

Joel L Sussman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7327216/publications.pdf>

Version: 2024-02-01

225
papers

24,228
citations

7069

78
h-index

7496

151
g-index

234
all docs

234
docs citations

234
times ranked

24171
citing authors

#	ARTICLE	IF	CITATIONS
1	The β / α hydrolase fold. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 197-211.	1.0	1,887
2	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
3	Quaternary ligand binding to aromatic residues in the active-site gorge of acetylcholinesterase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 9031-9035.	3.3	869
4	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008, 18, 756-764.	2.6	864
5	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	9.0	763
6	Structure of acetylcholinesterase complexed with E2020 (Aricept [®]): implications for the design of new anti-Alzheimer drugs. <i>Structure</i> , 1999, 7, 297-307.	1.6	667
7	Protein Data Bank (PDB): Database of Three-Dimensional Structural Information of Biological Macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1078-1084.	2.5	613
8	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
9	Acetylcholinesterase: From 3D structure to function. <i>Chemico-Biological Interactions</i> , 2010, 187, 10-22.	1.7	557
10	Relationship between sequence conservation and three-dimensional structure in a large family of esterases, lipases, and related proteins. <i>Protein Science</i> , 1993, 2, 366-382.	3.1	506
11	Specific chemical and structural damage to proteins produced by synchrotron radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 623-628.	3.3	438
12	Acetylcholinesterase: "classical" and "non-classical" functions and pharmacology. <i>Current Opinion in Pharmacology</i> , 2005, 5, 293-302.	1.7	438
13	Crystal structure of yeast phenylalanine transfer RNA. <i>Journal of Molecular Biology</i> , 1978, 123, 607-630.	2.0	377
14	Structure of acetylcholinesterase complexed with the nootropic alkaloid, (α)-huperzine A. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 57-63.	3.6	373
15	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
16	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
17	The X-ray Structure of a Transition State Analog Complex Reveals the Molecular Origins of the Catalytic Power and Substrate Specificity of Acetylcholinesterase. <i>Journal of the American Chemical Society</i> , 1996, 118, 2340-2346.	6.6	358
18	Crystal structure of yeast phenylalanine transfer RNA. <i>Journal of Molecular Biology</i> , 1978, 123, 631-660.	2.0	301

#	ARTICLE	IF	CITATIONS
19	Conversion of acetylcholinesterase to butyrylcholinesterase: modeling and mutagenesis.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 10827-10831.	3.3	292
20	Three-dimensional structures of <i>Drosophila melanogaster</i> acetylcholinesterase and of its complexes with two potent inhibitors. Protein Science, 2000, 9, 1063-1072.	3.1	282
21	Crystal Structures of Aged Phosphorylated Acetylcholinesterase: Nerve Agent Reaction Products at the Atomic Level,. Biochemistry, 1999, 38, 7032-7039.	1.2	268
22	Structure of acetylcholinesterase complexed with (â”)-galanthamine at 2.3 Å.. resolution. FEBS Letters, 1999, 463, 321-326.	1.3	265
23	Structures of recombinant native and E202Q mutant human acetylcholinesterase complexed with the snake-venom toxin fasciculin-II. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1385-1394.	2.5	260
24	X-ray structure of human acid phosphatase, the defective enzyme in Gaucher disease. EMBO Reports, 2003, 4, 704-709.	2.0	244
25	RNA - ligand interactions:(I) magnesium binding sites in yeast tRNAPhe. Nucleic Acids Research, 1977, 4, 2811-2820.	6.5	238
26	A 3D building blocks approach to analyzing and predicting structure of proteins. Proteins: Structure, Function and Bioinformatics, 1989, 5, 355-373.	1.5	234
27	Crystal structure of an acetylcholinesterase-fasciculin complex: interaction of a three-fingered toxin from snake venom with its target. Structure, 1995, 3, 1355-1366.	1.6	232
28	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT/JCSG+ strategy. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1426-1431.	2.5	228
29	Whatâ€™s in a name? Why these proteins are intrinsically disordered. Intrinsically Disordered Proteins, 2013, 1, e24157.	1.9	226
30	JSmol and the Next-Generation Web-Based Representation of 3D Molecular Structure as Applied to Proteopedia. Israel Journal of Chemistry, 2013, 53, 207-216.	1.0	210
31	Insights into protein adaptation to a saturated salt environment from the crystal structure of a halophilic 2Fe-2S ferredoxin. Nature Structural Biology, 1996, 3, 452-458.	9.7	207
32	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. Nature Chemical Biology, 2012, 8, 294-300.	3.9	205
33	How flexible is the furanose ring? 1. A comparison of experimental and theoretical studies. Journal of the American Chemical Society, 1982, 104, 270-278.	6.6	198
34	Refined crystal structure of dogfish M4 apo-lactate dehydrogenase. Journal of Molecular Biology, 1987, 198, 445-467.	2.0	195
35	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	6.5	195
36	Crystal structure of a naturally occurring dinucleoside phosphate: Uridylyl 3â€™,5â€™-adenosine phosphate model for RNA chain folding. Journal of Molecular Biology, 1972, 66, 403-421.	2.0	188

