



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4A1S / pdb_00004a1s
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 X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

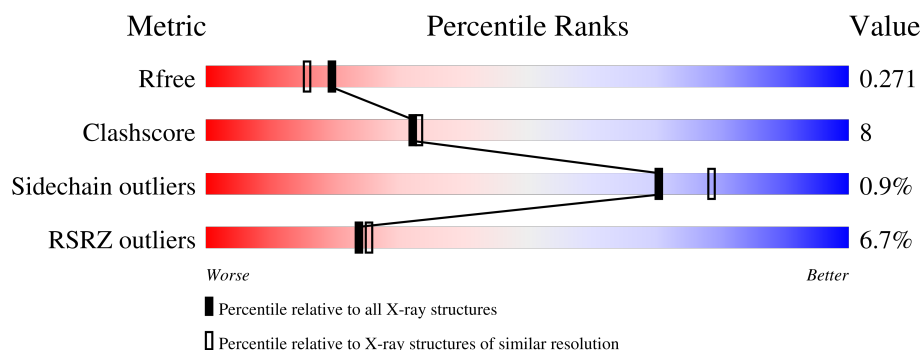
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	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 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 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, α , β , γ	160.20Å 64.23Å 107.60Å 90.00° 117.90° 90.00°	Depositor
Resolution (Å)	23.13 – 2.10 23.13 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.5 (23.13-2.10) 96.4 (23.13-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.208 , 0.256 (Not available) , 0.271	Depositor DCC
R_{free} test set	2164 reflections (3.91%)	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6240	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	1.10	2/2619 (0.1%)	1.11	5/3519 (0.1%)
1	B	1.12	2/2619 (0.1%)	1.13	5/3519 (0.1%)
2	C	1.09	0/247	1.07	0/336
2	E	1.12	0/231	1.01	0/313
All	All	1.11	4/5716 (0.1%)	1.11	10/7687 (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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	63	VAL	CA-CB	6.55	1.61	1.54
1	B	316	THR	CB-CG2	-6.39	1.31	1.52
1	B	76	ASP	CA-C	5.07	1.59	1.52
1	A	260	ALA	CA-CB	5.06	1.61	1.53

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	316	THR	OG1-CB-CG2	-8.66	91.97	109.30
1	B	66	PHE	N-CA-C	-6.30	104.49	111.36
1	B	109	THR	N-CA-C	-5.83	104.83	111.07
1	A	91	TYR	N-CA-C	-5.70	105.07	111.28
1	A	115	ASN	N-CA-C	5.61	118.92	111.30

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 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	2656	0	2502	40	0
1	B	2636	0	2498	40	0
2	C	239	0	223	9	0
2	E	224	0	212	4	0
3	A	231	0	0	14	0
3	B	228	0	0	12	0
3	C	13	0	0	1	0
3	E	13	0	0	1	0
All	All	6240	0	5435	90	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 8.

The worst 5 of 90 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)
2:C:6:HIS:HB2	2:C:7:PRO:HD3	1.36	1.06
1:B:67:GLN:OE1	3:B:2020:HOH:O	1.83	0.97
1:A:78:ARG:NH2	2:C:34:ILE:O	1.98	0.95
1:B:299:GLN:HE22	1:B:339:ARG:HH22	1.16	0.91
1:A:254:ARG:NH2	3:A:2178:HOH:O	2.02	0.91

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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%)	250 (98%)	4 (2%)	55	64
1	B	254/283 (90%)	253 (100%)	1 (0%)	84	89
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%)	554 (99%)	5 (1%)	70	78

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	LYS
1	A	112	LYS
1	A	294	ARG
1	A	316	THR
1	B	105	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	31	HIS
1	B	299	GLN
1	B	106	HIS
1	B	102	GLN
1	B	129	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 oligosaccharides 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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	368:ALA	C	375:UNK	N	4.93
1	A	368:ALA	C	371:UNK	N	4.06

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, 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	330/411 (80%)	0.16	20 (6%) 27 29	24, 37, 70, 93	0
1	B	330/411 (80%)	0.22	24 (7%) 21 22	24, 37, 68, 93	0
2	C	30/40 (75%)	0.11	2 (6%) 24 25	27, 40, 56, 76	0
2	E	28/40 (70%)	0.27	2 (7%) 22 23	27, 36, 49, 55	0
All	All	718/902 (79%)	0.19	48 (6%) 24 25	24, 37, 69, 93	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	113	SER	8.0
1	B	39	GLY	5.1
1	B	115	ASN	4.6
1	B	114	MET	4.1
1	A	39	GLY	3.8

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.