Full wwPDB X-ray Structure Validation Report (i)

Mar 13, 2024 – 06:16 PM JST

PDB ID	:	5IMX
Title	:	Anaplastic lymphoma kinase (ALK) catalytic domain complexed with novel inhibitor 3-sulfonylpyrazol-4-amino pyrimidine
Authors	:	Wang, C.; Zhang, P.; Dong, J.
Deposited on	:	2016-03-07
Resolution	:	2.12 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:

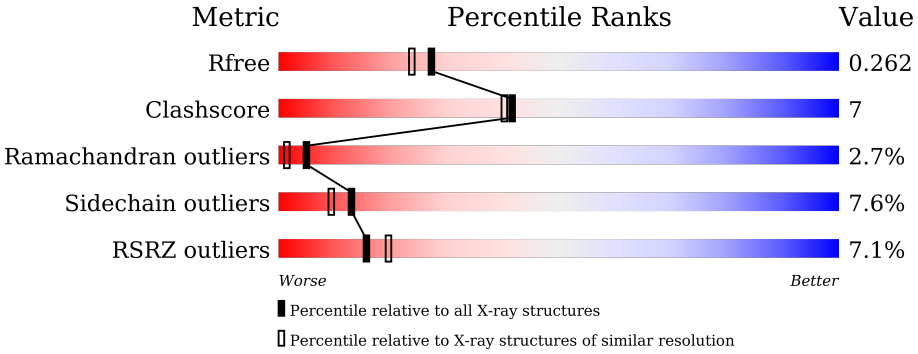
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

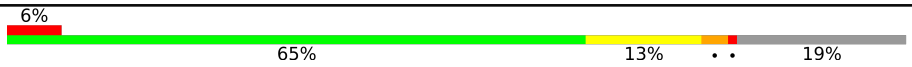
The reported resolution of this entry is 2.12 Å.

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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	327	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2135 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.

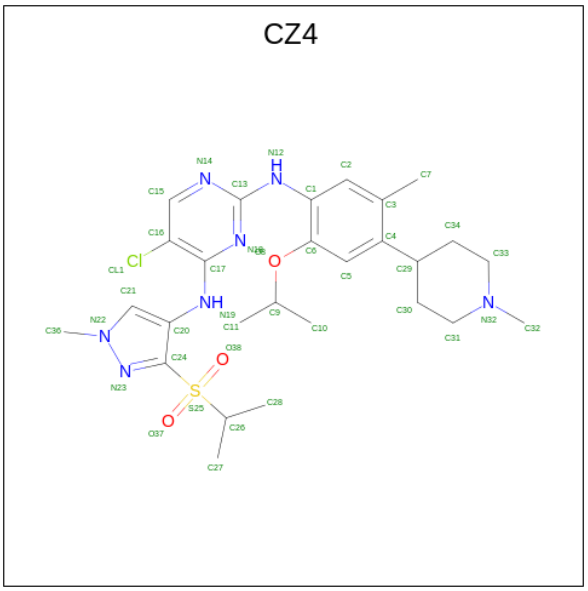
- Molecule 1 is a protein called ALK tyrosine kinase receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	266	2066	1322	352	375	17	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1085	MET	-	expression tag	UNP Q9UM73
A	1086	ALA	-	expression tag	UNP Q9UM73
A	1087	HIS	-	expression tag	UNP Q9UM73
A	1088	HIS	-	expression tag	UNP Q9UM73
A	1089	HIS	-	expression tag	UNP Q9UM73
A	1090	HIS	-	expression tag	UNP Q9UM73
A	1091	HIS	-	expression tag	UNP Q9UM73
A	1092	HIS	-	expression tag	UNP Q9UM73

- Molecule 2 is 5-chloro-N 2 -{5-methyl-4-(1-methylpiperidin-4-yl)-2-[(propan-2-yl)oxy]phenyl}-N 4 -{1-methyl-3-[(propan-2-yl)sulfonyl]-1H-pyrazol-4-yl}pyrimidine-2,4-diamine (three-letter code: CZ4) (formula: $C_{27}H_{38}ClN_7O_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Cl	N	O	S		
2	A	1	39	27	1	7	3	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	30	30	30	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: ALK tyrosine kinase receptor

