Susan S Taylor

List of Publications by Year
in descending order

252 papers	25,516 citations	8749 75 h-index	7340 152 g-index
269 all docs	269 docs citations	269 times ranked	17561 citing authors

#	Article	IF	Citations
1	Crystal structure of the catalytic subunit of cyclic adenosine monophosphate-dependent protein kinase. Science, 1991, 253, 407-414.	6.0	1,756
2	Identification of a signal for rapid export of proteins from the nucleus. Cell, 1995, 82, 463-473.	13.5	1,148
3	Structure of a peptide inhibitor bound to the catalytic subunit of cyclic adenosine monophosphate-dependent protein kinase. Science, 1991, 253, 414-420.	6.0	988
4	Regulation of Protein Kinases. Molecular Cell, 2004, 15, 661-675.	4.5	972
5	Protein kinases: evolution of dynamic regulatory proteins. Trends in Biochemical Sciences, 2011, 36, 65-77.	3.7	753
6	Matrix stiffness drives epithelialâ€“mesenchymal transition and tumour metastasis through a TWIST1â€“G3BP2 mechanotransduction pathway. Nature Cell Biology, 2015, 17, 678-688.	4.6	699
7	Fluorescence ratio imaging of cyclic AMP in single cells. Nature, 1991, 349, 694-697.	13.7	672
8	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.	3.3	632
9	Crystal structure of the catalytic subunit of cAMP-dependent protein kinase complexed with magnesium-ATP and peptide inhibitor. Biochemistry, 1993, 32, 2154-2161.	1.2	571
10	A genetically encoded, fluorescent indicator for cyclic AMP in living cells. Nature Cell Biology, 2000, 2, 25-29.	4.6	474
11	Primary structure of Torpedo californica acetylcholinesterase deduced from its cDNA sequence. Nature, 1986, 319, 407-409.	13.7	437
12	Regulatory subunit of protein kinase A: structure of deletion mutant with cAMP binding domains. Science, 1995, 269, 807-813.	6.0	378
13	Assembly of allosteric macromolecular switches: lessons from PKA. Nature Reviews Molecular Cell Biology, 2012, 13, 646-658.	16.1	374
14	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.	3.3	371
15	Direct evidence that oncogenic tyrosine kinases and cyclic AMP-dependent protein kinase have homologous ATP-binding sites. Nature, 1984, 310, 589-592.	13.7	369
16	Dynamics of cAMP-Dependent Protein Kinase. Chemical Reviews, 2001, 101, 2243-2270.	23.0	366
17	Three protein kinase structures define a common motif. Structure, 1994, 2, 345-355.	1.6	358
18	2.2 Ã… refined crystal structure of the catalytic subunit of cAMP-dependent protein kinase complexed with MnATP and a peptide inhibitor. Acta Crystallographica Section D: Biological Crystallography, 1993, 49, 362-365.	2.5	319

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19	Crystal Structure of a Complex Between the Catalytic and Regulatory (RIÂ) Subunits of PKA. Science, 2005, 307, 690-696.	6.0	309
20	Crystal structures of the myristylated catalytic subunit of cAMPâ€dependent protein kinase reveal open and closed conformations. Protein Science, 1993, 2, 1559-1573.	3.1	305
21	PKA-I Holoenzyme Structure Reveals a Mechanism for cAMP-Dependent Activation. Cell, 2007, 130, 1032-1043.	13.5	303
22	PKA: a portrait of protein kinase dynamics. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1697, 259-269.	1.1	269
23	cAMPâ€dependent protein kinase: Crystallographic insights into substrate recognition and phosphotransfer. Protein Science, 1994, 3, 176-187.	3.1	256
24	Identification of a Novel Protein Kinase A Anchoring Protein That Binds Both Type I and Type II Regulatory Subunits. Journal of Biological Chemistry, 1997, 272, 8057-8064.	1.6	256
25	Protein N-myristoylation in Escherichia coli: reconstitution of a eukaryotic protein modification in bacteria.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 1506-1510.	3.3	249
26	Dynamics-Driven Allostery in Protein Kinases. Trends in Biochemical Sciences, 2015, 40, 628-647.	3.7	237
27	Allosteric Activation of Functionally Asymmetric RAF Kinase Dimers. Cell, 2013, 154, 1036-1046.	13.5	236
28	PKA: Lessons learned after twenty years. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1271-1278.	1.1	232
29	Dynamics of signaling by PKA. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1754, 25-37.	1.1	215
30	D-AKAP2, a novel protein kinase A anchoring protein with a putative RGS domain. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 11184-11189.	3.3	212
31	A template for the protein kinase family. Trends in Biochemical Sciences, 1993, 18, 84-89.	3.7	210
32	Dynamic architecture of a protein kinase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4623-31.	3.3	205
33	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.	3.3	199
34	cAMP-dependent protein kinase. Model for an enzyme family. Journal of Biological Chemistry, 1989, 264, 8443-6.	1.6	198
35	Crystal structure of a transition state mimic of the catalytic subunit of cAMP-dependent protein kinase. Nature Structural Biology, 2002, 9, 273-277.	9.7	192
36	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.	3.3	190

