



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 10, 2023 – 04:08 PM EDT

PDB ID : 4KXN  
Title : Crystal structure of DNPH1 (RCL) with kinetine riboside monophosphate  
Authors : Padilla, A.; Labesse, G.; Kaminski, P.A.  
Deposited on : 2013-05-27  
Resolution : 1.90 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>.

---

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 : 2.35.1  
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

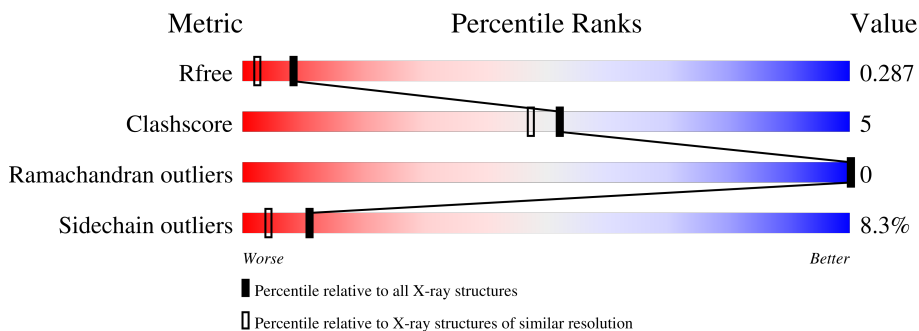
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	152	72% (green), 12% (yellow), 14% (grey)
1	B	152	74% (green), 9% (yellow), 17% (grey)
1	C	152	68% (green), 11% (yellow), 18% (grey)
1	D	152	70% (green), 14% (yellow), 14% (grey)

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4419 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 2'-deoxynucleoside 5'-phosphate N-hydrolase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	131	1032	651	186	191	4	0	1	0
1	B	126	1006	637	184	181	4	0	1	0
1	C	125	999	632	183	180	4	0	1	0
1	D	131	1023	646	185	188	4	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

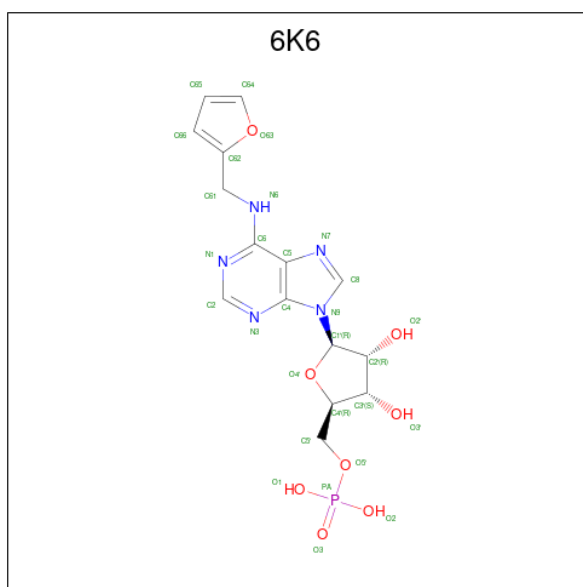
Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	expression tag	UNP O35820
A	9	ARG	-	expression tag	UNP O35820
A	10	ARG	-	expression tag	UNP O35820
A	69	ASN	ASP	engineered mutation	UNP O35820
A	152	VAL	-	expression tag	UNP O35820
A	153	GLU	-	expression tag	UNP O35820
A	154	HIS	-	expression tag	UNP O35820
A	155	HIS	-	expression tag	UNP O35820
A	156	HIS	-	expression tag	UNP O35820
A	157	HIS	-	expression tag	UNP O35820
A	158	HIS	-	expression tag	UNP O35820
A	159	HIS	-	expression tag	UNP O35820
B	8	MET	-	expression tag	UNP O35820
B	9	ARG	-	expression tag	UNP O35820
B	10	ARG	-	expression tag	UNP O35820
B	69	ASN	ASP	engineered mutation	UNP O35820
B	152	VAL	-	expression tag	UNP O35820
B	153	GLU	-	expression tag	UNP O35820
B	154	HIS	-	expression tag	UNP O35820
B	155	HIS	-	expression tag	UNP O35820
B	156	HIS	-	expression tag	UNP O35820

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	157	HIS	-	expression tag	UNP O35820
B	158	HIS	-	expression tag	UNP O35820
B	159	HIS	-	expression tag	UNP O35820
C	8	MET	-	expression tag	UNP O35820
C	9	ARG	-	expression tag	UNP O35820
C	10	ARG	-	expression tag	UNP O35820
C	69	ASN	ASP	engineered mutation	UNP O35820
C	152	VAL	-	expression tag	UNP O35820
C	153	GLU	-	expression tag	UNP O35820
C	154	HIS	-	expression tag	UNP O35820
C	155	HIS	-	expression tag	UNP O35820
C	156	HIS	-	expression tag	UNP O35820
C	157	HIS	-	expression tag	UNP O35820
C	158	HIS	-	expression tag	UNP O35820
C	159	HIS	-	expression tag	UNP O35820
D	8	MET	-	expression tag	UNP O35820
D	9	ARG	-	expression tag	UNP O35820
D	10	ARG	-	expression tag	UNP O35820
D	69	ASN	ASP	engineered mutation	UNP O35820
D	152	VAL	-	expression tag	UNP O35820
D	153	GLU	-	expression tag	UNP O35820
D	154	HIS	-	expression tag	UNP O35820
D	155	HIS	-	expression tag	UNP O35820
D	156	HIS	-	expression tag	UNP O35820
D	157	HIS	-	expression tag	UNP O35820
D	158	HIS	-	expression tag	UNP O35820
D	159	HIS	-	expression tag	UNP O35820

