Boris N Kholodenko

List of Publications by Year
in descending order

189 papers	13,075 citations	28190 55 h-index	27345 106 g-index
194 all docs	194 docs citations	194 times ranked	12186 citing authors

#	Article	IF	Citations
1	Relationship Between Dimensionality and Convergence of Optimization Algorithms: A Comparison Between Data-Driven Normalization and Scaling Factor-Based Methods Using PEPSSBI. Methods in Molecular Biology, 2022, 2385, 91-115.	0.4	0
2	Inhaled multi-walled carbon nanotubes differently modulate global gene and protein expression in rat lungs. Nanotoxicology, 2021, 15, 238-256.	1.6	14
3	Systems biology approaches to macromolecules: the role of dynamic protein assemblies in information processing. Current Opinion in Structural Biology, 2021, 67, 61-68.	2.6	2
4	A systematic analysis of signaling reactivation and drug resistance. Cell Reports, 2021, 35, 109157.	2.9	17
5	Reengineering protein-phosphorylation switches. Science, 2021, 373, 25-26.	6.0	0
6	Channeling macrophage polarization by rocaglates increases macrophage resistance to Mycobacterium tuberculosis. IScience, 2021, 24, 102845.	1.9	14
7	Modeling the Nonlinear Dynamics of Intracellular Signaling Networks. Bio-protocol, 2021, 11, e4089.	0.2	1
8	Can Systems Biology Advance Clinical Precision Oncology?. Cancers, 2021, 13, 6312.	1.7	10
9	Acute Phase Response as a Biological Mechanismâ€ofâ€Action of (Nano)particleâ€Induced Cardiovascular Disease. Small, 2020, 16, e1907476.	5.2	37
10	Extensive rewiring of the EGFR network in colorectal cancer cells expressing transforming levels of KRASG13D. Nature Communications, 2020, 11, 499.	5.8	42
11	Periodic propagating waves coordinate RhoGTPase network dynamics at the leading and trailing edges during cell migration. ELife, 2020, 9, .	2.8	40
12	An Integrative Computational Approach for a Prioritization of Key Transcription Regulators Associated With Nanomaterial-Induced Toxicity. Toxicological Sciences, 2019, 171, 303-314.	1.4	10
13	Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. PLoS Computational Biology, 2019, 15, e1006706.	1.5	8
14	Mapping connections in signaling networks with ambiguous modularity. Npj Systems Biology and Applications, 2019, 5, 19.	1.4	9
15	New insights into RAS biology reinvigorate interest in mathematical modeling of RAS signaling. Seminars in Cancer Biology, 2019, 54, 162-173.	4.3	16
16	Reconstructing static and dynamic models of signaling pathways using Modular Response Analysis. Current Opinion in Systems Biology, 2018, 9, 11-21.	1.3	22
17	Transcriptionally inducible Pleckstrin homology-like domain, family A, member 1, attenuates ErbB receptor activity by inhibiting receptor oligomerization. Journal of Biological Chemistry, 2018, 293, 2206-2218.	1.6	9
18	Rac1 and RhoA: Networks, loops and bistability. Small GTPases, 2018, 9, 316-321.	0.7	74

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19	Impact of measurement noise, experimental design, and estimation methods on Modular Response Analysis based network reconstruction. Scientific Reports, 2018, 8, 16217.	1.6	13
20	Dissecting RAF Inhibitor Resistance by Structure-based Modeling Reveals Ways to Overcome Oncogenic RAS Signaling. Cell Systems, 2018, 7, 161-179.e14.	2.9	53
21	Performance of objective functions and optimisation procedures for parameter estimation in system biology models. Npj Systems Biology and Applications, 2017, 3, 20.	1.4	57
22	Probing the Heterogeneity of Protein Kinase Activation in Cells by Super-resolution Microscopy. ACS Nano, 2017, 11, 249-257.	7.3	13
23	Modeling of Receptor Tyrosine Kinase Signaling: Computational and Experimental Protocols. Methods in Molecular Biology, 2017, 1636, 417-453.	0.4	8
24	SARAH Domain-Mediated MST2-RASSF Dimeric Interactions. PLoS Computational Biology, 2016, 12, e1005051.	1.5	15
