

# Manuela M Pereira

## List of Publications by Year in descending order

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87  
papers

3,527  
citations

136950

32  
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149698

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docs citations

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times ranked

3076  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms of Energy Transduction by Charge Translocating Membrane Proteins. <i>Chemical Reviews</i> , 2021, 121, 1804-1844.	47.7	30
2	Olfactory responses of <i>Anaphes nitens</i> (Hymenoptera, Mymaridae) to host and habitat cues. <i>Journal of Applied Entomology</i> , 2021, 145, 675-687.	1.8	1
3	The Ion-Translocating NrfD-Like Subunit of Energy-Transducing Membrane Complexes. <i>Frontiers in Chemistry</i> , 2021, 9, 663706.	3.6	10
4	Investigating the amino acid sequences of membrane bound dihydroorotate:quinone oxidoreductases (DHOQOs): Structural and functional implications. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2021, 1862, 148321.	1.0	11
5	Bioenergetics Theory and Components   Respiratory Alternative Complex III – Structural and Functional Insights. , 2021, , 143-149.		0
6	Coarse-Grained Parameterization of Nucleotide Cofactors and Metabolites: Protonation Constants, Partition Coefficients, and Model Topologies. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 335-346.	5.4	9
7	Modularity of membrane-bound charge-translocating protein complexes. <i>Biochemical Society Transactions</i> , 2021, , .	3.4	6
8	Identification of pheromone candidates for the eucalyptus weevil, <i>Gonipterus platensis</i> (Coleoptera, Curculionidae). <i>Journal of Applied Entomology</i> , 2020, 144, 41-53.	1.8	10
9	The plethora of membrane respiratory chains in the phyla of life. <i>Advances in Microbial Physiology</i> , 2019, 74, 331-414.	2.4	14
10	Taxonomic distribution, structure/function relationship and metabolic context of the two families of sulfide dehydrogenases: SQR and FCSD. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 742-753.	1.0	36
11	Structural basis for energy transduction by respiratory alternative complex III. <i>Nature Communications</i> , 2018, 9, 1728.	12.8	38
12	Catalytic Activity and Proton Translocation of Reconstituted Respiratory Complex I Monitored by Surface-Enhanced Infrared Absorption Spectroscopy. <i>Langmuir</i> , 2018, 34, 5703-5711.	3.5	13
13	Regulation of the mechanism of Type-II NADH: Quinone oxidoreductase from <i>S. aureus</i> . <i>Redox Biology</i> , 2018, 16, 209-214.	9.0	18
14	Functional and structural characterization of Alternative Complex III. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, e66.	1.0	0
15	In Silico Discovery of a Substituted 6-Methoxy-quinalidine with Leishmanicidal Activity in <i>Leishmania infantum</i> . <i>Molecules</i> , 2018, 23, 772.	3.8	20
16	The monoheme cytochrome c subunit of Alternative Complex III is a direct electron donor to caa3 oxygen reductase in <i>Rhodothermus marinus</i> . <i>Biological Chemistry</i> , 2017, 398, 1037-1044.	2.5	6
17	Structural and Functional insights into the catalytic mechanism of the Type II NADH:quinone oxidoreductase family. <i>Scientific Reports</i> , 2017, 7, 42303.	3.3	22
18	The key role of glutamate 172 in the mechanism of type II NADH:quinone oxidoreductase of <i>Staphylococcus aureus</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 823-832.	1.0	17

