



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 10:10 am BST

PDB ID : 5HCI  
Title : GPN-loop GTPase Npa3 in complex with GDP  
Authors : Niesser, J.; Wagner, F.R.; Kostrewa, D.; Muehlbacher, W.; Cramer, P.  
Deposited on : 2016-01-04  
Resolution : 2.30 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.

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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 : 2.11  
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) : 2.11

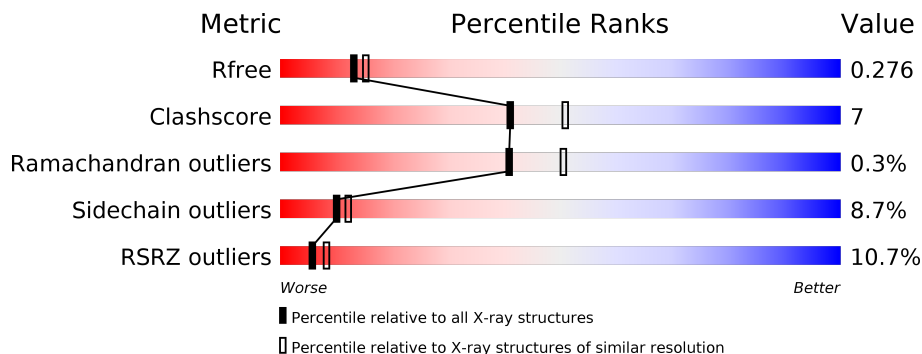
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	261	 4% (poor fit), 81% (0-1 outliers), 15% (2-3 outliers), 2% (not modelled)
1	B	261	 14% (poor fit), 75% (0-1 outliers), 17% (2-3 outliers), 5% (not modelled)
1	C	261	 11% (poor fit), 72% (0-1 outliers), 19% (2-3 outliers), 6% (not modelled)
1	D	261	 8% (poor fit), 84% (0-1 outliers), 12% (2-3 outliers), 3% (not modelled)
1	E	261	 7% (poor fit), 81% (0-1 outliers), 15% (2-3 outliers), 3% (not modelled)
1	F	261	 18% (poor fit), 82% (0-1 outliers), 12% (2-3 outliers), 5% (not modelled)

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
4	GOL	A	303	-	-	-	X
4	GOL	E	303	-	-	-	X

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 12383 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 GPN-loop GTPase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	257	2032	1300	324	391	17	0	0	0
1	B	258	2042	1306	327	392	17	0	0	0
1	C	246	1937	1238	309	374	16	0	0	0
1	D	258	2042	1306	327	392	17	0	0	0
1	E	259	2052	1312	330	393	17	0	0	0
1	F	249	1959	1252	314	377	16	0	0	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP P47122
A	?	-	ASN	deletion	UNP P47122
A	?	-	GLY	deletion	UNP P47122
A	?	-	ASP	deletion	UNP P47122
A	?	-	ASN	deletion	UNP P47122
A	?	-	GLY	deletion	UNP P47122
A	?	-	LEU	deletion	UNP P47122
A	?	-	GLY	deletion	UNP P47122
A	?	-	SER	deletion	UNP P47122
A	265	LYS	-	expression tag	UNP P47122
A	266	HIS	-	expression tag	UNP P47122
A	267	HIS	-	expression tag	UNP P47122
A	268	HIS	-	expression tag	UNP P47122
A	269	HIS	-	expression tag	UNP P47122
A	270	HIS	-	expression tag	UNP P47122
A	271	HIS	-	expression tag	UNP P47122
B	?	-	LEU	deletion	UNP P47122

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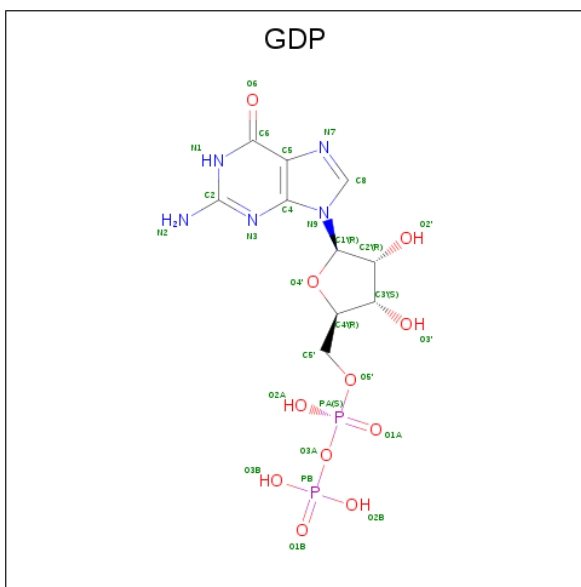
Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ASN	deletion	UNP P47122
B	?	-	GLY	deletion	UNP P47122
B	?	-	ASP	deletion	UNP P47122
B	?	-	ASN	deletion	UNP P47122
B	?	-	GLY	deletion	UNP P47122
B	?	-	LEU	deletion	UNP P47122
B	?	-	GLY	deletion	UNP P47122
B	?	-	SER	deletion	UNP P47122
B	265	LYS	-	expression tag	UNP P47122
B	266	HIS	-	expression tag	UNP P47122
B	267	HIS	-	expression tag	UNP P47122
B	268	HIS	-	expression tag	UNP P47122
B	269	HIS	-	expression tag	UNP P47122
B	270	HIS	-	expression tag	UNP P47122
B	271	HIS	-	expression tag	UNP P47122
C	?	-	LEU	deletion	UNP P47122
C	?	-	ASN	deletion	UNP P47122
C	?	-	GLY	deletion	UNP P47122
C	?	-	ASP	deletion	UNP P47122
C	?	-	ASN	deletion	UNP P47122
C	?	-	GLY	deletion	UNP P47122
C	?	-	LEU	deletion	UNP P47122
C	?	-	GLY	deletion	UNP P47122
C	?	-	SER	deletion	UNP P47122
C	265	LYS	-	expression tag	UNP P47122
C	266	HIS	-	expression tag	UNP P47122
C	267	HIS	-	expression tag	UNP P47122
C	268	HIS	-	expression tag	UNP P47122
C	269	HIS	-	expression tag	UNP P47122
C	270	HIS	-	expression tag	UNP P47122
C	271	HIS	-	expression tag	UNP P47122
D	?	-	LEU	deletion	UNP P47122
D	?	-	ASN	deletion	UNP P47122
D	?	-	GLY	deletion	UNP P47122
D	?	-	ASP	deletion	UNP P47122
D	?	-	ASN	deletion	UNP P47122
D	?	-	GLY	deletion	UNP P47122
D	?	-	LEU	deletion	UNP P47122
D	?	-	GLY	deletion	UNP P47122
D	?	-	SER	deletion	UNP P47122
D	265	LYS	-	expression tag	UNP P47122
D	266	HIS	-	expression tag	UNP P47122

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Chain	Residue	Modelled	Actual	Comment	Reference
D	267	HIS	-	expression tag	UNP P47122
D	268	HIS	-	expression tag	UNP P47122
D	269	HIS	-	expression tag	UNP P47122
D	270	HIS	-	expression tag	UNP P47122
D	271	HIS	-	expression tag	UNP P47122
E	?	-	LEU	deletion	UNP P47122
E	?	-	ASN	deletion	UNP P47122
E	?	-	GLY	deletion	UNP P47122
E	?	-	ASP	deletion	UNP P47122
E	?	-	ASN	deletion	UNP P47122
E	?	-	GLY	deletion	UNP P47122
E	?	-	LEU	deletion	UNP P47122
E	?	-	GLY	deletion	UNP P47122
E	?	-	SER	deletion	UNP P47122
E	265	LYS	-	expression tag	UNP P47122
E	266	HIS	-	expression tag	UNP P47122
E	267	HIS	-	expression tag	UNP P47122
E	268	HIS	-	expression tag	UNP P47122
E	269	HIS	-	expression tag	UNP P47122
E	270	HIS	-	expression tag	UNP P47122
E	271	HIS	-	expression tag	UNP P47122
F	?	-	LEU	deletion	UNP P47122
F	?	-	ASN	deletion	UNP P47122
F	?	-	GLY	deletion	UNP P47122
F	?	-	ASP	deletion	UNP P47122
F	?	-	ASN	deletion	UNP P47122
F	?	-	GLY	deletion	UNP P47122
F	?	-	LEU	deletion	UNP P47122
F	?	-	GLY	deletion	UNP P47122
F	?	-	SER	deletion	UNP P47122
F	265	LYS	-	expression tag	UNP P47122
F	266	HIS	-	expression tag	UNP P47122
F	267	HIS	-	expression tag	UNP P47122
F	268	HIS	-	expression tag	UNP P47122
F	269	HIS	-	expression tag	UNP P47122
F	270	HIS	-	expression tag	UNP P47122
F	271	HIS	-	expression tag	UNP P47122

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

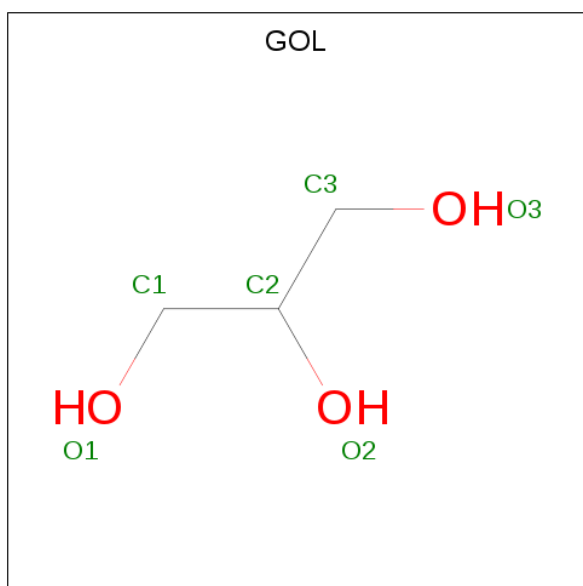


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	28	10	5	11	2	0	0
2	B	1	28	10	5	11	2	0	0
2	C	1	28	10	5	11	2	0	0
2	D	1	28	10	5	11	2	0	0
2	E	1	28	10	5	11	2	0	0
2	F	1	28	10	5	11	2	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	D	1	1	1	0	0
3	E	1	1	1	0	0
3	B	1	1	1	0	0
3	C	1	1	1	0	0
3	A	1	1	1	0	0
3	F	1	1	1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	C	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0
4	E	1	Total C O 6 3 3	0	0

- Molecule 5 is water.

