



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 21, 2020 – 05:05 PM BST

PDB ID : 2FAH  
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 Full wwPDB X-ray Structure Validation 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.14.6  
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) : 2.14.6

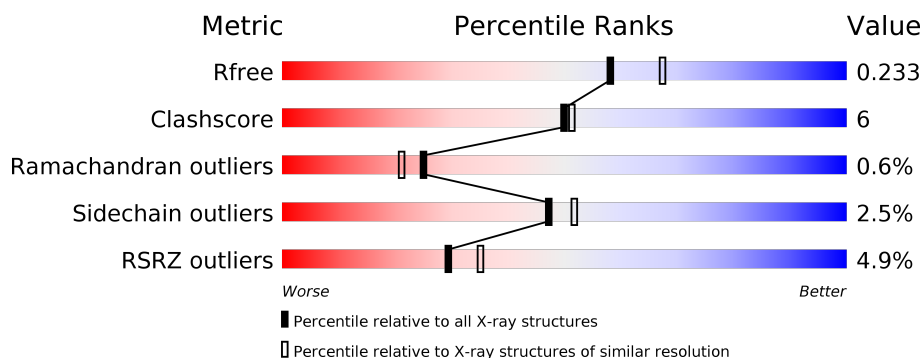
# 1 Overall quality at a glance

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))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (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 on 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	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>12%</div> </div> </div>
1	B	608	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>13%</div> </div> </div>
1	C	608	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>13%</div> </div> </div>
1	D	608	<div> <div>5%</div> <div> <div></div> <div>88%</div> <div>11%</div> </div> </div>
2	E	2	<div> <div></div> <div>100%</div> </div>
2	F	2	<div> <div></div> <div>100%</div> </div>

## 2 Entry composition

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

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

*Continued on next page...*

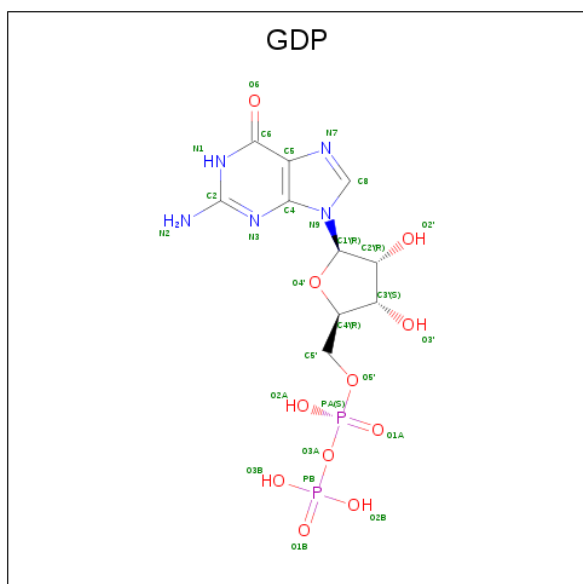
Continued from previous page...

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.

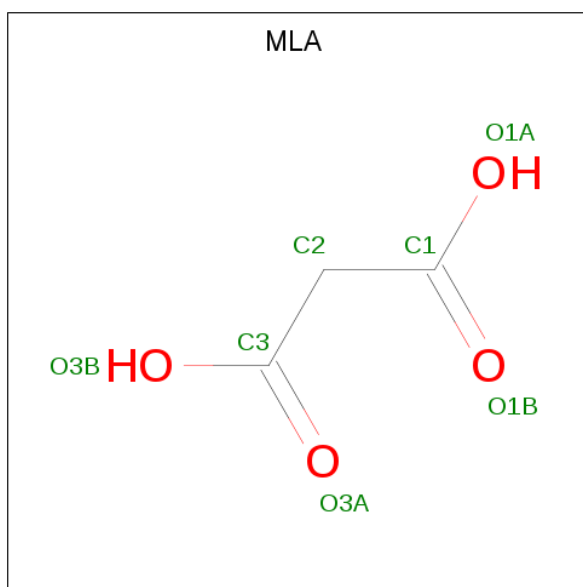
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			32	20	12			
2	F	2	Total	C	O	0	0	0
			32	20	12			

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



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

- Molecule 4 is MALONIC ACID (three-letter code: MLA) (formula:  $C_3H_4O_4$ ).



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

- Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

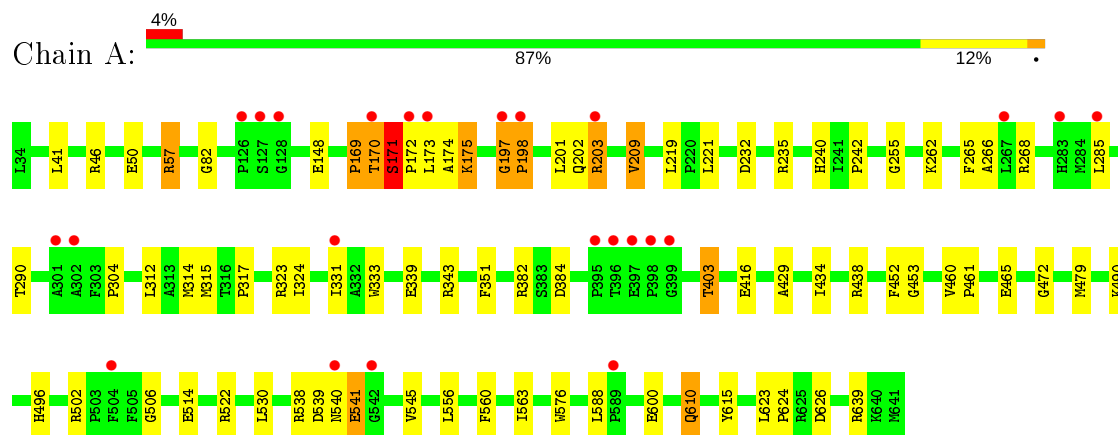
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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

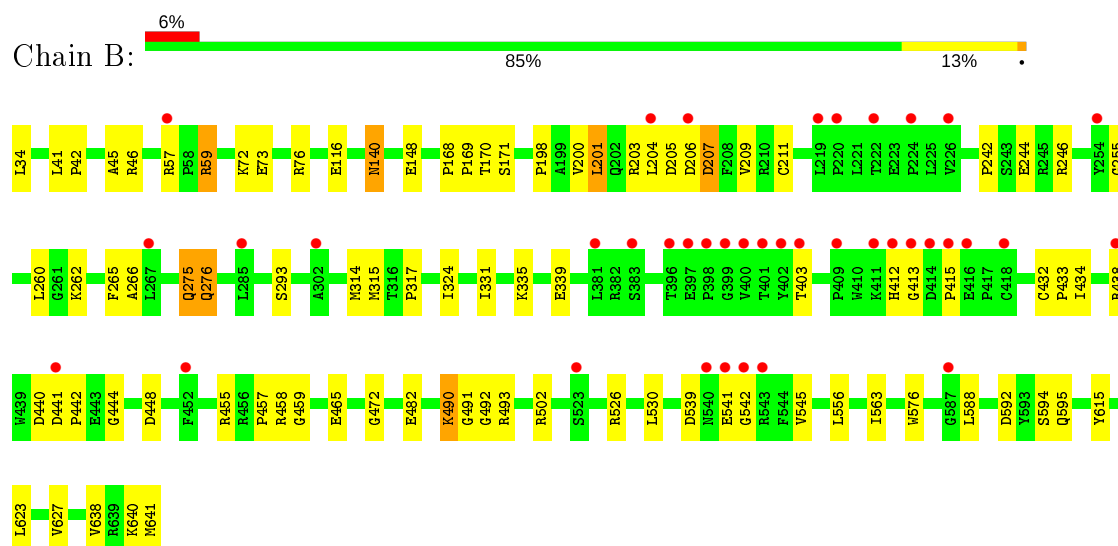
### 3 Residue-property plots [i](#)

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.

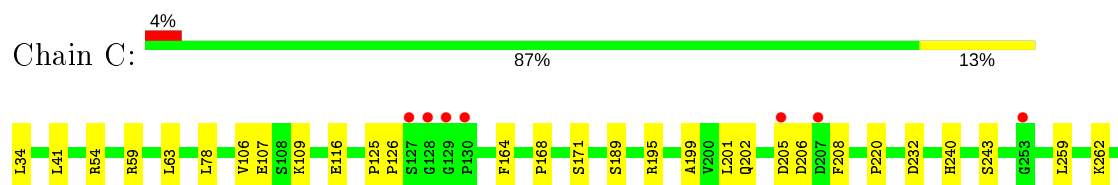
#### • Molecule 1: Phosphoenolpyruvate carboxykinase

