

Resource Summary Report

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IPD - Immuno Polymorphism Database

RRID:SCR_003004

Type: Tool

Proper Citation

IPD - Immuno Polymorphism Database (RRID:SCR_003004)

Resource Information

URL: <http://www.ebi.ac.uk/ipd/>

Proper Citation: IPD - Immuno Polymorphism Database (RRID:SCR_003004)

Description: A set of specialist databases related to the study of polymorphic genes in the immune system. The IPD project works with specialist groups or nomenclature committees who provide and curate individual sections before they are submitted to IPD for online publication. The IPD project stores all the data in a set of related databases. IPD currently consists of four databases: * IPD-KIR, contains the allelic sequences of Killer-cell Immunoglobulin-like Receptors, * IPD-MHC, is a database of sequences of the Major Histocompatibility Complex of different species; * IPD-human platelet antigens, alloantigens expressed only on platelets and * IPD-ESTDAB, which provides access to the European Searchable Tumour cell-line database, a cell bank of immunologically characterized melanoma cell lines.

Abbreviations: IPD

Synonyms: IPD-The Immuno Polymorphism Database, IPD - The Immuno Polymorphism Database

Resource Type: data or information resource, database

Defining Citation: [PMID:19875415](#), [PMID:18449992](#), [PMID:15608253](#)

Keywords: polymorphic gene, immune system, gene, gold standard, bio.tools

Funding: European Union contract QLRI-CT-2001-01325;
NCI P01 111412

Resource Name: IPD - Immuno Polymorphism Database

Resource ID: SCR_003004

Alternate IDs: biotools:ipd, nif-0000-03038, r3d100010797

Alternate URLs: <https://bio.tools/ipd>, <https://doi.org/10.17616/R3KK7K>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260905T133119+0000

Ratings and Alerts

No rating or validation information has been found for IPD - Immuno Polymorphism Database.

No alerts have been found for IPD - Immuno Polymorphism Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Chen A, et al. (2026) WGCNA and machine learning identify AURKA, CDK1, and other hub genes associated with immune infiltration as therapeutic targets in GIST: An integrative bioinformatics analysis. *Medicine*, 105(1), e46636.

Turganbekova A, et al. (2025) Genetic Diversity and Ethnic Tapestry of Kazakhstan as Inferred from HLA Polymorphism and Population Dynamics: A Comprehensive Review. *Genes*, 16(3).

Kowal K, et al. (2023) Canis MitoSNP database: a functional tool useful for comparative analyses of human and canine mitochondrial genomes. *Journal of applied genetics*, 64(3), 515.

Silwamba I, et al. (2023) High throughput analysis of MHC class I and class II diversity of Zambian indigenous cattle populations. *HLA*, 101(5), 458.

Deng Z, et al. (2021) Adaptive Admixture of HLA Class I Allotypes Enhanced Genetically Determined Strength of Natural Killer Cells in East Asians. *Molecular biology and evolution*, 38(6), 2582.

Eirin M, et al. (2020) BoLA-DRB3 exon2 polymorphisms among tuberculous cattle: Nucleotide and functional variability and their association with bovine tuberculosis pathology. *Research in veterinary science*, 130, 118.

Draganov DD, et al. (2019) Delivery of oncolytic vaccinia virus by matched allogeneic stem cells overcomes critical innate and adaptive immune barriers. *Journal of translational medicine*, 17(1), 100.

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- Shi C, et al. (2015) Allele Specific Expression of MICA Variants in Human Fibroblasts Suggests a Pathogenic Mechanism. *The open rheumatology journal*, 9, 60.
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- Gutiérrez AH, et al. (2015) Development and validation of an epitope prediction tool for swine (PigMatrix) based on the pocket profile method. *BMC bioinformatics*, 16, 290.
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