

Hafumi Nishi

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

1,131
citations

840776

11
h-index

996975

15
g-index

19
all docs

19
docs citations

19
times ranked

2091
citing authors

#	ARTICLE	IF	CITATIONS
1	New tools and functions in data activities at Protein Data Bank Japan (PDBj). <i>Protein Science</i> , 2018, 27, 95-102.	7.6	90
2	Dynamic recognition and linkage specificity in K63 di-ubiquitin and TAB2 NZF domain complex. <i>Scientific Reports</i> , 2018, 8, 16478.	3.3	3
3	Structural and Functional Characteristics of Protein Phosphorylation Revealed by Bioinformatic Approaches. <i>Seibutsu Butsuri</i> , 2016, 56, 207-211.	0.1	0
4	Structural characterization of single nucleotide variants at ligand binding sites and enzyme active sites of human proteins. <i>Biophysics and Physicobiology</i> , 2016, 13, 157-163.	1.0	7
5	H255Y and K508R missense mutations in tumour suppressor folliculin (FLCN) promote kidney cell proliferation. <i>Human Molecular Genetics</i> , 2016, 26, ddw392.	2.9	17
6	Distribution of single nucleotide variants on protein-protein interaction sites and its relationship with minor allele frequency. <i>Protein Science</i> , 2016, 25, 316-321.	7.6	14
7	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. <i>Journal of Molecular Biology</i> , 2015, 427, 511-520.	4.2	47
8	Physicochemical mechanisms of protein regulation by phosphorylation. <i>Frontiers in Genetics</i> , 2014, 5, 270.	2.3	152
9	3P267 Structural characteristics of phosphorylation sites on disordered binding regions(20. Origin) Tj ETQq1 1 0.784314 rgBT /Overl <i>Seibutsu Butsuri</i> , 2014, 54, S293.	0.1	0
10	Molecular Mechanisms of Disease-Causing Missense Mutations. <i>Journal of Molecular Biology</i> , 2013, 425, 3919-3936.	4.2	242
11	Regulation of protein-protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. <i>Molecular BioSystems</i> , 2013, 9, 1620.	2.9	60
12	Evolutionary, Physicochemical, and Functional Mechanisms of Protein Homooligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 3-24.	1.7	34
13	1P271 Crosstalk between signaling pathways revealed by database analysis of human phosphorylation sites(22B. Bioinformatics: Functional genomics, Poster). <i>Seibutsu Butsuri</i> , 2013, 53, S150.	0.1	0
14	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. <i>PLoS ONE</i> , 2013, 8, e66273.	2.5	102
15	Phosphorylation in Protein-Protein Binding: Effect on Stability and Function. <i>Structure</i> , 2011, 19, 1807-1815.	3.3	246
16	Caught in self-interaction: evolutionary and functional mechanisms of protein homooligomerization. <i>Physical Biology</i> , 2011, 8, 035007.	1.8	94
17	Cover and spacer insertions: Small nonhydrophobic accessories that assist protein oligomerization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2372-2379.	2.6	11
18	Amino acid substitutions at protein-protein interfaces that modulate the oligomeric state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1563-1574.	2.6	12