Christophe Lmj Verlinde

List of Publications by Year
in descending order

128	7,124	47006	64796
papers	citations	47 h-index	79 g-index

132	132	132	6884
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Efficient technique for screening drugs for activity against Trypanosoma cruzi using parasites expressing beta-galactosidase. Antimicrobial Agents and Chemotherapy, 1996, 40, 2592-2597.	3.2	457
2	Genomic-scale prioritization of drug targets: the TDR Targets database. Nature Reviews Drug Discovery, 2008, 7, 900-907.	46.4	282
3	Structure-based drug design: progress, results and challenges. Structure, 1994, 2, 577-587.	3.3	249
4	Missense Mutations in the Regulatory Domain of PKCÎ³: A New Mechanism for Dominant Nonepisodic Cerebellar Ataxia. American Journal of Human Genetics, 2003, 72, 839-849.	6.2	236
5	High-Affinity Pentavalent Ligands of Escherichia coli Heat-Labile Enterotoxin by Modular Structure-Based Design. Journal of the American Chemical Society, 2000, 122, 2663-2664.	13.7	231
6	Five Members of a Novel Ca2+-binding Protein (CABP) Subfamily with Similarity to Calmodulin. Journal of Biological Chemistry, 2000, 275, 1247-1260.	3.4	231
7	Glycolysis as a target for the design of new anti-trypanosome drugs. Drug Resistance Updates, 2001, 4, 50-65.	14.4	192
8	Toxoplasma gondii calcium-dependent protein kinase 1 is a target for selective kinase inhibitors. Nature Structural and Molecular Biology, 2010, 17, 602-607.	8.2	172
9	Rational Modification of a Candidate Cancer Drug for Use Against Chagas Disease. Journal of Medicinal Chemistry, 2009, 52, 1639-1647.	6.4	150
10	Three-dimensional structure of the diphtheria toxin repressor in complex with divalent cation co-repressors. Structure, 1995, 3, 87-100.	3.3	133
11	Discovery of Potent and Selective Inhibitors of CDPK1 from C. parvum and T. gondii. ACS Medicinal Chemistry Letters, 2010, 1, 331-335.	2.8	126
12	Structure-based design of submicromolar, biologically active inhibitors of trypanosomatid glyceraldehyde-3-phosphate dehydrogenase. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 4273-4278.	7.1	125
13	Solution and Crystallographic Studies of Branched Multivalent Ligands that Inhibit the Receptor-Binding of Cholera Toxin. Journal of the American Chemical Society, 2002, 124, 12991-12998.	13.7	124
14	AB5 toxins: structures and inhibitor design. Current Opinion in Structural Biology, 2000, 10, 680-686.	5.7	123
15	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. Biochemistry, 1995, 34, 14975-14986.	2.5	115
16	Adenosine Analogues as Selective Inhibitors of Glyceraldehyde-3-phosphate Dehydrogenase ofTrypanosomatidaevia Structure-Based Drug Design. Journal of Medicinal Chemistry, 2001, 44, 2080-2093.	6.4	115
17	Alternatively spliced isoforms of the human constitutive androstane receptor. Nucleic Acids Research, 2003, 31, 3194-3207.	14.5	113
18	Structure-Based Exploration of the Ganglioside GM1 Binding Sites ofEscherichia coliHeat-Labile Enterotoxin and Cholera Toxin for the Discovery of Receptor Antagonistsâ€. Biochemistry, 1999, 38, 5684-5692.	2.5	109

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19	Second Generation Analogues of the Cancer Drug Clinical Candidate Tipifarnib for Anti-Chagas Disease Drug Discovery. Journal of Medicinal Chemistry, 2010, 53, 3887-3898.	6.4	107
20	Rod and cone visual cycle consequences of a null mutation in the 11-cis-retinol dehydrogenase gene in man. Visual Neuroscience, 2000, 17, 667-678.	1.0	99
21	Structure of glycosomal glyceraldehyde-3-phosphate dehydrogenase from Trypanosoma brucei determined from Laue data.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 2355-2359.	7.1	91
