

Arne O Smalås

List of Publications by Year in descending order

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72
papers

2,300
citations

201674

27
h-index

223800

46
g-index

72
all docs

72
docs citations

72
times ranked

2015
citing authors

#	ARTICLE	IF	CITATIONS
1	Cold adapted enzymes. <i>Biotechnology Annual Review</i> , 2000, 6, 1-57.	2.1	200
2	Cold adaption of enzymes: Structural comparison between salmon and bovine trypsins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 149-166.	2.6	146
3	Interscaffolding additivity: binding of P 1 variants of bovine pancreatic trypsin inhibitor to four serine proteases 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 289, 175-186.	4.2	111
4	The hydrolytic water molecule in trypsin, revealed by time-resolved Laue crystallography. <i>Science</i> , 1993, 259, 669-673.	12.6	108
5	Temperature and pH sensitivity of trypsins from atlantic salmon (<i>Salmo salar</i>) in comparison with bovine and porcine trypsin. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 1996, 115, 33-45.	1.6	91
6	The crystal structures of the complexes between bovine \hat{I}^2 -trypsin and ten P1 variants of BPTI. <i>Journal of Molecular Biology</i> , 1999, 287, 923-942.	4.2	91
7	Structural comparison of psychrophilic and mesophilic trypsins. <i>FEBS Journal</i> , 2000, 267, 1039-1049.	0.2	83
8	Molecular Cloning and Characterization of Anionic and Cationic Variants of Trypsin from Atlantic Salmon. <i>FEBS Journal</i> , 1995, 232, 677-685.	0.2	80
9	Trypsin specificity as elucidated by LIE calculations, X-ray structures, and association constant measurements. <i>Protein Science</i> , 2004, 13, 1056-1070.	7.6	75
10	Substitutions at the P 1 $\hat{\epsilon}^2$ position in BPTI strongly affect the association energy with serine proteinases 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 301, 205-217.	4.2	71
11	Atomic resolution structures of trypsin provide insight into structural radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 488-497.	2.5	71
12	Increased Flexibility as a Strategy for Cold Adaptation. <i>Journal of Biological Chemistry</i> , 2005, 280, 18042-18048.	3.4	69
13	The structure of uracil-DNA glycosylase from Atlantic cod (<i>Gadus morhua</i>) reveals cold-adaptation features. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1357-1365.	2.5	59
14	Probing the Effect of Point Mutations at Protein-Protein Interfaces with Free Energy Calculations. <i>Biophysical Journal</i> , 2006, 90, 433-442.	0.5	59
15	Computational analysis of binding of P1 variants to trypsin. <i>Protein Science</i> , 2001, 10, 1584-1595.	7.6	47
16	Presence of acyl- ϵ -homoserine lactones in 57 members of the <i>Vibrionaceae</i> family. <i>Journal of Applied Microbiology</i> , 2013, 115, 835-847.	3.1	46
17	Comparative studies of endonuclease $\hat{\epsilon}$ fI from cold-adapted <i>Vibrio salmonicida</i> and mesophilic <i>Vibrio cholerae</i> . <i>FEBS Journal</i> , 2007, 274, 252-263.	4.7	45
18	Effect of fish skin mucus on the soluble proteome of <i>Vibrio salmonicida</i> analysed by 2-D gel electrophoresis and tandem mass spectrometry. <i>Microbial Pathogenesis</i> , 2007, 42, 36-45.	2.9	44