- Molecule 2 is N-(furan-2-ylmethyl)adenosine 5'-(dihydrogen phosphate) (three-letter code: 6K6) (formula: C<sub>15</sub>H<sub>18</sub>N<sub>5</sub>O<sub>8</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			29	15	5	8	1		
2	B	1	Total	C	N	O	P	0	0
			29	15	5	8	1		
2	C	1	Total	C	N	O	P	0	0
			29	15	5	8	1		
2	D	1	Total	C	N	O	P	0	0
			29	15	5	8	1		

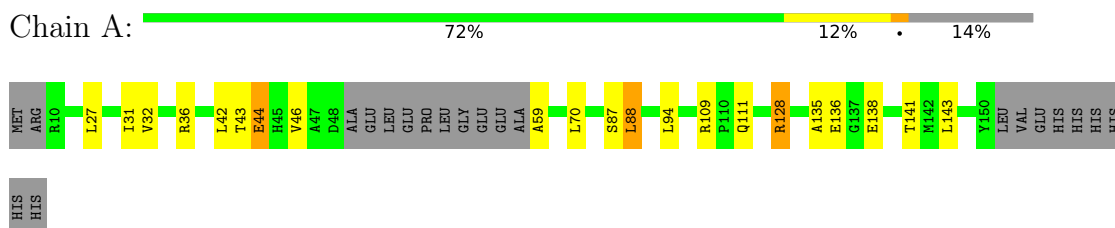
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	69	Total	O	0	0
			69	69		
3	B	67	Total	O	0	0
			67	67		
3	C	54	Total	O	0	0
			54	54		
3	D	53	Total	O	0	0
			53	53		

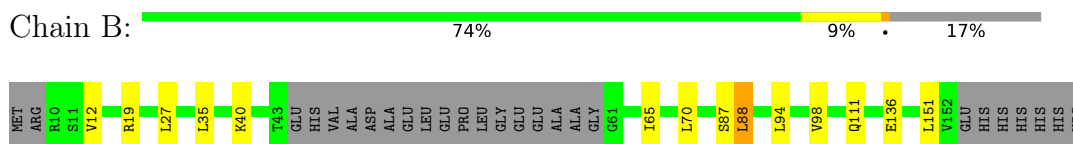
### 3 Residue-property plots [i](#)

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. 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. 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.

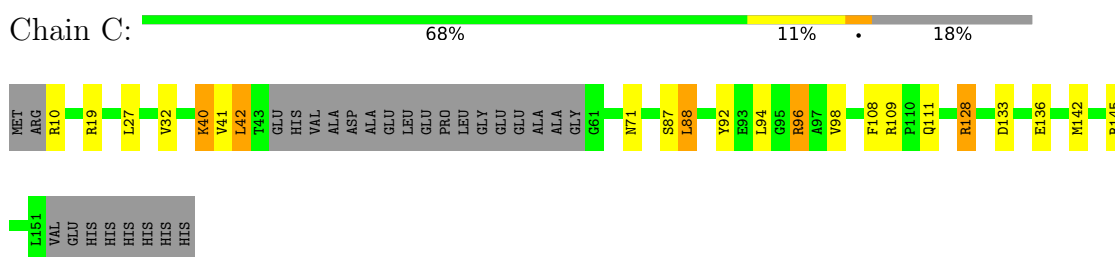
- Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1



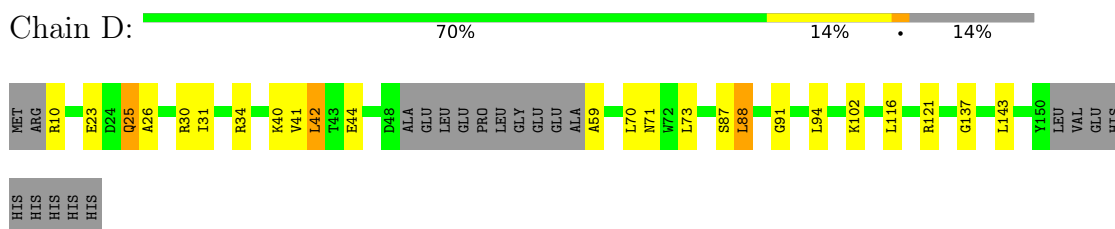
- Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1



- Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1



- Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	32.24Å 95.45Å 79.29Å 90.00° 101.56° 90.00°	Depositor
Resolution (Å)	23.86 – 1.90 23.77 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.3 (23.86-1.90) 97.6 (23.77-1.90)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.45 (at 1.90Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.232 , 0.286 0.232 , 0.287	Depositor DCC
$R_{free}$ test set	1818 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.9	Xtrriage
Anisotropy	0.154	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 32.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.20$	Xtrriage
Estimated twinning fraction	0.396 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4419	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.09% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 6K6

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	0.42	0/1055	0.56	0/1424
1	B	0.49	0/1029	0.63	0/1387
1	C	0.45	0/1022	0.64	0/1377
1	D	0.42	0/1042	0.58	0/1407
All	All	0.44	0/4148	0.60	0/5595

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	1032	0	1002	15	0
1	B	1006	0	999	6	0
1	C	999	0	990	15	0
1	D	1023	0	994	12	0
2	A	29	0	16	0	0
2	B	29	0	16	4	0
2	C	29	0	16	0	0
2	D	29	0	16	1	0
3	A	69	0	0	4	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	67	0	0	0	0
3	C	54	0	0	3	0
3	D	53	0	0	1	0
All	All	4419	0	4049	45	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.

