wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2023 – 10:16 AM EDT

PDB ID	:	1OPL
Title	:	Structural basis for the auto-inhibition of c-Abl tyrosine kinase
Authors	:	Nagar, B.; Hantschel, O.; Young, M.A.; Scheffzek, K.; Veach, D.; Bornmann, W.; Clarkson, B.; Superti-Furga, G.; Kuriyan, J.
Deposited on	:	2003-03-06
Resolution	:	3.42 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

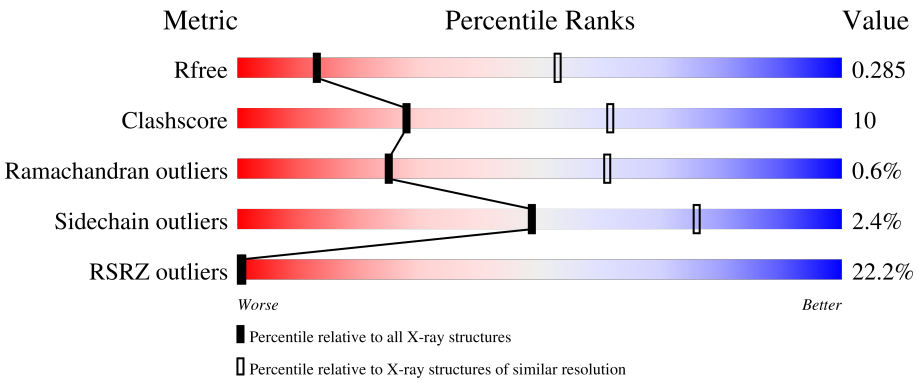
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.42 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	1486 (3.50-3.34)
Clashscore	141614	1572 (3.50-3.34)
Ramachandran outliers	138981	1534 (3.50-3.34)
Sidechain outliers	138945	1535 (3.50-3.34)
RSRZ outliers	127900	1395 (3.50-3.34)

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 <=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	537	4%, 72%, 11%, •, 16%
1	B	537	30%, 53%, 14%, •, 32%

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
2	MYR	A	538	-	-	-	X
3	P16	B	538	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6655 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.

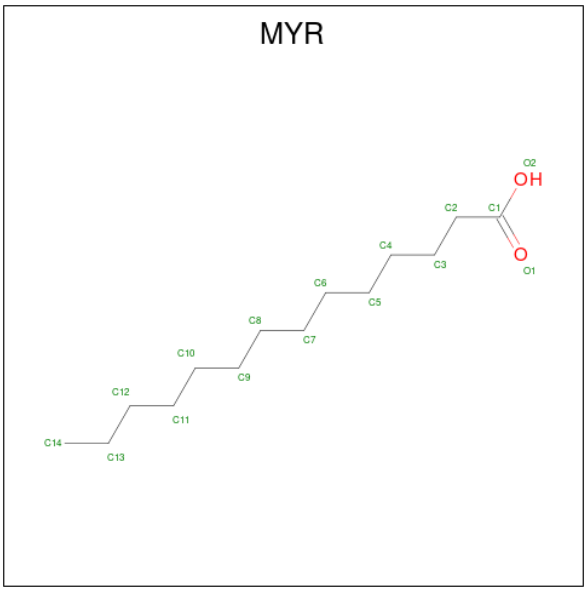
- Molecule 1 is a protein called proto-oncogene tyrosine-protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	451	3628	2314	611	685	18	0	0	0
1	B	365	2954	1889	497	551	17	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

