Michael W Parker

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/3880420/michael-w-parker-publications-by-year.pdf

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

332	16,509	70	114
papers	citations	h-index	g-index
354	18,120 ext. citations	7.9	6.18
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
332	Mechanism of Bloom syndrome complex assembly required for double Holliday junction dissolution and genome stability <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	1
331	Structural biology of cell surface receptors implicated in Alzheimer@ disease <i>Biophysical Reviews</i> , 2022 , 14, 233-255	3.7	O
330	Reaction hijacking of tyrosine tRNA synthetase as a new whole-of-life-cycle antimalarial strategy. <i>Science</i> , 2022 , 376, 1074-1079	33.3	3
329	Cytokine Receptors and their Ligands 2022 ,		
328	Structure of native HIV-1 cores and their interactions with IP6 and CypA. Science Advances, 2021, 7, eabj	5741\$	1
327	Messing with E : A unique receptor with many goals. <i>Seminars in Immunology</i> , 2021 , 54, 101513	10.7	О
326	A DARPin targeting activated Mac-1 is a novel diagnostic tool and potential anti-inflammatory agent in myocarditis, sepsis and myocardial infarction. <i>Basic Research in Cardiology</i> , 2021 , 116, 17	11.8	6
325	An ALYREF-MYCN coactivator complex drives neuroblastoma tumorigenesis through effects on USP3 and MYCN stability. <i>Nature Communications</i> , 2021 , 12, 1881	17.4	8
324	A novel combination therapy targeting ubiquitin-specific protease 5 in MYCN-driven neuroblastoma. <i>Oncogene</i> , 2021 , 40, 2367-2381	9.2	3
323	Role of nicotinic acetylcholine receptor subunits in the mode of action of neonicotinoid, sulfoximine and spinosyn insecticides in Drosophila melanogaster. <i>Insect Biochemistry and Molecular Biology</i> , 2021 , 131, 103547	4.5	14
322	Repurposing of drugs as STAT3 inhibitors for cancer therapy. Seminars in Cancer Biology, 2021, 68, 31-46	512.7	23
321	Functional and structural analysis of cytokine-selective IL6ST defects that cause recessive hyper-IgE syndrome. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 148, 585-598	11.5	5
320	Design of proteasome inhibitors with oral efficacy in vivo against and selectivity over the human proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
319	Drug repurposing: Misconceptions, challenges, and opportunities for academic researchers. <i>Science Translational Medicine</i> , 2021 , 13, eabd5524	17.5	12
318	Development of [F]MIPS15692, a radiotracer with inlivitro proof-of-concept for the imaging of MER tyrosine kinase (MERTK) in neuroinflammatory disease. <i>European Journal of Medicinal Chemistry</i> , 2021 , 226, 113822	6.8	1
317	X-ray crystallography shines a light on pore-forming toxins. <i>Methods in Enzymology</i> , 2021 , 649, 1-46	1.7	2
316	A structural view of PA2G4 isoforms with opposing functions in cancer. <i>Journal of Biological Chemistry</i> , 2020 , 295, 16100-16112	5.4	4

315	The structure of the extracellular domains of human interleukin 11Ireceptor reveals mechanisms of cytokine engagement. <i>Journal of Biological Chemistry</i> , 2020 , 295, 8285-8301	5.4	10	
314	Sequence comparisons of cytochrome P450 aromatases from Australian animals predict differences in enzymatic activity and/or efficiency <i>Biology of Reproduction</i> , 2020 , 102, 1261-1269	3.9	O	
313	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin. <i>PLoS ONE</i> , 2020 , 15, e0229000	3.7	6	•
312	Discovery of Acylsulfonohydrazide-Derived Inhibitors of the Lysine Acetyltransferase, KAT6A, as Potent Senescence-Inducing Anti-Cancer Agents. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 4655-4684	8.3	3	
311	Monoubiquitination by the human Fanconi anemia core complex clamps FANCI:FANCD2 on DNA in filamentous arrays. <i>ELife</i> , 2020 , 9,	8.9	35	
310	The Crystal Structure of the Manganese Superoxide Dismutase from Geobacillus stearothermophilus: Parker and Blake (1988) Revisited. <i>Australian Journal of Chemistry</i> , 2020 , 73, 145	1.2	1	
309	A Key Motif in the Cholesterol-Dependent Cytolysins Reveals a Large Family of Related Proteins. <i>MBio</i> , 2020 , 11,	7.8	8	
308	Long-chain fatty acyl-CoA esters regulate metabolism via allosteric control of AMPK ∄ isoforms. Nature Metabolism, 2020, 2, 873-881	14.6	34	
307	CaMKK2 is inactivated by cAMP-PKA signaling and 14-3-3 adaptor proteins. <i>Journal of Biological Chemistry</i> , 2020 , 295, 16239-16250	5.4	16	
306	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin 2020, 15, e022	9000		
305	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin 2020, 15, e022	9000		
304	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin 2020 , 15, e022	9000		
303	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin 2020, 15, e022	9000		
302	A Family of Dual-Activity Glycosyltransferase-Phosphorylases Mediates Mannogen Turnover and Virulence in Leishmania Parasites. <i>Cell Host and Microbe</i> , 2019 , 26, 385-399.e9	23.4	22	
301	Cholesterol-Dependent Cytolysins: Membrane and Protein Structural Requirements for Pore Formation. <i>Chemical Reviews</i> , 2019 , 119, 7721-7736	68.1	22	
300	A structure-based mechanism of cisplatin resistance mediated by glutathione transferase P1-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 13943-1395	1 ^{11.5}	47	
299	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. <i>MBio</i> , 2019 , 10,	7.8	7	
298	Repurposing the selective estrogen receptor modulator to suppress gastrointestinal cancer growth. <i>EMBO Molecular Medicine</i> , 2019 , 11,	12	22	

297	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. <i>Angewandte Chemie</i> , 2019 , 131, 16936-16940	3.6	3
296	Small Molecule Binding to Alzheimer Risk Factor CD33 Promotes APhagocytosis. <i>IScience</i> , 2019 , 19, 110-118	6.1	30
295	The structure of the PA28-20S proteasome complex from Plasmodium falciparum and implications for proteostasis. <i>Nature Microbiology</i> , 2019 , 4, 1990-2000	26.6	18
294	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 16780-16784	16.4	13
293	Discovery of Benzoylsulfonohydrazides as Potent Inhibitors of the Histone Acetyltransferase KAT6A. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 7146-7159	8.3	13
292	An Intermolecular Estacking Interaction Drives Conformational Changes Necessary to Barrel Formation in a Pore-Forming Toxin. <i>MBio</i> , 2019 , 10,	7.8	6
291	Structure and Function of the Proteasome Activator PA28 of the Malaria Parasite Plasmodium falciparum. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1324-1325	0.5	
2 90	Fluorescence Microscopy Assay to Measure HIV-1 Capsid Uncoating Kinetics. <i>Bio-protocol</i> , 2019 , 9, e329	76.9	5
289	Drugging MYCN Oncogenic Signaling through the MYCN-PA2G4 Binding Interface. <i>Cancer Research</i> , 2019 , 79, 5652-5667	10.1	17
288	The genetics, structure and function of the M1 aminopeptidase oxytocinase subfamily and their therapeutic potential in immune-mediated disease. <i>Human Immunology</i> , 2019 , 80, 281-289	2.3	11
287	Reaction mechanism of the bioluminescent protein mnemiopsin1 revealed by X-ray crystallography and QM/MM simulations. <i>Journal of Biological Chemistry</i> , 2019 , 294, 20-27	5.4	6
286	Structural Determinants for Small-Molecule Activation of Skeletal Muscle AMPK 位即 by the Glucose Importagog SC4. <i>Cell Chemical Biology</i> , 2018 , 25, 728-737.e9	8.2	24
285	A dual role for the N-terminal domain of the IL-3 receptor in cell signalling. <i>Nature Communications</i> , 2018 , 9, 386	17.4	20
284	Role of the Common (#) Family of Cytokines in Health and Disease. <i>Cold Spring Harbor Perspectives in Biology</i> , 2018 , 10,	10.2	13
283	Targeting of C-type lectin-like receptor or P2Y12 for the prevention of platelet activation by immunotherapeutic CpG oligodeoxynucleotides: comment. <i>Journal of Thrombosis and Haemostasis</i> , 2018 , 16, 181-185	15.4	1
282	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. <i>Nature</i> , 2018 , 560, 253-257	50.4	103
281	Kinetics of HIV-1 capsid uncoating revealed by single-molecule analysis. <i>ELife</i> , 2018 , 7,	8.9	58
2 80	EPO does not promote interaction between the erythropoietin and beta-common receptors. <i>Scientific Reports</i> , 2018 , 8, 12457	4.9	15

