Susan S Taylor

List of Publications by Year
in descending order

252	25,516	8755 75	7348 152
papers	citations	h-index	g-index

269	269	269	17561
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Tails of Protein Kinase A. Molecular Pharmacology, 2022, 101, 219-225.	2.3	15
2	A tribute to Eddy Fischer (April 6, 1920â€“August 27, 2021): Passionate biochemist and mentor. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121815119.	7.1	0
3	A non-catalytic herpesviral protein reconfigures ERK-RSK signaling by targeting kinase docking systems in the host. Nature Communications, 2022, 13, 472.	12.8	13
4	LRRK2 dynamics analysis identifies allosteric control of the crosstalk between its catalytic domains. PLoS Biology, 2022, 20, e3001427.	5.6	18
5	Nonâ€canonical Recruitment of PKA Catalytic Subunits to RIÎ±â€driven Biomolecular Condensates. FASEB Journal, 2022, 36, .	0.5	0
6	Integrated regulation of PKA by fast and slow neurotransmission in the nucleus accumbens controls plasticity and stress responses. Journal of Biological Chemistry, 2022, 298, 102245.	3.4	0
7	From structure to the dynamic regulation of a molecular switch: A journey over 3Âdecades. Journal of Biological Chemistry, 2021, 296, 100746.	3.4	49
8	Defective internal allosteric network imparts dysfunctional ATP/substrate-binding cooperativity in oncogenic chimera of protein kinase A. Communications Biology, 2021, 4, 321.	4.4	21
9	mTORC2 controls the activity of PKC and Akt by phosphorylating a conserved TOR interaction motif. Science Signaling, 2021, 14, .	3.6	64
10	Molecular Determinants of PKA RIÎ± Driven Liquidâ€Liquid Phase Separation. FASEB Journal, 2021, 35, .	0.5	0
11	Noncanonical protein kinase A activation by oligomerization of regulatory subunits as revealed by inherited Carney complex mutations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
12	PKA CÎ²: a forgotten catalytic subunit of cAMP-dependent protein kinase opens new windows for PKA signaling and disease pathologies. Biochemical Journal, 2021, 478, 2101-2119.	3.7	13
13	Conformation and dynamics of the kinase domain drive subcellular location and activation of LRRK2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
14	Drugging the Undruggable: How Isoquinolines and PKA Initiated the Era of Designed Protein Kinase Inhibitor Therapeutics. Biochemistry, 2021, 60, 3470-3484.	2.5	5
15	Is Disrupted Nucleotide-Substrate Cooperativity a Common Trait for Cushing's Syndrome Driving Mutations of Protein Kinase A?. Journal of Molecular Biology, 2021, 433, 167123.	4.2	8
16	G<i>Î±</i>sâ€“Protein Kinase A (PKA) Pathway Signalopathies: The Emerging Genetic Landscape and Therapeutic Potential of Human Diseases Driven by Aberrant G<i>Î±</i>s-PKA Signaling. Pharmacological Reviews, 2021, 73, 1326-1368.	16.0	27
17	Protein Kinase A in Human Retina: Differential Localization of CÎ², CÎ±, RIIÎ±, and RIIÎ² in Photoreceptors Highlights Non-redundancy of Protein Kinase A Subunits. Frontiers in Molecular Neuroscience, 2021, 14, 782041.	2.9	4
18	Germline and Mosaic Variants in PRKACA and PRKACB Cause a Multiple Congenital Malformation Syndrome. American Journal of Human Genetics, 2020, 107, 977-988.	6.2	33

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19	Hypothesis: Unifying model of domain architecture for conventional and novel protein kinase C isozymes. IUBMB Life, 2020, 72, 2584-2590.	3.4	9
20	The In Situ Structure of Parkinsonâ€™s Disease-Linked LRRK2. Cell, 2020, 182, 1508-1518.e16.	28.9	135
21	Kinase Domain Is a Dynamic Hub for Driving LRRK2 Allostery. Frontiers in Molecular Neuroscience, 2020, 13, 538219.	2.9	18