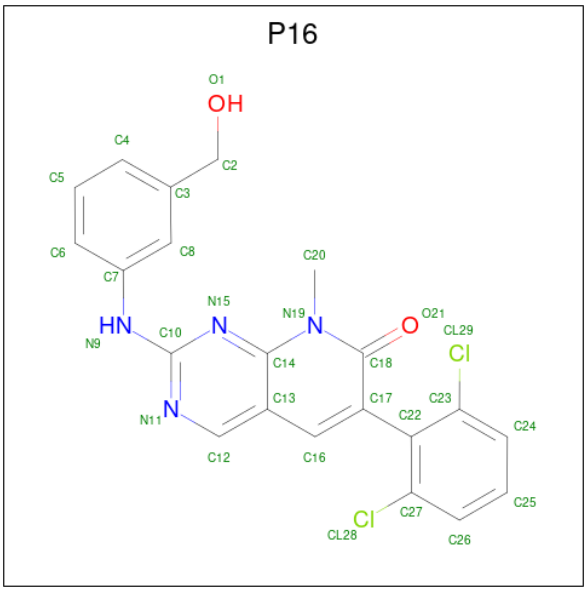
Chain	Residue	Modelled	Actual	Comment	Reference
A	29	ARG	LYS	engineered mutation	UNP P00519
A	30	ASP	GLU	engineered mutation	UNP P00519
A	382	ASN	ASP	engineered mutation	UNP P00519
A	532	GLU	-	cloning artifact	UNP P00519
A	533	ASN	-	cloning artifact	UNP P00519
A	534	LEU	-	cloning artifact	UNP P00519
A	535	TYR	-	cloning artifact	UNP P00519
A	536	PHE	-	cloning artifact	UNP P00519
A	537	GLN	-	cloning artifact	UNP P00519
B	29	ARG	LYS	engineered mutation	UNP P00519
B	30	ASP	GLU	engineered mutation	UNP P00519
B	382	ASN	ASP	engineered mutation	UNP P00519
B	532	GLU	-	cloning artifact	UNP P00519
B	533	ASN	-	cloning artifact	UNP P00519
B	534	LEU	-	cloning artifact	UNP P00519
B	535	TYR	-	cloning artifact	UNP P00519
B	536	PHE	-	cloning artifact	UNP P00519
B	537	GLN	-	cloning artifact	UNP P00519

- Molecule 2 is MYRISTIC ACID (three-letter code: MYR) (formula: $C_{14}H_{28}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	15	14	1	0	0

- Molecule 3 is 6-(2,6-DICHLOROPHENYL)-2-{[3-(HYDROXYMETHYL)PHENYL]AMINO}-8-METHYLPYRIDO[2,3-D]PYRIMIDIN-7(8H)-ONE (three-letter code: P16) (formula: $C_{21}H_{16}Cl_2N_4O_2$).



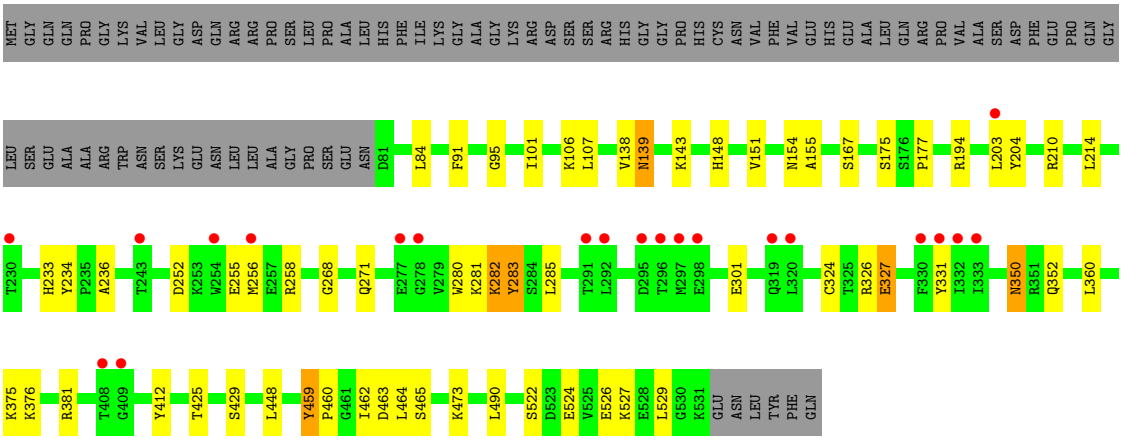
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
3	A	1	29	21	2	4	2	0	0
			Total	C	Cl	N	O		
3	B	1	29	21	2	4	2	0	0

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.

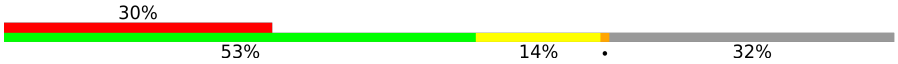
• Molecule 1: proto-oncogene tyrosine-protein kinase