(2016-2018)

279	Cholesterol-dependent cytolysins: from water-soluble state to membrane pore. <i>Biophysical Reviews</i> , 2018 , 10, 1337-1348	3.7	24
278	Cyclic Hexapeptide Mimics of the LEDGF Integrase Recognition Loop in Complex with HIV-1 Integrase. <i>ChemMedChem</i> , 2018 , 13, 1555-1565	3.7	4
277	Accumulation of JAK Activation-Loop Phosphorylation Promotes Type I JAK Inhibitor Withdrawal Syndrome in Myelofibrosis. <i>Blood</i> , 2018 , 132, 1787-1787	2.2	
276	AMP and adenosine are both ligands for adenosine 2B receptor signaling. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018 , 28, 202-206	2.9	7
275	Accumulation of JAK activation loop phosphorylation is linked to type I JAK inhibitor withdrawal syndrome in myelofibrosis. <i>Science Advances</i> , 2018 , 4, eaat3834	14.3	23
274	Protein structure and computational drug discovery. <i>Biochemical Society Transactions</i> , 2018 , 46, 1367-1	3 ₹ 9	17
273	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. <i>Structure</i> , 2018 , 26, 948-959.e5	5.2	2
272	The mechanism of GM-CSF inhibition by human GM-CSF auto-antibodies suggests novel therapeutic opportunities. <i>MAbs</i> , 2018 , 10, 1018-1029	6.6	1
271	Transitional changes in the CRP structure lead to the exposure of proinflammatory binding sites. <i>Nature Communications</i> , 2017 , 8, 14188	17.4	105
270	Glutathione transferase P1-1 as an arsenic drug-sequestering enzyme. <i>Protein Science</i> , 2017 , 26, 317-32	266.3	12
269	Promiscuous DNA-binding of a mutant zinc finger protein corrupts the transcriptome and diminishes cell viability. <i>Nucleic Acids Research</i> , 2017 , 45, 1130-1143	20.1	23
268	Ex vivo O-labeling mass spectrometry identifies a peripheral amyloid ⊯learance pathway. <i>Molecular Neurodegeneration</i> , 2017 , 12, 18	19	15
267	Nitric Oxide Interacting with Glutathione Transferases 2017 , 191-195		
266	Control of Virulence Gene Expression by the Master Regulator, CfaD, in the Prototypical Enterotoxigenic Strain, H10407. <i>Frontiers in Microbiology</i> , 2017 , 8, 1525	5.7	4
265	QM/MM simulations provide insight into the mechanism of bioluminescence triggering in ctenophore photoproteins. <i>PLoS ONE</i> , 2017 , 12, e0182317	3.7	6
264	A Homodimer Model Can Resolve the Conundrum as to How Cytochrome P450 Oxidoreductase and Cytochrome b5 Compete for the Same Binding Site on Cytochrome P450c17. <i>Current Protein and Peptide Science</i> , 2017 , 18, 515-521	2.8	5
263	Structural basis of allosteric and synergistic activation of AMPK by furan-2-phosphonic derivative C2 binding. <i>Nature Communications</i> , 2016 , 7, 10912	17.4	53
262	The Binding of Syndapin SH3 Domain to Dynamin Proline-rich Domain Involves Short and Long Distance Elements. <i>Journal of Biological Chemistry</i> , 2016 , 291, 9411-24	5.4	14

261	CSL311, a novel, potent, therapeutic monoclonal antibody for the treatment of diseases mediated by the common Ethain of the IL-3, GM-CSF and IL-5 receptors. <i>MAbs</i> , 2016 , 8, 436-53	6.6	22
260	Conformational Changes in the GM-CSF Receptor Suggest a Molecular Mechanism for Affinity Conversion and Receptor Signaling. <i>Structure</i> , 2016 , 24, 1271-1281	5.2	33
259	The C-terminal extension of human telomerase reverse transcriptase is necessary for high affinity binding to telomeric DNA. <i>Biochimie</i> , 2016 , 128-129, 114-21	4.6	5
258	Structural Basis for Receptor Recognition by the Human CD59-Responsive Cholesterol-Dependent Cytolysins. <i>Structure</i> , 2016 , 24, 1488-98	5.2	20
257	Structural Determinants Defining the Allosteric Inhibition of an Essential Antibiotic Target. <i>Structure</i> , 2016 , 24, 1282-1291	5.2	23
256	Determinants of oligosaccharide specificity of the carbohydrate-binding modules of AMP-activated protein kinase. <i>Biochemical Journal</i> , 2015 , 468, 245-57	3.8	19
255	Molecular basis for mid-region amyloid-Hapture by leading Alzheimer disease immunotherapies. <i>Scientific Reports</i> , 2015 , 5, 9649	4.9	54
254	A RIPK2 inhibitor delays NOD signalling events yet prevents inflammatory cytokine production. <i>Nature Communications</i> , 2015 , 6, 6442	17.4	74
253	The ₱ receptor family - Structural insights and their functional implications. <i>Cytokine</i> , 2015 , 74, 247-58	4	51
252	Abeta targets of the biosimilar antibodies of Bapineuzumab, Crenezumab, Solanezumab in comparison to an antibody against N-truncated Abeta in sporadic Alzheimer disease cases and mouse models. <i>Acta Neuropathologica</i> , 2015 , 130, 713-29	14.3	36
251	Discovery and SAR of novel pyrazolo[1,5-a]pyrimidines as inhibitors of CDK9. <i>Bioorganic and Medicinal Chemistry</i> , 2015 , 23, 6280-96	3.4	25
250	Evolutionary comparisons predict that dimerization of human cytochrome P450 aromatase increases its enzymatic activity and efficiency. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2015 , 154, 294-301	5.1	8
249	Crystal structure of human insulin-regulated aminopeptidase with specificity for cyclic peptides. <i>Protein Science</i> , 2015 , 24, 190-9	6.3	40
248	Propargyloxyproline Regio- and Stereoisomers for Click-Conjugation of Peptides: Synthesis and Application in Linear and Cyclic Peptides. <i>Australian Journal of Chemistry</i> , 2015 , 68, 1365	1.2	9
247	Structure of the lysine specific protease Kgp from Porphyromonas gingivalis, a target for improved oral health. <i>Protein Science</i> , 2015 , 24, 162-6	6.3	13
246	Crystal structure of Streptococcus pneumoniae pneumolysin provides key insights into early steps of pore formation. <i>Scientific Reports</i> , 2015 , 5, 14352	4.9	44
245	Two-step mechanism involving active-site conformational changes regulates human telomerase DNA binding. <i>Biochemical Journal</i> , 2015 , 465, 347-57	3.8	14
244	Phosphorothioate backbone modifications of nucleotide-based drugs are potent platelet activators. <i>Journal of Experimental Medicine</i> , 2015 , 212, 129-37	16.6	73