22	Transmission of malaria to mosquitoes blocked by bumped kinase inhibitors. Journal of Clinical Investigation, 2012, 122, 2301-2305.	8.2	90
23	Glycogen Synthase Kinase 3 Is a Potential Drug Target for African Trypanosomiasis Therapy. Antimicrobial Agents and Chemotherapy, 2008, 52, 3710-3717.	3.2	86
24	The Protein Farnesyltransferase Inhibitor Tipifarnib as a New Lead for the Development of Drugs against Chagas Disease. Journal of Medicinal Chemistry, 2005, 48, 5415-5418.	6.4	83
25	A Specific Inhibitor of PfCDPK4 Blocks Malaria Transmission: Chemical-genetic Validation. Journal of Infectious Diseases, 2014, 209, 275-284.	4.0	83
26	Selective Inhibition of Trypanosomal Glyceraldehyde-3-phosphate Dehydrogenase by Protein Structure-Based Design: Toward New Drugs for the Treatment of Sleeping Sickness. Journal of Medicinal Chemistry, 1994, 37, 3605-3613.	6.4	75
27	Selective Inhibitors of Methionyl-tRNA Synthetase Have Potent Activity against Trypanosoma brucei Infection in Mice. Antimicrobial Agents and Chemotherapy, 2011, 55, 1982-1989.	3.2	75
28	Characterization of Trypanosoma brucei dihydroorotate dehydrogenase as a possible drug target; structural, kinetic and RNAi studies. Molecular Microbiology, 2008, 68, 37-50.	2.5	73
29	Selective Tight Binding Inhibitors of Trypanosomal Glyceraldehyde-3-phosphate Dehydrogenase via Structure-Based Drug Design. Journal of Medicinal Chemistry, 1998, 41, 4790-4799.	6.4	72
30	Adenosine Analogues as Inhibitors of Trypanosoma brucei Phosphoglycerate Kinase:â€‰Elucidation of a Novel Binding Mode for a 2-Amino-N6-Substituted Adenosine. Journal of Medicinal Chemistry, 2000, 43, 4135-4150.	6.4	70
31	Identification of CD46 Binding Sites within the Adenovirus Serotype 35 Fiber Knob. Journal of Virology, 2007, 81, 12785-12792.	3.4	69
32	Distinct States of Methionyl-tRNA Synthetase Indicate Inhibitor Binding by Conformational Selection. Structure, 2012, 20, 1681-1691.	3.3	69
33	The Role of Waters in Docking Strategies with Incremental Flexibility for Carbohydrate Derivatives:Â Heat-Labile Enterotoxin, a Multivalent Test Case. Journal of Medicinal Chemistry, 1999, 42, 1778-1788.	6.4	67
34	Resistance to a Protein Farnesyltransferase Inhibitor in Plasmodium falciparum. Journal of Biological Chemistry, 2005, 280, 13554-13559.	3.4	66
35	Using Fragment Cocktail Crystallography To Assist Inhibitor Design ofTrypanosoma bruceiNucleoside 2-Deoxyribosyltransferaseâ€. Journal of Medicinal Chemistry, 2006, 49, 5939-5946.	6.4	66
36	Second Generation Tetrahydroquinoline-Based Protein Farnesyltransferase Inhibitors as Antimalarials. Journal of Medicinal Chemistry, 2007, 50, 4585-4605.	6.4	66

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37	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.	2.9	64
38	In-vitro and in-vivo effects of the CYP2C9*11 polymorphism on warfarin metabolism and dose. Pharmacogenetics and Genomics, 2005, 15, 475-481.	1.5	61
39	Urea-Based Inhibitors of Trypanosoma brucei Methionyl-tRNA Synthetase: Selectivity and in Vivo Characterization. Journal of Medicinal Chemistry, 2012, 55, 6342-6351.	6.4	60
40	Multiple Determinants for Selective Inhibition of Apicomplexan Calcium-Dependent Protein Kinase CDPK1. Journal of Medicinal Chemistry, 2012, 55, 2803-2810.	6.4	60
41	Conformational changes in Leishmania mexicana glyceraldehyde-3-phosphate dehydrogenase induced by designed inhibitors. Journal of Molecular Biology, 2001, 309, 423-435.	4.2	58
42	In Vitro and In Vivo Properties of Adenovirus Vectors with Increased Affinity to CD46. Journal of Virology, 2008, 82, 10567-10579.	3.4	56
43	Structure-Based Design of a Macrocyclic Inhibitor for Peptide Deformylase. Journal of Medicinal Chemistry, 2003, 46, 3771-3774.	6.4	54
