Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

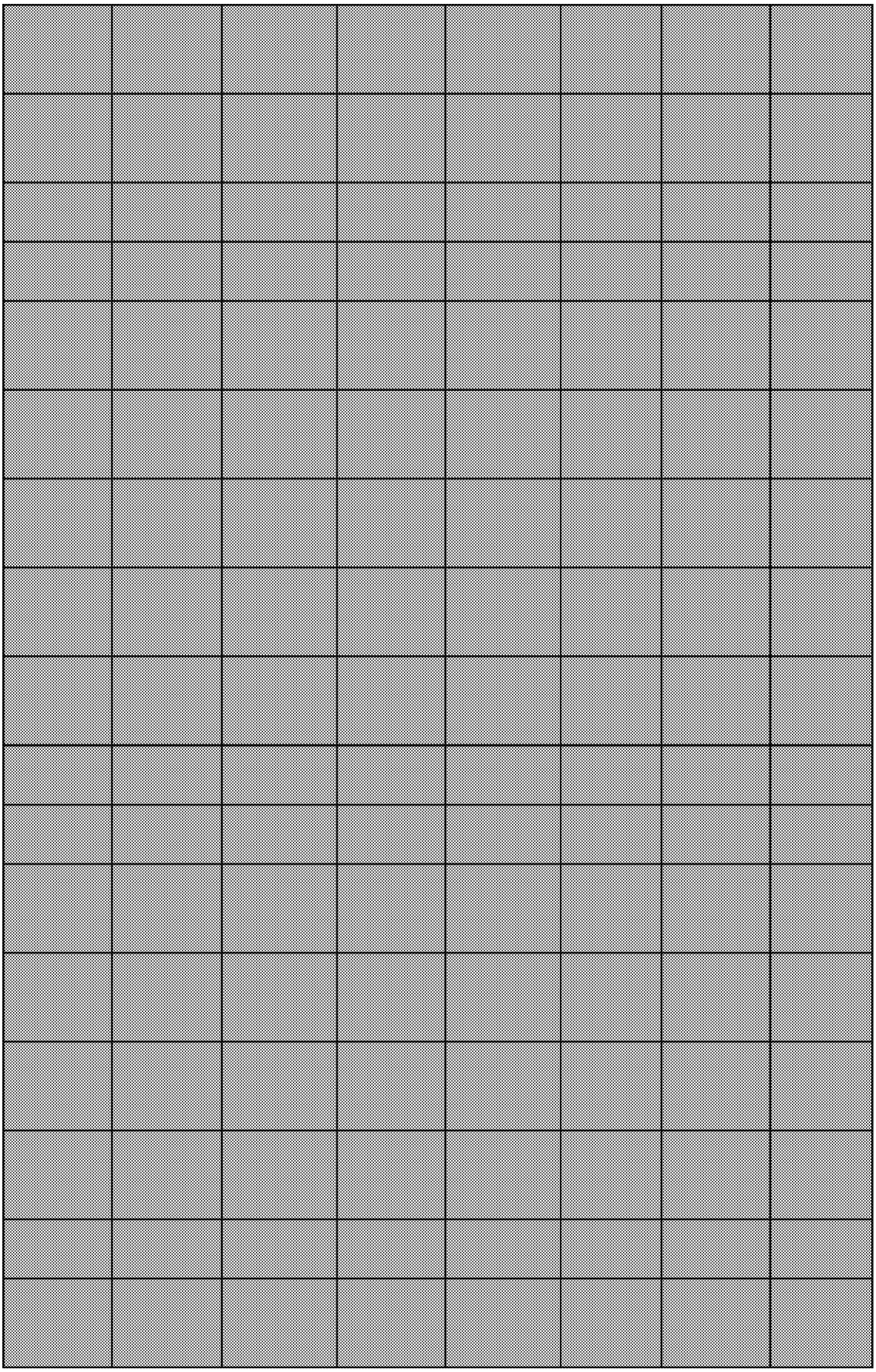
Level 1

Level 1

Level 1

Level 1

Level 1



2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090

M. Merkamm, A. Guyonvarch. Cloning of the sodA gene from Corynebacterium melassecola and role of superoxide dismutase in cellular viability. J Bacteriol. 2001. 183:1284-95
W. J. Paramchuk, S. O. Ismail, A. Bhatia, L. Gedamu. Cloning, characterization and overexpression of two iron superoxide dismutase cDNAs from Leishmania chagasi: role in pathogenesis. Mol Biochem Parasitol. 1997. 90:203-21
L. Liu, M. H. Wang. Cloning, expression, and characterization of a methionine sulfoxide reductase B gene from Nicotiana tabacum. Protein J. 2013. 32:543-50
T. Hunter, W. H. Bannister, G. J. Hunter. Cloning, expression, and characterization of two manganese superoxide dismutases from Caenorhabditis elegans. J Biol Chem. 1997. 272:28652-9
K. Sander, C. M. Wilson, M. Rodriguez, D. M. Klingeman, T. Rydzak, B. H. Davison, S. D. Brown. Clostridium thermocellum DSM 1313 transcriptional responses to redox perturbation. Biotechnol Biofuels. 2015. 8:211
Y. G. Kim. Collaborative effects of Photobacterium CuZn superoxide dismutase (SODs) and human AP endonuclease in DNA repair and SOD-deficient Escherichia coli under oxidative stress. Free Radic Biol Med. 2004. 36:173-9
S. Pohl, W. Y. Tu, P. D. Aldridge, C. Gillespie, H. Hahne, U. Mader, T. D. Read, C. R. Harwood. Combined proteomic and transcriptomic analysis of the response of Bacillus anthracis to oxidative stress. Proteomics. 2011. 11:3036-55
H. N. Koo, S. G. Lee, S. H. Yun, H. K. Kim, Y. S. Choi, G. H. Kim. Comparative Analyses of Cu-Zn Superoxide Dismutase (SOD1) and Thioredoxin Reductase (TrxR) at the mRNA Level between Apis mellifera L. and Apis cerana F. (Hymenoptera: Apidae) Under Stress Conditions. J Insect Sci. 2016. 16:#pages#
N. Yousef, E. K. Pistorius, K. P. Michel. Comparative analysis of idiA and isiA transcription under iron starvation and oxidative stress in Synechococcus elongatus PCC 7942 wild-type and selected mutants. Arch Microbiol. 2003. 180:471-83
K. S. Shin, H. S. Park, Y. H. Kim, J. H. Yu. Comparative proteomic analyses reveal that FlbA down-regulates gliT expression and SOD activity in Aspergillus fumigatus. J Proteomics. 2013. 87:40-52
S. P. Kernodle, J. G. Scandalios. A comparison of the structure and function of the highly homologous maize antioxidant Cu/Zn superoxide dismutase genes, Sod4 and Sod4A. Genetics. 1996. 144:317-28
C. Lu, W. E. Bentley, G. Rao. Comparisons of oxidative stress response genes in aerobic Escherichia coli fermentations. Biotechnol Bioeng. 2003. 83:864-70
J. J. LeBlanc, R. J. Davidson, P. S. Hoffman. Compensatory functions of two alkyl hydroperoxide reductases in the oxidative defense system of Legionella pneumophila. J Bacteriol. 2006. 188:6235-44
E. Vranova, S. Atichartpongkul, R. Villarroel, M. Van Montagu, D. Inze, W. Van Camp. Comprehensive analysis of gene expression in Nicotiana tabacum leaves acclimated to oxidative stress. Proc Natl Acad Sci U S A. 2002. 99:10870-5
M. J. Dougherty, D. M. Downs. A connection between iron-sulfur cluster metabolism and the biosynthesis of 4-amino-5-hydroxymethyl-2-methylpyrimidine pyrophosphate in Salmonella enterica. Microbiology. 2006. 152:2345-53
W. Wei, Z. Cao, Y. L. Zhu, X. Wang, G. Ding, H. Xu, P. Jia, D. Qu, A. Danchin, Y. Li. Conserved genes in a path from commensalism to pathogenicity: comparative phylogenetic profiles of Staphylococcus epidermidis RP62A and ATCC12228. BMC Genomics. 2006. 7:112
S. N. Wai, K. Nakayama, K. Umene, T. Moriya, K. Amako. Construction of a ferritin-deficient mutant of Campylobacter jejuni: contribution of ferritin to iron storage and protection against oxidative stress. Mol Microbiol. 1996. 20:1127-34

