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## [VO: Vaccine Ontology](#)

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#### Abstract:

Vaccine research, as well as the development, testing, clinical trials, and commercial uses of vaccines involve complex processes with various biological data that include gene and protein expression, analysis of molecular and cellular interactions, study of tissue and whole body responses, and extensive epidemiological modeling. Although many data resources are available to meet different aspects of vaccine needs, it remains a challenge how we are to standardize vaccine annotation, integrate data about varied vaccine types and resources, and support advanced vaccine data analysis and inference. To address these problems, the community-based Vaccine Ontology (VO, <http://www.violinet.org/vaccineontology>) has been developed through collaboration with vaccine researchers and many national and international centers and programs, including the National Center for Biomedical Ontology (NCBO), the Infectious Disease Ontology (IDO) Initiative, and the Ontology for Biomedical Investigations (OBI). VO utilizes the Basic Formal Ontology (BFO) as the top ontology and the Relation Ontology (RO) for definition of term relationships. VO is represented in the Web Ontology Language (OWL) and edited using the Protégé-OWL. Currently VO contains more than 2000 terms and relationships. VO emphasizes on classification of vaccines and vaccine components, vaccine quality and phenotypes, and host immune response to vaccines. These reflect different aspects of vaccine composition and biology and can thus be used to model individual vaccines. More than 200 licensed vaccines and many vaccine candidates in research or clinical trials have been modeled in VO. VO is being used for vaccine literature mining through collaboration with the National Center for Integrative Biomedical Informatics (NCIBI). Multiple VO applications will be presented.

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