



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:15 AM UTC

PDB ID : 2FAH / pdb\_00002fah  
Title : The structure of mitochondrial PEPCK, Complex with Mn and GDP  
Authors : Holyoak, T.; Sullivan, S.M.; Nowak, T.  
Deposited on : 2005-12-07  
Resolution : 2.09 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) 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

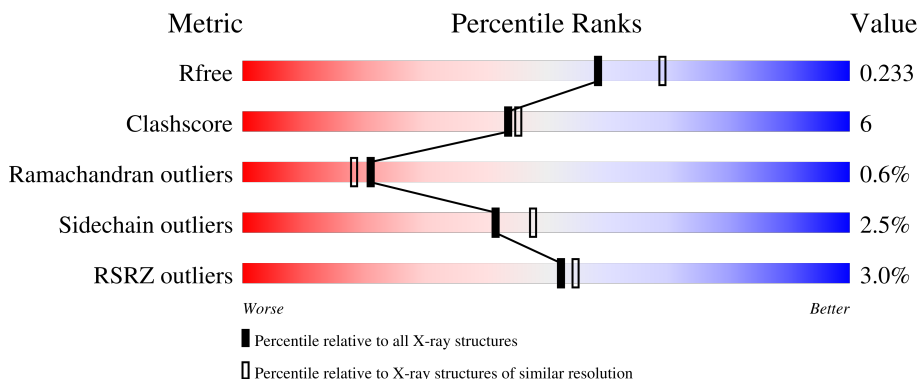
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.09 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.



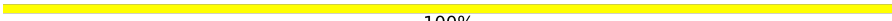
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	608	 3% 86% 12%
1	B	608	 5% 85% 14%
1	C	608	 2% 86% 13%
1	D	608	 0% 86% 13%
2	E	2	 100%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 20770 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 Phosphoenolpyruvate carboxykinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	608	4804	3048	865	858	33	0	11	0
1	B	608	4786	3039	855	859	33	0	13	0
1	C	608	4762	3021	857	851	33	0	6	0
1	D	608	4749	3017	848	851	33	0	5	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	GLY	-	insertion	UNP P21642
A	131	PRO	SER	SEE REMARK 999	UNP P21642
A	233	PRO	ARG	SEE REMARK 999	UNP P21642
A	268	ARG	ALA	SEE REMARK 999	UNP P21642
A	339	GLU	ARG	SEE REMARK 999	UNP P21642
A	502	ARG	SER	SEE REMARK 999	UNP P21642
B	129	GLY	-	insertion	UNP P21642
B	131	PRO	SER	SEE REMARK 999	UNP P21642
B	233	PRO	ARG	SEE REMARK 999	UNP P21642
B	268	ARG	ALA	SEE REMARK 999	UNP P21642
B	339	GLU	ARG	SEE REMARK 999	UNP P21642
B	502	ARG	SER	SEE REMARK 999	UNP P21642
C	129	GLY	-	insertion	UNP P21642
C	131	PRO	SER	SEE REMARK 999	UNP P21642
C	233	PRO	ARG	SEE REMARK 999	UNP P21642
C	268	ARG	ALA	SEE REMARK 999	UNP P21642
C	339	GLU	ARG	SEE REMARK 999	UNP P21642
C	502	ARG	SER	SEE REMARK 999	UNP P21642
D	129	GLY	-	insertion	UNP P21642
D	131	PRO	SER	SEE REMARK 999	UNP P21642
D	233	PRO	ARG	SEE REMARK 999	UNP P21642

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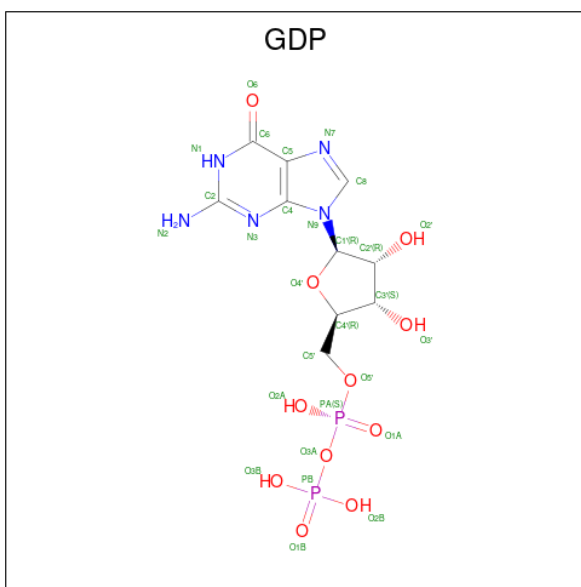
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Chain	Residue	Modelled	Actual	Comment	Reference
D	268	ARG	ALA	SEE REMARK 999	UNP P21642
D	339	GLU	ARG	SEE REMARK 999	UNP P21642
D	502	ARG	SER	SEE REMARK 999	UNP P21642

- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-6-O-octanoyl-alpha-D-glucopyranose.

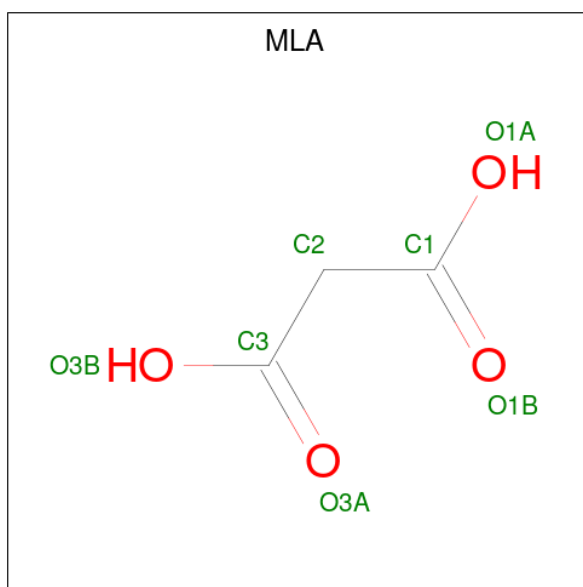
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			32	20	12			
2	F	2	Total	C	O	0	0	0
			32	20	12			

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 4 is MALONIC ACID (CCD ID: MLA) (formula: C<sub>3</sub>H<sub>4</sub>O<sub>4</sub>).