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37	Signaling through cAMP and cAMP-dependent protein kinase: Diverse strategies for drug design. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 16-26.	1.1	184
38	Dynamics connect substrate recognition to catalysis in protein kinase A. Nature Chemical Biology, 2010, 6, 821-828.	3.9	182
39	Evolution of the eukaryotic protein kinases as dynamic molecular switches. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2517-2528.	1.8	181
40	Phase Separation of a PKA Regulatory Subunit Controls cAMP Compartmentation and Oncogenic Signaling. Cell, 2020, 182, 1531-1544.e15.	13.5	177
41	A Dynamic Mechanism for AKAP Binding to RII Isoforms of cAMP-Dependent Protein Kinase. Molecular Cell, 2006, 24, 397-408.	4.5	176
42	How do protein kinases discriminate between serine/threonine and tyrosine? Structural insights from the insulin receptor proteinâ€tyrosine kinase. FASEB Journal, 1995, 9, 1255-1266.	0.2	174
43	Expression of the Catalytic Subunit of cAMP-Dependent Protein Kinase in Escherichia coli. Journal of Biological Chemistry, 1989, 264, 20940-20946.	1.6	174
44	Movement of the free catalytic subunit of cAMP-dependent protein kinase into and out of the nucleus can be explained by diffusion.. Molecular Biology of the Cell, 1993, 4, 993-1002.	0.9	164
45	Regulation of cAMP-dependent Protein Kinase Activity by Glutathionylation. Journal of Biological Chemistry, 2002, 277, 43505-43511.	1.6	159
46	Allosteric cooperativity in protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 506-511.	3.3	154
47	NH2-Terminal Targeting Motifs Direct Dual Specificity A-Kinaseâ€"anchoring Protein 1 (D-AKAP1) to Either Mitochondria or Endoplasmic Reticulum. Journal of Cell Biology, 1999, 145, 951-959.	2.3	147
48	Structure and Allostery of the PKA RIIÎ² Tetrameric Holoenzyme. Science, 2012, 335, 712-716.	6.0	142
49	The In Situ Structure of Parkinsonâ€™s Disease-Linked LRRK2. Cell, 2020, 182, 1508-1518.e16.	13.5	135
50	Inactivation of a GÎ±sâ€"PKA tumour suppressor pathway in skin stem cells initiates basal-cell carcinogenesis. Nature Cell Biology, 2015, 17, 793-803.	4.6	134
51	Molecular Basis for Regulatory Subunit Diversity in cAMP-Dependent Protein Kinase. Structure, 2001, 9, 73-82.	1.6	133
52	Dynamic Features of cAMP-dependent Protein Kinase Revealed by Apoenzyme Crystal Structure. Journal of Molecular Biology, 2003, 327, 159-171.	2.0	129
53	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.	3.3	129
54	Active Site Mutations Define the Pathway for the Cooperative Activation of cAMP-Dependent Protein Kinaseâ€. Biochemistry, 1996, 35, 2934-2942.	1.2	121

