

# Heini W Dirr

## List of Publications by Year in descending order

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98  
papers

3,344  
citations

147801

31  
h-index

155660

55  
g-index

98  
all docs

98  
docs citations

98  
times ranked

2081  
citing authors

#	ARTICLE	IF	CITATIONS
1	An empirical and theoretical description of <i>Schistosoma japonicum</i> glutathione transferase inhibition by bromosulphophthalein and indanyloxyacetic acid 94. <i>Journal of Molecular Structure</i> , 2021, 1223, 128892.	3.6	6
2	Molecular basis of inhibition of <i>Schistosoma japonicum</i> glutathione transferase by ellagic acid: Insights into biophysical and structural studies. <i>Molecular and Biochemical Parasitology</i> , 2020, 240, 111319.	1.1	11
3	Double trouble? Gag in conjunction with double insert in HIV protease contributes to reduced DRV susceptibility. <i>Biochemical Journal</i> , 2019, 476, 375-384.	3.7	5
4	Drug Susceptibility and Replication Capacity of a Rare HIV-1 Subtype C Protease Hinge Region Variant. <i>Antiviral Therapy</i> , 2019, 24, 333-342.	1.0	2
5	An update on the biophysical character of the human eukaryotic elongation factor 1 beta: Perspectives from interaction with elongation factor 1 gamma. <i>Journal of Molecular Recognition</i> , 2018, 31, e2708.	2.1	5
6	Molecular dynamics and ligand docking of a hinge region variant of South African HIV-1 subtype C protease. <i>Journal of Molecular Graphics and Modelling</i> , 2018, 82, 1-11.	2.4	15
7	The study of degradation mechanisms of glyco-engineered plant produced anti-rabies monoclonal antibodies E559 and 62-71-3. <i>PLoS ONE</i> , 2018, 13, e0209373.	2.5	3
8	Structural and biochemical characterization of <i>Plasmodium falciparum</i> Hsp70 $\alpha$ reveals functional versatility of its C-terminal EEVN motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1189-1201.	2.6	37
9	A conserved cation binding site in the DNA binding domain of forkhead box transcription factors regulates DNA binding by FOXP2. <i>Archives of Biochemistry and Biophysics</i> , 2018, 657, 56-64.	3.0	4
10	A Phosphomimetic Study Implicates Ser557 in Regulation of FOXP2 DNA Binding. <i>Protein Journal</i> , 2018, 37, 311-323.	1.6	8
11	Overexpression, Purification and Functional Characterisation of Wild-Type HIV-1 Subtype C Protease and Two Variants Using a Thioredoxin and His-Tag Protein Fusion System. <i>Protein Journal</i> , 2018, 37, 369-379.	1.6	3
12	The forkhead domain hinge-loop plays a pivotal role in DNA binding and transcriptional activity of FOXP2. <i>Biological Chemistry</i> , 2018, 399, 881-893.	2.5	5
13	The effects of mutating Tyr9 and Arg15 on the structure, stability, conformational dynamics and mechanism of GSTA3-3. <i>Biophysical Chemistry</i> , 2017, 224, 40-48.	2.8	4
14	The FOXP2 forkhead domain binds to a variety of DNA sequences with different rates and affinities. <i>Journal of Biochemistry</i> , 2017, 162, mvx003.	1.7	6
15	( $\alpha$ ) <sup>+</sup> -Epigallocatechin-3-Gallate Inhibits the Chaperone Activity of <i>Plasmodium falciparum</i> Hsp70 Chaperones and Abrogates Their Association with Functional Partners. <i>Molecules</i> , 2017, 22, 2139.	3.8	39
16	Energetics of Glutathione Binding to Human Eukaryotic Elongation Factor 1 Gamma: Isothermal Titration Calorimetry and Molecular Dynamics Studies. <i>Protein Journal</i> , 2016, 35, 448-458.	1.6	3
17	The Lyssavirus glycoprotein: A key to cross-immunity. <i>Virology</i> , 2016, 498, 250-256.	2.4	11
18	<i>Plasmodium falciparum</i> Hsp70-z, an Hsp110 homologue, exhibits independent chaperone activity and interacts with Hsp70-1 in a nucleotide-dependent fashion. <i>Cell Stress and Chaperones</i> , 2016, 21, 499-513.	2.9	41

