

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	Aneuploidy tolerance caused by BRG1 loss allows chromosome gains and recovery of fitness. <i>Nature Communications</i> , 2022, 13, 1731.	5.8	9
2	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
3	Uncovering an allosteric mode of action for a selective inhibitor of human Bloom syndrome protein. <i>ELife</i> , 2021, 10, .	2.8	18
4	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
5	PIK3CÎ expression by fibroblasts promotes triple-negative breast cancer progression. <i>Journal of Clinical Investigation</i> , 2020, 130, 3188-3204.	3.9	33
6	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
7	Predicting synthetic lethal interactions using conserved patterns in protein interaction networks. <i>PLoS Computational Biology</i> , 2019, 15, e1006888.	1.5	34
8	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
9	“Big data” approaches for novel anti-cancer drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 599-609.	2.5	9
10	Bioinformatics in translational drug discovery. <i>Bioscience Reports</i> , 2017, 37, .	1.1	68
11	Computational Approaches to Identify Genetic Interactions for Cancer Therapeutics. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	5
12	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
13	Identification and analysis of mutational hotspots in oncogenes and tumour suppressors. <i>Oncotarget</i> , 2017, 8, 21290-21304.	0.8	23
14	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
15	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
16	Mutational patterns in oncogenes and tumour suppressors. <i>Biochemical Society Transactions</i> , 2016, 44, 925-931.	1.6	16
17	Therapeutic opportunities within the DNA damage response. <i>Nature Reviews Cancer</i> , 2015, 15, 166-180.	12.8	442
18	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

#	ARTICLE	IF	CITATIONS
19	Deriving a Mutation Index of Carcinogenicity Using Protein Structure and Protein Interfaces. PLoS ONE, 2014, 9, e84598.	1.1	22
20	Conserved Regulation of Cardiac Calcium Uptake by Peptides Encoded in Small Open Reading Frames. Science, 2013, 341, 1116-1120.	6.0	311
21	MoKCa database—mutations of kinases in cancer. Nucleic Acids Research, 2009, 37, D824-D831.	6.5	51
22	The CATH Hierarchy Revisited—Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. Structure, 2009, 17, 1051-1062.	1.6	58
23	The CATH extended protein-family database: Providing structural annotations for genome sequences. Protein Science, 2009, 11, 233-244.	3.1	48
24	CATHEDRAL: A Fast and Effective Algorithm to Predict Folds and Domain Boundaries from Multidomain Protein Structures. PLoS Computational Biology, 2007, 3, e232.	1.5	90
25	The CATH domain structure database: new protocols and classification levels give a more comprehensive resource for exploring evolution. Nucleic Acids Research, 2007, 35, D291-D297.	6.5	274
26	The Cath Domain Structure Database. Methods of Biochemical Analysis, 2005, 44, 249-271.	0.2	50
27	The CATH domain structure database. , 2005, , .		0
28	The CATH Domain Structure Database and related resources Gene3D and DHS provide comprehensive domain family information for genome analysis. Nucleic Acids Research, 2004, 33, D247-D251.	6.5	226
29	The CATH database: an extended protein family resource for structural and functional genomics. Nucleic Acids Research, 2003, 31, 452-455.	6.5	218
30	Gene3D: structural assignments for the biologist and bioinformaticist alike. Nucleic Acids Research, 2003, 31, 469-473.	6.5	23
31	Recognizing the fold of a protein structure. Bioinformatics, 2003, 19, 1748-1759.	1.8	79
32	Gene3D: Structural Assignment for Whole Genes and Genomes Using the CATH Domain Structure Database. Genome Research, 2002, 12, 503-514.	2.4	55
33	Quantifying the Similarities within Fold Space. Journal of Molecular Biology, 2002, 323, 909-926.	2.0	133
34	Review: What Can Structural Classifications Reveal about Protein Evolution?. Journal of Structural Biology, 2001, 134, 145-165.	1.3	47
35	The CATH Database provides insights into protein structure/function relationships. Nucleic Acids Research, 1999, 27, 275-279.	6.5	172
36	Protein folds, functions and evolution. Journal of Molecular Biology, 1999, 293, 333-342.	2.0	163