



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 12, 2023 – 08:15 pm GMT

PDB ID : 3ZWO
Title : Crystal structure of ADP ribosyl cyclase complexed with reaction intermediate
Authors : Kotaka, M.; Graeff, R.; Zhang, L.H.; Lee, H.C.; Hao, Q.
Deposited on : 2011-08-02
Resolution : 2.00 Å(reported)

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We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

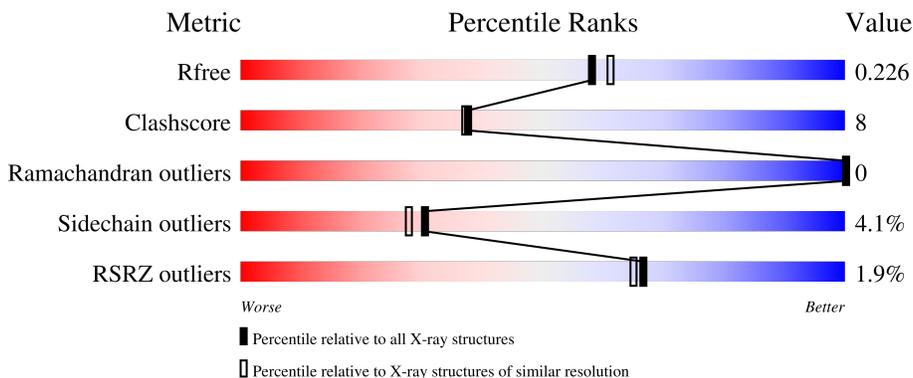
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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

Mol	Chain	Length	Quality of chain
1	A	259	 81% 13% . .
1	B	259	 86% 10% . .
1	C	259	 84% 10% . .
1	D	259	 81% 14% . .
1	E	259	 85% 11% . .

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Mol	Chain	Length	Quality of chain
1	F	259	
1	G	259	
1	H	259	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	G2Q	A	301	-	-	X	-
2	G2Q	B	301	-	-	X	-
2	G2Q	C	301	-	-	X	-
2	G2Q	E	301	-	-	X	-
2	G2Q	G	301	-	-	X	-

2 Entry composition

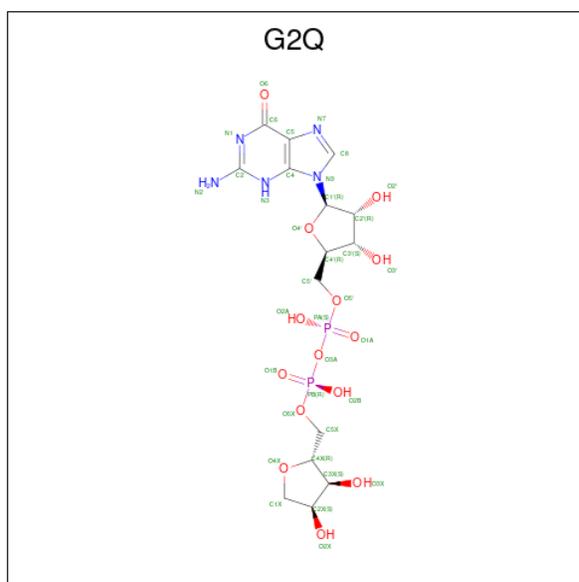
There are 4 unique types of molecules in this entry. The entry contains 17700 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ADP-RIBOSYL CYCLASE.

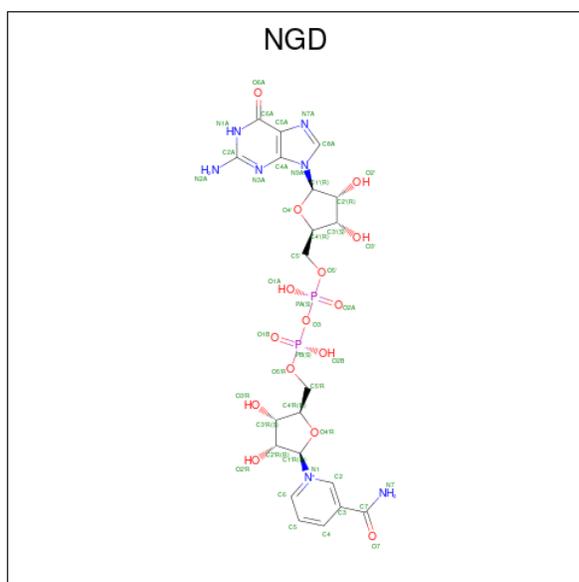
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	252	2017	1291	343	369	14	0	0	0
1	B	251	2012	1288	342	368	14	0	0	0
1	C	252	2017	1291	343	369	14	0	0	0
1	D	251	2012	1288	342	368	14	0	0	0
1	E	251	2012	1288	342	368	14	0	0	0
1	F	251	2012	1288	342	368	14	0	0	0
1	G	252	2017	1291	343	369	14	0	0	0
1	H	251	2012	1288	342	368	14	0	0	0

- Molecule 2 is GUANOSINE DIPHOSPHATE RIBOSE (three-letter code: G2Q) (formula: $C_{15}H_{23}N_5O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	B	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	C	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	E	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	G	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	H	1	Total	C	N	O	P	0	0
			36	15	5	14	2		

- Molecule 3 is 3-(AMINOCARBONYL)-1-[(2R,3R,4S,5R)-5-({[(S)-{(S)-{(2R,3S,4R,5R)-5-(2-AMINO-6-OXO-1,6-DIHYDRO-9H-PURIN-9-YL)-3,4-DIHYDROXYTETRAHYDROFURAN-2-YL]METHOXY}(HYDROXY)PHOSPHORYL]OXY}(HYDROXY)PHOSPHORYL]OXY}METHYL)-3,4-DIHYDROXYTETRAHYDROFURAN-2-YL]PYRIDINIUM (three-letter code: NGD) (formula: C₂₁H₂₈N₇O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	F	1	45	21	7	15	2	0	0

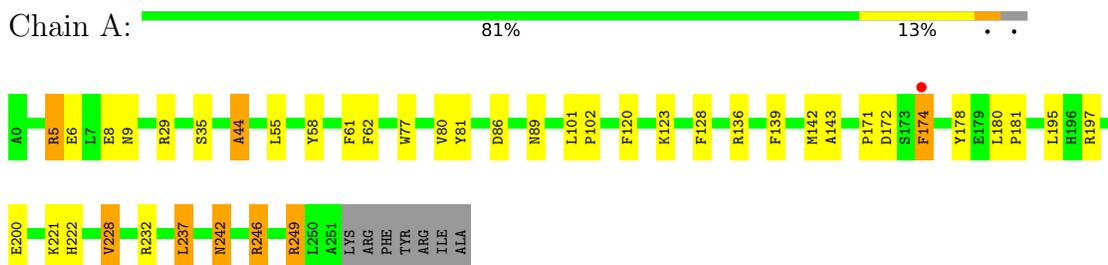
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	204	Total	O	0	0
			204	204		
4	B	194	Total	O	0	0
			194	194		
4	C	208	Total	O	0	0
			208	208		
4	D	204	Total	O	0	0
			204	204		
4	E	182	Total	O	0	0
			182	182		
4	F	138	Total	O	0	0
			138	138		
4	G	100	Total	O	0	0
			100	100		
4	H	98	Total	O	0	0
			98	98		

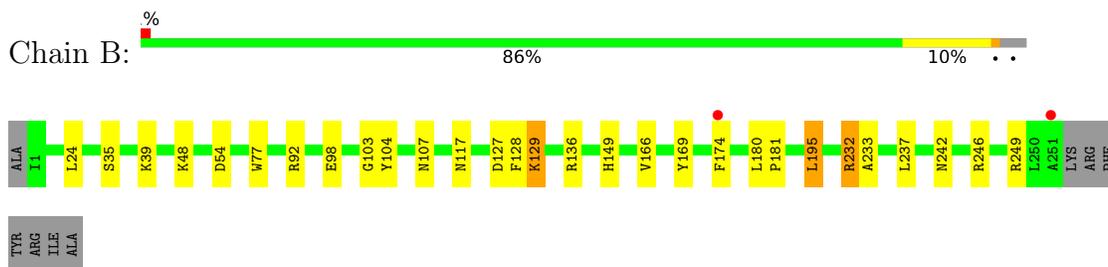
3 Residue-property plots [i](#)

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.

