



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 20, 2020 – 01:22 PM BST

PDB ID : 6KPR  
Title : Quadruple mutant (N51I+C59R+S108N+I164L) plasmodium falciparum dihydrofolate reductase-thymidylate synthase (PfDHFR-TS) complexed with B12155 inhibitor  
Authors : Vanichtanankul, J.; Vitsupakorn, D.  
Deposited on : 2019-08-15  
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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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 : 2.13.1  
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) : 2.13.1



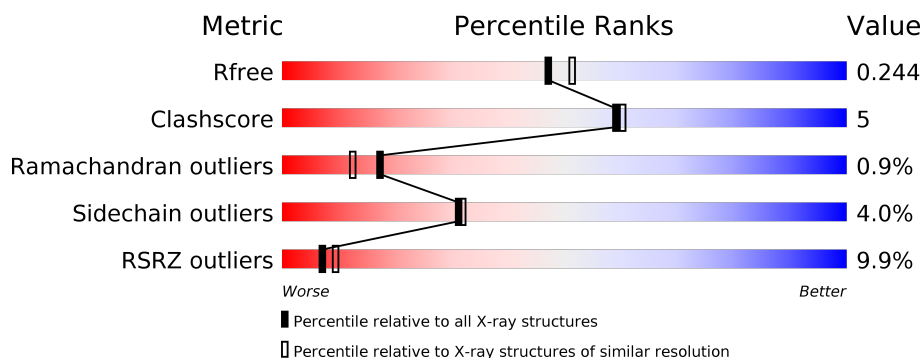
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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

Mol	Chain	Length	Quality of chain
1	A	608	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>10%</div> <div>12%</div> </div> </div>
1	B	608	<div> <div>12%</div> <div> <div></div> <div>75%</div> <div>11%</div> <div>12%</div> </div> </div>



## 2 Entry composition [i](#)

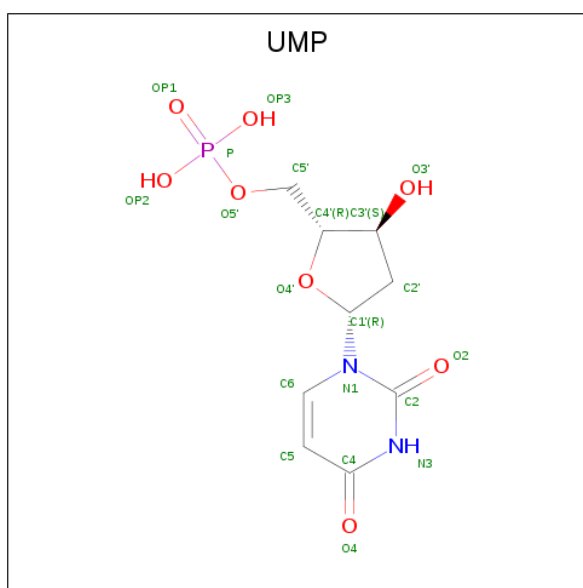
There are 6 unique types of molecules in this entry. The entry contains 9438 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional dihydrofolate reductase-thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	0	0
			4450	2878	736	811	25			
1	B	534	Total	C	N	O	S	0	0	0
			4444	2873	733	814	24			

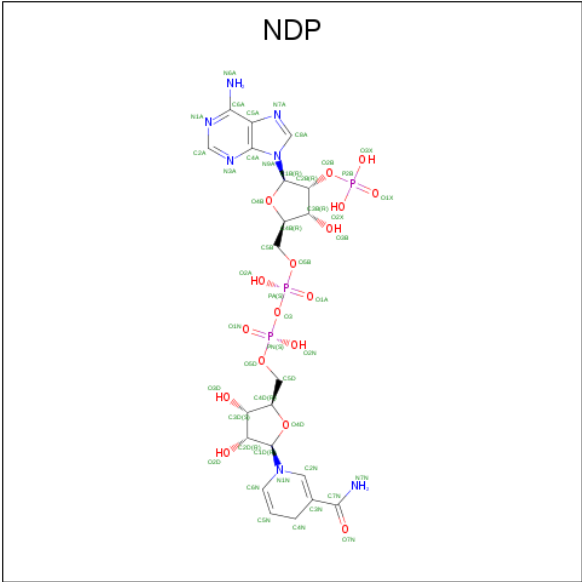
- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula:  $C_9H_{13}N_2O_8P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

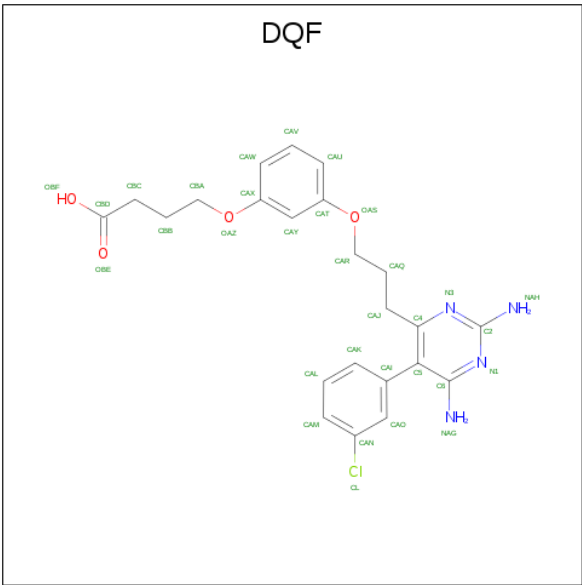
- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula:  $C_{21}H_{30}N_7O_{17}P_3$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is 4-[3-[3-[2,6-bis(azanyl)-5-(3-chlorophenyl)pyrimidin-4-yl]propoxy]phenoxy]butanoic acid (three-letter code: DQF) (formula: C<sub>23</sub>H<sub>25</sub>ClN<sub>4</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	0	0
			32	23	1	4	4		

