

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

NAPPA

RRID:SCR_003419

Type: Tool

Proper Citation

NAPPA (RRID:SCR_003419)

Resource Information

URL: <http://cran.r-project.org/web/packages/NAPPA/>

Proper Citation: NAPPA (RRID:SCR_003419)

Description: Software that enables the processing and normalization of the standard mRNA data output from the Nanostring nCounter software.

Abbreviations: NAPPA

Synonyms: NAPPA: Performs the processing and normalisation of Nanostring miRNA and mRNA data

Resource Type: software resource

Keywords: normalization, processing, nanostring, mirna, mrna, os x, windows

Availability: GNU General Public License, v3

Resource Name: NAPPA

Resource ID: SCR_003419

Alternate IDs: OMICS_02310

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260725T190541+0000

Ratings and Alerts

No rating or validation information has been found for NAPPA.

No alerts have been found for NAPPA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Liang T, et al. (2024) Antibody Profiling of Pan-Cancer Viral Proteome Reveals Biomarkers for Nasopharyngeal Carcinoma Diagnosis and Prognosis. Molecular & cellular proteomics : MCP, 23(3), 100729.

O'Kell AL, et al. (2022) Exploration of autoantibody responses in canine diabetes using protein arrays. Scientific reports, 12(1), 2490.

Mathilakathu A, et al. (2021) Mitogen signal-associated pathways, energy metabolism regulation, and mediation of tumor immunogenicity play essential roles in the cellular response of malignant pleural mesotheliomas to platinum-based treatment: a retrospective study. Translational lung cancer research, 10(7), 3030.

Brcic L, et al. (2021) Digital Gene Expression Analysis of Epithelioid and Sarcomatoid Mesothelioma Reveals Differences in Immunogenicity. Cancers, 13(8).

Cho S, et al. (2021) Automated analysis of lexical features in frontotemporal degeneration. Cortex; a journal devoted to the study of the nervous system and behavior, 137, 215.

Cho S, et al. (2020) Automated analysis of lexical features in Frontotemporal Degeneration. medRxiv : the preprint server for health sciences.

Gillen J, et al. (2019) Experimental Analysis of Viral-Host Interactions. Frontiers in physiology, 10, 425.

Nevler N, et al. (2019) Validated automatic speech biomarkers in primary progressive aphasia. Annals of clinical and translational neurology, 6(1), 4.

Wu C, et al. (2019) Prognostic Immune Cell Profiling of Malignant Pleural Effusion Patients by Computerized Immunohistochemical and Transcriptional Analysis. Cancers, 11(12).

Arévalo-Pinzón G, et al. (2018) Self-assembling functional programmable protein array for studying protein-protein interactions in malaria parasites. Malaria journal, 17(1), 270.

Yu X, et al. (2017) Multiplexed Nucleic Acid Programmable Protein Arrays. Theranostics, 7(16), 4057.

Gervits F, et al. (2016) Transcranial direct current stimulation for the treatment of primary progressive aphasia: An open-label pilot study. Brain and language, 162, 35.