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

- Molecule 5 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Mn 2 2	0	0
5	B	2	Total Mn 2 2	0	0
5	C	2	Total Mn 2 2	0	0
5	D	2	Total Mn 2 2	0	0

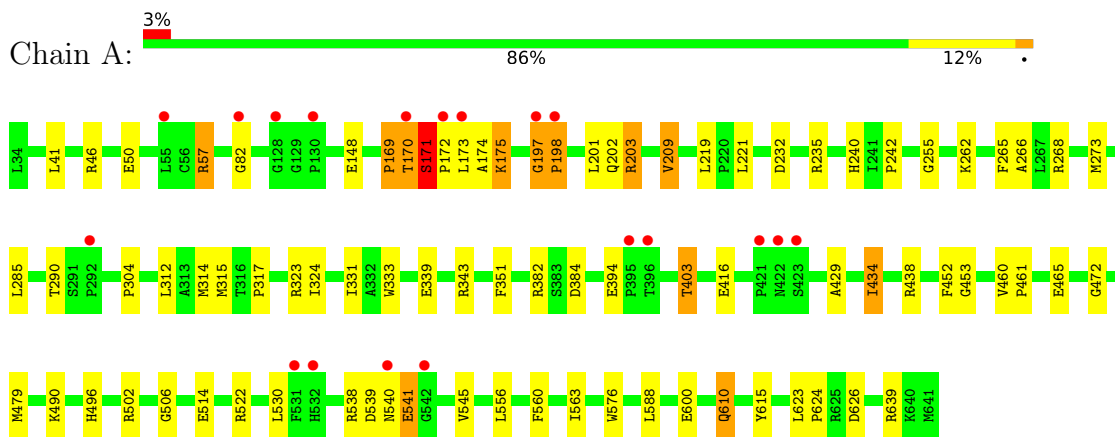
- Molecule 6 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	A	384	Total 384	O 384	0	0
6	B	305	Total 305	O 305	0	0
6	C	417	Total 417	O 417	0	0
6	D	344	Total 344	O 344	0	0

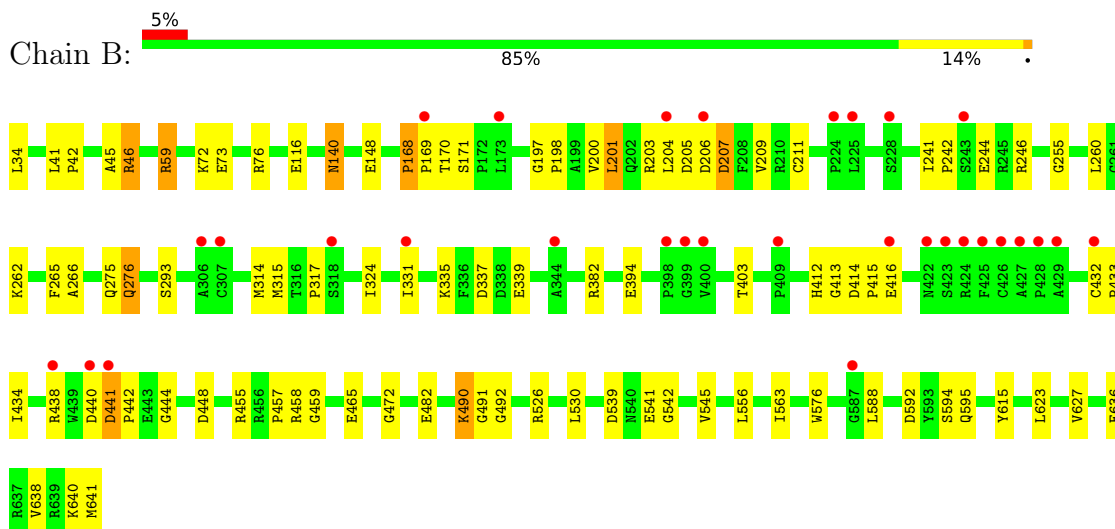
### 3 Residue-property plots [i](#)

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.

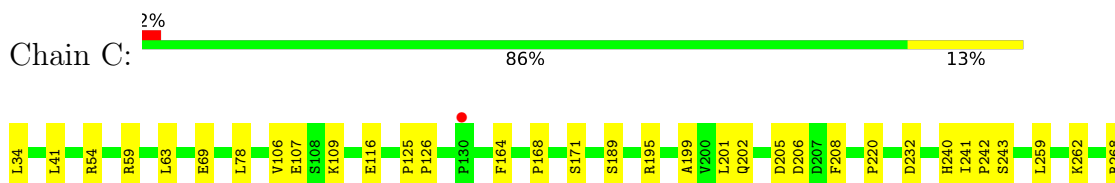
- Molecule 1: Phosphoenolpyruvate carboxykinase

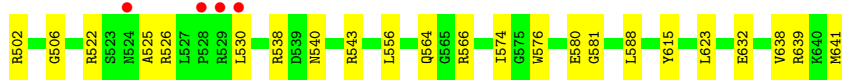
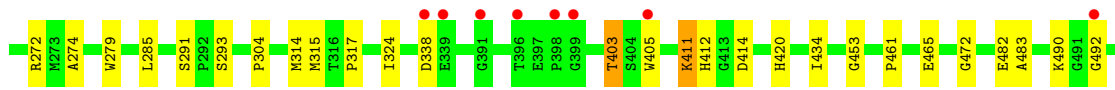


- Molecule 1: Phosphoenolpyruvate carboxykinase

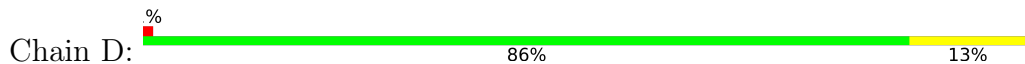


- Molecule 1: Phosphoenolpyruvate carboxykinase





- Molecule 1: Phosphoenolpyruvate carboxykinase



- Molecule 2: beta-D-fructofuranose-(2-1)-6-O-octanoyl-alpha-D-glucopyranose



- Molecule 2: beta-D-fructofuranose-(2-1)-6-O-octanoyl-alpha-D-glucopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.59Å 90.85Å 103.34Å 64.23° 73.74° 71.18°	Depositor
Resolution (Å)	32.81 – 2.09 32.81 – 2.09	Depositor EDS
% Data completeness (in resolution range)	94.7 (32.81-2.09) 94.7 (32.81-2.09)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 2.10Å)	Xtrriage
Refinement program	REFMAC, CNS	Depositor
R, $R_{free}$	0.187 , 0.234 0.186 , 0.233	Depositor DCC
$R_{free}$ test set	6402 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtrriage
Anisotropy	0.218	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 41.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	20770	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.66% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MLA, GDP, FRU, MN, TQY

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	0.65	0/4975	0.86	0/6766
1	B	0.60	0/4969	0.87	12/6761 (0.2%)
1	C	0.65	0/4923	0.87	5/6697 (0.1%)
1	D	0.63	0/4905	0.88	10/6677 (0.1%)
All	All	0.63	0/19772	0.87	27/26901 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	168	PRO	N-CA-C	11.10	124.24	110.70
1	D	167	GLY	CA-C-N	9.55	130.21	120.38
1	D	167	GLY	C-N-CA	9.55	130.21	120.38
1	B	197	GLY	CA-C-N	7.93	127.65	119.64
1	B	197	GLY	C-N-CA	7.93	127.65	119.64

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	A	170	THR	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	4804	0	4708	66	0
1	B	4786	0	4688	63	0
1	C	4762	0	4663	50	0
1	D	4749	0	4629	57	0
2	E	32	0	11	0	0
2	F	32	0	11	0	0
3	A	28	0	12	0	0
3	B	28	0	12	0	0
3	C	28	0	12	0	0
3	D	28	0	12	1	0
4	A	7	0	2	0	0
4	B	14	0	4	1	0
4	C	7	0	2	1	0
4	D	7	0	2	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	384	0	0	9	0
6	B	305	0	0	9	0
6	C	417	0	0	13	0
6	D	344	0	0	10	0
All	All	20770	0	18768	231	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 6.