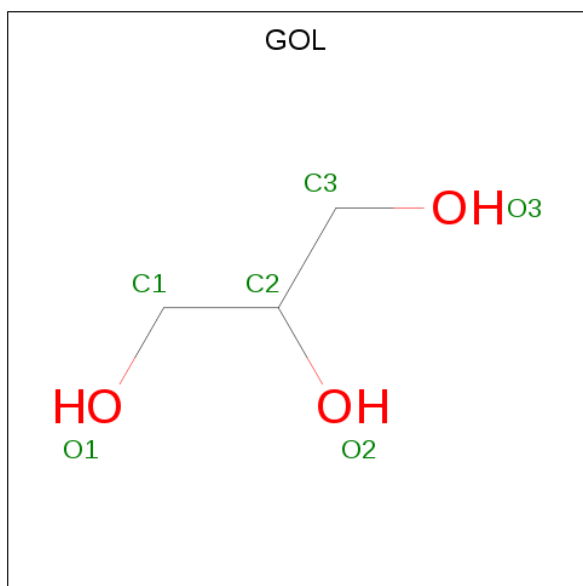
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	Cl	N	O	
			32	23	1	4	4	
								0
								0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O		
			6	3	3		
						0	0
5	B	1	Total	C	O		
			6	3	3		
						0	0

- Molecule 6 is water.

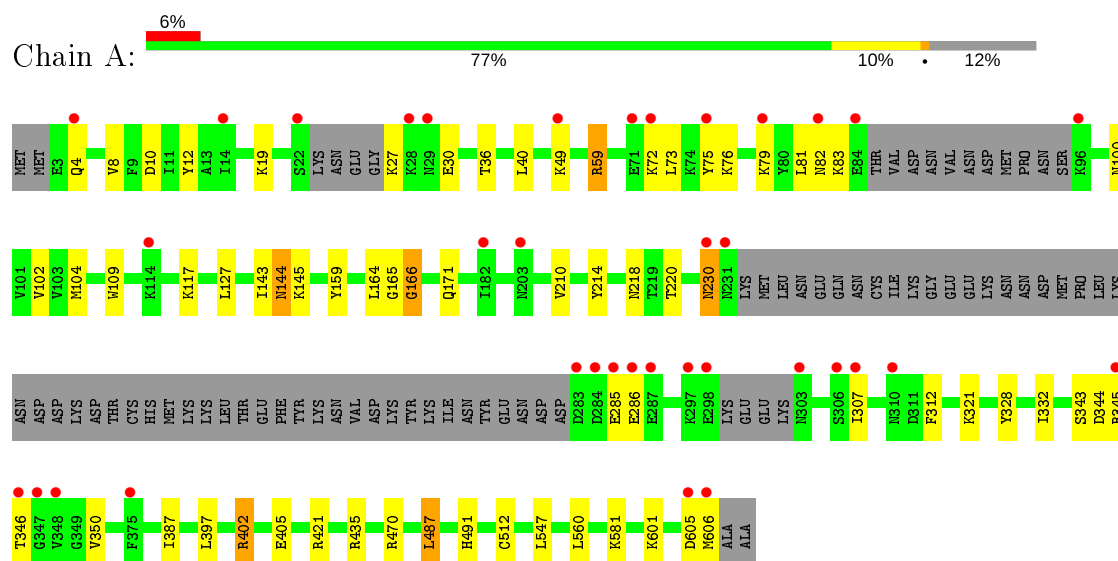
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	170	Total	O		
			170	170		
					0	0
6	B	162	Total	O		
			162	162		
					0	0



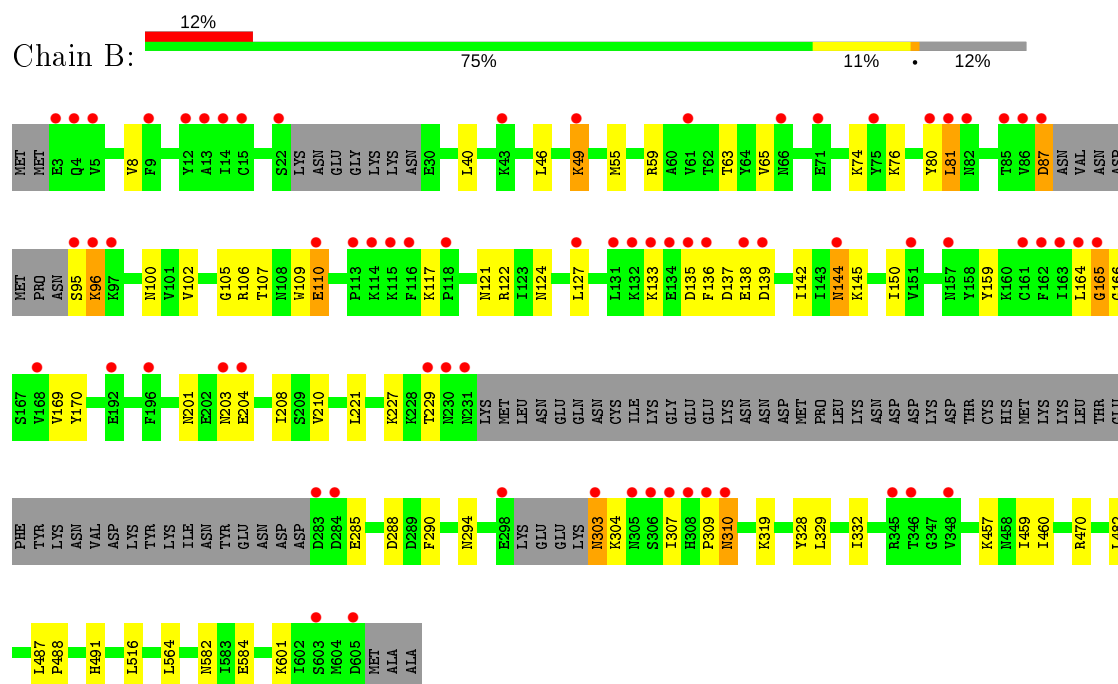
### 3 Residue-property plots [i](#)