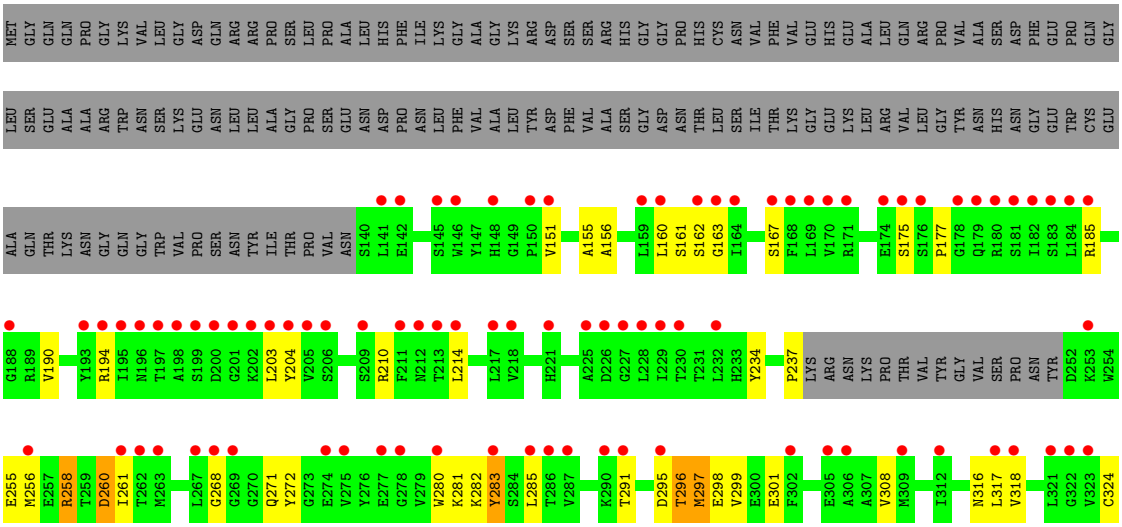
Chain A:

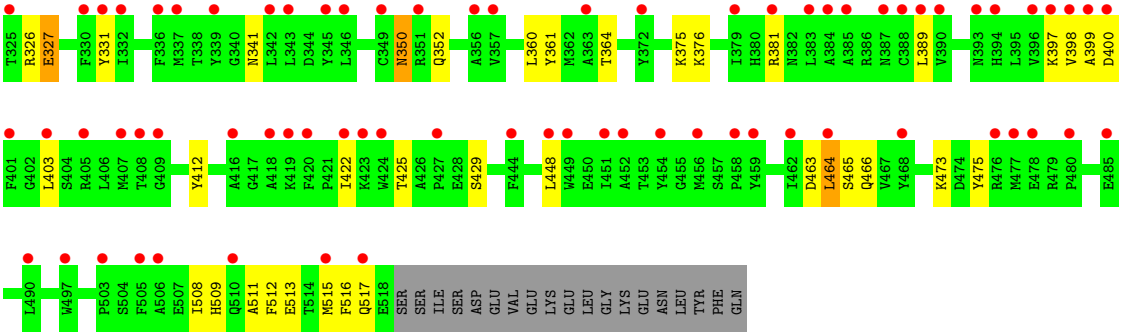


• Molecule 1: proto-oncogene tyrosine-protein kinase

Chain B:






T325 R326 E327 F330 Y331 I332 F336 M337 T338 Y339 G340 N341 L342 L343 D344 Y345 L346 C349 N350 R351 Q352 A356 V357 L360 Y361 M362 A363 T364 Y372 K375 K376 I379 H380 R381 N382 L383 A384 A385 R386 N387 C388 L389 V390 N393 H394 L395 V396 K397 V398 A399 D400
F401 G402 L403 S404 R405 L406 M407 T408 G409 Y412 A416 G417 A418 K419 F420 P421 I422 K423 W424 T425 A426 P427 E428 S429 F444 L448 W449 E450 I451 A452 T453 Y454 G455 M456 S457 P458 Y459 I462 D463 L464 S465 Q466 V467 Y468 K473 D474 Y475 R476 M477 E478 R479 P480 E485
L490 W497 P503 S504 F505 A506 E507 I508 H509 Q510 A511 F512 E513 T514 M515 F516 Q517 E518 SER SER ILE SER ASP GLU VAL GLU LYS GLU LEU GLY LYS GLU ASN LEU TYR PHE GLN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	77.02Å 273.38Å 124.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.95 – 3.42 74.13 – 3.42	Depositor EDS
% Data completeness (in resolution range)	89.1 (29.95-3.42) 89.2 (74.13-3.42)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	3.70 (at 3.41Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.306 , 0.315 0.270 , 0.285	Depositor DCC
R_{free} test set	1110 reflections (6.84%)	wwPDB-VP
Wilson B-factor (Å^2)	102.4	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 90.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	6655	wwPDB-VP
Average B, all atoms (Å^2)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MYR, P16

