

# 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	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
2	Three-dimensional structure of system I of photosynthesis at 6 Å... resolution. <i>Nature</i> , 1993, 361, 326-331.	27.8	411
3	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
4	The Complex Formed Between Tet Repressor and Tetracycline-Mg <sup>2+</sup>   ihsbop   +Reveals Mechanism of Antibiotic Resistance. <i>Journal of Molecular Biology</i> , 1995, 247, 260-280.	4.2	214
5	The Tetracycline Repressorâ€™A Paradigm for a Biological Switch. <i>Angewandte Chemie - International Edition</i> , 2000, 39, 2042-2052.	13.8	118
6	Conformational changes of the Tet repressor induced by tetracycline trapping. <i>Journal of Molecular Biology</i> , 1998, 279, 439-447.	4.2	113
7	The enzymatic activity of proteinase K is controlled by calcium. <i>FEBS Journal</i> , 1988, 176, 441-447.	0.2	98
8	Structural basis for a new tetracycline resistance mechanism relying on the TetX monooxygenase. <i>FEBS Letters</i> , 2011, 585, 1061-1066.	2.8	87
9	Ligandâ€™Field Control and Hydrogen Bonding as Design Elements in the Assembly and Crystallization of Poly(azoly)borateâ€™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
10	The crystal structure of an esterase from the hyperthermophilic microorganism <i>Pyrobaculum calidifontis</i> VA1 explains its enantioselectivity. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1061-1072.	3.6	64
11	Prion Protein Misfolding. <i>Current Molecular Medicine</i> , 2009, 9, 826-835.	1.3	63
12	Specific binding of divalent metal ions to tetracycline and to the Tet repressor/tetracycline complex. <i>Journal of Biological Inorganic Chemistry</i> , 2008, 13, 1097-1110.	2.6	62
13	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
14	Tetracycline-Chelated Mg <sup>2+</sup> -Ion Initiates Helix Unwinding in Tet Repressor Inductionâ€™. <i>Biochemistry</i> , 1999, 38, 191-198.	2.5	61
15	Long-range structural changes in proteinase K triggered by calcium ion removal. <i>Nature</i> , 1989, 337, 481-484.	27.8	59
16	Proximity Mapping of the Tet Repressor-Tetracycline-Fe <sup>2+</sup> Complex by Hydrogen Peroxide Mediated Protein Cleavage. <i>Biochemistry</i> , 1995, 34, 22-31.	2.5	59
17	Enzymatic Conversion of Flavonoids using Bacterial Chalcone Isomerase and Enoate Reductase. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1439-1442.	13.8	56
18	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

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19	A FRET Enzyme-Based Probe for Monitoring Hydrogen Sulfide. <i>Inorganic Chemistry</i> , 2012, 51, 11220-11222.	4.0	52
20	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
21	A Novel Tetranuclear Copper(I) Cluster with Alternate Bridging Halide and Triazolopyrimidine Ligands. <i>Angewandte Chemie International Edition in English</i> , 1988, 27, 856-858.	4.4	40
22	Crystal structure of the tet repressor in complex with a novel tetracycline, 9-( N , N ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Td (-dimer) Biology, 1999, 285, 455-461.	4.2	40
23	Protonation Patterns in Tetracycline:Tet Repressor Recognition: Simulations and Experiments. <i>ChemBioChem</i> , 2007, 8, 675-685.	2.6	40
24	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
25	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
26	Binding of vanadate (V) to ribonuclease-T1 and inosine, investigated by 15V NMR spectroscopy. <i>Journal of Inorganic Biochemistry</i> , 1989, 37, 141-150.	3.5	34
27	Tet Repressor Induction by Tetracycline: A Molecular Dynamics, Continuum Electrostatics, and Crystallographic Study. <i>Journal of Molecular Biology</i> , 2008, 378, 898-912.	4.2	34
28	Copper Coordination Polymers with Infinite Chloride Ion Channels and Different Directions of the Jahnâ€Teller Distortion, Built from Tris(1,2,4â€Triaazolyl)borate as a Modified Tris(pyrazolyl)borate Ligand. <i>Chemische Berichte</i> , 1996, 129, 991-995.	0.2	32
29	Crystallization of proteins under microgravity. <i>FEBS Letters</i> , 1989, 259, 194-198.	2.8	31
30	Structural and biochemical characterization of the dual substrate recognition of the (<i>R</i>)-selective amine transaminase from <i>AspergillusÂfumigatus</i>. <i>FEBS Journal</i> , 2015, 282, 407-415.	4.7	29
31	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
32	Nonantibiotic Properties of Tetracyclines: Structural Basis for Inhibition of Secretory Phospholipase A2. <i>Journal of Molecular Biology</i> , 2010, 398, 83-96.	4.2	27
33	Structure and electrical conductivity of TCNQ-2,3,7,8-tetramethoxychalcogenanthrene complexes. <i>Synthetic Metals</i> , 1987, 20, 357-364.	3.9	24
34	Modular organisation of inducer recognition and allostery in the tetracycline repressor. <i>FEBS Journal</i> , 2016, 283, 2102-2114.	4.7	23
35	The first crystallization of a vanadium-dependent peroxidase. <i>FEBS Letters</i> , 1988, 239, 292-294.	2.8	22
36	Human Î±<sub>2</sub>-â€M Macroglobulinâ€”Another Variation on the Venus Flytrap. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5045-5047.	13.8	21

