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 g-index
125 all docs	125 docs citations	125 times ranked	3466 citing authors

#	Article	IF	Citations
1	From nonpeptide toward noncarbon protease inhibitors: Metallacarboranes as specific and potent inhibitors of HIV protease. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15394-15399.	7.1	279
2	Link between a novel human gammaD-crystallin allele and a unique cataract phenotype explained by protein crystallography. Human Molecular Genetics, 2000, 9, 1779-1786.	2.9	133
3	Design of HIV Protease Inhibitors Based on Inorganic Polyhedral Metallacarboranes. Journal of Medicinal Chemistry, 2009, 52, 7132-7141.	6.4	132
4	A tick salivary protein targets cathepsin G and chymase and inhibits host inflammation and platelet aggregation. Blood, 2011, 117, 736-744.	1.4	122
5	Engineering Enzyme Stability and Resistance to an Organic Cosolvent by Modification of Residues in the Access Tunnel. Angewandte Chemie - International Edition, 2013, 52, 1959-1963.	13.8	113
6	Current and Novel Inhibitors of HIV Protease. Viruses, 2009, 1, 1209-1239.	3.3	102
7	Carboraneâ€Based Carbonic Anhydrase Inhibitors. Angewandte Chemie - International Edition, 2013, 52, 13760-13763.	13.8	93
8	Inorganic Polyhedral Metallacarborane Inhibitors of HIV Protease: A New Approach to Overcoming Antiviral Resistance. Journal of Medicinal Chemistry, 2008, 51, 4839-4843.	6.4	90
9	Engineering a de Novo Transport Tunnel. ACS Catalysis, 2016, 6, 7597-7610.	11.2	84
10	Molecular Analysis of the HIV-1 Resistance Development: Enzymatic Activities, Crystal Structures, and Thermodynamics of Nelfinavir-resistant HIV Protease Mutants. Journal of Molecular Biology, 2007, 374, 1005-1016.	4.2	74
11	Crystal structure and functional characterization of an immunomodulatory salivary cystatin from the soft tick Ornithodoros moubata. Biochemical Journal, 2010, 429, 103-112.	3.7	73
12	Structural Basis for Inhibition of Cathepsin B Drug Target from the Human Blood Fluke, Schistosoma mansoni. Journal of Biological Chemistry, 2011, 286, 35770-35781.	3.4	60
13	Structure-Aided Design of Novel Inhibitors of HIV Protease Based on a Benzodiazepine Scaffold. Journal of Medicinal Chemistry, 2012, 55, 10130-10135.	6.4	53
14	Multiple cellular proteins interact with LEDGF/p75 through a conserved unstructured consensus motif. Nature Communications, 2015, 6, 7968.	12.8	53
15	Metallacarborane Sulfamides: Unconventional, Specific, and Highly Selective Inhibitors of Carbonic Anhydrase IX. Journal of Medicinal Chemistry, 2019, 62, 9560-9575.	6.4	51
16	Thermodynamic and structural analysis of <scp>HIV</scp> protease resistance to darunavirÂâ€“Âanalysis of heavily mutated patientâ€derived <scp>HIV</scp>â€1 proteases. FEBS Journal, 2014, 281, 1834-1847.	4.7	48
17	QM/MM Calculations Reveal the Different Nature of the Interaction of Two Carborane-Based Sulfamide Inhibitors of Human Carbonic Anhydrase II. Journal of Physical Chemistry B, 2013, 117, 16096-16104.	2.6	47
18	Molecular Characterization of Clinical Isolates of Human Immunodeficiency Virus Resistant to the Protease Inhibitor Darunavir. Journal of Virology, 2009, 83, 8810-8818.	3.4	43

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19	Validation and Structural Characterization of the LEDGF/p75â€“MLL Interface as a New Target for the Treatment of MLL-Dependent Leukemia. Cancer Research, 2014, 74, 5139-5151.	0.9	41
20	Mutations in HIV-1gagandpolCompensate for the Loss of Viral Fitness Caused by a Highly Mutated Protease. Antimicrobial Agents and Chemotherapy, 2012, 56, 4320-4330.	3.2	40
21	Ninety-Nine Is Not Enough: Molecular Characterization of Inhibitor-Resistant Human Immunodeficiency Virus Type 1 Protease Mutants with Insertions in the Flap Region. Journal of Virology, 2008, 82, 5869-5878.	3.4	39
22	Balancing the Stabilityâ€“Activity Tradeâ€Off by Fineâ€Tuning Dehalogenase Access Tunnels. ChemCatChem, 2015, 7, 648-659.	3.7	39
23	Structural Basis for the Interaction Between Carbonic Anhydrase and 1,2,3,4-tetrahydroisoquinolin-2-ylsulfonamides. Journal of Medicinal Chemistry, 2011, 54, 2522-2526.	6.4	36
