

# Manuel A S Santos

## List of Publications by Year in descending order

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140  
papers

6,624  
citations

76326

40  
h-index

74163

75  
g-index

146  
all docs

146  
docs citations

146  
times ranked

9158  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of the genetic risk for COVID-19 outcomes in COPD and differences among worldwide populations. PLoS ONE, 2022, 17, e0264009.	2.5	11
2	The Role of MicroRNAs in Proteostasis Decline and Protein Aggregation during Brain and Skeletal Muscle Aging. International Journal of Molecular Sciences, 2022, 23, 3232.	4.1	8
3	Upregulation of tRNA-Ser-AGA-2-1 Promotes Malignant Behavior in Normal Bronchial Cells. Frontiers in Molecular Biosciences, 2022, 9, 809985.	3.5	6
4	tRNA-modifying enzyme mutations induce codon-specific mistranslation and protein aggregation in yeast. RNA Biology, 2021, 18, 563-575.	3.1	15
5	Developing New Marine Antifouling Surfaces: Learning from Single-Strain Laboratory Tests. Coatings, 2021, 11, 90.	2.6	10
6	All you need to know about sperm RNAs. Human Reproduction Update, 2021, 28, 67-91.	10.8	39
7	The role of micropeptides in biology. Cellular and Molecular Life Sciences, 2021, 78, 3285-3298.	5.4	28
8	Fighting Bisphenol A-Induced Male Infertility: The Power of Antioxidants. Antioxidants, 2021, 10, 289.	5.1	33
9	tRNAs as a Driving Force of Genome Evolution in Yeast. Frontiers in Microbiology, 2021, 12, 634004.	3.5	7
10	The association between initial adhesion and cyanobacterial biofilm development. FEMS Microbiology Ecology, 2021, 97, .	2.7	9
11	Optimizing CNT Loading in Antimicrobial Composites for Urinary Tract Application. Applied Sciences (Switzerland), 2021, 11, 4038.	2.5	15
12	The role of non-standard translation in <i>Candida albicans</i> pathogenesis. FEMS Yeast Research, 2021, 21, .	2.3	5
13	Unveiling the Antifouling Performance of Different Marine Surfaces and Their Effect on the Development and Structure of Cyanobacterial Biofilms. Microorganisms, 2021, 9, 1102.	3.6	17
14	Integration of segmented regression analysis with weighted gene correlation network analysis identifies genes whose expression is remodeled throughout physiological aging in mouse tissues. Aging, 2021, 13, 18150-18190.	3.1	9
15	Development of Chitosan-Based Surfaces to Prevent Single- and Dual-Species Biofilms of <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> . Molecules, 2021, 26, 4378.	3.8	11
16	Effect of <i>Lactobacillus plantarum</i> Biofilms on the Adhesion of <i>Escherichia coli</i> to Urinary Tract Devices. Antibiotics, 2021, 10, 966.	3.7	17
17	Detection and identification of fungal species by electronic nose technology: A systematic review. Fungal Biology Reviews, 2021, 37, 59-70.	4.7	21
18	Antimicrobial and anti-adhesive properties of carbon nanotube-based surfaces for medical applications: a systematic review. IScience, 2021, 24, 102001.	4.1	63