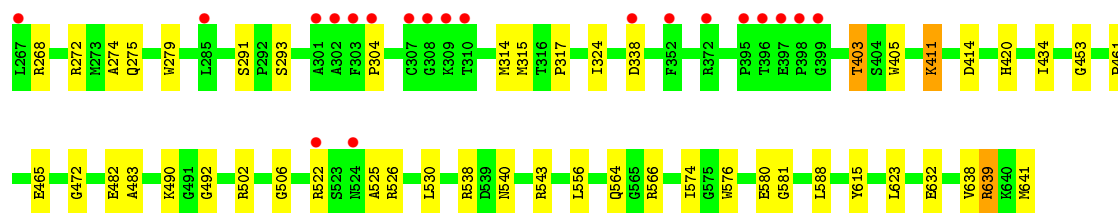


#### • Molecule 1: Phosphoenolpyruvate carboxykinase

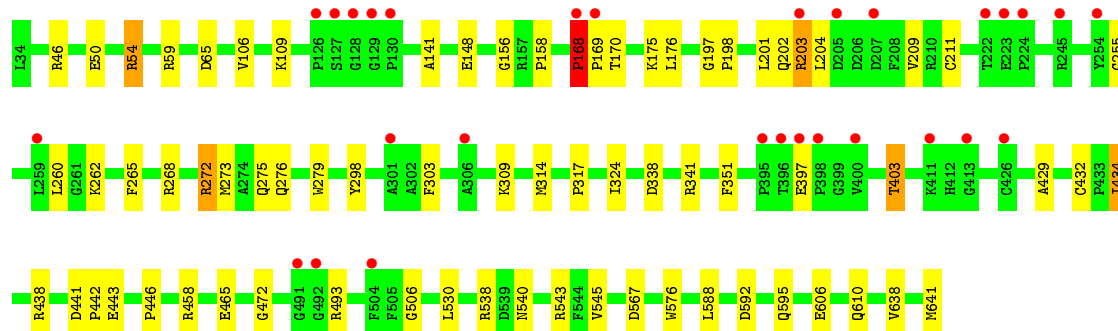
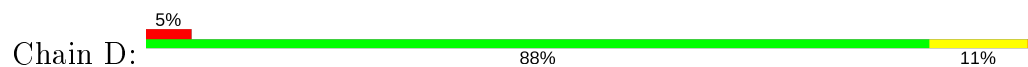


#### • Molecule 1: Phosphoenolpyruvate carboxykinase





● 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 32.80 – 2.09	Depositor EDS
% Data completeness (in resolution range)	94.7 (32.81-2.09) 94.7 (32.80-2.09)	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)	Xtriage
Refinement program	REFMAC, CNS	Depositor
R, $R_{free}$	0.187 , 0.234 0.187 , 0.233	Depositor DCC
$R_{free}$ test set	6402 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 43.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20770	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage'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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MLA, TQY, FRU, MN

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	0.52	0/4975	0.64	0/6766
1	B	0.49	0/4969	0.62	1/6761 (0.0%)
1	C	0.52	0/4923	0.63	1/6697 (0.0%)
1	D	0.50	0/4905	0.61	1/6677 (0.0%)
All	All	0.51	0/19772	0.62	3/26901 (0.0%)

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.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	502	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	C	639	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	D	168	PRO	C-N-CD	-5.58	108.33	120.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	PRO	Peptide
1	A	170	THR	Peptide

## 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	4804	0	4708	63	0
1	B	4786	0	4688	61	0
1	C	4762	0	4663	48	0
1	D	4749	0	4629	54	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	221	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.