24	Activation Route of the Schistosoma mansoni Cathepsin B1 Drug Target: Structural Map with a Glycosaminoglycan Switch. Structure, 2014, 22, 1786-1798.	3.3	34
25	The structure and function of Iristatin, a novel immunosuppressive tick salivary cystatin. Cellular and Molecular Life Sciences, 2019, 76, 2003-2013.	5.4	33
26	Ranking Power of the SQM/COSMO Scoring Function on Carbonic Anhydraseâ€…IIâ€“Inhibitor Complexes. ChemPhysChem, 2018, 19, 873-879.	2.1	29
27	Crystal structures of the effectorâ€binding domain of repressor Central glycolytic gene Regulator from Bacillus subtilis reveal ligandâ€induced structural changes upon binding of several glycolytic intermediates. Molecular Microbiology, 2008, 69, 895-910.	2.5	28
28	Stabilization of antibody structure upon association to a human carbonic anhydrase IX epitope studied by Xâ€ray crystallography, microcalorimetry, and molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1275-1287.	2.6	27
29	Relapsed acute lymphoblastic leukemia-specific mutations in NT5C2 cluster into hotspots driving intersubunit stimulation. Leukemia, 2018, 32, 1393-1403.	7.2	27
30	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
31	Structural Basis for Inhibition of Mycobacterial and Human Adenosine Kinase by 7-Substituted 7-(Het)aryl-7-deazaadenine Ribonucleosides. Journal of Medicinal Chemistry, 2014, 57, 8268-8279.	6.4	26
32	Structural Basis of HIV-1 and HIV-2 Protease Inhibition by a Monoclonal Antibody. Structure, 2001, 9, 887-895.	3.3	25
33	Triggering HIV polyprotein processing by light using rapid photodegradation of a tight-binding protease inhibitor. Nature Communications, 2015, 6, 6461.	12.8	25
34	Sulfonamido carboranes as highly selective inhibitors of cancer-specific carbonic anhydrase IX. European Journal of Medicinal Chemistry, 2020, 200, 112460.	5.5	25
35	Enzymatic and structural analysis of the I47A mutation contributing to the reduced susceptibility to HIV protease inhibitor lopinavir. Protein Science, 2008, 17, 1555-1564.	7.6	24
36	Synthesis, Structureâ€“Activity Relationship Studies, and X-ray Crystallographic Analysis of Arylsulfonamides as Potent Carbonic Anhydrase Inhibitors. Journal of Medicinal Chemistry, 2012, 55, 3891-3899.	6.4	24

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37	Carbonic anhydrase inhibitors: Design, synthesis and structural characterization of new heteroaryl-N-carbonylbenzenesulfonamides targeting druggable human carbonic anhydrase isoforms. European Journal of Medicinal Chemistry, 2015, 102, 223-232.	5.5	24
38	Crystal structure and putative function of small Toprim domainâ€¢containing protein from Bacillus stearothermophilus. Proteins: Structure, Function and Bioinformatics, 2008, 70, 311-319.	2.6	23
39	A Phenylnorstatine Inhibitor Binding to HIV-1 Protease:Â Geometry, Protonation, and Subsiteâ^'Pocket Interactions Analyzed at Atomic Resolution. Journal of Medicinal Chemistry, 2004, 47, 2030-2036.	6.4	22
40	Capturing a dynamically interacting inhibitor by paramagnetic NMR spectroscopy. Physical Chemistry Chemical Physics, 2019, 21, 5661-5673.	2.8	21
41	Structural and functional analysis of a novel haloalkane dehalogenase with two halide-binding sites. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1884-1897.	2.5	20
42	The crystal structure of the secreted aspartic protease 1 from Candida parapsilosis in complex with pepstatin A. Journal of Structural Biology, 2009, 167, 145-152.	2.8	19
43	Inhibitors of CA IX Enzyme Based on Polyhedral Boron Compounds. ChemBioChem, 2021, 22, 2741-2761.	2.6	19
44	Inhibitor binding at the protein interface in crystals of a HIV-1 protease complex. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1943-1948.	2.5	18
45	Structure of the mouse galectin-4 N-terminal carbohydrate-recognition domain reveals the mechanism of oligosaccharide recognition. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 204-211.	2.5	18
46	Carborane-Based Carbonic Anhydrase Inhibitors: Insight into CAII/CAIX Specificity from a High-Resolution Crystal Structure, Modeling, and Quantum Chemical Calculations. BioMed Research International, 2014, 2014, 1-9.	1.9	18
47	N-Glycosylation can selectively block or foster different receptorâ€“ligand binding modes. Scientific Reports, 2021, 11, 5239.	3.3	18