25	On the personalised modelling of cancer signalling * *Supported by EU FP7 grant â€œSynSignalâ€•(No.) Tj ETQq1 1 0.784314 rgBT /Ov	0.5	2
26	Phosphorylation of RAF Kinase Dimers Drives Conformational Changes that Facilitate Transactivation. Angewandte Chemie, 2016, 128, 995-998.	1.6	0
27	Three-factor models versus time series models: quantifying time-dependencies of interactions between stimuli in cell biology and psychobiology for short longitudinal data. Mathematical Medicine and Biology, 2016, 34, dqw001.	0.8	0
28	MAPK kinase signalling dynamics regulate cell fate decisions and drug resistance. Current Opinion in Structural Biology, 2016, 41, 151-158.	2.6	72
29	Integrating network reconstruction with mechanistic modeling to predict cancer therapies. Science Signaling, 2016, 9, ra114.	1.6	63
30	Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches. Cell Systems, 2016, 2, 38-48.	2.9	159
31	The complexities and versatility of the RAS-to-ERK signalling system in normal and cancer cells. Seminars in Cell and Developmental Biology, 2016, 58, 96-107.	2.3	51
32	Phosphorylation of RAF Kinase Dimers Drives Conformational Changes that Facilitate Transactivation. Angewandte Chemie - International Edition, 2016, 55, 983-986.	7.2	43
33	Feedback regulation in cell signalling: Lessons for cancer therapeutics. Seminars in Cell and Developmental Biology, 2016, 50, 85-94.	2.3	53
34	MST2-RASSF proteinâ€“protein interactions through SARAH domains. Briefings in Bioinformatics, 2016, 17, 593-602.	3.2	13
35	HER2-HER3 dimer quantification by FLIM-FRET predicts breast cancer metastatic relapse independently of HER2 IHC status. Oncotarget, 2016, 7, 51012-51026.	0.8	28
36	Frequency modulation of <scp>ERK</scp> activation dynamics rewires cell fate. Molecular Systems Biology, 2015, 11, 838.	3.2	189

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37	DYVIPAC: an integrated analysis and visualisation framework to probe multi-dimensional biological networks. Scientific Reports, 2015, 5, 12569.	1.6	23
38	Mitogen-Inducible Gene-6 Mediates Feedback Inhibition from Mutated BRAF towards the Epidermal Growth Factor Receptor and Thereby Limits Malignant Transformation. PLoS ONE, 2015, 10, e0129859.	1.1	8
39	Network-based identification of feedback modules that control RhoA activity and cell migration. Journal of Molecular Cell Biology, 2015, 7, 242-252.	1.5	20
40	Signaling pathway models as biomarkers: Patient-specific simulations of JNK activity predict the survival of neuroblastoma patients. Science Signaling, 2015, 8, ra130.	1.6	140
41	Feedforward regulation of mRNA stability by prolonged extracellular signalâ€regulated kinase activity. FEBS Journal, 2015, 282, 613-629.	2.2	14
42	Species differential regulation of COX2 can be described by an NFÎºB-dependent logic AND gate. Cellular and Molecular Life Sciences, 2015, 72, 2431-2443.	2.4	22
43	Signalling mechanisms regulating phenotypic changes in breast cancer cells. Bioscience Reports, 2015, 35, .	1.1	9
44	Silence on the relevant literature and errors in implementation. Nature Biotechnology, 2015, 33, 336-339.	9.4	14
45	Drug Resistance Resulting from Kinase Dimerization Is Rationalized by Thermodynamic Factors Describing Allosteric Inhibitor Effects. Cell Reports, 2015, 12, 1939-1949.	2.9	37
46	The dynamic control of signal transduction networks in cancer cells. Nature Reviews Cancer, 2015, 15, 515-527.	12.8	282
47	Proteinâ€"protein interactions generate hidden feedback and feed-forward loops to trigger bistable switches, oscillations and biphasic doseâ€"responses. Molecular BioSystems, 2015, 11, 2750-2762.	2.9	30
48	Competing to coordinate cell fate decisions: the MST2-Raf-1 signaling device. Cell Cycle, 2015, 14, 189-199.	1.3	23
