Michael J Sutcliffe

List of Publications by Year
in descending order

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140 papers	7,437 citations	36203 51 h-index	62479 80 g-index
143 all docs	143 docs citations	143 times ranked	6386 citing authors

#	Article	IF	Citations
1	To what extent is capital expenditure in UK higher education meeting the pedagogical needs of staff and students?. Journal of Higher Education Policy and Management, 2016, 38, 477-489.	1.5	17
2	Quantum Mechanics/Molecular Mechanics Studies on the Mechanism of Action of Cofactor Pyridoxal 5â€²â€Phosphate in Ornithine 4,5â€Aminomutase. Chemistry - A European Journal, 2014, 20, 11390-11401.	1.7	8
3	Pressure Effects on Enzyme-Catalyzed Quantum Tunneling Events Arise from Protein-Specific Structural and Dynamic Changes. Journal of the American Chemical Society, 2012, 134, 9749-9754.	6.6	27
4	Large-Scale Domain Conformational Change Is Coupled to the Activation of the Coâ€“C Bond in the B₁₂-Dependent Enzyme Ornithine 4,5-Aminomutase: A Computational Study. Journal of the American Chemical Society, 2012, 134, 2367-2377.	6.6	41
5	Temperatureâ€dependent study reveals that dynamics of hydrophobic residues plays an important functional role in the mitochondrial Tim9â€“Tim10 complex. Proteins: Structure, Function and Bioinformatics, 2012, 80, 602-615.	1.5	6
6	In-silico characterization of the effects of phosphorylated tyrosines 86 and 106 on structure and binding of MAL: insight into hyperinflammatory response to infection by the human malaria parasites. Journal of Receptor and Signal Transduction Research, 2011, 31, 53-65.	1.3	2
7	Cytochrome P450 6M2 from the malaria vector Anopheles gambiae metabolizes pyrethroids: Sequential metabolism of deltamethrin revealed. Insect Biochemistry and Molecular Biology, 2011, 41, 492-502.	1.2	217
8	How Does Pressure Affect Barrier Compression and Isotope Effects in an Enzymatic Hydrogen Tunneling Reaction?. Angewandte Chemie - International Edition, 2011, 50, 2129-2132.	7.2	25
9	Probing active site geometry using high pressure and secondary isotope effects in an enzymeâ€catalysed â€˜deepâ€™ Hâ€tunnelling reaction. Journal of Physical Organic Chemistry, 2010, 23, 696-701.	0.9	16
10	Proteinâ€“protein interactions. Biochemical Society Transactions, 2010, 38, 875-878.	1.6	45
11	Barrier Compression and Its Contribution to Both Classical and Quantum Mechanical Aspects of Enzyme Catalysis. Biophysical Journal, 2010, 98, 121-128.	0.2	43
12	Direct Analysis of Donorâ€“Acceptor Distance and Relationship to Isotope Effects and the Force Constant for Barrier Compression in Enzymatic H-Tunneling Reactions. Journal of the American Chemical Society, 2010, 132, 11329-11335.	6.6	74
13	New insights into the multi-step reaction pathway of the reductive half-reaction catalysed by aromatic amine dehydrogenase: a QM/MM study. Chemical Communications, 2010, 46, 3104.	2.2	10
14	Assignment of the Vibrational Spectra of Enzyme-Bound Tryptophan Tryptophyl Quinones Using a Combined QM/MM Approach. Journal of Physical Chemistry A, 2010, 114, 1212-1217.	1.1	7
15	Inhibition of CYP1A1 by Quassinoids Found inPicrasma excelsa. Planta Medica, 2009, 75, 137-141.	0.7	22
16	Parallel Pathways and Freeâ€Energy Landscapes for Enzymatic Hydride Transfer Probed by Hydrostatic Pressure. ChemBioChem, 2009, 10, 1379-1384.	1.3	22
17	Barrier Compression Enhances an Enzymatic Hydrogenâ€Transfer Reaction. Angewandte Chemie - International Edition, 2009, 48, 1452-1454.	7.2	52
