



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 02:57 am GMT

PDB ID : 2FBE  
Title : Crystal Structure of the PRYSPRY-domain  
Authors : Gruetter, C.; Briand, C.; Capitani, G.; Mittl, P.R.; Gruetter, M.G.  
Deposited on : 2005-12-09  
Resolution : 2.52 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

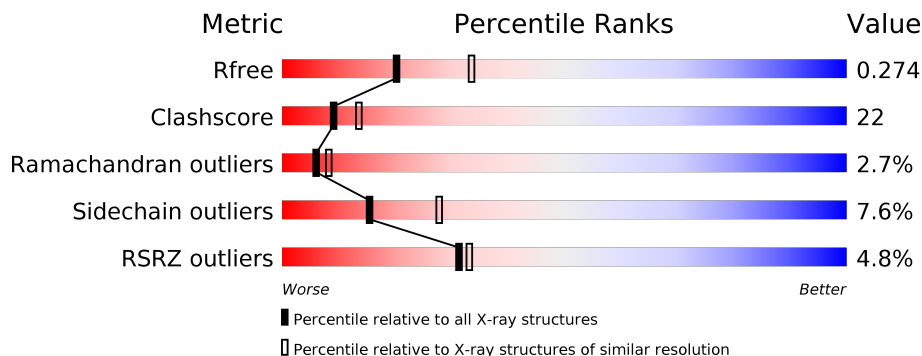
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.52 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))
$R_{free}$	100719	4636 (2.54-2.50)
Clashscore	112137	5382 (2.54-2.50)
Ramachandran outliers	110173	5282 (2.54-2.50)
Sidechain outliers	110143	5284 (2.54-2.50)
RSRZ outliers	101464	4669 (2.54-2.50)

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	201	<div> <div>4%</div> <div> <div></div> <div>65%</div> <div>25%</div> <div>6%</div> </div> </div>
1	B	201	<div> <div>7%</div> <div> <div></div> <div>58%</div> <div>30%</div> <div>9%</div> </div> </div>
1	C	201	<div> <div>5%</div> <div> <div></div> <div>62%</div> <div>31%</div> <div>• •</div> </div> </div>
1	D	201	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>23%</div> <div>• • 5%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6286 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 PREDICTED: similar to ret finger protein-like 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	Se	12	0	0
			1484	938	257	280	6	3			
1	B	198	Total	C	N	O	S	Se	4	0	0
			1544	974	267	294	6	3			
1	C	199	Total	C	N	O	S	Se	7	0	0
			1553	979	268	297	6	3			
1	D	190	Total	C	N	O	S	Se	3	0	0
			1497	946	259	283	6	3			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	GB 51474829
A	2	PRO	-	CLONING ARTIFACT	GB 51474829
A	3	LEU	-	CLONING ARTIFACT	GB 51474829
A	4	GLY	-	CLONING ARTIFACT	GB 51474829
A	5	SER	-	CLONING ARTIFACT	GB 51474829
A	6	PRO	-	CLONING ARTIFACT	GB 51474829
A	7	GLU	-	CLONING ARTIFACT	GB 51474829
A	12	MSE	MET	MODIFIED RESIDUE	GB 51474829
A	93	GLU	VAL	CLONING ARTIFACT	GB 51474829
A	118	MSE	MET	MODIFIED RESIDUE	GB 51474829
A	138	MSE	MET	MODIFIED RESIDUE	GB 51474829
B	1	GLY	-	CLONING ARTIFACT	GB 51474829
B	2	PRO	-	CLONING ARTIFACT	GB 51474829
B	3	LEU	-	CLONING ARTIFACT	GB 51474829
B	4	GLY	-	CLONING ARTIFACT	GB 51474829
B	5	SER	-	CLONING ARTIFACT	GB 51474829
B	6	PRO	-	CLONING ARTIFACT	GB 51474829
B	7	GLU	-	CLONING ARTIFACT	GB 51474829
B	12	MSE	MET	MODIFIED RESIDUE	GB 51474829
B	93	GLU	VAL	CLONING ARTIFACT	GB 51474829
B	118	MSE	MET	MODIFIED RESIDUE	GB 51474829

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Chain	Residue	Modelled	Actual	Comment	Reference
B	138	MSE	MET	MODIFIED RESIDUE	GB 51474829
C	1	GLY	-	CLONING ARTIFACT	GB 51474829
C	2	PRO	-	CLONING ARTIFACT	GB 51474829
C	3	LEU	-	CLONING ARTIFACT	GB 51474829
C	4	GLY	-	CLONING ARTIFACT	GB 51474829
C	5	SER	-	CLONING ARTIFACT	GB 51474829
C	6	PRO	-	CLONING ARTIFACT	GB 51474829
C	7	GLU	-	CLONING ARTIFACT	GB 51474829
C	12	MSE	MET	MODIFIED RESIDUE	GB 51474829
C	93	GLU	VAL	CLONING ARTIFACT	GB 51474829
C	118	MSE	MET	MODIFIED RESIDUE	GB 51474829
C	138	MSE	MET	MODIFIED RESIDUE	GB 51474829
D	1	GLY	-	CLONING ARTIFACT	GB 51474829
D	2	PRO	-	CLONING ARTIFACT	GB 51474829
D	3	LEU	-	CLONING ARTIFACT	GB 51474829
D	4	GLY	-	CLONING ARTIFACT	GB 51474829
D	5	SER	-	CLONING ARTIFACT	GB 51474829
D	6	PRO	-	CLONING ARTIFACT	GB 51474829
D	7	GLU	-	CLONING ARTIFACT	GB 51474829
D	12	MSE	MET	MODIFIED RESIDUE	GB 51474829
D	93	GLU	VAL	CLONING ARTIFACT	GB 51474829
D	118	MSE	MET	MODIFIED RESIDUE	GB 51474829
D	138	MSE	MET	MODIFIED RESIDUE	GB 51474829