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37	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
38	Selbststapelnde Systeme, IV 2,3,7,8-Tetramethoxythianthreniumsalze/Selfstacking Systems, Part IV 2.3.7.8-Tetramethoxythianthrenium Salts. <i>Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences</i> , 1987, 42, 169-176.	0.7	20
39	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
40	The structure of the left-handed antiparallel amylose double helix: Theoretical studies. <i>Biopolymers</i> , 1993, 33, 363-375.	2.4	17
41	Synergistic and strain-specific effects of bovine spongiform encephalopathy and scrapie prions in the cell-free conversion of recombinant prion protein. <i>Journal of General Virology</i> , 2006, 87, 3753-3761.	2.9	17
42	Tetracycline-Tet Repressor Binding Specificity: Insights from Experiments and Simulations. <i>Biophysical Journal</i> , 2009, 97, 2829-2838.	0.5	16
43	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
44	The growth of single crystal silver wires at the nitrobenzene   water interface. <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 12254.	2.8	14
45	Blocking tetracycline destruction. <i>Nature Chemical Biology</i> , 2017, 13, 694-695.	8.0	14
46	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
47	SELFSTACKING SYSTEMS, PART 6. <sup>1</sup> HOST LATTICE FUNCTION OF 2,3,8,9-TETRAMETHOXYDIBENZO[ <i>c,e</i> ][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
48	Tetracycline Repressor Allostery Does Not Depend on Divalent Metal Recognition. <i>Biochemistry</i> , 2014, 53, 7990-7998.	2.5	11
49	Selbststapelnde Systeme, I 4,4',5,5'-Tetramethoxy-2,2'-dithiobiphenyl-Iod (6/7), eine Verbindung mit Radikalkationen und Polyiodidketten / Selfstacking Systems, I 4,4',5,5'-Tetramethoxy-2,2'-dithiobiphenyl-Iodine (6/7), a Compound with Radical Cations and Polyiodide Chains. <i>Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences</i> , 1985, 40, 39-44.	0.7	10
50	Absolute configuration of Rp-uridine 3',5'-cyclic phosphorothioate. <i>Nucleic Acids Research</i> , 1987, 15, 4945-4955.	14.5	9
51	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(μ-chloro) (μ-2, 3, 7, 8-tetrahydro-1,4-benzodioxepin-1-yl) rhenium(I) tetrachloroplatinate(IV). <i>Acta Crystallographica Section B</i> , 1984, 40, 143-144.	0.7	9
52	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
53	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
54	Crystallization and preliminary X-ray diffraction studies of the (R)-selective amine transaminase from <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1415-1417.	0.7	9

