

Filip Van petegem

List of Publications by Year in descending order

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126
papers

4,630
citations

101543

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114465

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133
all docs

133
docs citations

133
times ranked

4738
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of phosphorylation in atrial fibrillation: a focus on mass spectrometry approaches. <i>Cardiovascular Research</i> , 2022, 118, 1205-1217.	3.8	1
2	Calcium-release channels: structure and function of IP ₃ receptors and ryanodine receptors. <i>Physiological Reviews</i> , 2022, 102, 209-268.	28.8	93
3	Cell Surface Xyloglucan Recognition and Hydrolysis by the Human Gut Commensal <i>Bacteroides uniformis</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0156621.	3.1	5
4	Cardiac ryanodine receptor N-terminal region biosensors identify novel inhibitors via FRET-based high-throughput screening. <i>Journal of Biological Chemistry</i> , 2022, 298, 101412.	3.4	2
5	Structural basis for diamide modulation of ryanodine receptor. <i>Journal of General Physiology</i> , 2022, 154, .	1.9	0
6	Multiple regions within junctin drive its interaction with calsequestrin-1 and its localization to triads in skeletal muscle. <i>Journal of Cell Science</i> , 2022, 135, .	2.0	3
7	Cryo-EM studies of ryanodine receptor disease mutant and modulation by calmodulin. <i>Biophysical Journal</i> , 2022, 121, 175a.	0.5	0
8	Structures of PKA-phospholamban complexes reveal a mechanism of familial dilated cardiomyopathy. <i>ELife</i> , 2022, 11, .	6.0	5
9	Structures of the junctophilin/voltage-gated calcium channel interface reveal hot spot for cardiomyopathy mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2120416119.	7.1	17
10	Altered cyclic nucleotide binding and pore opening in a diseased human HCN4 channel. <i>Biophysical Journal</i> , 2022, 121, 1166-1183.	0.5	1
11	Structural and electrophysiological basis for the modulation of KCNQ1 channel currents by ML277. <i>Nature Communications</i> , 2022, 13, .	12.8	15
12	It takes two to tango: Rycals and ATP snuggle up to bind ryanodine receptors. <i>Structure</i> , 2022, 30, 919-921.	3.3	0
13	Binding of calcium and magnesium to human cardiac troponin C. <i>Journal of Biological Chemistry</i> , 2021, 296, 100350.	3.4	13
14	Distinct protein architectures mediate species-specific beta-glucan binding and metabolism in the human gut microbiota. <i>Journal of Biological Chemistry</i> , 2021, 296, 100415.	3.4	17
15	Pathological conformations of disease mutant Ryanodine Receptors revealed by cryo-EM. <i>Nature Communications</i> , 2021, 12, 807.	12.8	38
16	Structural Insights into the Diamide Modulation of Ryanodine Receptor. <i>Biophysical Journal</i> , 2021, 120, 149a.	0.5	0
17	Homozygous <i>SCN1B</i> variants causing early infantile epileptic encephalopathy 52 affect voltage-gated sodium channel function. <i>Epilepsia</i> , 2021, 62, e82-e87.	5.1	9
18	Orthogonal Active-Site Labels for Mixed-Linkage endo- β -Glucanases. <i>ACS Chemical Biology</i> , 2021, 16, 1968-1984.	3.4	6