All (45) 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:C:96[A]:ARG:HH21	1:C:96[A]:ARG:HG3	1.25	1.02
1:A:36:ARG:NH2	1:A:44:GLU:OE2	2.23	0.71
1:A:109:ARG:HD2	1:A:136:GLU:HB3	1.75	0.69
1:D:31:ILE:HG23	1:D:143:LEU:HD11	1.77	0.67
1:A:59:ALA:HA	3:A:322:HOH:O	1.98	0.62
1:C:96[A]:ARG:NH1	3:C:352:HOH:O	2.31	0.62
1:C:96[A]:ARG:HG3	1:C:96[A]:ARG:NH2	2.00	0.61
1:A:46:VAL:CG2	3:A:364:HOH:O	2.48	0.61
1:D:30:ARG:HH22	1:D:137:GLY:HA2	1.65	0.61
1:A:87:SER:H	1:B:88:LEU:HD13	1.66	0.60
1:A:43:THR:HB	3:A:364:HOH:O	2.01	0.59
1:A:88:LEU:HD13	1:B:87:SER:H	1.68	0.58
1:C:111:GLN:HE22	1:C:136:GLU:H	1.53	0.57
1:C:87:SER:H	1:D:88:LEU:HD13	1.70	0.56
1:A:46:VAL:HG21	3:A:364:HOH:O	2.04	0.56
1:A:138:GLU:O	1:A:138:GLU:HG2	2.06	0.56
1:A:135:ALA:O	1:A:138:GLU:HB3	2.06	0.56
1:C:109:ARG:HG2	1:C:111:GLN:HG2	1.89	0.55
2:B:201:6K6:C8	2:B:201:6K6:H15	2.38	0.54
1:C:96[B]:ARG:HD2	3:C:302:HOH:O	2.09	0.53
1:C:88:LEU:HD13	1:D:87:SER:H	1.74	0.52
2:B:201:6K6:H15	2:B:201:6K6:H8	1.90	0.52
1:D:40:LYS:HE2	1:D:42:LEU:HD12	1.92	0.51
1:D:25:GLN:HG3	1:D:26:ALA:N	2.28	0.48
1:A:128:ARG:HA	1:A:128:ARG:HD2	1.55	0.48
1:C:32:VAL:HG13	1:C:41:VAL:HG11	1.96	0.48
1:A:31:ILE:HG23	1:A:143:LEU:HD11	1.96	0.47
1:B:65:ILE:HD13	2:B:201:6K6:H6	1.79	0.47
1:A:36:ARG:HH22	1:A:44:GLU:CD	2.15	0.47
1:C:19:ARG:HD2	3:C:324:HOH:O	2.15	0.47

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:LEU:O	1:C:98:VAL:HG23	2.16	0.46
1:D:73:LEU:O	1:D:102:LYS:HE3	2.16	0.45
1:C:128:ARG:NE	1:C:128:ARG:HA	2.32	0.45
1:C:92:TYR:HA	1:D:91:GLY:O	2.17	0.44
1:D:116:LEU:HD23	1:D:121:ARG:HG2	1.98	0.44
1:C:40:LYS:HE2	1:C:42:LEU:HD12	1.99	0.44
1:D:87:SER:OG	2:D:201:6K6:PA	2.75	0.44
1:D:41:VAL:O	1:D:44:GLU:HG3	2.18	0.44
1:B:19:ARG:NE	2:B:201:6K6:H3	2.33	0.43
1:A:32:VAL:O	1:A:36:ARG:HG3	2.20	0.42
1:C:108:PHE:O	1:C:133:ASP:HA	2.20	0.42
1:B:94:LEU:O	1:B:98:VAL:HG23	2.20	0.41
1:D:59:ALA:N	3:D:349:HOH:O	2.53	0.41
1:A:27:LEU:O	1:A:31:ILE:HG13	2.21	0.41
1:B:12:VAL:HG11	1:B:35:LEU:HD22	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	128/152 (84%)	126 (98%)	2 (2%)	0	100	100
1	B	123/152 (81%)	118 (96%)	5 (4%)	0	100	100
1	C	122/152 (80%)	119 (98%)	3 (2%)	0	100	100
1	D	127/152 (84%)	124 (98%)	3 (2%)	0	100	100
All	All	500/608 (82%)	487 (97%)	13 (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	104/122 (85%)	96 (92%)	8 (8%)	13	5
1	B	103/122 (84%)	96 (93%)	7 (7%)	16	7
1	C	102/122 (84%)	91 (89%)	11 (11%)	6	2
1	D	102/122 (84%)	93 (91%)	9 (9%)	10	4
All	All	411/488 (84%)	376 (92%)	35 (8%)	11	4