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	0.48	1/3723 (0.0%)	0.71	3/5049 (0.1%)
1	B	0.53	0/3031	0.77	2/4105 (0.0%)
All	All	0.50	1/6754 (0.0%)	0.74	5/9154 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	PRO	N-CD	5.29	1.55	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	464	LEU	CB-CA-C	6.88	123.28	110.20
1	A	95	GLY	N-CA-C	-6.14	97.75	113.10
1	A	459	TYR	CB-CG-CD1	6.11	124.66	121.00
1	B	234	TYR	N-CA-CB	-5.47	100.76	110.60
1	A	459	TYR	CB-CG-CD2	-5.05	117.97	121.00

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	3628	0	3525	46	0
1	B	2954	0	2875	86	0
2	A	15	0	27	3	0
3	A	29	0	16	1	0
3	B	29	0	16	3	0
All	All	6655	0	6459	130	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 10.

The worst 5 of 130 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:529:LEU:HD11	2:A:538:MYR:H42	1.55	0.88
1:B:162:SER:HB2	1:B:258:ARG:HG3	1.59	0.82
1:B:360:LEU:HD21	1:B:516:PHE:HA	1.61	0.80
1:B:360:LEU:CD2	1:B:516:PHE:HA	2.10	0.80
1:B:399:ALA:HB1	3:B:538:P16:CL28	2.21	0.77

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	449/537 (84%)	430 (96%)	17 (4%)	2 (0%)	34 69
1	B	361/537 (67%)	337 (93%)	21 (6%)	3 (1%)	19 56
All	All	810/1074 (75%)	767 (95%)	38 (5%)	5 (1%)	25 61

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	LYS
1	A	252	ASP
1	B	282	LYS
1	B	296	THR
1	B	298	GLU

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	393/463 (85%)	384 (98%)	9 (2%)	50	77
1	B	318/463 (69%)	310 (98%)	8 (2%)	47	75
All	All	711/926 (77%)	694 (98%)	17 (2%)	49	76

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	327	GLU
1	B	448	LEU
1	A	448	LEU
1	A	490	LEU
1	B	214	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	517	GLN
1	B	509	HIS
1	A	393	ASN
1	A	350	ASN
1	B	350	ASN

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)

3 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	P16	A	539	-	30,32,32	2.09	11 (36%)	36,46,46	1.13	4 (11%)
3	P16	B	538	-	30,32,32	2.08	10 (33%)	36,46,46	1.14	4 (11%)
2	MYR	A	538	-	14,14,15	0.57	0	13,13,15	0.59	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
3	P16	A	539	-	-	0/6/10/10	0/4/4/4
3	P16	B	538	-	-	0/6/10/10	0/4/4/4
2	MYR	A	538	-	-	5/11/12/13	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	539	P16	C17-C18	5.51	1.51	1.41
3	B	538	P16	C17-C18	5.46	1.51	1.41
3	B	538	P16	C18-N19	4.25	1.44	1.38
3	A	539	P16	C18-N19	4.22	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	539	P16	C26-C27	3.37	1.43	1.36

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	538	P16	C27-C22-C23	-3.33	117.78	125.49
3	A	539	P16	C27-C22-C23	-3.30	117.85	125.49
3	B	538	P16	C10-N15-C14	3.08	118.77	115.28
3	A	539	P16	C10-N15-C14	3.06	118.75	115.28
3	B	538	P16	N11-C10-N15	-2.25	124.35	126.52

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	538	MYR	C10-C11-C12-C13
2	A	538	MYR	C2-C3-C4-C5
2	A	538	MYR	C3-C4-C5-C6
2	A	538	MYR	C4-C5-C6-C7
2	A	538	MYR	C11-C12-C13-C14

