



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 10:32 pm BST

PDB ID : 6BRX
Title : Crystal Structure of Human DNA polymerase kappa in complex with DNA containing the major cisplatin lesion
Authors : Jha, V.K.; Ling, H.
Deposited on : 2017-12-01
Resolution : 2.80 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

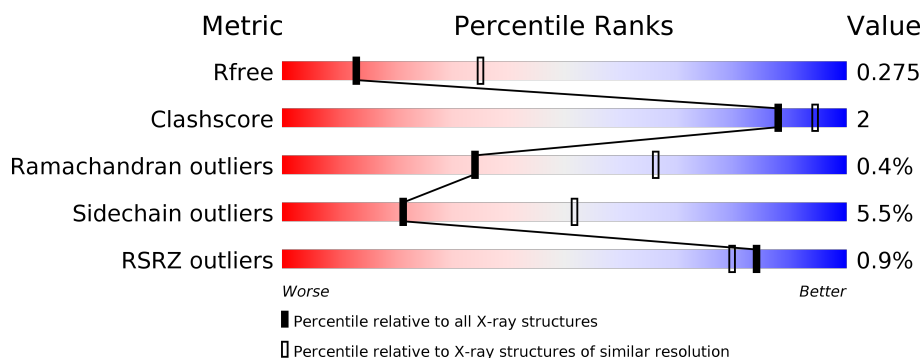
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 ≥ 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	551	<div> <div>%</div> <div> <div></div> <div>71%</div> <div>7%</div> <div>21%</div> </div> </div>
1	B	551	<div> <div>%</div> <div> <div></div> <div>72%</div> <div>6%</div> <div>22%</div> </div> </div>
2	C	9	<div> <div></div> <div> <div>78%</div> <div>22%</div> </div> </div>
2	P	9	<div> <div></div> <div> <div>89%</div> <div>11%</div> </div> </div>
3	D	13	<div> <div></div> <div> <div>54%</div> <div>46%</div> </div> </div>
3	T	13	<div> <div></div> <div> <div>77%</div> <div>23%</div> </div> </div>

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
6	PEG	D	601	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7902 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 DNA polymerase kappa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	S	0	0	0
			3375	2130	593	633	19			
1	B	430	Total	C	N	O	S	0	0	0
			3320	2097	583	620	20			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP Q9UBT6
A	-23	SER	-	expression tag	UNP Q9UBT6
A	-22	TYR	-	expression tag	UNP Q9UBT6
A	-21	TYR	-	expression tag	UNP Q9UBT6
A	-20	HIS	-	expression tag	UNP Q9UBT6
A	-19	HIS	-	expression tag	UNP Q9UBT6
A	-18	HIS	-	expression tag	UNP Q9UBT6
A	-17	HIS	-	expression tag	UNP Q9UBT6
A	-16	HIS	-	expression tag	UNP Q9UBT6
A	-15	HIS	-	expression tag	UNP Q9UBT6
A	-14	ASP	-	expression tag	UNP Q9UBT6
A	-13	TYR	-	expression tag	UNP Q9UBT6
A	-12	ASP	-	expression tag	UNP Q9UBT6
A	-11	ILE	-	expression tag	UNP Q9UBT6
A	-10	PRO	-	expression tag	UNP Q9UBT6
A	-9	THR	-	expression tag	UNP Q9UBT6
A	-8	THR	-	expression tag	UNP Q9UBT6
A	-7	GLU	-	expression tag	UNP Q9UBT6
A	-6	ASN	-	expression tag	UNP Q9UBT6
A	-5	LEU	-	expression tag	UNP Q9UBT6
A	-4	TYR	-	expression tag	UNP Q9UBT6
A	-3	PHE	-	expression tag	UNP Q9UBT6
A	-2	GLN	-	expression tag	UNP Q9UBT6
A	-1	GLY	-	expression tag	UNP Q9UBT6
A	0	ALA	-	expression tag	UNP Q9UBT6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-24	MET	-	initiating methionine	UNP Q9UBT6
B	-23	SER	-	expression tag	UNP Q9UBT6
B	-22	TYR	-	expression tag	UNP Q9UBT6
B	-21	TYR	-	expression tag	UNP Q9UBT6
B	-20	HIS	-	expression tag	UNP Q9UBT6
B	-19	HIS	-	expression tag	UNP Q9UBT6
B	-18	HIS	-	expression tag	UNP Q9UBT6
B	-17	HIS	-	expression tag	UNP Q9UBT6
B	-16	HIS	-	expression tag	UNP Q9UBT6
B	-15	HIS	-	expression tag	UNP Q9UBT6
B	-14	ASP	-	expression tag	UNP Q9UBT6
B	-13	TYR	-	expression tag	UNP Q9UBT6
B	-12	ASP	-	expression tag	UNP Q9UBT6
B	-11	ILE	-	expression tag	UNP Q9UBT6
B	-10	PRO	-	expression tag	UNP Q9UBT6
B	-9	THR	-	expression tag	UNP Q9UBT6
B	-8	THR	-	expression tag	UNP Q9UBT6
B	-7	GLU	-	expression tag	UNP Q9UBT6
B	-6	ASN	-	expression tag	UNP Q9UBT6
B	-5	LEU	-	expression tag	UNP Q9UBT6
B	-4	TYR	-	expression tag	UNP Q9UBT6
B	-3	PHE	-	expression tag	UNP Q9UBT6
B	-2	GLN	-	expression tag	UNP Q9UBT6
B	-1	GLY	-	expression tag	UNP Q9UBT6
B	0	ALA	-	expression tag	UNP Q9UBT6

