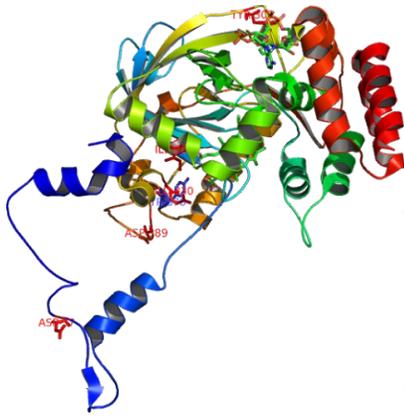


Catalase, the antioxidant heme enzyme one of three subgroups related to catalase deficiency in humans modulating the normal catalase reaction dependent on NADPH-binding catalases for function.

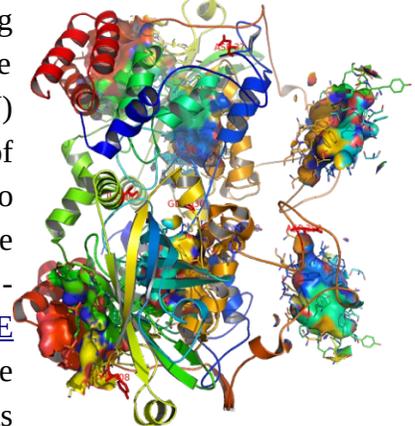
Catalase ([CAT](#)) is converted by decomposition and intracellular localization relationships of the [main](#) cellular [antioxidant](#) enzyme system like [superoxide](#) dismutase ([SOD](#)), [peroxiredoxins](#) ([Prdx](#)), and [glutathione](#) peroxidase ([GPX](#)) are peroxisomal matrix enzymes in the cytoplasm, [translocated](#) to the peroxisomes to catalyze hydrogen peroxide [H₂O₂](#) which is [decomposed](#) to oxygen and water, locus: [11p13](#) ([§](#), [‡](#)). Unlike catalase, the objective of this communication, SOD which [prevents](#) the formation of [Hydroxyl](#) radicals - ([HRGT](#)) determined from constant of [O₂](#)-dismutation, and generation of reversibly inactive (CAT)-compound II, [Panax ginseng](#) could induce both transcription factors. Catalase is composed of four identical subunits each of the subunits binds one heme-containing active site, and produces two catalase [compounds](#) HPI and HPII (PDB: [1p80](#)) is flipped [180 degrees](#) » with respect to the orientation of the heme related to the « root mean square to the [structure](#) of catalase, (Mutation [Location](#)) from peroxisomal catalases inactive state in compound II NADP+(H) binding pockets inverted remains similar to the structure of the wild type (Val111, PDB: [1A4E](#)) orientation on the heme [proximal](#) (PDB: [1GGK](#)) side, [inactivate](#) catalase can be prevented by [melatonin](#). Catalase (CAT; EC [1.11.1.6](#)) a free radical scavenging enzyme ([FRSE](#)) is a scavenger of [H₂O₂](#). Protoporphyrin - (ZnPPIX) (PDB: [1H6N](#)), from a heme group of the 'heme-pathway, which forms catalase,' is a scavenger of [antioxidant](#) ([HO-1](#)-HMOX1) [heme oxygenase](#), involving [ROS](#). Catalase is part of the enzymatic defense [system](#) constituting the [primary](#) defense against [ROS](#), zinc protoporphyrin IX ([ZnPPIX](#)) is an inhibitor of (HO-1) heme oxygenase. Catalase [protects](#) the cell from oxidative [damage](#) by the accumulation of cellular reactive oxygen species ([ROS](#)) generation systems, those [peroxisomal](#) enzymes that [breaks down](#) hydrogen peroxide after H(2)O(2) exposure, and thereby [mitigates*](#) (some [contradictory*](#) results) the toxic effects of hydrogen peroxide. In the process (The typical hydroperoxidases (CAT) known as [Compound I](#)) of the substrate of catalase, [NADP+](#) (an [inactive](#) state, [compound II](#)) is replaced by another molecule of NADP(H) to provide protection of catalase against [inactivation](#) by (H₂O₂) hydrogen peroxide. [Erythrocyte](#) [Human erythrocyte catalase ([HEC](#)), The [NADPH](#)-binding sites were empty - PDB: [1F4J](#), [1QQW](#)] and plasma [indices](#) (enzymatic-[antioxidants](#)) initially implies the thiobarbituric acid-reacting substances ([TBARS](#)) based on reaction with hydroxyl radicals ([OH](#)) can release thiobarbituric acid, [TBAR](#) inhibition [measures](#) malondialdehyde ([MDA](#) - impact of coenzyme [Q10](#)) correlated (with MPO-myeloperoxidase [activity](#) -generating ROS) as [co-variable](#), by which [mulberry leaf](#) polysaccharide (MLPII) via the decomposition of (certain) [MDA](#), products of [lipid](#) peroxidation ([LPO](#)) were reduced. Comparisons were to specific activities of catalase ([SNP](#)) single nucleotide [polymorphisms](#) (CAT-C-262 (rs1001179) the low-risk [allele](#)) of genetic variants in both, promoter a common [C/T](#) polymorphism (262-C/T), and in [nine](#) - [exonic](#) - regions and its boundaries, occur frequently associated distally in [genomic](#) mutations, similar to those of [normal catalase](#) demonstrating [changes](#) in catalase protein level targeted to the peroxisomal [matrix](#). The 262-C/T CAT low-risk allele is hypothetically related to the lower risk variant allele CAT [Tyr308](#) G to A point mutation ineducable in the Japanese acatalasemia allele. The common C/T polymorphism can be