#	ARTICLE	IF	CITATIONS
37	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
38	Acetylcholinesterase: How is structure related to function?. <i>Chemico-Biological Interactions</i> , 2008, 175, 3-10.	1.7	181
39	Directed evolution of hydrolases for prevention of G-type nerve agent intoxication. <i>Nature Chemical Biology</i> , 2011, 7, 120-125.	3.9	176
40	A server and database for dipole moments of proteins. <i>Nucleic Acids Research</i> , 2007, 35, W512-W521.	6.5	166
41	[29] Protein data bank archives of three-dimensional macromolecular structures. <i>Methods in Enzymology</i> , 1997, 277, 556-571.	0.4	163
42	Crystal structure of a eukaryotic initiator tRNA. <i>Nature</i> , 1979, 278, 188-190.	13.7	160
43	Structural insights into substrate traffic and inhibition in acetylcholinesterase. <i>EMBO Journal</i> , 2006, 25, 2746-2756.	3.5	160
44	Structure and dynamics of the active site gorge of acetylcholinesterase: Synergistic use of molecular dynamics simulation and X-ray crystallography. <i>Protein Science</i> , 1994, 3, 188-197.	3.1	158
45	Acetylcholinesterase: electrostatic steering increases the rate of ligand binding. <i>Biochemistry</i> , 1993, 32, 401-403.	1.2	150
46	Reaction Products of Acetylcholinesterase and VX Reveal a Mobile Histidine in the Catalytic Triad. <i>Journal of the American Chemical Society</i> , 1999, 121, 9883-9884.	6.6	150
47	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
48	Active-site gorge and buried water molecules in crystal structures of acetylcholinesterase from <i>Torpedo californica</i> 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 296, 713-735.	2.0	137
49	Proteomic signatures: Amino acid and oligopeptide compositions differentiate among phyla. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 20-40.	1.5	130
50	Hydrogen bonding in yeast phenylalanine transfer RNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1975, 72, 4866-4870.	3.3	127
51	Chapter 15: Structure and functions of acetylcholinesterase and butyrylcholinesterase. <i>Progress in Brain Research</i> , 1993, 98, 139-146.	0.9	125
52	The Binding Site of Acetylcholine Receptor as Visualized in the X-Ray Structure of a Complex between δ -Bungarotoxin and a Mimotope Peptide. <i>Neuron</i> , 2001, 32, 265-275.	3.8	125
53	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
54	The Complex of a Bivalent Derivative of Galanthamine with <i>Torpedo</i> Acetylcholinesterase Displays Drastic Deformation of the Active-Site Gorge: Implications for Structure-Based Drug Design. <i>Journal of the American Chemical Society</i> , 2004, 126, 15405-15411.	6.6	115

