



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 01:02 AM EDT

PDB ID : 7S5E  
Title : Crystal structure of a guanylate kinase from *Stenotrophomonas maltophilia* K279a with heterogeneous ligand states of GMP/ADP, GMP/-, GDP/-, and GMP/ATPgS  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2021-09-10  
Resolution : 2.40 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

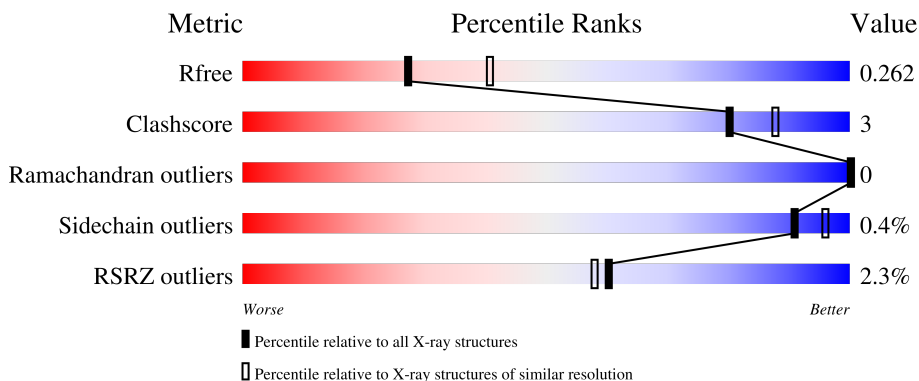
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	229	 3% 82% 7% 11%
1	B	229	 3% 79% 7% 14%
1	C	229	 4% 82% 5% 14%
1	D	229	 0% 84% 7% 10%

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Mol	Chain	Length	Quality of chain
1	E	229	 82% 7% 11%
1	F	229	 3% 79% 7% 14%
1	G	229	 4% 82% 5% 14%
1	H	229	 % 84% 7% 10%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12787 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 Guanylate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	203	Total 1565	C 986	N 286	O 288	S 5	0	0	0
1	B	198	Total 1461	C 928	N 257	O 272	S 4	0	1	0
1	C	198	Total 1469	C 934	N 262	O 269	S 4	0	0	0
1	D	207	Total 1562	C 985	N 284	O 288	S 5	0	0	0
1	E	203	Total 1561	C 983	N 285	O 288	S 5	0	0	0
1	F	198	Total 1455	C 924	N 256	O 271	S 4	0	0	0
1	G	198	Total 1459	C 929	N 258	O 268	S 4	0	0	0
1	H	207	Total 1562	C 985	N 284	O 288	S 5	0	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP B2FT06
A	-6	ALA	-	expression tag	UNP B2FT06
A	-5	HIS	-	expression tag	UNP B2FT06
A	-4	HIS	-	expression tag	UNP B2FT06
A	-3	HIS	-	expression tag	UNP B2FT06
A	-2	HIS	-	expression tag	UNP B2FT06
A	-1	HIS	-	expression tag	UNP B2FT06
A	0	HIS	-	expression tag	UNP B2FT06
B	-7	MET	-	initiating methionine	UNP B2FT06
B	-6	ALA	-	expression tag	UNP B2FT06
B	-5	HIS	-	expression tag	UNP B2FT06
B	-4	HIS	-	expression tag	UNP B2FT06
B	-3	HIS	-	expression tag	UNP B2FT06

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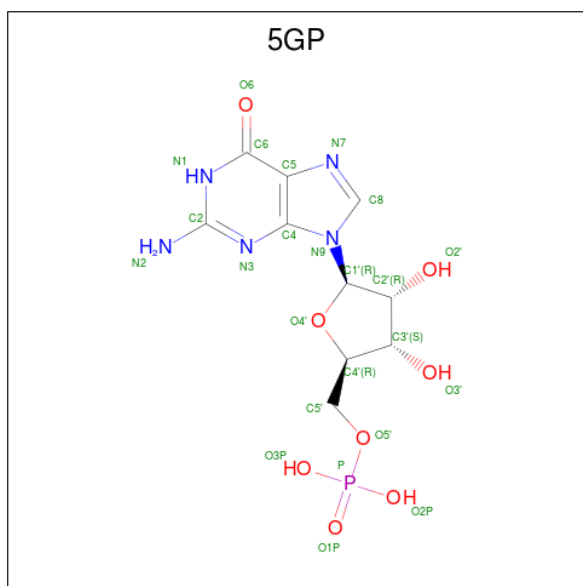
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP B2FT06
B	-1	HIS	-	expression tag	UNP B2FT06
B	0	HIS	-	expression tag	UNP B2FT06
C	-7	MET	-	initiating methionine	UNP B2FT06
C	-6	ALA	-	expression tag	UNP B2FT06
C	-5	HIS	-	expression tag	UNP B2FT06
C	-4	HIS	-	expression tag	UNP B2FT06
C	-3	HIS	-	expression tag	UNP B2FT06
C	-2	HIS	-	expression tag	UNP B2FT06
C	-1	HIS	-	expression tag	UNP B2FT06
C	0	HIS	-	expression tag	UNP B2FT06
D	-7	MET	-	initiating methionine	UNP B2FT06
D	-6	ALA	-	expression tag	UNP B2FT06
D	-5	HIS	-	expression tag	UNP B2FT06
D	-4	HIS	-	expression tag	UNP B2FT06
D	-3	HIS	-	expression tag	UNP B2FT06
D	-2	HIS	-	expression tag	UNP B2FT06
D	-1	HIS	-	expression tag	UNP B2FT06
D	0	HIS	-	expression tag	UNP B2FT06
E	-7	MET	-	initiating methionine	UNP B2FT06
E	-6	ALA	-	expression tag	UNP B2FT06
E	-5	HIS	-	expression tag	UNP B2FT06
E	-4	HIS	-	expression tag	UNP B2FT06
E	-3	HIS	-	expression tag	UNP B2FT06
E	-2	HIS	-	expression tag	UNP B2FT06
E	-1	HIS	-	expression tag	UNP B2FT06
E	0	HIS	-	expression tag	UNP B2FT06
F	-7	MET	-	initiating methionine	UNP B2FT06
F	-6	ALA	-	expression tag	UNP B2FT06
F	-5	HIS	-	expression tag	UNP B2FT06
F	-4	HIS	-	expression tag	UNP B2FT06
F	-3	HIS	-	expression tag	UNP B2FT06
F	-2	HIS	-	expression tag	UNP B2FT06
F	-1	HIS	-	expression tag	UNP B2FT06
F	0	HIS	-	expression tag	UNP B2FT06
G	-7	MET	-	initiating methionine	UNP B2FT06
G	-6	ALA	-	expression tag	UNP B2FT06
G	-5	HIS	-	expression tag	UNP B2FT06
G	-4	HIS	-	expression tag	UNP B2FT06
G	-3	HIS	-	expression tag	UNP B2FT06
G	-2	HIS	-	expression tag	UNP B2FT06
G	-1	HIS	-	expression tag	UNP B2FT06

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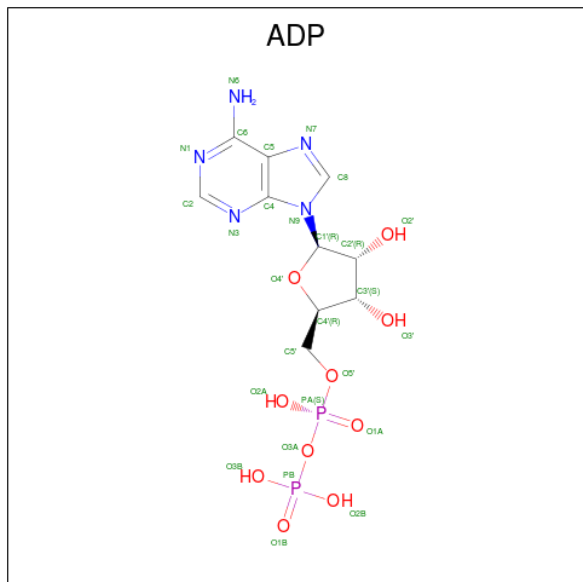
Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP B2FT06
H	-7	MET	-	initiating methionine	UNP B2FT06
H	-6	ALA	-	expression tag	UNP B2FT06
H	-5	HIS	-	expression tag	UNP B2FT06
H	-4	HIS	-	expression tag	UNP B2FT06
H	-3	HIS	-	expression tag	UNP B2FT06
H	-2	HIS	-	expression tag	UNP B2FT06
H	-1	HIS	-	expression tag	UNP B2FT06
H	0	HIS	-	expression tag	UNP B2FT06

- Molecule 2 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula:  $C_{10}H_{14}N_5O_8P$ ) (labeled as "Ligand of Interest" by depositor).



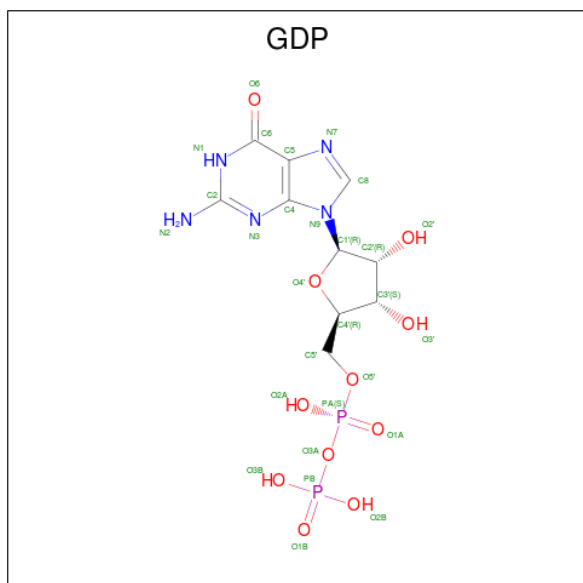
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	B	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	D	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	E	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	F	1	Total	C	N	O	P	0	0
			24	10	5	8	1		
2	H	1	Total	C	N	O	P	0	0
			24	10	5	8	1		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).



