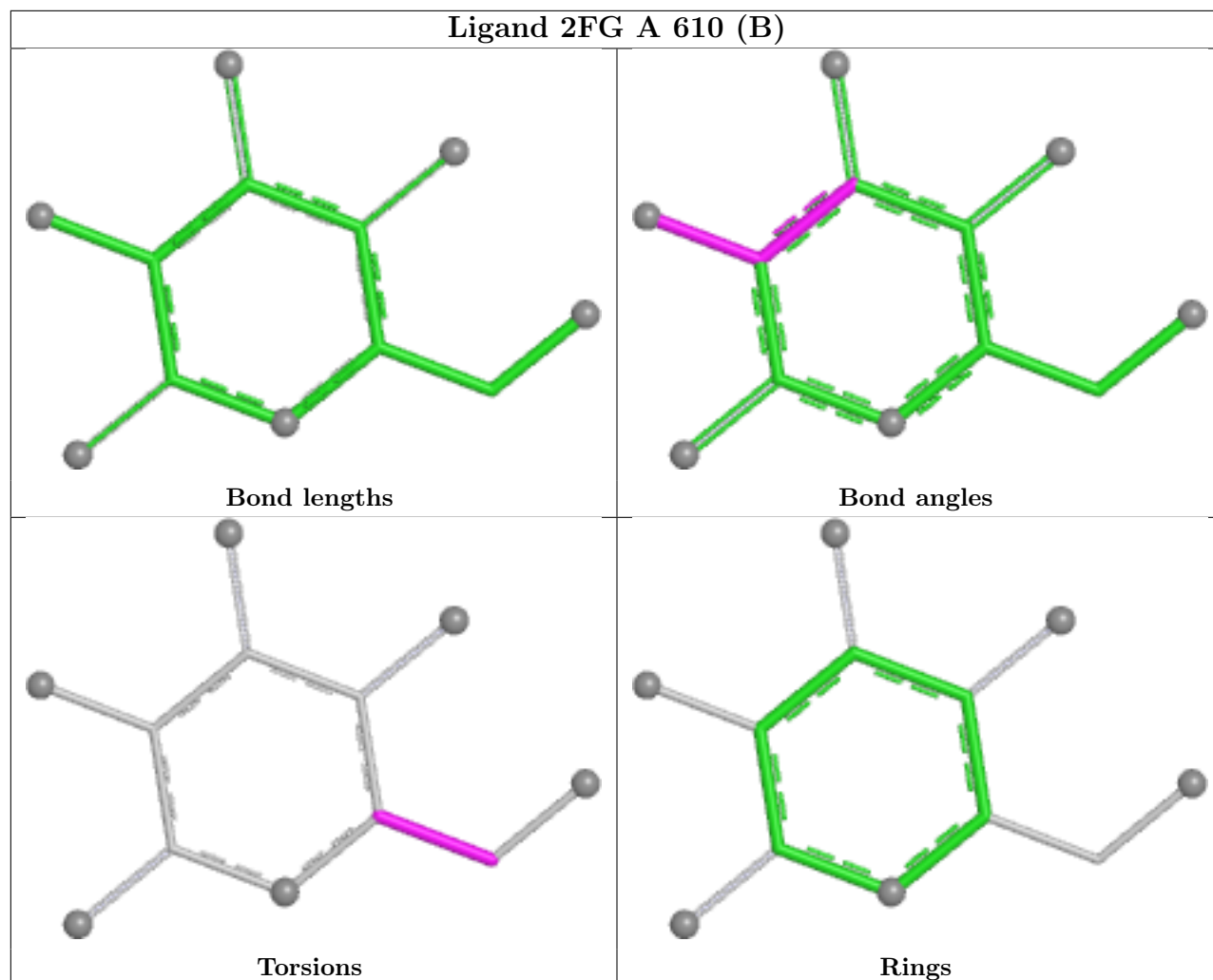
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	704	GOL	4	0
4	B	603	GOL	2	0
4	D	703	GOL	2	0
4	B	605	GOL	1	0
3	B	601	PEG	4	0
3	C	606	PEG	2	0
3	A	602	PEG	2	0
3	D	701	PEG	3	0
6	C	616[B]	2FG	1	0

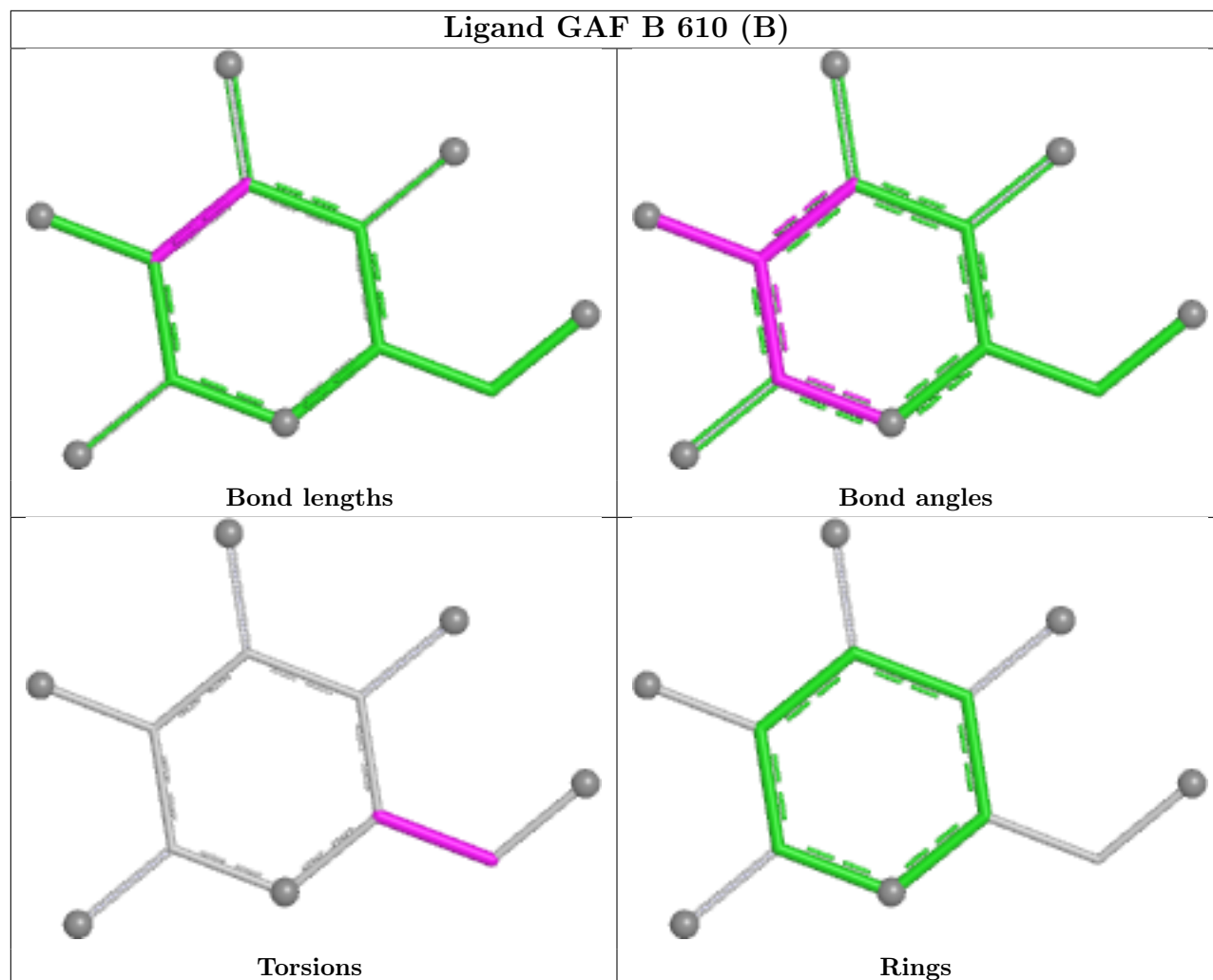
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