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	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
59	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
60	Assessment of disorder predictions in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 210-216.	1.5	104
61	Idealized atomic coordinates of yeast phenylalanine transfer RNA. <i>Biochemical and Biophysical Research Communications</i> , 1976, 68, 89-96.	1.0	103
62	The three-dimensional structure of a DNA duplex containing looped-out bases. <i>Nature</i> , 1988, 334, 82-84.	13.7	103
63	X-ray Structure of Human Acid- β -Glucosidase Covalently Bound to Conduritol-B-Epoxyde. <i>Journal of Biological Chemistry</i> , 2005, 280, 23815-23819.	1.6	102
64	The synaptic acetylcholinesterase tetramer assembles around a polyproline II helix. <i>EMBO Journal</i> , 2004, 23, 4394-4405.	3.5	98
65	Proteopedia - a scientific 'wiki' bridging the rift between 3D structure and function of biomacromolecules. <i>Genome Biology</i> , 2008, 9, R121.	13.9	98
66	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
67	New directions in the treatment of Gaucher disease. <i>Trends in Pharmacological Sciences</i> , 2004, 25, 147-151.	4.0	95
68	Three-dimensional structures of bulge-containing DNA fragments. <i>Journal of Molecular Biology</i> , 1992, 225, 397-431.	2.0	94
69	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
70	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
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	Assessment of CASP8 structure predictions for template free targets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 50-65.	1.5	89
74	Acetylcholinesterase: structure and use as a model for specific cation π protein interactions. <i>Current Opinion in Structural Biology</i> , 1992, 2, 721-729.	2.6	87
75	Three-dimensional structure of a complex of E2020 with acetylcholinesterase from <i>Torpedo californica</i> . <i>Journal of Physiology (Paris)</i> , 1998, 92, 191-194.	2.1	86
76	Adenine-guanine base pairing in ribosomal RNA. <i>Nucleic Acids Research</i> , 1982, 10, 2701-2708.	6.5	82
77	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
78	Evolved Stereoselective Hydrolases for Broad-Spectrum G-Type Nerve Agent Detoxification. <i>Chemistry and Biology</i> , 2012, 19, 456-466.	6.2	81
79	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1114-1124.	2.5	79
80	Crystal structure of 15-mer DNA duplex containing unpaired bases. <i>Nature</i> , 1988, 334, 85-86.	13.7	77
81	Context π dependent resistance to proteolysis of intrinsically disordered proteins. <i>Protein Science</i> , 2011, 20, 1285-1297.	3.1	77
82	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
83	Quantum/Classical Mechanical Comparison of Cation π Interactions between Tetramethylammonium and Benzene. <i>Journal of Physical Chemistry A</i> , 2001, 105, 1326-1333.	1.1	69
84	How Does Ammonium Interact with Aromatic Groups? A Density Functional Theory (DFT/B3LYP) Investigation. <i>Journal of Physical Chemistry A</i> , 2000, 104, 9573-9580.	1.1	68
85	External and internal electrostatic potentials of cholinesterase models. <i>Journal of Molecular Graphics and Modelling</i> , 1997, 15, 318-327.	1.3	63
86	Evidence for the formation of disulfide radicals in protein crystals upon X-ray irradiation. <i>Journal of Synchrotron Radiation</i> , 2002, 9, 342-346.	1.0	63
87	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
88	Backdoor opening mechanism in acetylcholinesterase based on X π ray crystallography and molecular dynamics simulations. <i>Protein Science</i> , 2011, 20, 1114-1118.	3.1	59
89	The structure of the complex between avidin and the dye, 2-(4'-hydroxyazobenzene) benzoic acid (HABA). <i>FEBS Letters</i> , 1993, 328, 165-168.	1.3	58
90	Site-directed mutants designed to test back-door hypotheses of acetylcholinesterase function. <i>FEBS Letters</i> , 1996, 386, 65-71.	1.3	58

#	ARTICLE	IF	CITATIONS
91	Catalytic Metal Ion Rearrangements Underline Promiscuity and Evolvability of a Metalloenzyme. <i>Journal of Molecular Biology</i> , 2013, 425, 1028-1038.	2.0	58
92	Crystal structure of demetallized concanavalin A: the metal-binding region. <i>Journal of Molecular Biology</i> , 1979, 131, 137-155.	2.0	57
93	Constrained-restrained least-squares (CORELS) refinement of proteins and nucleic acids. <i>Methods in Enzymology</i> , 1985, 115, 271-303.	0.4	57
94	Comparison of the crystal structures of genetically engineered human manganese superoxide dismutase and manganese superoxide dismutase from <i>thermus thermophilus</i> : Differences in dimer-dimer interaction. <i>Protein Science</i> , 1993, 2, 814-825.	3.1	57
95	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
96	Soluble monomeric acetylcholinesterase from mouse: Expression, purification, and crystallization in complex with fasciculin. <i>Protein Science</i> , 1996, 5, 672-679.	3.1	56
97	Dynamic Mechanism of E2020 Binding to Acetylcholinesterase: A Steered Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2005, 109, 23730-23738.	1.2	53
98	A Modular Treatment of Molecular Traffic Through the Active Site of Cholinesterase. <i>Biophysical Journal</i> , 1999, 77, 2430-2450.	0.2	52
99	A Structure-Based Design Approach to the Development of Novel, Reversible AChE Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2001, 44, 3203-3215.	2.9	52
100	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
101	Ë Turn is a conformational pattern in RNA loops and bends. <i>Nature</i> , 1976, 260, 645-646.	13.7	51
102	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
103	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
104	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
105	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
106	Mechanism of oligonucleotide loop formation in solution. <i>Biochemistry</i> , 1986, 25, 7417-7423.	1.2	48
107	Noncovalent interaction or chemical bonding between alkaline earth cations and benzene? A quantum chemistry study using MP2 and density-functional theory methods. <i>Chemical Physics Letters</i> , 2001, 349, 113-122.	1.2	48
108	G protein-coupled receptors show unusual patterns of intrinsic unfolding. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 103-110.	1.0	48

