

Wolfram Tempel

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.

33
papers

3,461
citations

25
h-index

39
g-index

39
ext. papers

3,964
ext. citations

9.4
avg. IF

4.07
L-index

#	Paper	IF	Citations
33	Pyruvate kinase M2 activators promote tetramer formation and suppress tumorigenesis. <i>Nature Chemical Biology</i> , 2012 , 8, 839-47	11.7	476
32	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. <i>Nature Chemical Biology</i> , 2011 , 7, 566-74	11.7	386
31	Structural basis for selective binding of m6A RNA by the YTHDC1 YTH domain. <i>Nature Chemical Biology</i> , 2014 , 10, 927-9	11.7	383
30	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. <i>Nature Communications</i> , 2012 , 3, 1288	17.4	209
29	Genome-scale protein expression and structural biology of Plasmodium falciparum and related Apicomplexan organisms. <i>Molecular and Biochemical Parasitology</i> , 2007 , 151, 100-10	1.9	199
28	Tet3 CXXC domain and dioxygenase activity cooperatively regulate key genes for Xenopus eye and neural development. <i>Cell</i> , 2012 , 151, 1200-13	56.2	188
27	In situ proteolysis for protein crystallization and structure determination. <i>Nature Methods</i> , 2007 , 4, 1019-21	21.6	181
26	Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. <i>EMBO Journal</i> , 2011 , 30, 2829-42	13	172
25	Structures of apicomplexan calcium-dependent protein kinases reveal mechanism of activation by calcium. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 596-601	17.6	167
24	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. <i>Nature Chemical Biology</i> , 2013 , 9, 184-91	11.7	129
23	Mechanism of class 1 (glycosylhydrolase family 47) α -mannosidases involved in N-glycan processing and endoplasmic reticulum quality control. <i>Journal of Biological Chemistry</i> , 2005 , 280, 16197-207	5.4	102
22	Binding of Rac1, Rnd1, and RhoD to a novel Rho GTPase interaction motif destabilizes dimerization of the plexin-B1 effector domain. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37215-24	5.4	101
21	A cellular chemical probe targeting the chromodomains of Polycomb repressive complex 1. <i>Nature Chemical Biology</i> , 2016 , 12, 180-7	11.7	100
20	Nicotinamide riboside kinase structures reveal new pathways to NAD ⁺ . <i>PLoS Biology</i> , 2007 , 5, e263	9.7	95
19	Structure and function of the intracellular region of the plexin-b1 transmembrane receptor. <i>Journal of Biological Chemistry</i> , 2009 , 284, 35962-72	5.4	71
18	Bromo-deaza-SAH: a potent and selective DOT1L inhibitor. <i>Bioorganic and Medicinal Chemistry</i> , 2013 , 21, 1787-1794	3.4	54
17	The xenograft antigen bound to Griffonia simplicifolia lectin 1-B(4). X-ray crystal structure of the complex and molecular dynamics characterization of the binding site. <i>Journal of Biological Chemistry</i> , 2002 , 277, 6615-21	5.4	52

16	Histone recognition by human malignant brain tumor domains. <i>Journal of Molecular Biology</i> , 2012 , 423, 702-18	6.5	45
15	Structure of mouse Golgi alpha-mannosidase IA reveals the molecular basis for substrate specificity among class 1 (family 47 glycosylhydrolase) alpha1,2-mannosidases. <i>Journal of Biological Chemistry</i> , 2004 , 279, 29774-86	5.4	43
14	Family-wide Characterization of Histone Binding Abilities of Human CW Domain-containing Proteins. <i>Journal of Biological Chemistry</i> , 2016 , 291, 9000-13	5.4	37
13	Sequence-specific recognition of a PxLPxI/L motif by an ankyrin repeat tumbler lock. <i>Science Signaling</i> , 2012 , 5, ra39	8.8	33
12	Structural basis of Rnd1 binding to plexin Rho GTPase binding domains (RBDs). <i>Journal of Biological Chemistry</i> , 2011 , 286, 26093-106	5.4	33
11	Structure and function of a G-actin sequestering protein with a vital role in malaria oocyst development inside the mosquito vector. <i>Journal of Biological Chemistry</i> , 2010 , 285, 11572-83	5.4	32
10	Structure-Based Design of a Covalent Inhibitor of the SET Domain-Containing Protein 8 (SETD8) Lysine Methyltransferase. <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 9881-9889	8.3	26
9	Structural basis for histone mimicry and hijacking of host proteins by influenza virus protein NS1. <i>Nature Communications</i> , 2014 , 5, 3952	17.4	25
8	IQGAP proteins reveal an atypical phosphoinositide (aPI) binding domain with a pseudo C2 domain fold. <i>Journal of Biological Chemistry</i> , 2012 , 287, 22483-96	5.4	21
7	Crystal structures of the Tudor domains of human PHF20 reveal novel structural variations on the Royal Family of proteins. <i>FEBS Letters</i> , 2012 , 586, 859-65	3.8	20
6	Structural genomics of <i>Pyrococcus furiosus</i> : X-ray crystallography reveals 3D domain swapping in rubrerythrin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 878-82	4.2	17
5	Plasticity at the DNA recognition site of the MeCP2 mCG-binding domain. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019 , 1862, 194409	6	12
4	First crystallographic models of human TBC domains in the context of a family-wide structural analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 497-502	4.2	9
3	Crystal structure of DPF3b in complex with an acetylated histone peptide. <i>Journal of Structural Biology</i> , 2016 , 195, 365-372	3.4	9
2	Three-dimensional structure of GlcNAc alpha1-4Gal releasing endo-beta-galactosidase from <i>Clostridium perfringens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 141-4	4.2	8
1	Structural Basis for the Binding Selectivity of Human CDY Chromodomains. <i>Cell Chemical Biology</i> , 2020 , 27, 827-838.e7	8.2	4