

Marco Vanoni

List of Publications by Year in descending order

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107
papers

3,124
citations

156536

32
h-index

223390

49
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114
all docs

114
docs citations

114
times ranked

4972
citing authors

#	ARTICLE	IF	CITATIONS
1	INTEGRATE: Model-based multi-omics data integration to characterize multi-level metabolic regulation. <i>PLoS Computational Biology</i> , 2022, 18, e1009337.	1.5	24
2	An Optimized Workflow for the Analysis of Metabolic Fluxes in Cancer Spheroids Using Seahorse Technology. <i>Cells</i> , 2022, 11, 866.	1.8	10
3	Profiling Metabolic and Signaling Phenotype of Bladder Cancer Cell Lines. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
4	Methotrexate inhibits SARS-CoV-2 virus replication <i>in vitro</i> . <i>Journal of Medical Virology</i> , 2021, 93, 1780-1785.	2.5	38
5	A microphysiological early metastatic niche on a chip reveals how heterotypic cell interactions and inhibition of integrin subunit $\beta 3$ impact breast cancer cell extravasation. <i>Lab on A Chip</i> , 2021, 21, 1061-1072.	3.1	21
6	The Multi-Level Mechanism of Action of a Pan-Ras Inhibitor Explains its Antiproliferative Activity on Cetuximab-Resistant Cancer Cells. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 625979.	1.6	7
7	The driving role of the Cdk5/Tln1/FAKs732 axis in cancer cell extravasation dissected by human vascularized microfluidic models. <i>Biomaterials</i> , 2021, 276, 120975.	5.7	16
8	Transcriptomics and Metabolomics Integration Reveals Redox-Dependent Metabolic Rewiring in Breast Cancer Cells. <i>Cancers</i> , 2021, 13, 5058.	1.7	10
9	Disruption of redox homeostasis for combinatorial drug efficacy in K-Ras tumors as revealed by metabolic connectivity profiling. <i>Cancer & Metabolism</i> , 2020, 8, 22.	2.4	10
10	Natural Products Attenuating Biosynthesis, Processing, and Activity of Ras Oncoproteins: State of the Art and Future Perspectives. <i>Biomolecules</i> , 2020, 10, 1535.	1.8	8
11	Tipifarnib as a Precision Therapy for <i>HRAS</i> -Mutant Head and Neck Squamous Cell Carcinomas. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1784-1796.	1.9	72
12	Profiling and Targeting of Energy and Redox Metabolism in Grade 2 Bladder Cancer Cells with Different Invasiveness Properties. <i>Cells</i> , 2020, 9, 2669.	1.8	15
13	Editorial overview: Network analysis and experimental models for the understanding of multifactorial human diseases. <i>Current Opinion in Biotechnology</i> , 2020, 63, vi-viii.	3.3	0
14	Systems metabolomics: from metabolomic snapshots to design principles. <i>Current Opinion in Biotechnology</i> , 2020, 63, 190-199.	3.3	36
15	Single-cell Digital Twins for Cancer Preclinical Investigation. <i>Methods in Molecular Biology</i> , 2020, 2088, 331-343.	0.4	17
16	Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata. <i>Lecture Notes in Computer Science</i> , 2020, , 207-215.	1.0	1
17	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. <i>PLoS Computational Biology</i> , 2019, 15, e1006733.	1.5	70
18	Qualitative behavior of a coarse-grain growth model. , 2019, , .		1