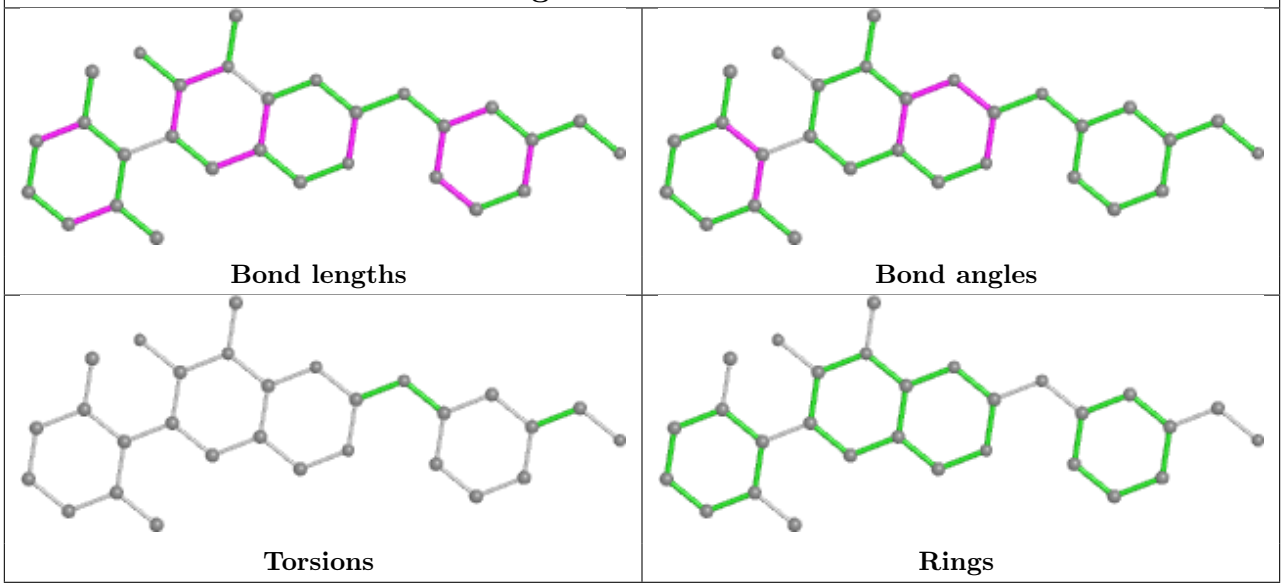
There are no ring outliers.

3 monomers are involved in 7 short contacts:

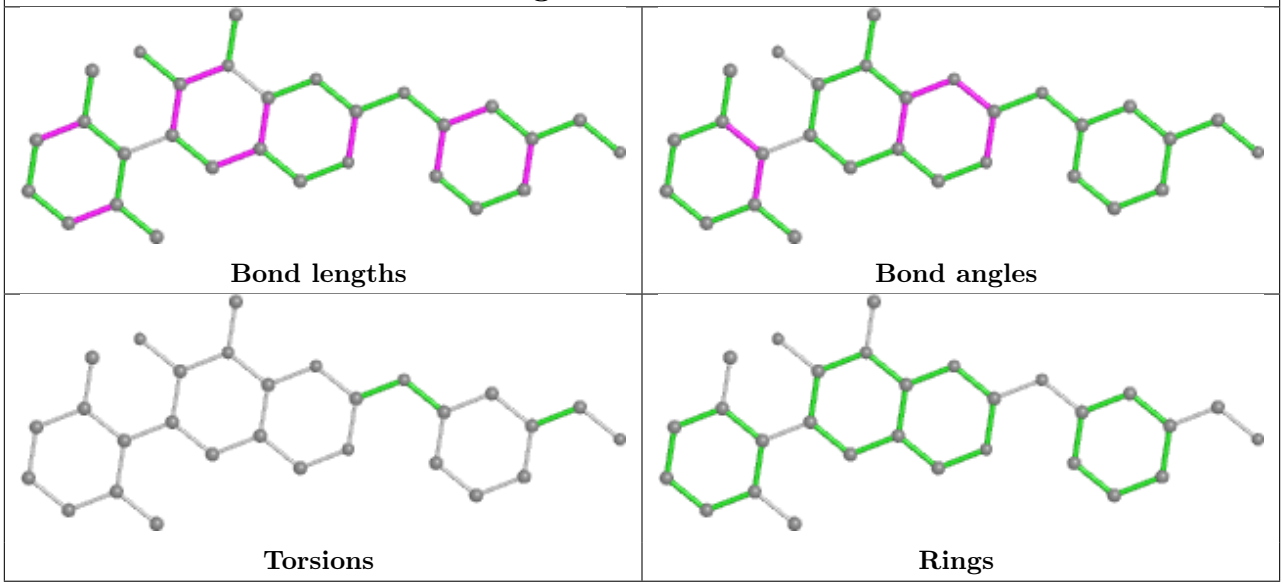
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	539	P16	1	0
3	B	538	P16	3	0
2	A	538	MYR	3	0

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 then 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 P16 A 539



