

Yvonne J Edwards

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

4,223
citations

201575

27
h-index

189801

50
g-index

58
all docs

58
docs citations

58
times ranked

7325
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Fugu rubripes</i> . <i>Science</i> , 2002, 297, 1301-1310.	6.0	1,432
2	Highly Conserved Non-Coding Sequences Are Associated with Vertebrate Development. <i>PLoS Biology</i> , 2004, 3, e7.	2.6	833
3	Whole-Exome Sequencing Links a Variant in <i>DHDDS</i> to Retinitis Pigmentosa. <i>American Journal of Human Genetics</i> , 2011, 88, 201-206.	2.6	155
4	Brown Fat <i>AKT2</i> Is a Cold-Induced Kinase that Stimulates ChREBP-Mediated De Novo Lipogenesis to Optimize Fuel Storage and Thermogenesis. <i>Cell Metabolism</i> , 2018, 27, 195-209.e6.	7.2	151
5	Whole-Exome Sequencing Efficiently Detects Rare Mutations in Autosomal Recessive Nonsyndromic Hearing Loss. <i>PLoS ONE</i> , 2012, 7, e50628.	1.1	143
6	Exome sequencing allows for rapid gene identification in a Charcot-Marie-Tooth family. <i>Annals of Neurology</i> , 2011, 69, 464-470.	2.8	107
7	Mutations in <i>OTOGL</i> , Encoding the Inner Ear Protein Otogelin-like, Cause Moderate Sensorineural Hearing Loss. <i>American Journal of Human Genetics</i> , 2012, 91, 872-882.	2.6	97
8	The mtDNA Mutation Spectrum of the Progeroid <i>Polg</i> Mutator Mouse Includes Abundant Control Region Multimers. <i>Cell Metabolism</i> , 2010, 12, 675-682.	7.2	86
9	Generation and Analysis of 25 Mb of Genomic DNA from the Pufferfish <i>Fugu rubripes</i> by Sequence Scanning. <i>Genome Research</i> , 1999, 9, 960-971.	2.4	81
10	The identification and characterization of microsatellites in the compact genome of the Japanese pufferfish, <i>Fugu rubripes</i> : perspectives in functional and comparative genomic analyses. <i>Journal of Molecular Biology</i> , 1998, 278, 843-854.	2.0	80
11	Identifying Consensus Disease Pathways in Parkinson's Disease Using an Integrative Systems Biology Approach. <i>PLoS ONE</i> , 2011, 6, e16917.	1.1	72
12	Comparison of Three Targeted Enrichment Strategies on the SOLiD Sequencing Platform. <i>PLoS ONE</i> , 2011, 6, e18595.	1.1	66
13	Insights into the regulation of intrinsically disordered proteins in the human proteome by analyzing sequence and gene expression data. <i>Genome Biology</i> , 2009, 10, R50.	13.9	65
14	Ligand-activated BMP signaling inhibits cell differentiation and death to promote melanoma. <i>Journal of Clinical Investigation</i> , 2017, 128, 294-308.	3.9	55
15	An alternative splicing program promotes adipose tissue thermogenesis. <i>ELife</i> , 2016, 5, .	2.8	55
16	Identification of the c3b binding site in a recombinant vWF-A domain of complement factor B by surface-enhanced laser desorption-ionisation affinity mass spectrometry and homology modelling: implications for the activity of factor B. <i>Journal of Molecular Biology</i> , 1999, 294, 587-599.	2.0	51
17	Recurrent and Private <i>MYO15A</i> Mutations Are Associated with Deafness in the Turkish Population. <i>Genetic Testing and Molecular Biomarkers</i> , 2010, 14, 543-550.	0.3	45
18	CRISPR-delivery particles targeting nuclear receptor-interacting protein 1 (<i>Nrip1</i>) in adipose cells to enhance energy expenditure. <i>Journal of Biological Chemistry</i> , 2018, 293, 17291-17305.	1.6	43