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19	The Influence of Nutrients Diffusion on a Metabolism-driven Model of a Multi-cellular System. <i>Fundamenta Informaticae</i> , 2019, 171, 279-295.	0.3	0
20	How do tree mortality models from combined tree-ring and inventory data affect projections of forest succession?. <i>Forest Ecology and Management</i> , 2019, 433, 606-617.	1.4	17
21	An Integrated Model Quantitatively Describing Metabolism, Growth and Cell Cycle in Budding Yeast. <i>Communications in Computer and Information Science</i> , 2018, , 165-180.	0.4	3
22	Modeling Biological Timing and Synchronization Mechanisms by Means of Interconnections of Stochastic Switches. , 2018, 2, 19-24.		2
23	Engineering an Environment for the Study of Fibrosis: A 3D Human Muscle Model with Endothelium Specificity and Endomysium. <i>Cell Reports</i> , 2018, 25, 3858-3868.e4.	2.9	56
24	A metabolic core model elucidates how enhanced utilization of glucose and glutamine, with enhanced glutamine-dependent lactate production, promotes cancer cell growth: The WarburQ effect. <i>PLoS Computational Biology</i> , 2017, 13, e1005758.	1.5	64
25	K-Ras Activation Induces Differential Sensitivity to Sulfur Amino Acid Limitation and Deprivation and to Oxidative and Anti-Oxidative Stress in Mouse Fibroblasts. <i>PLoS ONE</i> , 2016, 11, e0163790.	1.1	10
26	Drought and frost contribute to abrupt growth decreases before tree mortality in nine temperate tree species. <i>Forest Ecology and Management</i> , 2016, 382, 51-63.	1.4	76
27	Respiratory metabolism and calorie restriction relieve persistent endoplasmic reticulum stress induced by calcium shortage in yeast. <i>Scientific Reports</i> , 2016, 6, 27942.	1.6	11
28	Whi5 phosphorylation embedded in the G1/S network dynamically controls critical cell size and cell fate. <i>Nature Communications</i> , 2016, 7, 11372.	5.8	35
29	Quantifying the effects of drought on abrupt growth decreases of major tree species in Switzerland. <i>Ecology and Evolution</i> , 2016, 6, 3555-3570.	0.8	45
30	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. <i>Computational Biology and Chemistry</i> , 2016, 62, 60-69.	1.1	36
31	How Epigallocatechin gallate and Tetracycline Interact with the Josephin Domain of Ataxin-3 and Alter Its Aggregation Mode. <i>Chemistry - A European Journal</i> , 2015, 21, 18383-18393.	1.7	17
32	5-Fluorouracil resistant colon cancer cells are addicted to OXPHOS to survive and enhance stem-like traits. <i>Oncotarget</i> , 2015, 6, 41706-41721.	0.8	103
33	Computational Strategies for a System-Level Understanding of Metabolism. <i>Metabolites</i> , 2014, 4, 1034-1087.	1.3	54
34	Interactions of ataxin-3 with its molecular partners in the protein machinery that sorts protein aggregates to the aggresome. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 51, 58-64.	1.2	18
35	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. <i>Natural Computing</i> , 2014, 13, 321-331.	1.8	18
36	A Systems Biology Road Map for the Discovery of Drugs Targeting Cancer Cell Metabolism. <i>Current Pharmaceutical Design</i> , 2014, 20, 2648-2666.	0.9	11

