

# Ilkka Lappalainen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/365078/publications.pdf>

Version: 2024-02-01

23  
papers

1,490  
citations

430874

18  
h-index

552781

26  
g-index

26  
all docs

26  
docs citations

26  
times ranked

3921  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | ELIXIRâ€™EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.   | 7.8  | 18        |
| 2  | htsget: a protocol for securely streaming genomic data. <i>Bioinformatics</i> , 2019, 35, 119-121.   | 4.1  | 23        |
| 3  | Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.   | 16.3 | 69        |
| 4  | Federated discovery and sharing of genomic data using Beacons. <i>Nature Biotechnology</i> , 2019, 37, 220-224.  | 17.5 | 75        |
| 5  | Registered access: authorizing data access. <i>European Journal of Human Genetics</i> , 2018, 26, 1721-1731.   | 2.8  | 33        |
| 6  | Common ELIXIR Service for Researcher Authentication and Authorisation. <i>F1000Research</i> , 2018, 7, 1199.   | 1.6  | 23        |
| 7  | Orchestrating differential data access for translational research: a pilot implementation. <i>BMC Medical Informatics and Decision Making</i> , 2017, 17, 30.  | 3.0  | 5         |
| 8  | The European Genome-phenome Archive of human data consented for biomedical research. <i>Nature Genetics</i> , 2015, 47, 692-695.   | 21.4 | 338       |
| 9  | dbVar and DGVa: public archives for genomic structural variation. <i>Nucleic Acids Research</i> , 2012, 41, D936-D941.   | 14.5 | 222       |
| 10 | Public data archives for genomic structural variation. <i>Nature Genetics</i> , 2010, 42, 813-814.   | 21.4 | 71        |
| 11 | A System for Information Management in BioMedical Studiesâ€™SIMBioMS. <i>Bioinformatics</i> , 2009, 25, 2768-2769.   | 4.1  | 27        |
| 12 | Genome wide analysis of pathogenic SH2 domain mutations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 779-792.  | 2.6  | 56        |
| 13 | Plasticity Within the Obligatory Folding Nucleus of an Immunoglobulin-like Domain. <i>Journal of Molecular Biology</i> , 2008, 375, 547-559.   | 4.2  | 47        |
| 14 | Using Model Proteins to Quantify the Effects of Pathogenic Mutations in Ig-like Proteins. <i>Journal of Biological Chemistry</i> , 2006, 281, 24216-24226.   | 3.4  | 30        |
| 15 | Structure-Function Analysis of PrsA Reveals Roles for the Parvulin-like and Flanking N- and C-terminal Domains in Protein Folding and Secretion in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 19302-19314. | 3.4  | 91        |
| 16 | Structural basis of ICF-causing mutations in the methyltransferase domain of DNMT3B. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 1005-1014.   | 2.1  | 11        |
| 17 | Pattern of Somatic Androgen Receptor Gene Mutations in Patients with Hormone-Refractory Prostate Cancer. <i>Laboratory Investigation</i> , 2002, 82, 1591-1598.  | 3.7  | 64        |
| 18 | 4 Primary immunodeficiency mutation databases. <i>Advances in Genetics</i> , 2001, 43, 103-188.  | 1.8  | 70        |

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|----|--|-----|-----------|
| 19 | Six X-Linked Agammaglobulinemia-Causing Missense Mutations in the Src Homology 2 Domain of Bruton's Tyrosine Kinase: Phosphotyrosine-Binding and Circular Dichroism Analysis. <i>Journal of Immunology</i> , 2000, 164, 4170-4177. | 0.8 | 35        |
| 20 | The Metal Dependence of <i>Bacillus subtilis</i> Phytase. <i>Biochemical and Biophysical Research Communications</i> , 2000, 268, 365-369.   | 2.1 | 59        |
| 21 | Structural Basis for SH2D1A Mutations in X-Linked Lymphoproliferative Disease. <i>Biochemical and Biophysical Research Communications</i> , 2000, 269, 124-130.  | 2.1 | 29        |
| 22 | Registries of immunodeficiency patients and mutations. <i>Human Mutation</i> , 1997, 10, 261-267.  | 2.5 | 8         |
| 23 | Sequence specificity in CpG mutation hotspots. <i>FEBS Letters</i> , 1996, 396, 119-122.   | 2.8 | 65        |