

Pavlina Rezacova

List of Publications by Year in descending order

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121
papers

2,960
citations

201674

27
h-index

197818

49
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125
all docs

125
docs citations

125
times ranked

3466
citing authors

#	ARTICLE	IF	CITATIONS
1	3,5,7-Substituted Pyrazolo[4,3- <i>d</i>]Pyrimidine Inhibitors of Cyclin-Dependent Kinases and Cyclin K Degradors. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 8881-8896.	6.4	14
2	Druggable Hot Spots in the Schistosomiasis Cathepsin B1 Target Identified by Functional and Binding Mode Analysis of Potent Vinyl Sulfone Inhibitors. <i>ACS Infectious Diseases</i> , 2021, 7, 1077-1088.	3.8	9
3	Azanitrile Inhibitors of the SmCB1 Protease Target Are Lethal to <i>Schistosoma mansoni</i> : Structural and Mechanistic Insights into Chemotype Reactivity. <i>ACS Infectious Diseases</i> , 2021, 7, 189-201.	3.8	9
4	structural characterization of the interaction between the C-terminal domain of the influenza polymerase PA subunit and an optimized small peptide inhibitor. <i>Antiviral Research</i> , 2021, 185, 104971.	4.1	5
5	Cobalt Bis(dicarbollide) Alkylsulfonamides: Potent and Highly Selective Inhibitors of Tumor Specific Carbonic Anhydrase IX. <i>ChemPlusChem</i> , 2021, 86, 352-363.	2.8	11
6	N-Glycosylation can selectively block or foster different receptor-ligand binding modes. <i>Scientific Reports</i> , 2021, 11, 5239.	3.3	18
7	Imidazo[1,2- <i>c</i>]pyrimidin-5(6H)-one inhibitors of CDK2: Synthesis, kinase inhibition and co-crystal structure. <i>European Journal of Medicinal Chemistry</i> , 2021, 216, 113309.	5.5	6
8	Re-emerging Aspartic Protease Targets: Examining <i>Cryptococcus neoformans</i> Major Aspartyl Peptidase 1 as a Target for Antifungal Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 6706-6719.	6.4	14
9	Mialostatin, a Novel Midgut Cystatin from <i>Ixodes ricinus</i> Ticks: Crystal Structure and Regulation of Host Blood Digestion. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5371.	4.1	10
10	Inhibitors of CA IX Enzyme Based on Polyhedral Boron Compounds. <i>ChemBioChem</i> , 2021, 22, 2741-2761.	2.6	19
11	3- <i>H</i> -Pyrazolo[4,3- <i>f</i>]quinoline-Based Kinase Inhibitors Inhibit the Proliferation of Acute Myeloid Leukemia Cells In Vivo. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10981-10996.	6.4	10
12	Cobalt Bis(dicarbollide) Alkylsulfonamides: Potent and Highly Selective Inhibitors of Tumor Specific Carbonic Anhydrase IX. <i>ChemPlusChem</i> , 2021, 86, 351-351.	2.8	2
13	Structural insight into DNA recognition by bacterial transcriptional regulators of the SorC/DeoR family. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1411-1424.	2.3	3
14	Direct Introduction of an Alkylsulfonamido Group on C-sites of Isomeric Dicarba-closo-dodecaboranes: The Influence of Stereochemistry on Inhibitory Activity against the Cancer-Associated Carbonic Anhydrase IX Isoenzyme. <i>Chemistry - A European Journal</i> , 2020, 26, 16541-16553.	3.3	4
15	The structural basis for the selectivity of sulfonamido dicarbaboranes toward cancer-associated carbonic anhydrase IX. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2020, 35, 1800-1810.	5.2	8
16	Sulfonamido carboranes as highly selective inhibitors of cancer-specific carbonic anhydrase IX. <i>European Journal of Medicinal Chemistry</i> , 2020, 200, 112460.	5.5	25
17	Identification of Novel Carbonic Anhydrase IX Inhibitors Using High-Throughput Screening of Pooled Compound Libraries by DNA-Linked Inhibitor Antibody Assay (DIANA). <i>SLAS Discovery</i> , 2020, 25, 1026-1037.	2.7	2
18	Structural and catalytic effects of surface loop-helix transplantation within haloalkane dehalogenase family. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1352-1362.	4.1	2