49	Advances in dynamic modeling of colorectal cancer signaling-network regions, a path toward targeted therapies. Oncotarget, 2015, 6, 5041-5058.	0.8	24
50	Evaluating Strategies to Normalise Biological Replicates of Western Blot Data. PLoS ONE, 2014, 9, e87293.	1.1	174
51	Navigating the Multilayered Organization of Eukaryotic Signaling: A New Trend in Data Integration. PLoS Computational Biology, 2014, 10, e1003385.	1.5	9
52	Polyubiquitin chain assembly and organization determine the dynamics of protein activation and degradation. Frontiers in Physiology, 2014, 5, 4.	1.3	28
53	The ErbB4 CYT2 variant protects EGFR from ligand-induced degradation to enhance cancer cell motility. Science Signaling, 2014, 7, ra78.	1.6	34
54	The APC Network Regulates the Removal of Mutated Cells from Colonic Crypts. Cell Reports, 2014, 7, 94-103.	2.9	19

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55	Systems biology-embedded target validation: improving efficacy in drug discovery. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 1-11.	6.6	19
56	Protein interaction switches coordinate Raf-1 and MST2/Hippo signalling. Nature Cell Biology, 2014, 16, 673-684.	4.6	138
57	Nonlinear signalling networks and cell-to-cell variability transform external signals into broadly distributed or bimodal responses. Journal of the Royal Society Interface, 2014, 11, 20140383.	1.5	24
58	Ubiquitin chain specific autoâ€ubiquitination triggers sustained oscillation, bistable switches and excitable firing. IET Systems Biology, 2014, 8, 282-292.	0.8	8
59	Signalling by protein phosphatases and drug development: a systemsâ€centred view. FEBS Journal, 2013, 280, 751-765.	2.2	47
60	Integrating Bayesian variable selection with Modular Response Analysis to infer biochemical network topology. BMC Systems Biology, 2013, 7, 57.	3.0	34
61	Control of the G-protein cascade dynamics by GDP dissociation inhibitors. Molecular BioSystems, 2013, 9, 2454.	2.9	16
62	When ubiquitination meets phosphorylation: a systems biology perspective of EGFR/MAPK signalling. Cell Communication and Signaling, 2013, 11, 52.	2.7	154
63	It takes two to tango â€“ signalling by dimeric Raf kinases. Molecular BioSystems, 2013, 9, 551-558.	2.9	39
64	A dynamic model of the hypoxia-inducible factor 1-alpha (HIF-1Î±) network. Journal of Cell Science, 2013, 126, 1454-63.	1.2	112
65	Systems medicine: helping us understand the complexity of disease. QJM - Monthly Journal of the Association of Physicians, 2013, 106, 891-895.	0.2	30
66	Complexity of Receptor Tyrosine Kinase Signal Processing. Cold Spring Harbor Perspectives in Biology, 2013, 5, a009043-a009043.	2.3	70
67	Systems medicine: opportunities and challenges for systems biology approaches. FEBS Journal, 2013, 280, 5937-5937.	2.2	4
68	Pseudophosphatase STYX modulates cell-fate decisions and cell migration by spatiotemporal regulation of ERK1/2. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2934-43.	3.3	49
69	A dynamic model of the hypoxiaâ€inducible factor (HIF) network. FASEB Journal, 2013, 27, 717.12.	0.2	0
70	Crosstalk and Signaling Switches in Mitogen-Activated Protein Kinase Cascades. Frontiers in Physiology, 2012, 3, 355.	1.3	137
71	Mammalian protein expression noise: scaling principles and the implications for knockdown experiments. Molecular BioSystems, 2012, 8, 3068.	2.9	15
72	Computational Approaches for Analyzing Information Flow in Biological Networks. Science Signaling, 2012, 5, re1.	1.6	152

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73	Catching transcriptional regulation by thermostatistical modeling. Physical Biology, 2012, 9, 045007.	0.8	7
74	Emergence of bimodal cell population responses from the interplay between analog single-cell signaling and protein expression noise. BMC Systems Biology, 2012, 6, 109.	3.0	89