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19	A Single Amino Acid in the Hinge Loop Region of the FOXP Forkhead Domain is Significant for Dimerisation. <i>Protein Journal</i> , 2015, 34, 111-121.	1.6	16
20	The kinetics of the substitution of coordinated H <sub>2</sub> O on Co(III) by cyanide in aquacobalamin (vitamin B <sub>12</sub> )	3.9	4
21	Overexpression, Purification and Characterisation of the Plasmodium falciparum Hsp70-z (PfHsp70-z) Protein. <i>PLoS ONE</i> , 2015, 10, e0129445.	2.5	36
22	The Isomerization of $\Delta^5$ -Androstene-3,17-dione by the Human Glutathione Transferase A3-3 Proceeds via a Conjugated Heteroannular Diene Intermediate. <i>Journal of Biological Chemistry</i> , 2014, 289, 32243-32252.	3.4	4
23	Amide hydrogen exchange in HIV-1 subtype B and C proteases insights into reduced drug susceptibility and dimer stability. <i>FEBS Journal</i> , 2014, 281, 5395-5410.	4.7	7
24	Purification and characterisation of recombinant human eukaryotic elongation factor 1 gamma. <i>Protein Expression and Purification</i> , 2014, 99, 70-77.	1.3	17
25	Phosphorylation- and Nucleotide-Binding-Induced Changes to the Stability and Hydrogen Exchange Patterns of JNK1 $\Delta$ 1 Provide Insight into Its Mechanisms of Activation. <i>Journal of Molecular Biology</i> , 2014, 426, 3569-3589.	4.2	6
26	A Lys-Trp Cation- $\pi$ Interaction Mediates the Dimerization and Function of the Chloride Intracellular Channel Protein 1 Transmembrane Domain. <i>Biochemistry</i> , 2014, 53, 57-67.	2.5	21
27	A conserved cationic motif enhances membrane binding and insertion of the chloride intracellular channel protein 1 transmembrane domain. <i>European Biophysics Journal</i> , 2014, 43, 405-414.	2.2	6
28	Polymorphic Diversity: <i>N</i> -Phenylbenzamide as a Possible Polymorphophore. <i>Crystal Growth and Design</i> , 2013, 13, 3463-3474.	3.0	15
29	F99 is Critical for Dimerization and Activation of South African HIV-1 Subtype C Protease. <i>Protein Journal</i> , 2013, 32, 560-567.	1.6	2
30	JNK1 $\Delta$ 1 is phosphorylated during expression in <i>E. coli</i> and in vitro by MKK4 at three identical novel sites. <i>Biochemical and Biophysical Research Communications</i> , 2013, 432, 683-688.	2.1	5
31	High yield purification of JNK1 $\Delta$ 1 and activation by in vitro reconstitution of the MEKK1-MKK4-JNK MAPK phosphorylation cascade. <i>Protein Expression and Purification</i> , 2013, 87, 87-99.	1.3	13
32	<i>S</i> -Nitrosation Destabilizes Glutathione Transferase P1-1. <i>Biochemistry</i> , 2013, 52, 9394-9402.	2.5	7
33	Membrane Mimetics Induce Helix Formation and Oligomerization of the Chloride Intracellular Channel Protein 1 Transmembrane Domain. <i>Biochemistry</i> , 2013, 52, 2739-2749.	2.5	7
34	Structural insights into the South African HIV-1 subtype C protease: impact of hinge region dynamics and flap flexibility in drug resistance. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1370-1380.	3.5	36
35	<i>S</i> -Nitrosation of Glutathione Transferase P1-1 Is Controlled by the Conformation of a Dynamic Active Site Helix. <i>Journal of Biological Chemistry</i> , 2013, 288, 14973-14984.	3.4	10
36	Role of Arginine 29 and Glutamic Acid 81 Interactions in the Conformational Stability of Human Chloride Intracellular Channel 1. <i>Biochemistry</i> , 2012, 51, 7854-7862.	2.5	13

