Colin A M Semple

List of Publications by Year
in descending order

90	16,264	71102 41	48315 88
papers	citations	h-index	g-index

103	103	103	25180
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multiomic Characterization of High-Grade Serous Ovarian Carcinoma Enables High-Resolution Patient Stratification. Clinical Cancer Research, 2022, 28, 3546-3556.	7.0	5
2	Functional brain defects in a mouse model of a chromosomal t(1;11) translocation that disrupts DISC1 and confers increased risk of psychiatric illness. Translational Psychiatry, 2021, 11, 135.	4.8	3
3	Structural Variants at theBRCA1/2Loci are a Common Source of Homologous Repair Deficiency in High-grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2021, 27, 3201-3214.	7.0	27
4	Integrated molecular characterisation of endometrioid ovarian carcinoma identifies opportunities for stratification. Npj Precision Oncology, 2021, 5, 47.	5.4	10
5	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. Genome Research, 2021, 31, 1994-2007.	5.5	4
6	ISGylation drives basal breast tumour progression by promoting EGFR recycling and Akt signalling. Oncogene, 2021, 40, 6235-6247.	5.9	16
7	Gene Co-Expression Network Analysis Identifies Vitamin D-Associated Gene Modules in Adult Normal Rectal Epithelium Following Supplementation. Frontiers in Genetics, 2021, 12, 783970.	2.3	3
8	Molecular stratification of endometrioid ovarian carcinoma predicts clinical outcome. Nature Communications, 2020, 11, 4995.	12.8	70
9	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
10	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	27.8	36
11	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. Scientific Reports, 2019, 9, 10964.	3.3	17
12	Clinical and molecular characterization of ovarian carcinoma displaying isolated lymph node relapse. American Journal of Obstetrics and Gynecology, 2019, 221, 245.e1-245.e15.	1.3	22
13	Zebrafish MITF-Low Melanoma Subtype Models Reveal Transcriptional Subclusters and MITF-Independent Residual Disease. Cancer Research, 2019, 79, 5769-5784.	0.9	36
14	Modeling double strand break susceptibility to interrogate structural variation in cancer. Genome Biology, 2019, 20, 28.	8.8	11
15	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	3.5	17
16	Abstract 749: Multi-layer molecular characterization of high grade serous ovarian carcinomas. Cancer Research, 2019, 79, 749-749.	0.9	1
17	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. Open Biology, 2018, 8, 180011.	3.6	13
18	DISC1 regulates N-methyl-D-aspartate receptor dynamics: abnormalities induced by a Disc1 mutation modelling a translocation linked to major mental illness. Translational Psychiatry, 2018, 8, 184.	4.8	21

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19	Chromatin loop anchors are associated with genome instability in cancer and recombination hotspots in the germline. Genome Biology, 2018, 19, 101.	8.8	43
20	Enhanced response rate to pegylated liposomal doxorubicin in high grade serous ovarian carcinomas harbouring BRCA1 and BRCA2 aberrations. BMC Cancer, 2018, 18, 16.	2.6	13
21	Breaking point: the genesis and impact of structural variation in tumours. F1000Research, 2018, 7, 1814.	1.6	7
22	The circadian dynamics of small nucleolar RNA in the mouse liver. Journal of the Royal Society Interface, 2017, 14, 20170034.	3.4	13
23	Crossing Borders. , 2017, , 45-67.		0
24	When TADs go bad: chromatin structure and nuclear organisation in human disease. F1000Research, 2017, 6, 314.	1.6	52
25	Mutational Biases Drive Elevated Rates of Substitution at Regulatory Sites across Cancer Types. PLoS Genetics, 2016, 12, e1006207.	3.5	75
26	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changesÂin cellular differentiation. Molecular Systems Biology, 2015, 11, 852.	7.2	305
27	Integrative modeling reveals the principles of multi-scale chromatin boundary formation in human nuclear organization. Genome Biology, 2015, 16, 110.	8.8	33
28	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	2.9	27
29	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. PLoS Computational Biology, 2015, 11, e1004217.	3.2	22
30	Abundant local interactions in the 4p16.1 region suggest functional mechanisms underlying SLC2A9 associations with human serum uric acid. Human Molecular Genetics, 2014, 23, 5061-5068.	2.9	29
31	Sequence-Level Mechanisms of Human Epigenome Evolution. Genome Biology and Evolution, 2014, 6, 1758-1771.	2.5	17
32	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
33	The genomic signature of trait-associated variants. BMC Genomics, 2013, 14, 108.	2.8	45
34	Divergence of Mammalian Higher Order Chromatin Structure Is Associated with Developmental Loci. PLoS Computational Biology, 2013, 9, e1003017.	3.2	36
35	Side Effects: Substantial Non-Neutral Evolution Flanking Regulatory Sites. PLoS Genetics, 2013, 9, e1003528.	3.5	1
36	Corrigendum of 'High throughput analysis of epistasis in genome-wide association studies with BiForce'. Bioinformatics, 2013, 29, 2667-2668.	4.1	0