Chain A: 6% 65% 13% • • 19%

MET ALA HIS HIS HIS HIS HIS HIS ASN PRO ASN TYR CYS PHE ALA GLY LYS THR SER SER ILE SER ASP LEU K1109 E1110 V1111 P1112 R1113 K1114 N1115 I1116 T1117 L1118 I1119 H1124 G1125 G1128 E1129 S1136 GLY MET PRO ASN ASP PRO SER P1144 K1150 T1151 L1152 PRO GLU VAL CYS SER

GLU GLN ASP GLU L1162 D1163 F1164 L1165 M1166 E1167 A1168 L1169 S1172 Q1177 V1180 R1181 V1185 S1186 L1187 Q1188 S1189 L1190 P1191 R1192 F1193 E1197 D1203 R1214 P1215 S1216 Q1217 P1218 L1221 R1231 A1234 Q1238 R1253 L1256 G1272 M1273 A1274 R1275 D1276 T1277 TYR ARG

ALA SER TYR TYR ARG LYS GLY GLY C1288 A1289 M1290 L1319 N1375 L1380 L1397 P1398 I1399 E1400 TYR GLY PRO LEU VAL GLU GLU GLU GLU LYS VAL

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	51.70Å 56.76Å 104.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.34 – 2.12 46.34 – 2.12	Depositor EDS
% Data completeness (in resolution range)	87.9 (46.34-2.12) 87.9 (46.34-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.22 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.210 , 0.259 0.217 , 0.262	Depositor DCC
R_{free} test set	816 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	37.0	Xtriage
Anisotropy	0.628	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 46.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2135	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.49% 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: CZ4

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	0.75	0/2115	0.91	4/2871 (0.1%)

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	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1181	ARG	NE-CZ-NH2	-7.69	116.46	120.30
1	A	1380	LEU	CA-CB-CG	5.67	128.33	115.30
1	A	1181	ARG	NE-CZ-NH1	5.61	123.11	120.30
1	A	1319	LEU	CA-CB-CG	5.10	127.03	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1218	PRO	Peptide

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	2066	0	2034	28	0
2	A	39	0	0	2	0
3	A	30	0	0	0	0
All	All	2135	0	2034	29	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 7.

All (29) 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:1112:PRO:O	1:A:1113:ARG:HB2	1.91	0.70
1:A:1112:PRO:HG2	1:A:1115:ASN:HD22	1.55	0.69
1:A:1177:GLN:HE21	1:A:1177:GLN:H	1.40	0.68
1:A:1118:LEU:C	1:A:1119:ILE:HD12	2.15	0.67
1:A:1151:THR:HG22	1:A:1193:PHE:CE1	2.32	0.64
1:A:1162:LEU:O	1:A:1164:PHE:N	2.32	0.62
1:A:1112:PRO:O	1:A:1113:ARG:CB	2.49	0.60
1:A:1216:SER:O	1:A:1217:GLN:C	2.39	0.60
1:A:1180:VAL:HG13	1:A:1197:GLU:HB3	1.85	0.59
1:A:1125:GLY:N	1:A:1128:GLY:O	2.28	0.57
1:A:1215:PRO:C	1:A:1216:SER:O	2.42	0.56
1:A:1112:PRO:HG2	1:A:1115:ASN:ND2	2.21	0.56
1:A:1231:ARG:HH11	1:A:1231:ARG:HG2	1.73	0.54
1:A:1273:MET:O	1:A:1276:ASP:HB2	2.08	0.54
1:A:1203:ASP:HA	1:A:1256:LEU:HD23	1.92	0.52
1:A:1162:LEU:O	1:A:1165:LEU:N	2.41	0.52
1:A:1375:ASN:OD1	1:A:1375:ASN:C	2.51	0.49
1:A:1288:CYS:C	1:A:1290:MET:N	2.67	0.48
1:A:1234:ALA:HB3	1:A:1380:LEU:HD13	1.97	0.47
1:A:1288:CYS:C	1:A:1290:MET:H	2.18	0.46
1:A:1190:LEU:HG	1:A:1191:PRO:HA	1.97	0.46
1:A:1115:ASN:HB3	1:A:1136:SER:H	1.80	0.46
1:A:1165:LEU:HG	1:A:1169:LEU:HD12	1.99	0.45
1:A:1151:THR:HG22	1:A:1193:PHE:CD1	2.53	0.44
2:A:1501:CZ4:C2	2:A:1501:CZ4:N18	2.78	0.44
1:A:1124:HIS:CD2	1:A:1124:HIS:N	2.86	0.42
1:A:1214:ARG:O	1:A:1218:PRO:HB3	2.20	0.42
1:A:1221:LEU:O	1:A:1397:LEU:HD12	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1150:LYS:HE3	2:A:1501:CZ4:O38	2.21	0.41

