

John Kuriyan

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140
papers

25,753
citations

70
h-index

160
g-index

165
ext. papers

28,586
ext. citations

22.4
avg, IF

6.79
L-index

#	Paper	IF	Citations
140	Structural mechanism for STI-571 inhibition of abelson tyrosine kinase. <i>Science</i> , 2000 , 289, 1938-42	33.3	1546
139	Multiple BCR-ABL kinase domain mutations confer polyclonal resistance to the tyrosine kinase inhibitor imatinib (STI571) in chronic phase and blast crisis chronic myeloid leukemia. <i>Cancer Cell</i> , 2002 , 2, 117-25	24.3	1402
138	The conformational plasticity of protein kinases. <i>Cell</i> , 2002 , 109, 275-82	56.2	1355
137	An allosteric mechanism for activation of the kinase domain of epidermal growth factor receptor. <i>Cell</i> , 2006 , 125, 1137-49	56.2	1137
136	Crystal structure of the Src family tyrosine kinase Hck. <i>Nature</i> , 1997 , 385, 602-9	50.4	1075
135	Crystal structure of the eukaryotic DNA polymerase processivity factor PCNA. <i>Cell</i> , 1994 , 79, 1233-43	56.2	760
134	Three-dimensional structure of the catalytic subunit of protein serine/threonine phosphatase-1. <i>Nature</i> , 1995 , 376, 745-53	50.4	751
133	Three-dimensional structure of the beta subunit of E. coli DNA polymerase III holoenzyme: a sliding DNA clamp. <i>Cell</i> , 1992 , 69, 425-37	56.2	688
132	Structure of the C-terminal region of p21(WAF1/CIP1) complexed with human PCNA. <i>Cell</i> , 1996 , 87, 297-306	50.4	665
131	Structural basis for the autoinhibition of c-Abl tyrosine kinase. <i>Cell</i> , 2003 , 112, 859-71	56.2	661
130	Crystal structure of the phosphotyrosine recognition domain SH2 of v-src complexed with tyrosine-phosphorylated peptides. <i>Nature</i> , 1992 , 358, 646-53	50.4	651
129	Crystal structures of the kinase domain of c-Abl in complex with the small molecule inhibitors PD173955 and imatinib (STI-571). <i>Cancer Research</i> , 2002 , 62, 4236-43	10.1	634
128	The structural basis of the activation of Ras by Sos. <i>Nature</i> , 1998 , 394, 337-43	50.4	616
127	Activation of the Src-family tyrosine kinase Hck by SH3 domain displacement. <i>Nature</i> , 1997 , 385, 650-3	50.4	559
126	Modular peptide recognition domains in eukaryotic signaling. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997 , 26, 259-88		477
125	Mechanism for activation of the EGF receptor catalytic domain by the juxtamembrane segment. <i>Cell</i> , 2009 , 137, 1293-307	56.2	432
124	Crystal structure of Hck in complex with a Src family-selective tyrosine kinase inhibitor. <i>Molecular Cell</i> , 1999 , 3, 639-48	17.6	384