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37	Role of Individual Histidines in the pH-Dependent Global Stability of Human Chloride Intracellular Channel 1. <i>Biochemistry</i> , 2012, 51, 995-1004.	2.5	21
38	A Conserved Interdomain Interaction Is a Determinant of Folding Cooperativity in the GST Fold. <i>Biochemistry</i> , 2011, 50, 7067-7075.	2.5	4
39	Energetics of ligand binding to human glutathione transferase A1-1: Tyr-9 associated localisation of the C-terminal helix is ligand-dependent. <i>Biophysical Chemistry</i> , 2011, 156, 153-158.	2.8	3
40	Stability of the domain interface contributes towards the catalytic function at the H-site of class alpha glutathione transferase A1-1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 2228-2233.	2.3	15
41	Arginine 15 stabilizes an SNAr reaction transition state and the binding of anionic ligands at the active site of human glutathione transferase A1-1. <i>Biophysical Chemistry</i> , 2010, 146, 118-125.	2.8	20
42	The role of a topologically conserved isoleucine in glutathione transferase structure, stability and function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 776-780.	0.7	4
43	Class Pi Glutathione Transferase Unfolds via a Dimeric and Not Monomeric Intermediate: Functional Implications for an Unstable Monomer. <i>Biochemistry</i> , 2010, 49, 5074-5081.	2.5	17
44	Structural Dynamics of Soluble Chloride Intracellular Channel Protein CLIC1 Examined by Amide Hydrogen-Deuterium Exchange Mass Spectrometry. <i>Biochemistry</i> , 2009, 48, 8413-8421.	2.5	36
45	Impact of domain interchange on conformational stability and equilibrium folding of chimeric class $\gamma$ glutathione transferases. <i>Protein Science</i> , 2009, 11, 2208-2217.	7.6	17
46	Characterization of the binding of 8-anilinoanthralene sulfonate to rat class Mu GST M1-1. <i>Biophysical Chemistry</i> , 2008, 137, 100-104.	2.8	13
47	Formation of an Unfolding Intermediate State of Soluble Chloride Intracellular Channel Protein CLIC1 at Acidic pH. <i>Biochemistry</i> , 2008, 47, 11674-11681.	2.5	44
48	Stability and Unfolding of Reduced <i>Escherichia coli</i> Glutaredoxin 2: A Monomeric Structural Homologue of the Glutathione Transferase Family. <i>Biochemistry</i> , 2008, 47, 10801-10808.	2.5	2
49	Active-Site Mutations in the South African Human Immunodeficiency Virus Type 1 Subtype C Protease Have a Significant Impact on Clinical Inhibitor Binding: Kinetic and Thermodynamic Study. <i>Journal of Virology</i> , 2008, 82, 11476-11479.	3.4	38
50	Double Mutation at the Subunit Interface of Glutathione Transferase rGSTM1-1 Results in a Stable, Folded Monomer. <i>Biochemistry</i> , 2006, 45, 2267-2273.	2.5	28
51	The intersubunit lock-and-key motif in human glutathione transferase A1-1: role of the key residues Met51 and Phe52 in function and dimer stability. <i>Biochemical Journal</i> , 2006, 393, 523-528.	3.7	20
52	A Conserved N-capping Motif Contributes Significantly to the Stabilization and Dynamics of the C-terminal Region of Class Alpha Glutathione S-Transferases. <i>Journal of Biological Chemistry</i> , 2005, 280, 19480-19487.	3.4	20
53	Influence of the Dimer Interface on Glutathione Transferase Structure and Dynamics Revealed by Amide H/D Exchange Mass Spectrometry. <i>Biochemistry</i> , 2005, 44, 10605-10612.	2.5	21
54	Tertiary Interactions Stabilise the C-terminal Region of Human Glutathione Transferase A1-1: a Crystallographic and Calorimetric Study. <i>Journal of Molecular Biology</i> , 2005, 349, 825-838.	4.2	32

