

Winfried Hinrichs

List of Publications by Year in descending order

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90
papers

3,424
citations

159585

30
h-index

149698

56
g-index

99
all docs

99
docs citations

99
times ranked

3743
citing authors

#	ARTICLE	IF	CITATIONS
1	The induction mechanism of the flavonoid-responsive regulator FrrA. <i>FEBS Journal</i> , 2022, 289, 507-518.	4.7	2
2	Structural basis to repurpose boron-based proteasome inhibitors Bortezomib and Ixazomib as β -lactamase inhibitors. <i>Scientific Reports</i> , 2022, 12, 5510.	3.3	4
3	Hydrazones and Thiosemicarbazones Targeting Protein-Protein-Interactions of SARS-CoV-2 Papain-like Protease. <i>Frontiers in Chemistry</i> , 2022, 10, 832431.	3.6	5
4	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021, 372, 642-646.	12.6	240
5	The Komagataeibacter europaeus GqqA is the prototype of a novel bifunctional N-Acyl-homoserine lactone acylase with prephenate dehydratase activity. <i>Scientific Reports</i> , 2021, 11, 12255.	3.3	4
6	Thermodynamics, cooperativity and stability of the tetracycline repressor (TetR) upon tetracycline binding. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140404.	2.3	8
7	Structural and biochemical analysis of a phosin from <i>Streptomyces chartreusis</i> reveals a combined polyphosphate- and metal-binding fold. <i>FEBS Letters</i> , 2019, 593, 2019-2029.	2.8	9
8	Blocking tetracycline destruction. <i>Nature Chemical Biology</i> , 2017, 13, 694-695.	8.0	14
9	Assemblins as maturational proteases in herpesviruses. <i>Journal of General Virology</i> , 2017, 98, 1969-1984.	2.9	6
10	A Quantitative Real-Time RT-PCR Assay for the Detection of Venezuelan equine encephalitis virus Utilizing a Universal Alphavirus Control RNA. <i>BioMed Research International</i> , 2016, 2016, 1-7.	1.9	8
11	Modular organisation of inducer recognition and allostery in the tetracycline repressor. <i>FEBS Journal</i> , 2016, 283, 2102-2114.	4.7	23
12	Structural evidence of intramolecular propeptide inhibition of the aspzincin metalloendopeptidase AsaP1. <i>FEBS Letters</i> , 2016, 590, 3280-3294.	2.8	3
13	Structural analysis and knock-out of a <i>Burkholderia pseudomallei</i> homolog of the eukaryotic transcription coactivator PC4. <i>Gene</i> , 2016, 577, 140-147.	2.2	6
14	Dimerization-Induced Allosteric Changes of the Oxyanion-Hole Loop Activate the Pseudorabies Virus Assemblin pUL26N, a Herpesvirus Serine Protease. <i>PLoS Pathogens</i> , 2015, 11, e1005045.	4.7	15
15	Structure and catalytic mechanism of the evolutionarily unique bacterial chalcone isomerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 907-917.	2.5	21
16	Structural and biochemical characterization of the dual substrate recognition of the α -selective amine transaminase from <i>Aspergillus fumigatus</i> . <i>FEBS Journal</i> , 2015, 282, 407-415.	4.7	29
17	Tetracycline Repressor Allostery Does Not Depend on Divalent Metal Recognition. <i>Biochemistry</i> , 2014, 53, 7990-7998.	2.5	11
18	Enzymatic Conversion of Flavonoids using Bacterial Chalcone Isomerase and Enoate Reductase. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1439-1442.	13.8	56