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*AP*CP*AP*TP*AP*CP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	P	0	0	0
			181	87	33	52	9			
2	P	9	Total	C	N	O	P	0	0	0
			181	87	33	52	9			

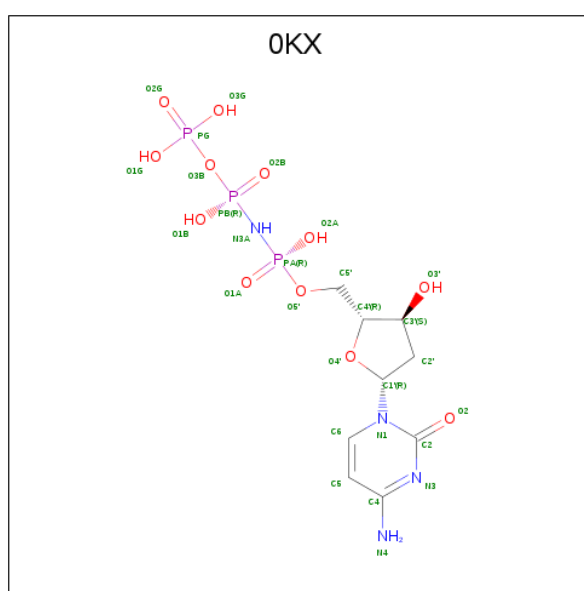
- Molecule 3 is a DNA chain called DNA (5'-D(*TP*AP*TP*GP*GP*TP*GP*TP*AP*TP*GP*TP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	13	Total	C	N	O	P	0	0	0
			267	130	47	78	12			
3	T	13	Total	C	N	O	P	0	0	0
			267	130	47	78	12			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	A	3	Total	Mg	0	0
			3	3		

- Molecule 5 is 2'-deoxy-5'-O-[(R)-hydroxy{[(R)-hydroxy(phosphonooxy)phosphoryl]amino}phosphoryl]cytidine (three-letter code: OKX) (formula: C₉H₁₇N₄O₁₂P₃).