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55	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.	3.3	116
56	Crystal Structure of a Polyhistidine-Tagged Recombinant Catalytic Subunit of cAMP-Dependent Protein Kinase Complexed with the Peptide Inhibitor PKI(5â^'24) and Adenosineâ€. Biochemistry, 1997, 36, 4438-4448.	1.2	113
57	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.	3.3	113
58	A-kinase-interacting protein localizes protein kinase A in the nucleus. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 349-354.	3.3	112
59	PKR and eIF2Î±: Integration of Kinase Dimerization, Activation, and Substrate Docking. Cell, 2005, 122, 823-825.	13.5	112
60	PKA Type IIÎ± Holoenzyme Reveals a Combinatorial Strategy for Isoform Diversity. Science, 2007, 318, 274-279.	6.0	103
61	Crystal Structure of the Potent Natural Product Inhibitor Balanol in Complex with the Catalytic Subunit of cAMP-Dependent Protein Kinaseâ€. Biochemistry, 1999, 38, 2367-2376.	1.2	98
62	Structure of D-AKAP2:PKA RI Complex: Insights into AKAP Specificity and Selectivity. Structure, 2010, 18, 155-166.	1.6	98
63	Kinase Regulation by Hydrophobic Spine Assembly in Cancer. Molecular and Cellular Biology, 2015, 35, 264-276.	1.1	98
64	cAMPâ€dependent protein kinase: prototype for a family of enzymes. FASEB Journal, 1988, 2, 2677-2685.	0.2	97
65	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.	1.6	97
66	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.	3.3	94
67	A dynamic hydrophobic core orchestrates allostery in protein kinases. Science Advances, 2017, 3, e1600663.	4.7	89
68	Identifying the molecular switches that determine whether (Rp)-cAMPS functions as an antagonist or an agonist in the activation of cAMP-dependent protein kinase I. Biochemistry, 1991, 30, 8710-8716.	1.2	87
69	Crosstalk between Domains in the Regulatory Subunit of cAMP-Dependent Protein Kinase: Influence of Amino Terminus on cAMP Binding and Holoenzyme Formation. Biochemistry, 1994, 33, 7485-7494.	1.2	87
70	Evolution of allostery in the cyclic nucleotide binding module. Genome Biology, 2007, 8, R264.	13.9	87
71	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.	3.3	86
72	AKAP1 Protects from Cerebral Ischemic Stroke by Inhibiting Drp1-Dependent Mitochondrial Fission. Journal of Neuroscience, 2018, 38, 8233-8242.	1.7	86