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19	Post-translational modification and extended glycosylation pattern of a plant latex peroxidase of native source characterized by X-ray crystallography. <i>FEBS Journal</i> , 2014, 281, 4319-4333.	4.7	9
20	Crystallographic characterization of the (<i>R</i>)-selective amine transaminase from <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1086-1093.	2.5	36
21	Structure and regulatory targets of SCO3201, a highly promiscuous TetR-like regulator of <i>Streptomyces coelicolor</i> M145. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 513-518.	2.1	8
22	Crystallization and preliminary X-ray diffraction studies of the (<i>R</i>)-selective amine transaminase from <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1415-1417.	0.7	9
23	Toxoid construction of AsaP1, a lethal toxic aspzincin metalloendopeptidase of <i>Aeromonas salmonicida</i> subsp. <i>achromogenes</i> , and studies of its activity and processing. <i>Veterinary Microbiology</i> , 2013, 162, 687-694.	1.9	5
24	Putative dioxygen-binding sites and recognition of tigecycline and minocycline in the tetracycline-degrading monooxygenase TetX. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1758-1767.	2.5	28
25	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. <i>Nucleic Acids Research</i> , 2012, 40, 4178-4192.	14.5	54
26	Purification, crystallization and preliminary crystallographic analysis of banyan peroxidase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 931-934.	0.7	1
27	A FRET Enzyme-Based Probe for Monitoring Hydrogen Sulfide. <i>Inorganic Chemistry</i> , 2012, 51, 11220-11222.	4.0	52
28	Human α_2 -Macroglobulin: Another Variation on the Venus Flytrap. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5045-5047.	13.8	21
29	The growth of single crystal silver wires at the nitrobenzene water interface. <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 12254.	2.8	14
30	Recognition of Drug Degradation Products by Target Proteins: Isotetracycline Binding to Tet Repressor. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 5108-5115.	6.4	9
31	Structural basis for a new tetracycline resistance mechanism relying on the TetX monooxygenase. <i>FEBS Letters</i> , 2011, 585, 1061-1066.	2.8	87
32	Cloning, functional expression, biochemical characterization, and structural analysis of a haloalkane dehalogenase from <i>Plesiocystis pacifica</i> SIR-1. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1049-1060.	3.6	36
33	The crystal structure of an esterase from the hyperthermophilic microorganism <i>Pyrobaculum caldifontis</i> VA1 explains its enantioselectivity. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1061-1072.	3.6	64
34	Influence of temperature during crystallization setup on precipitate formation and crystal shape of a metalloendopeptidase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 421-423.	0.7	4
35	Crystal structure of AsaP1 metalloendopeptidase in complex with its propeptide. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s143-s144.	0.3	0
36	Structure of the Ni(II) complex of <i>Escherichia coli</i> peptide deformylase and suggestions on deformylase activities depending on different metal(II) centres. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 195-201.	2.6	5

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37	Crystallization and preliminary X-ray crystallographic analysis of the tetracycline-degrading monooxygenase TetX2 from <i>Bacteroides thetaiotaomicron</i> . Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 611-614.	0.7	5
38	Crystallization and preliminary X-ray diffraction studies of the putative haloalkane dehalogenase DppA from <i>Plesiocystis pacifica</i> SIR-I. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 828-830.	0.7	3
39	Nonantibiotic Properties of Tetracyclines: Structural Basis for Inhibition of Secretory Phospholipase A2. Journal of Molecular Biology, 2010, 398, 83-96.	4.2	27
40	Structure of the tetracycline-degrading monooxygenase TetX2. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s144-s145.	0.3	0
41	Crystallization and preliminary X-ray diffraction studies of AsaP1_E294A and AsaP1_E294Q, two inactive mutants of the toxic zinc metallopeptidase AsaP1 from <i>Aeromonas salmonicida</i> subsp. <i>achromogenes</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 695-697.	0.7	2
42	Tetracycline-Tet Repressor Binding Specificity: Insights from Experiments and Simulations. Biophysical Journal, 2009, 97, 2829-2838.	0.5	16
43	Prion Protein Misfolding. Current Molecular Medicine, 2009, 9, 826-835.	1.3	63
44	Specific binding of divalent metal ions to tetracycline and to the Tet repressor/tetracycline complex. Journal of Biological Inorganic Chemistry, 2008, 13, 1097-1110.	2.6	62
45	Tryptophan π -Electron System Capping a Copper(I) Binding Site—A New Organometallic Bonding Mode in Proteins. ChemBioChem, 2008, 9, 1697-1699.	2.6	3
46	Tet Repressor Induction by Tetracycline: A Molecular Dynamics, Continuum Electrostatics, and Crystallographic Study. Journal of Molecular Biology, 2008, 378, 898-912.	4.2	34
47	Protonation Patterns in Tetracycline:Tet Repressor Recognition: Simulations and Experiments. ChemBioChem, 2007, 8, 675-685.	2.6	40
48	Structure of the apo form of the catabolite control protein A (CcpA) from <i>Bacillus megaterium</i> with a DNA-binding domain. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 253-257.	0.7	2
49	Synergistic and strain-specific effects of bovine spongiform encephalopathy and scrapie prions in the cell-free conversion of recombinant prion protein. Journal of General Virology, 2006, 87, 3753-3761.	2.9	17
50	Old Codons, New Amino Acids. Angewandte Chemie - International Edition, 2004, 43, 1190-1193.	13.8	6
51	Old Codons, New Amino Acids. ChemInform, 2004, 35, no.	0.0	0
52	How Unique Is the Genetic Code. ChemInform, 2003, 34, no.	0.0	0
53	How Unique Is the Genetic Code?. Angewandte Chemie - International Edition, 2003, 42, 606-610.	13.8	6
54	Gene regulation by the tetracycline-inducible Tet repressor-operator system—molecular mechanisms at atomic resolution. , 2001, , 107-123.		3

