Stevan R Hubbard

List of Publications by Year
in descending order

84 papers	14,498 citations	36303 51 h-index	62596 80 g-index
122 all docs	122 docs citations	122 times ranked	15702 citing authors

#	Article	IF	Citations
1	IRE1 couples endoplasmic reticulum load to secretory capacity by processing the XBP-1 mRNA. Nature, 2002, 415, 92-96.	27.8	2,452
2	Crystal structure of the tyrosine kinase domain of the human insulin receptor. Nature, 1994, 372, 746-754.	27.8	1,105
3	Structures of the Tyrosine Kinase Domain of Fibroblast Growth Factor Receptor in Complex with Inhibitors. Science, 1997, 276, 955-960.	12.6	1,047
4	Protein Tyrosine Kinase Structure and Function. Annual Review of Biochemistry, 2000, 69, 373-398.	11.1	996
5	Catalytic specificity of protein-tyrosine kinases is critical for selective signalling. Nature, 1995, 373, 536-539.	27.8	932
6	Structural Basis for FGF Receptor Dimerization and Activation. Cell, 1999, 98, 641-650.	28.9	575
7	Lrp4 Is a Receptor for Agrin and Forms a Complex with MuSK. Cell, 2008, 135, 334-342.	28.9	572
8	Receptor tyrosine kinases: mechanisms of activation and signaling. Current Opinion in Cell Biology, 2007, 19, 117-123.	5.4	388
9	Structure of the FGF Receptor Tyrosine Kinase Domain Reveals a Novel Autoinhibitory Mechanism. Cell, 1996, 86, 577-587.	28.9	378
10	Crystal Structures of Two FGF-FGFR Complexes Reveal the Determinants of Ligand-Receptor Specificity. Cell, 2000, 101, 413-424.	28.9	370
11	Structure and autoregulation of the insulin-like growth factor 1 receptor kinase. Nature Structural Biology, 2001, 8, 1058-1063.	9.7	308
12	Juxtamembrane autoinhibition in receptor tyrosine kinases. Nature Reviews Molecular Cell Biology, 2004, 5, 464-471.	37.0	264
13	Autoregulatory Mechanisms in Protein-tyrosine Kinases. Journal of Biological Chemistry, 1998, 273, 11987-11990.	3.4	262
14	The pseudokinase domain of JAK2 is a dual-specificity protein kinase that negatively regulates cytokine signaling. Nature Structural and Molecular Biology, 2011, 18, 971-976.	8.2	237
15	How IRE1 Reacts to ER Stress. Cell, 2008, 132, 24-26.	28.9	209
16	Crystal structures of the JAK2 pseudokinase domain and the pathogenic mutant V617F. Nature Structural and Molecular Biology, 2012, 19, 754-759.	8.2	196
17	Mechanism-based design of a protein kinase inhibitor. Nature Structural Biology, 2001, 8, 37-41.	9.7	185
18	Structural analysis of receptor tyrosine kinases. Progress in Biophysics and Molecular Biology, 1999, 71, 343-358.	2.9	181

