Heini W Dirr

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98	2,960	28	52
papers	citations	h-index	g-index
98	3,133	3.7	4.58
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
98	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	6.5	428
97	X-ray crystal structures of cytosolic glutathione S-transferases. Implications for protein architecture, substrate recognition and catalytic function. *FEBS Journal*, **1994**, 220, 645-61		361
96	Three-dimensional structure of class pi glutathione S-transferase from human placenta in complex with S-hexylglutathione at 2.8 A resolution. *Journal of Molecular Biology*, **1992**, 227, 214-26	6.5	261
95	Conformational stability of pGEX-expressed Schistosoma japonicum glutathione S-transferase: a detoxification enzyme and fusion-protein affinity tag. *Protein Science*, **1997**, 6, 399-406	6.3	113
94	Refined crystal structure of porcine class Pi glutathione S-transferase (pGST P1-1) at 2.1 A resolution. *Journal of Molecular Biology*, **1994**, 243, 72-92	6.5	86
93	Equilibrium and kinetic unfolding properties of dimeric human glutathione transferase A1-1. *Biochemistry*, **1998**, 37, 5320-8	3.2	71
92	Class pi glutathione S-transferase from pig lung. Purification, biochemical characterization, primary structure and crystallization. *FEBS Journal*, **1991**, 196, 693-8		62
91	Equilibrium unfolding of class pi glutathione S-transferase. *Biochemical and Biophysical Research Communications*, **1991**, 180, 294-300	3.4	58
90	Analysis of the levels of conservation of the J domain among the various types of DnaJ-like proteins. *Cell Stress and Chaperones*, **2000**, 5, 347-58	4	57
89	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, 319-22	6.5	57
88	Equilibrium folding of dimeric class mu glutathione transferases involves a stable monomeric intermediate. *Biochemistry*, **2000**, 39, 12336-44	3.2	55
87	Role of the C-terminal helix 9 in the stability and ligandin function of class alpha glutathione transferase A1-1. *Biochemistry*, **1999**, 38, 15631-40	3.2	52
86	The hydrophobic lock-and-key intersubunit motif of glutathione transferase A1-1: implications for catalysis, ligandin function and stability. *FEBS Letters*, **2000**, 465, 169-72	3.8	48
85	Folding and assembly of dimeric human glutathione transferase A1-1. *Biochemistry*, **1999**, 38, 16686-94	3.2	48
84	Native Dimer Stabilizes the Subunit Tertiary Structure of Porcine Class pi Glutathione S-transferase. *FEBS Journal*, **1995**, 230, 614-620		46
83	Formation of an unfolding intermediate state of soluble chloride intracellular channel protein CLIC1 at acidic pH. *Biochemistry*, **2008**, 47, 11674-81	3.2	38
82	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. *Biochemical Journal*, **2000**, 345, 645-651	3.8	38

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81	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, 15534-41	3.2	38
80	Molecular recognition at the dimer interface of a class mu glutathione transferase: role of a hydrophobic interaction motif in dimer stability and protein function. *Biochemistry*, **2002**, 41, 14238-47	3.2	37
79	Thermodynamics of the ligandin function of human class Alpha glutathione transferase A1-1: energetics of organic anion ligand binding. *Biochemical Journal*, **2002**, 363, 341-346	3.8	34
78	Protease inhibition in African subtypes of HIV-1. *AIDS Reviews*, **2003**, 5, 165-71	1.5	32
77	Structural dynamics of soluble chloride intracellular channel protein CLIC1 examined by amide hydrogen-deuterium exchange mass spectrometry. *Biochemistry*, **2009**, 48, 8413-21	3.2	30
76	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. *Journal of Virology*, **2008**, 82, 11476-9	6.6	30
75	The role of an evolutionarily conserved cis-proline in the thioredoxin-like domain of human class Alpha glutathione transferase A1-1. *Biochemical Journal*, **2003**, 372, 241-6	3.8	30
