John A L Armour

List of Publications by Year in descending order

100 papers	7,214 citations	70961 41 h-index	56606 83 g-index
101 all docs	101 docs citations	101 times ranked	6789 citing authors

#	Article	IF	Citations
1	Skin microbiome alters attractiveness to Anopheles mosquitoes. BMC Microbiology, 2022, 22, 98.	1.3	9
2	No Evidence for Association of BMI with Salivary Amylase Gene Copy Number in the UK 1958 Birth Cohort. Obesity, 2019, 27, 1533-1538.	1.5	13
3	Recurrent Rearrangements of Human Amylase Genes Create Multiple Independent CNV Series. Human Mutation, 2017, 38, 532-539.	1.1	29
4	Copy number variation of human AMY1 is a minor contributor to variation in salivary amylase expression and activity. Human Genomics, 2017, 11, 2.	1.4	35
5	Analysis of Multiallelic CNVs by Emulsion Haplotype Fusion PCR. Methods in Molecular Biology, 2017, 1492, 155-165.	0.4	1
6	Low Î±-defensin gene copy number increases the risk for IgA nephropathy and renal dysfunction. Science Translational Medicine, 2016, 8, 345ra88.	5.8	35
7	Selective sweep on human amylase genes postdates the split with Neanderthals. Scientific Reports, 2016, 6, 37198.	1.6	67
8	Heritability of Attractiveness to Mosquitoes. PLoS ONE, 2015, 10, e0122716.	1.1	46
9	Obesity, starch digestion and amylase: association between copy number variants at human salivary (AMY1) and pancreatic (AMY2) amylase genes. Human Molecular Genetics, 2015, 24, 3472-3480.	1.4	105
10	CCL3L1 copy number, CCR5genotype and susceptibility to tuberculosis. BMC Medical Genetics, 2014, 15, 5.	2.1	19
11	Genome-wide association study of handedness excludes simple genetic models. Heredity, 2014, 112, 221-225.	1.2	101
12	Inferring mechanisms of copy number change from haplotype structures at the human DEFA1A3 locus. BMC Genomics, 2014, 15, 614.	1.2	6
13	Accurate measurement of gene copy number for human alpha-defensin DEFA1A3. BMC Genomics, 2013, 14, 719.	1.2	22
14	Multilocus genetic models of handedness closely resemble singleâ€locus models in explaining family data and are compatible with genomeâ€wide association studies. Annals of the New York Academy of Sciences, 2013, 1288, 48-58.	1.8	129
15	Association of Î²-Defensin Copy Number and Psoriasis in Three Cohorts of European Origin. Journal of Investigative Dermatology, 2012, 132, 2407-2413.	0.3	50
16	Functional effects of CCL3L1 copy number. Genes and Immunity, 2012, 13, 374-379.	2.2	13
17	Association analysis of the CCL3L1 copy number locus by paralogue ratio test in Norwegian rheumatoid arthritis patients and healthy controls. Genes and Immunity, 2012, 13, 579-582.	2.2	10
18	Determination of haplotypes at structurally complex regions using emulsion haplotype fusion PCR. BMC Genomics, 2012, 13, 693.	1.2	4