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73	Dissection of the Nucleotide and Metalâ˘Phosphate Binding Sites in cAMP-Dependent Protein Kinaseâ€. Biochemistry, 1999, 38, 6352-6360.	1.2	84
74	Kinetic Analyses of Mutations in the Glycine-Rich Loop of cAMP-Dependent Protein Kinaseâ€. Biochemistry, 1998, 37, 7708-7715.	1.2	82
75	Allostery through the computational microscope: cAMP activation of a canonical signalling domain. Nature Communications, 2015, 6, 7588.	5.8	81
76	Divalent metal ions influence catalysis and activeâ€site accessibility in the campâ€dependent protein kinase. Protein Science, 1993, 2, 2177-2186.	3.1	79
77	Crystal Structure of a cAMP-dependent Protein Kinase Mutant at 1.26 Ã…: New Insights into the Catalytic Mechanism. Journal of Molecular Biology, 2004, 336, 473-487.	2.0	78
78	A conserved helix motif complements the protein kinase core.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 10618-10622.	3.3	77
79	Conserved water molecules contribute to the extensive network of interactions at the active site of protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 484-491.	3.3	76
80	Structural Basis for the Regulation of Protein Kinase A by Activation Loop Phosphorylation. Journal of Biological Chemistry, 2012, 287, 14672-14680.	1.6	76
81	Phosphoryl Transfer by Protein Kinase A Is Captured in a Crystal Lattice. Journal of the American Chemical Society, 2013, 135, 4788-4798.	6.6	74
82	Global Consequences of Activation Loop Phosphorylation on Protein Kinase A. Journal of Biological Chemistry, 2010, 285, 3825-3832.	1.6	73
83	Identification of a Partially Rate-Determining Step in the Catalytic Mechanism of cAMP-Dependent Protein Kinase:â€‰ A Transient Kinetic Study Using Stopped-Flow Fluorescence Spectroscopy. Biochemistry, 1997, 36, 6717-6724.	1.2	72
84	Identification of aspartate-184 as an essential residue in the catalytic subunit of cAMP-dependent protein kinase. Biochemistry, 1988, 27, 7356-7361.	1.2	71
85	Crystal Structures of RIÎ± Subunit of Cyclic Adenosine 5â€˜-Monophosphate (cAMP)-Dependent Protein Kinase Complexed with (Rp)-Adenosine 3â€˜,5â€˜-Cyclic Monophosphothioate and (Sp)-Adenosine 3â€˜,5â€˜-Cyclic Monophosphothioate, the Phosphothioate Analogues of cAMPâ€,â€¡. Biochemistry, 2004, 43, 6620-6629.	1.2	71
86	Consequences of Lysine 72 Mutation on the Phosphorylation and Activation State of cAMP-dependent Kinase. Journal of Biological Chemistry, 2005, 280, 8800-8807.	1.6	68
87	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.	1.6	67
88	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.	3.3	66
89	Dimerization/Docking Domain of the Type IÎ± Regulatory Subunit of cAMP-dependent Protein Kinase. Journal of Biological Chemistry, 1998, 273, 35048-35055.	1.6	65
90	2.0 Ã… refined crystal structure of the catalytic subunit of cAMP-dependent protein kinase complexed with a peptide inhibitor and detergent. Acta Crystallographica Section D: Biological Crystallography, 1993, 49, 357-361.	2.5	64

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91	mTORC2 controls the activity of PKC and Akt by phosphorylating a conserved TOR interaction motif. Science Signaling, 2021, 14, .	1.6	64
92	Importance of the A-helix of the catalytic subunit of cAMP-dependent protein kinase for stability and for orienting subdomains at the cleft interface. Protein Science, 1997, 6, 569-579.	3.1	62
93	Dissecting cAMP Binding Domain A in the RIÎ± Subunit of cAMP-dependent Protein Kinase. Journal of Biological Chemistry, 1998, 273, 26739-26746.	1.6	62
94	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.	2.5	62
95	Allosteric Network of cAMP-dependent Protein Kinase Revealed by Mutation of Tyr204 in the P+1 Loop. Journal of Molecular Biology, 2005, 346, 191-201.	2.0	60
96	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.	3.3	60
97	GPCR signaling inhibits mTORC1 via PKA phosphorylation of Raptor. ELife, 2019, 8, .	2.8	60
98	RIÎ± Subunit of PKA. Structure, 2004, 12, 1057-1065.	1.6	58
99	Divalent Metal Ions Mg²⁺ and Ca²⁺ Have Distinct Effects on Protein Kinase A Activity and Regulation. ACS Chemical Biology, 2015, 10, 2303-2315.	1.6	57
100	A Generalized Allosteric Mechanism for cis-Regulated Cyclic Nucleotide Binding Domains. PLoS Computational Biology, 2008, 4, e1000056.	1.5	55
101	Synchronous Opening and Closing Motions Are Essential for cAMP-Dependent Protein Kinase A Signaling. Structure, 2014, 22, 1735-1743.	1.6	55
102	cAMP-dependent Protein Kinase Regulatory Subunit Type IIÎ². Journal of Biological Chemistry, 2004, 279, 7029-7036.	1.6	54
103	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.	3.3	54
104	Identification of phosphorylation sites in the recombinant catalytic subunit of cAMP-dependent protein kinase. Journal of Biological Chemistry, 1993, 268, 18626-32.	1.6	54
105	Protein kinases: A diverse family of related proteins. BioEssays, 1987, 7, 24-29.	1.2	52
106	Selective protection of sulfhydryl groups in cAMP-dependent protein kinase II.. Journal of Biological Chemistry, 1983, 258, 10981-10987.	1.6	52
107	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.	1.2	50
108	600 ps Molecular dynamics reveals stable substructures and flexible hinge points in cAMP dependent protein kinase. , 1999, 50, 513-524.		49

