



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 01:44 AM GMT

PDB ID : 1TXD
Title : Crystal Structure of the DH/PH domains of Leukemia-associated RhoGEF
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Deposited on : 2004-07-03
Resolution : 2.13 Å(reported)

This is a wwPDB validation summary 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>

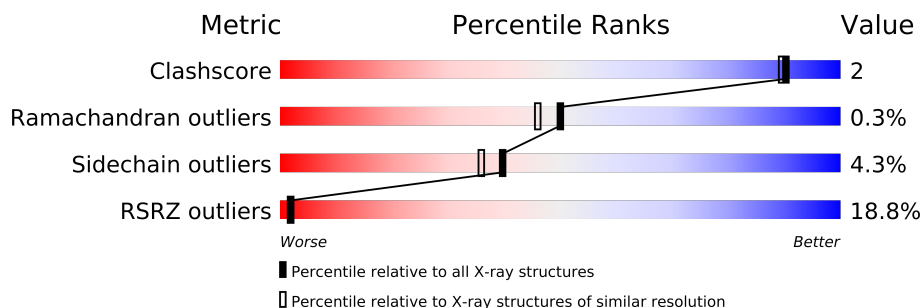
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
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 2.13 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	1302 (2.16-2.12)
Ramachandran outliers	78287	1281 (2.16-2.12)
Sidechain outliers	78261	1281 (2.16-2.12)
RSRZ outliers	66119	1116 (2.16-2.12)

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.

Mol	Chain	Length	Quality of chain
1	A	385	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2972 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 Rho guanine nucleotide exchange factor 12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	352	2881	1822	514	533	12	0	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	764	GLY	THR	CLONING ARTIFACT	UNP Q9NZN5
A	765	SER	ASP	CLONING ARTIFACT	UNP Q9NZN5
A	973	PHE	TYR	engineered	UNP Q9NZN5
A	1139	VAL	-	CLONING ARTIFACT	UNP Q9NZN5
A	1140	ASP	-	CLONING ARTIFACT	UNP Q9NZN5
A	1141	GLY	-	CLONING ARTIFACT	UNP Q9NZN5
A	1142	GLY	-	CLONING ARTIFACT	UNP Q9NZN5
A	1143	HIS	-	EXPRESSION TAG	UNP Q9NZN5
A	1144	HIS	-	EXPRESSION TAG	UNP Q9NZN5
A	1145	HIS	-	EXPRESSION TAG	UNP Q9NZN5
A	1146	HIS	-	EXPRESSION TAG	UNP Q9NZN5
A	1147	HIS	-	EXPRESSION TAG	UNP Q9NZN5
A	1148	HIS	-	EXPRESSION TAG	UNP Q9NZN5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	91	Total	O	0	0
			91	91		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	193.61Å 45.86Å 74.73Å 90.00° 107.49° 90.00°	Depositor
Resolution (Å)	24.85 – 2.13 24.83 – 2.07	Depositor EDS
% Data completeness (in resolution range)	97.5 (24.85-2.13) 97.4 (24.83-2.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.235 , 0.274 0.235 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 37667 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2972	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.77	1/2922 (0.0%)	0.89	9/3937 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	931	PRO	CG-CD	5.43	1.68	1.50

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	837	ASP	CB-CG-OD1	7.39	124.95	118.30
1	A	810	ASP	CB-CG-OD2	6.46	124.11	118.30
1	A	914	ASP	CB-CG-OD2	6.25	123.93	118.30
1	A	968	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	A	1014	ASP	CB-CG-OD2	5.37	123.13	118.30

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	2881	0	2972	12	0
2	A	91	0	0	0	0
All	All	2972	0	2972	12	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.

The worst 5 of 12 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:769:TRP:CD1	1:A:793:ASN:ND2	2.61	0.68
1:A:1020:MET:HE2	1:A:1041:LEU:HD22	1.86	0.58
1:A:930:ILE:N	1:A:931:PRO:CD	2.67	0.57
1:A:1095:LYS:HG2	1:A:1117:VAL:HG22	1.91	0.53
1:A:869:LEU:O	1:A:873:SER:OG	2.24	0.53

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	344/385 (89%)	331 (96%)	12 (4%)	1 (0%)	50	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	767	PRO

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	326/354 (92%)	312 (96%)	14 (4%)	40	36

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1018	ARG
1	A	1092	THR
1	A	1120	LYS
1	A	1017	LYS
1	A	1103	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1031	ASN
1	A	1094	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 ⓘ

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	352/385 (91%)	1.06	66 (18%) 2 2	10, 31, 69, 83	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1138	SER	8.0
1	A	1034	LYS	7.7
1	A	1048	VAL	6.3
1	A	1054	ASP	6.3
1	A	1047	LEU	6.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.