



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 22, 2017 – 04:32 PM EST

PDB ID : 5SXP  
Title : STRUCTURAL BASIS FOR THE INTERACTION BETWEEN ITCH PRR  
AND BETA-PIX  
Authors : Cappadocia, L.; Desrochers, G.; Lussier-Price, M.; Angers, A.; Omichinski,  
J.G.  
Deposited on : 2016-08-09  
Resolution : 1.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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)	:	rb-20028442

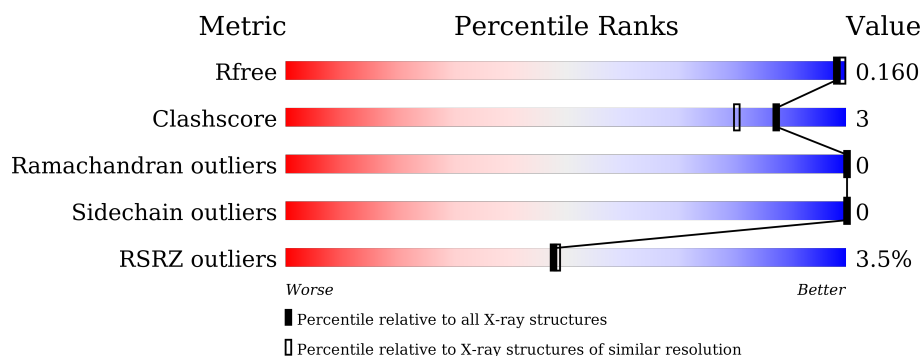
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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	62	<div> <div>2%</div> <div>95%</div> <div>5%</div> <div>••</div> </div>
1	B	62	<div> <div>6%</div> <div>94%</div> <div>5%</div> <div>•</div> </div>
1	C	62	<div> <div>89%</div> <div>8%</div> <div>•</div> </div>
1	D	62	<div> <div>2%</div> <div>97%</div> <div>•</div> </div>
2	F	27	<div> <div>11%</div> <div>70%</div> <div>30%</div> </div>
2	G	27	<div> <div>4%</div> <div>78%</div> <div>22%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4923 atoms, of which 2219 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 Rho guanine nucleotide exchange factor 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	61	Total	C	H	N	O	0	2	0
			988	320	478	91	99			
1	B	61	Total	C	H	N	O	0	0	0
			965	313	466	90	96			
1	C	60	Total	C	H	N	O	0	2	0
			996	320	487	95	94			
1	D	60	Total	C	H	N	O	0	0	0
			954	310	461	89	94			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	GLY	-	expression tag	UNP Q14155
B	182	GLY	-	expression tag	UNP Q14155
C	182	GLY	-	expression tag	UNP Q14155
D	182	GLY	-	expression tag	UNP Q14155

- Molecule 2 is a protein called E3 ubiquitin-protein ligase Itchy homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	19	Total	C	H	N	O	0	0	0
			303	91	155	34	23			
2	G	21	Total	C	H	N	O	0	0	0
			334	101	172	37	24			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	244	GLY	-	expression tag	UNP Q96J02
F	245	SER	-	expression tag	UNP Q96J02
F	246	GLY	-	expression tag	UNP Q96J02
F	247	GLY	-	expression tag	UNP Q96J02

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Chain	Residue	Modelled	Actual	Comment	Reference
F	248	GLY	-	expression tag	UNP Q96J02
F	270	TYR	-	expression tag	UNP Q96J02
G	244	GLY	-	expression tag	UNP Q96J02
G	245	SER	-	expression tag	UNP Q96J02
G	246	GLY	-	expression tag	UNP Q96J02
G	247	GLY	-	expression tag	UNP Q96J02
G	248	GLY	-	expression tag	UNP Q96J02
G	270	TYR	-	expression tag	UNP Q96J02

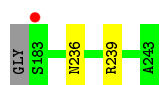
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	89	Total O 89 89	0	0
3	B	86	Total O 86 86	0	0
3	C	83	Total O 83 83	0	0
3	D	83	Total O 83 83	0	0
3	F	23	Total O 23 23	0	0
3	G	19	Total O 19 19	0	0

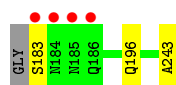
### 3 Residue-property plots [i](#)

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.

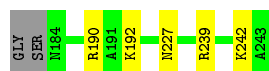
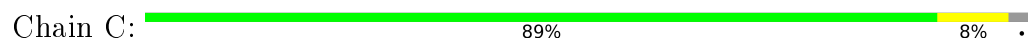
- Molecule 1: Rho guanine nucleotide exchange factor 7



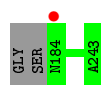
- Molecule 1: Rho guanine nucleotide exchange factor 7



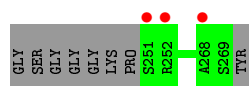
- Molecule 1: Rho guanine nucleotide exchange factor 7