(2014-2015)

243	An intermolecular electrostatic interaction controls the prepore-to-pore transition in a cholesterol-dependent cytolysin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 2204-9	11.5	34
242	Abstract 5371: PRMT5 inhibitors as novel treatment for cancers 2015 ,		3
241	Mechanistic Scrutiny Identifies a Kinetic Role for Cytochrome b5 Regulation of Human Cytochrome P450c17 (CYP17A1, P450 17A1). <i>PLoS ONE</i> , 2015 , 10, e0141252	3.7	22
240	Synthesis, structure-activity relationships and brain uptake of a novel series of benzopyran inhibitors of insulin-regulated aminopeptidase. <i>Journal of Medicinal Chemistry</i> , 2014 , 57, 1368-77	8.3	39
239	Oncogenic protein interfaces: small molecules, big challenges. <i>Nature Reviews Cancer</i> , 2014 , 14, 248-62	31.3	196
238	Tetraspanins as regulators of the tumour microenvironment: implications for metastasis and therapeutic strategies. <i>British Journal of Pharmacology</i> , 2014 , 171, 5462-90	8.6	64
237	A systematic and functional classification of Streptococcus pyogenes that serves as a new tool for molecular typing and vaccine development. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1325-38	7	187
236	Mechanism of activation of protein kinase JAK2 by the growth hormone receptor. <i>Science</i> , 2014 , 344, 1249783	33.3	269
235	78. Cytokine, 2014 , 70, 46	4	
234	Dual mechanism of interleukin-3 receptor blockade by an anti-cancer antibody. <i>Cell Reports</i> , 2014 , 8, 410-9	10.6	35
233	Do current therapeutic anti-Atantibodies for Alzheimer Q disease engage the target?. <i>Acta Neuropathologica</i> , 2014 , 127, 803-10	14.3	44
232	The role of Rdl in resistance to phenylpyrazoles in Drosophila melanogaster. <i>Insect Biochemistry and Molecular Biology</i> , 2014 , 54, 11-21	4.5	20
231	Structural studies of Streptococcus pyogenes streptolysin O provide insights into the early steps of membrane penetration. <i>Journal of Molecular Biology</i> , 2014 , 426, 785-92	6.5	44
230	Potent hepatitis C inhibitors bind directly to NS5A and reduce its affinity for RNA. <i>Scientific Reports</i> , 2014 , 4, 4765	4.9	86
229	Activity-modulating monoclonal antibodies to the human serine protease HtrA3 provide novel insights into regulating HtrA proteolytic activities. <i>PLoS ONE</i> , 2014 , 9, e108235	3.7	7
228	Computational Analysis of Amiloride Analogue Inhibitors of B3 RNA Polymerase. <i>Journal of Proteomics and Bioinformatics</i> , 2014 , Suppl 9, 004	2.1	1
227	Crystallization and preliminary X-ray diffraction analysis of the Fab portion of the AlzheimerQ disease immunotherapy candidate bapineuzumab complexed with amyloid-#Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 374-7	1.1	10
226	Unexpected mechanisms of action for a cytokine receptor-blocking antibody. <i>Molecular and Cellular Oncology</i> , 2014 , 1, e969129	1.2	1

225	Discovery of Phosphodiesterase-4 Inhibitors: Serendipity and Rational Drug Design. <i>Australian Journal of Chemistry</i> , 2014 , 67, 1780	1.2	2
224	Anti-Atantibody target engagement: a response to Siemers et al. <i>Acta Neuropathologica</i> , 2014 , 128, 611-4	14.3	4
223	Crystallization and preliminary X-ray diffraction analysis of the interleukin-3 alpha receptor bound to the Fab fragment of antibody CSL362. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 358-61	1.1	7
222	Lymphotoxin Induces apoptosis, necroptosis and inflammatory signals with the same potency as tumour necrosis factor. <i>FEBS Journal</i> , 2013 , 280, 5283-97	5.7	41
221	The impact of nitric oxide toxicity on the evolution of the glutathione transferase superfamily: a proposal for an evolutionary driving force. <i>Journal of Biological Chemistry</i> , 2013 , 288, 24936-47	5.4	23
220	Targeting acute myeloid leukemia by dual inhibition of PI3K signaling and Cdk9-mediated Mcl-1 transcription. <i>Blood</i> , 2013 , 122, 738-48	2.2	47
219	Synthetic dityrosine-linked 軸myloid dimers form stable, soluble, neurotoxic oligomers. <i>Chemical Science</i> , 2013 , 4, 4449	9.4	36
218	Molecular determinants of common gating of a ClC chloride channel. <i>Nature Communications</i> , 2013 , 4, 2507	17.4	31
217	Parallel screening of low molecular weight fragment libraries: do differences in methodology affect hit identification?. <i>Journal of Biomolecular Screening</i> , 2013 , 18, 147-59		57
216	Signalling by the # family of cytokines. <i>Cytokine and Growth Factor Reviews</i> , 2013 , 24, 189-201	17.9	62
215	Molecular and structural insight into lysine selection on substrate and ubiquitin lysine 48 by the ubiquitin-conjugating enzyme Cdc34. <i>Cell Cycle</i> , 2013 , 12, 1732-44	4.7	17
214	Bapineuzumab captures the N-terminus of the Alzheimer@disease amyloid-beta peptide in a helical conformation. <i>Scientific Reports</i> , 2013 , 3, 1302	4.9	78
213	Disarming bacterial virulence through chemical inhibition of the DNA binding domain of an AraC-like transcriptional activator protein. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31115-26	5.4	20
212	Phosphorylation of serine 779 in fibroblast growth factor receptor 1 and 2 by protein kinase C(epsilon) regulates Ras/mitogen-activated protein kinase signaling and neuronal differentiation. <i>Journal of Biological Chemistry</i> , 2013 , 288, 14874-85	5.4	12
211	Characterization of pathogenic human monoclonal autoantibodies against GM-CSF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 7832-7	11.5	36
210	Small molecule proprotein convertase inhibitors for inhibition of embryo implantation. <i>PLoS ONE</i> , 2013 , 8, e81380	3.7	2
209	From knock-out phenotype to three-dimensional structure of a promising antibiotic target from Streptococcus pneumoniae. <i>PLoS ONE</i> , 2013 , 8, e83419	3.7	21
208	Cytokine receptor activation at the cell surface. Current Opinion in Structural Biology, 2012, 22, 350-9	8.1	25