targeted by dietary and/or pharmacological antioxidants, and the endogenous antioxidant defense enzymes concentration can prevent cellular lipid (LPO) peroxidative reactions occurring. Catalase is a homotetramer complex of 4 identical monofunctional subunits. Catalase is located at the peroxisome of human cells associated with several (PBDs)-peroxisomal biogenesis disorders commonly caused by mutations in the PEX genes, peroxisomal targeting signal 1 (PTS1) protein affecting in peroxisomal biogenesis, the monomeric to homotetrameric transition in the forms of peroxisome biogenesis disorder. PBDs also include Acatalasemia the only disease known to be caused by the (CAT) gene. In human catalase, the antioxidant heme enzyme, is localized in the cytoplasm to the peroxisome, nucleus, or linked with mitochondria which in most cells lack catalase (Peroxisomes do not contain DNA), its mitochondrial fraction (microperoxisome), a secondary phenomena shows physiological decline, aging and age-related reactions in mitochondrial function and disfunction. NADPH is required for the prevention of forming an inactive state of the enzyme. Antioxidative defence mechanisms, capacity and redox cycle enzyme activities increasing with Tc treatment Tinospora cordifolia (Tc), T and B cells and antibody. Both RBCs and plasma were measured on parameters of oxidative stress. Syzygium cumini aqueous leaves extract (ASc) was able to remove oxidant species in a hyperglycemic state generated in red blood cells RBC-CAT levels. Catalase alone is unable to prevent in a hyperglycemic state. Macrophages recruit other types of immune cells such as lymphocytes white blood cells (WBCs). Catalase is dependent on the family of NADPH-binding catalases for function, the prevention and reversal of inactivation by its toxic substrate (H₂O₂) hydrogen peroxide. Amyloid-beta binds catalase and inhibits (H₂O₂) hydrogen peroxide, a reactive oxygen species, breakdown through efficient dismutation, and malonaldehyde (MDA) determined in plasma, as well as another member of the oxidoreductase family, myeloperoxidase (MPO (EC 1.11.1.7)) converting H₂O₂, the reducing equivalents produces (HOCl) hypochlorous acid a mechanism of cell-mediated antimicrobial immune defense for monofunctional catalases one of three subgroups related to catalase deficiency in humans, in micro-organisms manganese-containing catalases ('large catalases') determining in part the bifunctional activity of (KatG, PDB:1X7U) represented by bifunctional (heme) catalase-peroxidase based Bacterial-resistance mechanisms. Peroxiredoxins (Prxs, EC 1.11.1.21), bifunctional catalase-peroxidases (KatGs) two organelle systems are antioxidant enzymes of the peroxiredoxin family that oxidize and reduce H₂O₂ hydrogen peroxide thereby modulating the catalase reaction, KatGs are not found in plants and animals. Trx (thioredoxin) a redox-regulating protein also controls the antioxidant enzyme activity of the main cellular antioxidant enzymes (AOE) superoxide dismutase (SOD) and catalase.



The function of [NADPH](#) bound to [Catalase](#). The cytosine to thymidine transition of nucleotide-262 (-262C>T) Computer analysis indicated that the two variants bound promoter the Ile (-262 C/T) and (B) [Ile-262](#) in the [5'-flanking](#) region carrying the T allele best captured and characterized the generation of the hydroxyl radical site in (PDB: [1DGB](#)), (CAT) -[GLU] [330C>T](#) transition, is known also as -262C>T. The 'T allele in comparison to the C allele' is a common C/T polymorphism frequency in the [promoter](#) region association was observed between genotypes for locus11p13 risk alleles acatalasemia mutation Asp ([37C>T](#) in exon 9) was hypothetically related to the lower

risk Japanese acatalasemia allele [Tyr308](#) a single [G](#) to [A](#) (see: [rs7947841](#) to evaluate the link to [rs769214](#)) point mutation in exon 9 ([TC](#), [CC](#), [TT](#)) of the [CAT](#) gene to which variant changes in the promoter region C/T-262 polymorphism are more closely related to [CAT](#) T/C at codon [389](#) in exon 9 ([rs769217](#)) [polymorphism](#) did not [differ](#) significantly from those of healthy [controls](#) in both promoter (-262 C/T) and in exonic ([ASP-389](#) C/T) regions of the catalase ([CAT](#)). [Tyr 370](#) resolves the 25 Å-long (hydrogen peroxide) channel a constriction or narrowing of the channel leading to the heme cavity ('Parameters) situated in the entrance channel to a heme protoporphyrin (ZnPIX) (PDB: [1H6N](#)) from a heme group, capable of heme [biosynthesis](#)' in a wide range of organisms convert it into heme b, protoporphyrin [IX-heme](#). Two channels lead close to the distal side. A third channel reaching the heme [proximal side](#) Tyr 370, [Ile-262](#) is proposed as a the 'PDB: [1DGB](#) - variant with a substituted residue in the ASP 178 to the (Met) [D181E](#) variant PDB [1p80](#)'. These differences include the structure of the variant protein [Val111Ala](#) (*Saccharomyces cerevisiae*) related supports the existence of the 'Heme and NADP(H) binding pockets'. The omission of a 20-residue PDB: [1F4J](#), ([1QQW](#)) segment corresponds to the N-terminal (blue) of catalase from human erythrocytes (HEC), or in a [C-terminal](#) (red) domain organized with an extra [flavodoxin-like fold](#) topology may provide with weak coordination the [N- or C-terminal](#), that allows scrutiny of the origins (topology) in this report of what would otherwise remain speculative or [determined](#) with further verification.



Biological Xenobiotic Extracts Applications of note In the presence of Catalase:

green tea polyphenol (-)-epigallocatechin-3-gallate (EGCG)

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Diallyl

disulfide

(Allicin)

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aspera

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EGCG)

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