Stefan Janecek

List of Publications by Year
in descending order

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64	3,257	159358	149479
papers	citations	30 h-index	56 g-index

65	65	65	2497
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Relationship of sequence and structure to specificity in the Î±-amylase family of enzymes. BBA - Proteins and Proteomics, 2001, 1546, 1-20.	2.1	554
2	Î±-Amylase: an enzyme specificity found in various families of glycoside hydrolases. Cellular and Molecular Life Sciences, 2014, 71, 1149-1170.	2.4	272
3	Thermophilic archaeal amylolytic enzymes. Enzyme and Microbial Technology, 2000, 26, 3-14.	1.6	169
4	The carbohydrateâ€binding module familyâ€ƒ20 â€“ diversity, structure, and function. FEBS Journal, 2009, 276, 5006-5029.	2.2	168
5	Domain Evolution in the Î±-Amylase Family. Journal of Molecular Evolution, 1997, 45, 322-331.	0.8	157
6	Structural and evolutionary aspects of two families of non-catalytic domains present in starch and glycogen binding proteins from microbes, plants and animals. Enzyme and Microbial Technology, 2011, 49, 429-440.	1.6	112
7	Relation between domain evolution, specificity, and taxonomy of the Î±-amylase family members containing a C-terminal starch-binding domain. FEBS Journal, 2003, 270, 635-645.	0.2	102
8	Sequence Similarities and Evolutionary Relationships of Microbial, Plant and Animal alpha-amylases. FEBS Journal, 1994, 224, 519-524.	0.2	96
9	The evolution of starch-binding domain. FEBS Letters, 1999, 456, 119-125.	1.3	91
10	Starch-binding domains as CBM familiesâ€“history, occurrence, structure, function and evolution. Biotechnology Advances, 2019, 37, 107451.	6.0	83
11	Remarkable evolutionary relatedness among the enzymes and proteins from the Î±-amylase family. Cellular and Molecular Life Sciences, 2016, 73, 2707-2725.	2.4	81
12	Bioinformatics of the glycoside hydrolase family 57 and identification of catalytic residues in amylopullulanase from Thermococcusâ€hydrothermalis. FEBS Journal, 2004, 271, 2863-2872.	0.2	80
13	A new clan of CBM families based on bioinformatics of starch-binding domains from families CBM20 and CBM21. FEBS Journal, 2005, 272, 5497-5513.	2.2	62
14	The evolution of putative starch-binding domains. FEBS Letters, 2006, 580, 6349-6356.	1.3	62
15	Tracing the evolution of the Î±-amylase subfamily GH13_36 covering the amylolytic enzymes intermediate between oligo-1,6-glucosidases and neopullulanases. Carbohydrate Research, 2013, 367, 48-57.	1.1	61
16	Parallel Î²/Î±-barrels of Î±-amylase, cyclodextrin glycosyltransferase and oligo-1,6-glucosidase versus the barrel of Î²-amylase: Evolutionary distance is a reflection of unrelated sequences. FEBS Letters, 1994, 353, 119-123.	1.3	56
17	Sequence fingerprints of enzyme specificities from the glycoside hydrolase family GH57. Extremophiles, 2012, 16, 497-506.	0.9	54
18	Close Evolutionary Relatedness of Î±-Amylases from Archaea and Plants. Journal of Molecular Evolution, 1999, 48, 421-426.	0.8	52