All (221) 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

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:PRO:HG2	1:D:203:ARG:NH1	1.84	0.92
1:B:198:PRO:HA	1:B:201[A]:LEU:HD22	1.52	0.89
1:A:57:ARG:HG2	1:A:57:ARG:HH21	1.38	0.88
1:A:197:GLY:N	1:A:198:PRO:HD3	1.90	0.85
1:B:455:ARG:HB2	1:B:482:GLU:HG2	1.59	0.84
1:A:172:PRO:HB2	1:A:173:LEU:HA	1.64	0.80
1:A:209[B]:VAL:HG21	1:A:265:PHE:CE2	2.17	0.79
1:D:441:ASP:OD2	1:D:442:PRO:HD2	1.85	0.76
1:A:514[B]:GLU:HG2	1:A:624:PRO:HG3	1.67	0.76
1:A:416:GLU:HG3	6:A:2356:HOH:O	1.85	0.75
1:A:172:PRO:CB	1:A:173:LEU:HA	2.18	0.74
1:D:209:VAL:HG21	1:D:265:PHE:CD2	2.22	0.74
1:A:57:ARG:CG	1:A:57:ARG:HH21	2.02	0.73
1:D:50:GLU:O	1:D:54:ARG:HD3	1.87	0.73
1:D:403:THR:HG22	6:D:6005:HOH:O	1.89	0.71
1:D:158:PRO:HD2	6:D:6140:HOH:O	1.91	0.70
1:B:206:ASP:O	1:B:207:ASP:HB3	1.91	0.70
1:B:41:LEU:O	1:B:46:ARG:HD2	1.91	0.70
1:B:314:MET:HA	1:B:434:ILE:HD11	1.73	0.69
1:B:541:GLU:H	1:B:542:GLY:HA2	1.56	0.69
1:C:291[A]:SER:OG	1:C:293:SER:OG	2.10	0.69
1:C:54:ARG:HD2	6:C:6209:HOH:O	1.92	0.69
1:D:141:ALA:O	6:D:6122:HOH:O	2.11	0.68
1:B:59:ARG:HH11	1:B:59:ARG:CG	2.06	0.68
1:D:638:VAL:O	1:D:641:MET:HG2	1.94	0.67
4:C:4003:MLA:O1B	6:C:6273:HOH:O	2.11	0.67
1:B:72:LYS:O	1:B:76[A]:ARG:HG3	1.94	0.67
1:A:82:GLY:HA2	6:A:2008:HOH:O	1.95	0.67
1:A:626:ASP:OD1	6:A:2323:HOH:O	2.13	0.66
1:B:317:PRO:HG3	1:B:324:ILE:HG12	1.77	0.66
1:D:170:THR:HG23	1:D:442:PRO:HB3	1.78	0.65
1:D:458:ARG:NH2	1:D:540[B]:ASN:OD1	2.29	0.65
1:B:140[A]:ASN:ND2	1:B:140[A]:ASN:H	1.95	0.65
1:B:293[A]:SER:OG	6:B:6182:HOH:O	2.10	0.65
1:B:244[A]:GLU:HG2	1:B:246:ARG:HE	1.62	0.65
1:C:502[B]:ARG:NH1	6:C:6195:HOH:O	2.30	0.64
1:C:107:GLU:OE2	1:C:502[B]:ARG:NH1	2.24	0.63
1:B:276[A]:GLN:HG3	6:B:6294:HOH:O	1.97	0.63
1:D:209:VAL:CG2	1:D:265:PHE:CE2	2.76	0.63
1:A:197:GLY:N	1:A:198:PRO:CD	2.52	0.63
1:A:221:LEU:CD1	1:C:220:PRO:HD3	2.29	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:PRO:HG3	1:A:324:ILE:HG12	1.80	0.62
1:D:46:ARG:O	1:D:50:GLU:HG2	1.99	0.62
1:D:203:ARG:HD3	1:D:203:ARG:N	2.14	0.62
1:A:339:GLU:HG2	1:B:457:PRO:HB2	1.83	0.61
1:A:171:SER:CB	1:A:172:PRO:HA	2.30	0.61
1:C:580:GLU:O	6:C:6341:HOH:O	2.16	0.61
1:B:59:ARG:HH11	1:B:59:ARG:HG2	1.64	0.61
1:B:638:VAL:O	1:B:641:MET:HG2	2.01	0.61
1:A:539:ASP:HB3	1:A:545:VAL:HG22	1.83	0.61
1:D:169:PRO:HG2	1:D:203:ARG:HH12	1.64	0.61
1:D:175:LYS:HE3	1:D:273:MET:CE	2.31	0.60
1:D:314:MET:HA	1:D:434[B]:ILE:HD11	1.82	0.60
1:A:169:PRO:O	1:A:203:ARG:HG3	2.02	0.59
1:C:526:ARG:HD3	1:D:458:ARG:HH12	1.67	0.59
1:C:639:ARG:NH2	6:C:6298:HOH:O	2.36	0.58
1:A:343:ARG:HH12	1:A:438:ARG:HH22	1.52	0.57
1:A:472:GLY:HA3	1:A:530:LEU:HD12	1.85	0.57
1:C:59:ARG:HD2	6:C:6328:HOH:O	2.03	0.57
1:D:317:PRO:HG3	1:D:324[A]:ILE:HG12	1.87	0.57
1:B:209:VAL:HG21	1:B:265:PHE:CD2	2.40	0.56
1:C:314:MET:HA	1:C:434:ILE:HD11	1.87	0.56
1:A:171:SER:CB	1:A:172:PRO:CA	2.83	0.56
1:D:472:GLY:HA3	1:D:530:LEU:HD12	1.86	0.56
1:D:606:GLU:HG3	1:D:610:GLN:HE21	1.70	0.56
1:A:290:THR:HB	1:A:323:ARG:HB3	1.86	0.56
1:D:198:PRO:O	1:D:201:LEU:HB2	2.06	0.56
1:B:244[B]:GLU:OE2	6:B:6133:HOH:O	2.17	0.55
1:C:581:GLY:HA2	6:C:6235:HOH:O	2.06	0.55
1:D:175:LYS:HE3	1:D:273:MET:HE2	1.86	0.55
1:A:496:HIS:NE2	1:A:610[A]:GLN:NE2	2.54	0.55
1:B:200:VAL:HG23	6:B:6083:HOH:O	2.07	0.55
1:D:65:ASP:O	1:D:197:GLY:HA2	2.07	0.55
1:B:455:ARG:CB	1:B:482:GLU:HG2	2.31	0.55
1:A:403:THR:HG22	6:A:2025:HOH:O	2.07	0.54
1:A:203:ARG:HH21	1:A:203:ARG:HB3	1.73	0.54
1:B:45:ALA:HB2	1:B:204:LEU:HD11	1.90	0.54
1:B:168:PRO:HB3	1:B:440:ASP:O	2.08	0.54
1:D:465:GLU:HB3	1:D:576:TRP:HB2	1.90	0.54
1:D:338:ASP:HB3	6:D:6321:HOH:O	2.07	0.54
1:B:541:GLU:N	1:B:542:GLY:HA2	2.20	0.53
1:A:46:ARG:O	1:A:50:GLU:HG2	2.08	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:ARG:NH2	6:A:2101:HOH:O	2.41	0.53
1:D:59:ARG:NH2	1:D:156:GLY:O	2.41	0.53
1:D:538:ARG:HA	1:D:543:ARG:O	2.09	0.53
1:A:171:SER:HB3	1:A:172:PRO:CA	2.38	0.53
1:C:472:GLY:HA3	1:C:530:LEU:HD12	1.91	0.53
1:A:343:ARG:HH12	1:A:438:ARG:NH2	2.06	0.53
1:A:221:LEU:HD12	1:C:220:PRO:HD3	1.90	0.53
1:B:441:ASP:OD2	1:B:442:PRO:HD2	2.09	0.53
1:B:335:LYS:HG3	6:B:6248:HOH:O	2.09	0.52
1:C:199:ALA:HA	1:C:202:GLN:HE21	1.74	0.52
1:C:465:GLU:HB3	1:C:576:TRP:HB2	1.92	0.52
1:B:140[A]:ASN:HD22	1:B:140[A]:ASN:H	1.56	0.52
1:C:168:PRO:O	1:C:171:SER:HB3	2.10	0.51
1:C:411:LYS:HE2	1:C:414:ASP:OD2	2.10	0.51
1:D:317:PRO:HG3	1:D:324[B]:ILE:HG23	1.92	0.51
1:C:106:VAL:HG11	1:C:109:LYS:HD2	1.91	0.51
1:D:432:CYS:SG	1:D:434[A]:ILE:HD13	2.51	0.51
1:A:514[B]:GLU:HG3	6:A:2382:HOH:O	2.11	0.51
1:B:465:GLU:HB3	1:B:576:TRP:HB2	1.91	0.50
1:C:482:GLU:HB3	1:C:492:GLY:HA2	1.94	0.50
1:C:638:VAL:O	1:C:641:MET:HG2	2.12	0.49
1:A:171:SER:HB2	1:A:172:PRO:HA	1.93	0.49
1:B:448:ASP:HB3	1:B:563:ILE:HG21	1.94	0.49
1:B:491:GLY:HA2	6:B:6190:HOH:O	2.12	0.49
1:A:209[B]:VAL:HG21	1:A:265:PHE:CD2	2.47	0.49
1:A:540:ASN:HA	1:A:541:GLU:CD	2.33	0.48
1:A:465:GLU:HB3	1:A:576:TRP:HB2	1.96	0.48
1:B:627:VAL:HA	6:B:6224:HOH:O	2.14	0.48
1:C:232:ASP:OD1	6:C:6267:HOH:O	2.20	0.48
1:B:541:GLU:HB2	1:B:542:GLY:HA2	1.96	0.48
1:D:272:ARG:O	1:D:276:GLN:HG2	2.14	0.48
1:B:198:PRO:HA	1:B:201[B]:LEU:HD22	1.97	0.47
1:C:538:ARG:HA	1:C:543:ARG:O	2.14	0.47
1:D:202:GLN:HB3	1:D:203:ARG:HD3	1.96	0.47
1:D:351:PHE:CE2	1:D:429:ALA:HA	2.50	0.47
1:B:171:SER:HB2	1:B:442:PRO:HA	1.96	0.47
1:A:219:LEU:HD22	1:C:220:PRO:HD2	1.96	0.47
1:A:175:LYS:HG3	1:A:333:TRP:CZ3	2.49	0.47
1:B:198:PRO:HA	1:B:201[A]:LEU:CD2	2.35	0.47
1:D:169:PRO:HG2	1:D:203:ARG:CZ	2.43	0.47
1:D:176:LEU:HD11	1:D:203:ARG:HG2	1.96	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:592:ASP:O	1:D:595:GLN:HB2	2.14	0.46
1:A:315:MET:HE1	1:A:556:LEU:HD12	1.96	0.46
1:D:438:ARG:HD3	6:D:6314:HOH:O	2.16	0.46
1:B:592[B]:ASP:OD2	1:B:594:SER:OG	2.24	0.46
1:C:240:HIS:CE1	1:C:268:ARG:HD2	2.50	0.46
1:A:242:PRO:HG3	6:A:2175:HOH:O	2.14	0.46
1:B:34:LEU:HD12	1:B:73:GLU:CD	2.35	0.46
1:C:403:THR:HG22	6:C:6205:HOH:O	2.16	0.46
1:C:483:ALA:HB3	1:C:490:LYS:O	2.17	0.45
1:D:175:LYS:HE3	1:D:273:MET:HE1	1.97	0.45
1:A:171:SER:HB3	1:A:172:PRO:C	2.36	0.45
1:B:472:GLY:HA3	1:B:530:LEU:HD12	1.98	0.45
1:A:600:GLU:HB3	6:A:2182:HOH:O	2.16	0.45
1:C:205:ASP:CG	1:C:206:ASP:H	2.19	0.45
1:D:545:VAL:HG11	1:D:595:GLN:HB3	1.97	0.45
1:A:268:ARG:O	1:A:506:GLY:HA3	2.16	0.45
1:C:317:PRO:HG3	1:C:324:ILE:HG12	1.97	0.45
1:A:57:ARG:NH2	1:A:57:ARG:HG2	2.15	0.45
1:C:461:PRO:HG2	1:C:574:ILE:HD11	1.99	0.45
1:C:632:GLU:OE1	6:C:6222:HOH:O	2.20	0.44
1:A:172:PRO:HA	1:A:174:ALA:H	1.82	0.44
1:D:298:TYR:HB2	1:D:446:PRO:O	2.17	0.44
1:A:314:MET:HA	1:A:434[B]:ILE:HD11	1.99	0.44
1:B:482:GLU:HB2	1:B:492:GLY:O	2.18	0.44
1:C:268:ARG:O	1:C:506:GLY:HA3	2.18	0.44
1:D:324[B]:ILE:HD12	1:D:434[B]:ILE:HD12	1.98	0.44
1:D:324[B]:ILE:HD11	1:D:434[B]:ILE:CD1	2.47	0.44
1:C:63:LEU:HD21	1:C:201:LEU:HD11	1.98	0.44
1:D:567:ASP:OD2	6:D:6261:HOH:O	2.21	0.44
1:B:438:ARG:NH2	1:B:444:GLY:O	2.50	0.44
1:D:209:VAL:HG21	1:D:265:PHE:CZ	2.47	0.44
1:A:240:HIS:CE1	1:A:268:ARG:HD2	2.52	0.44
1:C:78:LEU:HD21	6:C:6225:HOH:O	2.18	0.44
1:D:175:LYS:HE2	1:D:279:TRP:CZ2	2.53	0.43
1:A:502[A]:ARG:NH2	6:A:2039:HOH:O	2.52	0.43
1:C:208:PHE:N	6:C:6353:HOH:O	2.50	0.43
1:C:615:TYR:HB3	1:C:623:LEU:HD22	2.00	0.43
1:C:338:ASP:OD1	1:D:493:ARG:HA	2.18	0.43
1:A:452:PHE:HB3	1:A:479:MET:SD	2.59	0.43
1:B:458:ARG:HG2	1:B:459:GLY:N	2.34	0.43
1:D:106:VAL:HG11	1:D:109:LYS:HD2	2.01	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:MET:HE1	1:B:556:LEU:HD12	2.00	0.43
1:C:315:MET:HE1	1:C:556:LEU:HD12	2.00	0.43
1:A:172:PRO:HB2	1:A:173:LEU:CA	2.42	0.43
1:A:221:LEU:HG	1:C:220:PRO:CD	2.48	0.43
1:B:432:CYS:HA	1:B:433:PRO:HD3	1.88	0.43
1:A:266:ALA:HB3	1:A:331:ILE:HD13	2.01	0.42
1:B:491:GLY:HA2	1:B:492:GLY:HA2	1.62	0.42
1:B:412:HIS:HA	1:B:413:GLY:HA2	1.79	0.42
1:B:242:PRO:HG3	6:B:6223:HOH:O	2.19	0.42
1:B:640:LYS:HE3	4:B:6001:MLA:HC22	2.02	0.42
1:C:34:LEU:N	6:C:6413:HOH:O	2.51	0.42
1:C:522:ARG:HB3	1:C:525:ALA:HB2	2.01	0.42
1:D:397:GLU:HG3	6:D:6345:HOH:O	2.18	0.42
1:A:460:VAL:HA	1:A:461:PRO:HD3	1.96	0.42
1:D:341:ARG:HD2	6:D:6075:HOH:O	2.18	0.42
1:C:41:LEU:HD23	1:C:201:LEU:HD21	2.02	0.42
1:D:268:ARG:O	1:D:506:GLY:HA3	2.20	0.42
3:D:5000:GDP:H3'	6:D:6164:HOH:O	2.18	0.42
1:A:351:PHE:CE2	1:A:429:ALA:HA	2.55	0.42
1:C:189:SER:HB2	1:C:259:LEU:HD21	2.01	0.42
1:C:564:GLN:OE1	1:C:566:ARG:NH1	2.53	0.42
1:A:232:ASP:OD2	1:A:235[B]:ARG:NE	2.32	0.42
1:B:262:LYS:O	1:B:266:ALA:HB3	2.19	0.42
1:D:303:PHE:HB2	1:D:309:LYS:HG3	2.01	0.42
1:B:211:CYS:HB3	1:B:260:LEU:HD12	2.02	0.42
1:A:41:LEU:HD23	1:A:201:LEU:HD21	2.00	0.42
1:C:405:TRP:CZ2	1:C:420:HIS:HD2	2.38	0.42
1:B:266:ALA:HB3	1:B:331:ILE:HD13	2.02	0.41
1:B:42:PRO:HG2	1:B:204:LEU:HD11	2.01	0.41
1:A:285:LEU:HD21	1:A:312:LEU:HD23	2.02	0.41
1:B:539:ASP:HB3	1:B:545:VAL:HG22	2.02	0.41
1:A:148:GLU:HB3	1:A:235[A]:ARG:HH22	1.86	0.41
1:C:304:PRO:HD3	1:C:453:GLY:O	2.20	0.41
1:B:545:VAL:HG11	1:B:595:GLN:HB3	2.02	0.41
1:A:382:ARG:HB2	1:A:384:ASP:OD1	2.21	0.41
1:B:275:GLN:HE21	1:B:275:GLN:HB3	1.78	0.41
1:B:491:GLY:CA	6:B:6190:HOH:O	2.68	0.41
1:B:59:ARG:CG	1:B:59:ARG:NH1	2.74	0.41
1:A:285:LEU:HD12	1:A:285:LEU:C	2.42	0.41
1:A:304:PRO:HD3	1:A:453:GLY:O	2.21	0.41
1:A:560:PHE:HA	1:A:563:ILE:HD12	2.03	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:615:TYR:HB3	1:A:623:LEU:HD22	2.03	0.41
1:B:200:VAL:HG12	1:B:204:LEU:HD23	2.03	0.41
1:C:164:PHE:HA	1:C:195:ARG:O	2.21	0.41
1:B:441:ASP:HA	1:B:442:PRO:HD2	1.76	0.40
1:B:490:LYS:HE3	1:B:490:LYS:HA	2.04	0.40
1:C:125:PRO:HA	1:C:126:PRO:HD3	1.98	0.40
1:C:274:ALA:HB1	1:C:279:TRP:O	2.22	0.40
1:D:211:CYS:HB3	1:D:260:LEU:HD12	2.04	0.40
1:B:615:TYR:HB3	1:B:623:LEU:HD22	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	617/608 (102%)	597 (97%)	14 (2%)	6 (1%)	15	11
1	B	619/608 (102%)	596 (96%)	19 (3%)	4 (1%)	25	21
1	C	612/608 (101%)	597 (98%)	14 (2%)	1 (0%)	47	49
1	D	611/608 (100%)	591 (97%)	17 (3%)	3 (0%)	29	26
All	All	2459/2432 (101%)	2381 (97%)	64 (3%)	14 (1%)	25	21

