

# Stefan Janecek

## List of Publications by Year in descending order

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64  
papers

3,257  
citations

159358

30  
h-index

149479

56  
g-index

65  
all docs

65  
docs citations

65  
times ranked

2497  
citing authors

#	ARTICLE	IF	CITATIONS
1	How many $\alpha$ -amylase GH families are there in the CAZy database?. <i>Amylase</i> , 2022, 6, 1-10.	0.7	18
2	A putative novel starch-binding domain revealed by in silico analysis of the N-terminal domain in bacterial amylomaltases from the family GH77. <i>3 Biotech</i> , 2021, 11, 229.	1.1	7
3	In Silico Analysis of Fungal and Chloride-Dependent $\alpha$ -Amylases within the Family GH13 with Identification of Possible Secondary Surface-Binding Sites. <i>Molecules</i> , 2021, 26, 5704.	1.7	4
4	A new GH13 subfamily represented by the $\alpha$ -amylase from the halophilic archaeon <i>Haloarcula hispanica</i> . <i>Extremophiles</i> , 2020, 24, 207-217.	0.9	17
5	A detailed in silico analysis of the amylolytic family GH126 and its possible relatedness to family GH76. <i>Carbohydrate Research</i> , 2020, 494, 108082.	1.1	7
6	Extension of the taxonomic coverage of the family GH126 outside Firmicutes and in silico characterization of its non-catalytic terminal domains. <i>3 Biotech</i> , 2020, 10, 420.	1.1	5
7	New groups of protein homologues in the $\alpha$ -amylase family GH57 closely related to $\alpha$ -glucan branching enzymes and $4\alpha$ -glucanotransferases. <i>Genetica</i> , 2020, 148, 77-86.	0.5	5
8	Characterization and diversity of the complete set of GH family 3 enzymes from <i>Rhodothermus marinus</i> DSM 4253. <i>Scientific Reports</i> , 2020, 10, 1329.	1.6	9
9	Fungal $\alpha$ -amylases from three GH13 subfamilies: their sequence-structural features and evolutionary relationships. <i>International Journal of Biological Macromolecules</i> , 2020, 159, 763-772.	3.6	13
10	Starch-binding domains as CBM familiesâ€“history, occurrence, structure, function and evolution. <i>Biotechnology Advances</i> , 2019, 37, 107451.	6.0	83
11	Identification of <i>Thermotoga maritima</i> MSB8 GH57 $\alpha$ -amylase AmyC as a glycogen-branching enzyme with high hydrolytic activity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6141-6151.	1.7	12
12	The unique evolution of the carbohydrate-binding module CBM 20 in laforin. <i>FEBS Letters</i> , 2018, 592, 586-598.	1.3	12
13	In silico analysis of the $\alpha$ -amylase family GH57: eventual subfamilies reflecting enzyme specificities. <i>3 Biotech</i> , 2018, 8, 307.	1.1	21
14	The starch-binding domain family CBM41â€“An <i>in silico</i> analysis of evolutionary relationships. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1480-1492.	1.5	18
15	A new group of glycoside hydrolase family 13 $\alpha$ -amylases with an aberrant catalytic triad. <i>Scientific Reports</i> , 2017, 7, 44230.	1.6	32
16	Fungal Hybrid B heme peroxidases â€“ unique fusions of a heme peroxidase domain with a carbohydrate-binding domain. <i>Scientific Reports</i> , 2017, 7, 9393.	1.6	9
17	New insight in cereal starch degradation: identification and structural characterization of four $\alpha$ -amylases in bread wheat. <i>Amylase</i> , 2017, 1, .	0.7	29
18	$\alpha$ -Amylases from Archaea: Sequences, Structures and Evolution. <i>Grand Challenges in Biology and Biotechnology</i> , 2016, , 505-524.	2.4	4

