



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2024 – 10:24 PM EST

PDB ID : 5W2A
Title : Structure of human DNA polymerase kappa in complex with Lucidin-derived DNA adduct and incoming dCMPNPP
Authors : Jha, V.K.; Ling, H.
Deposited on : 2017-06-06
Resolution : 2.90 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

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)
Xtrriage (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

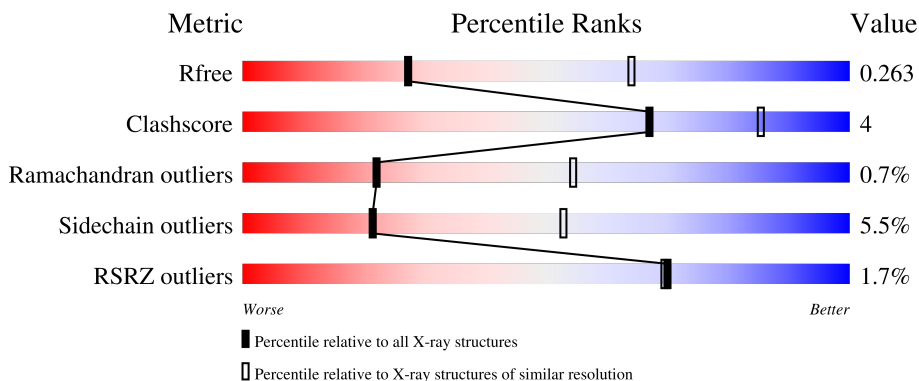
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 ≥ 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	 2% 70% 8% 22%
1	B	551	 2% 70% 7% 22%
2	C	9	 67% 33%
2	P	9	 67% 33%
3	D	13	 77% 23%

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Mol	Chain	Length	Quality of chain
3	T	13	 77% 23%

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
5	GOL	B	603	-	-	-	X
7	PGE	A	604	-	-	-	X
7	PGE	B	605	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7735 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
			Total	C	N	O	S			
1	A	431	3349	2117	593	620	19	0	0	0
1	B	431	3314	2101	585	608	20	0	0	0

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*GP*CP*GP*GP*AP*TP*CP*AP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	P	0	0	0
			188	88	38	53	9			
2	P	9	Total	C	N	O	P	0	0	0
			188	88	38	53	9			

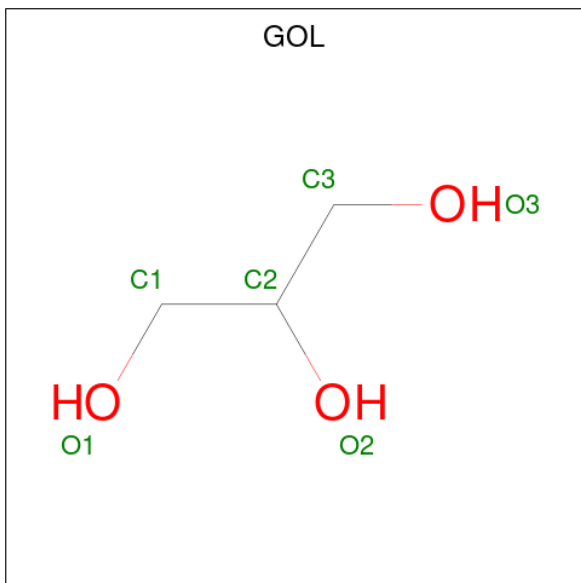
- Molecule 3 is a DNA chain called DNA (5'-D(*AP*TP*GP*(LDG)P*CP*TP*GP*AP*TP*CP*CP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	13	Total	C	N	O	P	0	0	0
			283	143	48	80	12			
3	T	13	Total	C	N	O	P	0	0	0
			283	143	48	80	12			

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

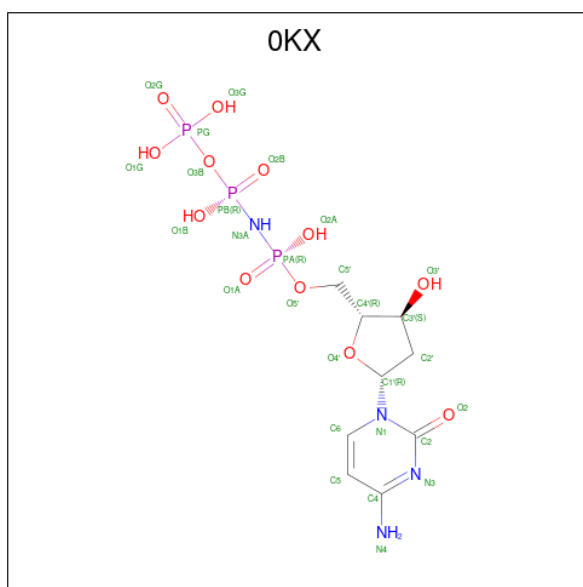
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0
4	B	1	Total Mg 1 1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