207	Structure of the lectin regulatory domain of the cholesterol-dependent cytolysin lectinolysin reveals the basis for its lewis antigen specificity. <i>Structure</i> , 2012 , 20, 248-58	5.2	43
206	Crystallization and preliminary X-ray diffraction analysis of human endoplasmic reticulum aminopeptidase 2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 468-71		6
205	The GM-CSF receptor family: mechanism of activation and implications for disease. <i>Growth Factors</i> , 2012 , 30, 63-75	1.6	50
204	Monomer-monomer interactions propagate structural transitions necessary for pore formation by the cholesterol-dependent cytolysins. <i>Journal of Biological Chemistry</i> , 2012 , 287, 24534-43	5.4	42
203	An Orally Available 3-Ethoxybenzisoxazole Capsid Binder with Clinical Activity against Human Rhinovirus. <i>ACS Medicinal Chemistry Letters</i> , 2012 , 3, 303-7	4.3	33
202	The GM-CSF/IL-3/IL-5 cytokine receptor family: from ligand recognition to initiation of signaling. <i>Immunological Reviews</i> , 2012 , 250, 277-302	11.3	157
201	PEGylation of a proprotein convertase peptide inhibitor for vaginal route of drug delivery: in vitro bioactivity, stability and in vivo pharmacokinetics. <i>Peptides</i> , 2012 , 38, 266-74	3.8	5
200	Structural approaches to probing metal interaction with proteins. <i>Journal of Inorganic Biochemistry</i> , 2012 , 115, 138-47	4.2	14
199	Phosphorylation of syndapin I F-BAR domain at two helix-capping motifs regulates membrane tubulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 3760-5	11.5	25
198	Manipulating the Lewis antigen specificity of the cholesterol-dependent cytolysin lectinolysin. <i>Frontiers in Immunology</i> , 2012 , 3, 330	8.4	7
197	Intracellular thicotinamide adenine dinucleotide inhibits the skeletal muscle ClC-1 chloride channel. <i>Journal of Biological Chemistry</i> , 2012 , 287, 25808-20	5.4	20
196	Selective Inhibitors of Arginine Methyl Transferase 5 (PRMT5) As a Novel Treatment for 町halassemia and Sickle Cell Disease <i>Blood</i> , 2012 , 120, 2129-2129	2.2	1
195	TRIM16 acts as an E3 ubiquitin ligase and can heterodimerize with other TRIM family members. <i>PLoS ONE</i> , 2012 , 7, e37470	3.7	71
194	Identification and development of specific inhibitors for insulin-regulated aminopeptidase as a new class of cognitive enhancers. <i>British Journal of Pharmacology</i> , 2011 , 164, 37-47	8.6	59
193	The extended catalysis of glutathione transferase. FEBS Letters, 2011, 585, 341-5	3.8	9
192	Thiophene inhibitors of PDE4: crystal structures show a second binding mode at the catalytic domain of PDE4D2. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011 , 21, 7089-93	2.9	17
191	Preparation, crystallization and preliminary X-ray diffraction analysis of two intestinal fatty-acid binding proteins in the presence of 11-(dansylamino)undecanoic acid. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 291-5		3
190	Purification, crystallization, small-angle X-ray scattering and preliminary X-ray diffraction analysis of the SH2 domain of the Csk-homologous kinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 336-9		15

189	Crystal structure of the Leishmania major MIX protein: a scaffold protein that mediates protein-protein interactions. <i>Protein Science</i> , 2011 , 20, 1060-8	6.3	2
188	Diuretic drug binding to human glutathione transferase P1-1: potential role of Cys-101 revealed in the double mutant C47S/Y108V. <i>Journal of Molecular Recognition</i> , 2011 , 24, 220-34	2.6	12
187	Fragment-based design of ligands targeting a novel site on the integrase enzyme of human immunodeficiency virus 1. <i>ChemMedChem</i> , 2011 , 6, 258-61	3.7	22
186	Studies of glutathione transferase P1-1 bound to a platinum(IV)-based anticancer compound reveal the molecular basis of its activation. <i>Chemistry - A European Journal</i> , 2011 , 17, 7806-16	4.8	66
185	Regulation of insulin-regulated membrane aminopeptidase activity by its C-terminal domain. <i>Biochemistry</i> , 2011 , 50, 2611-22	3.2	24
184	Amiloride is a competitive inhibitor of coxsackievirus B3 RNA polymerase. <i>Journal of Virology</i> , 2011 , 85, 10364-74	6.6	16
183	Mapping the intermedilysin-human CD59 receptor interface reveals a deep correspondence with the binding site on CD59 for complement binding proteins C8alpha and C9. <i>Journal of Biological Chemistry</i> , 2011 , 286, 20952-62	5.4	44
182	Direct involvement of the TEN domain at the active site of human telomerase. <i>Nucleic Acids Research</i> , 2011 , 39, 1774-88	20.1	41
181	An activation-specific platelet inhibitor that can be turned on/off by medically used hypothermia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology,</i> 2011 , 31, 2015-23	9.4	11
180	An Escherichia coli cell-free system for recombinant protein synthesis on a milligram scale. <i>Methods in Molecular Biology</i> , 2011 , 752, 17-28	1.4	1
179	Substrate-mediated stabilization of a tetrameric drug target reveals Achilles heel in anthrax. Journal of Biological Chemistry, 2010 , 285, 5188-95	5.4	41
178	Recognition and detoxification of the insecticide DDT by Drosophila melanogaster glutathione S-transferase D1. <i>Journal of Molecular Biology</i> , 2010 , 399, 358-66	6.5	48
177	Phenylalanine-544 plays a key role in substrate and inhibitor binding by providing a hydrophobic packing point at the active site of insulin-regulated aminopeptidase. <i>Molecular Pharmacology</i> , 2010 , 78, 600-7	4.3	20
176	Crystal structure of the HIV-1 integrase core domain in complex with sucrose reveals details of an allosteric inhibitory binding site. <i>FEBS Letters</i> , 2010 , 584, 1455-62	3.8	34
175	Molecular basis of cytokine receptor activation. <i>IUBMB Life</i> , 2010 , 62, 509-18	4.7	54
174	Crystallization of dihydrodipicolinate synthase from a clinical isolate of Streptococcus pneumoniae. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 32-6		11
173	Cloning, expression and crystallization of dihydrodipicolinate reductase from methicillin-resistant Staphylococcus aureus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 57-60		10
172	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the psychrophile Shewanella benthica. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1511-6		9

(2008-2009)

