



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 01:18 PM BST

PDB ID : 6Z4Z  
Title : Crystal structure of CLK1 in complex with macrocycle ODS2004070  
Authors : Chaikuad, A.; Benderitter, P.; Hoflack, J.; Denis, A.; Knapp, S.; Structural Genomics Consortium (SGC)  
Deposited on : 2020-05-26  
Resolution : 2.07 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.

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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

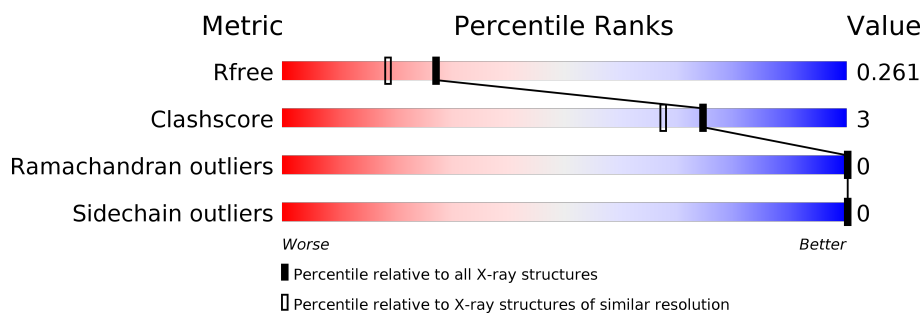
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.07 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)

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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	339	92% 8%
1	B	339	94% 6%
1	C	339	93% 6%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8825 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 Dual specificity protein kinase CLK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	337	2763	1767	482	497	17	0	1	0
1	B	339	2764	1765	483	499	17	0	1	0
1	C	337	2773	1773	481	502	17	0	4	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP P49759
A	0	MET	-	expression tag	UNP P49759
A	432	ALA	ARG	variant	UNP P49759
B	-1	SER	-	expression tag	UNP P49759
B	0	MET	-	expression tag	UNP P49759
B	432	ALA	ARG	variant	UNP P49759
C	-1	SER	-	expression tag	UNP P49759
C	0	MET	-	expression tag	UNP P49759
C	432	ALA	ARG	variant	UNP P49759

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



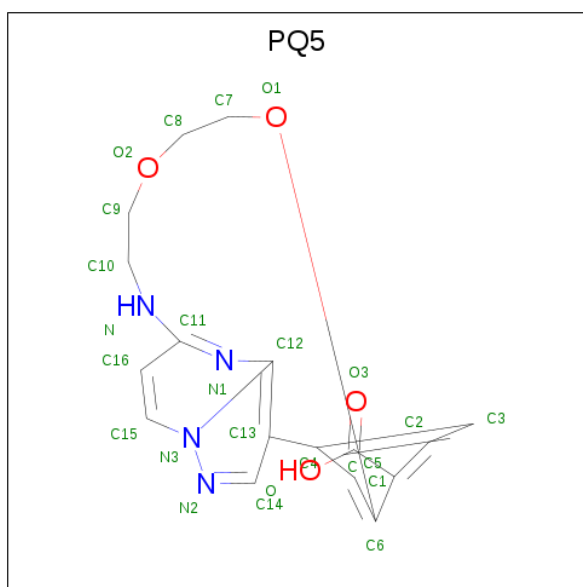
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			12	6	6		

- Molecule 4 is 7,10-Dioxa-13,17,18,21-tetrazatetracyclo[12.5.2.12,6.017,20]docosa-1(20),2(22),3,5,14(21),15,18-heptaene-5-carboxylic acid (three-letter code: PQ5) (formula: C<sub>17</sub>H<sub>16</sub>N<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	N	O	0	0
			25	17	4	4		
4	B	1	Total	C	N	O	0	0
			25	17	4	4		
4	C	1	Total	C	N	O	0	0
			25	17	4	4		

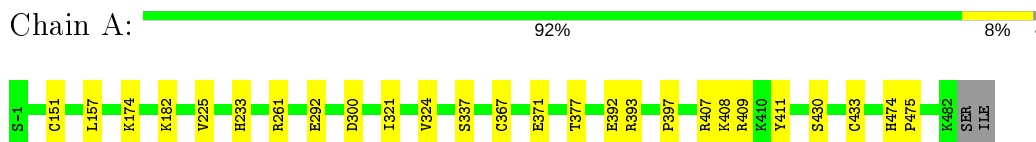
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	135	Total	O	0	0
			135	135		
5	B	143	Total	O	0	0
			143	143		
5	C	140	Total	O	0	0
			140	140		

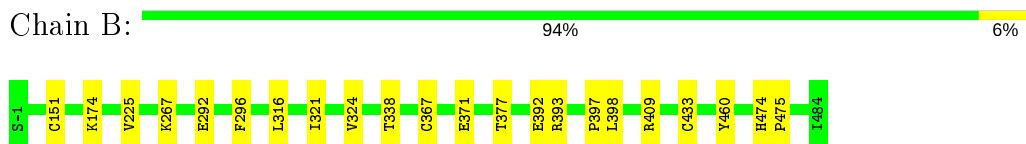
### 3 Residue-property plots [i](#)

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.