75	An Integrated Bayesian Framework for Identifying Phosphorylation Networks in Stimulated Cells. Advances in Experimental Medicine and Biology, 2012, 736, 59-80.	0.8	7
76	Versatility of Cooperative Transcriptional Activation: A Thermodynamical Modeling Analysis for Greater-Than-Additive and Less-Than-Additive Effects. PLoS ONE, 2012, 7, e34439.	1.1	16
77	Cross-talk between mitogenic Ras/MAPK and survival PI3K/Akt pathways: a fine balance. Biochemical Society Transactions, 2012, 40, 139-146.	1.6	385
78	The topology design principles that determine the spatiotemporal dynamics of G-protein cascades. Molecular BioSystems, 2012, 8, 730.	2.9	33
79	Bimodal Protein Distributions in Heterogeneous Oscillating Systems. Lecture Notes in Computer Science, 2012, , 17-28.	1.0	7
80	Understanding Cell Fate Decisions by Identifying Crucial System Dynamics. SIMAI Springer Series, 2012, , 83-104.	0.4	0
81	Prolactin-stimulated activation of ERK1/2 mitogen-activated protein kinases is controlled by PI3-kinase/Rac/PAK signaling pathway in breast cancer cells. Cellular Signalling, 2011, 23, 1794-1805.	1.7	89
82	Switches, Excitable Responses and Oscillations in the Ring1B/Bmi1 Ubiquitination System. PLoS Computational Biology, 2011, 7, e1002317.	1.5	33
83	Signalling ballet in space and time. Nature Reviews Molecular Cell Biology, 2010, 11, 414-426.	16.1	563
84	The Mammalian MAPK/ERK Pathway Exhibits Properties of a Negative Feedback Amplifier. Science Signaling, 2010, 3, ra90.	1.6	216
85	Formation of Intracellular Concentration Landscapes by Multisite Protein Modification. Biophysical Journal, 2010, 99, 59-66.	0.2	21
86	Signalling over a distance: gradient patterns and phosphorylation waves within single cells. Biochemical Society Transactions, 2010, 38, 1235-1241.	1.6	24
87	Ligand-Specific c-Fos Expression Emerges from the Spatiotemporal Control of ErbB Network Dynamics. Cell, 2010, 141, 884-896.	13.5	217
88	PI3K/Akt-sensitive MEK-independent compensatory circuit of ERK activation in ER-positive PI3K-mutant T47D breast cancer cells. Cellular Signalling, 2010, 22, 1369-1378.	1.7	84
89	Systemsâ€level interactions between insulinâ€“EGF networks amplify mitogenic signaling. Molecular Systems Biology, 2009, 5, 256.	3.2	205
90	Positional Information Generated by Spatially Distributed Signaling Cascades. PLoS Computational Biology, 2009, 5, e1000330.	1.5	36

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91	Spatially distributed cell signalling. FEBS Letters, 2009, 583, 4006-4012.	1.3	62
92	Signaling cascades as cellular devices for spatial computations. Journal of Mathematical Biology, 2009, 58, 35-55.	0.8	36
93	Fourâ€dimensional dynamics of MAPK informationâ€processing systems. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2009, 1, 28-44.	6.6	67
94	Toggle switches, pulses and oscillations are intrinsic properties of the Src activation/deactivation cycle. FEBS Journal, 2009, 276, 4102-4118.	2.2	35
95	Molecular Dynamics Simulations Reveal that Tyr-317 Phosphorylation Reduces Shc Binding Affinity for Phosphotyrosyl Residues of Epidermal Growth Factor Receptor. Biophysical Journal, 2009, 96, 2278-2288.	0.2	21
96	Endocytosis and signalling: A meeting with mathematics. Molecular Oncology, 2009, 3, 308-320.	2.1	30
97	Giving Space to Cell Signaling. Cell, 2008, 133, 566-567.	13.5	23
98	Multiâ€scale modeling of neuronal adaptation mediated by angiotensin II in the central regulation of blood pressure. FASEB Journal, 2008, 22, 756.2.	0.2	0
99	Spatio-temporal dynamics of protein modification cascades. SEB Experimental Biology Series, 2008, 61, 141-59.	0.1	2
100	Ligandâ€dependent responses of the ErbB signaling network: experimental and modeling analyses. Molecular Systems Biology, 2007, 3, 144.	3.2	203
101	Multistrip Western blotting to increase quantitative data output. Electrophoresis, 2007, 28, 3163-3173.	1.3	38