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	LEU
1	A	44	GLU
1	A	70	LEU
1	A	88	LEU
1	A	94	LEU
1	A	111	GLN
1	A	128	ARG
1	A	141	THR
1	B	27	LEU
1	B	40	LYS
1	B	70	LEU
1	B	88	LEU
1	B	111	GLN
1	B	136	GLU
1	B	151	LEU
1	C	10	ARG
1	C	27	LEU
1	C	40	LYS
1	C	42	LEU
1	C	71	ASN
1	C	88	LEU
1	C	96[A]	ARG
1	C	96[B]	ARG
1	C	128	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	142	MET
1	C	145	ARG
1	D	10	ARG
1	D	23	GLU
1	D	25	GLN
1	D	34	ARG
1	D	42	LEU
1	D	70	LEU
1	D	71	ASN
1	D	88	LEU
1	D	94	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	71	ASN
1	A	74	GLN
1	A	85	GLN
1	B	25	GLN
1	B	85	GLN
1	C	85	GLN
1	C	111	GLN
1	D	25	GLN
1	D	85	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

4 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	6K6	C	201	-	25,32,32	1.61	4 (16%)	28,47,47	3.47	9 (32%)
2	6K6	D	201	-	25,32,32	1.93	4 (16%)	28,47,47	3.35	12 (42%)
2	6K6	A	201	-	25,32,32	1.71	3 (12%)	28,47,47	3.44	12 (42%)
2	6K6	B	201	-	25,32,32	1.60	4 (16%)	28,47,47	3.51	9 (32%)

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	6K6	C	201	-	-	5/9/31/31	0/4/4/4
2	6K6	D	201	-	-	2/9/31/31	0/4/4/4
2	6K6	A	201	-	-	2/9/31/31	0/4/4/4
2	6K6	B	201	-	-	5/9/31/31	0/4/4/4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	6K6	O4'-C1'	6.08	1.49	1.41
2	B	201	6K6	C66-C62	-4.73	1.33	1.39
2	D	201	6K6	C66-C62	-4.65	1.33	1.39
2	A	201	6K6	C66-C62	-4.63	1.33	1.39
2	C	201	6K6	C66-C62	-4.56	1.33	1.39
2	A	201	6K6	PA-O3	4.28	1.64	1.50
2	B	201	6K6	PA-O3	3.63	1.62	1.50
2	A	201	6K6	O4'-C1'	3.54	1.46	1.41
2	D	201	6K6	PA-O3	3.19	1.60	1.50
2	C	201	6K6	PA-O1	3.07	1.66	1.54

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	6K6	O4'-C1'	3.04	1.45	1.41
2	C	201	6K6	O4'-C1'	2.96	1.45	1.41
2	C	201	6K6	PA-O2	2.86	1.65	1.54
2	D	201	6K6	PA-O2	2.38	1.64	1.54
2	B	201	6K6	C65-C66	-2.01	1.33	1.39

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	201	6K6	O1-PA-O5'	-11.11	77.18	106.73
2	D	201	6K6	O1-PA-O5'	-9.55	81.32	106.73
2	C	201	6K6	O5'-PA-O3	-9.42	80.05	106.47
2	C	201	6K6	O2-PA-O3	-8.38	77.86	110.68
2	A	201	6K6	O1-PA-O5'	-8.20	84.92	106.73
2	A	201	6K6	O1-PA-O3	-7.93	79.62	110.68
2	B	201	6K6	O1-PA-O3	-7.76	80.31	110.68
2	C	201	6K6	O1-PA-O3	-7.68	80.62	110.68
2	D	201	6K6	O1-PA-O2	-7.32	79.64	107.64
2	D	201	6K6	O1-PA-O3	-7.18	82.58	110.68
2	A	201	6K6	O1-PA-O2	-6.81	81.61	107.64
2	A	201	6K6	C2-N1-C6	6.24	121.94	116.59
2	B	201	6K6	O1-PA-O2	-6.05	84.51	107.64
2	C	201	6K6	C2-N1-C6	5.58	121.38	116.59
2	B	201	6K6	C2-N1-C6	5.13	120.99	116.59
2	B	201	6K6	O5'-PA-O3	5.11	120.82	106.47
2	D	201	6K6	N3-C2-N1	-5.09	120.72	128.68
2	D	201	6K6	C2-N1-C6	5.02	120.90	116.59
2	B	201	6K6	N3-C2-N1	-4.97	120.91	128.68
2	A	201	6K6	N3-C2-N1	-4.93	120.98	128.68
2	C	201	6K6	N3-C2-N1	-4.72	121.30	128.68
2	D	201	6K6	O2-PA-O5'	4.28	118.12	106.73
2	A	201	6K6	C5'-C4'-C3'	-3.94	100.42	115.18
2	C	201	6K6	C3'-C2'-C1'	3.80	106.69	100.98
2	A	201	6K6	O5'-PA-O3	3.73	116.95	106.47
2	A	201	6K6	PA-O5'-C5'	-3.65	108.25	118.30
2	C	201	6K6	O2-PA-O5'	3.63	116.39	106.73
2	C	201	6K6	O1-PA-O5'	3.57	116.22	106.73
2	A	201	6K6	O2-PA-O5'	3.47	115.96	106.73
2	B	201	6K6	O2-PA-O5'	3.39	115.76	106.73
2	B	201	6K6	C3'-C2'-C1'	3.13	105.70	100.98
2	D	201	6K6	O5'-PA-O3	3.00	114.90	106.47
2	A	201	6K6	C62-C61-N6	-2.91	106.40	112.71

