

Joel L Sussman

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223
papers

20,874
citations

74
h-index

142
g-index

234
ext. papers

22,420
ext. citations

7.7
avg, IF

6.2
L-index

#	Paper	IF	Citations
223	The alpha/beta hydrolase fold. <i>Protein Engineering, Design and Selection</i> , 1992 , 5, 197-211	1.9	1664
222	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, 9031-5	11.5	804
221	FoldIndex: a simple tool to predict whether a given protein sequence is intrinsically unfolded. <i>Bioinformatics</i> , 2005 , 21, 3435-8	7.2	776
220	Function and structure of inherently disordered proteins. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 756-64	8.1	746
219	Protein production and purification. <i>Nature Methods</i> , 2008 , 5, 135-46	21.6	655
218	Structure of acetylcholinesterase complexed with E2020 (Aricept): implications for the design of new anti-Alzheimer drugs. <i>Structure</i> , 1999 , 7, 297-307	5.2	571
217	Structure and evolution of the serum paraoxonase family of detoxifying and anti-atherosclerotic enzymes. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 412-9	17.6	494
216	Relationship between sequence conservation and three-dimensional structure in a large family of esterases, lipases, and related proteins. <i>Protein Science</i> , 1993 , 2, 366-82	6.3	442
215	Acetylcholinesterase: from 3D structure to function. <i>Chemico-Biological Interactions</i> , 2010 , 187, 10-22	5	420
214	Protein Data Bank (PDB): database of three-dimensional structural information of biological macromolecules. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1078-84		383
213	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, 623-8	11.5	383
212	Acetylcholinesterase: 'classical' and 'non-classical' functions and pharmacology. <i>Current Opinion in Pharmacology</i> , 2005 , 5, 293-302	5.1	362
211	Crystal structure of yeast phenylalanine transfer RNA. I. Crystallographic refinement. <i>Journal of Molecular Biology</i> , 1978 , 123, 607-30	6.5	344
210	Structure of acetylcholinesterase complexed with the nootropic alkaloid, (-)-huperzine A. <i>Nature Structural and Molecular Biology</i> , 1997 , 4, 57-63	17.6	343
209	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	16.4	325
208	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, 579-90	11.6	317
207	Conversion of acetylcholinesterase to butyrylcholinesterase: modeling and mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992 , 89, 10827-31	11.5	273

206	Crystal structure of yeast phenylalanine transfer RNA. II. Structural features and functional implications. <i>Journal of Molecular Biology</i> , 1978 , 123, 631-60	6.5	271
205	Crystal structures of aged phosphorylated acetylcholinesterase: nerve agent reaction products at the atomic level. <i>Biochemistry</i> , 1999 , 38, 7032-9	3.2	248
204	Three-dimensional structures of <i>Drosophila melanogaster</i> acetylcholinesterase and of its complexes with two potent inhibitors. <i>Protein Science</i> , 2000 , 9, 1063-72	6.3	246
203	Structures of recombinant native and E202Q mutant human acetylcholinesterase complexed with the snake-venom toxin fasciculin-II. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1385-94		229
202	Structure of acetylcholinesterase complexed with (-)-galanthamine at 2.3 Å resolution. <i>FEBS Letters</i> , 1999 , 463, 321-6	3.8	220
201	X-ray structure of human acid-beta-glucosidase, the defective enzyme in Gaucher disease. <i>EMBO Reports</i> , 2003 , 4, 704-9	6.5	218
200	Crystal structure of an acetylcholinesterase-fasciculin complex: interaction of a three-fingered toxin from snake venom with its target. <i>Structure</i> , 1995 , 3, 1355-66	5.2	217
199	RNA-ligand interactions. (I) Magnesium binding sites in yeast tRNAPhe. <i>Nucleic Acids Research</i> , 1977 , 4, 2811-20	20.1	212
198	A 3D building blocks approach to analyzing and predicting structure of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989 , 5, 355-73	4.2	209
197	Automated Structure- and Sequence-Based Design of Proteins for High Bacterial Expression and Stability. <i>Molecular Cell</i> , 2016 , 63, 337-346	17.6	204
196	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT/JCSG+ strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1426-31		191
195	Computational redesign of a mononuclear zinc metalloenzyme for organophosphate hydrolysis. <i>Nature Chemical Biology</i> , 2012 , 8, 294-300	11.7	189
194	Insights into protein adaptation to a saturated salt environment from the crystal structure of a halophilic 2Fe-2S ferredoxin. <i>Nature Structural Biology</i> , 1996 , 3, 452-8		185
193	How flexible is the furanose ring? 1. A comparison of experimental and theoretical studies. <i>Journal of the American Chemical Society</i> , 1982 , 104, 270-278	16.4	180
192	Refined crystal structure of dogfish M4 apo-lactate dehydrogenase. <i>Journal of Molecular Biology</i> , 1987 , 198, 445-67	6.5	178
191	Crystal structure of a naturally occurring dinucleoside phosphate: uridylyl 3',5'-adenosine phosphate model for RNA chain folding. <i>Journal of Molecular Biology</i> , 1972 , 66, 403-21	6.5	174
190	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157		171
189	Complexes of alkylene-linked tacrine dimers with <i>Torpedo californica</i> acetylcholinesterase: Binding of Bis5-tacrine produces a dramatic rearrangement in the active-site gorge. <i>Journal of Medicinal Chemistry</i> , 2006 , 49, 5491-500	8.3	170

