

Resource Summary Report

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CRAPome

RRID:SCR_025008

Type: Tool

Proper Citation

CRAPome (RRID:SCR_025008)

Resource Information

URL: <https://reprint-apms.org/?q=chooseworkflow>

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Description: Database of Mass Spectrometry contaminants and pipeline for Affinity Purification coupled with Mass Spectrometry analysis. Contaminant repository for affinity purification mass spectrometry data. Database of standardized negative controls. Used to identify protein-protein interactions.

Synonyms: CRAPome:Contaminant Repository for Affinity Purification

Resource Type: data access protocol, data or information resource, database, software resource, web service

Defining Citation: [PMID:23921808](#)

Keywords: Mass Spectrometry contaminants, standardized negative controls, contaminant repository, AP-MS analysis, affinity purification, mass spectrometry data,

Funding: Austrian Academy of Sciences ;
Austrian Federal Ministry for Science and Research ;
Austrian Science Fund ;
Canadian Institutes of Health Research ;
European Molecular Biology Organisation ;
European Research Council ;
European Union 7th Framework Program ;
government of Ontario ;
Human Frontier Science Program ;
NCI R21 CA16006001A1;
Netherlands Proteomics Center ;
NHLBI HL112618-01;
NIDA DP1DA026192;
NIGMS 5R01GM94231;

Stowers Institute for Medical Research

Availability: Free, Freely available,

Resource Name: CRAPome

Resource ID: SCR_025008

Alternate URLs: <https://reprint-apms.org/>

Record Creation Time: 20240214T050222+0000

Record Last Update: 20260919T200012+0000

Ratings and Alerts

No rating or validation information has been found for CRAPome.

No alerts have been found for CRAPome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Yang X, et al. (2026) A Brief Progress in Methods for Deciphering Protein-Protein Interaction Networks. International journal of molecular sciences, 27(4).

Tetenborg S, et al. (2026) Uncovering the electrical synapse proteome in retinal neurons via in vivo proximity labeling. eLife, 14.

Novoselov SS, et al. (2026) The P23H Rhodopsin Mouse Model Reveals a Novel Interaction Between the Endoplasmic Reticulum and Connecting Cilium Rootlet Within Photoreceptors. Investigative ophthalmology & visual science, 67(3), 57.

Justice JL, et al. (2025) Multi-epitope immunocapture of huntingtin reveals striatum-selective molecular signatures. Molecular systems biology, 21(5), 492.

Wang X, et al. (2025) DEAD-Box Helicase 6 Blockade in Brain-Derived A?? Oligomers From Alzheimer's Disease Patients Attenuates Neurotoxicity. MedComm, 6(5), e70156.

Yang Z, et al. (2025) Molecular basis of SIFI activity in the integrated stress response. Nature, 643(8073), 1117.

Arslanhan MD, et al. (2025) Kinase activity of DYRK family members is required for regulating primary cilium length, stability and morphology. Communications biology, 8(1),

1258.

Dillingham CM, et al. (2025) KDM3A and KDM3B regulate alternative splicing in mouse pluripotent stem cells. *iScience*, 28(6), 112612.

Ward JS, et al. (2025) Mapping *C. difficile* TcdB interactions with host cell-surface and intracellular factors using proximity-dependent biotinylation labeling. *mBio*, 16(2), e0333624.

Prince S, et al. (2025) Secreted Clever-1 modulates T cell responses and impacts cancer immunotherapy efficacy. *Theranostics*, 15(15), 7501.

Deretic J, et al. (2025) CCDC66 regulation of cytoskeleton and cilia stability is important for signaling and epithelial organization. *PLoS biology*, 23(7), e3003313.

Cipollone I, et al. (2025) The identification of adenylyl cyclase modulators as potential receptors for 6-nitrodopamine in human-induced pluripotent stem cell (hiPSC)-derived cardiomyocytes and their relevance in heart inotropism. *Frontiers in pharmacology*, 16, 1597035.

Yap K, et al. (2025) Enhanced hybridization-proximity labeling discovers protein interactomes of single RNA molecules. *Nature communications*, 16(1), 9257.

Gupta D, et al. (2025) A LisH-domain protein interaction map reveals a Lis1-ARIH2-dynein regulatory axis. *iScience*, 28(11), 113912.

Hsu E, et al. (2024) Reduction of ZFX levels decreases histone H4 acetylation and increases Pol2 pausing at target promoters. *Nucleic acids research*, 52(12), 6850.

Hamid A, et al. (2024) Interaction with IP6K1 supports pyrophosphorylation of substrate proteins by the inositol pyrophosphate 5-InsP7. *Bioscience reports*, 44(10).

Syriste L, et al. (2024) An acetyltransferase effector conserved across *Legionella* species targets the eukaryotic eIF3 complex to modulate protein translation. *mBio*, 15(3), e0322123.

Hsiao Y, et al. (2024) Analysis and visualization of quantitative proteomics data using FragPipe-Analyst. *bioRxiv : the preprint server for biology*.

Schreiber KJ, et al. (2024) Exploring Options for Proximity-Dependent Biotinylation Experiments: Comparative Analysis of Labeling Enzymes and Affinity Purification Resins. *Journal of proteome research*, 23(4), 1531.

Mettier J, et al. (2023) Comparison of PB1-F2 Proximity Interactomes Reveals Functional Differences between a Human and an Avian Influenza Virus. *Viruses*, 15(2).