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Function, kinetic properties, crystallization, and regulation of microbial malate dehydrogenase

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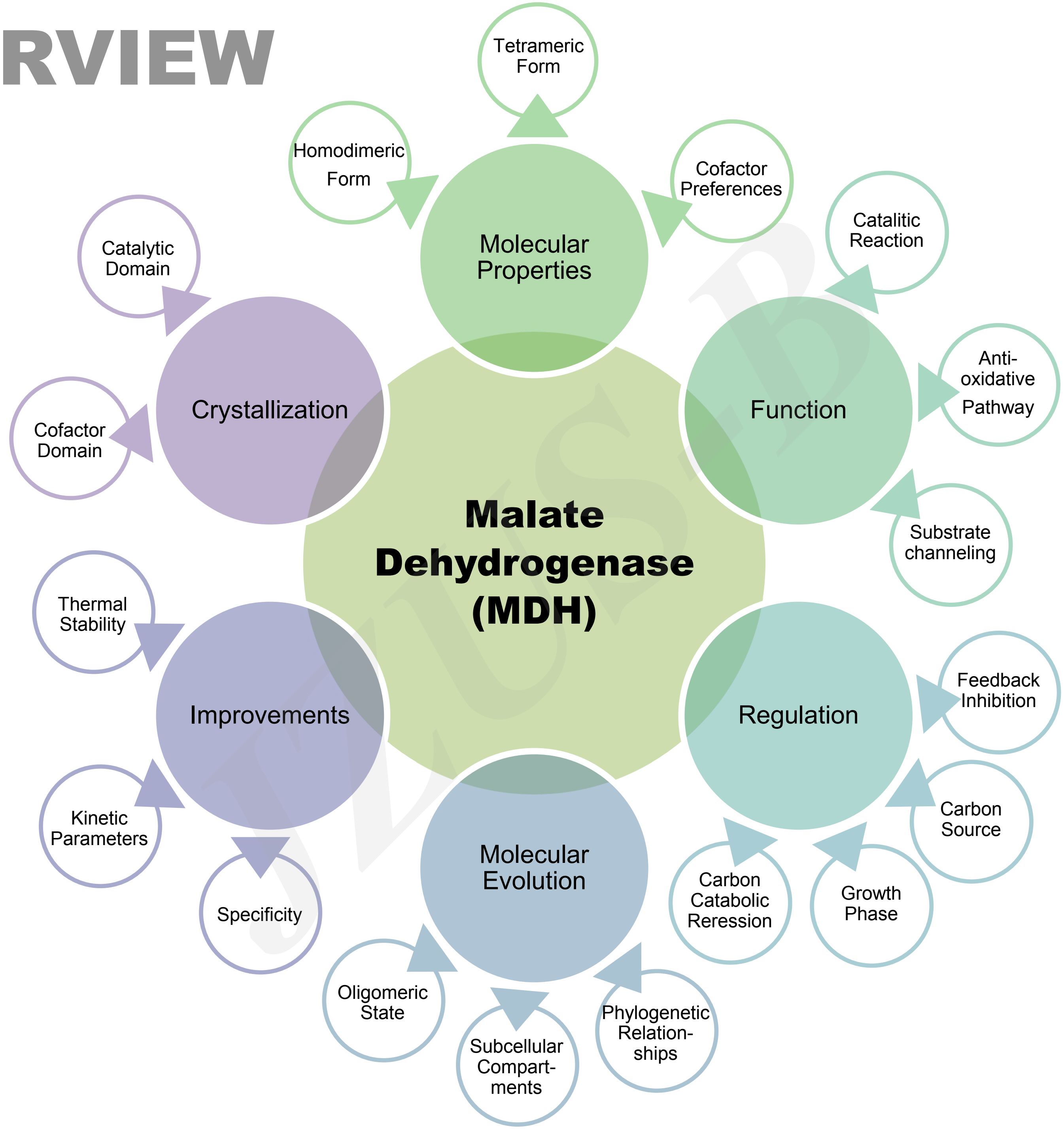
SCIENCE

Key words: Malate dehydrogenase, carbon metabolism, tricarboxylic acid cycle

OVERVIEW



Malate Dehydrogenase (MDH)

Molecular Properties
- Homodimeric Form
- Tetrameric Form
- Cofactor Preferences

Function
- Catalitic Reaction
- Anti-oxidative Pathway
- Substrate channeling

Regulation
- Feedback Inhibition
- Carbon Source
- Growth Phase
- Carbon Catabolic Reression

Molecular Evolution
- Phylogenetic Relation-ships
- Subcellular Compart-ments
- Oligomeric State

