

Lisa N Kinch

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

92
papers

4,620
citations

32
h-index

67
g-index

101
ext. papers

6,766
ext. citations

9.7
avg, IF

5.53
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 92 | Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021 , 373, 871-876 | 33.3 | 522 |
| 91 | Structure prediction for CASP8 with all-atom refinement using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 89-99 | 4.2 | 342 |
| 90 | AMPylation of Rho GTPases by Vibrio VopS disrupts effector binding and downstream signaling. <i>Science</i> , 2009 , 323, 269-72 | 33.3 | 287 |
| 89 | Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015 , 47, 13-21 | 36.3 | 247 |
| 88 | A Single Kinase Generates the Majority of the Secreted Phosphoproteome. <i>Cell</i> , 2015 , 161, 1619-32 | 56.2 | 187 |
| 87 | Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , 2016 , 533, 561-4 | 50.4 | 185 |
| 86 | ECOD: an evolutionary classification of protein domains. <i>PLoS Computational Biology</i> , 2014 , 10, e1003926 | | 184 |
| 85 | Large-scale determination of previously unsolved protein structures using evolutionary information. <i>ELife</i> , 2015 , 4, e09248 | 8.9 | 173 |
| 84 | Evolution of protein structures and functions. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 400-8 | 8.1 | 131 |
| 83 | Beclin 2 functions in autophagy, degradation of G protein-coupled receptors, and metabolism. <i>Cell</i> , 2013 , 154, 1085-1099 | 56.2 | 115 |
| 82 | A novel germline mutation in BAP1 predisposes to familial clear-cell renal cell carcinoma. <i>Molecular Cancer Research</i> , 2013 , 11, 1061-1071 | 6.6 | 111 |
| 81 | Fido, a novel AMPylation domain common to Fic, Doc, and AvrB. <i>PLoS ONE</i> , 2009 , 4, e5818 | 3.7 | 103 |
| 80 | Marker for type VI secretion system effectors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9271-6 | 11.5 | 98 |
| 79 | Protein AMPylation by an Evolutionarily Conserved Pseudokinase. <i>Cell</i> , 2018 , 175, 809-821.e19 | 56.2 | 87 |
| 78 | CASP9 assessment of free modeling target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79 Suppl 10, 59-73 | 4.2 | 82 |
| 77 | CASP5 assessment of fold recognition target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 395-409 | 4.2 | 82 |
| 76 | Succination of Keap1 and activation of Nrf2-dependent antioxidant pathways in FH-deficient papillary renal cell carcinoma type 2. <i>Cancer Cell</i> , 2011 , 20, 418-20 | 24.3 | 78 |

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|----|--|------|----|
| 75 | Site-2 protease regulated intramembrane proteolysis: sequence homologs suggest an ancient signaling cascade. <i>Protein Science</i> , 2006 , 15, 84-93 | 6.3 | 76 |
| 74 | Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 1194-1201 | 17.6 | 73 |
| 73 | Identification of novel restriction endonuclease-like fold families among hypothetical proteins. <i>Nucleic Acids Research</i> , 2005 , 33, 3598-605 | 20.1 | 70 |
| 72 | Kinetic and structural insights into the mechanism of AMPylation by VopS Fic domain. <i>Journal of Biological Chemistry</i> , 2010 , 285, 20155-63 | 5.4 | 62 |
| 71 | Pet10p is a yeast perilipin that stabilizes lipid droplets and promotes their assembly. <i>Journal of Cell Biology</i> , 2017 , 216, 3199-3217 | 7.3 | 61 |
| 70 | Evaluation of free modeling targets in CASP11 and ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 51-66 | 4.2 | 60 |
| 69 | CASP9 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79 Suppl 10, 21-36 | 4.2 | 54 |
| 68 | Acute Hepatopancreatic Necrosis Disease-Causing <i>Vibrio parahaemolyticus</i> Strains Maintain an Antibacterial Type VI Secretion System with Versatile Effector Repertoires. <i>Applied and Environmental Microbiology</i> , 2017 , 83, | 4.8 | 51 |
| 67 | Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015 , 11, e1005128 | 7.6 | 48 |
| 66 | Effectors of animal and plant pathogens use a common domain to bind host phosphoinositides. <i>Nature Communications</i> , 2013 , 4, 2973 | 17.4 | 46 |
| 65 | Realm of PD-(D/E)XK nuclease superfamily revisited: detection of novel families with modified transitive meta profile searches. <i>BMC Structural Biology</i> , 2007 , 7, 40 | 2.7 | 44 |
| 64 | Sec61beta—a component of the archaeal protein secretory system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 170-1 | 10.3 | 44 |
| 63 | Complete genome of <i>Plasmodium falciparum</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016 , 5, 2631 | 3.6 | 35 |
| 62 | Combined Blockade of Activating Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 277-289 | 12.9 | 35 |
| 61 | Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016 , 5, | 8.9 | 34 |
| 60 | ChSeq: A database of chameleon sequences. <i>Protein Science</i> , 2015 , 24, 1075-86 | 6.3 | 32 |
| 59 | A lytic polysaccharide monooxygenase-like protein functions in fungal copper import and meningitis. <i>Nature Chemical Biology</i> , 2020 , 16, 337-344 | 11.7 | 32 |
| 58 | Longin-like folds identified in CHiPS and DUF254 proteins: vesicle trafficking complexes conserved in eukaryotic evolution. <i>Protein Science</i> , 2006 , 15, 2669-74 | 6.3 | 31 |