123	Architecture and membrane interactions of the EGF receptor. <i>Cell</i> , 2013 , 152, 557-69	56.2	339
122	Conformational coupling across the plasma membrane in activation of the EGF receptor. <i>Cell</i> , 2013 , 152, 543-56	56.2	337
121	Structural evidence for feedback activation by Ras.GTP of the Ras-specific nucleotide exchange factor SOS. <i>Cell</i> , 2003 , 112, 685-95	56.2	337
120	Structural analysis of a eukaryotic sliding DNA clamp-clamp loader complex. <i>Nature</i> , 2004 , 429, 724-30	50.4	335
119	A myristoyl/phosphotyrosine switch regulates c-Abl. <i>Cell</i> , 2003 , 112, 845-57	56.2	332
118	Dynamic coupling between the SH2 and SH3 domains of c-Src and Hck underlies their inactivation by C-terminal tyrosine phosphorylation. <i>Cell</i> , 2001 , 105, 115-26	56.2	329
117	Activation of tyrosine kinases by mutation of the gatekeeper threonine. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1109-18	17.6	311
116	The origin of protein interactions and allostery in colocalization. <i>Nature</i> , 2007 , 450, 983-90	50.4	310
115	Structural basis for the autoinhibition of calcium/calmodulin-dependent protein kinase I. <i>Cell</i> , 1996 , 84, 875-87	56.2	295
114	Inhibition of the EGF receptor by binding of MIG6 to an activating kinase domain interface. <i>Nature</i> , 2007 , 450, 741-4	50.4	275
113	Structure of the kinase domain of an imatinib-resistant Abl mutant in complex with the Aurora kinase inhibitor VX-680. <i>Cancer Research</i> , 2006 , 66, 1007-14	10.1	256
112	Crystal structure of the processivity clamp loader gamma (gamma) complex of E. coli DNA polymerase III. <i>Cell</i> , 2001 , 106, 429-41	56.2	253
111	A Src-like inactive conformation in the abl tyrosine kinase domain. <i>PLoS Biology</i> , 2006 , 4, e144	9.7	244
110	Structure of the autoinhibited kinase domain of CaMKII and SAXS analysis of the holoenzyme. <i>Cell</i> , 2005 , 123, 849-60	56.2	242
109	Oncogenic mutations counteract intrinsic disorder in the EGFR kinase and promote receptor dimerization. <i>Cell</i> , 2012 , 149, 860-70	56.2	241
108	Structural analysis of the catalytically inactive kinase domain of the human EGF receptor 3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21608-13	11.5	241
107	Catalytic control in the EGF receptor and its connection to general kinase regulatory mechanisms. <i>Molecular Cell</i> , 2011 , 42, 9-22	17.6	239
106	Crystal structure of the delta' subunit of the clamp-loader complex of E. coli DNA polymerase III. <i>Cell</i> , 1997 , 91, 335-45	56.2	235

105	Structure of the amino-terminal protein interaction domain of STAT-4. <i>Science</i> , 1998 , 279, 1048-52	33.3	222
104	A conserved protonation-dependent switch controls drug binding in the Abl kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 139-44	11.5	216
103	Structural analysis of autoinhibition in the Ras activator Son of sevenless. <i>Cell</i> , 2004 , 119, 393-405	56.2	216
102	Mechanism of Processivity Clamp Opening by the Delta Subunit Wrench of the Clamp Loader Complex of E. coli DNA Polymerase III. <i>Cell</i> , 2001 , 106, 417-428	56.2	205
101	Molecular mechanisms in signal transduction at the membrane. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 659-65	17.6	204
100	Membrane-dependent signal integration by the Ras activator Son of sevenless. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 452-61	17.6	187
99	A structural perspective on the regulation of the epidermal growth factor receptor. <i>Annual Review of Biochemistry</i> , 2015 , 84, 739-64	29.1	184
98	Structural basis for the inhibition of tyrosine kinase activity of ZAP-70. <i>Cell</i> , 2007 , 129, 735-46	56.2	183
97	c-Src binds to the cancer drug imatinib with an inactive Abl/c-Kit conformation and a distributed thermodynamic penalty. <i>Structure</i> , 2007 , 15, 299-311	5.2	179
96	Structure of a sliding clamp on DNA. <i>Cell</i> , 2008 , 132, 43-54	56.2	175
95	High yield bacterial expression of active c-Abl and c-Src tyrosine kinases. <i>Protein Science</i> , 2005 , 14, 3135-0.3	17.6	175
94	Organization of the SH3-SH2 unit in active and inactive forms of the c-Abl tyrosine kinase. <i>Molecular Cell</i> , 2006 , 21, 787-98	17.6	174
93	A mechanism for tunable autoinhibition in the structure of a human Ca ²⁺ /calmodulin- dependent kinase II holoenzyme. <i>Cell</i> , 2011 , 146, 732-45	56.2	167
92	The structure, regulation, and function of ZAP-70. <i>Immunological Reviews</i> , 2009 , 228, 41-57	11.3	154
91	Crystal structure of a tetradecameric assembly of the association domain of Ca ²⁺ /calmodulin-dependent kinase II. <i>Molecular Cell</i> , 2003 , 11, 1241-51	17.6	144
90	A molecular assembly phase transition and kinetic proofreading modulate Ras activation by SOS. <i>Science</i> , 2019 , 363, 1098-1103	33.3	140
89	Crystal structure of the DNA polymerase processivity factor of T4 bacteriophage. <i>Journal of Molecular Biology</i> , 2000 , 296, 1215-23	6.5	139
88	Crystal structure of the catalytic alpha subunit of E. coli replicative DNA polymerase III. <i>Cell</i> , 2006 , 126, 881-92	56.2	136

