Xavier De la Cruz

List of Publications by Year
in descending order

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79 papers	3,588 citations	257101 24 h-index	143772 57 g-index
82 all docs	82 docs citations	82 times ranked	6692 citing authors

#	Article	IF	Citations
1	Cerebrospinal fluid-derived circulating tumour DNA better represents the genomic alterations of brain tumours than plasma. Nature Communications, 2015, 6, 8839.	5.8	605
2	PMUT: a web-based tool for the annotation of pathological mutations on proteins. Bioinformatics, 2005, 21, 3176-3178.	1.8	441
3	PupasView: a visual tool for selecting suitable SNPs, with putative pathological effect in genes, for genotyping purposes. Nucleic Acids Research, 2005, 33, W501-W505.	6.5	253
4	Do protein motifs read the histone code?. BioEssays, 2005, 27, 164-175.	1.2	220
5	Characterization of disease-associated single amino acid polymorphisms in terms of sequence and structure properties 1 1Edited by J. Thornton. Journal of Molecular Biology, 2002, 315, 771-786.	2.0	194
6	PMut: a web-based tool for the annotation of pathological variants on proteins, 2017 update. Nucleic Acids Research, 2017, 45, W222-W228.	6.5	184
7	Sequence-based prediction of pathological mutations. Proteins: Structure, Function and Bioinformatics, 2004, 57, 811-819.	1.5	156
8	Triplex-forming oligonucleotide target sequences in the human genome. Nucleic Acids Research, 2004, 32, 354-360.	6.5	149
9	Genome-wide analysis reveals that Smad3 and JMJD3 HDM co-activate the neural developmental program. Development (Cambridge), 2012, 139, 2681-2691.	1.2	100
10	Classical molecular interaction potentials: Improved setup procedure in molecular dynamics simulations of proteins. Proteins: Structure, Function and Bioinformatics, 2001, 45, 428-437.	1.5	87
11	Scoring by Intermolecular Pairwise Propensities of Exposed Residues (SIPPER): A New Efficient Potential for Proteinâ˜Protein Docking. Journal of Chemical Information and Modeling, 2011, 51, 370-377.	2.5	70
12	The (In)dependence of Alternative Splicing and Gene Duplication. PLoS Computational Biology, 2007, 3, e33.	1.5	66
13	Autoacetylation Regulates P/CAF Nuclear Localization. Journal of Biological Chemistry, 2009, 284, 1343-1352.	1.6	62
14	Exploring the Essential Dynamics of B-DNA. Journal of Chemical Theory and Computation, 2005, 1, 790-800.	2.3	61
15	Toward predicting protein topology: An approach to identifying Â hairpins. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11157-11162.	3.3	48
16	An Atomistic View to the Gas Phase Proteome. Structure, 2009, 17, 88-95.	1.6	44
17	Characterization of Compensated Mutations in Terms of Structural and Physico-Chemical Properties. Journal of Molecular Biology, 2007, 365, 249-256.	2.0	43
18	The Complementarity Between Protein-Specific and General Pathogenicity Predictors for Amino Acid Substitutions. Human Mutation, 2016, 37, 1013-1024.	1.1	42