#	ARTICLE	IF	CITATIONS
109	Theoretical Insight into the Interactions of TMA-Benzene and TMA-Pyrrole with B3LYP Density-Functional Theory (DFT) and ab Initio Second Order Møller-Plesset Perturbation Theory (MP2) Calculations. <i>Journal of Physical Chemistry A</i> , 2001, 105, 5431-5437.	1.1	45
110	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
111	Three-dimensional structures of acetylcholinesterase and of its complexes with anticholinesterase agents. <i>Biochemical Society Transactions</i> , 1994, 22, 745-749.	1.6	44
112	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
113	6-Amino-5,6-deoxy-5,6-dihydro-2-N ¹ -octyliminomethylidene)nojirimycin: Synthesis, Biological Evaluation, and Crystal Structure in Complex with Acid Î²-Glucosidase. <i>ChemBioChem</i> , 2009, 10, 1480-1485.	1.3	44
114	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
115	Acid Î²-glucosidase: insights from structural analysis and relevance to Gaucher disease therapy. <i>Biological Chemistry</i> , 2008, 389, 1361-1369.	1.2	43
116	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
117	PDBBrowse â€” a graphics interface to the Brookhaven Protein Data Bank. <i>Nature</i> , 1995, 374, 572-574.	13.7	42
118	Structural comparison of differently glycosylated forms of acid-Î²-glucosidase, the defective enzyme in Gaucher disease. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1458-1465.	2.5	42
119	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
120	Recommendations for Nomenclature in Cholinesterases. , 1992, , 285-288.		40
121	Effect of Mutations within the Peripheral Anionic Site on the Stability of Acetylcholinesterase. <i>Molecular Pharmacology</i> , 1999, 55, 982-992.	1.0	40
122	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
123	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
124	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
125	An unusual halotolerant Î±-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
126	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

#	ARTICLE	IF	CITATIONS
127	Structure of a complex of the potent and specific inhibitor BW284C51 with Torpedo californica acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1765-1771.	2.5	38
128	Catalytic Stimulation by Restrained Active-Site Floppiness—The Case of High Density Lipoprotein-Bound Serum Paraoxonase-1. <i>Journal of Molecular Biology</i> , 2015, 427, 1359-1374.	2.0	37
129	The Crystal Structure of the Complex of the Anticancer Prodrug 7-Ethyl-10-[4-(1-piperidino)-1-piperidino]-carbonyloxycamptothecin (CPT-11) with Torpedo californica Acetylcholinesterase Provides a Molecular Explanation for Its Cholinergic Action. <i>Molecular Pharmacology</i> , 2005, 67, 1874-1881.	1.0	36
130	Inhibition of acetylcholinesterase by the anticancer prodrug CPT-11. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 247-252.	1.7	35
131	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
132	Computational Studies on Acetylcholinesterases. <i>Molecules</i> , 2017, 22, 1324.	1.7	33
133	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
134	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
135	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
136	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
137	Static Laue Diffraction Studies on Acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1359-1366.	2.5	29
138	Additivity of Cation- π Interactions: An ab Initio Computational Study on Cation- π Sandwich Complexes. <i>Journal of Physical Chemistry A</i> , 2004, 108, 9400-9405.	1.1	29
139	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
140	Biochemical Evaluation of Photolabile Precursors of Choline and of Carbamylcholine for Potential Time-Resolved Crystallographic Studies on Cholinesterases. <i>Biochemistry</i> , 1996, 35, 10854-10861.	1.2	27
141	A preliminary comparison of structural models for catalytic intermediates of acetylcholinesterase. <i>Chemico-Biological Interactions</i> , 1999, 119-120, 43-52.	1.7	27
142	Natural protein engineering: a uniquely salt-tolerant, but not halophilic, β -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
143	eMovie: a storyboard-based tool for making molecular movies. <i>Trends in Biochemical Sciences</i> , 2007, 32, 199-204.	3.7	27
144	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

