

Rik K Wierenga

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99 papers	4,764 citations	35 h-index	67 g-index
100 ext. papers	5,102 ext. citations	5.2 avg, IF	4.95 L-index

#	Paper	IF	Citations
99	Prediction of the occurrence of the ADP-binding beta alpha beta-fold in proteins, using an amino acid sequence fingerprint. <i>Journal of Molecular Biology</i> , 1986 , 187, 101-7	6.5	1104
98	Crystal structure of a Src-homology 3 (SH3) domain. <i>Nature</i> , 1992 , 359, 851-5	50.4	436
97	The biochemistry of peroxisomal beta-oxidation in the yeast <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Reviews</i> , 2003 , 27, 35-64	15.1	231
96	The thiolase superfamily: condensing enzymes with diverse reaction specificities. <i>Trends in Biochemical Sciences</i> , 2006 , 31, 64-71	10.3	126
95	The crystal structure of triosephosphate isomerase (TIM) from <i>Thermotoga maritima</i> : A comparative thermostability structural analysis of ten different TIM structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 441-453	4.2	119
94	Triose-phosphate isomerase (TIM) of the psychrophilic bacterium <i>Vibrio marinus</i> . Kinetic and structural properties. <i>Journal of Biological Chemistry</i> , 1998 , 273, 2199-206	5.4	111
93	The crystal structure of enoyl-CoA hydratase complexed with octanoyl-CoA reveals the structural adaptations required for binding of a long chain fatty acid-CoA molecule. <i>Journal of Molecular Biology</i> , 1998 , 275, 847-59	6.5	99
92	The 1.8 Å crystal structure of the dimeric peroxisomal 3-ketoacyl-CoA thiolase of <i>Saccharomyces cerevisiae</i> : implications for substrate binding and reaction mechanism. <i>Journal of Molecular Biology</i> , 1997 , 273, 714-28	6.5	98
91	Crystallographic analysis of the reaction pathway of <i>Zoogloea ramigera</i> biosynthetic thiolase. <i>Journal of Molecular Biology</i> , 2000 , 297, 1171-82	6.5	92
90	Kinetic properties of triose-phosphate isomerase from <i>Trypanosoma brucei brucei</i> . A comparison with the rabbit muscle and yeast enzymes. <i>FEBS Journal</i> , 1987 , 168, 69-74		85
89	Structural and mutagenesis studies of leishmania triosephosphate isomerase: a point mutation can convert a mesophilic enzyme into a superstable enzyme without losing catalytic power. <i>Protein Engineering, Design and Selection</i> , 1999 , 12, 243-50	1.9	81
88	The crystal structure of dienoyl-CoA isomerase at 1.5 Å resolution reveals the importance of aspartate and glutamate sidechains for catalysis. <i>Structure</i> , 1998 , 6, 957-70	5.2	80
87	Crystal structure of triosephosphate isomerase complexed with 2-phosphoglycolate at 0.83-Å resolution. <i>Journal of Biological Chemistry</i> , 2003 , 278, 9544-51	5.4	79
86	The crystal structure of the "open" and the "closed" conformation of the flexible loop of trypanosomal triosephosphate isomerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 10, 33-49	4.2	79
85	The adaptability of the active site of trypanosomal triosephosphate isomerase as observed in the crystal structures of three different complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 10, 50-69	4.2	71
84	Crystallographic and kinetic studies of human mitochondrial acetoacetyl-CoA thiolase: the importance of potassium and chloride ions for its structure and function. <i>Biochemistry</i> , 2007 , 46, 4305-21	3.2	69
83	The cytosolic and glycosomal isoenzymes of glyceraldehyde-3-phosphate dehydrogenase in <i>Trypanosoma brucei</i> have a distant evolutionary relationship. <i>FEBS Journal</i> , 1991 , 198, 421-8		69

82	A biosynthetic thiolase in complex with a reaction intermediate: the crystal structure provides new insights into the catalytic mechanism. <i>Structure</i> , 1999 , 7, 1279-90	5.2	68
81	A double mutation at the tip of the dimer interface loop of triosephosphate isomerase generates active monomers with reduced stability. <i>Biochemistry</i> , 1997 , 36, 9655-62	3.2	66