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37	Lsh regulates LTR retrotransposon repression independently of Dnmt3b function. Genome Biology, 2013, 14, R146.	9.6	54
38	Properties of Local Interactions and Their Potential Value in Complementing Genome-Wide Association Studies. PLoS ONE, 2013, 8, e71203.	2.5	15
39	High-throughput analysis of epistasis in genome-wide association studies with BiForce. Bioinformatics, 2012, 28, 1957-1964.	4.1	49
40	BiForce Toolbox: powerful high-throughput computational analysis of gene-gene interactions in genome-wide association studies. Nucleic Acids Research, 2012, 40, W628-W632.	14.5	25
41	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
42	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. Epigenetics and Chromatin, 2012, 5, 6.	3.9	20
43	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E944-53.	7.1	332
44	Genome-wide methylation profiling in CrohnÊ¼s disease identifies altered epigenetic regulation of key host defense mechanisms including the Th17 pathway. Inflammatory Bowel Diseases, 2012, 18, 889-899.	1.9	152
45	The retroviral proteinase active site and the N-terminus of Ddi1 are required for repression of protein secretion. FEBS Letters, 2011, 585, 139-142.	2.8	26
46	Human Î²â€defensin 3 affects the activity of proâ€inflammatory pathways associated with MyD88 and TRIF. European Journal of Immunology, 2011, 41, 3291-3300.	2.9	122
47	Widespread signatures of recent selection linked to nucleosome positioning in the human lineage. Genome Research, 2011, 21, 1777-1787.	5.5	65
48	A High-Resolution Anatomical Atlas of the Transcriptome in the Mouse Embryo. PLoS Biology, 2011, 9, e1000582.	5.6	552
49	Thioredoxin Txnl1/TRP32 Is a Redox-active Cofactor of the 26 S Proteasome. Journal of Biological Chemistry, 2009, 284, 15246-15254.	3.4	68
50	The Structure of Change. Science, 2009, 323, 347-348.	12.6	7
51	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
52	New ATPase regulatorsâ€”p97 goes to the PUB. International Journal of Biochemistry and Cell Biology, 2009, 41, 2380-2388.	2.8	67
53	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	21.4	542
54	Rapidly evolving human promoter regions. Nature Genetics, 2008, 40, 1262-1263.	21.4	18

