



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:28 PM GMT

PDB ID : 4IGZ  
Title : Crystal structure of the SH3 domain of human sorbin and SH3 domain-containing protein 2  
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Deposited on : 2012-12-18  
Resolution : 1.33 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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  
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

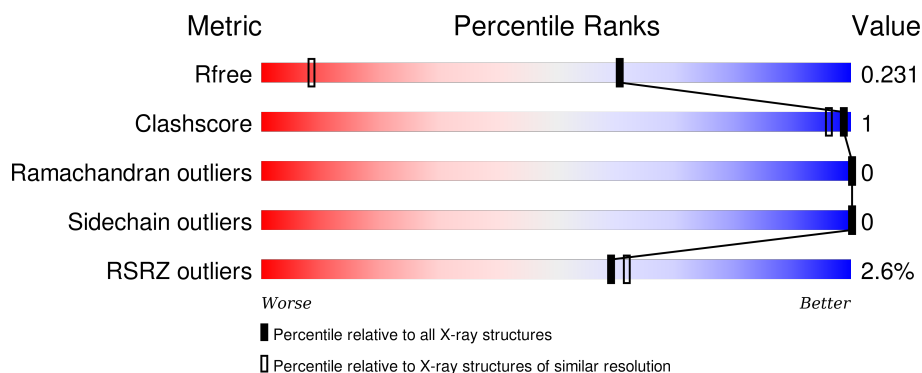
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.33 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	1723 (1.38-1.30)
Clashscore	102246	1806 (1.38-1.30)
Ramachandran outliers	100387	1749 (1.38-1.30)
Sidechain outliers	100360	1749 (1.38-1.30)
RSRZ outliers	91569	1721 (1.38-1.30)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	110	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	A	1003	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 668 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 Sorbin and SH3 domain-containing protein 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	76	Total	C	N	O	0	3	0
			612	398	101	113			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	832	MET	-	EXPRESSION TAG	UNP O94875
A	833	LYS	-	EXPRESSION TAG	UNP O94875
A	834	ILE	-	EXPRESSION TAG	UNP O94875
A	835	GLU	-	EXPRESSION TAG	UNP O94875
A	836	GLU	-	EXPRESSION TAG	UNP O94875
A	837	HIS	-	EXPRESSION TAG	UNP O94875
A	838	HIS	-	EXPRESSION TAG	UNP O94875
A	839	HIS	-	EXPRESSION TAG	UNP O94875
A	840	HIS	-	EXPRESSION TAG	UNP O94875
A	841	HIS	-	EXPRESSION TAG	UNP O94875
A	842	HIS	-	EXPRESSION TAG	UNP O94875
A	843	SER	-	EXPRESSION TAG	UNP O94875
A	844	SER	-	EXPRESSION TAG	UNP O94875
A	845	GLY	-	EXPRESSION TAG	UNP O94875
A	846	ARG	-	EXPRESSION TAG	UNP O94875
A	847	GLU	-	EXPRESSION TAG	UNP O94875
A	848	ASN	-	EXPRESSION TAG	UNP O94875
A	849	LEU	-	EXPRESSION TAG	UNP O94875
A	850	TYR	-	EXPRESSION TAG	UNP O94875
A	851	PHE	-	EXPRESSION TAG	UNP O94875
A	852	GLN	-	EXPRESSION TAG	UNP O94875
A	853	GLY	-	EXPRESSION TAG	UNP O94875
A	854	GLY	-	EXPRESSION TAG	UNP O94875
A	855	ALA	-	EXPRESSION TAG	UNP O94875
A	856	ALA	-	EXPRESSION TAG	UNP O94875
A	857	GLN	-	EXPRESSION TAG	UNP O94875
A	858	PRO	-	EXPRESSION TAG	UNP O94875

