

Resource Summary Report

Generated by NIF on Aug 29, 2026

Monster

RRID:SCR_006463

Type: Tool

Proper Citation

Monster (RRID:SCR_006463)

Resource Information

URL: <http://www.monster.com/>

Proper Citation: Monster (RRID:SCR_006463)

Description: Global online employment solution for people seeking jobs and the employers who need great people. They've been doing this for over ten years, and have expanded from their roots as a job board to a global provider of a full array of job seeking, career management, recruitment and talent management products and services.

Abbreviations: Monster

Synonyms: Monster.com

Resource Type: job resource

Keywords: career, advice, resume, community building portal

Resource Name: Monster

Resource ID: SCR_006463

Alternate IDs: nlx_144164

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260829T182237+0000

Ratings and Alerts

No rating or validation information has been found for Monster.

No alerts have been found for Monster.

Data and Source Information

Usage and Citation Metrics

We found 80 mentions in open access literature.

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

Lu Y, et al. (2025) Analyzing the labor market and salary determinants for big data talent based on job advertisements in China. PloS one, 20(2), e0317189.

Ara Z, et al. (2024) Collaborative Job Seeking for People with Autism: Challenges and Design Opportunities. Proceedings of the SIGCHI conference on human factors in computing systems. CHI Conference, 2024, 73.

Calia G, et al. (2024) Identification and characterization of specific motifs in effector proteins of plant parasites using MOnSTER. Communications biology, 7(1), 850.

Rossi N, et al. (2024) Rare variants at KCNJ2 are associated with LDL-cholesterol levels in a cross-population study. NPJ genomic medicine, 9(1), 36.

Calia G, et al. (2024) Definition of the effector landscape across 13 phytoplasma proteomes with LEAPH and EffectorComb. NAR genomics and bioinformatics, 6(3), lqae087.

Mueller SH, et al. (2023) Aggregation tests identify new gene associations with breast cancer in populations with diverse ancestry. Genome medicine, 15(1), 7.

Kumar D, et al. (2023) Fairness of recommender systems in the recruitment domain: an analysis from technical and legal perspectives. Frontiers in big data, 6, 1245198.

Ben Guebila M, et al. (2023) The Network Zoo: a multilingual package for the inference and analysis of gene regulatory networks. Genome biology, 24(1), 45.

Rosales R, et al. (2023) Recommendations for Recruitment and Retention of a Diverse Workforce: A Report from the Field. Behavior analysis in practice, 16(1), 346.

Volkmar N, et al. (2022) Regulation of membrane fluidity by RNF145-triggered degradation of the lipid hydrolase ADIPOR2. The EMBO journal, 41(19), e110777.

Seid M, et al. (2021) A science of collaborative learning health systems. Learning health systems, 5(3), e10278.

Miyabayashi H, et al. (2021) DNA Polymerase B1 Binding Protein 1 Is Important for DNA Repair by Holoenzyme PolB1 in the Extremely Thermophilic Crenarchaeon Sulfolobus acidocaldarius. Microorganisms, 9(2).

Miyabayashi H, et al. (2020) PolB1 Is Sufficient for DNA Replication and Repair Under Normal Growth Conditions in the Extremely Thermophilic Crenarchaeon Sulfolobus acidocaldarius. Frontiers in microbiology, 11, 613375.

Junghans BM, et al. (2019) Populations Norms for "SLURP"-An iPad App for Quantification of Visuomotor Coordination Testing. *Frontiers in neuroscience*, 13, 711.

Kember RL, et al. (2018) Genetic pleiotropy between mood disorders, metabolic, and endocrine traits in a multigenerational pedigree. *Translational psychiatry*, 8(1), 218.

Gilly A, et al. (2018) Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. *Nature communications*, 9(1), 4674.

Lee S, et al. (2018) WISARD: workbench for integrated superfast association studies for related datasets. *BMC medical genomics*, 11(Suppl 2), 39.

Temmink RJM, et al. (2018) Azolla along a phosphorus gradient: biphasic growth response linked to diazotroph traits and phosphorus-induced iron chlorosis. *Scientific reports*, 8(1), 4451.

Zhang Q, et al. (2018) Impact of rare and low-frequency sequence variants on reliability of genomic prediction in dairy cattle. *Genetics, selection, evolution : GSE*, 50(1), 62.

Hanschen FS, et al. (2017) Optimizing isothiocyanate formation during enzymatic glucosinolate breakdown by adjusting pH value, temperature and dilution in Brassica vegetables and *Arabidopsis thaliana*. *Scientific reports*, 7, 40807.