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19	CCL3L1 copy number and susceptibility to malaria. Infection, Genetics and Evolution, 2012, 12, 1147-1154.	1.0	20
20	Accuracy and differential bias in copy number measurement of CCL3L1 in association studies with three auto-immune disorders. BMC Genomics, 2011, 12, 418.	1.2	35
21	Meta-Analysis Confirms the LCE3C_LCE3B Deletion as a Risk Factor for Psoriasis in Several Ethnic Groups and Finds Interaction with HLA-Cw6. Journal of Investigative Dermatology, 2011, 131, 1105-1109.	0.3	89
22	Measurement methods and accuracy in copy number variation: failure to replicate associations of beta-defensin copy number with Crohn's disease. Human Molecular Genetics, 2010, 19, 4930-4938.	1.4	81
23	Deletion of Late Cornified Envelope 3B and 3C Genes Is Not Associated with Atopic Dermatitis. Journal of Investigative Dermatology, 2010, 130, 2057-2061.	0.3	25
24	Replication of LCE3Câ€“LCE3B CNV as a Risk Factor for Psoriasis and Analysis of Interaction with Other Genetic Risk Factors. Journal of Investigative Dermatology, 2010, 130, 979-984.	0.3	61
25	Î±-Cardiac myosin heavy chain (MYH6) mutations affecting myofibril formation are associated with congenital heart defects. Human Molecular Genetics, 2010, 19, 4007-4016.	1.4	131
26	Screening for common copy-number variants in cancer genes. Cancer Genetics and Cytogenetics, 2010, 203, 316-323.	1.0	2
27	Evolution of haplotypes at CCL3L1/CCL4L1. Genome Biology, 2010, 11, .	3.8	1
28	Allelic recombination between distinct genomic locations generates copy number diversity in human Î²-defensins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 853-858.	3.3	55
29	Quadruplex MAPH: improvement of throughput in high-resolution copy number screening. BMC Genomics, 2009, 10, 453.	1.2	3
30	Human Genetics: Measuring the Raw Material of Evolution. Current Biology, 2009, 19, R736-R738.	1.8	0
31	Constitutional trisomy 8 and BehÃ§et syndrome. American Journal of Medical Genetics, Part A, 2009, 149A, 982-986.	0.7	26
32	Sharp focus on the variable genome. Nature, 2009, 461, 735-736.	13.7	3
33	Deletion of the late cornified envelope LCE3B and LCE3C genes as a susceptibility factor for psoriasis. Nature Genetics, 2009, 41, 211-215.	9.4	482
34	Copy number variation and antigenic repertoire. Nature Genetics, 2009, 41, 1263-1264.	9.4	4
35	Experimental aspects of copy number variant assays at CCL3L1. Nature Medicine, 2009, 15, 1115-1117.	15.2	69
36	Multiplex Paralogue Ratio Tests for accurate measurement of multiallelic CNVs. Genomics, 2009, 93, 98-103.	1.3	43

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37	Genomic copy number variation, human health, and disease. Lancet, The, 2009, 374, 340-350.	6.3	172
38	Î²-Defensin-2 Protein Is a Serum Biomarker for Disease Activity in Psoriasis and Reaches Biologically Relevant Concentrations in Lesional Skin. PLoS ONE, 2009, 4, e4725.	1.1	151
39	Psoriasis is associated with increased Î²-defensin genomic copy number. Nature Genetics, 2008, 40, 23-25.	9.4	587
40	Directional and balancing selection in human beta-defensins. BMC Evolutionary Biology, 2008, 8, 113.	3.2	58
41	Defensins and the dynamic genome: What we can learn from structural variation at human chromosome band 8p23.1. Genome Research, 2008, 18, 1686-1697.	2.4	79
42	Accurate, high-throughput typing of copy number variation using paralogue ratios from dispersed repeats. Nucleic Acids Research, 2007, 35, e19-e19.	6.5	128
43	Evolutionary Conservation of a Coding Function for D4Z4, the Tandem DNA Repeat Mutated in Facioscapulohumeral Muscular Dystrophy. American Journal of Human Genetics, 2007, 81, 264-279.	2.6	142
44	Golli-MBP Copy Number Analysis by FISH, QMPSF and MAPH in 195 Patients with Hypomyelinating Leukodystrophies. Annals of Human Genetics, 2006, 70, 66-77.	0.3	16
45	PLP1 and GPM6B intragenic copy number analysis by MAPH in 262 patients with hypomyelinating leukodystrophies: identification of one partial triplication and two partial deletions of PLP1. Neurogenetics, 2006, 7, 31-37.	0.7	21
46	Tandemly repeated DNA: Why should anyone care?. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2006, 598, 6-14.	0.4	32
47	Microarray MAPH: accurate array-based detection of relative copy number in genomic DNA. BMC Genomics, 2006, 7, 163.	1.2	11
48	Duplications and copy number variants of 8p23.1 are cytogenetically indistinguishable but distinct at the molecular level. European Journal of Human Genetics, 2005, 13, 1131-1136.	1.4	46
49	High-resolution analysis of 16q22.1 in breast carcinoma using DNA amplifiable probes (multiplex) Tj ETQq1 1 0.784314 rgBT /Overloc Cancer, 2005, 114, 720-729.	2.3	22
50	Screening for exonic copy number mutations at MSH2 and MLH1 by MAPH. Familial Cancer, 2005, 4, 145-149.	0.9	10
51	Beta-defensin genomic copy number is not a modifier locus for cystic fibrosis. Journal of Negative Results in BioMedicine, 2005, 4, 9.	1.4	29
52	Copy number polymorphism and expression level variation of the human Î±-defensin genes DEFA1 and DEFA3. Human Molecular Genetics, 2005, 14, 2045-2052.	1.4	174
53	A 4q35.2 subtelomeric deletion identified in a screen of patients with co-morbid psychiatric illness and mental retardation. BMC Medical Genetics, 2004, 5, 21.	2.1	35
54	Compound haplotypes at Xp11.23 and human population growth in Eurasia. Annals of Human Genetics, 2004, 68, 428-437.	0.3	6