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19	The Use of Probiotics to Fight Biofilms in Medical Devices: A Systematic Review and Meta-Analysis. <i>Microorganisms</i> , 2021, 9, 27.	3.6	27
20	Antimicrobial coatings based on chitosan to prevent implant-associated infections: A systematic review. <i>IScience</i> , 2021, 24, 103480.	4.1	29
21	Human cells adapt to translational errors by modulating protein synthesis rate and protein turnover. <i>RNA Biology</i> , 2020, 17, 135-149.	3.1	15
22	Experimental Assessment of the Performance of Two Marine Coatings to Curb Biofilm Formation of Microfoulers. <i>Coatings</i> , 2020, 10, 893.	2.6	18
23	<i>De novo</i> sequencing of proteins by mass spectrometry. <i>Expert Review of Proteomics</i> , 2020, 17, 595-607.	3.0	19
24	Emerging Roles of tRNAs in RNA Virus Infections. <i>Trends in Biochemical Sciences</i> , 2020, 45, 794-805.	7.5	33
25	The Relative Importance of Shear Forces and Surface Hydrophobicity on Biofilm Formation by Coccoid Cyanobacteria. <i>Polymers</i> , 2020, 12, 653.	4.5	27
26	Antibacterial Action Mechanisms of Honey: Physiological Effects of Avocado, Chestnut, and Polyfloral Honey upon <i>Staphylococcus aureus</i> and <i>Escherichia coli</i> . <i>Molecules</i> , 2020, 25, 1252.	3.8	19
27	Does proteostasis get lost in translation? Implications for protein aggregation across the lifespan. <i>Ageing Research Reviews</i> , 2020, 62, 101119.	10.9	14
28	Evaluation of Physiological Effects Induced by Manuka Honey Upon <i>Staphylococcus aureus</i> and <i>Escherichia coli</i> . <i>Microorganisms</i> , 2019, 7, 258.	3.6	17
29	tRNA Deregulation and Its Consequences in Cancer. <i>Trends in Molecular Medicine</i> , 2019, 25, 853-865.	6.7	63
30	MicroRNA-186-5p controls GluA2 surface expression and synaptic scaling in hippocampal neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5727-5736.	7.1	39
31	Assessing the impact of Medical Microbiology classes using active strategies on short- and long-term retention on medical students: an innovative study. <i>Brazilian Journal of Microbiology</i> , 2019, 50, 165-173.	2.0	3
32	Epidemiology and susceptibility profile to classic antifungals and over-the-counter products of <i>Malassezia</i> clinical isolates from a Portuguese University Hospital: a prospective study. <i>Journal of Medical Microbiology</i> , 2019, 68, 778-784.	1.8	10
33	A Fluorescence-Based Sensor Assay that Monitors General Protein Aggregation in Human Cells. <i>Biotechnology Journal</i> , 2018, 13, e1700676.	3.5	21
34	Guanabenz inhibits TLR9 signaling through a pathway that is independent of eIF2 $\gamma$ dephosphorylation by the GADD34/PP1c complex. <i>Science Signaling</i> , 2018, 11, .	3.6	15
35	Codon misreading tRNAs promote tumor growth in mice. <i>RNA Biology</i> , 2018, 15, 1-14.	3.1	30
36	Impact of tRNA Modifications and tRNA-Modifying Enzymes on Proteostasis and Human Disease. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3738.	4.1	93

