

Joel L Sussman

List of Publications by Year in descending order

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225
papers

24,228
citations

7069

78
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7496

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234
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234
docs citations

234
times ranked

24171
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>IceBear</i> : an intuitive and versatile web application for research-data tracking from crystallization experiment to PDB deposition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 151-163.	1.1	13
2	<i>Torpedo californica</i> acetylcholinesterase is stabilized by binding of a divalent metal ion to a novel and versatile 4D motif. <i>Protein Science</i> , 2021, 30, 966-981.	3.1	8
3	A practical guide to teaching with Proteopedia. <i>Biochemistry and Molecular Biology Education</i> , 2021, 49, 707-719.	0.5	3
4	Enzyme Evolution: An Epistatic Ratchet versus a Smooth Reversible Transition. <i>Molecular Biology and Evolution</i> , 2020, 37, 1133-1147.	3.5	26
5	Computational studies on cholinesterases: Strengthening our understanding of the integration of structure, dynamics and function. <i>Neuropharmacology</i> , 2020, 179, 108265.	2.0	6
6	A Second Look at the Crystal Structures of <i>Drosophila melanogaster</i> Acetylcholinesterase in Complex with Tacrine Derivatives Provides Insights Concerning Catalytic Intermediates and the Design of Specific Insecticides. <i>Molecules</i> , 2020, 25, 1198.	1.7	11
7	Polyproline-rich peptides associated with <i>Torpedo californica</i> acetylcholinesterase tetramers. <i>Chemico-Biological Interactions</i> , 2020, 319, 109007.	1.7	2
8	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 T	0.8	12
9	The four-helix bundle in cholinesterase dimers: Structural and energetic determinants of stability. <i>Chemico-Biological Interactions</i> , 2019, 309, 108699.	1.7	4
10	Molecular dynamics simulations of the interaction of Mouse and <i>Torpedo</i> acetylcholinesterase with covalent inhibitors explain their differential reactivity: Implications for drug design. <i>Chemico-Biological Interactions</i> , 2019, 310, 108715.	1.7	11
11	Rivastigmine and metabolite analogues with putative Alzheimer's disease-modifying properties in a <i>Caenorhabditis elegans</i> model. <i>Communications Chemistry</i> , 2019, 2, .	2.0	25
12	Design, biological evaluation and X-ray crystallography of nanomolar multifunctional ligands targeting simultaneously acetylcholinesterase and glycogen synthase kinase-3. <i>European Journal of Medicinal Chemistry</i> , 2019, 168, 58-77.	2.6	51
13	Novel multitarget-directed ligands targeting acetylcholinesterase and β 1 receptors as lead compounds for treatment of Alzheimer's disease: Synthesis, evaluation, and structural characterization of their complexes with acetylcholinesterase. <i>European Journal of Medicinal Chemistry</i> , 2019, 162, 234-248.	2.6	35
14	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
15	On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field. , 2019, , .		0
16	Potent 3-Hydroxy-2-Pyridine Aldoxime Reactivators of Organophosphate-Inhibited Cholinesterases with Predicted Blood-Brain Barrier Penetration. <i>Chemistry - A European Journal</i> , 2018, 24, 9675-9691.	1.7	50
17	Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2331-2341.	2.0	13
18	Cryo-EM structure of the native butyrylcholinesterase tetramer reveals a dimer of dimers stabilized by a superhelical assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13270-13275.	3.3	24