18	The response of the tandem pore potassium channel TASKâ€3 (K_{2P}9.1) to voltage: gating at the cytoplasmic mouth. Journal of Physiology, 2009, 587, 4769-4783.	1.3	25

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19	Evidence To Support the Hypothesis That Promoting Vibrations Enhance the Rate of an Enzyme Catalyzed H-Tunneling Reaction. Journal of the American Chemical Society, 2009, 131, 17072-17073.	6.6	79
20	Quantum Mechanics/Molecular Mechanics Studies on the Sulfoxidation of Dimethyl Sulfide by Compound I and Compound 0 of Cytochrome P450: Which Is the Better Oxidant?. Journal of Physical Chemistry A, 2009, 113, 11635-11642.	1.1	56
21	OLDERADO: On-line database of ensemble representatives and domains. Protein Science, 2008, 6, 2628-2630.	3.1	53
22	Driving Force Analysis of Proton Tunnelling Across a Reactivity Series for an Enzymeâ€Substrate Complex. ChemBioChem, 2008, 9, 2839-2845.	1.3	20
23	Secondary Kinetic Isotope Effects as Probes of Environmentallyâ€Coupled Enzymatic Hydrogen Tunneling Reactions. ChemPhysChem, 2008, 9, 1536-1539.	1.0	16
24	Solvent as a Probe of Active Site Motion and Chemistry during the Hydrogen Tunnelling Reaction in Morphinone Reductase. ChemPhysChem, 2008, 9, 1875-1881.	1.0	16
25	Are Environmentally Coupled Enzymatic Hydrogen Tunneling Reactions Influenced by Changes in Solution Viscosity?. Angewandte Chemie - International Edition, 2008, 47, 537-540.	7.2	34
26	How Do Azoles Inhibit Cytochrome P450 Enzymes? A Density Functional Study. Journal of Physical Chemistry A, 2008, 112, 12911-12918.	1.1	76
27	Characterization of inhibitors and substrates of Anopheles gambiae CYP6Z2. Insect Molecular Biology, 2008, 17, 125-135.	1.0	92
28	The enzyme aromatic amine dehydrogenase induces a substrate conformation crucial for promoting vibration that significantly reduces the effective potential energy barrier to proton transfer. Journal of the Royal Society Interface, 2008, 5, 225-232.	1.5	29
29	Deep Tunneling Dominates the Biologically Important Hydride Transfer Reaction from NADH to FMN in Morphinone Reductase. Journal of the American Chemical Society, 2008, 130, 7092-7097.	6.6	75
30	Insight into the Mechanism of Inactivation and pH Sensitivity in Potassium Channels from Molecular Dynamics Simulations. Biochemistry, 2008, 47, 7414-7422.	1.2	50
31	Calculating Chemically Accurate Redox Potentials for Engineered Flavoproteins from Classical Molecular Dynamics Free Energy Simulations. Journal of Physical Chemistry A, 2008, 112, 13053-13057.	1.1	17
32	Multiple Substrate Binding by Cytochrome P450 3A4: Estimation of the Number of Bound Substrate Molecules. Drug Metabolism and Disposition, 2008, 36, 2136-2144.	1.7	50
33	Cysteine Substitution Mutagenesis and the Effects of Methanethiosulfonate Reagents at P2X2 and P2X4 Receptors Support a Core Common Mode of ATP Action at P2X Receptors. Journal of Biological Chemistry, 2008, 283, 20126-20136.	1.6	51
34	Atomistic insight into the origin of the temperature-dependence of kinetic isotope effects and H-tunnelling in enzyme systems is revealed through combined experimental studies and biomolecular simulation. Biochemical Society Transactions, 2008, 36, 16-21.	1.6	21
35	Activation Gating of hERG Potassium Channels. Journal of Biological Chemistry, 2007, 282, 31972-31981.	1.6	40