Ligand P16 B 538



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	451/537 (83%)	0.76	21 (4%)	31	32	36, 73, 158, 221	0
1	B	365/537 (67%)	2.08	160 (43%)	0	0	161, 161, 198, 198	0
All	All	816/1074 (75%)	1.35	181 (22%)	0	1	36, 140, 198, 221	0

The worst 5 of 181 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	400	ASP	15.5
1	B	398	VAL	11.4
1	B	388	CYS	11.0
1	B	214	LEU	10.3
1	B	291	THR	9.1

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)

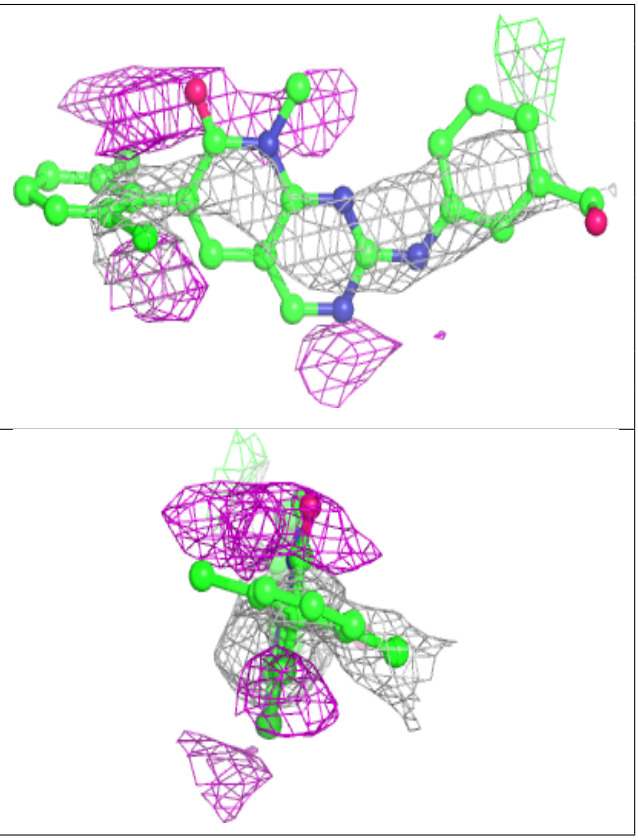
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	P16	B	538	29/29	0.55	1.08	152,152,152,152	0
2	MYR	A	538	15/16	0.65	1.06	81,83,87,87	0
3	P16	A	539	29/29	0.86	0.52	82,84,89,97	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.

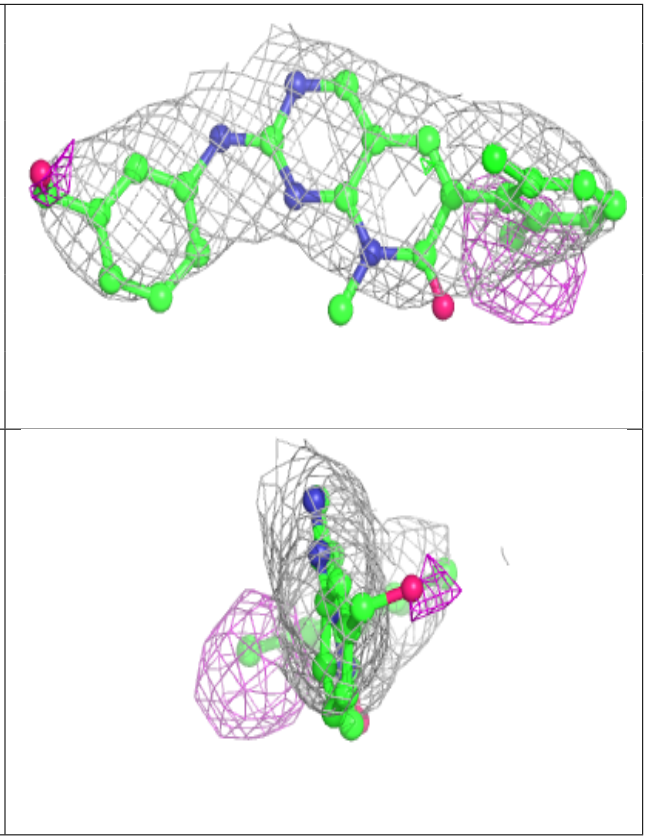
Electron density around P16 B 538:

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 P16 A 539:

$2mF_o$-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.