Xavier Soberon

List of Publications by Year
in descending order

59	3,274	257450 24	161849 54
papers	citations	h-index	g-index

61	61	61	6576
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The genomes of four tapeworm species reveal adaptations to parasitism. Nature, 2013, 496, 57-63.	27.8	603
2	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. Science, 2014, 344, 1280-1285.	12.6	420
3	Plasmid vector pBR322 and its special-purpose derivatives â€" a review. Gene, 1986, 50, 3-40.	2.2	321
4	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
5	Association of a Low-Frequency Variant inHNF1AWith Type 2 Diabetes in a Latino Population. JAMA - Journal of the American Medical Association, 2014, 311, 2305.	7.4	230
6	Combining metagenomics, metatranscriptomics and viromics to explore novel microbial interactions: towards a systems-level understanding of human microbiome. Computational and Structural Biotechnology Journal, 2015, 13, 390-401.	4.1	182
7	Construction and characterization of new cloning vehicles V. Mobilization and coding properties of pBR322 and several deletion derivatives including pBR327 and pBR328. Gene, 1981, 13, 25-35.	2.2	163
8	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	28.9	121
9	A proposed architecture for the central domain of the bacterial enhancer-binding proteins based on secondary structure prediction and fold recognition. Protein Science, 1997, 6, 543-555.	7.6	60
10	Genome analysis of Excretory/Secretory proteins in Taenia solium reveals their Abundance of Antigenic Regions (AAR). Scientific Reports, 2015, 5, 9683.	3.3	54
11	A Loss-of-Function Splice Acceptor Variant in IGF2 Is Protective for Type 2 Diabetes. Diabetes, 2017, 66, 2903-2914.	0.6	52
12	Demographic history and biologically relevant genetic variation of Native Mexicans inferred from whole-genome sequencing. Nature Communications, 2017, 8, 1005.	12.8	44
13	In vivo studies on the positive control function of NifA: a conserved hydrophobic amino acid patch at the central domain involved in transcriptional activation. Molecular Microbiology, 2002, 28, 55-67.	2.5	40
14	Â-Amylase from Bacillus licheniformis mutants near to the catalytic site: effects on hydrolytic and transglycosylation activity. Protein Engineering, Design and Selection, 2003, 16, 505-514.	2.1	40
15	Exploring the Structureâ€"Function Loop Adaptability of a (Î²/Î±)8-Barrel Enzyme through Loop Swapping and Hinge Variability. Journal of Molecular Biology, 2011, 411, 143-157.	4.2	37
16	Different strategies to recover the activity of monomeric triosephosphate isomerase by directed evolution. Protein Engineering, Design and Selection, 2001, 14, 149-155.	2.1	30
17	Improving a circularly permuted TEM-1 Î²-lactamase by directed evolution. Protein Engineering, Design and Selection, 2002, 15, 463-470.	2.1	30
18	Substitution of Asp for Asn at Position 132 in the Active Site of TEM Î² -Lactamase. Journal of Biological Chemistry, 1995, 270, 775-780.	3.4	29

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19	Saturation mutagenesis of His114 of EcoRI reveals relaxed-specificity mutants. Gene, 1995, 157, 295-301.	2.2	29
20	A New TEM Î² -Lactamase Double Mutant with Broadened Specificity Reveals Substrate-dependent Functional Interactions. Journal of Biological Chemistry, 1995, 270, 781-787.	3.4	28
21	Combinatorial codon-based amino acid substitutions. Nucleic Acids Research, 2004, 32, e158-e158.	14.5	28
22	Protein Design through Systematic Catalytic Loop Exchange in the (Î²/Î±)8 Fold. Journal of Molecular Biology, 2009, 387, 949-964.	4.2	28
23	Combinatorial mutagenesis of three major groove-contacting residues of EcoRI: single and double amino acid replacements retaining methyltransferase-sensitive activities. Gene, 1991, 106, 7-12.	2.2	26
24	Did cyclodextrin glycosyltransferases evolve from Î±-amylases?. FEBS Letters, 1997, 416, 221-224.	2.8	25
25	Introducing transglycosylation activity in a liquefying Î±-amylase. FEBS Letters, 1999, 453, 100-106.	2.8	25
26	Combination of DMT-mononucleotide and Fmoc-trinucleotide phosphoramidites in oligonucleotide synthesis affords an automatable codon-level mutagenesis method. Chemistry and Biology, 1998, 5, 519-527.	6.0	24
27	The Plasmid, pBR322. , 1988, 10, 5-41.		21
28	Protein evolution by codon-based random deletions. Nucleic Acids Research, 2004, 32, e136-e136.	14.5	20
29	Identification and characterization of Taenia solium enolase as a plasminogen-binding protein. Acta Tropica, 2018, 182, 69-79.	2.0	19
30	In vivo fragment complementation of a (Î²/Î±)8barrel protein: generation of variability by recombination. FEBS Letters, 2004, 560, 167-172.	2.8	18
31	Production of a fully functional, permuted single-chain penicillin G acylase. Protein Science, 2004, 13, 1677-1683.	7.6	17
32	Evolutionary Walk between (Î²/Î±)8 Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. Journal of Molecular Biology, 2012, 416, 255-270.	4.2	17
33	Temperature-sensitive mutants of the EcoRI endonuclease. Journal of Molecular Biology, 1997, 274, 722-737.	4.2	16
34	Exploring Variation in Known Pharmacogenetic Variants and its Association with Drug Response in Different Mexican Populations. Pharmaceutical Research, 2016, 33, 2644-2652.	3.5	16
35	Prediction of atorvastatin plasmatic concentrations in healthy volunteers using integrated pharmacogenetics sequencing. Pharmacogenomics, 2017, 18, 121-131.	1.3	16
36	The effect of amino acid deletions and substitutions in the longest loop of GFP. BMC Chemical Biology, 2007, 7, 1.	1.6	15