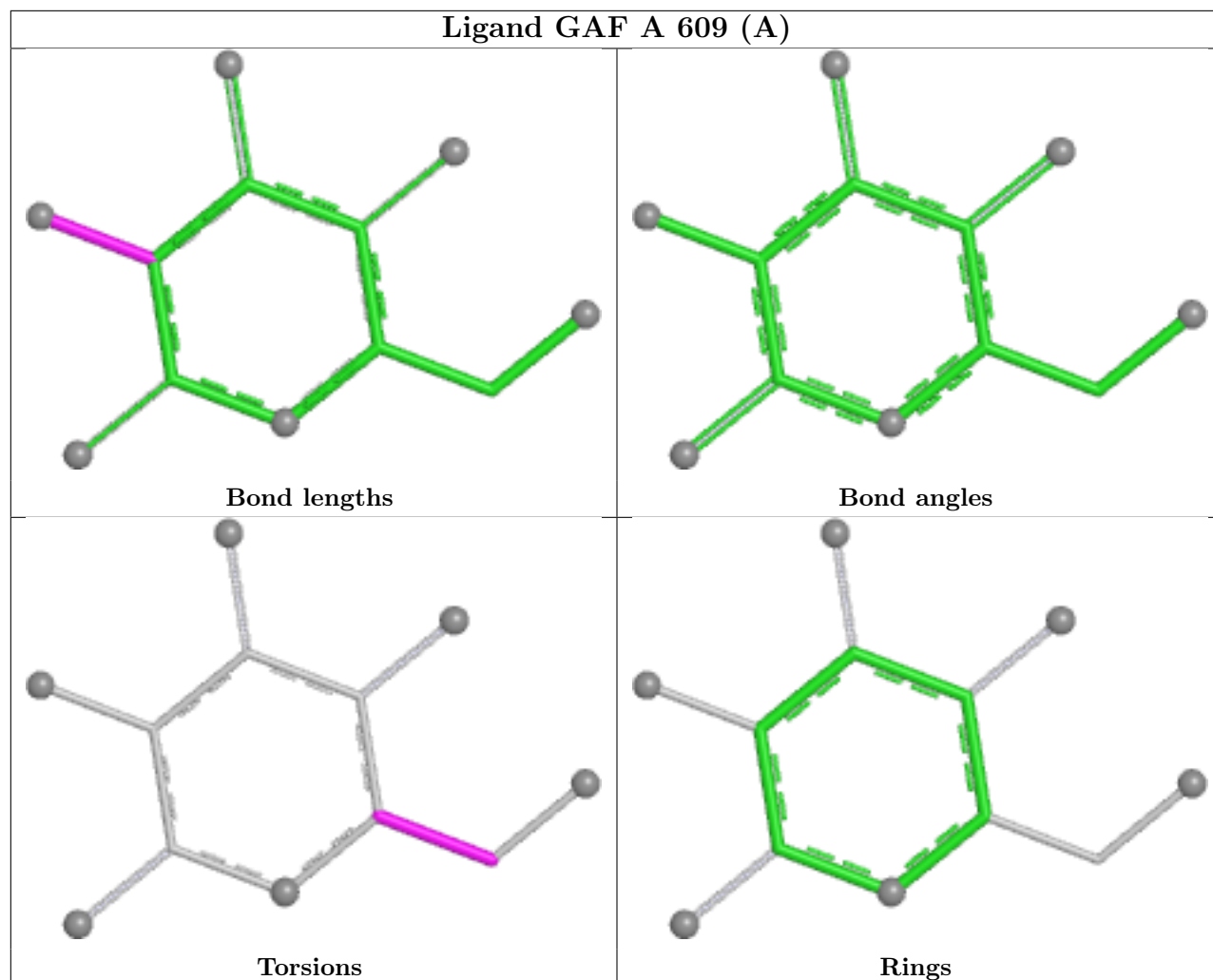
Ligand 2FG A 610 (B)