48	Crystal structure of native Î±-<scp>L</scp>-rhamnosidase from Aspergillus terreus. Acta Crystallographica Section D: Structural Biology, 2018, 74, 1078-1084.	2.3	17
49	Kinetic, Thermodynamic, and Structural Analysis of Drug Resistance Mutations in Neuraminidase from the 2009 Pandemic Influenza Virus. Viruses, 2018, 10, 339.	3.3	17
50	Inhibition of the HIVâ€1 and HIVâ€2 proteases by a monoclonal antibody. Protein Science, 1999, 8, 2686-2696.	7.6	16
51	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
52	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
53	Rutinosidase from Aspergillus niger: crystal structure and insight into the enzymatic activity. FEBS Journal, 2020, 287, 3315-3327.	4.7	15
54	New techniques for membrane protein crystallization tested on photosystem II core complex of PisumÂsativum. Photosynthesis Research, 2007, 90, 255-259.	2.9	14

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55	Feasibility and constraints of particle targeting using the antigenâ€“antibody interaction. Nanoscale, 2013, 5, 11490.	5.6	14
56	Re-emerging Aspartic Protease Targets: Examining Cryptococcus neoformans Major Aspartyl Peptidase 1 as a Target for Antifungal Drug Discovery. Journal of Medicinal Chemistry, 2021, 64, 6706-6719.	6.4	14
57	3,5,7-Substituted Pyrazolo[4,3-d]Pyrimidine Inhibitors of Cyclin-Dependent Kinases and Cyclin K Degraders. Journal of Medicinal Chemistry, 2022, 65, 8881-8896.	6.4	14
58	Crystallization and preliminary X-ray analysis of a novel haloalkane dehalogenase DbeA fromBradyrhizobium elkaniUSDA94. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 353-356.	0.7	13
59	Crystallization and diffraction analysis of the serpin IRS-2 from the hard tickIxodes ricinus. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1453-1457.	0.7	13
60	Molecular mechanism for the action of the anti-CD44 monoclonal antibody MEM-85. Journal of Structural Biology, 2015, 191, 214-223.	2.8	13
61	The crystal structure of the effectorâ€binding domain of the trehalose repressor TreR from Bacillus subtilis 168 reveals a unique quarternary assembly. Proteins: Structure, Function and Bioinformatics, 2007, 69, 679-682.	2.6	12
62	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. Journal of Proteome Research, 2010, 9, 5171-5179.	3.7	12
63	Medicinal Application ofÂCarboranes. , 2011, , 41-70.		12
64	Crystal structure of native Î²â€Nâ€acetylhexosaminidase isolated from AspergillusÂoryzae sheds light onto its substrate specificity, high stability, and regulation by propeptide. FEBS Journal, 2018, 285, 580-598.	4.7	12
65	Crystal structure of a cross-reaction complex between an anti-HIV-1 protease antibody and an HIV-2 protease peptide. Journal of Structural Biology, 2005, 149, 332-337.	2.8	11
66	Structure of the effector-binding domain of the arabinose repressor AraR fromBacillus subtilis. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 176-185.	2.5	11
67	Cobalt Bis(dicarbollide) Alkylsulfonamides: Potent and Highly Selective Inhibitors of Tumor Specific Carbonic Anhydrase IX. ChemPlusChem, 2021, 86, 352-363.	2.8	11
68	Structural basis of the interaction between the putative adhesion-involved and iron-regulated FrpD and FrpC proteins of Neisseria meningitidis. Scientific Reports, 2017, 7, 40408.	3.3	10
69	Inhibitorâ€“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
70	Mialostatin, a Novel Midgut Cystatin from Ixodes ricinus Ticks: Crystal Structure and Regulation of Host Blood Digestion. International Journal of Molecular Sciences, 2021, 22, 5371.	4.1	10
71	3H-Pyrazolo[4,3-f]quinoline-Based Kinase Inhibitors Inhibit the Proliferation of Acute Myeloid Leukemia Cells In Vivo. Journal of Medicinal Chemistry, 2021, 64, 10981-10996.	6.4	10
72	Structure of the effectorâ€binding domain of deoxyribonucleoside regulator DeoR from <scp>B</scp>acillusÂsubtilis. FEBS Journal, 2014, 281, 4280-4292.	4.7	9

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73	GS-8374, a Prototype Phosphonate-Containing Inhibitor of HIV-1 Protease, Effectively Inhibits Protease Mutants with Amino Acid Insertions. Journal of Virology, 2014, 88, 3586-3590.	3.4	9
