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Crystallography of NYSGRC Samples

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Metabolic Pathways—A list of metabolic pathways, and the enzymes involved in these pathways, could serve as a large and interesting basis for a target list aimed at determining the structure basis for catalytic activities in biology. Targets would be selected based on their biological relevance, unique sequence and structural signatures. The KEGG metabolic pathway database (www.genome.ad.jp/kegg/metabolism.html) was utilized to manually inspect, filter, and analyze those EC codes that represent enzymes with no known structures in the PDB. Large G-proteins—Sequence analysis across multiple genomes has revealed the existence of several highly conserved multi-domain GTP binding protein families. Since many of these families are poorly understood, we have initiated characterization and structure determination for several of these family members. Our aim will be to elucidate structure-function relationships between GTP-binding domains within these families, and to assign structure and putative function to the equally conserved but poorly understood domains associated with them.