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109	Tuning the â€œviolinâ€•of protein kinases: The role of dynamicsâ€based allostery. IUBMB Life, 2019, 71, 685-696.	1.5	49
110	From structure to the dynamic regulation of a molecular switch: A journey over 3Âdecades. Journal of Biological Chemistry, 2021, 296, 100746.	1.6	49
111	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.	3.3	47
112	Role of N-Terminal Myristylation in the Structure and Regulation of cAMP-Dependent Protein Kinase. Journal of Molecular Biology, 2012, 422, 215-229.	2.0	47
113	Intramolecular C2 Domain-Mediated Autoinhibition of Protein Kinase C Î²II. Cell Reports, 2015, 12, 1252-1260.	2.9	47
114	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.	3.3	47
115	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.	1.6	46
116	Contribution of Non-catalytic Core Residues to Activity and Regulation in Protein Kinase A. Journal of Biological Chemistry, 2009, 284, 6241-6248.	1.6	44
117	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.	1.1	43
118	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.	3.3	43
119	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.	3.3	43
120	Cushingâ€™s syndrome driver mutation disrupts protein kinase A allosteric network, altering both regulation and substrate specificity. Science Advances, 2019, 5, eaaw9298.	4.7	43
121	Effect of the thermostable protein kinase inhibitor on intracellular localization of the catalytic subunit of cAMP-dependent protein kinase. Journal of Biological Chemistry, 1992, 267, 16824-8.	1.6	43
122	Differential labeling and identification of the cysteine-containing tryptic peptides of catalytic subunit from porcine heart cAMP-dependent protein kinase. Journal of Biological Chemistry, 1981, 256, 3743-50.	1.6	43
123	p75 Neurotrophin Receptor Regulates Energy Balance in Obesity. Cell Reports, 2016, 14, 255-268.	2.9	42
124	Isoform-specific subcellular localization and function of protein kinase A identified by mosaic imaging of mouse brain. ELife, 2017, 6, .	2.8	42
125	Differential Binding of cAMP-dependent Protein Kinase Regulatory Subunit Isoforms IÎ± and IIÎ² to the Catalytic Subunit. Journal of Biological Chemistry, 2001, 276, 4102-4108.	1.6	40
126	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.	1.6	40

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127	Evolution of a dynamic molecular switch. IUBMB Life, 2019, 71, 672-684.	1.5	40
128	Globally correlated conformational entropy underlies positive and negative cooperativity in a kinaseâ€™s enzymatic cycle. Nature Communications, 2019, 10, 799.	5.8	40
129	A Conserved Gluâ€"Arg Salt Bridge Connects Coevolved Motifs That Define the Eukaryotic Protein Kinase Fold. Journal of Molecular Biology, 2012, 415, 666-679.	2.0	39
130	cAMP-dependent protein kinase defines a family of enzymes. Philosophical Transactions of the Royal Society B: Biological Sciences, 1993, 340, 315-324.	1.8	38
131	An Isoform-Specific Myristylation Switch Targets Type II PKA Holoenzymes to Membranes. Structure, 2015, 23, 1563-1572.	1.6	38
132	Disordered Protein Kinase Regions in Regulation of Kinase Domain Cores. Trends in Biochemical Sciences, 2019, 44, 300-311.	3.7	38
133	Backbone Flexibility of Five Sites on the Catalytic Subunit of cAMP-Dependent Protein Kinase in the Open and Closed Conformations. Biochemistry, 1998, 37, 13728-13735.	1.2	37
134	PKA RIÎ± Homodimer Structure Reveals an Intermolecular Interface with Implications for Cooperative cAMP Binding and Carney Complex Disease. Structure, 2014, 22, 59-69.	1.6	37
135	Examination of an activeâ€site electrostatic node in the cAMPâ€dependent protein kinase catalytic subunit. Protein Science, 1996, 5, 1316-1324.	3.1	36
136	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, .	3.3	35
137	Solution Scattering Reveals Large Differences in the Global Structures of Type II Protein Kinase A Isoforms. Journal of Molecular Biology, 2006, 357, 880-889.	2.0	34
138	A chimeric mechanism for polyvalent <i>trans</i>â€phosphorylation of PKA by PDK1. Protein Science, 2009, 18, 1486-1497.	3.1	33
139	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.	3.3	33
140	Germline and Mosaic Variants in PRKACA and PRKACB Cause a Multiple Congenital Malformation Syndrome. American Journal of Human Genetics, 2020, 107, 977-988.	2.6	33
141	Protein Kinase A (PKA) Type I Interacts with P-Rex1, a Rac Guanine Nucleotide Exchange Factor. Journal of Biological Chemistry, 2016, 291, 6182-6199.	1.6	32
142	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.	3.1	31
143	Selective protection of sulfhydryl groups in cAMP-dependent protein kinase II. Journal of Biological Chemistry, 1983, 258, 10981-7.	1.6	31
144	Consequences of cAMP-Binding Site Mutations on the Structural Stability of the Type I Regulatory Subunit of cAMP-Dependent Protein Kinase. Biochemistry, 2000, 39, 15022-15031.	1.2	30

