Karsten Niefind

List of Publications by Year
in descending order

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90 papers	3,727 citations	159525 30 h-index	138417 58 g-index
93 all docs	93 docs citations	93 times ranked	3507 citing authors

#	Article	IF	Citations
1	Crystal structure of human protein kinase CK2: insights into basic properties of the CK2 holoenzyme. EMBO Journal, 2001, 20, 5320-5331.	3.5	361
2	Structural Basis for Signaling by Exclusive EDS1 Heteromeric Complexes with SAG101 or PAD4 in Plant Innate Immunity. Cell Host and Microbe, 2013, 14, 619-630.	5.1	227
3	Different roles of Enhanced Disease Susceptibility1 (EDS1) bound to and dissociated from Phytoalexin Deficient4 (PAD4) in Arabidopsis immunity. New Phytologist, 2011, 191, 107-119.	3.5	206
4	Crystal structure of the catalytic subunit of protein kinase CK2 from Zea mays at 2.1Aresolution. EMBO Journal, 1998, 17, 2451-2462.	3.5	191
5	GTP plus water mimic ATP in the active site of protein kinase CK2. Nature Structural Biology, 1999, 6, 1100-1103.	9.7	176
6	Atomic Resolution Structures of R-specific Alcohol Dehydrogenase from Lactobacillus brevis Provide the Structural Bases of its Substrate and Cosubstrate Specificity. Journal of Molecular Biology, 2005, 349, 801-813.	2.0	135
7	The Structure of an Inverting GH43 Î²-Xylosidase from Geobacillus stearothermophilus with its Substrate Reveals the Role of the Three Catalytic Residues. Journal of Molecular Biology, 2006, 359, 97-109.	2.0	132
8	Crystal structure and snapshots along the reaction pathway of a family 51 Â-L-arabinofuranosidase. EMBO Journal, 2003, 22, 4922-4932.	3.5	127
9	The Crystal Structure of R-specific Alcohol Dehydrogenase from Lactobacillus brevis Suggests the Structural Basis of its Metal Dependency. Journal of Molecular Biology, 2003, 327, 317-328.	2.0	121
10	An EDS1 heterodimer signalling surface enforces timely reprogramming of immunity genes in Arabidopsis. Nature Communications, 2019, 10, 772.	5.8	103
11	Protein Kinase CK2 in Health and Disease. Cellular and Molecular Life Sciences, 2009, 66, 1800-1816.	2.4	90
12	The CK2Î±/CK2Î² Interface of Human Protein Kinase CK2 Harbors a Binding Pocket for Small Molecules. Chemistry and Biology, 2008, 15, 111-117.	6.2	89
13	X-ray Structure of a Dihydropyrimidinase from Thermus sp. at 1.3Ã... Resolution. Journal of Molecular Biology, 2002, 320, 143-156.	2.0	87
14	Crystal Structure ofd-Hydantoinase fromBacillus stearothermophilus:Â Insight into the Stereochemistry of Enantioselectivityâ€,â€¡. Biochemistry, 2002, 41, 9410-9417.	1.2	87
15	Crystal Structure of a C-terminal Deletion Mutant of Human Protein Kinase CK2 Catalytic Subunit. Journal of Molecular Biology, 2003, 330, 925-934.	2.0	72
16	The Structure of a Bacterial l-Amino Acid Oxidase from Rhodococcus opacus Gives New Evidence for the Hydride Mechanism for Dehydrogenation. Journal of Molecular Biology, 2007, 367, 234-248.	2.0	71
17	Crystal structure of cisâ€biphenylâ€2,3â€dihydrodiolâ€2,3â€dehydrogenase from a PCB degrader at 2.0 Ã... resolution. Protein Science, 1998, 7, 1286-1293.	3.1	69
18	The Structure of l-Hydantoinase from Arthobacter aurescens Leads to an Understanding of Dihydropyrimidinase Substrate and Enantio Specificity,. Biochemistry, 2002, 41, 8589-8597.	1.2	59