87	Clamp loaders and sliding clamps. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 217-24	8.1	122
86	How a DNA polymerase clamp loader opens a sliding clamp. <i>Science</i> , 2011 , 334, 1675-80	33.3	119
85	Equally potent inhibition of c-Src and Abl by compounds that recognize inactive kinase conformations. <i>Cancer Research</i> , 2009 , 69, 2384-92	10.1	117
84	The mechanism of ATP-dependent primer-template recognition by a clamp loader complex. <i>Cell</i> , 2009 , 137, 659-71	56.2	109
83	Reciprocal regulation of Hck activity by phosphorylation of Tyr(527) and Tyr(416). Effect of introducing a high affinity intramolecular SH2 ligand. <i>Journal of Biological Chemistry</i> , 2000 , 275, 2721-6	5.4	97
82	Molecular kinetics. Ras activation by SOS: allosteric regulation by altered fluctuation dynamics. <i>Science</i> , 2014 , 345, 50-4	33.3	94
81	Regulation of ras signaling dynamics by Sos-mediated positive feedback. <i>Current Biology</i> , 2006 , 16, 2173-6	6.3	94
80	Structural basis for the recognition of c-Src by its inactivator Csk. <i>Cell</i> , 2008 , 134, 124-34	56.2	93
79	Molecular basis for multimerization in the activation of the epidermal growth factor receptor. <i>ELife</i> , 2016 , 5,	8.9	91
78	Exploration of disorder in protein structures by X-ray restrained molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 10, 340-58	4.2	90
77	Protein-protein interactions in the allosteric regulation of protein kinases. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 702-9	8.1	89
76	Intersubunit capture of regulatory segments is a component of cooperative CaMKII activation. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 264-72	17.6	85
75	Regulation of the catalytic activity of the EGF receptor. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 777-84	8.1	80
74	Analysis of the role of PCNA-DNA contacts during clamp loading. <i>BMC Structural Biology</i> , 2010 , 10, 3	2.7	75
73	Oligomerization states of the association domain and the holoenzyme of Ca ²⁺ /CaM kinase II. <i>FEBS Journal</i> , 2006 , 273, 682-94	5.7	73
72	Structural insights into the role of iron-histidine bond cleavage in nitric oxide-induced activation of H-NOX gas sensor proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4156-64	11.5	70
71	Role of the histone domain in the autoinhibition and activation of the Ras activator Son of Sevenless. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 3430-5	11.5	70
70	A dimeric kinase assembly underlying autophosphorylation in the p21 activated kinases. <i>Journal of Molecular Biology</i> , 2006 , 361, 312-26	6.5	70

69	Cryo-EM structure of a dimeric B-Raf:14-3-3 complex reveals asymmetry in the active sites of B-Raf kinases. <i>Science</i> , 2019 , 366, 109-115	33.3	63
68	Prospective discovery of small molecule enhancers of an E3 ligase-substrate interaction. <i>Nature Communications</i> , 2019 , 10, 1402	17.4	61
67	A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. <i>Journal of Experimental Medicine</i> , 2016 , 213, 155-65	16.6	60
66	DNA polymerase clamp loaders and DNA recognition. <i>FEBS Letters</i> , 2005 , 579, 863-7	3.8	60
65	Phosphotyrosine-mediated LAT assembly on membranes drives kinetic bifurcation in recruitment dynamics of the Ras activator SOS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8218-23	11.5	60
64	Lck promotes Zap70-dependent LAT phosphorylation by bridging Zap70 to LAT. <i>Nature Immunology</i> , 2018 , 19, 733-741	19.1	59
63	Deconstruction of the Ras switching cycle through saturation mutagenesis. <i>ELife</i> , 2017 , 6,	8.9	58
62	Activation-triggered subunit exchange between CaMKII holoenzymes facilitates the spread of kinase activity. <i>ELife</i> , 2014 , 3, e01610	8.9	58
61	Structural analysis of autoinhibition in the Ras-specific exchange factor RasGRP1. <i>ELife</i> , 2013 , 2, e00813	8.9	57
60	Out-of-plane motions in open sliding clamps: molecular dynamics simulations of eukaryotic and archaeal proliferating cell nuclear antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13801-6	11.5	57
59	Emerging concepts in the regulation of the EGF receptor and other receptor tyrosine kinases. <i>Trends in Biochemical Sciences</i> , 2014 , 39, 437-46	10.3	56
58	Structural basis for activation of ZAP-70 by phosphorylation of the SH2-kinase linker. <i>Molecular and Cellular Biology</i> , 2013 , 33, 2188-201	4.8	56
57	Structural studies on the regulation of Ca ²⁺ /calmodulin dependent protein kinase II. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 292-301	8.1	55
56	Monovalent and multivalent ligation of the B cell receptor exhibit differential dependence upon Syk and Src family kinases. <i>Science Signaling</i> , 2013 , 6, ra1	8.8	55
55	Crystal structure of the FLT3 kinase domain bound to the inhibitor Quizartinib (AC220). <i>PLoS ONE</i> , 2015 , 10, e0121177	3.7	55
54	Mechanism of proliferating cell nuclear antigen clamp opening by replication factor C. <i>Journal of Biological Chemistry</i> , 2006 , 281, 17528-17539	5.4	55
53	Molecular mechanism of activation-triggered subunit exchange in Ca ²⁺ /calmodulin-dependent protein kinase II. <i>ELife</i> , 2016 , 5,	8.9	55
52	Autoinhibition of Bruton's tyrosine kinase (Btk) and activation by soluble inositol hexakisphosphate. <i>ELife</i> , 2015 , 4,	8.9	53