The worst 5 of 231 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:197:GLY:H	1:A:198:PRO:HD3	1.06	1.06
1:D:209:VAL:HG21	1:D:265:PHE:CE2	1.93	1.02
1:D:170:THR:HG22	6:D:6251:HOH:O	1.60	1.01
1:B:209:VAL:HG21	1:B:265:PHE:CE2	2.00	0.96
1:A:197:GLY:H	1:A:198:PRO:CD	1.81	0.93

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	617/608 (102%)	597 (97%)	14 (2%)	6 (1%)	12	9
1	B	619/608 (102%)	596 (96%)	19 (3%)	4 (1%)	21	18
1	C	612/608 (101%)	597 (98%)	14 (2%)	1 (0%)	43	44
1	D	611/608 (100%)	591 (97%)	17 (3%)	3 (0%)	24	22
All	All	2459/2432 (101%)	2381 (97%)	64 (3%)	14 (1%)	21	18

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	THR
1	B	207	ASP
1	D	168	PRO
1	A	255	GLY
1	B	255	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	509/499 (102%)	491 (96%)	18 (4%)	32	35
1	B	509/499 (102%)	489 (96%)	20 (4%)	28	31
1	C	503/499 (101%)	496 (99%)	7 (1%)	59	67
1	D	500/499 (100%)	487 (97%)	13 (3%)	40	46
All	All	2021/1996 (101%)	1963 (97%)	58 (3%)	42	42

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	205	ASP
1	D	434[B]	ILE
1	B	526	ARG
1	D	434[A]	ILE
1	D	203	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	365	ASN
1	C	135	ASN
1	D	275	GLN
1	C	132	GLN
1	C	202	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	TQY	E	1	2	20,20,21	1.95	3 (15%)	25,25,27	2.81	4 (16%)
2	FRU	E	2	2	11,12,12	0.77	1 (9%)	10,18,18	0.82	0
2	TQY	F	1	2	20,20,21	1.93	3 (15%)	25,25,27	2.83	5 (20%)
2	FRU	F	2	2	11,12,12	0.78	1 (9%)	10,18,18	0.70	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	TQY	E	1	2	-	3/12/29/32	0/1/1/1
2	FRU	E	2	2	-	0/5/24/24	0/1/1/1
2	TQY	F	1	2	-	2/12/29/32	0/1/1/1
2	FRU	F	2	2	-	2/5/24/24	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	TQY	C11-C10	-6.49	1.19	1.51
2	F	1	TQY	C11-C10	-6.22	1.20	1.51
2	F	1	TQY	O6-C13	4.01	1.45	1.33
2	E	1	TQY	C12-C11	-3.87	1.27	1.51
2	F	1	TQY	C12-C11	-3.84	1.27	1.51

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	TQY	C11-C10-C9	11.76	173.82	114.37
2	F	1	TQY	C11-C10-C9	11.61	173.07	114.37
2	F	1	TQY	C12-C11-C10	6.04	168.23	115.25
2	E	1	TQY	C12-C11-C10	5.99	167.83	115.25
2	E	1	TQY	O6-C13-O7	-2.66	116.97	123.63

There are no chirality outliers.

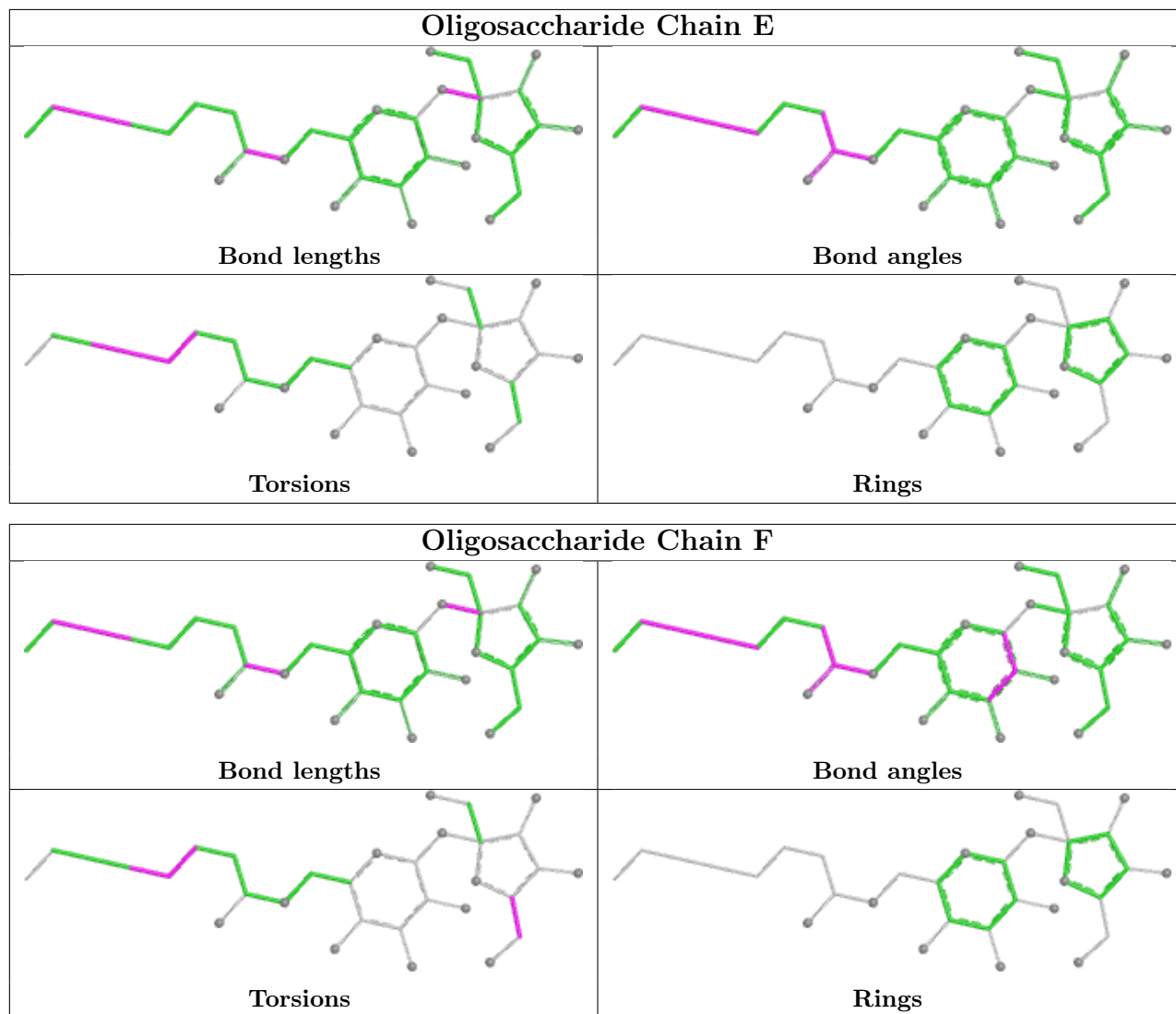
5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	2	FRU	O5-C5-C6-O6
2	E	1	TQY	C9-C10-C11-C12
2	E	1	TQY	C7-C8-C9-C10
2	E	1	TQY	C11-C10-C9-C8
2	F	1	TQY	C11-C10-C9-C8

