

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

cRAP protein sequences

RRID:SCR_018187

Type: Tool

Proper Citation

cRAP protein sequences (RRID:SCR_018187)

Resource Information

URL: <https://www.thegpm.org/crap/>

Proper Citation: cRAP protein sequences (RRID:SCR_018187)

Description: List of proteins commonly found in proteomics experiments that are present either by accident or through unavoidable contamination of protein samples. List is based on analysis of current version of GPMDB, as well as suggestions by users. Current version of cRAP in FASTA format can be obtained from the GPM FTP site.

Abbreviations: cRAP

Synonyms: common Repository of Adventitious Proteins

Resource Type: database, data repository, storage service resource, data or information resource, service resource

Keywords: Protein, collection, proteomic experiment, protein sample, contamination, Global Proteome Machine Data Base, data repository, data, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: cRAP protein sequences

Resource ID: SCR_018187

Alternate URLs: <ftp://ftp.thegpm.org/fasta/cRAP>

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260815T182715+0000

Ratings and Alerts

No rating or validation information has been found for cRAP protein sequences.

No alerts have been found for cRAP protein sequences.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 198 mentions in open access literature.

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

López-García M, et al. (2026) In vitro Host-Parasite Models Combined With Proteomics Reveal Cell Type-Specific Responses of Early Migrating *Fasciola hepatica* Juveniles. *Molecular & cellular proteomics : MCP*, 25(4), 101543.

Walker C, et al. (2026) Tumour specific HORMAD1 expression perturbs mitotic arrest and drives sensitivity to mitotic kinase inhibitors. *Nature communications*, 17(1).

Kyogoku H, et al. (2026) Cytoplasmic competition between separate parental pronuclei in zygotes. *Nature*, 654(8117), 189.

Rechsteiner SG, et al. (2026) Identification of *Fasciola hepatica* gut-associated glycoproteins as potential vaccine candidates by lectin-affinity chromatography, flukicidal monoclonal antibodies, and affinity-enrichment mass spectrometry. *Frontiers in parasitology*, 5, 1746419.

Fu Q, et al. (2026) Enamel proteins from six *Homo erectus* specimens across China. *Nature*, 655(8121), 141.

Muralidharan A, et al. (2026) Molecular basis for anti-jumbo phage immunity by AVAST type 5. *Molecular cell*, 86(4), 740.

Kamrad S, et al. (2026) Interspecies interactions drive bacterial proteome reorganization and emergent metabolism. *Nature ecology & evolution*, 10(6), 1127.

Kalidass M, et al. (2026) The C-terminal SUMOylation-dependent regulation of γ KNL2 governs its centromere targeting and interaction with CENH3. *Plant communications*, 7(2), 101617.

Al-Momani SS, et al. (2026) A Landscape Analysis of Human SUMOylation. *Molecular & cellular proteomics : MCP*, 25(5), 101571.

Boswell EL, et al. (2026) An AI-Ready Phosphorylation Meta-Analysis for *Saccharomyces cerevisiae*. *Journal of proteome research*, 25(6), 2915.

Velamuri R, et al. (2026) Multi-omics profiling finds synbio milk differs nutritionally from bovine milk and contains 93 uncharacterized fungal metabolites and 236 fungal proteins.

Scientific reports, 16(1).

Troian EA, et al. (2026) Harnessing toxin-mediated ribosome stalling as a complementary tool to annotate bacterial ORFs. *Nucleic acids research*, 54(7).

Inagaki S, et al. (2026) Endoplasmic reticulum patterns insect cuticle nanostructure. *The Journal of cell biology*, 225(2).

Zelter A, et al. (2026) Proteomic Profiling of Human Omental and Subcutaneous Adipose Tissue in Individuals with a Broad Range of BMI. *bioRxiv : the preprint server for biology*.

Aydin D, et al. (2026) Molecular mechanism of exchange coupling in CLC chloride/proton antiporters. *Nature communications*, 17(1), 1342.

Sazon LAR, et al. (2026) Stem nitrogen accumulation through vegetative storage proteins and mobilization to seeds supports high-yielding soybean. *Journal of experimental botany*, 77(10), 2998.

Zelter A, et al. (2026) Proteomic profiling of human omental and subcutaneous adipose tissue in individuals with a broad range of BMI. *Scientific data*, 13(1).

Végh EI, et al. (2026) Tiny Hopes? Assessing Protein Preservation in Collagen-Depleted Bones. *Journal of proteome research*, 25(7), 3443.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. *Microbiome*, 13(1), 200.

de Jesus Ramires M, et al. (2025) Host-specific targets of *Histomonas meleagridis* antigens revealed by immunoprecipitation. *Scientific reports*, 15(1), 5800.