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37	Plasmodium apicoplast tyrosyl-tRNA synthetase recognizes an unusual, simplified identity set in cognate tRNA <sup>Tyr</sup> . PLoS ONE, 2018, 13, e0209805.	2.5	4
38	Errors in protein synthesis increase the level of saturated fatty acids and affect the overall lipid profiles of yeast. PLoS ONE, 2018, 13, e0202402.	2.5	5
39	&lt;i>Saccharomyces cerevisiae</i> as a Model to Confirm the Ability of FTIR to Evaluate the Presence of Protein Aggregates. Spectral Analysis Review, 2018, 06, 1-11.	0.2	2
40	Protein synthesis inhibition and GADD34 control IFN $\alpha$ 2 heterogeneous expression in response to $\Delta$ sRNA. EMBO Journal, 2017, 36, 761-782.	7.8	64
41	Discovery and function of transfer <i>scp</i> RNA-derived fragments and their role in disease. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1423.	6.4	76
42	Adaptive Mistranslation Accelerates the Evolution of Fluconazole Resistance and Induces Major Genomic and Gene Expression Alterations in <i>Candida albicans</i> . MSphere, 2017, 2, .	2.9	29
43	Potential Impact of Flow Cytometry Antimicrobial Susceptibility Testing on the Clinical Management of Gram-Negative Bacteremia Using the FASTinov $\text{\textcircled{R}}$ Kit. Frontiers in Microbiology, 2017, 8, 2455.	3.5	23
44	Phenotypic heterogeneity promotes adaptive evolution. PLoS Biology, 2017, 15, e2000644.	5.6	128
45	The RNA-Binding Protein hnRNP K Mediates the Effect of BDNF on Dendritic mRNA Metabolism and Regulates Synaptic NMDA Receptors in Hippocampal Neurons. ENeuro, 2017, 4, ENEURO.0268-17.2017.	1.9	57
46	Flow Cytometry in Microbiology: The Reason and the Need. Series in Bioengineering, 2017, , 153-170.	0.6	3
47	The Fungus <i>Candida albicans</i> Tolerates Ambiguity at Multiple Codons. Frontiers in Microbiology, 2016, 7, 401.	3.5	15
48	A Flow Cytometric and Computational Approaches to Carbapenems Affinity to the Different Types of Carbapenemases. Frontiers in Microbiology, 2016, 7, 1259.	3.5	5
49	Unveiling the Synergistic Interaction Between Liposomal Amphotericin B and Colistin. Frontiers in Microbiology, 2016, 7, 1439.	3.5	10
50	Fluorescence In Vivo Hybridization (FIVH) for Detection of <i>Helicobacter pylori</i> Infection in a C57BL/6 Mouse Model. PLoS ONE, 2016, 11, e0148353.	2.5	16
51	Fungal Chitin Induces Trained Immunity in Human Monocytes during Cross-talk of the Host with <i>Saccharomyces cerevisiae</i> . Journal of Biological Chemistry, 2016, 291, 7961-7972.	3.4	90
52	EuGene: maximizing synthetic gene design for heterologous expression. Bioinformatics, 2016, 32, 1120-1120.	4.1	2
53	Conserved and highly expressed tRNA derived fragments in zebrafish. BMC Molecular Biology, 2015, 16, 22.	3.0	33
54	Non-Standard Genetic Codes Define New Concepts for Protein Engineering. Life, 2015, 5, 1610-1628.	2.4	24

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55	The effect of antibacterial and non-antibacterial compounds alone or associated with antifungals upon fungi. <i>Frontiers in Microbiology</i> , 2015, 6, 669.	3.5	50
56	Intrastrain genomic and phenotypic variability of the commercial <i>Saccharomyces cerevisiae</i> strain Zymaflore VL1 reveals microevolutionary adaptation to vineyard environments. <i>FEMS Yeast Research</i> , 2015, 15, fov063.	2.3	32
57	RUN and FYVE domain-containing protein 4 enhances autophagy and lysosome tethering in response to Interleukin-4. <i>Journal of Cell Biology</i> , 2015, 210, 1133-1152.	5.2	58
58	New Insights Regarding Yeast Survival following Exposure to Liposomal Amphotericin B. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 6181-6187.	3.2	9
59	Improving the accuracy of recombinant protein production through integration of bioinformatics, statistical and mass spectrometry methodologies. <i>FEBS Journal</i> , 2015, 282, 769-787.	4.7	9
60	Evolution of Robustness to Protein Mistranslation by Accelerated Protein Turnover. <i>PLoS Biology</i> , 2015, 13, e1002291.	5.6	29
61	TRNA mutations that affect decoding fidelity deregulate development and the proteostasis network in zebrafish. <i>RNA Biology</i> , 2014, 11, 1199-1213.	3.1	20
62	Hyperpolarization-Activated Cyclic Nucleotide-Gated Channels and cAMP-Dependent Modulation of Exocytosis in Cultured Rat Lactotrophs. <i>Journal of Neuroscience</i> , 2014, 34, 15638-15647.	3.6	20
63	High-throughput molecular profiling of a P-cadherin overexpressing breast cancer model reveals new targets for the anti-cancer bacterial protein azurin. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 50, 1-9.	2.8	22
64	Yap1 mediates tolerance to cobalt toxicity in the yeast <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 1977-1986.	2.4	24
65	Ischemic insults induce necroptotic cell death in hippocampal neurons through the up-regulation of endogenous RIP3. <i>Neurobiology of Disease</i> , 2014, 68, 26-36.	4.4	107
66	Protein mistranslation: friend or foe?. <i>Trends in Biochemical Sciences</i> , 2014, 39, 355-362.	7.5	134
67	Polyethyleneimine and polyethyleneimine-based nanoparticles: novel bacterial and yeast biofilm inhibitors. <i>Journal of Medical Microbiology</i> , 2014, 63, 1167-1173.	1.8	70
68	Rescue of wild-type E-cadherin expression from nonsense-mutated cancer cells by a suppressor-tRNA. <i>European Journal of Human Genetics</i> , 2014, 22, 1085-1092.	2.8	17
69	Differences in the expression pattern of HCN isoforms among mammalian tissues: sources and implications. <i>Molecular Biology Reports</i> , 2014, 41, 297-307.	2.3	22
70	In Vitro Ischemia Triggers a Transcriptional Response to Down-Regulate Synaptic Proteins in Hippocampal Neurons. <i>PLoS ONE</i> , 2014, 9, e99958.	2.5	20
71	Reversion of a fungal genetic code alteration links proteome instability with genomic and phenotypic diversification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11079-11084.	7.1	78
72	Selective Inhibition of an Apicoplastic Aminoacyl-tRNA Synthetase from <i>Plasmodium falciparum</i> . <i>ChemBioChem</i> , 2013, 14, 499-509.	2.6	30