44	Development of potent and selective Plasmodium falciparum calcium-dependent protein kinase 4 (PfCDPK4) inhibitors that block the transmission of malaria to mosquitoes. European Journal of Medicinal Chemistry, 2014, 74, 562-573.	5.5	54
45	2-Oxo-tetrahydro-1,8-naphthyridines as selective inhibitors of malarial protein farnesyltransferase and as anti-malarials. Bioorganic and Medicinal Chemistry Letters, 2008, 18, 494-497.	2.2	52
46	Structure of Leishmania major methionyl-tRNA synthetase in complex with intermediate products methionyladenylate and pyrophosphate. Biochimie, 2011, 93, 570-582.	2.6	50
47	Pharmacological Characterization, Structural Studies, andIn VivoActivities of Anti-Chagas Disease Lead Compounds Derived from Tipifarnib. Antimicrobial Agents and Chemotherapy, 2012, 56, 4914-4921.	3.2	50
48	Potent and Selective Inhibitors of CDPK1 from T. gondii and C. parvum Based on a 5-Aminopyrazole-4-carboxamide Scaffold. ACS Medicinal Chemistry Letters, 2014, 5, 40-44.	2.8	49
49	Protein crystallography and infectious diseases. Protein Science, 1994, 3, 1670-1686.	7.6	48
50	Synthesis and Structure-Activity Relationships of Analogs of 2'-Deoxy-2'-(3-methoxybenzamido)adenosine, a Selective Inhibitor of Trypanosomal Glycosomal Glyceraldehyde-3-phosphate Dehydrogenase. Journal of Medicinal Chemistry, 1995, 38, 3838-3849.	6.4	48
51	Conformational Changes in Guanylyl Cyclase-activating Protein 1 (GCAP1) and Its Tryptophan Mutants as a Function of Calcium Concentration. Journal of Biological Chemistry, 1999, 274, 19829-19837.	3.4	48
52	Characterization of Atrazine Biotransformation by Human and Murine Glutathione S-Transferases. Toxicological Sciences, 2004, 80, 230-238.	3.1	46
53	Benzoylbenzimidazole-based selective inhibitors targeting Cryptosporidium parvum and Toxoplasma gondii calcium-dependent protein kinase-1. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 5264-5267.	2.2	43
54	Buffer Optimization of Thermal Melt Assays of Plasmodium Proteins for Detection of Small-Molecule Ligands. Journal of Biomolecular Screening, 2009, 14, 700-707.	2.6	42

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55	Anchor-Based Design of Improved Cholera Toxin and E. coli Heat-Labile Enterotoxin Receptor Binding Antagonists that Display Multiple Binding Modes. Chemistry and Biology, 2002, 9, 215-224.	6.0	41
56	Efficacy, Pharmacokinetics, and Metabolism of Tetrahydroquinoline Inhibitors of Plasmodium falciparum Protein Farnesyltransferase. Antimicrobial Agents and Chemotherapy, 2007, 51, 3659-3671.	3.2	40
57	The Double-Length Tyrosyl-tRNA Synthetase from the Eukaryote Leishmania major Forms an Intrinsically Asymmetric Pseudo-Dimer. Journal of Molecular Biology, 2011, 409, 159-176.	4.2	40
58	Nonspanning Bivalent Ligands as Improved Surface Receptor Binding Inhibitors of the Cholera Toxin B Pentamer. Chemistry and Biology, 2004, 11, 1205-1215.	6.0	39
59	Ca2+-binding proteins in the retina: from discovery to etiology of human disease11The 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, AF1691152; human CaBP2, AF169154; bovine CaBP2, AF169155; short form of mouse. Biochimica Et Biophysica Acta - Molecular Cell Research, 2000, 1498, 233.	4.1	38
60	Structurally Simple Inhibitors of Lanosterol 14Î±-Demethylase Are Efficacious In a Rodent Model of Acute Chagas Disease. Journal of Medicinal Chemistry, 2009, 52, 3703-3715.	6.4	38
61	Structural Genomics of Pathogenic Protozoa: an Overview. Methods in Molecular Biology, 2008, 426, 497-513.	0.9	38
62	Structurally Simple Farnesyltransferase Inhibitors Arrest the Growth of Malaria Parasites. Angewandte Chemie - International Edition, 2005, 44, 4903-4906.	13.8	37