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19	Exploring membrane respiratory chains. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1039-1067.	1.0	70
20	Substrate-protein Interactions of Type II NADH:Quinone Oxidoreductase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2016, 55, 2722-2734.	2.5	13
21	Type II NADH:quinone oxidoreductase family: phylogenetic distribution, structural diversity and evolutionary divergences. <i>Environmental Microbiology</i> , 2016, 18, 4697-4709.	3.8	42
22	Respiratory complex I: A dual relation with H <sup>+</sup> and Na <sup>+</sup> ?. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 928-937.	1.0	20
23	Type II NADH:quinone oxidoreductase from <i>Staphylococcus aureus</i> has two distinct binding sites and is rate limited by quinone reduction. <i>Molecular Microbiology</i> , 2015, 98, 272-288.	2.5	39
24	Expression, purification, crystallization and preliminary X-ray diffraction analysis of a type II NADH:quinone oxidoreductase from the human pathogen <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 477-482.	0.8	3
25	Respiratory complex I from <i>Escherichia coli</i> does not transport Na <sup>+</sup> in the absence of its NuoL subunit. <i>FEBS Letters</i> , 2014, 588, 4520-4525.	2.8	8
26	Reconstitution of Respiratory Complex I on a Biomimetic Membrane Supported on Gold Electrodes. <i>Langmuir</i> , 2014, 30, 9007-9015.	3.5	22
27	The molecular selectivity of type II NADH:quinone oxidoreductase for quinones - A docking study. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, e84.	1.0	0
28	Protein-protein interaction in <i>Rhodothermus marinus</i> respiratory chain studied by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, e83-e84.	1.0	0
29	Structural composition of alternative complex III: Variations on the same theme. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 1378-1382.	1.0	22
30	A missing link between complex I and group 4 membrane-bound [NiFe] hydrogenases. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 198-209.	1.0	108
31	The antiporter-like subunit constituent of the universal adaptor of complex I, group 4 membrane-bound [NiFe]-hydrogenases and related complexes. <i>Biological Chemistry</i> , 2013, 394, 659-666.	2.5	16
32	Study of ion translocation by respiratory complex I. A new insight using <sup>23</sup> Na NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012, 1817, 1810-1816.	1.0	10
33	The Alternative complex III: Properties and possible mechanisms for electron transfer and energy conservation. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012, 1817, 1852-1859.	1.0	47
34	The role of proton and sodium ions in energy transduction by respiratory complex I. <i>IUBMB Life</i> , 2012, 64, 492-498.	3.4	13
35	The superfamily of heme-copper oxygen reductases: Types and evolutionary considerations. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012, 1817, 629-637.	1.0	163
36	Electron transfer dynamics of <i>Rhodothermus marinus</i> caa3 cytochrome c domains on biomimetic films. <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 18088.	2.8	12

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37	Decoupling of the Catalytic and Transport Activities of Complex I from <i>Rhodothermus marinus</i> by Sodium/Proton Antiporter Inhibitor. <i>ACS Chemical Biology</i> , 2011, 6, 477-483.	3.4	22
38	A Bioinformatics Classifier and Database for Heme-Copper Oxygen Reductases. <i>PLoS ONE</i> , 2011, 6, e19117.	2.5	60
39	Sodium influence on energy transduction by complexes I from <i>Escherichia coli</i> and <i>Paracoccus denitrificans</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2011, 1807, 286-292.	1.0	19
40	The removal of a disulfide bridge in CotA-laccase changes the slower motion dynamics involved in copper binding but has no effect on the thermodynamic stability. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 641-651.	2.6	14
41	Energy conservation by <i>Rhodothermus marinus</i> respiratory complex I. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 509-515.	1.0	24
42	The alternative complex III of <i>Rhodothermus marinus</i> and its structural and functional association with <i>caa3</i> oxygen reductase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 1477-1482.	1.0	33
43	The alternative complex III: A different architecture using known building modules. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 1869-1876.	1.0	55
44	Subunit composition of <i>Rhodothermus marinus</i> respiratory complex I. <i>Analytical Biochemistry</i> , 2010, 407, 104-110.	2.4	5
45	The role of Glu498 in the dioxygen reactivity of CotA-laccase from <i>Bacillus subtilis</i> . <i>Dalton Transactions</i> , 2010, 39, 2875.	3.3	49
46	The cytochrome <i>ba</i> complex from the thermoacidophilic crenarchaeote <i>Acidianus ambivalens</i> is an analog of <i>bc1</i> complexes. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 37-45.	1.0	24
47	Structural and Functional Insights into Sulfide:Quinone Oxidoreductase. <i>Biochemistry</i> , 2009, 48, 5613-5622.	2.5	118
48	Copper incorporation into recombinant CotA laccase from <i>Bacillus subtilis</i> : characterization of fully copper loaded enzymes. <i>Journal of Biological Inorganic Chemistry</i> , 2008, 13, 183-193.	2.6	173
49	The dihydrolipoamide dehydrogenase from the crenarchaeon <i>Acidianus ambivalens</i> . <i>FEMS Microbiology Letters</i> , 2008, 281, 147-154.	1.8	8
50	Looking for the minimum common denominator in haem-copper oxygen reductases: Towards a unified catalytic mechanism. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2008, 1777, 929-934.	1.0	64
51	Redox Properties of <i>Thermus thermophilus</i> <i>ba3</i> : Different Electron-Proton Coupling in Oxygen Reductases?. <i>Biophysical Journal</i> , 2008, 94, 2434-2441.	0.5	23
52	Thermodynamic Redox Behavior of the Heme Centers in A-Type Heme-Copper Oxygen Reductases: Comparison between the Two Subfamilies. <i>Biophysical Journal</i> , 2008, 95, 4448-4455.	0.5	6
53	SERR-Spectroelectrochemical Study of a <i>cbb<sub>3</sub></i> Oxygen Reductase in a Biomimetic Construct. <i>Journal of Physical Chemistry B</i> , 2008, 112, 16952-16959.	2.6	35
54	A Novel Type of Monoheme Cytochrome <i>c</i> : Biochemical and Structural Characterization at 1.23 Å... Resolution of <i>Rhodothermus marinus</i> Cytochrome <i>c</i> . <i>Biochemistry</i> , 2008, 47, 11953-11963.	2.5	44