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55	Posttranscriptional Regulation of miRNAs Harboring Conserved Terminal Loops. Molecular Cell, 2008, 32, 383-393.	9.7	316
56	Ubxd1 is a novel co-factor of the human p97 ATPase. International Journal of Biochemistry and Cell Biology, 2008, 40, 2927-2942.	2.8	42
57	Chromatin structure and evolution in the human genome. BMC Evolutionary Biology, 2007, 7, 72.	3.2	80
58	Characterisation of the nascent polypeptide-associated complex in fission yeast. Molecular Biology Reports, 2007, 34, 275-281.	2.3	16
59	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	21.4	1,201
60	Mutations in genes encoding ribonuclease H2 subunits cause Aicardi-GoutiÃ¨res syndrome and mimic congenital viral brain infection. Nature Genetics, 2006, 38, 910-916.	21.4	592
61	The changing of the guard: Molecular diversity and rapid evolution of Î²-defensins. Molecular Diversity, 2006, 10, 575-584.	3.9	75
62	Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. Nucleic Acids Research, 2006, 34, 3067-3081.	14.5	134
63	Disruption of Ledgf/Psip1 Results in Perinatal Mortality and HomeoticSkeletal Transformations. Molecular and Cellular Biology, 2006, 26, 7201-7210.	2.3	96
64	Heterotachy in Mammalian Promoter Evolution. PLoS Genetics, 2006, 2, e30.	3.5	102
65	Mouse MAELSTROM: the link between meiotic silencing of unsynapsed chromatin and microRNA pathway?. Human Molecular Genetics, 2006, 15, 2324-2334.	2.9	131
66	The complexity of selection at the major primate beta-defensin locus. BMC Evolutionary Biology, 2005, 5, 32.	3.2	38
67	Dazl binds in vivo to specific transcripts and can regulate the pre-meiotic translation of Mvh in germ cells. Human Molecular Genetics, 2005, 14, 3899-3909.	2.9	158
68	Two novel proteins recruited by synaptonemal complex protein 1 (SYCP1) are at the centre of meiosis. Journal of Cell Science, 2005, 118, 2755-2762.	2.0	190
69	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
70	Deep genomics in shallow times: the finished sequence of human chromosomes 13 and 19. European Journal of Human Genetics, 2004, 12, 875-876.	2.8	6
71	UBA domain containing proteins in fission yeast. International Journal of Biochemistry and Cell Biology, 2003, 35, 629-636.	2.8	30
72	POCUS: mining genomic sequence annotation to predict disease genes. Genome Biology, 2003, 4, R75.	9.6	199

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73	Duplication and selection in the evolution of primate beta-defensin genes. Genome Biology, 2003, 4, R31.	9.6	134
74	The Comparative Proteomics of Ubiquitination in Mouse. Genome Research, 2003, 13, 1389-1394.	5.5	122
75	Signal Sequence Conservation and Mature Peptide Divergence Within Subgroups of the Murine beta-Defensin Gene Family. Molecular Biology and Evolution, 2003, 20, 460-470.	8.9	81
76	SNP genotyping on pooled DNAs: comparison of genotyping technologies and a semi automated method for data storage and analysis. Nucleic Acids Research, 2002, 30, 74e-74.	14.5	114
77	Computational Comparison of Human Genomic Sequence Assemblies for a Region of Chromosome 4. Genome Research, 2002, 12, 424-429.	5.5	12
78	Sushi gets serious: the draft genome sequence of the pufferfish Fugu rubripes. Genome Biology, 2002, 3, reviews1025.1.	9.6	1
79	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548
80	A 6.9-Mb High-Resolution BAC/PAC Contig of Human 4p15.3â€“p16.1, a Candidate Region for Bipolar Affective Disorder. Genomics, 2001, 71, 315-323.	2.9	12
81	Identification of Genes from a Schizophrenia-Linked Translocation Breakpoint Region. Genomics, 2001, 73, 123-126.	2.9	21
82	Identification of polymorphisms within Disrupted in Schizophrenia 1 and Disrupted in Schizophrenia 2, and an investigation of their association with schizophrenia and bipolar affective disorder. Psychiatric Genetics, 2001, 11, 71-78.	1.1	116
83	Proteins containing the UBA domain are able to bind to multi-ubiquitin chains. Nature Cell Biology, 2001, 3, 939-943.	10.3	375
84	Physical mapping: integrating computational and molecular genetic data. Annals of Human Genetics, 2001, 65, 221-228.	0.8	2
85	Comparing Human Genome Mapping Data. Science, 2001, 293, 2394b-2395.	12.6	1
86	Disruption of two novel genes by a translocation co-segregating with schizophrenia. Human Molecular Genetics, 2000, 9, 1415-1423.	2.9	1,135
87	Chromosomal Location and Genomic Structure of the Human Translin-Associated Factor X Gene (TRAX; TSNAX) Revealed by Intergenic Splicing to DISC1, a Gene Disrupted by a Translocation Segregating with Schizophrenia. Genomics, 2000, 67, 69-77.	2.9	106
88	Gene Duplication and Gene Conversion in the Caenorhabditis elegans Genome. Journal of Molecular Evolution, 1999, 48, 555-564.	1.8	127
89	Assembling a View of the Human Genome. , 0, , 93-117.		2
90	Assembling a View of the Human Genome. , 0, , 59-84.		0