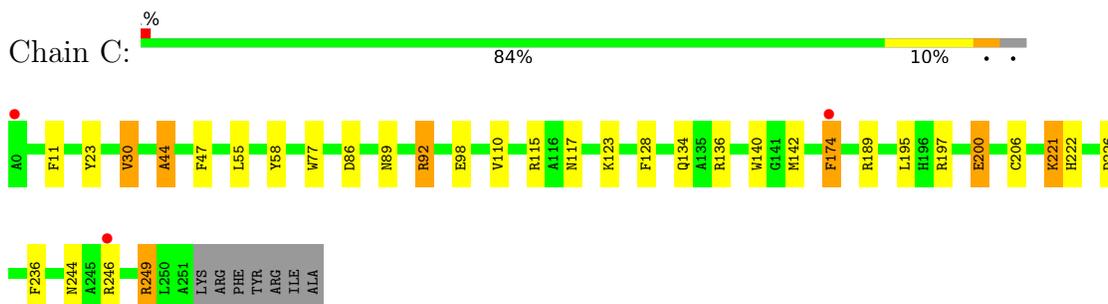
- Molecule 1: ADP-RIBOSYL CYCLASE



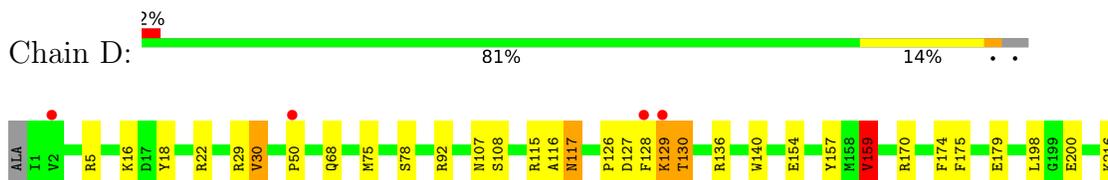
- Molecule 1: ADP-RIBOSYL CYCLASE



- Molecule 1: ADP-RIBOSYL CYCLASE

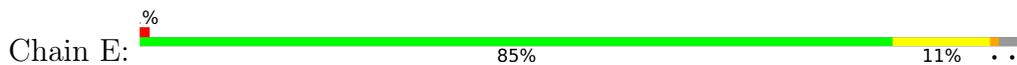


- Molecule 1: ADP-RIBOSYL CYCLASE

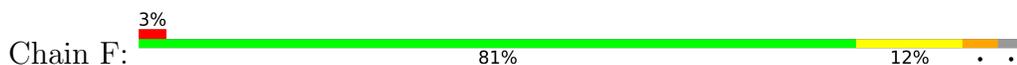




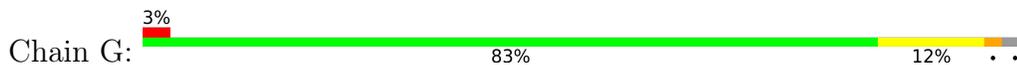
- Molecule 1: ADP-RIBOSYL CYCLASE



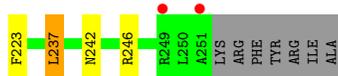
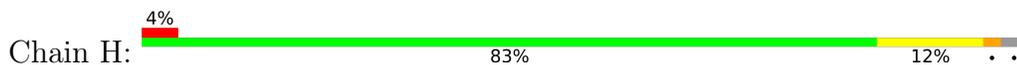
- Molecule 1: ADP-RIBOSYL CYCLASE



- Molecule 1: ADP-RIBOSYL CYCLASE



- Molecule 1: ADP-RIBOSYL CYCLASE



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.57Å 76.42Å 139.71Å 87.80° 89.09° 89.32°	Depositor
Resolution (Å)	30.00 – 2.00 29.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.1 (30.00-2.00) 83.4 (29.69-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.177 , 0.228 0.177 , 0.226	Depositor DCC
R_{free} test set	7075 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.059 for h,-k,-l 0.015 for -h,k,-l 0.004 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17700	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: G2Q, NGD

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	1.29	10/2069 (0.5%)	1.06	7/2800 (0.2%)
1	B	1.24	4/2064 (0.2%)	0.98	4/2793 (0.1%)
1	C	1.31	8/2069 (0.4%)	1.00	4/2800 (0.1%)
1	D	1.17	1/2064 (0.0%)	0.98	5/2793 (0.2%)
1	E	1.27	10/2064 (0.5%)	0.98	2/2793 (0.1%)
1	F	1.09	1/2064 (0.0%)	0.96	4/2793 (0.1%)
1	G	0.96	0/2069	0.87	4/2800 (0.1%)
1	H	0.94	0/2064	0.90	5/2793 (0.2%)
All	All	1.17	34/16527 (0.2%)	0.97	35/22365 (0.2%)

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	110	VAL	CB-CG2	8.40	1.70	1.52
1	B	166	VAL	CB-CG1	7.39	1.68	1.52
1	E	174	PHE	CE1-CZ	7.19	1.51	1.37
1	E	131	CYS	CB-SG	7.18	1.94	1.82
1	C	140	TRP	CE3-CZ3	6.95	1.50	1.38

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	172	ASP	CB-CG-OD2	-8.32	110.81	118.30
1	A	172	ASP	CB-CG-OD1	8.30	125.77	118.30
1	A	172	ASP	CB-CG-OD2	-7.59	111.47	118.30
1	H	237	LEU	CA-CB-CG	7.40	132.33	115.30
1	A	29	ARG	NE-CZ-NH1	-7.21	116.70	120.30

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	2017	0	1973	24	0
1	B	2012	0	1968	13	0
1	C	2017	0	1973	26	0
1	D	2012	0	1968	35	1
1	E	2012	0	1968	25	0
1	F	2012	0	1968	34	1
1	G	2017	0	1973	28	0
1	H	2012	0	1968	27	0
2	A	36	0	21	10	0
2	B	36	0	21	12	0
2	C	36	0	21	13	0
2	E	36	0	21	11	0
2	G	36	0	21	9	0
2	H	36	0	21	5	0
3	F	45	0	26	5	0
4	A	204	0	0	9	0
4	B	194	0	0	9	0
4	C	208	0	0	13	0
4	D	204	0	0	11	1
4	E	182	0	0	14	0
4	F	138	0	0	8	1
4	G	100	0	0	6	0
4	H	98	0	0	3	0
All	All	17700	0	15911	247	2

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

The worst 5 of 247 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)
2:C:301:G2Q:H1XA	4:C:2106:HOH:O	1.25	1.33
1:A:86:ASP:HB3	4:A:2108:HOH:O	1.26	1.30
1:C:86:ASP:HB3	4:C:2116:HOH:O	1.24	1.25
1:D:200:GLU:HG2	4:D:2168:HOH:O	1.41	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:49:ASN:HB2	1:F:115:ARG:HH22	1.05	1.13

All (2) 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:D:154:GLU:OE1	1:F:31:ARG:NH1[1_565]	1.48	0.72
4:D:2183:HOH:O	4:F:2025:HOH:O[1_565]	2.12	0.08

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	250/259 (96%)	243 (97%)	7 (3%)	0	100	100
1	B	249/259 (96%)	247 (99%)	2 (1%)	0	100	100
1	C	250/259 (96%)	241 (96%)	9 (4%)	0	100	100
1	D	249/259 (96%)	242 (97%)	7 (3%)	0	100	100
1	E	249/259 (96%)	245 (98%)	4 (2%)	0	100	100
1	F	249/259 (96%)	241 (97%)	8 (3%)	0	100	100
1	G	250/259 (96%)	243 (97%)	7 (3%)	0	100	100
1	H	249/259 (96%)	240 (96%)	9 (4%)	0	100	100
All	All	1995/2072 (96%)	1942 (97%)	53 (3%)	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	220/226 (97%)	211 (96%)	9 (4%)	30	28
1	B	220/226 (97%)	213 (97%)	7 (3%)	39	38
1	C	220/226 (97%)	213 (97%)	7 (3%)	39	38
1	D	220/226 (97%)	210 (96%)	10 (4%)	27	24
1	E	220/226 (97%)	213 (97%)	7 (3%)	39	38
1	F	220/226 (97%)	204 (93%)	16 (7%)	14	9
1	G	220/226 (97%)	212 (96%)	8 (4%)	35	34
1	H	220/226 (97%)	212 (96%)	8 (4%)	35	34
All	All	1760/1808 (97%)	1688 (96%)	72 (4%)	30	28