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19	Remarkable evolutionary relatedness among the enzymes and proteins from the $\alpha$ -amylase family. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2707-2725.	2.4	81
20	Amylolytic glycoside hydrolases. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2601-2602.	2.4	6
21	Domain evolution in enzymes of the neopullulanase subfamily. <i>Microbiology (United Kingdom)</i> , 2016, 162, 2099-2115.	0.7	28
22	A novel GH13 subfamily of $\alpha$ -amylases with a pair of tryptophans in the helix $\alpha$ 3 of the catalytic TIM-barrel, the LPDlx signature in the conserved sequence region V and a conserved aromatic motif at the C-terminus. <i>Biologia (Poland)</i> , 2015, 70, 1284-1294.	0.8	27
23	In silico analysis of family GH77 with focus on amylomaltases from borreliae and disproportionating enzymes DPE2 from plants and bacteria. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1260-1268.	1.1	17
24	Novel family GH3 $\beta$ -glucosidases or $\beta$ -xylosidases of unknown function found in various animal groups, including birds and reptiles. <i>Carbohydrate Research</i> , 2015, 408, 44-50.	1.1	5
25	Two structurally related starch-binding domain families CBM25 and CBM26. <i>Biologia (Poland)</i> , 2014, 69, 1087-1096.	0.8	17
26	$\alpha$ -Amylase: an enzyme specificity found in various families of glycoside hydrolases. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 1149-1170.	2.4	272
27	Protein engineering of selected residues from conserved sequence regions of a novel <i>Anoxybacillus</i> $\alpha$ -amylase. <i>Scientific Reports</i> , 2014, 4, 5850.	1.6	33
28	Gene make-up: rapid and massive intron gains after horizontal transfer of a bacterial $\alpha$ -amylase gene to Basidiomycetes. <i>BMC Evolutionary Biology</i> , 2013, 13, 40.	3.2	49
29	Tracing the evolution of the $\alpha$ -amylase subfamily GH13_36 covering the amylolytic enzymes intermediate between oligo-1,6-glucosidases and neopullulanases. <i>Carbohydrate Research</i> , 2013, 367, 48-57.	1.1	61
30	Two potentially novel amylolytic enzyme specificities in the prokaryotic glycoside hydrolase $\alpha$ -amylase family GH57. <i>Microbiology (United Kingdom)</i> , 2013, 159, 2584-2593.	0.7	18
31	In silico identification of catalytic residues and domain fold of the family GH119 sharing the catalytic machinery with the $\alpha$ -amylase family GH57. <i>FEBS Letters</i> , 2012, 586, 3360-3366.	1.3	26
32	Association of Novel Domain in Active Site of Archaic Hyperthermophilic Maltogenic Amylase from <i>Staphylothermus marinus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 7979-7989.	1.6	30
33	Sequence fingerprints of enzyme specificities from the glycoside hydrolase family GH57. <i>Extremophiles</i> , 2012, 16, 497-506.	0.9	54
34	Structural and evolutionary aspects of two families of non-catalytic domains present in starch and glycogen binding proteins from microbes, plants and animals. <i>Enzyme and Microbial Technology</i> , 2011, 49, 429-440.	1.6	112
35	Sequence-Structural Features and Evolutionary Relationships of Family GH57 $\alpha$ -Amylases and Their Putative $\alpha$ -Amylase-Like Homologues. <i>Protein Journal</i> , 2011, 30, 429-435.	0.7	37
36	Characterization of Maltase Clusters in the Genus <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2011, 72, 104-118.	0.8	26