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19	Structure and function of STAC proteins: Calcium channel modulators and critical components of muscle excitation–contraction coupling. <i>Journal of Biological Chemistry</i> , 2021, 297, 100874.	3.4	18
20	Functional characterization of a cellulose synthase, CtCESA1, from the marine red alga <i>Calliarthron tuberculatum</i> (Corallinales). <i>Journal of Experimental Botany</i> , 2021, , .	4.8	4
21	Cryo-EM structures of the ABCA4 importer reveal mechanisms underlying substrate binding and Stargardt disease. <i>Nature Communications</i> , 2021, 12, 5902.	12.8	25
22	Using hiPSC–CMs to Examine Mechanisms of Catecholaminergic Polymorphic Ventricular Tachycardia. <i>Current Protocols</i> , 2021, 1, e320.	2.9	3
23	Molecular interactions between sex hormone–binding globulin and nonsteroidal ligands that enhance androgen activity. <i>Journal of Biological Chemistry</i> , 2020, 295, 1202-1211.	3.4	7
24	Interleukin-10 and Small Molecule SHIP1 Allosteric Regulators Trigger Anti-inflammatory Effects through SHIP1/STAT3 Complexes. <i>IScience</i> , 2020, 23, 101433.	4.1	20
25	Sorcin is an early marker of neurodegeneration, Ca ²⁺ dysregulation and endoplasmic reticulum stress associated to neurodegenerative diseases. <i>Cell Death and Disease</i> , 2020, 11, 861.	6.3	29
26	A multi-dimensional analysis of genotype–phenotype discordance in malignant hyperthermia susceptibility. <i>British Journal of Anaesthesia</i> , 2020, 125, 995-1001.	3.4	5
27	Biophysical Investigation of Sodium Channel Interaction with β -Subunit Variants Associated with Arrhythmias. <i>Bioelectricity</i> , 2020, 2, 269-278.	1.1	1
28	Structural basis for diamide modulation of ryanodine receptor. <i>Nature Chemical Biology</i> , 2020, 16, 1246-1254.	8.0	75
29	The arrhythmogenic N53I variant subtly changes the structure and dynamics in the calmodulin N-terminal domain, altering its interaction with the cardiac ryanodine receptor. <i>Journal of Biological Chemistry</i> , 2020, 295, 7620-7634.	3.4	21
30	A rare CACNA1H variant associated with amyotrophic lateral sclerosis causes complete loss of Cav3.2–T-type channel activity. <i>Molecular Brain</i> , 2020, 13, 33.	2.6	14
31	Multiple Sequence Variants in STAC3 Affect Interactions with CaV1.1 and Excitation-Contraction Coupling. <i>Structure</i> , 2020, 28, 922-932.e5.	3.3	17
32	Crystal Structures of Calcium-Loaded Calmodulin in Complex with C-Terminal Domains of Voltage-Gated Sodium Channels. <i>Biophysical Journal</i> , 2020, 118, 576a.	0.5	0
33	Cardiac arrest in a mother and daughter and the identification of a novel <i>RYR2</i> variant, predisposing to low penetrant catecholaminergic polymorphic ventricular tachycardia in a four-generation Canadian family. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1151.	1.2	3
34	Nanodisc technology facilitates identification of monoclonal antibodies targeting multi-pass membrane proteins. <i>Scientific Reports</i> , 2020, 10, 1130.	3.3	11
35	Arrhythmia mutations in calmodulin can disrupt cooperativity of Ca ²⁺ -binding and cause misfolding. <i>Journal of Physiology</i> , 2020, 598, 1169-1186.	2.9	26
36	Synergy between Cell Surface Glycosidases and Glycan-Binding Proteins Dictates the Utilization of Specific Beta(1,3)-Glucans by Human Gut <i>Bacteroides</i> . <i>MBio</i> , 2020, 11, .	4.1	58

