

Resource Summary Report

Generated by [NIF](#) on Sep 4, 2026

VIOLIN: Vaccine Investigation and Online Information Network

RRID:SCR_012749

Type: Tool

Proper Citation

VIOLIN: Vaccine Investigation and Online Information Network (RRID:SCR_012749)

Resource Information

URL: <http://www.violinet.org>

Proper Citation: VIOLIN: Vaccine Investigation and Online Information Network (RRID:SCR_012749)

Description: A web-based central resource that integrates vaccine literature data mining, vaccine research data curation and storage, and curated vaccine data analysis for vaccines and vaccine candidates developed against various pathogens of high priority in public health and biological safety. The vaccine data includes research data from vaccine studies using humans, natural and laboratory animals. VIOLIN extracts and stores vaccine-related, peer-reviewed papers from PubMed. Several powerful literature searching and data mining programs have been developed. These include an advanced keywords search program, a natural language processing (NLP) based literature retrieval program, a MeSH-based literature browser, and a literature alert program. Registered users can subscribe to our email alert service and will be notified of any newly published vaccine papers in the areas of interest. These literature mining programs are designed to help the user and VIOLIN database curators to find efficiently needed vaccine articles and sentences within full-text articles that contain searched keywords or categories. A web-based literature mining and curation system (Limix) is available for registered users/curators to search, curate, and submit structured vaccine data into the VIOLIN database. The curated vaccine-related information contains many categories such as general pathogenesis, protective immunity, vaccine preparation and characteristics, host responses including vaccination protocol and efficacy against virulent pathogen infections. All data within the database is edited manually and is derived primarily from peer-reviewed publications. The curated data is stored in a relational database and can be queried using various VIOLIN search programs. Vaccine-related pathogen and host genes are annotated and available for searches based on a customized BLAST program. All VIOLIN data are available for download into an XML-based data exchange format. VIOLIN is designed to be a vital source of vaccine information and will provide researchers in basic and clinical sciences with curated data and bioinformatics tools to facilitate understanding

and development of vaccines to fight infectious diseases. Category: Other Molecular Biology Databases Subcategory: Drugs and drug design

Abbreviations: VIOLIN

Synonyms: Violin 2.0, Vaccine Investigation and Online Information Network

Resource Type: data or information resource, database

Keywords: immunology, infectious diseases, molecular biology, pathogen, public health, vaccine

Funding: NIAID U24 AI125008

Resource Name: VIOLIN: Vaccine Investigation and Online Information Network

Resource ID: SCR_012749

Alternate IDs: nif-0000-03629

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260904T000319+0000

Ratings and Alerts

No rating or validation information has been found for VIOLIN: Vaccine Investigation and Online Information Network.

No alerts have been found for VIOLIN: Vaccine Investigation and Online Information Network.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Hessami A, et al. (2026) Design of a novel proteome-derived scaffold presenting epitopes of *Pseudomonas aeruginosa* in native conformation. *Scientific reports*, 16(1).

Kudva IT, et al. (2026) The carbon starvation-inducible lipoprotein (Slp) influences differential adherence of *Escherichia coli* O157:H7 at the bovine rectoanal junction. *PLoS pathogens*, 22(5), e1013584.

Huffman A, et al. (2025) Systematic collection, annotation, and pattern analysis of viral vaccines in the VIOLIN vaccine knowledgebase. *Frontiers in cellular and infection*

microbiology, 15, 1509226.

Li X, et al. (2024) VaxLLM: Leveraging Fine-tuned Large Language Model for automated annotation of Brucella Vaccines. bioRxiv : the preprint server for biology.

Asfaw E, et al. (2024) CanVaxKB: a web-based cancer vaccine knowledgebase. NAR cancer, 6(1), zcad060.

Khan MT, et al. (2023) Multi-epitope vaccine against drug-resistant strains of Mycobacterium tuberculosis: a proteome-wide subtraction and immunoinformatics approach. Genomics & informatics, 21(3), e42.

Huang PC, et al. (2021) Cov19VaxKB: A Web-based Integrative COVID-19 Vaccine Knowledge Base. Vaccine: X, 10, 100139.

Khan MT, et al. (2021) Immunoinformatics and molecular dynamics approaches: Next generation vaccine design against West Nile virus. PloS one, 16(6), e0253393.

Berke K, et al. (2021) VaximmutorDB: A Web-Based Vaccine Immune Factor Database and Its Application for Understanding Vaccine-Induced Immune Mechanisms. Frontiers in immunology, 12, 639491.

Pritam M, et al. (2020) A cutting-edge immunoinformatics approach for design of multi-epitope oral vaccine against dreadful human malaria. International journal of biological macromolecules, 158, 159.

Hur J, et al. (2017) Ontology-based literature mining of E. coli vaccine-associated gene interaction networks. Journal of biomedical semantics, 8(1), 12.

Chambers MA, et al. (2016) Challenges in Veterinary Vaccine Development and Immunization. Methods in molecular biology (Clifton, N.J.), 1404, 3.

Xiang Z, et al. (2015) Ontorat: automatic generation of new ontology terms, annotations, and axioms based on ontology design patterns. Journal of biomedical semantics, 6, 4.

Powell BS, et al. (2015) Polyionic vaccine adjuvants: another look at aluminum salts and polyelectrolytes. Clinical and experimental vaccine research, 4(1), 23.

Ha??ar??z O, et al. (2015) Comparative transcriptome profiling approach to glean virulence and immunomodulation-related genes of Fasciola hepatica. BMC genomics, 16(1), 366.

Xiang Z, et al. (2013) Genome-wide prediction of vaccine targets for human herpes simplex viruses using Vaxign reverse vaccinology. BMC bioinformatics, 14 Suppl 4(Suppl 4), S2.

Sayers S, et al. (2012) Vaxjo: a web-based vaccine adjuvant database and its application for analysis of vaccine adjuvants and their uses in vaccine development. Journal of biomedicine & biotechnology, 2012, 831486.

He Y, et al. (2012) Analyses of Brucella pathogenesis, host immunity, and vaccine targets using systems biology and bioinformatics. Frontiers in cellular and infection microbiology, 2, 2.

Kudva IT, et al. (2012) Proteins other than the locus of enterocyte effacement-encoded proteins contribute to *Escherichia coli* O157:H7 adherence to bovine rectoanal junction stratified squamous epithelial cells. *BMC microbiology*, 12, 103.

Six A, et al. (2012) Systems biology in vaccine design. *Microbial biotechnology*, 5(2), 295.