

Christophe Lmj Verlinde

List of Publications by Year in descending order

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46918

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times ranked

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#	ARTICLE	IF	CITATIONS
1	Leishmania donovani tyrosyl-tRNA synthetase structure in complex with a tyrosyl adenylate analog and comparisons with human and protozoan counterparts. <i>Biochimie</i> , 2017, 138, 124-136.	1.3	13
2	Optimization of a binding fragment targeting the "enlarged methionine pocket" leads to potent <i>Trypanosoma brucei</i> methionyl-tRNA synthetase inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 2702-2707.	1.0	14
3	Structure-guided design of novel <i>Trypanosoma brucei</i> Methionyl-tRNA synthetase inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2016, 124, 1081-1092.	2.6	25
4	5-Fluoroimidazo[4,5- <i>b</i>]pyridine Is a Privileged Fragment That Conveys Bioavailability to Potent Trypanosomal Methionyl-tRNA Synthetase Inhibitors. <i>ACS Infectious Diseases</i> , 2016, 2, 399-404.	1.8	28
5	A binding hotspot in <i>Trypanosoma cruzi</i> histidyl-tRNA synthetase revealed by fragment-based crystallographic cocktail screens. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1684-1698.	2.5	19
6	Inhibitors of Methionyl-tRNA Synthetase Have Potent Activity against <i>Giardia intestinalis</i> Trophozoites. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7128-7131.	1.4	21
7	Identification of Potent Inhibitors of the <i>Trypanosoma brucei</i> Methionyl-tRNA Synthetase via High-Throughput Orthogonal Screening. <i>Journal of Biomolecular Screening</i> , 2015, 20, 122-130.	2.6	35
8	Structures of <i>Trypanosoma brucei</i> Methionyl-tRNA Synthetase with Urea-Based Inhibitors Provide Guidance for Drug Design against Sleeping Sickness. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2775.	1.3	37
9	Potent and Selective Inhibitors of CDPK1 from <i>T. gondii</i> and <i>C. parvum</i> Based on a 5-Aminopyrazole-4-carboxamide Scaffold. <i>ACS Medicinal Chemistry Letters</i> , 2014, 5, 40-44.	1.3	49
10	A Specific Inhibitor of PfCDPK4 Blocks Malaria Transmission: Chemical-genetic Validation. <i>Journal of Infectious Diseases</i> , 2014, 209, 275-284.	1.9	83
11	Development of potent and selective <i>Plasmodium falciparum</i> calcium-dependent protein kinase 4 (PfCDPK4) inhibitors that block the transmission of malaria to mosquitoes. <i>European Journal of Medicinal Chemistry</i> , 2014, 74, 562-573.	2.6	54
12	The structure of the D3 domain of <i>Plasmodium falciparum</i> myosin tail interacting protein MTIP in complex with a nanobody. <i>Molecular and Biochemical Parasitology</i> , 2013, 190, 87-91.	0.5	13
13	Dialkylimidazole inhibitors of <i>Trypanosoma cruzi</i> sterol 14 α -demethylase as anti-Chagas disease agents. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 6492-6499.	1.0	11
14	Crystal structures of <i>Plasmodium falciparum</i> cytosolic tryptophanyl-tRNA synthetase and its potential as a target for structure-guided drug design. <i>Molecular and Biochemical Parasitology</i> , 2013, 189, 26-32.	0.5	27
15	Induced Resistance to Methionyl-tRNA Synthetase Inhibitors in <i>Trypanosoma brucei</i> Is Due to Overexpression of the Target. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3021-3028.	1.4	19
16	Pharmacological Characterization, Structural Studies, and In Vivo Activities of Anti-Chagas Disease Lead Compounds Derived from Tipifarnib. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4914-4921.	1.4	50