188	JSmol and the Next-Generation Web-Based Representation of 3D Molecular Structure as Applied to Proteopedia. <i>Israel Journal of Chemistry</i> , 2013 , 53, 207-216	3.4	169
187	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014 , 42, D326-35	20.1	159
186	Directed evolution of hydrolases for prevention of G-type nerve agent intoxication. <i>Nature Chemical Biology</i> , 2011 , 7, 120-5	11.7	156
185	Crystal structure of a eukaryotic initiator tRNA. <i>Nature</i> , 1979 , 278, 188-90	50.4	149
184	A server and database for dipole moments of proteins. <i>Nucleic Acids Research</i> , 2007 , 35, W512-21	20.1	146
183	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	16.4	142
182	Structural insights into substrate traffic and inhibition in acetylcholinesterase. <i>EMBO Journal</i> , 2006 , 25, 2746-56	13	140
181	Acetylcholinesterase: electrostatic steering increases the rate of ligand binding. <i>Biochemistry</i> , 1993 , 32, 401-3	3.2	138
180	Protein Data Bank archives of three-dimensional macromolecular structures. <i>Methods in Enzymology</i> , 1997 , 277, 556-71	1.7	137
179	Acetylcholinesterase: how is structure related to function?. <i>Chemico-Biological Interactions</i> , 2008 , 175, 3-10	5	137
178	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, 188-97	6.3	136
177	Active-site gorge and buried water molecules in crystal structures of acetylcholinesterase from <i>Torpedo californica</i> . <i>Journal of Molecular Biology</i> , 2000 , 296, 713-35	6.5	128
176	Catalytic versatility and backups in enzyme active sites: the case of serum paraoxonase 1. <i>Journal of Molecular Biology</i> , 2012 , 418, 181-96	6.5	122
175	Proteomic signatures: amino acid and oligopeptide compositions differentiate among phyla. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 20-40	4.2	117
174	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, 7856-61	16.4	111
173	The binding site of acetylcholine receptor as visualized in the X-Ray structure of a complex between alpha-bungarotoxin and a mimotope peptide. <i>Neuron</i> , 2001 , 32, 265-75	13.9	110
172	Hydrogen bonding in yeast phenylalanine transfer RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1975 , 72, 4866-70	11.5	110
171	The complex of a bivalent derivative of galanthamine with torpedo 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, 15405-11	16.4	106