All (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
1	D	255	GLY

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	171	SER
1	A	198	PRO
1	C	262	LYS
1	D	262	LYS
1	A	262	LYS
1	B	415	PRO
1	A	197	GLY
1	B	169	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	509/499 (102%)	493 (97%)	16 (3%)	40	43
1	B	509/499 (102%)	489 (96%)	20 (4%)	32	33
1	C	503/499 (101%)	495 (98%)	8 (2%)	62	69
1	D	500/499 (100%)	488 (98%)	12 (2%)	49	53
All	All	2021/1996 (101%)	1965 (97%)	56 (3%)	47	47

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ARG
1	A	171	SER
1	A	175	LYS
1	A	202	GLN
1	A	203	ARG
1	A	209[A]	VAL
1	A	209[B]	VAL
1	A	403	THR
1	A	490	LYS
1	A	522	ARG
1	A	538[A]	ARG
1	A	538[B]	ARG
1	A	541	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	588	LEU
1	A	610[A]	GLN
1	A	610[B]	GLN
1	B	57	ARG
1	B	59	ARG
1	B	116	GLU
1	B	140[A]	ASN
1	B	140[B]	ASN
1	B	148	GLU
1	B	170	THR
1	B	201[A]	LEU
1	B	201[B]	LEU
1	B	203	ARG
1	B	205	ASP
1	B	275	GLN
1	B	276[A]	GLN
1	B	276[B]	GLN
1	B	339	GLU
1	B	403	THR
1	B	490	LYS
1	B	493	ARG
1	B	526	ARG
1	B	588	LEU
1	C	116	GLU
1	C	243	SER
1	C	272	ARG
1	C	275	GLN
1	C	403	THR
1	C	411	LYS
1	C	540	ASN
1	C	588	LEU
1	D	54	ARG
1	D	148	GLU
1	D	168	PRO
1	D	203	ARG
1	D	204	LEU
1	D	272	ARG
1	D	275	GLN
1	D	403	THR
1	D	434[A]	ILE
1	D	434[B]	ILE
1	D	443	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	588	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	HIS
1	A	117	GLN
1	A	135	ASN
1	A	275	GLN
1	A	311	ASN
1	A	412	HIS
1	B	117	GLN
1	B	135	ASN
1	B	202	GLN
1	B	275	GLN
1	B	311	ASN
1	B	524	ASN
1	C	135	ASN
1	C	202	GLN
1	C	275	GLN
1	C	311	ASN
1	C	540	ASN
1	D	85	HIS
1	D	135	ASN
1	D	140	ASN
1	D	275	GLN
1	D	311	ASN
1	D	412	HIS

### 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 ⓘ

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	1.77	3 (15%)	25,25,27	2.77	4 (16%)
2	FRU	E	2	2	11,12,12	0.76	1 (9%)	10,18,18	0.82	0
2	TQY	F	1	2	20,20,21	1.76	3 (15%)	25,25,27	2.81	5 (20%)
2	FRU	F	2	2	11,12,12	0.78	1 (9%)	10,18,18	0.73	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

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	TQY	C11-C10	-5.72	1.19	1.51
2	F	1	TQY	C11-C10	-5.48	1.20	1.51
2	F	1	TQY	O6-C13	4.01	1.45	1.33
2	E	1	TQY	O6-C13	3.72	1.44	1.33
2	E	1	TQY	C12-C11	-3.37	1.27	1.51
2	F	1	TQY	C12-C11	-3.35	1.27	1.51
2	F	2	FRU	O2-C2	2.40	1.44	1.40
2	E	2	FRU	O2-C2	2.18	1.44	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	TQY	C11-C10-C9	11.70	173.82	114.42
2	F	1	TQY	C11-C10-C9	11.55	173.07	114.42

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	TQY	C12-C11-C10	5.70	168.23	115.30
2	E	1	TQY	C12-C11-C10	5.66	167.83	115.30
2	E	1	TQY	O6-C13-O7	-2.62	116.97	123.59
2	F	1	TQY	O6-C13-C7	2.49	119.74	111.91
2	E	1	TQY	O6-C13-C7	2.46	119.61	111.91
2	F	1	TQY	C1-C2-C3	2.37	112.58	109.67
2	F	1	TQY	O6-C13-O7	-2.07	118.38	123.59

There are no chirality outliers.

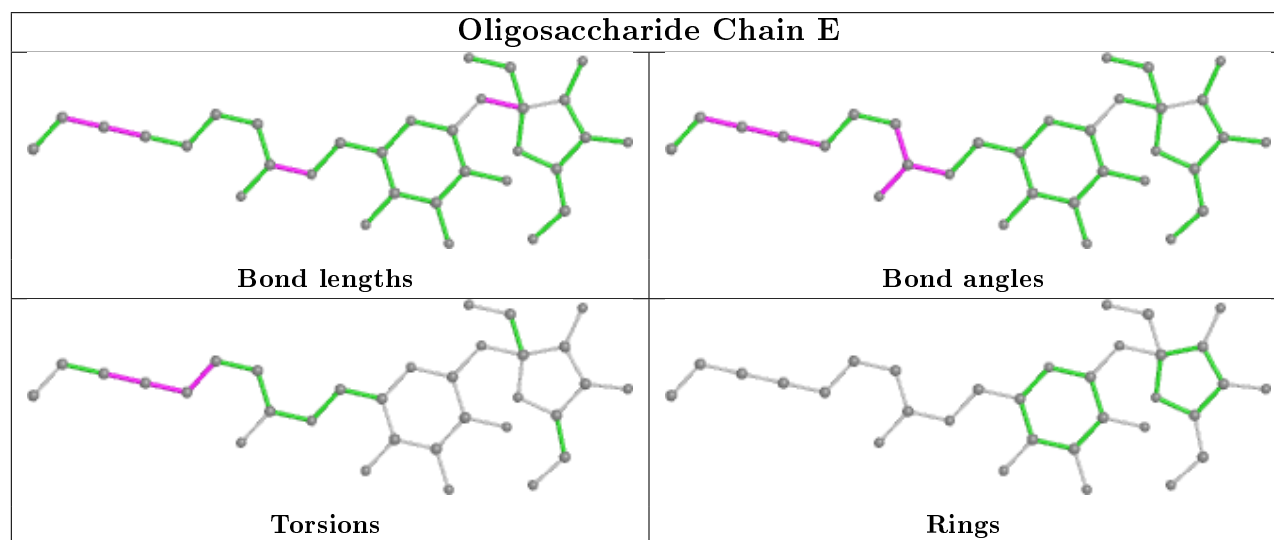
All (7) torsion outliers are listed below:

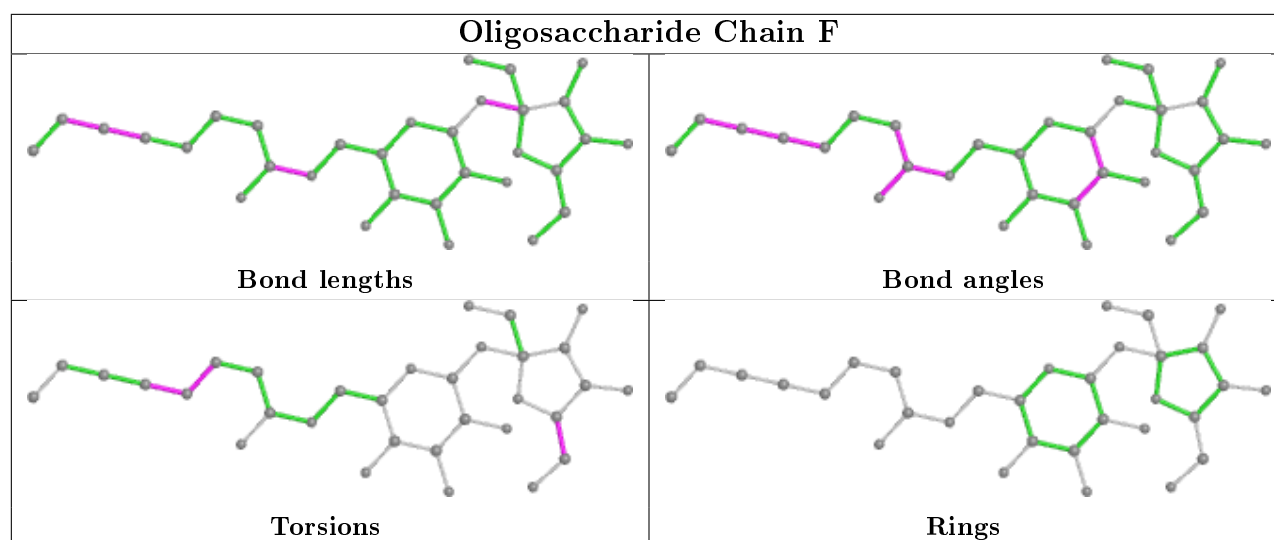
Mol	Chain	Res	Type	Atoms
2	F	2	FRU	O5-C5-C6-O6
2	E	1	TQY	C9-C10-C11-C12
2	E	1	TQY	C7-C8-C9-C10
2	E	1	TQY	C11-C10-C9-C8
2	F	1	TQY	C11-C10-C9-C8
2	F	1	TQY	C7-C8-C9-C10
2	F	2	FRU	C4-C5-C6-O6

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	$\# Z  > 2$
3	GDP	B	3000	5	24,30,30	1.08	1 (4%)	31,47,47	1.88	6 (19%)
3	GDP	D	5000	5	24,30,30	1.41	3 (12%)	31,47,47	2.04	7 (22%)
4	MLA	A	2001	5	0,6,6	0.00	-	0,7,7	0.00	-
4	MLA	D	5001	5	0,6,6	0.00	-	0,7,7	0.00	-
4	MLA	B	6001	-	0,6,6	0.00	-	0,7,7	0.00	-
3	GDP	C	4000	5	24,30,30	1.27	3 (12%)	31,47,47	1.98	7 (22%)
4	MLA	B	3001	5	0,6,6	0.00	-	0,7,7	0.00	-
4	MLA	C	4003	5	0,6,6	0.00	-	0,7,7	0.00	-
3	GDP	A	2000	5	24,30,30	1.19	4 (16%)	31,47,47	2.14	7 (22%)

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
3	GDP	B	3000	5	-	1/12/32/32	0/3/3/3
3	GDP	D	5000	5	-	0/12/32/32	0/3/3/3
4	MLA	A	2001	5	-	0/0/4/4	-
4	MLA	D	5001	5	-	0/0/4/4	-
4	MLA	B	6001	-	-	0/0/4/4	-
3	GDP	C	4000	5	-	0/12/32/32	0/3/3/3
4	MLA	B	3001	5	-	0/0/4/4	-
4	MLA	C	4003	5	-	0/0/4/4	-
3	GDP	A	2000	5	-	3/12/32/32	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	5000	GDP	C6-C5	4.42	1.49	1.41
3	C	4000	GDP	C6-C5	4.22	1.48	1.41
3	B	3000	GDP	C6-C5	3.71	1.47	1.41
3	A	2000	GDP	C6-C5	3.45	1.47	1.41
3	D	5000	GDP	O4'-C1'	3.03	1.45	1.41
3	D	5000	GDP	C5-C4	2.86	1.48	1.40
3	C	4000	GDP	C5-C4	2.49	1.47	1.40
3	A	2000	GDP	C5-C4	2.30	1.47	1.40
3	A	2000	GDP	O4'-C1'	2.21	1.44	1.41
3	C	4000	GDP	O4'-C1'	2.07	1.44	1.41
3	A	2000	GDP	C2-N2	2.03	1.38	1.33

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2000	GDP	C6-C5-C4	-5.55	115.50	120.80
3	C	4000	GDP	C2-N3-C4	5.26	121.36	115.36
3	C	4000	GDP	C6-C5-C4	-5.16	115.87	120.80
3	D	5000	GDP	C6-N1-C2	4.93	123.77	115.93
3	A	2000	GDP	C2-N3-C4	4.89	120.94	115.36
3	A	2000	GDP	C6-N1-C2	4.84	123.62	115.93
3	B	3000	GDP	C2-N3-C4	4.83	120.88	115.36
3	A	2000	GDP	N3-C2-N1	-4.82	120.79	127.22
3	D	5000	GDP	C2-N3-C4	4.46	120.45	115.36
3	D	5000	GDP	C5-C6-N1	-4.38	117.43	123.43
3	B	3000	GDP	C6-C5-C4	-4.21	116.78	120.80
3	B	3000	GDP	C6-N1-C2	4.11	122.47	115.93
3	D	5000	GDP	C6-C5-C4	-4.10	116.88	120.80
3	C	4000	GDP	N3-C2-N1	-3.99	121.90	127.22
3	D	5000	GDP	N3-C2-N1	-3.99	121.90	127.22

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4000	GDP	C6-N1-C2	3.94	122.19	115.93
3	B	3000	GDP	N3-C2-N1	-3.88	122.05	127.22
3	B	3000	GDP	C5-C6-N1	-3.61	118.49	123.43
3	A	2000	GDP	C5-C6-N1	-3.29	118.93	123.43
3	C	4000	GDP	C5-C6-N1	-2.93	119.42	123.43
3	A	2000	GDP	C1'-N9-C4	-2.87	121.59	126.64
3	D	5000	GDP	C4-C5-N7	-2.70	106.58	109.40
3	D	5000	GDP	PA-O3A-PB	-2.64	123.78	132.83
3	A	2000	GDP	PA-O3A-PB	-2.16	125.41	132.83
3	C	4000	GDP	PA-O3A-PB	-2.09	125.65	132.83
3	C	4000	GDP	C4-C5-N7	-2.04	107.28	109.40
3	B	3000	GDP	C4-C5-N7	-2.04	107.28	109.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