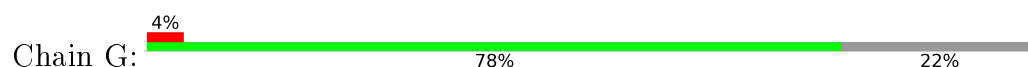
- Molecule 1: Rho guanine nucleotide exchange factor 7

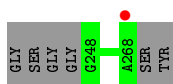


- Molecule 2: E3 ubiquitin-protein ligase Itchy homolog



- Molecule 2: E3 ubiquitin-protein ligase Itchy homolog





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	28.84Å 43.45Å 61.48Å 90.37° 101.01° 105.25°	Depositor
Resolution (Å)	41.85 – 1.65 41.85 – 1.65	Depositor EDS
% Data completeness (in resolution range)	95.7 (41.85-1.65) 93.0 (41.85-1.65)	Depositor EDS
$R_{merge}$	0.02	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.62 (at 1.65Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, $R_{free}$	0.139 , 0.161 0.138 , 0.160	Depositor DCC
$R_{free}$ test set	1361 reflections (4.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	14.9	Xtriage
Anisotropy	0.423	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 43.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4923	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.90% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	0.28	0/528	0.51	0/713
1	B	0.28	0/511	0.54	0/690
1	C	0.29	0/527	0.56	0/710
1	D	0.27	0/505	0.53	0/682
2	F	0.37	0/156	0.55	0/216
2	G	0.33	0/171	0.50	0/236
All	All	0.29	0/2398	0.53	0/3247

There are no bond length outliers.

There are no bond angle outliers.

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	510	478	478	4	0
1	B	499	466	466	5	0
1	C	509	487	487	6	0
1	D	493	461	461	0	0
2	F	148	155	154	0	0
2	G	162	172	172	0	0
3	A	89	0	0	1	1
3	B	86	0	0	2	1
3	C	83	0	0	5	0
3	D	83	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	23	0	0	0	0
3	G	19	0	0	0	0
All	All	2704	2219	2218	12	1

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 3.

All (12) 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:C:190:ARG:NH1	3:C:301:HOH:O	2.13	0.80
1:C:242:LYS:NZ	3:C:302:HOH:O	2.16	0.77
1:B:196:GLN:NE2	3:B:302:HOH:O	2.23	0.70
1:C:192:LYS:HD2	1:C:239[A]:ARG:HG2	1.87	0.55
1:C:227:ASN:O	3:C:303:HOH:O	2.19	0.50
1:A:236[A]:ASN:HD21	1:B:183:SER:N	2.09	0.50
1:C:239[A]:ARG:HD2	3:C:358:HOH:O	2.13	0.48
1:A:239:ARG:NH1	3:A:304:HOH:O	2.46	0.47
1:A:236[A]:ASN:HD21	1:B:183:SER:HA	1.82	0.44
1:C:227:ASN:OD1	3:C:304:HOH:O	2.21	0.44
1:A:236[A]:ASN:HD21	1:B:183:SER:CA	2.31	0.43
1:B:243:ALA:OXT	3:B:301:HOH:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:306:HOH:O	3:B:317:HOH:O[1_655]	2.10	0.10

## 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	61/62 (98%)	61 (100%)	0	0	100	100
1	B	59/62 (95%)	57 (97%)	2 (3%)	0	100	100
1	C	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
1	D	58/62 (94%)	58 (100%)	0	0	100	100
2	F	17/27 (63%)	17 (100%)	0	0	100	100
2	G	19/27 (70%)	19 (100%)	0	0	100	100
All	All	274/302 (91%)	271 (99%)	3 (1%)	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	55/53 (104%)	55 (100%)	0	100	100
1	B	53/53 (100%)	53 (100%)	0	100	100
1	C	54/53 (102%)	54 (100%)	0	100	100
1	D	52/53 (98%)	52 (100%)	0	100	100
2	F	18/22 (82%)	18 (100%)	0	100	100
2	G	19/22 (86%)	19 (100%)	0	100	100
All	All	251/256 (98%)	251 (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 ⓘ

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](#)

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](#)

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	61/62 (98%)	-0.41	1 (1%) 74 78	9, 13, 27, 57	0
1	B	61/62 (98%)	-0.22	4 (6%) 22 19	8, 13, 27, 75	0
1	C	60/62 (96%)	-0.16	0 100 100	9, 15, 32, 35	0
1	D	60/62 (96%)	-0.23	1 (1%) 73 76	8, 14, 28, 53	0
2	F	19/27 (70%)	0.31	3 (15%) 3 2	13, 18, 59, 63	0
2	G	21/27 (77%)	0.44	1 (4%) 34 32	13, 20, 61, 66	0
All	All	282/302 (93%)	-0.17	10 (3%) 48 48	8, 14, 45, 75	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	268	ALA	7.0
1	B	184	ASN	5.9
1	A	183	SER	4.4
2	F	251	SER	4.2
1	B	183	SER	3.6
2	F	252	ARG	3.4
1	B	186	GLN	3.0
1	B	185	ASN	3.0
2	F	268	ALA	2.4
1	D	184	ASN	2.4

### 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 [i](#)

There are no carbohydrates 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.