Frances M G Pearl

List of Publications by Year
in descending order

36	2,875	304743	361022
papers	citations	22	35
		h-index	g-index

41	41	41	4976
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Therapeutic opportunities within the DNA damage response. Nature Reviews Cancer, 2015, 15, 166-180.	28.4	442
2	Conserved Regulation of Cardiac Calcium Uptake by Peptides Encoded in Small Open Reading Frames. Science, 2013, 341, 1116-1120.	12.6	311
3	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.	14.5	274
4	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.	14.5	226
5	The CATH database: an extended protein family resource for structural and functional genomics. Nucleic Acids Research, 2003, 31, 452-455.	14.5	218
6	The CATH Database provides insights into protein structure/function relationships. Nucleic Acids Research, 1999, 27, 275-279.	14.5	172
7	Protein folds, functions and evolution. Journal of Molecular Biology, 1999, 293, 333-342.	4.2	163
8	Quantifying the Similarities within Fold Space. Journal of Molecular Biology, 2002, 323, 909-926.	4.2	133
9	CATHEDRAL: A Fast and Effective Algorithm to Predict Folds and Domain Boundaries from Multidomain Protein Structures. PLoS Computational Biology, 2007, 3, e232.	3.2	90
10	Recognizing the fold of a protein structure. Bioinformatics, 2003, 19, 1748-1759.	4.1	79
11	Cell-derived extracellular vesicles can be used as a biomarker reservoir for glioblastoma tumor subtyping. Communications Biology, 2019, 2, 315.	4.4	71
12	Bioinformatics in translational drug discovery. Bioscience Reports, 2017, 37, .	2.4	68
13	The CATH Hierarchy Revisited—Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. Structure, 2009, 17, 1051-1062.	3.3	58
14	Gene3D: Structural Assignment for Whole Genes and Genomes Using the CATH Domain Structure Database. Genome Research, 2002, 12, 503-514.	5.5	55
15	MoKCa database—mutations of kinases in cancer. Nucleic Acids Research, 2009, 37, D824-D831.	14.5	51
16	The Cath Domain Structure Database. Methods of Biochemical Analysis, 2005, 44, 249-271.	0.2	50
17	The CATH extended protein-family database: Providing structural annotations for genome sequences. Protein Science, 2009, 11, 233-244.	7.6	48
18	Review: What Can Structural Classifications Reveal about Protein Evolution?. Journal of Structural Biology, 2001, 134, 145-165.	2.8	47

#	Article	IF	Citations
19	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	8.2	47
20	Predicting synthetic lethal interactions using conserved patterns in protein interaction networks. PLoS Computational Biology, 2019, 15, e1006888.	3.2	34
21	PIK3CÎ´ expression by fibroblasts promotes triple-negative breast cancer progression. Journal of Clinical Investigation, 2020, 130, 3188-3204.	8.2	33
22	A first generation inhibitor of human Greatwall kinase, enabled by structural and functional characterisation of a minimal kinase domain construct. Oncotarget, 2016, 7, 71182-71197.	1.8	30
23	Mouse and Human Genetic Analyses Associate Kalirin with Ventral Striatal Activation during Impulsivity and with Alcohol Misuse. Frontiers in Genetics, 2016, 7, 52.	2.3	24
24	Gene3D: structural assignments for the biologist and bioinformaticist alike. Nucleic Acids Research, 2003, 31, 469-473.	14.5	23
25	Identification and analysis of mutational hotspots in oncogenes and tumour suppressors. Oncotarget, 2017, 8, 21290-21304.	1.8	23
26	Deriving a Mutation Index of Carcinogenicity Using Protein Structure and Protein Interfaces. PLoS ONE, 2014, 9, e84598.	2.5	22
27	Uncovering an allosteric mode of action for a selective inhibitor of human Bloom syndrome protein. ELife, 2021, 10, .	6.0	18
28	Mutational patterns in oncogenes and tumour suppressors. Biochemical Society Transactions, 2016, 44, 925-931.	3.4	16
29	â€˜Big dataâ€™ approaches for novel anti-cancer drug discovery. Expert Opinion on Drug Discovery, 2017, 12, 599-609.	5.0	9
30	Aneuploidy tolerance caused by BRG1 loss allows chromosome gains and recovery of fitness. Nature Communications, 2022, 13, 1731.	12.8	9
31	Defining Signatures of Arm-Wise Copy Number Change and Their Associated Drivers in Kidney Cancers. International Journal of Molecular Sciences, 2019, 20, 5762.	4.1	8
32	Definition of a Family of Tissue-Protective Cytokines Using Functional Cluster Analysis: A Proof-of-Concept Study. Frontiers in Immunology, 2014, 5, 115.	4.8	6
33	Computational Approaches to Identify Genetic Interactions for Cancer Therapeutics. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	5
34	Identifying the Impact of Inframe Insertions and Deletions on Protein Function in Cancer. Journal of Computational Biology, 2020, 27, 786-795.	1.6	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. Journal of Experimental Biology, 2022, 225, .	1.7	3
36	The CATH domain structure database. , 2005, , .		0