102	Oscillatory dynamics arising from competitive inhibition and multisite phosphorylation. Journal of Theoretical Biology, 2007, 244, 68-76.	0.8	68
103	Untangling the signalling wires. Nature Cell Biology, 2007, 9, 247-249.	4.6	66
104	Mechanisms Generating Ultrasensitivity, Bistability, and Oscillations in Signal Transduction. , 2007, , 282-299.		9
105	Employing Systems Biology to Quantify Receptor Tyrosine Kinase Signaling in Time and Space. , 2007, , 300-318.		0
106	Effects of sequestration on signal transduction cascades. FEBS Journal, 2006, 273, 895-906.	2.2	148
107	Bistability from double phosphorylation in signal transduction. FEBS Journal, 2006, 273, 3915-3926.	2.2	87
108	Cell-signalling dynamics in time and space. Nature Reviews Molecular Cell Biology, 2006, 7, 165-176.	16.1	1,241

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109	Trading the micro-world of combinatorial complexity for the macro-world of protein interaction domains. BioSystems, 2006, 83, 152-166.	0.9	36
110	A domain-oriented approach to the reduction of combinatorial complexity in signal transduction networks. BMC Bioinformatics, 2006, 7, 34.	1.2	78
111	Longâ€range signaling by phosphoprotein waves arising from bistability in protein kinase cascades. Molecular Systems Biology, 2006, 2, 61.	3.2	74
112	Scaffolding Protein Grb2-associated Binder 1 Sustains Epidermal Growth Factor-induced Mitogenic and Survival Signaling by Multiple Positive Feedback Loops*. Journal of Biological Chemistry, 2006, 281, 19925-19938.	1.6	153
113	Inference of signaling and gene regulatory networks by steady-state perturbation experiments: structure and accuracy. Journal of Theoretical Biology, 2005, 232, 427-441.	0.8	73
114	Signaling through Receptors and Scaffolds: Independent Interactions Reduce Combinatorial Complexity. Biophysical Journal, 2005, 89, 951-966.	0.2	91
115	News. IET Systems Biology, 2005, 152, 53.	2.0	1
116	Tyr-317 Phosphorylation Increases Shc Structural Rigidity and Reduces Coupling of Domain Motions Remote from the Phosphorylation Site as Revealed by Molecular Dynamics Simulations. Journal of Biological Chemistry, 2004, 279, 4657-4662.	1.6	30
117	Inferring dynamic architecture of cellular networks using time series of gene expression, protein and metabolite data. Bioinformatics, 2004, 20, 1877-1886.	1.8	148
118	Signal processing at the Ras circuit: what shapes Ras activation patterns?. IET Systems Biology, 2004, 1, 104-113.	2.0	51
119	Quantitative analysis of signaling networks. Progress in Biophysics and Molecular Biology, 2004, 86, 5-43.	1.4	188
120	Signaling switches and bistability arising from multisite phosphorylation in protein kinase cascades. Journal of Cell Biology, 2004, 164, 353-359.	2.3	620
121	Control of spatially heterogeneous and time-varying cellular reaction networks: a new summation law. Journal of Theoretical Biology, 2003, 225, 477-487.	0.8	38
122	Four-dimensional organization of protein kinase signaling cascades: the roles of diffusion, endocytosis and molecular motors. Journal of Experimental Biology, 2003, 206, 2073-2082.	0.8	146
123	Untangling the wires: A strategy to trace functional interactions in signaling and gene networks. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12841-12846.	3.3	386
124	Control Analysis for Autonomously Oscillating Biochemical Networks. Biophysical Journal, 2002, 82, 99-108.	0.2	69
125	Temperature Dependence of the Epidermal Growth Factor Receptor Signaling Network Can Be Accounted for by a Kinetic Modelâ€. Biochemistry, 2002, 41, 306-320.	1.2	74
126	Modular Response Analysis of Cellular Regulatory Networks. Journal of Theoretical Biology, 2002, 218, 507-520.	0.8	106

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127	MAP kinase cascade signaling and endocytic trafficking: a marriage of convenience?. Trends in Cell Biology, 2002, 12, 173-177.	3.6	96
