

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 8, 2026

VMD

RRID:SCR_004905

Type: Tool

Proper Citation

VMD (RRID:SCR_004905)

Resource Information

URL: <http://vmd.vbi.vt.edu/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. Database covering a range of plant pathogenic oomycetes, fungi and bacteria primarily those under study at Virginia Bioinformatics Institute. The data comes from different sources and has genomes of 3 oomycetes pathogens: *Phytophthora sojae*, *Phytophthora ramorum* and *Hyaloperonospora arabidopsidis*. The genome sequences (95 MB for *P.sojae* and 65 MB for *P.ramorum*) were annotated with approximately 19,000 and approximately 16,000 gene models, respectively. Two different statistical methods were used to validate these gene models, Fickett's and a log-likelihood method. Functional annotation of the gene models is based on results from BlastX and InterProScan screens. From the InterProScan results, putative functions to 17,694 genes in *P.sojae* and 14,700 genes in *P.ramorum* could be assigned. An easy-to-use genome browser was created to view the genome sequence data, which opens to detailed annotation pages for each gene model. A community annotation interface is available for registered community members to add or edit annotations. There are approximately 1600 gene models for *P.sojae* and approximately 700 models for *P.ramorum* that have already been manually curated. A toolkit is provided as an additional resource for users to perform a variety of sequence analysis jobs.

Abbreviations: PAMGO_VMD, VMD

Synonyms: VBI Microbial Database, Virginia Bioinformatics Institute Microbial Database

Resource Type: data or information resource, production service resource, data analysis service, database, analysis service resource, service resource

Defining Citation: [PMID:16381891](#)

Keywords: microbial genome sequence, genome, genome sequence, genome model, gene, image, oomycete, fungus, bacteria, phytophthora sojae, phytophthora ramorum,

hyaloperonospora arabidopsidis, plant

Funding: USDA Cooperative State Research Education and Extension Service 2002-35600-12747;
USDA Cooperative State Research Education and Extension Service 2004-35600-15055;
NSF MCB-0242131;
NSF EF-0412213;
NSF DBI-0211863

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: VMD

Resource ID: SCR_004905

Alternate IDs: nlx_87328

Old URLs: <http://phytophthora.vbi.vt.edu>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260808T190228+0000

Ratings and Alerts

No rating or validation information has been found for VMD.

No alerts have been found for VMD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Liu J, et al. (2023) A new approach for extracting information from protein dynamics. Proteins, 91(2), 183.

Randáková A, et al. (2020) Novel M2 -selective, Gi -biased agonists of muscarinic acetylcholine receptors. British journal of pharmacology, 177(9), 2073.

Latorraca NR, et al. (2017) Mechanism of Substrate Translocation in an Alternating Access Transporter. Cell, 169(1), 96.

Halbleib K, et al. (2017) Activation of the Unfolded Protein Response by Lipid Bilayer Stress. Molecular cell, 67(4), 673.

Chakrabarti KS, et al. (2017) Conformational Dynamics and Allostery in E2:E3 Interactions Drive Ubiquitination: gp78 and Ube2g2. *Structure* (London, England : 1993), 25(5), 794.

Glukhova A, et al. (2017) Structure of the Adenosine A1 Receptor Reveals the Basis for Subtype Selectivity. *Cell*, 168(5), 867.

Swanger SA, et al. (2016) Mechanistic Insight into NMDA Receptor Dysregulation by Rare Variants in the GluN2A and GluN2B Agonist Binding Domains. *American journal of human genetics*, 99(6), 1261.

Xin H, et al. (2013) Genome wide transcriptional profile analysis of *Vitis amurens* and *Vitis vinifera* in response to cold stress. *PloS one*, 8(3), e58740.