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: Bifunctional dihydrofolate reductase-thymidylate synthase



- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.90Å 156.50Å 165.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.99 – 2.10 26.97 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.2 (26.99-2.10) 97.3 (26.97-2.10)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.60 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.195 , 0.241 0.203 , 0.244	Depositor DCC
$R_{free}$ test set	4377 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.3	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9438	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, DQF, UMP, NDP

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	0.74	0/4553	0.88	2/6146 (0.0%)
1	B	0.73	0/4547	0.87	0/6142
All	All	0.74	0/9100	0.87	2/12288 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59	ARG	CG-CD-NE	-6.12	98.95	111.80
1	A	421	ARG	NE-CZ-NH2	-5.68	117.46	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	165	GLY	Mainchain,Peptide
1	A	350	VAL	Peptide
1	B	165	GLY	Peptide



## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4450	0	4405	38	0
1	B	4444	0	4389	47	0
2	A	20	0	11	1	0
2	B	20	0	11	1	0
3	A	48	0	26	3	0
3	B	48	0	26	4	0
4	A	32	0	0	0	0
4	B	32	0	0	1	0
5	A	6	0	8	0	0
5	B	6	0	8	0	0
6	A	170	0	0	5	0
6	B	162	0	0	5	0
All	All	9438	0	8884	84	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 5.

The worst 5 of 84 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:GLY:HA3	3:A:702:NDP:PA	2.20	0.82
1:A:166:GLY:HA3	3:A:702:NDP:O1A	1.82	0.79
1:B:109:TRP:CZ2	1:B:117:LYS:HD2	2.25	0.72
1:B:328:TYR:CZ	1:B:332:ILE:HD11	2.24	0.72
1:B:304:LYS:CD	1:B:304:LYS:H	2.03	0.71

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	524/608 (86%)	497 (95%)	23 (4%)	4 (1%)	19	15
1	B	524/608 (86%)	492 (94%)	27 (5%)	5 (1%)	15	11
All	All	1048/1216 (86%)	989 (94%)	50 (5%)	9 (1%)	17	12

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	345	ARG
1	B	49	LYS
1	A	166	GLY
1	B	96	LYS
1	A	82	ASN

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	500/570 (88%)	485 (97%)	15 (3%)	41	44
1	B	500/570 (88%)	475 (95%)	25 (5%)	24	23
All	All	1000/1140 (88%)	960 (96%)	40 (4%)	31	32

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	81	LEU
1	B	127	LEU
1	B	319	LYS
1	B	107	THR
1	B	133	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:



Mol	Chain	Res	Type
1	A	394	ASN
1	A	407	ASN
1	B	303	ASN
1	A	303	ASN
1	B	231	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

### 5.6 Ligand geometry ⓘ

8 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	$\# Z  > 2$
3	NDP	A	702	-	45,52,52	2.06	15 (33%)	53,80,80	1.51	10 (18%)
5	GOL	A	704	-	5,5,5	0.19	0	5,5,5	0.33	0
4	DQF	B	703	-	31,34,34	1.29	4 (12%)	41,45,45	2.32	13 (31%)
2	UMP	B	701	-	18,21,21	1.33	3 (16%)	21,31,31	1.23	1 (4%)
3	NDP	B	702	-	45,52,52	1.80	11 (24%)	53,80,80	1.61	6 (11%)
5	GOL	B	704	-	5,5,5	0.12	0	5,5,5	0.43	0
4	DQF	A	703	-	31,34,34	1.54	5 (16%)	41,45,45	2.61	15 (36%)
2	UMP	A	701	-	18,21,21	1.16	2 (11%)	21,31,31	1.23	1 (4%)



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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NDP	A	702	-	-	3/30/77/77	0/5/5/5
5	GOL	A	704	-	-	1/4/4/4	-
4	DQF	B	703	-	-	4/16/18/18	0/3/3/3
2	UMP	B	701	-	-	6/7/22/22	0/2/2/2
3	NDP	B	702	-	-	5/30/77/77	0/5/5/5
5	GOL	B	704	-	-	0/4/4/4	-
4	DQF	A	703	-	-	6/16/18/18	0/3/3/3
2	UMP	A	701	-	-	1/7/22/22	0/2/2/2

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	NDP	O4B-C1B	5.59	1.48	1.41
4	A	703	DQF	C5-CAI	-5.24	1.40	1.50
3	A	702	NDP	C2A-N3A	4.56	1.39	1.32
3	A	702	NDP	C2A-N1A	4.22	1.41	1.33
4	B	703	DQF	C5-CAI	-4.20	1.42	1.50

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	703	DQF	C2-N3-C4	10.94	125.36	116.24
4	B	703	DQF	C2-N3-C4	8.89	123.66	116.24
3	B	702	NDP	N3A-C2A-N1A	-6.30	118.83	128.68
3	A	702	NDP	N3A-C2A-N1A	-5.02	120.83	128.68
4	B	703	DQF	N3-C2-N1	-4.92	117.71	125.42

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	702	NDP	C2B-O2B-P2B-O2X
2	B	701	UMP	O4'-C4'-C5'-O5'
2	B	701	UMP	C5'-O5'-P-OP3
2	B	701	UMP	C3'-C4'-C5'-O5'
4	B	703	DQF	CAW-CAX-OAZ-CBA