63	Crystal Structures of Trypanosomal Histidyl-tRNA Synthetase Illuminate Differences between Eukaryotic and Prokaryotic Homologs. Journal of Molecular Biology, 2010, 397, 481-494.	4.2	37
64	Structures of Trypanosoma brucei Methionyl-tRNA Synthetase with Urea-Based Inhibitors Provide Guidance for Drug Design against Sleeping Sickness. PLoS Neglected Tropical Diseases, 2014, 8, e2775.	3.0	37
65	Structural biology and structure-based inhibitor design of cholera toxin and heat-labile enterotoxin. International Journal of Medical Microbiology, 2004, 294, 217-223.	3.6	36
66	Fragment-Based Cocktail Crystallography by the Medical Structural Genomics of Pathogenic Protozoa Consortium. Current Topics in Medicinal Chemistry, 2009, 9, 1678-1687.	2.1	36
67	Structure determination of glycogen synthase kinase-3 from Leishmania major and comparative inhibitor structureâ€“activity relationships with Trypanosoma brucei GSK-3. Molecular and Biochemical Parasitology, 2011, 176, 98-108.	1.1	35
68	Identification of Potent Inhibitors of the Trypanosoma brucei Methionyl-tRNA Synthetase via High-Throughput Orthogonal Screening. Journal of Biomolecular Screening, 2015, 20, 122-130.	2.6	35
69	Crystal structure of glyceraldehyde-3-phosphate dehydrogenase from Plasmodium falciparum at 2.25 Ã… resolution reveals intriguing extra electron density in the active site. Proteins: Structure, Function and Bioinformatics, 2005, 62, 570-577.	2.6	34
70	Protein Heterodimerization through Ligand-Bridged Multivalent Pre-organization:Â Enhancing Ligand Binding toward Both Protein Targets. Journal of the American Chemical Society, 2005, 127, 2044-2045.	13.7	33
71	Structures of Substrate- and Inhibitor-Bound Adenosine Deaminase from a Human Malaria Parasite Show a Dramatic Conformational Change and Shed Light on Drug Selectivity. Journal of Molecular Biology, 2008, 381, 975-988.	4.2	33
72	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.	6.4	32

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73	Methionine Sulfoxide and Proteolytic Cleavage Contribute to the Inactivation of Cathepsin G by Hypochlorous Acid. Journal of Biological Chemistry, 2005, 280, 29311-29321.	3.4	32
74	Structure of the complex between trypanosomal triosephosphate isomerase and Nâ€hydroxyâ€4â€phosphonoâ€butanamide: Binding at the active site despite an â€œopenâ€•flexible loop conformation. Protein Science, 1992, 1, 1578-1584.	7.6	30
75	Reengineering CCA-adding enzymes to function as (U,G)- or dCdCdA-adding enzymes or poly(C,A) and poly(U,G) polymerases. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 54-59.	7.1	30
76	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
77	Large Cyclic Peptides as Cores of Multivalent Ligands:Â Application to Inhibitors of Receptor Binding by Cholera Toxin. Journal of Organic Chemistry, 2004, 69, 7737-7740.	3.2	28
78	Resistance mutations at the lipid substrate binding site of Plasmodium falciparum protein farnesyltransferase. Molecular and Biochemical Parasitology, 2007, 152, 66-71.	1.1	28
79	Evaluation of Different Virtual Screening Programs for Docking in a Charged Binding Pocket. Journal of Chemical Information and Modeling, 2008, 48, 2010-2020.	5.4	28
80	2-Oxotetrahydroquinoline-Based Antimalarials with High Potency and Metabolic Stability. Journal of Medicinal Chemistry, 2008, 51, 384-387.	6.4	28
81	5-Fluoroimidazo[4,5-b]pyridine Is a Privileged Fragment That Conveys Bioavailability to Potent Trypanosomal Methionyl-tRNA Synthetase Inhibitors. ACS Infectious Diseases, 2016, 2, 399-404.	3.8	28
82	Crystal structures of Plasmodium falciparum cytosolic tryptophanyl-tRNA synthetase and its potential as a target for structure-guided drug design. Molecular and Biochemical Parasitology, 2013, 189, 26-32.	1.1	27
