

Ylva Lindqvist

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8695088/publications.pdf>

Version: 2024-02-01

113
papers

5,924
citations

61984

43
h-index

76900

74
g-index

119
all docs

119
docs citations

119
times ranked

5276
citing authors

#	ARTICLE	IF	CITATIONS
1	The manifold of vitamin B6 dependent enzymes. <i>Structure</i> , 2000, 8, R1-R6.	3.3	330
2	Crystal structure of nitrile hydratase reveals a novel iron centre in a novel fold. <i>Structure</i> , 1997, 5, 691-699.	3.3	294
3	Crystal structure of the active site of ribulose-bisphosphate carboxylase. <i>Nature</i> , 1989, 337, 229-234.	27.8	277
4	A thiamin diphosphate binding fold revealed by comparison of the crystal structures of transketolase, pyruvate oxidase and pyruvate decarboxylase. <i>Structure</i> , 1993, 1, 95-103.	3.3	193
5	Structure of the Complex between the Antibiotic Cerulenin and Its Target, β^2 -Ketoacyl-Acyl Carrier Protein Synthase. <i>Journal of Biological Chemistry</i> , 1999, 274, 6031-6034.	3.4	177
6	Three-dimensional structure of ribulose-1,5-bisphosphate carboxylase/oxygenase from <i>Rhodospirillum rubrum</i> at 2.9 Å... resolution. <i>EMBO Journal</i> , 1986, 5, 3409-3415.	7.8	163
7	Refined structure of spinach glycolate oxidase at 2 Å... resolution. <i>Journal of Molecular Biology</i> , 1989, 209, 151-166.	4.2	158
8	Circular permutations of natural protein sequences: structural evidence. <i>Current Opinion in Structural Biology</i> , 1997, 7, 422-427.	5.7	146
9	The crystal structure of phenol hydroxylase in complex with FAD and phenol provides evidence for a concerted conformational change in the enzyme and its cofactor during catalysis. <i>Structure</i> , 1998, 6, 605-617.	3.3	144
10	Crystal structure of scytalone dehydratase – a disease determinant of the rice pathogen, <i>Magnaporthe grisea</i> . <i>Structure</i> , 1994, 2, 937-944.	3.3	143
11	The enzymes of oxalate metabolism: unexpected structures and mechanisms. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 176-192.	3.0	141
12	Three-dimensional structure of a mammalian purple acid phosphatase at 2.2 Å... resolution with a $\frac{1}{4}$ -(hydr)oxo bridged di-iron center. <i>Journal of Molecular Biology</i> , 1999, 291, 135-147.	4.2	132
13	Crystal structures of rat acid phosphatase complexed with the transition-state analogs vanadate and molybdate. Implications for the reaction mechanism. <i>FEBS Journal</i> , 1994, 221, 139-142.	0.2	125
14	Crystallographic refinement and structure of ribulose-1,5-bisphosphate carboxylase from <i>Rhodospirillum rubrum</i> at 1.7 Å... resolution. <i>Journal of Molecular Biology</i> , 1990, 211, 989-1008.	4.2	114
15	Novel disease-causing mutations in the dihydropyrimidine dehydrogenase gene interpreted by analysis of the three-dimensional protein structure. <i>Biochemical Journal</i> , 2002, 364, 157-163.	3.7	102
16	Crystal structure of the FAD-containing fragment of corn nitrate reductase at 2.5 Å resolution: relationship to other flavoprotein reductases. <i>Structure</i> , 1994, 2, 809-821.	3.3	99
17	Crystal structure of diaminopelargonic acid synthase: evolutionary relationships between pyridoxal-5-phosphate-dependent enzymes. <i>Journal of Molecular Biology</i> , 1999, 291, 857-876.	4.2	99
18	Examination of Substrate Binding in Thiamin Diphosphate- dependent Transketolase by Protein Crystallography and Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 1997, 272, 1864-1869.	3.4	98