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37	Enhancement of the Alcoholytic Activity of Î±-Amylase AmyA fromThermotoga maritimaMSB8 (DSM 3109) by Site-Directed Mutagenesis. Applied and Environmental Microbiology, 2008, 74, 5168-5177.	3.1	15
38	Genotype frequencies of VKORC1 and CYP2C9 in Native and Mestizo populations from Mexico, potential impact for coumarin dosing. Gene, 2015, 558, 235-240.	2.2	15
39	Variation in Actionable Pharmacogenetic Markers in Natives and Mestizos From Mexico. Frontiers in Pharmacology, 2019, 10, 1169.	3.5	15
40	MutantEscherichia colipenicillin acylase with enhanced stability at alkaline pH. Biotechnology and Bioengineering, 1995, 48, 141-148.	3.3	13
41	Novel ceftazidime-resistance beta-lactamases generated by a codon-based mutagenesis method and selection. Nucleic Acids Research, 2002, 30, 84e-84.	14.5	12
42	Quantitative multiplexed proteomics of Taenia solium cysts obtained from the skeletal muscle and central nervous system of pigs. PLoS Neglected Tropical Diseases, 2017, 11, e0005962.	3.0	12
43	Fate of uptaken host proteins in Taenia solium and Taenia crassiceps cysticerci. Bioscience Reports, 2018, 38, .	2.4	11
44	Role of porcine serum haptoglobin in the host-parasite relationship of Taenia solium cysticercosis. Molecular and Biochemical Parasitology, 2016, 207, 61-67.	1.1	10
45	Microbial Systems and Directed Evolution of Protein Activities. Critical Reviews in Microbiology, 1994, 20, 107-116.	6.1	9
46	Microbial sensor for new-generation cephalosporins based in a protein-engineered Î²- lactamase. Applied Biochemistry and Biotechnology, 1998, 73, 243-256.	2.9	9
47	Identification and analysis of residues contained on Î² â†' Î± loops of the dualâ€substrate (Î²Î±)₈ phosphoribosyl isomerase A specific for its phosphoribosyl anthranilate isomerase activity. Protein Science, 2010, 19, 535-543.	7.6	9
48	Whole genome variation in 27 Mexican indigenous populations, demographic and biomedical insights. PLoS ONE, 2021, 16, e0249773.	2.5	8
49	Experimental and Theoretical Approaches To Investigate the Immunogenicity of Taenia solium-Derived KE7 Antigen. Infection and Immunity, 2017, 85, .	2.2	7
50	Pharmacogenetic Variation in Over 100 Genes in Patients Receiving Acenocumarol. Frontiers in Pharmacology, 2017, 8, 863.	3.5	7
51	Alternative Splice Variants in TIM Barrel Proteins from Human Genome Correlate with the Structural and Evolutionary Modularity of this Versatile Protein Fold. PLoS ONE, 2013, 8, e70582.	2.5	7
52	A more Efficient Starch Degradation by the Combination of Hydrolase and Transferase Activities ofÎ±-Amylase and Cyclomaltodextrin Glucanotransferase. Starch/Staerke, 2004, 56, 63-68.	2.1	6
53	Improvement of an Unusual Twin-Arginine Transporter Leader Peptide by a Codon-Based Randomization Approach. Applied and Environmental Microbiology, 2006, 72, 3797-3801.	3.1	4
54	Exploratory Analysis of Rare and Novel Variants in Mexican Patients Diagnosed with Schizophrenia and Dementia. Revista De Investigacion Clinica, 2019, 71, 246-254.	0.4	4

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55	An Engineered Penicillin Acylase with Altered Surface Charge Is More Stable in Alkaline pH. Annals of the New York Academy of Sciences, 1996, 799, 61-64.	3.8	2
56	Microbiome-MX 2018: microbiota and microbiome opportunities in Mexico, a megadiverse country. Research in Microbiology, 2019, 170, 235-241.	2.1	2
57	Association of FAAH p.Pro129Thr and COMT p.Ala72Ser with schizophrenia and comorbid substance use through next-generation sequencing: an exploratory analysis. Revista Brasileira De Psiquiatria, 2021, , .	1.7	2
58	Enzymes directly evolving toward commercial applications. Nature Biotechnology, 1999, 17, 539-540.	17.5	1
59	Generation of variability by in vivo recombination of halves of a (Î²/Î±)8 barrel protein. New Biotechnology, 2005, 22, 113-120.	2.7	1