

TIN-X Version 3: Update with expanded dataset and modernized architecture

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Overview

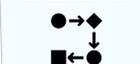
Target Importance and Novelty eXplorer (TIN-X)

An Interactive web-based visualization tool for illuminating associations between diseases and drug targets,¹ TIN-X uses natural language processing to identify disease and protein mentions within PubMed content. Two important metrics, **novelty** and **importance**, are computed from this data, and when plotted as log(importance) vs log(novelty), help users visually explore the novelty of drug targets and their associated importance to diseases. The primary data sources are TCRD/Pharos² and PubMed content. TIN-X is publicly available:

Version 2.0: newdrugtargets.org

Version 3.0 Demo: unmtid-devapps.net

Informatics Workflow



REST API



Public Web Application



New API, UI, and Database Improvements

TINX-API

- Upgraded the API from Python 2 to Python 3.8
- Includes support for Amazon RDS database
- Identified & fixed bugs



TINX-UI

- New table-view option where plot data is presented in a sortable, searchable table.
- Improving visibility & accessibility
- Fixed bugs and browser compatibility issues



TINX Database

- Now uses Cloud storage w/ Amazon RDS instead of MySQL
- Expanded Dataset to include full-text PubMed content³
- Improving process of updating data



TIN-X User Interface: Includes New Features

Browse Diseases or Browse Targets

A search for a specific Target associated with bacterial sepsis generates autocomplete suggestions:

Hovering over a data point brings up details:

Share & Export data

New Table View

Search table content; rows that don't contain the search query disappear.

Users can apply the same TDL and IDG Family filters available within the View Plot mode

Targets associated with bacterial sepsis

Name	TLR	Sym	Family	Detailed Family	TDL	Import	DBID	Novelty Score	Importance Score
Interleukin-4	IL4				Tcln	P05231		0.0002819	12.4296162
Interleukin-10	IL10				Tbio	P22301		0.0004352	3.97711031
Interleukin-8	CXCL8				Tchem	P10145	DTL_0500726	0.0005959	2.6801385
Interleukin-1 receptor	IL1R2				Tbio	P27930	DTL_0500233	0.00820359	0.12863064
Interleukin-1 receptor	IL1R1				Tchem	O99616	DTL_03100192	0.01001206	0.07144865
Interleukin-27 subunit	EBI3				Tbio	Q14213	DTL_05007313	0.09651194	0.02222222
Interleukin-1 beta	IL1B				Tcln	P01584		0.0003038	3.32590285
Interleukin-18 receptor	IL18R1				Tbio	Q13478	DTL_05002202	0.01634385	0.03752779
Interleukin-2	IL2				Tchem	P60568		0.0003129	0.9833349
Interleukin-10 receptor	IL10RA				Tbio	Q13631	DTL_0500694	0.0050698	0.11944579
Toll-like receptor 1	TLR1				Tbio	P59753		0.0005095	0.0999794
Interleukin-27 subunit	EBI3				Tbio	Q8N6V9		0.01469348	0.0230179
Interleukin-17A	IL17A				Tcln	Q14532		0.0011583	0.5236569
Interleukin-1 alpha	IL1A				Tchem	P01583		0.0019366	0.4370382
Interleukin-18	IL18				Tbio	Q14116		0.0002284	0.43171398
Interleukin-1 receptor	IL1R1				Tchem	P51617	DTL_03100190	0.00170873	0.20977101
Interleukin-4	IL4				Tbio	P05112		0.0005852	0.5740801
Interleukin-11	IL11				Tbio	P20809		0.00103994	0.19566029
Interleukin-1 receptor	IL1R1				Tchem	P14778	DTL_05002348	0.0014281	0.13466975
Interleukin-1 receptor	IL1R1				Tchem	Q9NWX3	DTL_03100193	0.00344058	0.07917905
Interleukin-26	IL26				Tbio	Q9N9V9		0.01233835	0.01577577

Table contents can be sorted by each of the fields, either ascending or descending.

Detailed View

When clicking on a single datapoint in the Plot View mode or when clicking on a row in the new Table View mode, the User is presented with details on the target/disease association.