17	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogen <i>Giardia lamblia</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1194-1200.	2.5	9
18	Urea-Based Inhibitors of <i>Trypanosoma brucei</i> Methionyl-tRNA Synthetase: Selectivity and in Vivo Characterization. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 6342-6351.	2.9	60

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19	Multiple Determinants for Selective Inhibition of Apicomplexan Calcium-Dependent Protein Kinase CDPK1. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 2803-2810.	2.9	60
20	Benzoylbenzimidazole-based selective inhibitors targeting <i>Cryptosporidium parvum</i> and <i>Toxoplasma gondii</i> calcium-dependent protein kinase-1. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 5264-5267.	1.0	43
21	Distinct States of Methionyl-tRNA Synthetase Indicate Inhibitor Binding by Conformational Selection. <i>Structure</i> , 2012, 20, 1681-1691.	1.6	69
22	Transmission of malaria to mosquitoes blocked by bumped kinase inhibitors. <i>Journal of Clinical Investigation</i> , 2012, 122, 2301-2305.	3.9	90
23	Structure of <i>Leishmania major</i> methionyl-tRNA synthetase in complex with intermediate products methionyladenylate and pyrophosphate. <i>Biochimie</i> , 2011, 93, 570-582.	1.3	50
24	The Double-Length Tyrosyl-tRNA Synthetase from the Eukaryote <i>Leishmania major</i> Forms an Intrinsically Asymmetric Pseudo-Dimer. <i>Journal of Molecular Biology</i> , 2011, 409, 159-176.	2.0	40
25	Structure determination of glycogen synthase kinase-3 from <i>Leishmania major</i> and comparative inhibitor structure-activity relationships with <i>Trypanosoma brucei</i> GSK-3. <i>Molecular and Biochemical Parasitology</i> , 2011, 176, 98-108.	0.5	35
26	Crystal structures of three protozoan homologs of tryptophanyl-tRNA synthetase. <i>Molecular and Biochemical Parasitology</i> , 2011, 177, 20-28.	0.5	16
27	Screening a fragment cocktail library using ultrafiltration. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 401, 1585-1591.	1.9	9
28	Selective Inhibitors of Methionyl-tRNA Synthetase Have Potent Activity against <i>Trypanosoma brucei</i> Infection in Mice. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 1982-1989.	1.4	75
29	An internal sequence targets <i>Trypanosoma brucei</i> triosephosphate isomerase to glycosomes. <i>Molecular and Biochemical Parasitology</i> , 2010, 171, 45-49.	0.5	25
30	Discovery of Potent and Selective Inhibitors of CDPK1 from <i>C. parvum</i> and <i>T. gondii</i> . <i>ACS Medicinal Chemistry Letters</i> , 2010, 1, 331-335.	1.3	126
31	Prediction of protein crystallization outcome using a hybrid method. <i>Journal of Structural Biology</i> , 2010, 171, 64-73.	1.3	17
32	The structure of tryptophanyl-tRNA synthetase from <i>Giardia lamblia</i> reveals divergence from eukaryotic homologs. <i>Journal of Structural Biology</i> , 2010, 171, 238-243.	1.3	12
33	The Crystal Structure and Activity of a Putative Trypanosomal Nucleoside Phosphorylase Reveal It to be a Homodimeric Uridine Phosphorylase. <i>Journal of Molecular Biology</i> , 2010, 396, 1244-1259.	2.0	16
34	Crystal Structures of Trypanosomal Histidyl-tRNA Synthetase Illuminate Differences between Eukaryotic and Prokaryotic Homologs. <i>Journal of Molecular Biology</i> , 2010, 397, 481-494.	2.0	37
35	<i>Toxoplasma gondii</i> calcium-dependent protein kinase 1 is a target for selective kinase inhibitors. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 602-607.	3.6	172
36	Crystal structure of the aspartyl-tRNA synthetase from <i>Entamoeba histolytica</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 169, 95-100.	0.5	14