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55	The Tetracycline Repressor – A Paradigm for a Biological Switch. <i>Angewandte Chemie - International Edition</i> , 2000, 39, 2042-2052.	13.8	118
56	Crystallization and preliminary X-ray analyses of catabolite control protein A, free and in complex with its DNA-binding site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 67-69.	2.5	2
57	Structural basis of gene regulation by the tetracycline inducible Tet repressor-operator system. <i>Nature Structural Biology</i> , 2000, 7, 215-219.	9.7	413
58	Proteolytic cleavage of Gram-positive λ 2 recombinase is required for crystallization. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 371-373.	2.1	6
59	Effect of the ionic environment on the molecular structure of bacteriophage SPP1 portal protein. <i>FEBS Journal</i> , 1999, 264, 724-735.	0.2	19
60	Tetracycline-Chelated Mg ²⁺ -Ion Initiates Helix Unwinding in Tet Repressor Induction. <i>Biochemistry</i> , 1999, 38, 191-198.	2.5	61
61	Crystal structure of the tet repressor in complex with a novel tetracycline, 9-(N , N) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 507 T Biology, 1999, 285, 455-461.	4.2	40
62	Crystallization and preliminary X-ray analysis of the Tet-repressor/operator complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 99-100.	2.5	9
63	Crystallization and preliminary X-ray crystallographic studies of the 13-fold symmetric portal protein of bacteriophage SPP1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1008-1011.	2.5	13
64	Conformational changes of the Tet repressor induced by tetracycline trapping. <i>Journal of Molecular Biology</i> , 1998, 279, 439-447.	4.2	113
65	Copper Coordination Polymers with Infinite Chloride Ion Channels and Different Directions of the Jahn-Teller Distortion, Built from Tris(1,2,4-triazolyl)borate as a Modified Tris(pyrazolyl)borate Ligand. <i>Chemische Berichte</i> , 1996, 129, 991-995.	0.2	32
66	Ligand-Field Control and Hydrogen Bonding as Design Elements in the Assembly and Crystallization of Poly(azolyl)borate-Metal Complexes: Chelate Complexes Versus Coordination Polymers and Symmetrical Versus Distorted Grid Sheets. <i>Chemistry - A European Journal</i> , 1995, 1, 637-644.	3.3	70
67	Characterization of non-inducible Tet repressor mutants suggests conformational changes necessary for induction. <i>Nature Structural Biology</i> , 1995, 2, 693-703.	9.7	61
68	Proximity Mapping of the Tet Repressor-Tetracycline-Fe ²⁺ Complex by Hydrogen Peroxide Mediated Protein Cleavage. <i>Biochemistry</i> , 1995, 34, 22-31.	2.5	59
69	The Complex Formed Between Tet Repressor and Tetracycline-Mg ²⁺ ihsbop +Reveals Mechanism of Antibiotic Resistance. <i>Journal of Molecular Biology</i> , 1995, 247, 260-280.	4.2	214
70	SELFSTACKING SYSTEMS, PART 6. HOST LATTICE FUNCTION OF 2,3,8,9-TETRAMETHOXYDIBENZO[1,2]-DICHALCOGENINS IN THEIR ELECTRICALLY CONDUCTING IODINE COMPLEXES. <i>Phosphorus, Sulfur and Silicon and the Related Elements</i> , 1995, 101, 235-244.	1.6	12
71	The structure of the left-handed antiparallel amylose double helix: Theoretical studies. <i>Biopolymers</i> , 1993, 33, 363-375.	2.4	17
72	Three-dimensional structure of system I of photosynthesis at 6 Å... resolution. <i>Nature</i> , 1993, 361, 326-331.	27.8	411