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37	Cardiac ryanodine receptor distribution is dynamic and changed by auxiliary proteins and post-translational modification. <i>ELife</i> , 2020, 9, .	6.0	44
38	Molecular interactions between sex hormone-binding globulin and nonsteroidal ligands that enhance androgen activity. <i>Journal of Biological Chemistry</i> , 2020, 295, 1202-1211.	3.4	13
39	Type 8 long QT syndrome: pathogenic variants in CACNA1C-encoded Cav1.2 cluster in STAC protein binding site. <i>Europace</i> , 2019, 21, 1725-1732.	1.7	15
40	Slaying a giant: Structures of calmodulin and protein kinase a bound to the cardiac ryanodine receptor. <i>Cell Calcium</i> , 2019, 83, 102079.	2.4	5
41	Binding and structural asymmetry governs ligand sensitivity in a cyclic nucleotide-gated ion channel. <i>Journal of General Physiology</i> , 2019, 151, 1190-1212.	1.9	5
42	The Cardiac Ryanodine Receptor Phosphorylation Hotspot Embraces PKA in a Phosphorylation-Dependent Manner. <i>Molecular Cell</i> , 2019, 75, 39-52.e4.	9.7	31
43	Crystal structures of Ca ²⁺ -calmodulin bound to Na ^V C-terminal regions suggest role for EF-hand domain in binding and inactivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10763-10772.	7.1	35
44	Surface glycan-binding proteins are essential for cereal beta-glucan utilization by the human gut symbiont <i>Bacteroides ovatus</i> . <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4319-4340.	5.4	35
45	In vitro analyses of suspected arrhythmogenic thin filament variants as a cause of sudden cardiac death in infants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6969-6974.	7.1	16
46	Structural Insights into Recognition of Ryanodine Receptors by PKA. <i>Biophysical Journal</i> , 2019, 116, 153a-154a.	0.5	0
47	Reply to Pitt and Lee: Occupancies of Ca ²⁺ in complexes of calmodulin with voltage-gated sodium channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26152-26152.	7.1	0
48	Subtle Changes in the Combining Site of the Chlamydiaceae-Specific mAb S25-23 Increase the Antibody-Carbohydrate Binding Affinity by an Order of Magnitude. <i>Biochemistry</i> , 2019, 58, 714-726.	2.5	2
49	Ca ²⁺ -dependent calmodulin binding to cardiac ryanodine receptor (RyR2) calmodulin-binding domains. <i>Biochemical Journal</i> , 2019, 476, 193-209.	3.7	24
50	Cardiac hypertrophy and arrhythmia in mice induced by a mutation in ryanodine receptor 2. <i>JCI Insight</i> , 2019, 4, .	5.0	18
51	STAC proteins associate to the IQ domain of Ca ^V 1.2 and inhibit calcium-dependent inactivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1376-1381.	7.1	40
52	The voltage-gated sodium channel EF-hands form an interaction with the III-IV linker that is disturbed by disease-causing mutations. <i>Scientific Reports</i> , 2018, 8, 4483.	3.3	25
53	The clinical and genetic spectrum of catecholaminergic polymorphic ventricular tachycardia: findings from an international multicentre registry. <i>Europace</i> , 2018, 20, 541-547.	1.7	91
54	Structural Insights into the STAC Adaptor Protein and Voltage-Gated Calcium Channel Interaction. <i>Biophysical Journal</i> , 2018, 114, 40a.	0.5	0