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	201	6K6	C3'-C2'-C1'	2.90	105.34	100.98
2	A	201	6K6	O2-PA-O3	2.73	121.36	110.68
2	C	201	6K6	O1-PA-O2	2.62	117.67	107.64
2	A	201	6K6	C3'-C2'-C1'	2.62	104.92	100.98
2	B	201	6K6	C62-C61-N6	-2.58	107.13	112.71
2	D	201	6K6	C61-N6-C6	-2.55	119.71	123.11
2	D	201	6K6	O2-PA-O3	2.38	120.02	110.68
2	D	201	6K6	C5'-C4'-C3'	-2.29	106.61	115.18
2	D	201	6K6	C4-C5-N7	-2.03	107.29	109.40

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	6K6	C5'-O5'-PA-O2
2	A	201	6K6	C5'-O5'-PA-O3
2	B	201	6K6	N1-C6-N6-C61
2	B	201	6K6	C5-C6-N6-C61
2	B	201	6K6	C5'-O5'-PA-O1
2	C	201	6K6	N1-C6-N6-C61
2	C	201	6K6	C5-C6-N6-C61
2	C	201	6K6	C5'-O5'-PA-O1
2	D	201	6K6	C5'-O5'-PA-O1
2	B	201	6K6	C3'-C4'-C5'-O5'
2	B	201	6K6	O4'-C4'-C5'-O5'
2	C	201	6K6	C5'-O5'-PA-O3
2	D	201	6K6	C5'-O5'-PA-O2
2	C	201	6K6	C3'-C4'-C5'-O5'

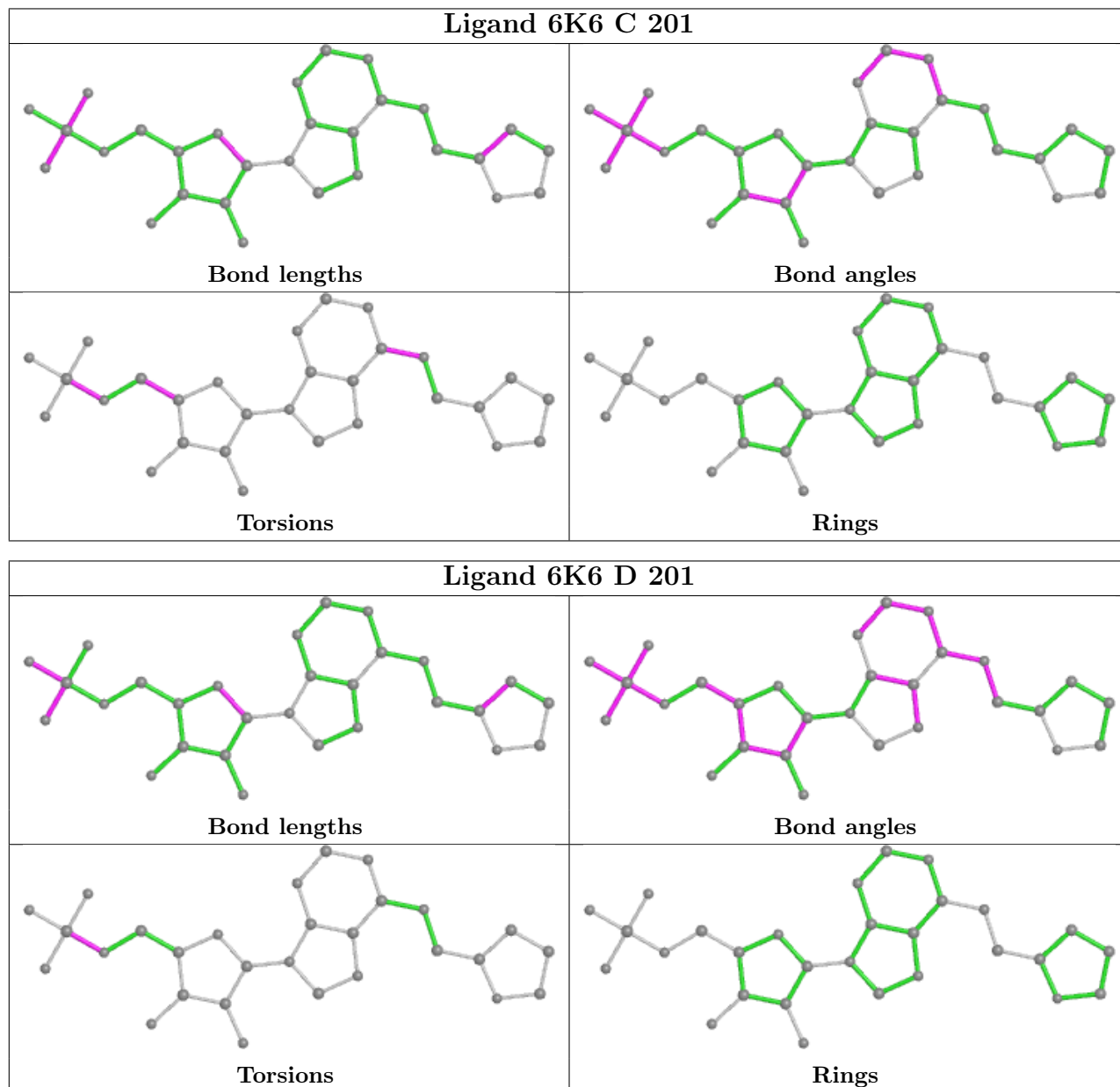
There are no ring outliers.

