

Resource Summary Report

Generated by [dkNET](#) on Sep 12, 2026

Exponentially Modified Protein Abundance Index

RRID:SCR_008616

Type: Tool

Proper Citation

Exponentially Modified Protein Abundance Index (RRID:SCR_008616)

Resource Information

URL: <http://empai.iab.keio.ac.jp/>

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Description: emPAI (exponentially modified protein abundance index), developed by Ishihama et al., is a measure to describe the protein composition in sample solutions. When the total protein amount in the sample is available, emPAI can be converted to the absolute amount of each protein in the sample. emPAI is derived from PAI, which is defined as the number of the observed peptides divided by the number of the observable peptides per protein. We recently found that $\log(\text{PAI})$ had linear relationship to the protein amounts, and that $\text{emPAI}, 10^{(\text{PAI})-1}$, was proportional to the protein amounts for whole cell lysate digested by trypsin. The accuracy of this method was within factor 5, similar or better than determination of abundance by protein staining

Synonyms: emPAI

Resource Type: data or information resource, database

Resource Name: Exponentially Modified Protein Abundance Index

Resource ID: SCR_008616

Alternate IDs: nif-0000-31967

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T200200+0000

Ratings and Alerts

No rating or validation information has been found for Exponentially Modified Protein Abundance Index.

No alerts have been found for Exponentially Modified Protein Abundance Index.

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](#) .

Walitang DI, et al. (2023) Microbe-Responsive Proteomes During Plant-Microbe Interactions Between Rice Genotypes and the Multifunctional Methylobacterium oryzae CBMB20. Rice (New York, N.Y.), 16(1), 23.

Vong YH, et al. (2021) The RNA-binding protein Igf2bp3 is critical for embryonic and germline development in zebrafish. PLoS genetics, 17(7), e1009667.

Tritten L, et al. (2021) Mining nematode protein secretomes to explain lifestyle and host specificity. PLoS neglected tropical diseases, 15(9), e0009828.

Altomare AA, et al. (2020) Silkworm pupae as source of high-value edible proteins and of bioactive peptides. Food science & nutrition, 8(6), 2652.

Ruiz-Ruiz S, et al. (2020) Functional microbiome deficits associated with ageing: Chronological age threshold. Aging cell, 19(1), e13063.

Nakashima Y, et al. (2019) Identification of Proteins Differentially Expressed by Adipose-derived Mesenchymal Stem Cells Isolated from Immunodeficient Mice. International journal of molecular sciences, 20(11).

Zawadzka K, et al. (2018) MukB ATPases are regulated independently by the N- and C-terminal domains of MukF kleisin. eLife, 7.

Yoshikawa K, et al. (2018) The human olfactory cleft mucus proteome and its age-related changes. Scientific reports, 8(1), 17170.

Madda R, et al. (2018) Plasma proteomic analysis of systemic lupus erythematosus patients using liquid chromatography/tandem mass spectrometry with label-free quantification. PeerJ, 6, e4730.

Nakashima Y, et al. (2018) A Liquid Chromatography with Tandem Mass Spectrometry-Based Proteomic Analysis of Cells Cultured in DMEM 10% FBS and Chemically Defined Medium Using Human Adipose-Derived Mesenchymal Stem Cells. International journal of molecular sciences, 19(7).

Dabbaghizadeh A, et al. (2018) Identification of proteins interacting with the mitochondrial small heat shock protein Hsp22 of Drosophila melanogaster: Implication in mitochondrial homeostasis. PloS one, 13(3), e0193771.

Lloyd-Lewis B, et al. (2018) Stat3-mediated alterations in lysosomal membrane protein composition. The Journal of biological chemistry, 293(12), 4244.

Sawafuji R, et al. (2017) Proteomic profiling of archaeological human bone. Royal Society open science, 4(6), 161004.

Abrahamian M, et al. (2017) Rethinking the evolution of eukaryotic metabolism: novel cellular partitioning of enzymes in stramenopiles links serine biosynthesis to glycolysis in mitochondria. BMC evolutionary biology, 17(1), 241.

Berthelot V, et al. (2016) The human DNA ends proteome uncovers an unexpected entanglement of functional pathways. Nucleic acids research, 44(10), 4721.

Ghosh S, et al. (2016) Proteometabolomic Study of Compatible Interaction in Tomato Fruit Challenged with *Sclerotinia rolfsii* Illustrates Novel Protein Network during Disease Progression. Frontiers in plant science, 7, 1034.

Isnard A, et al. (2015) Impact of Leishmania infection on host macrophage nuclear physiology and nucleopore complex integrity. PLoS pathogens, 11(3), e1004776.

Qin Y, et al. (2014) Profiling of concanavalin A-binding glycoproteins in human hepatic stellate cells activated with transforming growth factor- β 1. Molecules (Basel, Switzerland), 19(12), 19845.

Atanassov I, et al. (2013) Increased proteome coverage by combining PAGE and peptide isoelectric focusing: comparative study of gel-based separation approaches. Proteomics, 13(20), 2947.

Hassani K, et al. (2013) Immunomodulatory impact of leishmania-induced macrophage exosomes: a comparative proteomic and functional analysis. PLoS neglected tropical diseases, 7(5), e2185.