



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 12, 2017 – 08:08 pm GMT

PDB ID : 2ABL  
Title : SH3-SH2 DOMAIN FRAGMENT OF HUMAN BCR-ABL TYROSINE KINASE  
Authors : Nam, H.-J.; Frederick, C.A.  
Deposited on : 1996-11-17  
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/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  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

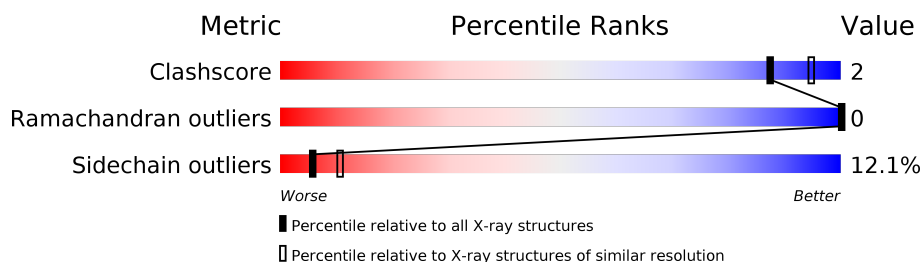
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	163	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1321 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 ABL TYROSINE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	0	0
			1281	803	226	250	2			

- Molecule 2 is water.

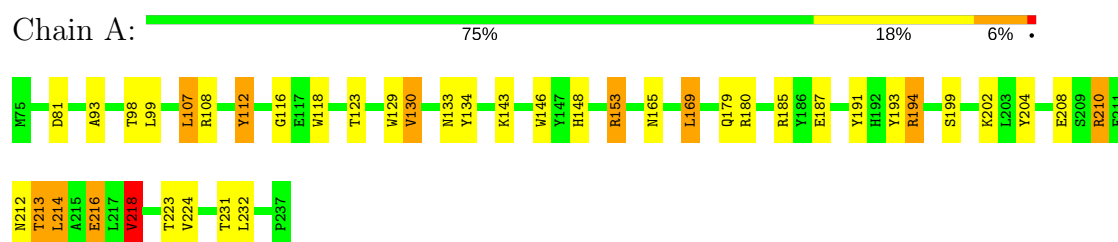
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	40	Total	O	0	0
			40	40		

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

These plots are drawn for all protein, RNA and DNA 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 ( $\text{RSRZ} > 2$ ). 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.

Note EDS was not executed.

#### • Molecule 1: ABL TYROSINE KINASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.62Å 45.85Å 54.45Å 90.00° 95.18° 90.00°	Depositor
Resolution (Å)	10.00 – 2.50	Depositor
% Data completeness (in resolution range)	99.1 (10.00-2.50)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.183 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1321	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	1.06	0/1316	1.83	38/1790 (2.1%)

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	ARG	NE-CZ-NH2	-11.86	114.37	120.30
1	A	108	ARG	NE-CZ-NH2	-11.17	114.72	120.30
1	A	169	LEU	CA-CB-CG	9.67	137.55	115.30
1	A	129	TRP	CD1-CG-CD2	7.95	112.66	106.30
1	A	146	TRP	CD1-CG-CD2	7.90	112.62	106.30
1	A	210	ARG	NE-CZ-NH1	7.71	124.15	120.30
1	A	210	ARG	NE-CZ-NH2	-7.44	116.58	120.30
1	A	180	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	A	146	TRP	CE2-CD2-CG	-7.35	101.42	107.30
1	A	129	TRP	CE2-CD2-CG	-7.28	101.47	107.30
1	A	118	TRP	CE2-CD2-CG	-7.14	101.59	107.30
1	A	146	TRP	CB-CG-CD1	-7.07	117.81	127.00
1	A	153	ARG	NE-CZ-NH2	-7.02	116.79	120.30
1	A	118	TRP	CD1-CG-CD2	6.67	111.63	106.30
1	A	118	TRP	CG-CD2-CE3	6.60	139.84	133.90
1	A	148	HIS	CA-C-N	6.59	129.38	116.20
1	A	146	TRP	CG-CD2-CE3	6.53	139.78	133.90
1	A	193	TYR	CB-CG-CD1	-6.44	117.14	121.00
1	A	129	TRP	CB-CG-CD1	-6.38	118.71	127.00
1	A	129	TRP	CG-CD2-CE3	6.29	139.57	133.90
1	A	218	VAL	CG1-CB-CG2	6.23	120.86	110.90
1	A	191	TYR	CB-CG-CD2	-5.99	117.41	121.00
1	A	223	THR	CA-CB-CG2	-5.87	104.18	112.40
1	A	129	TRP	CG-CD1-NE1	-5.84	104.25	110.10
1	A	143	LYS	CA-CB-CG	5.83	126.23	113.40
1	A	107	LEU	CA-CB-CG	5.81	128.67	115.30
1	A	93	ALA	CB-CA-C	-5.77	101.44	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	112	TYR	CB-CG-CD1	-5.71	117.57	121.00
1	A	81	ASP	CB-CG-OD1	5.70	123.43	118.30
1	A	179	GLN	CA-CB-CG	5.56	125.63	113.40
1	A	180	ARG	CG-CD-NE	-5.44	100.38	111.80
1	A	146	TRP	CG-CD1-NE1	-5.43	104.67	110.10
1	A	112	TYR	CD1-CG-CD2	5.39	123.83	117.90
1	A	134	TYR	CB-CG-CD2	-5.26	117.84	121.00
1	A	180	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	A	194	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	130	VAL	N-CA-CB	-5.07	100.35	111.50
1	A	204	TYR	CB-CG-CD2	-5.01	117.99	121.00

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	1281	0	1212	6	0
2	A	40	0	0	0	0
All	All	1321	0	1212	6	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 2.

All (6) 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:213:THR:HG23	1:A:216:GLU:HB2	1.62	0.81
1:A:214:LEU:O	1:A:218:VAL:HG13	2.11	0.49
1:A:202:LYS:HB3	1:A:210:ARG:HB3	1.97	0.47
1:A:165:ASN:ND2	1:A:187:GLU:H	2.15	0.45
1:A:112:TYR:HB3	1:A:116:GLY:HA2	1.99	0.43
1:A:99:LEU:HD21	1:A:123:THR:HG23	2.01	0.42

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	161/163 (99%)	152 (94%)	9 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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	140/140 (100%)	123 (88%)	17 (12%)	6	11

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

Mol	Chain	Res	Type
1	A	98	THR
1	A	107	LEU
1	A	130	VAL
1	A	133	ASN
1	A	153	ARG
1	A	169	LEU
1	A	194	ARG
1	A	199	SER
1	A	208	GLU
1	A	212	ASN

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Mol	Chain	Res	Type
1	A	213	THR
1	A	214	LEU
1	A	216	GLU
1	A	218	VAL
1	A	224	VAL
1	A	231	THR
1	A	232	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	122	GLN
1	A	127	GLN
1	A	133	ASN
1	A	165	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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.