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19	Structure-Based Optimization of Nonquaternary Reactivators of Acetylcholinesterase Inhibited by Organophosphorus Nerve Agents. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 7630-7639.	2.9	44
20	Overcoming an optimization plateau in the directed evolution of highly efficient nerve agent bioscavengers. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 333-345.	1.0	57
21	Recent developments in structural studies on acetylcholinesterase. <i>Journal of Neurochemistry</i> , 2017, 142, 19-25.	2.1	22
22	Computational Studies on Acetylcholinesterases. <i>Molecules</i> , 2017, 22, 1324.	1.7	33
23	The impact of crystallization conditions on structure-based drug design: A case study on the methylene blue/acetylcholinesterase complex. <i>Protein Science</i> , 2016, 25, 1096-1114.	3.1	31
24	InÂvitro evaluation of the catalytic activity of paraoxonases and phosphotriesterases predicts the enzyme circulatory levels required for inÂvivo protection against organophosphate intoxications. <i>Chemico-Biological Interactions</i> , 2016, 259, 252-256.	1.7	17
25	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. <i>Molecular Cell</i> , 2016, 63, 337-346.	4.5	363
26	Single treatment of VX poisoned guinea pigs with the phosphotriesterase mutant C23AL: Intraosseous versus intravenous injection. <i>Toxicology Letters</i> , 2016, 258, 198-206.	0.4	24
27	Catalytic efficiencies of directly evolved phosphotriesterase variants with structurally different organophosphorus compounds in vitro. <i>Archives of Toxicology</i> , 2016, 90, 2711-2724.	1.9	42
28	Catalytic Stimulation by Restrained Active-Site Floppinessâ€”The Case of High Density Lipoprotein-Bound Serum Paraoxonase-1. <i>Journal of Molecular Biology</i> , 2015, 427, 1359-1374.	2.0	37
29	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014, 42, D326-D335.	6.5	195
30	Post-exposure treatment of VX poisoned guinea pigs with the engineered phosphotriesterase mutant C23: A proof-of-concept study. <i>Toxicology Letters</i> , 2014, 231, 45-54.	0.4	40
31	Guest Editorial: Databases and Bioinformatics Tools. <i>Israel Journal of Chemistry</i> , 2013, 53, 143-143.	1.0	0
32	Catalytic Metal Ion Rearrangements Underline Promiscuity and Evolvability of a Metalloenzyme. <i>Journal of Molecular Biology</i> , 2013, 425, 1028-1038.	2.0	58
33	The specific interaction of the photosensitizer methylene blue with acetylcholinesterase provides a model system for studying the molecular consequences of photodynamic therapy. <i>Chemico-Biological Interactions</i> , 2013, 203, 63-66.	1.7	4
34	Whatâ€™s in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
35	JSmol and the Next-Generation Web-Based Representation of 3D Molecular Structure as Applied to <i>Proteopedia</i> . <i>Israel Journal of Chemistry</i> , 2013, 53, 207-216.	1.0	210
36	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. <i>Nature Chemical Biology</i> , 2012, 8, 294-300.	3.9	205

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37	Catalytic Versatility and Backups in Enzyme Active Sites: The Case of Serum Paraoxonase 1. <i>Journal of Molecular Biology</i> , 2012, 418, 181-196.	2.0	148
38	Flexibility of the flap in the active site of BACE1 as revealed by crystal structures and molecular dynamics simulations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 13-25.	2.5	91
39	Structural and functional characterization of the interaction of the photosensitizing probe methylene blue with <i>Torpedo californica</i> acetylcholinesterase. <i>Protein Science</i> , 2012, 21, 1138-1152.	3.1	14
40	Acetylcholinesterase: Substrate traffic and inhibition. <i>Biochemistry and Molecular Biology Education</i> , 2012, 40, 144-144.	0.5	0
41	Backbone and side chain NMR assignments for the intrinsically disordered cytoplasmic domain of human neuroligin-3. <i>Biomolecular NMR Assignments</i> , 2012, 6, 15-18.	0.4	7
42	Evolved Stereoselective Hydrolases for Broad-Spectrum G-Type Nerve Agent Detoxification. <i>Chemistry and Biology</i> , 2012, 19, 456-466.	6.2	81
43	Structure of recombinant human carboxylesterase 1 isolated from whole cabbage looper larvae. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 269-272.	0.7	6
44	Proteopedia: Exciting Advances in the 3D Encyclopedia of Biomolecular Structure. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 149-161.	0.5	0
45	Comparison of a molecular dynamics model with the X-ray structure of the N370S acid- β -glucosidase mutant that causes Gaucher disease. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 773-775.	1.0	13
46	Structure of Estradiol Metal Chelate and Estrogen Receptor Complex: The Basis for Designing a New Class of Selective Estrogen Receptor Modulators. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 3575-3580.	2.9	28
47	Expression of protein complexes using multiple <i>Escherichia coli</i> protein co-expression systems: A benchmarking study. <i>Journal of Structural Biology</i> , 2011, 175, 159-170.	1.3	39
48	Proteopedia: A status report on the collaborative, 3D web-encyclopedia of proteins and other biomolecules. <i>Journal of Structural Biology</i> , 2011, 175, 244-252.	1.3	49
49	From SPINE to SPINE-2 complexes and beyond. <i>Journal of Structural Biology</i> , 2011, 175, 105.	1.3	1
50	In vitro detoxification of cyclosarin in human blood pre-incubated ex vivo with recombinant serum paraoxonases. <i>Toxicology Letters</i> , 2011, 206, 24-28.	0.4	17
51	Cyclodextrin-mediated crystallization of acid β -glucosidase in complex with amphiphilic bicyclic nojirimycin analogues. <i>Organic and Biomolecular Chemistry</i> , 2011, 9, 4160.	1.5	31
52	Directed evolution of hydrolases for prevention of G-type nerve agent intoxication. <i>Nature Chemical Biology</i> , 2011, 7, 120-125.	3.9	176
53	Context-dependent resistance to proteolysis of intrinsically disordered proteins. <i>Protein Science</i> , 2011, 20, 1285-1297.	3.1	77
54	Backdoor opening mechanism in acetylcholinesterase based on X-ray crystallography and molecular dynamics simulations. <i>Protein Science</i> , 2011, 20, 1114-1118.	3.1	59