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19	Rutinosidase from <i>Aspergillus niger</i> : crystal structure and insight into the enzymatic activity. FEBS Journal, 2020, 287, 3315-3327.	4.7	15
20	A novel structurally characterized haloacid dehalogenase superfamily phosphatase from <i>Thermococcus thio-reducens</i> with diverse substrate specificity. Acta Crystallographica Section D: Structural Biology, 2019, 75, 743-752.	2.3	2
21	Metallacarborane Sulfamides: Unconventional, Specific, and Highly Selective Inhibitors of Carbonic Anhydrase IX. Journal of Medicinal Chemistry, 2019, 62, 9560-9575.	6.4	51
22	Crystal structure of the cold-adapted haloalkane dehalogenase DpcA from <i>Psychrobacter cryohalolentis</i> K5. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 324-331.	0.8	5
23	Investigation of flexibility of neuraminidase 150-loop using tamiflu derivatives in influenza A viruses H1N1 and H5N1. Bioorganic and Medicinal Chemistry, 2019, 27, 2935-2947.	3.0	15
24	Inhibitor-Polymer Conjugates as a Versatile Tool for Detection and Visualization of Cancer-Associated Carbonic Anhydrase Isoforms. ACS Omega, 2019, 4, 6746-6756.	3.5	10
25	3,5,7-Substituted Pyrazolo[4,3-d]pyrimidine Inhibitors of Cyclin-Dependent Kinases and Their Evaluation in Lymphoma Models. Journal of Medicinal Chemistry, 2019, 62, 4606-4623.	6.4	16
26	The structure and function of Iristatin, a novel immunosuppressive tick salivary cystatin. Cellular and Molecular Life Sciences, 2019, 76, 2003-2013.	5.4	33
27	Capturing a dynamically interacting inhibitor by paramagnetic NMR spectroscopy. Physical Chemistry Chemical Physics, 2019, 21, 5661-5673.	2.8	21
28	Relapsed acute lymphoblastic leukemia-specific mutations in NT5C2 cluster into hotspots driving intersubunit stimulation. Leukemia, 2018, 32, 1393-1403.	7.2	27
29	Ranking Power of the SQM/COSMO Scoring Function on Carbonic Anhydrase Inhibitor Complexes. ChemPhysChem, 2018, 19, 873-879.	2.1	29
30	In situ proteolysis of an N-terminal His tag with thrombin improves the diffraction quality of human aldo-keto reductase 1C3 crystals. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 300-306.	0.8	4
31	Crystal structure of native N-acetylhexosaminidase isolated from <i>Aspergillus oryzae</i> sheds light onto its substrate specificity, high stability, and regulation by propeptide. FEBS Journal, 2018, 285, 580-598.	4.7	12
32	DNA-linked inhibitor antibody assay (DIANA) as a new method for screening influenza neuraminidase inhibitors. Biochemical Journal, 2018, 475, 3847-3860.	3.7	5
33	Crystal structure of native L-rhamnosidase from <i>Aspergillus terreus</i> . Acta Crystallographica Section D: Structural Biology, 2018, 74, 1078-1084.	2.3	17
34	Structure-Based Optimization of Bisphosphonate Nucleoside Inhibitors of Human 3-deoxyribonucleotidases. European Journal of Organic Chemistry, 2018, 2018, 5144-5153.	2.4	1
35	Kinetic, Thermodynamic, and Structural Analysis of Drug Resistance Mutations in Neuraminidase from the 2009 Pandemic Influenza Virus. Viruses, 2018, 10, 339.	3.3	17
36	Affinity switching of the LEDGF/p75 IBD interactome is governed by kinase-dependent phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7053-E7062.	7.1	27