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55	Characterization of bromosulphophthalein binding to human glutathione S-transferase A1-1: thermodynamics and inhibition kinetics. <i>Biochemical Journal</i> , 2004, 382, 703-709.	3.7	30
56	Residue 219 Impacts on the Dynamics of the C-Terminal Region in Glutathione Transferase A1-1: Implications for Stability and Catalytic and Ligandin Functions. <i>Biochemistry</i> , 2003, 42, 15326-15332.	2.5	24
57	The role of an evolutionarily conserved cis-proline in the thioredoxin-like domain of human class Alpha glutathione transferase A1-1. <i>Biochemical Journal</i> , 2003, 372, 241-246.	3.7	31
58	Protease inhibition in African subtypes of HIV-1. <i>AIDS Reviews</i> , 2003, 5, 165-71.	1.0	34
59	Thermodynamics of the ligandin function of human class Alpha glutathione transferase A1-1: energetics of organic anion ligand binding. <i>Biochemical Journal</i> , 2002, 363, 341.	3.7	28
60	Thermodynamics of the ligandin function of human class Alpha glutathione transferase A1-1: energetics of organic anion ligand binding. <i>Biochemical Journal</i> , 2002, 363, 341-346.	3.7	40
61	Molecular Recognition at the Dimer Interface of a Class Mu Glutathione Transferase: Role of a Hydrophobic Interaction Motif in Dimer Stability and Protein Function. <i>Biochemistry</i> , 2002, 41, 14238-14247.	2.5	41
62	The Cochaperone Murine Stress-Inducible Protein 1: Overexpression, Purification, and Characterization. <i>Protein Expression and Purification</i> , 2001, 21, 462-469.	1.3	14
63	Heat shock cognate protein 70 chaperone-binding site in the co-chaperone murine stress-inducible protein 1 maps to within three consecutive tetratricopeptide repeat motifs. <i>Biochemical Journal</i> , 2000, 345, 645.	3.7	27
64	Electrostatic interactions affecting the active site of class Sigma glutathione S-transferase. <i>Biochemical Journal</i> , 2000, 347, 193.	3.7	10
65	Heat shock cognate protein 70 chaperone-binding site in the co-chaperone murine stress-inducible protein 1 maps to within three consecutive tetratricopeptide repeat motifs. <i>Biochemical Journal</i> , 2000, 345, 645-651.	3.7	41
66	Electrostatic interactions affecting the active site of class Sigma glutathione S-transferase. <i>Biochemical Journal</i> , 2000, 347, 193-197.	3.7	32
67	Domain-domain interface packing at conserved Trp-20 in class $\beta$ glutathione transferase impacts on protein stability. <i>BBA - Proteins and Proteomics</i> , 2000, 1478, 325-332.	2.1	21
68	Analysis of the levels of conservation of the J domain among the various types of DnaJ-like proteins. <i>Cell Stress and Chaperones</i> , 2000, 5, 347.	2.9	74
69	The hydrophobic lock-and-key intersubunit motif of glutathione transferase A1-1: implications for catalysis, ligandin function and stability. <i>FEBS Letters</i> , 2000, 465, 169-172.	2.8	58
70	Equilibrium Folding of Dimeric Class $\beta$ Glutathione Transferases Involves a Stable Monomeric Intermediate. <i>Biochemistry</i> , 2000, 39, 12336-12344.	2.5	56
71	Folding and Assembly of Dimeric Human Glutathione Transferase A1-1. <i>Biochemistry</i> , 1999, 38, 16686-16694.	2.5	52
72	Role of the C-Terminal Helix 9 in the Stability and Ligandin Function of Class $\beta$ Glutathione Transferase A1-1. <i>Biochemistry</i> , 1999, 38, 15631-15640.	2.5	59