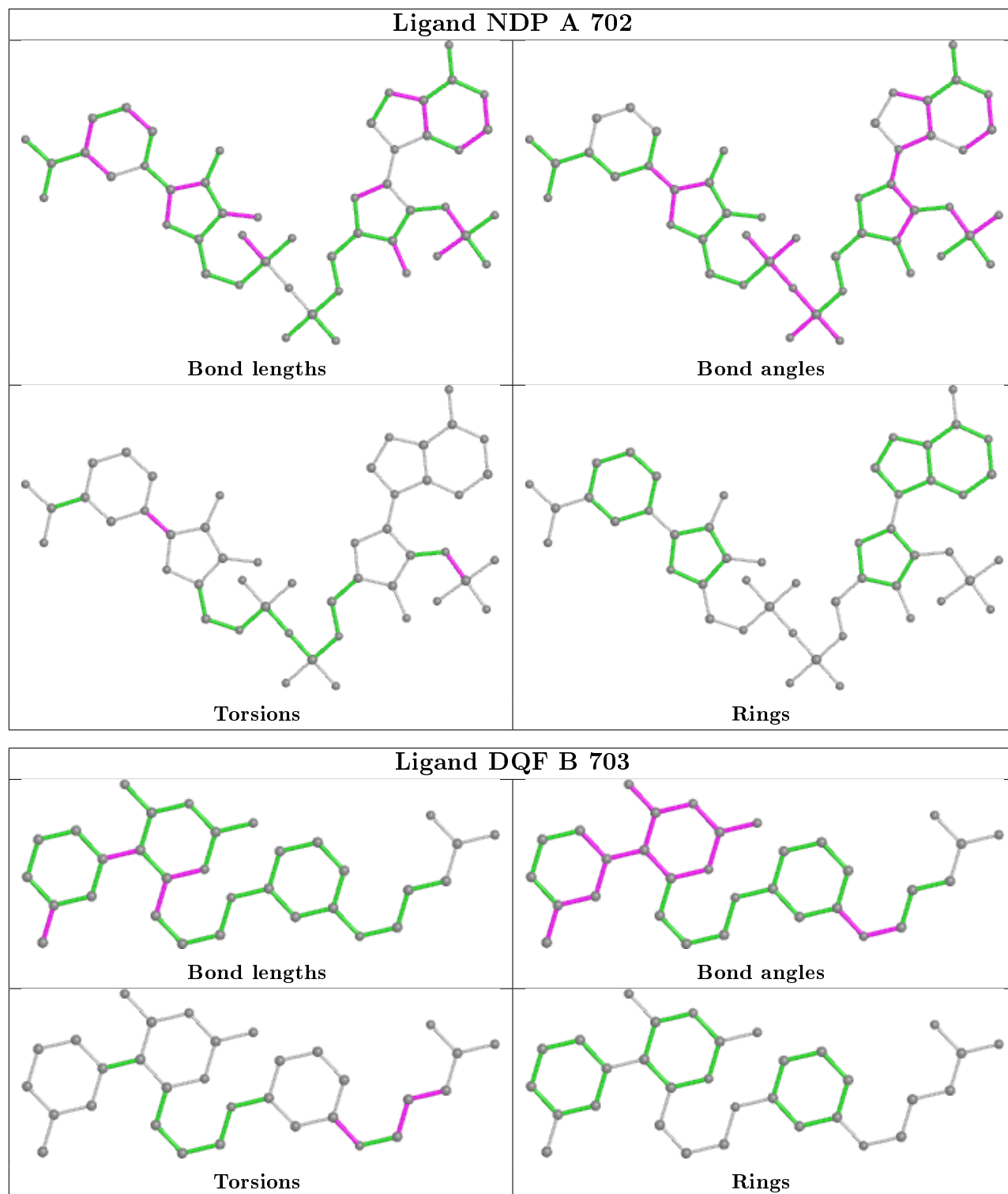
There are no ring outliers.

5 monomers are involved in 10 short contacts:

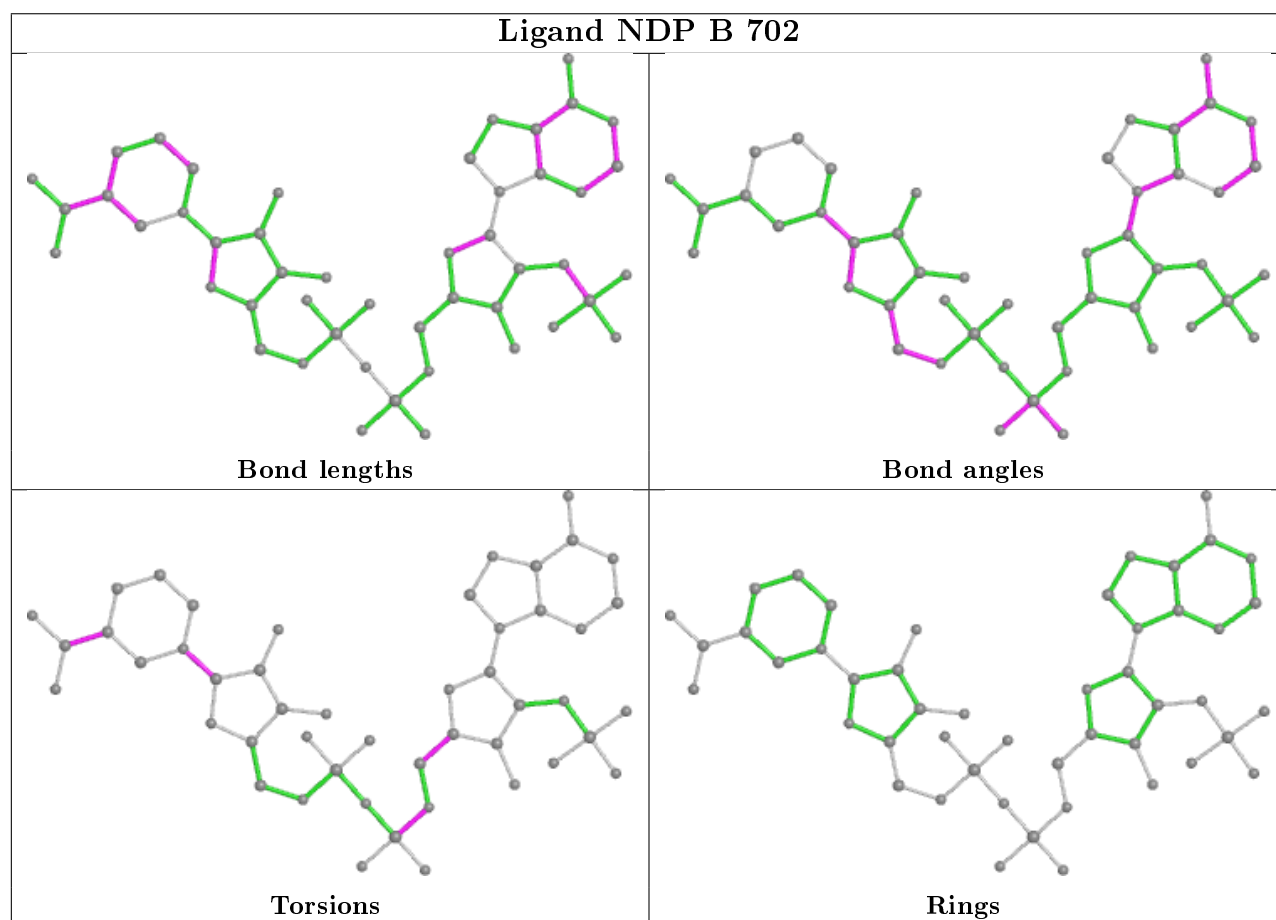
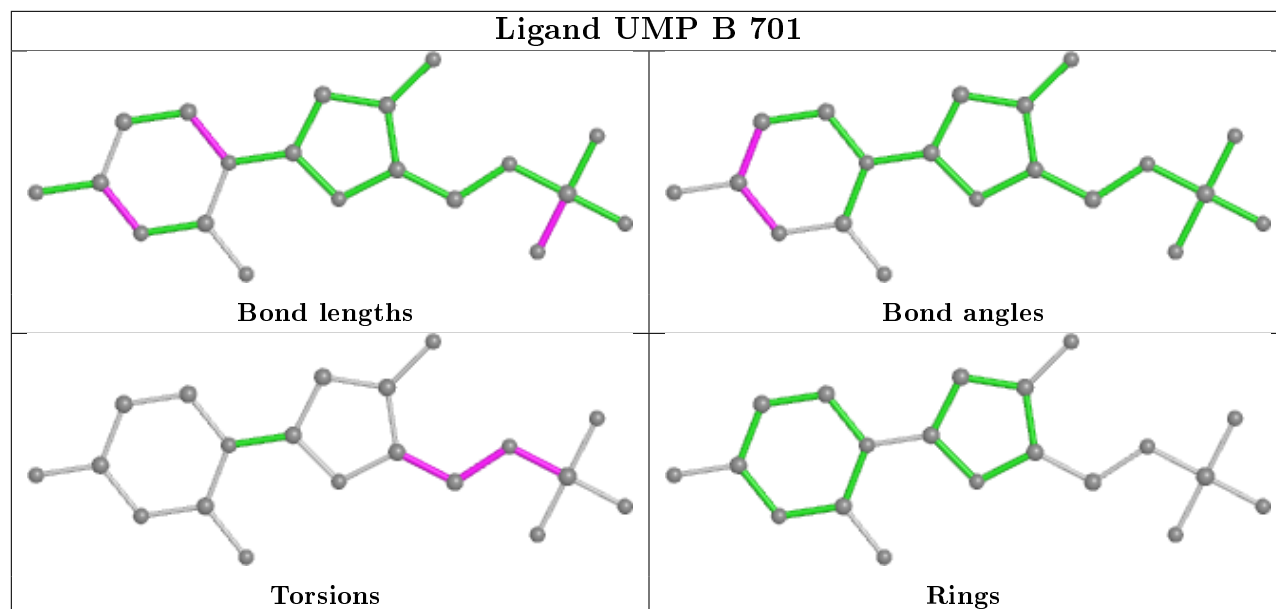
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	NDP	3	0
4	B	703	DQF	1	0
2	B	701	UMP	1	0
3	B	702	NDP	4	0
2	A	701	UMP	1	0

