

Yvonne J Edwards

List of Publications by Year in descending order

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53
papers

4,223
citations

201674
27
h-index

189892
50
g-index

58
all docs

58
docs citations

58
times ranked

7325
citing authors

#	ARTICLE	IF	CITATIONS
1	Glycosyltransferase ST6Gal-I promotes the epithelial to mesenchymal transition in pancreatic cancer cells. <i>Journal of Biological Chemistry</i> , 2021, 296, 100034.	3.4	35
2	Spt4 Promotes Pol I Processivity and Transcription Elongation. <i>Genes</i> , 2021, 12, 413.	2.4	6
3	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.	4.9	10
4	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.	2.4	5
5	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.	4.6	2
6	Human transcription factors responsive to initial reprogramming predominantly undergo legitimate reprogramming during fibroblast conversion to iPSCs. <i>Scientific Reports</i> , 2020, 10, 19710.	3.3	9
7	Oncogenic Pathways and Loss of the Rab11 GTPase Synergize To Alter Metabolism in Drosophila. <i>Genetics</i> , 2019, 212, 1227-1239.	2.9	12
8	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.	0.8	4
9	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.	11.2	11
10	Brown Fat AKT2 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.	16.2	151
11	CRISPR-delivery particles targeting nuclear receptor-interacting protein 1 (Nrip1) in adipose cells to enhance energy expenditure. <i>Journal of Biological Chemistry</i> , 2018, 293, 17291-17305.	3.4	43
12	The cJUN NH2-terminal kinase (JNK) signaling pathway promotes genome stability and prevents tumor initiation. <i>ELife</i> , 2018, 7, .	6.0	28
13	Activation of Inflammatory and Pro-Thrombotic Pathways in Acute Stress Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 2017, 4, 49.	2.4	18
14	Ligand-activated BMP signaling inhibits cell differentiation and death to promote melanoma. <i>Journal of Clinical Investigation</i> , 2017, 128, 294-308.	8.2	55
15	Endothelial Mitogen-Activated Protein Kinase Kinase Kinase 4 Is Critical for Lymphatic Vascular Development and Function. <i>Molecular and Cellular Biology</i> , 2016, 36, 1740-1749.	2.3	21
16	Gld2-catalyzed 3' monoadenylation of miRNAs in the hippocampus has no detectable effect on their stability or on animal behavior. <i>Rna</i> , 2016, 22, 1492-1499.	3.5	29
17	Cholesterol-Independent SREBP-1 Maturation Is Linked to ARF1 Inactivation. <i>Cell Reports</i> , 2016, 16, 9-18.	6.4	40
18	An alternative splicing program promotes adipose tissue thermogenesis. <i>ELife</i> , 2016, 5, .	6.0	55