74	Plasmodium falciparum Hsp70-z, an Hsp110 homologue, exhibits independent chaperone activity and interacts with Hsp70-1 in a nucleotide-dependent fashion. *Cell Stress and Chaperones*, **2016**, 21, 499-513	4	29
73	Structural insights into the South African HIV-1 subtype C protease: impact of hinge region dynamics and flap flexibility in drug resistance. *Journal of Biomolecular Structure and Dynamics*, **2013**, 31, 1370-80	3.6	29
72	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, 484-8		28
71	Overexpression, Purification and Characterisation of the Plasmodium falciparum Hsp70-z (PfHsp70-z) Protein. *PLoS ONE*, **2015**, 10, e0129445	3.7	28
70	Tertiary interactions stabilise the C-terminal region of human glutathione transferase A1-1: a crystallographic and calorimetric study. *Journal of Molecular Biology*, **2005**, 349, 825-38	6.5	27
69	Double mutation at the subunit interface of glutathione transferase rGSTM1-1 results in a stable, folded monomer. *Biochemistry*, **2006**, 45, 2267-73	3.2	26
68	Electrostatic interactions affecting the active site of class Sigma glutathione S-transferase. *Biochemical Journal*, **2000**, 347, 193-197	3.8	26
67	Porcine class pi glutathione S-transferase: anionic ligand binding and conformational analysis. *BBA - Proteins and Proteomics*, **1995**, 1247, 225-30		26
66	Structural and biochemical characterization of Plasmodium falciparum Hsp70-x reveals functional versatility of its C-terminal EEVN motif. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86, 1189-1201	4.2	26
65	Residue 219 impacts on the dynamics of the C-terminal region in glutathione transferase A1-1: implications for stability and catalytic and ligandin functions. *Biochemistry*, **2003**, 42, 15326-32	3.2	24
64	Thermodynamics of the ligandin function of human class Alpha glutathione transferase A1-1: energetics of organic anion ligand binding. *Biochemical Journal*, **2002**, 363, 341-6	3.8	24

63	(-)-Epigallocatechin-3-Gallate Inhibits the Chaperone Activity of Plasmodium falciparum Hsp70 Chaperones and Abrogates Their Association with Functional Partners. *Molecules*, **2017**, 22,	4.8	23
62	Characterization of bromosulphophthalein binding to human glutathione S-transferase A1-1: thermodynamics and inhibition kinetics. *Biochemical Journal*, **2004**, 382, 703-9	3.8	23
61	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. *Biochemical Journal*, **2000**, 345 Pt 3, 645-51	3.8	22
60	Domain-domain interface packing at conserved Trp-20 in class alpha glutathione transferase impacts on protein stability. *BBA - Proteins and Proteomics*, **2000**, 1478, 325-32		20
59	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, 383-90	4	20
58	A Lys-Trp cation-□nteraction mediates the dimerization and function of the chloride intracellular channel protein 1 transmembrane domain. *Biochemistry*, **2014**, 53, 57-67	3.2	19
57	Role of individual histidines in the pH-dependent global stability of human chloride intracellular channel 1. *Biochemistry*, **2012**, 51, 995-1004	3.2	19
56	Influence of the dimer interface on glutathione transferase structure and dynamics revealed by amide H/D exchange mass spectrometry. *Biochemistry*, **2005**, 44, 10605-12	3.2	18
55	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. *Biochemical Journal*, **2006**, 393, 523-8	3.8	18
54	Class Pi glutathione transferase unfolds via a dimeric and not monomeric intermediate: functional implications for an unstable monomer. *Biochemistry*, **2010**, 49, 5074-81	3.2	17
53	Arginine 15 stabilizes an S(N)Ar reaction transition state and the binding of anionic ligands at the active site of human glutathione transferase A1-1. *Biophysical Chemistry*, **2010**, 146, 118-25	3.5	17
52	Impact of domain interchange on conformational stability and equilibrium folding of chimeric class micro glutathione transferases. *Protein Science*, **2002**, 11, 2208-17	6.3	16
51	A conserved N-capping motif contributes significantly to the stabilization and dynamics of the C-terminal region of class Alpha glutathione S-transferases. *Journal of Biological Chemistry*, **2005**, 280, 19480-7	5.4	16
