



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:05 AM UTC

PDB ID : 3MYX / pdb_00003myx
Title : Crystal structure of a PSPTO_0244 (Protein with unknown function which belongs to Pfam DUF861 family) from Pseudomonas syringae pv. tomato str. DC3000 at 1.30 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2010-05-11
Resolution : 1.30 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

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	:	FAILED
Mogul	:	FAILED
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	FAILED
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

PERCENTILES INFOmissingINFO

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

GLOBAL-STATISTICS INFOmissingINFO

1 Model quality [i](#)

1.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

1.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

1.3 Torsion angles [i](#)

1.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

1.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

1.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

1.4 Non-standard residues in protein, DNA, RNA chains [i](#)

Mogul failed to run properly - this section is therefore empty.

1.5 Carbohydrates [i](#)

Mogul failed to run properly - this section is therefore empty.

1.6 Ligand geometry [i](#)

Mogul failed to run properly - this section is therefore empty.

1.7 Other polymers [i](#)

Mogul failed to run properly - this section is therefore empty.

1.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

2 Fit of model and data

2.1 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	1-A	8/238 (3%)	0.34	1 (12%) 8 9	7, 13, 24, 31	1 (12%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	3	GLN	3.1

MODRES-RSR INFOmissingINFO

SUGAR-RSR INFOmissingINFO

LIGAND-RSR INFOmissingINFO

OTHERPOLY-RSR INFOmissingINFO