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19	Crystal structure of a ternary complex of d -2-hydroxyisocaproate dehydrogenase from Lactobacillus casei , NAD + and 2-oxoisocaproate at 1.9 Ã... resolution 1 1Edited by R. Huber. Journal of Molecular Biology, 1997, 267, 640-660.	2.0	58
20	The Catalytic Subunit of Human Protein Kinase CK2 Structurally Deviates from Its Maize Homologue in Complex with the Nucleotide Competitive Inhibitor Emodin. Journal of Molecular Biology, 2008, 377, 1-8.	2.0	56
21	Evolved to Be Active: Sulfate Ions Define Substrate Recognition Sites of CK2Î± and Emphasise its Exceptional Role within the CMGC Family of Eukaryotic Protein Kinases. Journal of Molecular Biology, 2007, 370, 427-438.	2.0	54
22	Amino acid similarity coefficients for protein modeling and sequence alignment derived from main-chain folding angles. Journal of Molecular Biology, 1991, 219, 481-497.	2.0	53
23	Inclining the Purine Base Binding Plane in Protein Kinase CK2 by Exchanging the Flanking Side-chains Generates a Preference for ATP as a Cosubstrate. Journal of Molecular Biology, 2005, 347, 399-414.	2.0	53
24	The interaction of CK2Î± and CK2Î², the subunits of protein kinase CK2, requires CK2Î² in a preformed conformation and is enthalpically driven. Protein Science, 2008, 17, 2180-2186.	3.1	49
25	Structure of the Human Protein Kinase CK2 Catalytic Subunit CK2Î±â€² and Interaction Thermodynamics with the Regulatory Subunit CK2Î². Journal of Molecular Biology, 2011, 407, 1-12.	2.0	46
26	Primary and secondary interactions between CK2Î± and CK2Î² lead to ring-like structures in the crystals of the CK2 holoenzyme. Molecular and Cellular Biochemistry, 2005, 274, 3-14.	1.4	43
27	Conformational plasticity of the catalytic subunit of protein kinase CK2 and its consequences for regulation and drug design. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 484-492.	1.1	42
28	Unexpected Active-Site Flexibility in the Structure of Human Neutrophil Elastase in Complex with a New Dihydropyrimidone Inhibitor. Journal of Molecular Biology, 2011, 409, 681-691.	2.0	39
29	First Structure of Protein Kinase CK2 Catalytic Subunit with an Effective CK2Î²-Competitive Ligand. ACS Chemical Biology, 2013, 8, 901-907.	1.6	39
30	A subnanomolar fluorescent probe for protein kinase CK2 interaction studies. Organic and Biomolecular Chemistry, 2012, 10, 8645.	1.5	32
31	First Inactive Conformation of CK2Î±, the Catalytic Subunit of Protein Kinase CK2. Journal of Molecular Biology, 2009, 386, 1212-1221.	2.0	30
32	Expression, purification, and aggregation studies of His-tagged thermoalkalophilic lipase from Bacillus thermocatenulatus. Protein Expression and Purification, 2004, 34, 103-110.	0.6	28
33	Biochemical characterization of CK2Î± and Î±â€² paralogues and their derived holoenzymes: evidence for the existence of a heterotrimeric CK2Î±â€²-holoenzyme forming trimeric complexes. Molecular and Cellular Biochemistry, 2008, 316, 37-47.	1.4	28
34	The Protein Kinase CK2Andante Holoenzyme Structure Supports Proposed Models of Autoregulation and Trans-Autophosphorylation. Journal of Molecular Biology, 2014, 426, 1871-1882.	2.0	28
35	Protein kinase CK2 inhibition is associated with the destabilization of HIF-1Î± in human cancer cells. Cancer Letters, 2015, 356, 751-761.	3.2	27
36	Interaction between CK2Î± and CK2Î², the Subunits of Protein Kinase CK2: Thermodynamic Contributions of Key Residues on the CK2Î± Surface. Biochemistry, 2011, 50, 512-522.	1.2	26