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	258/327 (79%)	240 (93%)	11 (4%)	7 (3%)	5 1

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1163	ASP
1	A	1216	SER
1	A	1113	ARG
1	A	1272	GLY
1	A	1168	ALA
1	A	1215	PRO
1	A	1276	ASP

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	224/285 (79%)	207 (92%)	17 (8%)	13 9

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1109	LYS
1	A	1117	THR
1	A	1129	GLU
1	A	1162	LEU
1	A	1167	GLU
1	A	1172	SER
1	A	1177	GLN
1	A	1185	VAL
1	A	1186	SER
1	A	1189	SER
1	A	1217	GLN
1	A	1221	LEU
1	A	1238	GLN
1	A	1253	ARG
1	A	1273	MET
1	A	1276	ASP
1	A	1380	LEU

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	1124	HIS
1	A	1177	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)

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	$\#\|Z\| > 2$
2	CZ4	A	1501	-	38,42,42	2.03	6 (15%)	46,62,62	3.79	20 (43%)

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
2	CZ4	A	1501	-	-	4/20/38/38	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1501	CZ4	C3-C4	6.85	1.48	1.40
2	A	1501	CZ4	C20-C24	5.74	1.48	1.38
2	A	1501	CZ4	C26-S25	-5.14	1.69	1.79
2	A	1501	CZ4	C1-C6	3.81	1.48	1.40
2	A	1501	CZ4	C15-C16	-2.45	1.36	1.39
2	A	1501	CZ4	O37-S25	2.09	1.46	1.44

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1501	CZ4	O37-S25-O38	-13.73	106.11	118.71
2	A	1501	CZ4	C3-C4-C29	10.59	129.93	121.35
2	A	1501	CZ4	O37-S25-C26	6.74	112.50	107.97
2	A	1501	CZ4	O8-C6-C1	6.11	121.04	114.63
2	A	1501	CZ4	C36-N22-N23	-5.92	113.55	120.50
2	A	1501	CZ4	C5-C4-C29	-5.71	111.43	121.34
2	A	1501	CZ4	N14-C13-N18	-5.41	121.42	126.55

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1501	CZ4	O38-S25-C24	5.22	113.67	108.25
2	A	1501	CZ4	C6-O8-C9	5.12	129.40	119.53
2	A	1501	CZ4	C16-C15-N14	-4.39	119.07	122.84
2	A	1501	CZ4	C15-N14-C13	3.51	121.18	115.88
2	A	1501	CZ4	C20-N19-C17	-3.38	121.19	129.63
2	A	1501	CZ4	O38-S25-C26	-3.34	105.72	107.97
2	A	1501	CZ4	O8-C9-C11	3.31	119.55	107.93
2	A	1501	CZ4	C31-N32-C33	2.54	113.08	109.52
2	A	1501	CZ4	C13-N18-C17	2.42	121.92	116.39
2	A	1501	CZ4	C34-C29-C4	2.25	116.74	112.26
2	A	1501	CZ4	C31-C30-C29	-2.08	108.58	111.04
2	A	1501	CZ4	N19-C17-N18	2.07	122.21	119.12
2	A	1501	CZ4	C6-C5-C4	2.01	123.75	119.42