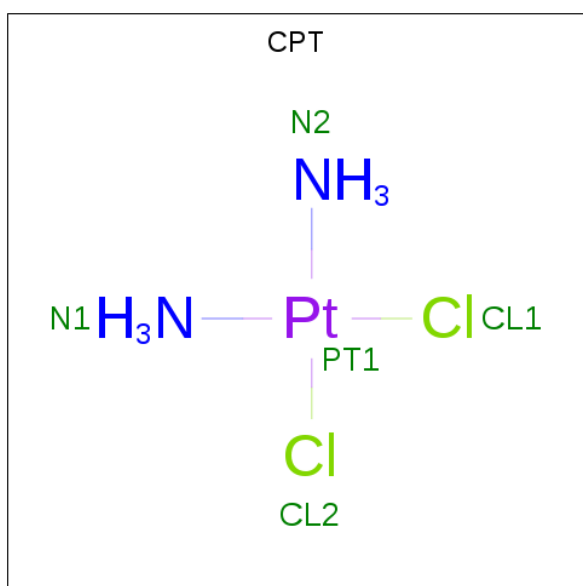
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			28	9	4	12	3		
5	B	1	Total	C	N	O	P	0	0
			28	9	4	12	3		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			7	4	3		
6	T	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is Cisplatin (three-letter code: CPT) (formula: $\text{Cl}_2\text{H}_6\text{N}_2\text{Pt}$).

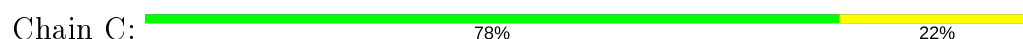


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	N	Pt	0	0
			3	2	1		
7	T	1	Total	N	Pt	0	0
			3	2	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	110	Total 110	O 110	0	0
8	B	78	Total 78	O 78	0	0
8	C	9	Total 9	O 9	0	0
8	D	11	Total 11	O 11	0	0
8	P	9	Total 9	O 9	0	0
8	T	13	Total 13	O 13	0	0

- Molecule 1: DNA polymerase kappa





- Molecule 2: DNA (5'-D(P*TP*AP*CP*AP*TP*AP*CP*AP*C)-3')

Chain P: 89% 11%



- Molecule 3: DNA (5'-D(*TP*AP*TP*GP*GP*TP*GP*TP*AP*TP*GP*TP*A)-3')

Chain D: 54% 46%



- Molecule 3: DNA (5'-D(*TP*AP*TP*GP*GP*TP*GP*TP*AP*TP*GP*TP*A)-3')

Chain T: 77% 23%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.69Å 129.06Å 168.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.47 – 2.80 48.42 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.47-2.80) 99.4 (48.42-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.214 , 0.269 0.218 , 0.275	Depositor DCC
R_{free} test set	1405 reflections (3.87%)	wwPDB-VP
Wilson B-factor (Å ²)	61.9	Xtriage
Anisotropy	0.846	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7902	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: 0KX, PEG, CPT, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/3427	0.67	0/4623
1	B	0.43	0/3373	0.67	0/4556
2	C	0.38	0/202	0.75	0/308
2	P	0.35	0/202	0.71	0/308
3	D	0.46	0/299	0.85	0/462
3	T	0.40	0/299	0.82	0/462
All	All	0.43	0/7802	0.69	0/10719

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	3375	0	3372	11	0
1	B	3320	0	3273	15	0
2	C	181	0	101	1	1
2	P	181	0	102	1	1
3	D	267	0	148	5	1
3	T	267	0	148	1	1
4	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	P	1	0	0	0	0
5	A	28	0	15	0	0
5	B	28	0	14	0	0
6	D	7	0	10	1	0
6	T	7	0	10	0	0
7	D	3	0	0	0	0
7	T	3	0	0	0	0
8	A	110	0	0	0	0
8	B	78	0	0	2	0
8	C	9	0	0	0	0
8	D	11	0	0	0	0
8	P	9	0	0	0	0
8	T	13	0	0	0	0
All	All	7902	0	7193	30	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 2.