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37	Structure analysis of haloalkane dehalogenase DbeA \hat{I}^{Cl} variant from <i>Bradyrhizobium elkanii</i> USDA94. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e212-e212.	0.1	0
38	Structure-assisted design of carborane inhibitors of human carbonic anhydrase IX. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e197-e197.	0.1	0
39	Structural characterization and comparison of crystallization behaviour of selected haloalkane dehalogenases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e185-e185.	0.1	0
40	Structural basis of the interaction between the putative adhesion-involved and iron-regulated FrpD and FrpC proteins of <i>Neisseria meningitidis</i> . <i>Scientific Reports</i> , 2017, 7, 40408.	3.3	10
41	Kinetic, thermodynamic and structural analysis of tamiphosphor binding to neuraminidase of H1N1 (2009) pandemic influenza. <i>European Journal of Medicinal Chemistry</i> , 2016, 121, 100-109.	5.5	9
42	Validation of the MLL-LEDGF/P75 interaction as a therapeutic target for mixed lineage leukemia. <i>Experimental Hematology</i> , 2016, 44, S69.	0.4	0
43	Engineering a de Novo Transport Tunnel. <i>ACS Catalysis</i> , 2016, 6, 7597-7610.	11.2	84
44	Oligomeric interface modulation causes misregulation of purine 5 \hat{A} -nucleotidase in relapsed leukemia. <i>BMC Biology</i> , 2016, 14, 91.	3.8	9
45	Atomic resolution crystal structure of Sapp2p, a secreted aspartic protease from <i>Candida parapsilosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2494-2504.	2.5	9
46	Structure-functional relationships of a novel haloalkane dehalogenase with two halide-binding sites. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s218-s218.	0.1	0
47	Balancing the Stability-Activity Trade-Off by Fine-Tuning Dehalogenase Access Tunnels. <i>ChemCatChem</i> , 2015, 7, 648-659.	3.7	39
48	Triggering HIV polyprotein processing by light using rapid photodegradation of a tight-binding protease inhibitor. <i>Nature Communications</i> , 2015, 6, 6461.	12.8	25
49	Multiple cellular proteins interact with LEDGF/p75 through a conserved unstructured consensus motif. <i>Nature Communications</i> , 2015, 6, 7968.	12.8	53
50	Structure-based design of a bisphosphonate 5 \hat{A} (3 \hat{A})-deoxyribonucleotidase inhibitor. <i>MedChemComm</i> , 2015, 6, 1635-1638.	3.4	2
51	Carbonic anhydrase inhibitors: Design, synthesis and structural characterization of new heteroaryl-N-carbonylbenzenesulfonamides targeting druggable human carbonic anhydrase isoforms. <i>European Journal of Medicinal Chemistry</i> , 2015, 102, 223-232.	5.5	24
52	Molecular mechanism for the action of the anti-CD44 monoclonal antibody MEM-85. <i>Journal of Structural Biology</i> , 2015, 191, 214-223.	2.8	13
53	Kinetic and structural characterization of an alternatively spliced variant of human mitochondrial 5 \hat{A} (3 \hat{A})-deoxyribonucleotidase. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2015, 30, 63-68.	5.2	0
54	Abstract 4492: Novel carborane based inhibitors of carbonic anhydrase IX. , 2015, , .		0