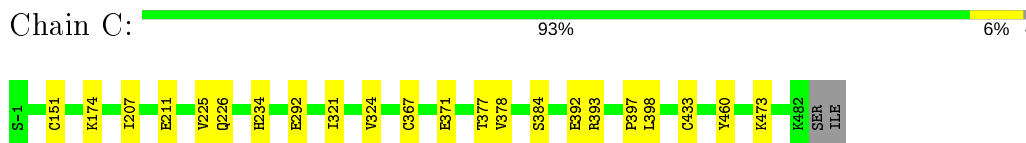
- Molecule 1: Dual specificity protein kinase CLK1



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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.29Å 116.67Å 91.29Å 90.00° 98.59° 90.00°	Depositor
Resolution (Å)	30.90 – 2.07 30.09 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.90-2.07) 99.9 (30.09-2.07)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.67 (at 2.06Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.175 , 0.213 0.234 , 0.261	Depositor DCC
$R_{free}$ test set	3463 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.0	Xtrriage
Anisotropy	0.218	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 41.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8825	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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: GOL, PO4, PQ5

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	1/2837 (0.0%)	0.75	0/3834
1	B	0.79	1/2839 (0.0%)	0.78	0/3841
1	C	0.75	1/2856 (0.0%)	0.76	0/3861
All	All	0.76	3/8532 (0.0%)	0.76	0/11536

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	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	292	GLU	CD-OE1	5.82	1.32	1.25
1	C	292	GLU	CD-OE1	5.63	1.31	1.25
1	B	292	GLU	CD-OE1	5.21	1.31	1.25

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	338	THR	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	2763	0	2724	22	0
1	B	2764	0	2696	14	0
1	C	2773	0	2731	16	0
2	A	15	0	0	0	0
2	C	5	0	0	1	0
3	A	12	0	16	3	0
4	A	25	0	0	1	0
4	B	25	0	0	0	0
4	C	25	0	0	0	0
5	A	135	0	0	5	0
5	B	143	0	0	1	0
5	C	140	0	0	5	0
All	All	8825	0	8167	53	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 3.