Improvements
- Specificity
- Kinetic Parameters
- Thermal Stability

Crystallization
- Cofactor Domain
- Catalytic Domain

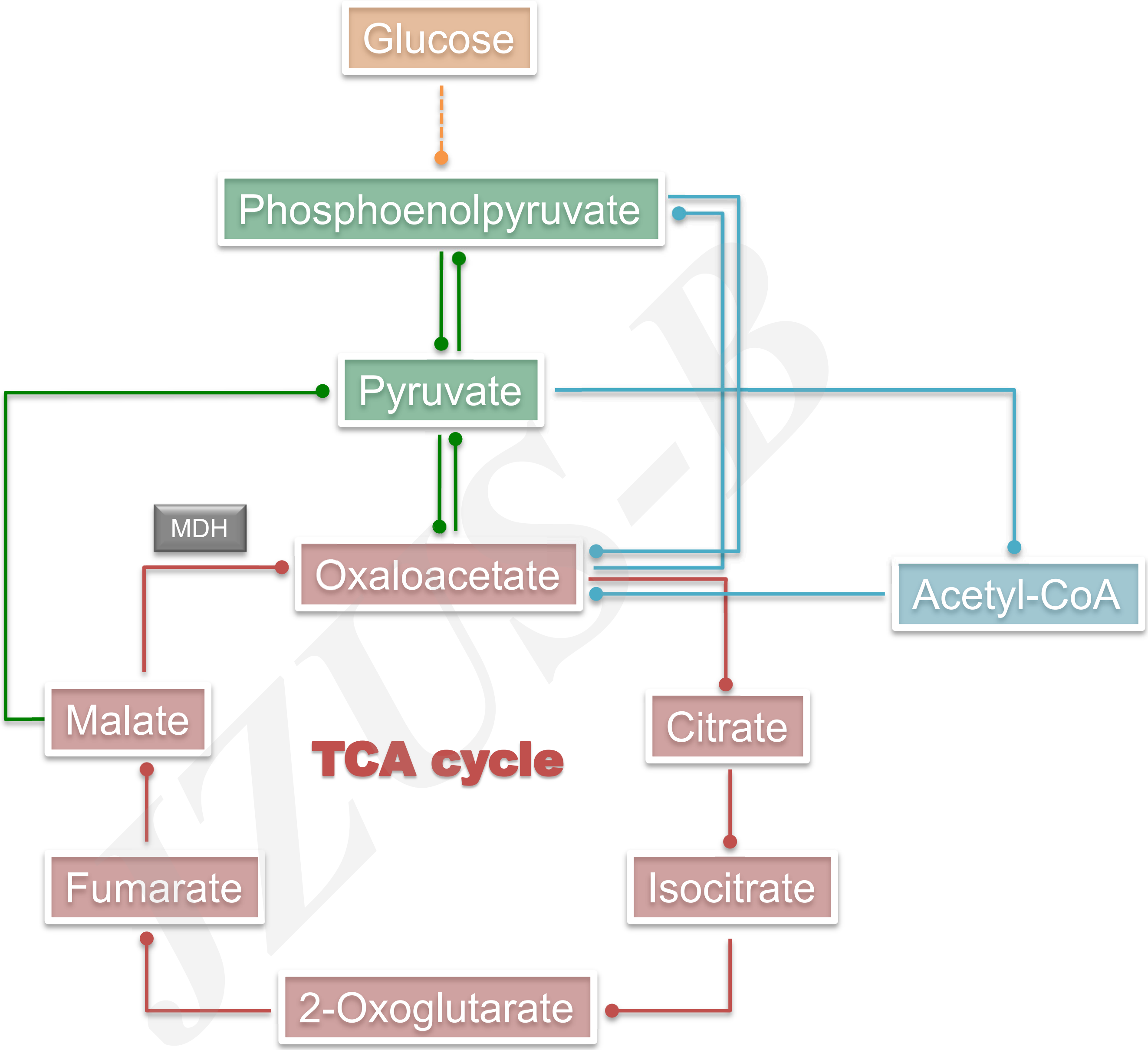


Figure shows phosphoenolpyruvate-pyruvate-oxaloacetate (PEP-Pyr-OAA) node (including pyruvate shunt), and tricarboxylic acid (TCA) cycle. These metabolic pathways are closely interconnected to malate dehydrogenase (MDH) enzyme catalysis.

MAIN FEATURES

- Malate dehydrogenase (MDH) carries out the interconversion between malate and oxaloacetate employing either NAD^+ or $NADP^+$ as a cofactor.
- MDH is part of the TCA cycle, the most important metabolic pathway for supplying ATP to aerobic organisms.
- It has been reported different affinities and specificities for substrate and cofactor among MDH enzymes of different microorganisms and celular compartiments.
- Its tertiary structure is widely conserved. In contrast to this, its amino acid sequence is poorly conserved making difficult to elucidate its molecular evolution.
- Being an ubiquitous enzyme, its subject to different mechanisms of regulation as activity inhibition and carbon catabolic repression.