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	108	SER
1	H	246	ARG
1	G	136	ARG
1	H	31	ARG
1	D	92	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	117	ASN
1	F	117	ASN
1	F	89	ASN
1	G	89	ASN
1	B	242	ASN

5.3.3 RNA

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](#)

7 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
2	G2Q	G	301	-	31,39,39	1.68	7 (22%)	38,60,60	1.77	8 (21%)
2	G2Q	C	301	-	31,39,39	2.53	10 (32%)	38,60,60	1.59	11 (28%)
3	NGD	F	5573	-	42,49,49	2.09	6 (14%)	51,75,75	2.04	12 (23%)
2	G2Q	E	301	-	31,39,39	3.02	13 (41%)	38,60,60	1.95	10 (26%)
2	G2Q	A	301	-	31,39,39	2.50	13 (41%)	38,60,60	1.85	13 (34%)
2	G2Q	H	301	-	31,39,39	1.42	4 (12%)	38,60,60	1.70	6 (15%)
2	G2Q	B	301	-	31,39,39	2.82	11 (35%)	38,60,60	1.79	10 (26%)

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	G2Q	G	301	-	-	6/18/51/51	0/4/4/4
2	G2Q	C	301	-	-	7/18/51/51	0/4/4/4
3	NGD	F	5573	-	-	5/26/62/62	0/5/5/5
2	G2Q	E	301	-	-	4/18/51/51	0/4/4/4
2	G2Q	A	301	-	-	4/18/51/51	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	G2Q	H	301	-	-	9/18/51/51	0/4/4/4
2	G2Q	B	301	-	-	4/18/51/51	0/4/4/4

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	G2Q	O4'-C1'	9.89	1.54	1.41
2	A	301	G2Q	O4X-C1X	7.95	1.61	1.43
2	B	301	G2Q	O4X-C4X	7.87	1.57	1.44
2	E	301	G2Q	O4'-C1'	7.83	1.52	1.41
3	F	5573	NGD	C2-N1	7.47	1.44	1.35

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	5573	NGD	C6-N1-C2	-8.98	113.79	121.97
2	H	301	G2Q	N2-C2-N3	5.55	128.51	116.72
2	E	301	G2Q	C1X-C2X-C3X	5.09	109.39	101.63
2	G	301	G2Q	C5'-C4'-C3'	-4.78	97.28	115.18
2	B	301	G2Q	C5X-C4X-C3X	-4.55	98.11	115.18

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	301	G2Q	C5'-O5'-PA-O1A
2	G	301	G2Q	C5'-O5'-PA-O1A
2	G	301	G2Q	O4'-C4'-C5'-O5'
2	H	301	G2Q	C5'-O5'-PA-O1A
2	H	301	G2Q	C5'-O5'-PA-O2A

There are no ring outliers.

7 monomers are involved in 65 short contacts:

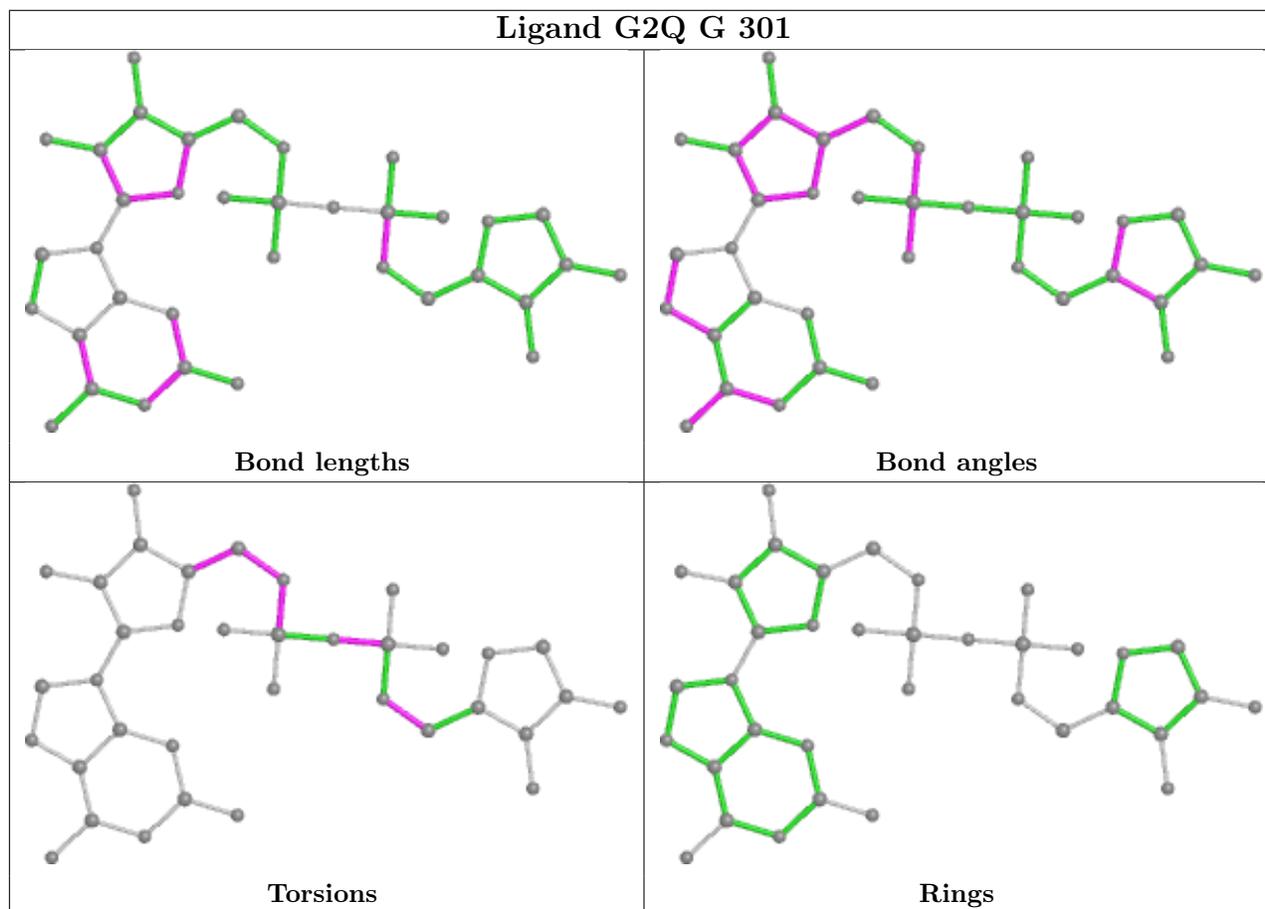
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	301	G2Q	9	0
2	C	301	G2Q	13	0
3	F	5573	NGD	5	0
2	E	301	G2Q	11	0
2	A	301	G2Q	10	0