#	ARTICLE	IF	CITATIONS
19	Structural Studies on Corn Nitrate Reductase: Refined Structure of the Cytochrome b ₅ Reductase Fragment at 2.5 Å..., its ADP Complex and an Active-site Mutant and Modeling of the Cytochrome b ₅ Domain. <i>Journal of Molecular Biology</i> , 1995, 248, 931-948.	4.2	93
20	Three-dimensional structure of human tissue inhibitor of metalloproteinases-2 at 2.1 Å... resolution. <i>Journal of Molecular Biology</i> , 1998, 284, 1133-1140.	4.2	91
21	Crystal structure of the ternary complex of 1,3,8-trihydroxynaphthalene reductase from <i>Magnaporthe grisea</i> with NADPH and an active-site inhibitor. <i>Structure</i> , 1996, 4, 1161-1170.	3.3	89
22	Crystallography and mutagenesis of transketolase: mechanistic implications for enzymatic thiamin catalysis. <i>BBA - Proteins and Proteomics</i> , 1998, 1385, 387-398.	2.1	85
23	Conversion of a β -Ketoacyl Synthase to a Malonyl Decarboxylase by Replacement of the Active-Site Cysteine with Glutamine. <i>Biochemistry</i> , 1999, 38, 11643-11650.	2.5	84
24	Crystal structure of transaldolase B from <i>Escherichia coli</i> suggests a circular permutation of the β / β ² barrel within the class I aldolase family. <i>Structure</i> , 1996, 4, 715-724.	3.3	80
25	Crystal Structure of the Carbohydrate Recognition Domain of p58/ERGIC-53, a Protein Involved in Glycoprotein Export from the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2002, 277, 15979-15984.	3.4	80
26	Identification of Catalytically Important Residues in Yeast Transketolase. <i>Biochemistry</i> , 1997, 36, 15643-15649.	2.5	75
27	Crystal structure of the reduced Schiff base intermediate complex of transaldolase B from <i>Escherichia coli</i> : Mechanistic implications for class I aldolases. <i>Protein Science</i> , 1997, 6, 119-124.	7.6	67
28	The crystal structure of β -ketoacyl-acyl carrier protein synthase II from <i>Synechocystis</i> sp. at 1.54 Å... resolution and its relationship to other condensing enzymes. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 305, 491-503.	4.2	66
29	Mechanism of an ATP-Dependent Carboxylase, Dethiobiotin Synthetase, Based on Crystallographic Studies of Complexes with Substrates and a Reaction Intermediate. <i>Biochemistry</i> , 1995, 34, 10985-10995.	2.5	63
30	Half-of-the-Sites Reactivity of the Castor Δ^9 -18:0-Acyl Carrier Protein Desaturase. <i>Plant Physiology</i> , 2015, 169, 432-441.	4.8	63
31	Three-dimensional structures of glycolate oxidase with bound active-site inhibitors. <i>Protein Science</i> , 1997, 6, 1009-1015.	7.6	60
32	The Crystal Structure of the Carbohydrate-recognition Domain of the Glycoprotein Sorting Receptor p58/ERGIC-53 Reveals an Unpredicted Metal-binding Site and Conformational Changes Associated with Calcium Ion Binding. <i>Journal of Molecular Biology</i> , 2003, 334, 845-851.	4.2	56
33	Structural Basis for Activation of the Thiamin Diphosphate-dependent Enzyme Oxalyl-CoA Decarboxylase by Adenosine Diphosphate*. <i>Journal of Biological Chemistry</i> , 2005, 280, 41645-41654.	3.4	54
34	Crystal Structure of the Productive Ternary Complex of Dihydropyrimidine Dehydrogenase with NADPH and 5-Iodouracil. <i>Journal of Biological Chemistry</i> , 2002, 277, 13155-13166.	3.4	51
35	Kinetic and Mechanistic Characterization of the Formyl-CoA Transferase from <i>Oxalobacter formigenes</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 36003-36012.	3.4	51
36	<i>Saccharomyces cerevisiae</i> phospholipid:diacylglycerol acyl transferase (PDAT) devoid of its membrane anchor region is a soluble and active enzyme retaining its substrate specificities. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2007, 1771, 1457-1463.	2.4	51