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37	Second Generation Analogues of the Cancer Drug Clinical Candidate Tipifarnib for Anti-Chagas Disease Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 3887-3898.	2.9	107
38	Buffer Optimization of Thermal Melt Assays of Plasmodium Proteins for Detection of Small-Molecule Ligands. <i>Journal of Biomolecular Screening</i> , 2009, 14, 700-707.	2.6	42
39	Fragment-Based Cocktail Crystallography by the Medical Structural Genomics of Pathogenic Protozoa Consortium. <i>Current Topics in Medicinal Chemistry</i> , 2009, 9, 1678-1687.	1.0	36
40	Rational Modification of a Candidate Cancer Drug for Use Against Chagas Disease. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 1639-1647.	2.9	150
41	Structurally Simple Inhibitors of Lanosterol 14 α -Demethylase Are Efficacious In a Rodent Model of Acute Chagas Disease. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 3703-3715.	2.9	38
42	2-Oxo-tetrahydro-1,8-naphthyridines as selective inhibitors of malarial protein farnesyltransferase and as anti-malarials. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 494-497.	1.0	52
43	Simplified YM-26734 inhibitors of secreted phospholipase A2 group IIA. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 5415-5419.	1.0	19
44	Multivalent Drug Design and Inhibition of Cholera Toxin by Specific and Transient Protein-Ligand Interactions. <i>Chemical Biology and Drug Design</i> , 2008, 71, 408-419.	1.5	25
45	Genomic-scale prioritization of drug targets: the TDR Targets database. <i>Nature Reviews Drug Discovery</i> , 2008, 7, 900-907.	21.5	282
46	Characterization of <i>Trypanosoma brucei</i> dihydroorotate dehydrogenase as a possible drug target; structural, kinetic and RNAi studies. <i>Molecular Microbiology</i> , 2008, 68, 37-50.	1.2	73
47	Design and Synthesis of bis-carbamate Analogs of Cyclic bis-(3 β -5 β -Diguanylic Acid (c-di-GMP) and the Acyclic Dimer PGPG. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2008, 27, 1282-1300.	0.4	24
48	Structures of Substrate- and Inhibitor-Bound Adenosine Deaminase from a Human Malaria Parasite Show a Dramatic Conformational Change and Shed Light on Drug Selectivity. <i>Journal of Molecular Biology</i> , 2008, 381, 975-988.	2.0	33
49	Evaluation of Different Virtual Screening Programs for Docking in a Charged Binding Pocket. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 2010-2020.	2.5	28
50	2-Oxotetrahydroquinoline-Based Antimalarials with High Potency and Metabolic Stability. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 384-387.	2.9	28
51	Glycogen Synthase Kinase 3 Is a Potential Drug Target for African Trypanosomiasis Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 3710-3717.	1.4	86
52	In Vitro and In Vivo Properties of Adenovirus Vectors with Increased Affinity to CD46. <i>Journal of Virology</i> , 2008, 82, 10567-10579.	1.5	56
53	Structural Genomics of Pathogenic Protozoa: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 497-513.	0.4	38
54	Reengineering CCA-adding enzymes to function as (U,G)- or dCdCdA-adding enzymes or poly(C,A) and poly(U,G) polymerases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 54-59.	3.3	30

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55	Efficacy, Pharmacokinetics, and Metabolism of Tetrahydroquinoline Inhibitors of <i>Plasmodium falciparum</i> Protein Farnesyltransferase. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3659-3671.	1.4	40
56	Second Generation Tetrahydroquinoline-Based Protein Farnesyltransferase Inhibitors as Antimalarials. <i>Journal of Medicinal Chemistry</i> , 2007, 50, 4585-4605.	2.9	66
