

Lisa N Kinch

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

8,592
citations

109321
35
h-index

54911
84
g-index

101
all docs

101
docs citations

101
times ranked

13200
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	12.6	2,843
2	Structure prediction for CASP8 with all-atom refinement using Rosetta. Proteins: Structure, Function and Bioinformatics, 2009, 77, 89-99.	2.6	425
3	AMPylation of Rho GTPases by <i>Vibrio</i> VopS Disrupts Effector Binding and Downstream Signaling. Science, 2009, 323, 269-272.	12.6	343
4	ECOD: An Evolutionary Classification of Protein Domains. PLoS Computational Biology, 2014, 10, e1003926.	3.2	321
5	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. Nature Genetics, 2015, 47, 13-21.	21.4	310
6	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. Cell, 2015, 161, 1619-1632.	28.9	264
7	Crystal structure of the human sterol transporter ABCG5/ABCG8. Nature, 2016, 533, 561-564.	27.8	233
8	Large-scale determination of previously unsolved protein structures using evolutionary information. ELife, 2015, 4, e09248.	6.0	229
9	Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. Nature Structural and Molecular Biology, 2020, 27, 1194-1201.	8.2	196
10	Marker for type VI secretion system effectors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9271-9276.	7.1	165
11	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. Cell, 2018, 175, 809-821.e19.	28.9	149
12	Evolution of protein structures and functions. Current Opinion in Structural Biology, 2002, 12, 400-408.	5.7	144
13	A Novel Germline Mutation in <i>BAP1</i> Predisposes to Familial Clear-Cell Renal Cell Carcinoma. Molecular Cancer Research, 2013, 11, 1061-1071.	3.4	135
14	Beclin 2 Functions in Autophagy, Degradation of G Protein-Coupled Receptors, and Metabolism. Cell, 2013, 154, 1085-1099.	28.9	130
15	Fido, a Novel AMPylation Domain Common to Fic, Doc, and AvrB. PLoS ONE, 2009, 4, e5818.	2.5	116
16	Site-2 protease regulated intramembrane proteolysis: Sequence homologs suggest an ancient signaling cascade. Protein Science, 2006, 15, 84-93.	7.6	97
17	Succination of Keap1 and Activation of Nrf2-Dependent Antioxidant Pathways in FH-Deficient Papillary Renal Cell Carcinoma Type 2. Cancer Cell, 2011, 20, 418-420.	16.8	92
18	Pet10p is a yeast perilipin that stabilizes lipid droplets and promotes their assembly. Journal of Cell Biology, 2017, 216, 3199-3217.	5.2	92

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19	CASP5 assessment of fold recognition target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 395-409.	2.6	91
20	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, .	3.1	88
21	CASP9 assessment of free modeling target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 59-73.	2.6	87
22	Identification of novel restriction endonuclease-like fold families among hypothetical proteins. <i>Nucleic Acids Research</i> , 2005, 33, 3598-3605.	14.5	83
23	Kinetic and Structural Insights into the Mechanism of AMPylation by VopS Fic Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 20155-20163.	3.4	77
24	Combined Blockade of Activating <i>ERBB2</i> Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 277-289.	7.0	74
25	Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015, 11, e1005128.	4.7	71
26	Evaluation of free modeling targets in CASP11 and ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 51-66.	2.6	70
27	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016, 5, .	6.0	68
28	Effectors of animal and plant pathogens use a common domain to bind host phosphoinositides. <i>Nature Communications</i> , 2013, 4, 2973.	12.8	62
29	CASP9 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 21-36.	2.6	61
30	A lytic polysaccharide monooxygenase-like protein functions in fungal copper import and meningitis. <i>Nature Chemical Biology</i> , 2020, 16, 337-344.	8.0	61
31	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.	2.3	57
32	Sec61 ^{Δ2} a component of the archaeal protein secretory system. <i>Trends in Biochemical Sciences</i> , 2002, 27, 170-171.	7.5	49
33	<sc>ChSeq</sc>: A database of chameleon sequences. <i>Protein Science</i> , 2015, 24, 1075-1086.	7.6	47
34	Complete genome of <i>Pieris rapae</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016, 5, 2631.	1.6	47
35	Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. <i>PLoS Computational Biology</i> , 2019, 15, e1007569.	3.2	45
36	Pyrimidine Salvage Enzymes Are Essential for De Novo Biosynthesis of Deoxypyrimidine Nucleotides in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2016, 12, e1006010.	4.7	39

