



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:01 AM GMT

PDB ID : 3D15
Title : Crystal structure of mouse Aurora A (Asn186->Gly, Lys240->Arg, Met302->Leu) in complex with 1-(3-chloro-phenyl)-3-{5-[2-(thieno[3,2-d]pyrimidin-4-ylamino)-ethyl]-thiazol-2-yl}-urea [SNS-314]
Authors : Elling, R.A.; Bui, M.; Allen, D.A.; Oslob, J.D.; Romanowski, M.J.
Deposited on : 2008-05-04
Resolution : 2.30 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

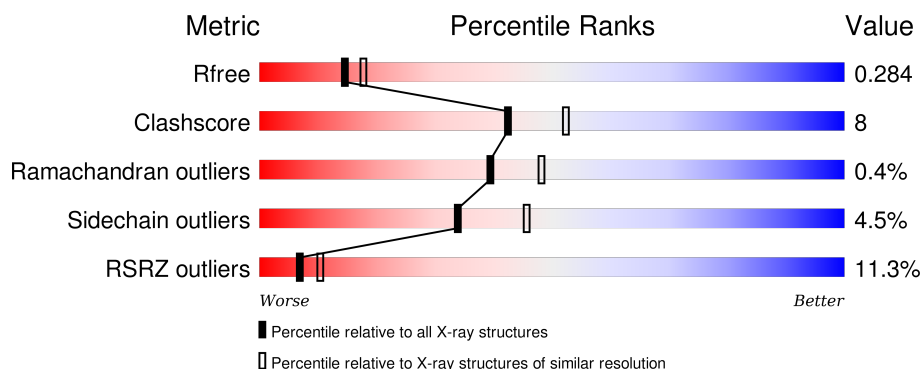
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	272	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2238 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.

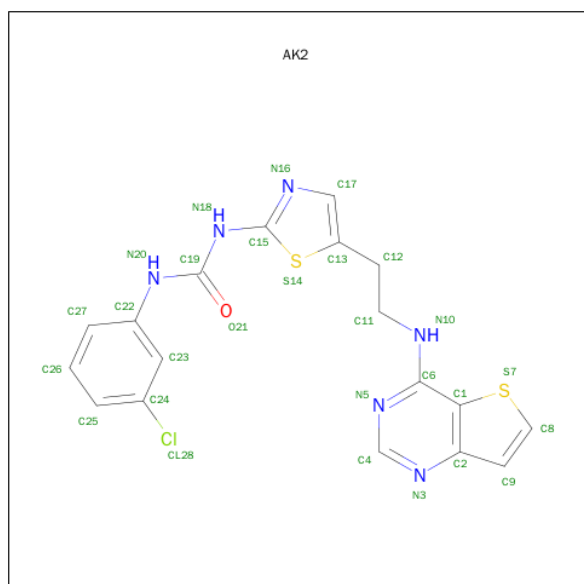
- Molecule 1 is a protein called serine/threonine kinase 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	256	2095	1347	367	376	5	0	3	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	133	GLY	-	EXPRESSION TAG	UNP Q8C3H8
A	134	PRO	-	EXPRESSION TAG	UNP Q8C3H8
A	135	LEU	-	EXPRESSION TAG	UNP Q8C3H8
A	136	GLY	-	EXPRESSION TAG	UNP Q8C3H8
A	137	SER	-	EXPRESSION TAG	UNP Q8C3H8
A	186	GLY	ASN	ENGINEERED	UNP Q8C3H8
A	240	ARG	LYS	ENGINEERED	UNP Q8C3H8
A	302	LEU	MET	ENGINEERED	UNP Q8C3H8

- Molecule 2 is 1-(3-CHLOROPHENYL)-3-{5-[2-(THIENO[3,2-D]PYRIMIDIN-4-YLAMINO)ETHYL]-1,3-THIAZOL-2-YL}UREA (three-letter code: AK2) (formula: C₁₈H₁₅ClN₆OS₂).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			28	18	1	6	1	2		