57	Identification of CD46 Binding Sites within the Adenovirus Serotype 35 Fiber Knob. <i>Journal of Virology</i> , 2007, 81, 12785-12792.	1.5	69
58	Resistance mutations at the lipid substrate binding site of <i>Plasmodium falciparum</i> protein farnesyltransferase. <i>Molecular and Biochemical Parasitology</i> , 2007, 152, 66-71.	0.5	28
59	Using Fragment Cocktail Crystallography To Assist Inhibitor Design of <i>Trypanosoma brucei</i> Nucleoside 2-Deoxyribosyltransferase. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5939-5946.	2.9	66
60	Structure of ribose 5-phosphate isomerase from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 427-431.	0.7	13
61	In-vitro and in-vivo effects of the CYP2C9*11 polymorphism on warfarin metabolism and dose. <i>Pharmacogenetics and Genomics</i> , 2005, 15, 475-481.	0.7	61
62	Structurally Simple Farnesyltransferase Inhibitors Arrest the Growth of Malaria Parasites. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 4903-4906.	7.2	37
63	Crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>Plasmodium falciparum</i> at 2.25 Å resolution reveals intriguing extra electron density in the active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 570-577.	1.5	34
64	Resistance to a Protein Farnesyltransferase Inhibitor in <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 13554-13559.	1.6	66
65	Archaeal CCA-adding Enzymes. <i>Journal of Biological Chemistry</i> , 2005, 280, 9555-9566.	1.6	24
66	The Protein Farnesyltransferase Inhibitor Tipifarnib as a New Lead for the Development of Drugs against Chagas Disease. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 5415-5418.	2.9	83
67	Protein Heterodimerization through Ligand-Bridged Multivalent Pre-organization: Enhancing Ligand Binding toward Both Protein Targets. <i>Journal of the American Chemical Society</i> , 2005, 127, 2044-2045.	6.6	33
68	Methionine Sulfoxide and Proteolytic Cleavage Contribute to the Inactivation of Cathepsin G by Hypochlorous Acid. <i>Journal of Biological Chemistry</i> , 2005, 280, 29311-29321.	1.6	32
69	Characterization of Atrazine Biotransformation by Human and Murine Glutathione S-Transferases. <i>Toxicological Sciences</i> , 2004, 80, 230-238.	1.4	46
70	Estradiol metabolites as isoform-specific inhibitors of human glutathione S-transferases. <i>Chemico-Biological Interactions</i> , 2004, 151, 21-32.	1.7	17
71	Nonspanning Bivalent Ligands as Improved Surface Receptor Binding Inhibitors of the Cholera Toxin B Pentamer. <i>Chemistry and Biology</i> , 2004, 11, 1205-1215.	6.2	39
72	Large Cyclic Peptides as Cores of Multivalent Ligands: Application to Inhibitors of Receptor Binding by Cholera Toxin. <i>Journal of Organic Chemistry</i> , 2004, 69, 7737-7740.	1.7	28

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73	Structural biology and structure-based inhibitor design of cholera toxin and heat-labile enterotoxin. <i>International Journal of Medical Microbiology</i> , 2004, 294, 217-223.	1.5	36
74	Structure-Based Design of a Macrocyclic Inhibitor for Peptide Deformylase. <i>Journal of Medicinal Chemistry</i> , 2003, 46, 3771-3774.	2.9	54
75	Cloning and analysis of <i>Trypanosoma cruzi</i> lanosterol 14 α -demethylase. <i>Molecular and Biochemical Parasitology</i> , 2003, 132, 75-81.	0.5	18
76	Missense Mutations in the Regulatory Domain of PKC δ : A New Mechanism for Dominant Nonepisodic Cerebellar Ataxia. <i>American Journal of Human Genetics</i> , 2003, 72, 839-849.	2.6	236
77	Alternatively spliced isoforms of the human constitutive androstane receptor. <i>Nucleic Acids Research</i> , 2003, 31, 3194-3207.	6.5	113