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 8 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MLA	D	5001	5	6,6,6	1.13	0	7,7,7	1.04	0
4	MLA	C	4003	5	6,6,6	1.26	0	7,7,7	1.22	0
4	MLA	A	2001	5	6,6,6	1.07	0	7,7,7	1.20	0
3	GDP	C	4000	5	29,30,30	1.22	3 (10%)	45,47,47	1.82	8 (17%)
4	MLA	B	6001	-	6,6,6	1.17	0	7,7,7	0.86	0
3	GDP	B	3000	5	29,30,30	1.21	4 (13%)	45,47,47	1.78	9 (20%)
3	GDP	D	5000	5	29,30,30	1.27	2 (6%)	45,47,47	1.71	7 (15%)
4	MLA	B	3001	5	6,6,6	1.16	0	7,7,7	1.05	0
3	GDP	A	2000	5	29,30,30	1.27	5 (17%)	45,47,47	1.72	7 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MLA	D	5001	5	-	4/4/4/4	-
4	MLA	C	4003	5	-	0/4/4/4	-
4	MLA	A	2001	5	-	4/4/4/4	-
3	GDP	C	4000	5	-	0/16/32/32	0/3/3/3
4	MLA	B	6001	-	-	2/4/4/4	-
3	GDP	B	3000	5	-	1/16/32/32	0/3/3/3
3	GDP	D	5000	5	-	0/16/32/32	0/3/3/3
4	MLA	B	3001	5	-	4/4/4/4	-
3	GDP	A	2000	5	-	3/16/32/32	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	5000	GDP	C5-C4	3.54	1.48	1.38
3	C	4000	GDP	C5-C4	3.19	1.47	1.38
3	A	2000	GDP	C5-C4	3.02	1.47	1.38
3	B	3000	GDP	PA-O3A	2.73	1.62	1.59
3	B	3000	GDP	C5-C4	2.64	1.46	1.38

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4000	GDP	C5-C4-N3	-5.77	119.21	128.39
3	B	3000	GDP	C5-C4-N3	-5.70	119.32	128.39
3	D	5000	GDP	C5-C4-N3	-5.54	119.57	128.39
3	C	4000	GDP	C2-N3-C4	5.26	121.36	112.30
3	A	2000	GDP	C5-C4-N3	-5.14	120.21	128.39

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2000	GDP	PA-O3A-PB-O2B
3	A	2000	GDP	PA-O3A-PB-O3B
3	A	2000	GDP	C5'-O5'-PA-O3A
4	B	3001	MLA	O1A-C1-C2-C3
4	B	3001	MLA	O1B-C1-C2-C3

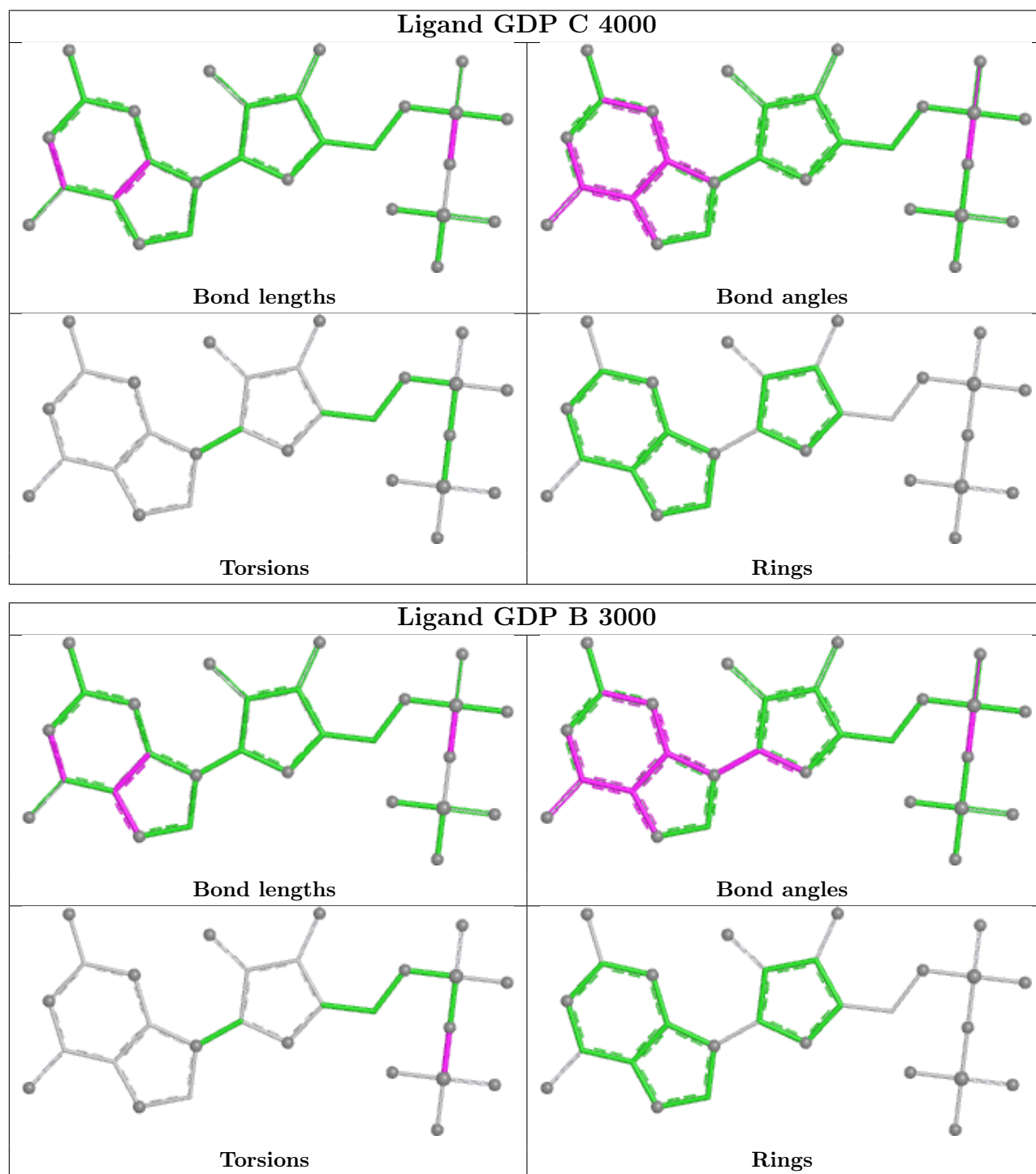
There are no ring outliers.