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55	Carborane-Based Carbonic Anhydrase Inhibitors: Insight into CAII/CAIX Specificity from a High-Resolution Crystal Structure, Modeling, and Quantum Chemical Calculations. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	18
56	Structure of the effector-binding domain of deoxyribonucleoside regulator DeoR from <i>Bacillus subtilis</i> . <i>FEBS Journal</i> , 2014, 281, 4280-4292.	4.7	9
57	Activation Route of the <i>Schistosoma mansoni</i> Cathepsin B1 Drug Target: Structural Map with a Glycosaminoglycan Switch. <i>Structure</i> , 2014, 22, 1786-1798.	3.3	34
58	Validation and Structural Characterization of the LEDGF/p75-MLL Interface as a New Target for the Treatment of MLL-Dependent Leukemia. <i>Cancer Research</i> , 2014, 74, 5139-5151.	0.9	41
59	Optimization of the crystallizability of a single-chain antibody fragment. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1701-1706.	0.8	1
60	GS-8374, a Prototype Phosphonate-Containing Inhibitor of HIV-1 Protease, Effectively Inhibits Protease Mutants with Amino Acid Insertions. <i>Journal of Virology</i> , 2014, 88, 3586-3590.	3.4	9
61	Structural and functional analysis of a novel haloalkane dehalogenase with two halide-binding sites. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1884-1897.	2.5	20
62	Backbone resonance assignments of the outer membrane lipoprotein FrpD from <i>Neisseria meningitidis</i> . <i>Biomolecular NMR Assignments</i> , 2014, 8, 53-55.	0.8	2
63	Thermodynamic and structural analysis of HIV-1 protease resistance to darunavir. Analysis of heavily mutated patient-derived HIV-1 proteases. <i>FEBS Journal</i> , 2014, 281, 1834-1847.	4.7	48
64	Structural Basis for Inhibition of Mycobacterial and Human Adenosine Kinase by 7-Substituted 7-(Het)aryl-7-deazaadenine Ribonucleosides. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 8268-8279.	6.4	26
65	Conformationally constrained nucleoside phosphonic acids are potent inhibitors of human mitochondrial and cytosolic 5 ² (3 ²)-nucleotidases. <i>Organic and Biomolecular Chemistry</i> , 2014, 12, 7971-7982.	2.8	5
66	Structures of human cytosolic and mitochondrial nucleotidases: implications for structure-based design of selective inhibitors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 461-470.	2.5	5
67	Crystal structure of the novel haloalkane dehalogenases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1678-C1678.	0.1	1
68	Engineering Enzyme Stability and Resistance to an Organic Cosolvent by Modification of Residues in the Access Tunnel. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 1959-1963.	13.8	113
69	QM/MM Calculations Reveal the Different Nature of the Interaction of Two Carborane-Based Sulfamide Inhibitors of Human Carbonic Anhydrase II. <i>Journal of Physical Chemistry B</i> , 2013, 117, 16096-16104.	2.6	47
70	Feasibility and constraints of particle targeting using the antigen-antibody interaction. <i>Nanoscale</i> , 2013, 5, 11490.	5.6	14
71	Crystallization of the Effector-Binding Domain of Repressor DeoR from <i>Bacillus subtilis</i> . <i>Crystal Growth and Design</i> , 2013, 13, 844-848.	3.0	5
72	Carborane-Based Carbonic Anhydrase Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 13760-13763.	13.8	93