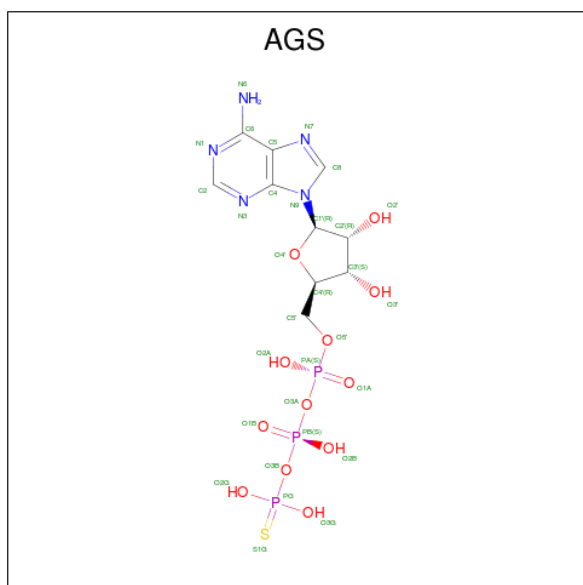
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	C	1	28	10	5	11	2	0	0
4	G	1	28	10	5	11	2	0	0

- Molecule 5 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	D	1	31	10	5	12	3	1	0	0
5	H	1	31	10	5	12	3	1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	58	Total	O	0	0
			58	58		
6	B	31	Total	O	0	0
			31	31		
6	C	45	Total	O	0	0
			45	45		
6	D	49	Total	O	0	0
			49	49		
6	E	62	Total	O	0	0
			62	62		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	F	36	Total 36	O 36	0	0
6	G	44	Total 44	O 44	0	0
6	H	52	Total 52	O 52	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: Guanylate kinase

Chain A: 




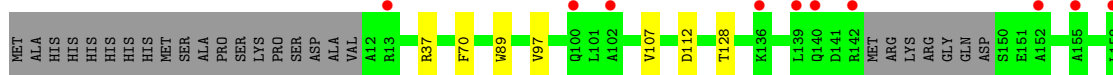
- Molecule 1: Guanylate kinase

Chain B: 




- Molecule 1: Guanylate kinase

Chain C: 



- Molecule 1: Guanylate kinase

Chain D: 



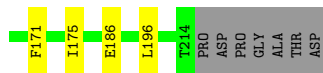
- Molecule 1: Guanylate kinase

Chain E: 82% 7% 11%



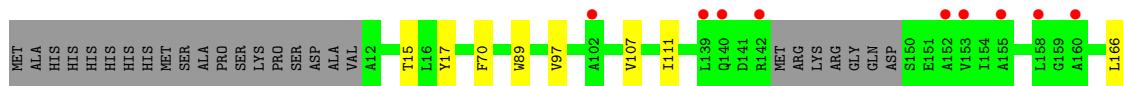
● Molecule 1: Guanylate kinase

Chain F: 3% 79% 7% 14%



● Molecule 1: Guanylate kinase

Chain G: 4% 82% 5% 14%



● Molecule 1: Guanylate kinase

Chain H: 0% 84% 7% 10%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.16Å 100.53Å 92.25Å 90.00° 95.21° 90.00°	Depositor
Resolution (Å)	45.93 – 2.40 45.93 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.9 (45.93-2.40) 96.8 (45.93-2.40)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.59 (at 2.39Å)	Xtrriage
Refinement program	PHENIX dev-4274	Depositor
R, $R_{free}$	0.226 , 0.265 0.227 , 0.262	Depositor DCC
$R_{free}$ test set	2064 reflections (3.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.7	Xtrriage
Anisotropy	0.272	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 37.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	0.034 for l,-k,h	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12787	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 99.50 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.3021e-13. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, ADP, AGS, 5GP

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	0.33	0/1596	0.57	0/2164
1	B	0.31	0/1494	0.52	0/2037
1	C	0.34	0/1500	0.55	0/2042
1	D	0.34	0/1593	0.57	0/2165
1	E	0.33	0/1592	0.57	0/2160
1	F	0.31	0/1485	0.52	0/2025
1	G	0.34	0/1490	0.54	0/2030
1	H	0.33	0/1593	0.56	0/2165
All	All	0.33	0/12343	0.55	0/16788

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	1565	0	1537	9	0
1	B	1461	0	1375	11	0
1	C	1469	0	1405	6	0
1	D	1562	0	1518	10	0
1	E	1561	0	1526	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1455	0	1367	11	0
1	G	1459	0	1388	7	0
1	H	1562	0	1518	9	0
2	A	24	0	12	1	0
2	B	24	0	12	1	0
2	D	24	0	12	0	0
2	E	24	0	12	1	0
2	F	24	0	12	1	0
2	H	24	0	12	0	0
3	A	27	0	12	1	0
3	E	27	0	12	1	0
4	C	28	0	12	0	0
4	G	28	0	12	1	0
5	D	31	0	12	0	0
5	H	31	0	12	0	0
6	A	58	0	0	1	0
6	B	31	0	0	0	0
6	C	45	0	0	1	0
6	D	49	0	0	1	0
6	E	62	0	0	1	0
6	F	36	0	0	0	0
6	G	44	0	0	0	0
6	H	52	0	0	1	0
All	All	12787	0	11778	65	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 3.

All (65) 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:131:ILE:HD13	1:B:175:ILE:HB	1.74	0.68
1:F:131:ILE:HD13	1:F:175:ILE:HB	1.77	0.66
1:G:97:VAL:HG12	1:G:107:VAL:HG11	1.78	0.64
1:C:97:VAL:HG12	1:C:107:VAL:HG11	1.79	0.63
1:E:146:ARG:NH1	3:E:302:ADP:O3B	2.38	0.56
1:A:144:ARG:NH2	1:A:151:GLU:OE1	2.36	0.56
1:B:111:ILE:HG22	2:B:301:5GP:C6	2.36	0.56
1:F:196:LEU:HD11	1:H:186:GLU:HB3	1.91	0.52
1:A:120:ARG:HD2	6:A:413:HOH:O	2.10	0.51
1:F:49:SER:HA	1:F:65:VAL:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:SER:HA	1:B:65:VAL:O	2.11	0.51
1:D:88:ASP:OD1	6:D:401:HOH:O	2.19	0.50
1:C:37:ARG:NH1	6:C:401:HOH:O	2.38	0.50
1:D:18:ILE:HD13	1:D:116:ALA:HA	1.93	0.50
1:F:111:ILE:HG22	2:F:301:5GP:C6	2.42	0.50
1:E:144:ARG:NH2	1:E:151:GLU:OE1	2.41	0.50
1:A:146:ARG:NH1	3:A:302:ADP:O3B	2.46	0.49
1:F:42:ALA:HB2	1:F:105:GLN:NE2	2.28	0.49
1:B:196:LEU:HD11	1:D:186:GLU:HB3	1.94	0.49
1:H:18:ILE:HD13	1:H:116:ALA:HA	1.94	0.49
1:C:187:LEU:O	1:C:191:PHE:HD1	1.96	0.48
1:E:120:ARG:HD2	6:E:409:HOH:O	2.13	0.48
1:E:38:ASP:CG	1:E:195:ARG:HH22	2.17	0.48
1:C:70:PHE:CE1	1:C:89:TRP:HB3	2.48	0.48
1:E:111:ILE:HG22	2:E:301:5GP:C6	2.43	0.48
1:A:111:ILE:HG22	2:A:301:5GP:C6	2.43	0.47
1:G:70:PHE:CE1	1:G:89:TRP:HB3	2.49	0.47
1:G:187:LEU:O	1:G:191:PHE:HD1	1.98	0.47
1:A:18:ILE:HB	1:A:128:THR:HG22	1.97	0.46
1:D:84:TRP:HB3	1:E:117:GLN:HE22	1.80	0.46
1:A:38:ASP:CG	1:A:195:ARG:HH22	2.18	0.46
1:H:13:ARG:HH21	1:H:101:LEU:HB2	1.81	0.46
1:B:166:LEU:HD23	1:D:213:LEU:HD22	1.99	0.45
1:D:62:TYR:HB2	1:D:64:PHE:CZ	2.51	0.45
1:E:205:HIS:NE2	1:G:176:VAL:HG21	2.32	0.45
1:F:166:LEU:HD23	1:H:213:LEU:HD22	1.99	0.45
1:B:18:ILE:HD11	1:B:119:VAL:HG11	1.99	0.44
1:F:120:ARG:HH11	1:F:128:THR:HG21	1.81	0.44
1:H:49:SER:OG	6:H:401:HOH:O	2.21	0.44
1:H:70:PHE:CE1	1:H:89:TRP:HB3	2.53	0.44
1:G:111:ILE:HG22	4:G:301:GDP:C6	2.53	0.44
1:B:128:THR:HB	1:B:171:PHE:CD2	2.53	0.44
1:A:100:GLN:HB3	1:A:105:GLN:HB3	2.00	0.44
1:B:42:ALA:HB2	1:B:105:GLN:NE2	2.33	0.43
1:G:15:THR:HB	1:G:17:TYR:CE2	2.53	0.43
1:D:62:TYR:HB2	1:D:64:PHE:CE2	2.54	0.43
1:A:70:PHE:CE1	1:A:89:TRP:HB3	2.54	0.42
1:F:18:ILE:HD11	1:F:119:VAL:HG11	2.00	0.42
1:F:100:GLN:OE1	1:F:100:GLN:N	2.46	0.42
1:D:100:GLN:OE1	1:D:100:GLN:N	2.42	0.42
1:E:100:GLN:HB3	1:E:105:GLN:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:70:PHE:CE1	1:E:89:TRP:HB3	2.55	0.42
1:F:186:GLU:HB3	1:H:196:LEU:HD11	2.02	0.42
1:H:21:ALA:HB2	1:H:131:ILE:HB	2.02	0.42
1:B:150:SER:HB3	1:B:153:VAL:HG23	2.01	0.42
1:B:128:THR:HB	1:B:171:PHE:HD2	1.85	0.41
1:E:213:LEU:HD22	1:G:166:LEU:HD23	2.01	0.41
1:D:21:ALA:HB2	1:D:131:ILE:HB	2.02	0.41
1:C:128:THR:HB	1:C:171:PHE:CD2	2.56	0.41
1:F:128:THR:HB	1:F:171:PHE:CD2	2.56	0.41
1:H:62:TYR:HB2	1:H:64:PHE:CZ	2.55	0.41
1:B:120:ARG:HH11	1:B:128:THR:HG21	1.86	0.41
1:D:23:SER:O	1:D:139:LEU:HD22	2.21	0.40
1:E:98:GLU:HB2	1:E:99:PRO:HD3	2.03	0.40
1:A:196:LEU:HD11	1:C:186:GLU:HB3	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	201/229 (88%)	198 (98%)	3 (2%)	0	100	100
1	B	195/229 (85%)	193 (99%)	2 (1%)	0	100	100
1	C	194/229 (85%)	191 (98%)	3 (2%)	0	100	100
1	D	205/229 (90%)	203 (99%)	2 (1%)	0	100	100
1	E	201/229 (88%)	198 (98%)	3 (2%)	0	100	100
1	F	194/229 (85%)	192 (99%)	2 (1%)	0	100	100
1	G	194/229 (85%)	191 (98%)	3 (2%)	0	100	100
1	H	205/229 (90%)	203 (99%)	2 (1%)	0	100	100
All	All	1589/1832 (87%)	1569 (99%)	20 (1%)	0	100	100



There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	158/183 (86%)	157 (99%)	1 (1%)	86	94
1	B	139/183 (76%)	139 (100%)	0	100	100
1	C	141/183 (77%)	140 (99%)	1 (1%)	84	92
1	D	154/183 (84%)	152 (99%)	2 (1%)	69	84
1	E	157/183 (86%)	157 (100%)	0	100	100
1	F	138/183 (75%)	138 (100%)	0	100	100
1	G	139/183 (76%)	139 (100%)	0	100	100
1	H	154/183 (84%)	153 (99%)	1 (1%)	86	94
All	All	1180/1464 (81%)	1175 (100%)	5 (0%)	91	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	LYS
1	C	112	ASP
1	D	112	ASP
1	D	157	ARG
1	H	112	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	GLN
1	E	117	GLN
1	F	105	GLN
1	H	140	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

12 ligands 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
5	AGS	D	302	-	26,33,33	0.80	1 (3%)	26,52,52	0.89	2 (7%)
3	ADP	A	302	-	24,29,29	0.67	0	29,45,45	0.70	1 (3%)
4	GDP	C	301	-	24,30,30	0.86	0	30,47,47	0.77	0
3	ADP	E	302	-	24,29,29	0.70	0	29,45,45	0.71	1 (3%)
2	5GP	H	301	-	22,26,26	0.68	0	26,40,40	0.87	0
4	GDP	G	301	-	24,30,30	0.86	0	30,47,47	0.75	0
2	5GP	A	301	-	22,26,26	0.97	3 (13%)	26,40,40	0.82	1 (3%)
5	AGS	H	302	-	26,33,33	0.82	1 (3%)	26,52,52	0.87	2 (7%)
2	5GP	F	301	-	22,26,26	0.83	1 (4%)	26,40,40	0.79	0
2	5GP	D	301	-	22,26,26	0.65	0	26,40,40	0.88	1 (3%)
2	5GP	E	301	-	22,26,26	0.86	2 (9%)	26,40,40	0.71	0
2	5GP	B	301	-	22,26,26	0.91	1 (4%)	26,40,40	0.88	1 (3%)

