

Lisa N Kinch

List of Publications by Year in Descending Order

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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	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
91	Completeness and Consistency in Structural Domain Classifications. <i>ACS Omega</i> , 2021 , 6, 15698-15707	3.9	0
90	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
89	Manipulation of IRE1-Dependent MAPK Signaling by a <i>Vibrio</i> Agonist-Antagonist Effector Pair. <i>MSystems</i> , 2021 , 6,	7.6	2
88	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
87	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021 , 373, 871-876	33.3	522
86	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
85	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
84	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
83	Germline and sporadic mTOR pathway mutations in low-grade oncocytic tumor of the kidney. <i>Modern Pathology</i> , 2021 ,	9.8	4
82	Genomics Reveals the Origins of Historical Specimens. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2166-2176	8.6	3
81	Regulation of Beclin 1-Mediated Autophagy by Oncogenic Tyrosine Kinases. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	14
80	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
79	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
78	β-strand-mediated interactions of protein domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1513-1527	4.2	1
77	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
76	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

75	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
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	Recent advances suggest increased influence of selective pressure in allostery. <i>Current Opinion in Structural Biology</i> , 2020 , 62, 183-188	8.1	8
72	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019 , 20, 18	2.7	9
71	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
70	Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019 , 40, 1463-1473	4.7	3
69	CASP13 target classification into tertiary structure prediction categories. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1021-1036	4.2	29
68	NK cell defects in X-linked pigmentary reticulate disorder. <i>JCI Insight</i> , 2019 , 4,	9.9	7
67	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
66	Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. <i>PLoS Computational Biology</i> , 2019 , 15, e1007569	5	14
65	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
64	Functional and evolutionary analysis of viral proteins containing a Rossmann-like fold. <i>Protein Science</i> , 2018 , 27, 1450-1463	6.3	9
63	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
62	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
61	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. <i>Cell</i> , 2018 , 175, 809-821.e19	56.2	87
60	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
59	Assessing predictions of fitness effects of missense mutations in SUMO-conjugating enzyme UBE2I. <i>Human Mutation</i> , 2017 , 38, 1051-1063	4.7	9
58	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

57	Proteomics Analysis Reveals Previously Uncharacterized Virulence Factors in <i>Vibrio proteolyticus</i> . <i>MBio</i> , 2016 , 7,	7.8	10
56	HP1BP3, a Chromatin Retention Factor for Co-transcriptional MicroRNA Processing. <i>Molecular Cell</i> , 2016 , 63, 420-32	17.6	21
55	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
54	Classification of proteins with shared motifs and internal repeats in the ECOD database. <i>Protein Science</i> , 2016 , 25, 1188-203	6.3	17
53	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
52	Complete genome of , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016 , 5, 2631	3.6	35
51	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016 , 5,	8.9	34
50	Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016 , 5,	8.9	23
49	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. <i>ELife</i> , 2016 , 5,	8.9	16
48	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
47	Assessment of CASP11 contact-assisted predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 164-80	4.2	19
46	CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 20-33	4.2	28
45	Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , 2016 , 533, 561-4	50.4	185
44	Compact Structure Patterns in Proteins. <i>Journal of Molecular Biology</i> , 2016 , 428, 4392-4412	6.5	10
43	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. <i>Cell</i> , 2015 , 161, 1619-32	56.2	187
42	ChSeq: A database of chameleon sequences. <i>Protein Science</i> , 2015 , 24, 1075-86	6.3	32
41	The secretory pathway kinases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 1687-93		27
40	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015 , 47, 13-21	36.3	247

39	Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015 , 11, e1005128	7.6	48
38	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
37	Large-scale determination of previously unsolved protein structures using evolutionary information. <i>ELife</i> , 2015 , 4, e09248	8.9	173
36	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
35	ECOD: an evolutionary classification of protein domains. <i>PLoS Computational Biology</i> , 2014 , 10, e1003926		184
34	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
33	Bioinformatics perspective on rhomboid intramembrane protease evolution and function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 2937-43	3.8	23
32	Beclin 2 functions in autophagy, degradation of G protein-coupled receptors, and metabolism. <i>Cell</i> , 2013 , 154, 1085-1099	56.2	115
31	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
30	Effectors of animal and plant pathogens use a common domain to bind host phosphoinositides. <i>Nature Communications</i> , 2013 , 4, 2973	17.4	46
29	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
28	Autoinhibition and Salt Sensing are Linked in the WNK1 Kinase. <i>FASEB Journal</i> , 2012 , 26, lb162	0.9	
27	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
26	CASP9 assessment of free modeling target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79 Suppl 10, 59-73	4.2	82
25	CASP9 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79 Suppl 10, 21-36	4.2	54
24	An automatic method for CASP9 free modeling structure prediction assessment. <i>Bioinformatics</i> , 2011 , 27, 3371-8	7.2	22
23	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
22	Fido, a novel AMPylation domain common to fic, doc, and AvrB. <i>PLoS ONE</i> , 2009 , 4, e5818	3.7	103

21	A database of domain definitions for proteins with complex interdomain geometry. <i>PLoS ONE</i> , 2009 , 4, e5084	3.7	18
20	Analysis of CASP8 targets, predictions and assessment methods. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap003	5	25
19	AMPylation of Rho GTPases by Vibrio VopS disrupts effector binding and downstream signaling. <i>Science</i> , 2009 , 323, 269-72	33.3	287
18	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
17	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
16	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
15	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
14	Site-2 protease regulated intramembrane proteolysis: sequence homologs suggest an ancient signaling cascade. <i>Protein Science</i> , 2006 , 15, 84-93	6.3	76
13	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
12	Identification of novel restriction endonuclease-like fold families among hypothetical proteins. <i>Nucleic Acids Research</i> , 2005 , 33, 3598-605	20.1	70
11	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
10	DCC proteins: a novel family of thiol-disulfide oxidoreductases. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 339-42	10.3	6
9	BTLCP proteins: a novel family of bacterial transglutaminase-like cysteine proteinases. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 392-5	10.3	24
8	BOF: a novel family of bacterial OB-fold proteins. <i>FEBS Letters</i> , 2004 , 567, 297-301	3.8	29
7	Deciphering a novel thioredoxin-like fold family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 323-31	4.2	12
6	CASP5 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 340-51	4.2	20
5	CASP5 assessment of fold recognition target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 395-409	4.2	82
4	Sec61beta—a component of the archaeal protein secretory system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 170-1	10.3	44

- 3 Evolution of protein structures and functions. *Current Opinion in Structural Biology*, **2002**, 12, 400-8 8.1 131
- 2 Expanding the nitrogen regulatory protein superfamily: Homology detection at below random sequence identity. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 75-84 4.2 15
- 1 Genomics reveals the origins of ancient specimens 8