

Resource Summary Report

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Osprey: Network Visualization System

RRID:SCR_007138

Type: Tool

Proper Citation

Osprey: Network Visualization System (RRID:SCR_007138)

Resource Information

URL: <http://biodata.mshri.on.ca/osprey/servlet/Index>

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Description: Osprey is a software platform for visualization of complex interaction networks. Osprey builds data-rich graphical representations from Geno Ontology (GO) annotated interaction data maintained by The Grid. The following list describes some of the important characteristics of the Osprey Network Visualization System: * Portability (cross platform availability) o Osprey is available on almost all Platforms that support the latest Java Plugin * Tools for Biological Analysis o Osprey provides many features such as network filters, connectivity filters, advanced layouts, and dataset superimposing which are extremely useful to biologists who are interested in analyzing their data * Powerful Support Database o Integrated with Osprey is a powerful database of interactions and annotation, see section 8. The GRID (The General Repository of Interaction Datasets). * Ease of use o Osprey provides an extremely user friendly interface for working with interaction data * Online Database Add-on Ability o Osprey can be incorporated as a standard visualization tool with online databases such as The GRID * Support for figures o Osprey networks can be saved in SVG, PNG and JPG format so they can be used with image programs Sponsors: Development of Osprey was funded by a grant from the Canadian Institutes of Health Research.

Synonyms: Osprey

Resource Type: data processing software, data visualization software, simulation software, software application, software resource

Keywords: filter, biological analysis, biologist, interaction, software, visualization

Resource Name: Osprey: Network Visualization System

Resource ID: SCR_007138

Alternate IDs: nif-0000-10394

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260912T195650+0000

Ratings and Alerts

No rating or validation information has been found for Osprey: Network Visualization System.

No alerts have been found for Osprey: Network Visualization System.

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 [Kravitz](#) .

Perica MI, et al. (2026) Age- and alcohol-related differences in adolescent neurometabolite levels. Alcohol, clinical & experimental research, 50(2), e70256.

Shams Z, et al. (2026) Identifying Out-of-Voxel Echoes in Edited MRS With Phase Cycle Inversion. Magnetic resonance in medicine, 95(4), 1921.

Archibald J, et al. (2026) The Impact and Reliability of Tissue Segmentation on In Vivo Magnetic Resonance Spectroscopy Metabolite Quantification. Magnetic resonance in medicine, 96(2), 516.

Malmros J, et al. (2026) The association among glutamate, GABA, and anterior cingulate connectivity in schizophrenia spectrum disorders: Implications for symptom domains. European psychiatry : the journal of the Association of European Psychiatrists, 69(1), e54.

Simegn GL, et al. (2026) Gradient Scheme Optimization for PRESS-Localized Edited MRS Using Weighted Pathway Suppression. NMR in biomedicine, 39(1), e70182.

Colaes R, et al. (2026) Identifying pre-treatment risk factors for cancer-related cognitive decline in patients with breast cancer. Breast (Edinburgh, Scotland), 88, 104788.

Remie LB, et al. (2026) MIND-NL diet adherence moderates the relation of low-grade systemic inflammation with neuroinflammatory metabolites and cognitive functioning: an exploratory cross-sectional study in older adults. Journal of neuroinflammation, 23(1).

Salsano I, et al. (2026) Elevated neurotransmitter levels in people with HIV are associated with attention function. Neurobiology of disease, 219, 107273.

Zöllner HJ, et al. (2026) Reproducibility of Metabolic Mapping Using 2D Multi-Slice Short-TE and GABA-Edited Spin-Echo MRSI at 3T in a Single Protocol. NMR in biomedicine,

39(1), e70175.

LaMaster J, et al. (2025) MRS-Sim: Open-Source Framework for Simulating In Vivo-Like Magnetic Resonance Spectra. *NMR in biomedicine*, 38(10), e70130.

Vandewouw MM, et al. (2025) Real-time neurofeedback, its neurotransmitter underpinnings, and therapeutic effects: study protocol for a randomized controlled trial in individuals at clinical high risk. *BMC psychiatry*, 26(1), 30.

Ehrler M, et al. (2025) Investigating brain maturation, neurodevelopmental and psychiatric outcomes in individuals with early-onset liver disease: protocol of a single-centre observational study. *BMJ open*, 15(11), e103290.

Salsano I, et al. (2025) Neurochemical changes in GABA+, Glx, and the excitatory/inhibitory ratio in the calcarine cortex with healthy aging. *NeuroImage*, 324, 121635.

Ganguly A, et al. (2017) Hsc70 chaperone activity is required for the cytosolic slow axonal transport of synapsin. *The Journal of cell biology*, 216(7), 2059.

Wang J, et al. (2015) Pathway and network approaches for identification of cancer signature markers from omics data. *Journal of Cancer*, 6(1), 54.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. *GigaScience*, 4, 38.

Hsiao HC, et al. (2014) The intrinsically disordered regions of the *Drosophila melanogaster* Hox protein ultrabithorax select interacting proteins based on partner topology. *PloS one*, 9(10), e108217.

O'Keefe DD, et al. (2014) Temporal regulation of Dpp signaling output in the *Drosophila* wing. *Developmental dynamics : an official publication of the American Association of Anatomists*, 243(6), 818.

Jain P, et al. (2013) Systems biology approach reveals genome to phenome correlation in type 2 diabetes. *PloS one*, 8(1), e53522.

Agapito G, et al. (2013) Visualization of protein interaction networks: problems and solutions. *BMC bioinformatics*, 14 Suppl 1(Suppl 1), S1.