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
5	AGS	D	302	-	-	3/17/38/38	0/3/3/3
3	ADP	A	302	-	-	7/12/32/32	0/3/3/3
4	GDP	C	301	-	-	3/12/32/32	0/3/3/3
3	ADP	E	302	-	-	7/12/32/32	0/3/3/3
2	5GP	H	301	-	-	0/6/26/26	0/3/3/3
4	GDP	G	301	-	-	5/12/32/32	0/3/3/3
2	5GP	A	301	-	-	0/6/26/26	0/3/3/3
5	AGS	H	302	-	-	3/17/38/38	0/3/3/3
2	5GP	F	301	-	-	0/6/26/26	0/3/3/3
2	5GP	D	301	-	-	0/6/26/26	0/3/3/3
2	5GP	E	301	-	-	0/6/26/26	0/3/3/3
2	5GP	B	301	-	-	0/6/26/26	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	302	AGS	PG-S1G	2.71	1.96	1.90
5	D	302	AGS	PG-S1G	2.64	1.96	1.90
2	A	301	5GP	C8-N7	-2.32	1.31	1.35
2	E	301	5GP	C8-N7	-2.29	1.31	1.35
2	A	301	5GP	C5-C4	-2.17	1.37	1.43
2	B	301	5GP	C5-C4	-2.17	1.37	1.43
2	E	301	5GP	C5-C4	-2.16	1.37	1.43
2	F	301	5GP	C5-C4	-2.15	1.37	1.43
2	A	301	5GP	C5-C6	-2.05	1.43	1.47

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	5GP	O3P-P-O2P	2.67	117.83	107.64
2	B	301	5GP	O3P-P-O2P	2.66	117.82	107.64
3	E	302	ADP	C5-C6-N6	2.37	123.95	120.35
3	A	302	ADP	C5-C6-N6	2.34	123.92	120.35
5	H	302	AGS	C5-C6-N6	2.29	123.83	120.35
5	D	302	AGS	C5-C6-N6	2.28	123.82	120.35
5	D	302	AGS	PA-O3A-PB	-2.12	125.57	132.83
5	H	302	AGS	O3G-PG-O3B	2.02	111.37	104.64
2	D	301	5GP	O2P-P-O1P	2.01	118.56	110.68

There are no chirality outliers.

All (28) torsion outliers are listed below:

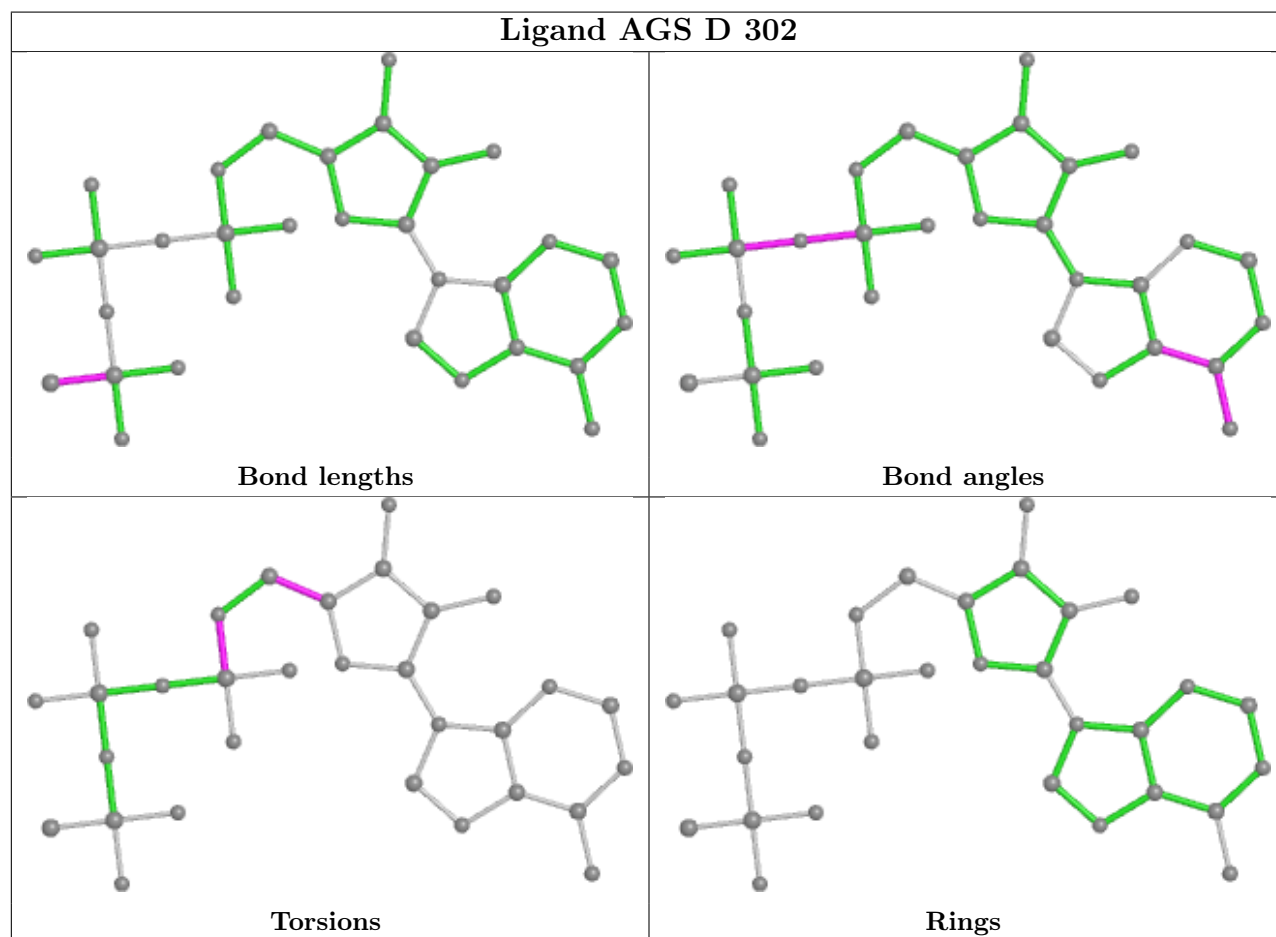
Mol	Chain	Res	Type	Atoms
3	A	302	ADP	PA-O3A-PB-O2B
3	A	302	ADP	C5'-O5'-PA-O2A
3	A	302	ADP	C5'-O5'-PA-O3A
3	A	302	ADP	O4'-C4'-C5'-O5'
3	E	302	ADP	PA-O3A-PB-O2B
3	E	302	ADP	C5'-O5'-PA-O2A
3	E	302	ADP	C5'-O5'-PA-O3A
3	E	302	ADP	O4'-C4'-C5'-O5'
4	C	301	GDP	C5'-O5'-PA-O1A
4	G	301	GDP	C5'-O5'-PA-O3A
4	G	301	GDP	C5'-O5'-PA-O1A
5	D	302	AGS	C5'-O5'-PA-O3A
5	H	302	AGS	PB-O3B-PG-O3G
3	A	302	ADP	C3'-C4'-C5'-O5'
3	E	302	ADP	C3'-C4'-C5'-O5'
5	D	302	AGS	O4'-C4'-C5'-O5'
4	G	301	GDP	PB-O3A-PA-O1A
4	C	301	GDP	C5'-O5'-PA-O3A
5	H	302	AGS	C5'-O5'-PA-O3A
5	D	302	AGS	C3'-C4'-C5'-O5'
3	A	302	ADP	C5'-O5'-PA-O1A
3	E	302	ADP	C5'-O5'-PA-O1A
4	G	301	GDP	C5'-O5'-PA-O2A
4	C	301	GDP	PB-O3A-PA-O1A
3	A	302	ADP	PA-O3A-PB-O1B
3	E	302	ADP	PA-O3A-PB-O1B
5	H	302	AGS	O4'-C4'-C5'-O5'
4	G	301	GDP	PB-O3A-PA-O2A

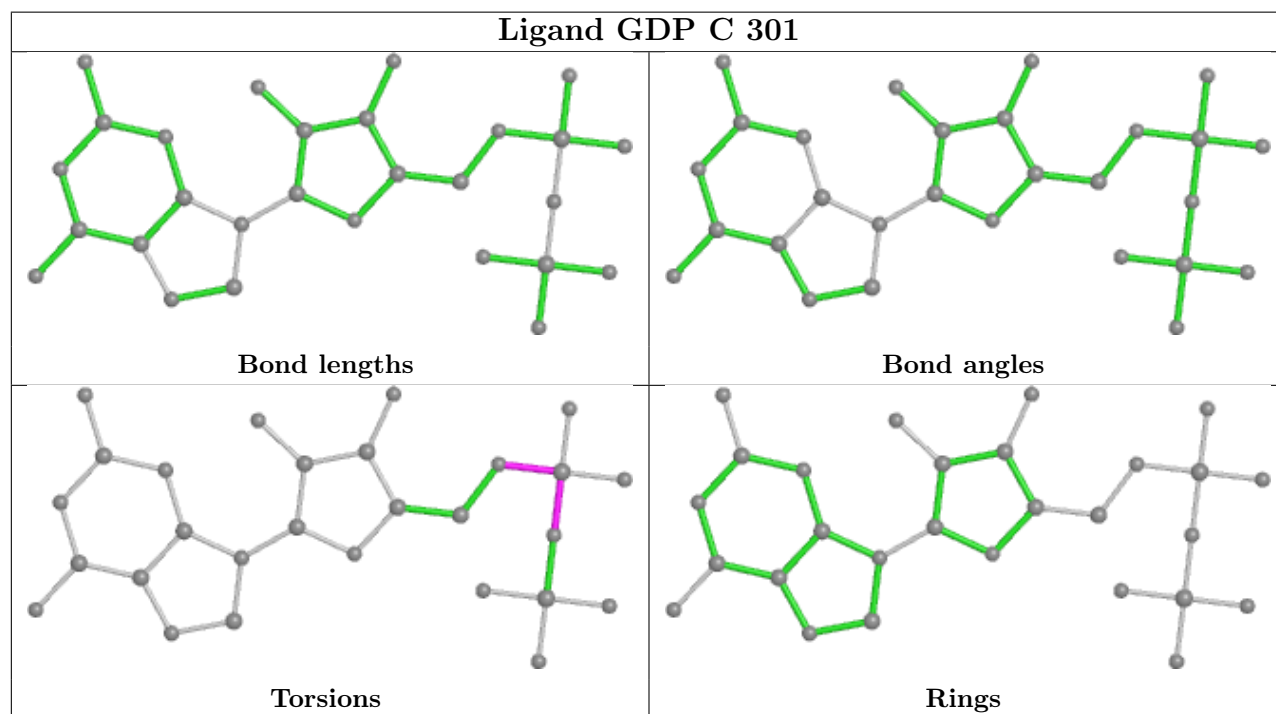
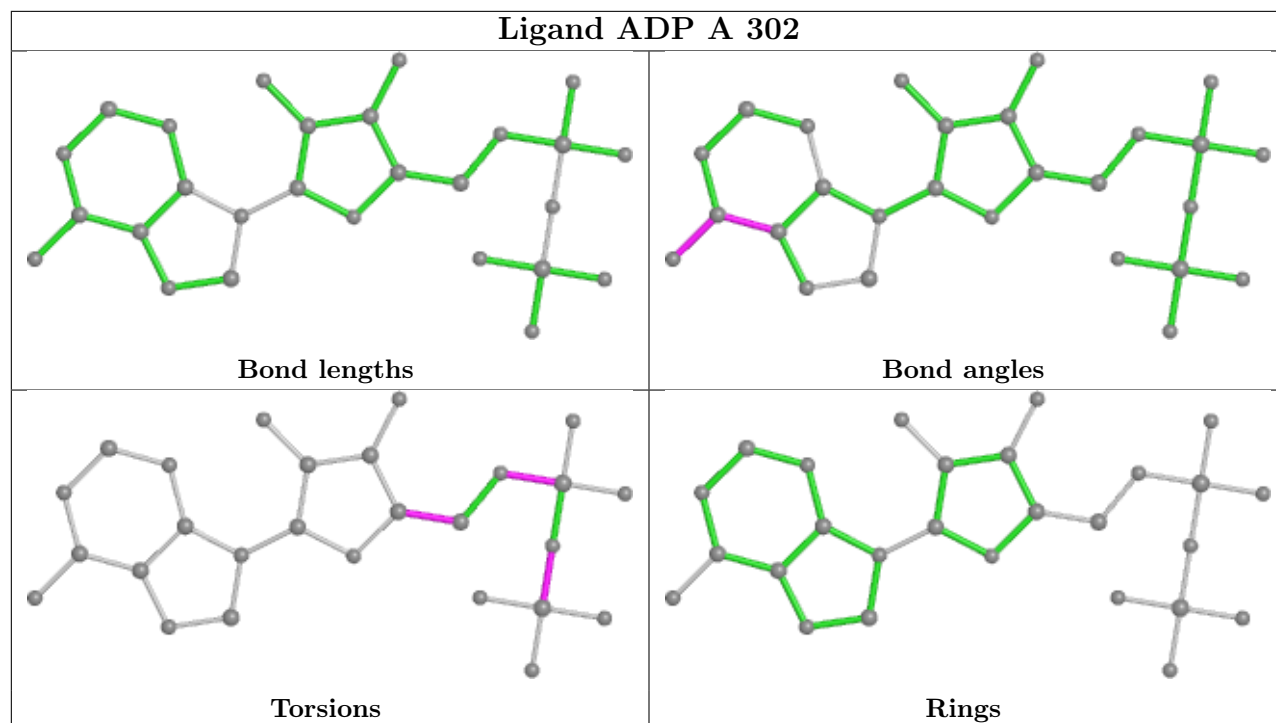
There are no ring outliers.