36	New Insights into the Reductive Half-reaction Mechanism of Aromatic Amine Dehydrogenase Revealed by Reaction with Carbinolamine Substrates*. Journal of Biological Chemistry, 2007, 282, 23766-23777.	1.6	16

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37	Promoting motions in enzyme catalysis probed by pressure studies of kinetic isotope effects. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 507-512.	3.3	98
38	Tunneling and Classical Paths for Proton Transfer in an Enzyme Reaction Dominated by Tunneling:Â Oxidation of Tryptamine by Aromatic Amine Dehydrogenase. Journal of Physical Chemistry B, 2007, 111, 3032-3047.	1.2	53
39	Mutagenesis of Morphinone Reductase Induces Multiple Reactive Configurations and Identifies Potential Ambiguity in Kinetic Analysis of Enzyme Tunneling Mechanisms. Journal of the American Chemical Society, 2007, 129, 13949-13956.	6.6	55
40	Proton Tunneling in Aromatic Amine Dehydrogenase is Driven by a Short-Range Sub-Picosecond Promoting Vibration:Â Consistency of Simulation and Theory with Experiment. Journal of Physical Chemistry B, 2007, 111, 2631-2638.	1.2	62
41	Analysis of Classical and Quantum Paths for Deprotonation of Methylamine by Methylamine Dehydrogenase. ChemPhysChem, 2007, 8, 1816-1835.	1.0	41
42	Drug block of the hERG potassium channel: Insight from modeling. Proteins: Structure, Function and Bioinformatics, 2007, 68, 568-580.	1.5	100
43	Molecular mechanisms for drug interactions with hERG that cause long QT syndrome. Expert Opinion on Drug Metabolism and Toxicology, 2006, 2, 81-94.	1.5	41
44	Computational studies of enzyme mechanism: linking theory with experiment in the analysis of enzymic H-tunnelling. Physical Chemistry Chemical Physics, 2006, 8, 4510.	1.3	14
45	Hydrogen tunnelling in enzyme-catalysed H-transfer reactions: flavoprotein and quinoprotein systems. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 1375-1386.	1.8	59
46	Design, synthesis and biological activity of new CDK4-specific inhibitors, based on fascaplysin. Organic and Biomolecular Chemistry, 2006, 4, 787.	1.5	42
47	IN SILICO PREDICTION OF DRUG BINDING TO CYP2D6: IDENTIFICATION OF A NEW METABOLITE OF METOCLOPRAMIDE. Drug Metabolism and Disposition, 2006, 34, 1386-1392.	1.7	41
48	Î±-Secondary Isotope Effects as Probes of â€œTunneling-Readyâ€•Configurations in Enzymatic H-Tunneling:Â Insight from Environmentally Coupled Tunneling Models. Journal of the American Chemical Society, 2006, 128, 14053-14058.	6.6	66
49	The preponderance of P450s in the Mycobacterium tuberculosis genome. Trends in Microbiology, 2006, 14, 220-228.	3.5	67
50	CA224, a non-planar analogue of fascaplysin, inhibits Cdk4 but not Cdk2 and arrests cells at G0/G1 inhibiting pRB phosphorylation. Bioorganic and Medicinal Chemistry Letters, 2006, 16, 4272-4278.	1.0	27
51	Inhibition of cancer cell growth by cyclin dependent kinase 4 inhibitors synthesized based on the structure of fascaplysin. Bioorganic Chemistry, 2006, 34, 287-297.	2.0	18
52	Insights into Drug Metabolism from Modelling Studies of Cytochrome P450-Drug Interactions. Current Topics in Medicinal Chemistry, 2006, 6, 1619-1626.	1.0	6
53	Drug Binding Interactions in the Inner Cavity of hERG Channels: Molecular Insights from Structure-Activity Relationships of Clofilium and Ibutilide Analogs. Molecular Pharmacology, 2006, 69, 509-519.	1.0	84
54	Introduction. Quantum catalysis in enzymes: beyond the transition state theory paradigm. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 1293-1294.	1.8	19

