

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 30, 2026

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%)., THIS RESOURCE IS NO LONGER IN SERVICE.
Documented on September 16,2025.

Abbreviations: CORUM

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

Resource Type: data or information resource, database

Defining Citation: [PMID:19884131](#), [PMID:17965090](#)

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

Funding: BMBF 031U212C

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CORUM

Resource ID: SCR_002254

Alternate IDs: nif-0000-02688, OMICS_01904, r3d100011272

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

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260729T044035+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 163 mentions in open access literature.

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

Dang V, et al. (2025) VerteBrain reveals novel neural and non-neural protein assemblies conserved across vertebrate evolution. bioRxiv : the preprint server for biology.

Frommelt F, et al. (2025) The solute carrier superfamily interactome. Molecular systems biology, 21(6), 632.

Le Minh G, et al. (2025) GATAD2B O-GlcNAcylation Regulates Breast Cancer Stem-like Potential and Drug Resistance. Cells, 14(6).

Pio-Lopez L, et al. (2025) Universal multilayer network embedding reveals a causal link between GABA neurotransmitter and cancer. BMC bioinformatics, 26(1), 149.

Liu X, et al. (2025) Mealtime alters daily rhythm in nuclear O-GlcNAc proteome to regulate hepatic gene expression. bioRxiv : the preprint server for biology.

Aç?kgöz MA, et al. (2025) Secondary Metabolites and Biological Activities From Achillea gypsicola Hub-Mor. Under Foliar Applications of Chitosan and Salicylic Acid. Food science & nutrition, 13(5), e70225.

Salovska B, et al. (2025) A robust multiplex-DIA workflow profiles protein turnover regulations associated with cisplatin resistance and aneuploidy. Nature communications, 16(1), 5034.

Girault V, et al. (2025) Multi-proteomic profiling of the varicella-zoster virus-host interface reveals host susceptibilities to severe infection. Nature microbiology, 10(8), 2048.

Soriaga LB, et al. (2025) Shared host genetic landscape of respiratory viral infection. Proceedings of the National Academy of Sciences of the United States of America,

122(20), e2414202122.

Kenaston MW, et al. (2025) Yellow Fever Virus Interactomes Reveal Common and Divergent Strategies of Replication and Evolution for Mosquito-borne Flaviviruses. *bioRxiv* : the preprint server for biology.

Lu Y, et al. (2025) Decoding the Effects of Bexarotene treatment on brain of AD-like model mice: Single-Cell Transcriptomics and Chromatin Accessibility Analysis. *Research square*.

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.

González JT, et al. (2025) Age-invariant genes: multi-tissue identification and characterization of murine reference genes. *Aging*, 17(1), 170.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1, a Structural Protein Complex Landscape of Human Endosomes. *bioRxiv* : the preprint server for biology.

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

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. *Nature*, 643(8070), 252.

Ibrahim IH, et al. (2025) Altered protein lipidation in cancer: A hidden link to sensory neuronal dysfunction. *Computational biology and chemistry*, 120(Pt 1), 108656.

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.

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.