

DECODING THE THERAPEUTIC BLUEPRINT OF INDOLE-3-CARBINOL THROUGH NETWORK-BASED BIOINFORMATICS

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ABSTRACT

Indole-3-carbinol, a naturally occurring phytochemical found in cruciferous vegetables, is recognized for its biological and nutritional benefits; however, its underlying molecular mechanisms remain largely underexplored. This study employed network-based computational approaches to comprehensively analyze its genomic and proteomic targets, along with the biological pathways it may influence. The compound exhibited high gastrointestinal absorption, blood-brain barrier permeability, favorable oral bioavailability, and non-toxic properties. A total of 139 protein-coding genes were identified as potential molecular targets. Protein-protein interaction analysis revealed strong functional associations among these genes, while functional classification indicated roles in regulating cell death, cellular signaling, and stress responses. Pathway enrichment analysis highlighted significant biological routes, including those related to apoptosis, cancer progression, and immune regulation. Overall, indole-3-carbinol shows multi-target therapeutic potential in oncology, immunology, and metabolic disorders, providing a bioinformatics framework for its future clinical development.