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19	Electrostatics of mesophilic and psychrophilic trypsin isoenzymes: Qualitative evaluation of electrostatic differences at the substrate binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 207-217.	2.6	40
20	Electrostatic effects play a central role in cold adaptation of trypsin. <i>FEBS Letters</i> , 2001, 499, 171-175.	2.8	38
21	Comparative Molecular Dynamics of Mesophilic and Psychrophilic Protein Homologues Studied by 1.2 ns Simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 1999, 17, 493-506.	3.5	32
22	The 1.8 Å crystal structure of a proteinase K-like enzyme from a psychrotroph <i>Serratia</i> species. <i>FEBS Journal</i> , 2006, 273, 61-71.	4.7	32
23	The crystal structure of anionic salmon trypsin in complex with bovine pancreatic trypsin inhibitor. <i>FEBS Journal</i> , 1998, 256, 317-324.	0.2	30
24	High-resolution structures of three new trypsin-squash-inhibitor complexes: a detailed comparison with other trypsins and their complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 139-148.	2.5	30
25	Optimisation of the Surface Electrostatics as a Strategy for Cold Adaptation of Uracil-DNA N-glycosylase (UNG) from Atlantic Cod (<i>Gadus morhua</i>). <i>Journal of Molecular Biology</i> , 2004, 343, 1221-1230.	4.2	30
26	Identification, cloning, and expression of uracil-DNA glycosylase from Atlantic cod (<i>Gadus morhua</i>): characterization and homology modeling of the cold-active catalytic domain. <i>Extremophiles</i> , 2002, 6, 73-86.	2.3	29
27	Structure of native pancreatic elastase from North Atlantic salmon at 1.61 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 925-937.	2.5	28
28	Structure of the uracil-DNA-glycosylase (UNG) from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1049-1056.	2.5	25
29	Structural adaptation of endonuclease I from the cold-adapted and halophilic bacterium <i>Vibrio salmonicida</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 368-376.	2.5	25
30	The first structure of a cold-active catalase from <i>Vibrio salmonicida</i> at 1.96 Å... reveals structural aspects of cold adaptation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 135-148.	2.5	24
31	Structure-Function Relationships in Serine Protease-Bovine Pancreatic Trypsin Inhibitor Interaction. <i>Protein and Peptide Letters</i> , 2005, 12, 403-407.	0.9	23
32	Evaluation of protein-protein association energies by free energy perturbation calculations. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 239-245.	2.1	22
33	Structure of a Non-psychrophilic Trypsin from a Cold-Adapted Fish Species. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 780-798.	2.5	21
34	Structural and functional characterization of two unusual endonuclease III enzymes from <i>Deinococcus radiodurans</i> . <i>Journal of Structural Biology</i> , 2015, 191, 87-99.	2.8	20
35	Comparative molecular dynamics simulation studies of salmon and bovine trypsins in aqueous solution. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 379-388.	2.1	19
36	The Crystal Structure of Mismatch-specific Uracil-DNA Glycosylase (MUG) from <i>Deinococcus radiodurans</i> Reveals a Novel Catalytic Residue and Broad Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2006, 281, 569-577.	3.4	19

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37	Comparative unfolding studies of psychrophilic and mesophilic uracil DNA glycosylase: MD simulations show reduced thermal stability of the cold-adapted enzyme. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 124-134.	2.4	19
38	Crystal Structures of Five Bovine Chymotrypsin Complexes with P1 BPTI Variants. <i>Journal of Molecular Biology</i> , 2004, 344, 1005-1020.	4.2	17
39	Free energy calculations show that acidic P1 variants undergo large pKa shifts upon binding to trypsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 740-748.	2.6	17
40	Crystallization and preliminary X-ray crystallographic studies of benzamidine-inhibited trypsin from the north atlantic salmon (<i>Salmo salar</i>). <i>Journal of Molecular Biology</i> , 1990, 214, 355-358.	4.2	15
41	Structural Consequences of Accommodation of Four Non-cognate Amino Acid Residues in the S1 Pocket of Bovine Trypsin and Chymotrypsin. <i>Journal of Molecular Biology</i> , 2003, 333, 845-861.	4.2	15
42	The structure of <i>Vibrio cholerae</i> extracellular endonuclease I reveals the presence of a buried chloride ion. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1387-1391.	2.5	14
43	Effects of salt on the kinetics and thermodynamic stability of endonuclease I from <i>Vibrio salmonicida</i> and <i>Vibrio cholerae</i> . <i>FEBS Journal</i> , 2008, 275, 1593-1605.	4.7	14
44	The antibody site in Atlantic salmon; phage display and modeling of scFv with anti-hapten binding ability.. <i>Developmental and Comparative Immunology</i> , 2002, 26, 201-206.	2.3	13
45	Structural evidence for lack of inhibition of fish goose-type lysozymes by a bacterial inhibitor of lysozyme. <i>Journal of Molecular Modeling</i> , 2008, 14, 777-788.	1.8	13
46	Electrostatic interactions play an essential role in DNA repair and cold-adaptation of Uracil DNA glycosylase. <i>Journal of Molecular Modeling</i> , 2008, 14, 201-213.	1.8	12
47	Sequence comparison and environmental adaptation of a bacterial endonuclease. <i>Computational Biology and Chemistry</i> , 2007, 31, 163-172.	2.3	11
48	Predicting proteinase specificities from free energy calculations. <i>Journal of Molecular Graphics and Modelling</i> , 2006, 25, 176-185.	2.4	10
49	Thermal unfolding studies of cold adapted uracil-DNA N-glycosylase (UNG) from Atlantic cod (<i>Gadus</i>) Tj ETQq1 1 0.784314 rgBT /Ove <i>Biochemistry and Molecular Biology</i> , 2012, 161, 60-68.	1.6	10
50	Characterization of the N-acetylneuraminic acid synthase (NeuB) from the psychrophilic fish pathogen <i>Moritella viscosa</i> . <i>Carbohydrate Research</i> , 2015, 402, 133-145.	2.3	10
51	Crystallization and preliminary X-ray diffraction analysis of a cold-adapted uracil-DNA glycosylase from Atlantic cod (<i>Gadus morhua</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1706-1708.	2.5	9
52	Structure of uracil-DNAN-glycosylase (UNG) from <i>Vibrio cholerae</i> : mapping temperature adaptation through structural and mutational analysis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 130-136.	0.7	9
53	Response. <i>Science</i> , 1993, 261, 621-622.	12.6	8
54	Environmental fate of chlorinated bornanes estimated by theoretical descriptors. <i>Chemosphere</i> , 2001, 43, 665-674.	8.2	8