74	Atomic resolution crystal structure of Sapp2p, a secreted aspartic protease fromCandida parapsilosis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2494-2504.	2.5	9
75	Kinetic, thermodynamic and structural analysis of tamiphosphor binding to neuraminidase of H1N1 (2009) pandemic influenza. European Journal of Medicinal Chemistry, 2016, 121, 100-109.	5.5	9
76	Oligomeric interface modulation causes misregulation of purine 5Â´-nucleotidase in relapsed leukemia. BMC Biology, 2016, 14, 91.	3.8	9
77	Druggable Hot Spots in the Schistosomiasis Cathepsin B1 Target Identified by Functional and Binding Mode Analysis of Potent Vinyl Sulfone Inhibitors. ACS Infectious Diseases, 2021, 7, 1077-1088.	3.8	9
78	Azanitrile Inhibitors of the SmCB1 Protease Target Are Lethal to Schistosoma mansoni: Structural and Mechanistic Insights into Chemotype Reactivity. ACS Infectious Diseases, 2021, 7, 189-201.	3.8	9
79	The crystal structure of protease Sapp1p from Candida parapsilosis in complex with the HIV protease inhibitor ritonavir. Journal of Enzyme Inhibition and Medicinal Chemistry, 2012, 27, 160-165.	5.2	8
80	Crystallographic analysis of new psychrophilic haloalkane dehalogenases: DpcA fromPsychrobacter cryohalolentisK5 and DmxA fromMarinobactersp. ELB17. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 683-688.	0.7	8
81	The structural basis for the selectivity of sulfonamido dicarbaboranes toward cancer-associated carbonic anhydrase IX. Journal of Enzyme Inhibition and Medicinal Chemistry, 2020, 35, 1800-1810.	5.2	8
82	Inhibition of HIV protease by monoclonal antibodies. Journal of Molecular Recognition, 2002, 15, 272-276.	2.1	7
83	Potent inhibition of drug-resistant HIV protease variants by monoclonal antibodies. Antiviral Research, 2008, 78, 275-277.	4.1	7
84	Crystallization and diffraction analysis of Î²-N-acetylhexosaminidase fromAspergillus oryzae. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 498-503.	0.7	6
85	Imidazo[1,2-c]pyrimidin-5(6H)-one inhibitors of CDK2: Synthesis, kinase inhibition and co-crystal structure. European Journal of Medicinal Chemistry, 2021, 216, 113309.	5.5	6
86	Crystallization and preliminary crystallographic characterization of the iron-regulated outer membrane lipoprotein FrpD fromNeisseria meningitidis. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1119-1123.	0.7	5
87	Crystallization of the Effector-Binding Domain of Repressor DeoR from Bacillus subtilis. Crystal Growth and Design, 2013, 13, 844-848.	3.0	5
88	Differences in crystallization of two LinB variants fromSphingobium japonicumUT26. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 284-287.	0.7	5
89	Conformationally constrained nucleoside phosphonic acids â€“ potent inhibitors of human mitochondrial and cytosolic 5â€²(3â€²)-nucleotidases. Organic and Biomolecular Chemistry, 2014, 12, 7971-7982.	2.8	5
90	Structures of human cytosolic and mitochondrial nucleotidases: implications for structure-based design of selective inhibitors. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 461-470.	2.5	5

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91	DNA-linked inhibitor antibody assay (DIANA) as a new method for screening influenza neuraminidase inhibitors. Biochemical Journal, 2018, 475, 3847-3860.	3.7	5
92	Crystal structure of the cold-adapted haloalkane dehalogenase DpcA fromPsychrobacter cryohalolentisK5. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 324-331.	0.8	5
93	structural characterization of the interaction between the C-terminal domain of the influenza polymerase PA subunit and an optimized small peptide inhibitor. Antiviral Research, 2021, 185, 104971.	4.1	5
94	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
95	Direct Introduction of an Alkylsulfonamido Group on Câ€sites of Isomeric Dicarbaâ€closoâ€dodecaboranes: The Influence of Stereochemistry on Inhibitory Activity against the Cancerâ€Associated Carbonic Anhydrase IX Isoenzyme. Chemistry - A European Journal, 2020, 26, 16541-16553.	3.3	4
96	Development of a Crystallization Protocol for the DbeA1 Variant of Novel Haloalkane Dehalogenase fromBradyrhizobium elkaniUSDA94. Crystal Growth and Design, 2011, 11, 516-519.	3.0	3