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55	IN SILICO AND IN VITRO SCREENING FOR INHIBITION OF CYTOCHROME P450 CYP3A4 BY COMEDICATIONS COMMONLY USED BY PATIENTS WITH CANCER. Drug Metabolism and Disposition, 2006, 34, 534-538.	1.7	58
56	Atomic Description of an Enzyme Reaction Dominated by Proton Tunneling. Science, 2006, 312, 237-241.	6.0	304
57	Kinetic isotope effects and ligand binding in PQQ-dependent methanol dehydrogenase. Biochemical Journal, 2005, 388, 123-133.	1.7	11
58	Flavoenzyme catalysed oxidation of amines: roles for flavin and protein-based radicals. Biochemical Society Transactions, 2005, 33, 754-757.	1.6	16
59	The design and synthesis of novel 3-[2-indol-1-yl-ethyl]-1H-indole derivatives as selective inhibitors of CDK4. Tetrahedron Letters, 2005, 46, 1423-1425.	0.7	44
60	Contribution of conserved glycine residues to ATP action at human P2X1 receptors: mutagenesis indicates that the glycine at position 250 is important for channel function. Journal of Neurochemistry, 2005, 95, 1746-1754.	2.1	21
61	The Design and Synthesis of Novel 3-[2-Indol-1-yl-ethyl]-1H-indole Derivatives as Selective Inhibitors of CDK4.. ChemInform, 2005, 36, no.	0.1	0
62	Why Is Quinidine an Inhibitor of Cytochrome P450 2D6?. Journal of Biological Chemistry, 2005, 280, 38617-38624.	1.6	63
63	TRAIL Receptor-Selective Mutants Signal to Apoptosis via TRAIL-R1 in Primary Lymphoid Malignancies. Cancer Research, 2005, 65, 11265-11270.	0.4	152
64	Biodiversity of cytochrome P450 redox systems. Biochemical Society Transactions, 2005, 33, 796-801.	1.6	107
65	Role of Active Site Residues and Solvent in Proton Transfer and the Modulation of Flavin Reduction Potential in Bacterial Morphinone Reductase. Journal of Biological Chemistry, 2005, 280, 27103-27110.	1.6	24
66	Progress in cytochrome P450 active site modeling. Archives of Biochemistry and Biophysics, 2005, 433, 361-368.	1.4	26
67	In Silico Methods for Predicting Ligand Binding Determinants of Cytochromes P450. Current Topics in Medicinal Chemistry, 2004, 4, 1803-1824.	1.0	67
68	Extensive Domain Motion and Electron Transfer in the Human Electron Transferring FlavoproteinÂ·Medium Chain Acyl-CoA Dehydrogenase Complex. Journal of Biological Chemistry, 2004, 279, 32904-32912.	1.6	82
69	A Copper-Bottomed Trafficking Solution. Structure, 2004, 12, 517-518.	1.6	1
70	Validation of Model of Cytochrome P450 2D6:â€‰ An in Silico Tool for Predicting Metabolism and Inhibition. Journal of Medicinal Chemistry, 2004, 47, 5340-5346.	2.9	78
71	Thermodynamic and Biophysical Characterization of Cytochrome P450 BioI fromBacillus subtilisâ€. Biochemistry, 2004, 43, 12410-12426.	1.2	57
72	New fascaplysin-based CDK4-specific inhibitors: design, synthesis and biological activity. Chemical Communications, 2004, , 1696-1697.	2.2	29

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73	Hydrogen tunneling in quinoproteins. Archives of Biochemistry and Biophysics, 2004, 428, 41-51.	1.4	59
74	Phe120 contributes to the regiospecificity of cytochrome P450 2D6: mutation leads to the formation of a novel dextromethorphan metabolite. Biochemical Journal, 2004, 380, 353-360.	1.7	69
75	Relationship between protein structure and function: Valuable insight from computational studies. Biochemist, 2004, 26, 13-16.	0.2	0
76	Extensive conformational sampling in a ternary electron transfer complex. Nature Structural and Molecular Biology, 2003, 10, 219-225.	3.6	112