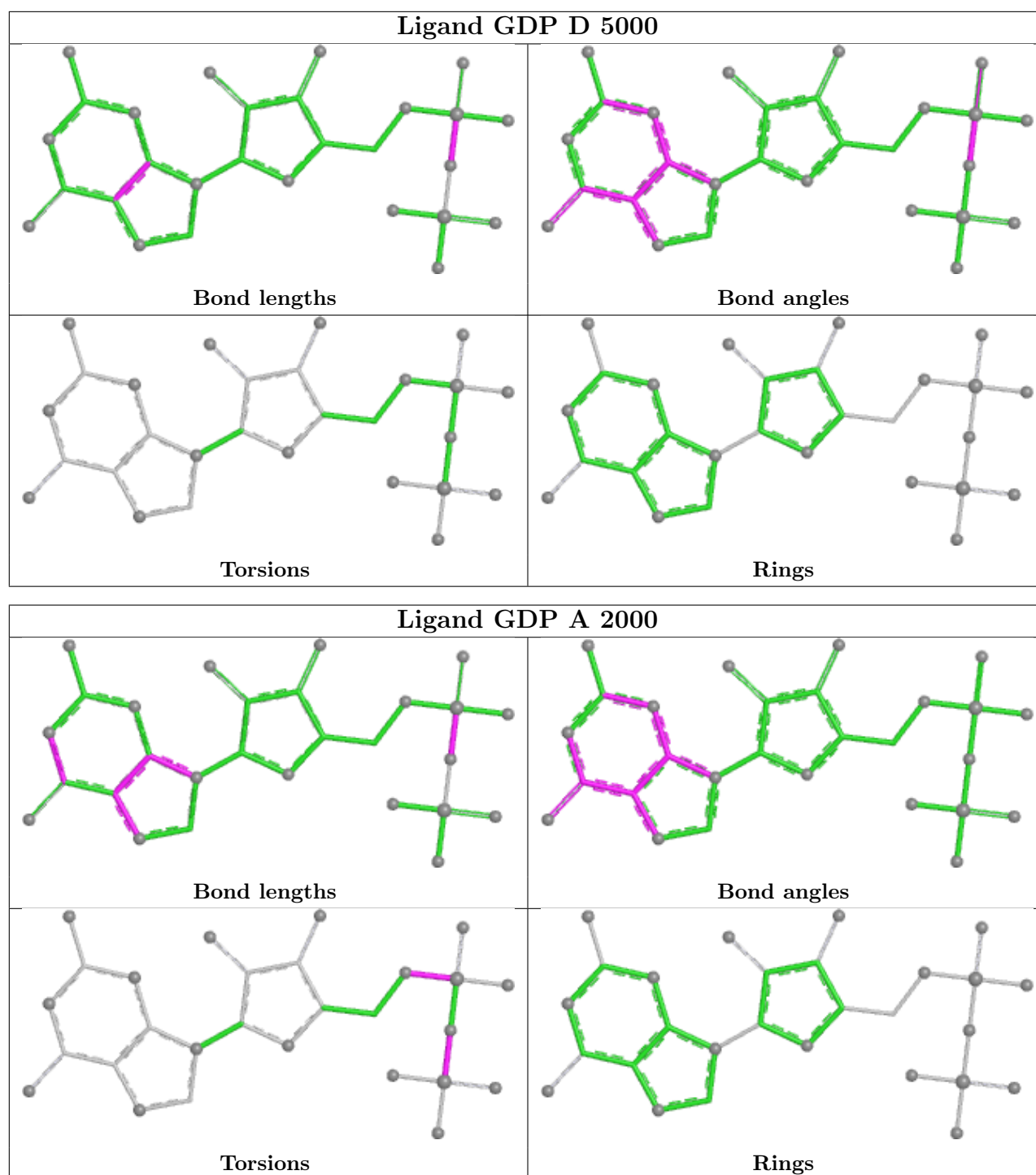
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	4003	MLA	1	0
4	B	6001	MLA	1	0
3	D	5000	GDP	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	608/608 (100%)	0.19	19 (3%) 51 54	6, 15, 19, 25	11 (1%)
1	B	608/608 (100%)	0.49	31 (5%) 33 35	8, 15, 19, 26	13 (2%)
1	C	608/608 (100%)	0.14	13 (2%) 63 66	8, 15, 19, 25	6 (0%)
1	D	608/608 (100%)	0.20	9 (1%) 72 74	7, 15, 19, 24	5 (0%)
All	All	2432/2432 (100%)	0.26	72 (2%) 52 55	6, 15, 19, 26	35 (1%)

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	530	LEU	6.8
1	B	426	CYS	6.4
1	B	427	ALA	6.1
1	B	429	ALA	6.1
1	B	428	PRO	5.9

