Full wwPDB X-ray Structure Validation Report (i)

Mar 3, 2024 – 10:58 PM EST

PDB ID	:	6OCU
Title	:	HUMAN PI3KDELTA IN COMPLEX WITH COMPOUND 29
Authors	:	Lesburg, C.A.; Augustin, M.A.
Deposited on	:	2019-03-25
Resolution	:	2.77 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 (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:

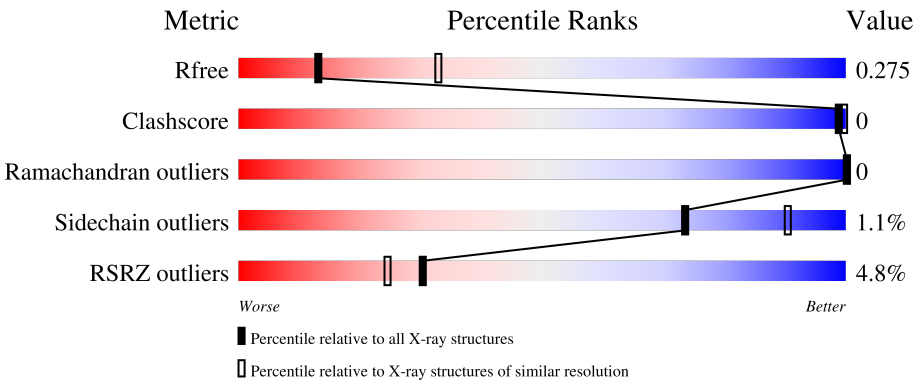
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.77 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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	1044	5% 85% • 13%
2	B	188	% 85% • 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8803 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 Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	910	7355	4711	1251	1340	53	153	0	0

- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

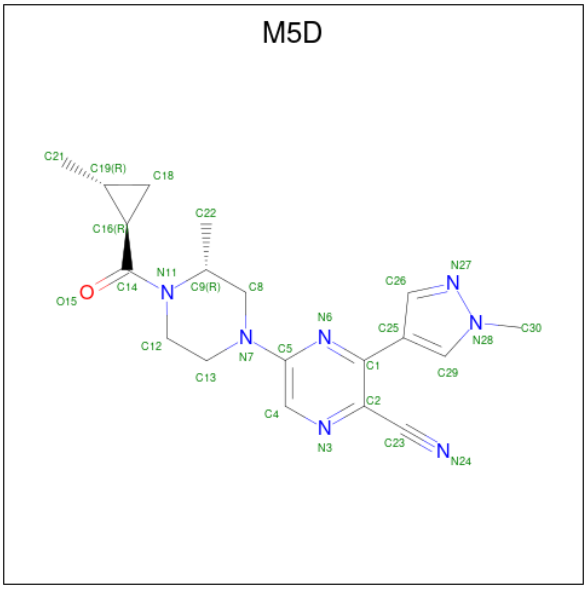
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	164	1421	881	259	276	5	41	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	430	MET	-	initiating methionine	UNP P23727
B	601	SER	-	expression tag	UNP P23727
B	602	ARG	-	expression tag	UNP P23727
B	603	ALA	-	expression tag	UNP P23727
B	604	CYS	-	expression tag	UNP P23727
B	605	SER	-	expression tag	UNP P23727
B	606	LEU	-	expression tag	UNP P23727
B	607	GLU	-	expression tag	UNP P23727
B	608	ALA	-	expression tag	UNP P23727
B	609	CYS	-	expression tag	UNP P23727
B	610	GLY	-	expression tag	UNP P23727
B	611	THR	-	expression tag	UNP P23727
B	612	LYS	-	expression tag	UNP P23727
B	613	LEU	-	expression tag	UNP P23727
B	614	VAL	-	expression tag	UNP P23727
B	615	GLU	-	expression tag	UNP P23727
B	616	LYS	-	expression tag	UNP P23727
B	617	TYR	-	expression tag	UNP P23727

- Molecule 3 is 5-{(3R)-3-methyl-4-[(1R,2R)-2-methylcyclopropane-1-carbonyl]piperazin-1-y

l}-3-(1-methyl-1H-pyrazol-4-yl)pyrazine-2-carbonitrile (three-letter code: M5D) (formula: $C_{19}H_{23}N_7O$) (labeled as "Ligand of Interest" by depositor).