77	Effects of Multiple Ligand Binding on Kinetic Isotope Effects in PQQ-Dependent Methanol Dehydrogenase. Biochemistry, 2003, 42, 3966-3978.	1.2	17
78	H-tunneling in the Multiple H-transfers of the Catalytic Cycle of Morphinone Reductase and in the Reductive Half-reaction of the Homologous Pentaerythritol Tetranitrate Reductase. Journal of Biological Chemistry, 2003, 278, 43973-43982.	1.6	98
79	Residues Glutamate 216 and Aspartate 301 Are Key Determinants of Substrate Specificity and Product Regioselectivity in Cytochrome P450 2D6. Journal of Biological Chemistry, 2003, 278, 4021-4027.	1.6	93
80	Spermine Is Fit to Block Inward Rectifier (Kir) Channels. Journal of General Physiology, 2003, 122, 481-484.	0.9	22
81	Role of conserved Asp293 of cytochrome P450 2C9 in substrate recognition and catalytic activity. Biochemical Journal, 2003, 370, 921-926.	1.7	31
82	Cytochromes P450: novel drug targets in the war against multidrug-resistant Mycobacterium tuberculosis. Biochemical Society Transactions, 2003, 31, 625-630.	1.6	32
83	Electron Transfer and Conformational Change in Complexes of Trimethylamine Dehydrogenase and Electron Transferring Flavoprotein. Journal of Biological Chemistry, 2002, 277, 8457-8465.	1.6	21
84	Comparative modelling of cytochromes P450. Advanced Drug Delivery Reviews, 2002, 54, 385-406.	6.6	47
85	A new conceptual framework for enzyme catalysis. FEBS Journal, 2002, 269, 3096-3102.	0.2	132
86	Impact of incorporating the 2C5 crystal structure into comparative models of cytochrome P450 2D6. Proteins: Structure, Function and Bioinformatics, 2002, 49, 216-231.	1.5	66
87	QM/MM Studies Show Substantial Tunneling for the Hydrogen-Transfer Reaction in Methylamine Dehydrogenase. Journal of the American Chemical Society, 2001, 123, 8604-8605.	6.6	62
88	Engineering the active site of ascorbate peroxidase. FEBS Journal, 2001, 268, 78-85.	0.2	24
89	Protein Dynamics Enhance Electronic Coupling in Electron Transfer Complexes. Journal of Biological Chemistry, 2001, 276, 34142-34147.	1.6	32
90	Î±Arg-237 in Methylophilus methylotrophus (sp. W3A1) Electron-transferring Flavoprotein Affords â^¼200-Millivolt Stabilization of the FAD Anionic Semiquinone and a Kinetic Block on Full Reduction to the Dihydroquinone. Journal of Biological Chemistry, 2001, 276, 20190-20196.	1.6	31

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91	Deuterium Isotope Effects during Carbonâ€“Hydrogen Bond Cleavage by Trimethylamine Dehydrogenase. Journal of Biological Chemistry, 2001, 276, 24581-24587.	1.6	70
92	Importance of Barrier Shape in Enzyme-catalyzed Reactions. Journal of Biological Chemistry, 2001, 276, 6234-6242.	1.6	98
93	Optimizing the Michaelis Complex of Trimethylamine Dehydrogenase. Journal of Biological Chemistry, 2001, 276, 42887-42892.	1.6	25
94	Engineering the active site of ascorbate peroxidase. Biochemical Society Transactions, 2001, 29, 105-11.	1.6	1
95	Trimethylamine Dehydrogenase and Electron Transferring Flavoprotein. Sub-Cellular Biochemistry, 2000, 35, 145-181.	1.0	6
96	Enzyme catalysis: over-the-barrier or through-the-barrier?. Trends in Biochemical Sciences, 2000, 25, 405-408.	3.7	54
97	Structural Insights Into NMDA Ionotropic Glutamate Receptors via Molecular Modelling. Journal of Molecular Modeling, 2000, 6, 16-25.	0.8	8
98	Enzymology takes a quantum leap forward. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2000, 358, 367-386.	1.6	46