171	Structural basis for antibody discrimination between two hormones that recognize the parathyroid hormone receptor. <i>Journal of Biological Chemistry</i> , 2009 , 284, 15557-63	5.4	10
170	Zanamivir-resistant influenza viruses with a novel neuraminidase mutation. <i>Journal of Virology</i> , 2009 , 83, 10366-73	6.6	196
169	Rational design of an organometallic glutathione transferase inhibitor. <i>Angewandte Chemie - International Edition</i> , 2009 , 48, 3854-7	16.4	159
168	Influence of the H-site residue 108 on human glutathione transferase P1-1 ligand binding: structure-thermodynamic relationships and thermal stability. <i>Protein Science</i> , 2009 , 18, 2454-70	6.3	14
167	Crystallization and preliminary X-ray analysis of dihydrodipicolinate synthase from Clostridium botulinum in the presence of its substrate pyruvate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 253-5		14
166	Expression, purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase from Bacillus anthracis in the presence of pyruvate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 188-91		15
165	Crystallization of the receptor-binding domain of parathyroid hormone-related protein in complex with a neutralizing monoclonal antibody Fab fragment. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 336-8		4
164	Crystallization and preliminary X-ray analysis of glutathione transferases from cyanobacteria. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 475-7		1
163	Dihydropyridine inhibition of the glycine receptor: subunit selectivity and a molecular determinant of inhibition. <i>Neuropharmacology</i> , 2009 , 56, 318-27	5.5	12
162	Oseltamivir resistance and the H274Y neuraminidase mutation in seasonal, pandemic and highly pathogenic influenza viruses. <i>Drugs</i> , 2009 , 69, 2523-31	12.1	88
161	Solid-phase synthesis of homodimeric peptides: preparation of covalently-linked dimers of amyloid beta peptide. <i>Chemical Communications</i> , 2009 , 6228-30	5.8	36
160	The granulocyte-macrophage colony-stimulating factor receptor: linking its structure to cell signaling and its role in disease. <i>Blood</i> , 2009 , 114, 1289-98	2.2	229
159	Development of cognitive enhancers based on inhibition of insulin-regulated aminopeptidase. <i>BMC Neuroscience</i> , 2008 , 9 Suppl 2, S14	3.2	46
158	Amyloid-beta-anti-amyloid-beta complex structure reveals an extended conformation in the immunodominant B-cell epitope. <i>Journal of Molecular Biology</i> , 2008 , 377, 181-92	6.5	45
157	The anti-cancer drug chlorambucil as a substrate for the human polymorphic enzyme glutathione transferase P1-1: kinetic properties and crystallographic characterisation of allelic variants. <i>Journal of Molecular Biology</i> , 2008 , 380, 131-44	6.5	43
156	The structure of the GM-CSF receptor complex reveals a distinct mode of cytokine receptor activation. <i>Cell</i> , 2008 , 134, 496-507	56.2	225
155	Preventing serpin aggregation: the molecular mechanism of citrate action upon antitrypsin unfolding. <i>Protein Science</i> , 2008 , 17, 2127-33	6.3	21
154	Identification and characterization of a new cognitive enhancer based on inhibition of insulin-regulated aminopeptidase. <i>FASEB Journal</i> , 2008 , 22, 4209-17	0.9	80

153	Structure and evolution of a novel dimeric enzyme from a clinically important bacterial pathogen. <i>Journal of Biological Chemistry</i> , 2008 , 283, 27598-27603	5.4	78
152	Identification of modulating residues defining the catalytic cleft of insulin-regulated aminopeptidase. <i>Biochemistry and Cell Biology</i> , 2008 , 86, 251-61	3.6	20
151	Copper binding to the Alzheimer@ disease amyloid precursor protein. <i>European Biophysics Journal</i> , 2008 , 37, 269-79	1.9	51
150	Federated repositories of X-ray diffraction images. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , D64, 810-4		35
149	The purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase from Clostridium botulinum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 206-8		13
148	Crystallization and preliminary X-ray diffraction analysis of the Fab fragment of WO2, an antibody specific for the Abeta peptides associated with Alzheimer@ disease. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 438-41		9
147	Purification, crystallization and preliminary X-ray diffraction studies to near-atomic resolution of dihydrodipicolinate synthase from methicillin-resistant Staphylococcus aureus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 659-61		19
146	Crystallization and preliminary X-ray diffraction analysis of the ternary human GM-CSF receptor complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 711-4		9
145	Structure of Alzheimer@ disease amyloid precursor protein copper-binding domain at atomic resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 819-24		24
144	Expression, purification, crystallization and preliminary X-ray diffraction analysis of chloride intracellular channel 2 (CLIC2). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 961-3		6
143	Tropisetron modulation of the glycine receptor: femtomolar potentiation and a molecular determinant of inhibition. <i>Journal of Neurochemistry</i> , 2007 , 100, 758-69	6	30
142	A proposed structural basis for picrotoxinin and picrotin binding in the glycine receptor pore. <i>Journal of Neurochemistry</i> , 2007 , 103, 580-9	6	51
141	Critical role for the second extracellular loop in the binding of both orthosteric and allosteric G protein-coupled receptor ligands. <i>Journal of Biological Chemistry</i> , 2007 , 282, 25677-86	5.4	122
140	Molecular evolution of glutathione S-transferases in the genus Drosophila. <i>Genetics</i> , 2007 , 177, 1363-7.	54	77
139	Inhibition of skeletal muscle ClC-1 chloride channels by low intracellular pH and ATP. <i>Journal of Biological Chemistry</i> , 2007 , 282, 32780-91	5.4	57
138	Real Value Solvent Accessibility Prediction using Adaptive Support Vector Regression 2007,		1
137	Structural studies of the Alzheimer@amyloid precursor protein copper-binding domain reveal how it binds copper ions. <i>Journal of Molecular Biology</i> , 2007 , 367, 148-61	6.5	85
136	Structures of perfringolysin O suggest a pathway for activation of cholesterol-dependent cytolysins. <i>Journal of Molecular Biology</i> , 2007 , 367, 1227-36	6.5	72

135	Structure of the Janus protein human CLIC2. Journal of Molecular Biology, 2007, 374, 719-31	6.5	56
134	Solving Protein Structures Using Molecular Replacement Via Protein Fragments. <i>Lecture Notes in Computer Science</i> , 2007 , 627-634	0.9	
133	Elucidation of the substrate binding site of Siah ubiquitin ligase. Structure, 2006, 14, 695-701	5.2	59
132	Hsp90 increases LIM kinase activity by promoting its homo-dimerization. FASEB Journal, 2006, 20, 1218-	-20 9	38
131	PROTEIN SECONDARY STRUCTURE PREDICTION USING SUPPORT VECTOR MACHINES AND A NEW FEATURE REPRESENTATION. <i>International Journal of Computational Intelligence and Applications</i> , 2006 , 06, 551-567	1.2	9
130	Molecular dissection of the interaction between amyloid precursor protein and its neuronal trafficking receptor SorLA/LR11. <i>Biochemistry</i> , 2006 , 45, 2618-28	3.2	144
129	Solution conformation and heparin-induced dimerization of the full-length extracellular domain of the human amyloid precursor protein. <i>Journal of Molecular Biology</i> , 2006 , 357, 493-508	6.5	56
128	Molecular determinants of ginkgolide binding in the glycine receptor pore. <i>Journal of Neurochemistry</i> , 2006 , 98, 395-407	6	36
127	A rivet model for channel formation by aerolysin-like pore-forming toxins. <i>EMBO Journal</i> , 2006 , 25, 457	-66	78
126	Calorimetric and structural studies of the nitric oxide carrier S-nitrosoglutathione bound to human glutathione transferase P1-1. <i>Protein Science</i> , 2006 , 15, 1093-105	6.3	21
125	Comparative three-dimensional structure of cholesterol-dependent cytolysins 2006, 659-670		3
124	Protein topology classification using two-stage support vector machines. <i>Genome Informatics</i> , 2006 , 17, 259-69		5
123	Human factor H-related protein 5 has cofactor activity, inhibits C3 convertase activity, binds heparin and C-reactive protein, and associates with lipoprotein. <i>Journal of Immunology</i> , 2005 , 174, 6250)- § ·3	115
122	Homology model of the GABAA receptor examined using Brownian dynamics. <i>Biophysical Journal</i> , 2005 , 88, 3286-99	2.9	57
121	Model for growth hormone receptor activation based on subunit rotation within a receptor dimer. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 814-21	17.6	313
120	Structural basis for glycogen recognition by AMP-activated protein kinase. <i>Structure</i> , 2005 , 13, 1453-62	5.2	163
119	Pore-forming protein toxins: from structure to function. <i>Progress in Biophysics and Molecular Biology</i> , 2005 , 88, 91-142	4.7	348
118	Crystallization of the glycogen-binding domain of the AMP-activated protein kinase beta subunit and preliminary X-ray analysis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 39-42		11