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55	Proximal mutations at the type I copper site of CotA laccase: spectroscopic, redox, kinetic and structural characterization of I494A and L386A mutants. <i>Biochemical Journal</i> , 2008, 412, 339-346.	3.7	66
56	The alternative complex III from <i>Rhodothermus marinus</i> – A prototype of a new family of quinol:electron acceptor oxidoreductases. <i>FEBS Letters</i> , 2007, 581, 4831-4835.	2.8	52
57	Thermodynamic Redox Behavior of the Heme Centers of <i>Cbb<sub>3</sub></i> Heme-Copper Oxygen Reductase from <i>Bradyrhizobium japonicum</i> . <i>Biochemistry</i> , 2007, 46, 13245-13253.	2.5	18
58	Aba <sub>3</sub> oxygen reductase from the thermohalophilic bacterium <i>Rhodothermus marinus</i> . <i>FEMS Microbiology Letters</i> , 2007, 269, 41-47.	1.8	16
59	A robust metallo-oxidase from the hyperthermophilic bacterium <i>Aquifex aeolicus</i> . <i>FEBS Journal</i> , 2007, 274, 2683-2694.	4.7	51
60	Electron Paramagnetic Resonance Studies of the Iron-Sulfur Centers from Complex I of <i>Rhodothermus marinus</i> . <i>Biochemistry</i> , 2006, 45, 1002-1008.	2.5	17
61	A tyrosine residue deprotonates during oxygen reduction by the <i>caa<sub>3</sub></i> reductase from <i>Rhodothermus marinus</i> . <i>FEBS Letters</i> , 2006, 580, 1350-1354.	2.8	18
62	Structure and coordination of Cu <sub>B</sub> in the <i>Acidianus ambivalens</i> <i>caa<sub>3</sub></i> quinol oxidase heme-copper center. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 625-635.	2.6	6
63	Midpoint Potentials of Hemes <i>a</i> and <i>b<sub>3</sub></i> in the Quinol Oxidase from <i>Acidianus ambivalens</i> are Inverted. <i>Journal of the American Chemical Society</i> , 2005, 127, 13561-13566.	13.7	38
64	Structure at 1.3 Å Resolution of <i>Rhodothermus marinus</i> <i>caa<sub>3</sub></i> Cytochrome c Domain. <i>Journal of Molecular Biology</i> , 2005, 345, 1047-1057.	4.2	19
65	Quinone reduction by <i>Rhodothermus marinus</i> succinate:menaquinone oxidoreductase is not stimulated by the membrane potential. <i>Biochemical and Biophysical Research Communications</i> , 2005, 330, 565-570.	2.1	14
66	A <i>nhaD</i> Na <sup>+</sup> /H <sup>+</sup> antiporter and a <i>pcd</i> homologues are among the <i>Rhodothermus marinus</i> complex I genes. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2005, 1709, 95-103.	1.0	8
67	Respiratory Chains from Aerobic Thermophilic Prokaryotes. <i>Journal of Bioenergetics and Biomembranes</i> , 2004, 36, 93-105.	2.3	35
68	Investigation of protonatable residues in <i>Rhodothermus marinus</i> <i>caa<sub>3</sub></i> haem-copper oxygen reductase: comparison with <i>Paracoccus denitrificans</i> <i>caa<sub>3</sub></i> haem-copper oxygen reductase. <i>Journal of Biological Inorganic Chemistry</i> , 2004, 9, 124-134.	2.6	21
69	Proton pathways, ligand binding and dynamics of the catalytic site in haem-copper oxygen reductases: a comparison between the three families. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2004, 1655, 340-346.	1.0	46
70	Active site structure of the <i>caa<sub>3</sub></i> quinol oxidase of <i>Acidianus ambivalens</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2004, 1655, 306-320.	1.0	17
71	Is a Q-cycle-like mechanism operative in dihaemic succinate:quinone and quinol:fumarate oxidoreductases?. <i>FEBS Letters</i> , 2003, 543, 1-4.	2.8	7
72	Quinol:fumarate oxidoreductases and succinate:quinone oxidoreductases: phylogenetic relationships, metal centres and membrane attachment. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2002, 1553, 158-170.	1.0	96