All (53) 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:261:ARG:HB2	3:A:504[A]:GOL:H32	1.70	0.72
1:A:393:ARG:NH2	1:A:430:SER:O	2.31	0.64
1:C:207:ILE:O	1:C:211:GLU:HG3	1.98	0.64
1:A:182:LYS:HB3	5:A:683:HOH:O	1.98	0.63
1:A:233:HIS:ND1	5:A:603:HOH:O	2.31	0.61
1:C:473:LYS:NZ	5:C:602:HOH:O	2.34	0.60
1:A:261:ARG:HB2	3:A:504[A]:GOL:C3	2.32	0.59
1:A:300:ASP:HB2	5:A:686:HOH:O	2.02	0.59
1:C:226:GLN:HG3	5:C:709:HOH:O	2.04	0.57
1:B:267:LYS:HE3	5:B:728:HOH:O	2.05	0.56
1:A:408:LYS:HD2	1:A:411:TYR:CE2	2.42	0.54
1:A:371:GLU:HG2	1:A:377:THR:HA	1.88	0.54
1:C:384:SER:OG	2:C:501:PO4:O4	2.19	0.53
1:C:392:GLU:HG3	1:C:397:PRO:HA	1.90	0.53
1:A:408:LYS:HD2	1:A:411:TYR:HE2	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392:GLU:HG3	1:B:397:PRO:HA	1.91	0.52
1:A:392:GLU:HG3	1:A:397:PRO:HA	1.91	0.51
1:C:225:VAL:HB	1:C:324:VAL:HG12	1.91	0.51
1:A:371:GLU:OE2	1:A:377:THR:HB	2.11	0.51
1:C:371:GLU:HG2	1:C:377:THR:HA	1.92	0.51
1:B:371:GLU:HG2	1:B:377:THR:HA	1.93	0.51
1:B:151:CYS:SG	1:B:174:LYS:NZ	2.77	0.50
1:C:151:CYS:SG	1:C:174:LYS:NZ	2.76	0.50
1:A:225:VAL:HB	1:A:324:VAL:HG12	1.93	0.50
1:B:371:GLU:OE2	1:B:377:THR:HB	2.13	0.49
1:A:151:CYS:SG	1:A:174:LYS:NZ	2.75	0.48
1:B:225:VAL:HB	1:B:324:VAL:HG12	1.95	0.48
1:C:234:HIS:ND1	5:C:603:HOH:O	2.35	0.48
1:C:473:LYS:CE	5:C:618:HOH:O	2.62	0.48
1:B:393:ARG:NH2	1:B:433:CYS:O	2.48	0.46
1:C:367:CYS:O	1:C:371:GLU:HG3	2.16	0.46
1:C:371:GLU:OE2	1:C:377:THR:HB	2.16	0.45
1:C:393:ARG:NH2	1:C:433:CYS:O	2.50	0.45
1:C:378:VAL:HG22	5:C:668:HOH:O	2.17	0.45
1:A:474:HIS:CG	1:A:475:PRO:HD2	2.52	0.44
4:A:505:PQ5:C8	4:A:505:PQ5:C5	2.96	0.44
1:A:407:ARG:NH1	5:A:607:HOH:O	2.49	0.44
1:C:321:ILE:HD12	1:C:321:ILE:C	2.38	0.44
1:C:398:LEU:HD12	1:C:460:TYR:CZ	2.52	0.44
1:B:296:PHE:CE1	1:B:316:LEU:HD21	2.52	0.44
1:B:409:ARG:HA	1:B:409:ARG:HD3	1.71	0.43
1:A:393:ARG:NH2	1:A:433:CYS:O	2.52	0.43
1:A:157:LEU:HD22	1:A:233:HIS:CD2	2.54	0.43
1:A:367:CYS:O	1:A:371:GLU:HG3	2.19	0.42
1:A:321:ILE:HD12	1:A:321:ILE:C	2.40	0.42
1:A:409:ARG:HA	1:A:409:ARG:HD3	1.65	0.42
1:B:321:ILE:HD12	1:B:321:ILE:C	2.40	0.41
1:B:367:CYS:O	1:B:371:GLU:HG3	2.19	0.41
1:B:398:LEU:HD12	1:B:460:TYR:CZ	2.55	0.41
1:A:337[A]:SER:HB3	5:A:625:HOH:O	2.20	0.41
1:B:474:HIS:CG	1:B:475:PRO:HD2	2.56	0.41
1:A:261:ARG:HB2	3:A:504[B]:GOL:H31	2.03	0.40
1:B:151:CYS:HB2	1:B:174:LYS:HD2	2.02	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	336/339 (99%)	327 (97%)	9 (3%)	0	100	100
1	B	338/339 (100%)	327 (97%)	11 (3%)	0	100	100
1	C	339/339 (100%)	328 (97%)	11 (3%)	0	100	100
All	All	1013/1017 (100%)	982 (97%)	31 (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	304/308 (99%)	304 (100%)	0	100	100
1	B	302/308 (98%)	302 (100%)	0	100	100
1	C	307/308 (100%)	307 (100%)	0	100	100
All	All	913/924 (99%)	913 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

9 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	GOL	A	504[A]	-	5,5,5	0.43	0	5,5,5	0.63	0
4	PQ5	A	505	-	20,28,28	1.15	2 (10%)	23,39,39	1.16	2 (8%)
2	PO4	A	503	-	4,4,4	0.64	0	6,6,6	0.87	0
4	PQ5	B	501	-	20,28,28	1.58	2 (10%)	23,39,39	1.19	2 (8%)
3	GOL	A	504[B]	-	5,5,5	0.45	0	5,5,5	0.25	0
2	PO4	A	502	-	4,4,4	0.42	0	6,6,6	0.93	0
2	PO4	C	501	-	4,4,4	1.08	0	6,6,6	0.69	0
2	PO4	A	501	-	4,4,4	0.78	0	6,6,6	0.59	0
4	PQ5	C	502	-	20,28,28	1.08	1 (5%)	23,39,39	1.33	3 (13%)