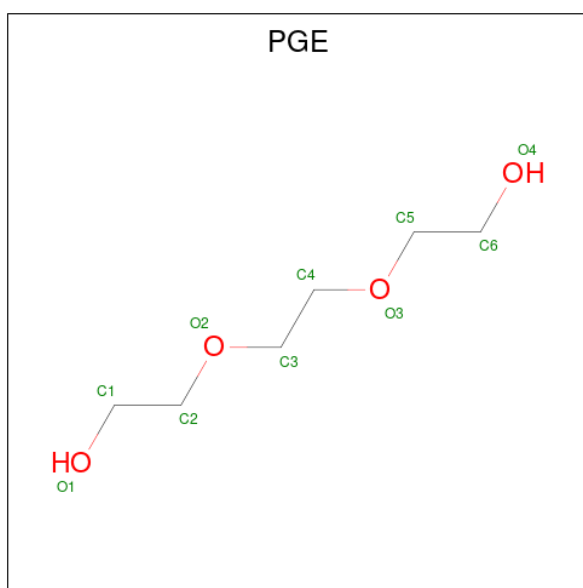
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	P	1	Total C O 6 3 3	0	0

- Molecule 6 is 2'-deoxy-5'-O-[(R)-hydroxy{[(R)-hydroxy(phosphonooxy)phosphoryl]amino}p
hosphoryl]cytidine (three-letter code: 0KX) (formula: C₉H₁₇N₄O₁₂P₃).



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

- Molecule 7 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	10	6	4	0	0
7	B	1	10	6	4	0	0

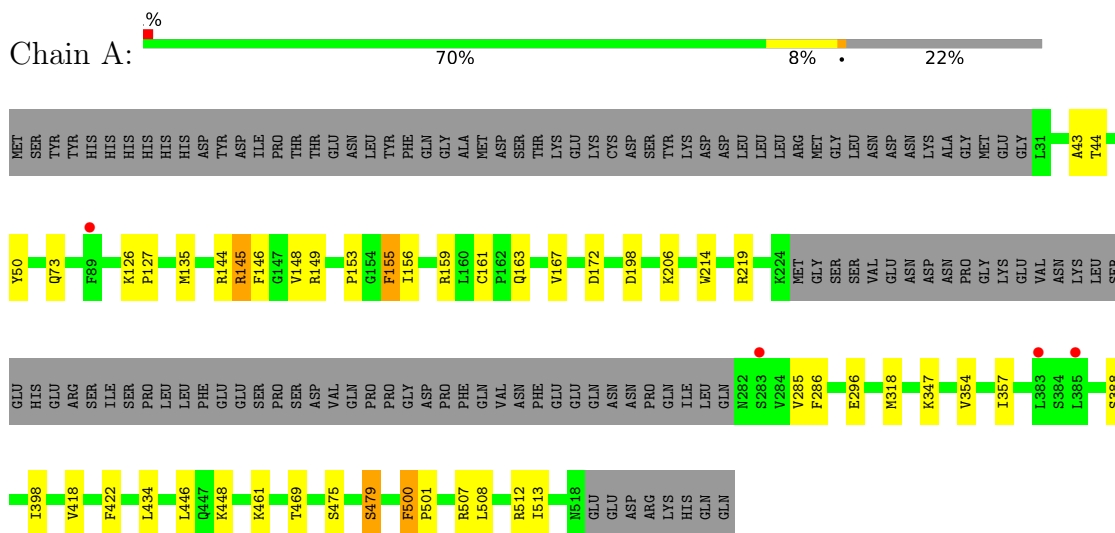
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	8	Total O 8 8	0	0
8	B	14	Total O 14 14	0	0
8	C	3	Total O 3 3	0	0
8	D	2	Total O 2 2	0	0
8	T	1	Total O 1 1	0	0