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19	Mutations in OTOGL , Encoding the Inner Ear Protein Otogelin-like, Cause Moderate Sensorineural Hearing Loss. American Journal of Human Genetics, 2012, 91, 872-882.	6.2	97
20	Whole-Exome Sequencing Efficiently Detects Rare Mutations in Autosomal Recessive Nonsyndromic Hearing Loss. PLoS ONE, 2012, 7, e50628.	2.5	143
21	Challenges in Whole Exome Sequencing: An Example from Hereditary Deafness. PLoS ONE, 2012, 7, e32000.	2.5	43
22	Identifying Consensus Disease Pathways in Parkinson's Disease Using an Integrative Systems Biology Approach. PLoS ONE, 2011, 6, e16917.	2.5	72
23	Comparison of Three Targeted Enrichment Strategies on the SOLiD Sequencing Platform. PLoS ONE, 2011, 6, e18595.	2.5	66
24	Whole-Exome Sequencing Links a Variant in DHDDS to Retinitis Pigmentosa. American Journal of Human Genetics, 2011, 88, 201-206.	6.2	155
25	Exome sequencing allows for rapid gene identification in a Charcotâ€Marieâ€Tooth family. Annals of Neurology, 2011, 69, 464-470.	5.3	107
26	Recurrent and Private <i>MYO15A</i> Mutations Are Associated with Deafness in the Turkish Population. Genetic Testing and Molecular Biomarkers, 2010, 14, 543-550.	0.7	45
27	The mtDNA Mutation Spectrum of the Progeroid Polg Mutator Mouse Includes Abundant Control Region Multimers. Cell Metabolism, 2010, 12, 675-682.	16.2	86
28	Insights into the regulation of intrinsically disordered proteins in the human proteome by analyzing sequence and gene expression data. Genome Biology, 2009, 10, R50.	9.6	65
29	A Meta-Analysis of Microarray Gene Expression in Mouse Stem Cells: Redefining Stemness. PLoS ONE, 2008, 3, e2712.	2.5	11
30	Divergent evolution of the myosin heavy chain gene family in fish and tetrapods: evidence from comparative genomic analysis. Physiological Genomics, 2007, 32, 1-15.	2.3	40
31	Characterisation of conserved non-coding sequences in vertebrate genomes using bioinformatics, statistics and functional studies. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2006, 1, 46-58.	1.0	5
32	A Fugu-Human Genome Synteny Viewer: web software for graphical display and annotation reports of synteny between Fugu genomic sequence and human genes. Nucleic Acids Research, 2004, 32, 2618-2622.	14.5	8
33	Highly Conserved Non-Coding Sequences Are Associated with Vertebrate Development. PLoS Biology, 2004, 3, e7.	5.6	833
34	Molecular characterisation of the SAND protein family: a study based on comparative genomics, structural bioinformatics and phylogeny. Cellular and Molecular Biology Letters, 2004, 9, 739-53.	7.0	11
35	Bioinformatics Methods to Predict Protein Structure and Function: A Practical Approach. Molecular Biotechnology, 2003, 23, 139-166.	2.4	34
36	AP1 genes in Fugu indicate a divergent transcriptional control to that of mammals. Mammalian Genome, 2003, 14, 514-525.	2.2	12

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37	Fugu ESTs: New Resources for Transcription Analysis and Genome Annotation. <i>Genome Research</i> , 2003, 13, 2747-2753.	5.5	41
38	Theatre: a software tool for detailed comparative analysis and visualization of genomic sequence. <i>Nucleic Acids Research</i> , 2003, 31, 3510-3517.	14.5	1
39	Cultural Connection and Transformation: Substance Abuse Treatment at Friendship House. <i>Journal of Psychoactive Drugs</i> , 2003, 35, 53-58.	1.7	19
40	Whole-Genome Shotgun Assembly and Analysis of the Genome of <i>Fugu rubripes</i> . <i>Science</i> , 2002, 297, 1301-1310.	12.6	1,432
41	Fugu orthologues of human major histocompatibility complex genes: a genome survey. <i>Immunogenetics</i> , 2002, 54, 367-380.	2.4	42
42	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
43	Prediction of Protein Structure and Function by Using Bioinformatics. , 2001, 175, 341-375.		8
44	Finding Genes in Genomic Nucleotide Sequences by Using Bioinformatics. , 2001, 175, 235-247.		0
45	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.	5.5	81
46	Sequence scanning chicken cosmid: a methodology for genome screening. <i>Gene</i> , 1999, 227, 223-230.	2.2	12
47	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.	4.2	51
48	Structural and functional modelling of von Willebrand factor type A domains in complement and coagulation. <i>Biochemical Society Transactions</i> , 1999, 27, 815-820.	3.4	9
49	STRUCTURE AND FUNCTION OF VWF-A DOMAINS IN COMPLEMENT AND COAGULATION. <i>Biochemical Society Transactions</i> , 1999, 27, A131-A131.	3.4	0
50	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.	4.2	80
51	Assessment of Protein Fold Predictions from Sequence Information: The Predicted $\hat{\alpha}/\hat{\beta}^2$ Doubly Wound Fold of the von Willebrand Factor Type A Domain is Similar to its Crystal Structure. <i>Journal of Molecular Biology</i> , 1996, 260, 277-285.	4.2	38
52	The protein fold of the von Willebrand factor type A domain is predicted to be similar to the open twisted β^2 -sheet flanked by α -helices found in human ras-p21. <i>FEBS Letters</i> , 1995, 358, 283-286.	2.8	33
53	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