#	ARTICLE	IF	CITATIONS
37	Trihydroxynaphthalene Reductase from <i>Magnaporthe grisea</i> : A Realization of an Active Center Inhibitor and Elucidation of the Kinetic Mechanism. <i>Biochemistry</i> , 1997, 36, 1852-1860.	2.5	47
38	Phosphatase and Oxygen Radical-Generating Activities of Mammalian Purple Acid Phosphatase Are Functionally Independent. <i>Biochemical and Biophysical Research Communications</i> , 2002, 292, 128-132.	2.1	47
39	Transketolase from <i>Leishmania mexicana</i> has a dual subcellular localization. <i>Biochemical Journal</i> , 2004, 382, 759-767.	3.7	47
40	Crystallographic Snapshots of Oxalyl-CoA Decarboxylase Give Insights into Catalysis by Nonoxidative ThDP-Dependent Decarboxylases. <i>Structure</i> , 2007, 15, 853-861.	3.3	47
41	Crystal structure of transketolase in complex with thiamine thiazolone diphosphate, an analogue of the reaction intermediate, at 2.3 Å... resolution. <i>FEBS Letters</i> , 1993, 326, 145-148.	2.8	45
42	Formyl-CoA transferase encloses the CoA binding site at the interface of an interlocked dimer. <i>EMBO Journal</i> , 2003, 22, 3210-3219.	7.8	45
43	Involvement of Tyr24 and Trp108 in Substrate Binding and Substrate Specificity of Glycolate Oxidase. <i>FEBS Journal</i> , 1995, 228, 408-416.	0.2	45
44	Divergent non-heme iron enzymes in the nogalamycin biosynthetic pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5251-5256.	7.1	44
45	Thiamin diphosphate dependent enzymes: transketolase, pyruvate oxidase and pyruvate decarboxylase. <i>Current Opinion in Structural Biology</i> , 1993, 3, 896-901.	5.7	43
46	Crystal Structure of Saccharopine Reductase from <i>Magnaporthe grisea</i> , an Enzyme of the $\hat{\pm}$ -Aminoacidate Pathway of Lysine Biosynthesis. <i>Structure</i> , 2000, 8, 1037-1047.	3.3	43
47	Crystal structure of an ATP-dependent carboxylase, dethiobiotin synthetase, at 1.65 Å resolution. <i>Structure</i> , 1994, 2, 407-414.	3.3	42
48	Protein-biotin interactions. <i>Current Opinion in Structural Biology</i> , 1996, 6, 798-803.	5.7	41
49	Structural Basis for the Thioredoxin-like Activity Profile of the Glutaredoxin-like NrdH-redoxin from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 35836-35841.	3.4	41
50	His103 in Yeast Transketolase is Required for Substrate Recognition and Catalysis. <i>FEBS Journal</i> , 1995, 233, 750-755.	0.2	38
51	Crystal Structure of Aclacinomycin-10-Hydroxylase, a S-Adenosyl-L-Methionine-dependent Methyltransferase Homolog Involved in Anthracycline Biosynthesis in <i>Streptomyces purpurascens</i> . <i>Journal of Molecular Biology</i> , 2003, 334, 269-280.	4.2	38
52	Dihydropyrimidine dehydrogenase: a flavoprotein with four iron-sulfur clusters. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1701, 61-74.	2.3	38
53	Structural Basis for Substrate Recognition and Specificity in Aklavinone-11-Hydroxylase from Rhodomycin Biosynthesis. <i>Journal of Molecular Biology</i> , 2009, 393, 966-977.	4.2	38
54	The EAL-like protein STM1697 regulates virulence phenotypes, motility and biofilm formation in <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 2013, 90, 1216-1232.	2.5	38

