

Ylva Lindqvist

List of Publications by Year in descending order

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papers

5,924
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61984

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76900

74
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119
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119
docs citations

119
times ranked

5276
citing authors

#	ARTICLE	IF	CITATIONS
1	Regioselectivity mechanism of the <i>Thunbergia alata</i> Δ^6 -16:0-acyl carrier protein desaturase. <i>Plant Physiology</i> , 2022, 188, 1537-1549.	4.8	3
2	The structure of the N-terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 912-923.	2.6	26
3	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 2018, 430, 3170-3189.	4.2	29
4	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
5	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
6	A novel protein quality control mechanism contributes to heat shock resistance of worldwide distributed <i>Pseudomonas aeruginosa</i> clone C strains. <i>Environmental Microbiology</i> , 2015, 17, 4511-4526.	3.8	36
7	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
8	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
9	Structure of Ldt _{Mt2} , an L,D-transpeptidase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 432-441.	2.5	36
10	Discovery of an Allosteric Inhibitor Binding Site in 3-Oxo-acyl-ACP Reductase from <i>Pseudomonas aeruginosa</i> . <i>ACS Chemical Biology</i> , 2013, 8, 2518-2527.	3.4	38
11	Crystal Structure of Bifunctional Aldos-2-Ulose Dehydratase/Isomerase from <i>Phanerochaete chrysosporium</i> with the Reaction Intermediate Ascopyrone M. <i>Journal of Molecular Biology</i> , 2012, 417, 279-293.	4.2	5
12	Crystal structure of the LMAN1-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
13	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
14	Crystal Structure of the Cofactor-Independent Monooxygenase SnoaB from <i>Streptomyces nogalater</i> : Implications for the Reaction Mechanism. <i>Biochemistry</i> , 2010, 49, 934-944.	2.5	34
15	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
16	Structural Basis for Substrate Recognition and Specificity in Aklavinone-11-Hydroxylase from <i>Rhodomyces</i> Biosynthesis. <i>Journal of Molecular Biology</i> , 2009, 393, 966-977.	4.2	38
17	New Insights into Multiple Coagulation Factor Deficiency from the Solution Structure of Human MCFD2. <i>Journal of Molecular Biology</i> , 2008, 381, 941-955.	4.2	37
18	<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

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19	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
20	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
21	Detection and characterization of merohedral twinning in crystals of oxalyl-coenzyme A decarboxylase from <i>Oxalobacter formigenes</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 122-128.	2.3	3
22	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
23	The enzymes of oxalate metabolism: unexpected structures and mechanisms. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 176-192.	3.0	141
24	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
25	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
26	Carl-Ivar Bränd, 1934-2004. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 371-371.	2.4	0
27	Crystal structure of 1-deoxy-d-xylulose-5-phosphate reductoisomerase from <i>Zymomonas mobilis</i> at 1.9-Å resolution. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1698, 37-44.	2.3	34
28	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
29	Transketolase from <i>Leishmania mexicana</i> has a dual subcellular localization. <i>Biochemical Journal</i> , 2004, 382, 759-767.	3.7	47
30	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
31	A New Kinase Fold. <i>Structure</i> , 2003, 11, 241-242.	3.3	0
32	Crystallization and preliminary crystallographic analysis of formyl-CoA transferase from <i>Oxalobacter formigenes</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1276-1277.	2.5	4
33	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
34	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
35	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
36	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

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37	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
38	Studies of the Mechanism of Phenol Hydroxylase: Effect of Mutation of Proline 364 to Serine. <i>Biochemistry</i> , 2002, 41, 13627-13636.	2.5	20
39	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
40	Conformational Changes During the Catalytic Cycle of Gluconate Kinase as Revealed by X-ray Crystallography. <i>Journal of Molecular Biology</i> , 2002, 318, 1057-1069.	4.2	37
41	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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 536-538.	2.5	7
42	The crystal structure of Î²-ketoacyl-acyl carrier protein synthase II from <i>Synechocystis</i> sp. at 1.54 Å... resolution and its relationship to other condensing enzymes11Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 305, 491-503.	4.2	66
43	Structural enzymology of biotin biosynthesis. <i>FEBS Letters</i> , 2001, 495, 7-11.	2.8	34
44	Crystallization and preliminary X-ray study of pig liver dihydropyrimidine dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 153-155.	2.5	8
45	Crystallization and preliminary X-ray crystallographic studies of recombinant thermoresistant gluconate kinase GntK from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1159-1161.	2.5	6
46	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
47	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
48	The manifold of vitamin B6 dependent enzymes. <i>Structure</i> , 2000, 8, R1-R6.	3.3	330
49	Crystal Structure of Saccharopine Reductase from <i>Magnaporthe grisea</i> , an Enzyme of the Î±-Amino adipate Pathway of Lysine Biosynthesis. <i>Structure</i> , 2000, 8, 1037-1047.	3.3	43
50	Structure of the Complex between the Antibiotic Cerulenin and Its Target, Î²-Ketoacyl-Acyl Carrier Protein Synthase. <i>Journal of Biological Chemistry</i> , 1999, 274, 6031-6034.	3.4	177
51	Murine class I major histocompatibility complex Hâ€²Dd: expression, refolding and crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 260-262.	2.5	29
52	Structure of dethiobiotin synthetase at 0.97â€¦Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 610-624.	2.5	34
53	Tartrate-Resistant Bone Acid Phosphatase: Large-Scale Production and Purification of the Recombinant Enzyme, Characterization, and Crystallization. <i>Journal of Bone and Mineral Research</i> , 1999, 14, 424-430.	2.8	29
54	The design and synthesis of inhibitors of dethiobiotin synthetase as potential herbicides. , 1999, 55, 236-247.		18