51	An electrostatic selection mechanism controls sequential kinase signaling downstream of the T cell receptor. <i>ELife</i> , 2016 , 5,	8.9	53
50	Clamp loader ATPases and the evolution of DNA replication machinery. <i>BMC Biology</i> , 2012 , 10, 34	7.3	50
49	The replication factor C clamp loader requires arginine finger sensors to drive DNA binding and proliferating cell nuclear antigen loading. <i>Journal of Biological Chemistry</i> , 2006 , 281, 35531-43	5.4	50
48	Macromolecular juggling by ubiquitylation enzymes. <i>BMC Biology</i> , 2013 , 11, 65	7.3	48
47	Analysis of the Role of the C-Terminal Tail in the Regulation of the Epidermal Growth Factor Receptor. <i>Molecular and Cellular Biology</i> , 2015 , 35, 3083-102	4.8	47
46	Mapping the interaction of DNA with the Escherichia coli DNA polymerase clamp loader complex. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 183-90	17.6	40
45	The catalytic activity of the kinase ZAP-70 mediates basal signaling and negative feedback of the T cell receptor pathway. <i>Science Signaling</i> , 2015 , 8, ra49	8.8	38
44	The Src module: an ancient scaffold in the evolution of cytoplasmic tyrosine kinases. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2018 , 53, 535-563	8.7	36
43	A Phosphosite within the SH2 Domain of Lck Regulates Its Activation by CD45. <i>Molecular Cell</i> , 2017 , 67, 498-511.e6	17.6	35
42	A structural atlas of kinases inhibited by clinically approved drugs. <i>Methods in Enzymology</i> , 2014 , 548, 23-67	1.7	32
41	CRISPR-Cas12a exploits R-loop asymmetry to form double-strand breaks. <i>ELife</i> , 2020 , 9,	8.9	32
40	Slow phosphorylation of a tyrosine residue in LAT optimizes T cell ligand discrimination. <i>Nature Immunology</i> , 2019 , 20, 1481-1493	19.1	27
39	Multiple interactions between an Arf/GEF complex and charged lipids determine activation kinetics on the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 11416-11421	11.5	27
38	Stability of an autoinhibitory interface in the structure of the tyrosine kinase ZAP-70 impacts T cell receptor response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 20699-704	11.5	26
37	Nucleotide-induced conformational changes in an isolated Escherichia coli DNA polymerase III clamp loader subunit. <i>Structure</i> , 2003 , 11, 253-63	5.2	24
36	Fine-tuning of substrate preferences of the Src-family kinase Lck revealed through a high-throughput specificity screen. <i>ELife</i> , 2018 , 7,	8.9	24
35	The Interdependent Activation of Son-of-Sevenless and Ras. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019 , 9,	5.4	23
34	The tyrosine kinase Csk dimerizes through Its SH3 domain. <i>PLoS ONE</i> , 2009 , 4, e7683	3.7	22