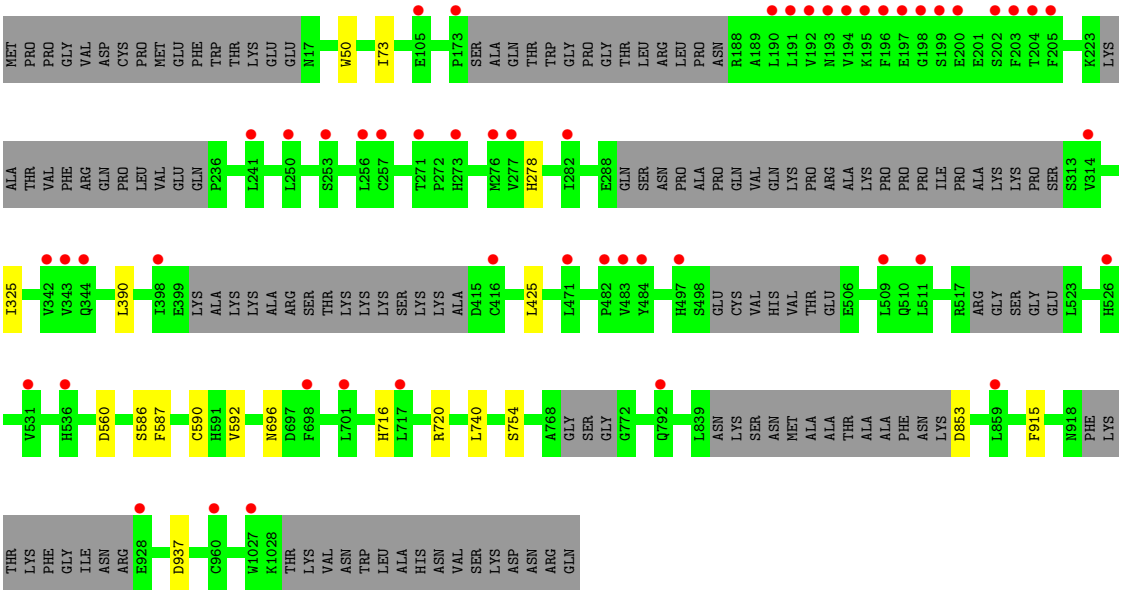
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	27	19	7	1	0	0

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: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit delta isoform

Chain A:



• Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit alpha

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	91.00Å 109.41Å 142.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.80 – 2.77 44.54 – 2.77	Depositor EDS
% Data completeness (in resolution range)	99.1 (86.80-2.77) 99.1 (44.54-2.77)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.88 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.219 , 0.287 0.219 , 0.275	Depositor DCC
R_{free} test set	755 reflections (2.06%)	wwPDB-VP
Wilson B-factor (Å^2)	79.6	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 55.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8803	wwPDB-VP
Average B, all atoms (Å^2)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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: M5D

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	0.39	0/7515	0.59	0/10158
2	B	0.41	0/1439	0.61	0/1917
All	All	0.39	0/8954	0.60	0/12075

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	7355	0	7338	5	0
2	B	1421	0	1409	3	0
3	A	27	0	0	0	0
All	All	8803	0	8747	7	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 0.

All (7) 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:73:ILE:HD11	2:B:493:ILE:HD12	1.89	0.55
1:A:390:LEU:HB2	1:A:425:LEU:HD21	1.96	0.47
2:B:509:ILE:HD11	2:B:521:ILE:HG23	2.01	0.42
1:A:587:PHE:HB3	1:A:592:VAL:HG11	2.01	0.41
1:A:325:ILE:HD13	1:A:390:LEU:HD21	2.02	0.41
1:A:716:HIS:O	1:A:720:ARG:HG2	2.20	0.41
2:B:488:ASN:OD1	2:B:542:ARG:CZ	2.70	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	890/1044 (85%)	859 (96%)	31 (4%)	0	100	100
2	B	160/188 (85%)	159 (99%)	1 (1%)	0	100	100
All	All	1050/1232 (85%)	1018 (97%)	32 (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	814/927 (88%)	803 (99%)	11 (1%)	67	87
2	B	155/176 (88%)	155 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	969/1103 (88%)	958 (99%)	11 (1%)	73 90

