Roberto Sanchez

List of Publications by Year
in descending order

60 papers	7,853 citations	136885 32 h-index	149623 56 g-index
62 all docs	62 docs citations	62 times ranked	12490 citing authors

#	Article	IF	Citations
1	Comparative Protein Structure Modeling of Genes and Genomes. Annual Review of Biophysics and Biomolecular Structure, 2000, 29, 291-325.	18.3	2,811
2	The PHD finger: a versatile epigenome reader. Trends in Biochemical Sciences, 2011, 36, 364-72.	3.7	343
3	Accuracy of structure-derived properties in simple comparative models of protein structures. Nucleic Acids Research, 2005, 33, 244-259.	6.5	329
4	A high-throughput chemical screen reveals that harmine-mediated inhibition of DYRK1A increases human pancreatic beta cell replication. Nature Medicine, 2015, 21, 383-388.	15.2	313
5	Statistical potentials for fold assessment. Protein Science, 2002, 11, 430-448.	3.1	304
6	Advances in comparative protein-structure modelling. Current Opinion in Structural Biology, 1997, 7, 206-214.	2.6	289
7	lynx1, an Endogenous Toxin-like Modulator of Nicotinic Acetylcholine Receptors in the Mammalian CNS. Neuron, 1999, 23, 105-114.	3.8	285
8	Structural Mechanism of the Bromodomain of the Coactivator CBP in p53 Transcriptional Activation. Molecular Cell, 2004, 13, 251-263.	4.5	285
9	Evaluation of comparative protein structure modeling by MODELLER-3. Proteins: Structure, Function and Bioinformatics, 1997, 29, 50-58.	1.5	207
10	Protein structure modeling for structural genomics. Nature Structural Biology, 2000, 7, 986-990.	9.7	199
11	Comparative Protein Structure Modeling: Introduction and Practical Examples with Modeller. , 2000, 143, 97-129.		193
12	SITEHOUND-web: a server for ligand binding site identification in protein structures. Nucleic Acids Research, 2009, 37, W413-W416.	6.5	181
13	Ligand Specificity of Brain Lipid-binding Protein. Journal of Biological Chemistry, 1996, 271, 24711-24719.	1.6	166
14	The bromodomain: From epigenome reader to druggable target. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 676-685.	0.9	157
15	Modern Homology Modeling of G-Protein Coupled Receptors: Which Structural Template to Use?. Journal of Medicinal Chemistry, 2009, 52, 5207-5216.	2.9	146
16	The role of human bromodomains in chromatin biology and gene transcription. Current Opinion in Drug Discovery & Development, 2009, 12, 659-65.	1.9	146
17	Small-molecule activation of SERCA2a SUMOylation for the treatment of heart failure. Nature Communications, 2015, 6, 7229.	5.8	102
18	Evaluation of comparative protein structure modeling by MODELLERâ€3. Proteins: Structure, Function and Bioinformatics, 1997, 29, 50-58.	1.5	88

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19	Improving accuracy and efficiency of blind proteinâ€ligand docking by focusing on predicted binding sites. Proteins: Structure, Function and Bioinformatics, 2009, 74, 417-424.	1.5	82
20	GLP-1 receptor agonists synergize with DYRK1A inhibitors to potentiate functional human Î² cell regeneration. Science Translational Medicine, 2020, 12, .	5.8	81
21	E<scp>asy</scp>MIF<scp>s</scp> and S<scp>ite</scp>H<scp>ound</scp>: a toolkit for the identification of ligand-binding sites in protein structures. Bioinformatics, 2009, 25, 3185-3186.	1.8	70
22	Privileged Diazepine Compounds and Their Emergence as Bromodomain Inhibitors. Chemistry and Biology, 2014, 21, 573-583.	6.2	59
23	Homology-based annotation yields 1,042 new candidate genes in the Drosophila melanogaster genome. Nature Genetics, 2001, 27, 337-340.	9.4	58
24	Variable gap penalty for protein sequenceâ€“structure alignment. Protein Engineering, Design and Selection, 2006, 19, 129-133.	1.0	58
25	Development of Kinase-Selective, Harmine-Based DYRK1A Inhibitors that Induce Pancreatic Human Î²-Cell Proliferation. Journal of Medicinal Chemistry, 2018, 61, 7687-7699.	2.9	58
26	Bacillus subtilis YhaM, a Member of a New Family of 3â€²-to-5â€² Exonucleases in Gram-Positive Bacteria. Journal of Bacteriology, 2002, 184, 6250-6259.	1.0	50
27	Suramin inhibits cullin-RING E3 ubiquitin ligases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2011-8.	3.3	50
28	Beyond structural genomics: computational approaches for the identification of ligand binding sites in protein structures. Journal of Structural and Functional Genomics, 2011, 12, 109-117.	1.2	44
29	Dissecting the Contributions of Cooperating Gene Mutations to Cancer Phenotypes and Drug Responses with Patient-Derived iPSCs. Stem Cell Reports, 2018, 10, 1610-1624.	2.3	43
30	An NR2F1-specific agonist suppresses metastasis by inducing cancer cell dormancy. Journal of Experimental Medicine, 2022, 219, .	4.2	42
31	SiteComp: a server for ligand binding site analysis in protein structures. Bioinformatics, 2012, 28, 1172-1173.	1.8	36
32	Synthesis and Biological Validation of a Harmine-Based, Central Nervous System (CNS)-Avoidant, Selective, Human Î²-Cell Regenerative Dual-Specificity Tyrosine Phosphorylation-Regulated Kinase A (DYRK1A) Inhibitor. Journal of Medicinal Chemistry, 2020, 63, 2986-3003.	2.9	36
33	Pharmacologic and genetic approaches define human pancreatic Î² cell mitogenic targets of DYRK1A inhibitors. JCI Insight, 2020, 5, .	2.3	35
34	Biochemical Profiling of Histone Binding Selectivity of the Yeast Bromodomain Family. PLoS ONE, 2010, 5, e8903.	1.1	33
35	Comparative Protein Structure Modeling in Genomics. Journal of Computational Physics, 1999, 151, 388-401.	1.9	29
36	Pivotal role for the ubiquitin Y59-E51 loop in lysine 48 polyubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8434-8439.	3.3	24