128	Modular Response Analysis of Cellular Regulatory Networks. Journal of Theoretical Biology, 2002, 218, 507-520.	0.8	95
129	Modular interaction strengths in regulatory networks; an example. Molecular Biology Reports, 2002, 29, 57-61.	1.0	6
130	Modular response analysis of cellular regulatory networks. Journal of Theoretical Biology, 2002, 218, 507-20.	0.8	51
131	Occurrence of paradoxical or sustained control by an enzyme when overexpressed: necessary conditions and experimental evidence with regard to hepatic glucokinase. Biochemical Journal, 2001, 355, 787-793.	1.7	11
132	Kinetics and control of oxidative phosphorylation in rat liver mitochondria after chronic ethanol feeding. Biochemical Journal, 2000, 349, 519.	1.7	22
133	Diffusion control of protein phosphorylation in signal transduction pathways. Biochemical Journal, 2000, 350, 901.	1.7	25
134	Kinetics and control of oxidative phosphorylation in rat liver mitochondria after chronic ethanol feeding. Biochemical Journal, 2000, 349, 519-526.	1.7	34
135	Diffusion control of protein phosphorylation in signal transduction pathways. Biochemical Journal, 2000, 350, 901-907.	1.7	72
136	Engineering a Living Cell to Desired Metabolite Concentrations and Fluxes: Pathways with Multifunctional Enzymes. Metabolic Engineering, 2000, 2, 1-13.	3.6	18
137	Negative feedback and ultrasensitivity can bring about oscillations in the mitogen-activated protein kinase cascades. FEBS Journal, 2000, 267, 1583-1588.	0.2	552
138	Cellular information transfer regarded from a stoichiometry and control analysis perspective. BioSystems, 2000, 55, 73-81.	0.9	14
139	Why cytoplasmic signalling proteins should be recruited to cell membranes. Trends in Cell Biology, 2000, 10, 173-178.	3.6	216
140	Metabolic Control From The Back Benches: Biochemistry Towards Biocomplexity. , 2000, , 235-242.		1
141	Quantification of Short Term Signaling by the Epidermal Growth Factor Receptor. Journal of Biological Chemistry, 1999, 274, 30169-30181.	1.6	507
142	Spatial gradients of cellular phospho-proteins. FEBS Letters, 1999, 457, 452-454.	1.3	175
143	Control Analysis of Stationary Forced Oscillations. Journal of Physical Chemistry B, 1999, 103, 10695-10710.	1.2	26
144	Subtleties in control by metabolic channelling and enzyme organization. Molecular and Cellular Biochemistry, 1998, 184, 311-320.	1.4	14

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145	Metabolic design: How to engineer a living cell to desired metabolite concentrations and fluxes. Biotechnology and Bioengineering, 1998, 59, 239-247.	1.7	36
146	The Intracellular Signaling Network as a Target for Ethanol. Alcoholism: Clinical and Experimental Research, 1998, 22, 224S-230S.	1.4	38
147	Control analysis of metabolic systems involving quasi-equilibrium reactions. Biochimica Et Biophysica Acta - General Subjects, 1998, 1379, 337-352.	1.1	15
148	Implications of macromolecular crowding for signal transduction and metabolite channeling. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 10547-10552.	3.3	102
149	Subtleties in control by metabolic channelling and enzyme organization. , 1998, , 311-320.		4
150	Control Analysis of Periodic Phenomena in Biological Systems. Journal of Physical Chemistry B, 1997, 101, 2070-2081.	1.2	47
151	Quantification of information transfer via cellular signal transduction pathways. FEBS Letters, 1997, 414, 430-434.	1.3	141
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154	Effect of channelling on the concentration of bulk-phase intermediates as cytosolic proteins become more concentrated. Biochemical Journal, 1996, 313, 921-926.	1.7	26
155	Ca2+ stimulates both the respiratory and phosphorylation subsystems in rat heart mitochondria. Biochemical Journal, 1996, 320, 329-334.	1.7	52
