

Srikrishna Subramanian

List of Publications by Year in descending order

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113
papers

2,945
citations

236833

25
h-index

197736

49
g-index

117
all docs

117
docs citations

117
times ranked

4482
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural classification of zinc fingers: SURVEY AND SUMMARY. <i>Nucleic Acids Research</i> , 2003, 31, 532-550.	6.5	732
2	Exploration of Uncharted Regions of the Protein Universe. <i>PLoS Biology</i> , 2009, 7, e1000205.	2.6	123
3	CASP5 assessment of fold recognition target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 395-409.	1.5	91
4	Structural Classification of Small, Disulfide-rich Protein Domains. <i>Journal of Molecular Biology</i> , 2006, 359, 215-237.	2.0	85
5	Complete genome sequence and comparative genomics of the probiotic yeast <i>Saccharomyces boulardii</i> . <i>Scientific Reports</i> , 2017, 7, 371.	1.6	85
6	Crystal structures of two novel dye-decolorizing peroxidases reveal a β -barrel fold with a conserved heme-binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 223-233.	1.5	81
7	Structural drift: a possible path to protein fold change. <i>Bioinformatics</i> , 2005, 21, 1308-1310.	1.8	75
8	Structural Basis of Murein Peptide Specificity of a β -D-Glutamyl-L-Diamino Acid Endopeptidase. <i>Structure</i> , 2009, 17, 303-313.	1.6	73
9	Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 234-243.	1.5	67
10	Structure of the β -glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L-Ala- β -D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364.	0.7	64
11	Complete Genome of the Starch-Degrading Myxobacteria <i>Sandaracinus amylolyticus</i> DSM 53668. <i>Genome Biology and Evolution</i> , 2016, 8, 2520-2529.	1.1	63
12	PALSSE: a program to delineate linear secondary structural elements from protein structures. <i>BMC Bioinformatics</i> , 2005, 6, 202.	1.2	56
13	Unravelling the Complete Genome of <i>Archangium gephyra</i> DSM 2261T and Evolutionary Insights into Myxobacterial Chitinases. <i>Genome Biology and Evolution</i> , 2017, 9, 1304-1311.	1.1	43
14	Three-dimensional Structure of <i>Physalis Mottle Virus</i> : Implications for the Viral Assembly. <i>Journal of Molecular Biology</i> , 1999, 289, 919-934.	2.0	42
15	4SCOPmap: automated assignment of protein structures to evolutionary superfamilies. <i>BMC Bioinformatics</i> , 2004, 5, 197.	1.2	42
16	Structurally Analogous Proteins Do Exist!. <i>Structure</i> , 2004, 12, 1125-1127.	1.6	41
17	Crystal Structure of the First Eubacterial Mre11 Nuclease Reveals Novel Features that May Discriminate Substrates During DNA Repair. <i>Journal of Molecular Biology</i> , 2010, 397, 647-663.	2.0	41
18	Composite genome sequence of <i>Bacillus clausii</i> , a probiotic commercially available as Enterogermina [®] , and insights into its probiotic properties. <i>BMC Microbiology</i> , 2019, 19, 307.	1.3	41

