

Stevan R Hubbard

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Unlocking the secrets to Janus kinase activation. <i>Science</i> , 2022, 376, 139-140. | 12.6 | 2 |
| 2 | Increased resistance of SARS-CoV-2 Omicron variant to neutralization by vaccine-elicited and therapeutic antibodies. <i>EBioMedicine</i> , 2022, 78, 103944. | 6.1 | 119 |
| 3 | Mechanism of homodimeric cytokine receptor activation and dysregulation by oncogenic mutations. <i>Science</i> , 2020, 367, 643-652. | 12.6 | 123 |
| 4 | KRAS4A directly regulates hexokinase 1. <i>Nature</i> , 2019, 576, 482-486. | 27.8 | 129 |
| 5 | Janus kinase 2 activation mechanisms revealed by analysis of suppressing mutations. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1549-1559.e6. | 2.9 | 21 |
| 6 | New Paradigms for the Mechanisms of Thrombopoietin Receptor Activation and Dysregulation By the JAK2V617F Mutation. <i>Blood</i> , 2019, 134, 2962-2962. | 1.4 | 0 |
| 7 | Crystal structure of the C-terminal four-helix bundle of the potassium channel KCa3.1. <i>PLoS ONE</i> , 2018, 13, e0199942. | 2.5 | 6 |
| 8 | Mechanistic Insights into Regulation of JAK2 Tyrosine Kinase. <i>Frontiers in Endocrinology</i> , 2017, 8, 361. | 3.5 | 69 |
| 9 | Histidine phosphorylation relieves copper inhibition in the mammalian potassium channel KCa3.1. <i>ELife</i> , 2016, 5, . | 6.0 | 46 |
| 10 | Insulin receptor Thr1160 phosphorylation mediates lipid-induced hepatic insulin resistance. <i>Journal of Clinical Investigation</i> , 2016, 126, 4361-4371. | 8.2 | 173 |
| 11 | Molecular insights into regulation of JAK2 in myeloproliferative neoplasms. <i>Blood</i> , 2015, 125, 3388-3392. | 1.4 | 65 |
| 12 | Proteasomal Control of Cytokinin Synthesis Protects Mycobacterium tuberculosis against Nitric Oxide. <i>Molecular Cell</i> , 2015, 57, 984-994. | 9.7 | 101 |
| 13 | Targeting the Inactive Conformation of JAK2 in Hematological Malignancies. <i>Cancer Cell</i> , 2015, 28, 1-2. | 16.8 | 21 |
| 14 | ATP binding to the pseudokinase domain of JAK2 is critical for pathogenic activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4642-4647. | 7.1 | 95 |
| 15 | The insulin and IGF1 receptor kinase domains are functional dimers in the activated state. <i>Nature Communications</i> , 2015, 6, 6406. | 12.8 | 60 |
| 16 | The MuSK Receptor Family. , 2015, , 359-372. | | 1 |
| 17 | IRAK4 Activation: A Cautious Embrace. <i>Molecular Cell</i> , 2014, 55, 805-806. | 9.7 | 2 |
| 18 | Molecular basis for pseudokinase-dependent autoinhibition of JAK2 tyrosine kinase. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 579-584. | 8.2 | 132 |

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|----|--|------|-----------|
| 19 | A DNA Sequence Recognition Loop on APOBEC3A Controls Substrate Specificity. <i>PLoS ONE</i> , 2014, 9, e97062. | 2.5 | 42 |
| 20 | Closing in on a mechanism for activation. <i>ELife</i> , 2014, 3, . | 6.0 | 4 |
| 21 | Structure and activation of MuSK, a receptor tyrosine kinase central to neuromuscular junction formation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2166-2169. | 2.3 | 38 |
| 22 | Insulin meets its receptor. <i>Nature</i> , 2013, 493, 171-172. | 27.8 | 13 |
| 23 | The Insulin Receptor: Both a Prototypical and Atypical Receptor Tyrosine Kinase. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a008946-a008946. | 5.5 | 116 |
| 24 | New insights into the structure and function of the pseudokinase domain in JAK2. <i>Biochemical Society Transactions</i> , 2013, 41, 1002-1007. | 3.4 | 35 |
| 25 | Structural Basis for the Interaction of the Adaptor Protein Grb14 with Activated Ras. <i>PLoS ONE</i> , 2013, 8, e72473. | 2.5 | 23 |
| 26 | <i>Mycobacterium tuberculosis</i> Prokaryotic Ubiquitin-like Protein-deconjugating Enzyme Is an Unusual Aspartate Amidase. <i>Journal of Biological Chemistry</i> , 2012, 287, 37522-37529. | 3.4 | 20 |
| 27 | Rap1-interacting adapter molecule (RIAM) associates with the plasma membrane via a proximity detector. <i>Journal of Cell Biology</i> , 2012, 199, 317-329. | 5.2 | 54 |
| 28 | Crystal structures of the JAK2 pseudokinase domain and the pathogenic mutant V617F. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 754-759. | 8.2 | 196 |
| 29 | The pseudokinase domain of JAK2 is a dual-specificity protein kinase that negatively regulates cytokine signaling. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 971-976. | 8.2 | 237 |
| 30 | Structure-Guided Identification of a Laminin Binding Site on the Laminin Receptor Precursor. <i>Journal of Molecular Biology</i> , 2011, 405, 24-32. | 4.2 | 22 |
| 31 | Cytokine Signaling Exposed. <i>Structure</i> , 2011, 19, 1-2. | 3.3 | 3 |
| 32 | 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). <i>Journal of Biological Chemistry</i> , 2011, 286, 40624-40630. | 3.4 | 123 |
| 33 | Molecular analysis of the prokaryotic ubiquitin-like protein (Pup) conjugation pathway in <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2010, 77, 1123-1135. | 2.5 | 90 |
| 34 | The Cytoplasmic Adaptor Protein Dok7 Activates the Receptor Tyrosine Kinase MuSK via Dimerization. <i>Molecular Cell</i> , 2010, 39, 100-109. | 9.7 | 109 |
| 35 | Structural and functional studies of the Ras-associating and pleckstrin-homology domains of Grb10 and Grb14. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 833-839. | 8.2 | 66 |
| 36 | The Juxtamembrane Region of EGFR Takes Center Stage. <i>Cell</i> , 2009, 137, 1181-1183. | 28.9 | 22 |

