

Alexander A Kanapin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	An account of Fusarium wilt resistance in flax : The disease severity data.. <i>Data in Brief</i> , 2022 , 41, 107869	1.2	1
55	A Genomic Blueprint of Flax Fungal Parasite <i>f. sp.</i> . <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
54	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	5.5	2
53	A comprehensive dataset of flax (<i>L.</i>) phenotypes. <i>Data in Brief</i> , 2021 , 37, 107224	1.2	0
52	The Genetic Landscape of Fiber Flax.. <i>Frontiers in Plant Science</i> , 2021 , 12, 764612	6.2	4
51	The Genome Sequence of Five Highly Pathogenic Isolates of <i>f. sp.</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 1112-1115	3.6	5
50	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	4.4	6
49	Current challenges and possible future developments in personalized psychiatry with an emphasis on psychotic disorders. <i>Heliyon</i> , 2020 , 6, e03990	3.6	4
48	PRMT5 promotes cancer cell migration and invasion through the E2F pathway. <i>Cell Death and Disease</i> , 2020 , 11, 572	9.8	7
47	Arginine methylation expands the regulatory mechanisms and extends the genomic landscape under E2F control. <i>Science Advances</i> , 2019 , 5, eaaw4640	14.3	9
46	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	8.1	77
45	RASSF1A uncouples Wnt from Hippo signalling and promotes YAP mediated differentiation via p73. <i>Nature Communications</i> , 2018 , 9, 424	17.4	47
44	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. <i>Mucosal Immunology</i> , 2018 , 11, 562-574	9.2	51
43	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	3.9	31
42	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	5.6	24
41	Interplay between RNA interference and heat shock response systems in <i>Drosophila melanogaster</i> . <i>Open Biology</i> , 2016 , 6,	7	8
40	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	10.6	54

39	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015 , 47, 717-726	36.3	244
38	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, 1092-103	10.7	96
37	Clinical whole-genome sequencing in severe early-onset epilepsy reveals new genes and improves molecular diagnosis. <i>Human Molecular Genetics</i> , 2014 , 23, 3200-11	5.6	179
36	Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , 2014 , 99, e201-4	6.6	14
35	Unfixed endogenous retroviral insertions in the human population. <i>Journal of Virology</i> , 2014 , 88, 9529-37.6	37.6	84
34	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014 , 6, 26	14.4	125
33	Whole-genome sequencing of bladder cancers reveals somatic CDKN1A mutations and clinicopathological associations with mutation burden. <i>Nature Communications</i> , 2014 , 5, 3756	17.4	66
32	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	40	2
31	Neanderthal and Denisovan retroviruses in modern humans. <i>Current Biology</i> , 2013 , 23, R994-R995	6.3	12
30	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, 304-7	36.3	146
29	Germline mutations affecting the proofreading domains of POLE and POLD1 predispose to colorectal adenomas and carcinomas. <i>Nature Genetics</i> , 2013 , 45, 136-44	36.3	686
28	Aberration Of SF3B1 Results In Deregulated Splicing Of Key Genes and Pathways In Myelodysplastic Syndromes. <i>Blood</i> , 2013 , 122, 2747-2747	2.2	
27	Recessive mutations in SPTBN2 implicate β III spectrin in both cognitive and motor development. <i>PLoS Genetics</i> , 2012 , 8, e1003074	6	74
26	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 Suppl 1, S4	4.5	2
25	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009 , 37, D619-22	20.1	675
24	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007 , 35, D224-8	20.1	397
23	InterPro as a new tool for complete genome analysis: An example of comparative analysis. <i>Biophysics (Russian Federation)</i> , 2006 , 51, 587-591	0.7	
22	Proteome Complexity Measures Based on Counting of Domain-to-Protein Links for Replicative and Non-Replicative Domains 2006 , 329-341		4

21	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
20	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , 2005 , 33, D297-302	20.1	116
19	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5	20.1	426
18	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
17	Supervised Learning-Aided Optimization of Expert-Driven Functional Protein Sequence Annotation. <i>Lecture Notes in Computer Science</i> , 2004 , 159-169	0.9	
16	Systematic functional analysis of the <i>Caenorhabditis elegans</i> genome using RNAi. <i>Nature</i> , 2003 , 421, 231-7	50.4	2758
15	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003 , 31, 414-7	20.1	55
14	Development and evaluation of an automated annotation pipeline and cDNA annotation system. <i>Genome Research</i> , 2003 , 13, 1542-51	9.7	24
13	Mouse proteome analysis. <i>Genome Research</i> , 2003 , 13, 1335-44	9.7	75
12	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
11	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002 , 420, 563-73	50.4	1350
10	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, 93-5	0.8	2
9	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002 , 3, 225-35	13.4	137
8	Interactive InterPro-based comparisons of proteins in whole genomes. <i>Bioinformatics</i> , 2002 , 18, 374-5	7.2	13
7	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002 , 3, 285-95	13.4	48
6	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, 277-84	2.3	4
5	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, 201-10	1.9	31
4	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, 44-8	20.1	63

3	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , 2001 , 29, 37-40	20.1	743
2	InterPro--an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , 2000 , 16, 1145-50	7.2	217
1	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> , 1994 , 150, 111-6	3.8	42