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	GOL	A	504[A]	-	-	4/4/4/4	-
4	PQ5	C	502	-	-	8/14/18/18	0/3/4/4
4	PQ5	A	505	-	-	9/14/18/18	0/3/4/4
4	PQ5	B	501	-	-	10/14/18/18	0/3/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	504[B]	-	-	1/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	PQ5	C1-C	5.24	1.52	1.47
4	C	502	PQ5	C13-C4	-3.78	1.42	1.49
4	A	505	PQ5	C13-C4	-3.72	1.43	1.49
4	B	501	PQ5	C12-N1	-3.11	1.30	1.35
4	A	505	PQ5	C1-C	2.63	1.50	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	502	PQ5	C11-N1-C12	-3.84	114.10	117.59
4	B	501	PQ5	C14-N2-N3	-3.54	101.12	103.70
4	C	502	PQ5	C2-C1-C	-2.71	116.16	120.20
4	C	502	PQ5	C10-N-C11	2.29	127.00	123.38
4	B	501	PQ5	C2-C1-C	-2.27	116.82	120.20
4	A	505	PQ5	C11-N1-C12	-2.04	115.74	117.59
4	A	505	PQ5	C3-C4-C13	-2.02	117.47	120.86

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	504[A]	GOL	O1-C1-C2-O2
3	A	504[A]	GOL	O1-C1-C2-C3
4	A	505	PQ5	C12-C13-C4-C3
4	A	505	PQ5	C12-C13-C4-C5
4	A	505	PQ5	C14-C13-C4-C3
4	A	505	PQ5	C14-C13-C4-C5
4	B	501	PQ5	C12-C13-C4-C3
4	B	501	PQ5	C12-C13-C4-C5
4	B	501	PQ5	C14-C13-C4-C3
4	B	501	PQ5	C14-C13-C4-C5
4	C	502	PQ5	C12-C13-C4-C3
4	C	502	PQ5	C12-C13-C4-C5
4	C	502	PQ5	C14-C13-C4-C3
4	C	502	PQ5	C14-C13-C4-C5
4	A	505	PQ5	C8-C7-O1-C6

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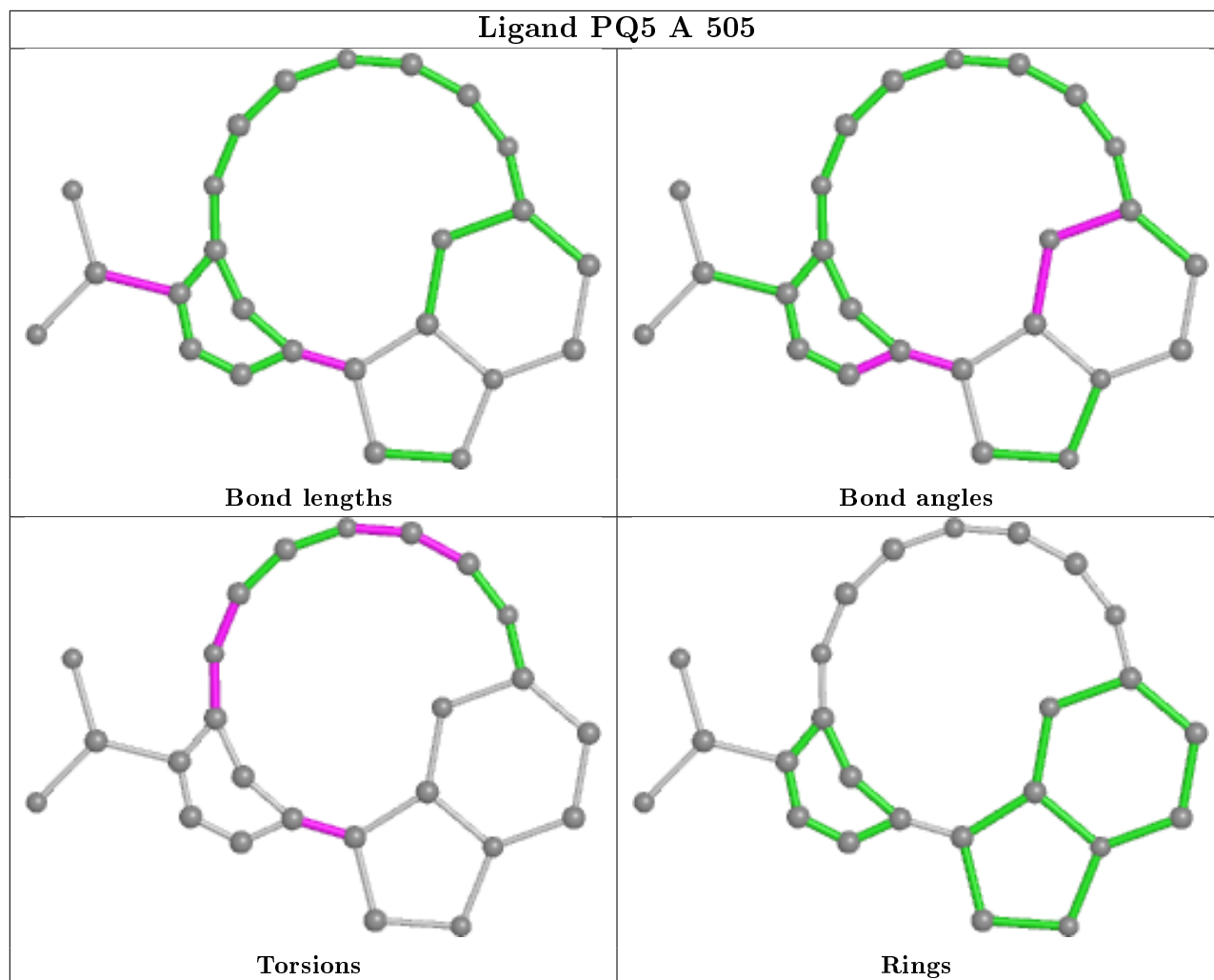
Mol	Chain	Res	Type	Atoms
4	A	505	PQ5	N-C10-C9-O2
3	A	504[A]	GOL	C1-C2-C3-O3
3	A	504[A]	GOL	O2-C2-C3-O3
4	C	502	PQ5	O1-C7-C8-O2
4	A	505	PQ5	C5-C6-O1-C7
4	B	501	PQ5	C9-C10-N-C11
4	C	502	PQ5	C9-C10-N-C11
4	C	502	PQ5	C10-C9-O2-C8
4	C	502	PQ5	C8-C7-O1-C6
4	A	505	PQ5	C1-C6-O1-C7
3	A	504[B]	GOL	O1-C1-C2-C3
4	B	501	PQ5	O1-C7-C8-O2
4	B	501	PQ5	C1-C6-O1-C7
4	B	501	PQ5	C5-C6-O1-C7
4	A	505	PQ5	C10-C9-O2-C8
4	B	501	PQ5	C8-C7-O1-C6
4	B	501	PQ5	C10-C9-O2-C8