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73	Cyclic ligands with fixed coordination geometry. Part 7 Cationic copper(I) complexes of composition [Cu(Vn3S3)L]+CF3SO3- (Vn3S3=5,10, 15-trithia-cyclo-triveratrylene, L=CO, CH3OH). Transition Metal Chemistry, 1991, 16, 76-81.	1.4	2
74	Crystal and molecular structure of the hexasaccharide complex (p-nitrophenyl) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 Td (.alpha.-mal 112, 2789-2796.	13.7	45
75	Binding of vanadate (V) to ribonuclease-T1 and inosine, investigated by 15V NMR spectroscopy. Journal of Inorganic Biochemistry, 1989, 37, 141-150.	3.5	34
76	A side chain of diastereomeric iloprost protrudes from the cage in the complex with cyclomaltoheptaose (Î²-cyclodextrin): Crystal structure of (Î²-cyclodextrin)2 iloprost·20.5 H2O. Carbohydrate Research, 1989, 192, 43-49.	2.3	3
77	Long-range structural changes in proteinase K triggered by calcium ion removal. Nature, 1989, 337, 481-484.	27.8	59
78	Crystallization of proteins under microgravity. FEBS Letters, 1989, 259, 194-198.	2.8	31
79	The enzymatic activity of proteinase K is controlled by calcium. FEBS Journal, 1988, 176, 441-447.	0.2	98
80	Ein neuartiger vierkerniger Kupfer(I)-Cluster " abwechselnd durch Halogeno- und Triazolopyrimidinliganden 1/4berbr1/4ckt. Angewandte Chemie, 1988, 100, 884-885.	2.0	7
81	A Novel Tetranuclear Copper(I) Cluster with Alternate Bridging Halide and Triazolopyrimidine Ligands. Angewandte Chemie International Edition in English, 1988, 27, 856-858.	4.4	40
82	The first crystallization of a vanadium-dependent peroxidase. FEBS Letters, 1988, 239, 292-294.	2.8	22
83	Selbststapelnde Systeme, IV 2,3,7,8-Tetramethoxythianthreniumsalze/Selfstacking Systems, Part IV 2.3.7.8-Tetramethoxythianthrenium Salts. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 1987, 42, 169-176.	0.7	20
84	Absolute configuration of Rp-uridine 3'-cyclic phosphorothioate. Nucleic Acids Research, 1987, 15, 4945-4955.	14.5	9
85	Structure and electrical conductivity of TCNQ-2,3,7,8-tetramethoxychalcogenanthrene complexes. Synthetic Metals, 1987, 20, 357-364.	3.9	24
86	Cyclic ligands with fixed co-ordination geometry. Part 6(1). Chalcogenanthrenes as bridging ligands in dinuclear complexes of rhenium(I) and platinum(IV)-X-ray crystal structure of di(?-chloro) (?-2, 3, 7,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50		
87	Elementorganische Verbindungen mit o-Phenylresten, XI [1] 3:1-Komplexe von Hexachlor-dibenzo-p-dioxin-2,3-chinon mit 2,3,7,8-Tetramethoxythianthren und -selenanthren / Organometallic Compounds with o-Phenylene Substituents, Part XI [1] 3:1 Complexes of Hexachloro-dibenzo-p-dioxin-2,3-quinone with 2,3,7,8-Tetramethoxythianthrene and Selenanthrene. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 1986, 41, 1109-1111	0.7	7
88	Structure, spectroscopy and magnetism of di-iodo-bridged tetrahedral cobalt(II) compounds. The crystal and molecular structures of di-1/4-iodo-bis[iodotriphenylphosphinecobalt(II)] bis(benzene) and di-1/4-iodo-bis[iodotriphenylphosphineoxidecobalt(II)] bis(benzene). Inorganica Chimica Acta, 1985, 105, 181-186.	2.4	7
89	Selbststapelnde Systeme, I 4,4'-2,5,5'-Tetramethoxy-2,2'-dithiobiphenyl-Iod (6/7), eine Verbindung mit Radikalkationen und Polyiodidketten / Selfstacking Systems, I 4,4'-2,5,5'-Tetramethoxy-2,2'-dithiobiphenyl-Iodine (6/7), a Compound with Radical Cations and Polyiodide Chains. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 1985, 40, 39-44.	0.7	10
90	Acyclische Liganden mit fixierter Koordinationsgeometrie, 1-2-Komplexe von Cobalt(II) mit den Anionen von 2,2'-Dihydroxydiphenyloxid und -sulfid - Kristall- und Molek1/4struktur von		