

Karsten Niefind

List of Publications by Year in descending order

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90
papers

3,727
citations

159525

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138417

58
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93
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93
docs citations

93
times ranked

3507
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Molecular Plasticity of Crystalline CK2 [±] Leads to KN2, a Bivalent Inhibitor of Protein Kinase CK2 with Extraordinary Selectivity. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 1302-1312. | 2.9 | 13 |
| 2 | Structural and Enzymological Evidence for an Altered Substrate Specificity in Okur-Chung Neurodevelopmental Syndrome Mutant CK2 [±] Lys198Arg. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 831693. | 1.6 | 3 |
| 3 | De novo variants of CSNK2B cause a new intellectual disability-craniodigital syndrome by disrupting the canonical Wnt signaling pathway. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100111. | 1.0 | 7 |
| 4 | Structural basis for the design of bisubstrate inhibitors of protein kinase CK2 provided by complex structures with the substrate-competitive inhibitor heparin. <i>European Journal of Medicinal Chemistry</i> , 2021, 214, 113223. | 2.6 | 5 |
| 5 | Expanding the Application Range of Microbial Oxidoreductases by an Alcohol Dehydrogenase from <i>Comamonas testosteroni</i> with a Broad Substrate Spectrum and pH Profile. <i>Catalysts</i> , 2020, 10, 1281. | 1.6 | 3 |
| 6 | Structural and Mechanistic Basis of the Inhibitory Potency of Selected 2-Aminothiazole Compounds on Protein Kinase CK2. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 7766-7772. | 2.9 | 10 |
| 7 | Unexpected CK2 [±] -antagonistic functionality of bisubstrate inhibitors targeting protein kinase CK2. <i>Bioorganic Chemistry</i> , 2020, 96, 103608. | 2.0 | 14 |
| 8 | Arabidopsis immunity regulator EDS1 in a PAD4/SAG101-unbound form is a monomer with an inherently inactive conformation. <i>Journal of Structural Biology</i> , 2019, 208, 107390. | 1.3 | 19 |
| 9 | Diacritic Binding of an Indenoindole Inhibitor by CK2 [±] Paralogs Explored by a Reliable Path to Atomic Resolution CK2 [±] Structures. <i>ACS Omega</i> , 2019, 4, 5471-5478. | 1.6 | 18 |
| 10 | An EDS1 heterodimer signalling surface enforces timely reprogramming of immunity genes in Arabidopsis. <i>Nature Communications</i> , 2019, 10, 772. | 5.8 | 103 |
| 11 | Design of CK2 [±] -Mimicking Peptides as Tools To Study the CK2 [±] /CK2 [±] Interaction in Cancer Cells. <i>ChemMedChem</i> , 2019, 14, 833-841. | 1.6 | 16 |
| 12 | Improved protein-crystal identification by using 2,2,2-trichloroethanol as a fluorescence enhancer. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 307-314. | 0.4 | 2 |
| 13 | Biological properties and structural study of new aminoalkyl derivatives of benzimidazole and benzotriazole, dual inhibitors of CK2 and PIM1 kinases. <i>Bioorganic Chemistry</i> , 2018, 80, 266-275. | 2.0 | 17 |
| 14 | A π -Halogen Bond of Dibenzofuranones with the Gatekeeper Phe113 in Human Protein Kinase CK2 Leads to Potent Tight Binding Inhibitors. <i>Pharmaceuticals</i> , 2018, 11, 23. | 1.7 | 6 |
| 15 | Crystal structure of highly glycosylated human leukocyte elastase in complex with an S2 site binding inhibitor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 480-489. | 0.4 | 15 |
| 16 | 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 CK2 [±] and Its Paralog CK2 [±] . <i>Pharmaceuticals</i> , 2017, 10, 98. | 1.7 | 13 |
| 17 | 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. <i>Pharmaceuticals</i> , 2017, 10, 9. | 1.7 | 12 |
| 18 | A novel esterase subfamily with β -hydrolase fold suggested by structures of two bacterial enzymes homologous to <i>hsc70</i> homoserine <i>acetyl</i> transferases. <i>FEBS Letters</i> , 2016, 590, 174-184. | 1.3 | 5 |