99	X-ray Scattering Studies of Methylophilus methylotrophus (sp. W3A1) Electron-transferring Flavoprotein. Journal of Biological Chemistry, 2000, 275, 21349-21354.	1.6	15
100	Amino Acid 305 Determines Catalytic Center Accessibility in CYP3A4â€. Biochemistry, 2000, 39, 4406-4414.	1.2	38
101	Structural and Biochemical Characterization of Recombinant Wild Type and a C30A Mutant of Trimethylamine Dehydrogenase fromMethylophilus methylotrophus(sp. W3A1)â€,â€¡. Biochemistry, 2000, 39, 7678-7688.	1.2	44
102	Differential Coupling through Val-344 and Tyr-442 of Trimethylamine Dehydrogenase in Electron Transfer Reactions with Ferricenium Ions and Electron Transferring Flavoproteinâ€. Biochemistry, 2000, 39, 9188-9200.	1.2	21
103	Structure of the Complex of Cdc42Hs with a Peptide Derived from P-21 Activated Kinase,. Biochemistry, 2000, 39, 3963-3971.	1.2	43
104	Kinetic Studies of the Mechanism of Carbonâˆ’Hydrogen Bond Breakage by the Heterotetrameric Sarcosine Oxidase ofArthrobactersp. 1-INâ€. Biochemistry, 2000, 39, 1189-1198.	1.2	98
105	Cysteine Mutagenesis and Homology Modeling of the Ligand-binding Site of a Kainate-binding Protein. Journal of Biological Chemistry, 1999, 274, 37210-37218.	1.6	9
106	The Role of Tyr-169 of Trimethylamine Dehydrogenase in Substrate Oxidation and Magnetic Interaction between FMN Cofactor and the 4Fe/4S Center. Journal of Biological Chemistry, 1999, 274, 13155-13161.	1.6	21
107	New insights into enzyme catalysis. Ground state tunnelling driven by protein dynamics. FEBS Journal, 1999, 264, 666-671.	0.2	78
108	Topology of the Pore Region of an Inward Rectifier K+ Channel, Kir2.1. Annals of the New York Academy of Sciences, 1999, 868, 414-417.	1.8	0

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109	Three-dimensional models of glutamate receptors. Faraday Discussions, 1999, 111, 259-272.	1.6	3
110	Enzymatic H-Transfer Requires Vibration-Driven Extreme Tunneling. Biochemistry, 1999, 38, 3218-3222.	1.2	245
111	Reductive half-reaction of the H172Q mutant of trimethylamine dehydrogenase: evidence against a carbanion mechanism and assignment of kinetically influential ionizations in the enzymeâ€'substrate complex. Biochemical Journal, 1999, 341, 307.	1.7	8
112	Reductive half-reaction of the H172Q mutant of trimethylamine dehydrogenase: evidence against a carbanion mechanism and assignment of kinetically influential ionizations in the enzymeâ€"substrate complex. Biochemical Journal, 1999, 341, 307-314.	1.7	14
113	Identification of the Binding Surface on Cdc42Hs for p21-Activated Kinaseâ€. Biochemistry, 1998, 37, 14030-14037.	1.2	38
114	[32] Molecular modeling of ligand-gated ion channels. Methods in Enzymology, 1998, 293, 589-620.	0.4	17
115	Determinants of the substrate specificity of human cytochrome P-450 CYP2D6: design and construction of a mutant with testosterone hydroxylase activity. Biochemical Journal, 1998, 331, 783-792.	1.7	67
116	An Exposed Tyrosine on the Surface of Trimethylamine Dehydrogenase Facilitates Electron Transfer to Electron Transferring Flavoprotein:â€‰ Kinetics of Transfer in Wild-Type and Mutant Complexes. Biochemistry, 1997, 36, 41-48.	1.2	40
117	A Single Mutation in Cytochrome P450 BM3 Changes Substrate Orientation in a Catalytic Intermediate and the Regiospecificity of Hydroxylationâ€. Biochemistry, 1997, 36, 1567-1572.	1.2	141
118	Definition of the Switch Surface in the Solution Structure of Cdc42Hsâ€,â€¡. Biochemistry, 1997, 36, 8755-8766.	1.2	95