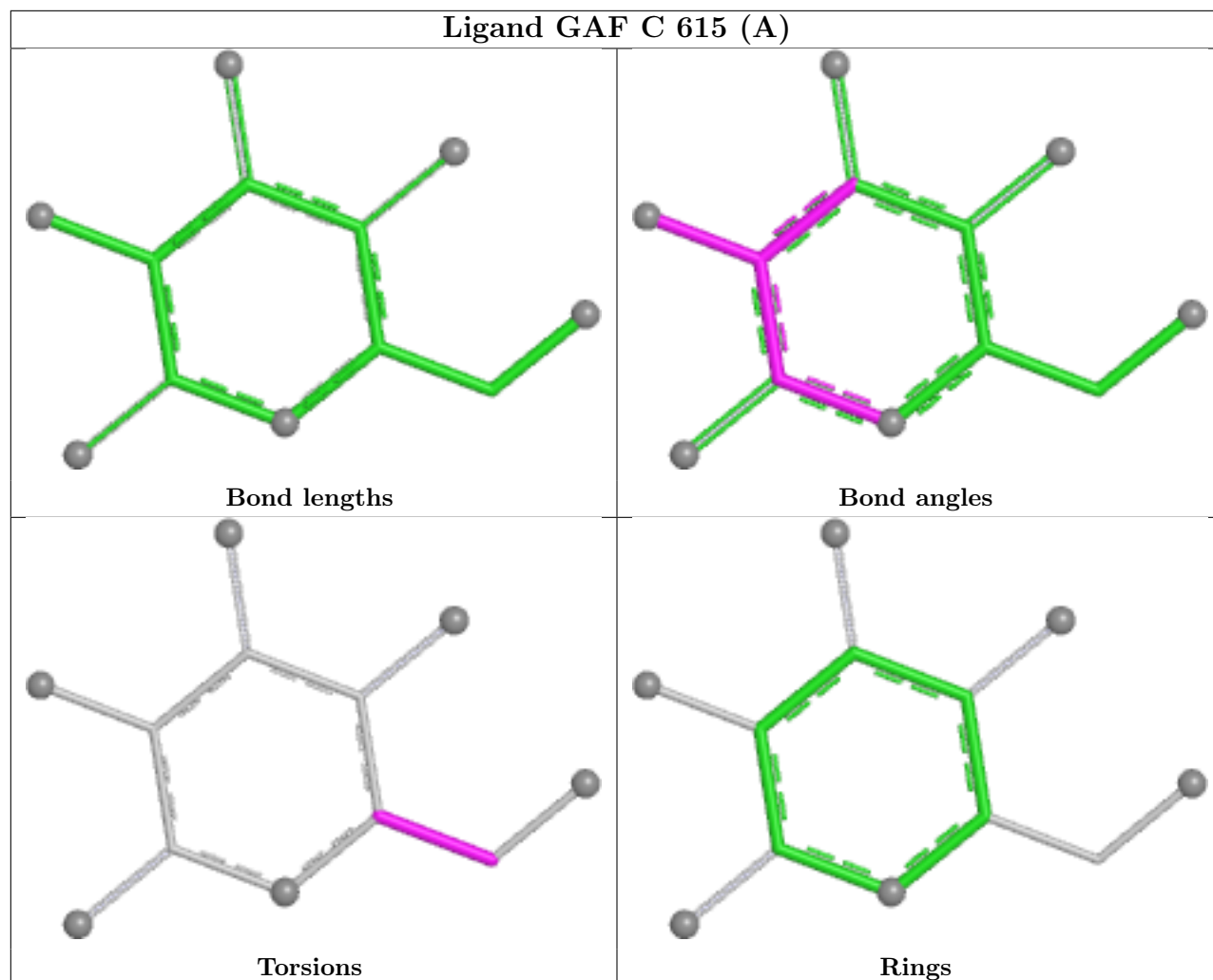
Ligand GAF B 610 (B)

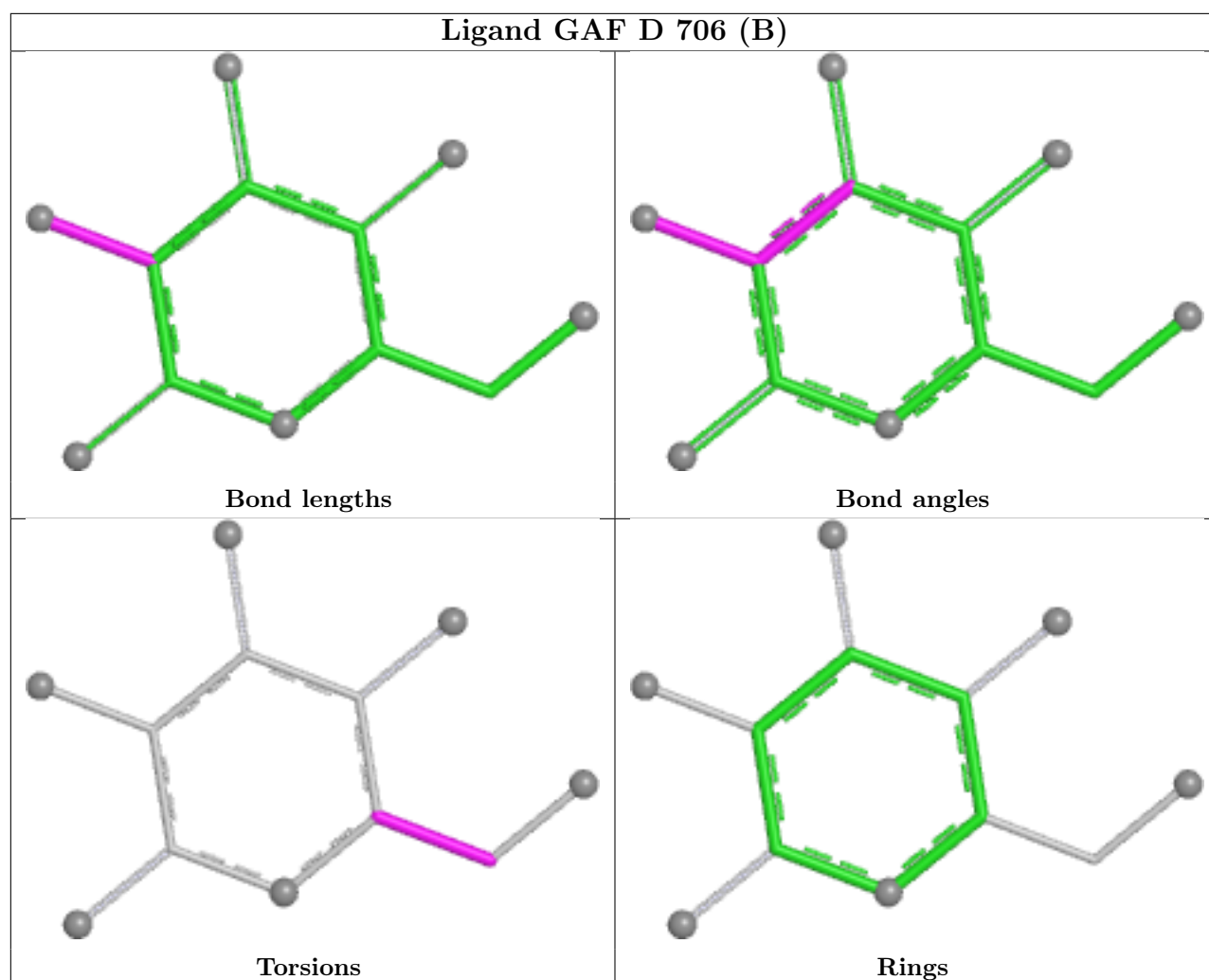


Ligand GAF A 609 (A)