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19	Î±-Amylases and approaches leading to their enhanced stability. FEBS Letters, 1992, 304, 1-3.	1.3	51
20	Domain evolution in the GH13 pullulanase subfamily with focus on the carbohydrate-binding module family 48. Biologia (Poland), 2008, 63, 1057-1068.	0.8	50
21	Gene make-up: rapid and massive intron gains after horizontal transfer of a bacterial Î±-amylase gene to Basidiomycetes. BMC Evolutionary Biology, 2013, 13, 40.	3.2	49
22	Location of repeat elements in glucansucrases of Leuconostoc and Streptococcus species. FEMS Microbiology Letters, 2000, 192, 53-57.	0.7	45
23	A motif of a microbial starch-binding domain found in human genethonin. Bioinformatics, 2002, 18, 1534-1537.	1.8	40
24	Close evolutionary relatedness among functionally distantly related members of the (Î±/Î²)8-barrel glycosyl hydrolases suggested by the similarity of their fifth conserved sequence region. FEBS Letters, 1995, 377, 6-8.	1.3	39
25	A remote but significant sequence homology between glycoside hydrolase clan GH-H and family GH31. FEBS Letters, 2007, 581, 1261-1268.	1.3	39
26	Sequence-Structural Features and Evolutionary Relationships of Family GH57 Î±-Amylases and Their Putative Î±-Amylase-Like Homologues. Protein Journal, 2011, 30, 429-435.	0.7	37
27	Looking for the ancestry of the heavyâ€chain subunits of heteromeric amino acid transporters rBAT and 4F2hc within the GH13 Î±â€amylase family. FEBS Journal, 2009, 276, 7265-7278.	2.2	34
28	Gene Sequence, Bioinformatics and Enzymatic Characterization of Î±-Amylase from Saccharomycopsis fibuligera KZ. Protein Journal, 2010, 29, 355-364.	0.7	33
29	Protein engineering of selected residues from conserved sequence regions of a novel Anoxybacillus Î±-amylase. Scientific Reports, 2014, 4, 5850.	1.6	33
30	A new group of glycoside hydrolase family 13 Î±-amylases with an aberrant catalytic triad. Scientific Reports, 2017, 7, 44230.	1.6	32
31	Association of Novel Domain in Active Site of Archaic Hyperthermophilic Maltogenic Amylase from Staphylothermus marinus. Journal of Biological Chemistry, 2012, 287, 7979-7989.	1.6	30
32	New insight in cereal starch degradation: identification and structural characterization of four Î±-amylases in bread wheat. Amylase, 2017, 1, .	0.7	29
33	Domain evolution in enzymes of the neopullulanase subfamily. Microbiology (United Kingdom), 2016, 162, 2099-2115.	0.7	28
34	The unique glycoside hydrolase family 77 amylomaltase fromBorrelia burgdorferiwith only catalytic triad conserved. FEMS Microbiology Letters, 2008, 284, 84-91.	0.7	27
35	A novel GH13 subfamily of Î±-amylases with a pair of tryptophans in the helix Î±3 of the catalytic TIM-barrel, the LPDlx signature in the conserved sequence region V and a conserved aromatic motif at the C-terminus. Biologia (Poland), 2015, 70, 1284-1294.	0.8	27
36	Characterization of Maltase Clusters in the Genus Drosophila. Journal of Molecular Evolution, 2011, 72, 104-118.	0.8	26