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| 57 | CASP13 target classification into tertiary structure prediction categories. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1021-1036 | 4.2 | 29 |
| 56 | BOF: a novel family of bacterial OB-fold proteins. <i>FEBS Letters</i> , 2004 , 567, 297-301 | 3.8 | 29 |
| 55 | The human Ago2 MC region does not contain an eIF4E-like mRNA cap binding motif. <i>Biology Direct</i> , 2009 , 4, 2 | 7.2 | 28 |
| 54 | Human herpesvirus 1 UL24 gene encodes a potential PD-(D/E)XK endonuclease. <i>Journal of Virology</i> , 2006 , 80, 2575-7 | 6.6 | 28 |
| 53 | CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 20-33 | 4.2 | 28 |
| 52 | The secretory pathway kinases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 1687-93 | 4.9 | 27 |
| 51 | Analysis of CASP8 targets, predictions and assessment methods. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap003 | 5 | 25 |
| 50 | BTLCP proteins: a novel family of bacterial transglutaminase-like cysteine proteinases. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 392-5 | 10.3 | 24 |
| 49 | Bioinformatics perspective on rhomboid intramembrane protease evolution and function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 2937-43 | 3.8 | 23 |
| 48 | Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016 , 5, | 8.9 | 23 |
| 47 | An automatic method for CASP9 free modeling structure prediction assessment. <i>Bioinformatics</i> , 2011 , 27, 3371-8 | 7.2 | 22 |
| 46 | HP1BP3, a Chromatin Retention Factor for Co-transcriptional MicroRNA Processing. <i>Molecular Cell</i> , 2016 , 63, 420-32 | 17.6 | 21 |
| 45 | CASP5 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 340-51 | 4.2 | 20 |
| 44 | Assessment of CASP11 contact-assisted predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 164-80 | 4.2 | 19 |
| 43 | A database of domain definitions for proteins with complex interdomain geometry. <i>PLoS ONE</i> , 2009 , 4, e5084 | 3.7 | 18 |
| 42 | Vibrio type III effector VPA1380 is related to the cysteine protease domain of large bacterial toxins. <i>PLoS ONE</i> , 2014 , 9, e104387 | 3.7 | 18 |
| 41 | Pyrimidine Salvage Enzymes Are Essential for De Novo Biosynthesis of Deoxypyrimidine Nucleotides in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2016 , 12, e1006010 | 7.6 | 18 |
| 40 | Classification of proteins with shared motifs and internal repeats in the ECOD database. <i>Protein Science</i> , 2016 , 25, 1188-203 | 6.3 | 17 |