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55	Acetylcholinesterase: From 3D structure to function. <i>Chemico-Biological Interactions</i> , 2010, 187, 10-22.	1.7	557
56	Proteopedia: A collaborative, virtual 3D web resource for protein and biomolecule structure and function. <i>Biochemistry and Molecular Biology Education</i> , 2010, 38, 341-342.	0.5	14
57	Long Route or Shortcut? A Molecular Dynamics Study of Traffic of Thiocholine within the Active-Site Gorge of Acetylcholinesterase. <i>Biophysical Journal</i> , 2010, 99, 4003-4011.	0.2	26
58	Molecular Basis of Reduced Glucosylceramidase Activity in the Most Common Gaucher Disease Mutant, N370S. <i>Journal of Biological Chemistry</i> , 2010, 285, 42105-42114.	1.6	31
59	New trends in protein expression. <i>Journal of Structural Biology</i> , 2010, 172, 1-2.	1.3	2
60	Characterization of gene-activated human acid- β -glucosidase: Crystal structure, glycan composition, and internalization into macrophages. <i>Glycobiology</i> , 2010, 20, 24-32.	1.3	113
61	Design, expression and characterization of mutants of fasciculin optimized for interaction with its target, acetylcholinesterase. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 641-648.	1.0	13
62	An encyclopedic effort to make 3D structures easier to understand. <i>Trends in Biochemical Sciences</i> , 2009, 34, 100-101.	3.7	12
63	6- <i>N</i> -deoxy-5,6-dia- <i>N</i> -octyliminomethylidene)nojirimycin: Synthesis, Biological Evaluation, and Crystal Structure in Complex with Acid β -Glucosidase. <i>ChemBioChem</i> , 2009, 10, 1480-1485.	1.3	44
64	Assessment of disorder predictions in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 210-216.	1.5	104
65	Assessment of CASP8 structure predictions for template free targets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 50-65.	1.5	89
66	Amalgam, an axon guidance <i>Drosophila</i> adhesion protein belonging to the immunoglobulin superfamily: Over-expression, purification and biophysical characterization. <i>Protein Expression and Purification</i> , 2009, 63, 147-157.	0.6	13
67	The Quaternary Structure of Amalgam, a <i>Drosophila</i> Neuronal Adhesion Protein, Explains Its Dual Adhesion Properties. <i>Biophysical Journal</i> , 2009, 97, 2316-2326.	0.2	11
68	Structural Studies on Acetylcholinesterase and Paraoxonase Directed Towards Development of Therapeutic Biomolecules for the Treatment of Degenerative Diseases and Protection Against Chemical Threat Agents. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2009, , 183-199.	0.5	0
69	Directed Evolution of Serum Paraoxonase PON3 by Family Shuffling and Ancestor/Consensus Mutagenesis, and Its Biochemical Characterization. <i>Biochemistry</i> , 2009, 48, 6644-6654.	1.2	43
70	The Crystal Structure of a Complex of Acetylcholinesterase with a Bis-($\hat{\alpha}$)- <i>m</i> -meptazinol Derivative Reveals Disruption of the Catalytic Triad. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 2543-2549.	2.9	22
71	Crystallographic Snapshots of Nonaged and Aged Conjugates of Soman with Acetylcholinesterase, and of a Ternary Complex of the Aged Conjugate with Pralidoxime. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 7593-7603.	2.9	81
72	Tools to Make 3D Structural Data More Comprehensible: Emovie & Proteopedia. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2009, , 169-182.	0.5	0