78	Solution and Crystallographic Studies of Branched Multivalent Ligands that Inhibit the Receptor-Binding of Cholera Toxin. <i>Journal of the American Chemical Society</i> , 2002, 124, 12991-12998.	6.6	124
79	Anchor-Based Design of Improved Cholera Toxin and <i>E. coli</i> Heat-Labile Enterotoxin Receptor Binding Antagonists that Display Multiple Binding Modes. <i>Chemistry and Biology</i> , 2002, 9, 215-224.	6.2	41
80	Protein structure-based design of anti-protozoal drugs. <i>Journal of the Brazilian Chemical Society</i> , 2002, 13, 843-844.	0.6	8
81	Conformational changes in <i>Leishmania mexicana</i> glyceraldehyde-3-phosphate dehydrogenase induced by designed inhibitors. <i>Journal of Molecular Biology</i> , 2001, 309, 423-435.	2.0	58
82	Glycolysis as a target for the design of new anti-trypanosome drugs. <i>Drug Resistance Updates</i> , 2001, 4, 50-65.	6.5	192
83	Adenosine Analogues as Selective Inhibitors of Glyceraldehyde-3-phosphate Dehydrogenase of <i>Trypanosomatida</i> . <i>Structure-Based Drug Design. Journal of Medicinal Chemistry</i> , 2001, 44, 2080-2093.	2.9	115
84	Rod and cone visual cycle consequences of a null mutation in the 11-cis-retinol dehydrogenase gene in man. <i>Visual Neuroscience</i> , 2000, 17, 667-678.	0.5	99
85	Structure of <i>m</i> -carboxyphenyl- β -D-galactopyranoside complexed to heat-labile enterotoxin at 1.3 \AA resolution: surprising variations in ligand-binding modes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 795-804.	2.5	10
86	AB5 toxins: structures and inhibitor design. <i>Current Opinion in Structural Biology</i> , 2000, 10, 680-686.	2.6	123
87	High-Affinity Pentavalent Ligands of <i>Escherichia coli</i> Heat-Labile Enterotoxin by Modular Structure-Based Design. <i>Journal of the American Chemical Society</i> , 2000, 122, 2663-2664.	6.6	231
88	Five Members of a Novel Ca ²⁺ -binding Protein (CABP) Subfamily with Similarity to Calmodulin. <i>Journal of Biological Chemistry</i> , 2000, 275, 1247-1260.	1.6	231
89	Ca ²⁺ -binding proteins in the retina: from discovery to etiology of human disease. The nucleotide sequences reported in this manuscript have been submitted to the GenBank, EMBL databank with the following accession numbers: short form of human CaBP1, AF169148; long form of human CaBP1, AF169149; short form of bovine CaBP1, AF169150; long form of bovine CaBP1, AF169151; short form of mouse CaBP1, AF169153; long form of mouse CaBP1, AF169152; human CaBP2, AF169154; bovine CaBP2, AF169155; short form of mouse. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2000, 1498,	1.9	38
90	Adenosine Analogues as Inhibitors of <i>Trypanosoma brucei</i> Phosphoglycerate Kinase: Elucidation of a Novel Binding Mode for a 2-Amino-N ⁶ -Substituted Adenosine. <i>Journal of Medicinal Chemistry</i> , 2000, 43, 4135-4150.	2.9	70

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91	Using a Galactose Library for Exploration of a Novel Hydrophobic Pocket in the Receptor Binding Site of the Escherichia coli Heat-labile Enterotoxin. <i>Journal of Biological Chemistry</i> , 1999, 274, 33469-33473.	1.6	25
92	Structure-based design of submicromolar, biologically active inhibitors of trypanosomatid glyceraldehyde-3-phosphate dehydrogenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 4273-4278.	3.3	125
93	Conformational Changes in Guanylyl Cyclase-activating Protein 1 (GCAP1) and Its Tryptophan Mutants as a Function of Calcium Concentration. <i>Journal of Biological Chemistry</i> , 1999, 274, 19829-19837.	1.6	48