80	The catalytic cycle of biosynthetic thiolase: a conformational journey of an acetyl group through four binding modes and two oxyanion holes. <i>Biochemistry</i> , 2002 , 41, 15543-56	3.2	59
79	Overexpression of trypanosomal triosephosphate isomerase in Escherichia coli and characterisation of a dimer-interface mutant. <i>FEBS Journal</i> , 1993 , 211, 703-10		58
78	Structures of the "open" and "closed" state of trypanosomal triosephosphate isomerase, as observed in a new crystal form: implications for the reaction mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 16, 311-26	4.2	53
77	High resolution crystal structures of human cytosolic thiolase (CT): a comparison of the active sites of human CT, bacterial thiolase, and bacterial KAS I. <i>Journal of Molecular Biology</i> , 2005 , 347, 189-201	6.5	50
76	The thiolase reaction mechanism: the importance of Asn316 and His348 for stabilizing the enolate intermediate of the Claisen condensation. <i>Biochemistry</i> , 2009 , 48, 11011-25	3.2	49
75	The active site of an algal prolyl 4-hydroxylase has a large structural plasticity. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37112-23	5.4	49
74	The crystal structure of an algal prolyl 4-hydroxylase complexed with a proline-rich peptide reveals a novel buried tripeptide binding motif. <i>Journal of Biological Chemistry</i> , 2009 , 284, 25290-301	5.4	47
73	Mutagenic and enzymological studies of the hydratase and isomerase activities of 2-enoyl-CoA hydratase-1. <i>Biochemistry</i> , 1999 , 38, 2991-9	3.2	47
72	The crystal structure of delta(3)-delta(2)-enoyl-CoA isomerase. <i>Journal of Molecular Biology</i> , 2001 , 309, 845-53	6.5	45
71	The ionization of a buried glutamic acid is thermodynamically linked to the stability of Leishmania mexicana triose phosphate isomerase. <i>FEBS Journal</i> , 2000 , 267, 2516-24		44
70	Selective Inhibition of Trypanosomal Triosephosphate Isomerase by a Thiopeptide. <i>Angewandte Chemie International Edition in English</i> , 1992 , 31, 328-330		41
69	Active site properties of monomeric triosephosphate isomerase (monoTIM) as deduced from mutational and structural studies. <i>Protein Science</i> , 1996 , 5, 229-39	6.3	40
68	The 1.3 Å crystal structure of human mitochondrial Delta3-Delta2-enoyl-CoA isomerase shows a novel mode of binding for the fatty acyl group. <i>Journal of Molecular Biology</i> , 2004 , 342, 1197-208	6.5	36
67	Three new crystal structures of point mutation variants of monoTIM: conformational flexibility of loop-1, loop-4 and loop-8. <i>Structure</i> , 1995 , 3, 669-79	5.2	36
66	Atomic resolution crystallography of a complex of triosephosphate isomerase with a reaction-intermediate analog: new insight in the proton transfer reaction mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 1878-88	4.2	35
65	Alpha-methylacyl-CoA racemase from Mycobacterium tuberculosis. Mutational and structural characterization of the active site and the fold. <i>Journal of Biological Chemistry</i> , 2005 , 280, 12611-20	5.4	35

64	Functional role of the conserved active site proline of triosephosphate isomerase. <i>Biochemistry</i> , 2006 , 45, 15483-94	3.2	34
63	The catalysis of the 1,1-proton transfer by alpha-methyl-acyl-CoA racemase is coupled to a movement of the fatty acyl moiety over a hydrophobic, methionine-rich surface. <i>Journal of Molecular Biology</i> , 2007 , 367, 1145-61	6.5	33
62	Structural determinants for ligand binding and catalysis of triosephosphate isomerase. <i>FEBS Journal</i> , 2001 , 268, 5189-96		33
61	Triose-phosphate isomerase of <i>Leishmania mexicana mexicana</i> . Cloning and characterization of the gene, overexpression in <i>Escherichia coli</i> and analysis of the protein. <i>FEBS Journal</i> , 1994 , 220, 331-8		33
