QIAGEN Ingenuity® Pathway Analysis (IPA®) | QIAGEN® Digital Insights

Analyze, compare and contextualize your biological data

Find biological meaning in your ‘omics data using advanced pathway analysis

It’s no small feat to understand the nuances in your biological data. Within there’s incredible power for discovery. Yet as a researcher, you need to unlock the secrets it holds by analyzing, comparing and contextualizing your results.

Luckily, QIAGEN IPA’s integrative analysis and visualization tools enable biologically meaningful data interpretation with evidence-backed insights. It lets you analyze your experimental data in the context of known biology, quickly narrow in on what is most important in your datasets and discover novel relationships.
IPA also helps you search for targeted biological information, build your own biological models and refine hypotheses to test at the bench.

Sample to Insight

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QIAGEN IPA’s Knowledge Base helps you uncover the “hidden” information in your biological data

✓ **IPA enables exploration and visualization of your hypotheses**

- Explore across >12 million findings
- Create your own interactive pathways and diagrams

✓ **Analyze** using IPA Core Analysis: Go beyond basic pathway analysis

- Discover the hidden causal relationships in your datasets
- Interpret your data with pathways, upstream drivers and downstream disease and functions among >12 million findings

✓ **Compare** using IPA Analysis Match: Automatically compare with more than $100 million worth of ’omics data

- Automatically match and compare your Core Analysis to our entire collection of 100,000+ disease-focused statistical comparisons
- Explore the activity of any pathway, regulator or disease of interest across our entire dataset collection
- Search any expression pattern subset in your dataset with Pattern Search

✓ **Contextualize** using Land Explorer for IPA: Find biological meaning using a massive collection of ’omics data

- Discover key differences between groups of samples within a Land database, by expression, mutation, metadata and more
- Quickly create survival plots from thousands of samples, grouped on metadata or ’omics data
- Explore sample-level data – expression, variations, fusions and more – from 600,000+ datasets
- Export ’omics comparison data for downstream analytics

Explore QIAGEN IPA’s comprehensive and integrated knowledge base for ’omics interpretation

- Causal networks
- Clinical trials (clinicaltrials.gov)
- Clinical databases (ClinVar, OMIM)
- Conserved domain database
- COSMIC
- Curated molecule-to-function, molecule-to-molecule and molecule-to-disease content
- Disease, signaling and metabolic pathways
- Drug and chemical data from DrugBank, Human Metabolome Database (HMDB), PubChem
- Expression atlases (GNF, NCI-60, The Human Protein Atlas)
- Gene identifiers/models: RefSeq, Ensembl, miRBase
- Gene ontology (GO)
- Human phenotype Ontology (HPO)
- HumanCyc metabolic pathways
- Isoform content: (GTEx tissue expression, APPRIS, literature curation)
- microRNA-target databases (TargetScan, TarBase, miRbase, miRecords)
- Mouse genome database (JAX)
- OncoTree
- Orphanet
- Protein-protein interaction databases (BioGRID, BIND, IntAct)
- Subcellular locations

Ready to try advanced pathway analysis with your own data?
Visit **digitalinsights.qiagen.com/IPA** to start your free trial.

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