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| 39 | Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. <i>ELife</i> , 2016 , 5, | 8.9 | 16 |
| 38 | EDD, a novel phosphotransferase domain common to mannose transporter EIIA, dihydroxyacetone kinase, and DegV. <i>Protein Science</i> , 2005 , 14, 360-7 | 6.3 | 15 |
| 37 | Expanding the nitrogen regulatory protein superfamily: Homology detection at below random sequence identity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 75-84 | 4.2 | 15 |
| 36 | Regulation of Beclin 1-Mediated Autophagy by Oncogenic Tyrosine Kinases. <i>International Journal of Molecular Sciences</i> , 2020 , 21, | 6.3 | 14 |
| 35 | RUVBL1/RUVBL2 ATPase Activity Drives PAQosome Maturation, DNA Replication and Radioresistance in Lung Cancer. <i>Cell Chemical Biology</i> , 2020 , 27, 105-121.e14 | 8.2 | 14 |
| 34 | Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. <i>PLoS Computational Biology</i> , 2019 , 15, e1007569 | 5 | 14 |
| 33 | Topology evaluation of models for difficult targets in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1673-1686 | 4.2 | 14 |
| 32 | Hyperactivation of TORC1 Drives Resistance to the Pan-HER Tyrosine Kinase Inhibitor Neratinib in HER2-Mutant Cancers. <i>Cancer Cell</i> , 2020 , 37, 183-199.e5 | 24.3 | 13 |
| 31 | The effector RavD binds phosphatidylinositol-3-phosphate and helps suppress endolysosomal maturation of the -containing vacuole. <i>Journal of Biological Chemistry</i> , 2019 , 294, 6405-6415 | 5.4 | 12 |
| 30 | Direct Demonstration That Loop1 of Scap Binds to Loop7: A CRUCIAL EVENT IN CHOLESTEROL HOMEOSTASIS. <i>Journal of Biological Chemistry</i> , 2016 , 291, 12888-12896 | 5.4 | 12 |
| 29 | Deciphering a novel thioredoxin-like fold family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 323-31 | 4.2 | 12 |
| 28 | Definition and classification of evaluation units for tertiary structure prediction in CASP12 facilitated through semi-automated metrics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 16-26 | 4.2 | 10 |
| 27 | Proteomics Analysis Reveals Previously Uncharacterized Virulence Factors in <i>Vibrio proteolyticus</i> . <i>MBio</i> , 2016 , 7, | 7.8 | 10 |
| 26 | Compact Structure Patterns in Proteins. <i>Journal of Molecular Biology</i> , 2016 , 428, 4392-4412 | 6.5 | 10 |
| 25 | Target classification in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1618-1632 | 4.2 | 10 |
| 24 | ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019 , 20, 18 | 2.7 | 9 |
| 23 | Functional and evolutionary analysis of viral proteins containing a Rossmann-like fold. <i>Protein Science</i> , 2018 , 27, 1450-1463 | 6.3 | 9 |
| 22 | Assessing predictions of fitness effects of missense mutations in SUMO-conjugating enzyme UBE2I. <i>Human Mutation</i> , 2017 , 38, 1051-1063 | 4.7 | 9 |

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| 21 | Solution structure of the WNK1 autoinhibitory domain, a WNK-specific PF2 domain. <i>Journal of Molecular Biology</i> , 2013 , 425, 1245-52 | 6.5 | 8 |
| 20 | Genomics reveals the origins of ancient specimens | | 8 |
| 19 | Recent advances suggest increased influence of selective pressure in allostery. <i>Current Opinion in Structural Biology</i> , 2020 , 62, 183-188 | 8.1 | 8 |
| 18 | NK cell defects in X-linked pigmentary reticulate disorder. <i>JCI Insight</i> , 2019 , 4, | 9.9 | 7 |
| 17 | Using homology relations within a database markedly boosts protein sequence similarity search. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7003-8 | 11.5 | 6 |
| 16 | DCC proteins: a novel family of thiol-disulfide oxidoreductases. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 339-42 | 10.3 | 6 |
| 15 | Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , 2020 , 16, e1007775 | 5 | 5 |
| 14 | Role of Two Metacaspases in Development and Pathogenicity of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2021 , 12, | 7.8 | 5 |
| 13 | Assessment of domain interactions in the fourteenth round of the Critical Assessment of Structure Prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1700-1710 | 4.2 | 4 |
| 12 | Germline and sporadic mTOR pathway mutations in low-grade oncocytic tumor of the kidney. <i>Modern Pathology</i> , 2021 , | 9.8 | 4 |
| 11 | Schnyder corneal dystrophy-associated UBIAD1 is defective in MK-4 synthesis and resists autophagy-mediated degradation. <i>Journal of Lipid Research</i> , 2020 , 61, 746-757 | 6.3 | 3 |
| 10 | FlyXCDB-A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018 , 430, 3353-3411 | 6.5 | 3 |
| 9 | Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019 , 40, 1463-1473 | 4.7 | 3 |
| 8 | Identification of residues critical for topology inversion of the transmembrane protein TM4SF20 through regulated alternative translocation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 6054-6061 | 5.4 | 3 |
| 7 | Genomics Reveals the Origins of Historical Specimens. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2166-2176 | 11.6 | 3 |
| 6 | A combined RAD-Seq and WGS approach reveals the genomic basis of yellow color variation in bumble bee <i>Bombus terrestris</i> . <i>Scientific Reports</i> , 2021 , 11, 7996 | 4.9 | 2 |
| 5 | Manipulation of IRE1-Dependent MAPK Signaling by a Vibrio Agonist-Antagonist Effector Pair. <i>MSystems</i> , 2021 , 6, | 7.6 | 2 |
| 4 | A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. <i>Journal of Molecular Biology</i> , 2021 , 433, 166788 | 6.5 | 2 |

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| 3 | β-strand-mediated interactions of protein domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1513-1527 | 4.2 | 1 |
| 2 | Completeness and Consistency in Structural Domain Classifications. <i>ACS Omega</i> , 2021 , 6, 15698-15707 | 3.9 | 0 |
| 1 | Autoinhibition and Salt Sensing are Linked in the WNK1 Kinase. <i>FASEB Journal</i> , 2012 , 26, lb162 | 0.9 | |