

Alastair R W Kerr

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

5,461
citations

126907

33
h-index

175258

52
g-index

61
all docs

61
docs citations

61
times ranked

8327
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome Analysis in a Primary Human Muscle Cell Differentiation Model for Myotonic Dystrophy Type 1. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8607.	4.1	9
2	Soluble guanylate cyclase signalling mediates etoposide resistance in progressing small cell lung cancer. <i>Nature Communications</i> , 2021, 12, 6652.	12.8	14
3	TIAM1-RAC1 promote small-cell lung cancer cell survival through antagonizing Nur77-induced BCL2 conformational change. <i>Cell Reports</i> , 2021, 37, 109979.	6.4	13
4	A multistage sequencing strategy pinpoints novel candidate alleles for Emery-Dreifuss muscular dystrophy and supports gene misregulation as its pathomechanism. <i>EBioMedicine</i> , 2020, 51, 102587.	6.1	40
5	The Rare YAP1 Subtype of SCLC Revisited in a Biobank of 39 Circulating Tumor Cell Patient Derived Explant Models: A Brief Report. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1836-1843.	1.1	45
6	Convergent genes shape budding yeast pericentromeres. <i>Nature</i> , 2020, 582, 119-123.	27.8	50
7	A biobank of small cell lung cancer CDX models elucidates inter- and intratumoral phenotypic heterogeneity. <i>Nature Cancer</i> , 2020, 1, 437-451.	13.2	103
8	A model of k-mer surprisal to quantify local sequence information content surrounding splice regions. <i>PeerJ</i> , 2020, 8, e10063.	2.0	1
9	Telomere elongation through hTERT immortalization leads to chromosome repositioning in control cells and genomic instability in Hutchinsonâ€™Gilford progeria syndrome fibroblasts, expressing a novel SUN1 isoform. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 341-356.	2.8	27
10	A rapid computational approach identifies SPICE1 as an Aurora kinase substrate. <i>Molecular Biology of the Cell</i> , 2019, 30, 312-323.	2.1	8
11	Toxicity of overexpressed MeCP2 is independent of HDAC3 activity. <i>Genes and Development</i> , 2018, 32, 1514-1524.	5.9	23
12	PuLSE: Quality control and quantification of peptide sequences explored by phage display libraries. <i>PLoS ONE</i> , 2018, 13, e0193332.	2.5	6
13	Analysis of RNA-Seq datasets reveals enrichment of tissue-specific splice variants for nuclear envelope proteins. <i>Nucleus</i> , 2018, 9, 410-430.	2.2	10
14	Constrained release of lamina-associated enhancers and genes from the nuclear envelope during T-cell activation facilitates their association in chromosome compartments. <i>Genome Research</i> , 2017, 27, 1126-1138.	5.5	97
15	Tissue-specific NETs alter genome organization and regulation even in a heterologous system. <i>Nucleus</i> , 2017, 8, 81-97.	2.2	35
16	Lin28a uses distinct mechanisms of binding to RNA and affects miRNA levels positively and negatively. <i>Rna</i> , 2017, 23, 317-332.	3.5	36
17	The SNF2 family ATPase LSH promotes cell-autonomous de novo DNA methylation in somatic cells. <i>Nucleic Acids Research</i> , 2016, 44, 7592-7604.	14.5	24
18	Loss of Tet1-Associated 5-Hydroxymethylcytosine Is Concomitant with Aberrant Promoter Hypermethylation in Liver Cancer. <i>Cancer Research</i> , 2016, 76, 3097-3108.	0.9	71