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19	Challenges in Whole Exome Sequencing: An Example from Hereditary Deafness. PLoS ONE, 2012, 7, e32000.	1.1	43
20	Fugu orthologues of human major histocompatibility complex genes: a genome survey. Immunogenetics, 2002, 54, 367-380.	1.2	42
21	Fugu ESTs: New Resources for Transcription Analysis and Genome Annotation. Genome Research, 2003, 13, 2747-2753.	2.4	41
22	Divergent evolution of the myosin heavy chain gene family in fish and tetrapods: evidence from comparative genomic analysis. Physiological Genomics, 2007, 32, 1-15.	1.0	40
23	Cholesterol-Independent SREBP-1 Maturation Is Linked to ARF1 Inactivation. Cell Reports, 2016, 16, 9-18.	2.9	40
24	Assessment of Protein Fold Predictions from Sequence Information: The Predicted $\hat{I}\pm/\hat{I}^2$ Doubly Wound Fold of the von Willebrand Factor Type A Domain is Similar to its Crystal Structure. Journal of Molecular Biology, 1996, 260, 277-285.	2.0	38
25	Glycosyltransferase ST6Gal-I promotes the epithelial to mesenchymal transition in pancreatic cancer cells. Journal of Biological Chemistry, 2021, 296, 100034.	1.6	35
26	Bioinformatics Methods to Predict Protein Structure and Function: A Practical Approach. Molecular Biotechnology, 2003, 23, 139-166.	1.3	34
27	The protein fold of the von Willebrand factor type A domain is predicted to be similar to the open twisted \hat{I}^2 -sheet flanked by $\hat{I}\pm$ -helices found in human ras-p21. FEBS Letters, 1995, 358, 283-286.	1.3	33
28	Gld2-catalyzed 3' monoadenylation of miRNAs in the hippocampus has no detectable effect on their stability or on animal behavior. Rna, 2016, 22, 1492-1499.	1.6	29
29	The cJUN NH2-terminal kinase (JNK) signaling pathway promotes genome stability and prevents tumor initiation. ELife, 2018, 7, .	2.8	28
30	Endothelial Mitogen-Activated Protein Kinase Kinase Kinase Kinase 4 Is Critical for Lymphatic Vascular Development and Function. Molecular and Cellular Biology, 2016, 36, 1740-1749.	1.1	21
31	Cultural Connection and Transformation: Substance Abuse Treatment at Friendship House. Journal of Psychoactive Drugs, 2003, 35, 53-58.	1.0	19
32	Activation of Inflammatory and Pro-Thrombotic Pathways in Acute Stress Cardiomyopathy. Frontiers in Cardiovascular Medicine, 2017, 4, 49.	1.1	18
33	Sequence scanning chicken cosmids: a methodology for genome screening. Gene, 1999, 227, 223-230.	1.0	12
34	AP1 genes in Fugu indicate a divergent transcriptional control to that of mammals. Mammalian Genome, 2003, 14, 514-525.	1.0	12
35	Oncogenic Pathways and Loss of the Rab11 GTPase Synergize To Alter Metabolism in Drosophila. Genetics, 2019, 212, 1227-1239.	1.2	12
36	A Meta-Analysis of Microarray Gene Expression in Mouse Stem Cells: Redefining Stemness. PLoS ONE, 2008, 3, e2712.	1.1	11

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37	The cJUN NH2-terminal kinase (JNK) pathway contributes to mouse mammary gland remodeling during involution. <i>Cell Death and Differentiation</i> , 2018, 25, 1702-1715.	5.0	11
38	Molecular characterisation of the SAND protein family: a study based on comparative genomics, structural bioinformatics and phylogeny. <i>Cellular and Molecular Biology Letters</i> , 2004, 9, 739-53.	2.7	11
39	Disruptor of telomeric silencing 1-like promotes ovarian cancer tumor growth by stimulating pro-tumorigenic metabolic pathways and blocking apoptosis. <i>Oncogenesis</i> , 2021, 10, 48.	2.1	10
40	Structural and functional modelling of von Willebrand factor type A domains in complement and coagulation. <i>Biochemical Society Transactions</i> , 1999, 27, 815-820.	1.6	9
41	Human transcription factors responsive to initial reprogramming predominantly undergo legitimate reprogramming during fibroblast conversion to iPSCs. <i>Scientific Reports</i> , 2020, 10, 19710.	1.6	9
42	Prediction of Protein Structure and Function by Using Bioinformatics. , 2001, 175, 341-375.		8
43	A Fugu-Human Genome Synteny Viewer: web software for graphical display and annotation reports of synteny between Fugu genomic sequence and human genes. <i>Nucleic Acids Research</i> , 2004, 32, 2618-2622.	6.5	8
44	SAND, a New Protein Family: From Nucleic Acid to Protein Structure and Function Prediction. <i>Comparative and Functional Genomics</i> , 2001, 2, 226-235.	2.0	6
45	Spt4 Promotes Pol I Processivity and Transcription Elongation. <i>Genes</i> , 2021, 12, 413.	1.0	6
46	Characterisation of conserved non-coding sequences in vertebrate genomes using bioinformatics, statistics and functional studies. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2006, 1, 46-58.	0.4	5
47	Defining the Influence of the A12.2 Subunit on Transcription Elongation and Termination by RNA Polymerase I In Vivo. <i>Genes</i> , 2021, 12, 1939.	1.0	5
48	Cutting Edge: Early Attrition of Memory T Cells during Inflammation and Costimulation Blockade Is Regulated Concurrently by Proapoptotic Proteins Fas and Bim. <i>Journal of Immunology</i> , 2019, 202, 647-651.	0.4	4
49	JAGN1, tetraspanins, and Erv proteins: is common topology indicative of common function in cargo sorting?. <i>American Journal of Physiology - Cell Physiology</i> , 2020, 319, C667-C674.	2.1	2
50	Theatre: a software tool for detailed comparative analysis and visualization of genomic sequence. <i>Nucleic Acids Research</i> , 2003, 31, 3510-3517.	6.5	1
51	The Effects of Local Environments on the Pattern of Amino-Acid Substitution in Homologous Protein Structures: the Role of Side-Chain to Main-Chain Van Der Waals Interactions. <i>Techniques in Protein Chemistry</i> , 1994, , 405-412.	0.3	1
52	STRUCTURE AND FUNCTION OF VWF-A DOMAINS IN COMPLEMENT AND COAGULATION. <i>Biochemical Society Transactions</i> , 1999, 27, A131-A131.	1.6	0
53	Finding Genes in Genomic Nucleotide Sequences by Using Bioinformatics. , 2001, 175, 235-247.		0