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19	PHF2 histone demethylase prevents DNA damage and genome instability by controlling cell cycle progression of neural progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19464-19473.	3.3	35
20	The SV40 T antigen modulates CBP histone acetyltransferase activity. Nucleic Acids Research, 2003, 31, 3114-3122.	6.5	34
21	Epigenetic signature for attention-deficit/hyperactivity disorder: identification of miR-26b-5p, miR-185-5p, and miR-191-5p as potential biomarkers in peripheral blood mononuclear cells. Neuropsychopharmacology, 2019, 44, 890-897.	2.8	31
22	EZH2 regulates neuroepithelium structure and neuroblast proliferation by repressing p21. Open Biology, 2016, 6, 150227.	1.5	30
23	Exploring the Binding Mode of Semicarbazide-Sensitive Amine Oxidase/VAP-1:Â Identification of Novel Substrates with Insulin-like Activity. Journal of Medicinal Chemistry, 2004, 47, 4865-4874.	2.9	27
24	Elucidating the molecular basis of MSH2â€deficient tumors by combined germline and somatic analysis. International Journal of Cancer, 2017, 141, 1365-1380.	2.3	26
25	hSos1 Contains a New Amino-terminal Regulatory Motif with Specific Binding Affinity for Its Pleckstrin Homology Domain. Journal of Biological Chemistry, 2002, 277, 44171-44179.	1.6	25
26	Lineage specific transcription factors and epigenetic regulators mediate TGFÎ²-dependent enhancer activation. Nucleic Acids Research, 2018, 46, 3351-3365.	6.5	24
27	Molecular damage in <scp>F</scp>abry disease: Characterization and prediction of alphaâ€galactosidase <scp>A</scp> pathological mutations. Proteins: Structure, Function and Bioinformatics, 2015, 83, 91-104.	1.5	23
28	A new procedure for constructing peptides into a given C. Folding & Design, 1998, 3, 1-10.	4.5	22
29	Alternative Splicing Mechanisms for the Modulation of Protein Function: Conservation Between Human and Other Species. Journal of Molecular Biology, 2004, 335, 495-502.	2.0	21
30	Involvement of chromatin and histone deacetylation in SV40 T antigen transcription regulation. Nucleic Acids Research, 2007, 35, 1958-1968.	6.5	20
31	Use of bioinformatics tools for the annotation of disease-associated mutations in animal models. Proteins: Structure, Function and Bioinformatics, 2005, 61, 878-887.	1.5	19
32	Prediction of pathological mutations in proteins: the challenge of integrating sequence conservation and structure stability principles. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2014, 4, 249-268.	6.2	19
33	Functional consequences of transferrin receptorâ€2 mutations causing hereditary hemochromatosis type 3. Molecular Genetics & Genomic Medicine, 2015, 3, 221-232.	0.6	19
34	Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. Human Mutation, 2019, 40, 1546-1556.	1.1	19
35	Factors limiting the performance of predictionâ€based fold recognition methods. Protein Science, 1999, 8, 750-759.	3.1	18
36	Structural and Computational Characterization of Disease-Related Mutations Involved in Protein-Protein Interfaces. International Journal of Molecular Sciences, 2019, 20, 1583.	1.8	17

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37	Investigation of shape variations in the antibody binding site by molecular dynamics computer simulation. Journal of Molecular Biology, 1994, 236, 1186-1195.	2.0	16
38	The functional modulation of epigenetic regulators by alternative splicing. BMC Genomics, 2007, 8, 252.	1.2	14
39	Alternative Splicing of Transcription Factors' Genes: Beyond the Increase of Proteome Diversity. Comparative and Functional Genomics, 2009, 2009, 1-6.	2.0	14
40	Clinical and structural impact of mutations affecting the residue Phe367 of FOXP3 in patients with IPEX syndrome. Clinical Immunology, 2016, 163, 60-65.	1.4	14
41	Development of pathogenicity predictors specific for variants that do not comply with clinical guidelines for the use of computational evidence. BMC Genomics, 2017, 18, 569.	1.2	14
42	Increased dNTP pools rescue mtDNA depletion in human POLGâ€deficient fibroblasts. FASEB Journal, 2019, 33, 7168-7179.	0.2	14
43	A Collaborative Effort to Define Classification Criteria forATMVariants in Hereditary Cancer Patients. Clinical Chemistry, 2021, 67, 518-533.	1.5	14
44	Novel Mutations Causing C5 Deficiency in Three North-African Families. Journal of Clinical Immunology, 2016, 36, 388-396.	2.0	13
45	Early Versus Late Diagnosis of Complement Factor I Deficiency: Clinical Consequences Illustrated in Two Families with Novel Homozygous CFI Mutations. Journal of Clinical Immunology, 2017, 37, 781-789.	2.0	13
46	New genes involved in Angelman syndrome-like: Expanding the genetic spectrum. PLoS ONE, 2021, 16, e0258766.	1.1	13
47	Data Mining of Molecular Dynamics Trajectories of Nucleic Acids. Journal of Biomolecular Structure and Dynamics, 2006, 23, 447-455.	2.0	12
48	The histone demethylase PHF8 is a molecular safeguard of the IFNÎ³ response. Nucleic Acids Research, 2017, 45, gkw1346.	6.5	12
49	Preservation of protein clefts in comparative models. BMC Structural Biology, 2008, 8, 2.	2.3	11
50	BRCA1 â€and BRCA2 â€specific in silico tools for variant interpretation in the CAGI 5 ENIGMA challenge. Human Mutation, 2019, 40, 1593-1611.	1.1	11
51	The structural homology between uteroglobin and the poreâ€forming domain of colicin A suggests a possible mechanism of action for uteroglobin. Protein Science, 1996, 5, 857-861.	3.1	10
52	Identification and characterization of a novel splice site mutation in the SERPING1 gene in a family with hereditary angioedema. Clinical Immunology, 2014, 150, 143-148.	1.4	10
53	Molecular Dynamics Study of Naturally Existing Cavity Couplings in Proteins. PLoS ONE, 2015, 10, e0119978.	1.1	10
54	Representation of noncovalent interactions in protein structures. Journal of Molecular Graphics, 1992, 10, 96-100.	1.7	8