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73	Candida albicans CUG Mistranslation Is a Mechanism To Create Cell Surface Variation. MBio, 2013, 4, .	4.1	77
74	mRNA secondary structure optimization using a correlated stem-loop prediction. Nucleic Acids Research, 2013, 41, e73-e73.	14.5	67
75	Molecular reconstruction of a fungal genetic code alteration. RNA Biology, 2013, 10, 968-980.	3.1	6
76	Analysis of the Effects of Sex Hormone Background on the Rat Choroid Plexus Transcriptome by cDNA Microarrays. PLoS ONE, 2013, 8, e60199.	2.5	34
77	Involvement of Yeast HSP90 Isoforms in Response to Stress and Cell Death Induced by Acetic Acid. PLoS ONE, 2013, 8, e71294.	2.5	21
78	Ethanol Exposure Induces Upregulation of Specific MicroRNAs in Zebrafish Embryos. Toxicological Sciences, 2012, 127, 18-28.	3.1	53
79	Novel Method for Evaluating <i>In Vitro</i> Activity of Anidulafungin in Combination with Amphotericin B or Azoles. Journal of Clinical Microbiology, 2012, 50, 2748-2754.	3.9	7
80	An integrative approach for codon repeats evolutionary analyses. International Journal of Data Mining and Bioinformatics, 2012, 6, 369.	0.1	0
81	Next-Generation Sequencing of miRNAs with Roche 454 GS-FLX Technology: Steps for a Successful Application. Methods in Molecular Biology, 2012, 822, 189-204.	0.9	9
82	EuGene: maximizing synthetic gene design for heterologous expression. Bioinformatics, 2012, 28, 2683-2684.	4.1	54
83	Low level genome mistranslations deregulate the transcriptome and translome and generate proteotoxic stress in yeast. BMC Biology, 2012, 10, 55.	3.8	31
84	Cancer syndromes and therapy by stop-codon readthrough. Trends in Molecular Medicine, 2012, 18, 667-678.	6.7	61
85	Dre-miR-2188 Targets Nrp2a and Mediates Proper Intersegmental Vessel Development in Zebrafish Embryos. PLoS ONE, 2012, 7, e39417.	2.5	11
86	Lack of microRNA-101 causes E-cadherin functional deregulation through EZH2 up-regulation in intestinal gastric cancer. Journal of Pathology, 2012, 228, 31-44.	4.5	125
87	Differential gene expression analysis in Enchytraeus albidus exposed to natural and chemical stressors at different exposure periods. Ecotoxicology, 2012, 21, 213-224.	2.4	11
88	Genetic Diversity and Population Structure of Saccharomyces cerevisiae Strains Isolated from Different Grape Varieties and Winemaking Regions. PLoS ONE, 2012, 7, e32507.	2.5	81
89	The genetic code of the fungal CTG clade. Comptes Rendus - Biologies, 2011, 334, 607-611.	0.2	90
90	Systems biology of infectious diseases: a focus on fungal infections. Immunobiology, 2011, 216, 1212-1227.	1.9	30