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19	Insulin receptor Thr1160 phosphorylation mediates lipid-induced hepatic insulin resistance. Journal of Clinical Investigation, 2016, 126, 4361-4371.	8.2	173
20	Molecular basis for pseudokinase-dependent autoinhibition of JAK2 tyrosine kinase. Nature Structural and Molecular Biology, 2014, 21, 579-584.	8.2	132
21	KRAS4A directly regulates hexokinase 1. Nature, 2019, 576, 482-486.	27.8	129
22	Agrin Binds to the N-terminal Region of Lrp4 Protein and Stimulates Association between Lrp4 and the First Immunoglobulin-like Domain in Muscle-specific Kinase (MuSK). Journal of Biological Chemistry, 2011, 286, 40624-40630.	3.4	123
23	Mechanism of homodimeric cytokine receptor activation and dysregulation by oncogenic mutations. Science, 2020, 367, 643-652.	12.6	123
24	Crystal Structure of the MuSK Tyrosine Kinase. Structure, 2002, 10, 1187-1196.	3.3	122
25	Increased resistance of SARS-CoV-2 Omicron variant to neutralization by vaccine-elicited and therapeutic antibodies. EBioMedicine, 2022, 78, 103944.	6.1	119
26	The Insulin Receptor: Both a Prototypical and Atypical Receptor Tyrosine Kinase. Cold Spring Harbor Perspectives in Biology, 2013, 5, a008946-a008946.	5.5	116
27	Expression, Characterization, and Crystallization of the Catalytic Core of the Human Insulin Receptor Protein-tyrosine Kinase Domain. Journal of Biological Chemistry, 1995, 270, 8122-8130.	3.4	114
28	Anomalous small-angle x-ray scattering from a sulfonated polystyrene ionomer. Macromolecules, 1988, 21, 1698-1703.	4.8	113
29	Structural Basis for Recruitment of the Adaptor Protein APS to the Activated Insulin Receptor. Molecular Cell, 2003, 12, 1379-1389.	9.7	113
30	The Cytoplasmic Adaptor Protein Dok7 Activates the Receptor Tyrosine Kinase MuSK via Dimerization. Molecular Cell, 2010, 39, 100-109.	9.7	109
31	Structural Basis for Inhibition of the Insulin Receptor by the Adaptor Protein Grb14. Molecular Cell, 2005, 20, 325-333.	9.7	105
32	Proteasomal Control of Cytokinin Synthesis Protects Mycobacterium tuberculosis against Nitric Oxide. Molecular Cell, 2015, 57, 984-994.	9.7	101
33	ATP binding to the pseudokinase domain of JAK2 is critical for pathogenic activation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4642-4647.	7.1	95
34	Structural and biochemical characterization of the KRLB region in insulin receptor substrate-2. Nature Structural and Molecular Biology, 2008, 15, 251-258.	8.2	94
35	Molecular analysis of the prokaryotic ubiquitin-like protein (Pup) conjugation pathway in Mycobacterium tuberculosis. Molecular Microbiology, 2010, 77, 1123-1135.	2.5	90
36	X-ray crystal structure of a recombinant human myoglobin mutant at 2Â·8 Ã… resolution. Journal of Molecular Biology, 1990, 213, 215-218.	4.2	87

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37	The BPS domain of Grb10 inhibits the catalytic activity of the insulin and IGF1 receptors. FEBS Letters, 2001, 493, 106-111.	2.8	81
38	Small-molecule inhibition and activation-loop trans-phosphorylation of the IGF1 receptor. EMBO Journal, 2008, 27, 1985-1994.	7.8	75
39	Protein tyrosine kinases: autoregulation and small-molecule inhibition. Current Opinion in Structural Biology, 2002, 12, 735-741.	5.7	72
40	Alternative splicing, gene localization, and binding of SH2-B to the insulin receptor kinase domain. Mammalian Genome, 1999, 10, 1160-1167.	2.2	70
41	Structural Characterization of a Novel Cbl Phosphotyrosine Recognition Motif in the APS Family of Adapter Proteins. Journal of Biological Chemistry, 2005, 280, 18943-18949.	3.4	70
42	Crystallographic and Solution Studies of an Activation Loop Mutant of the Insulin Receptor Tyrosine Kinase. Journal of Biological Chemistry, 2001, 276, 10049-10055.	3.4	69
43	Mechanistic Insights into Regulation of JAK2 Tyrosine Kinase. Frontiers in Endocrinology, 2017, 8, 361.	3.5	69
44	Structural and functional studies of the Ras-associating and pleckstrin-homology domains of Grb10 and Grb14. Nature Structural and Molecular Biology, 2009, 16, 833-839.	8.2	66
45	Molecular insights into regulation of JAK2 in myeloproliferative neoplasms. Blood, 2015, 125, 3388-3392.	1.4	65
46	Crystal Structure of the Frizzled-Like Cysteine-Rich Domain of the Receptor Tyrosine Kinase MuSK. Journal of Molecular Biology, 2009, 393, 1-9.	4.2	63
47	Crystal Structure of the Agrin-responsive Immunoglobulin-like Domains 1 and 2 of the Receptor Tyrosine Kinase MuSK. Journal of Molecular Biology, 2006, 364, 424-433.	4.2	61
48	The insulin and IGF1 receptor kinase domains are functional dimers in the activated state. Nature Communications, 2015, 6, 6406.	12.8	60
49	Structural Basis for Dimerization of the Grb10 Src Homology 2 Domain. Journal of Biological Chemistry, 2003, 278, 13257-13264.	3.4	56
50	Structural and Biochemical Evidence for an Autoinhibitory Role for Tyrosine 984 in the Juxtamembrane Region of the Insulin Receptor. Journal of Biological Chemistry, 2003, 278, 26007-26014.	3.4	55
51	Rap1-interacting adapter molecule (RIAM) associates with the plasma membrane via a proximity detector. Journal of Cell Biology, 2012, 199, 317-329.	5.2	54
52	Src autoinhibition: let us count the ways. , 1999, 6, 711-714.		50
53	Structural Basis for Phosphotyrosine Recognition by Suppressor of Cytokine Signaling-3. Structure, 2006, 14, 1285-1292.	3.3	48
54	Crystal Structure of the Human Laminin Receptor Precursor. Journal of Biological Chemistry, 2008, 283, 3002-3005.	3.4	46