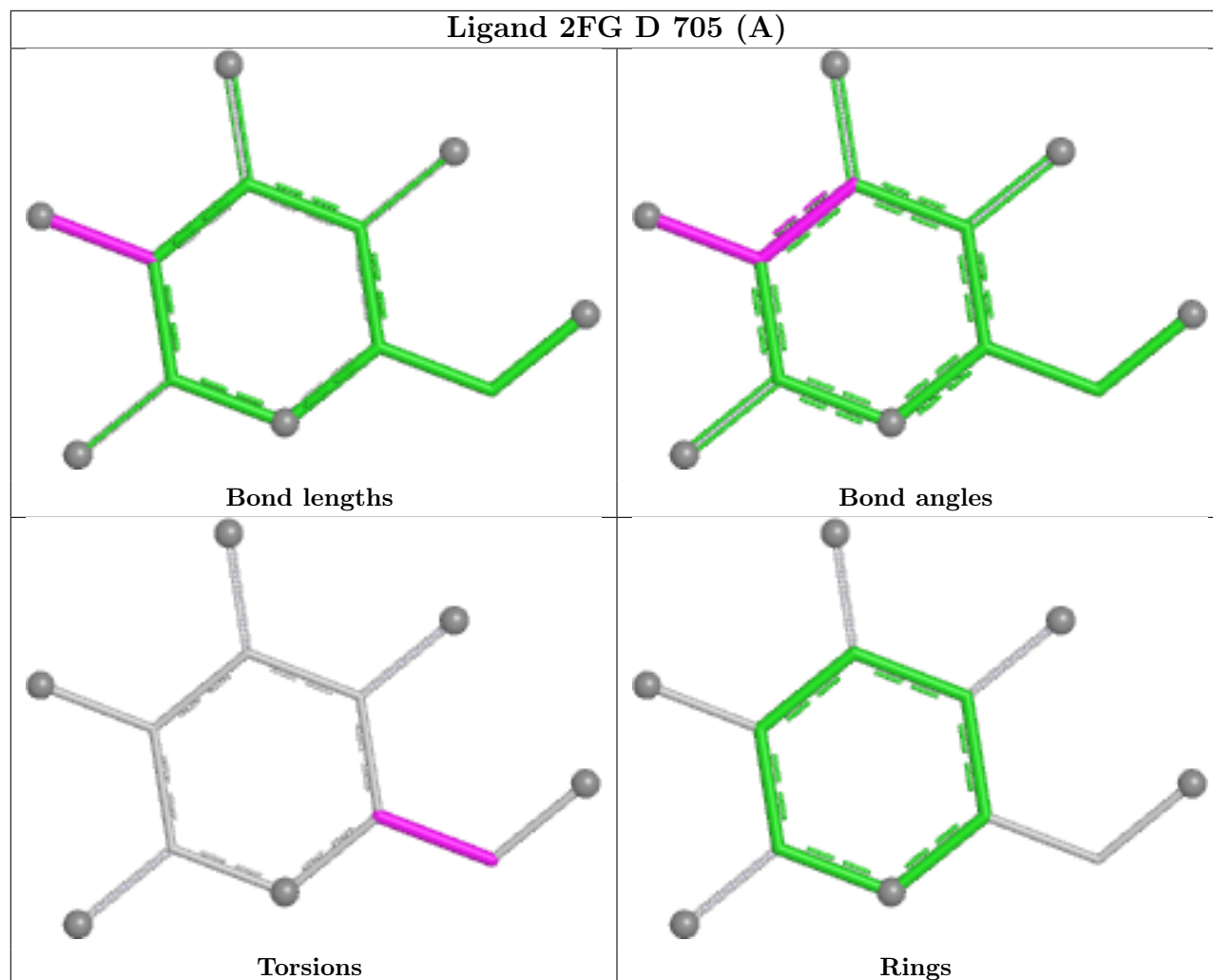


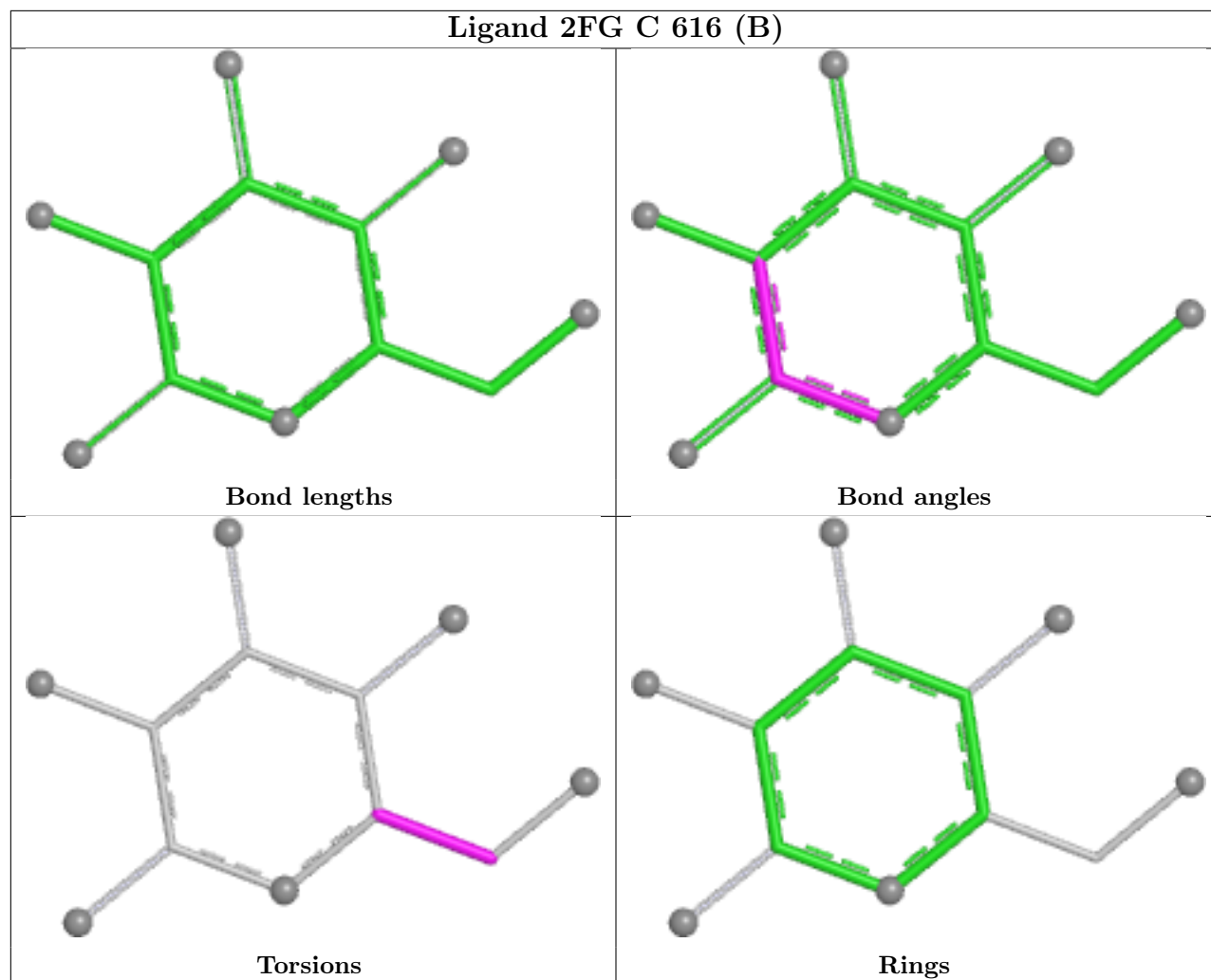
Ligand GAF C 615 (A)





Ligand 2FG D 705 (A)





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%)	-0.53	1 (0%) 95 95	10, 16, 28, 56	6 (1%)
1	B	418/429 (97%)	-0.48	3 (0%) 87 88	11, 17, 30, 97	2 (0%)
1	C	419/429 (97%)	-0.52	3 (0%) 87 88	12, 18, 30, 55	7 (1%)
1	D	418/429 (97%)	-0.47	3 (0%) 87 88	13, 20, 34, 77	5 (1%)
All	All	1673/1716 (97%)	-0.50	10 (0%) 89 90	10, 18, 31, 97	20 (1%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	LEU	9.8
1	D	243	LEU	7.3
1	C	419	ALA	5.1
1	D	244	ASN	4.1
1	B	418[A]	LEU	3.6

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 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(\AA^2)	Q<0.9
9	PGE	C	611	10/10	0.75	0.15	32,34,39,41	10
4	GOL	D	707	6/6	0.76	0.17	27,30,32,35	6
4	GOL	B	603	6/6	0.76	0.16	31,37,39,43	6
9	PGE	C	609	10/10	0.78	0.16	29,37,47,52	10
2	MES	A	606	12/12	0.79	0.21	23,32,42,43	12
3	PEG	B	608	7/7	0.79	0.21	26,28,35,36	7
3	PEG	B	606	7/7	0.80	0.14	30,36,39,40	7
4	GOL	A	608	6/6	0.81	0.27	21,30,33,34	6
4	GOL	B	605	6/6	0.82	0.21	28,32,35,44	6
4	GOL	C	608	6/6	0.82	0.16	21,25,26,30	6
4	GOL	C	612	6/6	0.82	0.16	25,27,34,38	6
3	PEG	C	617	7/7	0.83	0.16	22,26,31,35	7
4	GOL	A	605	6/6	0.83	0.19	26,28,32,37	6