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73	Plasticity of proton pathways in haem-copper oxygen reductases. <i>FEBS Letters</i> , 2002, 522, 14-18.	2.8	35
74	Molecular and Biochemical Characterization of a Highly Stable Bacterial Laccase That Occurs as a Structural Component of the <i>Bacillus subtilis</i> Endospore Coat. <i>Journal of Biological Chemistry</i> , 2002, 277, 18849-18859.	3.4	456
75	A ferredoxin from the thermohalophilic bacterium <i>Rhodothermus marinus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2002, 1601, 1-8.	2.3	13
76	Purification and characterization of the complex I from the respiratory chain of <i>Rhodothermus marinus</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 2002, 34, 413-421.	2.3	21
77	A novel scenario for the evolution of haem-copper oxygen reductases. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2001, 1505, 185-208.	1.0	408
78	Ligand Binding and the Catalytic Reaction of Cytochrome <i>caa3</i> from the Thermophilic Bacterium <i>Rhodothermus marinus</i> . <i>Biochemistry</i> , 2001, 40, 10578-10585.	2.5	12
79	The succinate dehydrogenase from the thermohalophilic bacterium <i>Rhodothermus marinus</i> : redox-Bohr effect on heme bL. <i>Journal of Bioenergetics and Biomembranes</i> , 2001, 33, 343-352.	2.3	27
80	Gene Cluster of <i>Rhodothermus marinus</i> High-Potential Iron-Sulfur Protein: Oxygen Oxidoreductase, a <i>caa3</i> -Type Oxidase Belonging to the Superfamily of Heme-Copper Oxidases. <i>Journal of Bacteriology</i> , 2001, 183, 687-699.	2.2	35
81	Heme centers of <i>Rhodothermus marinus</i> respiratory chain. Characterization of its <i>cbb3</i> oxidase. <i>Journal of Bioenergetics and Biomembranes</i> , 2000, 32, 143-152.	2.3	33
82	The <i>caa3</i> Terminal Oxidase of <i>Rhodothermus marinus</i> Lacking the Key Glutamate of the D-Channel Is a Proton Pump. <i>Biochemistry</i> , 2000, 39, 6336-6340.	2.5	40
83	Membrane-Bound Electron Transfer Chain of the Thermohalophilic Bacterium <i>Rhodothermus marinus</i> : A Novel Multihemic Cytochrome <i>bc</i> , a New Complex III. <i>Biochemistry</i> , 1999, 38, 1268-1275.	2.5	88
84	The <i>caa3</i> terminal oxidase of the thermohalophilic bacterium <i>Rhodothermus marinus</i> : a HiPIP: oxygen oxidoreductase lacking the key glutamate of the D-channel. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1999, 1413, 1-13.	1.0	49
85	Membrane-Bound Electron Transfer Chain of the Thermohalophilic Bacterium <i>Rhodothermus marinus</i> : Characterization of the Iron-Sulfur Centers from the Dehydrogenases and Investigation of the High-Potential Iron-Sulfur Protein Function by in Vitro Reconstitution of the Respiratory Chain. <i>Biochemistry</i> , 1999, 38, 1276-1283.	2.5	55
86	Isolation and characterization of a high molecular weight cytochrome from the sulfate reducing bacterium <i>Desulfovibrio gigas</i> . <i>FEBS Letters</i> , 1994, 347, 295-299.	2.8	25
87	A membrane-bound HiPIP type center in the thermohalophile <i>Rhodothermus marinus</i> . <i>FEBS Letters</i> , 1994, 352, 327-330.	2.8	35