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73	Differences in crystallization of two LinB variants from <i>Sphingobium japonicum</i> UT26. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 284-287.	0.7	5
74	Crystallographic analysis of new psychrophilic haloalkane dehalogenases: DpcA from <i>Psychrobacter cryohalolentis</i> K5 and DmxA from <i>Marinobacter</i> sp. ELB17. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 683-688.	0.7	8
75	Crystal structure of haloalkane dehalogenase DpcA from psychrophilic <i>Psychrobacter cryohalolentis</i> K5. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s605-s606.	0.3	0
76	The crystal structure of protease Sapp1p from <i>Candida parapsilosis</i> in complex with the HIV protease inhibitor ritonavir. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2012, 27, 160-165.	5.2	8
77	Mutations in HIV-1 gag and pol Compensate for the Loss of Viral Fitness Caused by a Highly Mutated Protease. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4320-4330.	3.2	40
78	Synthesis, Structure-Activity Relationship Studies, and X-ray Crystallographic Analysis of Arylsulfonamides as Potent Carbonic Anhydrase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 3891-3899.	6.4	24
79	Structure-Aided Design of Novel Inhibitors of HIV Protease Based on a Benzodiazepine Scaffold. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10130-10135.	6.4	53
80	Structure of the effector-binding domain of the arabinose repressor AraR from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 176-185.	2.5	11
81	Recombinant fragment of an antibody tailored for direct radioiodination. <i>Journal of Labelled Compounds and Radiopharmaceuticals</i> , 2012, 55, 52-56.	1.0	0
82	Structural Basis for the Interaction Between Carbonic Anhydrase and 1,2,3,4-tetrahydroisoquinolin-2-ylsulfonamides. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 2522-2526.	6.4	36
83	Structural Basis for Inhibition of Cathepsin B Drug Target from the Human Blood Fluke, <i>Schistosoma mansoni</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 35770-35781.	3.4	60
84	A tick salivary protein targets cathepsin G and chymase and inhibits host inflammation and platelet aggregation. <i>Blood</i> , 2011, 117, 736-744.	1.4	122
85	Medicinal Application of Carboranes. , 2011, , 41-70.		12
86	Development of a Crystallization Protocol for the DbeA1 Variant of Novel Haloalkane Dehalogenase from <i>Bradyrhizobium elkani</i> USDA94. <i>Crystal Growth and Design</i> , 2011, 11, 516-519.	3.0	3
87	Structure of the mouse galectin-4 N-terminal carbohydrate-recognition domain reveals the mechanism of oligosaccharide recognition. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 204-211.	2.5	18
88	Crystallization and diffraction analysis of $\hat{1}^2$ -N-acetylhexosaminidase from <i>Aspergillus oryzae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 498-503.	0.7	6
89	Crystallization and diffraction analysis of thioredoxin reductase from <i>Streptomyces coelicolor</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 917-921.	0.7	1
90	Crystal structure and functional characterization of an immunomodulatory salivary cystatin from the soft tick <i>Ornithodoros moubata</i> . <i>Biochemical Journal</i> , 2010, 429, 103-112.	3.7	73

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91	Crystallization and preliminary crystallographic characterization of the iron-regulated outer membrane lipoprotein FrpD from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1119-1123.	0.7	5
92	Crystallization and diffraction analysis of the serpin IRS-2 from the hard tick <i>Ixodes ricinus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1453-1457.	0.7	13
93	Identification of Carbonic Anhydrase I Immunodominant Epitopes Recognized by Specific Autoantibodies Which Indicate an Improved Prognosis in Patients with Malignancy after Autologous Stem Cell Transplantation. <i>Journal of Proteome Research</i> , 2010, 9, 5171-5179.	3.7	12
94	Toward the Crystallization of Photosystem II Core Complex from <i>Pisum sativum</i> L.. <i>Crystal Growth and Design</i> , 2010, 10, 3391-3396.	3.0	1
95	Molecular Characterization of Clinical Isolates of Human Immunodeficiency Virus Resistant to the Protease Inhibitor Darunavir. <i>Journal of Virology</i> , 2009, 83, 8810-8818.	3.4	43
96	Crystallization and preliminary X-ray analysis of a novel haloalkane dehalogenase DbeA from <i>Bradyrhizobium elkanii</i> USDA94. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 353-356.	0.7	13
97	The crystal structure of the secreted aspartic protease 1 from <i>Candida parapsilosis</i> in complex with pepstatin A. <i>Journal of Structural Biology</i> , 2009, 167, 145-152.	2.8	19
98	Current and Novel Inhibitors of HIV Protease. <i>Viruses</i> , 2009, 1, 1209-1239.	3.3	102
99	Design of HIV Protease Inhibitors Based on Inorganic Polyhedral Metallacarboranes. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 7132-7141.	6.4	132
100	Structural analysis of a novel type of haloalkane dehalogenase DbeA and mutant DbeA1. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s136-s137.	0.3	1
101	Crystal structure and putative function of small Toprim domain-containing protein from <i>Bacillus stearothermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 311-319.	2.6	23
102	Stabilization of antibody structure upon association to a human carbonic anhydrase IX epitope studied by X-ray crystallography, microcalorimetry, and molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1275-1287.	2.6	27
103	Crystallization and preliminary X-ray diffraction analysis of mouse galectin-4 N-terminal carbohydrate recognition domain in complex with lactose. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 665-667.	0.7	2
104	Crystal structures of the effector-binding domain of repressor Central glycolytic gene Regulator from <i>Bacillus subtilis</i> reveal ligand-induced structural changes upon binding of several glycolytic intermediates. <i>Molecular Microbiology</i> , 2008, 69, 895-910.	2.5	28
105	Potent inhibition of drug-resistant HIV protease variants by monoclonal antibodies. <i>Antiviral Research</i> , 2008, 78, 275-277.	4.1	7
106	Enzymatic and structural analysis of the I47A mutation contributing to the reduced susceptibility to HIV protease inhibitor lopinavir. <i>Protein Science</i> , 2008, 17, 1555-1564.	7.6	24
107	Inorganic Polyhedral Metallacarborane Inhibitors of HIV Protease: A New Approach to Overcoming Antiviral Resistance. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 4839-4843.	6.4	90
108	Ninety-Nine Is Not Enough: Molecular Characterization of Inhibitor-Resistant Human Immunodeficiency Virus Type 1 Protease Mutants with Insertions in the Flap Region. <i>Journal of Virology</i> , 2008, 82, 5869-5878.	3.4	39

