P K Vinod

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Pan-Renal Cell Carcinoma classification and survival prediction from histopathology images using deep learning. Scientific Reports, 2019, 9, 10509.	1.6	127
2	MolGPT: Molecular Generation Using a Transformer-Decoder Model. Journal of Chemical Information and Modeling, 2022, 62, 2064-2076.	2.5	105
3	Meiotic Prophase Requires Proteolysis of M Phase Regulators Mediated by the Meiosis-Specific APC/CAma1. Cell, 2012, 151, 603-618.	13.5	93
4	Atypical Flexibility in Dynamic Functional Connectivity Quantifies the Severity in Autism Spectrum Disorder. Frontiers in Human Neuroscience, 2019, 13, 6.	1.0	78
5	Integration of Global Signaling Pathways, cAMP-PKA, MAPK and TOR in the Regulation of FLO11. PLoS ONE, 2008, 3, e1663.	1.1	75
6	Machine Learning Based Clinical Decision Support System for Early COVID-19 Mortality Prediction. Frontiers in Public Health, 2021, 9, 626697.	1.3	72
7	mTOR inhibition increases cell viability via autophagy induction during endoplasmic reticulum stress – An experimental and modeling study. FEBS Open Bio, 2014, 4, 704-713.	1.0	71
8	Dependency of the Spindle Assembly Checkpoint on Cdk1 Renders the Anaphase Transition Irreversible. Current Biology, 2014, 24, 630-637.	1.8	63
9	A cellular stress-directed bistable switch controls the crosstalk between autophagy and apoptosis. Molecular BioSystems, 2013, 9, 296-306.	2.9	62
10	Molecular mechanisms creating bistable switches at cell cycle transitions. Open Biology, 2013, 3, 120179.	1.5	62
11	Network-based metabolic characterization of renal cell carcinoma. Scientific Reports, 2020, 10, 5955.	1.6	61
12	Integrative Analysis of Hippocampus Gene Expression Profiles Identifies Network Alterations in Aging and Alzheimer's Disease. Frontiers in Aging Neuroscience, 2018, 10, 153.	1.7	58
13	PP2A/B55 and Fcp1 Regulate Greatwall and Ensa Dephosphorylation during Mitotic Exit. PLoS Genetics, 2014, 10, e1004004.	1.5	55
14	Host metabolic reprogramming in response to SARS-CoV-2 infection: A systems biology approach. Microbial Pathogenesis, 2021, 158, 105114.	1.3	44
15	Machine learning models to predict the progression from early to late stages of papillary renal cell carcinoma. Computers in Biology and Medicine, 2018, 100, 92-99.	3.9	31
16	Quantification of the effect of amino acids on an integrated mTOR and insulin signaling pathway. Molecular BioSystems, 2009, 5, 1163.	2.9	29
17	Computational modelling of mitotic exit in budding yeast: the role of separase and Cdc14 endocycles. Journal of the Royal Society Interface, 2011, 8, 1128-1141.	1.5	24
18	Crosstalk between cAMP-PKA and MAP kinase pathways is a key regulatory design necessary to regulate FLO11 expression. Biophysical Chemistry, 2007, 125, 59-71.	1.5	23

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19	Systems-level organization of non-alcoholic fatty liver disease progression network. Molecular BioSystems, 2017, 13, 1898-1911.	2.9	22
20	Integrative analysis of DNA methylation and gene expression in papillary renal cell carcinoma. Molecular Genetics and Genomics, 2020, 295, 807-824.	1.0	22
21	Model scenarios for switchâ€like mitotic transitions. FEBS Letters, 2015, 589, 667-671.	1.3	21
22	The role of APC/C inhibitor Emi2/XErp1 in oscillatory dynamics of early embryonic cell cycles. Biophysical Chemistry, 2013, 177-178, 1-6.	1.5	16
23	COVID-19 Risk Stratification and Mortality Prediction in Hospitalized Indian Patients: Harnessing clinical data for public health benefits. PLoS ONE, 2022, 17, e0264785.	1.1	16
24	Genome-scale metabolic modelling predicts biomarkers and therapeutic targets for neuropsychiatric disorders. Computers in Biology and Medicine, 2020, 125, 103994.	3.9	14
25	Systems-level feedback in cell-cycle control. Biochemical Society Transactions, 2010, 38, 1242-1246.	1.6	12
26	Multiple systemâ€level feedback loops control lifeâ€andâ€death decisions in endoplasmic reticulum stress. FEBS Letters, 2020, 594, 1112-1123.	1.3	11
27	Clinico-Genomic Analysis Reveals Mutations Associated with COVID-19 Disease Severity: Possible Modulation by RNA Structure. Pathogens, 2021, 10, 1109.	1.2	9
28	Interplay of transcriptional and proteolytic regulation in driving robust cell cycle progression. Molecular BioSystems, 2012, 8, 863.	2.9	5
29	In-Silico Pharmacodynamics. Applied Bioinformatics, 2006, 5, 141-150.	1.7	4
30	Mathematical modelling of reversible transition between quiescence and proliferation. PLoS ONE, 2018, 13, e0198420.	1.1	4
31	Specificity of MAPK signaling towards FLO11 expression is established by crosstalk from cAMP pathway. Systems and Synthetic Biology, 2007, 1, 99-108.	1.0	3
32	Computational modelling of meiotic entry and commitment. Scientific Reports, 2018, 8, 180.	1.6	3
33	Modeling the Control of Meiotic Cell Divisions: Entry, Progression, and Exit. Biophysical Journal, 2020, 119, 1015-1024.	0.2	3
34	Systems-level feedback regulation of cell cycle transitions in Ostreococcus tauri. Plant Physiology and Biochemistry, 2018, 126, 39-46.	2.8	2
35	Single-cell transcriptomic analysis of pancreatic islets in health and type 2 diabetes. International Journal of Advances in Engineering Sciences and Applied Mathematics, 2019, 11, 105-118.	0.7	2
36	Systems-level analysis of transcriptome reorganization during liver regeneration. Molecular Omics, 2022, 18, 315-327.	1.4	2

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37	Exploring Histological Similarities Across Cancers From a Deep Learning Perspective. Frontiers in Oncology, 2022, 12, 842759.	1.3	1

Cell Cycle Transitions, Mitotic Exit. , 2013, , 333-336.