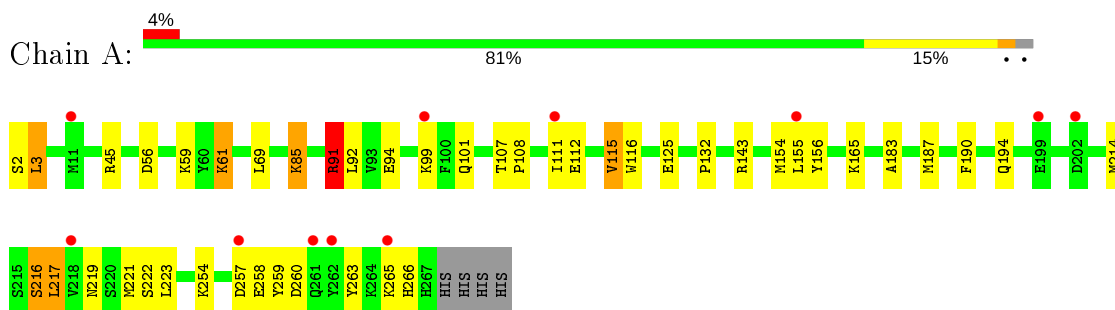
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	33	Total O 33 33	0	0
5	B	30	Total O 30 30	0	0
5	C	16	Total O 16 16	0	0
5	D	16	Total O 16 16	0	0
5	E	21	Total O 21 21	0	0
5	F	5	Total O 5 5	0	0



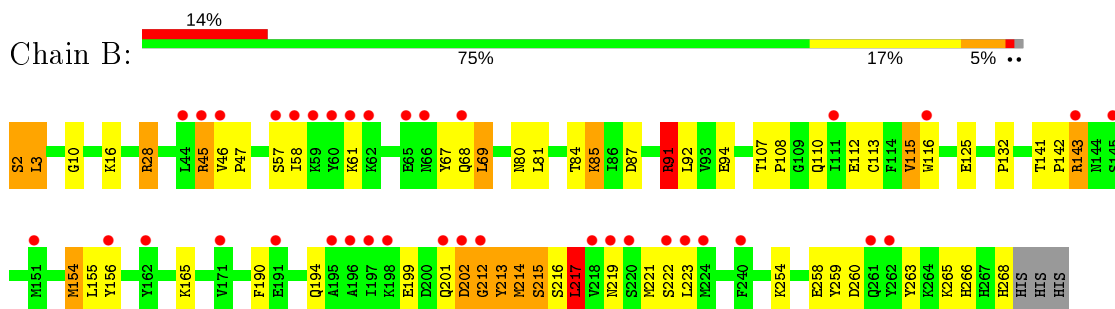
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

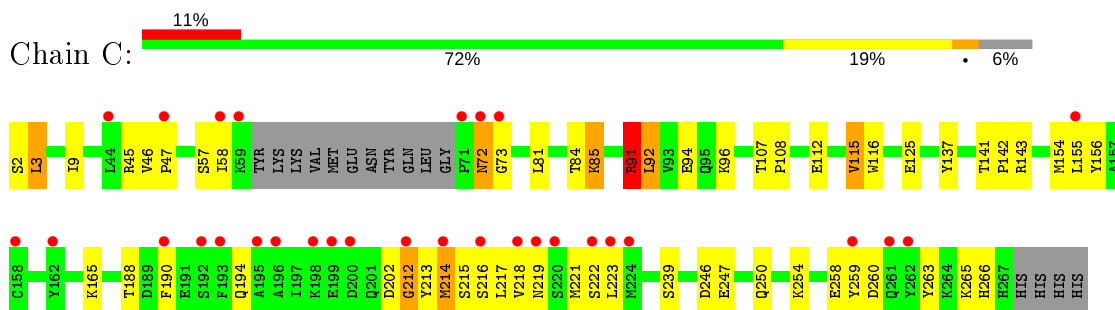
- Molecule 1: GPN-loop GTPase 1



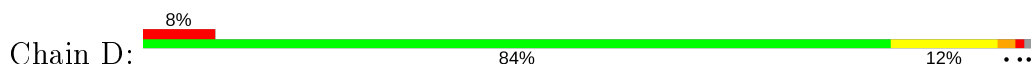
- Molecule 1: GPN-loop GTPase 1

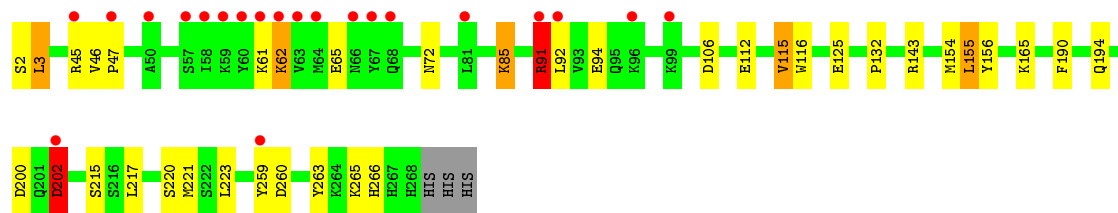


- Molecule 1: GPN-loop GTPase 1

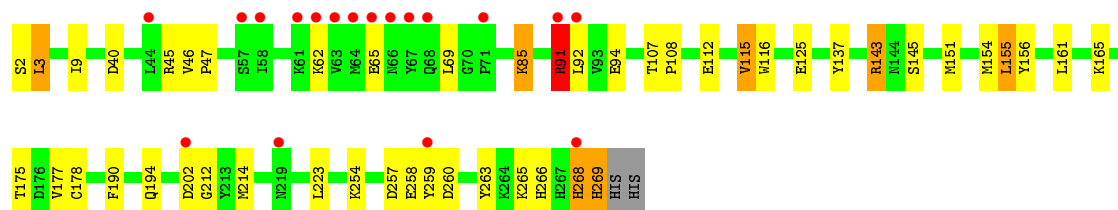
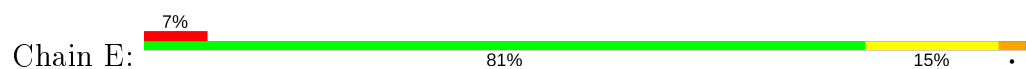


- Molecule 1: GPN-loop GTPase 1

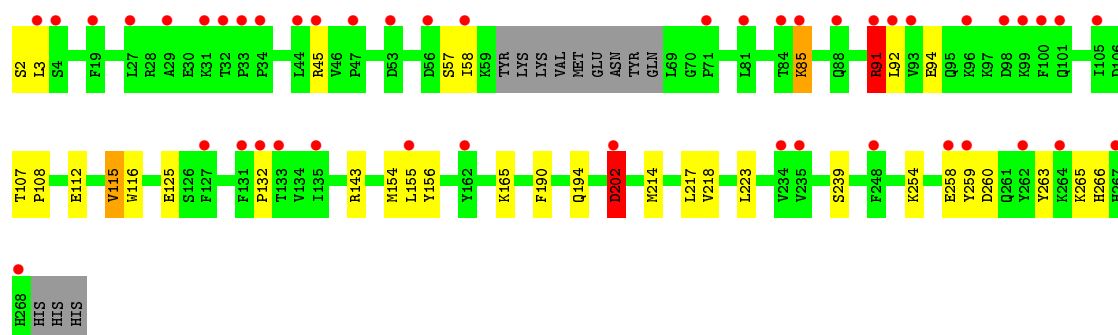
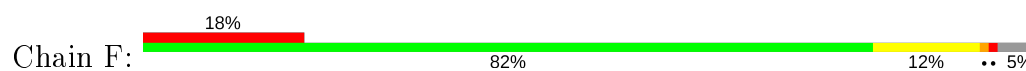




● Molecule 1: GPN-loop GTPase 1



● Molecule 1: GPN-loop GTPase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.99Å 119.18Å 347.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.25 – 2.30 49.15 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.25-2.30) 99.8 (49.15-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.50 (at 2.29Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.238 , 0.276 0.241 , 0.276	Depositor DCC
$R_{free}$ test set	1988 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.6	Xtrriage
Anisotropy	0.533	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 54.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12383	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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: GDP, GOL, MG

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	0.55	0/2075	0.65	2/2806 (0.1%)
1	B	0.58	0/2086	0.90	7/2821 (0.2%)
1	C	0.62	1/1977 (0.1%)	0.70	2/2673 (0.1%)
1	D	0.40	0/2086	0.60	3/2821 (0.1%)
1	E	0.57	0/2097	0.68	3/2836 (0.1%)
1	F	0.38	0/2000	0.58	1/2705 (0.0%)
All	All	0.52	1/12321 (0.0%)	0.69	18/16662 (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	C	0	1
1	D	0	1
1	F	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	73	GLY	N-CA	-5.39	1.38	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	45	ARG	NE-CZ-NH1	-20.10	110.25	120.30
1	B	45	ARG	NE-CZ-NH2	19.68	130.14	120.30
1	E	91	ARG	NE-CZ-NH1	10.69	125.64	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	45	ARG	CD-NE-CZ	9.86	137.40	123.60
1	D	91	ARG	NE-CZ-NH1	9.20	124.90	120.30
1	B	91	ARG	NE-CZ-NH1	8.53	124.56	120.30
1	C	91	ARG	NE-CZ-NH1	8.53	124.56	120.30
1	E	91	ARG	NE-CZ-NH2	-8.46	116.07	120.30
1	A	91	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	F	91	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	B	28	ARG	NE-CZ-NH2	-7.36	116.62	120.30
1	B	217	LEU	CA-CB-CG	6.89	131.15	115.30
1	C	3	LEU	CA-CB-CG	5.42	127.77	115.30
1	D	91	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	E	3	LEU	CA-CB-CG	5.30	127.49	115.30
1	D	3	LEU	CA-CB-CG	5.24	127.35	115.30
1	A	3	LEU	CA-CB-CG	5.20	127.25	115.30
1	B	3	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	72	ASN	Peptide
1	D	202	ASP	Peptide
1	F	202	ASP	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	2032	0	2009	22	1
1	B	2042	0	2016	58	0
1	C	1937	0	1914	52	0
1	D	2042	0	2016	20	0
1	E	2052	0	2023	26	1
1	F	1959	0	1933	22	0
2	A	28	0	12	0	0
2	B	28	0	12	0	0
2	C	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	28	0	12	0	0
2	E	28	0	12	0	0
2	F	28	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	6	0	8	1	0
4	C	6	0	8	0	0
4	E	12	0	16	1	0
5	A	33	0	0	2	0
5	B	30	0	0	2	0
5	C	16	0	0	0	0
5	D	16	0	0	1	0
5	E	21	0	0	3	0
5	F	5	0	0	0	0
All	All	12383	0	12015	173	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 7.