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

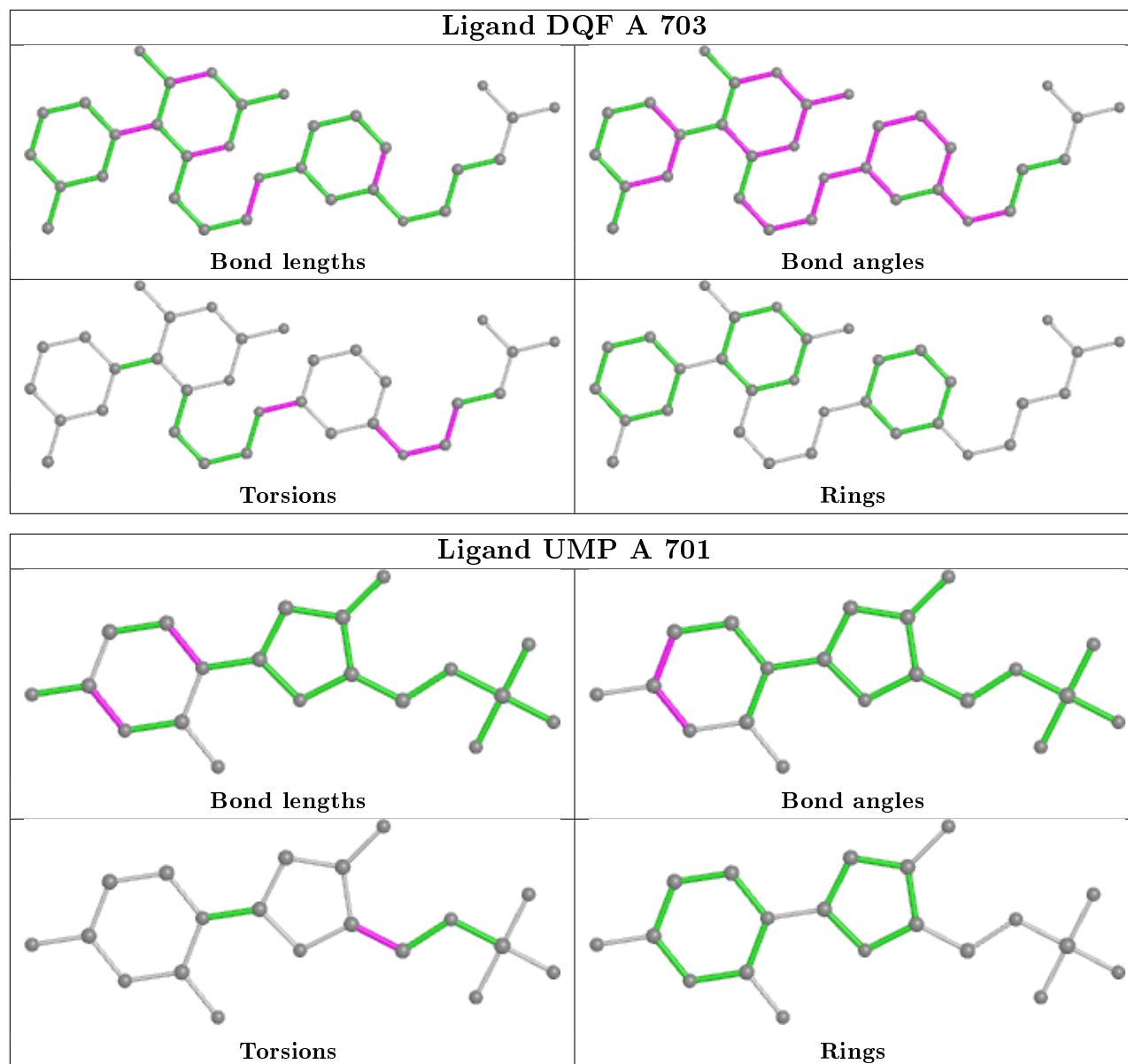












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	534/608 (87%)	0.23	36 (6%) 17 22	13, 26, 73, 116	0
1	B	534/608 (87%)	0.62	70 (13%) 3 4	13, 32, 87, 121	0
All	All	1068/1216 (87%)	0.42	106 (9%) 7 9	13, 28, 81, 121	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	231	ASN	8.4
1	B	116	PHE	7.9
1	B	95	SER	7.8
1	B	114	LYS	7.2
1	A	75	TYR	6.8

### 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.

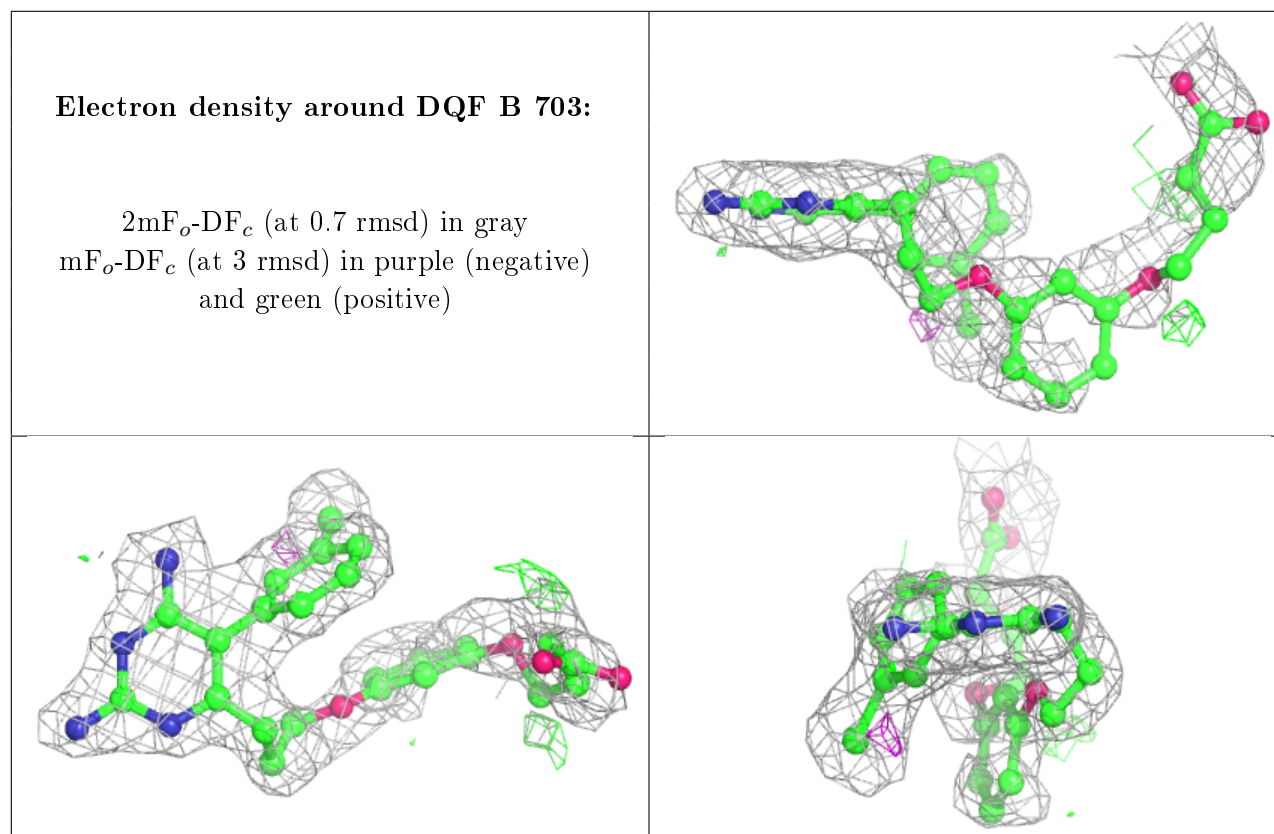
### 6.4 Ligands [i](#)