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37	Morphological, physiological, molecular and phylogenetic characterization of new environmental isolates of <i>Acanthamoeba</i> spp. from the region of Bratislava, Slovakia. <i>Biologia (Poland)</i> , 2010, 65, 81-91.	0.8	15
38	Tyrosine 39 of GH13 $\alpha$ -amylase from <i>Thermococcus hydrothermalis</i> contributes to its thermostability. <i>Biologia (Poland)</i> , 2010, 65, 408-415.	0.8	9
39	Gene Sequence, Bioinformatics and Enzymatic Characterization of $\alpha$ -Amylase from <i>Saccharomycopsis fibuligera</i> KZ. <i>Protein Journal</i> , 2010, 29, 355-364.	0.7	33
40	New Insight into Structure/Function Relationships in Plant $\alpha$ -Amylase Family GH13 Members. <i>Journal of Applied Glycoscience</i> (1999), 2010, 57, 157-162.	0.3	4
41	The carbohydrate-binding module family 20 diversity, structure, and function. <i>FEBS Journal</i> , 2009, 276, 5006-5029.	2.2	168
42	Looking for the ancestry of the heavy chain subunits of heteromeric amino acid transporters rBAT and 4F2hc within the GH13 $\alpha$ -amylase family. <i>FEBS Journal</i> , 2009, 276, 7265-7278.	2.2	34
43	Domain evolution in the GH13 pullulanase subfamily with focus on the carbohydrate-binding module family 48. <i>Biologia (Poland)</i> , 2008, 63, 1057-1068.	0.8	50
44	The 3 rd Symposium on the Alpha-Amylase Family, Smolenice Castle, Slovakia, September 23-27, 2007. <i>Biologia (Poland)</i> , 2008, 63, 963-966.	0.8	0
45	The unique glycoside hydrolase family 77 amylomaltase from <i>Borrelia burgdorferi</i> with only catalytic triad conserved. <i>FEMS Microbiology Letters</i> , 2008, 284, 84-91.	0.7	27
46	Sequence Fingerprints in the Evolution of the $\alpha$ -Amylase Family. , 2008, , 45-63.		1
47	A remote but significant sequence homology between glycoside hydrolase clan GH-H and family GH31. <i>FEBS Letters</i> , 2007, 581, 1261-1268.	1.3	39
48	The evolution of putative starch-binding domains. <i>FEBS Letters</i> , 2006, 580, 6349-6356.	1.3	62
49	$\alpha$ -Amylase from <i>Thermococcus hydrothermalis</i> : Re-cloning aimed at the improved expression and hydrolysis of corn starch. <i>Enzyme and Microbial Technology</i> , 2006, 39, 1300-1305.	1.6	14
50	A new clan of CBM families based on bioinformatics of starch-binding domains from families CBM20 and CBM21. <i>FEBS Journal</i> , 2005, 272, 5497-5513.	2.2	62
51	Bioinformatics of the glycoside hydrolase family 57 and identification of catalytic residues in amylopullulanase from <i>Thermococcus hydrothermalis</i> . <i>FEBS Journal</i> , 2004, 271, 2863-2872.	0.2	80
52	Relation between domain evolution, specificity, and taxonomy of the $\alpha$ -amylase family members containing a C-terminal starch-binding domain. <i>FEBS Journal</i> , 2003, 270, 635-645.	0.2	102
53	A motif of a microbial starch-binding domain found in human genethonin. <i>Bioinformatics</i> , 2002, 18, 1534-1537.	1.8	40
54	Relationship of sequence and structure to specificity in the $\alpha$ -amylase family of enzymes. <i>BBA - Proteins and Proteomics</i> , 2001, 1546, 1-20.	2.1	554

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55	Thermophilic archaeal amylolytic enzymes. <i>Enzyme and Microbial Technology</i> , 2000, 26, 3-14.	1.6	169
56	Location of repeat elements in glucansucrases of <i>Leuconostoc</i> and <i>Streptococcus</i> species. <i>FEMS Microbiology Letters</i> , 2000, 192, 53-57.	0.7	45
57	New Horizons of Carbohydrate Bioengineering. Proteins without Enzymatic Function with Sequence Relatedness to the .ALPHA.-Amylase Family.. <i>Trends in Glycoscience and Glycotechnology</i> , 2000, 12, 363-371.	0.0	2
58	Close Evolutionary Relatedness of $\hat{1}\pm$ -Amylases from Archaea and Plants. <i>Journal of Molecular Evolution</i> , 1999, 48, 421-426.	0.8	52
59	The evolution of starch-binding domain. <i>FEBS Letters</i> , 1999, 456, 119-125.	1.3	91
60	Domain Evolution in the $\hat{1}\pm$ -Amylase Family. <i>Journal of Molecular Evolution</i> , 1997, 45, 322-331.	0.8	157
61	Close evolutionary relatedness among functionally distantly related members of the ( $\hat{1}\pm/\hat{1}^2$ )8-barrel glycosyl hydrolases suggested by the similarity of their fifth conserved sequence region. <i>FEBS Letters</i> , 1995, 377, 6-8.	1.3	39
62	Sequence Similarities and Evolutionary Relationships of Microbial, Plant and Animal alpha-amylases. <i>FEBS Journal</i> , 1994, 224, 519-524.	0.2	96
63	Parallel $\hat{1}^2/\hat{1}\pm$ -barrels of $\hat{1}\pm$ -amylase, cyclodextrin glycosyltransferase and oligo-1,6-glucosidase versus the barrel of $\hat{1}^2$ -amylase: Evolutionary distance is a reflection of unrelated sequences. <i>FEBS Letters</i> , 1994, 353, 119-123.	1.3	56
64	$\hat{1}\pm$ -Amylases and approaches leading to their enhanced stability. <i>FEBS Letters</i> , 1992, 304, 1-3.	1.3	51