(GSEA) (also functional enrichment analysis) is a method to identify classes of genes or proteins that are over-represented in a large set of genes or proteins and may have an association with disease phenotypes. The method uses statistical approaches to identify significantly enriched or depleted groups of genes. Transcriptomics technologies and proteomics results often identify thousands of genes that are used for the analysis.

Example: Zou YF, Meng LB, Wang QQ, He ZK, Hu CH, Shan MJ, Wang DY, Yu X. Identification and Functional Enrichment Analysis of Potential Diagnostic and Therapeutic Targets in Adamantinomatous Craniopharyngioma. J Comput Biol. 2019 Aug 19. doi: 10.1089/cmb.2019.0184. [Epub ahead of print] PubMed PMID: 31424286.