33	Structural Insights into the Regulation of Ca/Calmodulin-Dependent Protein Kinase II (CaMKII). <i>Cold Spring Harbor Perspectives in Biology</i> , 2020 , 12,	10.2	22
32	Crystal structure of an SH2-kinase construct of c-Abl and effect of the SH2 domain on kinase activity. <i>Biochemical Journal</i> , 2015 , 468, 283-91	3.8	19
31	A Histidine pH sensor regulates activation of the Ras-specific guanine nucleotide exchange factor RasGRP1. <i>ELife</i> , 2017 , 6,	8.9	19
30	Understanding molecular mechanisms in cell signaling through natural and artificial sequence variation. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 25-34	17.6	18
29	Structural basis for dimerization quality control. <i>Nature</i> , 2020 , 586, 452-456	50.4	17
28	Modification by covalent reaction or oxidation of cysteine residues in the tandem-SH2 domains of ZAP-70 and Syk can block phosphopeptide binding. <i>Biochemical Journal</i> , 2015 , 465, 149-61	3.8	16
27	Comparative analysis of mutant tyrosine kinase chemical rescue. <i>Biochemistry</i> , 2009 , 48, 3378-86	3.2	16
26	Crystal Structure of a Ube2S-Ubiquitin Conjugate. <i>PLoS ONE</i> , 2016 , 11, e0147550	3.7	16
25	Switch-like activation of Bruton's tyrosine kinase by membrane-mediated dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10798-10803	11.5	15
24	Deep mutational analysis reveals functional trade-offs in the sequences of EGFR autophosphorylation sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E7303-E7312	11.5	15
23	Flexible linkers in CaMKII control the balance between activating and inhibitory autophosphorylation. <i>ELife</i> , 2020 , 9,	8.9	15
22	Identification of Inhibitors of the Association of ZAP-70 with the T Cell Receptor by High-Throughput Screen. <i>SLAS Discovery</i> , 2017 , 22, 324-331	3.4	13
21	Allostery and coupled sequence variation in nuclear hormone receptors. <i>Cell</i> , 2004 , 116, 354-6	56.2	10
20	Breakage of the oligomeric CaMKII hub by the regulatory segment of the kinase. <i>ELife</i> , 2020 , 9,	8.9	10
19	Variation in assembly stoichiometry in non-metazoan homologs of the hub domain of Ca/calmodulin-dependent protein kinase II. <i>Protein Science</i> , 2019 , 28, 1071-1082	6.3	8
18	GHB analogs confer neuroprotection through specific interaction with the CaMKII hub domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
17	Structural basis and regulation of the reductive stress response. <i>Cell</i> , 2021 , 184, 5375-5390.e16	56.2	8
16	Allosteric communication in DNA polymerase clamp loaders relies on a critical hydrogen-bonded junction. <i>ELife</i> , 2021 , 10,	8.9	7

15	A molecular mechanism for the generation of ligand-dependent differential outputs by the epidermal growth factor receptor. <i>ELife</i> , 2021 , 10,	8.9	6
14	A highly efficient peptide substrate for EGFR activates the kinase by inducing aggregation. <i>Biochemical Journal</i> , 2013 , 453, 337-44	3.8	4
13	Phosphorylation control of the ubiquitin ligase Cbl is conserved in choanoflagellates. <i>Protein Science</i> , 2018 , 27, 923-932	6.3	3
12	Author response: Molecular mechanism of activation-triggered subunit exchange in Ca ²⁺ /calmodulin-dependent protein kinase II 2016 ,		3
11	A molecular mechanism for the generation of ligand-dependent differential outputs by the epidermal growth factor receptor		3
10	Author response: Deconstruction of the Ras switching cycle through saturation mutagenesis 2017 ,		2
9	Author response: Breakage of the oligomeric CaMKII hub by the regulatory segment of the kinase 2020 ,		2
8	Differences in the dynamics of the tandem-SH2 modules of the Syk and ZAP-70 tyrosine kinases. <i>Protein Science</i> , 2021 , 30, 2373-2384	6.3	2
7	Switch-like activation of Bruton's tyrosine kinase by membrane-mediated dimerization		2
6	New insights into Raf regulation from structural analyses. <i>Current Opinion in Structural Biology</i> , 2021 , 71, 223-231	8.1	2
5	A saturation-mutagenesis analysis of the interplay between stability and activation in Ras.. <i>ELife</i> , 2022 , 11,	8.9	2
4	A two-component protein condensate of the EGFR cytoplasmic tail and Grb2 regulates Ras activation by SOS at the membrane.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2122531119	11.5	2
3	Relating cellular signaling timescales to single-molecule kinetics: A first-passage time analysis of Ras activation by SOS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
2	Molecular Mechanisms of DNA Polymerase Clamp Loaders. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012 , 103-114	0.1	0
1	Allosteric Mechanisms in Receptor Tyrosine Kinase Activation. <i>FASEB Journal</i> , 2009 , 23, 313.1	0.9	