The sodA gene encoding the Corynebacterium melassecola manganese-cofactored superoxide dismutase (SOD) has beer
We have isolated and characterized two superoxide dismutase (SOD) cDNAs from a Leishmania chagasi promastigote cDI
Reactive oxygen species (ROS) are generated during normal aerobic metabolism and in plants exposed to environmental
Two genes encoding manganese superoxide dismutase (sod-2 and sod-3) have been identified in the nematode Caenorh
BACKGROUND: Clostridium thermocellum is a promising consolidated bioprocessing candidate organism capable of direc
The defenses against free radical damage include specialized repair enzymes that correct oxidative damage in DNA and c
The endospore-forming Gram-positive pathogen Bacillus anthracis is responsible for the usually fatal disease, inhalationa
This study compared stress-induced expression of Cu-Zn superoxide dismutase (SOD1) and thioredoxin reductase (TrxR) g
In the mesophilic cyanobacterium Synechococcus elongatus PCC 7942, iron starvation induces the expression of a numbe
FlbA is a regulator of G-protein signaling protein that plays a central role in attenuating heterotrimeric G-protein mediate
Two highly similar cytosolic Cu/Zn Sod (Sod4 and Sod4A) genes have been isolated from maize. Sod4A contains eight exo
The promoter regions of five SoxRS regulon genes (sodA, fumC, zwf, acnA, and acrAB) and one SoxRS regulatory protein g
Legionella pneumophila expresses two catalase-peroxidase enzymes that exhibit strong peroxidatic but weak catalatic ac
The molecular mechanisms by which plants acclimate to oxidative stress are poorly understood. To identify the processe
Several cellular pathways have been identified which affect the efficiency of thiamine biosynthesis in Salmonella enterica
BACKGROUND: Staphylococcus epidermidis, long regarded as an innocuous commensal bacterium of the human skin, is t
The ferritin-encoding gene (cft) of Campylobacter jejuni was cloned and sequenced. The nucleotide sequence of cft had a

Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

Level 1

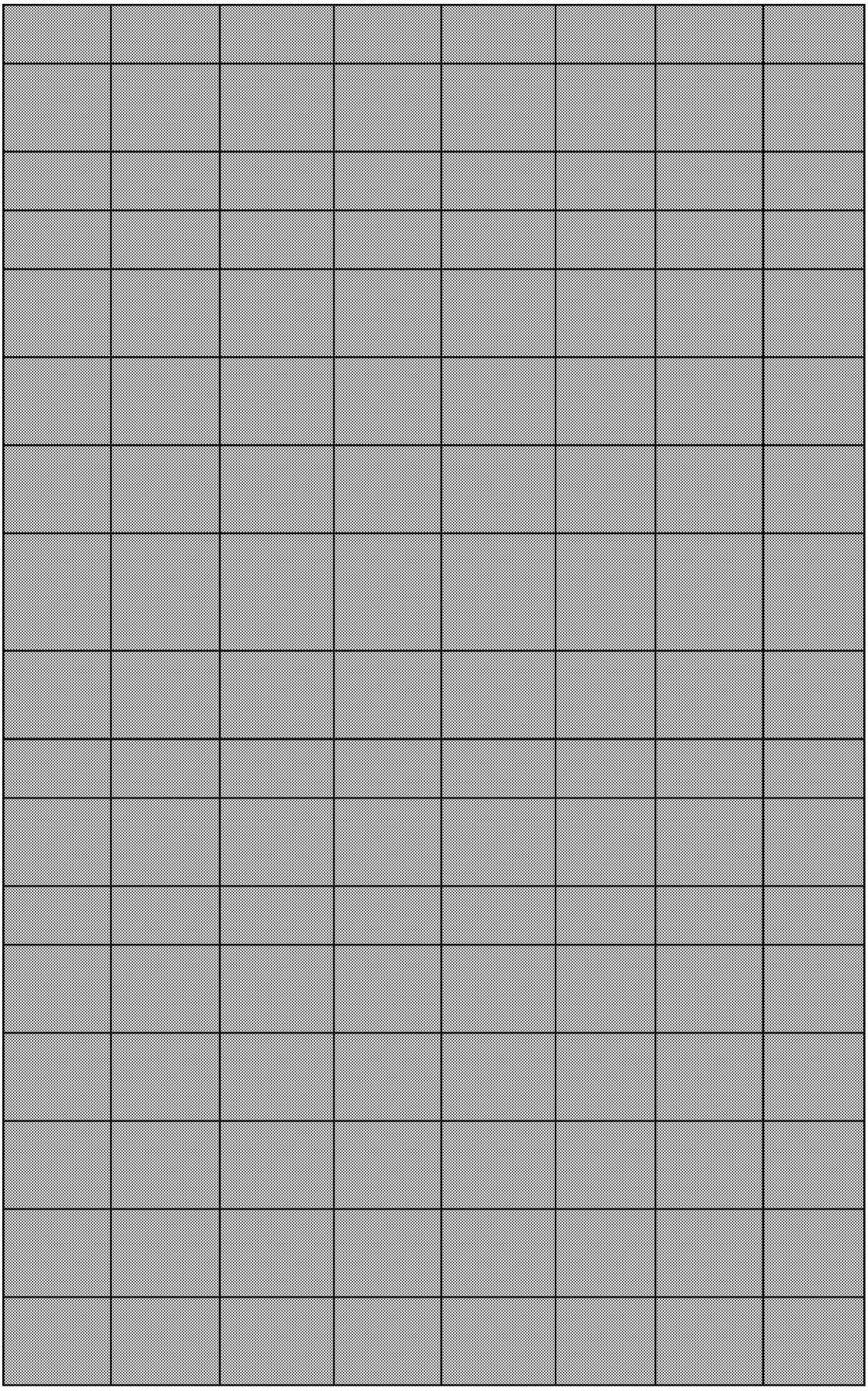
Level 1

Level 1

Level 1

Level 1

Level 1



2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108

H. J. Lee, M. B. Gu. Construction of a sodA::luxCDABE fusion Escherichia coli: comparison with a katG fusion strain through their responses to oxidative stresses. Appl Microbiol Biotechnol. 2003. 60:577-80
C. Poyart, E. Pellegrini, O. Gaillot, C. Boumaila, M. Baptista, P. Trieu-Cuot. Contribution of Mn-cofactored superoxide dismutase (SodA) to the virulence of Streptococcus agalactiae. Infect Immun. 2001. 69:5098-106
C. M. Gibson, T. C. Mallett, A. Claiborne, M. G. Caparon. Contribution of NADH oxidase to aerobic metabolism of Streptococcus pyogenes. J Bacteriol. 2000. 182:448-55
G. Wang, A. A. Olczak, J. P. Walton, R. J. Maier. Contribution of the Helicobacter pylori thiol peroxidase bacterioferritin comigratory protein to oxidative stress resistance and host colonization. Infect Immun. 2005. 73:378-84
M. Sabri, M. Caza, J. Proulx, M. H. Lymberopoulos, A. Bree, M. Moulin-Schouleur, R. Curtiss, C. M. Dozois. Contribution of the SitABCD, MntH, and FeoB metal transporters to the virulence of avian pathogenic Escherichia coli O78 strain chi7122. Infect Immun. 2008. 76:601-11
A. Reder, D. Hoper, U. Gerth, M. Hecker. Contributions of individual sigmaB-dependent general stress genes to oxidative stress resistance of Bacillus subtilis. J Bacteriol. 2012. 194:3601-10
A. Kaur, P. T. Van, C. R. Busch, C. K. Robinson, M. Pan, W. L. Pang, D. J. Reiss, J. DiRuggiero, N. S. Baliga. Coordination of frontline defense mechanisms under severe oxidative stress. Mol Syst Biol. 2010. 6:393
C. Borghouts, A. Werner, T. Elthon, H. D. Osiewacz. Copper-modulated gene expression and senescence in the filamentous fungus Podospora anserina. Mol Cell Biol. 2001. 21:390-9
S. Langsrud, G. Sundheim, A. L. Holck. Cross-resistance to antibiotics of Escherichia coli adapted to benzalkonium chloride or exposed to stress-inducers. J Appl Microbiol. 2004. 96:201-8