170	Crystal structures of complexes of N-butyl- and N-nonyl-deoxynojirimycin bound to acid beta-glucosidase: insights into the mechanism of chemical chaperone action in Gaucher disease. <i>Journal of Biological Chemistry</i> , 2007 , 282, 29052-29058	5.4	102
169	Structure and functions of acetylcholinesterase and butyrylcholinesterase. <i>Progress in Brain Research</i> , 1993 , 98, 139-46	2.9	102
168	The three-dimensional structure of a DNA duplex containing looped-out bases. <i>Nature</i> , 1988 , 334, 82-4	50.4	98
167	Characterization of gene-activated human acid-beta-glucosidase: crystal structure, glycan composition, and internalization into macrophages. <i>Glycobiology</i> , 2010 , 20, 24-32	5.8	97
166	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, 1232-42		94
165	Assessment of disorder predictions in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 210-6	4.2	93
164	Idealized atomic coordinates of yeast phenylalanine transfer RNA. <i>Biochemical and Biophysical Research Communications</i> , 1976 , 68, 89-96	3.4	92
163	New directions in the treatment of Gaucher disease. <i>Trends in Pharmacological Sciences</i> , 2004 , 25, 147-51	13.2	91
162	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, 11340-9	16.4	87
161	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, 363-73	16.4	86
160	Proteopedia - a scientific 'wiki' bridging the rift between three-dimensional structure and function of biomacromolecules. <i>Genome Biology</i> , 2008 , 9, R121	18.3	85
159	The synaptic acetylcholinesterase tetramer assembles around a polyproline II helix. <i>EMBO Journal</i> , 2004 , 23, 4394-405	13	85
158	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, 369-83	3.3	85
157	X-ray structure of human acid-beta-glucosidase covalently bound to conduritol-B-epoxide. Implications for Gaucher disease. <i>Journal of Biological Chemistry</i> , 2005 , 280, 23815-9	5.4	85
156	Three-dimensional structures of bulge-containing DNA fragments. <i>Journal of Molecular Biology</i> , 1992 , 225, 397-431	6.5	85
155	Flexibility of aromatic residues in the active-site gorge of acetylcholinesterase: X-ray versus molecular dynamics. <i>Biophysical Journal</i> , 2008 , 95, 2500-11	2.9	84
154	Structural disorder serves as a weak signal for intracellular protein degradation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 903-9	4.2	84
153	Assessment of CASP8 structure predictions for template free targets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 50-65	4.2	83

152	Operational definition of intrinsically unstructured protein sequences based on susceptibility to the 20S proteasome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 70, 1357-66	4.2	80
151	Acetylcholinesterase: structure and use as a model for specific cation-protein interactions. <i>Current Opinion in Structural Biology</i> , 1992 , 2, 721-729	8.1	77
150	Three-dimensional structure of a complex of E2020 with acetylcholinesterase from Torpedo californica. <i>Journal of Physiology (Paris)</i> , 1998 , 92, 191-4		75
149	Evolved stereoselective hydrolases for broad-spectrum G-type nerve agent detoxification. <i>Chemistry and Biology</i> , 2012 , 19, 456-66		74
148	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, 7593-603	8.3	73
147	Crystal structure of 15-mer DNA duplex containing unpaired bases. <i>Nature</i> , 1988 , 334, 85-6	50.4	72
146	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		70
145	Adenine-guanine base pairing ribosomal RNA. <i>Nucleic Acids Research</i> , 1982 , 10, 2701-8	20.1	68
144	Eukaryotic expression: developments for structural proteomics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1114-24		67
143	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, 7493-8	11.5	67
142	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	2.8	64
141	Quantum/Classical Mechanical Comparison of Cation-Interactions between Tetramethylammonium and Benzene. <i>Journal of Physical Chemistry A</i> , 2001 , 105, 1326-1333	2.8	63
140	External and internal electrostatic potentials of cholinesterase models. <i>Journal of Molecular Graphics and Modelling</i> , 1997 , 15, 318-27, 335-7	2.8	59
139	Evidence for the formation of disulfide radicals in protein crystals upon X-ray irradiation. <i>Journal of Synchrotron Radiation</i> , 2002 , 9, 342-6	2.4	59
138	Context-dependent resistance to proteolysis of intrinsically disordered proteins. <i>Protein Science</i> , 2011 , 20, 1285-97	6.3	56
137	Soluble monomeric acetylcholinesterase from mouse: expression, purification, and crystallization in complex with fasciculon. <i>Protein Science</i> , 1996 , 5, 672-9	6.3	54
136	The structure of the complex between avidin and the dye, 2-(4'-hydroxyazobenzene) benzoic acid (HABA). <i>FEBS Letters</i> , 1993 , 328, 165-8	3.8	54
135	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, 814-25	6.3	53

