

Bjarni Ásgeirsson

List of Publications by Year in descending order

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docs citations

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#	ARTICLE	IF	CITATIONS
1	The high catalytic rate of the cold-active <i>Vibrio</i> alkaline phosphatase requires a hydrogen bonding network involving a large interface loop. <i>FEBS Open Bio</i> , 2021, 11, 173-184.	2.3	3
2	X-ray crystal structure of <i>Vibrio</i> alkaline phosphatase with the non-competitive inhibitor cyclohexylamine. <i>Biochemistry and Biophysics Reports</i> , 2020, 24, 100830.	1.3	4
3	Chloride promotes refolding of active <i>Vibrio</i> alkaline phosphatase through an inactive dimeric intermediate with an altered interface. <i>FEBS Open Bio</i> , 2019, 9, 169-184.	2.3	6
4	pH-Dependent Binding of Chloride to a Marine Alkaline Phosphatase Affects the Catalysis, Active Site Stability, and Dimer Equilibrium. <i>Biochemistry</i> , 2017, 56, 5075-5089.	2.5	11
5	Cold-active alkaline phosphatase is irreversibly transformed into an inactive dimer by low urea concentrations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 755-765.	2.3	18
6	Directed evolution induces tributyrin hydrolysis in a virulence factor of <i>Xylella fastidiosa</i> using a duplicated gene as a template. <i>F1000Research</i> , 2014, 3, 215.	1.6	1
7	Characterizing alpha helical properties of Ebola viral proteins as potential targets for inhibition of alpha-helix mediated protein-protein interactions. <i>F1000Research</i> , 2014, 3, 251.	1.6	9
8	The PDB database is a rich source of alpha-helical anti-microbial peptides to combat disease causing pathogens. <i>F1000Research</i> , 2014, 3, 295.	1.6	9
9	The PDB database is a rich source of alpha-helical anti-microbial peptides to combat disease causing pathogens. <i>F1000Research</i> , 2014, 3, 295.	1.6	8
10	Characterizing alpha helical properties of Ebola viral proteins as potential targets for inhibition of alpha-helix mediated protein-protein interactions. <i>F1000Research</i> , 2014, 3, 251.	1.6	7
11	Dynamics fingerprint and inherent asymmetric flexibility of a cold-adapted homodimeric enzyme. A case study of the <i>Vibrio</i> alkaline phosphatase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 2970-2980.	2.4	19
12	Structural phylogeny by profile extraction and multiple superimposition using electrostatic congruence as a discriminator. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e25463.	1.9	7
13	Protein structure quality assessment based on the distance profiles of consecutive backbone C α atoms. <i>F1000Research</i> , 2013, 2, 211.	1.6	12
14	The dipeptidyl peptidase IV inhibitors vildagliptin and K-579 inhibit a phospholipase C: a case of promiscuous scaffolds in proteins. <i>F1000Research</i> , 2013, 2, 286.	1.6	7
15	A Computational Module Assembled from Different Protease Family Motifs Identifies PI PLC from <i>Bacillus cereus</i> as a Putative Prolyl Peptidase with a Serine Protease Scaffold. <i>PLoS ONE</i> , 2013, 8, e70923.	2.5	21
16	The electrostatic profile of consecutive C α atoms applied to protein structure quality assessment. <i>F1000Research</i> , 2013, 2, 243.	1.6	5
17	The electrostatic profile of consecutive C α atoms applied to protein structure quality assessment. <i>F1000Research</i> , 2013, 2, 243.	1.6	4
18	Nervonic Acid (24:1n-9) is a Dominant Unsaturated Fatty Acid in the Intestinal Brush Border of Atlantic Cod. <i>Lipid Insights</i> , 2012, 5, LPI.S10291.	1.0	3