22	Phase Separation of a PKA Regulatory Subunit Controls cAMP Compartmentation and Oncogenic Signaling. Cell, 2020, 182, 1531-1544.e15.	28.9	177
23	Allosteric pluripotency as revealed by protein kinase A. Science Advances, 2020, 6, eabb1250.	10.3	25
24	Protein kinase A in the neutron beam: Insights for catalysis from directly observing protons. Methods in Enzymology, 2020, 634, 311-331.	1.0	0
25	Structural analyses of the PKA RIIÎ² holoenzyme containing the oncogenic DnaJB1-PKAc fusion protein reveal protomer asymmetry and fusion-induced allosteric perturbations in fibrolamellar hepatocellular carcinoma. PLoS Biology, 2020, 18, e3001018.	5.6	22
26	Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A. ELife, 2020, 9, .	6.0	16
27	Title is missing!. , 2020, 18, e3001018.		0
28	Title is missing!. , 2020, 18, e3001018.		0
29	Title is missing!. , 2020, 18, e3001018.		0
30	Title is missing!. , 2020, 18, e3001018.		0
31	Title is missing!. , 2020, 18, e3001018.		0
32	Title is missing!. , 2020, 18, e3001018.		0
33	BRAF inhibitors promote intermediate BRAF(V600E) conformations and binary interactions with activated RAS. Science Advances, 2019, 5, eaav8463.	10.3	25
34	The dynamic switch mechanism that leads to activation of LRRK2 is embedded in the DFGÏˆ motif in the kinase domain. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14979-14988.	7.1	66
35	Two PKA RIÎ± holoenzyme states define ATP as an isoform-specific orthosteric inhibitor that competes with the allosteric activator, cAMP. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16347-16356.	7.1	28
36	Dynamic allostery-based molecular workings of kinase:peptide complexes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15052-15061.	7.1	33

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37	Cardiac ischemia-reperfusion injury induces ROS-dependent loss of PKA regulatory subunit RIÎ±. American Journal of Physiology - Heart and Circulatory Physiology, 2019, 317, H1231-H1242.	3.2	23
38	Cushingâ€™s syndrome driver mutation disrupts protein kinase A allosteric network, altering both regulation and substrate specificity. Science Advances, 2019, 5, eaaw9298.	10.3	43
39	Activation of PKA via asymmetric allosteric coupling of structurally conserved cyclic nucleotide binding domains. Nature Communications, 2019, 10, 3984.	12.8	18
40	Tuning the â€œviolinâ€•of protein kinases: The role of dynamicsâ€based allostery. IUBMB Life, 2019, 71, 685-696.	3.4	49
41	Evolution of a dynamic molecular switch. IUBMB Life, 2019, 71, 672-684.	3.4	40
42	Structures of the PKA RIÎ± Holoenzyme with the FLHCC Driver J-PKAcÎ± or Wild-Type PKAcÎ±. Structure, 2019, 27, 816-828.e4.	3.3	27
43	Zooming in on protons: Neutron structure of protein kinase A trapped in a product complex. Science Advances, 2019, 5, eaav0482.	10.3	26
44	Globally correlated conformational entropy underlies positive and negative cooperativity in a kinaseâ€™s enzymatic cycle. Nature Communications, 2019, 10, 799.	12.8	40
45	Disordered Protein Kinase Regions in Regulation of Kinase Domain Cores. Trends in Biochemical Sciences, 2019, 44, 300-311.	7.5	38
46	Crystal structure of the WD40 domain dimer of LRRK2. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1579-1584.	7.1	60
47	GPCR signaling inhibits mTORC1 via PKA phosphorylation of Raptor. ELife, 2019, 8, .	6.0	60
48	A Cushing Syndrome Mutation of Protein Kinase A Câ€subunit Disrupts the Internal Allosteric Network Affecting Regulation and Substrate Specificity. FASEB Journal, 2019, 33, 478.11.	0.5	1
49	A Catalytically Disabled Double Mutant of Src Tyrosine Kinase Can Be Stabilized into an Active-Like Conformation. Journal of Molecular Biology, 2018, 430, 881-889.	4.2	10