All (173) 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:B:91:ARG:HG3	1:D:202:ASP:HB3	1.23	1.13
1:C:202:ASP:O	1:C:213:TYR:N	1.85	1.07
1:C:91:ARG:HG3	1:F:202:ASP:HB3	1.48	0.94
1:B:143:ARG:NH2	5:B:401:HOH:O	2.01	0.92
1:C:91:ARG:CG	1:F:202:ASP:HB3	2.08	0.82
1:C:214:MET:HB3	1:C:217:LEU:HD13	1.62	0.80
1:C:91:ARG:HG3	1:F:202:ASP:CB	2.12	0.79
1:B:28:ARG:HE	1:C:250:GLN:CD	1.91	0.74
1:B:28:ARG:HH22	1:C:247:GLU:N	1.86	0.73
1:B:45:ARG:NH2	1:C:188:THR:OG1	2.24	0.71
1:F:190:PHE:HD2	1:F:194:GLN:HE21	1.38	0.71
1:B:28:ARG:HE	1:C:250:GLN:NE2	1.87	0.71
1:B:190:PHE:HD2	1:B:194:GLN:HE21	1.39	0.70
1:C:190:PHE:HD2	1:C:194:GLN:HE21	1.40	0.70
1:B:199:GLU:OE2	5:B:402:HOH:O	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ASP:OD2	5:A:401:HOH:O	2.10	0.69
1:E:263:TYR:OH	5:E:401:HOH:O	2.10	0.69
1:B:212:GLY:O	1:B:215:SER:N	2.27	0.67
1:D:91:ARG:HH11	1:D:91:ARG:HG3	1.60	0.67
1:E:190:PHE:HD2	1:E:194:GLN:HE21	1.43	0.66
1:B:28:ARG:HH22	1:C:246:ASP:C	2.00	0.66
1:F:91:ARG:HH11	1:F:91:ARG:HG3	1.61	0.65
1:B:45:ARG:HB3	1:C:188:THR:CG2	2.26	0.65
1:A:91:ARG:HH11	1:A:91:ARG:HG3	1.62	0.65
1:B:91:ARG:HG3	1:D:202:ASP:CB	2.15	0.65
1:D:190:PHE:HD2	1:D:194:GLN:HE21	1.45	0.64
1:C:217:LEU:HB3	1:C:221:MET:SD	2.38	0.64
1:C:214:MET:N	1:C:214:MET:SD	2.71	0.63
1:A:190:PHE:HD2	1:A:194:GLN:HE21	1.46	0.62
1:A:59:LYS:HD2	1:A:61:LYS:HZ2	1.64	0.62
1:B:217:LEU:O	1:B:221:MET:HG3	1.99	0.62
1:A:99:LYS:HG3	1:B:2:SER:OG	1.99	0.62
1:E:91:ARG:HG3	1:E:91:ARG:HH11	1.66	0.61
1:B:45:ARG:HD2	1:C:188:THR:HG21	1.82	0.61
1:B:115:VAL:HG22	1:B:116:TRP:CE3	2.36	0.60
1:B:28:ARG:NH2	1:C:246:ASP:C	2.56	0.59
1:B:201:GLN:HG2	1:B:213:TYR:H	1.68	0.59
1:B:212:GLY:HA3	1:B:215:SER:HB3	1.84	0.59
1:C:214:MET:O	1:C:217:LEU:HB2	2.02	0.59
1:A:115:VAL:HG22	1:A:116:TRP:CE3	2.37	0.59
1:E:115:VAL:HG22	1:E:116:TRP:CE3	2.36	0.59
1:E:257:ASP:HB3	4:E:303:GOL:H31	1.84	0.58
1:B:28:ARG:NH2	1:C:247:GLU:N	2.52	0.58
1:F:115:VAL:HG22	1:F:116:TRP:CE3	2.39	0.58
1:B:202:ASP:O	1:B:212:GLY:C	2.42	0.56
1:B:201:GLN:HG2	1:B:213:TYR:HB3	1.86	0.56
1:C:212:GLY:HA2	1:C:215:SER:HB3	1.86	0.56
1:B:45:ARG:HB3	1:C:188:THR:HG21	1.86	0.56
1:D:115:VAL:HG22	1:D:116:TRP:CE3	2.41	0.56
1:C:91:ARG:HH11	1:C:91:ARG:HG3	1.70	0.56
1:A:91:ARG:HH11	1:A:91:ARG:CG	2.19	0.55
1:F:165:LYS:HE3	1:F:266:HIS:HD2	1.72	0.54
1:E:91:ARG:CG	1:E:91:ARG:HH11	2.20	0.54
1:F:91:ARG:HH11	1:F:91:ARG:CG	2.19	0.54
1:D:165:LYS:HE3	1:D:266:HIS:HD2	1.72	0.54
1:D:91:ARG:HH11	1:D:91:ARG:CG	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165:LYS:HE3	1:E:266:HIS:HD2	1.73	0.53
1:C:115:VAL:HG22	1:C:116:TRP:CE3	2.42	0.53
1:A:165:LYS:HE3	1:A:266:HIS:HD2	1.73	0.52
1:F:214:MET:O	1:F:218:VAL:HG23	2.10	0.52
1:B:80:ASN:HB3	1:E:177:VAL:O	2.10	0.51
1:E:254:LYS:NZ	1:E:258:GLU:OE2	2.34	0.51
1:B:212:GLY:O	1:B:214:MET:N	2.44	0.51
1:B:165:LYS:HE3	1:B:266:HIS:HD2	1.76	0.51
1:C:165:LYS:HE3	1:C:266:HIS:HD2	1.75	0.51
1:B:91:ARG:CG	1:B:91:ARG:HH11	2.24	0.50
1:A:216:SER:O	1:A:219:ASN:HB2	2.11	0.50
1:B:91:ARG:HG3	1:B:91:ARG:HH11	1.77	0.50
1:D:265:LYS:HG3	1:D:266:HIS:ND1	2.26	0.50
1:C:91:ARG:HG3	1:F:202:ASP:CG	2.30	0.50
1:F:265:LYS:HG3	1:F:266:HIS:ND1	2.27	0.50
1:C:91:ARG:HH11	1:C:91:ARG:CG	2.24	0.50
1:B:28:ARG:NE	1:C:250:GLN:NE2	2.56	0.49
1:C:265:LYS:HG3	1:C:266:HIS:ND1	2.28	0.49
1:D:155:LEU:HD23	1:E:155:LEU:HD23	1.94	0.48
1:B:28:ARG:NH2	1:C:246:ASP:HB3	2.29	0.48
1:D:165:LYS:HE2	1:D:266:HIS:HB3	1.96	0.48
1:C:215:SER:O	1:C:218:VAL:N	2.46	0.48
1:E:161:LEU:HD21	5:E:401:HOH:O	2.13	0.47
1:E:202:ASP:OD1	1:E:202:ASP:N	2.47	0.47
1:A:265:LYS:HG3	1:A:266:HIS:ND1	2.29	0.47
1:B:110:GLN:HB2	1:B:113:CYS:SG	2.54	0.47
1:E:40:ASP:OD2	5:E:402:HOH:O	2.20	0.47
1:E:165:LYS:HE2	1:E:266:HIS:HB3	1.96	0.47
1:F:202:ASP:OD1	1:F:202:ASP:N	2.47	0.47
1:B:201:GLN:HE21	1:B:213:TYR:HB3	1.80	0.47
1:E:175:THR:HA	1:E:178:CYS:O	2.15	0.47
1:F:254:LYS:NZ	1:F:258:GLU:OE2	2.38	0.47
1:E:265:LYS:HG3	1:E:266:HIS:ND1	2.29	0.47
1:B:265:LYS:HG3	1:B:266:HIS:ND1	2.29	0.47
1:F:165:LYS:HE2	1:F:266:HIS:HB3	1.97	0.47
1:B:45:ARG:HB3	1:C:188:THR:HG23	1.95	0.46
1:C:222:SER:OG	1:C:223:LEU:N	2.48	0.46
1:D:220:SER:HB2	1:E:156:TYR:CE2	2.50	0.46
1:A:85:LYS:N	1:A:85:LYS:HD2	2.30	0.46
1:C:91:ARG:HG2	1:F:202:ASP:HB3	1.92	0.46
1:B:222:SER:OG	1:B:223:LEU:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:THR:HB	1:C:142:PRO:HD3	1.96	0.46
1:B:254:LYS:NZ	1:B:258:GLU:OE2	2.38	0.46
1:F:223:LEU:HD23	1:F:223:LEU:HA	1.79	0.46
1:D:259:TYR:HA	1:D:263:TYR:HB2	1.97	0.46
1:B:141:THR:HB	1:B:142:PRO:HD3	1.97	0.46
1:E:151:MET:O	1:E:155:LEU:HD22	2.15	0.46
1:C:212:GLY:HA2	1:C:215:SER:CB	2.46	0.46
1:C:259:TYR:HA	1:C:263:TYR:HB2	1.97	0.46
1:A:165:LYS:HE2	1:A:266:HIS:HB3	1.98	0.45
1:B:201:GLN:HE21	1:B:213:TYR:CB	2.29	0.45
1:B:202:ASP:O	1:B:213:TYR:N	2.49	0.45
1:B:259:TYR:HA	1:B:263:TYR:HB2	1.97	0.45
1:C:85:LYS:N	1:C:85:LYS:HD2	2.31	0.45
1:D:62:LYS:HE3	1:D:62:LYS:HB2	1.78	0.45
1:E:259:TYR:HA	1:E:263:TYR:HB2	1.98	0.45
1:E:46:VAL:HA	1:E:47:PRO:HD3	1.80	0.45
1:B:81:LEU:O	1:B:84:THR:HB	2.15	0.45
1:B:165:LYS:HE2	1:B:266:HIS:HB3	1.98	0.45
1:C:165:LYS:HE2	1:C:266:HIS:HB3	1.98	0.45
1:F:259:TYR:HA	1:F:263:TYR:HB2	1.98	0.44
1:A:259:TYR:HA	1:A:263:TYR:HB2	1.99	0.44
1:C:219:ASN:O	1:C:222:SER:HB3	2.17	0.44
1:D:106:ASP:OD1	5:D:402:HOH:O	2.21	0.44
1:B:87:ASP:CG	1:E:143:ARG:HH22	2.21	0.44
1:F:85:LYS:N	1:F:85:LYS:HD2	2.33	0.44
1:C:84:THR:HG22	1:C:85:LYS:HD2	2.00	0.44
1:E:85:LYS:HD2	1:E:85:LYS:N	2.33	0.44
1:C:46:VAL:HA	1:C:47:PRO:HD3	1.84	0.44
1:D:85:LYS:N	1:D:85:LYS:HD2	2.33	0.44
1:B:84:THR:HG22	1:B:85:LYS:HD2	1.99	0.43
1:E:268:HIS:CD2	1:E:269:HIS:HB3	2.53	0.43
1:A:254:LYS:NZ	1:A:258:GLU:OE2	2.38	0.43
1:C:107:THR:HB	1:C:108:PRO:HD2	2.00	0.43
1:F:57:SER:OG	1:F:58:ILE:HD12	2.18	0.43
1:C:9:ILE:O	1:C:137:TYR:HA	2.18	0.43
1:F:239:SER:N	2:F:301:GDP:O6	2.51	0.43
1:B:107:THR:HB	1:B:108:PRO:HD2	1.99	0.43
1:B:28:ARG:NH2	1:C:247:GLU:HA	2.33	0.43
1:D:46:VAL:HA	1:D:47:PRO:HD3	1.82	0.43
1:C:81:LEU:O	1:C:84:THR:HB	2.19	0.43
1:C:217:LEU:O	1:C:221:MET:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:ARG:NH2	1:D:200:ASP:O	2.52	0.42
1:A:219:ASN:O	1:A:222:SER:HB3	2.19	0.42
1:B:57:SER:OG	1:B:58:ILE:HD12	2.19	0.42
1:C:202:ASP:OD1	1:C:202:ASP:N	2.50	0.42
1:B:154:MET:CE	1:B:154:MET:HA	2.49	0.42
1:A:107:THR:HB	1:A:108:PRO:HD2	2.02	0.42
1:A:183:ALA:O	1:A:187:MET:HG3	2.19	0.42
1:B:132:PRO:HA	1:B:259:TYR:CE1	2.55	0.42
1:B:219:ASN:O	1:B:222:SER:HB3	2.19	0.42
1:B:69:LEU:HD13	1:B:69:LEU:HA	1.86	0.42
1:C:254:LYS:NZ	1:C:258:GLU:OE2	2.39	0.42
1:C:239:SER:N	2:C:301:GDP:O6	2.52	0.42
1:E:223:LEU:HD23	1:E:223:LEU:HA	1.88	0.42
1:A:111:ILE:HA	5:A:417:HOH:O	2.20	0.41
1:C:223:LEU:HD23	1:C:223:LEU:HA	1.90	0.41
1:B:85:LYS:HD2	1:B:85:LYS:N	2.35	0.41
1:C:190:PHE:CZ	1:C:222:SER:HA	2.55	0.41
1:F:132:PRO:HA	1:F:259:TYR:CE1	2.55	0.41
1:E:107:THR:HB	1:E:108:PRO:HD2	2.01	0.41
1:C:57:SER:OG	1:C:58:ILE:HD12	2.21	0.41
1:C:92:LEU:O	1:C:96:LYS:HG2	2.20	0.41
1:A:223:LEU:HA	1:A:223:LEU:HD23	1.79	0.41
1:B:10:GLY:N	1:B:16:LYS:HD3	2.35	0.41
1:B:67:TYR:HB3	1:B:69:LEU:HD22	2.02	0.41
1:B:46:VAL:HA	1:B:47:PRO:HD3	1.81	0.41
1:D:223:LEU:HA	1:D:223:LEU:HD23	1.81	0.41
1:E:9:ILE:O	1:E:137:TYR:HA	2.21	0.41
1:A:132:PRO:HA	1:A:259:TYR:CE1	2.56	0.41
1:F:107:THR:HB	1:F:108:PRO:HD2	2.03	0.41
1:A:101:GLN:CD	4:A:303:GOL:H32	2.41	0.40
1:A:217:LEU:HD12	1:A:221:MET:SD	2.61	0.40
1:B:190:PHE:CZ	1:B:222:SER:HA	2.57	0.40
1:D:217:LEU:O	1:D:221:MET:HG3	2.21	0.40
1:B:202:ASP:OD1	1:B:202:ASP:N	2.48	0.40
1:D:132:PRO:HA	1:D:259:TYR:CE1	2.56	0.40

