

Resource Summary Report

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ProRata

RRID:SCR_002988

Type: Tool

Proper Citation

ProRata (RRID:SCR_002988)

Resource Information

URL: <https://code.google.com/p/prorata/>

Proper Citation: ProRata (RRID:SCR_002988)

Description: A quantitative proteomics software program for accurate protein abundance ratio estimation with confidence interval evaluation.

Synonyms: ProRata: A quantitative proteomics program for accurate protein abundance ratio estimation with confidence interval evaluation, prorata - Quantitative Proteomics Software

Resource Type: software resource

Defining Citation: [PMID:17037911](#)

Keywords: standalone software, mass spectrometry, proteomics, stable isotope labeling, quantitative proteomics, proteomics, bio.tools

Availability: GNU General Public License, v3

Resource Name: ProRata

Resource ID: SCR_002988

Alternate IDs: biotools:prorata, OMICS_02502

Alternate URLs: <https://bio.tools/prorata>

License: GNU General Public License, v3

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260815T182222+0000

Ratings and Alerts

No rating or validation information has been found for ProRata.

No alerts have been found for ProRata.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Pickens CP, et al. (2025) Absence of biofilm adhesin proteins changes surface attachment and cell strategy for *Desulfovibrio vulgaris* Hildenborough. *Journal of bacteriology*, 207(1), e0037924.

Wang D, et al. (2023) Cross-Feedings, Competition, and Positive and Negative Synergies in a Four-Species Synthetic Community for Anaerobic Degradation of Cellulose to Methane. *mBio*, 14(2), e0318922.

Voiriot G, et al. (2021) Combined use of a broad-panel respiratory multiplex PCR and procalcitonin to reduce duration of antibiotics exposure in patients with severe community-acquired pneumonia (MULTI-CAP): a multicentre, parallel-group, open-label, individual randomised trial conducted in French intensive care units. *BMJ open*, 11(8), e048187.

Li Z, et al. (2019) Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using $^{13}\text{CO}_2$ and ^{13}C -Methanol. *Frontiers in microbiology*, 10, 2706.

Mosier AC, et al. (2016) Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. *Frontiers in microbiology*, 7, 238.

Li Z, et al. (2014) Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. *Nature communications*, 5, 4405.

Wolff D, et al. (2013) Combined application of targeted and untargeted proteomics identifies distinct metabolic alterations in the tetraacetylphytosphingosine (TAPS) producing yeast *Wickerhamomyces ciferrii*. *Journal of proteomics*, 82, 274.

Hausmann U, et al. (2012) Global proteome survey of protocatechuate- and glucose-grown *Corynebacterium glutamicum* reveals multiple physiological differences. *Journal of proteomics*, 75(9), 2649.

Fr??nzl B, et al. (2010) Quantitative proteomic overview on the *Corynebacterium glutamicum* l-lysine producing strain DM1730. *Journal of proteomics*, 73(12), 2336.