60	Structural biology of the thioester-dependent degradation and synthesis of fatty acids. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 621-8	8.1	32
59	The importance of the conserved Arg191-Asp227 salt bridge of triosephosphate isomerase for folding, stability, and catalysis. <i>FEBS Letters</i> , 2002 , 518, 39-42	3.8	30
58	The purification and characterization of the catalytic domain of Src expressed in <i>Schizosaccharomyces pombe</i> . Comparison of unphosphorylated and tyrosine phosphorylated species. <i>FEBS Journal</i> , 1996 , 240, 756-64		29
57	High resolution crystal structures of unliganded and liganded human liver ACBP reveal a new mode of binding for the acyl-CoA ligand. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 66, 229-38	4.2	28
56	The peptide-substrate-binding domain of collagen prolyl 4-hydroxylases is a tetratricopeptide repeat domain with functional aromatic residues. <i>Journal of Biological Chemistry</i> , 2004 , 279, 52255-61	5.4	28
55	Insights into mitochondrial fatty acid synthesis from the structure of heterotetrameric 3-ketoacyl-ACP reductase/3R-hydroxyacyl-CoA dehydrogenase. <i>Nature Communications</i> , 2014 , 5, 4805	17.4	27
54	The structural motifs for substrate binding and dimerization of the β subunit of collagen prolyl 4-hydroxylase. <i>Structure</i> , 2013 , 21, 2107-18	5.2	25
53	Structure of mycobacterial α -oxidation trifunctional enzyme reveals its altered assembly and putative substrate channeling pathway. <i>ACS Chemical Biology</i> , 2013 , 8, 1063-73	4.9	24
52	Structural mutations that probe the interactions between the catalytic and dianion activation sites of triosephosphate isomerase. <i>Biochemistry</i> , 2013 , 52, 5928-40	3.2	24
51	Modeling, mutagenesis, and structural studies on the fully conserved phosphate-binding loop (loop 8) of triosephosphate isomerase: toward a new substrate specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 383-9	4.2	24
50	Anion binding at the active site of trypanosomal triosephosphate isomerase. Monohydrogen phosphate does not mimic sulphate. <i>FEBS Journal</i> , 1991 , 198, 53-7		23
49	Phylogenetic relationships and classification of thiolases and thiolase-like proteins of <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium smegmatis</i> . <i>Tuberculosis</i> , 2014 , 94, 405-12	2.6	22
48	The isomerase and hydratase reaction mechanism of the crotonase active site of the multifunctional enzyme (type-1), as deduced from structures of complexes with 3S-hydroxy-acyl-CoA. <i>FEBS Journal</i> , 2013 , 280, 3160-75	5.7	20
47	Crystal structure of liganded rat peroxisomal multifunctional enzyme type 1: a flexible molecule with two interconnected active sites. <i>Journal of Biological Chemistry</i> , 2010 , 285, 24089-98	5.4	20

46	Structural studies on delta(3)-delta(2)-enoyl-CoA isomerase: the variable mode of assembly of the trimeric disks of the crotonase superfamily. <i>FEBS Letters</i> , 2004 , 557, 81-7	3.8	20
45	The crystal structure of human mitochondrial 3-ketoacyl-CoA thiolase (T1): insight into the reaction mechanism of its thiolase and thioesterase activities. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 3212-25		19
44	The first case in Asia of 2-methyl-3-hydroxybutyryl-CoA dehydrogenase deficiency (HSD10 disease) with atypical presentation. <i>Journal of Human Genetics</i> , 2014 , 59, 609-14	4.3	18
43	Organization of the multifunctional enzyme type 1: interaction between N- and C-terminal domains is required for the hydratase-1/isomerase activity. <i>Biochemical Journal</i> , 2002 , 367, 433-41	3.8	18
42	Comparison of the structures and the crystal contacts of trypanosomal triosephosphate isomerase in four different crystal forms. <i>Protein Science</i> , 1994 , 3, 779-87	6.3	18
41	ATGme: Open-source web application for rare codon identification and custom DNA sequence optimization. <i>BMC Bioinformatics</i> , 2015 , 16, 303	3.6	17