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

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

### 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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.

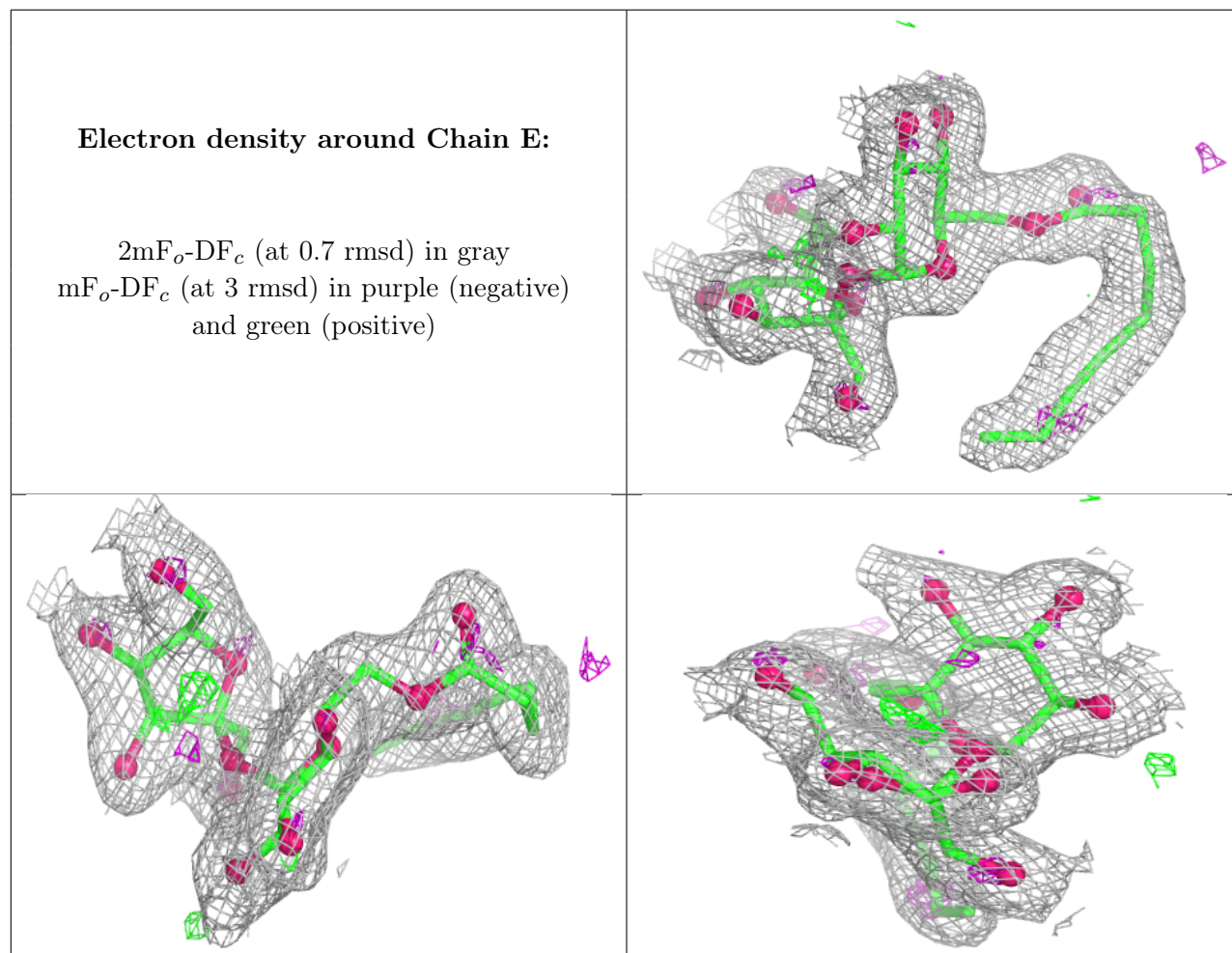
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	FRU	F	2	12/12	0.93	0.07	14,15,18,19	0
2	FRU	E	2	12/12	0.94	0.07	10,12,13,14	0

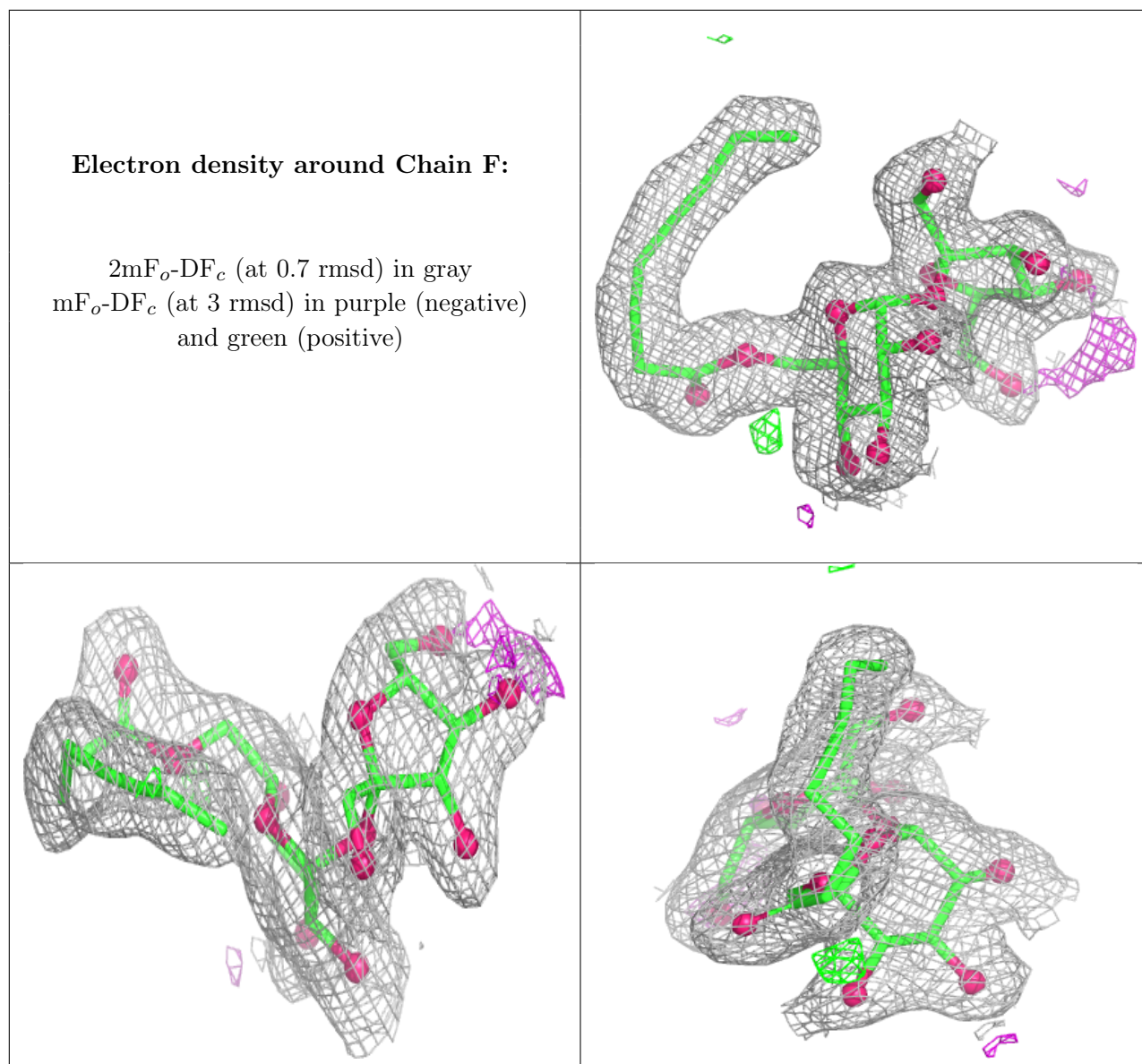
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	TQY	F	1	20/21	0.94	0.07	11,14,19,20	0
2	TQY	E	1	20/21	0.94	0.07	8,13,18,18	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





## 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, 95<sup>th</sup> 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.