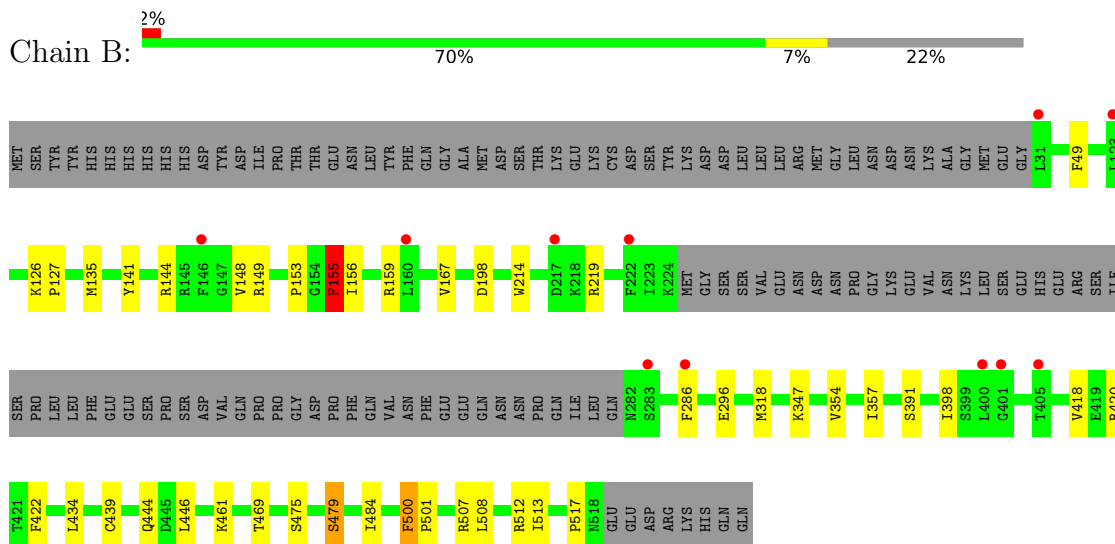
3 Residue-property plots i

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: DNA polymerase kappa



- Molecule 1: DNA polymerase kappa



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






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

Chain P:  67% 33%




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

Chain D:  77% 23%



- Molecule 3: DNA (5'-D(*AP*TP*GP*(LDG)P*CP*TP*GP*AP*TP*CP*CP*GP*C)-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	63.89Å 129.01Å 167.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.25 – 2.90 47.25 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.25-2.90) 99.0 (47.25-2.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.91Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.231 , 0.270 0.231 , 0.263	Depositor DCC
R_{free} test set	1228 reflections (3.94%)	wwPDB-VP
Wilson B-factor (Å ²)	76.8	Xtrriage
Anisotropy	1.008	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 70.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7735	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% 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: LDG, MG, PGE, 0KX, GOL

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	0.45	0/3401	0.71	0/4590
1	B	0.45	0/3367	0.70	1/4548 (0.0%)
2	C	0.45	0/211	0.79	0/324
2	P	0.41	0/211	0.83	0/324
3	D	0.45	0/267	0.80	0/408
3	T	0.48	0/267	0.77	0/408
All	All	0.45	0/7724	0.72	1/10602 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	155	PHE	CB-CG-CD1	5.46	124.62	120.80

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	3349	0	3342	29	0
1	B	3314	0	3275	28	0
2	C	188	0	101	1	2
2	P	188	0	101	1	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	283	0	134	6	1
3	T	283	0	134	10	2
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	6	0	8	0	0
5	B	12	0	16	0	0
5	P	6	0	8	0	0
6	A	28	0	16	0	0
6	B	28	0	14	0	0
7	A	10	0	14	0	0
7	B	10	0	14	0	0
8	A	8	0	0	0	0
8	B	14	0	0	0	0
8	C	3	0	0	0	0
8	D	2	0	0	0	0
8	T	1	0	0	0	0
All	All	7735	0	7177	58	3

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 4.