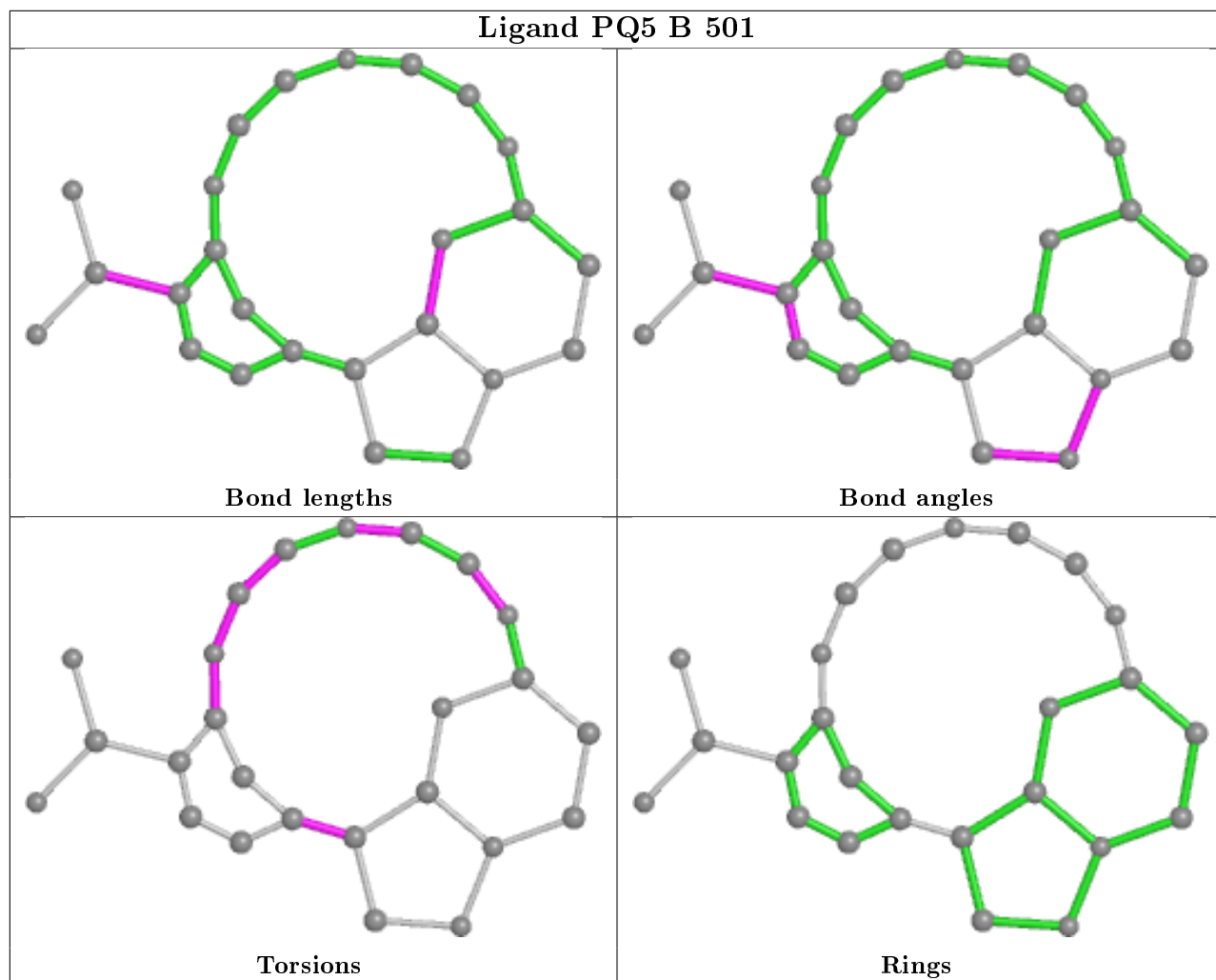
There are no ring outliers.

