Liskin Swint-Kruse

List of Publications by Year
in descending order

59 papers	1,898 citations	279798 23 h-index	276875 41 g-index
66 all docs	66 docs citations	66 times ranked	1559 citing authors

#	Article	IF	Citations
1	The lactose repressor system: paradigms for regulation, allosteric behavior and protein folding. Cellular and Molecular Life Sciences, 2007, 64, 3-16.	5.4	151
2	Thermodynamics of unfolding for turkey ovomucoid third domain: Thermal and chemical denaturation. Protein Science, 1993, 2, 2037-2049.	7.6	137
3	Allostery in the LacI/GalR family: variations on a theme. Current Opinion in Microbiology, 2009, 12, 129-137.	5.1	128
4	Temperature and pH Dependences of Hydrogen Exchange and Global Stability for Ovomucoid Third Domainâ€. Biochemistry, 1996, 35, 171-180.	2.5	103
5	Hydrogen Bonds and the pH dependence of Ovomucoid Third Domain Stability. Biochemistry, 1995, 34, 4724-4732.	2.5	99
6	Resmap: automated representation of macromolecular interfaces as two-dimensional networks. Bioinformatics, 2005, 21, 3327-3328.	4.1	99
7	Modular, Multi-Input Transcriptional Logic Gating with Orthogonal LacI/GalR Family Chimeras. ACS Synthetic Biology, 2014, 3, 645-651.	3.8	79
8	Novel insights from hybrid LacI/GalR proteins: family-wide functional attributes and biologically significant variation in transcription repression. Nucleic Acids Research, 2012, 40, 11139-11154.	14.5	74
9	Ligand-induced Conformational Changes and Conformational Dynamics in the Solution Structure of the Lactose Repressor Protein. Journal of Molecular Biology, 2008, 376, 466-481.	4.2	61
10	Allosteric transition pathways in the lactose repressor protein core domains: Asymmetric motions in a homodimer. Protein Science, 2009, 12, 2523-2541.	7.6	54
11	Rheostats and Toggle Switches for Modulating Protein Function. PLoS ONE, 2013, 8, e83502.	2.5	51
12	Plasticity of quaternary structure: Twenty-two ways to form a LacI dimer. Protein Science, 2001, 10, 262-276.	7.6	43
13	Fine-tuning function: Correlation of hinge domain interactions with functional distinctions between LacI and PurR. Protein Science, 2002, 11, 778-794.	7.6	40
14	Perturbation from a Distance:â€‰ Mutations that Alter LacI Function through Long-Range Effects. Biochemistry, 2003, 42, 14004-14016.	2.5	39
15	Extrinsic Interactions Dominate Helical Propensity in Coupled Binding and Folding of the Lactose Repressor Protein Hinge Helix. Biochemistry, 2006, 45, 5896-5906.	2.5	39
16	Using Networks To Identify Fine Structural Differences between Functionally Distinct Protein Statesâ€. Biochemistry, 2004, 43, 10886-10895.	2.5	36
17	Using Evolution to Guide Protein Engineering: The Devil IS in the Details. Biophysical Journal, 2016, 111, 10-18.	0.5	36
18	Functional consequences of exchanging domains between LacI and PurR are mediated by the intervening linker sequence. Proteins: Structure, Function and Bioinformatics, 2007, 68, 375-388.	2.6	35

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19	Integrated Insights from Simulation, Experiment, and Mutational Analysis Yield New Details of LacI Functionâ€. Biochemistry, 2005, 44, 11201-11213.	2.5	32
20	Functionally important positions can comprise the majority of a protein's architecture. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1589-1608.	2.6	32
21	Comparing the Functional Roles of Nonconserved Sequence Positions in Homologous Transcription Repressors: Implications for Sequence/Function Analyses. Journal of Molecular Biology, 2010, 395, 785-802.	4.2	31
22	Experimental identification of specificity determinants in the domain linker of a LacI/GalR protein: Bioinformaticsâ€based predictions generate true positives and false negatives. Proteins: Structure, Function and Bioinformatics, 2008, 73, 941-957.	2.6	30
23	Substitutions at Nonconserved Rheostat Positions Modulate Function by Rewiring Long-Range, Dynamic Interactions. Molecular Biology and Evolution, 2021, 38, 201-214.	8.9	30
24	Relieving repression. Nature Structural Biology, 2000, 7, 184-187.	9.7	29
25	Subdividing Repressor Function: DNA Binding Affinity, Selectivity, and Allostery Can Be Altered by Amino Acid Substitution of Nonconserved Residues in a LacI/GalR Homologue. Biochemistry, 2008, 47, 8058-8069.	2.5	27
26	Designed Disulfide between N-terminal Domains of Lactose Repressor Disrupts Allosteric Linkage. Journal of Biological Chemistry, 1997, 272, 26818-26821.	3.4	26
27	Multiple Co-Evolutionary Networks Are Supported by the Common Tertiary Scaffold of the LacI/GalR Proteins. PLoS ONE, 2013, 8, e84398.	2.5	26
28	Comparison of Simulated and Experimentally Determined Dynamics for a Variant of the LacI DNA-Binding Domain, Nlac-P. Biophysical Journal, 1998, 74, 413-421.	0.5	23
29	Enzymatic reaction sequences as coupled multiple traces on a multidimensional landscape. Trends in Biochemical Sciences, 2008, 33, 104-112.	7.5	23
30	In vivo tests of thermodynamic models of transcription repressor function. Biophysical Chemistry, 2011, 159, 142-151.	2.8	23
31	Amino acid positions subject to multiple coevolutionary constraints can be robustly identified by their eigenvector network centrality scores. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2293-2306.	2.6	23
32	RheoScale: A tool to aggregate and quantify experimentally determined substitution outcomes for multiple variants at individual protein positions. Human Mutation, 2018, 39, 1814-1826.	2.5	23
33	Flexibility and Disorder in Gene Regulation: LacI/GalR and Hox Proteins. Journal of Biological Chemistry, 2015, 290, 24669-24677.	3.4	19
34	The strengths and limitations of using biolayer interferometry to monitor equilibrium titrations of biomolecules. Protein Science, 2020, 29, 1004-1020.	7.6	19
35	A clinically relevant polymorphism in the Na+/taurocholate cotransporting polypeptide (NTCP) occurs at a rheostat position. Journal of Biological Chemistry, 2021, 296, 100047.	3.4	19
36	AlloRep: A Repository of Sequence, Structural and Mutagenesis Data for the LacI/GalR Transcription Regulators. Journal of Molecular Biology, 2016, 428, 671-678.	4.2	18