All (58) 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:500:PHE:HD1	1:A:501:PRO:HA	1.32	0.95
1:B:500:PHE:HD1	1:B:501:PRO:HA	1.34	0.92
1:B:155:PHE:CE1	1:B:156:ILE:HG13	2.21	0.75
1:B:155:PHE:HD1	1:B:156:ILE:N	1.87	0.73
1:A:500:PHE:CD1	1:A:501:PRO:HA	2.22	0.70
1:A:155:PHE:CE1	1:A:156:ILE:HG13	2.25	0.70
1:B:155:PHE:CD2	3:T:3:DT:C5	2.80	0.70
1:B:500:PHE:CD1	1:B:501:PRO:HA	2.23	0.68
1:A:155:PHE:HD1	1:A:156:ILE:N	1.94	0.64
1:A:161:CYS:SG	1:A:163:GLN:HG3	2.40	0.62
1:A:155:PHE:HD2	3:D:3:DT:C5	2.18	0.61
1:B:155:PHE:CD2	3:T:3:DT:C6	2.89	0.61
1:A:354:VAL:HG11	1:A:398:ILE:HD12	1.83	0.61
1:B:155:PHE:CD2	3:T:3:DT:C4	2.89	0.60
1:A:155:PHE:HD2	3:D:3:DT:C4	2.20	0.59
1:A:155:PHE:CD2	3:D:3:DT:C5	2.91	0.59
1:B:155:PHE:HD2	3:T:3:DT:C6	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:354:VAL:HG11	1:B:398:ILE:HD12	1.84	0.58
1:A:144:ARG:O	1:A:146:PHE:N	2.37	0.57
1:B:155:PHE:HD2	3:T:3:DT:C4	2.23	0.57
1:B:155:PHE:HD2	3:T:3:DT:C5	2.21	0.56
1:A:500:PHE:HD1	1:A:501:PRO:CA	2.14	0.56
1:B:500:PHE:HD1	1:B:501:PRO:CA	2.15	0.54
1:A:155:PHE:CD1	1:A:156:ILE:N	2.76	0.53
2:P:12:DA:H2''	2:P:13:DG:H5'	1.90	0.53
1:A:286:PHE:CE2	1:A:296:GLU:HA	2.43	0.53
1:B:155:PHE:CD1	1:B:156:ILE:HG13	2.44	0.52
1:B:286:PHE:CE2	1:B:296:GLU:HA	2.44	0.52
1:B:141:TYR:HA	1:B:144:ARG:HD2	1.92	0.52
1:B:155:PHE:HE1	1:B:156:ILE:HG13	1.73	0.51
1:A:214:TRP:O	1:A:219:ARG:NH1	2.44	0.50
2:C:12:DA:H2''	2:C:13:DG:H5'	1.93	0.50
1:B:214:TRP:O	1:B:219:ARG:NH1	2.45	0.50
1:A:135:MET:HA	1:A:153:PRO:HA	1.93	0.49
1:A:388:SER:OG	3:D:12:DC:OP1	2.30	0.49
1:A:144:ARG:O	1:A:145:ARG:C	2.50	0.49
1:B:155:PHE:CE2	3:T:3:DT:C5	3.01	0.48
1:A:155:PHE:HD1	1:A:156:ILE:H	1.59	0.47
1:B:155:PHE:HD2	3:T:3:DT:C2	2.33	0.47
1:A:155:PHE:CD1	1:A:156:ILE:HG13	2.50	0.46
1:B:439:CYS:SG	1:B:484:ILE:HG22	2.55	0.46
1:A:126:LYS:HG2	1:A:127:PRO:HD2	1.98	0.46
1:A:155:PHE:CD2	3:D:3:DT:C4	3.03	0.46
1:A:43:ALA:HB1	1:A:159:ARG:HE	1.81	0.45
1:A:44:THR:HG22	1:A:50:TYR:CD1	2.51	0.44
1:B:135:MET:HA	1:B:153:PRO:HA	2.00	0.44
1:B:155:PHE:CE2	3:T:3:DT:C6	3.06	0.44
1:B:155:PHE:CD1	1:B:156:ILE:N	2.76	0.43
1:B:126:LYS:HG2	1:B:127:PRO:HD2	2.00	0.43
1:A:461:LYS:HB3	1:A:508:LEU:HB3	2.01	0.43
1:B:446:LEU:HD11	1:B:513:ILE:HG21	2.01	0.42
1:A:155:PHE:HD2	3:D:3:DT:C6	2.38	0.42
1:A:172:ASP:OD2	1:B:420:ARG:HD2	2.20	0.42
1:B:461:LYS:HB3	1:B:508:LEU:HB3	2.02	0.41
1:A:285:VAL:C	1:A:286:PHE:HD1	2.24	0.41
1:B:49:PHE:CE2	3:T:4:DG:C2	3.08	0.41
1:A:354:VAL:HG11	1:A:398:ILE:CD1	2.50	0.41
1:A:446:LEU:HD11	1:A:513:ILE:HG21	2.02	0.40