40	Kinetic and expression analyses of seven novel mutations in mitochondrial acetoacetyl-CoA thiolase (T2): identification of a Km mutant and an analysis of the mutational sites in the structure. <i>Molecular Genetics and Metabolism</i> , 2007 , 90, 370-8	3.7	16
39	Structure-Function Studies of Hydrophobic Residues That Clamp a Basic Glutamate Side Chain during Catalysis by Triosephosphate Isomerase. <i>Biochemistry</i> , 2016 , 55, 3036-47	3.2	15
38	The sulfur atoms of the substrate CoA and the catalytic cysteine are required for a productive mode of substrate binding in bacterial biosynthetic thiolase, a thioester-dependent enzyme. <i>FEBS Journal</i> , 2008 , 275, 6136-48	5.7	15
37	Inhibition of triosephosphate isomerase from <i>Trypanosoma brucei</i> with cyclic hexapeptides. <i>FEBS Journal</i> , 1992 , 207, 441-7		15
36	De novo biosynthesis of sterols and fatty acids in the <i>Trypanosoma brucei</i> procyclic form: Carbon source preferences and metabolic flux redistributions. <i>PLoS Pathogens</i> , 2018 , 14, e1007116	7.6	14
35	The enolization chemistry of a thioester-dependent racemase: the 1.4 Å crystal structure of a reaction intermediate complex characterized by detailed QM/MM calculations. <i>Journal of Physical Chemistry B</i> , 2012 , 116, 3619-29	3.4	14
34	Crystal structures of SCP2-thiolases of Trypanosomatidae, human pathogens causing widespread tropical diseases: the importance for catalysis of the cysteine of the unique HDCF loop. <i>Biochemical Journal</i> , 2013 , 455, 119-30	3.8	14
33	The characterization and evolutionary relationships of a trypanosomal thiolase. <i>International Journal for Parasitology</i> , 2011 , 41, 1273-83	4.3	14
32	Oxyanion Holes and Their Mimics		14
31	Stereoelectronic requirements for optimal hydrogen-bond-catalyzed enolization. <i>Chemistry - A European Journal</i> , 2011 , 17, 2859-66	4.8	13
30	Human Δ ³ -enoyl-CoA isomerase, type 2: a structural enzymology study on the catalytic role of its ACBP domain and helix-10. <i>FEBS Journal</i> , 2015 , 282, 746-68	5.7	12
29	Crystallization and preliminary X-ray diffraction studies of an alpha-methylacyl-CoA racemase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 353-5		12

28	Structure-based protein engineering efforts with a monomeric TIM variant: the importance of a single point mutation for generating an active site with suitable binding properties. <i>Protein Engineering, Design and Selection</i> , 2008 , 21, 257-66	1.9	11
27	Crystallographic binding studies with an engineered monomeric variant of triosephosphate isomerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 934-44		10
26	Structural studies show that the A178L mutation in the C-terminal hinge of the catalytic loop-6 of triosephosphate isomerase (TIM) induces a closed-like conformation in dimeric and monomeric TIM. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , 64, 178-88		9
25	Assembly of the elongated collagen prolyl 4-hydroxylase \square heterotetramer around a central \square dimer. <i>Biochemical Journal</i> , 2017 , 474, 751-769	3.8	8
24	High resolution crystal structures of triosephosphate isomerase complexed with its suicide inhibitors: the conformational flexibility of the catalytic glutamate in its closed, liganded active site. <i>Protein Science</i> , 2011 , 20, 1387-97	6.3	8
23	Structural studies of MFE-1: the 1.9 Å crystal structure of the dehydrogenase part of rat peroxisomal MFE-1. <i>Journal of Molecular Biology</i> , 2006 , 355, 734-46	6.5	7
22	Crystal structure of a thiolase from Escherichia coli at 1.8 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 534-44	1.1	6
21	The peroxisomal zebrafish SCP2-thiolase (type-1) is a weak transient dimer as revealed by crystal structures and native mass spectrometry. <i>Biochemical Journal</i> , 2019 , 476, 307-332	3.8	6