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:A:257:ASP:O	1:E:91:ARG:NH2[5_455]	2.13	0.07

## 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	255/261 (98%)	251 (98%)	4 (2%)	0	100	100
1	B	256/261 (98%)	250 (98%)	4 (2%)	2 (1%)	19	23
1	C	242/261 (93%)	236 (98%)	5 (2%)	1 (0%)	34	42
1	D	256/261 (98%)	252 (98%)	4 (2%)	0	100	100
1	E	257/261 (98%)	252 (98%)	4 (2%)	1 (0%)	34	42
1	F	245/261 (94%)	241 (98%)	4 (2%)	0	100	100
All	All	1511/1566 (96%)	1482 (98%)	25 (2%)	4 (0%)	41	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	212	GLY
1	C	212	GLY
1	B	213	TYR
1	E	212	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	231/235 (98%)	211 (91%)	20 (9%)	10	12
1	B	232/235 (99%)	209 (90%)	23 (10%)	8	9
1	C	221/235 (94%)	203 (92%)	18 (8%)	11	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	232/235 (99%)	211 (91%)	21 (9%)	9	11
1	E	233/235 (99%)	212 (91%)	21 (9%)	9	11
1	F	223/235 (95%)	206 (92%)	17 (8%)	13	16
All	All	1372/1410 (97%)	1252 (91%)	120 (9%)	10	12

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	3	LEU
1	A	45	ARG
1	A	61	LYS
1	A	69	LEU
1	A	85	LYS
1	A	91	ARG
1	A	92	LEU
1	A	94	GLU
1	A	112	GLU
1	A	115	VAL
1	A	125	GLU
1	A	143	ARG
1	A	154	MET
1	A	155	LEU
1	A	156	TYR
1	A	214	MET
1	A	216	SER
1	A	217	LEU
1	A	260	ASP
1	B	2	SER
1	B	3	LEU
1	B	61	LYS
1	B	68	GLN
1	B	69	LEU
1	B	85	LYS
1	B	91	ARG
1	B	92	LEU
1	B	94	GLU
1	B	112	GLU
1	B	115	VAL
1	B	125	GLU
1	B	143	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	154	MET
1	B	155	LEU
1	B	156	TYR
1	B	202	ASP
1	B	214	MET
1	B	215	SER
1	B	216	SER
1	B	217	LEU
1	B	260	ASP
1	B	268	HIS
1	C	2	SER
1	C	3	LEU
1	C	45	ARG
1	C	72	ASN
1	C	85	LYS
1	C	91	ARG
1	C	92	LEU
1	C	94	GLU
1	C	112	GLU
1	C	115	VAL
1	C	125	GLU
1	C	143	ARG
1	C	154	MET
1	C	155	LEU
1	C	156	TYR
1	C	214	MET
1	C	216	SER
1	C	260	ASP
1	D	2	SER
1	D	3	LEU
1	D	45	ARG
1	D	61	LYS
1	D	62	LYS
1	D	65	GLU
1	D	72	ASN
1	D	85	LYS
1	D	91	ARG
1	D	92	LEU
1	D	94	GLU
1	D	112	GLU
1	D	115	VAL
1	D	125	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	143	ARG
1	D	154	MET
1	D	155	LEU
1	D	156	TYR
1	D	202	ASP
1	D	215	SER
1	D	260	ASP
1	E	2	SER
1	E	3	LEU
1	E	45	ARG
1	E	62	LYS
1	E	65	GLU
1	E	69	LEU
1	E	85	LYS
1	E	91	ARG
1	E	92	LEU
1	E	94	GLU
1	E	112	GLU
1	E	115	VAL
1	E	125	GLU
1	E	143	ARG
1	E	145	SER
1	E	154	MET
1	E	155	LEU
1	E	214	MET
1	E	260	ASP
1	E	268	HIS
1	E	269	HIS
1	F	2	SER
1	F	3	LEU
1	F	45	ARG
1	F	85	LYS
1	F	91	ARG
1	F	92	LEU
1	F	94	GLU
1	F	112	GLU
1	F	115	VAL
1	F	125	GLU
1	F	143	ARG
1	F	154	MET
1	F	155	LEU
1	F	156	TYR

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Mol	Chain	Res	Type
1	F	202	ASP
1	F	217	LEU
1	F	260	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	GLN
1	B	194	GLN
1	B	201	GLN
1	C	194	GLN
1	C	250	GLN
1	D	194	GLN
1	E	194	GLN
1	F	194	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	GOL	E	304	-	5,5,5	0.37	0	5,5,5	0.54	0
2	GDP	F	301	3	24,30,30	1.19	2 (8%)	31,47,47	1.96	7 (22%)
2	GDP	D	301	3	24,30,30	1.29	2 (8%)	31,47,47	1.99	8 (25%)
4	GOL	A	303	-	5,5,5	0.36	0	5,5,5	0.63	0
4	GOL	C	303	-	5,5,5	0.36	0	5,5,5	0.29	0
4	GOL	E	303	-	5,5,5	0.35	0	5,5,5	0.21	0
2	GDP	C	301	-	24,30,30	1.39	3 (12%)	31,47,47	2.12	7 (22%)
2	GDP	A	301	3	24,30,30	1.18	2 (8%)	31,47,47	1.99	8 (25%)
2	GDP	E	301	3	24,30,30	1.32	2 (8%)	31,47,47	2.42	10 (32%)
2	GDP	B	301	3	24,30,30	1.23	2 (8%)	31,47,47	1.98	9 (29%)