#	ARTICLE	IF	CITATIONS
55	Discovery of an Allosteric Inhibitor Binding Site in 3-Oxo-acyl-ACP Reductase from <i>Pseudomonas aeruginosa</i> . ACS Chemical Biology, 2013, 8, 2518-2527.	3.4	38
56	Structure of glycolate oxidase from spinach at a resolution of 5.5 Å.... Journal of Molecular Biology, 1980, 143, 201-211.	4.2	37
57	Conformational Changes During the Catalytic Cycle of Gluconate Kinase as Revealed by X-ray Crystallography. Journal of Molecular Biology, 2002, 318, 1057-1069.	4.2	37
58	New Insights into Multiple Coagulation Factor Deficiency from the Solution Structure of Human MCFD2. Journal of Molecular Biology, 2008, 381, 941-955.	4.2	37
59	Primary structure of glycolate oxidase from spinach. FEBS Journal, 1988, 173, 523-527.	0.2	36
60	Role of tyrosine 129 in the active site of spinach glycolate oxidase. FEBS Journal, 1993, 213, 1047-1054.	0.2	36
61	Structure of Ldt _{Mt2} , an L _D -D-transpeptidase from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 432-441.	2.5	36
62	A novel protein quality control mechanism contributes to heat shock resistance of worldwide distributed <i>Pseudomonas aeruginosa</i> clone C strains. Environmental Microbiology, 2015, 17, 4511-4526.	3.8	36
63	High-resolution structures of scytalone dehydratase-inhibitor complexes crystallized at physiological pH. , 1999, 35, 425-439.		35
64	Structure of dethiobiotin synthetase at 0.97 Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 610-624.	2.5	34
65	Structural enzymology of biotin biosynthesis. FEBS Letters, 2001, 495, 7-11.	2.8	34
66	Crystal structure of 1-deoxy-d-xylulose-5-phosphate reductoisomerase from <i>Zymomonas mobilis</i> at 1.9 Å... resolution. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1698, 37-44.	2.3	34
67	Crystal Structure of the Cofactor-Independent Monooxygenase SnoaB from <i>Streptomyces nogalater</i> : Implications for the Reaction Mechanism. Biochemistry, 2010, 49, 934-944.	2.5	34
68	Active Site Mutants of <i>Escherichia coli</i> Dethiobiotin Synthetase: Effects of Mutations on Enzyme Catalytic and Structural Properties. Biochemistry, 1997, 36, 4751-4760.	2.5	30
69	Murine class I major histocompatibility complex H-2Dd: expression, refolding and crystallization. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 260-262.	2.5	29
70	Tartrate-Resistant Bone Acid Phosphatase: Large-Scale Production and Purification of the Recombinant Enzyme, Characterization, and Crystallization. Journal of Bone and Mineral Research, 1999, 14, 424-430.	2.8	29
71	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in <i>Salmonella typhimurium</i> . Journal of Molecular Biology, 2018, 430, 3170-3189.	4.2	29
72	The structure of the N-terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. Proteins: Structure, Function and Bioinformatics, 2018, 86, 912-923.	2.6	26

#	ARTICLE	IF	CITATIONS
73	Preliminary crystallographic data for stearyl-acyl carrier protein desaturase from castor seed. <i>Journal of Molecular Biology</i> , 1992, 225, 561-564.	4.2	25
74	A flexible lid controls access to the active site in 1,3,8-trihydroxynaphthalene reductase. <i>FEBS Letters</i> , 1997, 400, 173-176.	2.8	25
75	Structure of human glycolate oxidase in complex with the inhibitor 4-carboxy-5-[(4-chlorophenyl)sulfanyl]-1,2,3-thiadiazole. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1246-1253.	0.7	24
76	Crystal structure of the LMAN1â€CRD/MCFD2 transport receptor complex provides insight into combined deficiency of factor V and factor VIII. <i>FEBS Letters</i> , 2010, 584, 878-882.	2.8	23
77	Insights into the mechanism of dihydropyrimidine dehydrogenase from site-directed mutagenesis targeting the active site loop and redox cofactor coordination. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 2198-2206.	2.3	22
78	Studies of the Mechanism of Phenol Hydroxylase:â€‰ Effect of Mutation of Proline 364 to Serine. <i>Biochemistry</i> , 2002, 41, 13627-13636.	2.5	20
79	Crystal structure of two quaternary complexes of dethiobiotin synthetase, enzymeâ€MgADPâ€AlF₃â€diaminopelargonic acid and enzymeâ€MgADPâ€dethiobiotinâ€phosphate;7.6 implications for catalysis. <i>Protein Science</i> , 1998, 7, 2560-2566.		19
80	The design and synthesis of inhibitors of dethiobiotin synthetase as potential herbicides. , 1999, 55, 236-247.		18
81	NrdH-redoxin of <i>Corynebacterium ammoniagenes</i> forms a domain-swapped dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 613-619.	2.6	17
82	Crystal structure of apo-glycolate oxidase. <i>FEBS Letters</i> , 1993, 327, 361-365.	2.8	14
83	Crystallization and preliminary X-ray diffraction study of 1,3,8-trihydroxynaphthalene reductase from <i>Magnaporthe grisea</i> . , 1996, 24, 525-527.		13
84	Insulin-like Growth Factor II in the Mink (<i>Mustela vison</i>): Determination of a cDNA Nucleotide Sequence and Developmental Regulation of Its Expression. <i>General and Comparative Endocrinology</i> , 1993, 90, 243-250.	1.8	11
85	Crystallization and preliminary crystallographic studies of the FAD domain of corn NADH: Nitrate reductase. <i>Journal of Molecular Biology</i> , 1992, 224, 277-279.	4.2	10
86	Electrostatic fields at the active site of ribulose-1,5-bisphosphate carboxylase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 117-127.	2.6	9
87	Crystallization and Preliminary X-ray Analysis of Phenol Hydroxylase from <i>Trichosporon cutaneum</i> . <i>Journal of Molecular Biology</i> , 1994, 238, 128-130.	4.2	9
88	High-Level Expression, Purification, and Crystallization of Recombinant Spinach Glycolate Oxidase in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 1996, 8, 295-298.	1.3	9
89	Cloning, expression, purification and crystallization of saccharopine reductase from <i>Magnaporthe grisea</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 662-664.	2.5	9
90	Involvement of Tyr24 and Trp108 in Substrate Binding and Substrate Specificity of Glycolate Oxidase. <i>FEBS Journal</i> , 1995, 228, 408-416.	0.2	8