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55	Ion pairs and their role in modulating stability of cold- and warm-active uracil DNA glycosylase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1219-1230.	2.6	8
56	Structure of a highly stable mutant of human fibroblast growth factor 1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 67-73.	2.5	8
57	Draft Genome Sequence of the Actinomycete <i>Rhodococcus</i> sp. Strain AW25M09, Isolated from the Hadsel Fjord, Northern Norway. <i>Genome Announcements</i> , 2013, 1, e0005513.	0.8	8
58	Structure determination and refinement of benzamidine-inhibited trypsin from the North Atlantic salmon (<i>Salmo salar</i>) at 1.82 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 318-330.	2.5	7
59	Thermodynamics and structure of a salmon cold active goose-type lysozyme. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2010, 156, 254-263.	1.6	7
60	Characterization of the sialic acid synthase from <i>Aliivibrio salmonicida</i> suggests a novel pathway for bacterial synthesis of 7-O-acetylated sialic acids. <i>Glycobiology</i> , 2013, 23, 806-819.	2.5	7
61	Laue diffraction as a tool in dynamic studies: hydrolysis of a transiently stable intermediate in catalysis by trypsin. <i>Philosophical Transactions of the Royal Society: Physical and Engineering Sciences</i> , 1992, 340, 285-300.	1.0	6
62	Refined crystal structure of lysozyme from the rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 354-367.	2.5	6
63	Structural and biophysical analysis of interactions between cod and human uracil-DNA N-glycosylase (UNG) and UNG inhibitor (Ugi). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2093-2100.	2.5	6
64	Structure of anionic salmon trypsin in a second crystal form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 725-730.	2.5	5
65	The primary structure and specificity determining residues displayed by recombinant salmon antibody domains. <i>Molecular Immunology</i> , 2004, 40, 1347-1360.	2.2	5
66	High quality draft genome sequence of <i>Streptomyces</i> sp. strain AW19M42 isolated from a sea squirt in Northern Norway. <i>Standards in Genomic Sciences</i> , 2014, 9, 676-686.	1.5	5
67	Features and structure of a cold active N-acetylneuraminase lyase. <i>PLoS ONE</i> , 2019, 14, e0217713.	2.5	5
68	Uracil-DNA N-glycosylase (UNG) from the marine, psychrophilic bacterium <i>Vibrio salmonicida</i> shows cold adapted features. <i>Enzyme and Microbial Technology</i> , 2008, 42, 594-600.	3.2	4
69	Molecular Cloning and Characterization of Anionic and Cationic Variants of Trypsin from Atlantic Salmon. <i>FEBS Journal</i> , 1995, 232, 677-685.	0.2	4
70	Crystallization and preliminary X-ray crystallographic studies of native elastase from North Atlantic salmon (<i>Salmo salar</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 393-394.	2.5	1
71	Draft Genome Sequence of the Symbiotically Competent Cyanobacterium <i>Nostoc</i> sp. Strain KVJ20. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
72	Consideration in the choice of a wavelength range for white-beam Laue diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 305-307.	2.5	0