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|----|---|-----|-----------|
| 19 | A Note of Caution on the Role of Halogen Bonds for Protein Kinase/Inhibitor Recognition Suggested by High- And Low-Salt CK2 α Complex Structures. <i>ACS Chemical Biology</i> , 2015, 10, 1654-1660. | 1.6 | 22 |
| 20 | Synthesis, biological activity and structural study of new benzotriazole-based protein kinase CK2 inhibitors. <i>RSC Advances</i> , 2015, 5, 72482-72494. | 1.7 | 21 |
| 21 | Protein kinase CK2 inhibition is associated with the destabilization of HIF-1 α in human cancer cells. <i>Cancer Letters</i> , 2015, 356, 751-761. | 3.2 | 27 |
| 22 | Development of a high-throughput screening-compatible assay to identify inhibitors of the CK2 α /CK2 β interaction. <i>Analytical Biochemistry</i> , 2015, 468, 4-14. | 1.1 | 18 |
| 23 | Impressions from the Conformational and Configurational Space Captured by Protein Kinase CK2. , 2015, , 17-33. | | 1 |
| 24 | Evidence for aggregation of protein kinase CK2 in the cell: a novel strategy for studying CK2 holoenzyme interaction by BRET2. <i>Molecular and Cellular Biochemistry</i> , 2014, 397, 285-293. | 1.4 | 22 |
| 25 | The Protein Kinase CK2 Andante Holoenzyme Structure Supports Proposed Models of Autoregulation and Trans-Autophosphorylation. <i>Journal of Molecular Biology</i> , 2014, 426, 1871-1882. | 2.0 | 28 |
| 26 | Structural Basis for Signaling by Exclusive EDS1 Heteromeric Complexes with SAG101 or PAD4 in Plant Innate Immunity. <i>Cell Host and Microbe</i> , 2013, 14, 619-630. | 5.1 | 227 |
| 27 | First Structure of Protein Kinase CK2 Catalytic Subunit with an Effective CK2 β -Competitive Ligand. <i>ACS Chemical Biology</i> , 2013, 8, 901-907. | 1.6 | 39 |
| 28 | Enzyme-substrate complexes of the quinate/shikimate dehydrogenase from <i>Corynebacterium glutamicum</i> enable new insights in substrate and cofactor binding, specificity, and discrimination. <i>Biological Chemistry</i> , 2013, 394, 1505-1516. | 1.2 | 8 |
| 29 | 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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 883-892. | 2.5 | 16 |
| 30 | A subnanomolar fluorescent probe for protein kinase CK2 interaction studies. <i>Organic and Biomolecular Chemistry</i> , 2012, 10, 8645. | 1.5 | 32 |
| 31 | Interaction between CK2 α and CK2 β , the Subunits of Protein Kinase CK2: Thermodynamic Contributions of Key Residues on the CK2 α Surface. <i>Biochemistry</i> , 2011, 50, 512-522. | 1.2 | 26 |
| 32 | Structure of the Human Protein Kinase CK2 Catalytic Subunit CK2 α and Interaction Thermodynamics with the Regulatory Subunit CK2 β . <i>Journal of Molecular Biology</i> , 2011, 407, 1-12. | 2.0 | 46 |
| 33 | Unexpected Active-Site Flexibility in the Structure of Human Neutrophil Elastase in Complex with a New Dihydropyrimidone Inhibitor. <i>Journal of Molecular Biology</i> , 2011, 409, 681-691. | 2.0 | 39 |
| 34 | Different roles of Enhanced Disease Susceptibility1 (EDS1) bound to and dissociated from Phytoalexin Deficient4 (PAD4) in Arabidopsis immunity. <i>New Phytologist</i> , 2011, 191, 107-119. | 3.5 | 206 |
| 35 | Protein kinase CK2: a catalyst for biology, medicine and structural biochemistry. <i>Molecular and Cellular Biochemistry</i> , 2011, 356, 1-3. | 1.4 | 8 |
| 36 | Enzymatic activity with an incomplete catalytic spine: insights from a comparative structural analysis of human CK2 α and its paralogous isoform CK2 α . <i>Molecular and Cellular Biochemistry</i> , 2011, 356, 57-65. | 1.4 | 21 |