S. X. Tan, M. Teo, Y. T. Lam, I. W. Dawes, G. G. Perrone. Cu, Zn superoxide dismutase and NADP(H) homeostasis are required for tolerance of endoplasmic reticulum stress in Saccharomyces cerevisiae. Mol Biol Cell. 2009. 20:1493-508
D. J. Thomas, T. J. Avenson, J. B. Thomas, S. K. Herbert. A cyanobacterium lacking iron superoxide dismutase is sensitized to oxidative stress induced with methyl viologen but Is not sensitized to oxidative stress induced with norflurazon. Plant Physiol. 1998. 116:1593-602
T. M. Bradley, E. Hidalgo, V. Leautaud, H. Ding, B. Demple. Cysteine-to-alanine replacements in the Escherichia coli SoxR protein and the role of the [2Fe-2S] centers in transcriptional activation. Nucleic Acids Res. 1997. 25:1469-75
V. S. Braz, J. F. da Silva Neto, V. C. Italiani, M. V. Marques. CztR, a LysR-type transcriptional regulator involved in zinc homeostasis and oxidative stress defense in Caulobacter crescentus. J Bacteriol. 2010. 192:5480-8
X. Lu, H. Kim, S. Zhong, H. Chen, Z. Hu, B. Zhou. De novo transcriptome assembly for rudimentary leaves in Litchi chinesis Sonn. and identification of differentially expressed genes in response to reactive oxygen species. BMC Genomics. 2014. 15:805
Y. Nemoto-Sasaki, K. Kasai. Deletion of lec-10, a galectin-encoding gene, increases susceptibility to oxidative stress in Caenorhabditis elegans. Biol Pharm Bull. 2009. 32:1973-7
W. Zhao, J. C. Panepinto, J. R. Fortwendel, L. Fox, B. G. Oliver, D. S. Askew, J. C. Rhodes. Deletion of the regulatory subunit of protein kinase A in Aspergillus fumigatus alters morphology, sensitivity to oxidative damage, and virulence. Infect Immun. 2006. 74:4865-74
R. C. Rodrigues, A. L. Pocheron, M. Hernould, N. Haddad, O. Tresse, J. M. Cappelier. Description of Campylobacter jejuni Bf, an atypical aero-tolerant strain. Gut Pathog. 2015. 7:30
M. S. Dhar, V. Gupta, J. S. Virdi. Detection, distribution and characterization of novel superoxide dismutases from Yersinia enterocolitica Biovar 1A. PLoS One. 2013. 8:e63919