119	Chemical, Spectroscopic and Structural Investigation of the Substrate-Binding Site in Ascorbate Peroxidase. FEBS Journal, 1997, 248, 347-354.	0.2	23
120	Steady-State and Picosecond-Time-Resolved Fluorenscence Studies on the Recombinant Heme Domain of Bacillus megaterium Cytochrome P-450. FEBS Journal, 1997, 244, 361-370.	0.2	15
121	NMR Studies of the Mode of Binding of Corepressors and Inducers to Escherichia coli Trp Repressor. FEBS Journal, 1996, 235, 804-813.	0.2	10
122	The catalytic mechanism of cytochrome P450 BM3 involves a 6 Ã… movement of the bound substrate on reduction. Nature Structural Biology, 1996, 3, 414-417.	9.7	123
123	Crystal structure of a PDZ domain. Nature, 1996, 382, 649-652.	13.7	322
124	Ligand Binding to Integrin Î±IIbÎ²3 Is Dependent on a MIDAS-like Domain in the Î²3 Subunit. Journal of Biological Chemistry, 1996, 271, 21978-21984.	1.6	161
125	An automated approach for clustering an ensemble of NMR-derived protein structures into conformationally related subfamilies. Protein Engineering, Design and Selection, 1996, 9, 1063-1065.	1.0	426
126	Steroid Recognition by Chloramphenicol Acetyltransferase: Engineering and Structural Analysis of a High Affinity Fusidic Acid Binding Site. Journal of Molecular Biology, 1995, 254, 993-1005.	2.0	17

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127	[23] Protein-ligand interactions: Exchange processes and determination of ligand conformation and protein-ligand contacts. Methods in Enzymology, 1994, 239, 657-700.	0.4	75
128	Another turn for Eâ€“F hands. Nature Structural and Molecular Biology, 1994, 1, 209-212.	3.6	4
129	Three-dimensional structure of the RGD-containing neurotoxin homologue dendroaspin. Nature Structural Biology, 1994, 1, 802-807.	9.7	47
130	1H-NMR Assignments and Secondary Structure of Dendroaspin, an RGD-Containing Glycoprotein IIb-IIIa (alphaIIb-beta3) Antagonist with a Neurotoxin Fold. FEBS Journal, 1994, 226, 861-868.	0.2	13
131	Model Building Predicts an Additional Conformational Switch when GTP Binds to the CDC42HS Protein. Protein and Peptide Letters, 1994, 1, 84-91.	0.4	6
132	Representing an ensemble of NMRâ€derived protein structures by a single structure. Protein Science, 1993, 2, 936-944.	3.1	40
133	Structure of Hen Lysozyme in Solution. Journal of Molecular Biology, 1993, 229, 930-944.	2.0	147
134	Structure and mechanism of Streptococcal protein G. Biochemical Society Transactions, 1993, 21, 333S-333S.	1.6	3
135	Determination of the solution structures of domains II and III of protein G from Streptococcus by 1H nuclear magnetic resonance. Journal of Molecular Biology, 1992, 228, 1219-1234.	2.0	69
136	Solution structure of neuronal bungarotoxin determined by two-dimensional NMR spectroscopy: sequence-specific assignments, secondary structure, and dimer formation. Biochemistry, 1991, 30, 4901-4909.	1.2	48
137	Relaxation data in NMR structure determination: Model calculations for the lysozyme-Gd3+ complex. Proteins: Structure, Function and Bioinformatics, 1991, 10, 117-129.	1.5	7
138	Molecular anatomy: Phyletic relationships derived from three-dimensional structures of proteins. Journal of Molecular Evolution, 1990, 30, 43-59.	0.8	103
139	Hydrogen Tunneling in Enzyme-Catalyzed Hydrogen Transfer: Aspects from Flavoprotein Catalysed Reactions. , 0, , 1341-1359.		0
140	Homology Models Applied to Toxicology. , 0, , 433-468.		0