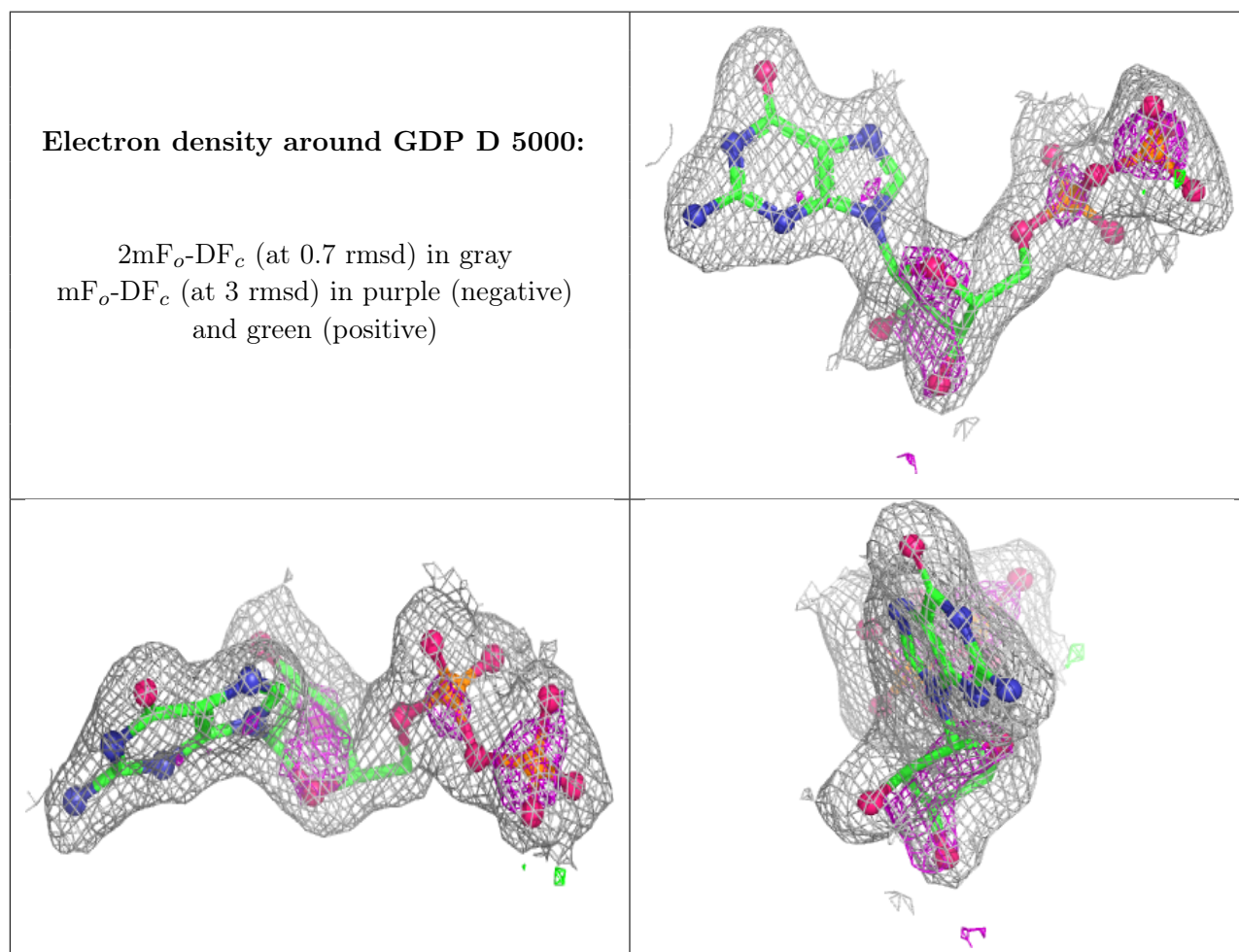
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MLA	A	2001	7/7	0.83	0.15	34,36,38,38	0
4	MLA	D	5001	7/7	0.83	0.12	27,30,32,32	0
4	MLA	B	3001	7/7	0.87	0.14	27,27,29,29	0
4	MLA	C	4003	7/7	0.89	0.14	21,21,26,30	0
4	MLA	B	6001	7/7	0.89	0.10	30,32,34,36	0

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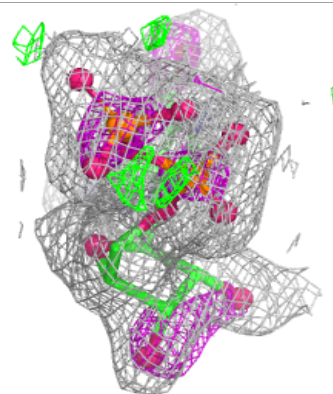
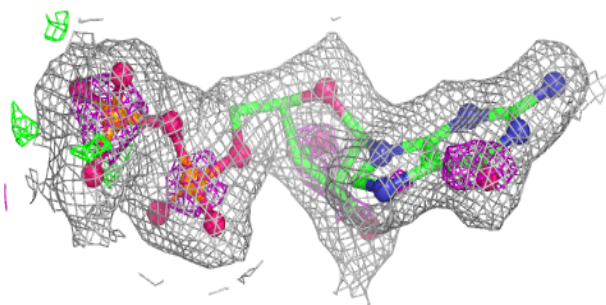
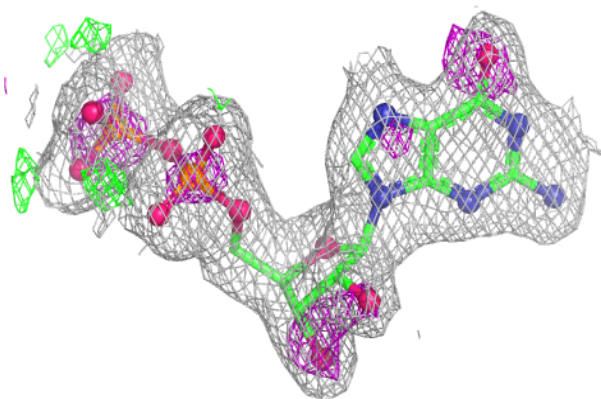
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	MN	B	3003	1/1	0.89	0.15	23,23,23,23	1
5	MN	C	4002	1/1	0.93	0.08	9,9,9,9	1
5	MN	D	5003	1/1	0.93	0.06	14,14,14,14	1
3	GDP	D	5000	28/28	0.94	0.08	16,18,23,24	0
5	MN	A	2003	1/1	0.94	0.10	21,21,21,21	1
5	MN	B	3002	1/1	0.94	0.13	28,28,28,28	1
3	GDP	C	4000	28/28	0.96	0.07	9,11,13,14	0
3	GDP	A	2000	28/28	0.96	0.06	9,11,14,15	0
5	MN	D	5002	1/1	0.96	0.14	38,38,38,38	1
3	GDP	B	3000	28/28	0.96	0.07	15,18,18,19	0
5	MN	A	2002	1/1	0.99	0.09	15,15,15,15	1
5	MN	C	4001	1/1	1.00	0.09	9,9,9,9	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.