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55	Gene Dosage Analysis by Multiplex Amplifiable Probe Hybridization. , 2004, 92, 125-140.		3
56	No evidence for DNA copy number change associated with the DUP25 cytogenetic phenotype. European Journal of Human Genetics, 2003, 11, 911-912.	1.4	6
57	Extensive Normal Copy Number Variation of a Î²-Defensin Antimicrobial-Gene Cluster. American Journal of Human Genetics, 2003, 73, 591-600.	2.6	315
58	Evolution and population genetics of the H-ras minisatellite and cancer predisposition. Human Molecular Genetics, 2003, 12, 891-900.	1.4	14
59	DNA copy number analysis by MAPH: molecular diagnostic applications. Expert Review of Molecular Diagnostics, 2002, 2, 370-378.	1.5	23
60	The detection of large deletions or duplications in genomic DNA. Human Mutation, 2002, 20, 325-337.	1.1	110
61	Screening for subtelomeric chromosome abnormalities in children with idiopathic mental retardation using multiprobe telomeric FISH and the new MAPH telomeric assay. European Journal of Human Genetics, 2001, 9, 527-532.	1.4	67
62	A New Triplex STR System Without Irregular Alleles by Silver Staining and Its Potential Application to Forensic Analysis. Journal of Forensic Sciences, 2001, 46, 448-452.	0.9	1
63	Measurement of locus copy number by hybridisation with amplifiable probes. Nucleic Acids Research, 2000, 28, 605-609.	6.5	178
64	Integrated analysis of sequence evolution and population history using hypervariable compound haplotypes. Human Molecular Genetics, 2000, 9, 2675-2681.	1.4	14
65	Recombination and Human Diversity. Stadler Genetics Symposia Series, 2000, , 81-89.	0.0	0
66	Evaluation of two new STR loci 9q2h2 and wg3f12 in a Japanese population. Legal Medicine, 1999, 1, 25-28.	0.6	4
67	Tetrameric short tandem repeat (STR) system D15S233 (wg1d1): sequencing and frequency data in the japanese and Chinese populations. Legal Medicine, 1999, 1, 119-126.	0.6	4
68	Sequence analysis of alleles at a microsatellite locus D14S299 (wg1c5) and population genetic comparisons. International Journal of Legal Medicine, 1999, 113, 15-18.	1.2	8
69	Direct analysis by small-pool PCR of MS205 minisatellite mutation rates in sperm after mutagenic therapies. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 1999, 445, 73-80.	0.9	28
70	Cis-regulation of inter-allelic exchanges in mutation at human minisatellite MS205 in yeast. Gene, 1999, 232, 143-153.	1.0	12
71	MS205 Minisatellite Diversity in Basques: Evidence for a Pre-Neolithic Component. Genome Research, 1998, 8, 1289-1298.	2.4	21
72	Distribution of tandem repeat polymorphism within minisatellite MS621 (D5S110). Annals of Human Genetics, 1996, 60, 11-20.	0.3	18