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55	Histidine phosphorylation relieves copper inhibition in the mammalian potassium channel KCa3.1. ELife, 2016, 5, .	6.0	46
56	Crystal Structure of a Complex between Protein Tyrosine Phosphatase 1B and the Insulin Receptor Tyrosine Kinase. Structure, 2005, 13, 1643-1651.	3.3	43
57	A DNA Sequence Recognition Loop on APOBEC3A Controls Substrate Specificity. PLoS ONE, 2014, 9, e97062.	2.5	42
58	EGF receptor inhibition: Attacks on multiple fronts. Cancer Cell, 2005, 7, 287-288.	16.8	40
59	Structure and activation of MuSK, a receptor tyrosine kinase central to neuromuscular junction formation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2166-2169.	2.3	38
60	Theme and Variations. Molecular Cell, 2001, 8, 481-482.	9.7	37
61	Autoinhibitory mechanisms in receptor tyrosine kinases. Frontiers in Bioscience - Landmark, 2002, 7, d330-340.	3.0	35
62	New insights into the structure and function of the pseudokinase domain in JAK2. Biochemical Society Transactions, 2013, 41, 1002-1007.	3.4	35
63	Structural Basis for Phosphotyrosine Recognition by the Src Homology-2 Domains of the Adapter Proteins SH2-B and APS. Journal of Molecular Biology, 2006, 361, 69-79.	4.2	32
64	Probing the Catalytic Mechanism of the Insulin Receptor Kinase with a Tetrafluorotyrosine-containing Peptide Substrate. Journal of Biological Chemistry, 2000, 275, 30394-30398.	3.4	30
65	Oncogenic Mutations in B-Raf. Cell, 2004, 116, 764-766.	28.9	28
66	Bisubstrate analog probes for the insulin receptor protein tyrosine kinase: Molecular yardsticks for analyzing catalytic mechanism and inhibitor design. Bioorganic Chemistry, 2005, 33, 285-297.	4.1	25
67	EGF Receptor Activation: Push Comes to Shove. Cell, 2006, 125, 1029-1031.	28.9	24
68	Structural Basis for the Interaction of the Adaptor Protein Grb14 with Activated Ras. PLoS ONE, 2013, 8, e72473.	2.5	23
69	The Juxtamembrane Region of EGFR Takes Center Stage. Cell, 2009, 137, 1181-1183.	28.9	22
70	Structure-Guided Identification of a Laminin Binding Site on the Laminin Receptor Precursor. Journal of Molecular Biology, 2011, 405, 24-32.	4.2	22
71	Targeting the Inactive Conformation of JAK2 in Hematological Malignancies. Cancer Cell, 2015, 28, 1-2.	16.8	21
72	Janus kinase 2 activation mechanisms revealed by analysis of suppressing mutations. Journal of Allergy and Clinical Immunology, 2019, 143, 1549-1559.e6.	2.9	21

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73	Mycobacterium tuberculosis Prokaryotic Ubiquitin-like Protein-deconjugating Enzyme Is an Unusual Aspartate Amidase. Journal of Biological Chemistry, 2012, 287, 37522-37529.	3.4	20
74	Agrin / MuSK signaling: willing and Abl. Nature Neuroscience, 2003, 6, 653-654.	14.8	14
75	Insulin meets its receptor. Nature, 2013, 493, 171-172.	27.8	13
76	Crystal structure of the C-terminal four-helix bundle of the potassium channel KCa3.1. PLoS ONE, 2018, 13, e0199942.	2.5	6
77	Closing in on a mechanism for activation. ELife, 2014, 3, .	6.0	4
78	Cytokine Signaling Exposed. Structure, 2011, 19, 1-2.	3.3	3
79	IRAK4 Activation: A Cautious Embrace. Molecular Cell, 2014, 55, 805-806.	9.7	2
80	Unlocking the secrets to Janus kinase activation. Science, 2022, 376, 139-140.	12.6	2
81	The MuSK Receptor Family. , 2015, , 359-372.		1
82	IRE1 couples endoplasmic reticulum load to secretory capacity by processing the XBP-1 mRNA. , 0, .		1
83	[13] Characterization of the cysteine-rich zinc-binding domains of protein kinase C by X-ray absorption spectroscopy. Methods in Enzymology, 1995, 252, 123-132.	1.0	0
84	New Paradigms for the Mechanisms of Thrombopoietin Receptor Activation and Dysregulation By the JAK2V617F Mutation. Blood, 2019, 134, 2962-2962.	1.4	0