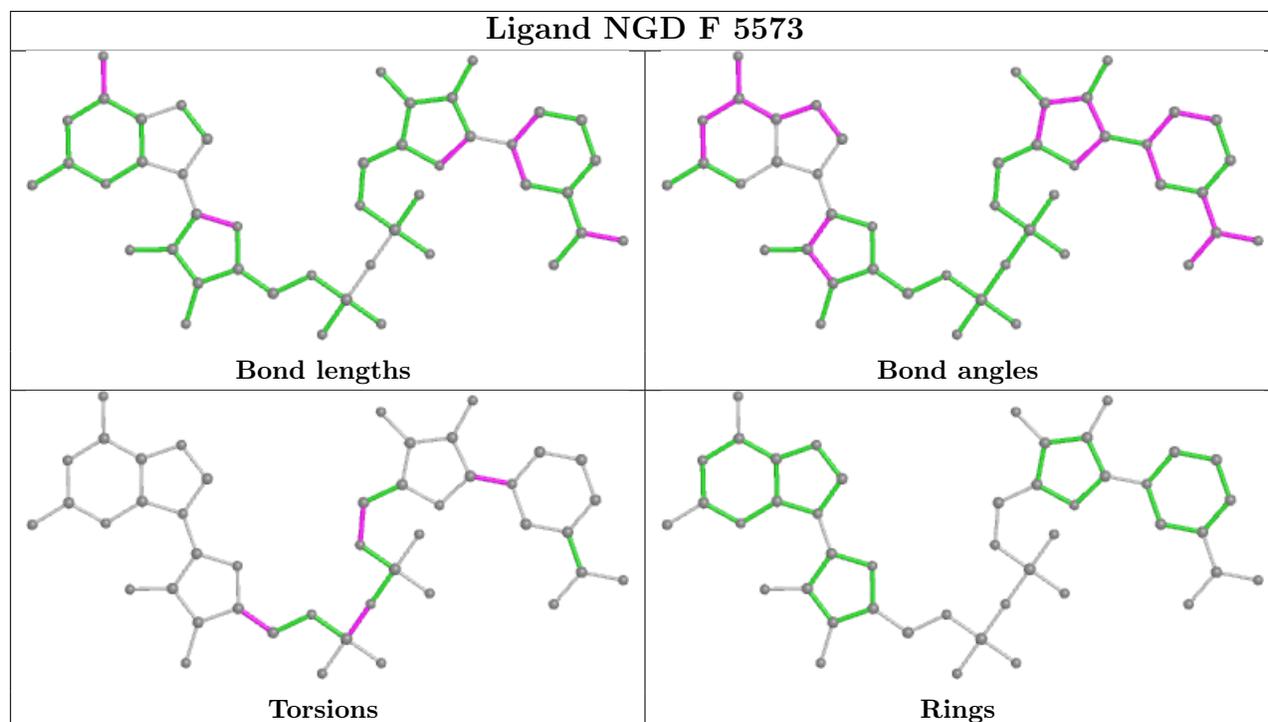
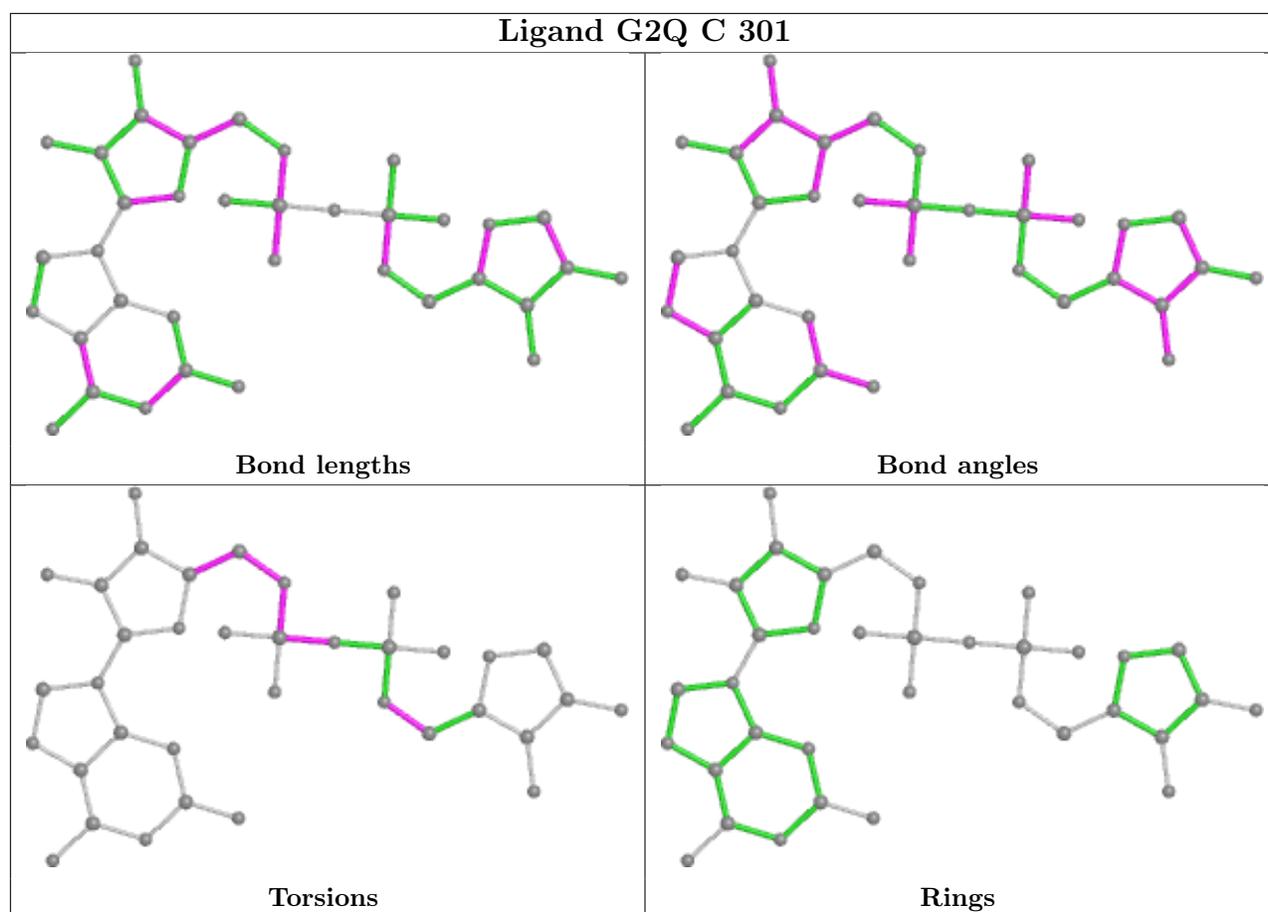
Continued on next page...

