

# Alexander A Kanapin

## List of Publications by Citations

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56  
papers

12,893  
citations

31  
h-index

63  
g-index

63  
ext. papers

14,416  
ext. citations

12  
avg. IF

4.61  
L-index

#	Paper	IF	Citations
56	The transcriptional landscape of the mammalian genome. <i>Science</i> , <b>2005</b> , 309, 1559-63	33.3	2807
55	Systematic functional analysis of the <i>Caenorhabditis elegans</i> genome using RNAi. <i>Nature</i> , <b>2003</b> , 421, 231-7	50.4	2758
54	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , <b>2002</b> , 420, 563-73	50.4	1350
53	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 37-40	20.1	743
52	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. <i>Nature Genetics</i> , <b>2013</b> , 45, 136-44	36.3	686
51	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D619-22	20.1	675
50	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 315-8	20.1	556
49	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D201-5	20.1	426
48	New developments in the InterPro database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D224-8	20.1	397
47	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , <b>2004</b> , 2, e162	9.7	255
46	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , <b>2015</b> , 47, 717-726	36.3	244
45	InterPro--an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , <b>2000</b> , 16, 1145-50	7.2	217
44	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 3200-11	5.6	179
43	Mutations in TCF12, encoding a basic helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis. <i>Nature Genetics</i> , <b>2013</b> , 45, 304-7	36.3	146
42	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 225-35	13.4	137
41	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , <b>2014</b> , 6, 26	14.4	125
40	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D297-302	20.1	116

39	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> , <b>2015</b> , 29, 1092-103	10.7	96
38	Unfixed endogenous retroviral insertions in the human population. <i>Journal of Virology</i> , <b>2014</b> , 88, 9529-37.6		84
37	Clinical whole-genome sequencing from routine formalin-fixed, paraffin-embedded specimens: pilot study for the 100,000 Genomes Project. <i>Genetics in Medicine</i> , <b>2018</b> , 20, 1196-1205	8.1	77
36	Mouse proteome analysis. <i>Genome Research</i> , <b>2003</b> , 13, 1335-44	9.7	75
35	Recessive mutations in SPTBN2 implicate $\beta$ III spectrin in both cognitive and motor development. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003074	6	74
34	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. <i>Nature Communications</i> , <b>2014</b> , 5, 3756	17.4	66
33	Proteome Analysis Database: online application of InterPro and CluSTR for the functional classification of proteins in whole genomes. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 44-8	20.1	63
32	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 414-7	20.1	55
31	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. <i>Cell Reports</i> , <b>2016</b> , 17, 2724-2737	10.6	54
30	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. <i>Mucosal Immunology</i> , <b>2018</b> , 11, 562-574	9.2	51
29	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 285-95	13.4	48
28	RASSF1A uncouples Wnt from Hippo signalling and promotes YAP mediated differentiation via p73. <i>Nature Communications</i> , <b>2018</b> , 9, 424	17.4	47
27	The pss4 gene from <i>Rhizobium leguminosarum</i> by <i>viciae</i> VF39: cloning, sequence and the possible role in polysaccharide production and nodule formation. <i>Gene</i> , <b>1994</b> , 150, 111-6	3.8	42
26	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> , <b>2018</b> , 10, 166-188	3.9	31
25	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> , <b>2001</b> , 118, 201-10	1.9	31
24	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> , <b>2017</b> , 26, 3869-3882	5.6	24
23	Development and evaluation of an automated annotation pipeline and cDNA annotation system. <i>Genome Research</i> , <b>2003</b> , 13, 1542-51	9.7	24
22	Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , <b>2014</b> , 99, e201-4	6.6	14

21	Interactive InterPro-based comparisons of proteins in whole genomes. <i>Bioinformatics</i> , <b>2002</b> , 18, 374-5	7.2	13
20	Neanderthal and Denisovan retroviruses in modern humans. <i>Current Biology</i> , <b>2013</b> , 23, R994-R995	6.3	12
19	Arginine methylation expands the regulatory mechanisms and extends the genomic landscape under E2F control. <i>Science Advances</i> , <b>2019</b> , 5, eaaw4640	14.3	9
18	Interplay between RNA interference and heat shock response systems in <i>Drosophila melanogaster</i> . <i>Open Biology</i> , <b>2016</b> , 6,	7	8
17	PRMT5 promotes cancer cell migration and invasion through the E2F pathway. <i>Cell Death and Disease</i> , <b>2020</b> , 11, 572	9.8	7
16	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> , <b>2020</b> , 11, 9	4.4	6
15	The Genome Sequence of Five Highly Pathogenic Isolates of <i>f. sp.</i> . <i>Molecular Plant-Microbe Interactions</i> , <b>2020</b> , 33, 1112-1115	3.6	5
14	Application of InterPro for the functional classification of the proteins of fish origin in SWISS-PROT and TrEMBL. <i>Journal of Biosciences</i> , <b>2001</b> , 26, 277-84	2.3	4
13	Current challenges and possible future developments in personalized psychiatry with an emphasis on psychotic disorders. <i>Heliyon</i> , <b>2020</b> , 6, e03990	3.6	4
12	Proteome Complexity Measures Based on Counting of Domain-to-Protein Links for Replicative and Non-Replicative Domains <b>2006</b> , 329-341		4
11	The Genetic Landscape of Fiber Flax.. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 764612	6.2	4
10	Mutations of TCF12, encoding a basic-helix-loop-helix partner of TWIST1, are a frequent cause of coronal craniosynostosis. <i>Lancet, The</i> , <b>2013</b> , 381, S114	4.0	2
9	Projection of gene-protein networks to the functional space of the proteome and its application to analysis of organism complexity. <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 1, S4	4.5	2
8	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> , <b>2002</b> , 383, 93-5	0.8	2
7	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> , <b>2021</b> , 105, 110134	5.5	2
6	An account of Fusarium wilt resistance in flax : The disease severity data.. <i>Data in Brief</i> , <b>2022</b> , 41, 107869	1.2	1
5	A Genomic Blueprint of Flax Fungal Parasite <i>f. sp.</i> . <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	1
4	A comprehensive dataset of flax ( <i>L.</i> ) phenotypes. <i>Data in Brief</i> , <b>2021</b> , 37, 107224	1.2	0

- 3 InterPro as a new tool for complete genome analysis: An example of comparative analysis. *Biophysics (Russian Federation)*, **2006**, 51, 587-591 0.7
- 2 Supervised Learning-Aided Optimization of Expert-Driven Functional Protein Sequence Annotation. *Lecture Notes in Computer Science*, **2004**, 159-169 0.9
- 1 Aberration Of SF3B1 Results In Deregulated Splicing Of Key Genes and Pathways In Myelodysplastic Syndromes. *Blood*, **2013**, 122, 2747-2747 2.2