This view presents the User with details about the target and an accompanying list of the specific PubMed articles which form the basis of the predicted association between the target and disease. In this example, the target TLR4 is associated with the disease bacterial sepsis. This view includes external links to Pharos, DrugCentral, and disease-ontology.org. The listed publication titles and abstracts link to the corresponding paper. We now prominently feature the publication date.

DTO/DO Disease Ontology

TDL Colors

IDG Families

Above screenshots are from TIN-X Version 3.0, temporarily available at <https://unmtid-devapps.net>

Development History

2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Conceived and Prototyped by Cristian Bologa	Work began on what would become TIN-X		Version 1.0 is first published online by Cannon et al ¹		Version 2.0 of TIN-X released Feb 18, 2019		Work on Version 3.0 of TIN-X begins	Jensen Lab DISEASES 2.0 released ³	Version 3.0 launching Spring 2023

NEW: TIN-X Dataset Expanded via Jensen Lab DISEASES 2.0³

TIN-X relies on the DISEASES³ resource for text-mined PubMed associations

For text-mined associations, the number of disease-gene associations increased by at least **9-fold** at all confidence cutoffs (compared to the previous version of DISEASES)³

How is this achieved?

1. Primarily by adding full-text articles to the collection in addition to the titles and abstracts previously included
2. To a lesser extent, improvements to the disease and gene dictionaries used for Named Entity Recognition

DISEASES
Disease-gene associations mined from literature

Search Downloads About

The DISEASES resource is available for download:

Text mining channel: full filtered

Knowledge channel: full filtered

Experiments channel: full filtered

Integrated channel (experimental): full

The files contain all links in the DISEASES database. All files start with the following four columns: gene identifier, gene name, disease identifier, and disease name. The **knowledge** files further contain the source database, the evidence type, and the confidence score. The **experiments** files instead contain the source database, the source score, and the confidence score. Finally, the **textmining** files contain the z-score, the confidence score, and a URL to a viewer of the underlying abstracts.

Download files from earlier versions are archived on [figshare](https://figshare.com).

DISEASES tagger and the latest dictionary of human gene and disease names can also be downloaded for installation on Linux platforms. We also make available a list of PubMed IDs for excluded publications from research papers.

Developed by Sune Frankild, Alexander Junge, Albert Palieja, Dhouha Grissa, Kalliope Tsafou, and Lars Juhl Jensen from the Novo Nordisk Foundation Center for Protein Research.

Note: Jensen Lab DISEASES resource updated **weekly**

Background & Contributions

TIN-X relies on text mining of PubMed content by JensenLab³, the Target Central Resource Database (TCRD)² for target and Drug Target Ontology (DTO) data, and the DISEASES³ dictionary for disease ontology. Since 2017, TIN-X has been continually maintained, updated, and improved. The development work highlighted in this poster is being finalized in preparation for a public launch of TIN-X Version 3.0 in Spring 2023, replacing the Version 2.0 which is presently accessible at newdrugtargets.org. Also, TIN-X is among several REST APIs made available at pharos-api.newdrugtargets.org as part of the CFDE Gene Pages Partnership Project. These improvements support the Resource Sharing Plan of KMC, the CFDE, and NIH policies and principles concerning digital resource sharing (e.g. FAIR) as emphasized by the NIH Strategic Plan for Data Science⁴.

References:

- 1) DC Cannon, JJ Yang, SL Mathias, O Ursu, S Mani, A Waller, SC Schürer, LJ Jensen, LA Sklar, CG Bologa, and TI Oprea, "TIN-X: Target Importance and Novelty Explorer." (2017) *Bioinformatics*, btx200, doi: 10.1093/bioinformatics/btx200
- 2) Sheils, T., Mathias, S. et al, "TCRD and Pharos 2021: mining the human proteome for disease biology." (2021) *Nucl. Acids Res.*, DOI: 10.1093/nar/gkaa993
- 3) Dhouha Grissa, Alexander Junge, Tudor I. Oprea, and Lars Juhl Jensen. "DISEASES 2.0: a weekly updated database of disease-gene associations from text mining and data integration." (2022) *Database*, 1-8; doi/10.1093/database/baac019/6554833
- 4) NIH Strategic Plan for Data Science, accessed Feb 2022, https://datascience.nih.gov/sites/default/files/NIH_Strategic_Plan_for_Data_Science_Final_508.pdf