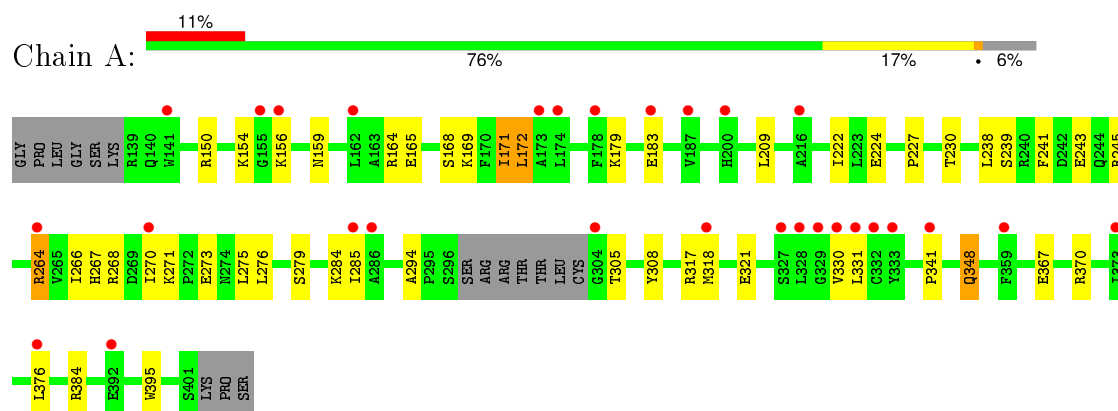
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	115	Total	O	0	0
			115	115		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: serine/threonine kinase 6



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	82.35Å 82.35Å 172.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.30 29.74 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-2.30) 98.9 (29.74-2.30)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.234 , 0.287 0.228 , 0.284	Depositor DCC
R_{free} test set	1131 reflections (7.69%)	DCC
Wilson B-factor (Å ²)	58.7	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 15884 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2238	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AK2

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	0.44	0/2147	0.60	0/2904

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

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	2095	0	2070	34	0
2	A	28	0	15	2	0
3	A	115	0	0	4	0
All	All	2238	0	2085	35	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 8.

All (35) 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:270:ILE:HD13	1:A:285:ILE:HD11	1.53	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:ILE:CD1	1:A:285:ILE:CD1	2.54	0.83
1:A:308:TYR:HE2	3:A:488:HOH:O	1.64	0.80
1:A:270:ILE:CD1	1:A:285:ILE:HD11	2.14	0.77
1:A:270:ILE:CD1	1:A:285:ILE:HD12	2.20	0.72
1:A:270:ILE:HD13	1:A:285:ILE:CD1	2.18	0.71
1:A:275:LEU:HD11	1:A:331:LEU:HD11	1.72	0.71
1:A:271:LYS:HG3	1:A:273:GLU:HG2	1.78	0.65
1:A:370:ARG:NH2	3:A:469:HOH:O	2.29	0.65
1:A:348:GLN:HE21	1:A:348:GLN:H	1.50	0.59
1:A:172:LEU:HD13	1:A:222:ILE:HG23	1.86	0.57
1:A:270:ILE:HD11	1:A:285:ILE:CD1	2.35	0.57
1:A:179:LYS:O	1:A:183:GLU:HG2	2.05	0.57
1:A:266:ILE:HG21	1:A:321:GLU:HA	1.88	0.55
1:A:330:VAL:HG13	1:A:341:PRO:HD2	1.88	0.54
1:A:243:GLU:HG3	1:A:395:TRP:HZ2	1.73	0.54
1:A:241:PHE:HB3	1:A:245:ARG:HG2	1.91	0.53
1:A:317:ARG:NH2	3:A:442:HOH:O	2.39	0.52
1:A:243:GLU:HG3	1:A:395:TRP:CZ2	2.46	0.51
1:A:224:GLU:O	2:A:1:AK2:H4	2.11	0.51
1:A:266:ILE:CG2	1:A:321:GLU:HA	2.44	0.48
1:A:230:THR:HG22	1:A:276:LEU:CD2	2.45	0.46
2:A:1:AK2:O21	2:A:1:AK2:H27	2.17	0.44
1:A:230:THR:HG22	1:A:276:LEU:HD22	2.00	0.44
1:A:318:MET:HE2	1:A:318:MET:HA	1.98	0.44
1:A:168:SER:O	1:A:169:LYS:HB2	2.18	0.43
1:A:267:HIS:O	1:A:268:ARG:HB2	2.19	0.43
1:A:238:LEU:O	1:A:239:SER:HB2	2.18	0.43
1:A:305:THR:HG23	3:A:502:HOH:O	2.18	0.43
1:A:227:PRO:HG2	1:A:279:SER:HB3	2.01	0.42
1:A:264:ARG:HD2	1:A:294:ALA:HB3	2.00	0.42
1:A:154:LYS:CB	1:A:159:ASN:ND2	2.83	0.42
1:A:264:ARG:HD3	1:A:264:ARG:HA	1.80	0.41
1:A:156:LYS:HA	1:A:156:LYS:HD2	1.78	0.41
1:A:164:ARG:HG3	1:A:171:ILE:HG12	2.01	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	252/272 (93%)	243 (96%)	8 (3%)	1 (0%)	39	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	ARG

