

Resource Summary Report

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Harmony

RRID:SCR_023543

Type: Tool

Proper Citation

Harmony (RRID:SCR_023543)

Resource Information

URL: <https://www.perkinelmer.com/product/harmony-5-1-office-hh17000012>

Proper Citation: Harmony (RRID:SCR_023543)

Description: Software tool designed by PerkinElmer for high content screening systems. Used to quantify complex cellular phenotypes. High content analysis software.

Synonyms: Harmony High-Content Imaging and Analysis Software, Harmony 5.0, Harmony 5.1

Resource Type: software resource, data processing software, software application, data analysis software

Keywords: PerkinElmer, high content screening systems, quantify complex cellular phenotypes,

Availability: Restricted

Resource Name: Harmony

Resource ID: SCR_023543

Record Creation Time: 20230504T050216+0000

Record Last Update: 20260806T054751+0000

Ratings and Alerts

No rating or validation information has been found for Harmony.

No alerts have been found for Harmony.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Pan J, et al. (2026) Cannabidiol suppresses emergency MDSCs generation by disturbing EEF1B2-mediated C/EBP β protein synthesis in colorectal adenomas. *Journal for immunotherapy of cancer*, 14(1).

Figueras-Novoa C, et al. (2025) Caspase cleavage of influenza A virus M2 disrupts M2-LC3 interaction and regulates virion production. *EMBO reports*, 26(7), 1768.

Hou Z, et al. (2025) Tertiary lymphoid structure-related RNA indicator as metastasis risk factor in nasopharyngeal carcinoma. *Clinical and translational medicine*, 15(12), e70539.

Wang H, et al. (2025) Phenotypic plasticity and increased infiltration of peripheral blood-derived TREM1⁺ mono-macrophages following radiotherapy in rectal cancer. *Cell reports. Medicine*, 6(1), 101887.

Geraud M, et al. (2025) Protocol for single-cell analysis of DNA double-strand break production and repair in cell-cycle phases by automated high-content microscopy. *STAR protocols*, 6(1), 103662.

Krieg K, et al. (2025) Cortical organoid-derived models of the melanoma brain metastatic niche enable prioritization of cancer-targeting drugs. *Cell reports methods*, 5(12), 101236.

Mendelsohn AI, et al. (2025) Segregated basal ganglia output pathways correspond to genetically divergent neuronal subclasses. *Cell reports*, 44(4), 115454.

Hölbling BV, et al. (2025) A multimodal screening platform for endogenous dipeptide repeat proteins in C9orf72 patient iPSC neurons. *Cell reports*, 44(5), 115695.

Saez-Atienzar S, et al. (2024) Mechanism-free repurposing of drugs for C9orf72-related ALS/FTD using large-scale genomic data. *Cell genomics*, 4(11), 100679.

Jiang Y, et al. (2024) Nicotinamide metabolism face-off between macrophages and fibroblasts manipulates the microenvironment in gastric cancer. *Cell metabolism*, 36(8), 1806.

Geraud M, et al. (2024) TDP1 mutation causing SCAN1 neurodegenerative syndrome hampers the repair of transcriptional DNA double-strand breaks. *Cell reports*, 43(5), 114214.

Ariey-Bonnet J, et al. (2023) Combination drug screen targeting glioblastoma core vulnerabilities reveals pharmacological synergisms. *EBioMedicine*, 95, 104752.

Garretti F, et al. (2023) Interaction of an α -synuclein epitope with HLA-DRB1*15:01 triggers enteric features in mice reminiscent of prodromal Parkinson's disease. *Neuron*,

111(21), 3397.

Wali G, et al. (2023) Generation of human-induced pluripotent-stem-cell-derived cortical neurons for high-throughput imaging of neurite morphology and neuron maturation. STAR protocols, 4(2), 102325.

Lin Y, et al. (2022) Allele-specific regulatory effects on the pig transcriptome. GigaScience, 12.