

Charalampos Kalodimos

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,731
citations

471509

17
h-index

642732

23
g-index

28
all docs

28
docs citations

28
times ranked

2331
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis for Signal-Sequence Recognition by the Translocase Motor SecA as Determined by NMR. <i>Cell</i> , 2007, 131, 756-769.	28.9	381
2	Structural Basis for Protein Antiaggregation Activity of the Trigger Factor Chaperone. <i>Science</i> , 2014, 344, 1250-1254.	12.6	254
3	Structural basis for cAMP-mediated allosteric control of the catabolite activator protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6927-6932.	7.1	197
4	Structural basis for the antifolding activity of a molecular chaperone. <i>Nature</i> , 2016, 537, 202-206.	27.8	135
5	Conformational states dynamically populated by a kinase determine its function. <i>Science</i> , 2020, 370, .	12.6	134
6	A microscale protein NMR sample screening pipeline. <i>Journal of Biomolecular NMR</i> , 2010, 46, 11-22.	2.8	106
7	Structures of chaperone-substrate complexes docked onto the export gate in a type III secretion system. <i>Nature Communications</i> , 2018, 9, 1773.	12.8	72
8	Structures of Large Protein Complexes Determined by Nuclear Magnetic Resonance Spectroscopy. <i>Annual Review of Biophysics</i> , 2017, 46, 317-336.	10.0	62
9	¹⁵ N and ¹³ C-SOFAST-HMQC editing enhances 3D-NOESY sensitivity in highly deuterated, selectively [¹ H, ¹³ C]-labeled proteins. <i>Journal of Biomolecular NMR</i> , 2016, 66, 259-271.	2.8	56
10	Oligomerization of a molecular chaperone modulates its activity. <i>ELife</i> , 2018, 7, .	6.0	51
11	Automatic methyl assignment in large proteins by the MAGIC algorithm. <i>Journal of Biomolecular NMR</i> , 2017, 69, 215-227.	2.8	44
12	A hybrid NMR/SAXS-based approach for discriminating oligomeric protein interfaces using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 309-317.	2.6	33
13	Structural elucidation of the Cys-His-Glu-Asn proteolytic relay in the secreted CHAP domain enzyme from the human pathogen <i>Staphylococcus saprophyticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 515-519.	2.6	30
14	Exploiting <i>E. coli</i> auxotrophs for leucine, valine, and threonine specific methyl labeling of large proteins for NMR applications. <i>Journal of Biomolecular NMR</i> , 2016, 65, 99-108.	2.8	29
15	Mechanism for the activation of the anaplastic lymphoma kinase receptor. <i>Nature</i> , 2021, 600, 153-157.	27.8	28
16	Structural and sequencing analysis of local target DNA recognition by MLV integrase. <i>Nucleic Acids Research</i> , 2015, 43, 5647-5663.	14.5	26
17	Recognition and targeting mechanisms by chaperones in flagellum assembly and operation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9798-9803.	7.1	25
18	A community resource of experimental data for NMR / X-ray crystal structure pairs. <i>Protein Science</i> , 2016, 25, 30-45.	7.6	24

#	ARTICLE	IF	CITATIONS
19	Toolkit for NMR Studies of Methyl-Labeled Proteins. <i>Methods in Enzymology</i> , 2019, 614, 107-142.	1.0	17
20	Structures of apo- and ssDNA-bound YdbC from <i>Lactococcus lactis</i> uncover the function of protein domain family DUF2128 and expand the single-stranded DNA-binding domain proteome. <i>Nucleic Acids Research</i> , 2013, 41, 2756-2768.	14.5	10
21	Imatinib can act as an Allosteric Activator of Abl Kinase. <i>Journal of Molecular Biology</i> , 2022, 434, 167349.	4.2	9
22	Synthesis of Isotopically Labeled, Spin-Isolated Tyrosine and Phenylalanine for Protein NMR Applications. <i>Organic Letters</i> , 2021, 23, 6288-6292.	4.6	4
23	Progress toward automated methyl assignments for methyl-TROSY applications. <i>Structure</i> , 2022, 30, 69-79.e2.	3.3	4