

# Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

## [PIDFinder](#)

RRID:SCR\_005833

Type: Tool

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### Proper Citation

PIDFinder (RRID:SCR\_005833)

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### Resource Information

**URL:** <http://pidfinder.appspot.com/>

**Proper Citation:** PIDFinder (RRID:SCR\_005833)

**Description:** PIDFinder is a tool for the exploration of the Primary Immunodeficiency Disease Ontology. Apart from browsing the knowledge contained in the ontology, it can also be used for the identification of PIDs based on a set of observed Phenotypes. The PidFinder web application is a developing prototype application that allows non-bioinformaticians to quickly view and use the knowledge contained in the Primary Immunodeficiency Disease Ontology. The application consists of a number of components: \* The PIDFinder: allows the selection of a set of phenotypes and subsequently compares the set with the canonical set of phenotypes defined in the PID Ontology. The phenotypes, that can be selected are grouped by biomarker and are thus available in a number of different facets. Once phenotypes have been selected, the application compares them to canonical phenotypes associated with PIDs in the PID Ontology, by computing a semantic similarity measure. The similarity is determined using a Tanimoto Distance - the more closely related an observed phenotype is to a canonical ontology phenotype, the closer the calculated Tanimoto Distance is to 1 - with increasing dissimilarity, the Tanimoto Coefficient tends towards 0. \* The Phenotype Explorer: a rudimentary browser for phenotypes currently contained in the PID Ontology. The browser allows the user to find phenotypes based on biomarker categories and provides some basic definitions (not all definitions are available at this stage) and disease association information. \* A Heatmap comparing the phenotypic overlap of PIDs: In essence, the heatmap is a many-to-many comparison of the phenotypic overlap between all Primary Immunodeficiency Diseases contained in the PID Ontology. Again, overlap is calculated using a Tanimoto Distance. The heatmap is a matrix, plotting the Tanimoto coefficients for every PID/PID pair. Increased off-diagonal overlap between PIDs most likely indicates genes in the same pathway. \* A Phenotype Frequency Visualization: The phenotype frequency visualization is a simple bar chart indicating how often a particular phenotype is associated with a Primary Immunodeficiency Disease in the Ontology. \* A PID Expert map: All of the phenotypes and knowledge contained in the Primary Immunodeficiency Disease Ontology has been extracted from primary clinical or research literature. To

construct the map, we have extracted the affiliations and locations of the authors of the literature sources and overlayed them on a map. The hope is that this will facilitate the identification of (local) experts on primary immunodeficiency diseases.

**Abbreviations:** PIDFinder

**Synonyms:** Primary Immunodeficiency Disease Finder

**Resource Type:** analysis service resource, data analysis service, production service resource, service resource

**Keywords:** phenotype, disease, immunodeficiency, biomarker, ontology

**Related Condition:** Primary Immunodeficiency Disease

**Resource Name:** PIDFinder

**Resource ID:** SCR\_005833

**Alternate IDs:** nlx\_149343

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260905T133132+0000

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## Ratings and Alerts

No rating or validation information has been found for PIDFinder.

No alerts have been found for PIDFinder.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.