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73	Operational definition of intrinsically unstructured protein sequences based on susceptibility to the 20S proteasome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1357-1366.	1.5	93
74	Control of the rate of evaporation in protein crystallization by the 'microbatch under oil' method. <i>Journal of Applied Crystallography</i> , 2008, 41, 969-971.	1.9	15
75	Structural disorder serves as a weak signal for intracellular protein degradation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 903-909.	1.5	96
76	Crystal structure of YagE, a putative DHPS-like protein from <i>Escherichia coli</i> K12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2102-2108.	1.5	5
77	Induced-fit or preexisting equilibrium dynamics? Lessons from protein crystallography and MD simulations on acetylcholinesterase and implications for structure-based drug design. <i>Protein Science</i> , 2008, 17, 601-605.	3.1	51
78	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	9.0	763
79	Acetylcholinesterase: How is structure related to function?. <i>Chemico-Biological Interactions</i> , 2008, 175, 3-10.	1.7	181
80	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008, 18, 756-764.	2.6	864
81	Biophysical Characterization of the Unstructured Cytoplasmic Domain of the Human Neuronal Adhesion Protein Neuroligin 3. <i>Biophysical Journal</i> , 2008, 95, 1928-1944.	0.2	45
82	Flexibility of Aromatic Residues in the Active-Site Gorge of Acetylcholinesterase: X-ray versus Molecular Dynamics. <i>Biophysical Journal</i> , 2008, 95, 2500-2511.	0.2	104
83	Acid β -glucosidase: insights from structural analysis and relevance to Gaucher disease therapy. <i>Biological Chemistry</i> , 2008, 389, 1361-1369.	1.2	43
84	Proteopedia - a scientific 'wiki' bridging the rift between 3D structure and function of biomacromolecules. <i>Genome Biology</i> , 2008, 9, R121.	13.9	98
85	Crystal Structure of Thioflavin T Bound to the Peripheral Site of <i>Torpedo californica</i> Acetylcholinesterase Reveals How Thioflavin T Acts as a Sensitive Fluorescent Reporter of Ligand Binding to the Acylation Site. <i>Journal of the American Chemical Society</i> , 2008, 130, 7856-7861.	6.6	119
86	Shoot-and-Trap: Use of specific x-ray damage to study structural protein dynamics by temperature-controlled cryo-crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11742-11747.	3.3	52
87	Structural Genomics and Structural Proteomics: A Global Perspective. , 2008, , 505-537.		0
88	Crystal Structures of Complexes of N-Butyl- and N-Nonyl-Deoxynojirimycin Bound to Acid β -Glucosidase. <i>Journal of Biological Chemistry</i> , 2007, 282, 29052-29058.	1.6	109
89	An idea whose time has come. <i>Genome Biology</i> , 2007, 8, 408.	13.9	6
90	3-D Structure of Serum Paraoxonase 1 Sheds Light on Its Activity, Stability, Solubility and Crystallizability. <i>Arhiv Za Higijenu Rada I Toksikologiju</i> , 2007, 58, 347-353.	0.4	30

