

# Alexander A Kanapin

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

15,537  
citations

126708

33  
h-index

143772

57  
g-index

63  
all docs

63  
docs citations

63  
times ranked

23973  
citing authors

| #  | ARTICLE                                                                                                                                                                                                  | IF   | CITATIONS |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1  | Systematic functional analysis of the <i>Caenorhabditis elegans</i> genome using RNAi. <i>Nature</i> , 2003, 421, 231-237.                                                                               | 13.7 | 3,343     |
| 2  | The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.                                                                                                            | 6.0  | 3,227     |
| 3  | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.                                                                      | 13.7 | 1,548     |
| 4  | The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , 2001, 29, 37-40.                                         | 6.5  | 928       |
| 5  | Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. <i>Nature Genetics</i> , 2013, 45, 136-144.                                    | 9.4  | 851       |
| 6  | Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009, 37, D619-D622.                                                                                  | 6.5  | 760       |
| 7  | The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.                                                                               | 6.5  | 640       |
| 8  | InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.                                                                                                              | 6.5  | 478       |
| 9  | New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.                                                                                                          | 6.5  | 444       |
| 10 | Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.                                                              | 9.4  | 310       |
| 11 | InterPro—an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , 2000, 16, 1145-1150.                                                           | 1.8  | 301       |
| 12 | Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.                                                                                  | 2.6  | 290       |
| 13 | Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. <i>Human Molecular Genetics</i> , 2014, 23, 3200-3211.                               | 1.4  | 222       |
| 14 | Mutations in TCF12, encoding a basic helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis. <i>Nature Genetics</i> , 2013, 45, 304-307.                                   | 9.4  | 181       |
| 15 | Disruption of SF3B1 results in deregulated expression and splicing of key genes and pathways in myelodysplastic syndrome hematopoietic stem and progenitor cells. <i>Leukemia</i> , 2015, 29, 1092-1103. | 3.3  | 161       |
| 16 | Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014, 6, 26.                                                                                       | 3.6  | 158       |
| 17 | InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.                                                | 3.2  | 155       |
| 18 | Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , 2004, 33, D297-D302.                                                                     | 6.5  | 125       |

| #  | ARTICLE                                                                                                                                                                                                    | IF  | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Clinical whole-genome sequencing from routine formalin-fixed, paraffin-embedded specimens: pilot study for the 100,000 Genomes Project. <i>Genetics in Medicine</i> , 2018, 20, 1196-1205.                 | 1.1 | 125       |
| 20 | Unfixed Endogenous Retroviral Insertions in the Human Population. <i>Journal of Virology</i> , 2014, 88, 9529-9537.                                                                                        | 1.5 | 118       |
| 21 | Recessive Mutations in SPTBN2 Implicate Î²-III Spectrin in Both Cognitive and Motor Development. <i>PLoS Genetics</i> , 2012, 8, e1003074.                                                                 | 1.5 | 94        |
| 22 | Mouse Proteome Analysis. <i>Genome Research</i> , 2003, 13, 1335-1344.                                                                                                                                     | 2.4 | 91        |
| 23 | Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. <i>Cell Reports</i> , 2016, 17, 2724-2737.                                        | 2.9 | 86        |
| 24 | Proteome Analysis Database: online application of InterPro and CluSTr for the functional classification of proteins in whole genomes. <i>Nucleic Acids Research</i> , 2001, 29, 44-48.                     | 6.5 | 84        |
| 25 | Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. <i>Nature Communications</i> , 2014, 5, 3756.                       | 5.8 | 81        |
| 26 | RASSF1A uncouples Wnt from Hippo signalling and promotes YAP mediated differentiation via p73. <i>Nature Communications</i> , 2018, 9, 424.                                                                | 5.8 | 72        |
| 27 | NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. <i>Mucosal Immunology</i> , 2018, 11, 562-574.                                                                         | 2.7 | 71        |
| 28 | The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 414-417.                                                                   | 6.5 | 64        |
| 29 | Human Accelerated Regions and Other Human-Specific Sequence Variations in the Context of Evolution and Their Relevance for Brain Development. <i>Genome Biology and Evolution</i> , 2018, 10, 166-188.     | 1.1 | 61        |
| 30 | Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002, 3, 285-295.                                                                                 | 3.2 | 54        |
| 31 | The pss4 gene from <i>Rhizobium leguminosarum</i> bv viciae VF39: cloning, sequence and the possible role in polysaccharide production and nodule formation. <i>Gene</i> , 1994, 150, 111-116.             | 1.0 | 45        |
| 32 | Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species. <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 201-210.        | 0.5 | 40        |
| 33 | Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , 2014, 99, e201-e204.                                                                                     | 1.7 | 35        |
| 34 | A point mutation in the ion conduction pore of AMPA receptor GRIA3 causes dramatically perturbed sleep patterns as well as intellectual disability. <i>Human Molecular Genetics</i> , 2017, 26, 3869-3882. | 1.4 | 35        |
| 35 | Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. <i>Genome Research</i> , 2003, 13, 1542-1551.                                                                   | 2.4 | 34        |
| 36 | PRMT5 promotes cancer cell migration and invasion through the E2F pathway. <i>Cell Death and Disease</i> , 2020, 11, 572.                                                                                  | 2.7 | 20        |