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37	Rheostat positions: A new classification of protein positions relevant to pharmacogenomics. Medicinal Chemistry Research, 2020, 29, 1133-1146.	2.4	16
38	Homolog comparisons further reconcile in vitro and in vivo correlations of protein activities by revealing overâ€looked physiological factors. Protein Science, 2019, 28, 1806-1818.	7.6	15
39	Functional tunability from a distance: Rheostat positions influence allosteric coupling between two distant binding sites. Scientific Reports, 2019, 9, 16957.	3.3	15
40	Thermodynamics, Protein Modification, and Molecular Dynamics in Characterizing Lactose Repressor Protein: Strategies for Complex Analyses of Protein Structureâ€"Function. Methods in Enzymology, 2004, 379, 188-209.	1.0	14
41	Identification of biochemically neutral positions in liver pyruvate kinase. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1340-1350.	2.6	14
42	Linker Regions of the RhaS and RhaR Proteins. Journal of Bacteriology, 2007, 189, 269-271.	2.2	12
43	Ligand interactions with lactose repressor protein and the repressor-operator complex: The effects of ionization and oligomerization on binding. Biophysical Chemistry, 2007, 126, 94-105.	2.8	12
44	Rheostat functional outcomes occur when substitutions are introduced at nonconserved positions that diverge with speciation. Protein Science, 2021, 30, 1833-1853.	7.6	12
45	Substitutions at a rheostat position in human aldolase A cause a shift in the conformational population. Protein Science, 2022, 31, 357-370.	7.6	7
46	Structural Plasticity Is a Feature of Rheostat Positions in the Human Na+/Taurocholate Cotransporting Polypeptide (NTCP). International Journal of Molecular Sciences, 2022, 23, 3211.	4.1	4
47	Spectroscopic evidence of tetanus toxin translocation domain bilayer-induced refolding and insertion. Biophysical Journal, 2021, 120, 4763-4776.	0.5	3
48	Data on publications, structural analyses, and queries used to build and utilize the AlloRep database. Data in Brief, 2016, 8, 948-957.	1.0	2
49	Rheostats and Toggle Switches for Modifying Protein Function. Biophysical Journal, 2014, 106, 207a.	0.5	1
50	A Tale of Two Proteins. FASEB Journal, 2015, 29, 232.1.	0.5	1
51	Correlating in Vitro Measurements of Protein-DNA Binding Affinities with in Vivo Repression and Impact on the Growth Rate of the Host Organism. Biophysical Journal, 2011, 100, 321a.	0.5	0
52	Multiple Co-Evolutionary Networks have Evolved on the Common Tertiary Scaffold of the LacI/GalR Proteins. Biophysical Journal, 2012, 102, 184a.	0.5	0
53	In Vitro Thermodynamics of DNA Binding Correlate with InÂVivo Transcription Repression by a Synthetic LacI/Galr Paralog. Biophysical Journal, 2013, 104, 576a.	0.5	0
54	A New Pattern in Protein Evolutionary Sequence Information Robustly Identifies Functionally-Important Amino Acid Positions. Biophysical Journal, 2016, 110, 188a.	0.5	0

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55	Transcription | lac Operon Regulation. , 2021, , 455-465.		0
56	Allosteric regulation within the highly interconnected structural scaffold of <scp>AraC</scp>/<scp>XylS</scp> homologs tolerates a wide range of amino acid changes. Proteins: Structure, Function and Bioinformatics, 2022, 90, 186-199.	2.6	0
57	lac Operon. , 2004, , 529-534.		0
58	Characterization of the Expression and Function of Rheostat Locations within the Na + /Taurocholate Cotransporting Polypeptide. FASEB Journal, 2019, 33, 507.10.	0.5	0
59	Functional Characterization of Position 271 in NTCP, a Predicted Rheostat Location. FASEB Journal, 2020, 34, 1-1.	0.5	0