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109	Molecular Analysis of the HIV-1 Resistance Development: Enzymatic Activities, Crystal Structures, and Thermodynamics of Nelfinavir-resistant HIV Protease Mutants. <i>Journal of Molecular Biology</i> , 2007, 374, 1005-1016.	4.2	74
110	The crystal structure of the effector-binding domain of the trehalose repressor TreR from <i>Bacillus subtilis</i> 168 reveals a unique quaternary assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 679-682.	2.6	12
111	New techniques for membrane protein crystallization tested on photosystem II core complex of <i>Pisum sativum</i> . <i>Photosynthesis Research</i> , 2007, 90, 255-259.	2.9	14
112	Regular arrangement of periodates bound to lysozyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1181-1189.	2.5	1
113	From nonpeptide toward noncarbon protease inhibitors: Metallacarboranes as specific and potent inhibitors of HIV protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15394-15399.	7.1	279
114	Crystal structure of a cross-reaction complex between an anti-HIV-1 protease antibody and an HIV-2 protease peptide. <i>Journal of Structural Biology</i> , 2005, 149, 332-337.	2.8	11
115	Inhibitor binding at the protein interface in crystals of a HIV-1 protease complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1943-1948.	2.5	18
116	A Phenylnorstatine Inhibitor Binding to HIV-1 Protease: Geometry, Protonation, and Subsite Pocket Interactions Analyzed at Atomic Resolution. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 2030-2036.	6.4	22
117	Structure of a single-chain Fv fragment of an antibody that inhibits the HIV-1 and HIV-2 proteases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 955-957.	2.5	2
118	Inhibition of HIV protease by monoclonal antibodies. <i>Journal of Molecular Recognition</i> , 2002, 15, 272-276.	2.1	7
119	Structural Basis of HIV-1 and HIV-2 Protease Inhibition by a Monoclonal Antibody. <i>Structure</i> , 2001, 9, 887-895.	3.3	25
120	Link between a novel human gammaD-crystallin allele and a unique cataract phenotype explained by protein crystallography. <i>Human Molecular Genetics</i> , 2000, 9, 1779-1786.	2.9	133
121	Inhibition of the HIV-1 and HIV-2 proteases by a monoclonal antibody. <i>Protein Science</i> , 1999, 8, 2686-2696.	7.6	16