83	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	2.6	26
84	Using a Galactose Library for Exploration of a Novel Hydrophobic Pocket in the Receptor Binding Site of the Escherichia coliHeat-labile Enterotoxin. Journal of Biological Chemistry, 1999, 274, 33469-33473.	3.4	25
85	Multivalent Drug Design and Inhibition of Cholera Toxin by Specific and Transient Proteinâ€“Ligand Interactions. Chemical Biology and Drug Design, 2008, 71, 408-419.	3.2	25
86	An internal sequence targets Trypanosoma brucei triosephosphate isomerase to glycosomes. Molecular and Biochemical Parasitology, 2010, 171, 45-49.	1.1	25
87	Structure-guided design of novel Trypanosoma brucei Methionyl-tRNA synthetase inhibitors. European Journal of Medicinal Chemistry, 2016, 124, 1081-1092.	5.5	25
88	Archaeal CCA-adding Enzymes. Journal of Biological Chemistry, 2005, 280, 9555-9566.	3.4	24
89	Design and Synthesis ofbis-carbamate Analogs of Cyclicbis-(3â€²-5â€²)-Diguanylic Acid (c-di-GMP) and the Acyclic Dimer PGPG. Nucleosides, Nucleotides and Nucleic Acids, 2008, 27, 1282-1300.	1.1	24
90	Inhibitors of Methionyl-tRNA Synthetase Have Potent Activity against Giardia intestinalis Trophozoites. Antimicrobial Agents and Chemotherapy, 2015, 59, 7128-7131.	3.2	21

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91	Synthesis and Conformational Analysis of 2?-Deoxy-2?-(3-methoxybenzamido)adenosine, a rational-designed inhibitor of trypanosomal glyceraldehyde phosphate dehydrogenase (GAPDH). Helvetica Chimica Acta, 1994, 77, 631-644.	1.6	20
92	Simplified YM-26734 inhibitors of secreted phospholipase A2 group IIA. Bioorganic and Medicinal Chemistry Letters, 2008, 18, 5415-5419.	2.2	19
93	Induced Resistance to Methionyl-tRNA Synthetase Inhibitors in Trypanosoma brucei Is Due to Overexpression of the Target. Antimicrobial Agents and Chemotherapy, 2013, 57, 3021-3028.	3.2	19
94	A binding hotspot inTrypanosoma cruzihistidyl-tRNA synthetase revealed by fragment-based crystallographic cocktail screens. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1684-1698.	2.5	19
95	Cloning and analysis of Trypanosoma cruzi lanosterol 14Î±-demethylase. Molecular and Biochemical Parasitology, 2003, 132, 75-81.	1.1	18
96	Estradiol metabolites as isoform-specific inhibitors of human glutathione S-transferases. Chemico-Biological Interactions, 2004, 151, 21-32.	4.0	17
97	Prediction of protein crystallization outcome using a hybrid method. Journal of Structural Biology, 2010, 171, 64-73.	2.8	17
98	The Crystal Structure and Activity of a Putative Trypanosomal Nucleoside Phosphorylase Reveal It to be a Homodimeric Uridine Phosphorylase. Journal of Molecular Biology, 2010, 396, 1244-1259.	4.2	16
99	Crystal structures of three protozoan homologs of tryptophanyl-tRNA synthetase. Molecular and Biochemical Parasitology, 2011, 177, 20-28.	1.1	16
100	Crystal structure of the aspartyl-tRNA synthetase from Entamoeba histolytica. Molecular and Biochemical Parasitology, 2010, 169, 95-100.	1.1	14
101	Optimization of a binding fragment targeting the â€œenlarged methionine pocketâ€•leads to potent Trypanosoma brucei methionyl-tRNA synthetase inhibitors. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 2702-2707.	2.2	14
102	Structure of ribose 5-phosphate isomerase fromPlasmodium falciparum. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 427-431.	0.7	13
103	The structure of the D3 domain of Plasmodium falciparum myosin tail interacting protein MTIP in complex with a nanobody. Molecular and Biochemical Parasitology, 2013, 190, 87-91.	1.1	13
104	Leishmania donovani tyrosyl-tRNA synthetase structure in complex with a tyrosyl adenylate analog and comparisons with human and protozoan counterparts. Biochimie, 2017, 138, 124-136.	2.6	13