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1501	CZ4	C34-C29-C4-C3
2	A	1501	CZ4	C34-C29-C4-C5
2	A	1501	CZ4	C11-C9-O8-C6
2	A	1501	CZ4	C5-C6-O8-C9

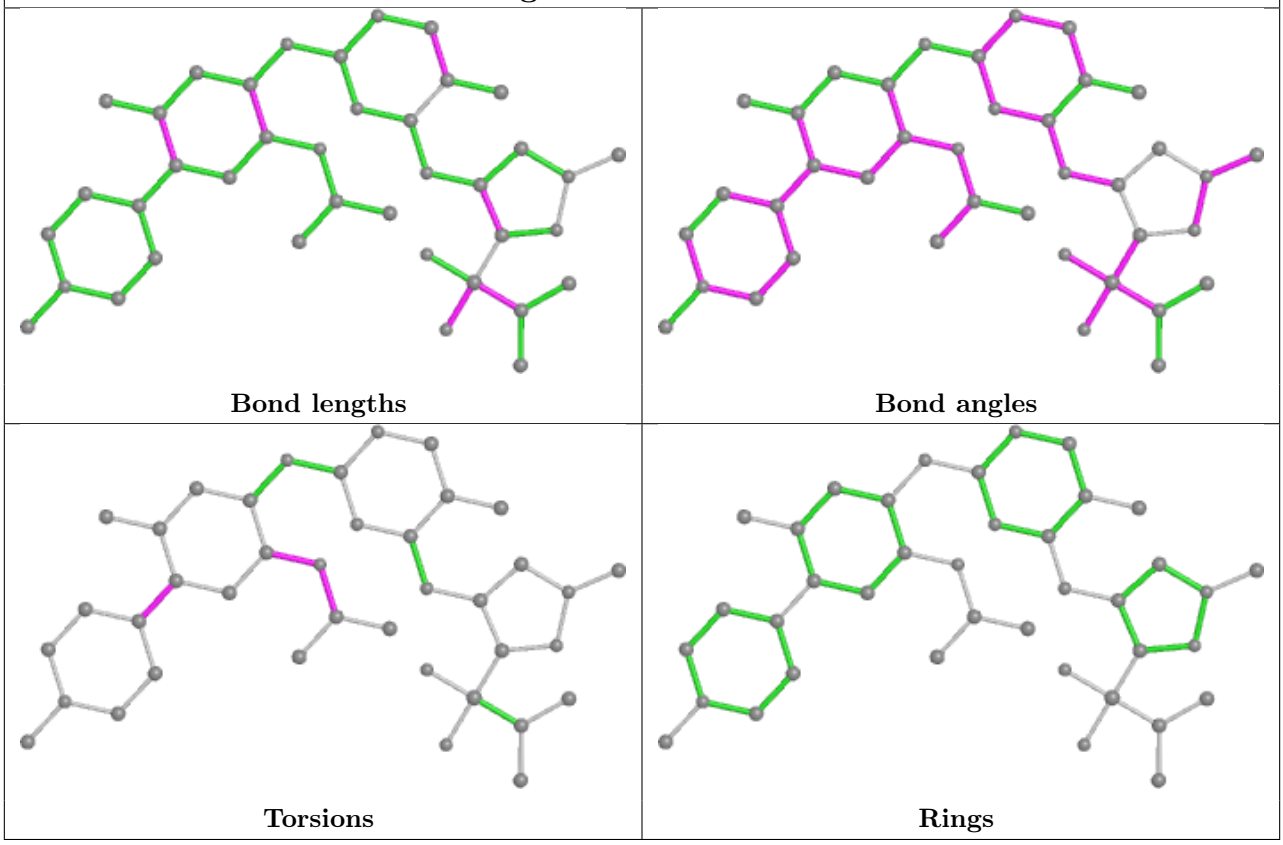
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1501	CZ4	2	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 CZ4 A 1501



