Curt Scharfe

List of Publications by Year
in descending order

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32 papers	4,042 citations	361413 20 h-index	454955 30 g-index
35 all docs	35 docs citations	35 times ranked	5873 citing authors

#	Article	IF	Citations
1	A multipurpose panel of microhaplotypes for use with STR markers in casework. Forensic Science International: Genetics, 2022, 60, 102729.	3.1	6
2	Multi-frequency impedance sensing for detection and sizing of DNA fragments. Scientific Reports, 2021, 11, 6490.	3.3	17
3	Massively parallel discovery of human-specific substitutions that alter enhancer activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	67
4	The population genetics characteristics of a 90 locus panel of microhaplotypes. Human Genetics, 2021, 140, 1753-1773.	3.8	15
5	Reducing False-Positive Results in Newborn Screening Using Machine Learning. International Journal of Neonatal Screening, 2020, 6, 16.	3.2	33
6	Ethnic variability in newborn metabolic screening markers associated with falseâ€positive outcomes. Journal of Inherited Metabolic Disease, 2020, 43, 934-943.	3.6	23
7	Validation of novel forensic DNA markers using multiplex microhaplotype sequencing. Forensic Science International: Genetics, 2020, 47, 102275.	3.1	42
8	Timing of Newborn Blood Collection Alters Metabolic Disease Screening Performance. Frontiers in Pediatrics, 2020, 8, 623184.	1.9	14
9	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. Genetics in Medicine, 2019, 21, 896-903.	2.4	31
10	Elevated methylmalonic acidemia (MMA) screening markers in Hispanic and preterm newborns. Molecular Genetics and Metabolism, 2019, 126, 39-42.	1.1	6
11	Transplant Virus Detection Using Multiplex Targeted Sequencing. journal of applied laboratory medicine, The, 2018, 2, 757-769.	1.3	4
12	Next-Generation Molecular Testing of Newborn Dried Blood Spots for Cystic Fibrosis. Journal of Molecular Diagnostics, 2016, 18, 267-282.	2.8	26
13	Mitochondrial Disease Sequence Data Resource (MSeqDR): A global grass-roots consortium to facilitate deposition, curation, annotation, and integrated analysis of genomic data for the mitochondrial disease clinical and research communities. Molecular Genetics and Metabolism, 2015, 114, 388-396.	1.1	76
14	A Rapid, High-Quality, Cost-Effective, Comprehensive and Expandable Targeted Next-Generation Sequencing Assay for Inherited Heart Diseases. Circulation Research, 2015, 117, 603-611.	4.5	34
15	Multiplex target capture with double-stranded DNA probes. Genome Medicine, 2013, 5, 50.	8.2	18
16	Rare variant detection using family-based sequencing analysis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3985-3990.	7.1	54
17	Forward Chemical Genetics in Yeast for Discovery of Chemical Probes Targeting Metabolism. Molecules, 2012, 17, 13098-13115.	3.8	14
18	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. Nucleic Acids Research, 2011, 39, 44-58.	14.5	37

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19	High-quality DNA sequence capture of 524 disease candidate genes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6549-6554.	7.1	52
20	Mitochondrial DNA analysis by multiplex denaturing high-performance liquid chromatography and selective sequencing in pediatric patients with cardiomyopathy. Genetics in Medicine, 2009, 11, 118-126.	2.4	6
21	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. PLoS Computational Biology, 2009, 5, e1000374.	3.2	74
22	Proteome analysis of mitochondrial outer membrane fromNeurospora crassa. Proteomics, 2006, 6, 72-80.	2.2	74
23	The Role of Selection in the Evolution of Human Mitochondrial Genomes. Genetics, 2006, 172, 373-387.	2.9	395
24	Identifying new candidate genes for hereditary facial paresis on chromosome 3q21â€“q22 by RNA in situ hybridization in mouse. Genomics, 2005, 86, 55-67.	2.9	16
25	Integrative Analysis of the Mitochondrial Proteome in Yeast. PLoS Biology, 2004, 2, e160.	5.6	181
26	Role of duplicate genes in genetic robustness against null mutations. Nature, 2003, 421, 63-66.	27.8	790
27	Evolutionary Rate in the Protein Interaction Network. Science, 2002, 296, 750-752.	12.6	798
28	Systematic screen for human disease genes in yeast. Nature Genetics, 2002, 31, 400-404.	21.4	503
29	The complete form of X-linked congenital stationary night blindness is caused by mutations in a gene encoding a leucine-rich repeat protein. Nature Genetics, 2000, 26, 324-327.	21.4	231
30	Correction: The MITOP database â€“ a one-stop shop for mitochondrial information. Trends in Genetics, 1999, 15, 82.	6.7	0
31	The MITOP databaseâ€”a one-stop shop for mitochondrial information. Trends in Genetics, 1998, 14, 519.	6.7	0
32	Diabetes insipidus, diabetes mellitus, optic atrophy and deafness (DIDMOAD) caused by mutations in a novel gene (wolframin) coding for a predicted transmembrane protein. Human Molecular Genetics, 1998, 7, 2021-2028.	2.9	403