



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 06:12 PM GMT

PDB ID : 4A1S  
Title : Crystallographic structure of the Pins:Insc complex  
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Deposited on : 2011-09-19  
Resolution : 2.10 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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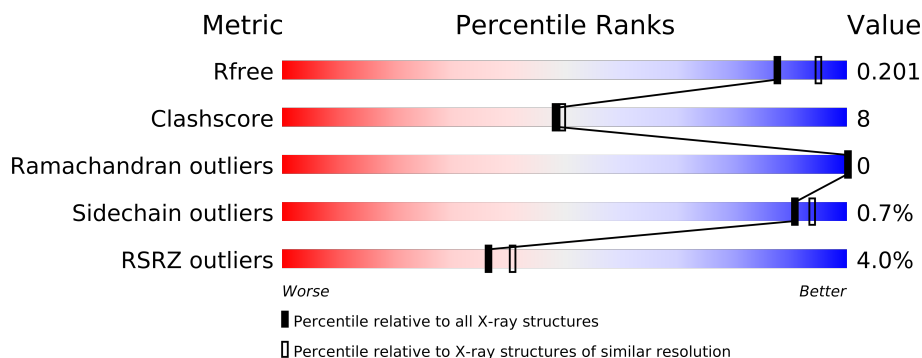
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 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 2.10 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))
$R_{free}$	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. 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	411	
1	B	411	
2	C	40	
2	E	40	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6240 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 PARTNER OF INSCUTEABLE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	0	0
			2656	1638	501	504	13			
1	B	342	Total	C	N	O	S	0	0	0
			2636	1626	497	500	13			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	EXPRESSION TAG	UNP Q9NH88
A	-3	PRO	-	EXPRESSION TAG	UNP Q9NH88
A	-2	LEU	-	EXPRESSION TAG	UNP Q9NH88
A	-1	GLY	-	EXPRESSION TAG	UNP Q9NH88
A	0	SER	-	EXPRESSION TAG	UNP Q9NH88
B	-4	GLY	-	EXPRESSION TAG	UNP Q9NH88
B	-3	PRO	-	EXPRESSION TAG	UNP Q9NH88
B	-2	LEU	-	EXPRESSION TAG	UNP Q9NH88
B	-1	GLY	-	EXPRESSION TAG	UNP Q9NH88
B	0	SER	-	EXPRESSION TAG	UNP Q9NH88

- Molecule 2 is a protein called RE60102P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	30	Total	C	N	O	S	0	0	0
			239	150	42	44	3			
2	E	28	Total	C	N	O	S	0	0	0
			224	141	38	42	3			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	231	Total	O	0	0
			231	231		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	228	Total 228	O 228	0	0
3	C	13	Total 13	O 13	0	0
3	E	13	Total 13	O 13	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	160.20Å 64.23Å 107.60Å 90.00° 117.90° 90.00°	Depositor
Resolution (Å)	23.13 – 2.10 23.59 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.5 (23.13-2.10) 96.5 (23.59-2.10)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.43 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.208 , 0.256 0.201 , 0.201	Depositor DCC
$R_{free}$ test set	2163 reflections (3.96%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.3	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 54.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 54635 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6240	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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	0.89	1/2619 (0.0%)	0.83	0/3519
1	B	0.94	5/2619 (0.2%)	0.87	6/3519 (0.2%)
2	C	0.86	0/247	0.78	0/336
2	E	0.97	0/231	0.78	0/313
All	All	0.91	6/5716 (0.1%)	0.85	6/7687 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	316	THR	CB-CG2	-6.33	1.31	1.52
1	A	54	CYS	CB-SG	-5.66	1.72	1.81
1	B	275	GLU	CD-OE1	5.33	1.31	1.25
1	B	113	SER	CB-OG	5.32	1.49	1.42
1	B	146	ARG	CZ-NH1	-5.11	1.26	1.33

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	316	THR	OG1-CB-CG2	-7.84	91.97	110.00
1	B	244	ARG	NE-CZ-NH2	-7.35	116.62	120.30
1	B	323	ARG	NE-CZ-NH1	-5.78	117.41	120.30
1	B	114	MET	CG-SD-CE	5.59	109.14	100.20
1	B	116	ASP	CB-CG-OD1	5.35	123.11	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	39	GLY	Peptide
1	B	39	GLY	Peptide

## 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	2656	0	26	20	0
1	B	2636	0	26	22	0
2	C	239	0	0	5	0
2	E	224	0	0	4	0
3	A	231	0	0	14	0
3	B	228	0	0	12	0
3	C	13	0	0	0	0
3	E	13	0	0	1	0
All	All	6240	0	52	45	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 8.

The worst 5 of 45 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:67:GLN:OE1	3:B:2020:HOH:O	1.83	0.97
1:B:78:ARG:NH2	3:B:2028:HOH:O	1.96	0.96
1:A:78:ARG:NH2	2:C:34:ILE:O	1.98	0.95
1:A:254:ARG:NH2	3:A:2178:HOH:O	2.02	0.91
1:B:60:ARG:NH2	3:B:2018:HOH:O	2.09	0.85

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	328/411 (80%)	321 (98%)	7 (2%)	0	100	100
1	B	328/411 (80%)	321 (98%)	7 (2%)	0	100	100
2	C	28/40 (70%)	27 (96%)	1 (4%)	0	100	100
2	E	26/40 (65%)	25 (96%)	1 (4%)	0	100	100
All	All	710/902 (79%)	694 (98%)	16 (2%)	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	254/283 (90%)	251 (99%)	3 (1%)	82	87
1	B	254/283 (90%)	253 (100%)	1 (0%)	95	97
2	C	26/34 (76%)	26 (100%)	0	100	100
2	E	25/34 (74%)	25 (100%)	0	100	100
All	All	559/634 (88%)	555 (99%)	4 (1%)	91	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	LYS
1	A	244	ARG
1	A	316	THR
1	B	244	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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, 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	330/411 (80%)	0.12	11 (3%) 44 49	24, 37, 70, 93	0
1	B	330/411 (80%)	0.14	15 (4%) 32 35	24, 37, 68, 93	0
2	C	30/40 (75%)	-0.07	2 (6%) 17 19	27, 40, 56, 77	0
2	E	28/40 (70%)	-0.07	1 (3%) 41 45	27, 36, 49, 55	0
All	All	718/902 (79%)	0.11	29 (4%) 36 41	24, 37, 69, 93	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	366	GLN	4.5
1	A	352	GLY	4.0
1	B	181	ARG	3.6
1	B	365	LEU	3.6
1	B	355	GLU	3.3

### 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.