All (3) 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)
2:C:5:DG:OP2	3:T:14:DC:O3'[3_555]	1.78	0.42
2:C:5:DG:P	3:T:14:DC:O3'[3_555]	2.07	0.13
3:D:14:DC:O3'	2:P:5:DG:OP1[3_555]	2.15	0.05

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	427/551 (78%)	402 (94%)	22 (5%)	3 (1%)	22	54
1	B	427/551 (78%)	401 (94%)	23 (5%)	3 (1%)	22	54
All	All	854/1102 (78%)	803 (94%)	45 (5%)	6 (1%)	22	54

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	517	PRO
1	A	145	ARG
1	A	347	LYS
1	B	347	LYS
1	A	479	SER
1	B	479	SER

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	353/495 (71%)	334 (95%)	19 (5%)	22	54
1	B	342/495 (69%)	323 (94%)	19 (6%)	21	52
All	All	695/990 (70%)	657 (94%)	38 (6%)	21	53

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	148	VAL
1	A	149	ARG
1	A	155	PHE
1	A	167	VAL
1	A	198	ASP
1	A	206	LYS
1	A	318	MET
1	A	357	ILE
1	A	418	VAL
1	A	422	PHE
1	A	434	LEU
1	A	448	LYS
1	A	469	THR
1	A	475	SER
1	A	479	SER
1	A	500	PHE
1	A	507	ARG
1	A	512	ARG
1	B	148	VAL
1	B	149	ARG
1	B	155	PHE
1	B	159	ARG
1	B	167	VAL
1	B	198	ASP
1	B	318	MET
1	B	357	ILE
1	B	391	SER
1	B	418	VAL
1	B	422	PHE
1	B	434	LEU
1	B	444	GLN
1	B	469	THR
1	B	475	SER
1	B	479	SER

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Mol	Chain	Res	Type
1	B	500	PHE
1	B	507	ARG
1	B	512	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	212	GLN
1	B	212	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	GOL	P	101	-	5,5,5	0.48	0	5,5,5	0.33	0
6	OKX	B	604	4	28,29,29	1.64	4 (14%)	40,45,45	1.03	1 (2%)
5	GOL	B	603	-	5,5,5	0.47	0	5,5,5	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	OKX	A	603	4	28,29,29	1.03	1 (3%)	40,45,45	0.93	0
5	GOL	A	602	-	5,5,5	0.45	0	5,5,5	0.38	0
5	GOL	B	602	-	5,5,5	0.43	0	5,5,5	0.40	0
7	PGE	A	604	-	9,9,9	0.52	0	8,8,8	0.36	0
7	PGE	B	605	-	9,9,9	0.51	0	8,8,8	0.33	0

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	GOL	P	101	-	-	0/4/4/4	-
6	OKX	B	604	4	-	2/19/34/34	0/2/2/2
5	GOL	B	603	-	-	3/4/4/4	-
6	OKX	A	603	4	-	2/19/34/34	0/2/2/2
5	GOL	A	602	-	-	2/4/4/4	-
5	GOL	B	602	-	-	1/4/4/4	-
7	PGE	A	604	-	-	4/7/7/7	-
7	PGE	B	605	-	-	4/7/7/7	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	604	OKX	PB-O1B	-4.04	1.45	1.56
6	B	604	OKX	PA-O2A	-3.83	1.46	1.56
6	B	604	OKX	PB-O2B	3.71	1.52	1.46
6	B	604	OKX	PA-O1A	3.56	1.51	1.46
6	A	603	OKX	C6-C5	2.10	1.39	1.35

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	604	OKX	O3G-PG-O3B	2.13	111.78	104.64