50	Conformational Landscape of the PRKACA-DNAJB1 Chimeric Kinase, the Driver for Fibrolamellar Hepatocellular Carcinoma. Scientific Reports, 2018, 8, 720.	3.3	23
51	The gene product of a Trypanosoma equiperdum ortholog of the cAMP-dependent protein kinase regulatory subunit is a monomeric protein that is not capable of binding cyclic nucleotides. Biochimie, 2018, 146, 166-180.	2.6	17
52	Expression of an active GÎ± _s mutant in skeletal stem cells is sufficient and necessary for fibrous dysplasia initiation and maintenance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E428-E437.	7.1	43
53	Switching of the folding-energy landscape governs the allosteric activation of protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7478-E7485.	7.1	15
54	AKAP1 Protects from Cerebral Ischemic Stroke by Inhibiting Drp1-Dependent Mitochondrial Fission. Journal of Neuroscience, 2018, 38, 8233-8242.	3.6	86

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55	Kinase domain dimerization drives RIPK3-dependent necroptosis. Science Signaling, 2018, 11, .	3.6	29
56	GNAS â€PKA Oncosignaling Network in Colorectal Cancer. FASEB Journal, 2018, 32, 695.9.	0.5	2
57	PKA RIÎ± Holoenzyme Crystal Structure Reveals Its Allosteric Regulation and Carney Complex Disease Implications. FASEB Journal, 2018, 32, lb50.	0.5	1
58	Mutation of a kinase allosteric node uncouples dynamics linked to phosphotransfer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E931-E940.	7.1	47
59	Electrostatic Interactions as Mediators in the Allosteric Activation of Protein Kinase A RIÎ±. Biochemistry, 2017, 56, 1536-1545.	2.5	16
60	A dynamic hydrophobic core orchestrates allostery in protein kinases. Science Advances, 2017, 3, e1600663.	10.3	89
61	Integrated Method to Attach DNA Handles and Functionally Select Proteins to Study Folding and Protein-Ligand Interactions with Optical Tweezers. Scientific Reports, 2017, 7, 10843.	3.3	28
62	Sub-mitochondrial localization of genetic-tagged MIB interacting partners: Mic19, Mic60 and Sam50. Journal of Cell Science, 2017, 130, 3248-3260.	2.0	26
63	Isoform-specific subcellular localization and function of protein kinase A identified by mosaic imaging of mouse brain. ELife, 2017, 6, .	6.0	42
64	Gpr161 anchoring of PKA consolidates GPCR and cAMP signaling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7786-7791.	7.1	86
65	Structure of a PKA RIÎ± Recurrent Acrodysostosis Mutant Explains Defective cAMP-Dependent Activation. Journal of Molecular Biology, 2016, 428, 4890-4904.	4.2	19
66	Protein Kinase A (PKA) Type I Interacts with P-Rex1, a Rac Guanine Nucleotide Exchange Factor. Journal of Biological Chemistry, 2016, 291, 6182-6199.	3.4	32
67	Structure of sm<scp>AKAP</scp> and its regulation by <scp>PKA</scp>â€mediated phosphorylation. FEBS Journal, 2016, 283, 2132-2148.	4.7	19
68	Uncoupling Catalytic and Binding Functions in the Cyclic AMP-Dependent Protein Kinase A. Structure, 2016, 24, 353-363.	3.3	19
69	p75 Neurotrophin Receptor Regulates Energy Balance in Obesity. Cell Reports, 2016, 14, 255-268.	6.4	42
70	Decoding the Interactions Regulating the Active State Mechanics of Eukaryotic Protein Kinases. PLoS Biology, 2016, 14, e2000127.	5.6	27
71	Mapping the Free Energy Landscape of PKA Inhibition and Activation: A Double-Conformational Selection Model for the Tandem cAMP-Binding Domains of PKA RIÎ±. PLoS Biology, 2015, 13, e1002305.	5.6	28
72	Discovery of allostery in PKA signaling. Biophysical Reviews, 2015, 7, 227-238.	3.2	14

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73	Mapping the Hydrogen Bond Networks in the Catalytic Subunit of Protein Kinase A Using H/D Fractionation Factors. Biochemistry, 2015, 54, 4042-4049.	2.5	16