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	223/240 (93%)	213 (96%)	10 (4%)	34	46

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	ARG
1	A	165	GLU
1	A	171	ILE
1	A	172	LEU
1	A	209	LEU
1	A	264	ARG
1	A	284	LYS
1	A	348	GLN
1	A	367	GLU
1	A	376	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	159	ASN
1	A	198	GLN
1	A	274	ASN
1	A	348	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 carbohydrates 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	AK2	A	1	-	25,31,31	2.44	6 (24%)	23,42,42	2.93	6 (26%)

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	AK2	A	1	-	-	0/10/14/14	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	AK2	C13-S14	-7.81	1.57	1.73
2	A	1	AK2	C17-N16	-5.49	1.28	1.36
2	A	1	AK2	C17-C13	-4.18	1.27	1.37
2	A	1	AK2	C9-C2	-3.23	1.29	1.42
2	A	1	AK2	C9-C8	-2.44	1.26	1.36
2	A	1	AK2	C19-N20	-2.16	1.33	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	AK2	N3-C4-N5	-9.50	121.62	128.89
2	A	1	AK2	C15-N18-C19	-3.82	125.45	130.13
2	A	1	AK2	C12-C11-N10	-2.59	107.23	111.04
2	A	1	AK2	C1-C6-N10	2.24	124.16	120.58
2	A	1	AK2	C4-N3-C2	4.08	118.96	115.19
2	A	1	AK2	C4-N5-C6	7.14	121.62	116.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	AK2	2	0

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	256/272 (94%)	0.60	29 (11%) 7 10	38, 57, 81, 105	2 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	156	LYS	7.1
1	A	328	LEU	4.5
1	A	318	MET	4.2
1	A	155	GLY	3.9
1	A	332	CYS	3.9
1	A	359	PHE	3.8
1	A	200	HIS	3.8
1	A	329	GLY	3.6
1	A	286	ALA	3.5
1	A	270	ILE	3.4
1	A	327	SER	3.3
1	A	392	GLU	3.1
1	A	330	VAL	2.9
1	A	373	ILE	2.9
1	A	285	ILE	2.8
1	A	178	PHE	2.6
1	A	331	LEU	2.6
1	A	187	VAL	2.6
1	A	141	TRP	2.5
1	A	183	GLU	2.5
1	A	264	ARG	2.5
1	A	174	LEU	2.2
1	A	376	LEU	2.2
1	A	341	PRO	2.2
1	A	216	ALA	2.2
1	A	333	TYR	2.1
1	A	304	GLY	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	162	LEU	2.0
1	A	173	ALA	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	AK2	A	1	28/28	0.93	0.14	-0.43	41,47,55,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.