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55	Catecholaminergic polymorphic ventricular tachycardia patients with multiple genetic variants in the PACES CPVT Registry. <i>PLoS ONE</i> , 2018, 13, e0205925.	2.5	31
56	Arrhythmia mutations in calmodulin cause conformational changes that affect interactions with the cardiac voltage-gated calcium channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10556-E10565.	7.1	36
57	Calcium Channelopathies: Structural Insights into Disorders of the Muscle Excitation- Contraction Complex. <i>Annual Review of Genetics</i> , 2018, 52, 373-396.	7.6	25
58	Ryanodine Receptor (RyR). , 2018, , 4786-4792.		0
59	Ligand binding to Ryanodine Receptors revealed through cryo-electron microscopy. <i>Cell Calcium</i> , 2017, 61, 50-52.	2.4	4
60	The Arrhythmogenic Calmodulin p.Phe142Leu Mutation Impairs C-domain Ca ²⁺ Binding but Not Calmodulin-dependent Inhibition of the Cardiac Ryanodine Receptor. <i>Journal of Biological Chemistry</i> , 2017, 292, 1385-1395.	3.4	35
61	Structural insights into binding of STAC proteins to voltage-gated calcium channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9520-E9528.	7.1	63
62	Catecholaminergic polymorphic ventricular tachycardia. <i>Current Opinion in Cardiology</i> , 2017, 32, 78-85.	1.8	19
63	Crystallographic insight into the evolutionary origins of xyloglucan endotransglycosylases and endohydrolases. <i>Plant Journal</i> , 2017, 89, 651-670.	5.7	33
64	A novel RYR2 loss-of-function mutation (I4855M) is associated with left ventricular non-compaction and atypical catecholaminergic polymorphic ventricular tachycardia. <i>Journal of Electrocardiology</i> , 2017, 50, 227-233.	0.9	47
65	CPVT-associated cardiac ryanodine receptor mutation G357S with reduced penetrance impairs Ca ²⁺ release termination and diminishes protein expression. <i>PLoS ONE</i> , 2017, 12, e0184177.	2.5	12
66	Characterization of Zebrafish Cardiac and Slow Skeletal Troponin C Paralogs by MD Simulation and AITC. <i>Biophysical Journal</i> , 2016, 111, 38-49.	0.5	16
67	How to open a Ryanodine Receptor. <i>Cell Research</i> , 2016, 26, 1073-1074.	12.0	9
68	Defining the stoichiometry of inositol 1,4,5-trisphosphate binding required to initiate Ca ²⁺ release. <i>Science Signaling</i> , 2016, 9, ra35.	3.6	140
69	Identification of Avian Corticosteroid-binding Globulin (Serpina6) Reveals the Molecular Basis of Evolutionary Adaptations in SerpinA6 Structure and Function as a Steroid-binding Protein. <i>Journal of Biological Chemistry</i> , 2016, 291, 11300-11312.	3.4	16
70	Cyclic Purine and Pyrimidine Nucleotides Bind to the HCN2 Ion Channel and Variably Promote C-Terminal Domain Interactions and Opening. <i>Structure</i> , 2016, 24, 1629-1642.	3.3	16
71	Ryanodine receptors under the magnifying lens: Insights and limitations of cryo-electron microscopy and X-ray crystallography studies. <i>Cell Calcium</i> , 2016, 59, 209-227.	2.4	52
72	Binary architecture of the Nav1.2-β2 signaling complex. <i>ELife</i> , 2016, 5, .	6.0	37

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73	The H29D Mutation Does Not Enhance Cytosolic Ca ²⁺ Activation of the Cardiac Ryanodine Receptor. PLoS ONE, 2015, 10, e0139058.	2.5	4
74	Roles of the NH ₂ -terminal Domains of Cardiac Ryanodine Receptor in Ca ²⁺ Release Activation and Termination. Journal of Biological Chemistry, 2015, 290, 7736-7746.	3.4	17
75	Crystal structures of ryanodine receptor SPRY1 and tandem-repeat domains reveal a critical FKBP12 binding determinant. Nature Communications, 2015, 6, 7947.	12.8	56
76	Paramagnetic Ligand Tagging To Identify Protein Binding Sites. Journal of the American Chemical Society, 2015, 137, 11391-11398.	13.7	34
77	Ryanodine Receptors: Allosteric Ion Channel Giants. Journal of Molecular Biology, 2015, 427, 31-53.	4.2	137
78	Deciphering the Binding of Caveolin-1 to Client Protein Endothelial Nitric-oxide Synthase (eNOS). Journal of Biological Chemistry, 2014, 289, 13273-13283.	3.4	54
79	Mapping the sevoflurane-binding sites of calmodulin. Pharmacology Research and Perspectives, 2014, 2, 5.	2.4	5
80	Lobe-Specific Calmodulin Binding to Different Ryanodine Receptor Isoforms. Biochemistry, 2014, 53, 932-946.	2.5	43
81	Crystal structures of wild type and disease mutant forms of the ryanodine receptor SPRY2 domain. Nature Communications, 2014, 5, 5397.	12.8	58
82	The Cardiac Ryanodine Receptor N-Terminal Region Contains an Anion Binding Site that Is Targeted by Disease Mutations. Structure, 2013, 21, 1440-1449.	3.3	51
83	Talin Autoinhibition Is Required for Morphogenesis. Current Biology, 2013, 23, 1825-1833.	3.9	43
84	Conformational Dynamics inside Amino-Terminal Disease Hotspot of Ryanodine Receptor. Structure, 2013, 21, 2051-2060.	3.3	25
85	The General Anaesthetic Binding Site of Calmodulin Disrupts Ryanodine Peptide Binding. Biophysical Journal, 2013, 104, 445a.	0.5	1
86	Type 2 Ryanodine Receptor Domain A Contains a Unique and Dynamic α -Helix That Transitions to a β -Strand in a Mutant Linked with a Heritable Cardiomyopathy. Journal of Molecular Biology, 2013, 425, 4034-4046.	4.2	38
87	Disease mutations in the ryanodine receptor N-terminal region couple to a mobile intersubunit interface. Nature Communications, 2013, 4, 1506.	12.8	74
88	The CPVT-associated RyR2 mutation G230C enhances store overload-induced Ca ²⁺ release and destabilizes the N-terminal domains. Biochemical Journal, 2013, 454, 123-131.	3.7	25
89	Crystallographic insights into sodium-channel modulation by the β 4 subunit. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E5016-24.	7.1	79
90	Structures and allosteric motions of Ryanodine Receptor Domains. FASEB Journal, 2013, 27, 590.6.	0.5	0