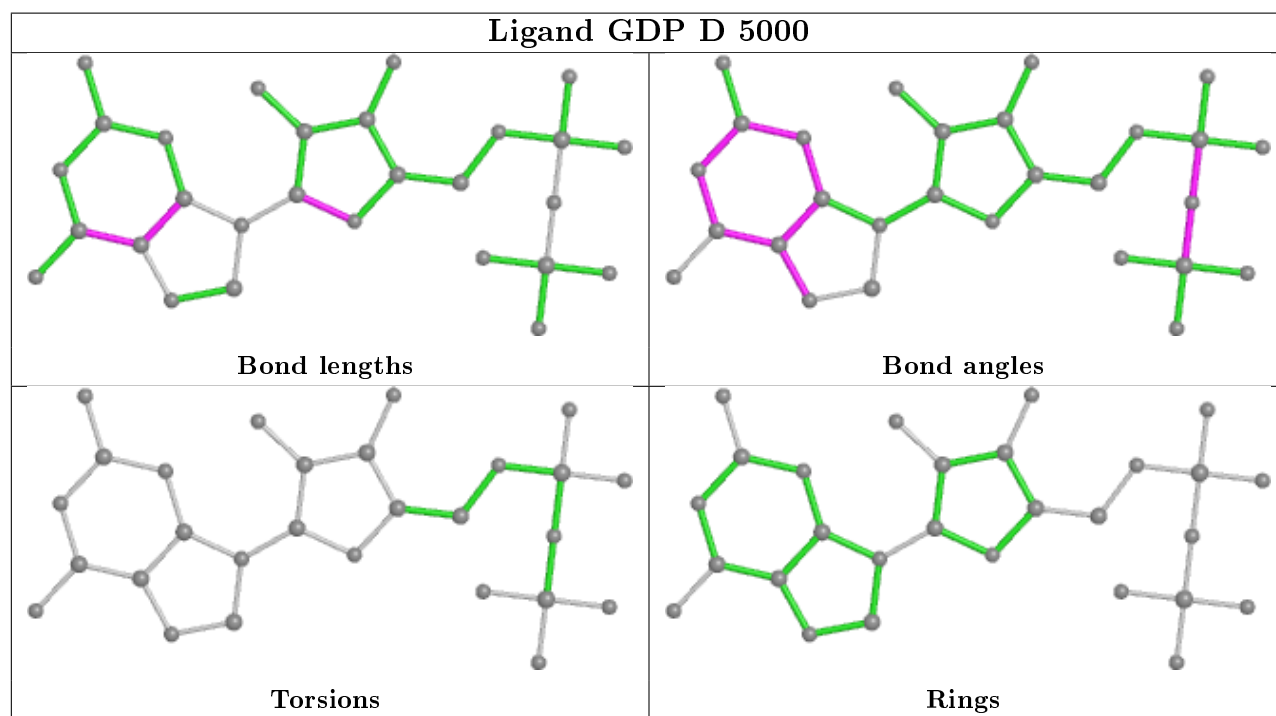
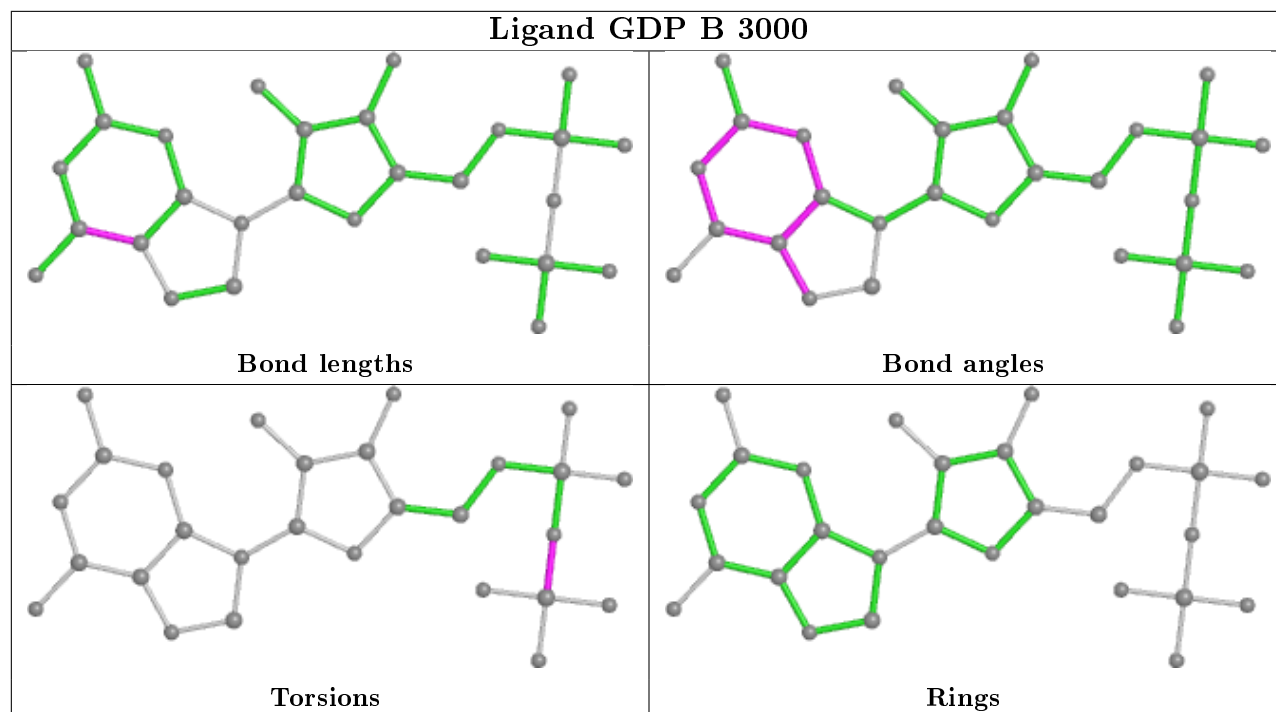
Mol	Chain	Res	Type	Atoms
3	A	2000	GDP	PA-O3A-PB-O2B
3	A	2000	GDP	PA-O3A-PB-O3B
3	A	2000	GDP	C5'-O5'-PA-O3A
3	B	3000	GDP	PA-O3A-PB-O3B

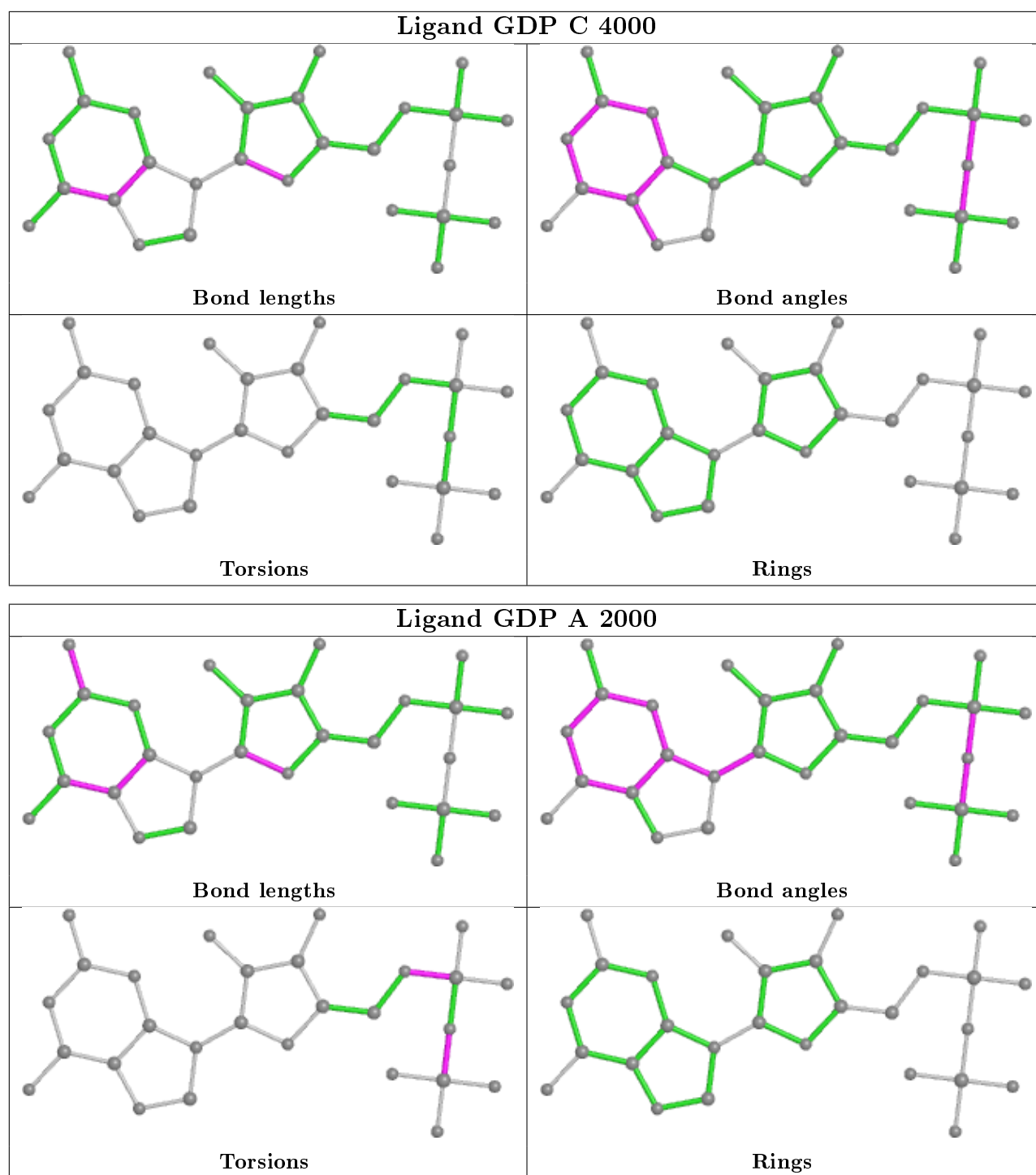
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	5000	GDP	1	0
4	B	6001	MLA	1	0
4	C	4003	MLA	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