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91	Use of a 'caged' analogue to study the traffic of choline within acetylcholinesterase by kinetic crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1115-1128.	2.5	40
92	RIKEN aids international structural genomics efforts. <i>Nature</i> , 2007, 445, 21-21.	13.7	14
93	Production of glucocerebrosidase with terminal mannose glycans for enzyme replacement therapy of Gaucher's disease using a plant cell system. <i>Plant Biotechnology Journal</i> , 2007, 5, 579-590.	4.1	371
94	eMovie: a storyboard-based tool for making molecular movies. <i>Trends in Biochemical Sciences</i> , 2007, 32, 199-204.	3.7	27
95	A server and database for dipole moments of proteins. <i>Nucleic Acids Research</i> , 2007, 35, W512-W521.	6.5	166
96	Complexes of Alkylene-Linked Tacrine Dimers with <i>Torpedo californica</i> Acetylcholinesterase: Binding of Bis(5)-tacrine Produces a Dramatic Rearrangement in the Active-Site Gorge. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5491-5500.	2.9	186
97	The X-Ray Structure of Human Acid-beta-Glucosidase. , 2006, , 85-96.		0
98	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1114-1124.	2.5	79
99	Co-expression of protein complexes in prokaryotic and eukaryotic hosts: experimental procedures, database tracking and case studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1232-1242.	2.5	113
100	Structural comparison of differently glycosylated forms of acid-β-glucosidase, the defective enzyme in Gaucher disease. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1458-1465.	2.5	42
101	Structural insights into substrate traffic and inhibition in acetylcholinesterase. <i>EMBO Journal</i> , 2006, 25, 2746-2756.	3.5	160
102	Shedding UV Light on the Phase Problem. <i>Structure</i> , 2006, 14, 629-630.	1.6	1
103	Database and Comparative Identification of Prophages. , 2006, , 863-868.		0
104	The Crystal Structure of the Complex of the Anticancer Prodrug 7-Ethyl-10-[4-(1-piperidino)-1-piperidino]-carbonyloxycamptothecin (CPT-11) with <i>Torpedo californica</i> Acetylcholinesterase Provides a Molecular Explanation for Its Cholinergic Action. <i>Molecular Pharmacology</i> , 2005, 67, 1874-1881.	1.0	36
105	The 3D structure of the anticancer prodrug CPT-11 with <i>Torpedo californica</i> acetylcholinesterase rationalizes its inhibitory action on AChE and its hydrolysis by butyrylcholinesterase and carboxylesterase. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 153-157.	1.7	14
106	Inhibition of acetylcholinesterase by the anticancer prodrug CPT-11. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 247-252.	1.7	35
107	HalX: an open-source LIMS (Laboratory Information Management System) for small- to large-scale laboratories. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 671-678.	2.5	23
108	Three-dimensional structure determination of proteins related to human health in their functional context at The Israel Structural Proteomics Center (ISPC). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1364-1372.	2.5	8