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37	In silico identification of catalytic residues and domain fold of the family GH119 sharing the catalytic machinery with the Î±â€amylase family GH57. FEBS Letters, 2012, 586, 3360-3366.	1.3	26
38	In silico analysis of the Î±-amylase family GH57: eventual subfamilies reflecting enzyme specificities. 3 Biotech, 2018, 8, 307.	1.1	21
39	Two potentially novel amylolytic enzyme specificities in the prokaryotic glycoside hydrolase Î±-amylase family GH57. Microbiology (United Kingdom), 2013, 159, 2584-2593.	0.7	18
40	The starchâ€binding domain family CBM41â€"An in silico analysis of evolutionary relationships. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1480-1492.	1.5	18
41	How many Î±-amylase GH families are there in the CAZy database?. Amylase, 2022, 6, 1-10.	0.7	18
42	Two structurally related starch-binding domain families CBM25 and CBM26. Biologia (Poland), 2014, 69, 1087-1096.	0.8	17
43	In silico analysis of family GH77 with focus on amylomaltases from borreliae and disproportionating enzymes DPE2 from plants and bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1260-1268.	1.1	17
44	A new GH13 subfamily represented by the Î±-amylase from the halophilic archaeon Haloarcula hispanica. Extremophiles, 2020, 24, 207-217.	0.9	17
45	Morphological, physiological, molecular and phylogenetic characterization of new environmental isolates of Acanthamoeba spp. from the region of Bratislava, Slovakia. Biologia (Poland), 2010, 65, 81-91.	0.8	15
46	Î±-Amylase from Thermococcus hydrothermalis: Re-cloning aimed at the improved expression and hydrolysis of corn starch. Enzyme and Microbial Technology, 2006, 39, 1300-1305.	1.6	14
47	Fungal Î±-amylases from three GH13 subfamilies: their sequence-structural features and evolutionary relationships. International Journal of Biological Macromolecules, 2020, 159, 763-772.	3.6	13
48	The unique evolution of the carbohydrateâ€binding module CBM 20 in laforin. FEBS Letters, 2018, 592, 586-598.	1.3	12
49	Identification of Thermotoga maritima MSB8 GH57 Î±-amylase AmyC as a glycogen-branching enzyme with high hydrolytic activity. Applied Microbiology and Biotechnology, 2019, 103, 6141-6151.	1.7	12
50	Tyrosine 39 of GH13 Î±-amylase from Thermococcus hydrothermalis contributes to its thermostability. Biologia (Poland), 2010, 65, 408-415.	0.8	9
51	Fungal Hybrid B heme peroxidases â€“ unique fusions of a heme peroxidase domain with a carbohydrate-binding domain. Scientific Reports, 2017, 7, 9393.	1.6	9
52	Characterization and diversity of the complete set of GH family 3 enzymes from Rhodothermus marinus DSM 4253. Scientific Reports, 2020, 10, 1329.	1.6	9
53	A detailed in silico analysis of the amylolytic family GH126 and its possible relatedness to family GH76. Carbohydrate Research, 2020, 494, 108082.	1.1	7
54	A putative novel starch-binding domain revealed by in silico analysis of the N-terminal domain in bacterial amylomaltases from the family GH77. 3 Biotech, 2021, 11, 229.	1.1	7

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55	Amylolytic glycoside hydrolases. Cellular and Molecular Life Sciences, 2016, 73, 2601-2602.	2.4	6
56	Novel family GH3 Î²-glucosidases or Î²-xylosidases of unknown function found in various animal groups, including birds and reptiles. Carbohydrate Research, 2015, 408, 44-50.	1.1	5
57	Extension of the taxonomic coverage of the family GH126 outside Firmicutes and in silico characterization of its non-catalytic terminal domains. 3 Biotech, 2020, 10, 420.	1.1	5
58	New groups of protein homologues in the Îą-amylase family GH57 closely related to Îą-glucan branching enzymes and 4-Îą-glucanotransferases. Genetica, 2020, 148, 77-86.	0.5	5
59	Îą-Amylases from Archaea: Sequences, Structures and Evolution. Grand Challenges in Biology and Biotechnology, 2016, , 505-524.	2.4	4
60	In Silico Analysis of Fungal and Chloride-Dependent Îą-Amylases within the Family GH13 with Identification of Possible Secondary Surface-Binding Sites. Molecules, 2021, 26, 5704.	1.7	4
61	New Insight into Structure/Function Relationships in Plant .ALPHA.-Amylase Family GH13 Members. Journal of Applied Glycoscience (1999), 2010, 57, 157-162.	0.3	4
62	New Horizons of Carbohydrate Bioengineering. Proteins without Enzymatic Function with Sequence Relatedness to the .ALPHA.-Amylase Family.. Trends in Glycoscience and Glycotechnology, 2000, 12, 363-371.	0.0	2
63	Sequence Fingerprints in the Evolution of the Îą-Amylase Family. , 2008, , 45-63.		1
64	The 3 rd Symposium on the Alpha-Amylase Family, Smolenice Castle, Slovakia, September 23â€“27, 2007. Biologia (Poland), 2008, 63, 963-966.	0.8	0