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55	High-resolution structures of scytalone dehydratase-inhibitor complexes crystallized at physiological pH. , 1999, 35, 425-439.		35
56	Conversion of a β^2 -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
57	Three-dimensional structure of a mammalian purple acid phosphatase at 2.2 Å... resolution with a μ_4 -(hydr)oxo bridged di-iron center. <i>Journal of Molecular Biology</i> , 1999, 291, 135-147.	4.2	132
58	Crystal structure of diaminopelargonic acid synthase: evolutionary relationships between pyridoxal-5 α -phosphate-dependent enzymes. <i>Journal of Molecular Biology</i> , 1999, 291, 857-876.	4.2	99
59	Crystallography and mutagenesis of transketolase: mechanistic implications for enzymatic thiamin catalysis. <i>BBA - Proteins and Proteomics</i> , 1998, 1385, 387-398.	2.1	85
60	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
61	Crystal structure of two quaternary complexes of dethiobiotin synthetase, enzyme \cdot MgADP \cdot AlF ₃ \cdot diaminopelargonic acid and enzyme \cdot MgADP \cdot dethiobiotin \cdot phosphate;7.6 implications for catalysis. <i>Protein Science</i> , 1998, 7, 2560-2566.		19
62	Purification and preliminary X-ray crystallographic studies of recombinant 7,8-diaminopelargonic acid synthase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1397-1398.	2.5	7
63	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
64	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
65	[40] Structure of ATP-dependent carboxylase, dethiobiotin synthase. <i>Methods in Enzymology</i> , 1997, 279, 376-385.	1.0	3
66	Trihydroxynaphthalene Reductase from <i>Magnaporthe grisea</i> : \hat{A} Realization of an Active Center Inhibitor and Elucidation of the Kinetic Mechanism. <i>Biochemistry</i> , 1997, 36, 1852-1860.	2.5	47
67	Identification of Catalytically Important Residues in Yeast Transketolase \hat{E} . <i>Biochemistry</i> , 1997, 36, 15643-15649.	2.5	75
68	Active Site Mutants of <i>Escherichia coli</i> Dethiobiotin Synthetase: \hat{A} Effects of Mutations on Enzyme Catalytic and Structural Properties. <i>Biochemistry</i> , 1997, 36, 4751-4760.	2.5	30
69	Circular permutations of natural protein sequences: structural evidence. <i>Current Opinion in Structural Biology</i> , 1997, 7, 422-427.	5.7	146
70	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
71	Crystal structure of nitrile hydratase reveals a novel iron centre in a novel fold. <i>Structure</i> , 1997, 5, 691-699.	3.3	294
72	Crystal structure of the reduced Schiff \hat{E} 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