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	GOL	E	304	-	-	1/4/4/4	-
2	GDP	F	301	3	-	5/12/32/32	0/3/3/3
2	GDP	D	301	3	-	4/12/32/32	0/3/3/3
4	GOL	A	303	-	-	2/4/4/4	-
4	GOL	C	303	-	-	2/4/4/4	-
4	GOL	E	303	-	-	2/4/4/4	-
2	GDP	C	301	-	-	3/12/32/32	0/3/3/3
2	GDP	A	301	3	-	0/12/32/32	0/3/3/3
2	GDP	E	301	3	-	1/12/32/32	0/3/3/3
2	GDP	B	301	3	-	0/12/32/32	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	GDP	C6-C5	5.28	1.50	1.41
2	E	301	GDP	C6-C5	4.49	1.49	1.41
2	D	301	GDP	C6-C5	4.42	1.49	1.41
2	B	301	GDP	C6-C5	4.23	1.48	1.41
2	A	301	GDP	C6-C5	4.16	1.48	1.41
2	F	301	GDP	C6-C5	3.98	1.48	1.41
2	D	301	GDP	C5-C4	2.70	1.48	1.40
2	F	301	GDP	C5-C4	2.54	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	GDP	C5-C4	2.48	1.47	1.40
2	A	301	GDP	C5-C4	2.34	1.47	1.40
2	C	301	GDP	C5-C4	2.29	1.47	1.40
2	E	301	GDP	C5-C4	2.13	1.46	1.40
2	C	301	GDP	O4'-C1'	2.10	1.44	1.41

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	GDP	C2-N3-C4	7.25	123.64	115.36
2	C	301	GDP	C2-N3-C4	6.38	122.65	115.36
2	A	301	GDP	C5-C6-N1	-5.13	116.42	123.43
2	B	301	GDP	C5-C6-N1	-4.97	116.63	123.43
2	D	301	GDP	C2-N3-C4	4.94	121.00	115.36
2	E	301	GDP	C6-C5-C4	-4.70	116.31	120.80
2	A	301	GDP	C6-N1-C2	4.64	123.31	115.93
2	F	301	GDP	C6-N1-C2	4.53	123.13	115.93
2	F	301	GDP	C2-N3-C4	4.52	120.51	115.36
2	F	301	GDP	C6-C5-C4	-4.47	116.53	120.80
2	A	301	GDP	C2-N3-C4	4.30	120.27	115.36
2	E	301	GDP	C5'-C4'-C3'	-4.29	99.11	115.18
2	E	301	GDP	N3-C2-N1	-4.27	121.53	127.22
2	B	301	GDP	C6-N1-C2	4.25	122.69	115.93
2	F	301	GDP	C5-C6-N1	-4.23	117.65	123.43
2	C	301	GDP	C6-N1-C2	4.04	122.36	115.93
2	D	301	GDP	PA-O3A-PB	-4.03	119.01	132.83
2	C	301	GDP	N3-C2-N1	-4.01	121.88	127.22
2	D	301	GDP	C5-C6-N1	-3.85	118.16	123.43
2	D	301	GDP	C6-C5-C4	-3.83	117.14	120.80
2	D	301	GDP	C6-N1-C2	3.83	122.01	115.93
2	C	301	GDP	C5-C6-N1	-3.79	118.25	123.43
2	E	301	GDP	C6-N1-C2	3.66	121.74	115.93
2	F	301	GDP	N3-C2-N1	-3.63	122.38	127.22
2	C	301	GDP	C6-C5-C4	-3.60	117.36	120.80
2	E	301	GDP	PA-O3A-PB	-3.55	120.64	132.83
2	E	301	GDP	C4-C5-N7	-3.52	105.73	109.40
2	D	301	GDP	C4-C5-N7	-3.51	105.74	109.40
2	A	301	GDP	N3-C2-N1	-3.50	122.55	127.22
2	B	301	GDP	C2-N3-C4	3.44	119.29	115.36
2	B	301	GDP	C6-C5-C4	-3.25	117.69	120.80
2	C	301	GDP	C4-C5-N7	-3.25	106.01	109.40
2	B	301	GDP	PA-O3A-PB	-3.22	121.78	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	GDP	C5-C6-N1	-3.16	119.11	123.43
2	A	301	GDP	C4-C5-N7	-3.15	106.11	109.40
2	A	301	GDP	C6-C5-C4	-2.87	118.06	120.80
2	D	301	GDP	N3-C2-N1	-2.86	123.40	127.22
2	F	301	GDP	PA-O3A-PB	-2.79	123.24	132.83
2	B	301	GDP	C4-C5-N7	-2.75	106.53	109.40
2	B	301	GDP	N3-C2-N1	-2.67	123.66	127.22
2	D	301	GDP	O4'-C1'-C2'	-2.60	103.12	106.93
2	E	301	GDP	N2-C2-N1	2.37	120.94	117.25
2	A	301	GDP	O3B-PB-O3A	2.34	112.49	104.64
2	C	301	GDP	PA-O3A-PB	-2.26	125.06	132.83
2	E	301	GDP	O4'-C4'-C3'	2.20	109.48	105.11
2	B	301	GDP	C2'-C3'-C4'	2.16	106.84	102.64
2	B	301	GDP	C1'-N9-C4	-2.06	123.02	126.64
2	A	301	GDP	O2B-PB-O3A	2.02	111.42	104.64
2	F	301	GDP	C4-C5-N7	-2.02	107.30	109.40

There are no chirality outliers.

All (20) torsion outliers are listed below:

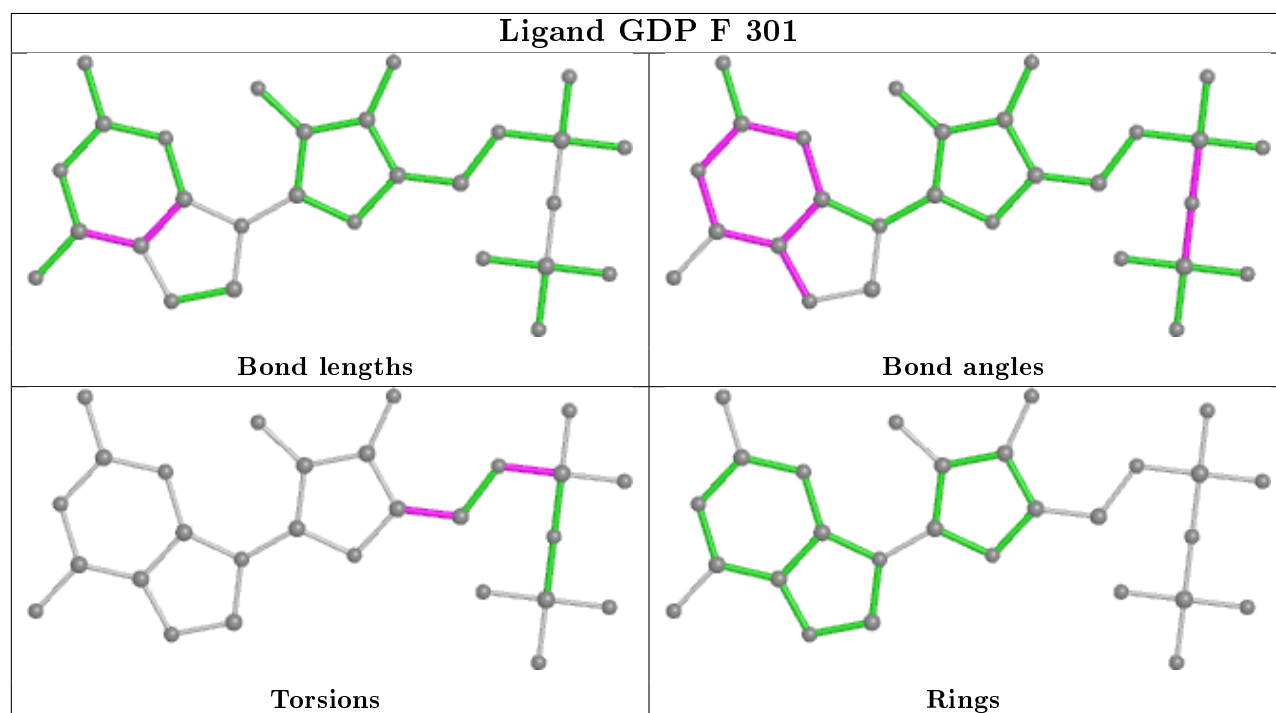
Mol	Chain	Res	Type	Atoms
2	F	301	GDP	C5'-O5'-PA-O1A
2	F	301	GDP	O4'-C4'-C5'-O5'
4	A	303	GOL	O1-C1-C2-C3
4	C	303	GOL	O1-C1-C2-C3
4	E	303	GOL	C1-C2-C3-O3
2	F	301	GDP	C3'-C4'-C5'-O5'
4	C	303	GOL	O1-C1-C2-O2
4	E	304	GOL	C1-C2-C3-O3
4	A	303	GOL	O1-C1-C2-O2
4	E	303	GOL	O2-C2-C3-O3
2	F	301	GDP	C5'-O5'-PA-O3A
2	F	301	GDP	C5'-O5'-PA-O2A
2	D	301	GDP	O4'-C4'-C5'-O5'
2	D	301	GDP	PA-O3A-PB-O1B
2	C	301	GDP	PA-O3A-PB-O1B
2	E	301	GDP	PA-O3A-PB-O1B
2	D	301	GDP	PA-O3A-PB-O2B
2	D	301	GDP	PA-O3A-PB-O3B
2	C	301	GDP	PA-O3A-PB-O2B
2	C	301	GDP	PA-O3A-PB-O3B