4 monomers are involved in 5 short contacts:

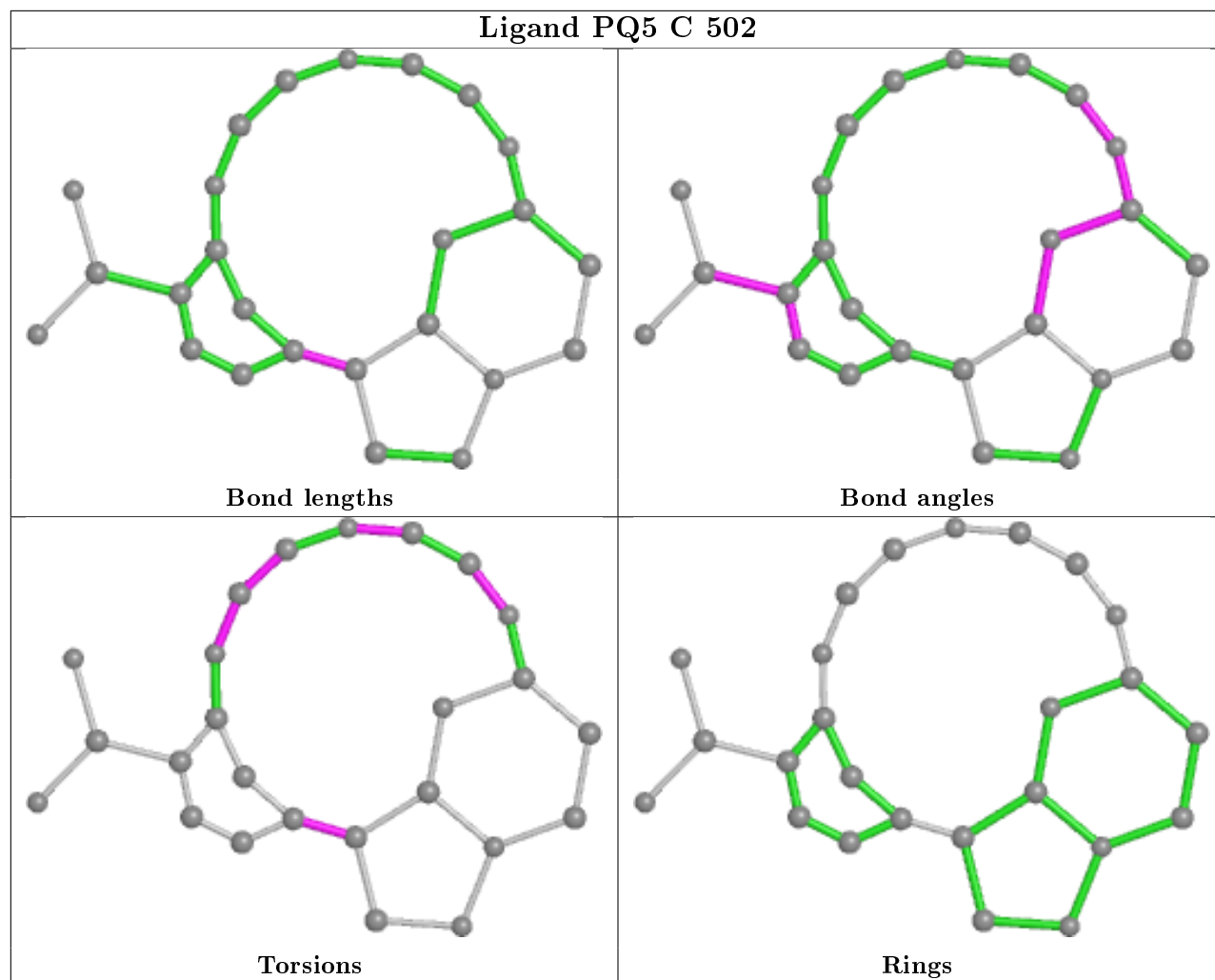
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504[A]	GOL	2	0
4	A	505	PQ5	1	0
3	A	504[B]	GOL	1	0
2	C	501	PO4	1	0