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109	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT//CSG+ strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1426-1431.	2.5	228
110	Analysis of Genetic Polymorphisms in Acetylcholinesterase as Reflected in Different Populations. <i>Current Alzheimer Research</i> , 2005, 2, 207-218.	0.7	16
111	FoldIndex(C): a simple tool to predict whether a given protein sequence is intrinsically unfolded. <i>Bioinformatics</i> , 2005, 21, 3435-3438.	1.8	886
112	G protein-coupled receptors show unusual patterns of intrinsic unfolding. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 103-110.	1.0	48
113	Three-dimensional structure of a halotolerant algal carbonic anhydrase predicts halotolerance of a mammalian homolog. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7493-7498.	3.3	71
114	X-ray Structure of Human Acid-Î²-Glucosidase Covalently Bound to Conduritol-B-Epoxyde. <i>Journal of Biological Chemistry</i> , 2005, 280, 23815-23819.	1.6	102
115	Acetylcholinesterase: â€˜classicalâ€™ and â€˜non-classicalâ€™ functions and pharmacology. <i>Current Opinion in Pharmacology</i> , 2005, 5, 293-302.	1.7	438
116	Dynamic Mechanism of E2020 Binding to Acetylcholinesterase:â€‰ A Steered Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2005, 109, 23730-23738.	1.2	53
117	Crystal Packing Mediates Enantioselective Ligand Recognition at the Peripheral Site of Acetylcholinesterase. <i>Journal of the American Chemical Society</i> , 2005, 127, 11029-11036.	6.6	44
118	Molecular Determinants of Protein Halotolerance: Structural and Functional Studies of the Extremely Salt Tolerant Carbonic Anhydrases from <i>Dunaliella salina</i> . , 2005, , 503-515.		0
119	Natural protein engineering: a uniquely salt-tolerant, but not halophilic, Î±-type carbonic anhydrase from algae proliferating in low- to hyper-saline environments. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 191-200.	1.0	27
120	The synaptic acetylcholinesterase tetramer assembles around a polyproline II helix. <i>EMBO Journal</i> , 2004, 23, 4394-4405.	3.5	98
121	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 412-419.	3.6	569
122	A paradigm for single nucleotide polymorphism analysis: The case of the acetylcholinesterase gene. <i>Human Mutation</i> , 2004, 24, 408-416.	1.1	25
123	Additivity of Cation-Î± Interactions:â€‰ An ab Initio Computational Study on Î±-Cation-Î± Sandwich Complexes. <i>Journal of Physical Chemistry A</i> , 2004, 108, 9400-9405.	1.1	29
124	The Complex of a Bivalent Derivative of Galanthamine with Torpedo Acetylcholinesterase Displays Drastic Deformation of the Active-Site Gorge:â€‰ Implications for Structure-Based Drug Design. <i>Journal of the American Chemical Society</i> , 2004, 126, 15405-15411.	6.6	115
125	New directions in the treatment of Gaucher disease. <i>Trends in Pharmacological Sciences</i> , 2004, 25, 147-151.	4.0	95
126	Acetylcholinesterase: A Multifaceted Target for Structure-Based Drug Design of Anticholinesterase Agents for the Treatment of Alzheimer's Disease. <i>Journal of Molecular Neuroscience</i> , 2003, 20, 369-384.	1.1	104

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127	The Binding Site of Acetylcholine Receptor. <i>Annals of the New York Academy of Sciences</i> , 2003, 998, 93-100.	1.8	20
128	Design and Synthesis of Peptides That Bind α -Bungarotoxin with High Affinity and Mimic the Three-Dimensional Structure of the Binding Site of Acetylcholine Receptor. <i>ChemInform</i> , 2003, 34, no.	0.1	0
129	Identification, cDNA cloning, expression, crystallization and preliminary X-ray analysis of an exceptionally halotolerant carbonic anhydrase from <i>Dunaliella salina</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1084-1086.	2.5	8
130	The intracellular domain of the <i>Drosophila</i> cholinesterase-like neural adhesion protein, gliotactin, is natively unfolded. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 758-767.	1.5	60
131	Proteomic signatures: Amino acid and oligopeptide compositions differentiate among phyla. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 20-40.	1.5	130
132	X-ray structure of human acid α -glucosidase, the defective enzyme in Gaucher disease. <i>EMBO Reports</i> , 2003, 4, 704-709.	2.0	244
133	How Does Huperzine A Enter and Leave the Binding Gorge of Acetylcholinesterase? Steered Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2003, 125, 11340-11349.	6.6	94
134	An unusual halotolerant α -type carbonic anhydrase from the alga <i>Dunaliella salina</i> functionally expressed in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2003, 28, 151-157.	0.6	39
135	Acetylcholinesterase Complexed with Bivalent Ligands Related to Huperzine A: Experimental Evidence for Species-Dependent Protein-Ligand Complementarity. <i>Journal of the American Chemical Society</i> , 2003, 125, 363-373.	6.6	94
136	STRUCTURAL FEATURE OF AChE INHIBITOR HUPERZINE B IN NATURE AND IN THE BINDING SITE OF AChE: DENSITY FUNCTIONAL THEORY STUDY COMBINED WITH IR DETERMINATION. <i>Journal of Theoretical and Computational Chemistry</i> , 2002, 01, 81-92.	1.8	0
137	The Relationship between Binding Models of TMA with Furan and Imidazole and the Molecular Electrostatic Potentials: DFT and MP2 Computational Studies. <i>Journal of Physical Chemistry A</i> , 2002, 106, 157-164.	1.1	19
138	A Neutral Molecule in a Cation-binding Site: Specific Binding of a PEG-SH to Acetylcholinesterase from <i>Torpedo californica</i> . <i>Journal of Molecular Biology</i> , 2002, 320, 721-725.	2.0	40
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