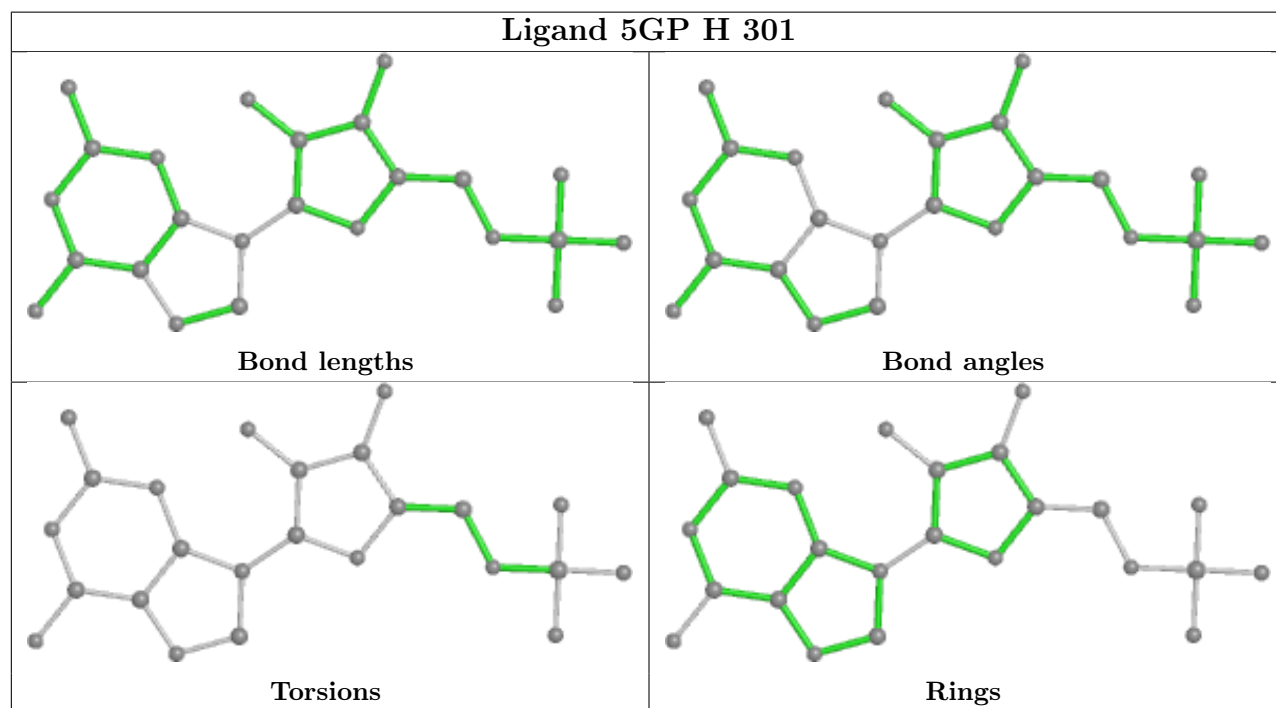
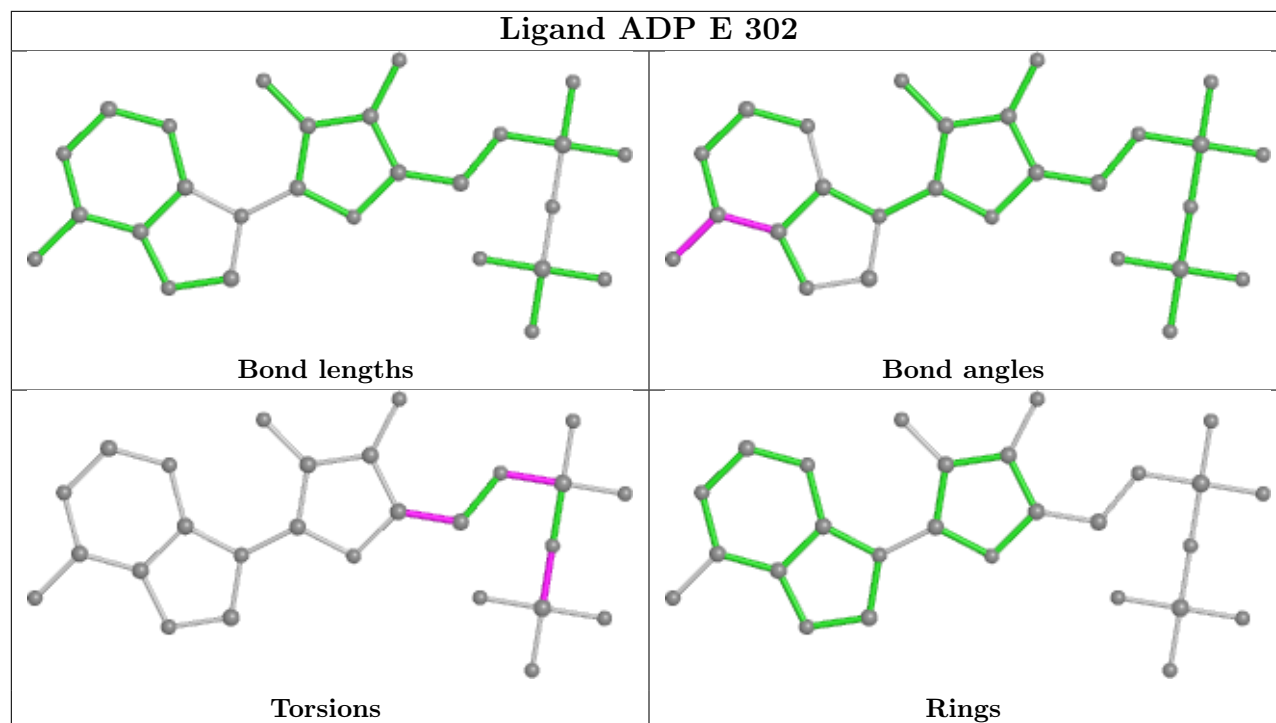
7 monomers are involved in 7 short contacts:

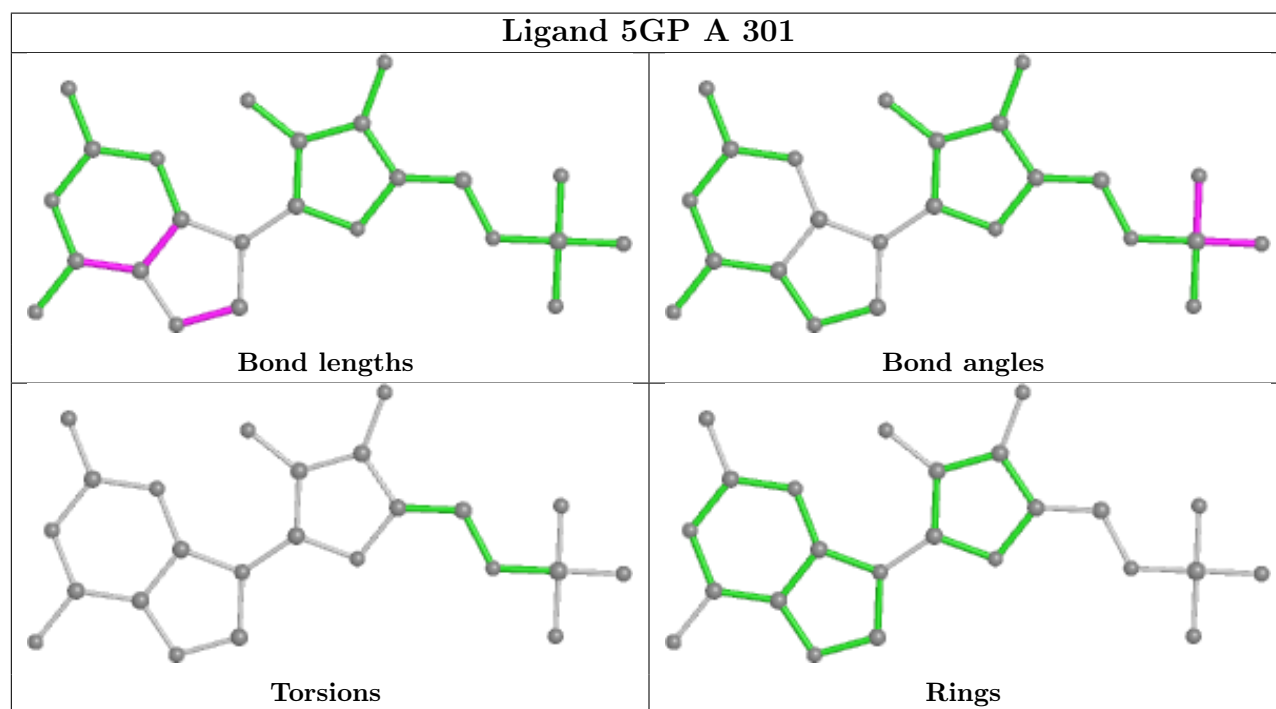
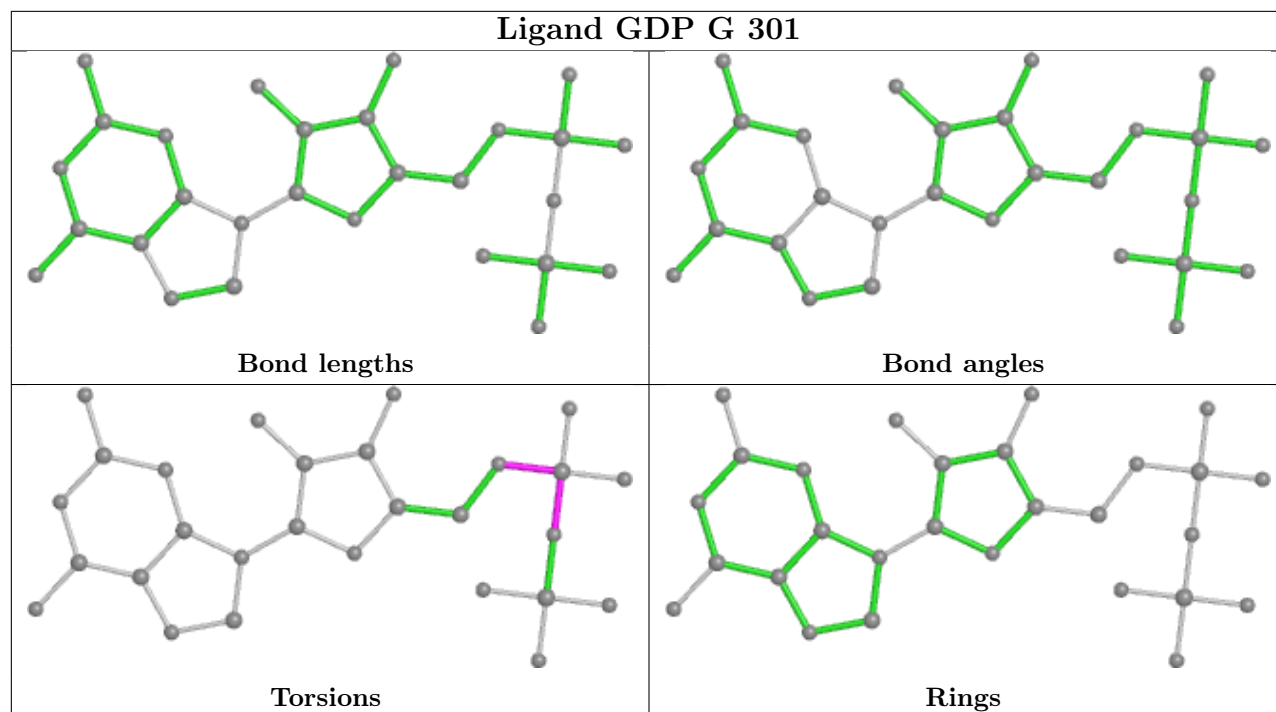
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	ADP	1	0
3	E	302	ADP	1	0
4	G	301	GDP	1	0
2	A	301	5GP	1	0
2	F	301	5GP	1	0
2	E	301	5GP	1	0
2	B	301	5GP	1	0

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.

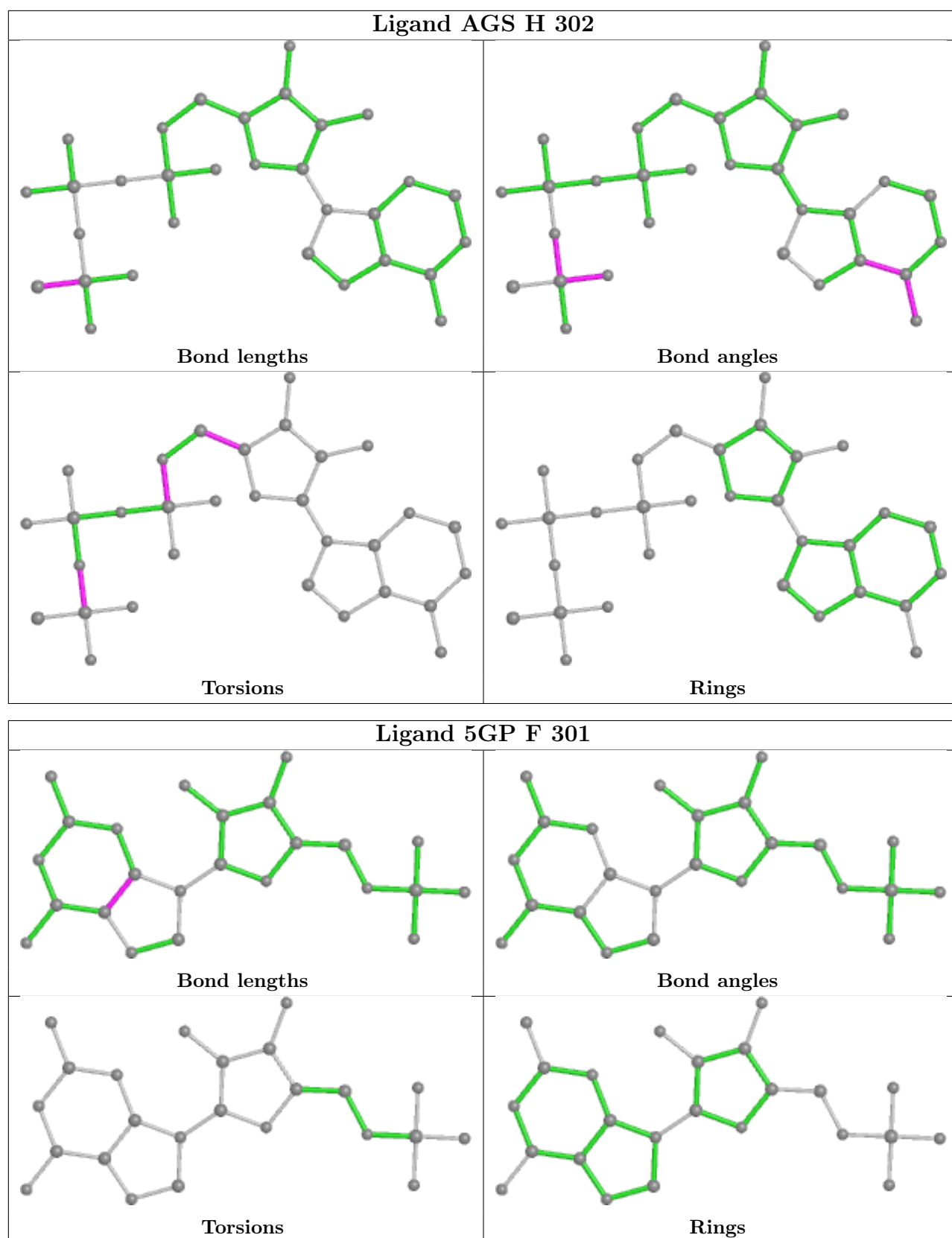


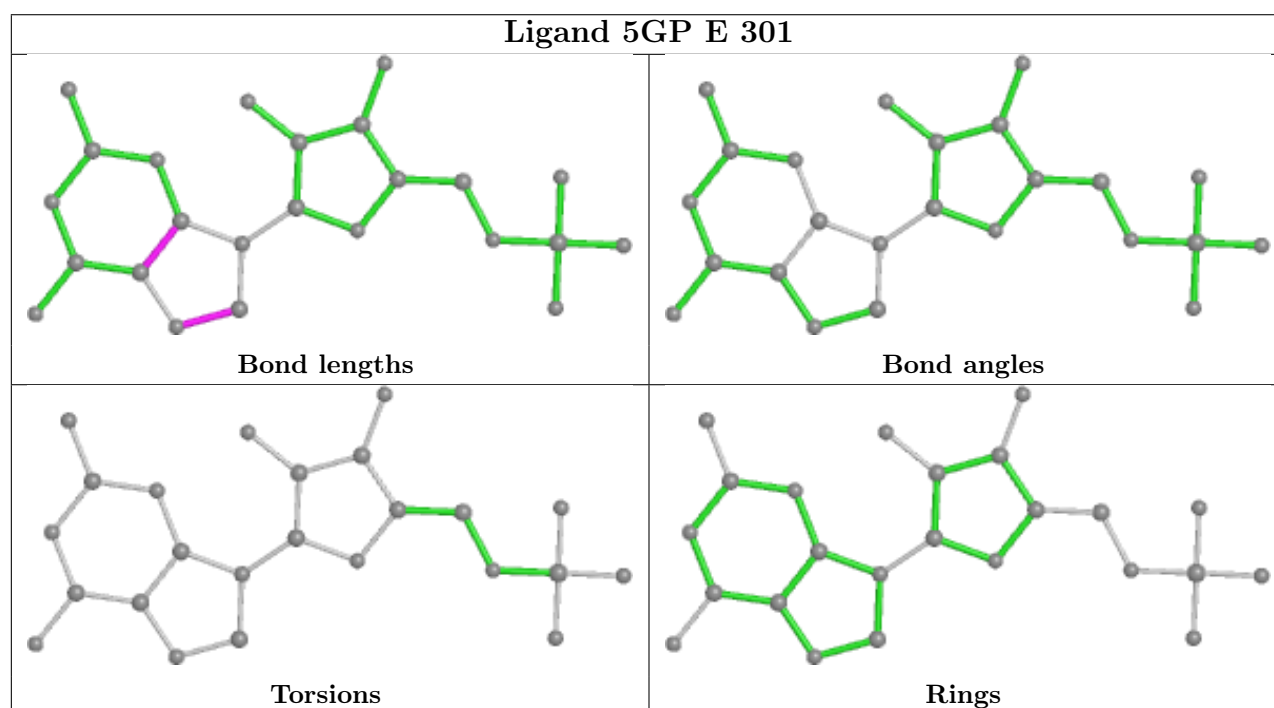
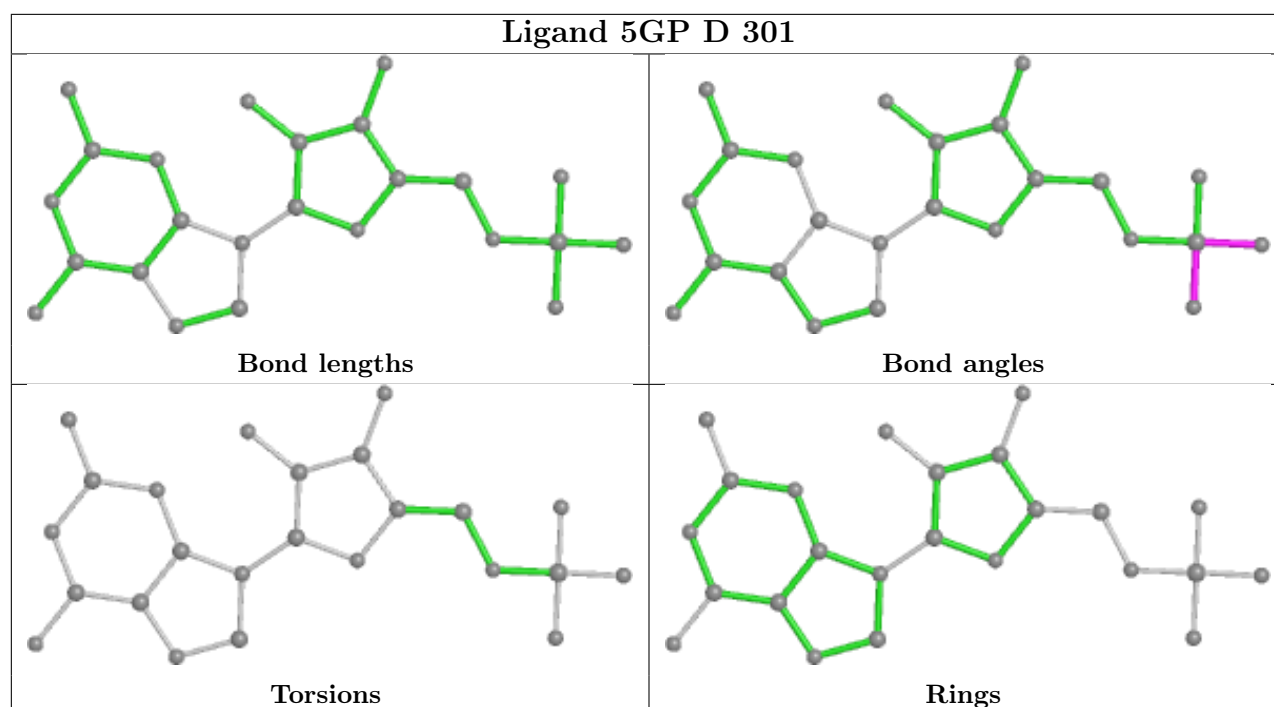