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91	Crystallographic basis for calcium regulation of sodium channels. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3558-3563.	7.1	128
92	Seeing the Forest through the Trees: towards a Unified View on Physiological Calcium Regulation of Voltage-Gated Sodium Channels. Biophysical Journal, 2012, 103, 2243-2251.	0.5	52
93	Conformational Dynamics Inside Amino-Terminal Disease Hotspot of Ryanodine Receptor. Biophysical Journal, 2012, 102, 304a.	0.5	1
94	Ryanodine Receptors: Structure and Function. Journal of Biological Chemistry, 2012, 287, 31624-31632.	3.4	205
95	Energetics of Cyclic AMP Binding to HCN Channel C Terminus Reveal Negative Cooperativity. Journal of Biological Chemistry, 2012, 287, 600-606.	3.4	39
96	The Ryanodine Receptor N-Terminal Disease Hot Spot Intersubunit Interface is Disrupted by Channel Opening and Affected by Disease Mutations Acting via Long-Range Structural Changes. Biophysical Journal, 2012, 102, 304a.	0.5	0
97	Molecular and structural characterization of the SH3 domain of AHI-1 in regulation of cellular resistance of BCR-ABL+ chronic myeloid leukemia cells to tyrosine kinase inhibitors. Proteomics, 2012, 12, 2094-2106.	2.2	8
98	Disease Mutations in the Ryanodine Receptor Central Region: Crystal Structures of a Phosphorylation Hot Spot Domain. Structure, 2012, 20, 1201-1211.	3.3	97
99	The Deletion of Exon 3 in the Cardiac Ryanodine Receptor Is Rescued by β Strand Switching. Structure, 2011, 19, 790-798.	3.3	47
100	The structural biology of ryanodine receptors. Science China Life Sciences, 2011, 54, 712-724.	4.9	39
101	Common allosteric mechanisms between ryanodine and inositol-1,4,5-trisphosphate receptors. Channels, 2011, 5, 120-123.	2.8	14
102	Molecular and Structural Characterization of the SH3 Domain of AHI-1 in Regulation of Cellular Resistance of BCR-ABL+ Chronic Myeloid Leukemia Cells to Tyrosine Kinase Inhibitors. Blood, 2011, 118, 966-966.	1.4	0
103	Folding properties of the hepatitis B core as a carrier protein for vaccination research. Amino Acids, 2010, 38, 1617-1626.	2.7	14
104	Multiple C-terminal tail Ca ²⁺ /CaMs regulate CaV1.2 function but do not mediate channel dimerization. EMBO Journal, 2010, 29, 3924-3938.	7.8	66
105	Multiple C-terminal tail Ca ²⁺ /CaMs regulate CaV1.2 function but do not mediate channel dimerization. EMBO Journal, 2010, 29, 4062-4062.	7.8	1
106	The amino-terminal disease hotspot of ryanodine receptors forms a cytoplasmic vestibule. Nature, 2010, 468, 585-588.	27.8	190
107	AnhE, a Metallochaperone Involved in the Maturation of a Cobalt-dependent Nitrile Hydratase. Journal of Biological Chemistry, 2010, 285, 25126-25133.	3.4	30
108	A Double Tyrosine Motif in the Cardiac Sodium Channel Domain III-IV Linker Couples Calcium-dependent Calmodulin Binding to Inactivation Gating. Journal of Biological Chemistry, 2009, 284, 33265-33274.	3.4	49