| #  | ARTICLE                                                                                                                                                                                                                                    | IF  | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Arginine methylation expands the regulatory mechanisms and extends the genomic landscape under E2F control. <i>Science Advances</i> , 2019, 5, eaaw4640.                                                                                   | 4.7 | 19        |
| 38 | Neanderthal and Denisovan retroviruses in modern humans. <i>Current Biology</i> , 2013, 23, R994-R995.                                                                                                                                     | 1.8 | 17        |
| 39 | Current challenges and possible future developments in personalized psychiatry with an emphasis on psychotic disorders. <i>Heliyon</i> , 2020, 6, e03990.                                                                                  | 1.4 | 15        |
| 40 | Interactive InterPro-based comparisons of proteins in whole genomes. <i>Bioinformatics</i> , 2002, 18, 374-375.                                                                                                                            | 1.8 | 14        |
| 41 | The Genome Sequence of Five Highly Pathogenic Isolates of <i>Fusarium oxysporum</i> f. sp. lini. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1112-1115.                                                                        | 1.4 | 14        |
| 42 | Characterising a human endogenous retrovirus (HERV)-derived tumour-associated antigen: enriched RNA-Seq analysis of HERV-K(HML-2) in mantle cell lymphoma cell lines. <i>Mobile DNA</i> , 2020, 11, 9.                                     | 1.3 | 13        |
| 43 | The Genetic Landscape of Fiber Flax. <i>Frontiers in Plant Science</i> , 2021, 12, 764612.                                                                                                                                                 | 1.7 | 11        |
| 44 | Interplay between RNA interference and heat shock response systems in <i>Drosophila melanogaster</i> . <i>Open Biology</i> , 2016, 6, 160224.                                                                                              | 1.5 | 9         |
| 45 | Proteome Complexity Measures Based on Counting of Domain-to-Protein Links for Replicative and Non-Replicative Domains. , 2006, , 329-341.                                                                                                  |     | 9         |
| 46 | A Genomic Blueprint of Flax Fungal Parasite <i>Fusarium oxysporum</i> f. sp. lini. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2665.                                                                                    | 1.8 | 6         |
| 47 | Application of InterPro for the functional classification of the proteins of fish origin in SWISS-PROT and TrEMBL. <i>Journal of Biosciences</i> , 2001, 26, 277-284.                                                                      | 0.5 | 5         |
| 48 | Mutations of TCF12, encoding a basic-helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis. <i>Lancet, The</i> , 2013, 381, S114.                                                                           | 6.3 | 5         |
| 49 | A comprehensive dataset of flax ( <i>Linum uitatissimum</i> L.) phenotypes. <i>Data in Brief</i> , 2021, 37, 107224.                                                                                                                       | 0.5 | 5         |
| 50 | A genome-wide association study identifies a gene network associated with paranoid schizophrenia and antipsychotics-induced tardive dyskinesia. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 105, 110134. | 2.5 | 4         |
| 51 | Projection of gene-protein networks to the functional space of the proteome and its application to analysis of organism complexity. <i>BMC Genomics</i> , 2010, 11, S4.                                                                    | 1.2 | 3         |
| 52 | Antisense oligodeoxyribonucleotides for fragments of the reverse transcriptase gene of the LINE-1 element of rats disturb the formation of long-term memory. <i>Doklady Biochemistry and Biophysics</i> , 2002, 383, 93-95.                | 0.3 | 2         |
| 53 | Stochastic Effects in Retrotransposon Dynamics Revealed by Modeling under Competition for Cellular Resources. <i>Life</i> , 2021, 11, 1209.                                                                                                | 1.1 | 2         |
| 54 | An account of <i>Fusarium</i> wilt resistance in flax <i>Linum usitatissimum</i> : The disease severity data. <i>Data in Brief</i> , 2022, 41, 107869.                                                                                     | 0.5 | 2         |

| #  | ARTICLE                                                                                                                                             | IF  | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | Regions Of 3D Similarity in Potential ORF1 Prducts of Mobile Genetics Classes. Protein Engineering, Design and Selection, 0, , .                    | 1.0 | 0         |
| 56 | Supervised Learning-Aided Optimization of Expert-Driven Functional Protein Sequence Annotation. Lecture Notes in Computer Science, 2004, , 159-169. | 1.0 | 0         |
| 57 | InterPro as a new tool for complete genome analysis: An example of comparative analysis. Biophysics (Russian Federation), 2006, 51, 587-591.        | 0.2 | 0         |
| 58 | Reactome - a knowledgebase of human biological pathways. Nature Precedings, 2009, , .                                                               | 0.1 | 0         |
| 59 | Aberration Of SF3B1 Results In Deregulated Splicing Of Key Genes and Pathways In Myelodysplastic Syndromes. Blood, 2013, 122, 2747-2747.            | 0.6 | 0         |