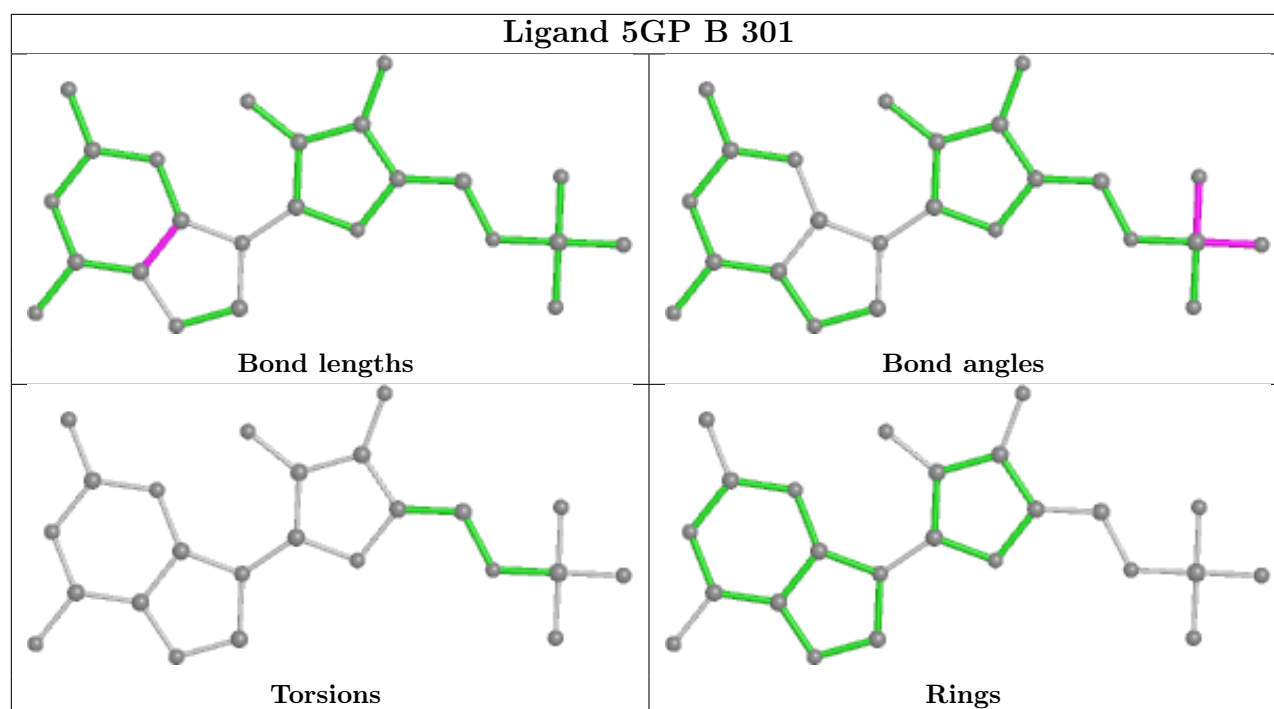












## 5.7 Other polymers [i](#)

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	203/229 (88%)	-0.15	1 (0%) 91 89	34, 47, 75, 96	0
1	B	198/229 (86%)	-0.11	6 (3%) 50 49	39, 59, 92, 117	0
1	C	198/229 (86%)	0.12	10 (5%) 28 26	36, 53, 96, 123	0
1	D	207/229 (90%)	-0.03	2 (0%) 82 80	35, 47, 64, 81	0
1	E	203/229 (88%)	-0.23	0 100 100	35, 47, 78, 98	0
1	F	198/229 (86%)	-0.11	6 (3%) 50 49	39, 60, 91, 118	0
1	G	198/229 (86%)	0.12	10 (5%) 28 26	37, 51, 95, 120	0
1	H	207/229 (90%)	-0.00	2 (0%) 82 80	39, 47, 62, 76	0
All	All	1612/1832 (87%)	-0.05	37 (2%) 60 58	34, 51, 84, 123	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	152	ALA	4.3
1	C	140	GLN	4.0
1	C	139	LEU	3.9
1	B	11	VAL	3.8
1	B	152	ALA	3.5
1	H	13	ARG	3.4
1	G	139	LEU	3.1
1	F	11	VAL	3.1
1	G	140	GLN	3.0
1	C	13	ARG	3.0
1	B	36	ALA	3.0
1	G	152	ALA	2.9
1	F	45	ILE	2.9
1	C	155	ALA	2.8
1	G	155	ALA	2.6
1	B	153	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	45	ILE	2.5
1	C	136	LYS	2.5
1	H	94	ARG	2.5
1	G	160	ALA	2.4
1	C	102	ALA	2.4
1	G	102	ALA	2.4
1	C	152	ALA	2.3
1	F	140	GLN	2.3
1	G	153	VAL	2.3
1	F	36	ALA	2.3
1	G	142	ARG	2.2
1	F	153	VAL	2.2
1	D	181	ASP	2.2
1	G	158	LEU	2.2
1	G	179	VAL	2.2
1	D	94	ARG	2.2
1	C	100	GLN	2.1
1	C	142	ARG	2.1
1	C	158	LEU	2.1
1	B	150	SER	2.1
1	A	206	ALA	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

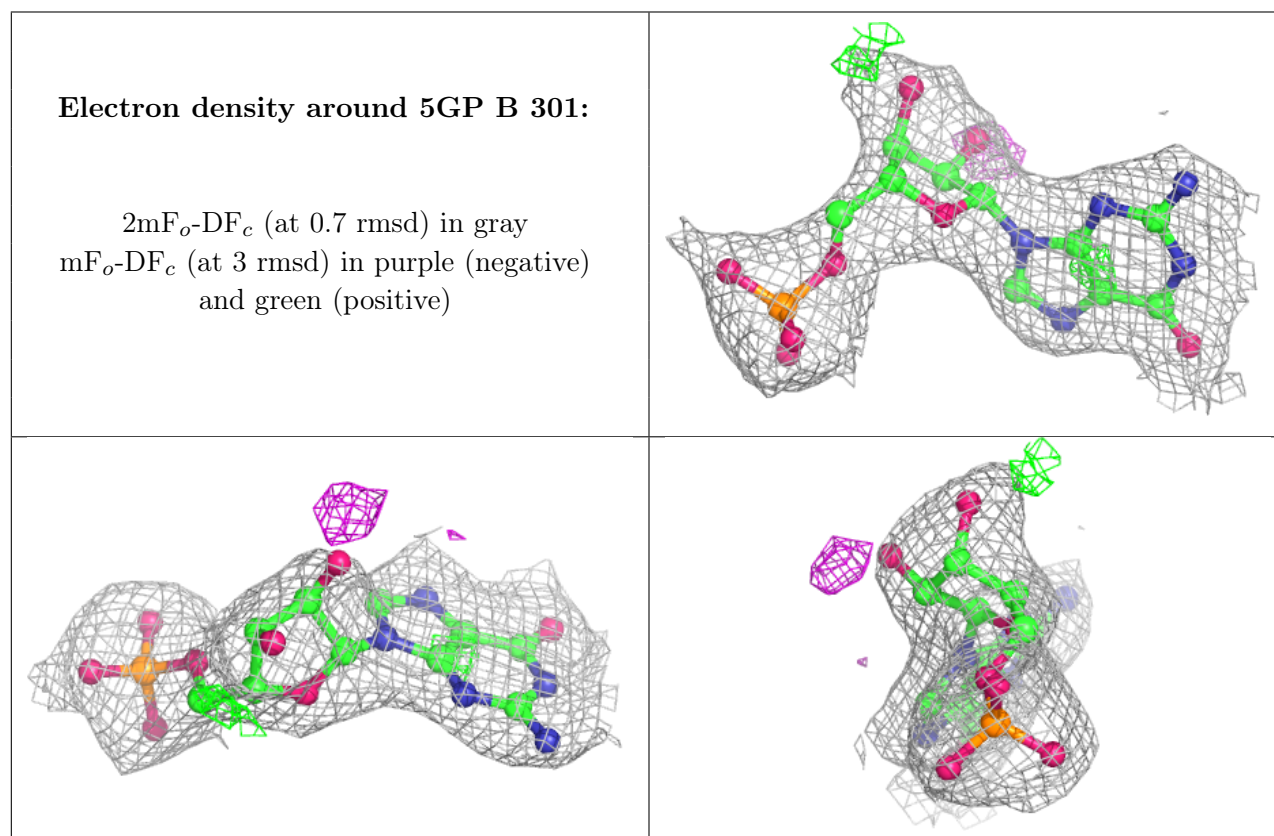
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	5GP	B	301	24/24	0.93	0.16	45,48,62,64	0
2	5GP	F	301	24/24	0.93	0.17	46,50,64,65	0

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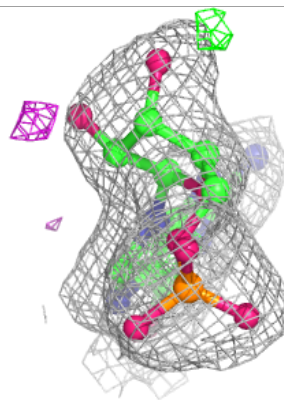
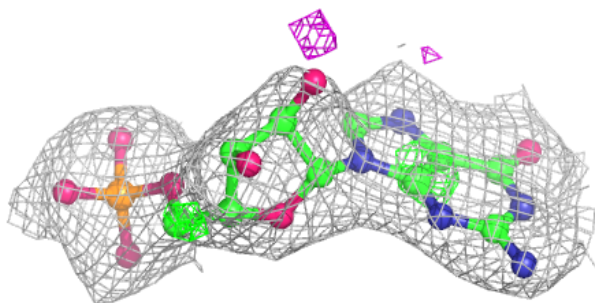
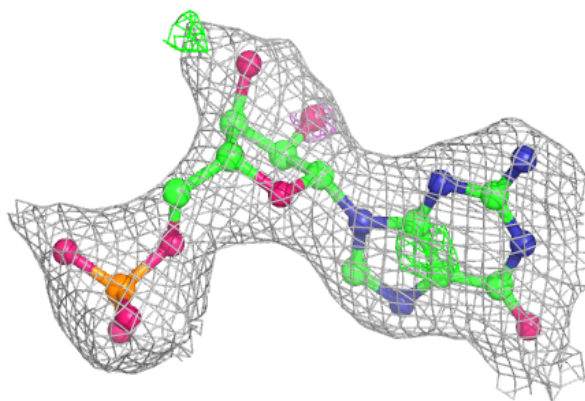
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GDP	C	301	28/28	0.93	0.12	37,48,58,62	0
4	GDP	G	301	28/28	0.94	0.12	36,47,57,62	0
5	AGS	D	302	31/31	0.94	0.14	47,50,62,67	0
5	AGS	H	302	31/31	0.94	0.14	48,50,58,67	0
2	5GP	D	301	24/24	0.95	0.18	37,40,43,50	0
2	5GP	H	301	24/24	0.95	0.19	39,42,46,53	0
3	ADP	A	302	27/27	0.95	0.14	49,53,57,62	0
3	ADP	E	302	27/27	0.95	0.14	49,52,58,63	0
2	5GP	A	301	24/24	0.96	0.12	38,41,53,54	0
2	5GP	E	301	24/24	0.96	0.13	35,40,52,53	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.