All (30) 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:394:TYR:CE1	1:B:398:ILE:HD11	2.33	0.63
1:B:335:ILE:HD11	1:B:345:PHE:CD1	2.37	0.59
1:B:454:ARG:NH2	2:P:5:DT:OP2	2.36	0.59
1:B:354:VAL:HG11	1:B:398:ILE:HG12	1.88	0.55
1:A:108:MET:HB2	1:A:198:ASP:HB2	1.91	0.53
1:B:108:MET:HB2	1:B:198:ASP:HB2	1.90	0.52
1:B:504:LEU:HB3	1:B:506:LEU:HD13	1.93	0.50
1:B:171:PHE:CD2	1:B:175:ARG:NH2	2.80	0.50
3:D:2:DT:H2''	3:D:3:DA:H5'	1.94	0.49
1:A:351:ILE:HG12	1:A:357:ILE:HG21	1.94	0.49
1:A:444:GLN:HE21	1:B:444:GLN:NE2	2.11	0.49
1:B:171:PHE:CE2	1:B:175:ARG:NH2	2.82	0.47
1:B:352:ARG:NH2	8:B:702:HOH:O	2.48	0.46
3:D:2:DT:H2''	3:D:3:DA:C5'	2.45	0.46
1:A:214:TRP:O	1:A:219:ARG:NH1	2.49	0.46
3:T:5:DG:H2''	3:T:6:DG:O5'	2.17	0.45
1:A:32:ASP:O	1:A:36:ILE:HG13	2.16	0.45
2:C:10:DA:C2	3:D:10:DA:C2	3.07	0.43
1:A:354:VAL:HG11	1:A:398:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:5:DG:C2	6:D:601:PEG:H21	2.52	0.43
1:A:444:GLN:HG2	1:B:444:GLN:HE21	1.84	0.43
1:B:500:PHE:CG	1:B:501:PRO:HA	2.54	0.42
1:B:512:ARG:NH2	8:B:705:HOH:O	2.53	0.42
1:A:153:PRO:HG2	1:A:156:ILE:HD12	2.02	0.42
1:B:153:PRO:HG2	1:B:156:ILE:HD12	2.02	0.41
1:A:35:LYS:O	1:A:39:ILE:HG13	2.20	0.41
1:B:425:ILE:CD1	1:B:434:LEU:HD13	2.51	0.41
3:D:5:DG:H2''	3:D:6:DG:O5'	2.21	0.40
1:A:500:PHE:CG	1:A:501:PRO:HA	2.56	0.40
1:A:394:TYR:CE1	1:A:398:ILE:HD11	2.56	0.40

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)
3:D:14:DA:O3'	2:P:5:DT:P[3_555]	1.92	0.28
2:C:5:DT:P	3:T:14:DA:O3'[3_555]	1.92	0.28

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	429/551 (78%)	416 (97%)	11 (3%)	2 (0%)	29	61
1	B	426/551 (77%)	411 (96%)	14 (3%)	1 (0%)	47	78
All	All	855/1102 (78%)	827 (97%)	25 (3%)	3 (0%)	34	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	409	ARG

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Mol	Chain	Res	Type
1	A	479	SER
1	B	479	SER

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	361/495 (73%)	338 (94%)	23 (6%)	17	45
1	B	348/495 (70%)	332 (95%)	16 (5%)	27	60
All	All	709/990 (72%)	670 (94%)	39 (6%)	21	52

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ILE
1	A	74	ILE
1	A	122	GLU
1	A	123	LEU
1	A	126	LYS
1	A	132	SER
1	A	148	VAL
1	A	167	VAL
1	A	181	VAL
1	A	198	ASP
1	A	212	GLN
1	A	283	SER
1	A	284	VAL
1	A	288	THR
1	A	304	LYS
1	A	306	THR
1	A	318	MET
1	A	351	ILE
1	A	402	LEU
1	A	434	LEU
1	A	475	SER

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Mol	Chain	Res	Type
1	A	506	LEU
1	A	507	ARG
1	B	60	VAL
1	B	62	GLN
1	B	123	LEU
1	B	148	VAL
1	B	163	GLN
1	B	181	VAL
1	B	191	ASN
1	B	198	ASP
1	B	283	SER
1	B	284	VAL
1	B	288	THR
1	B	390	THR
1	B	433	SER
1	B	434	LEU
1	B	475	SER
1	B	507	ARG