74	Intramolecular C2 Domain-Mediated Autoinhibition of Protein Kinase C Î²II. Cell Reports, 2015, 12, 1252-1260.	6.4	47
75	Molecular Features of Product Release for the PKA Catalytic Cycle. Biochemistry, 2015, 54, 2-10.	2.5	26
76	Divalent Metal Ions Mg²⁺ and Ca²⁺ Have Distinct Effects on Protein Kinase A Activity and Regulation. ACS Chemical Biology, 2015, 10, 2303-2315.	3.4	57
77	Allostery through the computational microscope: cAMP activation of a canonical signalling domain. Nature Communications, 2015, 6, 7588.	12.8	81
78	Isoform-specific interactions between meprin metalloproteases and the catalytic subunit of protein kinase A: significance in acute and chronic kidney injury. American Journal of Physiology - Renal Physiology, 2015, 308, F56-F68.	2.7	15
79	Integration of signaling in the kinome: Architecture and regulation of the Î±C Helix. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1567-1574.	2.3	43
80	Matrix stiffness drives epithelialâ€“mesenchymal transition and tumour metastasis through a TWIST1â€“G3BP2 mechanotransduction pathway. Nature Cell Biology, 2015, 17, 678-688.	10.3	699
81	Inactivation of a GÎ±sâ€“PKA tumour suppressor pathway in skin stem cells initiates basal-cell carcinogenesis. Nature Cell Biology, 2015, 17, 793-803.	10.3	134
82	Dysfunctional conformational dynamics of protein kinase A induced by a lethal mutant of phospholamban hinder phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3716-3721.	7.1	43
83	Dynamics-Driven Allostery in Protein Kinases. Trends in Biochemical Sciences, 2015, 40, 628-647.	7.5	237
84	Mechanisms of cyclic AMP/protein kinase A- and glucocorticoid-mediated apoptosis using S49 lymphoma cells as a model system. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12681-12686.	7.1	9
85	An Isoform-Specific Myristylation Switch Targets Type II PKA Holoenzymes to Membranes. Structure, 2015, 23, 1563-1572.	3.3	38
86	Proteomic and Metabolic Analyses of S49 Lymphoma Cells Reveal Novel Regulation of Mitochondria by cAMP and Protein Kinase A. Journal of Biological Chemistry, 2015, 290, 22274-22286.	3.4	9
87	Kinase Regulation by Hydrophobic Spine Assembly in Cancer. Molecular and Cellular Biology, 2015, 35, 264-276.	2.3	98
88	Single Turnover Autophosphorylation Cycle of the PKA RIIÎ² Holoenzyme. PLoS Biology, 2015, 13, e1002192.	5.6	30
89	Cyclic AMP/PKAâ€Mediated Regulation of Mitochondria and Branchedâ€Chain Amino Acid Metabolism in S49 Lymphoma Cells. FASEB Journal, 2015, 29, 896.5.	0.5	0
90	Using Markov State Models to Develop a Mechanistic Understanding of Protein Kinase A Regulatory Subunit RIÎ± Activation in Response to cAMP Binding. Journal of Biological Chemistry, 2014, 289, 30040-30051.	3.4	29

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91	Allosteric linkers in cAMP signalling. Biochemical Society Transactions, 2014, 42, 139-144.	3.4	16
92	Synchronous Opening and Closing Motions Are Essential for cAMP-Dependent Protein Kinase A Signaling. Structure, 2014, 22, 1735-1743.	3.3	55
93	Dynamic architecture of a protein kinase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4623-31.	7.1	205
94	The Roles of the RIIÎ² Linker and N-terminal Cyclic Nucleotide-binding Domain in Determining the Unique Structures of the Type IIÎ² Protein Kinase A. Journal of Biological Chemistry, 2014, 289, 28505-28512.	3.4	5
95	PKA RIÎ± Homodimer Structure Reveals an Intermolecular Interface with Implications for Cooperative cAMP Binding and Carney Complex Disease. Structure, 2014, 22, 59-69.	3.3	37