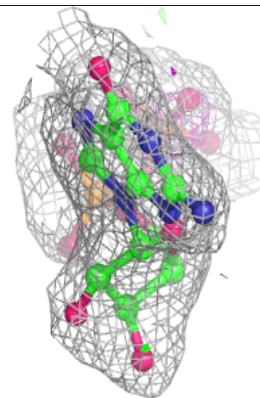
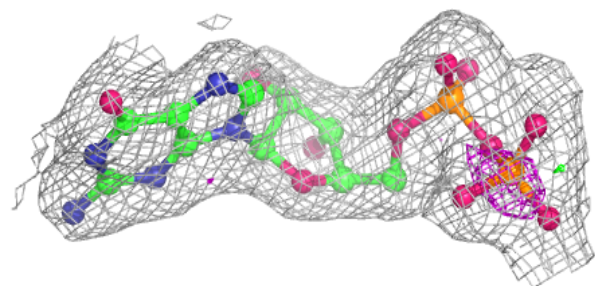
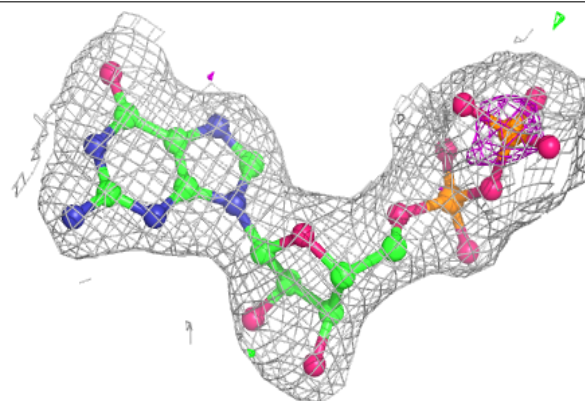


**Electron density around 5GP F 301:**

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

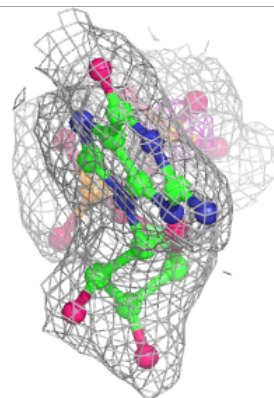
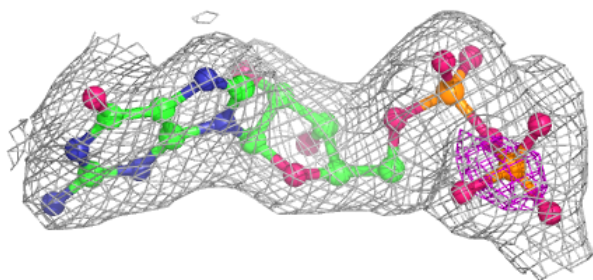
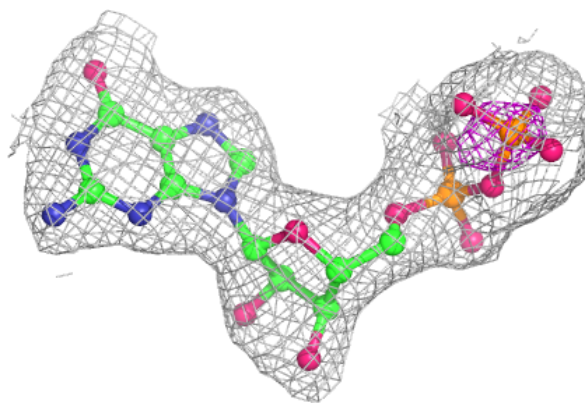
**Electron density around GDP C 301:**

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

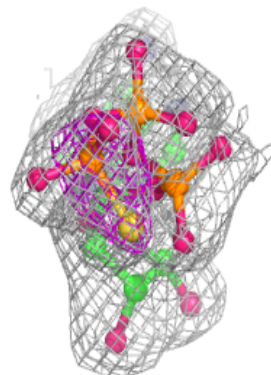
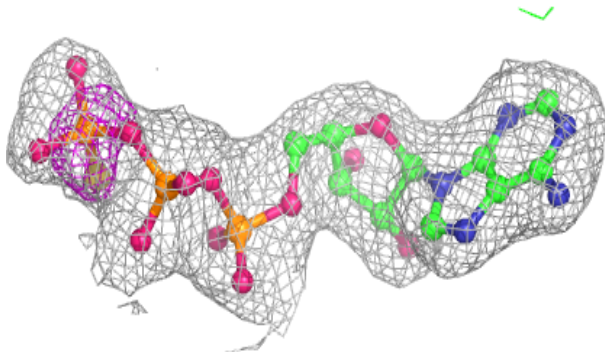
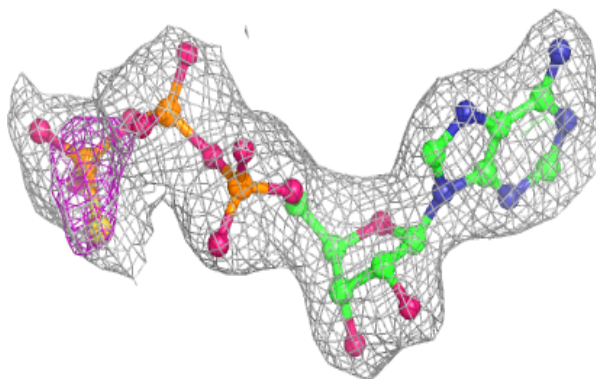


**Electron density around GDP G 301:**

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

**Electron density around AGS D 302:**

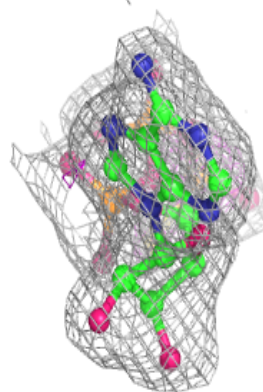
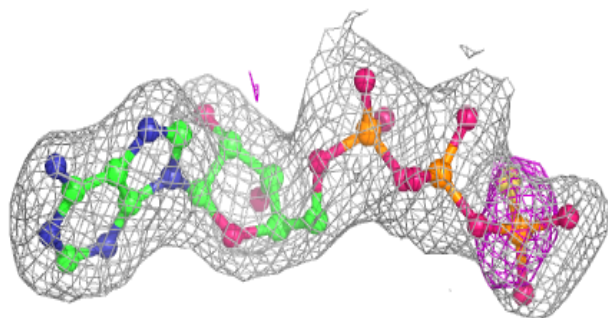
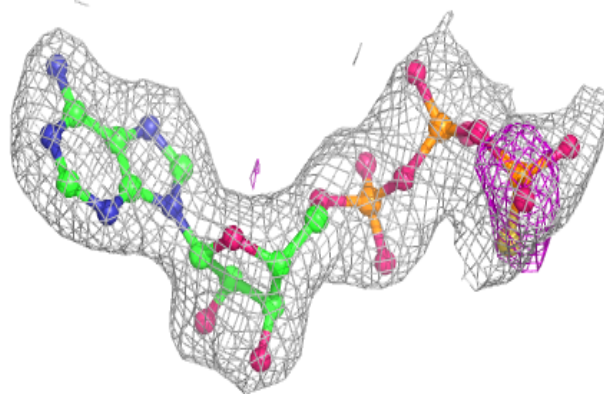
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



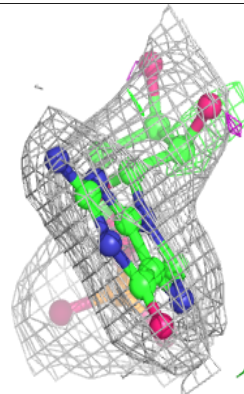
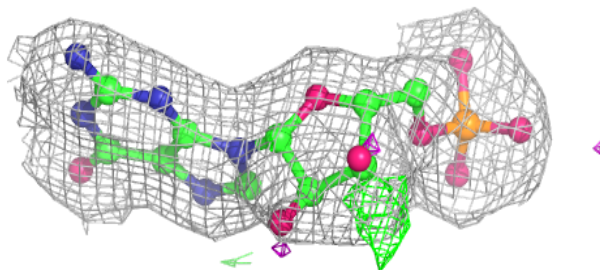
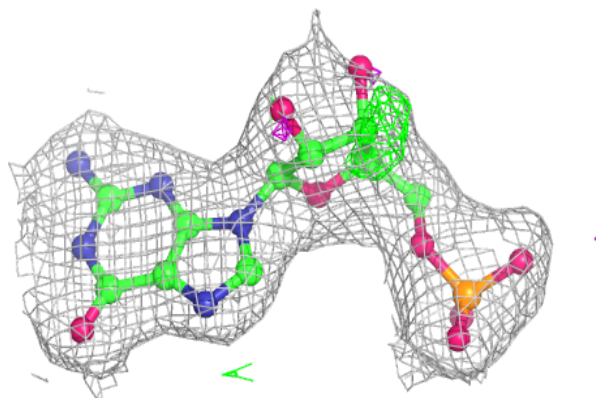


**Electron density around AGS H 302:**

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

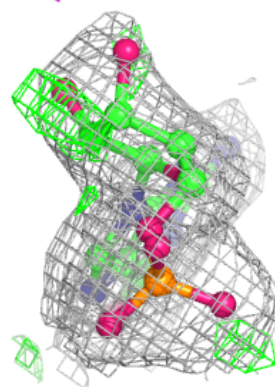
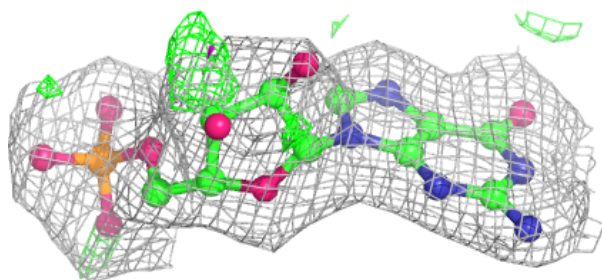
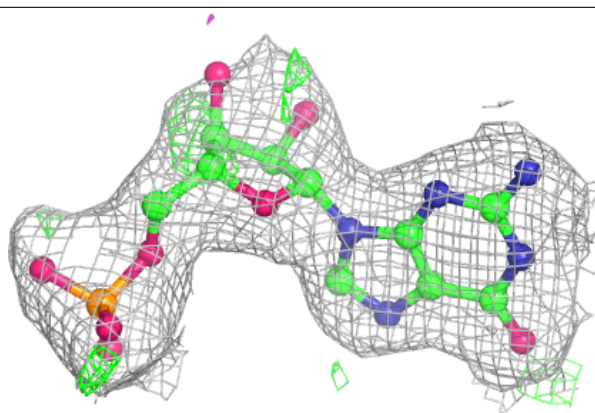
**Electron density around 5GP D 301:**