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91	Protein translation in Plasmodium parasites. Trends in Parasitology, 2011, 27, 467-476.	3.3	79
92	Purification, crystallization and preliminary X-ray diffraction analysis of the seryl-tRNA synthetase from <i>Candida albicans</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 153-156.	0.7	5
93	Expression variability of co-regulated genes differentiates <i>Saccharomyces cerevisiae</i> strains. BMC Genomics, 2011, 12, 201.	2.8	16
94	Genotyping of <i>Saccharomyces cerevisiae</i> strains by interdelta sequence typing using automated microfluidics. Electrophoresis, 2011, 32, 1447-1455.	2.4	19
95	Unveiling the structural basis for translational ambiguity tolerance in a human fungal pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14091-14096.	7.1	43
96	Species-Specific Codon Context Rules Unveil Non-Neutrality Effects of Synonymous Mutations. PLoS ONE, 2011, 6, e26817.	2.5	34
97	Low Complexity Regions behave as tRNA sponges to help co-translational folding of plasmodial proteins. FEBS Letters, 2010, 584, 448-454.	2.8	32
98	Development of the genetic code: Insights from a fungal codon reassignment. FEBS Letters, 2010, 584, 334-341.	2.8	36
99	MicroRNA Expression Variability in Human Cervical Tissues. PLoS ONE, 2010, 5, e11780.	2.5	155
100	An Application for Studying Tandem Repeats in Orthologous Genes. Advances in Intelligent and Soft Computing, 2010, , 109-115.	0.2	0
101	MicroRNA-155 modulates the interleukin-1 signaling pathway in activated human monocyte-derived dendritic cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2735-2740.	7.1	672
102	Parallel DNA pyrosequencing unveils new zebrafish microRNAs. BMC Genomics, 2009, 10, 195.	2.8	65
103	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. Nature, 2009, 459, 657-662.	27.8	963
104	Genetic code ambiguity: an unexpected source of proteome innovation and phenotypic diversity. Current Opinion in Microbiology, 2009, 12, 631-637.	5.1	30
105	The Yeast PNC1 Longevity Gene Is Up-Regulated by mRNA Mistranslation. PLoS ONE, 2009, 4, e5212.	2.5	15
106	Analysing the Evolution of Repetitive Strands in Genomes. Lecture Notes in Computer Science, 2009, , 1047-1054.	1.3	2
107	Comparative genomics of wild type yeast strains unveils important genome diversity. BMC Genomics, 2008, 9, 524.	2.8	111
108	Exploiting Codon-Triplets Association for Genome Primary Structure Analysis. , 2008, , .		0