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37	Archaeal Serine Proteases. , 2013, , 3224-3233.		0
38	A comparative study of Whi5 and retinoblastoma proteins: from sequence and structure analysis to intracellular networks. <i>Frontiers in Physiology</i> , 2013, 4, 315.	1.3	17
39	Cancer cell growth and survival as a system-level property sustained by enhanced glycolysis and mitochondrial metabolic remodeling. <i>Frontiers in Physiology</i> , 2012, 3, 362.	1.3	24
40	Approaches to Ras signaling modulation and treatment of Ras-dependent disorders: a patent review (2007 – present). <i>Expert Opinion on Therapeutic Patents</i> , 2012, 22, 1263-1287.	2.4	15
41	Novel RasGRF1-derived Tat-fused peptides inhibiting Ras-dependent proliferation and migration in mouse and human cancer cells. <i>Biotechnology Advances</i> , 2012, 30, 233-243.	6.0	19
42	Cell growth and cell cycle in <i>Saccharomyces cerevisiae</i> : Basic regulatory design and protein–protein interaction network. <i>Biotechnology Advances</i> , 2012, 30, 52-72.	6.0	48
43	Regulation of hSos1 activity is a system-level property generated by its multi-domain structure. <i>Biotechnology Advances</i> , 2012, 30, 154-168.	6.0	8
44	Overexpression of Far1, a cyclin-dependent kinase inhibitor, induces a large transcriptional reprogramming in which RNA synthesis senses Far1 in a Sfp1-mediated way. <i>Biotechnology Advances</i> , 2012, 30, 185-201.	6.0	8
45	Comparative analysis of the molecular mechanisms controlling the initiation of chromosomal DNA replication in yeast and in mammalian cells. <i>Biotechnology Advances</i> , 2012, 30, 73-98.	6.0	22
46	Systems biology for biomedical innovation. <i>Biotechnology Advances</i> , 2012, 30, 1-3.	6.0	6
47	Loop 7 of E2 Enzymes: An Ancestral Conserved Functional Motif Involved in the E2-Mediated Steps of the Ubiquitination Cascade. <i>PLoS ONE</i> , 2012, 7, e40786.	1.1	26
48	Binding properties and biological characterization of new sugar-derived Ras ligands. <i>MedChemComm</i> , 2011, 2, 396.	3.5	16
49	Nutritional Limitation Sensitizes Mammalian Cells to GSK-3 ^{Î²} Inhibitors and Leads to Growth Impairment. <i>American Journal of Pathology</i> , 2011, 178, 1814-1823.	1.9	10
50	An Acidic Loop and Cognate Phosphorylation Sites Define a Molecular Switch That Modulates Ubiquitin Charging Activity in Cdc34-Like Enzymes. <i>PLoS Computational Biology</i> , 2011, 7, e1002056.	1.5	29
51	Glucose Signaling-Mediated Coordination of Cell Growth and Cell Cycle in <i>Saccharomyces Cerevisiae</i> . <i>Sensors</i> , 2010, 10, 6195-6240.	2.1	102
52	Snf1/AMPK promotes S-phase entrance by controlling <i>CLB5</i> transcription in budding yeast. <i>Cell Cycle</i> , 2010, 9, 2189-2200.	1.3	30
53	CK2 activity is modulated by growth rate in <i>Saccharomyces cerevisiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 398, 44-50.	1.0	12
54	The Insulin-Like Growth Factor Receptor I Promotes Motility and Invasion of Bladder Cancer Cells through Akt- and Mitogen-Activated Protein Kinase-Dependent Activation of Paxillin. <i>American Journal of Pathology</i> , 2010, 176, 2997-3006.	1.9	91

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55	Abstract 5057: The insulin-like growth factor receptor I promotes motility and invasion of bladder cancer cells through Akt- and MAPK-dependent activation of paxillin. , 2010, , .		0
56	Glutamine Deprivation Induces Abortive S-Phase Rescued by Deoxyribonucleotides in K-Ras Transformed Fibroblasts. PLoS ONE, 2009, 4, e4715.	1.1	131
57	Data recovery and integration from public databases uncovers transformation-specific transcriptional downregulation of cAMP-PKA pathway-encoding genes. BMC Bioinformatics, 2009, 10, S1.	1.2	6
58	Towards a systems biology approach to mammalian cell cycle: modeling the entrance into S phase of quiescent fibroblasts after serum stimulation. BMC Bioinformatics, 2009, 10, S16.	1.2	37
59	Analysis and modeling of growing budding yeast populations at the single cell level. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 114-120.	1.1	37
60	Order propensity of an intrinsically disordered protein, the cyclin-dependent kinase inhibitor Sic1. Proteins: Structure, Function and Bioinformatics, 2009, 76, 731-746.	1.5	64
61	Molecular networks and system-level properties. Journal of Biotechnology, 2009, 144, 224-233.	1.9	37
62	First experimental identification of Ras-inhibitor binding interface using a water-soluble Ras ligand. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 4217-4222.	1.0	36
63	Proteomic and biochemical analyses unveil tight interaction of ataxin-3 with tubulin. International Journal of Biochemistry and Cell Biology, 2009, 41, 2485-2492.	1.2	21
64	Selective cytotoxicity of a bicyclic Ras inhibitor in cancer cells expressing K-RasG13D. Biochemical and Biophysical Research Communications, 2009, 386, 593-597.	1.0	35
65	Functional coupling of the mammalian EGF receptor to the Ras/cAMP pathway in the yeast <i>Saccharomyces cerevisiae</i> . Current Genetics, 2008, 53, 153-162.	0.8	9
66	The CK2 phosphorylation of catalytic domain of Cdc34 modulates its activity at the G ₁ to S transition in <i>Saccharomyces cerevisiae</i> . Cell Cycle, 2008, 7, 1391-1401.	1.3	44
67	Proteomic Analysis of a Nutritional Shift-up in <i>Saccharomyces cerevisiae</i> Identifies Gvp36 as a BAR-containing Protein Involved in Vesicular Traffic and Nutritional Adaptation. Journal of Biological Chemistry, 2008, 283, 4730-4743.	1.6	15
68	RAS and PKA pathways in cancer: new insight from transcriptional analysis. Frontiers in Bioscience - Landmark, 2008, Volume, 5257.	3.0	27
69	Cell Size at S Phase Initiation: An Emergent Property of the G ₁ /S Network. PLoS Computational Biology, 2007, 3, e64.	1.5	96
70	In CK2 inactivated cells the cyclin dependent kinase inhibitor Sic1 is involved in cell-cycle arrest before the onset of S phase. Biochemical and Biophysical Research Communications, 2007, 359, 921-927.	1.0	31
71	Glucose-Derived Ras Pathway Inhibitors: Evidence of Ras-Ligand Binding and Ras-GEF (Cdc25) Interaction Inhibition. ChemBioChem, 2007, 8, 1376-1379.	1.3	23
72	Rapamycin-mediated G ₁ arrest involves regulation of the Cdk inhibitor Sic1 in <i>Saccharomyces cerevisiae</i> . Molecular Microbiology, 2007, 63, 1482-1494.	1.2	63

