

Resource Summary Report

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Qiagen: QIAxcel Genetic Analyzer

RRID:SCR_018624

Type: Tool

Proper Citation

Qiagen: QIAxcel Genetic Analyzer (RRID:SCR_018624)

Resource Information

URL: <https://www.qiagen.com/us/service-and-support/learning-hub/technologies-and-research-topics/sample-quality-control/instruments/qiaxcel-advanced/>

Proper Citation: Qiagen: QIAxcel Genetic Analyzer (RRID:SCR_018624)

Description: Genetic analyzer that automates electrophoresis analysis of your DNA and RNA samples.

Synonyms: QIAxcel Advanced, Qiagen QIAxcel Advanced

Resource Type: instrument resource

Keywords: Genetic Analyzer, Instrument, Equipment, Qiagen, USEDit, ABRF

Availability: Commercially available

Resource Name: Qiagen: QIAxcel Genetic Analyzer

Resource ID: SCR_018624

Alternate IDs: SCR_020418, Model_Number_QIAxcel

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260725T190853+0000

Ratings and Alerts

No rating or validation information has been found for Qiagen: QIAxcel Genetic Analyzer.

No alerts have been found for Qiagen: QIAxcel Genetic Analyzer.

Data and Source Information

Usage and Citation Metrics

We found 57 mentions in open access literature.

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

Filippou C, et al. (2025) Transcriptomic Analysis Reveals Molecular Mechanisms Underpinning Mycovirus-Mediated Hypervirulence in *Beauveria bassiana* Infecting *Tenebrio molitor*. *Journal of fungi* (Basel, Switzerland), 11(1).

Liefferinckx C, et al. (2025) The identification of blood-derived response eQTLs reveals complex effects of regulatory variants on inflammatory and infectious disease risk. *PLoS genetics*, 21(4), e1011599.

Stenger PL, et al. (2025) A Multimarker Approach to Identify Microbial Bioindicators for Coral Reef Health Monitoring-Case Study in La Réunion Island. *Microbial ecology*, 87(1), 179.

Charlesson B, et al. (2025) Training load influences gut microbiome of highly trained rowing athletes. *Journal of the International Society of Sports Nutrition*, 22(1), 2507952.

de Lana M, et al. (2025) Parasitological cure and clinical benefits of benznidazole treatment in patients from the Jequitinhonha Valley, MG, Brazil, with recent chronic infection by *Trypanosoma cruzi* II. *Memorias do Instituto Oswaldo Cruz*, 120, e240229.

Mawarda PC, et al. (2025) Unveiling the ecological processes driving soil and lichen microbiome assembly along an urbanization gradient. *NPJ biofilms and microbiomes*, 11(1), 99.

Battle-Masó L, et al. (2025) De Novo or inherited: gonosomal mosaicism in hereditary angioedema due to C1 inhibitor deficiency. *Frontiers in immunology*, 16, 1550380.

Beaumont C, et al. (2025) hnRNP A1 induces aberrant CFTR exon 9 splicing via a newly discovered ESS element. *Life science alliance*, 8(9).

Oganezovi N, et al. (2024) Long-term effects of myo-inositol on traumatic brain injury: Epigenomic and transcriptomic studies. *IBRO neuroscience reports*, 16, 291.

Modak RV, et al. (2024) Targeting CCL2/CCR2 Signaling Overcomes MEK Inhibitor Resistance in Acute Myeloid Leukemia. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(10), 2245.

Jiraskova Zakostelska Z, et al. (2024) Lysate of *Parabacteroides distasonis* prevents severe forms of experimental autoimmune encephalomyelitis by modulating the priming of T cell response. *Frontiers in immunology*, 15, 1475126.

VanInsberghe D, et al. (2024) Genetic drift and purifying selection shape within-host influenza A virus populations during natural swine infections. *PLoS pathogens*, 20(4), e1012131.

Delfosse K, et al. (2023) High-throughput functional analysis of regulatory variants using a massively parallel reporter assay. STAR protocols, 4(4), 102731.

Ally HM, et al. (2023) Genetic diversity, distribution, and structure of Bemisia tabaci whitefly species in potential invasion and hybridization regions of East Africa. PloS one, 18(5), e0285967.

Phumee A, et al. (2023) Genetic diversity and phylogenetic analyses of Asian lineage Zika virus whole genome sequences derived from Culex quinquefasciatus mosquitoes and urine of patients during the 2020 epidemic in Thailand. Scientific reports, 13(1), 18470.

Liu H, et al. (2023) Inflammatory stress-mediated chromatin changes underlie dysfunction in endothelial cells. bioRxiv : the preprint server for biology.

VanInsberghe D, et al. (2023) Genetic drift and purifying selection shape within-host influenza A virus populations during natural swine infections. bioRxiv : the preprint server for biology.

Nganyewo NN, et al. (2023) Recent increase in low complexity polygenomic infections and sialic acid-independent invasion pathways in Plasmodium falciparum from Western Gambia. Parasites & vectors, 16(1), 309.

Popovi? Dragonji? L, et al. (2023) Cordylobia anthropophaga Myiasis Mimicking Hyperproliferative Skin Disorder in Traveler Returning from Sub-Saharan Africa. Tropical medicine and infectious disease, 8(11).

Kieran TJ, et al. (2023) Influenza A Virus Multicycle Replication Yields Comparable Viral Population Emergence in Human Respiratory and Ocular Cell Types. Microbiology spectrum, 11(4), e0116623.