2 monomers are involved in 5 short contacts:

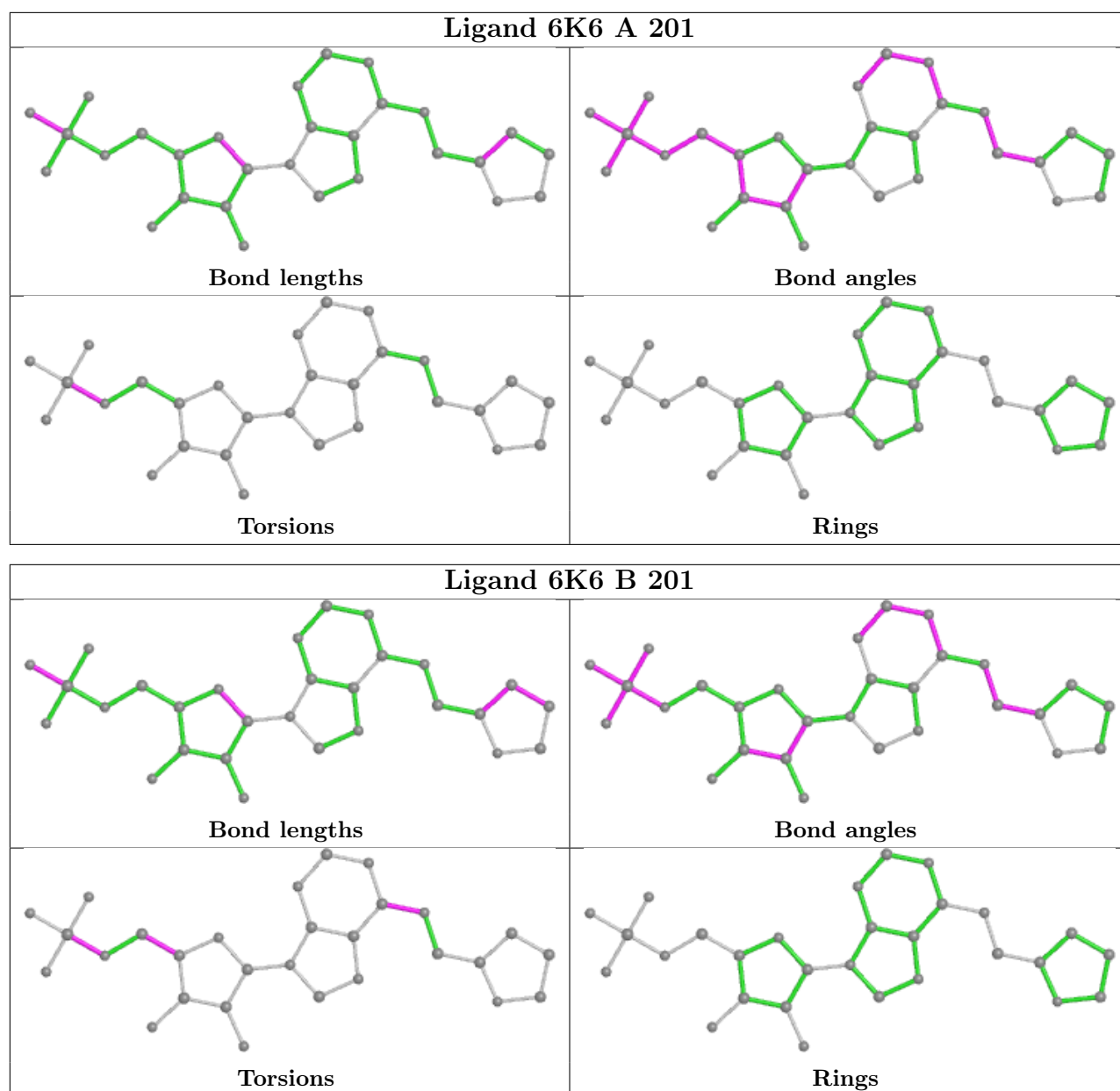
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	201	6K6	1	0
2	B	201	6K6	4	0