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| 37 | Crystallization and preliminary crystallographic analysis of <i>Arabidopsis thaliana</i> EDS1, a key component of plant immunity, in complex with its signalling partner SAG101. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 245-248. | 0.7 | 4 |
| 38 | Conformational plasticity of the catalytic subunit of protein kinase CK2 and its consequences for regulation and drug design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 484-492. | 1.1 | 42 |
| 39 | Crystallization and preliminary crystallographic analysis of Gre2p, an NADP ⁺ -dependent alcohol dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 838-841. | 0.7 | 9 |
| 40 | Structural Basis of the Constitutive Activity of Protein Kinase CK2. <i>Methods in Enzymology</i> , 2010, 484, 515-529. | 0.4 | 17 |
| 41 | The Three-Dimensional Structure of AKR11B4, a Glycerol Dehydrogenase from <i>Gluconobacter oxydans</i> , Reveals a Tryptophan Residue as an Accelerator of Reaction Turnover. <i>Journal of Molecular Biology</i> , 2010, 404, 353-362. | 2.0 | 15 |
| 42 | Protein Kinase CK2 in Health and Disease. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 1800-1816. | 2.4 | 90 |
| 43 | Crystallization and preliminary crystallographic analysis of <i>CgHle</i> , a homoserine acetyltransferase homologue, from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 34-38. | 0.7 | 6 |
| 44 | First Inactive Conformation of CK2 α , the Catalytic Subunit of Protein Kinase CK2. <i>Journal of Molecular Biology</i> , 2009, 386, 1212-1221. | 2.0 | 30 |
| 45 | Biochemical characterization of CK2 α and β paralogues and their derived holoenzymes: evidence for the existence of a heterotrimeric CK2 α β -holoenzyme forming trimeric complexes. <i>Molecular and Cellular Biochemistry</i> , 2008, 316, 37-47. | 1.4 | 28 |
| 46 | Insights from soft X-rays: the chlorine and sulfur sub-structures of a CK2 α /DRB complex. <i>Molecular and Cellular Biochemistry</i> , 2008, 316, 15-23. | 1.4 | 14 |
| 47 | 1.6 Å... structure of an NAD ⁺ -dependent quinate dehydrogenase from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 803-809. | 2.5 | 7 |
| 48 | The CK2 α /CK2 β Interface of Human Protein Kinase CK2 Harbors a Binding Pocket for Small Molecules. <i>Chemistry and Biology</i> , 2008, 15, 111-117. | 6.2 | 89 |
| 49 | Exploring the intramolecular phosphorylation sites in human Chk2. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 646, 50-59. | 0.4 | 3 |
| 50 | The interaction of CK2 α and CK2 β , the subunits of protein kinase CK2, requires CK2 β in a preformed conformation and is enthalpically driven. <i>Protein Science</i> , 2008, 17, 2180-2186. | 3.1 | 49 |
| 51 | The Catalytic Subunit of Human Protein Kinase CK2 Structurally Deviates from Its Maize Homologue in Complex with the Nucleotide Competitive Inhibitor Emodin. <i>Journal of Molecular Biology</i> , 2008, 377, 1-8. | 2.0 | 56 |
| 52 | The Structure of a Bacterial l-Amino Acid Oxidase from <i>Rhodococcus opacus</i> Gives New Evidence for the Hydride Mechanism for Dehydrogenation. <i>Journal of Molecular Biology</i> , 2007, 367, 234-248. | 2.0 | 71 |
| 53 | Evolved to Be Active: Sulfate Ions Define Substrate Recognition Sites of CK2 α and Emphasise its Exceptional Role within the CMGC Family of Eukaryotic Protein Kinases. <i>Journal of Molecular Biology</i> , 2007, 370, 427-438. | 2.0 | 54 |
| 54 | The Structure of an Inverting GH43 β -Xylosidase from <i>Geobacillus stearothermophilus</i> with its Substrate Reveals the Role of the Three Catalytic Residues. <i>Journal of Molecular Biology</i> , 2006, 359, 97-109. | 2.0 | 132 |