3	PEG	A	604	7/7	0.84	0.15	32,39,49,56	0
3	PEG	C	602	7/7	0.84	0.17	19,23,27,29	7
3	PEG	A	602	7/7	0.84	0.19	22,25,32,36	7
4	GOL	B	602	6/6	0.85	0.18	29,29,38,38	4
4	GOL	C	604	6/6	0.85	0.14	24,29,34,39	6
4	GOL	A	603	6/6	0.85	0.18	17,26,28,32	6
4	GOL	C	610	6/6	0.85	0.17	22,22,28,39	6
3	PEG	C	603	7/7	0.86	0.18	17,23,34,35	7
8	EDO	C	607	4/4	0.86	0.19	37,39,44,46	0
4	GOL	D	703	6/6	0.87	0.18	28,32,34,37	6
3	PEG	D	701	7/7	0.87	0.19	19,24,34,35	7
8	EDO	B	607	4/4	0.87	0.16	24,28,33,34	4
3	PEG	C	605	7/7	0.88	0.18	26,30,33,37	7
3	PEG	C	614	7/7	0.88	0.17	28,32,34,38	7
3	PEG	A	607	7/7	0.89	0.13	31,37,40,46	7
4	GOL	D	702[B]	6/6	0.90	0.34	39,39,44,44	6
3	PEG	C	618	7/7	0.90	0.18	24,31,35,39	5
4	GOL	D	704	6/6	0.90	0.15	16,29,32,34	6
4	GOL	D	702[A]	6/6	0.90	0.34	35,37,38,39	6
3	PEG	B	604	7/7	0.91	0.16	21,24,30,30	7
3	PEG	C	601	7/7	0.92	0.12	22,28,37,37	7
3	PEG	C	606	7/7	0.93	0.16	15,29,31,33	7
5	GAF	D	706[B]	12/12	0.93	0.09	15,17,18,20	12
3	PEG	C	613	7/7	0.93	0.17	21,22,25,36	7
3	PEG	B	601	7/7	0.94	0.17	20,25,37,48	7
6	2FG	D	705[A]	12/12	0.94	0.10	19,22,26,31	12
7	CL	B	611	1/1	0.96	0.08	62,62,62,62	0
5	GAF	B	610[B]	12/12	0.96	0.07	12,13,14,17	12
6	2FG	B	609[A]	12/12	0.96	0.07	15,20,23,26	12
6	2FG	C	616[B]	12/12	0.96	0.08	13,15,17,22	12

