

Jens Erik Nielsen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3751335/publications.pdf>

Version: 2024-02-01

35
papers

3,126
citations

393982

19
h-index

377514

34
g-index

35
all docs

35
docs citations

35
times ranked

4779
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of a GH51 β -D-arabinofuranosidase from <i>Meripilus giganteus</i> : conserved substrate recognition from bacteria to fungi. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1124-1133.	1.1	8
2	Structure and Dynamics of a Promiscuous Xanthan Lyase from <i>Paenibacillus nanensis</i> and the Design of Variants with Increased Stability and Activity. <i>Cell Chemical Biology</i> , 2019, 26, 191-202.e6.	2.5	13
3	Investigation of Ionization Pattern of the Adjacent Acidic Residues in the DXDXE Motif of GH-18 Chitinases Using Theoretical pK _a Calculations. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 572-583.	2.5	7
4	Coupled effect of salt and pH on proteins probed with NMR spectroscopy. <i>Chemical Physics Letters</i> , 2013, 579, 114-121.	1.2	13
5	Protein Dielectric Constants Determined from NMR Chemical Shift Perturbations. <i>Journal of the American Chemical Society</i> , 2013, 135, 16968-16976.	6.6	82
6	Highly Perturbed pKa Values in the Unfolded State of Hen Egg White Lysozyme. <i>Biophysical Journal</i> , 2012, 102, 1636-1645.	0.2	9
7	DataPipeline: Automated importing and fitting of large amounts of biophysical data. <i>Journal of Computational Chemistry</i> , 2012, 33, 2357-2362.	1.5	2
8	Toward Fast Determination of Protein Stability Maps: Experimental and Theoretical Analysis of Mutants of a <i>Nocardioopsis prasina</i> Serine Protease. <i>Biochemistry</i> , 2012, 51, 5339-5347.	1.2	6
9	A collaborative environment for developing and validating predictive tools for protein biophysical characteristics. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 387-396.	1.3	1
10	Predicting the open conformations of protein kinases using molecular dynamics simulations. <i>Biopolymers</i> , 2012, 97, 65-72.	1.2	7
11	Constructing and Evaluating Predictive Models for Protein Biophysical Characteristics. <i>Annual Reports in Computational Chemistry</i> , 2011, , 101-124.	0.9	2
12	Integrated prediction of the effect of mutations on multiple protein characteristics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 165-178.	1.5	19
13	Remeasuring HEWL pK _a values by NMR spectroscopy: Methods, analysis, accuracy, and implications for theoretical pK _a calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 685-702.	1.5	89
14	On the development of protein pK _a calculation algorithms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3287-3298.	1.5	19
15	Progress in the prediction of pK _a values in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3260-3275.	1.5	229
16	Calculating pK _a values in the cAMP-dependent protein kinase: The effect of conformational change and ligand binding. <i>Protein Science</i> , 2010, 19, 2485-2497.	3.1	4
17	Titration_DB: Storage and analysis of NMR-monitored protein pH titration curves. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 843-857.	1.5	37
18	Improving the analysis of NMR spectra tracking pH-induced conformational changes: Removing artefacts of the electric field on the NMR chemical shift. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 971-984.	1.5	20

#	ARTICLE	IF	CITATIONS
19	Capturing, sharing and analysing biophysical data from protein engineering and protein characterization studies. <i>Nucleic Acids Research</i> , 2010, 38, e186-e186.	6.5	5
20	Electrostatics in proteins and protein-ligand complexes. <i>Future Medicinal Chemistry</i> , 2010, 2, 647-666.	1.1	75
21	Designed Human Serum Hyaluronidase 1 Variant, HYAL1 ^L , Exhibits Activity up to pH 5.9. <i>Journal of Biological Chemistry</i> , 2009, 284, 19173-19177.	1.6	8
22	Structural Artifacts in Protein-Ligand X-ray Structures: Implications for the Development of Docking Scoring Functions. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 5673-5684.	2.9	49
23	Chapter 9 Analyzing Enzymatic pH Activity Profiles and Protein Titration Curves Using Structure-Based pKa Calculations and Titration Curve Fitting. <i>Methods in Enzymology</i> , 2009, 454, 233-258.	0.4	20
24	Analyzing Protein NMR pH-Titration Curves. <i>Annual Reports in Computational Chemistry</i> , 2008, 4, 89-106.	0.9	4
25	Determination of Electrostatic Interaction Energies and Protonation State Populations in Enzyme Active Sites. <i>Journal of Molecular Biology</i> , 2008, 376, 269-287.	2.0	28
26	Analysing the pH-dependent properties of proteins using pKa calculations. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 25, 691-699.	1.3	38
27	Redesigning protein pKa values. <i>Protein Science</i> , 2006, 16, 239-249.	3.1	59
28	pKD: re-designing protein pKa values. <i>Nucleic Acids Research</i> , 2006, 34, W48-W51.	6.5	33
29	Calculating pKa values in enzyme active sites. <i>Protein Science</i> , 2003, 12, 1894-1901.	3.1	147
30	On the evaluation and optimization of protein X-ray structures for pKa calculations. <i>Protein Science</i> , 2003, 12, 313-326.	3.1	108
31	Rational Redesign of Enzymes. , 2003, , .		0
32	Predicting Changes in the Stability of Proteins and Protein Complexes: A Study of More Than 1000 Mutations. <i>Journal of Molecular Biology</i> , 2002, 320, 369-387.	2.0	1,609
33	The determinants of α -amylase pH-activity profiles. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 505-512.	1.0	92
34	The ionization of a buried glutamic acid is thermodynamically linked to the stability of <i>Leishmania mexicana</i> triose phosphate isomerase. <i>FEBS Journal</i> , 2000, 267, 2516-2524.	0.2	49
35	Protein engineering of bacterial α -amylases. <i>BBA - Proteins and Proteomics</i> , 2000, 1543, 253-274.	2.1	235