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|----|--|-----|-----------|
| 55 | Purification and characterization of the CK2 β -based holoenzyme, an isozyme of CK2 α : A comparative analysis. <i>Protein Expression and Purification</i> , 2006, 47, 651-661. | 0.6 | 24 |
| 56 | Crystallization and preliminary X-ray analysis of a bacterial L-amino-acid oxidase from <i>Rhodococcus opacus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 279-281. | 0.7 | 5 |
| 57 | Cloning, expression, purification and preliminary crystallographic characterization of a shikimate dehydrogenase from <i>Corynebacterium glutamicum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 635-637. | 0.7 | 3 |
| 58 | The ϵ -regulatory β -subunit of protein kinase CK2 negatively influences p53-mediated allosteric effects on Chk2 activation. <i>Oncogene</i> , 2005, 24, 6194-6200. | 2.6 | 16 |
| 59 | Biochemical characterization of the recombinant human <i>Drosophila</i> homologues Timekeeper and Andante involved in the <i>Drosophila</i> circadian oscillator. <i>Molecular and Cellular Biochemistry</i> , 2005, 274, 151-161. | 1.4 | 14 |
| 60 | Primary and secondary interactions between CK2 α and CK2 β lead to ring-like structures in the crystals of the CK2 holoenzyme. <i>Molecular and Cellular Biochemistry</i> , 2005, 274, 3-14. | 1.4 | 43 |
| 61 | Crystallization and preliminary crystallographic analysis of a flavoprotein NADH oxidase from <i>Lactobacillus brevis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 528-530. | 0.7 | 5 |
| 62 | Crystallization and preliminary crystallographic analysis of a family 43 β -D-xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1054-1057. | 0.7 | 4 |
| 63 | Inclining the Purine Base Binding Plane in Protein Kinase CK2 by Exchanging the Flanking Side-chains Generates a Preference for ATP as a Cosubstrate. <i>Journal of Molecular Biology</i> , 2005, 347, 399-414. | 2.0 | 53 |
| 64 | Atomic Resolution Structures of R-specific Alcohol Dehydrogenase from <i>Lactobacillus brevis</i> Provide the Structural Bases of its Substrate and Cosubstrate Specificity. <i>Journal of Molecular Biology</i> , 2005, 349, 801-813. | 2.0 | 135 |
| 65 | Expression, purification, and aggregation studies of His-tagged thermoalkalophilic lipase from <i>Bacillus thermocatenulatus</i> . <i>Protein Expression and Purification</i> , 2004, 34, 103-110. | 0.6 | 28 |
| 66 | Crystal structure and snapshots along the reaction pathway of a family 51 α -L-arabinofuranosidase. <i>EMBO Journal</i> , 2003, 22, 4922-4932. | 3.5 | 127 |
| 67 | Crystallization and preliminary X-ray analysis of a family 51 glycoside hydrolase, the β -L-arabinofuranosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 913-915. | 2.5 | 12 |
| 68 | The Crystal Structure of R-specific Alcohol Dehydrogenase from <i>Lactobacillus brevis</i> Suggests the Structural Basis of its Metal Dependency. <i>Journal of Molecular Biology</i> , 2003, 327, 317-328. | 2.0 | 121 |
| 69 | Crystal Structure of a C-terminal Deletion Mutant of Human Protein Kinase CK2 Catalytic Subunit. <i>Journal of Molecular Biology</i> , 2003, 330, 925-934. | 2.0 | 72 |
| 70 | Crystal Structure of Creatininase from <i>Pseudomonas putida</i> : A Novel Fold and a Case of Convergent Evolution. <i>Journal of Molecular Biology</i> , 2003, 332, 287-301. | 2.0 | 18 |
| 71 | The Structure of L-Hydantoinase from <i>Arthobacter aurescens</i> Leads to an Understanding of Dihydropyrimidinase Substrate and Enantio Specificity. <i>Biochemistry</i> , 2002, 41, 8589-8597. | 1.2 | 59 |
| 72 | X-ray Structure of a Dihydropyrimidinase from <i>Thermus</i> sp. at 1.3 Å Resolution. <i>Journal of Molecular Biology</i> , 2002, 320, 143-156. | 2.0 | 87 |