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

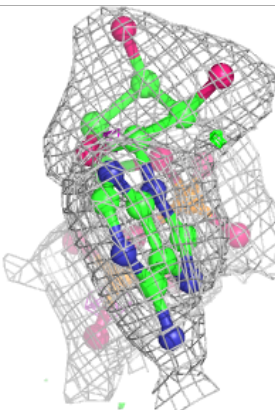
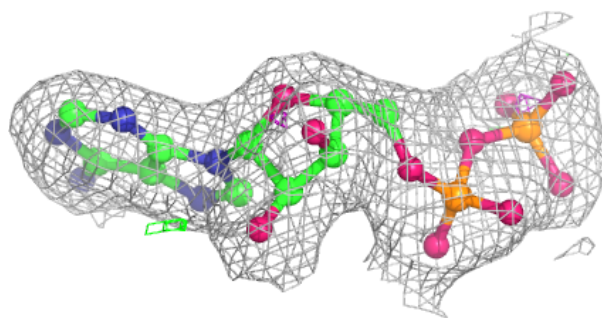
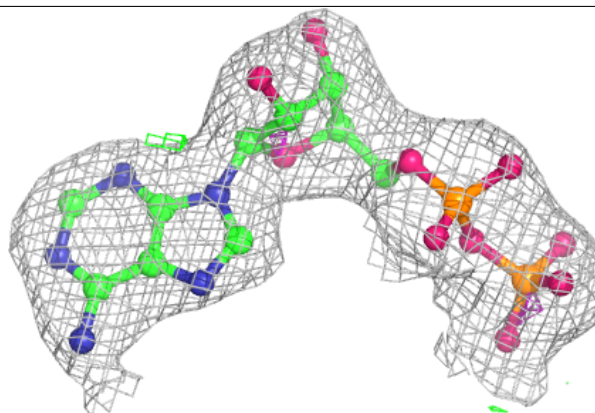


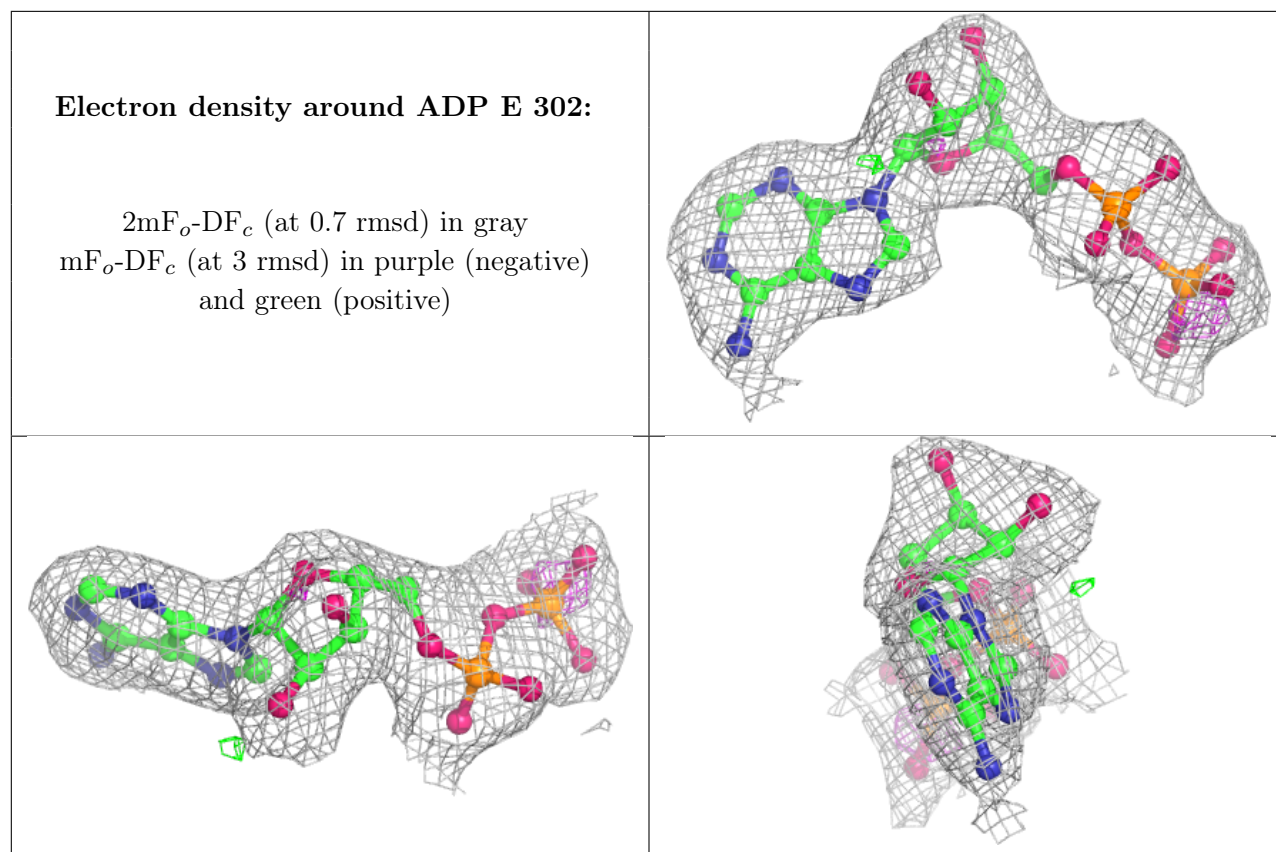
**Electron density around 5GP H 301:**

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

**Electron density around ADP A 302:**

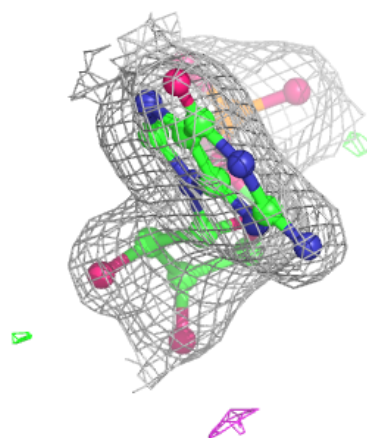
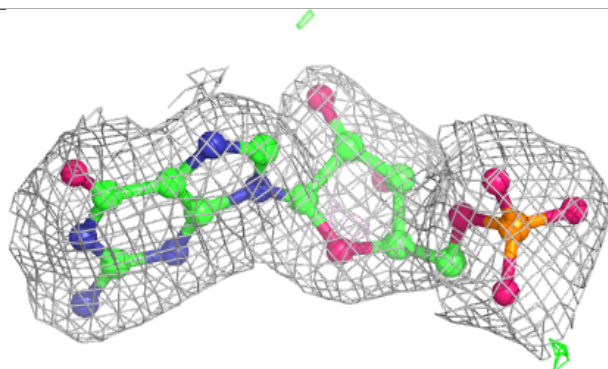
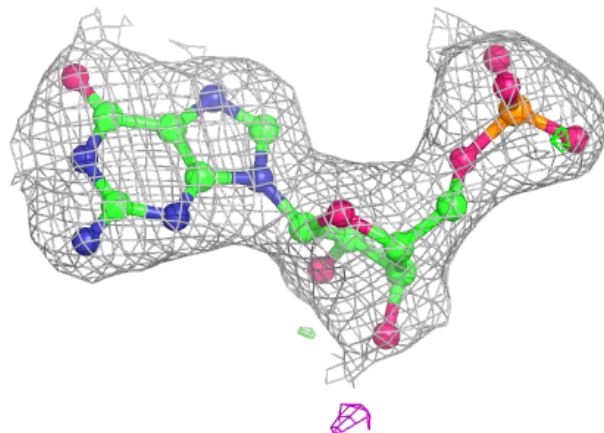
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

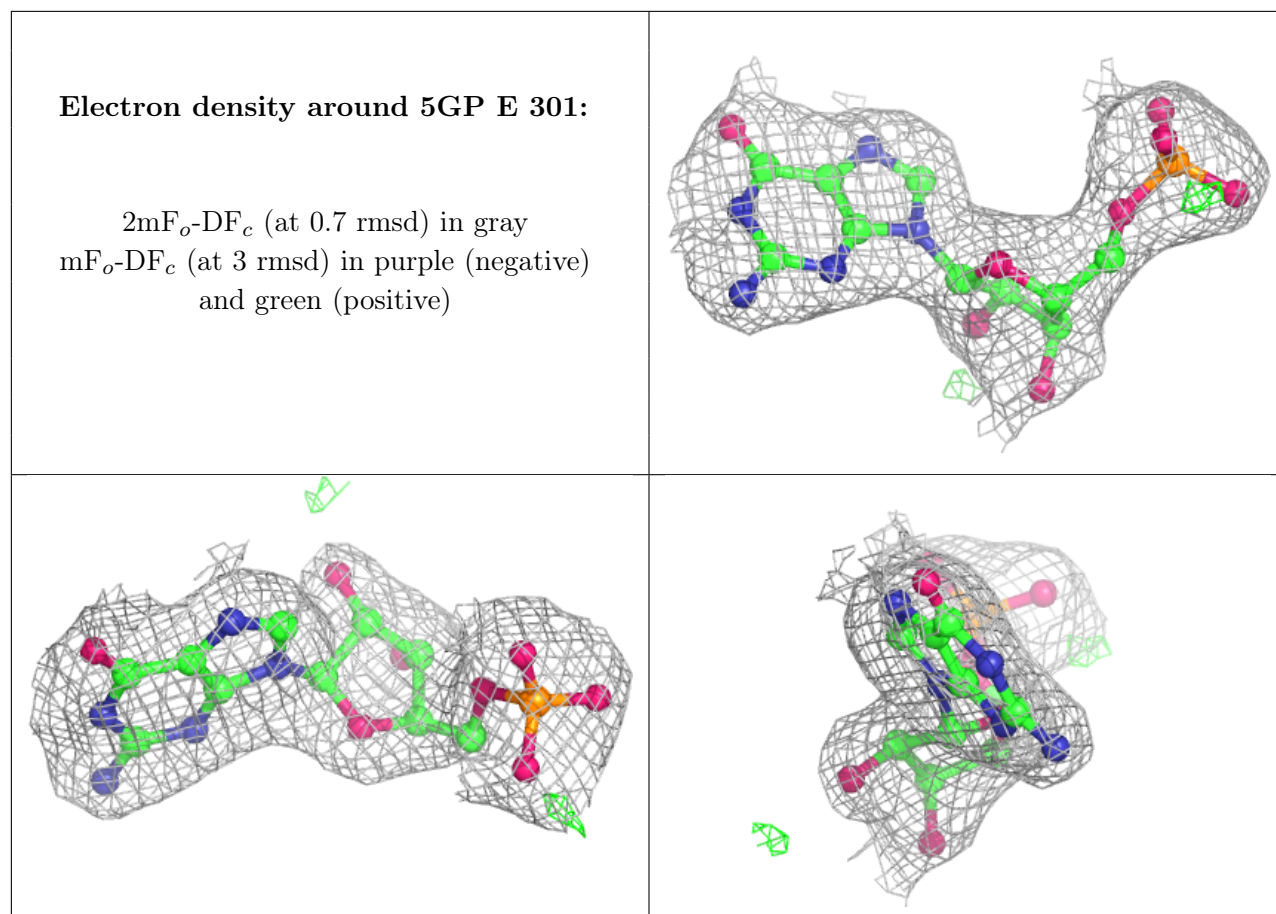




**Electron density around 5GP A 301:**

$2mF_o-DF_c$  (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.