96	Allosteric Activation of Functionally Asymmetric RAF Kinase Dimers. Cell, 2013, 154, 1036-1046.	28.9	236
97	Insights into the Phosphoryl Transfer Catalyzed by cAMP-Dependent Protein Kinase: An X-ray Crystallographic Study of Complexes with Various Metals and Peptide Substrate SP20. Biochemistry, 2013, 52, 3721-3727.	2.5	24
98	Phosphoryl Transfer by Protein Kinase A Is Captured in a Crystal Lattice. Journal of the American Chemical Society, 2013, 135, 4788-4798.	13.7	74
99	PKA: Lessons learned after twenty years. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1271-1278.	2.3	232
100	Signaling through dynamic linkers as revealed by PKA. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14231-14236.	7.1	94
101	Proteomic analysis of the cAMP/protein kinase A (PKA) signaling pathway identifies PKA as a regulator of cellular response to oxidative stress. FASEB Journal, 2013, 27, 1143.16.	0.5	0
102	AKIP1 protects against cardiac injury via enhanced mitochondrial function. FASEB Journal, 2013, 27, 657.3.	0.5	0
103	Dynamic expression and localization of Protein Kinase A regulatory subunit RIÎ± in cardiac mitochondria controls response to oxidative stress. FASEB Journal, 2013, 27, 1209.22.	0.5	0
104	Cotranslational <i>cis</i> -phosphorylation of the COOH-terminal tail is a key priming step in the maturation of cAMP-dependent protein kinase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1221-9.	7.1	47
105	Structural Basis for the Regulation of Protein Kinase A by Activation Loop Phosphorylation. Journal of Biological Chemistry, 2012, 287, 14672-14680.	3.4	76
106	A Small Novel A-Kinase Anchoring Protein (AKAP) That Localizes Specifically Protein Kinase A-Regulatory Subunit I (PKA-RI) to the Plasma Membrane. Journal of Biological Chemistry, 2012, 287, 43789-43797.	3.4	67
107	Localization and quaternary structure of the PKA RIÎ² holoenzyme. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12443-12448.	7.1	54
108	Evolution of the eukaryotic protein kinases as dynamic molecular switches. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2517-2528.	4.0	181

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109	Conformational Equilibrium of N-Myristoylated cAMP-Dependent Protein Kinase A by Molecular Dynamics Simulations. Biochemistry, 2012, 51, 10186-10196.	2.5	27
110	Structure and Allostery of the PKA RIIÎ² Tetrameric Holoenzyme. Science, 2012, 335, 712-716.	12.6	142
111	Assembly of allosteric macromolecular switches: lessons from PKA. Nature Reviews Molecular Cell Biology, 2012, 13, 646-658.	37.0	374
112	A Conserved Gluâ€"Arg Salt Bridge Connects Coevolved Motifs That Define the Eukaryotic Protein Kinase Fold. Journal of Molecular Biology, 2012, 415, 666-679.	4.2	39
113	Role of N-Terminal Myristylation in the Structure and Regulation of cAMP-Dependent Protein Kinase. Journal of Molecular Biology, 2012, 422, 215-229.	4.2	47
114	Protein kinases: evolution of dynamic regulatory proteins. Trends in Biochemical Sciences, 2011, 36, 65-77.	7.5	753
115	Isoform-specific targeting of PKA to multivesicular bodies. Journal of Cell Biology, 2011, 193, 347-363.	5.2	30
116	Mutation that blocks ATP binding creates a pseudokinase stabilizing the scaffolding function of kinase suppressor of Ras, CRAF and BRAF. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6067-6072.	7.1	116
117	Dynamically committed, uncommitted, and quenched states encoded in protein kinase A revealed by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6969-6974.	7.1	129
118	Cyclic AMP Analog Blocks Kinase Activation by Stabilizing Inactive Conformation: Conformational Selection Highlights a New Concept in Allosteric Inhibitor Design. Molecular and Cellular Proteomics, 2011, 10, M110.004390.	3.8	62
