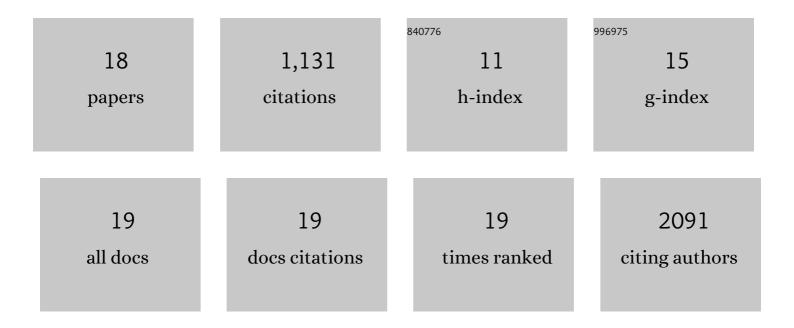
## Hafumi Nishi

List of Publications by Year in descending order

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HAFLIMI NISHI

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