

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

pBuild

RRID:SCR_002929

Type: Tool

Proper Citation

pBuild (RRID:SCR_002929)

Resource Information

URL: <http://pfind.ict.ac.cn/software/pBuild/index.html>

Proper Citation: pBuild (RRID:SCR_002929)

Description: A software tool that can compare several search engines' results and combine them together.

Resource Type: software resource

Keywords: mass spectrometry, proteomics

Resource Name: pBuild

Resource ID: SCR_002929

Alternate IDs: OMICS_02468

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260801T190215+0000

Ratings and Alerts

No rating or validation information has been found for pBuild.

No alerts have been found for pBuild.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Damm M, et al. (2024) Venomics and Peptidomics of Palearctic Vipers: A Clade-Wide Analysis of Seven Taxa of the Genera *Vipera*, *Montivipera*, *Macrovipera*, and *Daboia* across Turkey. *Journal of proteome research*, 23(8), 3524.

Avella I, et al. (2023) One Size Fits All-Venomics of the Iberian Adder (*Vipera seoanei*, Lataste 1878) Reveals Low Levels of Venom Variation across Its Distributional Range. *Toxins*, 15(6).

Zhu D, et al. (2022) Iso-seco-tanapartholide activates Nrf2 signaling pathway through Keap1 modification and oligomerization to exert anti-inflammatory effects. *Free radical biology & medicine*, 178, 398.

Zhu H, et al. (2022) Ac-LysargiNase efficiently helps genome reannotation of *Mycobacterium smegmatis* MC2 155. *Journal of proteomics*, 264, 104622.

Shu Q, et al. (2020) Large-scale Identification of N-linked Intact Glycopeptides in Human Serum using HILIC Enrichment and Spectral Library Search. *Molecular & cellular proteomics : MCP*, 19(4), 672.

Thompson JJ, et al. (2019) Classic motor chunking theory fails to account for behavioural diversity and speed in a complex naturalistic task. *PloS one*, 14(6), e0218251.

Ma C, et al. (2016) Improvement of core-fucosylated glycoproteome coverage via alternating HCD and ETD fragmentation. *Journal of proteomics*, 146, 90.

Gao Z, et al. (2015) Experimental Validation of *Bacillus anthracis* A16R Proteogenomics. *Scientific reports*, 5, 14608.