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	602	GOL	O1-C1-C2-C3

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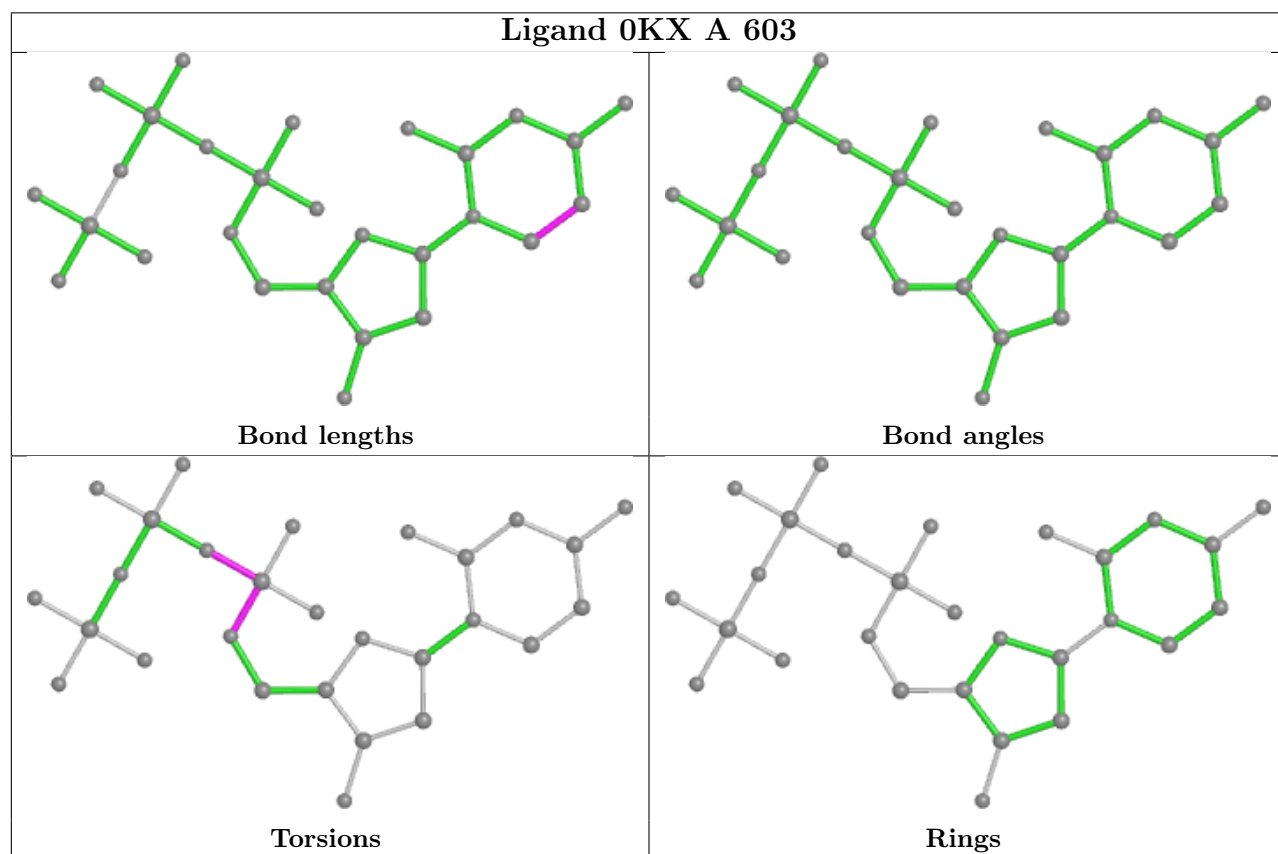
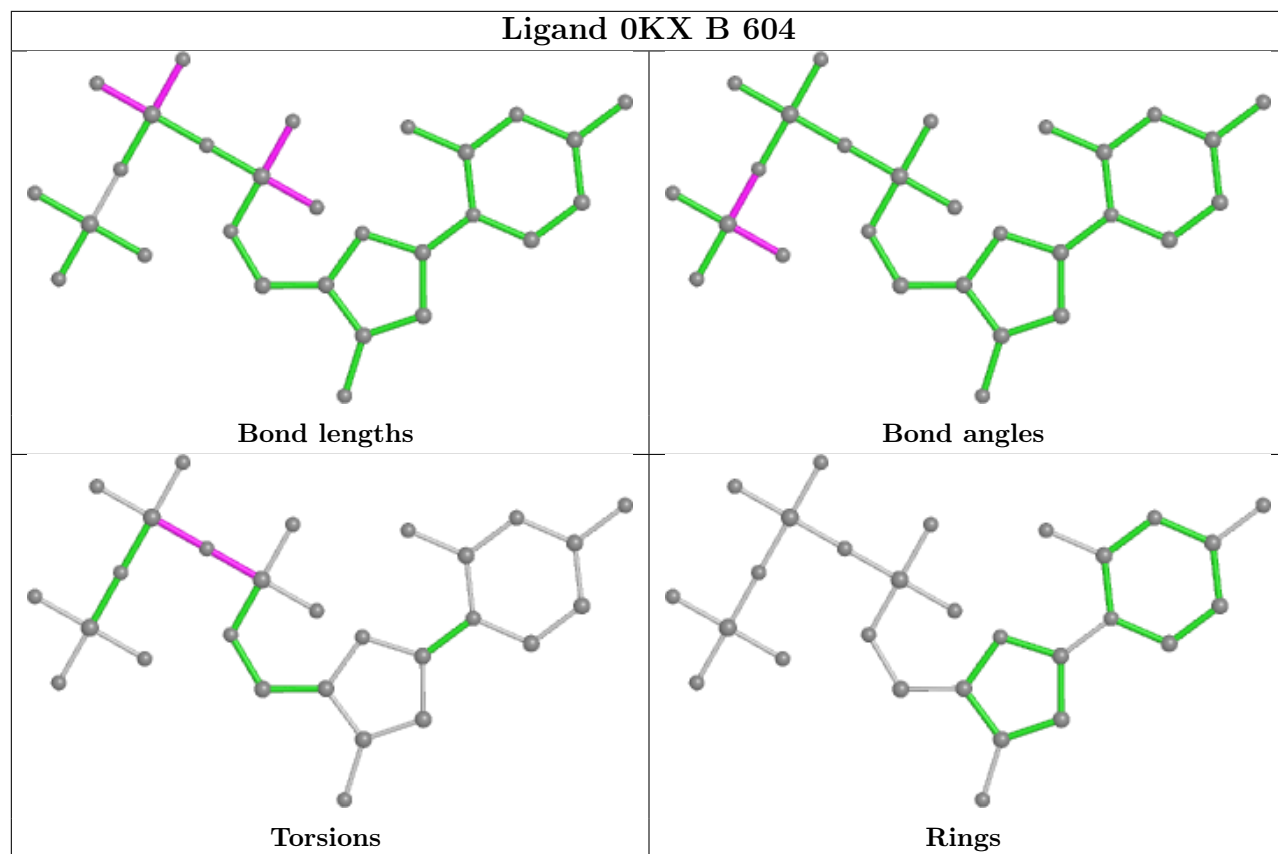
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Mol	Chain	Res	Type	Atoms
5	B	603	GOL	O1-C1-C2-C3
6	A	603	0KX	PB-N3A-PA-O1A
6	A	603	0KX	C5'-O5'-PA-O2A
6	B	604	0KX	PA-N3A-PB-O2B
6	B	604	0KX	PB-N3A-PA-O5'
7	B	605	PGE	O1-C1-C2-O2
7	B	605	PGE	O2-C3-C4-O3
7	A	604	PGE	O3-C5-C6-O4
7	B	605	PGE	O3-C5-C6-O4
5	A	602	GOL	O1-C1-C2-O2
7	A	604	PGE	O1-C1-C2-O2
7	B	605	PGE	C1-C2-O2-C3
5	B	603	GOL	O1-C1-C2-O2
7	A	604	PGE	C3-C4-O3-C5
7	A	604	PGE	O2-C3-C4-O3
5	B	602	GOL	O2-C2-C3-O3
5	B	603	GOL	C1-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	431/551 (78%)	0.12	4 (0%) 84 84	75, 110, 142, 188	0
1	B	431/551 (78%)	0.12	11 (2%) 56 52	70, 112, 148, 191	0
2	C	9/9 (100%)	-0.53	0 100 100	92, 99, 118, 124	0
2	P	9/9 (100%)	-0.37	0 100 100	90, 100, 110, 113	0
3	D	12/13 (92%)	-0.20	0 100 100	86, 111, 133, 138	0
3	T	12/13 (92%)	-0.27	0 100 100	76, 108, 124, 127	0
All	All	904/1146 (78%)	0.10	15 (1%) 70 69	70, 111, 145, 191	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	160	LEU	3.9
1	B	400	LEU	3.6
1	B	146	PHE	3.6
1	B	222	PHE	3.3
1	B	31	LEU	2.8
1	B	286	PHE	2.7
1	A	89	PHE	2.4
1	B	405	THR	2.4
1	B	283	SER	2.4
1	A	383	LEU	2.4
1	A	385	LEU	2.2
1	B	217	ASP	2.1
1	B	401	GLY	2.1
1	A	283	SER	2.1
1	B	123	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