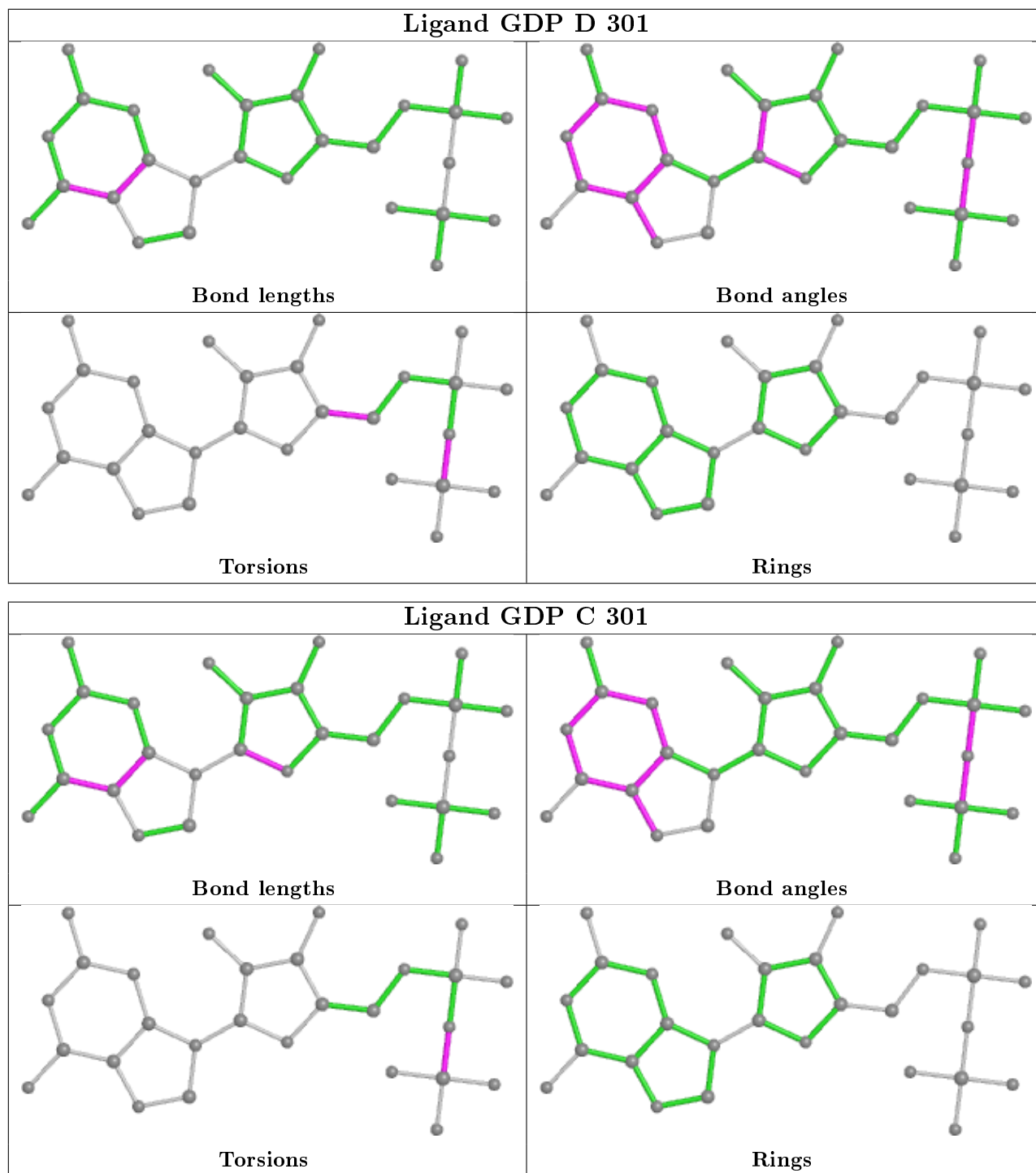
There are no ring outliers.

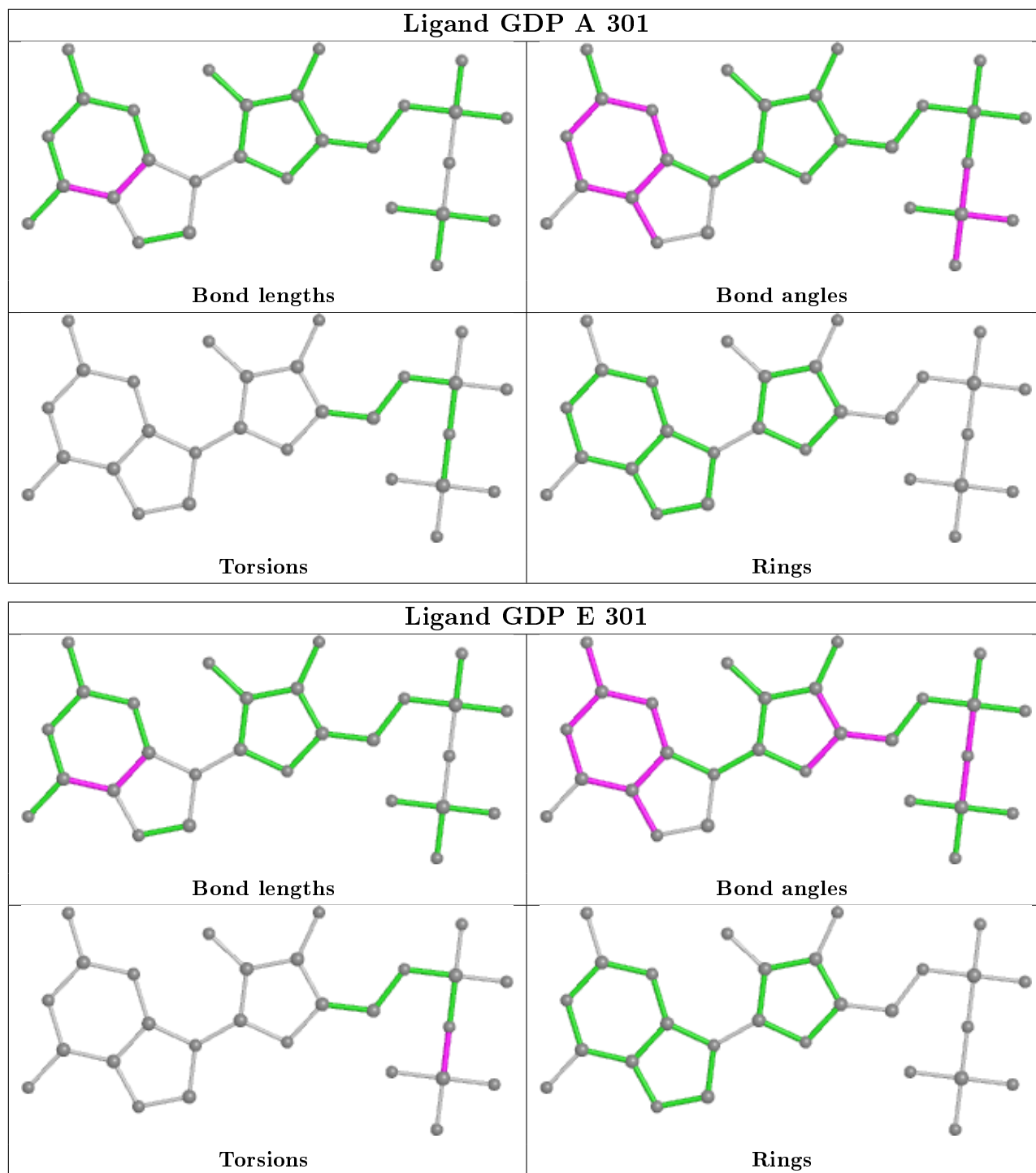
4 monomers are involved in 4 short contacts:

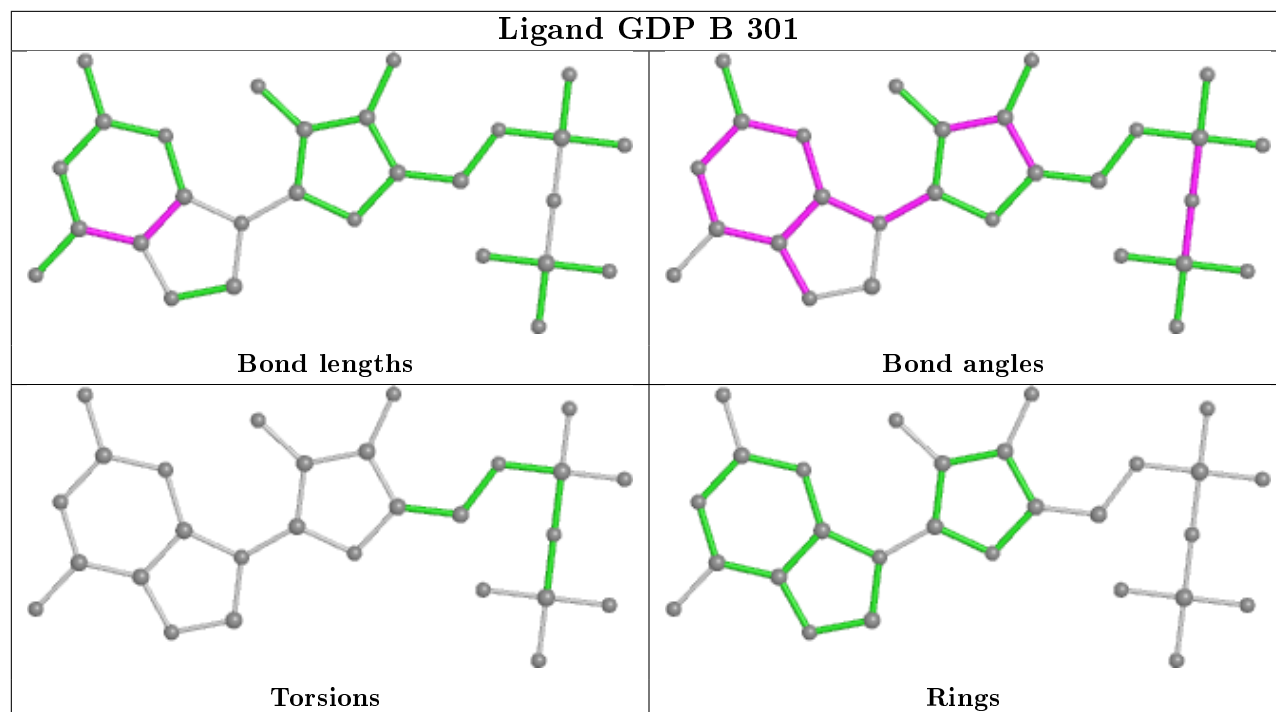
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	GDP	1	0
4	A	303	GOL	1	0
4	E	303	GOL	1	0
2	C	301	GDP	1	0

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

### 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	257/261 (98%)	0.39	11 (4%) 35 42	42, 60, 106, 198	0
1	B	258/261 (98%)	1.01	37 (14%) 2 3	44, 69, 146, 237	0
1	C	246/261 (94%)	0.86	30 (12%) 4 6	48, 72, 158, 280	0
1	D	258/261 (98%)	0.62	21 (8%) 12 16	56, 83, 135, 186	0
1	E	259/261 (99%)	0.50	18 (6%) 16 22	44, 63, 127, 211	0
1	F	249/261 (95%)	1.19	46 (18%) 1 1	55, 104, 146, 195	0
All	All	1527/1566 (97%)	0.76	163 (10%) 6 8	42, 74, 141, 280	0

