

# Evangelia Petsalaki

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

4,529  
citations

304743

22  
h-index

361022

35  
g-index

45  
all docs

45  
docs citations

45  
times ranked

7733  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phase Transition of a Disordered Nuage Protein Generates Environmentally Responsive Membraneless Organelles. <i>Molecular Cell</i> , 2015, 57, 936-947.	9.7	1,408
2	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2007, 36, D919-D922.	14.5	518
3	WD40 proteins propel cellular networks. <i>Trends in Biochemical Sciences</i> , 2010, 35, 565-574.	7.5	518
4	Peptide-mediated interactions in biological systems: new discoveries and applications. <i>Current Opinion in Biotechnology</i> , 2008, 19, 344-350.	6.6	232
5	Structural Basis and Sequence Rules for Substrate Recognition by Tankyrase Explain the Basis for Cherubism Disease. <i>Cell</i> , 2011, 147, 1340-1354.	28.9	214
6	PepSite: prediction of peptide-binding sites from protein surfaces. <i>Nucleic Acids Research</i> , 2012, 40, W423-W427.	14.5	174
7	Systems analysis of RhoGEF and RhoGAP regulatory proteins reveals spatially organized RAC1 signalling from integrin adhesions. <i>Nature Cell Biology</i> , 2020, 22, 498-511.	10.3	154
8	Diagnostic accuracy of elastography and magnetic resonance imaging in patients with NAFLD: A systematic review and meta-analysis. <i>Journal of Hepatology</i> , 2021, 75, 770-785.	3.7	149
9	Accurate Prediction of Peptide Binding Sites on Protein Surfaces. <i>PLoS Computational Biology</i> , 2009, 5, e1000335.	3.2	138
10	PredSL: A Tool for the N-terminal Sequence-based Prediction of Protein Subcellular Localization. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 48-55.	6.9	125
11	Pooled matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	7.2	102
12	Transcription factors: Bridge between cell signaling and gene regulation. <i>Proteomics</i> , 2021, 21, e2000034.	2.2	79
13	Cell Surface Mechanics Gate Embryonic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2021, 28, 209-216.e4.	11.1	73
14	Combinatorial proteomic analysis of intercellular signaling applied to the CD28 T-cell costimulatory receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1594-603.	7.1	65
15	The identification of short linear motif-mediated interfaces within the human interactome. <i>Bioinformatics</i> , 2012, 28, 976-982.	4.1	63
16	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. <i>PLoS Computational Biology</i> , 2015, 11, e1004147.	3.2	59
17	Interaction Domains of Sos1/Grb2 Are Finely Tuned for Cooperative Control of Embryonic Stem Cell Fate. <i>Cell</i> , 2013, 152, 1008-1020.	28.9	53
18	Systematic identification of phosphorylation-mediated protein interaction switches. <i>PLoS Computational Biology</i> , 2017, 13, e1005462.	3.2	44

#	ARTICLE	IF	CITATIONS
19	Application of CRISPR-Cas9 Based Genome-Wide Screening Approaches to Study Cellular Signalling Mechanisms. <i>International Journal of Molecular Sciences</i> , 2018, 19, 933.	4.1	42
20	Dynamic regulation of hypoxia-inducible factor-1 $\alpha$ activity is essential for normal B cell development. <i>Nature Immunology</i> , 2020, 21, 1408-1420.	14.5	40
21	Proteomics and phosphoproteomics in precision medicine: applications and challenges. <i>Briefings in Bioinformatics</i> , 2019, 20, 767-777.	6.5	34
22	A recombinant <i>Fasciola gigantica</i> 14-3-3 epsilon protein (rFg14-3-3e) modulates various functions of goat peripheral blood mononuclear cells. <i>Parasites and Vectors</i> , 2018, 11, 152.	2.5	26
23	SELPHI: correlation-based identification of kinase-associated networks from global phospho-proteomics data sets. <i>Nucleic Acids Research</i> , 2015, 43, W276-W282.	14.5	24
24	Prediction of Signed Protein Kinase Regulatory Circuits. <i>Cell Systems</i> , 2020, 10, 384-396.e9.	6.2	23
25	Interactions between the Fyn SH3 domain and adaptor protein Cbp/PAG derived ligands, effects on kinase activity and affinity. <i>FEBS Journal</i> , 2008, 275, 4863-4874.	4.7	21
26	iTRAQ-Based Global Phosphoproteomics Reveals Novel Molecular Differences Between <i>Toxoplasma gondii</i> Strains of Different Genotypes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 307.	3.9	20
27	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. <i>Journal of Molecular Biology</i> , 2019, 431, 336-350.	4.2	20
28	Suppression of insulin-induced gene 1 (INSIG1) function promotes hepatic lipid remodelling and restrains NASH progression. <i>Molecular Metabolism</i> , 2021, 48, 101210.	6.5	20
29	Src Homology 2 Domain Containing Protein 5 (SH2D5) Binds the Breakpoint Cluster Region Protein, BCR, and Regulates Levels of Rac1-GTP. <i>Journal of Biological Chemistry</i> , 2014, 289, 35397-35408.	3.4	15
30	<scp>CEN</scp> tools: an integrative platform to identify the contexts of essential genes. <i>Molecular Systems Biology</i> , 2020, 16, e9698.	7.2	14
31	Phosphoproteomics identifies a bimodal EPHA2 receptor switch that promotes embryonic stem cell differentiation. <i>Nature Communications</i> , 2020, 11, 1357.	12.8	12
32	The pervasive effects of recombinant <i>Fasciola gigantica</i> Ras-related protein Rab10 on the functions of goat peripheral blood mononuclear cells. <i>Parasites and Vectors</i> , 2018, 11, 579.	2.5	11
33	Use of viral motif mimicry improves the proteome-wide discovery of human linear motifs. <i>Cell Reports</i> , 2022, 39, 110764.	6.4	10
34	Large-scale datasets uncovering cell signalling networks in cancer: context matters. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 118-124.	3.3	9
35	Identification of phenotype-specific networks from paired gene expression and cell shape imaging data. <i>Genome Research</i> , 2022, 32, 750-765.	5.5	5