

Nicholas H Keep

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.

49
papers

3,250
citations

29
h-index

51
g-index

51
ext. papers

3,617
ext. citations

6.1
avg, IF

4.67
L-index

#	Paper	IF	Citations
49	Characterization of the MurT/GatD complex in towards validating a novel anti-tubercular drug target. <i>JAC-Antimicrobial Resistance</i> , 2021 , 3, dlab028	2.9	1
48	Chemoenzymatic Cascades toward Methylated Tetrahydroprotoberberine and Protoberberine Alkaloids. <i>Organic Letters</i> , 2021 , 23, 6342-6347	6.2	2
47	Pictet-Spenglerases in alkaloid biosynthesis: Future applications in biocatalysis. <i>Current Opinion in Chemical Biology</i> , 2020 , 55, 69-76	9.7	37
46	Single step syntheses of (1S)-aryl-tetrahydroisoquinolines by norcoclaurine synthases. <i>Communications Chemistry</i> , 2020 , 3,	6.3	7
45	Acceptance and Kinetic Resolution of α -Methyl-Substituted Aldehydes by Norcoclaurine Synthases. <i>ACS Catalysis</i> , 2019 , 9, 9640-9649	13.1	24
44	Cell wall peptidoglycan in Mycobacterium tuberculosis: An Achilles Wheel for the TB-causing pathogen. <i>FEMS Microbiology Reviews</i> , 2019 , 43, 548-575	15.1	63
43	Critical Role of a Sheath Phosphorylation Site On the Assembly and Function of an Atypical Type VI Secretion System. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2418-2432	7.6	5
42	Terminal Regions Confer Plasticity to the Tetrameric Assembly of Human HspB2 and HspB3. <i>Journal of Molecular Biology</i> , 2018 , 430, 3297-3310	6.5	24
41	Structural Evidence for the Dopamine-First Mechanism of Norcoclaurine Synthase. <i>Biochemistry</i> , 2017 , 56, 5274-5277	3.2	29
40	Crystal Structures and Binding Dynamics of Odorant-Binding Protein 3 from two aphid species Megoura viciae and Nasonovia ribisnigri. <i>Scientific Reports</i> , 2016 , 6, 24739	4.9	35
39	Human BRCA1-BARD1 ubiquitin ligase activity counteracts chromatin barriers to DNA resection. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 647-55	17.6	166
38	Structure of the stationary phase survival protein YuiC from B.subtilis. <i>BMC Structural Biology</i> , 2015 , 15, 12	2.7	4
37	Dopamine-first mechanism enables the rational engineering of the norcoclaurine synthase aldehyde activity profile. <i>FEBS Journal</i> , 2015 , 282, 1137-51	5.7	51
36	Crystal structures of the human Dysferlin inner DysF domain. <i>BMC Structural Biology</i> , 2014 , 14, 3	2.7	19
35	Dbl3 drives Cdc42 signaling at the apical margin to regulate junction position and apical differentiation. <i>Journal of Cell Biology</i> , 2014 , 204, 111-27	7.3	41
34	The RpfC (Rv1884) atomic structure shows high structural conservation within the resuscitation-promoting factor catalytic domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1022-6	1.1	13
33	Characterisation of ATP-dependent Mur ligases involved in the biogenesis of cell wall peptidoglycan in Mycobacterium tuberculosis. <i>PLoS ONE</i> , 2013 , 8, e60143	3.7	56