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|----|---|------|-----------|
| 37 | Crystal Structure of the Frizzled-Like Cysteine-Rich Domain of the Receptor Tyrosine Kinase MuSK. <i>Journal of Molecular Biology</i> , 2009, 393, 1-9. | 4.2 | 63 |
| 38 | Small-molecule inhibition and activation-loop trans-phosphorylation of the IGF1 receptor. <i>EMBO Journal</i> , 2008, 27, 1985-1994. | 7.8 | 75 |
| 39 | Structural and biochemical characterization of the KRLB region in insulin receptor substrate-2. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 251-258. | 8.2 | 94 |
| 40 | How IRE1 Reacts to ER Stress. <i>Cell</i> , 2008, 132, 24-26. | 28.9 | 209 |
| 41 | Lrp4 Is a Receptor for Agrin and Forms a Complex with MuSK. <i>Cell</i> , 2008, 135, 334-342. | 28.9 | 572 |
| 42 | Crystal Structure of the Human Laminin Receptor Precursor. <i>Journal of Biological Chemistry</i> , 2008, 283, 3002-3005. | 3.4 | 46 |
| 43 | Receptor tyrosine kinases: mechanisms of activation and signaling. <i>Current Opinion in Cell Biology</i> , 2007, 19, 117-123. | 5.4 | 388 |
| 44 | EGF Receptor Activation: Push Comes to Shove. <i>Cell</i> , 2006, 125, 1029-1031. | 28.9 | 24 |
| 45 | Structural Basis for Phosphotyrosine Recognition by the Src Homology-2 Domains of the Adapter Proteins SH2-B and APS. <i>Journal of Molecular Biology</i> , 2006, 361, 69-79. | 4.2 | 32 |
| 46 | Crystal Structure of the Agrin-responsive Immunoglobulin-like Domains 1 and 2 of the Receptor Tyrosine Kinase MuSK. <i>Journal of Molecular Biology</i> , 2006, 364, 424-433. | 4.2 | 61 |
| 47 | Structural Basis for Phosphotyrosine Recognition by Suppressor of Cytokine Signaling-3. <i>Structure</i> , 2006, 14, 1285-1292. | 3.3 | 48 |
| 48 | Bisubstrate analog probes for the insulin receptor protein tyrosine kinase: Molecular yardsticks for analyzing catalytic mechanism and inhibitor design. <i>Bioorganic Chemistry</i> , 2005, 33, 285-297. | 4.1 | 25 |
| 49 | EGF receptor inhibition: Attacks on multiple fronts. <i>Cancer Cell</i> , 2005, 7, 287-288. | 16.8 | 40 |
| 50 | Crystal Structure of a Complex between Protein Tyrosine Phosphatase 1B and the Insulin Receptor Tyrosine Kinase. <i>Structure</i> , 2005, 13, 1643-1651. | 3.3 | 43 |
| 51 | Structural Characterization of a Novel Cbl Phosphotyrosine Recognition Motif in the APS Family of Adapter Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 18943-18949. | 3.4 | 70 |
| 52 | Structural Basis for Inhibition of the Insulin Receptor by the Adaptor Protein Grb14. <i>Molecular Cell</i> , 2005, 20, 325-333. | 9.7 | 105 |
| 53 | Juxtamembrane autoinhibition in receptor tyrosine kinases. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 464-471. | 37.0 | 264 |
| 54 | Oncogenic Mutations in B-Raf. <i>Cell</i> , 2004, 116, 764-766. | 28.9 | 28 |