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Chain	Residue	Modelled	Actual	Comment	Reference
A	859	ALA	-	EXPRESSION TAG	UNP O94875
A	860	MET	-	EXPRESSION TAG	UNP O94875
A	861	ALA	-	EXPRESSION TAG	UNP O94875
A	862	GLN	-	EXPRESSION TAG	UNP O94875
A	863	GLY	-	EXPRESSION TAG	UNP O94875
A	864	ALA	-	EXPRESSION TAG	UNP O94875
A	865	LEU	-	EXPRESSION TAG	UNP O94875
A	922	GLY	-	EXPRESSION TAG	UNP O94875
A	923	SER	-	EXPRESSION TAG	UNP O94875
A	924	ALA	-	EXPRESSION TAG	UNP O94875
A	925	ALA	-	EXPRESSION TAG	UNP O94875
A	926	ALA	-	EXPRESSION TAG	UNP O94875
A	927	LEU	-	EXPRESSION TAG	UNP O94875
A	928	ARG	-	EXPRESSION TAG	UNP O94875
A	929	THR	-	EXPRESSION TAG	UNP O94875
A	930	GLY	-	EXPRESSION TAG	UNP O94875
A	931	GLU	-	EXPRESSION TAG	UNP O94875
A	932	ALA	-	EXPRESSION TAG	UNP O94875
A	933	TYR	-	EXPRESSION TAG	UNP O94875
A	934	LEU	-	EXPRESSION TAG	UNP O94875
A	935	ARG	-	EXPRESSION TAG	UNP O94875
A	936	TYR	-	EXPRESSION TAG	UNP O94875
A	937	VAL	-	EXPRESSION TAG	UNP O94875
A	938	ASP	-	EXPRESSION TAG	UNP O94875
A	939	ALA	-	EXPRESSION TAG	UNP O94875
A	940	ALA	-	EXPRESSION TAG	UNP O94875
A	941	ALA	-	EXPRESSION TAG	UNP O94875

- Molecule 2 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	6	Total X 6 6	0	0

- Molecule 3 is water.

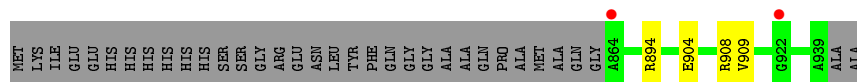
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	50	Total O 50 50	0	0

### 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 (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: Sorbin and SH3 domain-containing protein 2

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.20Å 27.50Å 58.85Å 90.00° 101.01° 90.00°	Depositor
Resolution (Å)	39.52 – 1.33 39.52 – 1.33	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.52-1.33) 99.7 (39.52-1.33)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 1.33Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.159 , 0.222 0.174 , 0.231	Depositor DCC
$R_{free}$ test set	821 reflections (5.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.7	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 53.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 16885 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	668	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.13% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.82	0/633	0.95	2/854 (0.2%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	894	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	A	908	ARG	NE-CZ-NH1	5.11	122.85	120.30

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	612	0	601	1	0
2	A	6	0	0	0	0
3	A	50	0	0	0	0
All	All	668	0	601	1	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 1.

All (1) 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:904:GLU:HG2	1:A:909:VAL:HG22	1.90	0.54

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	75/110 (68%)	73 (97%)	2 (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	60/85 (71%)	60 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are unknown - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	76/110 (69%)	-0.41	2 (2%) 59 62	12, 21, 37, 55	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	864[A]	ALA	2.2
1	A	922	GLY	2.1

### 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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
2	UNX	A	1003	1/1	0.97	0.07	2.42	25,25,25,25	0
2	UNX	A	1001	1/1	0.96	0.08	0.38	27,27,27,27	0
2	UNX	A	1004	1/1	0.95	0.18	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	UNX	A	1005	1/1	0.91	0.07	-	38,38,38,38	0
2	UNX	A	1002	1/1	0.95	0.06	-	38,38,38,38	0
2	UNX	A	1006	1/1	0.98	0.26	-	34,34,34,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.