117	Crystallization and preliminary crystallographic studies of the copper-binding domain of the amyloid precursor protein of Alzheimer@disease. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 93-5		7
116	Nitrosylation of human glutathione transferase P1-1 with dinitrosyl diglutathionyl iron complex in vitro and in vivo. <i>Journal of Biological Chemistry</i> , 2005 , 280, 42172-80	5.4	102
115	Insights into the action of the superfamily of cholesterol-dependent cytolysins from studies of intermedilysin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 600-5	11.5	118
114	Cytoplasmic ATP-sensing domains regulate gating of skeletal muscle ClC-1 chloride channels. Journal of Biological Chemistry, 2005 , 280, 32452-8	5.4	99
113	Insights into interactions between the alpha-helical region of the salmon calcitonin antagonists and the human calcitonin receptor using photoaffinity labeling. <i>Journal of Biological Chemistry</i> , 2005 , 280, 28610-22	5.4	27
112	The identification and structure of the membrane-spanning domain of the Clostridium septicum alpha toxin. <i>Journal of Biological Chemistry</i> , 2004 , 279, 14315-22	5.4	77
111	Binding and kinetic mechanisms of the Zeta class glutathione transferase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 33336-42	5.4	15
110	Crystallization and preliminary X-ray analysis of the human-specific toxin intermedilysin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 347-9		11
109	Crystallization and preliminary X-ray diffraction analysis of the unliganded human growth hormone receptor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 2380-2		1
108	Intrasteric control of AMPK via the gamma1 subunit AMP allosteric regulatory site. <i>Protein Science</i> , 2004 , 13, 155-65	6.3	130
107	Optimised expression and purification of recombinant human indoleamine 2,3-dioxygenase. <i>Protein Expression and Purification</i> , 2004 , 37, 392-8	2	36
106	Crystal structure of a putative methyltransferase from Mycobacterium tuberculosis: misannotation of a genome clarified by protein structural analysis. <i>Journal of Bacteriology</i> , 2003 , 185, 4057-65	3.5	26
105	Clarification of the role of key active site residues of glutathione transferase zeta/maleylacetoacetate isomerase by a new spectrophotometric technique. <i>Biochemical Journal</i> , 2003 , 374, 731-7	3.8	39
104	Glutathione transferase P1-1: self-preservation of an anti-cancer enzyme. <i>Biochemical Journal</i> , 2003 , 376, 71-6	3.8	32
103	AMPK beta subunit targets metabolic stress sensing to glycogen. Current Biology, 2003, 13, 867-71	6.3	355
102	Structural characterization of respiratory syncytial virus fusion inhibitor escape mutants: homology model of the F protein and a syncytium formation assay. <i>Virology</i> , 2003 , 311, 275-88	3.6	57
101	Naturally occurring Phe151Leu substitution near a conserved folding module lowers stability of glutathione transferase P1-1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003 , 1649, 16-23	4	10
100	Structure of the Alzheimer@ disease amyloid precursor protein copper binding domain. A regulator of neuronal copper homeostasis. <i>Journal of Biological Chemistry</i> , 2003 , 278, 17401-7	5.4	208

(2001-2003)

99	Insights into the structural basis for zinc inhibition of the glycine receptor. <i>Journal of Biological Chemistry</i> , 2003 , 278, 28985-92	5.4	46
98	Engineering a new C-terminal tail in the H-site of human glutathione transferase P1-1: structural and functional consequences. <i>Journal of Molecular Biology</i> , 2003 , 325, 111-22	6.5	17
97	Cryptic clues as to how water-soluble protein toxins form pores in membranes. <i>Toxicon</i> , 2003 , 42, 1-6	2.8	22
96	Contribution of glycine 146 to a conserved folding module affecting stability and refolding of human glutathione transferase p1-1. <i>Journal of Biological Chemistry</i> , 2003 , 278, 1291-302	5.4	20
95	Thermodynamic description of the effect of the mutation Y49F on human glutathione transferase P1-1 in binding with glutathione and the inhibitor S-hexylglutathione. <i>Journal of Biological Chemistry</i> , 2003 , 278, 46938-48	5.4	18
94	Contrasting, species-dependent modulation of copper-mediated neurotoxicity by the Alzheimer@ disease amyloid precursor protein. <i>Journal of Neuroscience</i> , 2002 , 22, 365-76	6.6	72
93	Anxiety over GABA(A) receptor structure relieved by AChBP. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 280-7	10.3	161
92	From glutathione transferase to pore in a CLIC. European Biophysics Journal, 2002, 31, 356-64	1.9	81
91	Siah ubiquitin ligase is structurally related to TRAF and modulates TNF-alpha signaling. <i>Nature Structural Biology</i> , 2002 , 9, 68-75		113
90	Conversion of a transmembrane to a water-soluble protein complex by a single point mutation. <i>Nature Structural Biology</i> , 2002 , 9, 729-33		51
89	Altered kinetics and benzodiazepine sensitivity of a GABAA receptor subunit mutation [gamma 2(R43Q)] found in human epilepsy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 15170-5	11.5	90
88	GSTB1-1 from Proteus mirabilis: a snapshot of an enzyme in the evolutionary pathway from a redox enzyme to a conjugating enzyme. <i>Journal of Biological Chemistry</i> , 2002 , 277, 18777-84	5.4	40
87	Identification of essential residues in the Erm(B) rRNA methyltransferase of Clostridium perfringens. <i>Antimicrobial Agents and Chemotherapy</i> , 2002 , 46, 1253-61	5.9	20
86	Glutamic acid-65 is an essential residue for catalysis in Proteus mirabilis glutathione S-transferase B1-1. <i>Biochemical Journal</i> , 2002 , 363, 189-93	3.8	6
85	Identification and characterization of GSTT3, a third murine Theta class glutathione transferase. <i>Biochemical Journal</i> , 2002 , 366, 323-32	3.8	22
84	Properties and utility of the peculiar mixed disulfide in the bacterial glutathione transferase B1-1. <i>Biochemistry</i> , 2002 , 41, 4686-93	3.2	12
83	GSTZ1d: a new allele of glutathione transferase zeta and maleylacetoacetate isomerase. <i>Pharmacogenetics and Genomics</i> , 2001 , 11, 671-8		43
82	Dichloromethane mediated in vivo selection and functional characterization of rat glutathione S-transferase theta 1-1 variants. <i>FEBS Journal</i> , 2001 , 268, 4001-10		4