50	Aflatoxin B1 and sulphobromophthalein binding to the dimeric human glutathione S-transferase A1-1: a fluorescence spectroscopic analysis. *FEBS Journal*, **1998**, 257, 434-42		15
49	Stability of the domain interface contributes towards the catalytic function at the H-site of class alpha glutathione transferase A1-1. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2010**, 1804, 2228-33	4	14
48	The cochaperone murine stress-inducible protein 1: overexpression, purification, and characterization. *Protein Expression and Purification*, **2001**, 21, 462-9	2	14
47	High yield purification of JNK1□ and activation by in vitro reconstitution of the MEKK1□MKK4□JNK MAPK phosphorylation cascade. *Protein Expression and Purification*, **2013**, 87, 87-99	2	13
46	Role of arginine 29 and glutamic acid 81 interactions in the conformational stability of human chloride intracellular channel 1. *Biochemistry*, **2012**, 51, 7854-62	3.2	13

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44	Purification and characterisation of recombinant human eukaryotic elongation factor 1 gamma. *Protein Expression and Purification*, **2014**, 99, 70-7	2	12
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41	Characterization of the binding of 8-anilinonaphthalene sulfonate to rat class Mu GST M1-1. *Biophysical Chemistry*, **2008**, 137, 100-4	3.5	11
40	Purification and properties of an esterase from Cucurbita maxima fruit tissue. *Phytochemistry*, **1989**, 28, 379-383	4	11
39	A Single Amino Acid in the Hinge Loop Region of the FOXP Forkhead Domain is Significant for Dimerisation. *Protein Journal*, **2015**, 34, 111-21	3.9	10
38	Molecular dynamics and ligand docking of a hinge region variant of South African HIV-1 subtype C protease. *Journal of Molecular Graphics and Modelling*, **2018**, 82, 1-11	2.8	10
37	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 (Pt 2), 413-8	3.8	10
36	Conformational stability of Cys45-alkylated and hydrogen peroxide-oxidised glutathione S-transferase. *FEBS Letters*, **1995**, 371, 94-8	3.8	9
35	Solvent effects on the spectroscopic properties of aflatoxin B1. *International Journal of Biochemistry & Cell Biology*, **1987**, 19, 1137-40		9
34	S-nitrosation of glutathione transferase p1-1 is controlled by the conformation of a dynamic active site helix. *Journal of Biological Chemistry*, **2013**, 288, 14973-84	5.4	8
33	Electrostatic interactions affecting the active site of class Sigma glutathione S-transferase. *Biochemical Journal*, **2000**, 347, 193	3.8	8
32	S-Nitrosation destabilizes glutathione transferase P1-1. *Biochemistry*, **2013**, 52, 9394-402	3.2	7
31	The Lyssavirus glycoprotein: A key to cross-immunity. *Virology*, **2016**, 498, 250-256	3.6	6
30	Phosphorylation- and nucleotide-binding-induced changes to the stability and hydrogen exchange patterns of JNK1▯ provide insight into its mechanisms of activation. *Journal of Molecular Biology*, **2014**, 426, 3569-89	6.5	6
29	Membrane mimetics induce helix formation and oligomerization of the chloride intracellular channel protein 1 transmembrane domain. *Biochemistry*, **2013**, 52, 2739-49	3.2	6
28	Purification and partial characterization of the glutathione S-transferase of rat erythrocytes. *BBA - Proteins and Proteomics*, **1988**, 957, 173-7		6

27	A conserved cationic motif enhances membrane binding and insertion of the chloride intracellular channel protein 1 transmembrane domain. *European Biophysics Journal*, **2014**, 43, 405-14	1.9	5
26	The FOXP2 forkhead domain binds to a variety of DNA sequences with different rates and affinities. *Journal of Biochemistry*, **2017**, 162, 45-54	3.1	5
25	Amide hydrogen exchange in HIV-1 subtype B and C proteases--insights into reduced drug susceptibility and dimer stability. *FEBS Journal*, **2014**, 281, 5395-410	5.7	5
24	JNK1▯ is phosphorylated during expression in E. coli and in vitro by MKK4 at three identical novel sites. *Biochemical and Biophysical Research Communications*, **2013**, 432, 683-8	3.4	4