156	Paradoxical control properties of enzymes within pathways: can activation cause an enzyme to have increased control?. Biochemical Journal, 1996, 314, 753-760.	1.7	16
157	Steady-State Characterization of Systems with Moiety-Conservations Made Easy: Matrix Equations of Metabolic Control Analysis and Biochemical System Theory. Journal of Theoretical Biology, 1996, 178, 1-6.	0.8	9
158	Molecular Control Analysis: Control within Proteins and Molecular Processes. Journal of Theoretical Biology, 1996, 182, 389-396.	0.8	17
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160	Direct Transfer of Control and Multidrug Resistance. , 1996, , 283-292.		3
161	The macroworld versus the microworld of biochemical regulation and control. Trends in Biochemical Sciences, 1995, 20, 52-54.	3.7	56
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164	Control in channelled pathways. A matrix method calculating the enzyme control coefficients. Biophysical Chemistry, 1995, 53, 247-258.	1.5	19
165	Defining control coefficients in non-ideal metabolic pathways. Biophysical Chemistry, 1995, 56, 215-226.	1.5	47
166	How to reveal various aspects of regulation in group-transfer pathways. Biochimica Et Biophysica Acta - Bioenergetics, 1995, 1229, 275-289.	0.5	6
167	Control theory of group transfer pathways. Biochimica Et Biophysica Acta - Bioenergetics, 1995, 1229, 256-274.	0.5	16
168	Calcium Indirectly Increases the Control Exerted by the Adenine Nucleotide Translocator over 2-Oxoglutarate Oxidation in Rat Heart Mitochondria. Archives of Biochemistry and Biophysics, 1995, 324, 130-134.	1.4	44
169	Composite control of cell function: metabolic pathways behaving as single control units. FEBS Letters, 1995, 368, 1-4.	1.3	33
170	Control theory of metabolic channelling. Molecular and Cellular Biochemistry, 1994, 133-134, 313-331.	1.4	17
171	Getting to the inside of cells using metabolic control analysis. Biophysical Chemistry, 1994, 50, 273-283.	1.5	35
172	Control theory of one enzyme. BBA - Proteins and Proteomics, 1994, 1208, 294-305.	2.1	24
173	Control by Enzymes, Coenzymes and Conserved Moieties. A Generalisation of the Connectivity Theorem of Metabolic Control Analysis. FEBS Journal, 1994, 225, 179-186.	0.2	29
174	Rate limitation within a single enzyme is directly related to enzyme intermediate levels. FEBS Letters, 1994, 349, 131-134.	1.3	12
175	Control theory of metabolic channelling. , 1994, , 313-331.		0
176	Kinetic models of coupling between H+ and Na+-translocation and ATP synthesis/hydrolysis by F0F1-ATPases: Can a cell utilize both $$Delta ar mu _{H^ + } $$ and $$Delta ar mu _{Na^ + } $$ for ATP synthesis underin vivo conditions using the same enzyme?. Journal of Bioenergetics and Biomembranes, 1993, 25, 285-295.	1.0	3
177	The sum of the control coefficients of all enzymes on the flux through a group-transfer pathway can be as high as two. FEBS Journal, 1993, 212, 791-799.	0.2	56
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182	Sum of the Flux Control Coefficients: What is it Equal to in Different Systems?. , 1993, , 205-210.		1
183	Control of the metabolic flux in a system with high enzyme concentrations and moiety-conserved cycles. The sum of the flux control coefficients can drop significantly below unity. FEBS Journal, 1992, 210, 147-153.	0.2	40
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187	Dynamic stability of steady states and static stabilization in unbranched metabolic pathways. Journal of Mathematical Biology, 1982, 15, 51-63.	0.8	27
188	The Regulation of Glycolysis in Human Erythrocytes. The Dependence of the Glycolytic Flux on the ATP Concentration. FEBS Journal, 1981, 115, 359-365.	0.2	37
189	Mechanistic and modular approaches to modeling and inference of cellular regulatory networks. , 0, , 143-159.		11