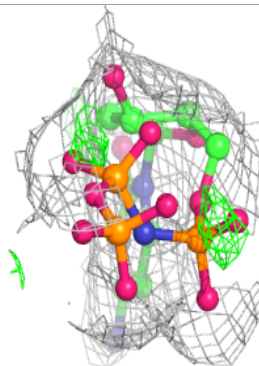
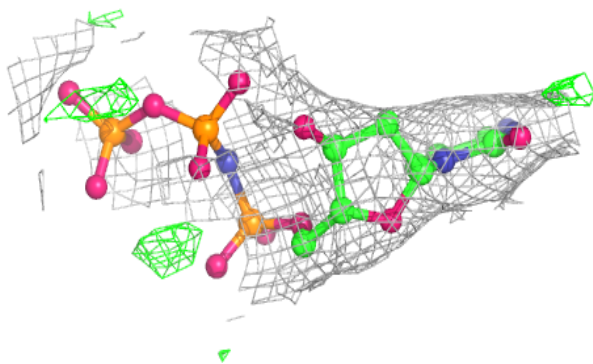
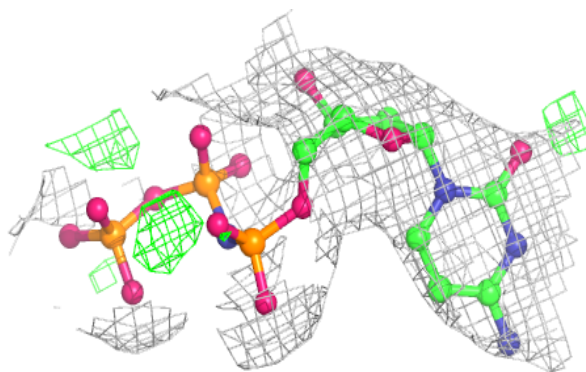
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GOL	B	602	6/6	0.62	0.23	119,133,137,141	0
7	PGE	A	604	10/10	0.63	0.44	113,134,145,149	0
5	GOL	A	602	6/6	0.67	0.22	113,120,120,121	0
5	GOL	B	603	6/6	0.68	0.47	120,128,133,135	0
7	PGE	B	605	10/10	0.73	0.54	128,135,139,143	0
5	GOL	P	101	6/6	0.78	0.40	91,104,109,110	0
4	MG	A	601	1/1	0.94	0.26	79,79,79,79	0
4	MG	B	601	1/1	0.94	0.23	91,91,91,91	0
6	OKX	A	603	28/28	0.96	0.26	85,93,99,101	0
6	OKX	B	604	28/28	0.97	0.23	83,96,102,105	0