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73	Expression of transforming K-Ras oncogene affects mitochondrial function and morphology in mouse fibroblasts. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2006, 1757, 1338-1356.	0.5	68
74	Catalytic competence of the Ras-GEF domain of hSos1 requires intra-REM domain interactions mediated by Phenylalanine 577. <i>FEBS Letters</i> , 2006, 580, 6322-6328.	1.3	8
75	Sic1 is phosphorylated by CK2 on Ser201 in budding yeast cells. <i>Biochemical and Biophysical Research Communications</i> , 2006, 346, 786-793.	1.0	24
76	In <i>Saccharomyces cerevisiae</i> an unbalanced level of tyrosine phosphorylation down-regulates the Ras/PKA pathway. <i>International Journal of Biochemistry and Cell Biology</i> , 2006, 38, 444-460.	1.2	10
77	A modular systems biology analysis of cell cycle entrance into S-phase. <i>Topics in Current Genetics</i> , 2005, , 325-347.	0.7	5
78	The yeast cyclin-dependent kinase inhibitor Sic1 and mammalian p27Kip1 are functional homologues with a structurally conserved inhibitory domain. <i>Biochemical Journal</i> , 2005, 387, 639-647.	1.7	66
79	Identification and in silico analysis of a new group of double-histone fold-containing proteins. <i>Journal of Molecular Modeling</i> , 2005, 12, 76-84.	0.8	3
80	Subcellular Localization of the Cyclin Dependent Kinase Inhibitor Sic1 is Modulated by the Carbon Source in Budding Yeast. <i>Cell Cycle</i> , 2005, 4, 1798-1807.	1.3	25
81	CK2 regulates in vitro the activity of the yeast cyclin-dependent kinase inhibitor Sic1. <i>Biochemical and Biophysical Research Communications</i> , 2005, 336, 1040-1048.	1.0	15
82	The isolated catalytic hairpin of the Ras-specific guanine nucleotide exchange factor Cdc25Mmretains nucleotide dissociation activity but has impaired nucleotide exchange activity. <i>FEBS Letters</i> , 2005, 579, 6851-6858.	1.3	8
83	A cell sizer network involving Cln3 and Far1 controls entrance into S phase in the mitotic cycle of budding yeast. <i>Journal of Cell Biology</i> , 2004, 167, 433-443.	2.3	49
84	Mutations of the CK2 phosphorylation site of Sic1 affect cell size and S-Cdk kinase activity in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2004, 51, 447-460.	1.2	41
85	Systems Biology and the Molecular Circuits of Cancer. <i>ChemBioChem</i> , 2004, 5, 1322-1333.	1.3	38
86	Systems Biology and the Molecular Circuits of Cancer. <i>ChemInform</i> , 2004, 35, no.	0.1	2
87	Conglutin α , a lupin seed protein, binds insulin in vitro and reduces plasma glucose levels of hyperglycemic rats. <i>Journal of Nutritional Biochemistry</i> , 2004, 15, 646-650.	1.9	129
88	Structure Determination and Dynamics of Peptides Overlapping the Catalytic Hairpin of the Ras-Specific GEF Cdc25Mm. <i>Biochemistry</i> , 2003, 42, 12154-12162.	1.2	6
89	The Ras GDP/GTP cycle is regulated by oxidizing agents at the level of Ras regulators and effectors. <i>FEBS Letters</i> , 2001, 492, 139-145.	1.3	22
90	The Sso7d DNA-binding protein from <i>Sulfolobus solfataricus</i> has ribonuclease activity. <i>FEBS Letters</i> , 2001, 497, 131-136.	1.3	22