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	TRP
1	A	278	HIS
1	A	560	ASP
1	A	586	SER
1	A	590	CYS
1	A	696	ASN
1	A	740	LEU
1	A	754	SER
1	A	853	ASP
1	A	915	PHE
1	A	937	ASP

Sometimes 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)

1 ligand is 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	M5D	A	1101	-	27,30,30	1.00	0	32,44,44	2.03	10 (31%)

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	M5D	A	1101	-	-	0/12/36/36	0/4/4/4

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1101	M5D	C30-N28-N27	5.02	126.40	120.50
3	A	1101	M5D	C26-N27-N28	3.71	108.09	104.23
3	A	1101	M5D	C29-N28-N27	-3.36	108.64	111.56
3	A	1101	M5D	C4-N3-C2	3.35	121.66	116.67
3	A	1101	M5D	C4-C5-N6	-3.15	117.05	121.32
3	A	1101	M5D	N6-C5-N7	3.07	120.00	116.55
3	A	1101	M5D	C1-N6-C5	3.04	122.95	115.32
3	A	1101	M5D	C2-C23-N24	-2.98	172.51	177.60
3	A	1101	M5D	C1-C2-C23	2.59	123.66	120.64
3	A	1101	M5D	O15-C14-C16	-2.54	117.41	121.88

There are no chirality outliers.

There are no torsion outliers.

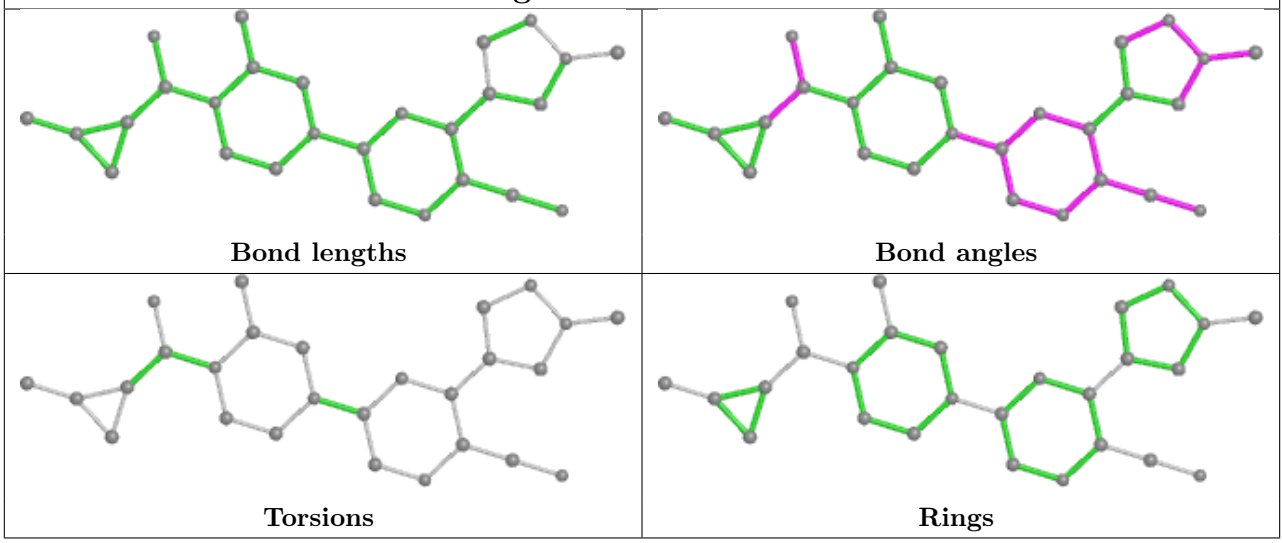
There are no ring outliers.