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
4	DQF	B	703	32/32	0.81	0.22	34,55,94,96	0
5	GOL	B	704	6/6	0.88	0.17	27,34,38,40	0
3	NDP	B	702	48/48	0.89	0.15	44,67,90,92	0
4	DQF	A	703	32/32	0.91	0.17	17,25,51,54	0
2	UMP	B	701	20/20	0.94	0.17	28,46,58,63	0
5	GOL	A	704	6/6	0.94	0.19	23,26,30,32	0
2	UMP	A	701	20/20	0.96	0.16	25,44,51,52	0
3	NDP	A	702	48/48	0.97	0.09	23,33,39,40	0

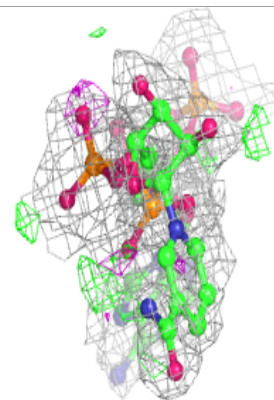
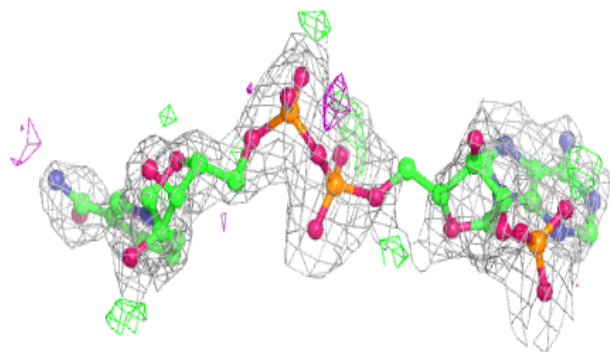
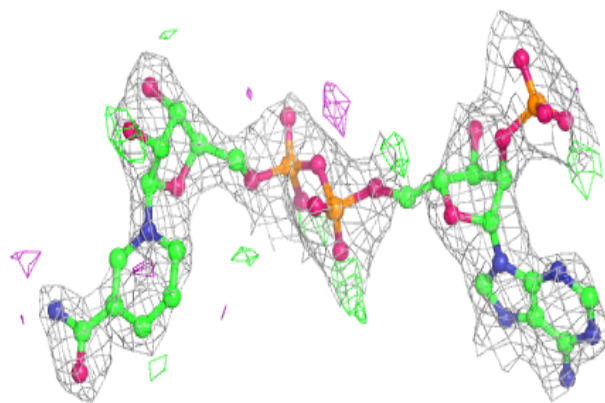
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



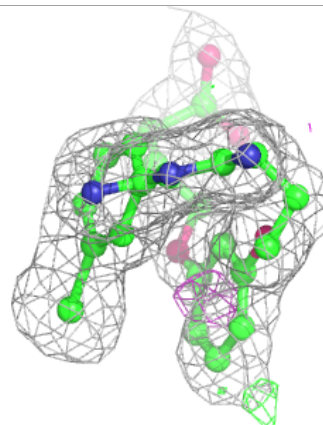
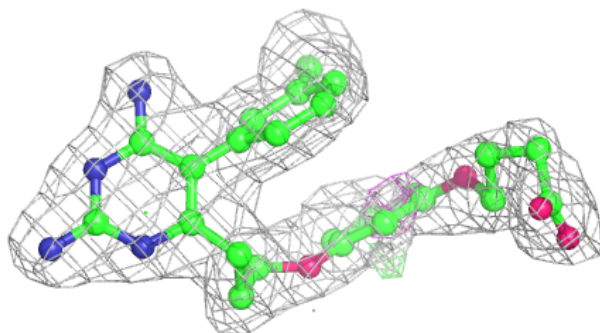
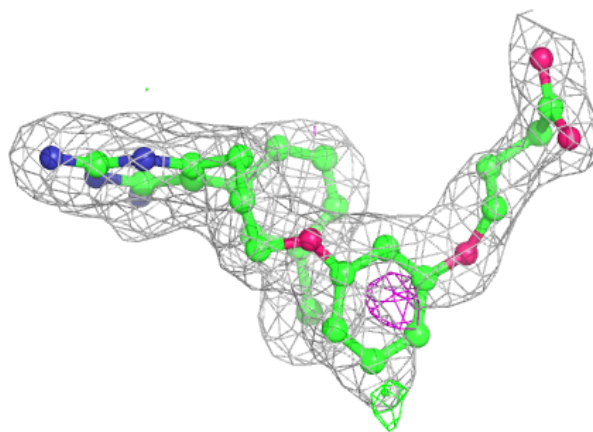


**Electron density around NDP B 702:**

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

**Electron density around DQF A 703:**

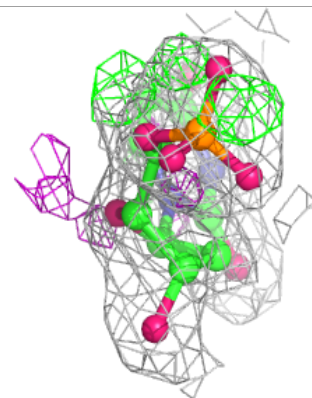
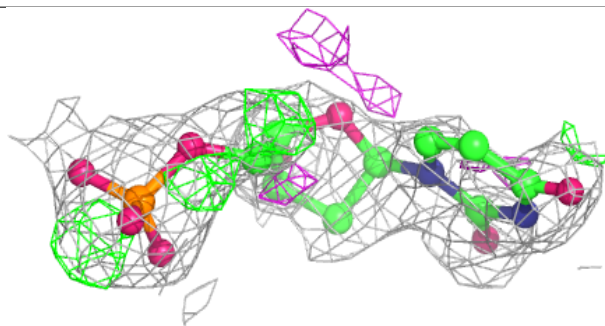
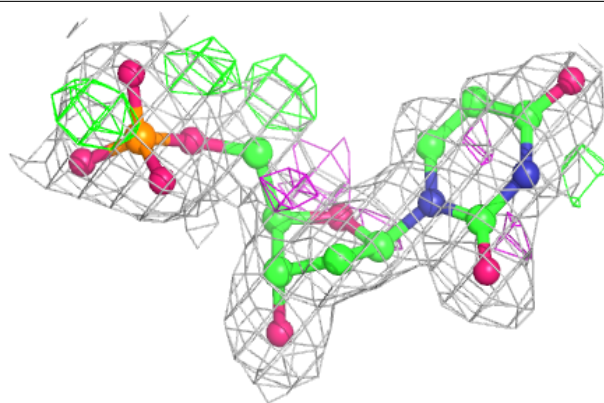
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