134	Catalytic metal ion rearrangements underline promiscuity and evolvability of a metalloenzyme. <i>Journal of Molecular Biology</i> , 2013 , 425, 1028-38	6.5	52
133	The intracellular domain of the Drosophila cholinesterase-like neural adhesion protein, gliotactin, is natively unfolded. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 758-67	4.2	52
132	Crystal structure of demetallized concanavalin A: the metal-binding region. <i>Journal of Molecular Biology</i> , 1979 , 131, 137-55	6.5	52
131	Site-directed mutants designed to test back-door hypotheses of acetylcholinesterase function. <i>FEBS Letters</i> , 1996 , 386, 65-71	3.8	51
130	Constrained-restrained least-squares (CORELS) refinement of proteins and nucleic acids. <i>Methods in Enzymology</i> , 1985 , 115, 271-303	1.7	50
129	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, 11742-7	11.5	49
128	A structure-based design approach to the development of novel, reversible AChE inhibitors. <i>Journal of Medicinal Chemistry</i> , 2001 , 44, 3203-15	8.3	49
127	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, 601-5	6.3	48
126	pi turn is a conformational pattern in RNA loops and bends. <i>Nature</i> , 1976 , 260, 645-6	50.4	48
125	Backdoor opening mechanism in acetylcholinesterase based on X-ray crystallography and molecular dynamics simulations. <i>Protein Science</i> , 2011 , 20, 1114-8	6.3	47
124	Dynamic mechanism of E2020 binding to acetylcholinesterase: a steered molecular dynamics simulation. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 23730-8	3.4	47
123	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	2.5	47
122	Mechanism of oligonucleotide loop formation in solution. <i>Biochemistry</i> , 1986 , 25, 7417-23	3.2	47
121	A modular treatment of molecular traffic through the active site of cholinesterase. <i>Biophysical Journal</i> , 1999 , 77, 2430-50	2.9	46
120	Proteopedia: a status report on the collaborative, 3D web-encyclopedia of proteins and other biomolecules. <i>Journal of Structural Biology</i> , 2011 , 175, 244-52	3.4	42
119	6-Amino-6-deoxy-5,6-di-N-(N'-octyliminomethylidene)nojirimycin: synthesis, biological evaluation, and crystal structure in complex with acid beta-glucosidase. <i>ChemBioChem</i> , 2009 , 10, 1480-5	3.8	42
118	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	1.9	41
117	Crystal packing mediates enantioselective ligand recognition at the peripheral site of acetylcholinesterase. <i>Journal of the American Chemical Society</i> , 2005 , 127, 11029-36	16.4	40

116	G protein-coupled receptors show unusual patterns of intrinsic unfolding. <i>Protein Engineering, Design and Selection</i> , 2005 , 18, 103-10	1.9	40
115	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	2.8	40
114	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, 721-5	6.5	39
113	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, 1115-28		38
112	Structural comparison of differently glycosylated forms of acid-beta-glucosidase, the defective enzyme in Gaucher disease. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1458-65		38
111	An unusual halotolerant alpha-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, 151-7	2	38
110	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	4.8	37
109	Effect of mutations within the peripheral anionic site on the stability of acetylcholinesterase. <i>Molecular Pharmacology</i> , 1999 , 55, 982-92	4.3	36
108	Three-dimensional structures of acetylcholinesterase and of its complexes with anticholinesterase agents. <i>Biochemical Society Transactions</i> , 1994 , 22, 745-9	5.1	36
107	Catalytic efficiencies of directly evolved phosphotriesterase variants with structurally different organophosphorus compounds in vitro. <i>Archives of Toxicology</i> , 2016 , 90, 2711-2724	5.8	35
106	Directed evolution of serum paraoxonase PON3 by family shuffling and ancestor/consensus mutagenesis, and its biochemical characterization. <i>Biochemistry</i> , 2009 , 48, 6644-54	3.2	35
105	Acid beta-glucosidase: insights from structural analysis and relevance to Gaucher disease therapy. <i>Biological Chemistry</i> , 2008 , 389, 1361-9	4.5	35
104	PDBbrowse--a graphics interface to the Brookhaven Protein Data Bank. <i>Nature</i> , 1995 , 374, 572-4	50.4	35
103	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	4.4	34
102	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, 159-70	3.4	34
101	Biophysical characterization of the unstructured cytoplasmic domain of the human neuronal adhesion protein neuroligin 3. <i>Biophysical Journal</i> , 2008 , 95, 1928-44	2.9	34
100	Structure of a complex of the potent and specific inhibitor BW284C51 with <i>Torpedo californica</i> acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1765-71		34
99	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, 1874-81	4.3	34

