

Alexander A Kanapin

List of Publications by Year in descending order

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59
papers

15,537
citations

126708

33
h-index

143772

57
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63
all docs

63
docs citations

63
times ranked

23973
citing authors

#	ARTICLE	IF	CITATIONS
1	An account of Fusarium wilt resistance in flax <i>Linum usitatissimum</i> : The disease severity data. <i>Data in Brief</i> , 2022, 41, 107869.	0.5	2
2	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
3	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
4	A comprehensive dataset of flax (<i>Linum usitatissimum</i> L.) phenotypes. <i>Data in Brief</i> , 2021, 37, 107224.	0.5	5
5	Stochastic Effects in Retrotransposon Dynamics Revealed by Modeling under Competition for Cellular Resources. <i>Life</i> , 2021, 11, 1209.	1.1	2
6	The Genetic Landscape of Fiber Flax. <i>Frontiers in Plant Science</i> , 2021, 12, 764612.	1.7	11
7	Current challenges and possible future developments in personalized psychiatry with an emphasis on psychotic disorders. <i>Heliyon</i> , 2020, 6, e03990.	1.4	15
8	PRMT5 promotes cancer cell migration and invasion through the E2F pathway. <i>Cell Death and Disease</i> , 2020, 11, 572.	2.7	20
9	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
10	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
11	Arginine methylation expands the regulatory mechanisms and extends the genomic landscape under E2F control. <i>Science Advances</i> , 2019, 5, eaaw4640.	4.7	19
12	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
13	RASSF1A uncouples Wnt from Hippo signalling and promotes YAP mediated differentiation via p73. <i>Nature Communications</i> , 2018, 9, 424.	5.8	72
14	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. <i>Mucosal Immunology</i> , 2018, 11, 562-574.	2.7	71
15	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
16	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
17	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
18	Interplay between RNA interference and heat shock response systems in <i>Drosophila melanogaster</i> . <i>Open Biology</i> , 2016, 6, 160224.	1.5	9

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19	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. <i>Nature Genetics</i> , 2015, 47, 717-726.	9.4	310
20	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
21	Unfixed Endogenous Retroviral Insertions in the Human Population. <i>Journal of Virology</i> , 2014, 88, 9529-9537.	1.5	118
22	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014, 6, 26.	3.6	158
23	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
24	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
25	Erythrocytosis associated with a novel missense mutation in the BPGM gene. <i>Haematologica</i> , 2014, 99, e201-e204.	1.7	35
26	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
27	Neanderthal and Denisovan retroviruses in modern humans. <i>Current Biology</i> , 2013, 23, R994-R995.	1.8	17
28	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
29	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
30	Aberration Of SF3B1 Results In Deregulated Splicing Of Key Genes and Pathways In Myelodysplastic Syndromes. <i>Blood</i> , 2013, 122, 2747-2747.	0.6	0
31	Recessive Mutations in SPTBN2 Implicate Î²-III Spectrin in Both Cognitive and Motor Development. <i>PLoS Genetics</i> , 2012, 8, e1003074.	1.5	94
32	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
33	Reactome - a knowledgebase of human biological pathways. <i>Nature Precedings</i> , 2009, , .	0.1	0
34	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009, 37, D619-D622.	6.5	760
35	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	6.5	444
36	InterPro as a new tool for complete genome analysis: An example of comparative analysis. <i>Biophysics (Russian Federation)</i> , 2006, 51, 587-591.	0.2	0

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37	Proteome Complexity Measures Based on Counting of Domain-to-Protein Links for Replicative and Non-Replicative Domains. , 2006, , 329-341.		9
38	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	6.0	3,227
39	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. Nucleic Acids Research, 2004, 33, D297-D302.	6.5	125
40	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	6.5	478
41	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	2.6	290
42	Supervised Learning-Aided Optimization of Expert-Driven Functional Protein Sequence Annotation. Lecture Notes in Computer Science, 2004, , 159-169.	1.0	0
43	Systematic functional analysis of the Caenorhabditis elegans genome using RNAi. Nature, 2003, 421, 231-237.	13.7	3,343
44	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. Nucleic Acids Research, 2003, 31, 414-417.	6.5	64
45	Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. Genome Research, 2003, 13, 1542-1551.	2.4	34
46	Mouse Proteome Analysis. Genome Research, 2003, 13, 1335-1344.	2.4	91
47	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	6.5	640
48	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	3.2	155
49	Interactive InterPro-based comparisons of proteins in whole genomes. Bioinformatics, 2002, 18, 374-375.	1.8	14
50	Applications of InterPro in protein annotation and genome analysis. Briefings in Bioinformatics, 2002, 3, 285-295.	3.2	54
51	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	13.7	1,548
52	Antisense oligodeoxyribonucleotides for fragments of the reverse transcriptase gene of the LINE-1 element of rats disturb the formation of long-term memory. Doklady Biochemistry and Biophysics, 2002, 383, 93-95.	0.3	2
53	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. Nucleic Acids Research, 2001, 29, 37-40.	6.5	928
54	Application of InterPro for the functional classification of the proteins of fish origin in SWISS-PROT and TrEMBL. Journal of Biosciences, 2001, 26, 277-284.	0.5	5

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55	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
56	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
57	InterPro--an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , 2000, 16, 1145-1150.	1.8	301
58	The pss4 gene from <i>Rhizobium leguminosarum</i> bv <i>viciae</i> VF39: cloning, sequence and the possible role in polysaccharide production and nodule formation. <i>Gene</i> , 1994, 150, 111-116.	1.0	45
59	Regions Of 3D Similarity in Potential ORF1 Products of Mobile Genetics Classes. <i>Protein Engineering, Design and Selection</i> , 0, , .	1.0	0