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37	RUVBL1/RUVBL2 ATPase Activity Drives PAQosome Maturation, DNA Replication and Radioresistance in Lung Cancer. <i>Cell Chemical Biology</i> , 2020, 27, 105-121.e14.	5.2	38
38	BOF: a novel family of bacterial OB-fold proteins. <i>FEBS Letters</i> , 2004, 567, 297-301.	2.8	36
39	Human Herpesvirus 1 <i>UL24</i> Gene Encodes a Potential PD-(D/E)XK Endonuclease. <i>Journal of Virology</i> , 2006, 80, 2575-2577.	3.4	35
40	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.	2.6	35
41	CASP13 target classification into tertiary structure prediction categories. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1021-1036.	2.6	34
42	Germline and sporadic mTOR pathway mutations in low-grade oncocyctic tumor of the kidney. <i>Modern Pathology</i> , 2022, 35, 333-343.	5.5	34
43	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.	16.8	33
44	Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016, 5, .	6.0	33
45	Longin-like folds identified in CHiPS and DUF254 proteins: Vesicle trafficking complexes conserved in eukaryotic evolution. <i>Protein Science</i> , 2006, 15, 2669-2674.	7.6	32
46	HP1BP3, a Chromatin Retention Factor for Co-transcriptional MicroRNA Processing. <i>Molecular Cell</i> , 2016, 63, 420-432.	9.7	32
47	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.	2.6	32
48	The secretory pathway kinases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1687-1693.	2.3	31
49	CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 20-33.	2.6	31
50	BTLCp proteins: a novel family of bacterial transglutaminase-like cysteine proteinases. <i>Trends in Biochemical Sciences</i> , 2004, 29, 392-395.	7.5	29
51	Analysis of CASP8 targets, predictions and assessment methods. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap003-bap003.	3.0	29
52	The human Ago2 MC region does not contain an eIF4E-like mRNA cap binding motif. <i>Biology Direct</i> , 2009, 4, 2.	4.6	29
53	Regulation of Beclin 1-Mediated Autophagy by Oncogenic Tyrosine Kinases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9210.	4.1	27
54	Bioinformatics perspective on rhomboid intramembrane protease evolution and function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2937-2943.	2.6	26