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109	Studying the Evolution of Codon Context in Conserved Gene Sequences. , 2008, , .		0
110	Surfactants as Microbicides and Contraceptive Agents: A Systematic In Vitro Study. PLoS ONE, 2008, 3, e2913.	2.5	52
111	A genetic code alteration generates a proteome of high diversity in the human pathogen <i>Candida albicans</i> . Genome Biology, 2007, 8, R206.	9.6	99
112	Large Scale Comparative Codon-Pair Context Analysis Unveils General Rules that Fine-Tune Evolution of mRNA Primary Structure. PLoS ONE, 2007, 2, e847.	2.5	90
113	A Genetic Code Alteration Is a Phenotype Diversity Generator in the Human Pathogen <i>Candida albicans</i> . PLoS ONE, 2007, 2, e996.	2.5	45
114	Yeast proteome map (update 2006). Proteomics, 2007, 7, 1117-1120.	2.2	16
115	Critical roles for a genetic code alteration in the evolution of the genus <i>Candida</i> . EMBO Journal, 2007, 26, 4555-4565.	7.8	43
116	Codon-triplet context unveils unique features of the <i>Candida albicans</i> protein coding genome. BMC Genomics, 2007, 8, 444.	2.8	8
117	Computational and Statistical Methodologies for ORFeome Primary Structure Analysis. Methods in Molecular Biology, 2007, 395, 449-462.	0.9	3
118	Evolution of the genetic code in yeasts. Yeast, 2006, 23, 203-213.	1.7	67
119	Comparative context analysis of codon pairs on an ORFeome scale. Genome Biology, 2005, 6, R28.	9.6	85
120	Yeast as a model organism for studying the evolution of nonstandard genetic codes. Briefings in Functional Genomics & Proteomics, 2004, 3, 35-46.	3.8	12
121	A Gene from the Mesophilic Bacterium <i>Dehalococcoides ethenogenes</i> Encodes a Novel Mannosylglycerate Synthase. Journal of Bacteriology, 2004, 186, 4075-4084.	2.2	36
122	Driving change: the evolution of alternative genetic codes. Trends in Genetics, 2004, 20, 95-102.	6.7	133
123	Extant Variations in the Genetic Code. , 2004, , 183-200.		5
124	Comparative Evolutionary Genomics Unveils the Molecular Mechanism of Reassignment of the CTG Codon in <i>Candida</i> spp.. Genome Research, 2003, 13, 544-557.	5.5	111
125	Stop codon decoding in <i>Candida albicans</i> : from non-standard back to standard. Yeast, 2002, 19, 727-733.	1.7	4
126	The <i>Candida albicans</i> gene encoding the cytoplasmic leucyl-tRNA synthetase: implications for the evolution of CUG codon reassignment. Gene, 2001, 275, 133-140.	2.2	7



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127	Seryl-tRNA synthetase is not responsible for the evolution of CUG codon reassignment in <i>Candida albicans</i> . <i>Yeast</i> , 2001, 18, 313-322.	1.7	7
128	Selective advantages created by codon ambiguity allowed for the evolution of an alternative genetic code in <i>Candida</i> spp.. <i>Molecular Microbiology</i> , 1999, 31, 937-947.	2.5	99
129	The <i>Candida albicans</i> CUG-decoding ser-tRNA has an atypical anticodon stem-loop structure 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 293, 1039-1053.	4.2	25
130	beta, a novel repetitive DNA element associated with tRNA genes in the pathogenic yeast <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 1997, 25, 229-236.	2.5	10
131	The non- $\epsilon$ standard genetic code of <i>Candida</i> spp.: an evolving genetic code or a novel mechanism for adaptation?. <i>Molecular Microbiology</i> , 1997, 26, 423-431.	2.5	77
132	Codon reassignment in <i>Candida</i> species: An evolutionary conundrum. <i>Biochimie</i> , 1996, 78, 993-999.	2.6	28
133	The CUG codon is decoded in vivo as serine and not leucine in <i>Candida albicans</i> . <i>Nucleic Acids Research</i> , 1995, 23, 1481-1486.	14.5	244
134	Transfer RNA profiling: A new method for the identification of pathogenic <i>Candida</i> species. <i>Yeast</i> , 1994, 10, 625-636.	1.7	13
135	New insights into mRNA decoding $\hat{\epsilon}$ implications for heterologous protein synthesis. <i>Trends in Biotechnology</i> , 1993, 11, 500-505.	9.3	22
136	Presence and coding properties of 2-O-methyl-5-carbamoylmethyluridine (ncm <sup>5</sup> Um) in the wobble position of the anticodon of tRNA <sup>Leu</sup> (U <sup>3</sup> AA) from brewer's yeast. <i>FEBS Letters</i> , 1992, 314, 381-385.	2.8	24
137	<i>Candida albicans</i> and three other <i>Candida</i> species contain an elongation factor structurally and functionally analogous to elongation factor 3. <i>FEMS Microbiology Letters</i> , 1991, 80, 45-50.	1.8	25
138	Efficient translation of the UAG termination codon in <i>Candida</i> species. <i>Current Genetics</i> , 1990, 17, 487-491.	1.7	33
139	The Genetic Code of the <i>Candida</i> CTG Clade. , 0, , 45-55.		0
140	Computational and Statistical Methodologies for ORFeome Primary Structure Analysis. , 0, , 449-462.		0