A recombinant bioluminescent Escherichia coli strain, EBHJ, (sodA::luxCDABE), containing the promoter for the mangane
Superoxide dismutases convert superoxide anions to molecular oxygen and hydrogen peroxide, which, in turn, is metabo
An understanding of how the heme-deficient gram-positive bacterium Streptococcus pyogenes establishes infections in (
Peroxiredoxins, the enzymes that catalyze the reduction of hydrogen peroxide and organic hydroperoxides, are ubiquito
The roles of SitABCD, MntH, and FeoB metal transporters in the virulence of avian pathogenic Escherichia coli (APEC) O78
The general stress regulon of Bacillus subtilis comprises approximately 200 genes and is under the control of the alternat
Complexity of cellular response to oxidative stress (OS) stems from its wide-ranging damage to nucleic acids, proteins, ca
We have previously shown that the control of cellular copper homeostasis by the copper-modulated transcription factor
AIMS: To study the effects of adaptation and stress on the resistance to benzalkonium chloride (BC) and cross-resistance
Genome-wide screening for sensitivity to chronic endoplasmic reticulum (ER) stress induced by dithiothreitol and tunicar
A strain of Synechococcus sp. strain PCC 7942 with no functional Fe superoxide dismutase (SOD), designated sodB-, was c
The Escherichia coli soxRS regulon activates oxidative stress and antibiotic resistance genes in two transcriptional stages.
Caulobacter crescentus is a free-living alphaproteobacterium that has 11 predicted LysR-type transcriptional regulators (
BACKGROUND: Litchi is an evergreen woody tree widely cultivated in subtropical and tropical regions. Defective flowerin
Galectins are a family of beta-galactoside-binding lectins. They are involved in the regulation of a variety of biological ph
Aspergillus fumigatus is an important opportunistic fungal pathogen. The cAMP-dependent protein kinase (PKA) signalin
BACKGROUND: Campylobacter jejuni is a leading cause of bacterial enteritis worldwide. This microaerophilic bacterium c
BACKGROUND: Superoxide dismutases (SODs) cause dismutation of superoxide radicals to hydrogen peroxide and oxyge

Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant
Not Relevant