119	Structure of D-AKAP2:PKA RI Complex: Insights into AKAP Specificity and Selectivity. Structure, 2010, 18, 155-166.	3.3	98
120	Dynamics connect substrate recognition to catalysis in protein kinase A. Nature Chemical Biology, 2010, 6, 821-828.	8.0	182
121	Cyclic AMP- and (Rp)-cAMPS-induced Conformational Changes in a Complex of the Catalytic and Regulatory (RIÎ±) Subunits of Cyclic AMP-dependent Protein Kinase. Molecular and Cellular Proteomics, 2010, 9, 2225-2237.	3.8	28
122	Global Consequences of Activation Loop Phosphorylation on Protein Kinase A. Journal of Biological Chemistry, 2010, 285, 3825-3832.	3.4	73
123	Communication between Tandem cAMP Binding Domains in the Regulatory Subunit of Protein Kinase A-IÎ± as Revealed by Domain-silencing Mutations. Journal of Biological Chemistry, 2010, 285, 15523-15537.	3.4	46
124	Disruption of Protein Kinase A Localization Using a Trans-activator of Transcription (TAT)-conjugated A-kinase-anchoring Peptide Reduces Cardiac Function. Journal of Biological Chemistry, 2010, 285, 27632-27640.	3.4	40
125	Yet another â€œactiveâ€• pseudokinase, Erb3. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8047-8048.	7.1	16
126	Structure of Dâ€AKAP2â€PKA RI isoform complex: Insights into AKAP specificity and selectivity. FASEB Journal, 2010, 24, 866.3.	0.5	0

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127	Defining the Conserved Internal Architecture of a Protein Kinase. FASEB Journal, 2010, 24, 864.3.	0.5	0
128	ChChd3, an Inner Mitochondrial Membrane Protein is Essential for Maintaining Cristae Integrity and Mitochondrial Function. FASEB Journal, 2010, 24, 510.4.	0.5	1
129	Dynamics of PKA Signaling. FASEB Journal, 2010, 24, 309.1.	0.5	0
130	Contribution of Non-catalytic Core Residues to Activity and Regulation in Protein Kinase A. Journal of Biological Chemistry, 2009, 284, 6241-6248.	3.4	44
131	The Chaperones Hsp90 and Cdc37 Mediate the Maturation and Stabilization of Protein Kinase C through a Conserved PXXP Motif in the C-terminal Tail*. Journal of Biological Chemistry, 2009, 284, 4921-4935.	3.4	97
132	A chimeric mechanism for polyvalent <i>trans</i>â€phosphorylation of PKA by PDK1. Protein Science, 2009, 18, 1486-1497.	7.6	33
133	A Transition Path Ensemble Study Reveals a Linchpin Role for Mg²⁺ during Rate-Limiting ADP Release from Protein Kinase A. Biochemistry, 2009, 48, 11532-11545.	2.5	50
134	Identifying Critical Non-Catalytic Residues that Modulate Protein Kinase A Activity. PLoS ONE, 2009, 4, e4746.	2.5	15
135	Regulation of NFâ€ĸB Nuclear Translocation by AKIP and PKAc. FASEB Journal, 2009, 23, .	0.5	0
136	Architecture of the PKA RIIÎ² Holoenzyme. FASEB Journal, 2009, 23, 709.11.	0.5	0
137	Evolution of PKA Signaling: Structure of Yeast Regulatory Subunit. FASEB Journal, 2009, 23, 709.10.	0.5	0
138	Dâ€AKAP2 interacts with Rab4 and Rab11 through its RGS domains and regulates transferrin recycling. FASEB Journal, 2009, 23, 877.6.	0.5	0
139	Signaling through cAMP and cAMP-dependent protein kinase: Diverse strategies for drug design. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 16-26.	2.3	184
140	Allosteric cooperativity in protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 506-511.	7.1	154
141	A helix scaffold for the assembly of active protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14377-14382.	7.1	371
142	A Generalized Allosteric Mechanism for cis-Regulated Cyclic Nucleotide Binding Domains. PLoS Computational Biology, 2008, 4, e1000056.	3.2	55