81	Human glutathione transferase T2-2 discloses some evolutionary strategies for optimization of substrate binding to the active site of glutathione transferases. <i>Journal of Biological Chemistry</i> , 2001 , 276, 5427-31	5.4	22
80	Human glutathione transferase T2-2 discloses some evolutionary strategies for optimization of the catalytic activity of glutathione transferases. <i>Journal of Biological Chemistry</i> , 2001 , 276, 5432-7	5.4	11
79	Human glutathione transferase P1-1 and nitric oxide carriers; a new role for an old enzyme. <i>Journal of Biological Chemistry</i> , 2001 , 276, 42138-45	5.4	79
78	Arresting pore formation of a cholesterol-dependent cytolysin by disulfide trapping synchronizes the insertion of the transmembrane beta-sheet from a prepore intermediate. <i>Journal of Biological Chemistry</i> , 2001 , 276, 8261-8	5.4	105
77	Crystal structure of maleylacetoacetate isomerase/glutathione transferase zeta reveals the molecular basis for its remarkable catalytic promiscuity. <i>Biochemistry</i> , 2001 , 40, 1567-76	3.2	108
76	Cleaved antitrypsin polymers at atomic resolution. <i>Protein Science</i> , 2000 , 9, 417-20	6.3	67
75	Kinetic properties of missense mutations in patients with glutathione synthetase deficiency. <i>Biochemical Journal</i> , 2000 , 349, 275-9	3.8	16
74	Evaluation of the role of two conserved active-site residues in Beta class glutathione S-transferases. <i>Biochemical Journal</i> , 2000 , 351, 341	3.8	8
73	Evaluation of the role of two conserved active-site residues in Beta class glutathione S-transferases. <i>Biochemical Journal</i> , 2000 , 351, 341-346	3.8	20
72	Structure of the activation domain of the GM-CSF/IL-3/IL-5 receptor common	2.2	47
71	Structures of thermolabile mutants of human glutathione transferase P1-1. <i>Journal of Molecular Biology</i> , 2000 , 302, 295-302	6.5	15
70	Valine 10 may act as a driver for product release from the active site of human glutathione transferase P1-1. <i>Biochemistry</i> , 2000 , 39, 15961-70	3.2	3
69	Crystal structure of the N-terminal, growth factor-like domain of Alzheimer amyloid precursor protein. <i>Nature Structural Biology</i> , 1999 , 6, 327-31		199
68	Functional analysis of the evolutionarily conserved proline 53 residue in Proteus mirabilis glutathione transferase B1-1. <i>FEBS Letters</i> , 1999 , 445, 347-50	3.8	30
67	Two structural transitions in membrane pore formation by pneumolysin, the pore-forming toxin of Streptococcus pneumoniae. <i>Cell</i> , 1999 , 97, 647-55	56.2	163
66	The mechanism of membrane insertion for a cholesterol-dependent cytolysin: a novel paradigm for pore-forming toxins. <i>Cell</i> , 1999 , 99, 293-9	56.2	320
65	The ligandin (non-substrate) binding site of human Pi class glutathione transferase is located in the electrophile binding site (H-site). <i>Journal of Molecular Biology</i> , 1999 , 291, 913-26	6.5	101
64	Studies on the structure and mechanism of a bacterial protein toxin by analytical ultracentrifugation and small-angle neutron scattering. <i>Journal of Molecular Biology</i> , 1999 , 293, 1145-6	50 ^{6.5}	39

63	Proton release on binding of glutathione to Alpha, Mu and Delta class glutathione transferases. <i>Biochemical Journal</i> , 1999 , 344, 419-425	3.8	49
62	Proton release on binding of glutathione to Alpha, Mu and Delta class glutathione transferases. <i>Biochemical Journal</i> , 1999 , 344, 419	3.8	19
61	Human theta class glutathione transferase: the crystal structure reveals a sulfate-binding pocket within a buried active site. <i>Structure</i> , 1998 , 6, 309-22	5.2	139
60	A mixed disulfide bond in bacterial glutathione transferase: functional and evolutionary implications. <i>Structure</i> , 1998 , 6, 721-34	5.2	134
59	Crystal structure of a colicin N fragment suggests a model for toxicity. <i>Structure</i> , 1998 , 6, 863-74	5.2	120
58	Preliminary X-ray crystallographic studies of a newly defined human theta-class glutathione transferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 148-50		4
57	Site-directed mutagenesis of the Proteus mirabilis glutathione transferase B1-1 G-site. <i>FEBS Letters</i> , 1998 , 423, 122-4	3.8	35
56	Evidence for an induced-fit mechanism operating in pi class glutathione transferases. <i>Biochemistry</i> , 1998 , 37, 9912-7	3.2	53
55	Solution structure of glutathione bound to human glutathione transferase P1-1: comparison of NMR measurements with the crystal structure. <i>Biochemistry</i> , 1998 , 37, 3020-7	3.2	27
54	Movement of a loop in domain 3 of aerolysin is required for channel formation. <i>Biochemistry</i> , 1998 , 37, 741-6	3.2	34
53	Shifting substrate specificity of human glutathione transferase (from class Pi to class alpha) by a single point mutation. <i>Biochemical and Biophysical Research Communications</i> , 1998 , 252, 184-9	3.4	19
52	The molecular mechanism of pneumolysin, a virulence factor from Streptococcus pneumoniae. <i>Journal of Molecular Biology</i> , 1998 , 284, 449-61	6.5	94
51	Self-interaction of pneumolysin, the pore-forming protein toxin of Streptococcus pneumoniae. <i>Journal of Molecular Biology</i> , 1998 , 284, 1223-37	6.5	67
50	Mutations of Gly to Ala in human glutathione transferase P1-1 affect helix 2 (G-site) and induce positive cooperativity in the binding of glutathione. <i>Journal of Molecular Biology</i> , 1998 , 284, 1717-25	6.5	26
49	Aerolysina paradigm for membrane insertion of beta-sheet protein toxins?. <i>Journal of Structural Biology</i> , 1998 , 121, 92-100	3.4	49
48	Identification of a membrane-spanning domain of the thiol-activated pore-forming toxin Clostridium perfringens perfringolysin O: an alpha-helical to beta-sheet transition identified by fluorescence spectroscopy. <i>Biochemistry</i> , 1998 , 37, 14563-74	3.2	285
47	Catalytic mechanism and role of hydroxyl residues in the active site of theta class glutathione S-transferases. Investigation of Ser-9 and Tyr-113 in a glutathione S-transferase from the Australian sheep blowfly, Lucilia cuprina. <i>Journal of Biological Chemistry</i> , 1997 , 272, 29681-6	5.4	64
46	The three-dimensional structure of the human Pi class glutathione transferase P1-1 in complex with the inhibitor ethacrynic acid and its glutathione conjugate. <i>Biochemistry</i> , 1997 , 36, 576-85	3.2	111