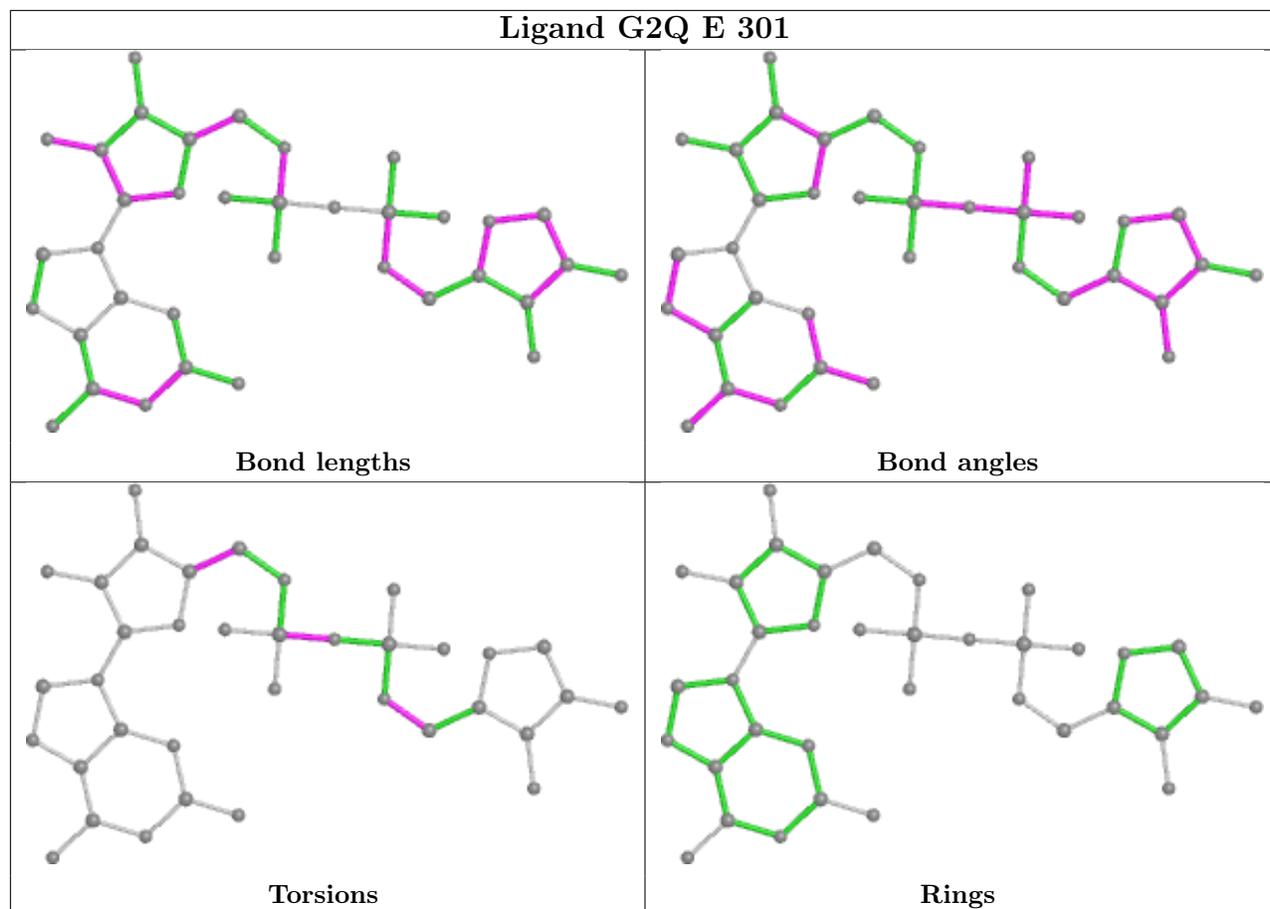
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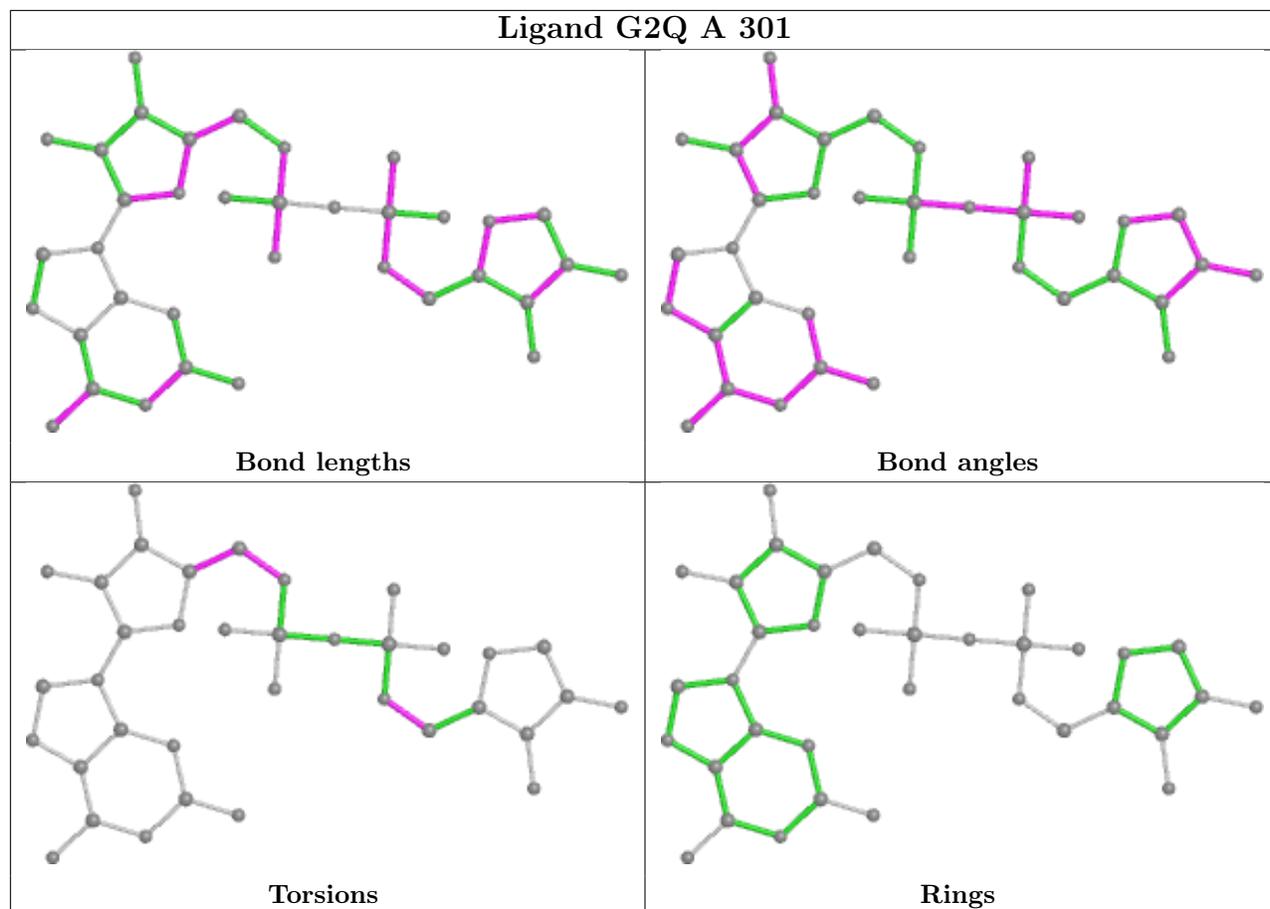
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	301	G2Q	5	0
2	B	301	G2Q	12	0

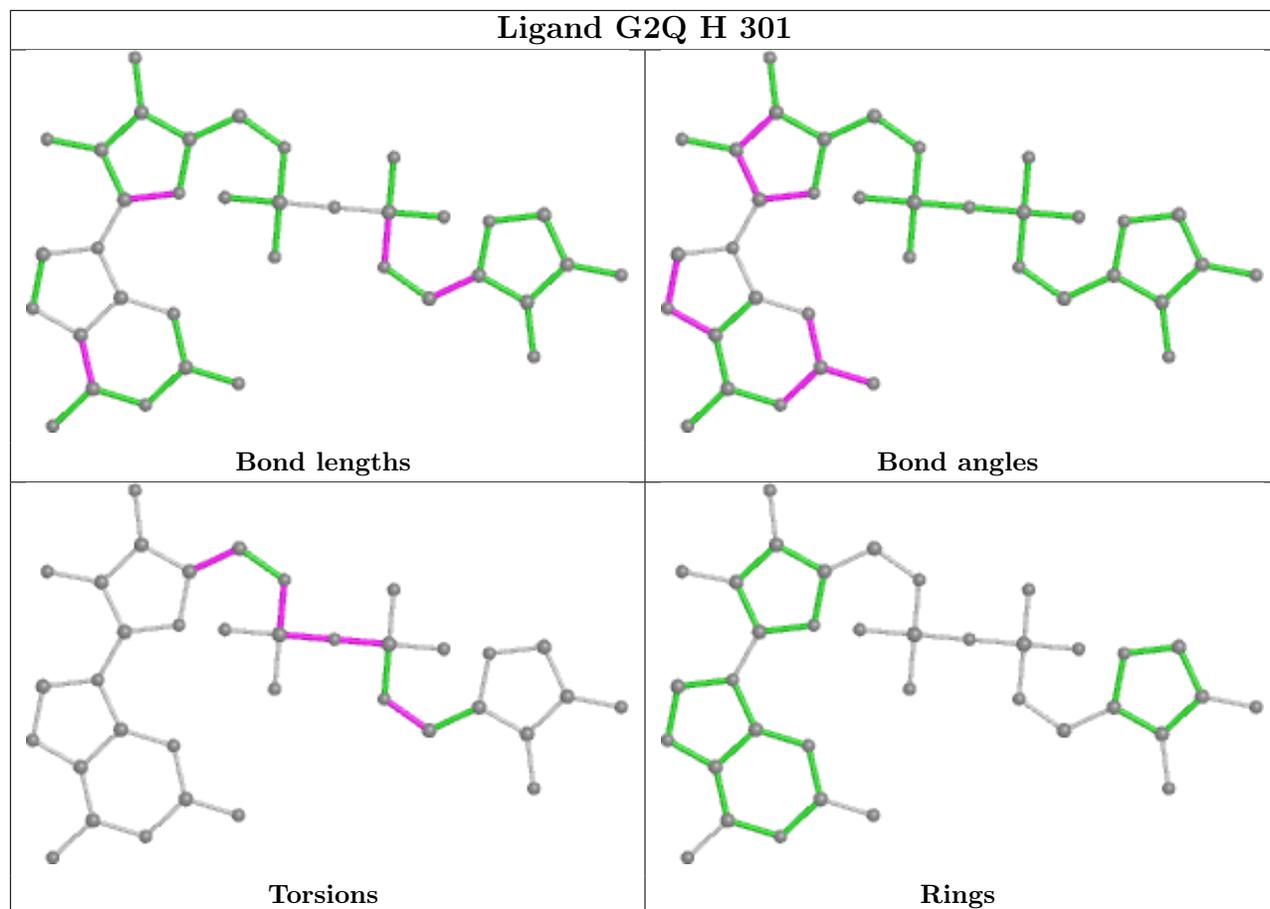
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

