



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 12:42 AM 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 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/ValidationPDFNotes.html>

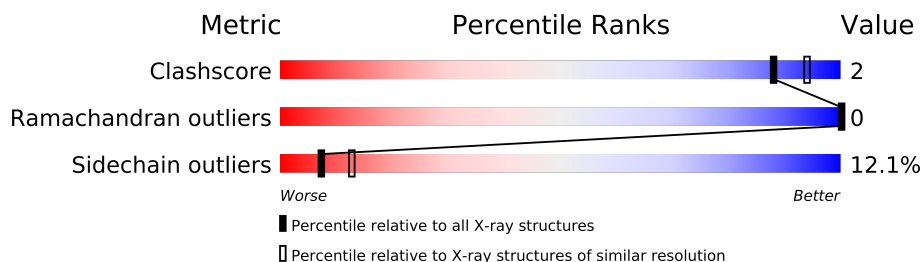
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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 hydrogen and 0 are deuterium.

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		

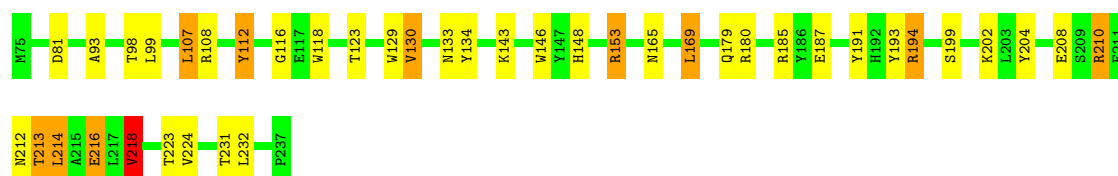
3 Residue-property plots

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.

Note EDS was not executed.

• Molecule 1: ABL TYROSINE KINASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	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 ²)	13.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

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

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (6) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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%)	7	13

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
1	A	213	THR
1	A	214	LEU
1	A	216	GLU

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Mol	Chain	Res	Type
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 ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.