105	The structure of tryptophanyl-tRNA synthetase from Giardia lamblia reveals divergence from eukaryotic homologs. Journal of Structural Biology, 2010, 171, 238-243.	2.8	12
106	Structure-based Discovery of a Pore-binding Ligand: Towards Assembly Inhibitors for Cholera and Related AB5Toxins. Journal of Molecular Biology, 1999, 285, 1169-1178.	4.2	11
107	Dialkylimidazole inhibitors of Trypanosoma cruzi sterol 14Î±-demethylase as anti-Chagas disease agents. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 6492-6499.	2.2	11
108	Structure ofm-carboxyphenyl-Î±-D-galactopyranoside complexed to heat-labile enterotoxin at 1.3â€…Ã… resolution: surprising variations in ligand-binding modes. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 795-804.	2.5	10

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109	The kappa-active oxygen in the opioid pharmacophore of some benzomorphans: Charges, proton affinties and binding modelling. Neuropeptides, 1984, 5, 209-212.	2.2	9
110	Screening a fragment cocktail library using ultrafiltration. Analytical and Bioanalytical Chemistry, 2011, 401, 1585-1591.	3.7	9
111	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogenGiardia lamblia. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1194-1200.	2.5	9
112	Protein structure-based design of anti-protozoal drugs. Journal of the Brazilian Chemical Society, 2002, 13, 843-844.	0.6	8
113	5-Ethyl-2'-hydroxy-2-[(1-hydroxycyclopropyl)methyl]-9,9-dimethyl-6,7-benzomorphan hydrochloride (bremazocine), C20H29NO2.HCl. Acta Crystallographica Section C: Crystal Structure Communications, 1984, 40, 1759-1761.	0.4	6
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	Assessment of the Î¹-opioid activity of a series of 6,7-benzomorphans in the rabbit vas deferens. European Journal of Pharmacology, 1988, 153, 83-87.	3.5	5
116	Static disorder in (â€“)-(1R,5R,9R,13S)-2'-hydroxy-5,9-dimethyl-2-(2-methyltetrahydrofurfuryl)-6,7-benzomorphan, C20H29NO2. Crystal structure and MM2 pucker analysis of the tetrahydrofuran ring. Acta Crystallographica Section B: Structural Science, 1989, 45, 107-112.	1.8	5
117	(1S,5R,9R)-2-Cyclopropylmethyl-2'-hydroxy-5,9-dimethyl-8-oxo-6,7-benzomorphan hydrochloride monohydrate (ketazocine), C18H23NO2.HCl.H2O. Acta Crystallographica Section C: Crystal Structure Communications, 1983, 39, 1703-1706.	0.4	4
118	Structure-based Reevaluation of the Mechanism of Class I Fructose-1,6-bisphosphate Aldolase. Journal of Molecular Modeling, 1999, 5, 37-45.	1.8	4
119	(â€“)-(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
120	Structure of a Î¹-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
121	Structure and conformational analysis of the opioid antagonist (â€“)-(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
122	Drug or tool, design or serendipity?. Nature Structural and Molecular Biology, 1995, 2, 429-432.	8.2	2
123	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
124	(â€“)-(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
125	(â€“)-(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
126	(â€“)-(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

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127	Structure and absolute configuration of two stereoisomers of Î±,Î±'-[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
128	Structure of the opioid Î¼-agonist (â^')-(1R,5R,9R,2''S)-2'-hydroxy-2-(2-methoxypropyl)-5,9-dimethyl-6,7-benzomorphan hydrobromide (I) and its inactive (â^')-(1R,5R,9R,2''R) diastereomer (II). Acta Crystallographica Section C: Crystal Structure Communications, 1990, 46, 663-666.	0.4	0