45	Multifunctional role of Tyr 108 in the catalytic mechanism of human glutathione transferase P1-1. Crystallographic and kinetic studies on the Y108F mutant enzyme. <i>Biochemistry</i> , 1997 , 36, 6207-17	3.2	58
44	Conformational changes in aerolysin during the transition from the water-soluble protoxin to the membrane channel. <i>Biochemistry</i> , 1997 , 36, 15224-32	3.2	42
43	Crystallization, structural determination and analysis of a novel parasite vaccine candidate: Fasciola hepatica glutathione S-transferase. <i>Journal of Molecular Biology</i> , 1997 , 273, 857-72	6.5	48
42	The structures of human glutathione transferase P1-1 in complex with glutathione and various inhibitors at high resolution. <i>Journal of Molecular Biology</i> , 1997 , 274, 84-100	6.5	158
41	Structure of a cholesterol-binding, thiol-activated cytolysin and a model of its membrane form. <i>Cell</i> , 1997 , 89, 685-92	56.2	412
40	The glutathione conjugate of ethacrynic acid can bind to human pi class glutathione transferase P1-1 in two different modes. <i>FEBS Letters</i> , 1997 , 419, 32-6	3.8	45
39	Regulation and crystallization of phosphorylated and dephosphorylated forms of truncated dimeric phenylalanine hydroxylase. <i>Protein Science</i> , 1997 , 6, 1352-7	6.3	17
38	Crystallization and preliminary X-ray analysis of a thiol-activated cytolysin. FEBS Letters, 1996, 397, 290-	- 2 3.8	12
37	Mutagenesis of the active site of the human Theta-class glutathione transferase GSTT2-2: catalysis with different substrates involves different residues. <i>Biochemical Journal</i> , 1996 , 319 (Pt 1), 315-21	3.8	67
36	Aerolysinthe ins and outs of a model channel-forming toxin. <i>Molecular Microbiology</i> , 1996 , 19, 205-12	4.1	95
35	Ca2+/S100 regulation of giant protein kinases. <i>Nature</i> , 1996 , 380, 636-9	50.4	127
34	A structurally derived consensus pattern for theta class glutathione transferases. <i>Protein Engineering, Design and Selection</i> , 1996 , 9, 327-32	1.9	31
33	Membrane topology of the colicin A pore-forming domain analyzed by disulfide bond engineering. Journal of Biological Chemistry, 1996 , 271, 15401-6	5.4	24
32	Structural flexibility modulates the activity of human glutathione transferase P1-1. Influence of a poor co-substrate on dynamics and kinetics of human glutathione transferase. <i>Journal of Biological Chemistry</i> , 1996 , 271, 16193-8	5.4	45
31	Protein Toxin Structure. Molecular Biology Intelligence Unit, 1996,		4
30	Insights into Membrane Insertion Based on Studies of Colicins. <i>Molecular Biology Intelligence Unit</i> , 1996 , 5-23		5
29	Structure and Assembly of the Channel-Forming Aeromonas Toxin Aerolysin. <i>Molecular Biology Intelligence Unit</i> , 1996 , 79-95		1
28	Vibrio spp. secrete proaerolysin as a folded dimer without the need for disulphide bond formation. Molecular Microbiology, 1995 , 17, 1035-44	4.1	72

(1990-1995)

27	Site-directed mutagenesis of human glutathione transferase P1-1. Mutation of Cys-47 induces a positive cooperativity in glutathione transferase P1-1. <i>Journal of Biological Chemistry</i> , 1995 , 270, 1243-8	8 ^{5.4}	81
26	Protonation of histidine-132 promotes oligomerization of the channel-forming toxin aerolysin. <i>Biochemistry</i> , 1995 , 34, 16450-5	3.2	45
25	Protein crystallography in Australia. Australian and New Zealand Journal of Medicine, 1995, 25, 876-82		1
24	A single amino acid substitution can restore the solubility of aggregated colicin A mutants in Escherichia coli. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 1495-500	1.9	18
23	Structure and function of glutathione S-transferases. BBA - Proteins and Proteomics, 1994, 1205, 1-18		455
22	Substrate and pseudosubstrate interactions with protein kinases: determinants of specificity. <i>Trends in Biochemical Sciences</i> , 1994 , 19, 440-4	10.3	120
21	Structure of the Aeromonas toxin proaerolysin in its water-soluble and membrane-channel states. <i>Nature</i> , 1994 , 367, 292-5	50.4	378
20	Insights into autoregulation from the crystal structure of twitchin kinase. <i>Nature</i> , 1994 , 369, 581-4	50.4	196
19	The role of electrostatic charge in the membrane insertion of colicin A. Calculation and mutation. <i>FEBS Journal</i> , 1994 , 220, 155-63		29
18	Crystallization and preliminary X-ray analysis of the auto-inhibited twitchin kinase. <i>Journal of Molecular Biology</i> , 1994 , 236, 1259-61	6.5	9
17	Crystallization and preliminary X-ray diffraction studies of a glutathione S-transferase from the Australian sheep blowfly, Lucilia cuprina. <i>Journal of Molecular Biology</i> , 1994 , 236, 1407-9	6.5	13
16	Rendering a membrane protein soluble in water: a common packing motif in bacterial protein toxins. <i>Trends in Biochemical Sciences</i> , 1993 , 18, 391-5	10.3	117
15	Refined structure of the pore-forming domain of colicin A at 2.4 A resolution. <i>Journal of Molecular Biology</i> , 1992 , 224, 639-57	6.5	211
14	Three-dimensional structure of class pi glutathione S-transferase from human placenta in complex with S-hexylglutathione at 2.8 A resolution. <i>Journal of Molecular Biology</i> , 1992 , 227, 214-26	6.5	261
13	Membrane insertion of the pore-forming domain of colicin A. A spectroscopic study. <i>FEBS Journal</i> , 1991 , 196, 599-607		79
12	Crystallization and preliminary X-ray analysis of phosphoporin from the outer membrane of Escherichia coli. <i>Journal of Molecular Biology</i> , 1991 , 222, 881-4	6.5	7
11	A common channel-forming motif in evolutionarily distant porins. <i>Journal of Structural Biology</i> , 1991 , 107, 136-45	3.4	54
10	Crystallization of glutathione S-transferase from human placenta. <i>Journal of Molecular Biology</i> , 1990 , 213, 221-2	6.5	7°

9	Crystallization of a proform of aerolysin, a hole-forming toxin from Aeromonas hydrophila. <i>Journal of Molecular Biology</i> , 1990 , 212, 561-2	6.5	30	
8	Insights into membrane insertion based on studies of colicins. <i>Trends in Biochemical Sciences</i> , 1990 , 15, 126-9	10.3	115	
7	Crystallographic phases through genetic engineering: experiences with colicin A. <i>Protein Engineering, Design and Selection</i> , 1989 , 2, 399-405	1.9	15	
6	Iron- and manganese-containing superoxide dismutases can be distinguished by analysis of their primary structures. <i>FEBS Letters</i> , 1988 , 229, 377-82	3.8	204	
5	Crystal structure of manganese superoxide dismutase from Bacillus stearothermophilus at 2.4 A resolution. <i>Journal of Molecular Biology</i> , 1988 , 199, 649-61	6.5	145	
4	Purification, crystallisation and preliminary X-ray diffraction characterisation of methanol dehydrogenase from Methylosinus trichosporium OB3b. <i>FEBS Journal</i> , 1987 , 164, 223-7		13	
3	Histidine H-2 n.m.r. resonances of sperm whale oxy-, carbonyl-, and met-myoglobin. <i>Journal of the Chemical Society Chemical Communications</i> , 1981 , 208		3	
2	Monoubiquitination by the Fanconi Anemia core complex locks FANCI:FANCD2 on DNA in filamentous arrays		2	
1	SARS-CoV-2 Spike receptor-binding domain with a G485R mutation in complex with human ACE2		2	