20	Structure-based directed evolution of a monomeric triosephosphate isomerase: toward a pentose sugar isomerase. <i>Protein Engineering, Design and Selection</i> , 2015 , 28, 187-97	1.9	5
19	Structures of yeast peroxisomal (B),(2)-enoyl-CoA isomerase complexed with acyl-CoA substrate analogues: the importance of hydrogen-bond networks for the reactivity of the catalytic base and the oxyanion hole. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 2178-91		5
18	Crystallization and characterization of the dehydrogenase domain from rat peroxisomal multifunctional enzyme type 1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 690-3		5
17	Insights into the stability and substrate specificity of the E. coli aerobic \square -oxidation trifunctional enzyme complex. <i>Journal of Structural Biology</i> , 2020 , 210, 107494	3.4	4
16	Structural enzymology binding studies of the peptide-substrate-binding domain of human collagen prolyl 4-hydroxylase (type-II): High affinity peptides have a PxGP sequence motif. <i>Protein Science</i> , 2018 , 27, 1692-1703	6.3	4
15	Crystallographic substrate binding studies of Leishmania mexicana SCP2-thiolase (type-2): unique features of oxyanion hole-1. <i>Protein Engineering, Design and Selection</i> , 2017 , 30, 225-233	1.9	3
14	Neutron structures of triosephosphate isomerase in complex with reaction-intermediate mimics shed light on the proton-shuttling steps. <i>IUCrJ</i> , 2021 , 8, 633-643	4.7	3
13	IceBear: an intuitive and versatile web application for research-data tracking from crystallization experiment to PDB deposition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 151-163	5.5	3
12	Complementary substrate specificity and distinct quaternary assembly of the aerobic and anaerobic \square -oxidation trifunctional enzyme complexes. <i>Biochemical Journal</i> , 2019 , 476, 1975-1994	3.8	2
11	Crystal structure of human anterior gradient protein 3. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 425-430	1.1	2

10	Structural enzymology comparisons of multifunctional enzyme, type-1 (MFE1): the flexibility of its dehydrogenase part. <i>FEBS Open Bio</i> , 2017 , 7, 1830-1842	2.7	2
9	The SCP2-thiolase-like protein (SLP) of <i>Trypanosoma brucei</i> is an enzyme involved in lipid metabolism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 1075-96	4.2	2
8	Structure of transmembrane prolyl 4-hydroxylase reveals unique organization of EF and dioxygenase domains. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100197	5.4	2
7	Crystallization and preliminary X-ray diffraction studies of the C-terminal domain of <i>Chlamydia trachomatis</i> CdsD. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1431-3	1.1	1
6	Crystallographic binding studies of rat peroxisomal multifunctional enzyme type 1 with 3-ketodecanoyl-CoA: capturing active and inactive states of its hydratase and dehydrogenase catalytic sites. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020 , 76, 1256-1269	5.5	1
5	The crystal structure of triosephosphate isomerase (TIM) from <i>Thermotoga maritima</i> : A comparative thermostability structural analysis of ten different TIM structures 1999 , 37, 441		1
4	Substrate specificity and conformational flexibility properties of the <i>Mycobacterium tuberculosis</i> α -oxidation trifunctional enzyme. <i>Journal of Structural Biology</i> , 2021 , 213, 107776	3.4	0
3	Crystal structures of two monomeric triosephosphate isomerase variants identified via a directed-evolution protocol selecting for L-arabinose isomerase activity. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 490-9	1.1	
2	Toward New Nonnatural TIM-Barrel Enzymes Using Computational Design and Directed Evolution Approaches 2016 , 561-611		
1	The extended structure of the periplasmic region of CdsD, a structural protein of the type III secretion system of <i>Chlamydia trachomatis</i> . <i>Protein Science</i> , 2016 , 25, 987-98	6.3	