All (163) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	220	SER	14.7
1	D	67	TYR	11.1
1	B	223	LEU	10.0
1	C	223	LEU	9.7
1	D	63	VAL	8.7
1	C	222	SER	8.7
1	B	219	ASN	8.5
1	C	198	LYS	8.5
1	C	58	ILE	8.2
1	B	198	LYS	7.8
1	C	219	ASN	7.3
1	D	60	TYR	7.2
1	F	93	VAL	6.8
1	D	64	MET	6.4
1	D	66	ASN	6.4
1	F	202	ASP	6.3
1	F	3	LEU	6.2
1	E	66	ASN	6.0
1	B	220	SER	5.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	58	ILE	5.6
1	F	32	THR	5.3
1	F	58	ILE	5.0
1	E	61	LYS	4.7
1	E	63	VAL	4.7
1	E	68	GLN	4.7
1	F	259	TYR	4.7
1	C	190	PHE	4.7
1	F	131	PHE	4.7
1	C	72	ASN	4.7
1	B	58	ILE	4.6
1	F	91	ARG	4.5
1	B	195	ALA	4.5
1	E	92	LEU	4.5
1	B	59	LYS	4.4
1	D	99	LYS	4.4
1	E	62	LYS	4.3
1	C	59	LYS	4.3
1	F	268	HIS	4.2
1	F	84	THR	4.2
1	A	202	ASP	4.2
1	F	33	PRO	4.1
1	F	262	TYR	4.1
1	C	224	MET	4.1
1	B	262	TYR	4.1
1	E	268	HIS	4.1
1	B	45	ARG	4.0
1	C	195	ALA	4.0
1	F	105	ILE	4.0
1	F	4	SER	4.0
1	B	212	GLY	4.0
1	F	85	LYS	3.9
1	F	27	LEU	3.9
1	C	212	GLY	3.9
1	D	59	LYS	3.9
1	F	234	VAL	3.9
1	F	98	ASP	3.9
1	C	73	GLY	3.7
1	B	162	TYR	3.7
1	C	192	SER	3.7
1	C	218	VAL	3.7
1	B	218	VAL	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	224	MET	3.6
1	B	222	SER	3.6
1	C	44	LEU	3.6
1	F	81	LEU	3.6
1	C	214	MET	3.5
1	F	44	LEU	3.4
1	F	92	LEU	3.4
1	F	248	PHE	3.4
1	C	199	GLU	3.3
1	F	47	PRO	3.3
1	D	45	ARG	3.3
1	E	65	GLU	3.3
1	B	46	VAL	3.3
1	B	196	ALA	3.2
1	E	57	SER	3.2
1	A	257	ASP	3.2
1	C	196	ALA	3.2
1	D	92	LEU	3.1
1	D	62	LYS	3.1
1	F	127	PHE	3.0
1	A	199	GLU	3.0
1	B	202	ASP	3.0
1	A	262	TYR	2.9
1	F	132	PRO	2.9
1	B	68	GLN	2.9
1	E	58	ILE	2.8
1	D	96	LYS	2.8
1	F	258	GLU	2.8
1	F	100	PHE	2.8
1	F	99	LYS	2.7
1	D	91	ARG	2.7
1	D	202	ASP	2.7
1	D	50	ALA	2.7
1	C	216	SER	2.7
1	B	60	TYR	2.7
1	E	202	ASP	2.7
1	D	61	LYS	2.7
1	B	66	ASN	2.7
1	B	197	ILE	2.6
1	D	259	TYR	2.6
1	A	111	ILE	2.6
1	B	201	GLN	2.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	F	88	GLN	2.6
1	B	151	MET	2.5
1	D	68	GLN	2.5
1	F	29	ALA	2.5
1	C	71	PRO	2.5
1	F	19	PHE	2.5
1	A	265	LYS	2.5
1	B	240	PHE	2.5
1	E	219	ASN	2.5
1	F	133	THR	2.5
1	B	145	SER	2.5
1	C	47	PRO	2.5
1	F	162	TYR	2.5
1	E	44	LEU	2.5
1	A	155	LEU	2.4
1	B	116	TRP	2.4
1	E	67	TYR	2.4
1	D	57	SER	2.4
1	B	156	TYR	2.4
1	C	155	LEU	2.4
1	F	267	HIS	2.4
1	D	47	PRO	2.4
1	F	96	LYS	2.4
1	A	99	LYS	2.3
1	F	101	GLN	2.3
1	B	143	ARG	2.3
1	B	44	LEU	2.3
1	F	264	LYS	2.3
1	B	191	GLU	2.3
1	F	235	VAL	2.3
1	E	64	MET	2.2
1	B	61	LYS	2.2
1	A	11	MET	2.2
1	B	111	ILE	2.2
1	B	62	LYS	2.2
1	F	45	ARG	2.2
1	A	218	VAL	2.2
1	F	135	ILE	2.2
1	F	34	PRO	2.2
1	B	57	SER	2.2
1	B	261	GLN	2.2
1	F	31	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	53	ASP	2.2
1	B	65	GLU	2.1
1	F	155	LEU	2.1
1	C	162	TYR	2.1
1	A	261	GLN	2.1
1	F	56	ASP	2.1
1	D	81	LEU	2.1
1	C	158	CYS	2.1
1	E	259	TYR	2.1
1	C	261	GLN	2.0
1	C	200	ASP	2.0
1	E	71	PRO	2.0
1	F	71	PRO	2.0
1	C	193	PHE	2.0
1	C	259	TYR	2.0
1	E	91	ARG	2.0
1	B	171	VAL	2.0
1	C	262	TYR	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](#)

There are no carbohydrates 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, 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.

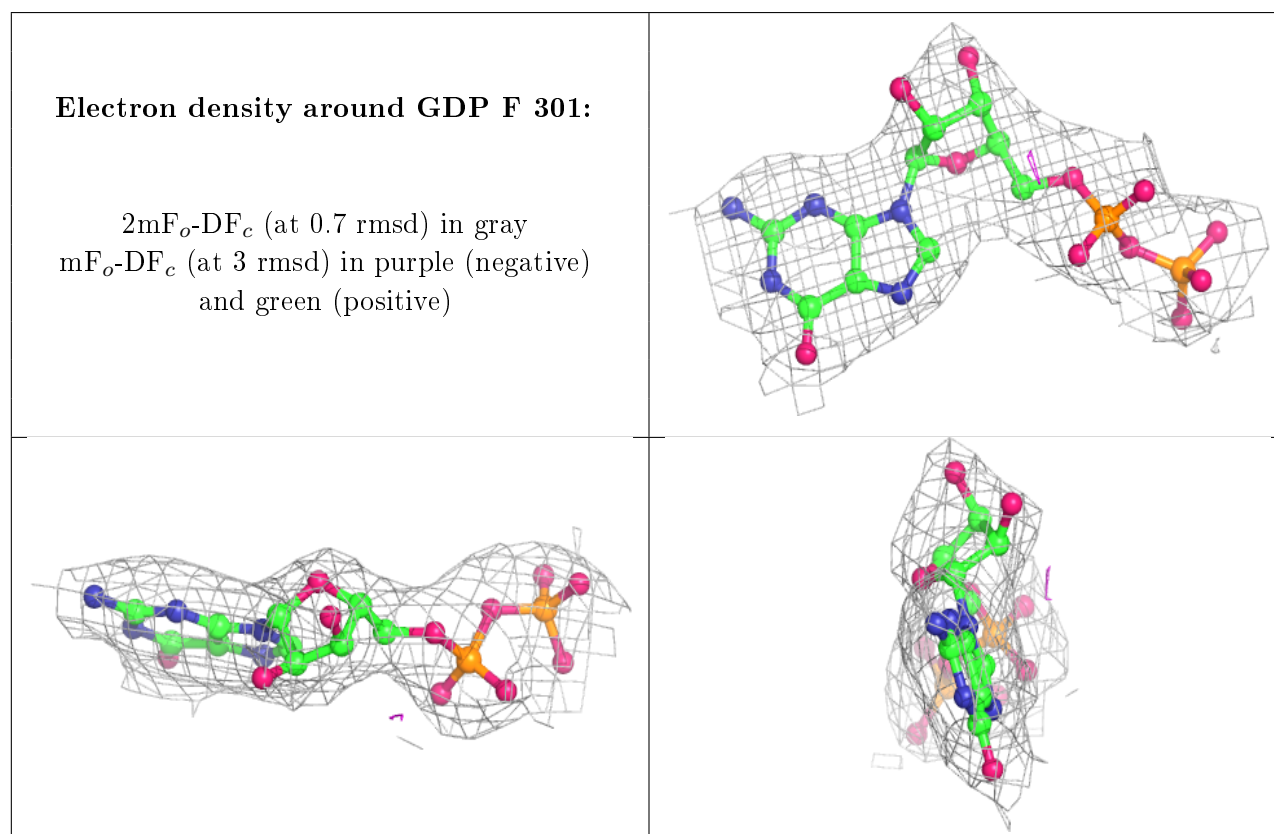
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	E	303	6/6	0.60	0.46	91,102,106,108	0
4	GOL	A	303	6/6	0.64	0.47	104,119,129,129	0
4	GOL	C	303	6/6	0.72	0.23	90,102,119,125	0
4	GOL	E	304	6/6	0.86	0.26	69,98,110,124	0
2	GDP	F	301	28/28	0.93	0.13	71,93,103,114	0