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

Mol	Chain	Res	Type
1	B	62	GLN
1	B	66	ASN
1	B	406	HIS
1	B	444	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	0KX	B	602	4	26,29,29	1.57	2 (7%)	33,45,45	1.09	1 (3%)
6	PEG	D	601	-	6,6,6	0.49	0	5,5,5	0.26	0
5	0KX	A	604	4	26,29,29	1.56	2 (7%)	33,45,45	1.03	2 (6%)
7	CPT	D	602	3	0,2,4	0.00	-	-		
6	PEG	T	601	-	6,6,6	0.86	0	5,5,5	0.59	0
7	CPT	T	602	3	0,2,4	0.00	-	-		

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	0KX	B	602	4	-	6/16/34/34	0/2/2/2
6	PEG	D	601	-	-	1/4/4/4	-
6	PEG	T	601	-	-	3/4/4/4	-
5	0KX	A	604	4	-	3/16/34/34	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	604	0KX	PB-O2B	6.48	1.56	1.46
5	B	602	0KX	PA-O1A	6.45	1.56	1.46
5	B	602	0KX	PA-O2A	-3.83	1.46	1.56
5	A	604	0KX	PB-O1B	-3.82	1.46	1.56

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	602	0KX	C2-N3-C4	3.71	120.10	116.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	604	0KX	C2-N3-C4	3.65	120.04	116.34
5	A	604	0KX	C2'-C1'-N1	-2.03	109.59	114.27

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	602	0KX	PB-O3B-PG-O3G
5	B	602	0KX	PA-N3A-PB-O2B
5	B	602	0KX	PB-N3A-PA-O1A
5	B	602	0KX	O4'-C1'-N1-C6
5	A	604	0KX	PB-O3B-PG-O3G
6	T	601	PEG	O1-C1-C2-O2
6	T	601	PEG	C4-C3-O2-C2
6	T	601	PEG	O2-C3-C4-O4
6	D	601	PEG	C1-C2-O2-C3
5	B	602	0KX	PB-O3B-PG-O1G
5	A	604	0KX	PB-O3B-PG-O1G
5	B	602	0KX	PB-N3A-PA-O5'
5	A	604	0KX	PB-N3A-PA-O5'

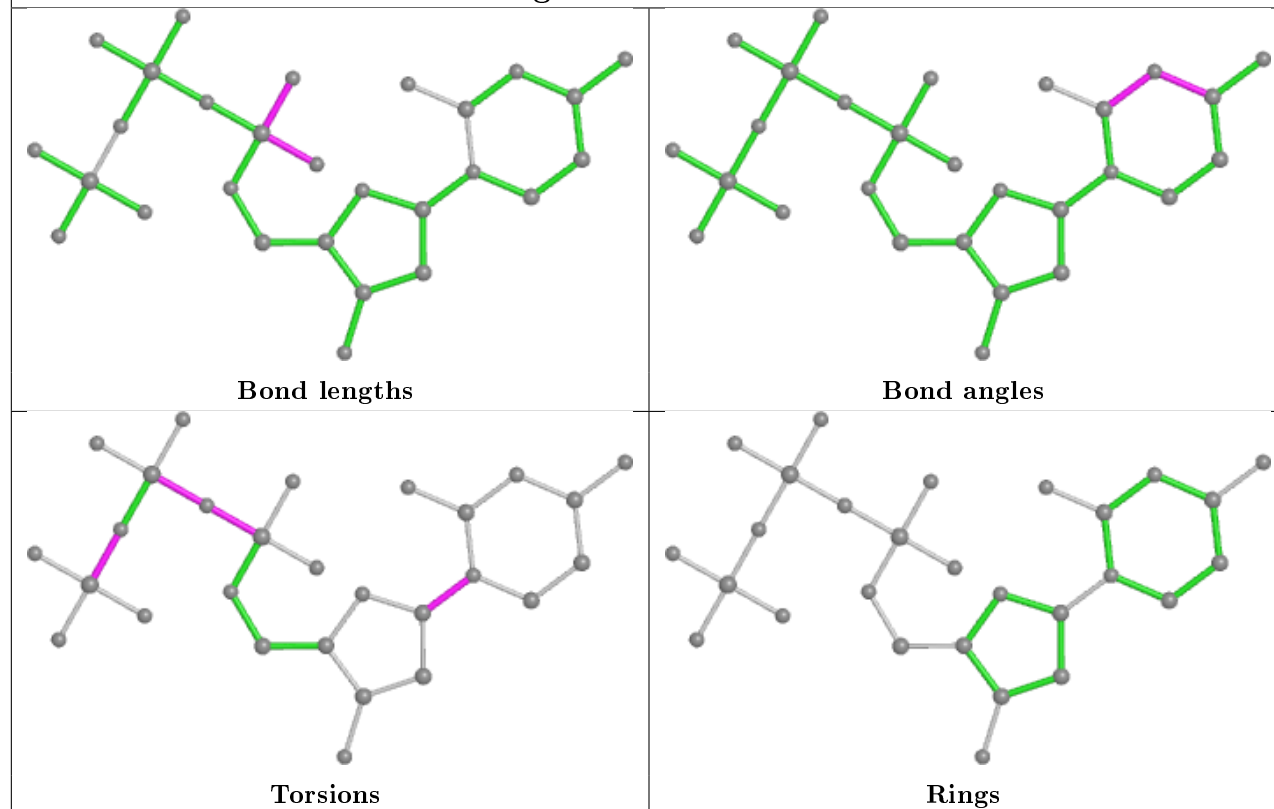
There are no ring outliers.