32	Crystal structure of reduced MsAcg, a putative nitroreductase from <i>Mycobacterium smegmatis</i> and a close homologue of <i>Mycobacterium tuberculosis</i> Acg. <i>Journal of Biological Chemistry</i> , 2012 , 287, 44372-83	5.4	11
31	Crystal structure of R120G disease mutant of human B-crystallin domain dimer shows closure of a groove. <i>Journal of Molecular Biology</i> , 2011 , 408, 118-34	6.5	95
30	Characterization of an oxidoreductase from the arylamine N-acetyltransferase operon in <i>Mycobacterium smegmatis</i> . <i>FEBS Journal</i> , 2011 , 278, 4824-32	5.7	2
29	Essential residues for the enzyme activity of ATP-dependent MurE ligase from <i>Mycobacterium tuberculosis</i> . <i>Protein and Cell</i> , 2010 , 1, 1011-22	7.2	26
28	ATP-dependent MurE ligase in <i>Mycobacterium tuberculosis</i> : biochemical and structural characterisation. <i>Tuberculosis</i> , 2010 , 90, 16-24	2.6	41
27	Characterisation of <i>Bombyx mori</i> Odorant-binding proteins reveals that a general odorant-binding protein discriminates between sex pheromone components. <i>Journal of Molecular Biology</i> , 2009 , 389, 529-45	6.5	198
26	Crystal structures of alpha-crystallin domain dimers of alphaB-crystallin and Hsp20. <i>Journal of Molecular Biology</i> , 2009 , 392, 1242-52	6.5	233
25	Solution structure of the inner DysF domain of myoferlin and implications for limb girdle muscular dystrophy type 2b. <i>Journal of Molecular Biology</i> , 2008 , 379, 981-90	6.5	25
24	N-terminus-mediated dimerization of ROCK-I is required for RhoE binding and actin reorganization. <i>Biochemical Journal</i> , 2008 , 411, 407-14	3.8	18
23	Proteomics study reveals cross-talk between Rho guanidine nucleotide dissociation inhibitor 1 post-translational modifications in epidermal growth factor stimulated fibroblasts. <i>Journal of Proteome Research</i> , 2007 , 6, 2623-30	5.6	8
22	Bacterial resuscitation factors: revival of viable but non-culturable bacteria. <i>Cellular and Molecular Life Sciences</i> , 2006 , 63, 2555-9	10.3	36
21	Genetic analysis of BRCA1 ubiquitin ligase activity and its relationship to breast cancer susceptibility. <i>Human Molecular Genetics</i> , 2006 , 15, 599-606	5.6	85
20	Wake up! Peptidoglycan lysis and bacterial non-growth states. <i>Trends in Microbiology</i> , 2006 , 14, 271-6	12.4	114
19	The structure of a resuscitation-promoting factor domain from <i>Mycobacterium tuberculosis</i> shows homology to lysozymes. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 270-3	17.6	116
18	Dodecameric structure of the small heat shock protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 33419-25	5.4	82
17	The GDP-GTP exchange factor collybistin: an essential determinant of neuronal gephyrin clustering. <i>Journal of Neuroscience</i> , 2004 , 24, 5816-26	6.6	210
16	Resuscitation-promoting factors possess a lysozyme-like domain. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 7-10	10.3	57
15	(1)H, (15)N, and (13)C chemical shift assignments of the resuscitation promoting factor domain of Rv1009 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biomolecular NMR</i> , 2004 , 30, 373-4	3	12

14	The X-ray crystal structure and putative ligand-derived peptide binding properties of gamma-aminobutyric acid receptor type A receptor-associated protein. <i>Journal of Biological Chemistry</i> , 2002 , 277, 5556-61	5.4	57
13	Identification of residues required for the interaction of BARD1 with BRCA1. <i>Journal of Biological Chemistry</i> , 2002 , 277, 9382-6	5.4	31
12	Crystal structure of the core domain of RhoE/Rnd3: a constitutively activated small G protein. <i>Biochemistry</i> , 2002 , 41, 6303-10	3.2	25
11	Backbone 1H, 13C, and 15N resonance assignments for a 14 kD protein, GABA(A) receptor associated protein (GABARAP). <i>Journal of Biomolecular NMR</i> , 2001 , 21, 185-6	3	6
10	The 2.7 Å crystal structure of the activated FERM domain of moesin: an analysis of structural changes on activation. <i>Biochemistry</i> , 2001 , 40, 7061-8	3.2	71
9	Mapping the binding site for the GTP-binding protein Rac-1 on its inhibitor RhoGDI-1. <i>Structure</i> , 2000 , 8, 47-55	5.2	66
8	The structure of the N-terminal actin-binding domain of human dystrophin and how mutations in this domain may cause Duchenne or Becker muscular dystrophy. <i>Structure</i> , 2000 , 8, 481-91	5.2	132
7	Structure of the utrophin actin-binding domain bound to F-actin reveals binding by an induced fit mechanism. <i>Journal of Molecular Biology</i> , 2000 , 297, 465-80	6.5	60
6	Crystal structure of the actin-binding region of utrophin reveals a head-to-tail dimer. <i>Structure</i> , 1999 , 7, 1539-46	5.2	86
5	The 2.0 Å structure of the second calponin homology domain from the actin-binding region of the dystrophin homologue utrophin. <i>Journal of Molecular Biology</i> , 1999 , 285, 1257-64	6.5	42
4	A modulator of rho family G proteins, rhoGDI, binds these G proteins via an immunoglobulin-like domain and a flexible N-terminal arm. <i>Structure</i> , 1997 , 5, 623-33	5.2	98
3	How coenzyme B12 radicals are generated: the crystal structure of methylmalonyl-coenzyme A mutase at 2 Å resolution. <i>Structure</i> , 1996 , 4, 339-50	5.2	45 ^o
2	X-CGDbase: a database of X-CGD-causing mutations. <i>Trends in Immunology</i> , 1996 , 17, 517-521		3
1	Chronic granulomatous disease. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 1994 , 1227, 1-24	6.9	176