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 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 M5D A 1101



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	910/1044 (87%)	0.25	51 (5%)	24	19	52, 93, 149, 198	48 (5%)
2	B	164/188 (87%)	-0.08	1 (0%)	89	88	65, 90, 129, 152	11 (6%)
All	All	1074/1232 (87%)	0.20	52 (4%)	30	24	52, 92, 148, 198	59 (5%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	204	THR	5.5
1	A	509	LEU	5.0
1	A	717	LEU	4.8
1	A	198	GLY	4.7
1	A	203	PHE	4.4
1	A	195	LYS	4.2
1	A	191	LEU	4.0
1	A	197	GLU	3.9
1	A	241	LEU	3.8
1	A	205	PHE	3.8
1	A	511	LEU	3.6
1	A	196	PHE	3.4
1	A	193	ASN	3.4
1	A	416	CYS	3.4
1	A	471	LEU	3.4
1	A	497	HIS	3.3
1	A	276	MET	3.3
1	A	190	LEU	3.1
1	A	277	VAL	3.1
1	A	105	GLU	3.1
1	A	344	GLN	2.9
1	A	536	HIS	2.8
1	A	192	VAL	2.8
1	A	173	PRO	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	273	HIS	2.7
1	A	526	HIS	2.7
1	A	200	GLU	2.7
1	A	701	LEU	2.7
1	A	271	THR	2.6
1	A	928	GLU	2.6
1	A	698	PHE	2.6
1	A	342	VAL	2.6
1	A	194	VAL	2.5
1	A	343	VAL	2.5
1	A	257	CYS	2.5
1	A	398	ILE	2.5
1	A	859	LEU	2.5
1	A	250	LEU	2.4
1	A	199	SER	2.4
1	A	483	VAL	2.4
1	A	484	TYR	2.4
1	A	482	PRO	2.4
1	A	1027	TRP	2.4
1	A	253	SER	2.3
2	B	449	LEU	2.2
1	A	314	VAL	2.2
1	A	282	ILE	2.2
1	A	202	SER	2.2
1	A	960	CYS	2.1
1	A	256	LEU	2.1
1	A	792	GLN	2.1
1	A	531	VAL	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,

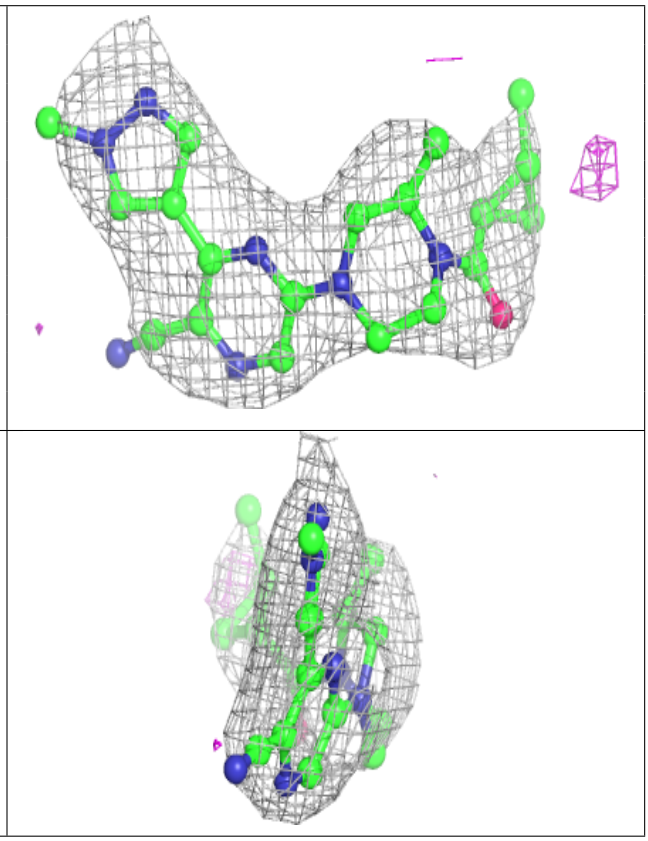
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	M5D	A	1101	27/27	0.95	0.23	67,81,94,101	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 M5D A 1101:

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.