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55	A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. Journal of Molecular Biology, 2021, 433, 166788.	4.2	26
56	An automatic method for CASP9 free modeling structure prediction assessment. Bioinformatics, 2011, 27, 3371-3378.	4.1	24
57	Assessment of CASP11 contact-assisted predictions. Proteins: Structure, Function and Bioinformatics, 2016, 84, 164-180.	2.6	24
58	Genomics Reveals the Origins of Historical Specimens. Molecular Biology and Evolution, 2021, 38, 2166-2176.	8.9	24
59	Classification of proteins with shared motifs and internal repeats in the <scp>ECOD</scp> database. Protein Science, 2016, 25, 1188-1203.	7.6	23
60	The Legionella effector RavD binds phosphatidylinositol-3-phosphate and helps suppress endolysosomal maturation of the Legionella-containing vacuole. Journal of Biological Chemistry, 2019, 294, 6405-6415.	3.4	22
61	Vibrio Type III Effector VPA1380 Is Related to the Cysteine Protease Domain of Large Bacterial Toxins. PLoS ONE, 2014, 9, e104387.	2.5	22
62	Proteomics Analysis Reveals Previously Uncharacterized Virulence Factors in Vibrio proteolyticus. MBio, 2016, 7, .	4.1	21
63	CASP5 target classification. Proteins: Structure, Function and Bioinformatics, 2003, 53, 340-351.	2.6	20
64	Compact Structure Patterns in Proteins. Journal of Molecular Biology, 2016, 428, 4392-4412.	4.2	20
65	A Database of Domain Definitions for Proteins with Complex Interdomain Geometry. PLoS ONE, 2009, 4, e5084.	2.5	19
66	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. ELife, 2016, 5, .	6.0	19
67	Functional and evolutionary analysis of viral proteins containing a Rossmann-like fold. Protein Science, 2018, 27, 1450-1463.	7.6	18
68	Direct Demonstration That Loop1 of Scap Binds to Loop7. Journal of Biological Chemistry, 2016, 291, 12888-12896.	3.4	17
69	NK cell defects in X-linked pigmentary reticulate disorder. JCI Insight, 2019, 4, .	5.0	17
70	Expanding the nitrogen regulatory protein superfamily: Homology detection at below random sequence identity. Proteins: Structure, Function and Bioinformatics, 2002, 48, 75-84.	2.6	16
71	EDD, a novel phosphotransferase domain common to mannose transporter EIIA, dihydroxyacetone kinase, and DegV. Protein Science, 2005, 14, 360-367.	7.6	16
72	Role of Two Metacaspases in Development and Pathogenicity of the Rice Blast Fungus Magnaporthe oryzae. MBio, 2021, 12, .	4.1	14

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73	Co-component signal transduction systems: Fast-evolving virulence regulation cassettes discovered in enteric bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	14
74	Deciphering a novel thioredoxin-like fold family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 323-331.	2.6	13
75	Solution Structure of the WNK1 Autoinhibitory Domain, a WNK-Specific PF2 Domain. <i>Journal of Molecular Biology</i> , 2013, 425, 1245-1252.	4.2	13
76	FlyXCDBâ€”A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018, 430, 3353-3411.	4.2	13
77	Recent advances suggest increased influence of selective pressure in allostery. <i>Current Opinion in Structural Biology</i> , 2020, 62, 183-188.	5.7	13
78	Assessing predictions of fitness effects of missense mutations in SUMOâ€™conjugating enzyme UBE2I. <i>Human Mutation</i> , 2017, 38, 1051-1063.	2.5	12
79	Definition and classification of evaluation units for tertiary structure prediction in CASP12 facilitated through semiâ€™automated metrics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 16-26.	2.6	12
80	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 18.	2.0	12
81	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.	4.2	12
82	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , 2020, 16, e1007775.	3.2	11
83	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, 7003-7008.	7.1	8
84	Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019, 40, 1463-1473.	2.5	8
85	Completeness and Consistency in Structural Domain Classifications. <i>ACS Omega</i> , 2021, 6, 15698-15707.	3.5	8
86	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.	2.6	8
87	DCC proteins: a novel family of thiol-disulfide oxidoreductases. <i>Trends in Biochemical Sciences</i> , 2004, 29, 339-342.	7.5	7
88	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.	3.3	7
89	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.	3.4	5
90	Manipulation of IRE1-Dependent MAPK Signaling by a <i>Vibrio</i> Agonist-Antagonist Effector Pair. <i>MSystems</i> , 2021, 6, .	3.8	3

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91	α-Strand-mediated interactions of protein domains. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1513-1527.	2.6	2
92	Autoinhibition and Salt Sensing are Linked in the WNK1 Kinase. FASEB Journal, 2012, 26, lb162.	0.5	0
93	Hyperactivation of Torc1 Drives Resistance to the Pan-Her Tyrosine Kinase Inhibitor Neratinib in Her2-Mutant Cancers. SSRN Electronic Journal, 0, , .	0.4	0
94	Enzymatic Specificity of Conserved Rho GTPase Deamidases Promotes Invasion of Vibrio parahaemolyticus at the Expense of Infection. MBio, 2022, 13, .	4.1	0