#	ARTICLE	IF	CITATIONS
145	Enzyme Evolution: An Epistatic Ratchet versus a Smooth Reversible Transition. <i>Molecular Biology and Evolution</i> , 2020, 37, 1133-1147.	3.5	26
146	Design and synthesis of peptides that bind Î±-bungarotoxin with high affinity and mimic the three-dimensional structure of the binding-site of acetylcholine receptor. <i>Biophysical Chemistry</i> , 2002, 100, 293-305.	1.5	25
147	A paradigm for single nucleotide polymorphism analysis: The case of the acetylcholinesterase gene. <i>Human Mutation</i> , 2004, 24, 408-416.	1.1	25
148	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
149	Characterization of crystals of genetically engineered human manganese superoxide dismutase. <i>Journal of Molecular Biology</i> , 1989, 206, 787-788.	2.0	24
150	A Metastable State of <i>Torpedo californica</i> Acetylcholinesterase Generated by Modification with Organomercurials. <i>Biochemistry</i> , 1994, 33, 14407-14418.	1.2	24
151	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
152	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
153	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
154	The Crystal Structure of a Complex of Acetylcholinesterase with a Bis-($\hat{\alpha}$)-meptazinol Derivative Reveals Disruption of the Catalytic Triad. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 2543-2549.	2.9	22
155	Recent developments in structural studies on acetylcholinesterase. <i>Journal of Neurochemistry</i> , 2017, 142, 19-25.	2.1	22
156	The Protein Data Bank: Current status and future challenges. <i>Journal of Research of the National Institute of Standards and Technology</i> , 1996, 101, 231.	0.4	21
157	The Binding Site of Acetylcholine Receptor. <i>Annals of the New York Academy of Sciences</i> , 2003, 998, 93-100.	1.8	20
158	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
159	Site-directed mutagenesis of active-site-related residues in <i>Torpedo</i> acetylcholinesterase Presence of a glutamic acid in the catalytic triad. <i>FEBS Letters</i> , 1992, 309, 421-423.	1.3	18
160	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
161	In vitro evaluation of the catalytic activity of paraoxonases and phosphotriesterases predicts the enzyme circulatory levels required for in vivo protection against organophosphate intoxications. <i>Chemico-Biological Interactions</i> , 2016, 259, 252-256.	1.7	17
162	Conformational transitions of synthetic DNA sequences with inserted bases, related to the dodecamer d(CGCGAATTCGCG). <i>Nucleic Acids Research</i> , 1987, 15, 3877-3890.	6.5	16

#	ARTICLE	IF	CITATIONS
163	Analysis of Genetic Polymorphisms in Acetylcholinesterase as Reflected in Different Populations. <i>Current Alzheimer Research</i> , 2005, 2, 207-218.	0.7	16
164	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
165	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
166	RIKEN aids international structural genomics efforts. <i>Nature</i> , 2007, 445, 21-21.	13.7	14
167	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
168	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
169	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
170	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
171	Comparison of a molecular dynamics model with the X-ray structure of the N370S acid- α -glucosidase mutant that causes Gaucher disease. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 773-775.	1.0	13
172	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
173	<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
174	AutoDep: a web-based system for deposition and validation of macromolecular structural information. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 828-841.	2.5	12
175	An encyclopedic effort to make 3D structures easier to understand. <i>Trends in Biochemical Sciences</i> , 2009, 34, 100-101.	3.7	12
176	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
177	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	12
178	Structural studies on vertebrate and invertebrate acetylcholinesterases and their complexes with functional ligands. <i>Drug Development Research</i> , 2000, 50, 573-583.	1.4	11
179	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
180	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