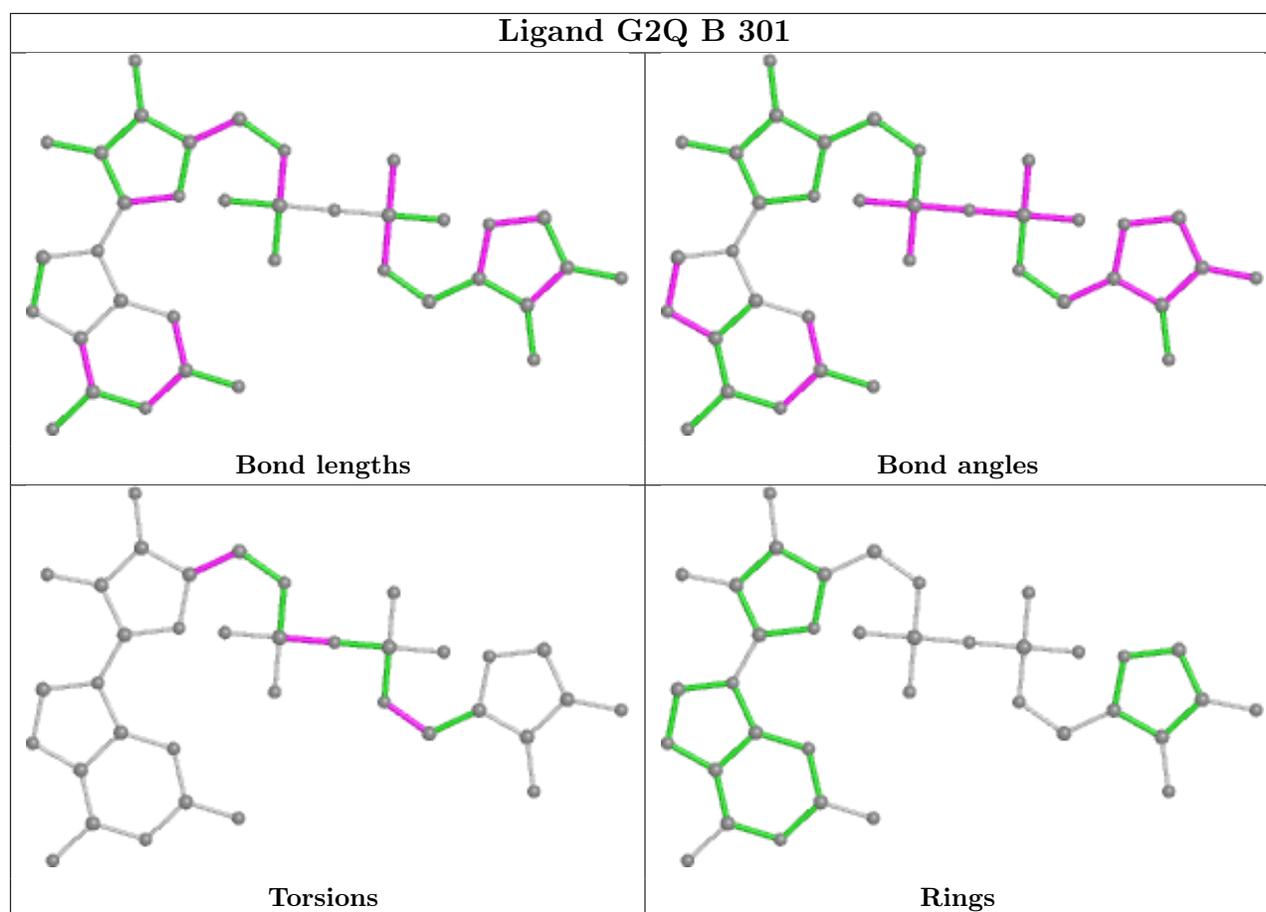












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	252/259 (97%)	-0.25	1 (0%) 92 92	15, 30, 48, 57	0
1	B	251/259 (96%)	-0.29	2 (0%) 86 85	19, 31, 49, 61	0
1	C	252/259 (97%)	-0.26	3 (1%) 79 78	17, 29, 48, 57	0
1	D	251/259 (96%)	-0.17	4 (1%) 72 70	18, 32, 53, 76	0
1	E	251/259 (96%)	-0.27	3 (1%) 79 78	19, 31, 47, 60	0
1	F	251/259 (96%)	-0.13	7 (2%) 53 51	19, 36, 56, 75	0
1	G	252/259 (97%)	-0.00	9 (3%) 42 42	29, 46, 62, 76	0
1	H	251/259 (96%)	-0.03	10 (3%) 38 37	30, 45, 63, 74	0
All	All	2011/2072 (97%)	-0.18	39 (1%) 66 65	15, 35, 56, 76	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	128	PHE	6.9
1	F	128	PHE	6.8
1	D	128	PHE	6.5
1	G	128	PHE	6.5
1	E	251	ALA	4.9

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands

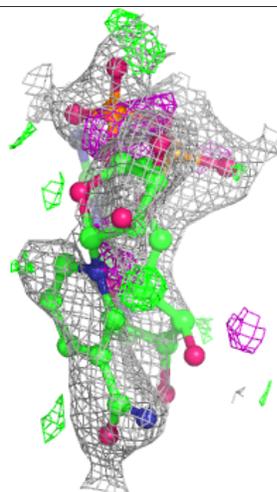
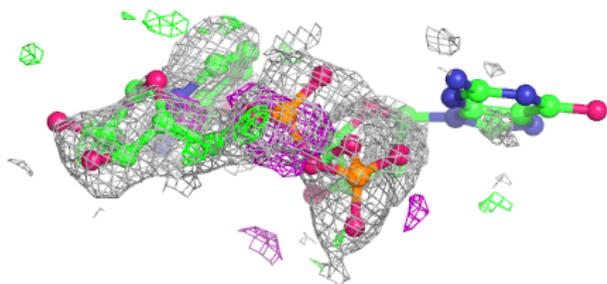
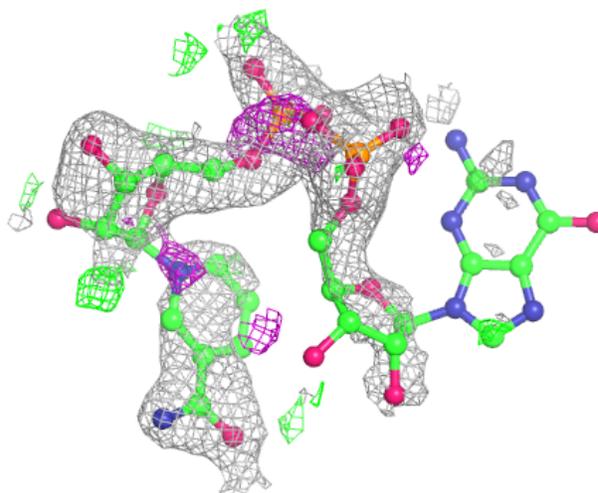
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NGD	F	5573	45/45	0.59	0.33	64,99,123,125	0
2	G2Q	A	301	36/36	0.86	0.16	20,43,54,56	0
2	G2Q	C	301	36/36	0.87	0.17	27,50,61,62	0
2	G2Q	B	301	36/36	0.88	0.16	31,48,54,56	0
2	G2Q	E	301	36/36	0.89	0.15	27,51,57,59	0
2	G2Q	G	301	36/36	0.90	0.16	60,69,78,81	0
2	G2Q	H	301	36/36	0.91	0.16	58,72,78,81	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.