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19	Inhibition of a cold-active alkaline phosphatase by imipenem revealed by <i>in silico</i> modeling of metallo-β-lactamase active sites. <i>FEBS Letters</i> , 2012, 586, 3710-3715.	2.8	28
20	A Measure of the Broad Substrate Specificity of Enzymes Based on "Duplicate" Catalytic Residues. <i>PLoS ONE</i> , 2012, 7, e49313.	2.5	14
21	Isolation and biochemical characterisation of lipid rafts from Atlantic cod (<i>Gadus morhua</i>) intestinal enterocytes. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2010, 155, 86-95.	1.6	15
22	Structural features and dynamics of a cold-adapted alkaline phosphatase studied by EPR spectroscopy. <i>FEBS Journal</i> , 2009, 276, 2725-2735.	4.7	13
23	The 1.4 Å crystal structure of the large and cold-active <i>Vibrio</i> sp. alkaline phosphatase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 297-308.	2.3	48
24	Effects of replacing active site residues in a cold-active alkaline phosphatase with those found in its mesophilic counterpart from <i>Escherichia coli</i> . <i>FEBS Journal</i> , 2008, 275, 117-127.	4.7	20
25	Engineered disulfide bonds increase active-site local stability and reduce catalytic activity of a cold-adapted alkaline phosphatase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 679-687.	2.3	27
26	Microscopic rate-constants for substrate binding and acylation in cold-adaptation of trypsin I from Atlantic cod. <i>FEBS Letters</i> , 2006, 580, 4639-4644.	2.8	17
27	Reversible inactivation of alkaline phosphatase from Atlantic cod (<i>Gadus morhua</i>) in urea. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 190-198.	2.3	11
28	Amino acid sequence of the cold-active alkaline phosphatase from Atlantic cod (<i>Gadus morhua</i>). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2003, 136, 45-60.	1.6	16
29	Primary structure of cold-adapted alkaline phosphatase from a <i>Vibrio</i> sp. as deduced from the nucleotide gene sequence. <i>BBA - Proteins and Proteomics</i> , 2001, 1549, 99-111.	2.1	20
30	Dissociation and unfolding of cold-active alkaline phosphatase from Atlantic cod in the presence of guanidinium chloride. <i>FEBS Journal</i> , 2000, 267, 6403-6412.	0.2	20
31	Heat-labile bacterial alkaline phosphatase from a marine <i>Vibrio</i> sp.. <i>Enzyme and Microbial Technology</i> , 2000, 27, 66-73.	3.2	54
32	The third serine proteinase with chymotrypsin specificity isolated from Atlantic cod (<i>Gadus morhua</i>) is a type-II elastase. <i>FEBS Journal</i> , 1998, 255, 638-646.	0.2	7
33	Hereditary cystatin C amyloid angiopathy: monitoring the presence of the Leu-68→Gln cystatin C variant in cerebrospinal fluids and monocyte cultures by MS. <i>Biochemical Journal</i> , 1998, 329, 497-503.	3.7	24
34	Serine Proteinases from Cold-Adapted Organisms. <i>Advances in Experimental Medicine and Biology</i> , 1997, 415, 27-46.	1.6	13
35	Structure of chymotrypsin variant B from Atlantic cod, <i>Gadus morhua</i> . <i>BBA - Proteins and Proteomics</i> , 1996, 1297, 49-56.	2.1	24
36	Alkaline phosphatase from Atlantic cod (<i>Gadus morhua</i>). Kinetic and structural properties which indicate adaptation to low temperatures. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 1995, 110, 315-329.	1.6	44

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37	Properties of elastase from Atlantic cod a cold-adapted proteinase. BBA - Proteins and Proteomics, 1993, 1164, 91-100.	2.1	46
38	On the role of monocytes/macrophages in the pathogenesis of central nervous system lesions in hereditary cystatin C amyloid angiopathy. Journal of the Neurological Sciences, 1992, 108, 121-128.	0.6	30
39	Structural and kinetic properties of chymotrypsin from atlantic cod (<i>Gadus morhua</i>). Comparison with bovine chymotrypsin. Comparative Biochemistry and Physiology Part B: Comparative Biochemistry, 1991, 99, 327-335.	0.2	62
40	Calcium-dependent protein phosphorylation in bovine anterior pituitary membranes and intact cells. Molecular and Cellular Endocrinology, 1984, 34, 183-190.	3.2	2
41	Dipeptidyl peptidase-IV inhibitors used in type-2 diabetes inhibit a phospholipase C: a case of promiscuous scaffolds in proteins. F1000Research, 0, 2, 286.	1.6	8
42	Correlating the ability of VP24 protein from Ebola and Marburg viruses to bind human karyopherin to their immune suppression mechanism and pathogenicity using computational methods. F1000Research, 0, 3, 265.	1.6	8
43	Correlating the ability of VP24 protein from Ebola and Marburg viruses to bind human karyopherin to their immune suppression mechanism and pathogenicity using computational methods. F1000Research, 0, 3, 265.	1.6	3
44	Promiscuous scaffolds in proteins - non-native, non-additive and non-trivial. F1000Research, 0, 2, 260.	1.6	0
45	The electrostatic profile of consecutive C $\hat{\alpha}$ atoms applied to protein structure quality assessment. F1000Research, 0, 2, 243.	1.6	1
46	Promiscuous scaffolds in proteins - non-native, non-additive and non-trivial. F1000Research, 0, 2, 260.	1.6	0
47	PREMONITION - Preprocessing motifs in protein structures for search acceleration. F1000Research, 0, 3, 217.	1.6	3
48	Protein structure quality assessment based on the distance profiles of consecutive backbone C $\hat{\alpha}$ atoms. F1000Research, 0, , .	1.6	5