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37	Purification and characterization of the CK2Î±â€²-based holoenzyme, an isozyme of CK2Î±: A comparative analysis. Protein Expression and Purification, 2006, 47, 651-661.	0.6	24
38	Expression, purification and crystallization of the catalytic subunit of protein kinase CK2 from Zea mays. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 143-145.	2.5	22
39	Evidence for aggregation of protein kinase CK2 in the cell: a novel strategy for studying CK2 holoenzyme interaction by BRET2. Molecular and Cellular Biochemistry, 2014, 397, 285-293.	1.4	22
40	A Note of Caution on the Role of Halogen Bonds for Protein Kinase/Inhibitor Recognition Suggested by High- And Low-Salt CK2Î± Complex Structures. ACS Chemical Biology, 2015, 10, 1654-1660.	1.6	22
41	Enzymatic activity with an incomplete catalytic spine: insights from a comparative structural analysis of human CK2Î± and its paralogous isoform CK2Î±â€². Molecular and Cellular Biochemistry, 2011, 356, 57-65.	1.4	21
42	Synthesis, biological activity and structural study of new benzotriazole-based protein kinase CK2 inhibitors. RSC Advances, 2015, 5, 72482-72494.	1.7	21
43	Crystal Structure of l-2-Hydroxyisocaproate Dehydrogenase fromLactobacillus confususat 2.2 Ã… Resolution. An Example of Strong Asymmetry Between Subunits. Journal of Molecular Biology, 1995, 251, 256-281.	2.0	20
44	Arabidopsis immunity regulator EDS1 in a PAD4/SAG101-unbound form is a monomer with an inherently inactive conformation. Journal of Structural Biology, 2019, 208, 107390.	1.3	19
45	Crystal Structure of Creatininase from Pseudomonas putida: A Novel Fold and a Case of Convergent Evolution. Journal of Molecular Biology, 2003, 332, 287-301.	2.0	18
46	Development of a high-throughput screening-compatible assay to identify inhibitors of the CK2Î±/CK2Î² interaction. Analytical Biochemistry, 2015, 468, 4-14.	1.1	18
47	Diacritic Binding of an Indenoindole Inhibitor by CK2Î± Paralogs Explored by a Reliable Path to Atomic Resolution CK2Î±â€² Structures. ACS Omega, 2019, 4, 5471-5478.	1.6	18
48	Crystallization and preliminary characterization of crystals of human protein kinase CK2. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1680-1684.	2.5	17
49	Structural Basis of the Constitutive Activity of Protein Kinase CK2. Methods in Enzymology, 2010, 484, 515-529.	0.4	17
50	Biological properties and structural study of new aminoalkyl derivatives of benzimidazole and benzotriazole, dual inhibitors of CK2 and PIM1 kinases. Bioorganic Chemistry, 2018, 80, 266-275.	2.0	17
51	The â€˜regulatoryâ€™ Î²-subunit of protein kinase CK2 negatively influences p53-mediated allosteric effects on Chk2 activation. Oncogene, 2005, 24, 6194-6200.	2.6	16
52	Low-density crystal packing of human protein kinase CK2 catalytic subunit in complex with resorufin or other ligands: a tool to study the unique hinge-region plasticity of the enzyme without packing bias. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 883-892.	2.5	16
53	Design of CK2Î²â€Mimicking Peptides as Tools To Study the CK2Î±/CK2Î² Interaction in Cancer Cells. ChemMedChem, 2019, 14, 833-841.	1.6	16
54	The Three-Dimensional Structure of AKR11B4, a Glycerol Dehydrogenase from Gluconobacter oxydans, Reveals a Tryptophan Residue as an Accelerator of Reaction Turnover. Journal of Molecular Biology, 2010, 404, 353-362.	2.0	15

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55	Crystal structure of highly glycosylated human leukocyte elastase in complex with an S2â€² site binding inhibitor. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 480-489.	0.4	15
56	Biochemical characterization of the recombinant human Drosophila homologues Timekeeper and Andante involved in the Drosophila circadian oscillator. Molecular and Cellular Biochemistry, 2005, 274, 151-161.	1.4	14
57	Insights from soft X-rays: the chlorine and sulfur sub-structures of a CK2Î±/DRB complex. Molecular and Cellular Biochemistry, 2008, 316, 15-23.	1.4	14
58	Unexpected CK2Î²-antagonistic functionality of bisubstrate inhibitors targeting protein kinase CK2. Bioorganic Chemistry, 2020, 96, 103608.	2.0	14
59	Unexpected Binding Mode of a Potent Indeno[1,2-b]indole-Type Inhibitor of Protein Kinase CK2 Revealed by Complex Structures with the Catalytic Subunit CK2Î± and Its Paralog CK2Î±â€². Pharmaceuticals, 2017, 10, 98.	1.7	13
60	Molecular Plasticity of Crystalline CK2Î±â€² Leads to KN2, a Bivalent Inhibitor of Protein Kinase CK2 with Extraordinary Selectivity. Journal of Medicinal Chemistry, 2022, 65, 1302-1312.	2.9	13
61	Crystallization and preliminary X-ray analysis of a family 51 glycoside hydrolase, the Î±-L-arabinofuranosidase fromGeobacillus stearothermophilusT-6. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 913-915.	2.5	12
62	Structural Hypervariability of the Two Human Protein Kinase CK2 Catalytic Subunit Paralogs Revealed by Complex Structures with a Flavonol- and a Thieno[2,3-d]pyrimidine-Based Inhibitor. Pharmaceuticals, 2017, 10, 9.	1.7	12
63	Crystallization and preliminary characterization of crystals ofR-alcohol dehydrogenase fromLactobacillus brevis. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1696-1698.	2.5	11
64	Structural and Mechanistic Basis of the Inhibitory Potency of Selected 2-Aminothiazole Compounds on Protein Kinase CK2. Journal of Medicinal Chemistry, 2020, 63, 7766-7772.	2.9	10
65	Crystallization and preliminary crystallographic analysis of Gre2p, an NADP⁺-dependent alcohol dehydrogenase fromSaccharomyces cerevisiae. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 838-841.	0.7	9
66	Characterization of CK2 holoenzyme variants with regard to crystallization. Molecular and Cellular Biochemistry, 2001, 227, 3-11.	1.4	8
67	Protein kinase CK2: a catalyst for biology, medicine and structural biochemistry. Molecular and Cellular Biochemistry, 2011, 356, 1-3.	1.4	8
68	Enzyme-substrate complexes of the quinate/shikimate dehydrogenase from Corynebacterium glutamicum enable new insights in substrate and cofactor binding, specificity, and discrimination. Biological Chemistry, 2013, 394, 1505-1516.	1.2	8
69	1.6 Ã... structure of an NAD+-dependent quinate dehydrogenase fromCorynebacterium glutamicum. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 803-809.	2.5	7
70	De novo variants of CSNK2B cause a new intellectual disability-craniodigital syndrome by disrupting the canonical Wnt signaling pathway. Human Genetics and Genomics Advances, 2022, 3, 100111.	1.0	7
71	Crystallization and preliminary crystallographic analysis ofcgHle, a homoserine acetyltransferase homologue, fromCorynebacterium glutamicum. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 34-38.	0.7	6
72	A Ï€-Halogen Bond of Dibenzofuranones with the Gatekeeper Phe113 in Human Protein Kinase CK2 Leads to Potent Tight Binding Inhibitors. Pharmaceuticals, 2018, 11, 23.	1.7	6