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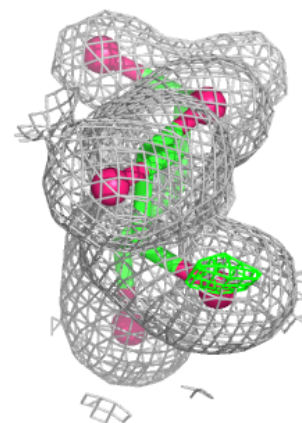
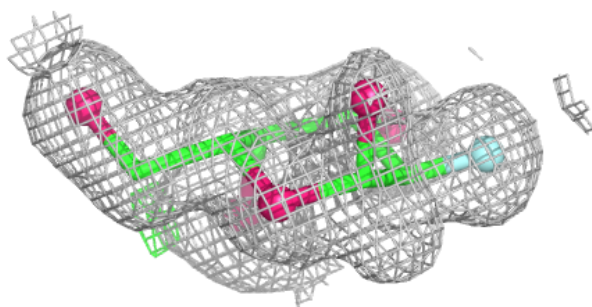
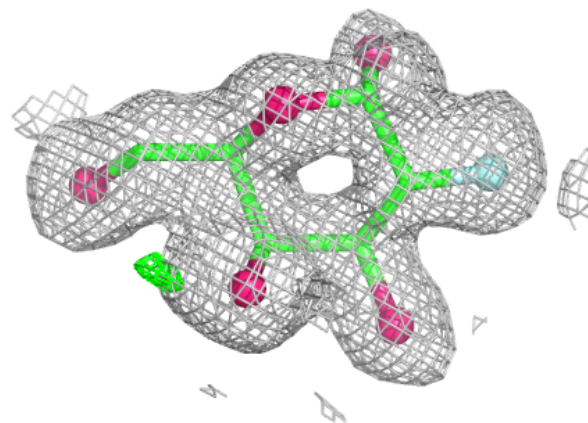
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	GAF	C	615[A]	12/12	0.96	0.09	13,16,20,20	12
6	2FG	A	610[B]	12/12	0.97	0.07	16,18,20,25	12
7	CL	D	708	1/1	0.97	0.04	55,55,55,55	0
5	GAF	A	609[A]	12/12	0.97	0.07	9,14,15,17	12
2	MES	A	601	12/12	0.98	0.11	19,26,29,30	12
7	CL	C	619	1/1	0.99	0.05	25,25,25,25	0
7	CL	A	611	1/1	1.00	0.04	19,19,19,19	0
7	CL	C	620	1/1	1.00	0.03	18,18,18,18	0
7	CL	B	612	1/1	1.00	0.05	18,18,18,18	0
7	CL	D	709	1/1	1.00	0.04	20,20,20,20	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.

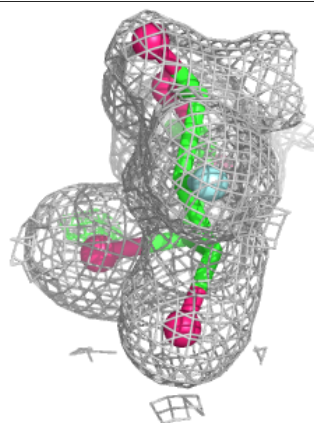
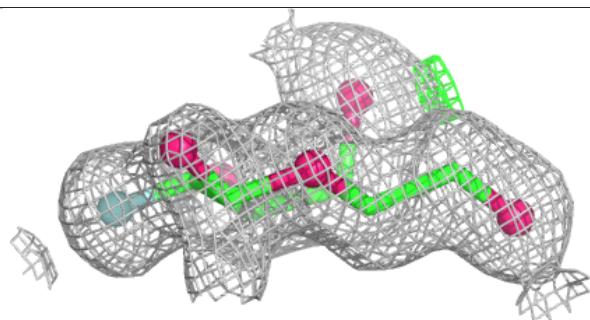
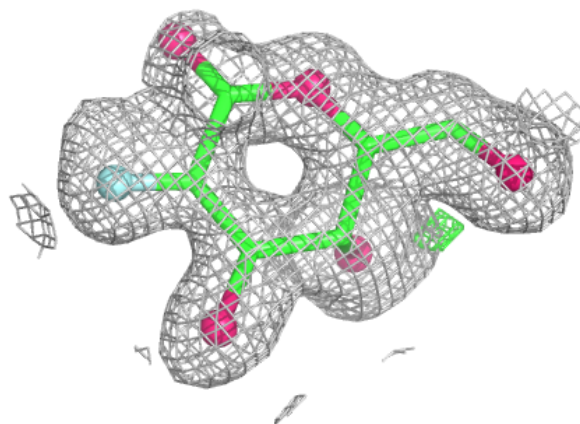
Electron density around GAF D 706 (B):

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



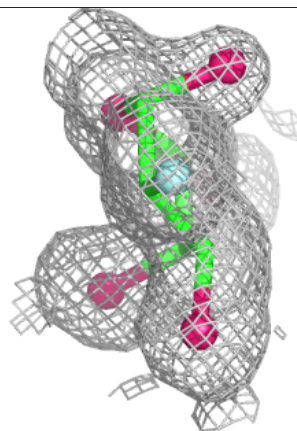
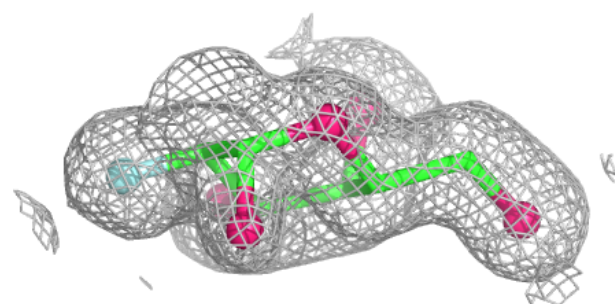
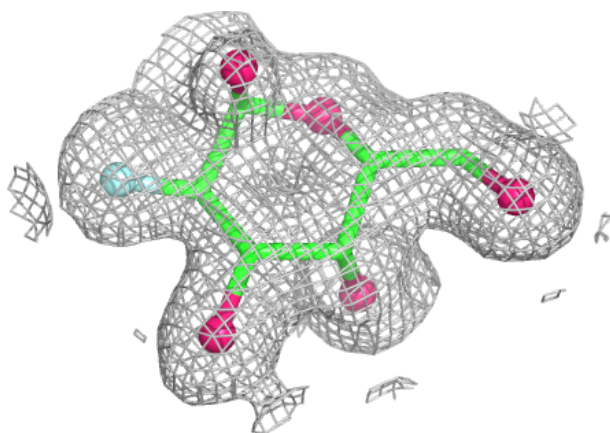
Electron density around 2FG D 705 (A):