1 monomer is involved in 1 short contact:

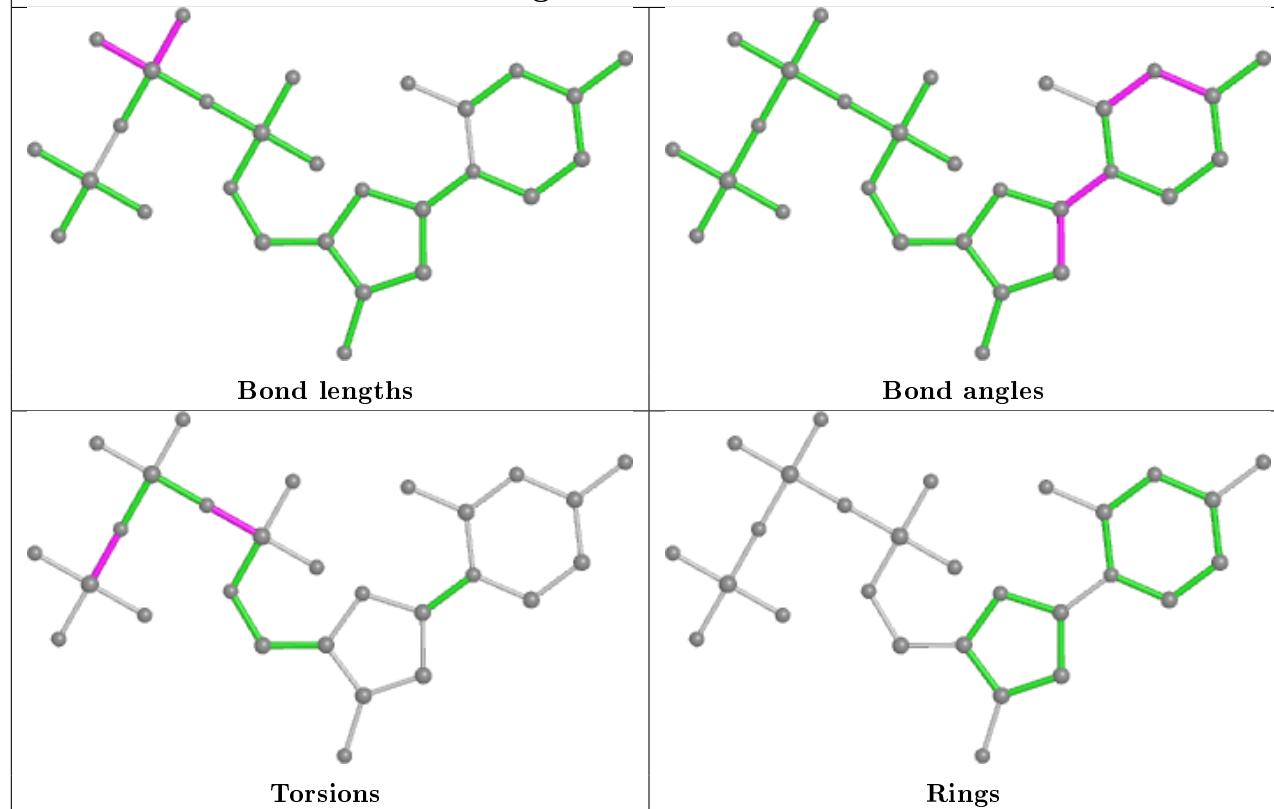
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	601	PEG	1	0