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19	Complete Genomes of <i>Bacillus coagulans</i> S-lac and <i>Bacillus subtilis</i> TO-A JPC, Two Phylogenetically Distinct Probiotics. <i>PLoS ONE</i> , 2016, 11, e0156745.	1.1	40
20	Genome Sequence, Comparative Analysis, and Evolutionary Insights into Chitinases of Entomopathogenic Fungus <i>Hirsutella thompsonii</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 916-930.	1.1	39
21	TOPSAN: use of a collaborative environment for annotating, analyzing and disseminating data on JCSC and PSI structures. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1143-1147.	0.7	33
22	Complete Genome Sequence and Comparative Genomics of a Novel Myxobacterium <i>Myxococcus hansupus</i> . <i>PLoS ONE</i> , 2016, 11, e0148593.	1.1	33
23	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. <i>Journal of Molecular Biology</i> , 2010, 396, 31-46.	2.0	32
24	Structure of a membrane-attack complex/perforin (MACPF) family protein from the human gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1297-1305.	0.7	30
25	Crystal structure of acireductone dioxygenase (ARD) from <i>Mus musculus</i> at 2.06 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 808-813.	1.5	28
26	A tale of two ferredoxins: sequence similarity and structural differences. <i>BMC Structural Biology</i> , 2006, 6, 8.	2.3	26
27	Prevalence of the F-type lectin domain. <i>Glycobiology</i> , 2015, 25, 888-901.	1.3	25
28	Identification of a Discrete Intermediate in the Assembly/Disassembly of <i>Physalis Mottle Tymovirus</i> through Mutational Analysis. <i>Journal of Molecular Biology</i> , 1999, 289, 905-918.	2.0	24
29	Metagenomics analysis reveals features unique to Indian distal gut microbiota. <i>PLoS ONE</i> , 2020, 15, e0231197.	1.1	24
30	Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. <i>Journal of Biological Chemistry</i> , 2009, 284, 25268-25279.	1.6	23
31	Crystal structure of the Fic (Filamentation induced by cAMP) family protein SO4266 (gi 24375750) from <i>Shewanella oneidensis</i> MRâ€1 at 1.6 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 264-271.	1.5	23
32	Structural studies on the empty capsids of <i>physalis mottle virus 1</i> Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 307, 1035-1047.	2.0	22
33	Evolutionary convergence and divergence in archaeal chromosomal proteins and Chromo-like domains from bacteria and eukaryotes. <i>Scientific Reports</i> , 2018, 8, 6196.	1.6	22
34	Identification of novel small RNAs in <i>Burkholderia cenocepacia</i> KC-01 expressed under iron limitation and oxidative stress conditions. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1924-1936.	0.7	22
35	The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1160-1166.	0.7	20
36	Structure of a tryptophanyl-tRNA synthetase containing an iron-sulfur cluster. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1326-1334.	0.7	19

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37	Crystal structure of a novel Smâ€like protein of putative cyanophage origin at 2.60 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 296-307.	1.5	18
38	Structure of the first representative of Pfam family PF09410 (DUF2006) reveals a structural signature of the calycin superfamily that suggests a role in lipid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1153-1159.	0.7	18
39	Gleaning evolutionary insights from the genome sequence of a probiotic yeast <i>Saccharomyces boulardii</i> . <i>Gut Pathogens</i> , 2013, 5, 30.	1.6	18
40	Comparative Genomics of Myxobacterial Chemosensory Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	18
41	Structure of an essential bacterial protein YeaZ (TM0874) from <i>Thermotoga maritima</i> at 2.5 Å... resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1230-1236.	0.7	17
42	The bridge-region of the Ku superfamily is an atypical zinc ribbon domain. <i>Journal of Structural Biology</i> , 2010, 172, 294-299.	1.3	17
43	Classification of the treble clef zinc finger: noteworthy lessons for structure and function evolution. <i>Scientific Reports</i> , 2016, 6, 32070.	1.6	17
44	Draft Genome Sequence of the Nitrophenol-Degrading Actinomycete <i>Rhodococcus imtechensis</i> RKJ300. <i>Journal of Bacteriology</i> , 2012, 194, 3543-3543.	1.0	16
45	Genome sequencing and annotation of <i>Acinetobacter haemolyticus</i> strain MTCC 9819T. <i>Genomics Data</i> , 2014, 2, 10-12.	1.3	16
46	Crystal structure of a single-stranded DNA-binding protein (TM0604) from <i>Thermotoga maritima</i> at 2.60 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 256-260.	1.5	15
47	Examination into the taxonomic position of <i>Bacillus thermotolerans</i> Yang et al., 2013, proposal for its reclassification into a new genus and species <i>Quasibacillus thermotolerans</i> gen. nov., comb. nov. and reclassification of <i>B. encimensis</i> Dastager et al., 2015 as a later heterotypic synonym of <i>B. badius</i> . <i>Systematic and Applied Microbiology</i> , 2017, 40, 411-422.	1.2	14
48	Crystal structure of homoserine O-succinyltransferase from <i>Bacillus cereus</i> at 2.4 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 999-1005.	1.5	13
49	Crystal Structure of Histidine Phosphotransfer Protein ShpA, an Essential Regulator of Stalk Biogenesis in <i>Caulobacter crescentus</i> . <i>Journal of Molecular Biology</i> , 2009, 390, 686-698.	2.0	13
50	Ablation of RNA interference and retrotransposons accompany acquisition and evolution of transposases to heterochromatin protein CENPB. <i>Molecular Biology of the Cell</i> , 2017, 28, 1132-1146.	0.9	13
51	The crystal structure of a bacterial Sufuâ€like protein defines a novel group of bacterial proteins that are similar to the Nâ€terminal domain of human Sufu. <i>Protein Science</i> , 2010, 19, 2131-2140.	3.1	12
52	Genome sequence and comparative analysis of clavicipitaceous insect-pathogenic fungus <i>Aschersonia badia</i> with <i>Metarhizium</i> spp.. <i>BMC Genomics</i> , 2016, 17, 367.	1.2	12
53	Influence of a mutation in the ATP-binding region of Ca ²⁺ /calmodulin-dependent protein kinase II on its interaction with peptide substrates. <i>Biochemical Journal</i> , 2004, 378, 391-397.	1.7	11
54	Representing and comparing protein structures as paths in three-dimensional space. <i>BMC Bioinformatics</i> , 2006, 7, 460.	1.2	11