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73	Crystallization and preliminary crystallographic analysis of a flavoprotein NADH oxidase fromLactobacillus brevis. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 528-530.	0.7	5
74	Crystallization and preliminary X-ray analysis of a bacterialL-amino-acid oxidase fromRhodococcus opacus. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 279-281.	0.7	5
75	A novel esterase subfamily with Î±/Î²â€hydrolase fold suggested by structures of two bacterial enzymes homologous to <scp>l</scp>â€homoserine Oâ€acetyl transferases. FEBS Letters, 2016, 590, 174-184.	1.3	5
76	Structural basis for the design of bisubstrate inhibitors of protein kinase CK2 provided by complex structures with the substrate-competitive inhibitor heparin. European Journal of Medicinal Chemistry, 2021, 214, 113223.	2.6	5
77	Crystallization and preliminary X-ray analysis of a hydantoinase from Artrobacter aurescens DSM 3745. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 1209-1210.	2.5	4
78	Crystallization, preliminary X-ray analysis of a native and selenomethionineD-hydantoinase fromThermussp.. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1166-1169.	2.5	4
79	Crystallization and preliminary crystallographic analysis of a family 43 Î²-D-xylosidase fromGeobacillus stearothermophilusT-6. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1054-1057.	0.7	4
80	Crystallization and preliminary crystallographic analysis ofArabidopsis thalianaEDS1, a key component of plant immunity, in complex with its signalling partner SAG101. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 245-248.	0.7	4
81	Patterns of Sequence Variation in Families of Homologous Proteins. , 1991, , 373-385.		4
82	Crystallization and preliminary crystallographic analysis of creatininase from Pseudomonas putida. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1356-1358.	2.5	3
83	Cloning, expression, purification and preliminary crystallographic characterization of a shikimate dehydrogenase fromCorynebacterium glutamicum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 635-637.	0.7	3
84	Exploring the intramolecular phosphorylation sites in human Chk2. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 646, 50-59.	0.4	3
85	Expanding the Application Range of Microbial Oxidoreductases by an Alcohol Dehydrogenase from Comamonas testosteroni with a Broad Substrate Spectrum and pH Profile. Catalysts, 2020, 10, 1281.	1.6	3
86	Structural and Enzymological Evidence for an Altered Substrate Specificity in Okur-Chung Neurodevelopmental Syndrome Mutant CK2Î±Lys198Arg. Frontiers in Molecular Biosciences, 2022, 9, 831693.	1.6	3
87	Crystallization and Preliminary Characterization of Crystals of d-2-hydroxyisocaproate Dehydrogenase from Lactobacillus casei. Journal of Molecular Biology, 1994, 240, 400-402.	2.0	2
88	Improved protein-crystal identification by using 2,2,2-trichloroethanol as a fluorescence enhancer. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 307-314.	0.4	2
89	Biochemie und Molekulargenetik 1994. Nachrichten Aus Der Chemie, 1995, 43, 173-192.	0.0	1
90	Impressions from the Conformational and Configurational Space Captured by Protein Kinase CK2. , 2015, , 17-33.		1