23	The isomerization of ▯-androstene-3,17-dione by the human glutathione transferase A3-3 proceeds via a conjugated heteroannular diene intermediate. *Journal of Biological Chemistry*, **2014**, 289, 32243-32252	5.4	4
22	A conserved interdomain interaction is a determinant of folding cooperativity in the GST fold. *Biochemistry*, **2011**, 50, 7067-75	3.2	4
21	X-ray structure methods for glutathione binding. *Methods in Enzymology*, **1995**, 251, 243-54	1.7	4
20	The effects of mutating Tyr9 and Arg15 on the structure, stability, conformational dynamics and mechanism of GSTA3-3. *Biophysical Chemistry*, **2017**, 224, 40-48	3.5	3
19	The kinetics of the substitution of coordinated H2O on Co(III) by cyanide in aquacobalamin (vitamin B12a) and in a corrole analogue. *Inorganic Chemistry Communication*, **2015**, 57, 15-17	3.1	3
18	An update on the biophysical character of the human eukaryotic elongation factor 1 beta: Perspectives from interaction with elongation factor 1 gamma. *Journal of Molecular Recognition*, **2018**, 31, e2708	2.6	3
17	A Phosphomimetic Study Implicates Ser557 in Regulation of FOXP2 DNA Binding. *Protein Journal*, **2018**, 37, 311-323	3.9	3
16	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. *Protein Journal*, **2018**, 37, 369-379	3.9	3
15	The forkhead domain hinge-loop plays a pivotal role in DNA binding and transcriptional activity of FOXP2. *Biological Chemistry*, **2018**, 399, 881-893	4.5	3
14	Energetics of ligand binding to human glutathione transferase A1-1: Tyr-9 associated localisation of the C-terminal helix is ligand-dependent. *Biophysical Chemistry*, **2011**, 156, 153-8	3.5	3
13	The role of a topologically conserved isoleucine in glutathione transferase structure, stability and function. *Acta Crystallographica Section F: Structural Biology Communications*, **2010**, 66, 776-80		3
12	Characterization of the aflatoxin B1-binding site of rat albumin. *BBA - Proteins and Proteomics*, **1987** , 913, 300-7		3
11	Energetics of Glutathione Binding to Human Eukaryotic Elongation Factor 1 Gamma: Isothermal Titration Calorimetry and Molecular Dynamics Studies. *Protein Journal*, **2016**, 35, 448-458	3.9	2
10	F99 is critical for dimerization and activation of South African HIV-1 subtype C protease. *Protein Journal*, **2013**, 32, 560-7	3.9	2

9	Stability and unfolding of reduced Escherichia coli glutaredoxin 2: a monomeric structural homologue of the glutathione transferase family. *Biochemistry*, **2008**, 47, 10801-8	3.2	2
8	Molecular basis of inhibition of Schistosoma japonicum glutathione transferase by ellagic acid: Insights into biophysical and structural studies. *Molecular and Biochemical Parasitology*, **2020**, 240, 111319	1.9	2
7	Double trouble? Gag in conjunction with double insert in HIV protease contributes to reduced DRV susceptibility. *Biochemical Journal*, **2019**, 476, 375-384	3.8	2
6	The study of degradation mechanisms of glyco-engineered plant produced anti-rabies monoclonal antibodies E559 and 62-71-3. *PLoS ONE*, **2018**, 13, e0209373	3.7	2
5	A conserved cation binding site in the DNA binding domain of forkhead box transcription factors regulates DNA binding by FOXP2. *Archives of Biochemistry and Biophysics*, **2018**, 657, 56-64	4.1	2
4	Accessibility of the tryptophan residues and flavin prosthetic group of □cyclopiazonate oxidocyclase to solvent studied by fluorescence quenching. *International Journal of Biochemistry & Cell Biology*, **1988**, 20, 109-111		1
3	Drug susceptibility and replication capacity of a rare HIV-1 subtype C protease hinge region variant. *Antiviral Therapy*, **2019**, 24, 333-342	1.6	1
2	An empirical and theoretical description of Schistosoma japonicum glutathione transferase inhibition by bromosulfophthalein and indanyloxyacetic acid 94. *Journal of Molecular Structure*, **2021**, 1223, 128892	3.4	0
1	X-ray crystal structures of cytosolic glutathione S-transferases **1994**, 57-73		