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145	Isoform-specific targeting of PKA to multivesicular bodies. Journal of Cell Biology, 2011, 193, 347-363.	2.3	30
146	Single Turnover Autophosphorylation Cycle of the PKA RIIÎ² Holoenzyme. PLoS Biology, 2015, 13, e1002192.	2.6	30
147	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.	1.6	29
148	Kinase domain dimerization drives RIPK3-dependent necroptosis. Science Signaling, 2018, 11, .	1.6	29
149	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.	2.5	28
150	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.	2.6	28
151	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.	1.6	28
152	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.	3.3	28
153	Conformational Equilibrium of N-Myristoylated cAMP-Dependent Protein Kinase A by Molecular Dynamics Simulations. Biochemistry, 2012, 51, 10186-10196.	1.2	27
154	Structures of the PKA RIÎ± Holoenzyme with the FLHCC Driver J-PKAcÎ± or Wild-Type PKAcÎ±. Structure, 2019, 27, 816-828.e4.	1.6	27
155	Decoding the Interactions Regulating the Active State Mechanics of Eukaryotic Protein Kinases. PLoS Biology, 2016, 14, e2000127.	2.6	27
156	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.	7.1	27
157	Molecular Features of Product Release for the PKA Catalytic Cycle. Biochemistry, 2015, 54, 2-10.	1.2	26
158	Sub-mitochondrial localization of genetic-tagged MIB interacting partners: Mic19, Mic60 and Sam50. Journal of Cell Science, 2017, 130, 3248-3260.	1.2	26
159	Zooming in on protons: Neutron structure of protein kinase A trapped in a product complex. Science Advances, 2019, 5, eaav0482.	4.7	26
160	Recombinant Strategies for Rapid Purification of Catalytic Subunits of cAMP-Dependent Protein Kinase. Analytical Biochemistry, 1997, 245, 115-122.	1.1	25
161	Two wellâ€defined motifs in the cAMPâ€dependent protein kinase inhibitor (PKIÎ±) correlate with inhibitory and nuclear export function. Protein Science, 1999, 8, 545-553.	3.1	25
162	BRAF inhibitors promote intermediate BRAF(V600E) conformations and binary interactions with activated RAS. Science Advances, 2019, 5, eaav8463.	4.7	25

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163	Allosteric pluripotency as revealed by protein kinase A. Science Advances, 2020, 6, eabb1250.	4.7	25
164	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.	1.2	24
165	cAMP-dependent Protein Kinase: A Framework for a Diverse Family of Enzymes. Cold Spring Harbor Symposia on Quantitative Biology, 1988, 53, 121-130.	2.0	24
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