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55	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 Å... resolution provides a structural scaffold for nonclassical, eukaryotic-like phosphatases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 415-421.	1.5	11
56	The structure of Haemophilus influenzae prephenate dehydrogenase suggests unique features of bifunctional TyrA enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1317-1325.	0.7	11
57	Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1274-1280.	0.7	11
58	Ethanolamine utilization in <i>Vibrio alginolyticus</i> . <i>Biology Direct</i> , 2012, 7, 45; discussion 45.	1.9	11
59	Repurposing TRASH: Emergence of the enzyme organomercurial lyase from a non-catalytic zinc finger scaffold. <i>Journal of Structural Biology</i> , 2014, 188, 16-21.	1.3	11
60	Crystal structure of a glycerate kinase (TM1585) from <i>Thermotoga maritima</i> at 2.70 Å... resolution reveals a new fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 243-248.	1.5	10
61	The structure of the first representative of Pfam family PF06475 reveals a new fold with possible involvement in glycolipid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1211-1217.	0.7	10
62	Genome Sequence of the Marine Bacterium <i>Marinilabilia salmonicolor</i> JCM 21150. <i>Journal of Bacteriology</i> , 2012, 194, 3746-3746.	1.0	10
63	Draft Genome Sequence of a Plant Growth-Promoting Rhizobacterium, <i>Serratia fonticola</i> Strain AU-P3(3). <i>Genome Announcements</i> , 2013, 1, .	0.8	10
64	The structure of Jann_2411 (DUF1470) from <i>Jannaschia</i> sp. at 1.45 Å... resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1198-1204.	0.7	9
65	A conserved fold for fimbrial components revealed by the crystal structure of a putative fimbrial assembly protein (BT1062) from <i>Bacteroides thetaiotaomicron</i> at 2.2 Å... resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1281-1286.	0.7	9
66	Evolutionary relationships between heme-binding ferredoxin α -barrels. <i>BMC Bioinformatics</i> , 2016, 17, 168.	1.2	9
67	Comparative structural analysis of a novel glutathione S-transferase (ATU5508) from <i>Agrobacterium tumefaciens</i> at 2.0 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 527-537.	1.5	8
68	Crystal structure of a novel archaeal AAA+ ATPase SSO1545 from <i>Sulfolobus solfataricus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 1041-1049.	1.5	8
69	The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1174-1181.	0.7	8
70	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1245-1253.	0.7	8
71	The structure of BVU2987 from <i>Bacteroides vulgatus</i> reveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1265-1273.	0.7	8
72	Structures of the first representatives of Pfam family PF06938 (DUF1285) reveal a new fold with repeated structural motifs and possible involvement in signal transduction. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1218-1225.	0.7	8