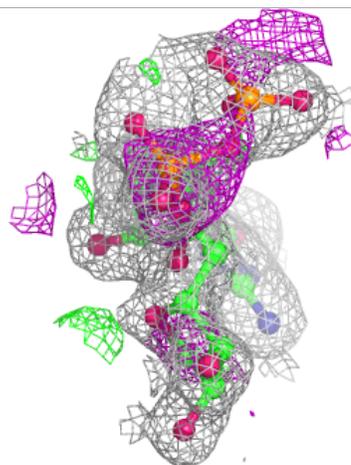
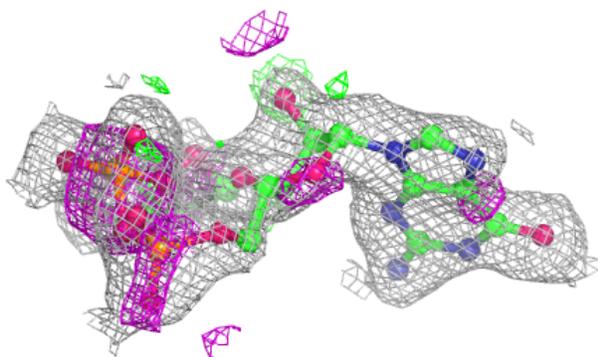
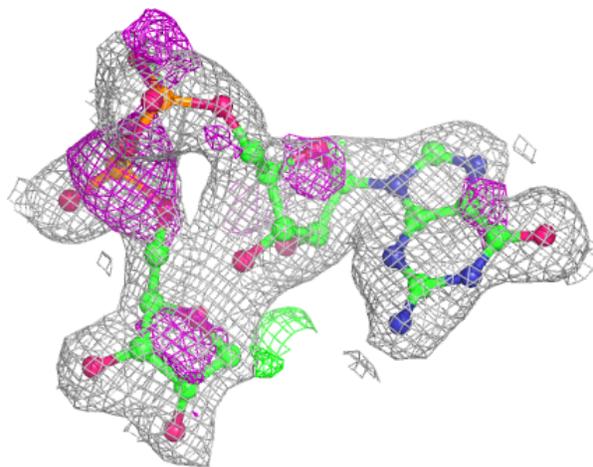
Electron density around NGD F 5573:

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



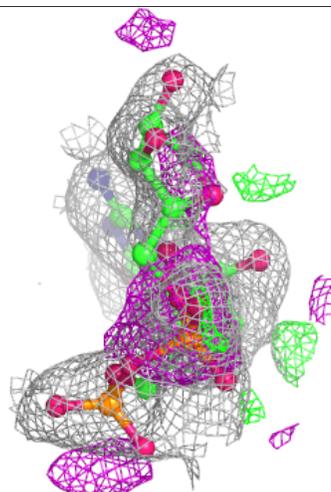
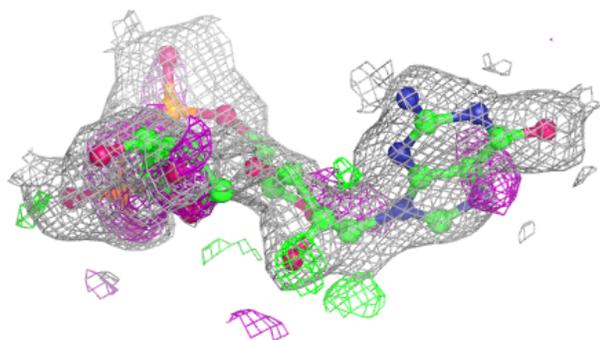
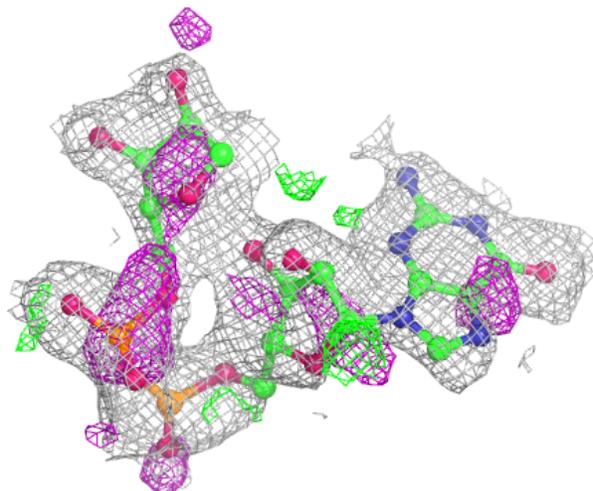
Electron density around G2Q A 301:

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



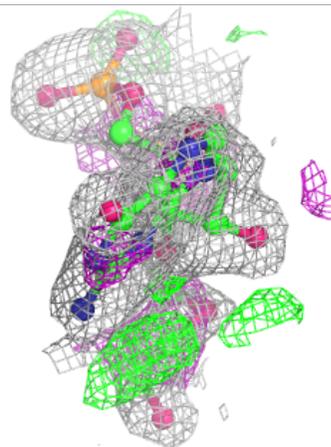
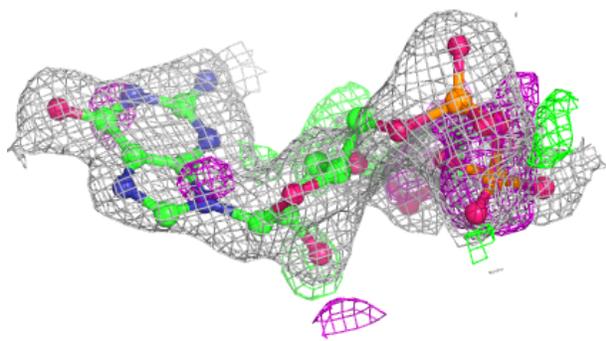
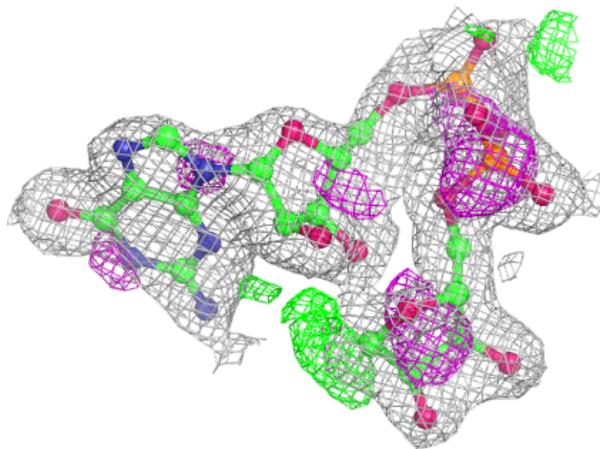
Electron density around G2Q C 301:

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



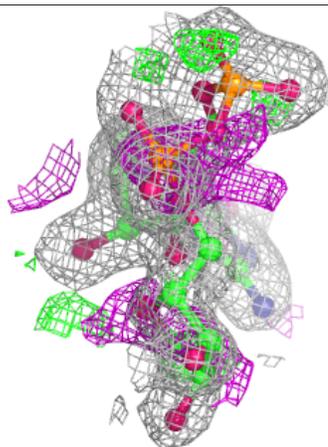
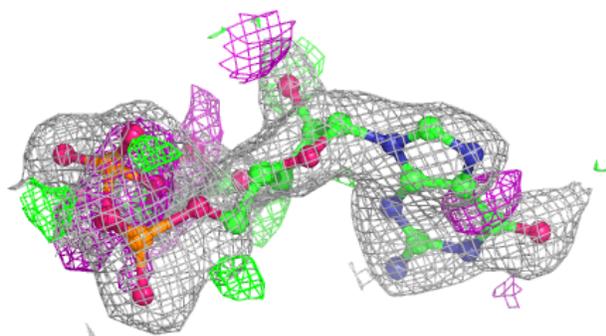
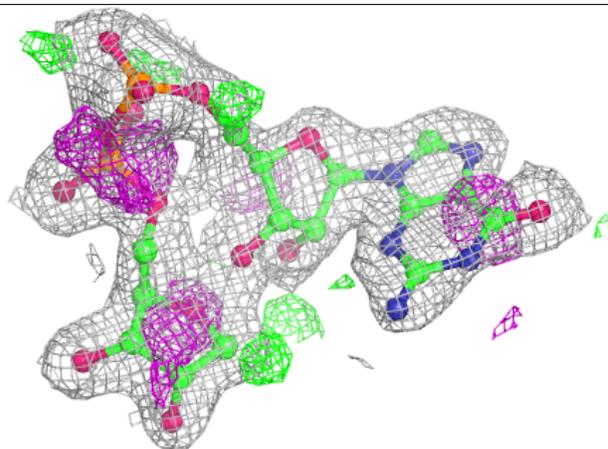
Electron density around G2Q B 301:

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



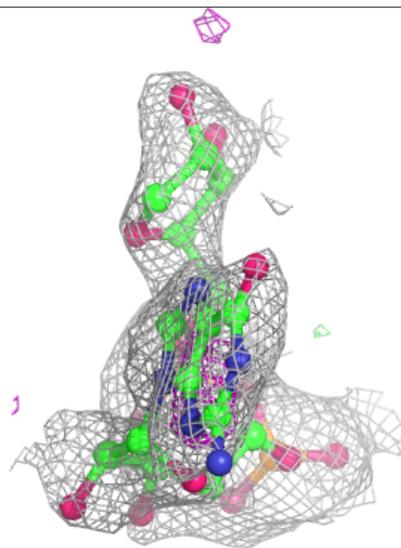
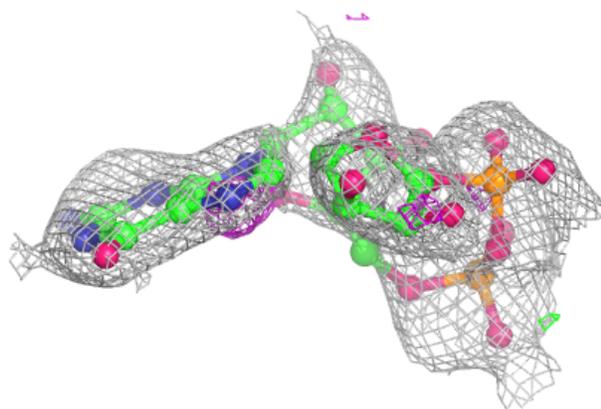
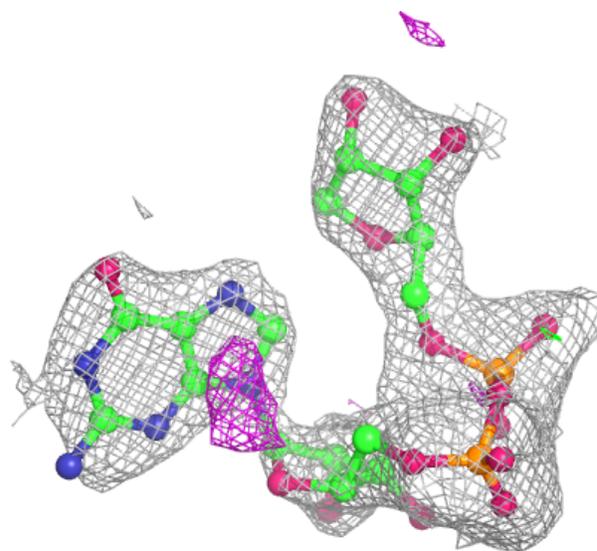
Electron density around G2Q E 301:

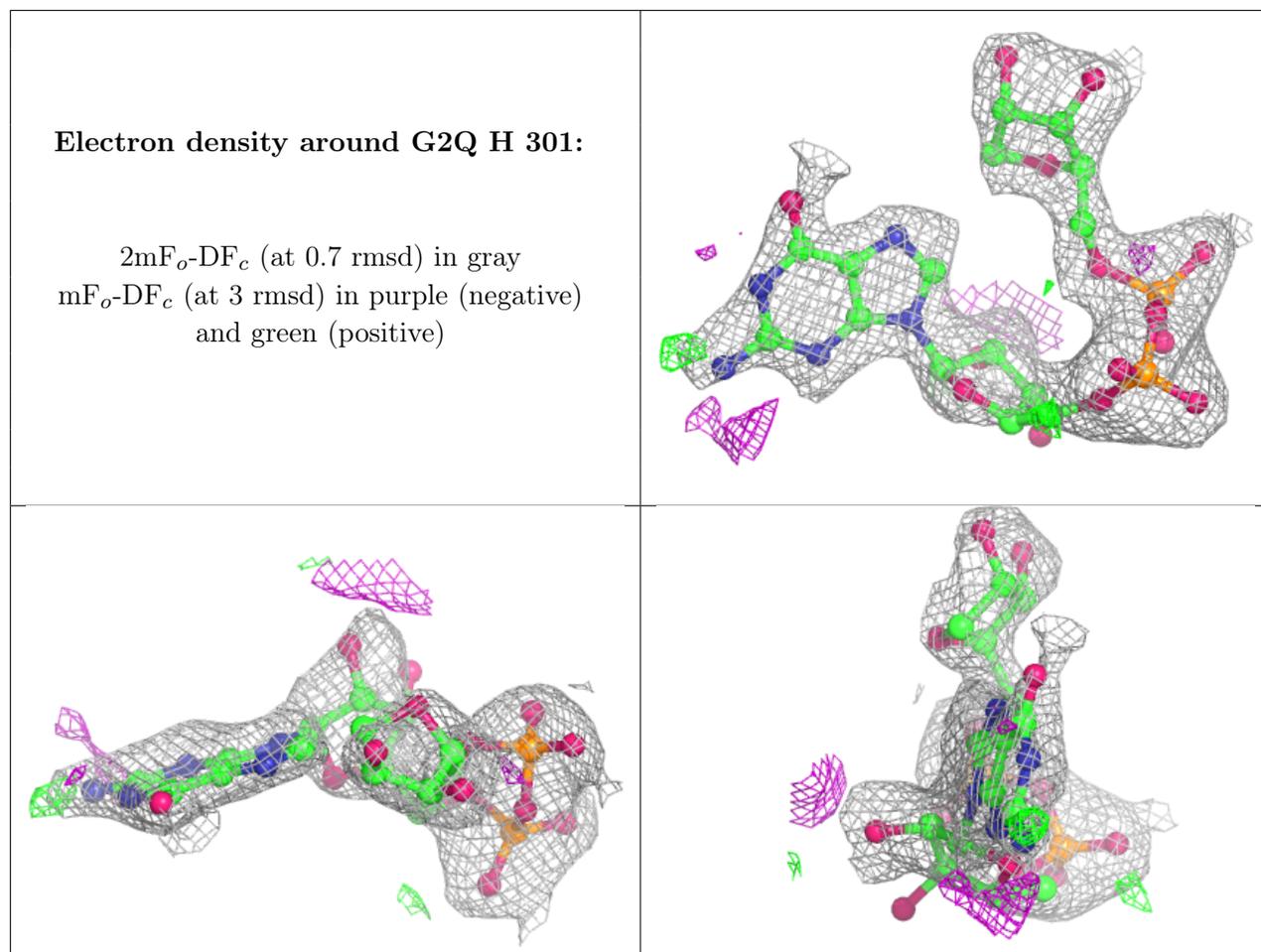
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around G2Q 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.