98	Recommendations for Nomenclature in Cholinesterases 1992 , 285-288		33
97	Molecular basis of reduced glucosylceramidase activity in the most common Gaucher disease mutant, N370S. <i>Journal of Biological Chemistry</i> , 2010 , 285, 42105-14	5.4	31
96	Inhibition of acetylcholinesterase by the anticancer prodrug CPT-11. <i>Chemico-Biological Interactions</i> , 2005 , 157-158, 247-52	5	31
95	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	6.8	31
94	Structure-Based Optimization of Nonquaternary Reactivators of Acetylcholinesterase Inhibited by Organophosphorus Nerve Agents. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 7630-7639	8.3	30
93	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	6.5	30
92	Cyclodextrin-mediated crystallization of acid β -glucosidase in complex with amphiphilic bicyclic nojirimycin analogues. <i>Organic and Biomolecular Chemistry</i> , 2011 , 9, 4160-7	3.9	30
91	Novel multitarget-directed ligands targeting acetylcholinesterase and β -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	6.8	28
90	Static Laue diffraction studies on acetylcholinesterase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1359-66		26
89	eMovie: a storyboard-based tool for making molecular movies. <i>Trends in Biochemical Sciences</i> , 2007 , 32, 199-204	10.3	26
88	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	2.8	26
87	Natural protein engineering: a uniquely salt-tolerant, but not halophilic, alpha-type carbonic anhydrase from algae proliferating in low- to hyper-saline environments. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 191-200	1.9	25
86	A preliminary comparison of structural models for catalytic intermediates of acetylcholinesterase. <i>Chemico-Biological Interactions</i> , 1999 , 119-120, 43-52	5	25
85	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, 3575-80	8.3	24
84	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, 347-53	1.7	23
83	Design and synthesis of peptides that bind alpha-bungarotoxin with high affinity and mimic the three-dimensional structure of the binding-site of acetylcholine receptor. <i>Biophysical Chemistry</i> , 2003 , 100, 293-305	3.5	23
82	Characterization of crystals of genetically engineered human manganese superoxide dismutase. <i>Journal of Molecular Biology</i> , 1989 , 206, 787-8	6.5	23
81	The crystal structure of a complex of acetylcholinesterase with a bis(-)-nor-meptazinol derivative reveals disruption of the catalytic triad. <i>Journal of Medicinal Chemistry</i> , 2009 , 52, 2543-9	8.3	22

80	Biochemical evaluation of photolabile precursors of choline and of carbamylcholine for potential time-resolved crystallographic studies on cholinesterases. <i>Biochemistry</i> , 1996 , 35, 10854-61	3.2	22
79	A metastable state of <i>Torpedo californica</i> acetylcholinesterase generated by modification with organomercurials. <i>Biochemistry</i> , 1994 , 33, 14407-18	3.2	22
78	Single treatment of VX poisoned guinea pigs with the phosphotriesterase mutant C23AL: Intraosseous versus intravenous injection. <i>Toxicology Letters</i> , 2016 , 258, 198-206	4.4	21
77	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, 1096-114	6.3	21
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