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73	Three-dimensional structures of glycolate oxidase with bound active-site inhibitors. <i>Protein Science</i> , 1997, 6, 1009-1015.	7.6	60
74	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
75	Protein-biotin interactions. <i>Current Opinion in Structural Biology</i> , 1996, 6, 798-803.	5.7	41
76	Crystal structure of transaldolase B from <i>Escherichia coli</i> suggests a circular permutation of the β_2 barrel within the class I aldolase family. <i>Structure</i> , 1996, 4, 715-724.	3.3	80
77	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
78	Crystallization and preliminary X-ray diffraction study of 1,3,8-trihydroxynaphthalene reductase from <i>Magnaporthe grisea</i> . , 1996, 24, 525-527.		13
79	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
80	His103 in Yeast Transketolase is Required for Substrate Recognition and Catalysis. <i>FEBS Journal</i> , 1995, 233, 750-755.	0.2	38
81	Three-dimensional model of the β_2 -subunit of bacterial luciferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 241-255.	2.6	5
82	Purification and preliminary X-ray crystallographic studies of recombinant <i>Escherichia coli</i> ribulose-5-phosphate 4-epimerase from <i>Escherichia coli</i> . <i>Protein Science</i> , 1995, 4, 1648-1650.	7.6	7
83	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
84	Structural Studies on Corn Nitrate Reductase: Refined Structure of the Cytochrome b Reductase Fragment at 2.5 Å., its ADP Complex and an Active-site Mutant and Modeling of the Cytochrome b Domain. <i>Journal of Molecular Biology</i> , 1995, 248, 931-948.	4.2	93
85	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
86	Crystal structure of an ATP-dependent carboxylase, dethiobiotin synthetase, at 1.65 Å resolution. <i>Structure</i> , 1994, 2, 407-414.	3.3	42
87	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
88	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
89	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
90	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

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91	Role of tyrosine 129 in the active site of spinach glycolate oxidase. FEBS Journal, 1993, 213, 1047-1054.	0.2	36
92	A thiamin diphosphate binding fold revealed by comparison of the crystal structures of transketolase, pyruvate oxidase and pyruvate decarboxylase. Structure, 1993, 1, 95-103.	3.3	193
93	Insulin-like Growth Factor II in the Mink (<i>Mustela vison</i>): Determination of a cDNA Nucleotide Sequence and Developmental Regulation of Its Expression. General and Comparative Endocrinology, 1993, 90, 243-250.	1.8	11
94	Crystal structure of apo-glycolate oxidase. FEBS Letters, 1993, 327, 361-365.	2.8	14
95	Crystal structure of transketolase in complex with thiamine thiazolone diphosphate, an analogue of the reaction intermediate, at 2.3 Å... resolution. FEBS Letters, 1993, 326, 145-148.	2.8	45
96	Thiamin diphosphate dependent enzymes: transketolase, pyruvate oxidase and pyruvate decarboxylase. Current Opinion in Structural Biology, 1993, 3, 896-901.	5.7	43
97	Crystallization and preliminary crystallographic studies of the FAD domain of corn NADH: Nitrate reductase. Journal of Molecular Biology, 1992, 224, 277-279.	4.2	10
98	Preliminary crystallographic data for stearyl-acyl carrier protein desaturase from castor seed. Journal of Molecular Biology, 1992, 225, 561-564.	4.2	25
99	Electrostatic fields at the active site of ribulose-1,5-bisphosphate carboxylase. Proteins: Structure, Function and Bioinformatics, 1992, 12, 117-127.	2.6	9
100	Structural and Functional Aspects of Rubisco. , 1992, , 585-592.		0
101	CHARACTERIZATION OF GLYOOLATE OXIDASE AND AN ACTIVE SITE MUTANT. , 1991, , 119-122.		0
102	THE STRUCTURE OF GLYCOLATE OXIDASE. , 1991, , 107-114.		0
103	Crystallographic refinement and structure of ribulose-1,5-bisphosphate carboxylase from <i>Rhodospirillum rubrum</i> at 1.7 Å... resolution. Journal of Molecular Biology, 1990, 211, 989-1008.	4.2	114
104	Crystal structure of the active site of ribulose-bisphosphate carboxylase. Nature, 1989, 337, 229-234.	27.8	277
105	Refined structure of spinach glycolate oxidase at 2 Å... resolution. Journal of Molecular Biology, 1989, 209, 151-166.	4.2	158
106	Primary structure of glycolate oxidase from spinach. FEBS Journal, 1988, 173, 523-527.	0.2	36
107	Primary structure of glycolate oxidase from spinach. FEBS Journal, 1988, 173, 527-530.	0.2	0
108	Crystallization and structure of a recombinant ribulose-1,5-bisphosphate carboxylase. Journal of Crystal Growth, 1988, 90, 188-192.	1.5	0

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109	Three-Dimensional Structure of Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase from <i>Rhodospirillum Rubrum</i> . , 1987, , 1-8.		0
110	Three-dimensional structure of ribulose-1,5-bisphosphate carboxylase/oxygenase from <i>Rhodospirillum rubrum</i> at 2.9 Å... resolution. EMBO Journal, 1986, 5, 3409-3415.	7.8	163
111	The structure of glycolate oxidase from spinach. , 1984, , 277-288.		1
112	X-ray Studies on Glycolate Oxidase from Spinach. , 1984, , 849-850.		0
113	Structure of glycolate oxidase from spinach at a resolution of 5.5 Å.... Journal of Molecular Biology, 1980, 143, 201-211.	4.2	37