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

### 6.1 Protein, DNA and RNA chains

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

### 6.2 Non-standard residues in protein, DNA, RNA chains

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

### 6.3 Carbohydrates

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

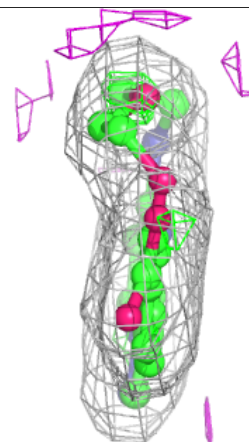
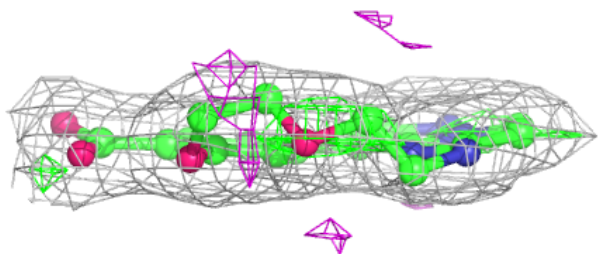
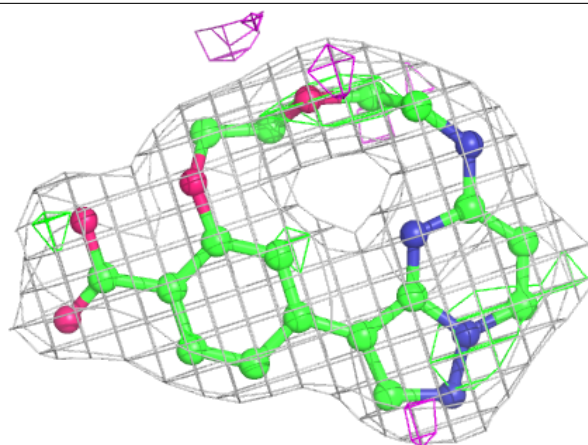
### 6.4 Ligands

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.

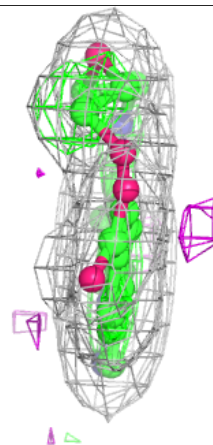
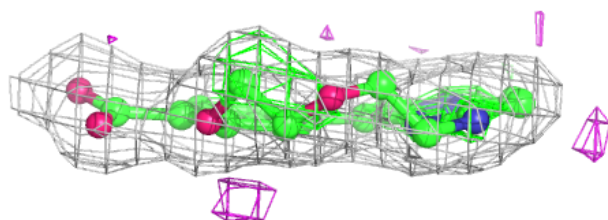
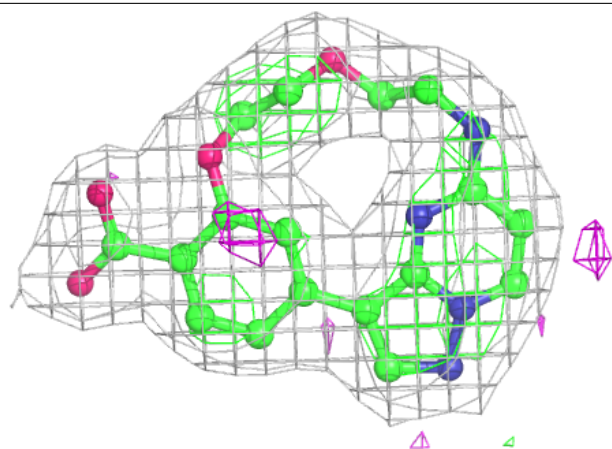
**Electron density around PQ5 A 505:**