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73	Aflatoxin B1 and sulphobromophthalein binding to the dimeric human glutathione S-transferase A1-1 : a fluorescence spectroscopic analysis. FEBS Journal, 1998, 257, 434-442.	0.2	16
74	Class Sigma Glutathione Transferase Unfolds via a Dimeric and a Monomeric Intermediate: Impact of Subunit Interface on Conformational Stability in the Superfamily. Biochemistry, 1998, 37, 15534-15541.	2.5	42
75	Equilibrium and Kinetic Unfolding Properties of Dimeric Human Glutathione Transferase A1-1. Biochemistry, 1998, 37, 5320-5328.	2.5	75
76	A topologically conserved aliphatic residue in $\alpha$ -helix 6 stabilizes the hydrophobic core in domain II of glutathione transferases and is a structural determinant for the unfolding pathway. Biochemical Journal, 1998, 336, 413-418.	3.7	11
77	Conformational stability of pGEX-expressed <i>Schistosoma japonicum</i> glutathione S-transferase: A detoxification enzyme and fusion protein affinity tag. Protein Science, 1997, 6, 399-406.	7.6	121
78	Effect of glutathione, glutathione sulphonate and S-hexylglutathione on the conformational stability of class pi glutathione S-transferase. FEBS Letters, 1996, 391, 313-316.	2.8	15
79	Determination of a Binding Site for a Non-Substrate Ligand in Mammalian Cytosolic Glutathione S-Transferases by means of Fluorescence-Resonance Energy Transfer. FEBS Journal, 1996, 241, 484-488.	0.2	32
80	Class-pi Glutathione S-Transferase is Unable to Regain Its Native Conformation After Oxidative Inactivation by Hydrogen Peroxide. FEBS Journal, 1996, 242, 301-307.	0.2	13
81	Native Dimer Stabilizes the Subunit Tertiary Structure of Porcine Class pi Glutathione S-transferase. FEBS Journal, 1995, 230, 614-620.	0.2	51
82	Porcine class pi glutathione S-transferase: anionic ligand binding and conformational analysis. BBA - Proteins and Proteomics, 1995, 1247, 225-230.	2.1	29
83	[22] X-ray structure methods for glutathione binding. Methods in Enzymology, 1995, 251, 243-254.	1.0	4
84	Conformational stability of Cys45-alkylated and hydrogen peroxide-oxidised glutathione S-transferase. FEBS Letters, 1995, 371, 94-98.	2.8	10
85	X-ray crystal structures of cytosolic glutathione S-transferases. Implications for protein architecture, substrate recognition and catalytic function. FEBS Journal, 1994, 220, 645-661.	0.2	400
86	Refined Crystal Structure of Porcine Class Pi Glutathione S-Transferase (pGST P1-1) at 2.1 Å Resolution. Journal of Molecular Biology, 1994, 243, 72-92.	4.2	93
87	X-ray crystal structures of cytosolic glutathione S-transferases. , 1994, , 57-73.		0
88	Structure Determination and Refinement of Human Alpha Class Glutathione Transferase A1-1, and a Comparison with the Mu and Pi Class Enzymes. Journal of Molecular Biology, 1993, 232, 192-212.	4.2	453
89	Three-dimensional structure of class pi glutathione S-transferase from human placenta in complex with S-hexylglutathione at 2.8 Å resolution. Journal of Molecular Biology, 1992, 227, 214-226.	4.2	273
90	Mutational substitution of residues implicated by crystal structure in binding the substrate glutathione to human glutathione S-transferase pi. Journal of Molecular Biology, 1992, 226, 319-322.	4.2	58

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91	Equilibrium unfolding of class $\gamma$ glutathione S-transferase. Biochemical and Biophysical Research Communications, 1991, 180, 294-300.	2.1	61
92	Class $\pi$ glutathione S-transferase from pig lung. Purification, biochemical characterization, primary structure and crystallization. FEBS Journal, 1991, 196, 693-698.	0.2	67
93	Purification and properties of an esterase from Cucurbita maxima fruit tissue. Phytochemistry, 1989, 28, 379-383.	2.9	12
94	Accessibility of the tryptophan residues and flavin prosthetic group of $\beta^2$ -cyclopiazonate oxidocyclase to solvent studied by fluorescence quenching. International Journal of Biochemistry & Cell Biology, 1988, 20, 109-111.	0.5	2
95	Purification and partial characterization of the glutathione S-transferase of rat erythrocytes. BBA - Proteins and Proteomics, 1988, 957, 173-177.	2.1	7
96	Solvent effects on the spectroscopic properties of aflatoxin B1. International Journal of Biochemistry & Cell Biology, 1987, 19, 1137-1140.	0.5	9
97	Characterization of the aflatoxin B1-binding site of rat albumin. BBA - Proteins and Proteomics, 1987, 913, 300-307.	2.1	8
98	Aflatoxin B1 transport in rat blood plasma. Binding to albumin in vivo and in vitro and spectrofluorimetric studies into the nature of the interaction. Biochimica Et Biophysica Acta - General Subjects, 1986, 881, 383-390.	2.4	22