Resource Summary Report

Generated by dkNET on Apr 16, 2025

CORUM

RRID:SCR_002254
Type: Tool

Proper Citation

CORUM (RRID:SCR_002254)

Resource Information

URL: http://mips.helmholtz-muenchen.de/genre/proj/corum

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Description: Database of manually annotated protein complexes from mammalian organisms. Annotation includes protein complex function, localization, subunit composition, literature references and more. All information is obtained from individual experiments published in scientific articles, but data from high-throughput experiments is excluded.
The majority of protein complexes in CORUM originates from man (65%), followed by mouse (14%) and rat (14%).

Abbreviations: CORUM

Synonyms: CORUM the Comprehensive Resource of Mammalian protein complexes, CORUM - the Comprehensive Resource of Mammalian protein complexes

Resource Type: database, data or information resource

Defining Citation: PMID:19884131, PMID:17965090

Keywords: mammalian protein, protein, protein complex, protein function, FASEB list

Funding: BMBF 031U212C

Resource Name: CORUM

Resource ID: SCR_002254

Alternate IDs: nif-0000-02688, OMICS_01904

Alternate URLs: http://mips.gsf.de/genre/proj/corum

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250412T054658+0000

Ratings and Alerts

No rating or validation information has been found for CORUM.

No alerts have been found for CORUM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 148 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Buzzao D, et al. (2025) FunCoup 6: advancing functional association networks across species with directed links and improved user experience. Nucleic acids research, 53(D1), D658.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Sweeney KM, et al. (2024) CRISPR screen for protein inclusion formation uncovers a role for SRRD in the regulation of intermediate filament dynamics and aggresome assembly. PLoS genetics, 20(2), e1011138.

Wang K, et al. (2024) Longitudinal molecular profiling elucidates immunometabolism dynamics in breast cancer. Nature communications, 15(1), 3837.

Bhakuni T, et al. (2024) FOXC1 regulates endothelial CD98 (LAT1/4F2hc) expression in retinal angiogenesis and blood-retina barrier formation. Nature communications, 15(1), 4097.

Malone CF, et al. (2024) The KAT module of the SAGA complex maintains the oncogenic gene expression program in MYCN-amplified neuroblastoma. Science advances, 10(22), eadm9449.

van Strien J, et al. (2024) Analysis of Complexome Profiles with the Gaussian Interaction Profiler (GIP) Reveals Novel Protein Complexes in Plasmodium falciparum. Journal of proteome research, 23(10), 4467.

Laulumaa S, et al. (2024) Structure and interactions of the endogenous human Commander complex. Nature structural & molecular biology, 31(6), 925.

Salovska B, et al. (2024) A Comprehensive and Robust Multiplex-DIA Workflow Profiles Protein Turnover Regulations Associated with Cisplatin Resistance. bioRxiv : the preprint server for biology.

Tilk S, et al. (2024) Cancers adapt to their mutational load by buffering protein misfolding stress. eLife, 12.

González JT, et al. (2024) Age-Invariant Genes: Multi-Tissue Identification and Characterization of Murine Reference Genes. bioRxiv : the preprint server for biology.

Keele GR, et al. (2023) Global and tissue-specific aging effects on murine proteomes. Cell reports, 42(7), 112715.

Yin K, et al. (2023) Investigation of Cellular Response to the HSP90 Inhibition in Human Cells Through Thermal Proteome Profiling. Molecular & cellular proteomics : MCP, 22(6), 100560.

Peng H, et al. (2023) ProInfer: An interpretable protein inference tool leveraging on biological networks. PLoS computational biology, 19(3), e1010961.

Yiu SPT, et al. (2023) An Epstein-Barr virus protein interaction map reveals NLRP3 inflammasome evasion via MAVS UFMylation. Molecular cell, 83(13), 2367.

van Strien J, et al. (2023) Comparative Clustering (CompaCt) of eukaryote complexomes identifies novel interactions and sheds light on protein complex evolution. PLoS computational biology, 19(8), e1011090.

Leblanc S, et al. (2023) Newfound Coding Potential of Transcripts Unveils Missing Members of Human Protein Communities. Genomics, proteomics & bioinformatics, 21(3), 515.

Renaux A, et al. (2023) A knowledge graph approach to predict and interpret disease-causing gene interactions. BMC bioinformatics, 24(1), 324.

Calzada-Fraile D, et al. (2023) Immune synapse formation promotes lipid peroxidation and MHC-I upregulation in licensed dendritic cells for efficient priming of CD8+ T cells. Nature communications, 14(1), 6772.

Jarecki W, et al. (2023) Soybean Response to Seed Inoculation or Coating with Bradyrhizobium japonicum and Foliar Fertilization with Molybdenum. Plants (Basel, Switzerland), 12(13).