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73	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved $\hat{I}\pm\hat{I}^2$ core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1335-1346.	0.7	8
74	Crystal structure of phosphoribosylformylglycinamide synthase II (smPurL) from <i>Thermotoga maritima</i> at 2.15 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1106-1111.	1.5	7
75	Crystal structure of an ORFan protein (TM1622) from <i>Thermotoga maritima</i> at 1.75 Å... resolution reveals a fold similar to the Ran-binding protein Mog1p. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 777-782.	1.5	7
76	Crystal structure of AICAR transformylase IMP cyclohydrolase (TM1249) from <i>Thermotoga maritima</i> at 1.88 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1042-1049.	1.5	7
77	A novel RING finger in the C-terminal domain of the coatomer protein $\hat{I}\pm$ -COP. <i>Biology Direct</i> , 2015, 10, 70.	1.9	7
78	The UBR-box and its relationship to binuclear RING-like treble clef zinc fingers. <i>Biology Direct</i> , 2015, 10, 36.	1.9	7
79	The Ku "Mar zinc finger: A segment-swapped zinc ribbon in MarR-like transcription regulators related to the Ku bridge. <i>Journal of Structural Biology</i> , 2015, 191, 281-289.	1.3	7
80	<i>Grimontia indica</i> AK16T, sp. nov., Isolated from a Seawater Sample Reports the Presence of Pathogenic Genes Similar to <i>Vibrio</i> Genus. <i>PLoS ONE</i> , 2014, 9, e85590.	1.1	7
81	Crystal structure of TM1367 from <i>Thermotoga maritima</i> at 1.90 Å... resolution reveals an atypical member of the cyclophilin (peptidylprolyl isomerase) fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1112-1118.	1.5	6
82	Crystal structure of phosphoribosylformyl-glycinamide synthase II, PurS subunit (TM1244) from <i>Thermotoga maritima</i> at 1.90 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 249-254.	1.5	6
83	Crystal structure of MtnX phosphatase from <i>Bacillus subtilis</i> at 2.0 Å... resolution provides a structural basis for bipartite phosphomonoester hydrolysis of 2-hydroxy-3-keto-5-methylthiopentenylophosphate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 433-439.	1.5	6
84	Crystal structure of an ADP-ribosylated protein with a cytidine deaminase-like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1546-1552.	1.5	6
85	Draft Genome Sequence of the Opportunistic Human Pathogen <i>Morganella morganii</i> SC01. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
86	Draft Genome Sequence of Plant-Growth-Promoting Rhizobacterium <i>Serratia fonticola</i> Strain AU-AP2C, Isolated from the Pea Rhizosphere. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
87	Complete genome sequence and identification of polyunsaturated fatty acid biosynthesis genes of the myxobacterium <i>Minicycstis rosea</i> DSM 24000T. <i>BMC Genomics</i> , 2021, 22, 655.	1.2	6
88	Crystal structure of a transcription regulator (TM1602) from <i>Thermotoga maritima</i> at 2.3 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 247-252.	1.5	5
89	Conformational changes associated with the binding of zinc acetate at the putative active site of XcTcmJ, a cupin from <i>Xanthomonas campestris</i> sp. <i>campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1347-1353.	0.7	5
90	Evidence of a new metabolic capacity in an emerging diarrheal pathogen: lessons from the draft genomes of <i>Vibrio fluvialis</i> strains PG41 and I21563. <i>Gut Pathogens</i> , 2013, 5, 20.	1.6	5