### 6.1 Protein, DNA and RNA chains

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%)	0.21	24 (3%)	39 45	9, 15, 19, 25	0
1	B	608/608 (100%)	0.32	39 (6%)	19 24	11, 15, 19, 26	0
1	C	608/608 (100%)	0.26	27 (4%)	34 40	12, 15, 19, 25	0
1	D	608/608 (100%)	0.23	29 (4%)	30 36	11, 15, 19, 24	0
All	All	2432/2432 (100%)	0.25	119 (4%)	29 35	9, 15, 19, 26	0

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	398	PRO	6.5
1	B	400	VAL	6.5
1	C	396	THR	5.7
1	A	396	THR	5.1
1	C	130	PRO	4.9
1	B	222	THR	4.7
1	D	396	THR	4.7
1	D	492	GLY	4.5
1	D	169	PRO	4.4
1	A	398	PRO	4.4
1	D	395	PRO	4.3
1	C	128	GLY	4.3
1	A	197	GLY	4.2
1	D	128	GLY	4.1
1	A	542	GLY	4.0
1	D	254[A]	TYR	4.0
1	A	170	THR	3.9
1	C	399	GLY	3.9
1	B	224	PRO	3.8
1	D	222	THR	3.8
1	C	338	ASP	3.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	401	THR	3.5
1	B	540	ASN	3.4
1	A	397	GLU	3.4
1	A	173	LEU	3.4
1	B	409	PRO	3.4
1	B	412	HIS	3.3
1	C	129	GLY	3.3
1	B	381	LEU	3.2
1	D	398	PRO	3.2
1	B	399	GLY	3.2
1	D	223	GLU	3.1
1	C	309[A]	LYS	3.1
1	B	587	GLY	3.1
1	C	302	ALA	3.1
1	B	397	GLU	3.1
1	D	400	VAL	3.1
1	D	129	GLY	3.0
1	B	542	GLY	3.0
1	A	540	ASN	3.0
1	B	413	GLY	3.0
1	C	398	PRO	3.0
1	C	397	GLU	2.9
1	C	307	CYS	2.9
1	B	396	THR	2.9
1	C	524	ASN	2.9
1	A	198	PRO	2.9
1	D	130	PRO	2.9
1	C	127	SER	2.9
1	A	267	LEU	2.8
1	D	203	ARG	2.8
1	D	126	PRO	2.8
1	A	589	PRO	2.7
1	B	226	VAL	2.7
1	A	128	GLY	2.7
1	A	285	LEU	2.7
1	D	491	GLY	2.6
1	A	504	PHE	2.6
1	B	416	GLU	2.6
1	C	301	ALA	2.6
1	D	259	LEU	2.6
1	A	301	ALA	2.5
1	D	413	GLY	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	285	LEU	2.5
1	D	207	ASP	2.5
1	B	402	TYR	2.5
1	B	206	ASP	2.5
1	D	301	ALA	2.5
1	C	522	ARG	2.4
1	D	205	ASP	2.4
1	B	543	ARG	2.4
1	B	403	THR	2.4
1	B	438	ARG	2.4
1	B	383	SER	2.4
1	B	415	PRO	2.4
1	C	395	PRO	2.4
1	D	224	PRO	2.4
1	A	302	ALA	2.4
1	B	441	ASP	2.4
1	C	207	ASP	2.4
1	B	285	LEU	2.3
1	D	411	LYS	2.3
1	C	303	PHE	2.3
1	B	219	LEU	2.3
1	C	205	ASP	2.3
1	D	306	ALA	2.3
1	B	204	LEU	2.3
1	D	397	GLU	2.3
1	B	414	ASP	2.3
1	D	426	CYS	2.3
1	A	203	ARG	2.2
1	A	127	SER	2.2
1	D	168	PRO	2.2
1	B	254[A]	TYR	2.2
1	A	126	PRO	2.2
1	C	310	THR	2.2
1	A	331	ILE	2.2
1	D	127	SER	2.2
1	C	267	LEU	2.2
1	B	411	LYS	2.2
1	B	302	ALA	2.2
1	C	372	ARG	2.2
1	A	395	PRO	2.1
1	C	352	PHE	2.1
1	D	245	ARG	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	308	GLY	2.1
1	A	172	PRO	2.1
1	B	220	PRO	2.1
1	A	399	GLY	2.1
1	B	523	SER	2.1
1	D	504	PHE	2.1
1	B	267	LEU	2.1
1	C	304	PRO	2.1
1	C	253	GLY	2.1
1	B	418	CYS	2.1
1	B	541	GLU	2.0
1	A	283	HIS	2.0
1	B	452	PHE	2.0
1	B	57	ARG	2.0

## 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](#)

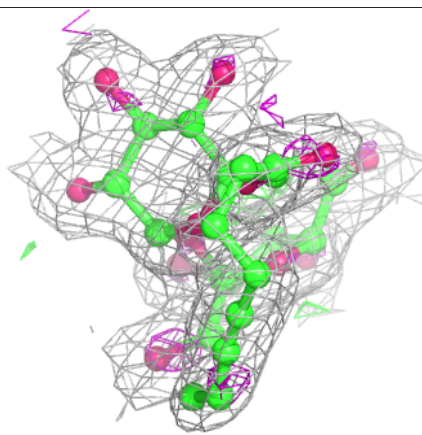
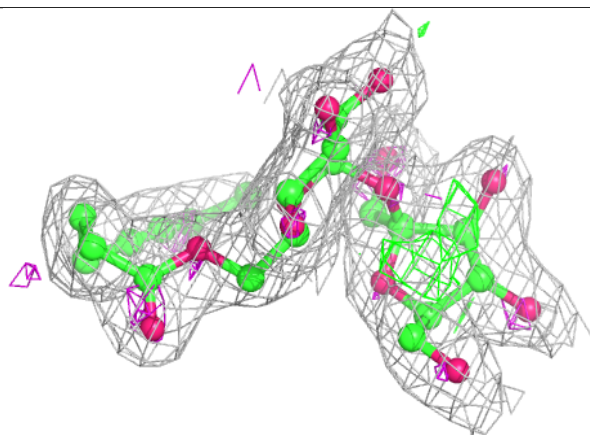
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

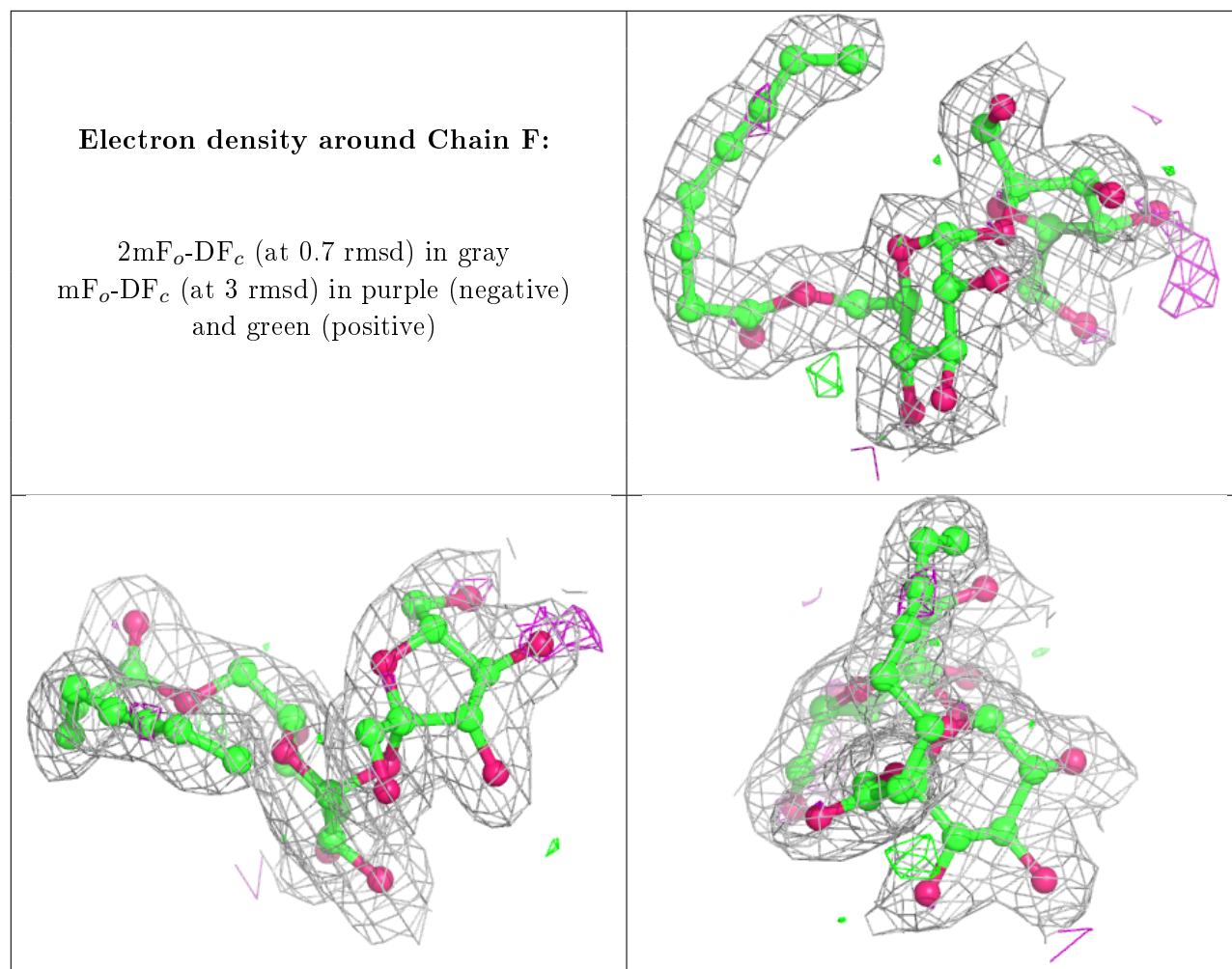
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FRU	E	2	12/12	0.95	0.08	10,12,13,14	0
2	FRU	F	2	12/12	0.95	0.09	14,15,18,19	0
2	TQY	E	1	20/21	0.96	0.09	8,13,18,18	0
2	TQY	F	1	20/21	0.96	0.08	11,14,19,20	0

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.