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| 73 | Crystal Structure of d-Hydantoinase from <i>Bacillus stearothermophilus</i> : Insight into the Stereochemistry of Enantioselectivity. <i>Biochemistry</i> , 2002, 41, 9410-9417. | 1.2 | 87 |
| 74 | Crystallization and preliminary crystallographic analysis of creatininase from <i>Pseudomonas putida</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1356-1358. | 2.5 | 3 |
| 75 | Characterization of CK2 holoenzyme variants with regard to crystallization. <i>Molecular and Cellular Biochemistry</i> , 2001, 227, 3-11. | 1.4 | 8 |
| 76 | Crystal structure of human protein kinase CK2: insights into basic properties of the CK2 holoenzyme. <i>EMBO Journal</i> , 2001, 20, 5320-5331. | 3.5 | 361 |
| 77 | Crystallization, preliminary X-ray analysis of a native and selenomethionine D-hydantoinase from <i>Thermus sp.</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1166-1169. | 2.5 | 4 |
| 78 | Crystallization and preliminary characterization of crystals of R-alcohol dehydrogenase from <i>Lactobacillus brevis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1696-1698. | 2.5 | 11 |
| 79 | Crystallization and preliminary characterization of crystals of human protein kinase CK2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1680-1684. | 2.5 | 17 |
| 80 | GTP plus water mimic ATP in the active site of protein kinase CK2. <i>Nature Structural Biology</i> , 1999, 6, 1100-1103. | 9.7 | 176 |
| 81 | Crystal structure of the catalytic subunit of protein kinase CK2 from <i>Zea mays</i> at 2.1 Å resolution. <i>EMBO Journal</i> , 1998, 17, 2451-2462. | 3.5 | 191 |
| 82 | Crystal structure of cis-biphenyl-2,3-dihydrodiol-2,3-dihydrogenase from a PCB degrader at 2.0 Å resolution. <i>Protein Science</i> , 1998, 7, 1286-1293. | 3.1 | 69 |
| 83 | Expression, purification and crystallization of the catalytic subunit of protein kinase CK2 from <i>Zea mays</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 143-145. | 2.5 | 22 |
| 84 | Crystal structure of a ternary complex of d-2-hydroxyisocaproate dehydrogenase from <i>Lactobacillus casei</i> , NAD ⁺ and 2-oxoisocaproate at 1.9 Å resolution. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1997, 267, 640-660. | 2.0 | 58 |
| 85 | Crystallization and preliminary X-ray analysis of a hydantoinase from <i>Arthro bacter aurescens</i> DSM 3745. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 1209-1210. | 2.5 | 4 |
| 86 | Biochemie und Molekulargenetik 1994. <i>Nachrichten Aus Der Chemie</i> , 1995, 43, 173-192. | 0.0 | 1 |
| 87 | Crystal Structure of L-2-Hydroxyisocaproate Dehydrogenase from <i>Lactobacillus confusus</i> at 2.2 Å Resolution. An Example of Strong Asymmetry Between Subunits. <i>Journal of Molecular Biology</i> , 1995, 251, 256-281. | 2.0 | 20 |
| 88 | Crystallization and Preliminary Characterization of Crystals of d-2-hydroxyisocaproate Dehydrogenase from <i>Lactobacillus casei</i> . <i>Journal of Molecular Biology</i> , 1994, 240, 400-402. | 2.0 | 2 |
| 89 | Amino acid similarity coefficients for protein modeling and sequence alignment derived from main-chain folding angles. <i>Journal of Molecular Biology</i> , 1991, 219, 481-497. | 2.0 | 53 |
| 90 | Patterns of Sequence Variation in Families of Homologous Proteins. , 1991, , 373-385. | | 4 |