

Srikrishna Subramanian

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112
papers

2,290
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h-index

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117
ext. papers

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ext. citations

4.6
avg, IF

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L-index

#	Paper	IF	Citations
112	Structural classification of zinc fingers: survey and summary. <i>Nucleic Acids Research</i> , 2003 , 31, 532-50	20.1	583
111	Exploration of uncharted regions of the protein universe. <i>PLoS Biology</i> , 2009 , 7, e1000205	9.7	98
110	CASP5 assessment of fold recognition target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 395-409	4.2	82
109	Structural classification of small, disulfide-rich protein domains. <i>Journal of Molecular Biology</i> , 2006 , 359, 215-37	6.5	80
108	Crystal structures of two novel dye-decolorizing peroxidases reveal a beta-barrel fold with a conserved heme-binding motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 223-33	4.2	68
107	Identification and structural characterization of heme binding in a novel dye-decolorizing peroxidase, TyrA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 234-43	4.2	61
106	Structural drift: a possible path to protein fold change. <i>Bioinformatics</i> , 2005 , 21, 1308-10	7.2	61
105	Structural basis of murein peptide specificity of a gamma-D-glutamyl-L-diamino acid endopeptidase. <i>Structure</i> , 2009 , 17, 303-13	5.2	57
104	Complete genome sequence and comparative genomics of the probiotic yeast <i>Saccharomyces boulardii</i> . <i>Scientific Reports</i> , 2017 , 7, 371	4.9	55
103	PALSSE: a program to delineate linear secondary structural elements from protein structures. <i>BMC Bioinformatics</i> , 2005 , 6, 202	3.6	48
102	Structure of the D-glutamyl-L-diamino acid endopeptidase Ykfc from <i>Bacillus cereus</i> in complex with L-Ala-D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1354-64		45
101	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, 647-63	6.5	37
100	Three-dimensional structure of physalis mottle virus: implications for the viral assembly. <i>Journal of Molecular Biology</i> , 1999 , 289, 919-34	6.5	35
99	Complete Genome of the Starch-Degrading Myxobacteria <i>Sandaracinus amylolyticus</i> DSM 53668T. <i>Genome Biology and Evolution</i> , 2016 , 8, 2520-9	3.9	34
98	TOPSAN: use of a collaborative environment for annotating, analyzing and disseminating data on JCSG and PSI structures. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1143-7		33
97	Genome sequence, comparative analysis, and evolutionary insights into chitinases of entomopathogenic fungus <i>Hirsutella thompsonii</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 916-30	3.9	30
96	4SCOPmap: automated assignment of protein structures to evolutionary superfamilies. <i>BMC Bioinformatics</i> , 2004 , 5, 197	3.6	30

95	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	3.7	27
94	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, 1297-305		26
93	Bacterial pleckstrin homology domains: a prokaryotic origin for the PH domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 31-46	6.5	25
92	Crystal structure of acireductone dioxygenase (ARD) from <i>Mus musculus</i> at 2.06 angstrom resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 808-13	4.2	25
91	Complete Genome Sequence and Comparative Genomics of a Novel Myxobacterium <i>Myxococcus hansupus</i> . <i>PLoS ONE</i> , 2016 , 11, e0148593	3.7	23
90	Prevalence of the F-type lectin domain. <i>Glycobiology</i> , 2015 , 25, 888-901	5.8	22
89	Identification of a discrete intermediate in the assembly/disassembly of physalis mottle tymovirus through mutational analysis. <i>Journal of Molecular Biology</i> , 1999 , 289, 905-18	6.5	22
88	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	3.9	21
87	A tale of two ferredoxins: sequence similarity and structural differences. <i>BMC Structural Biology</i> , 2006 , 6, 8	2.7	21
86	Structural studies on the empty capsids of Physalis mottle virus. <i>Journal of Molecular Biology</i> , 2001 , 307, 1035-47	6.5	20
85	Crystal structure of the Fic (Filamentation induced by cAMP) family protein SO4266 (gi 24375750) from <i>Shewanella oneidensis</i> MR-1 at 1.6 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 264-71	4.2	19
84	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, 25268-79	5.4	17
83	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	4.5	17
82	Structure of a tryptophanyl-tRNA synthetase containing an iron-sulfur cluster. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1326-34		16
81	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, 1153-9		15
80	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, 1160-6		15
79	Gleaning evolutionary insights from the genome sequence of a probiotic yeast <i>Saccharomyces boulardii</i> . <i>Gut Pathogens</i> , 2013 , 5, 30	5.4	14
78	Crystal structure of a novel Sm-like protein of putative cyanophage origin at 2.60 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 296-307	4.2	14