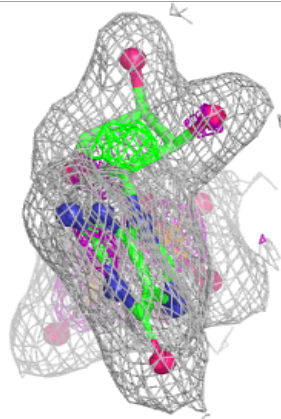
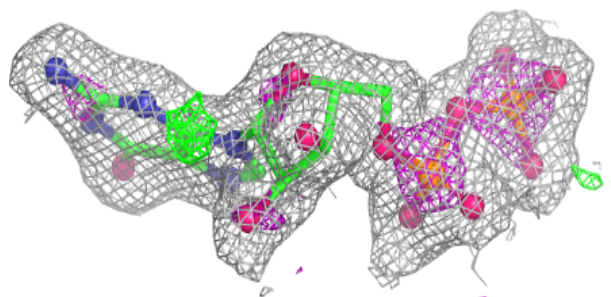
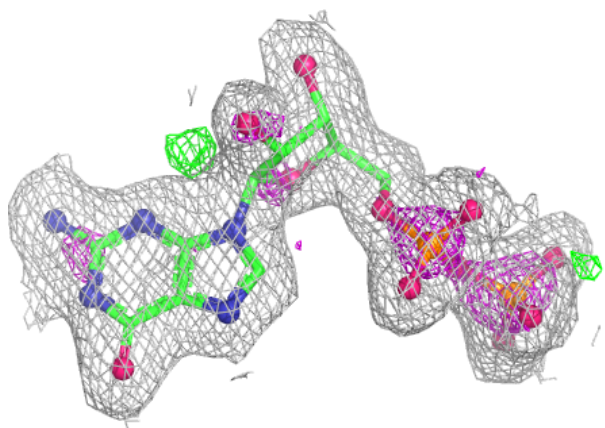


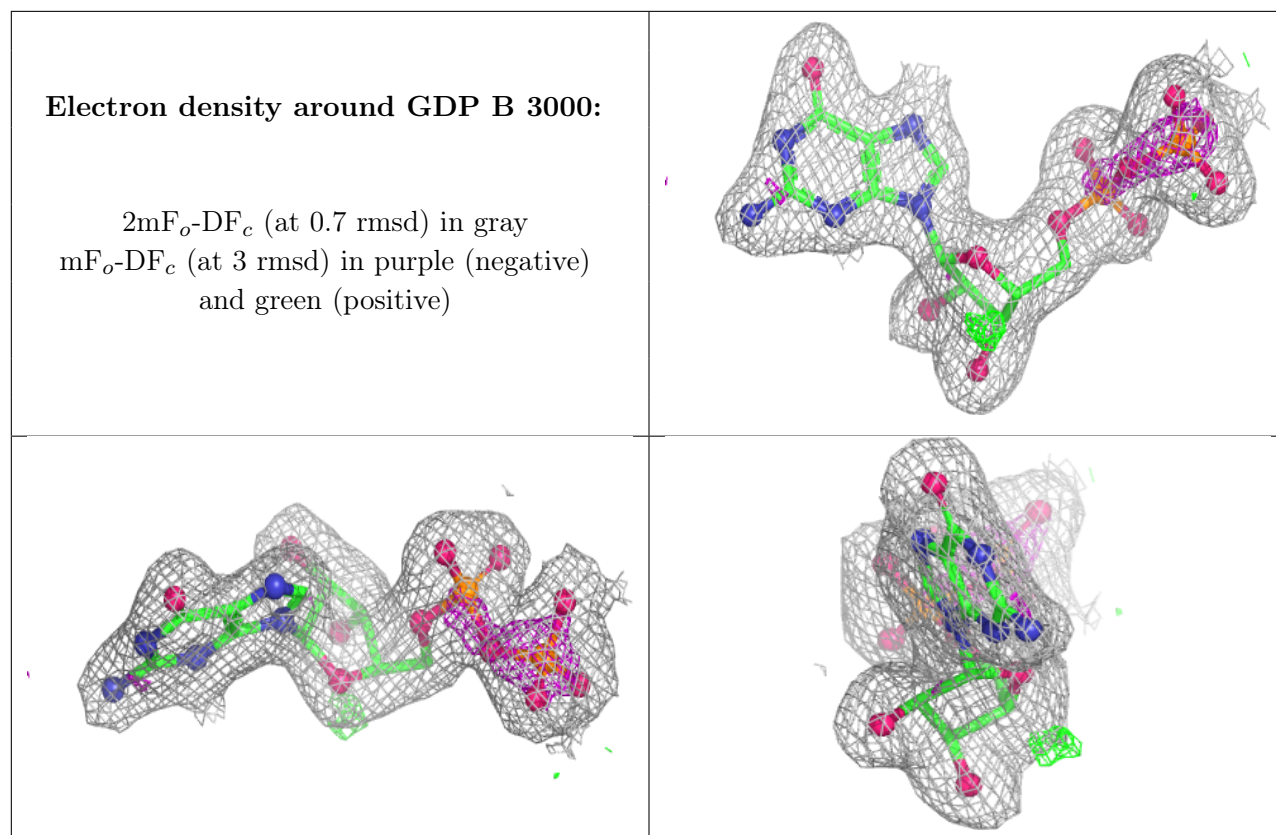
**Electron density around GDP C 4000:**

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

**Electron density around GDP A 2000:**

$2mF_o-DF_c$  (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.