143	PKA Type IIa Holoenzyme Structure Reveals Isoform Diversity for Inhibition of Catalysis. FASEB Journal, 2008, 22, 1011.3.	0.5	0
144	Mitochondrial ChChD3 acts as a Scaffold for Mitofilin, Sam50 and PKA. FASEB Journal, 2008, 22, 645.20.	0.5	4

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145	Crystallization of PKA regulatory subunit from Saccharomyces cerevisiae. FASEB Journal, 2008, 22, 1050.13.	0.5	0
146	Evolution of allostery in the cyclic nucleotide binding module: A comparative genomics study. FASEB Journal, 2008, 22, 828.3.	0.5	0
147	The RGS homology domains of Dâ€AKAP2 regulate the endocytic recycling compartment through complexes with Rab4 and Rab11. FASEB Journal, 2008, 22, 816.6.	0.5	0
148	Conserved hydrophobic ensembles in protein kinases: their integrating and regulatory roles. FASEB Journal, 2008, 22, 1048.12.	0.5	0
149	Deciphering the Role of Disulfide Bonds in RIalpha. FASEB Journal, 2008, 22, 1044.14.	0.5	0
150	The hallmark of AGC kinase functional divergence is its C-terminal tail, a cis-acting regulatory module. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1272-1277.	7.1	199
151	cAMP activation of PKA defines an ancient signaling mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 93-98.	7.1	113
152	PKA-I Holoenzyme Structure Reveals a Mechanism for cAMP-Dependent Activation. Cell, 2007, 130, 1032-1043.	28.9	303
153	Evolution of allostery in the cyclic nucleotide binding module. Genome Biology, 2007, 8, R264.	9.6	87
154	PKA Type IIÎ± Holoenzyme Reveals a Combinatorial Strategy for Isoform Diversity. Science, 2007, 318, 274-279.	12.6	103
155	AKIP1, PKA, and AIF: Human Embryonic Stem Cells Dance Towards Death. FASEB Journal, 2007, 21, A987.	0.5	0
156	Characterization of chchd3; A novel cAMP dependent protein kinase A substrate in mitochondria. FASEB Journal, 2007, 21, A986.	0.5	0
157	The mitochondrial targeting form of PKA anchoring protein Dâ€AKAP1a may affect the structure of mitochondria cristae and the function of mitochondria. FASEB Journal, 2007, 21, A987.	0.5	0
158	Dynamics of Signaling by PKA. FASEB Journal, 2007, 21, A204.	0.5	0
159	Solution Scattering Reveals Large Differences in the Global Structures of Type II Protein Kinase A Isoforms. Journal of Molecular Biology, 2006, 357, 880-889.	4.2	34
160	A Dynamic Mechanism for AKAP Binding to RII Isoforms of cAMP-Dependent Protein Kinase. Molecular Cell, 2006, 24, 397-408.	9.7	176
161	Surface comparison of active and inactive protein kinases identifies a conserved activation mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17783-17788.	7.1	632
162	The role of Dâ€AKAP2 scaffolding in integration of PKA signaling. FASEB Journal, 2006, 20, LB73.	0.5	0

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163	Crystal Structure of Type IIa Holoenzyme of PKA Defines the Molecular Basis of Isoform Diversity. FASEB Journal, 2006, 20, LB59.	0.5	0
164	Crystal structure of a complex between the catalytic and regulatory (RI alpha 91â€379) subunits of PKA. FASEB Journal, 2006, 20, A492.	0.5	2
165	Dynamics of signaling by PKA. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1754, 25-37.	2.3	215
166	Crystal structure of the E230Q mutant of cAMP-dependent protein kinase reveals an unexpected apoenzyme conformation and an extended N-terminal A helix. Protein Science, 2005, 14, 2871-2879.	7.6	31
167	Consequences of Lysine 72 Mutation on the Phosphorylation and Activation State of cAMP-dependent Kinase. Journal of Biological Chemistry, 2005, 280, 8800-8807.	3.4	68
168	The cAMP binding domain: An ancient signaling module. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 45-50.	7.1	190
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