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91	Draft Genome Sequence of Plant Growth-Promoting Rhizobacterium <i>Pantoea</i> sp. Strain AS-PWVM4. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
92	Genome sequencing and annotation of <i>Amycolatopsis azurea</i> DSM 43854T. <i>Genomics Data</i> , 2014, 2, 44-45.	1.3	5
93	The insertion domain 1 of class IIA dimeric glycyl-tRNA synthetase is a rubredoxin-like zinc ribbon. <i>Journal of Structural Biology</i> , 2015, 190, 38-46.	1.3	5
94	Draft Genome Sequence of <i>Kocuria palustris</i> PEL. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
95	Taxonomic insights into the phylogeny of <i>Bacillus badius</i> and proposal for its reclassification to the genus <i>Pseudobacillus</i> as <i>Pseudobacillus badius</i> comb. nov. and reclassification of <i>Bacillus wudalianchiensis</i> Liu et al., 2017 as <i>Pseudobacillus wudalianchiensis</i> comb. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 360-372.	1.2	4
96	Crystal structure of 2-phosphosulfolactate phosphatase (ComB) from <i>Clostridium acetobutylicum</i> at 2.6 Å... resolution reveals a new fold with a novel active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 771-776.	1.5	3
97	Crystal structures of MW1337R and lin2004: Representatives of a novel protein family that adopt a four-helical bundle fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1589-1596.	1.5	3
98	The structure of KPN03535 (gi 152972051), a novel putative lipoprotein from <i>Klebsiella pneumoniae</i> , reveals an OB-fold. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1254-1260.	0.7	3
99	Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1205-1210.	0.7	3
100	Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of the <i>Bacillus</i> chorismate mutase fold and suggest a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1182-1189.	0.7	3
101	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1167-1173.	0.7	3
102	Genome Sequence of the Halotolerant Bacterium <i>Haloterrigena halotolerans</i> K1. <i>Journal of Bacteriology</i> , 2012, 194, 3731-3731.	1.0	3
103	Draft Genome Sequence of <i>Rhodovulum</i> sp. Strain PH10, a Phototrophic Alphaproteobacterium Isolated from a Soil Sample of Mangrove of Namkhana, India. <i>Journal of Bacteriology</i> , 2012, 194, 6363-6363.	1.0	3
104	Evolutionary analysis of a novel zinc ribbon in the N-terminal region of threonine synthase. <i>Cell Cycle</i> , 2017, 16, 1918-1926.	1.3	3
105	Structure of a putative NTP pyrophosphohydrolase: YP_001813558.1 from <i>Exiguobacterium sibiricum</i> 255-15. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1237-1244.	0.7	2
106	Structure of <i>Bacteroides thetaiotaomicron</i> BT2081 at 2.05 Å... resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1287-1296.	0.7	2
107	Draft Genome Sequence of an Alphaproteobacterium, <i>Caenispirillum salinarum</i> AK4 T, Isolated from a Solar Saltern. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
108	Genome sequencing and annotation of <i>Acinetobacter gernerii</i> strain MTCC 9824T. <i>Genomics Data</i> , 2014, 2, 7-9.	1.3	2

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109	Genome sequencing and annotation of <i>Acinetobacter gyllenbergii</i> strain MTCC 11365T. <i>Genomics Data</i> , 2014, 2, 4-6.	1.3	1
110	Genome sequencing and annotation of <i>Acinetobacter junii</i> strain MTCC 11364. <i>Genomics Data</i> , 2014, 2, 13-15.	1.3	1
111	An atypical segment swap in the DN and DC domains of the Acr_tran family resistance-nodulation-cell division pump. <i>Journal of Structural Biology</i> , 2016, 196, 358-363.	1.3	1
112	Evolutionary relationship between the cysteine and histidine rich domains (CHORDs) and Btk-type zinc fingers. <i>Bioinformatics</i> , 2018, 34, 1981-1985.	1.8	1
113	Genome sequencing and annotation of <i>Acinetobacter guillouiae</i> strain MSP 4-18. <i>Genomics Data</i> , 2014, 2, 1-3.	1.3	0