94	Structure-based Reevaluation of the Mechanism of Class I Fructose-1,6-bisphosphate Aldolase. <i>Journal of Molecular Modeling</i> , 1999, 5, 37-45.	0.8	4
95	The Role of Waters in Docking Strategies with Incremental Flexibility for Carbohydrate Derivatives: A Heat-Labile Enterotoxin, a Multivalent Test Case. <i>Journal of Medicinal Chemistry</i> , 1999, 42, 1778-1788.	2.9	67
96	Structure-Based Exploration of the Ganglioside GM1 Binding Sites of Escherichia coli Heat-Labile Enterotoxin and Cholera Toxin for the Discovery of Receptor Antagonists. <i>Biochemistry</i> , 1999, 38, 5684-5692.	1.2	109
97	Structure-based Discovery of a Pore-binding Ligand: Towards Assembly Inhibitors for Cholera and Related AB5 Toxins. <i>Journal of Molecular Biology</i> , 1999, 285, 1169-1178.	2.0	11
98	Selective Tight Binding Inhibitors of Trypanosomal Glyceraldehyde-3-phosphate Dehydrogenase via Structure-Based Drug Design. <i>Journal of Medicinal Chemistry</i> , 1998, 41, 4790-4799.	2.9	72
99	Efficient technique for screening drugs for activity against Trypanosoma cruzi using parasites expressing beta-galactosidase. <i>Antimicrobial Agents and Chemotherapy</i> , 1996, 40, 2592-2597.	1.4	457
100	Three-dimensional structure of the diphtheria toxin repressor in complex with divalent cation co-repressors. <i>Structure</i> , 1995, 3, 87-100.	1.6	133
101	Drug or tool, design or serendipity?. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 429-432.	3.6	2
102	Crystal Structure of Glycosomal Glyceraldehyde-3-phosphate Dehydrogenase from Leishmania mexicana: Implications for Structure-Based Drug Design and a New Position for the Inorganic Phosphate Binding Site. <i>Biochemistry</i> , 1995, 34, 14975-14986.	1.2	115
103	Synthesis and Structure-Activity Relationships of Analogs of 2'-Deoxy-2'-(3-methoxybenzamido)adenosine, a Selective Inhibitor of Trypanosomal Glycosomal Glyceraldehyde-3-phosphate Dehydrogenase. <i>Journal of Medicinal Chemistry</i> , 1995, 38, 3838-3849.	2.9	48
104	Protein crystallography and infectious diseases. <i>Protein Science</i> , 1994, 3, 1670-1686.	3.1	48
105	Synthesis and Conformational Analysis of 2'-Deoxy-2'-(3-methoxybenzamido)adenosine, a rational-designed inhibitor of trypanosomal glyceraldehyde phosphate dehydrogenase (GAPDH). <i>Helvetica Chimica Acta</i> , 1994, 77, 631-644.	1.0	20
106	Structure-based drug design: progress, results and challenges. <i>Structure</i> , 1994, 2, 577-587.	1.6	249
107	Selective Inhibition of Trypanosomal Glyceraldehyde-3-phosphate Dehydrogenase by Protein Structure-Based Design: Toward New Drugs for the Treatment of Sleeping Sickness. <i>Journal of Medicinal Chemistry</i> , 1994, 37, 3605-3613.	2.9	75
108	Structure of glycosomal glyceraldehyde-3-phosphate dehydrogenase from Trypanosoma brucei determined from Laue data.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 2355-2359.	3.3	91

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109	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	1.5	26
110	In search of new lead compounds for trypanosomiasis drug design: A protein structure-based linked-fragment approach. Journal of Computer-Aided Molecular Design, 1992, 6, 131-147.	1.3	64
111	Structure of the complex between trypanosomal triosephosphate isomerase and α -D-glucose-1-phosphono-L-proline: Binding at the active site despite an "open" flexible loop conformation. Protein Science, 1992, 1, 1578-1584.	3.1	30
112	Crystallographic and molecular modeling studies on trypanosomal triosephosphate isomerase: a critical assessment of the predicted and observed structures of the complex with 2-phosphoglycerate. Journal of Medicinal Chemistry, 1991, 34, 2709-2718.	2.9	32