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19	The molecular basis of variable phenotypic severity among common missense mutations causing Rett syndrome. <i>Human Molecular Genetics</i> , 2016, 25, 558-570.	2.9	76
20	Tissue-Specific Gene Repositioning by Muscle Nuclear Membrane Proteins Enhances Repression of Critical Developmental Genes during Myogenesis. <i>Molecular Cell</i> , 2016, 62, 834-847.	9.7	165
21	Inter-individual variability contrasts with regional homogeneity in the human brain DNA methylome. <i>Nucleic Acids Research</i> , 2015, 43, 732-744.	14.5	42
22	TD-60 links RalA GTPase function to the CPC in mitosis. <i>Nature Communications</i> , 2015, 6, 7678.	12.8	43
23	Lipids contribute to epigenetic control via chromatin structure and functions. <i>ScienceOpen Research</i> , 2015, .	0.6	4
24	Lipids contribute to epigenetic control via chromatin structure and functions. <i>ScienceOpen Research</i> , 2015, .	0.6	1
25	Structural evidence for Scc4-dependent localization of cohesin loading. <i>ELife</i> , 2015, 4, e06057.	6.0	69
26	The kinetochore prevents centromere-proximal crossover recombination during meiosis. <i>ELife</i> , 2015, 4, .	6.0	108
27	Genome-Wide Distribution of RNA-DNA Hybrids Identifies RNase H Targets in tRNA Genes, Retrotransposons and Mitochondria. <i>PLoS Genetics</i> , 2014, 10, e1004716.	3.5	179
28	Shugoshin biases chromosomes for biorientation through condensin recruitment to the pericentromere. <i>ELife</i> , 2014, 3, e01374.	6.0	74
29	Identical sets of methylated and nonmethylated genes in <i>Ciona intestinalis</i> sperm and muscle cells. <i>Epigenetics and Chromatin</i> , 2013, 6, 38.	3.9	29
30	Tissue specificity in the nuclear envelope supports its functional complexity. <i>Nucleus</i> , 2013, 4, 460-477.	2.2	77
31	The nuclear envelope proteome differs notably between tissues. <i>Nucleus</i> , 2012, 3, 552-564.	2.2	177
32	Co-transcriptional degradation of aberrant pre-mRNA by Xrn2. <i>EMBO Journal</i> , 2012, 31, 2566-2578.	7.8	81
33	Mitotic chromosomes are compacted laterally by KIF4 and condensin and axially by topoisomerase II β . <i>Journal of Cell Biology</i> , 2012, 199, 755-770.	5.2	155
34	Cfp1 integrates both CpG content and gene activity for accurate H3K4me3 deposition in embryonic stem cells. <i>Genes and Development</i> , 2012, 26, 1714-1728.	5.9	253
35	Many mechanisms, one entrance: membrane protein translocation into the nucleus. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2205-2216.	5.4	46
36	Cell type-specific DNA methylation at intragenic CpG islands in the immune system. <i>Genome Research</i> , 2011, 21, 1074-1086.	5.5	256

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37	System analysis shows distinct mechanisms and common principles of nuclear envelope protein dynamics. <i>Journal of Cell Biology</i> , 2011, 193, 109-123.	5.2	97
38	FG repeats facilitate integral protein trafficking to the inner nuclear membrane. <i>Communicative and Integrative Biology</i> , 2011, 4, 557-559.	1.4	8
39	Several Novel Nuclear Envelope Transmembrane Proteins Identified in Skeletal Muscle Have Cytoskeletal Associations. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003129.	3.8	118
40	FG repeats facilitate integral protein trafficking to the inner nuclear membrane. <i>Communicative and Integrative Biology</i> , 2011, 4, 557-9.	1.4	6
41	The Leukocyte Nuclear Envelope Proteome Varies with Cell Activation and Contains Novel Transmembrane Proteins That Affect Genome Architecture. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2571-2585.	3.8	120
42	Hairpin RNA induces secondary small interfering RNA synthesis and silencing in <i>S. pombe</i> in fission yeast. <i>EMBO Reports</i> , 2010, 11, 112-118.	4.5	64
43	CpG islands influence chromatin structure via the CpG-binding protein Cfp1. <i>Nature</i> , 2010, 464, 1082-1086.	27.8	577
44	Orphan CpG Islands Identify Numerous Conserved Promoters in the Mammalian Genome. <i>PLoS Genetics</i> , 2010, 6, e1001134.	3.5	445
45	Neuronal MeCP2 Is Expressed at Near Histone-Octamer Levels and Globally Alters the Chromatin State. <i>Molecular Cell</i> , 2010, 37, 457-468.	9.7	609
46	H3 K36 Methylation Helps Determine the Timing of Cdc45 Association with Replication Origins. <i>PLoS ONE</i> , 2009, 4, e5882.	2.5	51
47	Comparative proteomic analyses of the nuclear envelope and pore complex suggests a wide range of heretofore unexpected functions. <i>Journal of Proteomics</i> , 2009, 72, 56-70.	2.4	24
48	Evolution by leaps: gene duplication in bacteria. <i>Biology Direct</i> , 2009, 4, 46.	4.6	58
49	A Novel CpG Island Set Identifies Tissue-Specific Methylation at Developmental Gene Loci. <i>PLoS Biology</i> , 2008, 6, e22.	5.6	533
50	A promoter-hijack strategy for conditional shutdown of multiply spliced essential cell cycle genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2457-2462.	7.1	22
51	Bioinformatics for Geneticists: A Bioinformatics Primer for the Analysis of Genetic Data. 2nd Edn. Ed. M.ÂR. Barnes. Wiley. 2007. 528 pages. ISBN 978-0-470-02620-5. Price Â£45. (paperback). <i>Genetical Research</i> , 2007, 89, 123-124.	0.9	1
52	CpG methylation is targeted to transcription units in an invertebrate genome. <i>Genome Research</i> , 2007, 17, 625-631.	5.5	217
53	Systematic base composition variation around the genome of <i>Mycoplasma genitalium</i> , but not <i>Mycoplasma pneumoniae</i> . <i>Molecular Microbiology</i> , 1997, 25, 1177-1179.	2.5	51