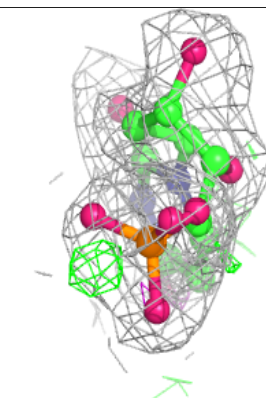
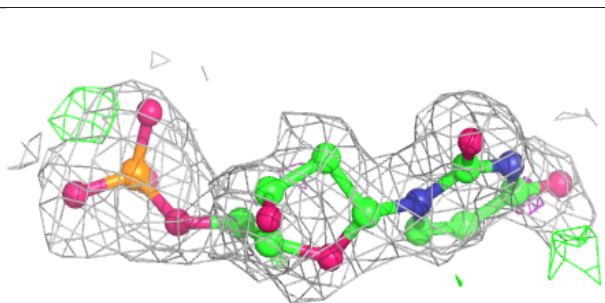
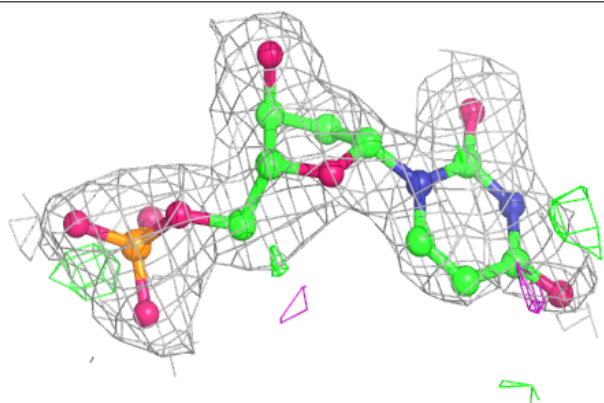


**Electron density around UMP B 701:**

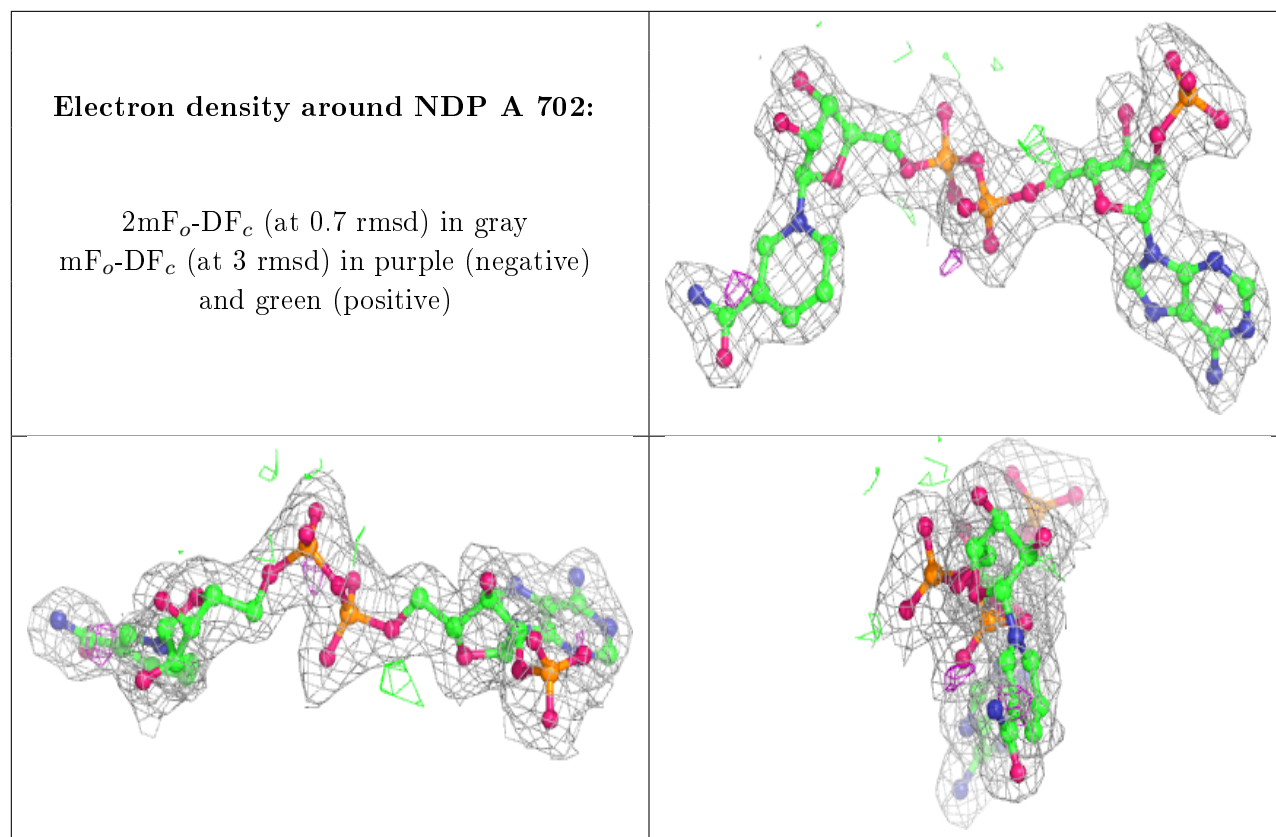
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around UMP A 701:**

$2mF_o-DF_c$  (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.