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55	Discrete representations of the protein CÎ± chain. Folding & Design, 1997, 2, 223-234.	4.5	8
56	Use of surface area computations to describe atom-atom interactions. , 2001, 15, 521-532.		8
57	Linear response theory: An alternative to PB and GB methods for the analysis of molecular dynamics trajectories?. Proteins: Structure, Function and Bioinformatics, 2004, 57, 458-467.	1.5	8
58	Partition of protein solvation into group contributions from molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2004, 58, 101-109.	1.5	8
59	Identification and characterization of the novel point mutation m.3634A>G in the mitochondrial MT - ND1 gene associated with LHON syndrome. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 182-187.	1.8	8
60	Loss of microRNA-135b Enhances Bone Metastasis in Prostate Cancer and Predicts Aggressiveness in Human Prostate Samples. Cancers, 2021, 13, 6202.	1.7	8
61	Characterization of structural variability sheds light on the specificity determinants of the interaction between effector domains and histone tails. Epigenetics, 2010, 5, 137-148.	1.3	7
62	The computational approach to variant interpretation. , 2021, , 89-119.		6
63	A procedure for identifying homologous alternative splicing events. BMC Bioinformatics, 2007, 8, 260.	1.2	5
64	Characterization of the impact of alternative splicing on protein dynamics: The cases of glutathione Sâ€transferase and ectodysplasinâ€A isoforms. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2235-2249.	1.5	5
65	The histone demethylase PHF8 regulates astrocyte differentiation and function. Development (Cambridge), 2021, 148, .	1.2	5
66	The Relationship between Gene Isoform Multiplicity, Number of Exons and Protein Divergence. PLoS ONE, 2013, 8, e72742.	1.1	5
67	Atomic accessible and contact surfaces as restraints in the Hendrickson & Konnert refinement program. Journal of Applied Crystallography, 1991, 24, 941-946.	1.9	4
68	Use of structure comparison methods for the refinement of protein structure predictions. I. Identifying the structural family of a protein from low-resolution models. Proteins: Structure, Function and Bioinformatics, 2002, 46, 72-84.	1.5	4
69	FHLdb: A Comprehensive Database on the Molecular Basis of Familial Hemophagocytic Lymphohistiocytosis. Frontiers in Immunology, 2020, 11, 107.	2.2	4
70	A fast method for the determination of fractional contributions to solvation in proteins. Protein Science, 2006, 15, 2525-2533.	3.1	3
71	Elucidating the clinical significance of two PMS2 missense variants coexisting in a family fulfilling hereditary cancer criteria. Familial Cancer, 2017, 16, 501-507.	0.9	3
72	Improving the diagnosis of cobalamin and related defects by genomic analysis, plus functional and structural assessment of novel variants. Orphanet Journal of Rare Diseases, 2018, 13, 125.	1.2	3

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73	Compensated pathogenic variants in coagulation factors VIII and IX present complex mapping between molecular impact and hemophilia severity. Scientific Reports, 2019, 9, 9538.	1.6	3
74	Molecular analysis of the novel L243R mutation in STXBP2 reveals impairment of degranulation activity. International Journal of Hematology, 2020, 111, 440-450.	0.7	2
75	Alternative Splicing as a Source of Phenotypic Differences Between Species: Protein-Level Mechanisms. , 2012, , 343-356.		1
76	PirePred. Journal of Molecular Diagnostics, 2022, 24, 406-425.	1.2	1
77	Front Cover, Volume 40, Issue 9. Human Mutation, 2019, 40, i.	1.1	0
78	F5EPIGENETIC SIGNATURE FOR ATTENTION DEFICIT HYPERACTIVITY DISORDER: IDENTIFICATION OF MIR-23A-5P, MIR-26B-5P, MIR-185-5P AND MIR-191-5P AS A POTENTIAL BIOMARKER IN PERIPHERAL BLOOD MONONUCLEAR CELLS. European Neuropsychopharmacology, 2019, 29, S1112.	0.3	0
79	Towards a New, Endophenotype-Based Strategy for Pathogenicity Prediction in BRCA1 and BRCA2: In Silico Modeling of the Outcome of HDR/SGE Assays for Missense Variants. International Journal of Molecular Sciences, 2021, 22, 6226.	1.8	0