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

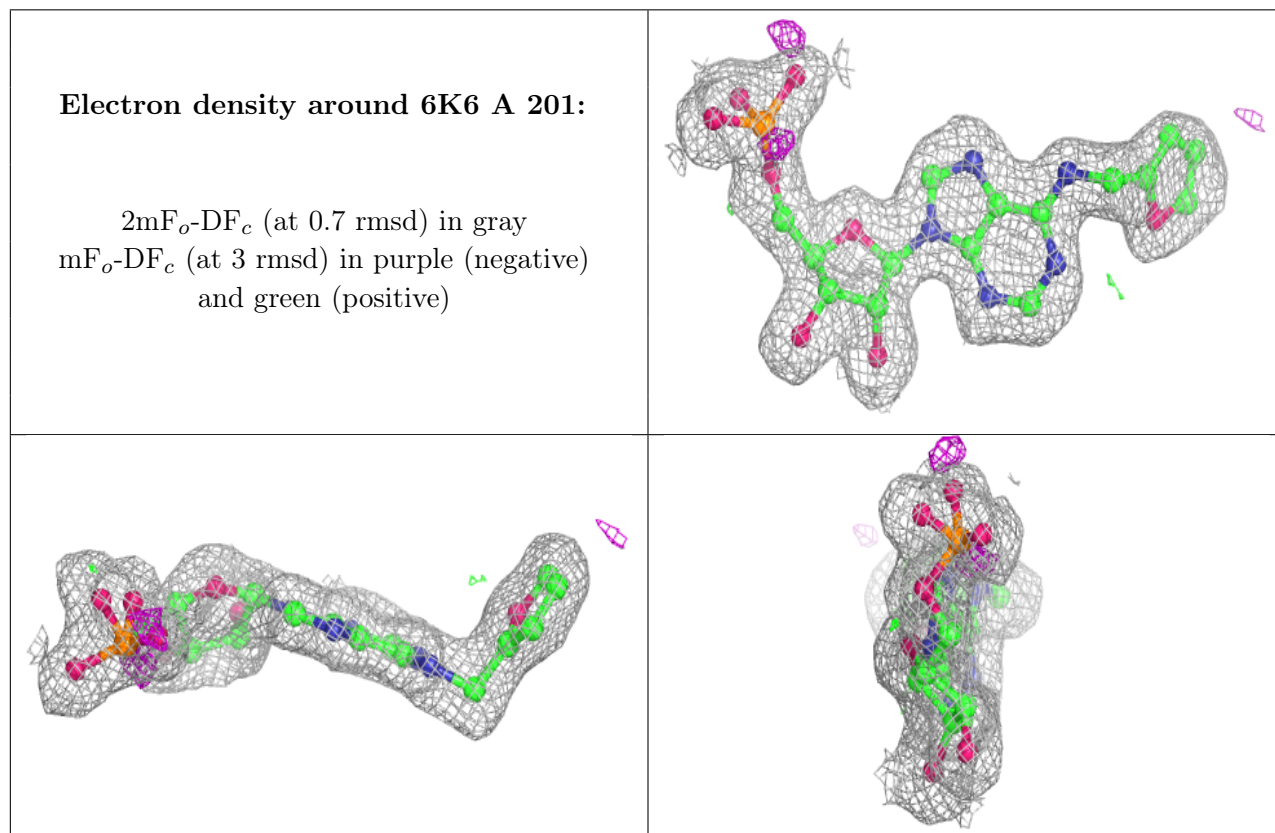
### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

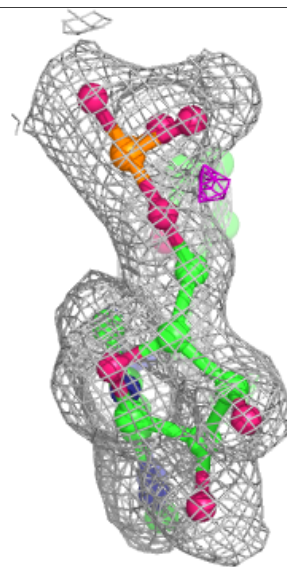
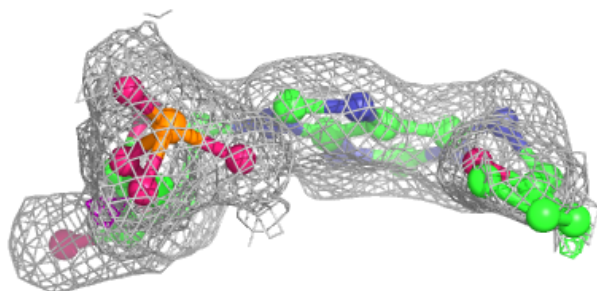
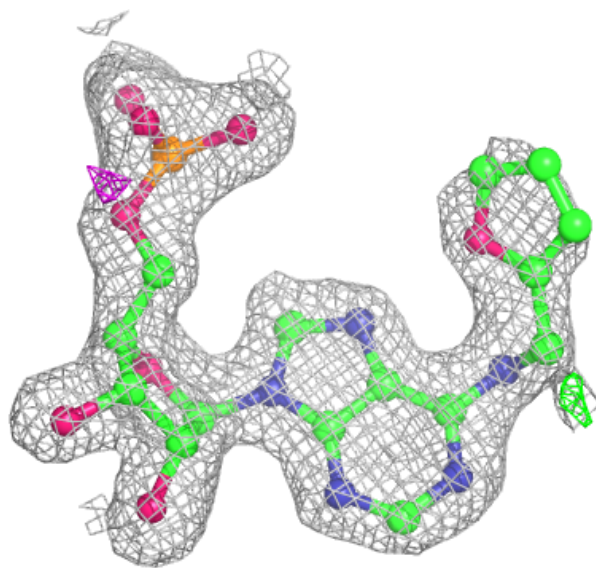
Unable to reproduce the depositors R factor - this section is therefore empty.

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.



