# Resource Summary Report

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## Roche NimbleGen

RRID:SCR_008571
Type: Tool

### Proper Citation

Roche NimbleGen (RRID:SCR_008571)

### Resource Information

**URL:** http://www.nimblegen.com

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**Description:** Roche NimbleGen, Inc. is a leading innovator, manufacturer and supplier of a proprietary suite of DNA microarrays, consumables, instruments and services. Roche NimbleGen uniquely produces high-density arrays of long oligo probes that provide greater information content and higher data quality necessary for studying the full diversity of genomic and epigenomic variation. Roche NimbleGen is enabling a new era of High-Definition Genomics by providing scientists with cost-effective, high-throughput tools for extracting and integrating complex data on important forms of genomic and epigenomic variation not previously accessible on a genome-wide scale. Scientists can thus obtain a clearer understanding of genomic and epigenomic structure and function and how they impact biology and medicine. This improved performance is made possible by Roche NimbleGen''s proprietary Maskless Array Synthesis (MAS) technology, which uses digital light processing and rapid, high-yield photochemistry to synthesize long oligo, high-density DNA microarrays with extreme flexibility. NimbleGen Systems was established in 1999. The MAS technology is the result of research collaborations between the departments of biotechnology, genetics, physics, and semiconductor engineering at the University of Wisconsin - Madison. Roche NimbleGen has the exclusive worldwide license to the MAS technology from the Wisconsin Alumni Research Foundation (WARF).

**Abbreviations:** Roche NimbleGen

**Resource Type:** instrument manufacture, material service resource, production service resource, service resource

**Resource Name:** Roche NimbleGen

**Resource ID:** SCR_008571

**Alternate IDs:** nif-0000-31466

**Record Creation Time:** 20220129T080248+0000

**Record Last Update:** 20260912T195706+0000

## Ratings and Alerts

No rating or validation information has been found for Roche NimbleGen.

No alerts have been found for Roche NimbleGen.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 233 mentions in open access literature.

**Listed below are recent publications.** The full list is available at Kravitz .


Beheshti ST, et al. (2025) Expanding the Clinical and Molecular Spectrum of TUBB2B Through Distinct Variants Identified Across Multiple Families. medRxiv : the preprint server for health sciences.

Elli FM, et al. (2024) Targeted silencing of GNAS in a human model of osteoprogenitor cells results in the deregulation of the osteogenic differentiation program. Frontiers in endocrinology, 15, 1296886.

Mougeot JC, et al. (2023) Identification of single nucleotide polymorphisms (SNPs) associated with chronic graft-versus-host disease in patients undergoing allogeneic hematopoietic cell transplantation. Supportive care in cancer : official journal of the Multinational Association of Supportive Care in Cancer, 31(10), 587.

Xu Q, et al. (2022) Gene interaction analysis of psoriasis in Chinese Han population. Molecular genetics & genomic medicine, 10(5), e1858.

Yang K, et al. (2022) Two heterozygous mutations in the calcium/calmodulin-dependent serine protein kinase gene (CASK) in cases with developmental disorders. Molecular genetics & genomic medicine, 10(11), e2065.

Zhang H, et al. (2021) Genomic Copy Number Variants in CML Patients With the Philadelphia Chromosome (Ph+): An Update. Frontiers in genetics, 12, 697009.

Wang M, et al. (2020) Identification of a novel mutation in CRYM in a Chinese family with hearing loss using whole-exome sequencing. Experimental and therapeutic medicine, 20(2), 1447.

Van Winkle LJ, et al. (2020) Lysine Deprivation during Maternal Consumption of Low-Protein Diets Could Adversely Affect Early Embryo Development and Health in Adulthood. International journal of environmental research and public health, 17(15).

Edwards JJ, et al. (2020) Systems Analysis Implicates WAVE2 Complex in the Pathogenesis of Developmental Left-Sided Obstructive Heart Defects. JACC. Basic to translational science, 5(4), 376.

Preston JL, et al. (2020) Epigenetic loss of heterozygosity of Apc and an inflammation-associated mutational signature detected in Lrig1+/--driven murine colonic adenomas. BMC cancer, 20(1), 126.

Zou ZV, et al. (2020) Genomic profiling of the transcription factor Zfp148 and its impact on the p53 pathway. Scientific reports, 10(1), 14156.

Martin PB, et al. (2020) NEMF mutations that impair ribosome-associated quality control are associated with neuromuscular disease. Nature communications, 11(1), 4625.

Shi Y, et al. (2020) Circulating tumor DNA predicts response in Chinese patients with relapsed or refractory classical hodgkin lymphoma treated with sintilimab. EBioMedicine, 54, 102731.

Jamil MA, et al. (2019) F8 Inversions at Xq28 Causing Hemophilia A Are Associated With Specific Methylation Changes: Implication for Molecular Epigenetic Diagnosis. Frontiers in genetics, 10, 508.

Alcala N, et al. (2019) Integrative and comparative genomic analyses identify clinically relevant pulmonary carcinoid groups and unveil the supra-carcinoids. Nature communications, 10(1), 3407.

Gardiner LJ, et al. (2019) Integrating genomic resources to present full gene and putative promoter capture probe sets for bread wheat. GigaScience, 8(4).

Kumar M, et al. (2019) Strigolactone Signaling Genes Showing Differential Expression Patterns in Arabidopsis max Mutants. Plants (Basel, Switzerland), 8(9).

Shetty AC, et al. (2019) Genomic structure and diversity of Plasmodium falciparum in Southeast Asia reveal recent parasite migration patterns. Nature communications, 10(1), 2665.

Li P, et al. (2019) Natural Variation and Domestication Selection of ZmPGP1 Affects Plant Architecture and Yield-Related Traits in Maize. Genes, 10(9).

Pehlivan D, et al. (2019) The Genomics of Arthrogryposis, a Complex Trait: Candidate Genes and Further Evidence for Oligogenic Inheritance. American journal of human genetics, 105(1), 132.