#	ARTICLE	IF	CITATIONS
181	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
182	Preliminary X-ray diffraction studies on 2 fe-ferredoxin from <i>Halobacterium</i> of the Dead Sea. <i>Journal of Molecular Biology</i> , 1979, 134, 375-377.	2.0	9
183	The effect of binding of metal ions on the three-dimensional structure of demetallized concanavalin A. <i>FEBS Letters</i> , 1978, 95, 54-56.	1.3	8
184	Analysis of dihedral angles distribution: The doublets distribution determines polypeptides conformations. <i>Biopolymers</i> , 1990, 30, 499-508.	1.2	8
185	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
186	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
187	<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
188	Protein Data Bank Deposits. , 1998, 282, 1991f-1991.		8
189	A Structural Model For Sequence-Specific Proflavin-DNA Interactions During <i>In Vitro</i> Frameshift Mutagenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 1992, 10, 317-331.	2.0	7
190	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
191	An idea whose time has come. <i>Genome Biology</i> , 2007, 8, 408.	13.9	6
192	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
193	Computational studies on cholinesterases: Strengthening our understanding of the integration of structure, dynamics and function. <i>Neuropharmacology</i> , 2020, 179, 108265.	2.0	6
194	[9] Crystal forms of avidin. <i>Methods in Enzymology</i> , 1990, 184, 90-93.	0.4	5
195	Crystal structure of YagE, a putative DHDPs-like protein from <i>Escherichia coli</i> K12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2102-2108.	1.5	5
196	Apotheosis, not apocalypse: methods in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1510-1511.	2.5	4
197	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
198	The four-helix bundle in cholinesterase dimers: Structural and energetic determinants of stability. <i>Chemico-Biological Interactions</i> , 2019, 309, 108699.	1.7	4

#	ARTICLE	IF	CITATIONS
199	Bridging the gap. <i>Nature Structural Biology</i> , 1997, 4, 517-517.	9.7	3
200	A practical guide to teaching with Proteopedia. <i>Biochemistry and Molecular Biology Education</i> , 2021, 49, 707-719.	0.5	3
201	Site-Directed Mutagenesis of Functional Residues in <i>Torpedo</i> Acetylcholinesterase. , 1992, , 177-183.		3
202	Crystal Structures of α -Aged α -Phosphorylated and Phosphonylated <i>Torpedo</i> Californica Acetylcholinesterase. , 1998, , 425-431.		3
203	New trends in protein expression. <i>Journal of Structural Biology</i> , 2010, 172, 1-2.	1.3	2
204	Polyproline-rich peptides associated with <i>Torpedo californica</i> acetylcholinesterase tetramers. <i>Chemico-Biological Interactions</i> , 2020, 319, 109007.	1.7	2
205	Assembly of Acetylcholinesterase Subunits in vitro. , 1998, , 442-443.		2
206	Histochemical method for characterization of enzyme crystals: application to crystals of <i>Torpedo californica</i> acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1348-1350.	2.5	1
207	Shedding UV Light on the Phase Problem. <i>Structure</i> , 2006, 14, 629-630.	1.6	1
208	From SPINE to SPINE-2 complexes and beyond. <i>Journal of Structural Biology</i> , 2011, 175, 105.	1.3	1
209	How Three-Fingered Snake Toxins Recognise Their Targets. , 1997, , 303-315.		1
210	Structural and Functional Studies on Acetylcholinesterase. , 1998, , 25-33.		1
211	Letter to the Editor. <i>Journal of Biomolecular Structure and Dynamics</i> , 1996, 13, 583-583.	2.0	0
212	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
213	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
214	The X-Ray Structure of Human Acid-beta-Glucosidase. , 2006, , 85-96.		0
215	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
216	Acetylcholinesterase: Substrate traffic and inhibition. <i>Biochemistry and Molecular Biology Education</i> , 2012, 40, 144-144.	0.5	0

#	ARTICLE	IF	CITATIONS
217	Guest Editorial: Databases and Bioinformatics Tools. Israel Journal of Chemistry, 2013, 53, 143-143.	1.0	0
218	Structural Genomics and Structural Proteomics: A Global Perspective. , 2008, , 505-537.		0
219	Tools to Make 3D Structural Data More Comprehensible: Emovie & Proteopedia. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 169-182.	0.5	0
220	Proteopedia: Exciting Advances in the 3D Encyclopedia of Biomolecular Structure. NATO Science for Peace and Security Series A: Chemistry and Biology, 2012, , 149-161.	0.5	0
221	3D Structure of a Complex of the Anti-Alzheimer Drug, E2020, with Acetylcholinesterase at 2.5Å... Resolution. , 1998, , 469-475.		0
222	Crystallographic Studies on Complexes of Acetylcholinesterase with the Natural Cholinesterase Inhibitors Fasciculin and Huperzine A. Advances in Behavioral Biology, 1998, , 523-530.	0.2	0
223	On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field. , 2019, , .		0
224	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
225	Database and Comparative Identification of Prophages. , 2006, , 863-868.		0