77	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, 1230-6		14
76	The bridge-region of the Ku superfamily is an atypical zinc ribbon domain. <i>Journal of Structural Biology</i> , 2010 , 172, 294-9	3-4	13
75	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, 256-60	4-2	13
74	Classification of the treble clef zinc finger: noteworthy lessons for structure and function evolution. <i>Scientific Reports</i> , 2016 , 6, 32070	4-9	13
73	Evolutionary convergence and divergence in archaeal chromosomal proteins and Chromo-like domains from bacteria and eukaryotes. <i>Scientific Reports</i> , 2018 , 8, 6196	4-9	12
72	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, 686-98	6-5	12
71	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. <i>Protein Science</i> , 2010 , 19, 2131-40	6-3	12
70	Identification of novel small RNAs in KC-01 expressed under iron limitation and oxidative stress conditions. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1924-1936	2-9	12
69	Draft genome sequence of the nitrophenol-degrading actinomycete <i>Rhodococcus imtechensis</i> RKJ300. <i>Journal of Bacteriology</i> , 2012 , 194, 3543	3-5	11
68	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	4-2	11
67	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	3-4	10
66	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, 243-8	4-2	10
65	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	3-5	9
64	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	4-5	9
63	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, 1198-204		9
62	The structure of <i>Haemophilus influenzae</i> prephenate dehydrogenase suggests unique features of bifunctional TyrA enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1317-25		9
61	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, 1274-80		9
60	Representing and comparing protein structures as paths in three-dimensional space. <i>BMC Bioinformatics</i> , 2006 , 7, 460	3-6	9

59	Metagenomics analysis reveals features unique to Indian distal gut microbiota. <i>PLoS ONE</i> , 2020 , 15, e0231197	9
58	Crystal structure of a novel archaeal AAA+ ATPase SSO1545 from <i>Sulfolobus solfataricus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 74, 1041-9	4.2 8
57	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, 1211-7	8
56	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, 1245-53	8
55	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, 1281-6	8
54	Comparative structural analysis of a novel glutathioneS-transferase (ATU5508) from <i>Agrobacterium tumefaciens</i> at 2.0 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 527-37	4.2 8
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, 391-7	3.8 8
52	Ethanolamine utilization in <i>Vibrio alginolyticus</i> . <i>Biology Direct</i> , 2012 , 7, 45; discussion 45	7.2 7
51	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, 1174-81	7
50	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, 1218-25	7
49	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1335-46	7
48	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 angstroms resolution provides a structural scaffold for nonclassical, eukaryotic-like phosphatases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 415-21	4.2 7
47	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, 1106-11	4.2 7
46	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, 777-82	4.2 7
45	Comparative Genomics of Myxobacterial Chemosensory Systems. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5 7
44	Evolutionary relationships between heme-binding ferredoxin β-barrels. <i>BMC Bioinformatics</i> , 2016 , 17, 168	3.6 6
43	Draft Genome Sequence of a Plant Growth-Promoting Rhizobacterium, <i>Serratia fonticola</i> Strain AU-P3(3). <i>Genome Announcements</i> , 2013 , 1,	6
42	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, 1265-73	6