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



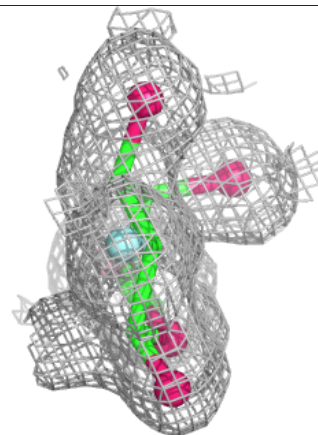
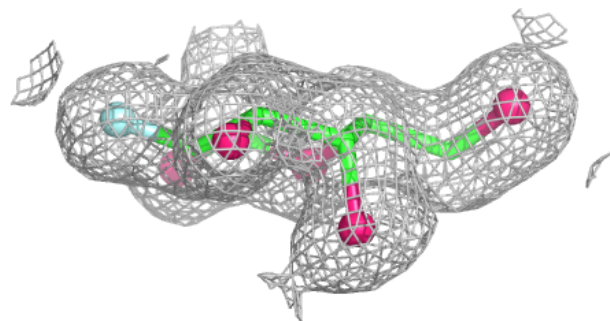
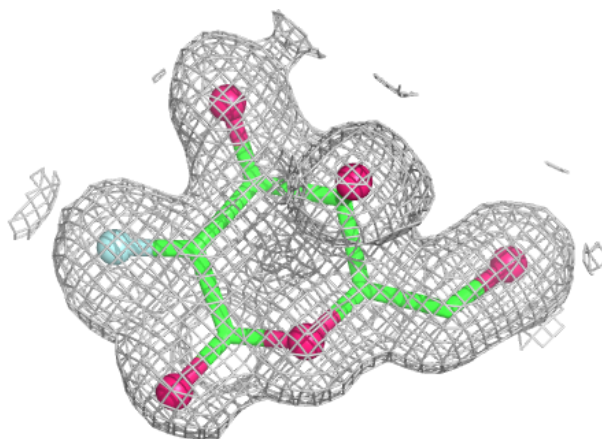
Electron density around GAF B 610 (B):

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



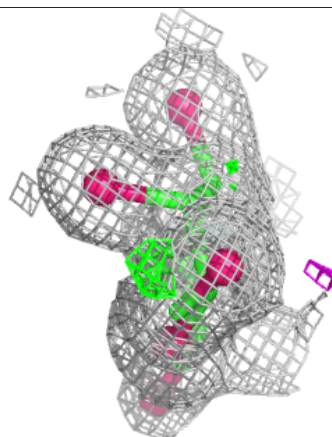
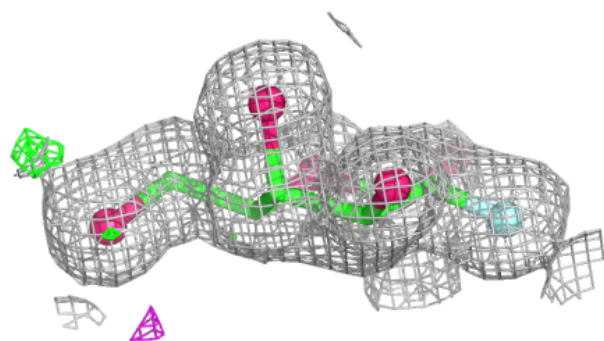
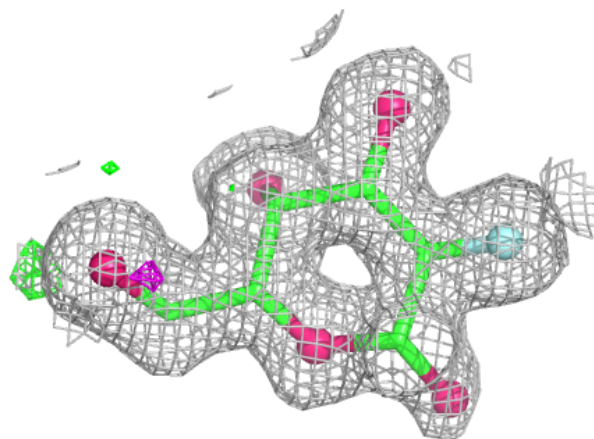
Electron density around 2FG B 609 (A):

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



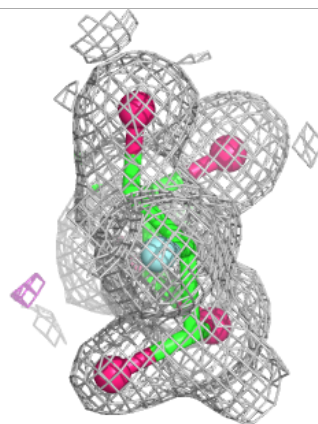
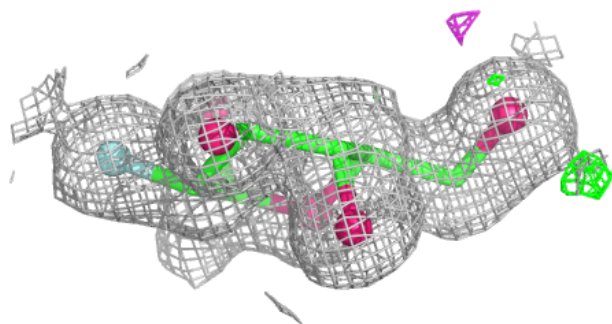
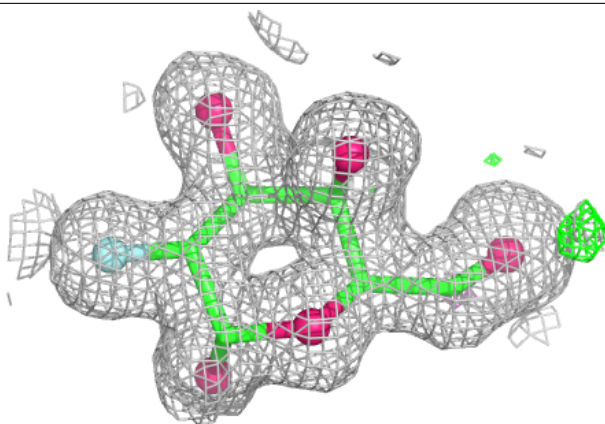
Electron density around 2FG C 616 (B):

