

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 [dkNET](#) .

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.

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.

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).

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.

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.

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.

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.

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

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.

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

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.

Liu H, et al. (2023) Inflammatory stress-mediated chromatin changes underlie dysfunction in endothelial cells. *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.

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*.

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.

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.