113	Anion binding at the active site of trypanosomal triosephosphate isomerase. Monohydrogen phosphate does not mimic sulphate. FEBS Journal, 1991, 198, 53-57.	0.2	28
114	Structure of the neuroleptic drug 4-amino-N-1-[(1-ethyl-2-pyrrolidinyl)methyl]-5-(ethylsulfonyl)-2-methoxybenzamide (amisulpride). Acta Crystallographica Section C: Crystal Structure Communications, 1990, 46, 313-317.	0.4	6
115	Structure of the opioid μ -agonist (\pm) -[(1R,5R,9R,2'S)-2'-hydroxy-2-(2-methoxypropyl)-5,9-dimethyl-6,7-benzomorphan hydrobromide (I) and its inactive (\pm) -[(1R,5R,9R,2''R)-2''-hydroxy-2-(2-methoxypropyl)-5,9-dimethyl-6,7-benzomorphan hydrobromide (II)]. Acta Crystallographica Section C: Crystal Structure Communications, 1990, 46, 663-666.	0.4	0
116	Structure of a μ -opioid receptor misfit: (1S,5R,8R,9R)-2'-hydroxy-5,9-dimethyl-8,2-epoxyethano-6,7-benzomorphan hydrochloride. Acta Crystallographica Section C: Crystal Structure Communications, 1989, 45, 799-803.	0.4	2
117	Structure and conformational analysis of the opioid antagonist (\pm) -[(1R,5R,9R)-5,9-diethyl-2-(3-furylmethyl)-2'-hydroxy-6,7-benzomorphan (Mr2266)]. Acta Crystallographica Section C: Crystal Structure Communications, 1989, 45, 1797-1802.	0.4	2
118	Structure and absolute configuration of two stereoisomers of (\pm) -[iminobis(methylene)]bis(3,4-dihydro-2H-1-benzopyran-2-methanol) hydrobromide. Acta Crystallographica Section C: Crystal Structure Communications, 1989, 45, 1930-1933.	0.4	0
119	Static disorder in (\pm) -[(1R,5R,9R,13S)-2'-hydroxy-5,9-dimethyl-2-(2-methyltetrahydrofurfuryl)-6,7-benzomorphan, C ₂₀ H ₂₉ NO ₂]. Crystal structure and MM2 pucker analysis of the tetrahydrofuran ring. Acta Crystallographica Section B: Structural Science, 1989, 45, 107-112.	1.8	5
120	Structure of 8-chloro-2-[(3-furoyl)aminomethyl]-1-methyl-5-phenyl-2,3-dihydro-1H-1,4-benzodiazepine hydrochloride. Acta Crystallographica Section C: Crystal Structure Communications, 1988, 44, 1125-1127.	0.4	1
121	(\pm) -[(1R,5R,9R,2''R)-2''-hydroxy-5,9-dimethyl-2-[2-(tetrahydro-2-furyl)ethyl]-6,7-benzomorphan hydrobromide. Acta Crystallographica Section C: Crystal Structure Communications, 1988, 44, 1611-1614.	0.4	2
122	(\pm) -[(1R,5R,9R)-2'-hydroxy-2-methoxyethyl-5,9-dimethyl-6,7-benzomorphan hydrobromide monohydrate. Acta Crystallographica Section C: Crystal Structure Communications, 1988, 44, 1792-1794.	0.4	1
123	(\pm) -[(1R,5R,9R)-2-Ethoxyethyl-2'-hydroxy-5,9-dimethyl-6,7-benzomorphan hydrobromide. Acta Crystallographica Section C: Crystal Structure Communications, 1988, 44, 1789-1791.	0.4	1
124	Assessment of the μ -opioid activity of a series of 6,7-benzomorphan in the rabbit vas deferens. European Journal of Pharmacology, 1988, 153, 83-87.	1.7	5
125	(\pm) -[(1R,5R,9R)-2'-hydroxy-2-(3-methoxypropyl)-5,9-dimethyl-6,7-benzomorphan hydrobromide monohydrate. Acta Crystallographica Section C: Crystal Structure Communications, 1988, 44, 1609-1611.	0.4	1
126	5-Ethyl-2'-hydroxy-2-[(1-hydroxycyclopropyl)methyl]-9,9-dimethyl-6,7-benzomorphan hydrochloride (bremazocine), C ₂₀ H ₂₉ NO ₂ .HCl. Acta Crystallographica Section C: Crystal Structure Communications, 1984, 40, 1759-1761.	0.4	6

#	ARTICLE	IF	CITATIONS
127	The kappa-active oxygen in the opioid pharmacophore of some benzomorphans: Charges, proton affinities and binding modelling. <i>Neuropeptides</i> , 1984, 5, 209-212.	0.9	9
128	(1S,5R,9R)-2-Cyclopropylmethyl-2'-hydroxy-5,9-dimethyl-8-oxo-6,7-benzomorphan hydrochloride monohydrate (ketazocine), C ₁₈ H ₂₃ NO ₂ .HCl.H ₂ O. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 1983, 39, 1703-1706.	0.4	4