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| 55 | Agrin / MuSK signaling: willing and Abl. <i>Nature Neuroscience</i> , 2003, 6, 653-654. | 14.8 | 14 |
| 56 | Structural Basis for Dimerization of the Grb10 Src Homology 2 Domain. <i>Journal of Biological Chemistry</i> , 2003, 278, 13257-13264. | 3.4 | 56 |
| 57 | Structural Basis for Recruitment of the Adaptor Protein APS to the Activated Insulin Receptor. <i>Molecular Cell</i> , 2003, 12, 1379-1389. | 9.7 | 113 |
| 58 | Structural and Biochemical Evidence for an Autoinhibitory Role for Tyrosine 984 in the Juxtamembrane Region of the Insulin Receptor. <i>Journal of Biological Chemistry</i> , 2003, 278, 26007-26014. | 3.4 | 55 |
| 59 | Autoinhibitory mechanisms in receptor tyrosine kinases. <i>Frontiers in Bioscience - Landmark</i> , 2002, 7, d330-340. | 3.0 | 35 |
| 60 | Crystal Structure of the MuSK Tyrosine Kinase. <i>Structure</i> , 2002, 10, 1187-1196. | 3.3 | 122 |
| 61 | Protein tyrosine kinases: autoregulation and small-molecule inhibition. <i>Current Opinion in Structural Biology</i> , 2002, 12, 735-741. | 5.7 | 72 |
| 62 | IRE1 couples endoplasmic reticulum load to secretory capacity by processing the XBP-1 mRNA. <i>Nature</i> , 2002, 415, 92-96. | 27.8 | 2,452 |
| 63 | Theme and Variations. <i>Molecular Cell</i> , 2001, 8, 481-482. | 9.7 | 37 |
| 64 | The BPS domain of Grb10 inhibits the catalytic activity of the insulin and IGF1 receptors. <i>FEBS Letters</i> , 2001, 493, 106-111. | 2.8 | 81 |
| 65 | Mechanism-based design of a protein kinase inhibitor. <i>Nature Structural Biology</i> , 2001, 8, 37-41. | 9.7 | 185 |
| 66 | Structure and autoregulation of the insulin-like growth factor 1 receptor kinase. <i>Nature Structural Biology</i> , 2001, 8, 1058-1063. | 9.7 | 308 |
| 67 | Crystallographic and Solution Studies of an Activation Loop Mutant of the Insulin Receptor Tyrosine Kinase. <i>Journal of Biological Chemistry</i> , 2001, 276, 10049-10055. | 3.4 | 69 |
| 68 | Probing the Catalytic Mechanism of the Insulin Receptor Kinase with a Tetrafluorotyrosine-containing Peptide Substrate. <i>Journal of Biological Chemistry</i> , 2000, 275, 30394-30398. | 3.4 | 30 |
| 69 | Protein Tyrosine Kinase Structure and Function. <i>Annual Review of Biochemistry</i> , 2000, 69, 373-398. | 11.1 | 996 |
| 70 | Crystal Structures of Two FGF-FGFR Complexes Reveal the Determinants of Ligand-Receptor Specificity. <i>Cell</i> , 2000, 101, 413-424. | 28.9 | 370 |
| 71 | Src autoinhibition: let us count the ways. , 1999, 6, 711-714. | | 50 |
| 72 | Alternative splicing, gene localization, and binding of SH2-B to the insulin receptor kinase domain. <i>Mammalian Genome</i> , 1999, 10, 1160-1167. | 2.2 | 70 |

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|----|--|------|-----------|
| 73 | Structural analysis of receptor tyrosine kinases. Progress in Biophysics and Molecular Biology, 1999, 71, 343-358. | 2.9 | 181 |
| 74 | Structural Basis for FGF Receptor Dimerization and Activation. Cell, 1999, 98, 641-650. | 28.9 | 575 |
| 75 | Autoregulatory Mechanisms in Protein-tyrosine Kinases. Journal of Biological Chemistry, 1998, 273, 11987-11990. | 3.4 | 262 |
| 76 | Structures of the Tyrosine Kinase Domain of Fibroblast Growth Factor Receptor in Complex with Inhibitors. Science, 1997, 276, 955-960. | 12.6 | 1,047 |
| 77 | Structure of the FGF Receptor Tyrosine Kinase Domain Reveals a Novel Autoinhibitory Mechanism. Cell, 1996, 86, 577-587. | 28.9 | 378 |
| 78 | [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 |
| 79 | Catalytic specificity of protein-tyrosine kinases is critical for selective signalling. Nature, 1995, 373, 536-539. | 27.8 | 932 |
| 80 | 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 |
| 81 | Crystal structure of the tyrosine kinase domain of the human insulin receptor. Nature, 1994, 372, 746-754. | 27.8 | 1,105 |
| 82 | X-ray crystal structure of a recombinant human myoglobin mutant at 2.8 Å resolution. Journal of Molecular Biology, 1990, 213, 215-218. | 4.2 | 87 |
| 83 | Anomalous small-angle x-ray scattering from a sulfonated polystyrene ionomer. Macromolecules, 1988, 21, 1698-1703. | 4.8 | 113 |
| 84 | IRE1 couples endoplasmic reticulum load to secretory capacity by processing the XBP-1 mRNA. , 0, . | | 1 |