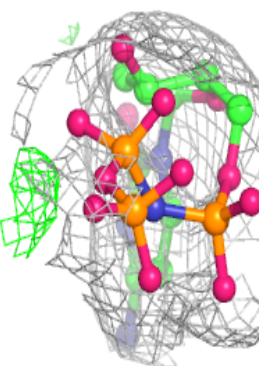
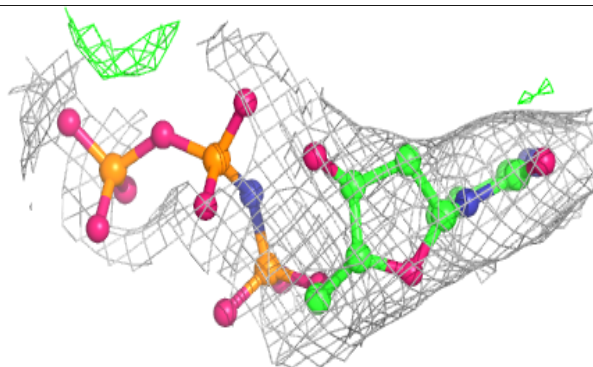
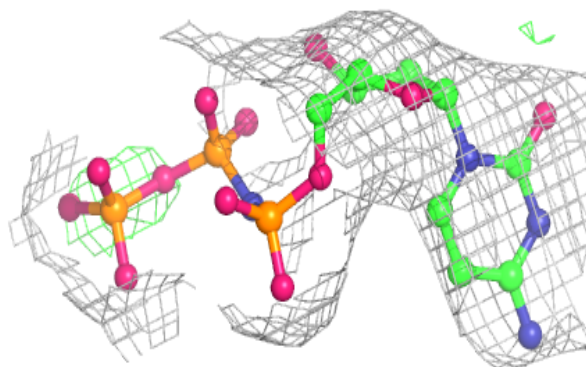
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 0KX A 603:

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

**Electron density around 0KX B 604:**

$2mF_o-DF_c$ (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.