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109	Crystal Structures of the N-Terminal Domains of Cardiac and Skeletal Muscle Ryanodine Receptors: Insights into Disease Mutations. <i>Structure</i> , 2009, 17, 1505-1514.	3.3	109
110	Crystal Structure of the Talin Integrin Binding Domain 2. <i>Journal of Molecular Biology</i> , 2009, 387, 787-793.	4.2	6
111	Alanine-Scanning Mutagenesis Defines a Conserved Energetic Hotspot in the CaV1 AID-CaV2 Interaction Site that Is Critical for Channel Modulation. <i>Structure</i> , 2008, 16, 280-294.	3.3	73
112	Structures of CaV2 Ca2+/CaM-IQ Domain Complexes Reveal Binding Modes that Underlie Calcium-Dependent Inactivation and Facilitation. <i>Structure</i> , 2008, 16, 1455-1467.	3.3	96
113	Crystal structure of <i>Sulfolobus acidocaldarius</i> aspartate carbamoyltransferase in complex with its allosteric activator CTP. <i>Biochemical and Biophysical Research Communications</i> , 2008, 372, 40-44.	2.1	3
114	Understanding Nicotinamide Dinucleotide Cofactor and Substrate Specificity in Class I Flavoprotein Disulfide Oxidoreductases: Crystallographic Analysis of a Glutathione Amide Reductase. <i>Journal of Molecular Biology</i> , 2007, 374, 883-889.	4.2	9
115	The structural biology of voltage-gated calcium channel function and regulation. <i>Biochemical Society Transactions</i> , 2006, 34, 887-893.	3.4	39
116	Insights into voltage-gated calcium channel regulation from the structure of the CaV1.2 IQ domain-Ca2+/calmodulin complex. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 1108-1115.	8.2	221
117	Structure of a complex between a voltage-gated calcium channel β_2 -subunit and an β_1 -subunit domain. <i>Nature</i> , 2004, 429, 671-675.	27.8	402
118	Protein Dynamics in the Region of the Sixth Ligand Methionine Revealed by Studies of Imidazole Binding To <i>Rhodobacter capsulatus</i> Cytochrome c2 Hinge Mutants,. <i>Biochemistry</i> , 2004, 43, 7717-7724.	2.5	19
119	Crystal Structure of T State Aspartate Carbamoyltransferase of the Hyperthermophilic Archaeon <i>Sulfolobus acidocaldarius</i> . <i>Journal of Molecular Biology</i> , 2004, 339, 887-900.	4.2	11
120	Crystal structures of a psychrophilic metalloprotease reveal new insights into catalysis by cold-adapted proteases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 636-647.	2.6	106
121	The Structure of a Cold-adapted Family 8 Xylanase at 1.3 Å... Resolution. <i>Journal of Biological Chemistry</i> , 2003, 278, 7531-7539.	3.4	124
122	Atomic resolution structure of the major endoglucanase from <i>Thermoascus aurantiacus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2002, 296, 161-166.	2.1	22
123	Crystallization and preliminary X-ray crystallographic analysis of glutathione amide reductase from <i>Chromatium gracile</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 339-340.	2.5	2
124	Crystallization and preliminary X-ray analysis of a xylanase from the psychrophile <i>Pseudoalteromonas haloplanktis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1494-1496.	2.5	14
125	<i>Trichoderma reesei</i> β -1,2-mannosidase: structural basis for the cleavage of four consecutive mannose residues 1 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2001, 312, 157-165.	4.2	34
126	A DNA ligase from the psychrophile <i>Pseudoalteromonas haloplanktis</i> gives insights into the adaptation of proteins to low temperatures. <i>FEBS Journal</i> , 2000, 267, 3502-3512.	0.2	63