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.

Ligand 0KX B 602



Ligand 0KX A 604



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	433/551 (78%)	-0.12	3 (0%) 87 84	46, 71, 106, 126	0
1	B	430/551 (78%)	-0.14	5 (1%) 79 73	48, 79, 114, 140	0
2	C	9/9 (100%)	-0.44	0 100 100	56, 59, 65, 66	0
2	P	9/9 (100%)	-0.37	0 100 100	60, 66, 75, 77	0
3	D	13/13 (100%)	-0.28	0 100 100	51, 67, 80, 89	0
3	T	13/13 (100%)	-0.33	0 100 100	57, 69, 80, 83	0
All	All	907/1146 (79%)	-0.14	8 (0%) 84 80	46, 75, 109, 140	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	31	LEU	3.7
1	A	29	GLU	2.9
1	B	410	ASP	2.6
1	B	222	PHE	2.6
1	B	283	SER	2.5
1	A	224	LYS	2.3
1	B	411	GLY	2.2
1	B	412	GLU	2.2

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

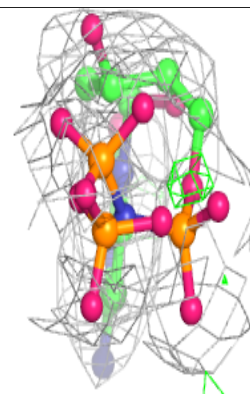
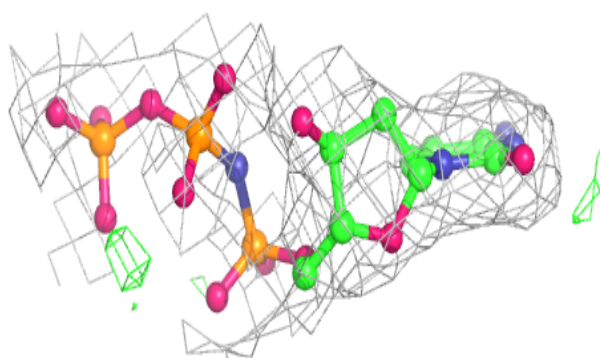
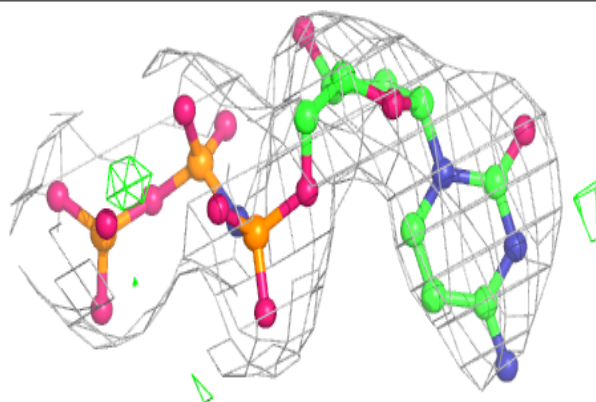
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