97	Structural insight into DNA recognition by bacterial transcriptional regulators of the SorC/DeoR family. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1411-1424.	2.3	3
98	Structure of a single-chain Fv fragment of an antibody that inhibits the HIV-1 and HIV-2 proteases. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 955-957.	2.5	2
99	Crystallization and preliminary X-ray diffraction analysis of mouse galectin-4 N-terminal carbohydrate recognition domain in complex with lactose. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 665-667.	0.7	2
100	Backbone resonance assignments of the outer membrane lipoprotein FrpD from Neisseria meningitidis. Biomolecular NMR Assignments, 2014, 8, 53-55.	0.8	2
101	Structure-based design of a bisphosphonate 5â€²(3â€²)-deoxyribonucleotidase inhibitor. MedChemComm, 2015, 6, 1635-1638.	3.4	2
102	A novel structurally characterized haloacid dehalogenase superfamily phosphatase from Thermococcus thioreducens with diverse substrate specificity. Acta Crystallographica Section D: Structural Biology, 2019, 75, 743-752.	2.3	2
103	Identification of Novel Carbonic Anhydrase IX Inhibitors Using High-Throughput Screening of Pooled Compound Libraries by DNA-Linked Inhibitor Antibody Assay (DIANA). SLAS Discovery, 2020, 25, 1026-1037.	2.7	2
104	Structural and catalytic effects of surface loop-helix transplantation within haloalkane dehalogenase family. Computational and Structural Biotechnology Journal, 2020, 18, 1352-1362.	4.1	2
105	Cobalt Bis(dicarbollide) Alkylsulfonamides: Potent and Highly Selective Inhibitors of Tumor Specific Carbonic Anhydrase IX. ChemPlusChem, 2021, 86, 351-351.	2.8	2
106	Regular arrangement of periodates bound to lysozyme. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1181-1189.	2.5	1
107	Toward the Crystallization of Photosystem II Core Complex from Pisum sativum L.. Crystal Growth and Design, 2010, 10, 3391-3396.	3.0	1
108	Crystallization and diffraction analysis of thioredoxin reductase fromStreptomyces coelicolor. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 917-921.	0.7	1

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109	Optimization of the crystallizability of a single-chain antibody fragment. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1701-1706.	0.8	1
110	Structureâ€Based Optimization of Bisphosphonate Nucleoside Inhibitors of Human 5â€²(3â€²)â€deoxyribonucleotidases. European Journal of Organic Chemistry, 2018, 2018, 5144-5153.	2.4	1
111	Structural analysis of a novel type of haloalkane dehalogenase DbeA and mutant DbeA1. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s136-s137.	0.3	1
112	Crystal structure of the novel haloalkane dehalogenases. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1678-C1678.	0.1	1
113	Recombinant fragment of an antibody tailored for direct radioiodination. Journal of Labelled Compounds and Radiopharmaceuticals, 2012, 55, 52-56.	1.0	0
114	Structure-functional relationships of a novel haloalkane dehalogenase with two halide-binding sites. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s218-s218.	0.1	0
115	Kinetic and structural characterization of an alternatively spliced variant of human mitochondrial 5â€²(3â€²)-deoxyribonucleotidase. Journal of Enzyme Inhibition and Medicinal Chemistry, 2015, 30, 63-68.	5.2	0
116	Validation of the MLL-LEDGF/P75 interaction as a therapeutic target for mixed lineage leukemia. Experimental Hematology, 2016, 44, S69.	0.4	0
117	Crystal structure of haloalkane dehalogenase DpcA from psychrophilicPsychrobacter cryohalolentisK5. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, s605-s606.	0.3	0
118	Abstract 4492: Novel carborane based inhibitors of carbonic anhydrase IX. , 2015, , .		0
119	Structure analysis of haloalkane dehalogenase DbeA Î”Cl variant from Bradyrhizobium elkanii USDA94. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e212-e212.	0.1	0
120	Structure-assisted design of carborane inhibitors of human carbonic anhydrase IX. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e197-e197.	0.1	0
121	Structural characterization and comparison of crystallization behaviour of selected haloalkane dehalogenases. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e185-e185.	0.1	0