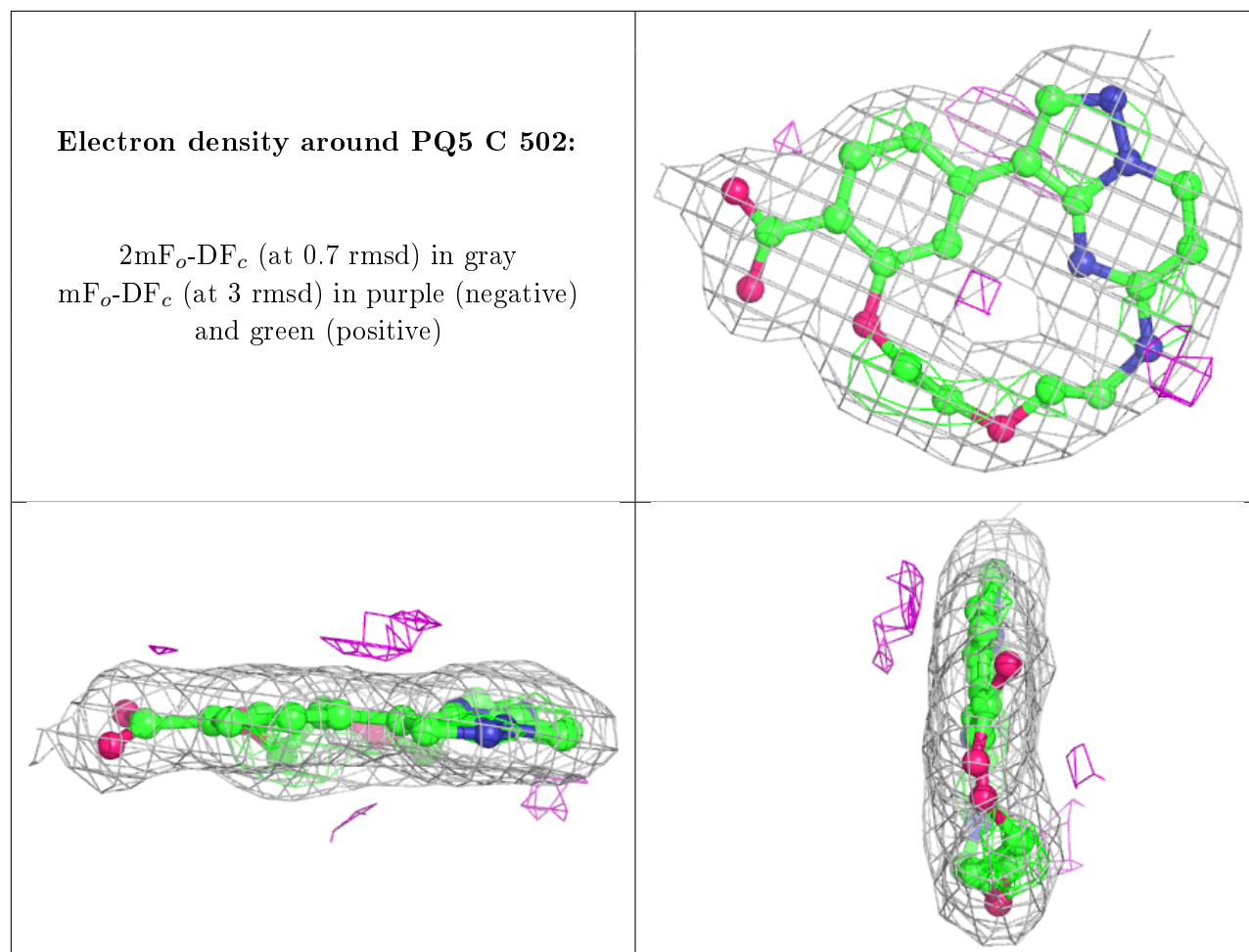
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around PQ5 B 501:**

$2mF_o-DF_c$  (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.