Filipa L Sousa

List of Publications by Year
in descending order

47 papers	3,259 citations	257101 24 h-index	189595 50 g-index
53 all docs	53 docs citations	53 times ranked	3856 citing authors

#	Article	IF	Citations
1	DiSCo: a sequence-based type-specific predictor of Dsr-dependent dissimilatory sulphur metabolism in microbial data. Microbial Genomics, 2021, 7, .	1.0	16
2	Energy at Origins: Favorable Thermodynamics of Biosynthetic Reactions in the Last Universal Common Ancestor (LUCA). Frontiers in Microbiology, 2021, 12, 793664.	1.5	23
3	Identification of the sirohaem biosynthesis pathway in StaphylococcusÂaureus. FEBS Journal, 2020, 287, 1537-1553.	2.2	2
4	Dissimilatory sulfate reduction in the archaeon â€˜Candidatus Vulcanisaeta moutnovskiaâ€™ sheds light on the evolution of sulfur metabolism. Nature Microbiology, 2020, 5, 1428-1438.	5.9	27
5	The Future of Origin of Life Research: Bridging Decades-Old Divisions. Life, 2020, 10, 20.	1.1	63
6	Meet the relatives of our cellular ancestor. Nature, 2020, 577, 478-479.	13.7	8
7	Metagenomes from Coastal Marine Sediments Give Insights into the Ecological Role and Cellular Features of <i>Loki</i> - and <i>Thorarchaeota</i>. MBio, 2019, 10, .	1.8	16
8	Metabopolis: scalable network layout for biological pathway diagrams in urban map style. BMC Bioinformatics, 2019, 20, 187.	1.2	8
9	Oxygen Reductases in Alphaproteobacterial Genomes: Physiological Evolution From Low to High Oxygen Environments. Frontiers in Microbiology, 2019, 10, 499.	1.5	30
10	Native metals, electron bifurcation, and CO2 reduction in early biochemical evolution. Current Opinion in Microbiology, 2018, 43, 77-83.	2.3	48
11	An electrogenic redox loop in sulfate reduction reveals a likely widespread mechanism of energy conservation. Nature Communications, 2018, 9, 5448.	5.8	27
12	Serpentinization: Connecting Geochemistry, Ancient Metabolism and Industrial Hydrogenation. Life, 2018, 8, 41.	1.1	61
13	<i>Staphylococcus aureus</i> haem biosynthesis and acquisition pathways are linked through haem monooxygenase IsdG. Molecular Microbiology, 2018, 109, 385-400.	1.2	18
14	The physiology of trace elements in biological methane production. Bioresource Technology, 2017, 241, 775-786.	4.8	28
15	Physiology, phylogeny, and LUCA. Microbial Cell, 2016, 3, 582-587.	1.4	31
16	Energy for two: New archaeal lineages and the origin of mitochondria. BioEssays, 2016, 38, 850-856.	1.2	31
17	One step beyond a ribosome: The ancient anaerobic core. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 1027-1038.	0.5	51
18	Data on publications, structural analyses, and queries used to build and utilize the AlloRep database. Data in Brief, 2016, 8, 948-957.	0.5	2

#	Article	IF	Citations
19	Reply to â€˜Is LUCA a thermophilic progenote?â€™. Nature Microbiology, 2016, 1, 16230.	5.9	14
20	The physiology and habitat of the last universal common ancestor. Nature Microbiology, 2016, 1, 16116.	5.9	739
21	Lokiarchaeon is hydrogen dependent. Nature Microbiology, 2016, 1, 16034.	5.9	107
22	AlloRep: A Repository of Sequence, Structural and Mutagenesis Data for the LacI/GalR Transcription Regulators. Journal of Molecular Biology, 2016, 428, 671-678.	2.0	18
23	Early Microbial Evolution: The Age of Anaerobes. Cold Spring Harbor Perspectives in Biology, 2016, 8, a018127.	2.3	78
24	Autocatalytic sets in E. coli metabolism. Journal of Systems Chemistry, 2015, 6, 4.	1.7	68
25	YCF1: A Green TIC?. Plant Cell, 2015, 27, 1827-1833.	3.1	115
26	Endosymbiotic origin and differential loss of eukaryotic genes. Nature, 2015, 524, 427-432.	13.7	251
27	Origins of major archaeal clades correspond to gene acquisitions from bacteria. Nature, 2015, 517, 77-80.	13.7	238
28	Plastid origin: who, when and why?. Acta Societatis Botanicorum Poloniae, 2014, 83, 281-289.	0.8	10
29	Biochemical fossils of the ancient transition from geoenergetics to bioenergetics in prokaryotic one carbon compound metabolism. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 964-981.	0.5	78
30	Energy at life's origin. Science, 2014, 344, 1092-1093.	6.0	121
31	Chlorophyll Biosynthesis Gene Evolution Indicates Photosystem Gene Duplication, Not Photosystem Merger, at the Origin of Oxygenic Photosynthesis. Genome Biology and Evolution, 2013, 5, 200-216.	1.1	79
32	Early bioenergetic evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130088.	1.8	199
33	The emergence of protein complexes: quaternary structure, dynamics and allostery. Biochemical Society Transactions, 2012, 40, 475-491.	1.6	75
34	The superfamily of hemeâ€“copper oxygen reductases: Types and evolutionary considerations. Biochimica Et Biophysica Acta - Bioenergetics, 2012, 1817, 629-637.	0.5	163
35	A Bioinformatics Classifier and Database for Heme-Copper Oxygen Reductases. PLoS ONE, 2011, 6, e19117.	1.1	60
36	The alternative complex III: A different architecture using known building modules. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 1869-1876.	0.5	55

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37	The alternative complex III: A different architecture using known building modules. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 116.	0.5	1
38	Structural and Functional Insights into Sulfide:Quinone Oxidoreductase[,]. Biochemistry, 2009, 48, 5613-5622.	1.2	118
39	Looking for the minimum common denominator in haemâ€“copper oxygen reductases: Towards a unified catalytic mechanism. Biochimica Et Biophysica Acta - Bioenergetics, 2008, 1777, 929-934.	0.5	64
40	Redox Properties of Thermus thermophilus ba3: Different Electron-Proton Coupling in Oxygen Reductases?. Biophysical Journal, 2008, 94, 2434-2441.	0.2	23
41	Thermodynamic Redox Behavior of the Heme Centers in A-Type Heme-Copper Oxygen Reductases: Comparison between the Two Subfamilies. Biophysical Journal, 2008, 95, 4448-4455.	0.2	6
42	Thermodynamic Redox Behavior of the Heme Centers of <i>cbb</i>₃ Heme-Copper Oxygen Reductase from <i>Bradyrhizobium japonicum</i>. Biochemistry, 2007, 46, 13245-13253.	1.2	18
43	Electron Paramagnetic Resonance Studies of the Ironâˆ'Sulfur Centers from Complex I ofRhodothermus marinusâ€. Biochemistry, 2006, 45, 1002-1008.	1.2	17
44	A tyrosine residue deprotonates during oxygen reduction by thecaa3 reductase fromRhodothermus marinus. FEBS Letters, 2006, 580, 1350-1354.	1.3	18
45	Structure at 1.3Ã… Resolution of Rhodothermus marinus caa3 Cytochrome c Domain. Journal of Molecular Biology, 2005, 345, 1047-1057.	2.0	19
46	A nhaD Na+/H+antiporter and a pcd homologues are among the Rhodothermus marinus complex I genes. Biochimica Et Biophysica Acta - Bioenergetics, 2005, 1709, 95-103.	0.5	8
47	9 Early life. , 0, , .		1