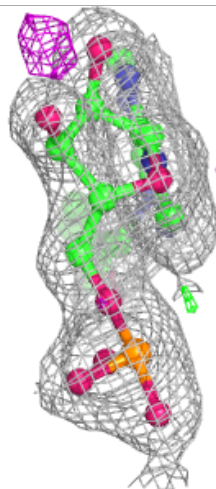
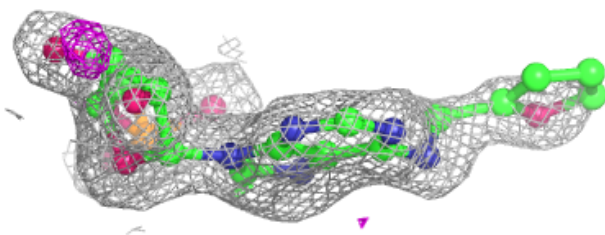
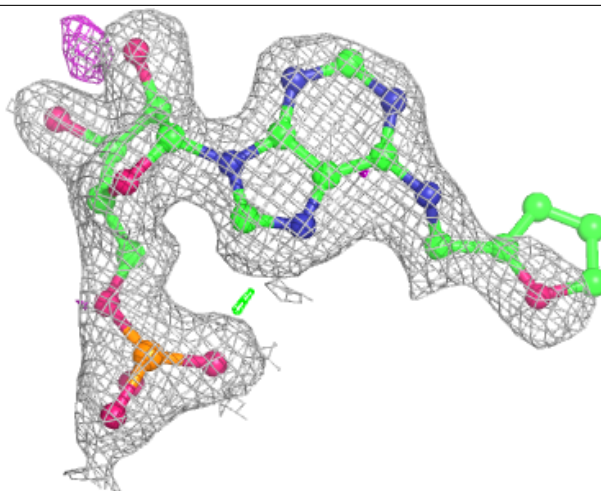
**Electron density around 6K6 B 201:**

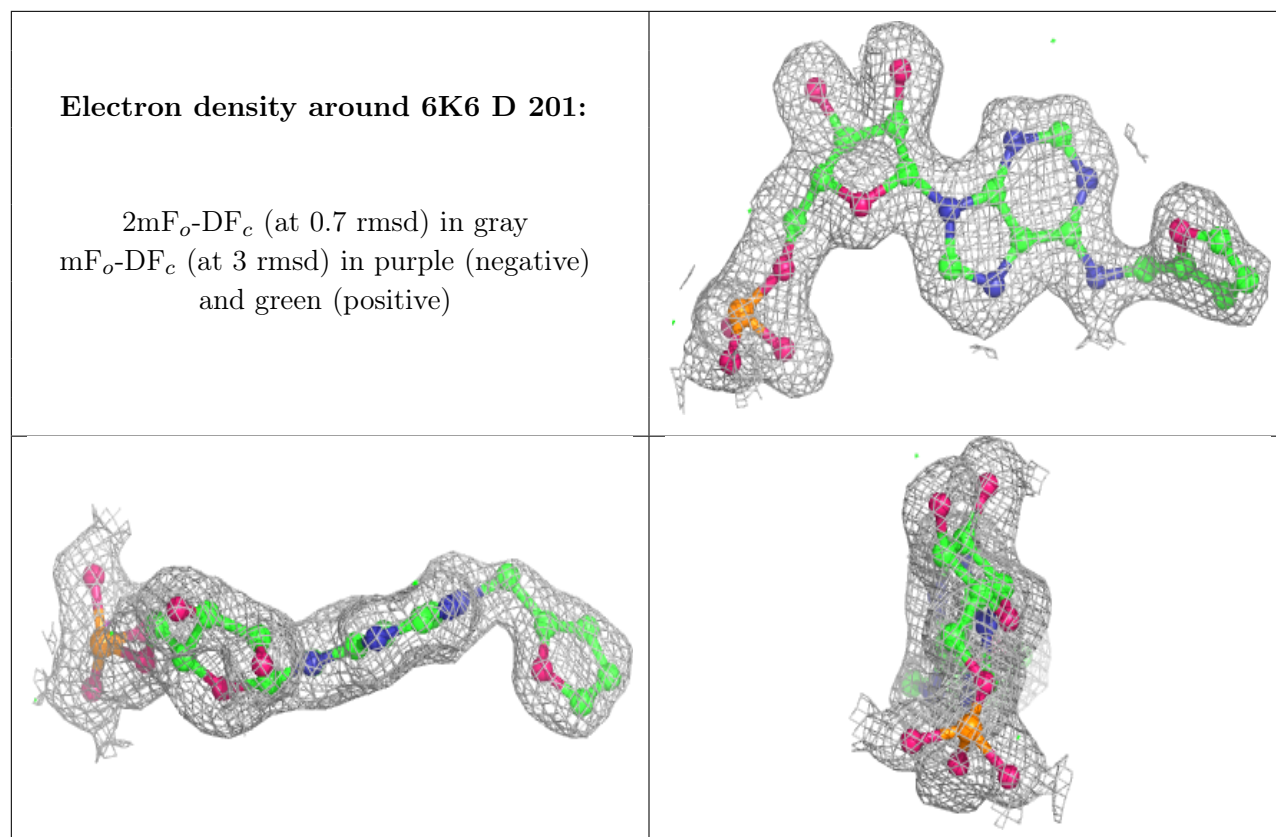
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 6K6 C 201:**

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





## 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.