#	ARTICLE	IF	CITATIONS
91	Crystallization and preliminary X-ray study of pig liver dihydropyrimidine dehydrogenase. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 153-155.	2.5	8
92	Purification and preliminary X-ray crystallographic studies of recombinant ribulose-5-phosphate 4-epimerase from <i>Escherichia coli</i> . Protein Science, 1995, 4, 1648-1650.	7.6	7
93	Purification and preliminary X-ray crystallographic studies of recombinant 7,8-diaminopelargonic acid synthase from <i>Escherichia coli</i> . Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1397-1398.	2.5	7
94	Expression, purification, refolding and crystallization of the carbohydrate-recognition domain of p58/ERGIC-53, an animal C-type lectin involved in export of glycoproteins from the endoplasmic reticulum. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 536-538.	2.5	7
95	Crystallization and preliminary X-ray crystallographic studies of recombinant thermoresistant gluconate kinase GntK from <i>Escherichia coli</i> . Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1159-1161.	2.5	6
96	Three-dimensional model of the β -subunit of bacterial luciferase. Proteins: Structure, Function and Bioinformatics, 1995, 23, 241-255.	2.6	5
97	Crystal Structure of Bifunctional Aldos-2-Ulose Dehydratase/Isomerase from <i>Phanerochaete chrysosporium</i> with the Reaction Intermediate Ascopyrone M. Journal of Molecular Biology, 2012, 417, 279-293.	4.2	5
98	Crystallization and preliminary crystallographic analysis of formyl-CoA transferase from <i>Oxalobacter formigenes</i> . Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1276-1277.	2.5	4
99	[40] Structure of ATP-dependent carboxylase, dethiobiotin synthase. Methods in Enzymology, 1997, 279, 376-385.	1.0	3
100	Detection and characterization of merohedral twinning in crystals of oxalyl-coenzyme A decarboxylase from <i>Oxalobacter formigenes</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 122-128.	2.3	3
101	Regioselectivity mechanism of the <i>Thunbergia alata</i> Δ^6 -16:0-acyl carrier protein desaturase. Plant Physiology, 2022, 188, 1537-1549.	4.8	3
102	The structure of glycolate oxidase from spinach. , 1984, , 277-288.		1
103	Primary structure of glycolate oxidase from spinach. FEBS Journal, 1988, 173, 527-530.	0.2	0
104	Crystallization and structure of a recombinant ribulose-1,5-bisphosphate carboxylase. Journal of Crystal Growth, 1988, 90, 188-192.	1.5	0
105	CHARACTERIZATION OF GLYCOLATE OXIDASE AND AN ACTIVE SITE MUTANT. , 1991, , 119-122.		0
106	THE STRUCTURE OF GLYCOLATE OXIDASE. , 1991, , 107-114.		0
107	A New Kinase Fold. Structure, 2003, 11, 241-242.	3.3	0
108	Carl-Ivar BrändÅ©n, 1934Å©2004. Journal of Synchrotron Radiation, 2004, 11, 371-371.	2.4	0

#	ARTICLE	IF	CITATIONS
109	Going through the motions; lessons from haemoglobin, hard work driven by ATP, dealing with ammonia and frustrations in drug discovery. <i>Current Opinion in Structural Biology</i> , 2007, 17, 631-632.	5.7	0
110	X-ray Studies on Glycolate Oxidase from Spinach. , 1984, , 849-850.		0
111	Three-Dimensional Structure of Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase from <i>Rhodospirillum Rubrum</i> . , 1987, , 1-8.		0
112	Structural and Functional Aspects of Rubisco. , 1992, , 585-592.		0
113	Crystal structure of the flavoenzyme PA4991 from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 105-111.	0.8	0