

Frances M G Pearl

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,875
citations

304602

22
h-index

360920

35
g-index

41
all docs

41
docs citations

41
times ranked

4976
citing authors

#	ARTICLE	IF	CITATIONS
1	Therapeutic opportunities within the DNA damage response. <i>Nature Reviews Cancer</i> , 2015, 15, 166-180.	12.8	442
2	Conserved Regulation of Cardiac Calcium Uptake by Peptides Encoded in Small Open Reading Frames. <i>Science</i> , 2013, 341, 1116-1120.	6.0	311
3	The CATH domain structure database: new protocols and classification levels give a more comprehensive resource for exploring evolution. <i>Nucleic Acids Research</i> , 2007, 35, D291-D297.	6.5	274
4	The CATH Domain Structure Database and related resources Gene3D and DHS provide comprehensive domain family information for genome analysis. <i>Nucleic Acids Research</i> , 2004, 33, D247-D251.	6.5	226
5	The CATH database: an extended protein family resource for structural and functional genomics. <i>Nucleic Acids Research</i> , 2003, 31, 452-455.	6.5	218
6	The CATH Database provides insights into protein structure/function relationships. <i>Nucleic Acids Research</i> , 1999, 27, 275-279.	6.5	172
7	Protein folds, functions and evolution. <i>Journal of Molecular Biology</i> , 1999, 293, 333-342.	2.0	163
8	Quantifying the Similarities within Fold Space. <i>Journal of Molecular Biology</i> , 2002, 323, 909-926.	2.0	133
9	CATHEDRAL: A Fast and Effective Algorithm to Predict Folds and Domain Boundaries from Multidomain Protein Structures. <i>PLoS Computational Biology</i> , 2007, 3, e232.	1.5	90
10	Recognizing the fold of a protein structure. <i>Bioinformatics</i> , 2003, 19, 1748-1759.	1.8	79
11	Cell-derived extracellular vesicles can be used as a biomarker reservoir for glioblastoma tumor subtyping. <i>Communications Biology</i> , 2019, 2, 315.	2.0	71
12	Bioinformatics in translational drug discovery. <i>Bioscience Reports</i> , 2017, 37, .	1.1	68
13	The CATH Hierarchy Revisited—Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. <i>Structure</i> , 2009, 17, 1051-1062.	1.6	58
14	Gene3D: Structural Assignment for Whole Genes and Genomes Using the CATH Domain Structure Database. <i>Genome Research</i> , 2002, 12, 503-514.	2.4	55
15	MoKCa database—mutations of kinases in cancer. <i>Nucleic Acids Research</i> , 2009, 37, D824-D831.	6.5	51
16	The Cath Domain Structure Database. <i>Methods of Biochemical Analysis</i> , 2005, 44, 249-271.	0.2	50
17	The CATH extended protein-family database: Providing structural annotations for genome sequences. <i>Protein Science</i> , 2009, 11, 233-244.	3.1	48
18	Review: What Can Structural Classifications Reveal about Protein Evolution?. <i>Journal of Structural Biology</i> , 2001, 134, 145-165.	1.3	47

#	ARTICLE	IF	CITATIONS
19	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017, 9, 113.	3.6	47
20	Predicting synthetic lethal interactions using conserved patterns in protein interaction networks. <i>PLoS Computational Biology</i> , 2019, 15, e1006888.	1.5	34
21	PIK3CÎ´ expression by fibroblasts promotes triple-negative breast cancer progression. <i>Journal of Clinical Investigation</i> , 2020, 130, 3188-3204.	3.9	33
22	A first generation inhibitor of human Greatwall kinase, enabled by structural and functional characterisation of a minimal kinase domain construct. <i>Oncotarget</i> , 2016, 7, 71182-71197.	0.8	30
23	Mouse and Human Genetic Analyses Associate Kalirin with Ventral Striatal Activation during Impulsivity and with Alcohol Misuse. <i>Frontiers in Genetics</i> , 2016, 7, 52.	1.1	24
24	Gene3D: structural assignments for the biologist and bioinformaticist alike. <i>Nucleic Acids Research</i> , 2003, 31, 469-473.	6.5	23
25	Identification and analysis of mutational hotspots in oncogenes and tumour suppressors. <i>Oncotarget</i> , 2017, 8, 21290-21304.	0.8	23
26	Deriving a Mutation Index of Carcinogenicity Using Protein Structure and Protein Interfaces. <i>PLoS ONE</i> , 2014, 9, e84598.	1.1	22
27	Uncovering an allosteric mode of action for a selective inhibitor of human Bloom syndrome protein. <i>ELife</i> , 2021, 10, .	2.8	18
28	Mutational patterns in oncogenes and tumour suppressors. <i>Biochemical Society Transactions</i> , 2016, 44, 925-931.	1.6	16
29	“Big data” approaches for novel anti-cancer drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 599-609.	2.5	9
30	Aneuploidy tolerance caused by BRG1 loss allows chromosome gains and recovery of fitness. <i>Nature Communications</i> , 2022, 13, 1731.	5.8	9
31	Defining Signatures of Arm-Wise Copy Number Change and Their Associated Drivers in Kidney Cancers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5762.	1.8	8
32	Definition of a Family of Tissue-Protective Cytokines Using Functional Cluster Analysis: A Proof-of-Concept Study. <i>Frontiers in Immunology</i> , 2014, 5, 115.	2.2	6
33	Computational Approaches to Identify Genetic Interactions for Cancer Therapeutics. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	5
34	Identifying the Impact of Inframe Insertions and Deletions on Protein Function in Cancer. <i>Journal of Computational Biology</i> , 2020, 27, 786-795.	0.8	3
35	A combined bioinformatics and LC-MS-based approach for the development and benchmarking of a comprehensive database of <i>Lymnaea</i> CNS proteins. <i>Journal of Experimental Biology</i> , 2022, 225, .	0.8	3
36	The CATH domain structure database. , 2005, , .		0