**Electron density around Chain E:**

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





## 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	0.85	0.18	34,36,38,38	0
4	MLA	B	6001	7/7	0.90	0.16	30,32,34,36	0
4	MLA	D	5001	7/7	0.91	0.15	27,30,32,32	0
4	MLA	B	3001	7/7	0.92	0.14	27,27,29,29	0
4	MLA	C	4003	7/7	0.94	0.13	21,21,26,30	0
5	MN	B	3002	1/1	0.95	0.07	28,28,28,28	1
3	GDP	D	5000	28/28	0.96	0.09	16,18,23,24	0
5	MN	C	4002	1/1	0.96	0.15	9,9,9,9	1
5	MN	A	2003	1/1	0.97	0.19	21,21,21,21	1
5	MN	D	5002	1/1	0.97	0.07	38,38,38,38	1

*Continued on next page...*

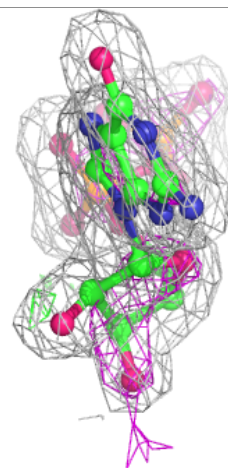
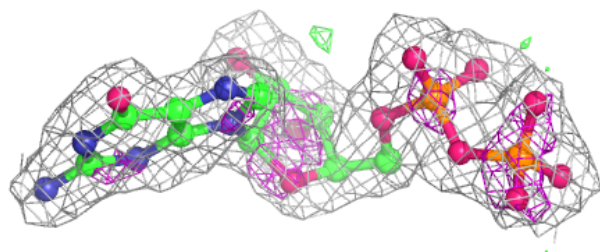
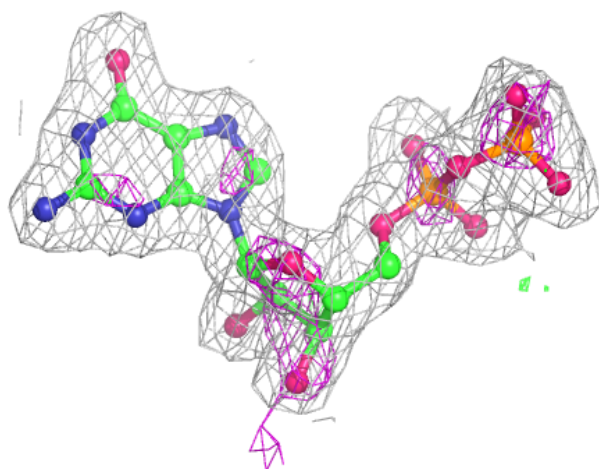
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GDP	B	3000	28/28	0.97	0.07	15,18,18,19	0
3	GDP	C	4000	28/28	0.97	0.08	9,11,13,14	0
5	MN	B	3003	1/1	0.98	0.13	23,23,23,23	1
5	MN	D	5003	1/1	0.98	0.18	14,14,14,14	1
3	GDP	A	2000	28/28	0.98	0.07	9,11,14,15	0
5	MN	A	2002	1/1	0.99	0.05	15,15,15,15	1
5	MN	C	4001	1/1	1.00	0.04	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.

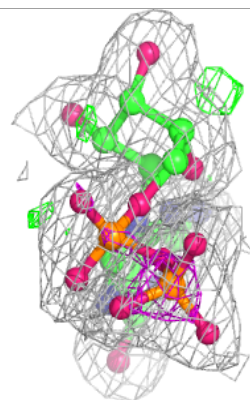
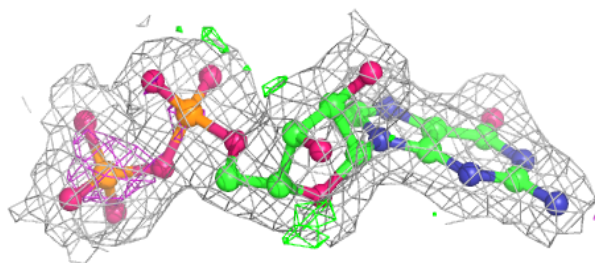
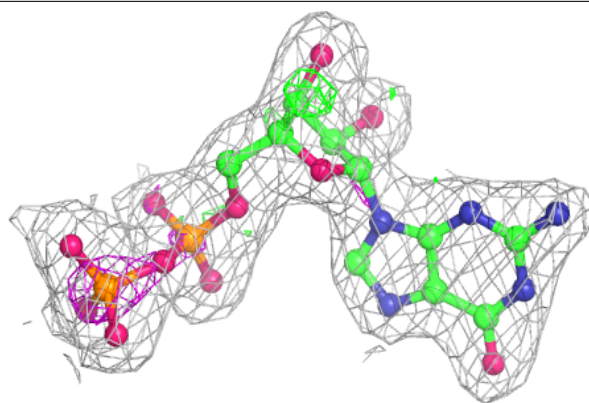
**Electron density around GDP D 5000:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

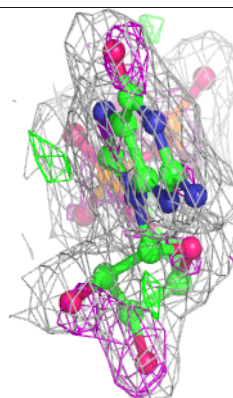
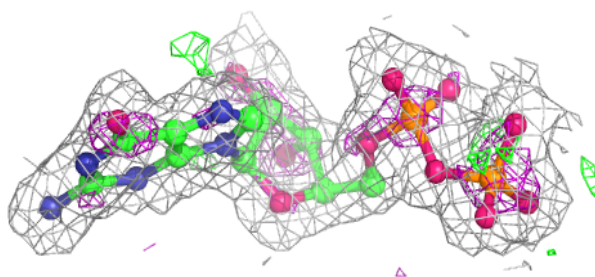
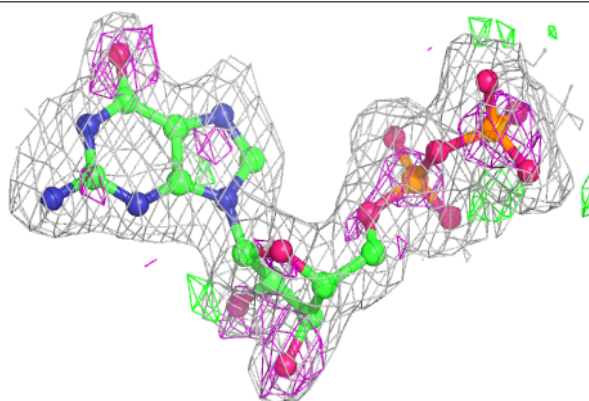


**Electron density around GDP B 3000:**

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

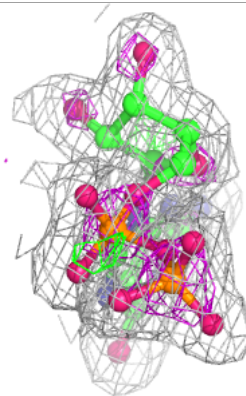
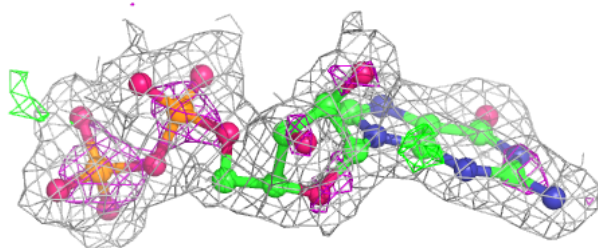
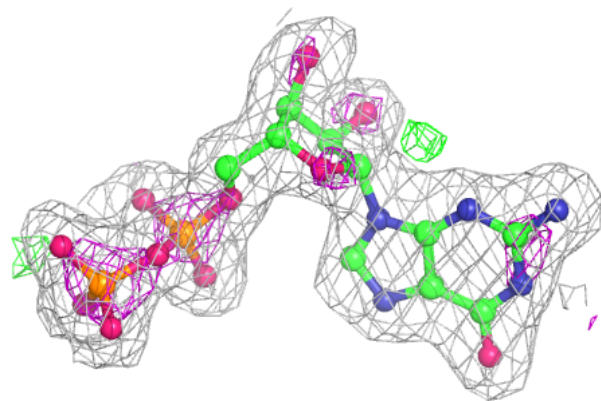
**Electron density around GDP C 4000:**

$2mF_o-DF_c$  (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.