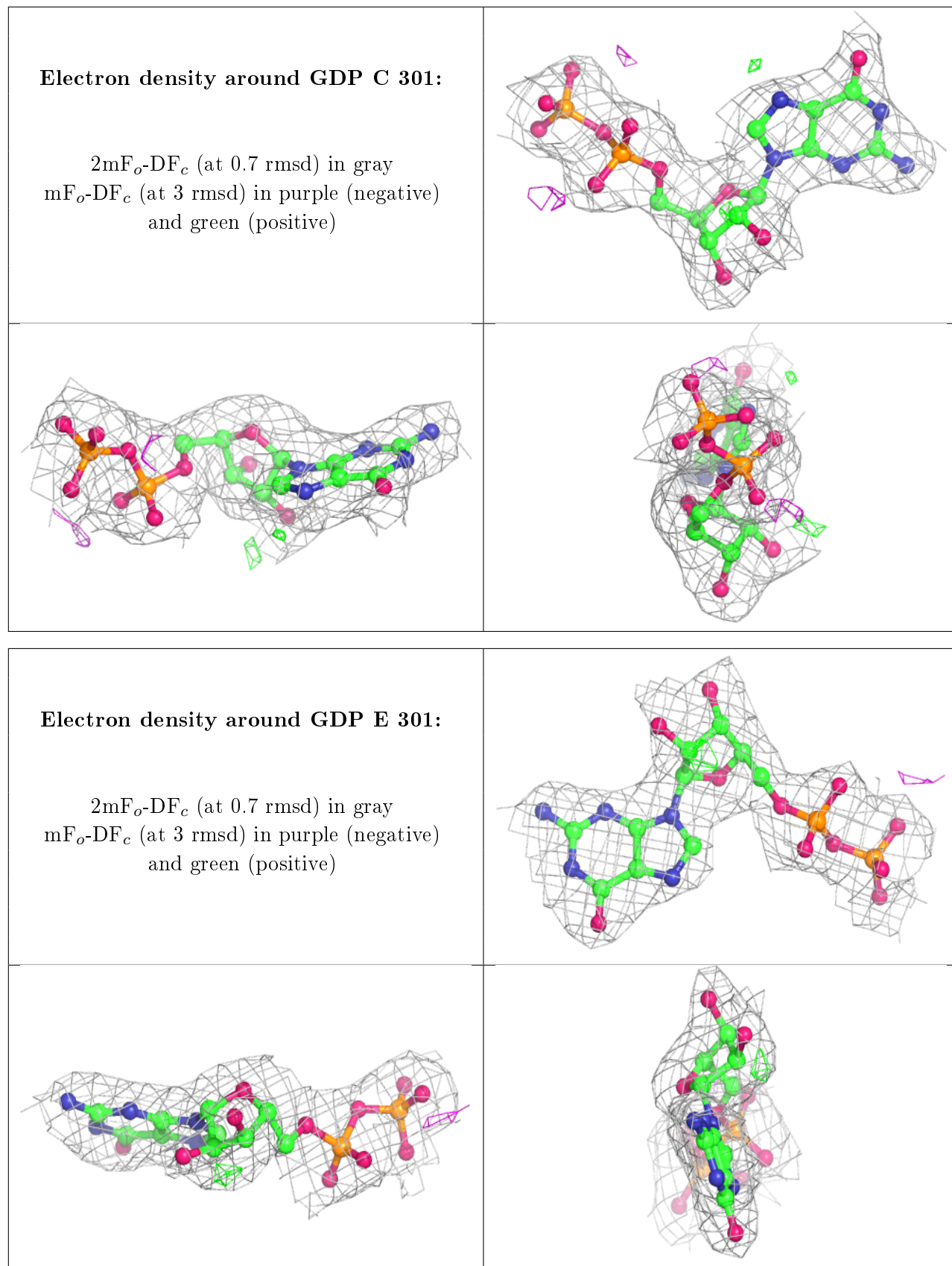
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GDP	C	301	28/28	0.93	0.16	45,66,77,84	0
3	MG	D	302	1/1	0.93	0.05	65,65,65,65	0
3	MG	A	302	1/1	0.94	0.24	55,55,55,55	0
3	MG	B	302	1/1	0.94	0.12	52,52,52,52	0
2	GDP	E	301	28/28	0.95	0.20	54,61,86,110	0
3	MG	C	302	1/1	0.96	0.19	63,63,63,63	0
2	GDP	D	301	28/28	0.96	0.11	55,68,91,136	0
3	MG	F	302	1/1	0.97	0.21	85,85,85,85	0
3	MG	E	302	1/1	0.97	0.07	61,61,61,61	0
2	GDP	B	301	28/28	0.97	0.14	51,53,63,65	0
2	GDP	A	301	28/28	0.98	0.18	57,59,77,79	0

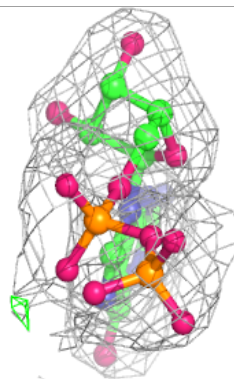
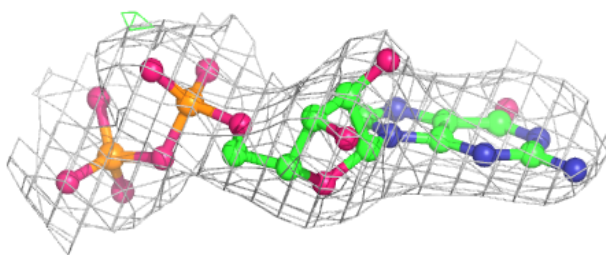
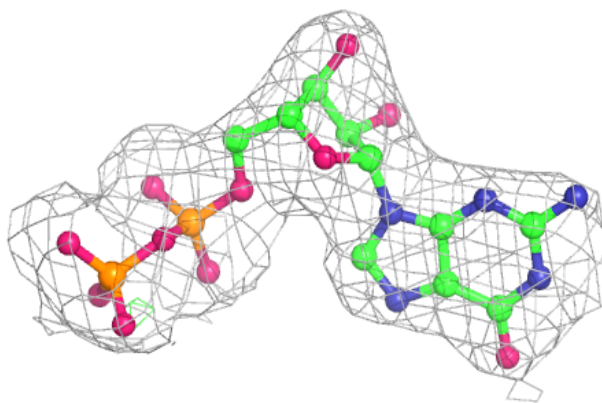
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



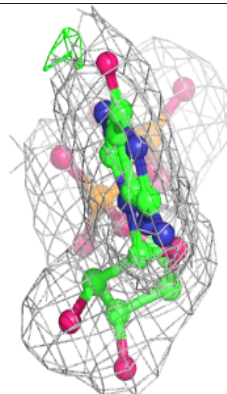
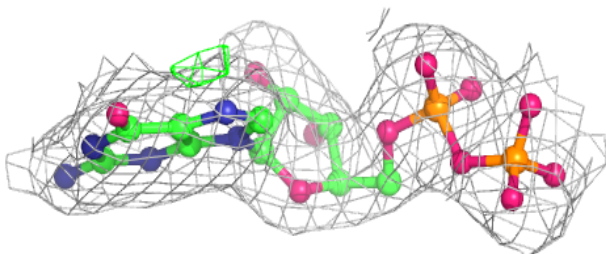
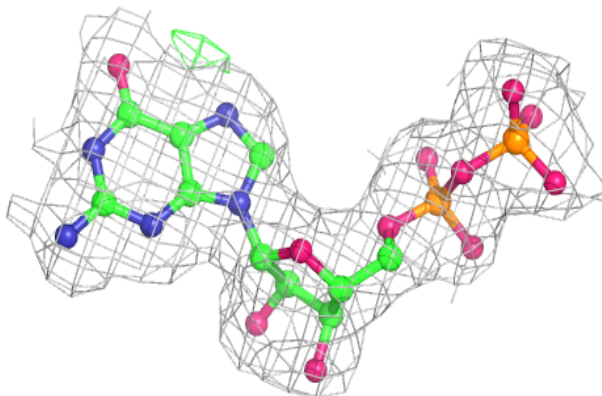


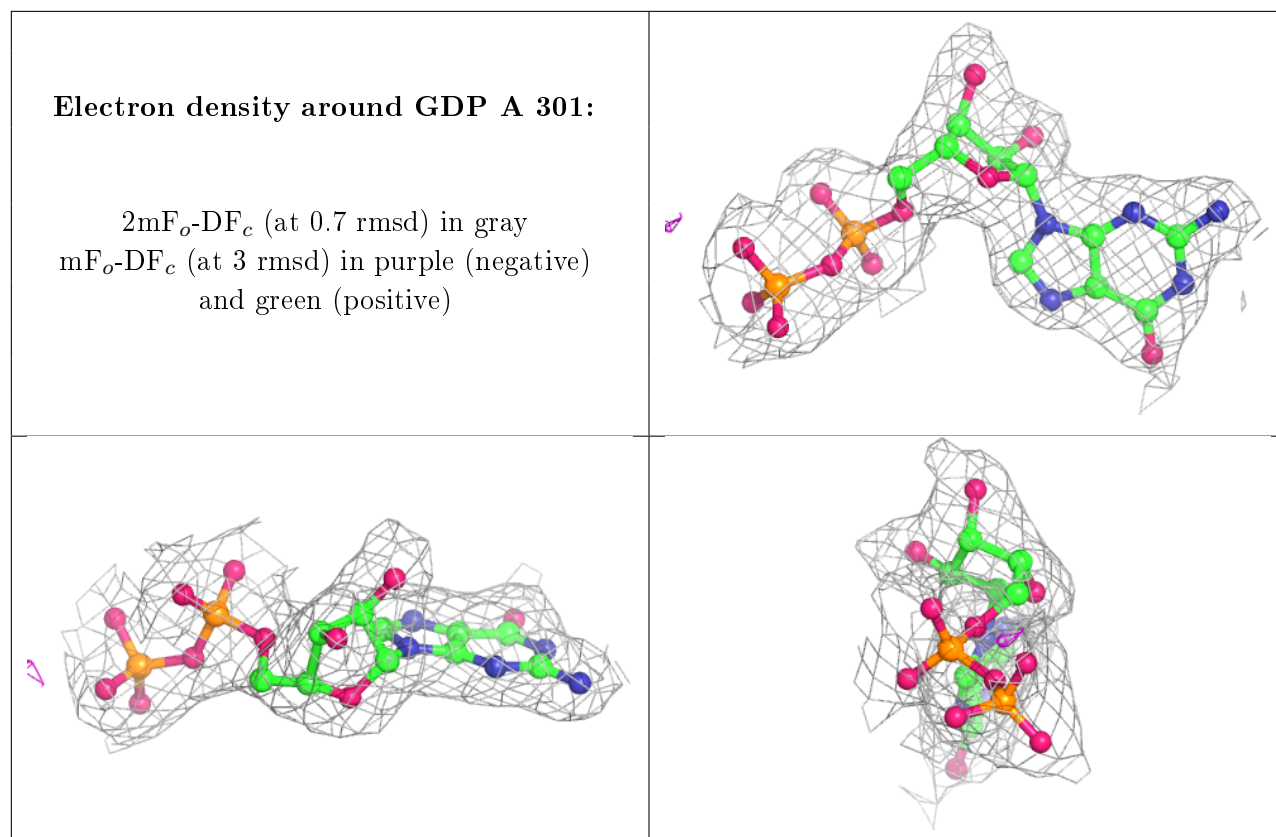
**Electron density around GDP D 301:**

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

**Electron density around GDP B 301:**

$2mF_o-DF_c$  (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.