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73	Thyroid peroxidase: evidence for disease gene exclusion in Pendred's syndrome. Clinical Endocrinology, 1996, 44, 441-446.	1.2	13
74	Evaluation of tetranucleotide repeat locus D7S809 (wg1g9) in the Japanese population. Forensic Science International, 1996, 81, 133-140.	1.3	9
75	Pendred syndrome (goitre and sensorineural hearing loss) maps to chromosome 7 in the region containing the nonsyndromic deafness gene DFNB4. Nature Genetics, 1996, 12, 421-423.	9.4	146
76	Minisatellite diversity supports a recent African origin for modern humans. Nature Genetics, 1996, 13, 154-160.	9.4	173
77	Mutation rate heterogeneity and the generation of allele diversity at the human minisatellite MS205 (D16S309). Human Molecular Genetics, 1996, 5, 1823-1833.	1.4	77
78	Mutation processes at human minisatellites. Electrophoresis, 1995, 16, 1577-1585.	1.3	62
79	Allelic imbalance on chromosome I in human breast cancer. I. Minisatellite and rflp analysis. Genes Chromosomes and Cancer, 1995, 12, 16-23.	1.5	31
80	Loss of heterozygosity on the X chromosome in human breast cancer. Genes Chromosomes and Cancer, 1995, 13, 229-238.	1.5	21
81	The tetranucleotide repeat polymorphism D21S1245 demonstrates hypermutability in germline and somatic cells. Human Molecular Genetics, 1995, 4, 1193-1199.	1.4	59
82	Complex gene conversion events in germline mutation at human minisatellites. Nature Genetics, 1994, 6, 136-145.	9.4	524
83	CEPH Consortium Map of Chromosome 9. Genomics, 1994, 19, 203-214.	1.3	24
84	Isolation of human simple repeat loci by hybridization selection. Human Molecular Genetics, 1994, 3, 599-605.	1.4	438
85	Abnormal Segregation of Alleles in CEPH Pedigree DNAs Arising from Allele Loss in Lymphoblastoid DNA. Genomics, 1993, 15, 119-122.	1.3	10
86	Allelic diversity at minisatellite MS205 (D16S309): evidence for polarized variability. Human Molecular Genetics, 1993, 2, 1137-1145.	1.4	98
87	Isolation of human minisatellite loci detected by synthetic tandem repeat probes: direct comparison with cloned DNA fingerprinting probes. Human Molecular Genetics, 1992, 1, 319-323.	1.4	10
88	The Frequency of Uniparental Disomy in Prader-Willi Syndrome. New England Journal of Medicine, 1992, 326, 1599-1607.	13.9	257
89	A hypervariable locus D16S309 located at the distal end of 16p. Nucleic Acids Research, 1992, 20, 1164-1164.	6.5	20
90	Human minisatellite alleles detectable only after PCR amplification. Genomics, 1992, 12, 116-124.	1.3	23

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91	Biology and applications of human minisatellite loci. Current Opinion in Genetics and Development, 1992, 2, 850-856.	1.5	64
92	Recent advances in minisatellite biology. FEBS Letters, 1992, 307, 113-115.	1.3	9
93	Uniparental paternal disomy in Angelman's syndrome. Lancet, The, 1991, 337, 694-697.	6.3	330
94	Hypervariable minisatellite DNA sequences in the Indian peafowl Pavo cristatus. Genomics, 1991, 9, 587-597.	1.3	58
95	STS for minisatellite MS607 (D22S163). Nucleic Acids Research, 1991, 19, 3158-3158.	6.5	6
96	33.6 (D1S111) and pMLAJ1 (D1S61) identify the same VNTR on chromosome 1. Nucleic Acids Research, 1991, 19, 4801-4801.	6.5	0
97	STS for minisatellite 33.1 (D9S49): direct typing by PCR. Nucleic Acids Research, 1991, 19, 4788-4788.	6.5	0
98	Systematic cloning of human minisatellites from ordered array charomid libraries. Genomics, 1990, 8, 501-512.	1.3	153
99	Sequences flanking the repeat arrays of human minlsatellites: association with tandem and dispersed repeat elements. Nucleic Acids Research, 1989, 17, 4925-4936.	6.5	117
100	Analysis of somatic mutations at human minisatellite loci in tumors and cell lines. Genomics, 1989, 4, 328-334.	1.3	113