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	266/327 (81%)	0.18	19 (7%) 16 19	26, 43, 91, 128	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1164	PHE	7.9
1	A	1277	ILE	5.9
1	A	1188	GLN	5.4
1	A	1152	LEU	4.5
1	A	1169	LEU	4.5
1	A	1275	ARG	4.0
1	A	1400	GLU	3.7
1	A	1217	GLN	3.6
1	A	1399	ILE	3.3
1	A	1216	SER	3.2
1	A	1165	LEU	3.2
1	A	1151	THR	2.7
1	A	1190	LEU	2.6
1	A	1215	PRO	2.6
1	A	1124	HIS	2.5
1	A	1189	SER	2.3
1	A	1163	ASP	2.3
1	A	1273	MET	2.2
1	A	1111	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)

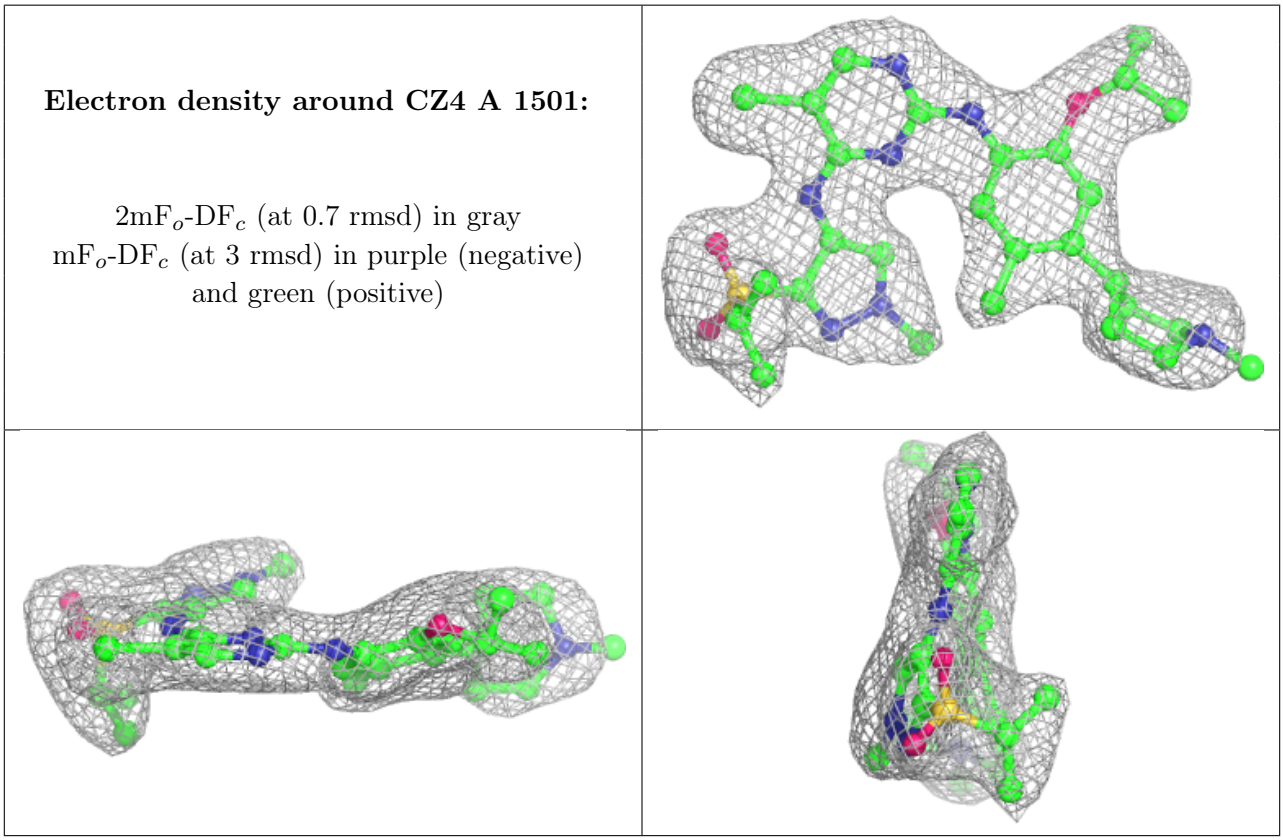
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CZ4	A	1501	39/39	0.97	0.12	37,48,63,66	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 CZ4 A 1501:

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.