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91	The role of hexose transport and phosphorylation in cAMP signalling in the yeast <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2001, 1, 33-45.	1.1	49
92	A dominant negative RAS-specific guanine nucleotide exchange factor reverses neoplastic phenotype in K-ras transformed mouse fibroblasts. <i>Oncogene</i> , 2000, 19, 2147-2154.	2.6	27
93	Mutations at position 1122 in the catalytic domain of the mouse ras-specific guanine nucleotide exchange factor CDC25Mmoriginate both loss-of-function and gain-of-function proteins. <i>FEBS Letters</i> , 1998, 440, 291-296.	1.3	9
94	Redox-Mediated Regulation of p21Waf1/Cip1 Expression Involves a Post-Transcriptional Mechanism and Activation of the Mitogen-Activated Protein Kinase Pathway. <i>FEBS Journal</i> , 1997, 245, 730-737.	0.2	97
95	In <i>Saccharomyces cerevisiae</i> a short amino acid sequence facilitates excretion in the growth medium of periplasmic proteins. <i>Molecular Microbiology</i> , 1997, 23, 997-1007.	1.2	16
96	Identification of Gene encoding a Putative RNA-Helicase, Homologous to SKI2, in Chromosome VII of <i>Saccharomyces cerevisiae</i> . , 1997, 13, 391-397.		19
97	¹ H-NMR and photo-CIDNP spectroscopies show a possible role for Trp23 and Phe31 in nucleic acid binding by P2 ribonuclease from the archaeon <i>Sulfolobus solfataricus</i> . <i>FEBS Letters</i> , 1995, 372, 135-139.	1.3	7
98	In <i>Saccharomyces cerevisiae</i> overexpression of hybrid Virus-Like-Particles correlates with altered cell volume distributions. <i>Biotechnology Letters</i> , 1994, 16, 1131-1134.	1.1	1
99	Molecular cloning, nucleotide sequence and expression of a <i>Sulfolobus solfataricus</i> gene encoding a class II fumarase. <i>FEBS Letters</i> , 1994, 337, 93-98.	1.3	19
100	Isolation and characterization of maltose non utilizing (mnu) mutants mapping outside the MAL1 locus in <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Letters</i> , 1991, 77, 233-236.	0.7	0
101	Overexpression of the CDC25 gene, an upstream element of the ras/adenylyl cyclase pathway in <i>Saccharomyces cerevisiae</i> , allows immunological identification and characterization of its gene product. <i>Biochemical and Biophysical Research Communications</i> , 1990, 172, 61-69.	1.0	23
102	Regulation of MAL gene expression in yeast: Gene dosage effects. <i>Molecular Genetics and Genomics</i> , 1987, 209, 508-517.	2.4	43
103	Macromolecular syntheses in the cell cycle mutant cdc25 of budding yeast. <i>FEBS Journal</i> , 1984, 144, 205-210.	0.2	38
104	A Computer algorithm for the analysis of protein distribution in budding yeast. <i>Cytometry</i> , 1984, 5, 81-85.	1.8	23
105	Effects of temperature on the yeast cell cycle analyzed by flow cytometry. <i>Cytometry</i> , 1984, 5, 530-533.	1.8	17
106	Analysis of protein distribution in budding yeast. <i>Biotechnology and Bioengineering</i> , 1983, 25, 1295-1310.	1.7	66
107	An ensemble approach to the study of the emergence of metabolic and proliferative disorders via Flux Balance Analysis. <i>Electronic Proceedings in Theoretical Computer Science, EPTCS</i> , 0, 130, 92-97.	0.8	0