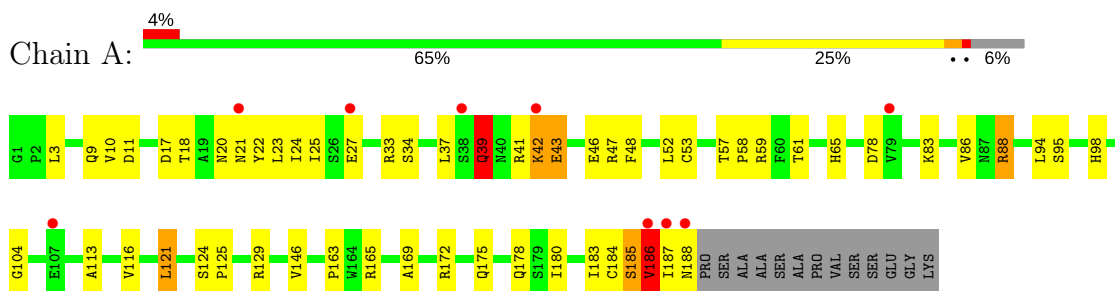
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	44	Total O 44 44	0	0
2	B	48	Total O 48 48	0	0
2	C	50	Total O 50 50	0	0
2	D	66	Total O 66 66	0	0

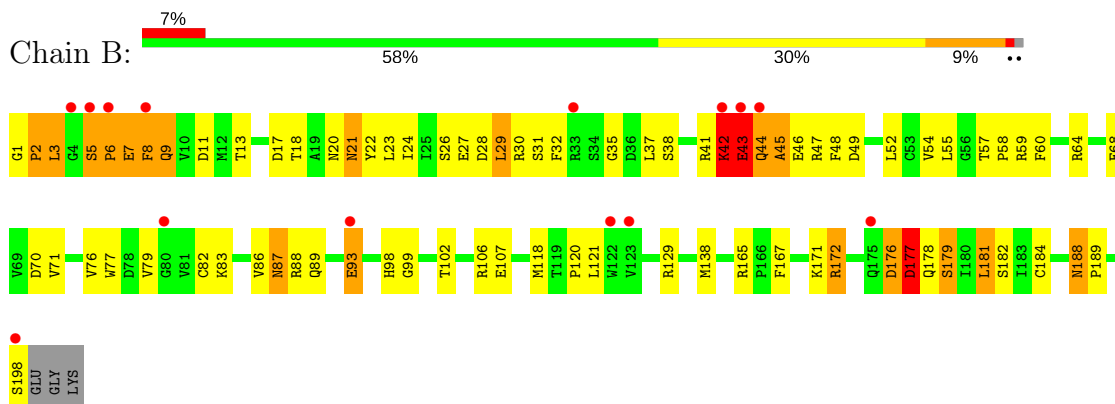
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

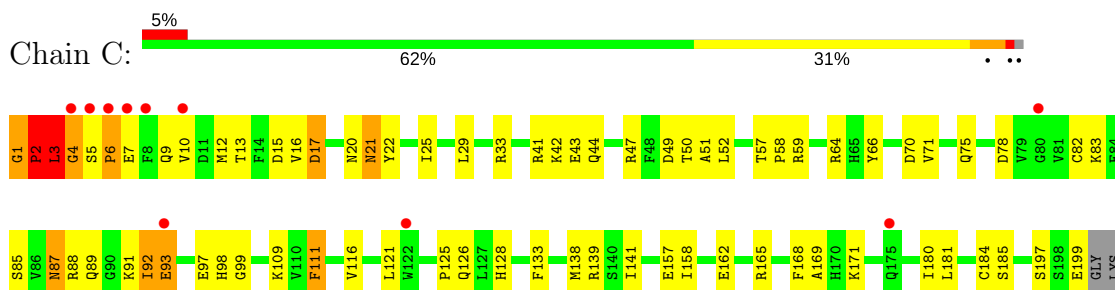
- Molecule 1: PREDICTED: similar to ret finger protein-like 1