41	Crystal structure of MtnX phosphatase from <i>Bacillus subtilis</i> at 2.0 angstroms resolution provides a structural basis for bipartite phosphomonoester hydrolysis of 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 433-9	4.2	6
40	Crystal structure of AICAR transformylase IMP cyclohydrolase (TM1249) from <i>Thermotoga maritima</i> at 1.88 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1042-9	4.2	6
39	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 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 1546-52	4.2	6
38	Crystal structure of TM1367 from <i>Thermotoga maritima</i> at 1.90 A resolution reveals an atypical member of the cyclophilin (peptidylprolyl isomerase) fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 1112-8	4.2	6
37	Crystal structure of phosphoribosylformyl-glycinamidase II, PurS subunit (TM1244) from <i>Thermotoga maritima</i> at 1.90 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 65, 249-54	4.2	6
36	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	3.4	5
35	The UBR-box and its relationship to binuclear RING-like treble clef zinc fingers. <i>Biology Direct</i> , 2015 , 10, 36	7.2	5
34	Draft Genome Sequence of the Opportunistic Human Pathogen <i>Morganella morganii</i> SC01. <i>Genome Announcements</i> , 2013 , 1,		5
33	Genome sequence of the marine bacterium <i>Marinilabilia salmonicolor</i> JCM 21150T. <i>Journal of Bacteriology</i> , 2012 , 194, 3746	3.5	5
32	Crystal structure of a transcription regulator (TM1602) from <i>Thermotoga maritima</i> at 2.3 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 247-52	4.2	5
31	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, 281-9	3.4	4
30	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	5.4	4
29	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	4.2	4
28	A novel RING finger in the C-terminal domain of the coatomer protein ECOP. <i>Biology Direct</i> , 2015 , 10, 70	7.2	4
27	Conformational changes associated with the binding of zinc acetate at the putative active site of XcTcmJ, a cupin from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1347-53		4
26	<i>Grimontia indica</i> AK16(T), 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	3.7	4
25	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	4.2	3
24	Genome sequencing and annotation of <i>Amycolatopsis azurea</i> DSM 43854(T). <i>Genomics Data</i> , 2014 , 2, 44-5		3

23	Evolutionary analysis of a novel zinc ribbon in the N-terminal region of threonine synthase. <i>Cell Cycle</i> , 2017 , 16, 1918-1926	4-7	3
22	Draft Genome Sequence of Plant Growth-Promoting Rhizobacterium <i>Pantoea</i> sp. Strain AS-PWVM4. <i>Genome Announcements</i> , 2013 , 1,		3
21	Genome sequence of the halotolerant bacterium <i>Imtechella halotolerans</i> K1T. <i>Journal of Bacteriology</i> , 2012 , 194, 3731	3-5	3
20	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	3-5	3
19	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, 1254-60		3
18	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, 1167-73		3
17	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, 1589-96	4-2	3
16	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, 771-6	4-2	3
15	Genome sequencing and annotation of <i>Acinetobacter haemolyticus</i> strain MTCC 9819(T). <i>Genomics Data</i> , 2014 , 2, 10-2		2
14	Draft Genome Sequence of <i>Kocuria palustris</i> PEL. <i>Genome Announcements</i> , 2014 , 2,		2
13	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,		2
12	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, 1205-10		2
11	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, 1182-9		2
10	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, 1237-44		2
9	Complete genome sequence and identification of polyunsaturated fatty acid biosynthesis genes of the myxobacterium <i>Minicystis rosea</i> DSM 24000. <i>BMC Genomics</i> , 2021 , 22, 655	4-5	2
8	Evolutionary relationship between the cysteine and histidine rich domains (CHORDs) and Btk-type zinc fingers. <i>Bioinformatics</i> , 2018 , 34, 1981-1985	7-2	1
7	Genome sequencing and annotation of <i>Acinetobacter gyllenbergii</i> strain MTCC 11365(T). <i>Genomics Data</i> , 2014 , 2, 4-6		1
6	Genome sequencing and annotation of <i>Acinetobacter junii</i> strain MTCC 11364. <i>Genomics Data</i> , 2014 , 2, 13-5		1

- 5 Draft Genome Sequence of an Alphaproteobacterium, *Caenispirillum salinarum* AK4(T), Isolated from a Solar Saltern. *Genome Announcements*, **2013**, 1, 1
- 4 Structure of *Bacteroides thetaiotaomicron* BT2081 at 2.05 Å resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. *Acta Crystallographica Section F: Structural Biology Communications*, **2010**, 66, 1287-96 1
- 3 Genome sequencing and annotation of *Acinetobacter gernerii* strain MTCC 9824(T). *Genomics Data*, **2014**, 2, 7-9 0
- 2 Genome sequencing and annotation of *Acinetobacter guillouiae* strain MSP 4-18. *Genomics Data*, **2014**, 2, 1-3
- 1 An atypical segment swap in the DN and DC domains of the Acr_{tran} family resistance-nodulation-cell division pump. *Journal of Structural Biology*, **2016**, 196, 358-363 3-4