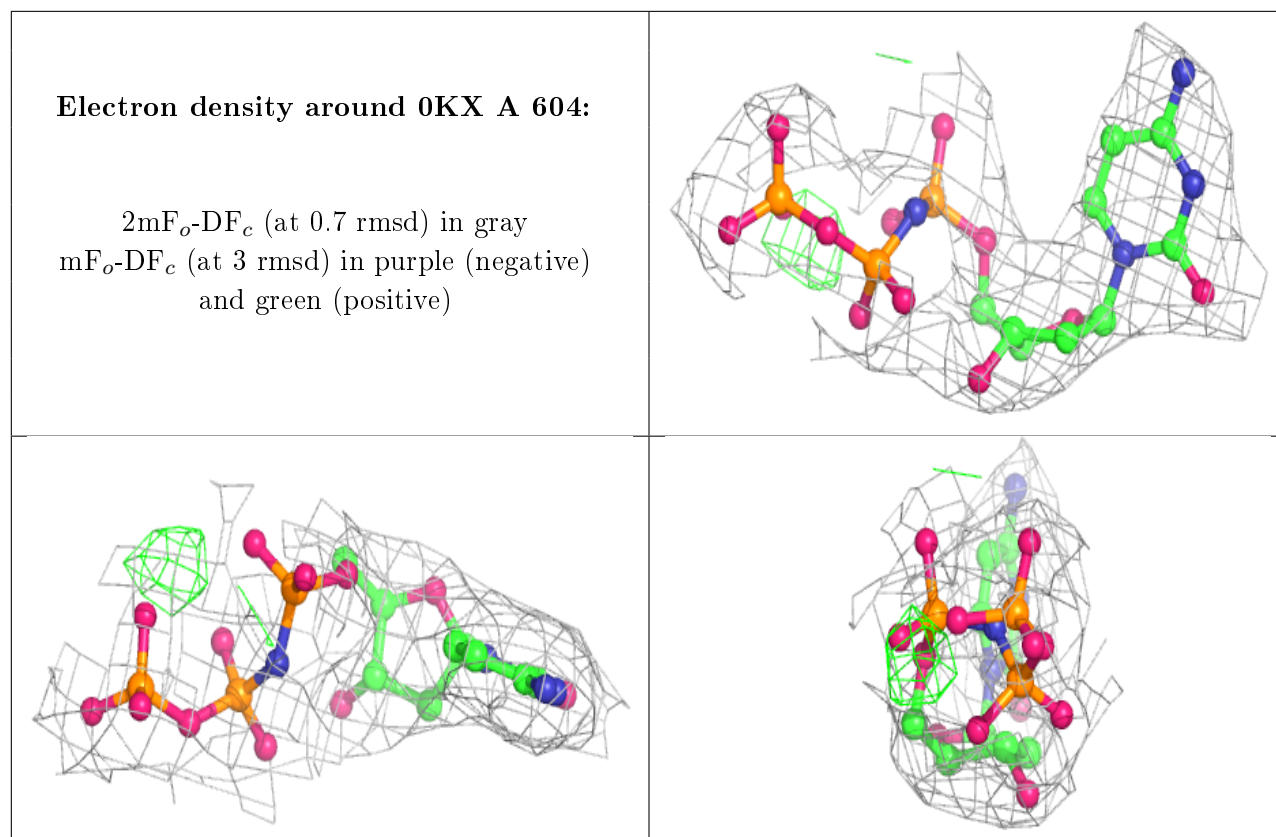
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MG	P	101	1/1	0.55	0.34	79,79,79,79	0
4	MG	A	602	1/1	0.60	0.21	66,66,66,66	0
6	PEG	D	601	7/7	0.78	0.47	75,82,86,86	0
6	PEG	T	601	7/7	0.85	0.26	44,46,47,48	0
4	MG	A	601	1/1	0.94	0.28	52,52,52,52	0
4	MG	B	601	1/1	0.94	0.24	66,66,66,66	0
4	MG	A	603	1/1	0.95	0.09	66,66,66,66	0
5	OKX	B	602	28/28	0.96	0.18	71,79,84,86	0
5	OKX	A	604	28/28	0.97	0.19	56,64,74,75	0
7	CPT	T	602	3/5	0.99	0.11	57,57,59,73	0
7	CPT	D	602	3/5	0.99	0.11	58,58,61,72	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 OKX B 602:

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.