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55	Post-translational modification and extended glycosylation pattern of a plant latex peroxidase of native source characterized by X-ray crystallography. FEBS Journal, 2014, 281, 4319-4333.	4.7	9
56	Structural and biochemical analysis of a phosin from <i>Streptomyces chartreusis</i> reveals a combined polyphosphate and metal-binding fold. FEBS Letters, 2019, 593, 2019-2029.	2.8	9
57	Structure and regulatory targets of SCO3201, a highly promiscuous TetR-like regulator of <i>Streptomyces coelicolor</i> M145. Biochemical and Biophysical Research Communications, 2014, 450, 513-518.	2.1	8
58	A Quantitative Real-Time RT-PCR Assay for the Detection of Venezuelan equine encephalitis virus Utilizing a Universal Alphavirus Control RNA. BioMed Research International, 2016, 2016, 1-7.	1.9	8
59	Thermodynamics, cooperativity and stability of the tetracycline repressor (TetR) upon tetracycline binding. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140404.	2.3	8
60	Structure, spectroscopy and magnetism of di-iodo-bridged tetrahedral cobalt(II) compounds. The crystal and molecular structures of di-iodo-bis[iodotriphenylphosphinecobalt(II)] bis(benzene) and di-iodo-bis[iodotriphenylphosphineoxidecobalt(II)] bis(benzene). Inorganica Chimica Acta, 1985, 105, 181-186.	2.4	7
61	Elementorganische Verbindungen mit Ar-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 für Naturforschung - Section B Journal of Chemical Sciences, 1986, 41, 1133-1141.	0.7	7
62	Ein neuartiger vierkerniger Kupfer(I)-Cluster abwechselnd durch Halogeno- und Triazolopyrimidinliganden überbrückt. Angewandte Chemie, 1988, 100, 884-885.	2.0	7
63	Struktur und Kristallstruktur von 2,2'-Dihydroxydiphenyloxid und -sulfid		

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73	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
74	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
75	Structural basis to repurpose boron-based proteasome inhibitors Bortezomib and Ixazomib as $\beta$ -lactamase inhibitors. <i>Scientific Reports</i> , 2022, 12, 5510.	3.3	4
76	A side chain of diastereomeric iloprost protrudes from the cage in the complex with cyclomaltoheptaose ( $\beta$ -cyclodextrin): Crystal structure of ( $\beta$ -cyclodextrin) <sub>2</sub> iloprost·20.5 H <sub>2</sub> O. <i>Carbohydrate Research</i> , 1989, 192, 43-49.	2.3	3
77	Gene regulation by the tetracycline-inducible Tet repressor-operator system – molecular mechanisms at atomic resolution. , 2001, , 107-123.		3
78	Tryptophan – Electron System Capping a Copper(I) Binding Site – A New Organometallic Bonding Mode in Proteins. <i>ChemBioChem</i> , 2008, 9, 1697-1699.	2.6	3
79	Crystallization and preliminary X-ray diffraction studies of the putative haloalkane dehalogenase DppA from <i>Plesiocystis pacifica</i> SIR-I. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 828-830.	0.7	3
80	Structural evidence of intramolecular propeptide inhibition of the aspzincin metalloendopeptidase AsaP1. <i>FEBS Letters</i> , 2016, 590, 3280-3294.	2.8	3
81	Cyclic ligands with fixed coordination geometry. Part 7 Cationic copper(I) complexes of composition [Cu(Vn3S3)L]+CF <sub>3</sub> SO <sub>3</sub> - (Vn3S3=5,10, 15-trithia-cyclo-triveratrylene, L=CO, CH <sub>3</sub> OH). <i>Transition Metal Chemistry</i> , 1991, 16, 76-81.	1.4	2
82	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
83	Structure of the apo form of the catabolite control protein A (CcpA) from <i>Bacillus megaterium</i> with a DNA-binding domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 253-257.	0.7	2
84	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> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 695-697.	0.7	2
85	The induction mechanism of the flavonoid-responsive regulator FrrA. <i>FEBS Journal</i> , 2022, 289, 507-518.	4.7	2
86	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
87	How Unique Is the Genetic Code. <i>ChemInform</i> , 2003, 34, no.	0.0	0
88	Old Codons, New Amino Acids. <i>ChemInform</i> , 2004, 35, no.	0.0	0
89	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
90	Structure of the tetracycline-degrading monooxygenase TetX2. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s144-s145.	0.3	0