- Molecule 1: PREDICTED: similar to ret finger protein-like 1

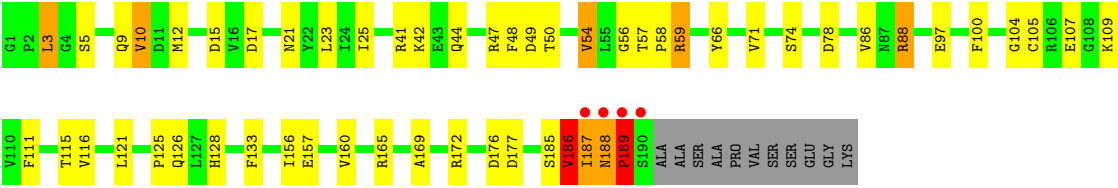


- Molecule 1: PREDICTED: similar to ret finger protein-like 1



- Molecule 1: PREDICTED: similar to ret finger protein-like 1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.22Å 77.22Å 297.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.46 – 2.52 34.30 – 2.52	Depositor EDS
% Data completeness (in resolution range)	96.1 (30.46-2.52) 96.1 (34.30-2.52)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.97 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.227 , 0.277 0.225 , 0.274	Depositor DCC
$R_{free}$ test set	1502 reflections (4.95%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.5	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 60.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6286	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.38% 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	0.42	0/1518	0.80	4/2055 (0.2%)
1	B	0.54	1/1580 (0.1%)	0.93	6/2142 (0.3%)
1	C	0.52	1/1589 (0.1%)	0.82	8/2154 (0.4%)
1	D	0.48	0/1532	0.83	2/2075 (0.1%)
All	All	0.49	2/6219 (0.0%)	0.85	20/8426 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1	GLY	N-CA	6.58	1.55	1.46
1	B	8	PHE	CD2-CE2	-5.01	1.29	1.39

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	189	PRO	N-CA-C	13.85	148.10	112.10
1	C	2	PRO	C-N-CA	8.47	142.89	121.70
1	A	185	SER	N-CA-C	8.31	133.45	111.00
1	A	185	SER	N-CA-CB	-7.49	99.26	110.50
1	B	42	LYS	CA-C-N	-7.46	100.78	117.20

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	1484	0	1431	41	3
1	B	1544	0	1489	94	3
1	C	1553	0	1495	84	0
1	D	1497	0	1443	53	0
2	A	44	0	0	4	0
2	B	48	0	0	6	0
2	C	50	0	0	6	0
2	D	66	0	0	2	0
All	All	6286	0	5858	264	3

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 22.

The worst 5 of 264 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:B:42:LYS:O	1:B:47:ARG:NH1	1.70	1.23
1:C:97:GLU:CD	1:D:189:PRO:HB3	1.60	1.22
1:B:42:LYS:HE3	1:B:44:GLN:OE1	1.39	1.20
1:C:4:GLY:HA2	2:C:244:HOH:O	1.42	1.15
1:B:22:TYR:CE1	1:B:38:SER:OG	2.01	1.12

All (3) 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)
1:A:22:TYR:OH	1:B:43:GLU:OE2[1_655]	1.64	0.56
1:A:22:TYR:OH	1:B:43:GLU:CD[1_655]	2.10	0.10
1:A:22:TYR:OH	1:B:43:GLU:OE1[1_655]	2.11	0.09

## 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	186/201 (92%)	165 (89%)	18 (10%)	3 (2%)	11	19
1	B	196/201 (98%)	176 (90%)	11 (6%)	9 (5%)	3	3
1	C	197/201 (98%)	173 (88%)	17 (9%)	7 (4%)	4	4
1	D	188/201 (94%)	178 (95%)	8 (4%)	2 (1%)	17	28
All	All	767/804 (95%)	692 (90%)	54 (7%)	21 (3%)	6	8

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	VAL
1	B	43	GLU
1	B	45	ALA
1	C	3	LEU
1	C	6	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	166/172 (96%)	157 (95%)	9 (5%)	26	45
1	B	173/172 (101%)	156 (90%)	17 (10%)	9	17
1	C	174/172 (101%)	160 (92%)	14 (8%)	14	25
1	D	168/172 (98%)	156 (93%)	12 (7%)	17	31
All	All	681/688 (99%)	629 (92%)	52 (8%)	15	28

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	181	LEU
1	C	21	ASN
1	D	126	GLN
1	B	188	ASN
1	C	2	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	20	ASN
1	C	75	GLN
1	D	178	GLN
1	C	21	ASN
1	C	44	GLN

### 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](#)

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 [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	185/201 (92%)	0.08	9 (4%) 30 32	23, 46, 87, 115	7 (3%)
1	B	195/201 (97%)	0.26	14 (7%) 16 17	29, 53, 88, 100	3 (1%)
1	C	196/201 (97%)	0.10	10 (5%) 29 30	24, 47, 84, 106	4 (2%)
1	D	187/201 (93%)	-0.28	4 (2%) 64 66	18, 34, 59, 127	3 (1%)
All	All	763/804 (94%)	0.04	37 (4%) 31 33	18, 45, 86, 127	17 (2%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	187	ILE	7.5
1	D	189	PRO	7.4
1	D	190	SER	7.4
1	C	5	SER	6.0
1	D	188	ASN	5.6

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.