

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

[CRAPome](#)

RRID:SCR_025008

Type: Tool

Proper Citation

CRAPome (RRID:SCR_025008)

Resource Information

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

Proper Citation: CRAPome (RRID:SCR_025008)

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

Defining Citation: [PMID:23921808](#)

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

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

NCI R21 CA16006001A1

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: 20260805T044539+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 16 mentions in open access literature.

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

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.

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.

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.

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

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

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

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

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

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

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

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).

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.

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

Arslanhan MD, et al. (2023) CCDC15 localizes to the centriole inner scaffold and controls centriole length and integrity. *The Journal of cell biology*, 222(12).