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



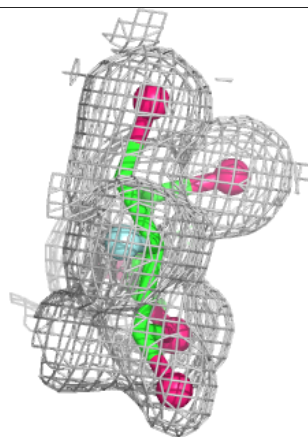
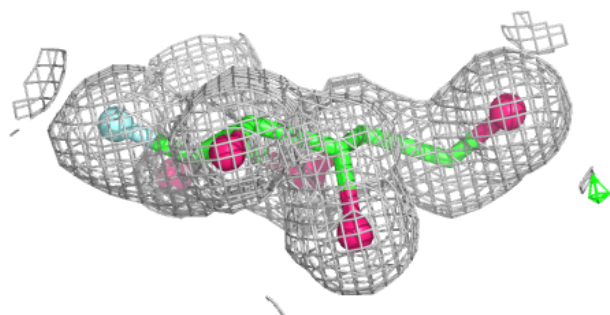
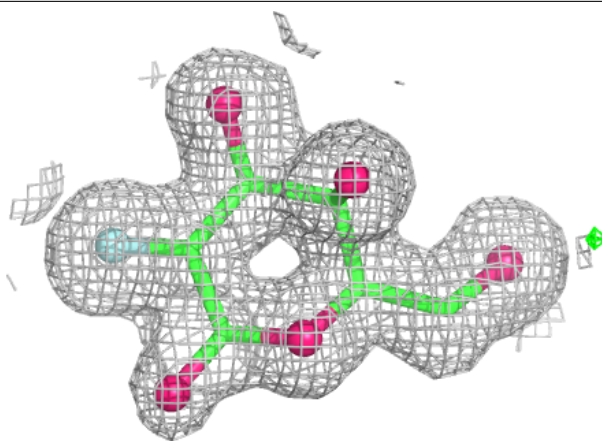
Electron density around GAF C 615 (A):

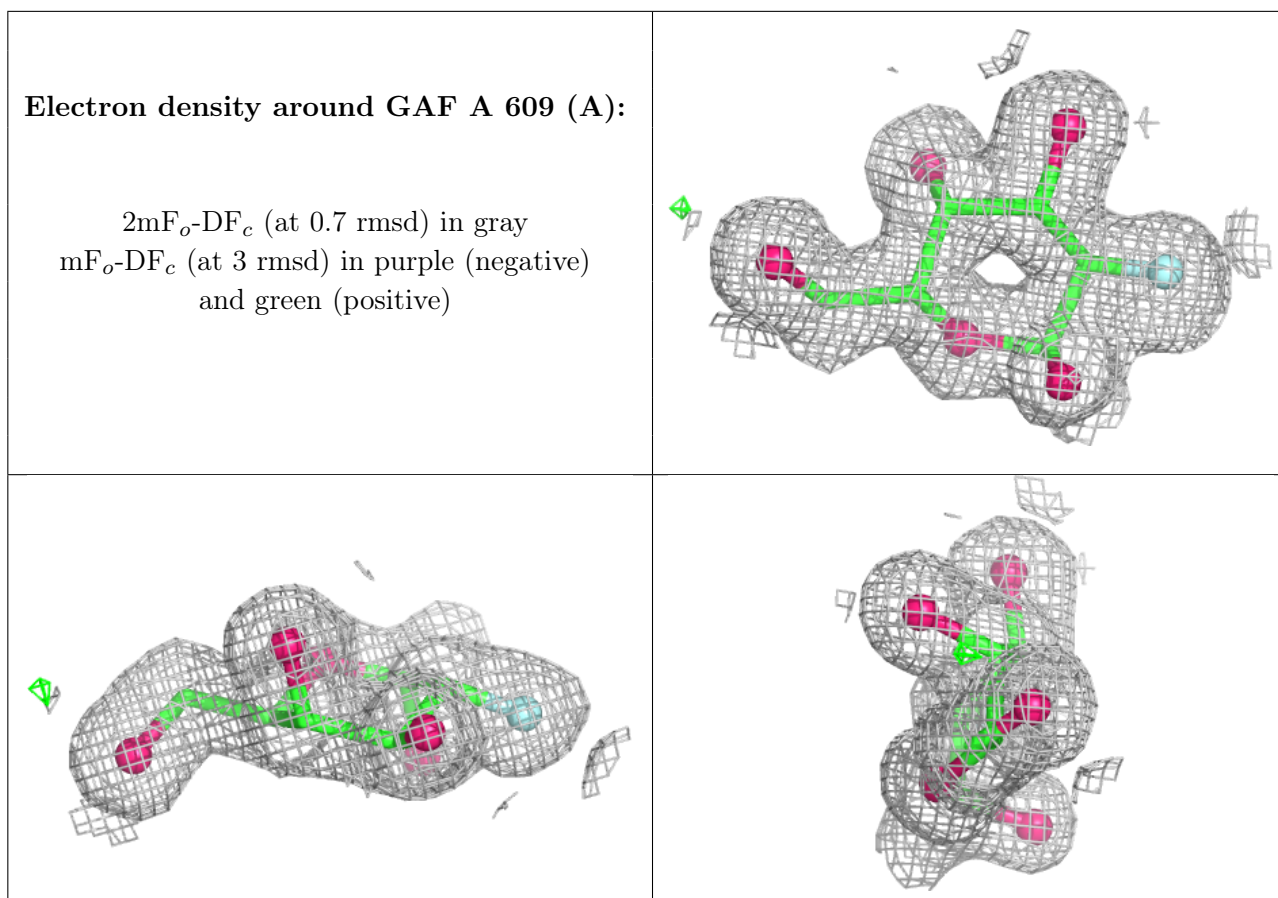
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 2FG A 610 (B):

$2mF_o - DF_c$ (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.