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37	Structural features and inhibitors of bromodomains. Drug Discovery Today: Technologies, 2016, 19, 3-15.	4.0	23
38	Systematic analysis of the effect of multiple templates on the accuracy of comparative models of protein structure. BMC Structural Biology, 2008, 8, 31.	2.3	22
39	Convallatoxin-Induced Reduction of Methionine Import Effectively Inhibits Human Cytomegalovirus Infection and Replication. Journal of Virology, 2016, 90, 10715-10727.	1.5	22
40	DHTKD1 and OGDH display substrate overlap in cultured cells and form a hybrid 2-oxo acid dehydrogenase complex in vivo. Human Molecular Genetics, 2020, 29, 1168-1179.	1.4	21
41	A human liver cell-based system modeling a clinical prognostic liver signature for therapeutic discovery. Nature Communications, 2021, 12, 5525.	5.8	21
42	Scaling the Druggability Landscape of Human Bromodomains, a New Class of Drug Targets. Journal of Medicinal Chemistry, 2012, 55, 7342-7345.	2.9	20
43	Systematic Analysis of Added-Value in Simple Comparative Models of Protein Structure. Structure, 2004, 12, 1461-1470.	1.6	19
44	Evaluation of comparative protein structure modeling by MODELLER-3. Proteins: Structure, Function and Bioinformatics, 1997, 29, 50-58.	1.5	19
45	Bacillus subtilis YhcR, a High-Molecular-Weight, Nonspecific Endonuclease with a Unique Domain Structure. Journal of Bacteriology, 2004, 186, 5376-5383.	1.0	15
46	Inhibition and Crystal Structure of the Human DHTKD1-Thiamin Diphosphate Complex. ACS Chemical Biology, 2020, 15, 2041-2047.	1.6	14
47	Structureâ€“Activity Relationships and Biological Evaluation of 7-Substituted Harmine Analogs for Human Î²-Cell Proliferation. Molecules, 2020, 25, 1983.	1.7	13
48	Discovery and characterization of small-molecule inhibitors of NLRP3 and NLRC4 inflammasomes. Journal of Biological Chemistry, 2021, 296, 100597.	1.6	13
49	Comparative protein structure modeling as an optimization problem. Computational and Theoretical Chemistry, 1997, 398-399, 489-496.	1.5	12
50	Cell type-specific pharmacological kinase inhibition for cancer chemoprevention. Nanomedicine: Nanotechnology, Biology, and Medicine, 2018, 14, 317-325.	1.7	12
51	ChEpiMod: a knowledgebase for chemical modulators of epigenome reader domains. Bioinformatics, 2014, 30, 1481-1483.	1.8	11
52	Inhibitors of cullin-RING E3 ubiquitin ligase 4 with antitumor potential. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	9
53	Photochemical Control of Drug Efficacy: A Comparison of Uncaging and Photoswitching Ifenprodil on NMDA Receptors. ChemPhotoChem, 2021, 5, 445-454.	1.5	8
54	Comparative Protein Structure Modeling. , 2001, , .		5

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55	Automated identification of binding sites for phosphorylated ligands in protein structures. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2347-2358.	1.5	3
56	Systematic assessment of accuracy of comparative model of proteins belonging to different structural fold classes. Journal of Molecular Modeling, 2011, 17, 2831-2837.	0.8	2
57	In Silico Modeling of Novel Drug Ligands for Treatment of Concussion Associated Tauopathy. Journal of Cellular Biochemistry, 2016, 117, 2241-2248.	1.2	1
58	P3-060: ACTIVATION OF ECTOPICALLY EXPRESSED OLFACTORY RECEPTORS IN THE BRAIN ATTENUATES TAU-PROCESSING IN RESPONSE TO MILD TRAUMATIC BRAIN INJURY. , 2014, 10, P649-P650.		0
59	Recovering Bound Forms of Protein Structures Using the Elastic Network Model and Molecular Interaction Fields. , 2016, , .		0
60	Identification of small molecule ligands targeting GPR83, a Gâ€protein coupled receptor activated by the abundant neuropeptide PEN. FASEB Journal, 2018, 32, 829.9.	0.2	0