



Discover the power of gene regulation
with German accuracy and precision

We integrate biology, chemistry,
computer science, and mathematics to
generate new theories and applications
for future health research

geneXplain GmbH, Wolfenbüttel, Germany



THE COMPANY

About us

Located in Wolfenbuettel, at the geographical center of Germany, geneXplain GmbH is one of the strategic life science units of the Lower Saxony region.

Worldwide known for its best-in-class biological databases and bio and chemo informatics software tools, our company serves as a reliable partner in life science research for pharma and biotech companies, as well as academic institutions all around the world.



OUR MISSION

Our mission is in supporting translational research and bringing the latest advances of systems biology, chemo and bio informatics to the clinic. We provide solutions for personalized and cohort drug target identification, selection and optimization of prospective drug compounds, as well as treatment response prediction and modeling.



THE TEAM

Uniting specialists in bioinformatics, biology, chemistry, programming, and applied mathematics, our team holds an outstanding expertise in life sciences, mainly in the context of precision medicine and pharmaco-genomics, with a special focus on gene regulation studies, where we are a recognized leader.



COLLABORATION

Being a highly active partner and coordinator in a big number of international biomedical research projects, the geneXplain name have become a recognizable brand in the global scientific community. We provide our clients and partners with top scientific expertise in gene regulation, making their research more effective and profitable.



OUR SOLUTIONS

We aim at supporting your research with the best-in-class biological databases and software tools for solving a broad range of bioinformatics, cheminformatics systems biology, and pharmacogenomics tasks.

OUR DATABASES

TRANSFAC[®] database of eukaryotic transcription factors, their genomic binding sites and DNA-binding profiles with a history of over 30 years behind, offering its users the biggest and most complete collection of positional weight matrices (DNA-binding models) suitable for a comprehensive analysis of genomic sequences for potential transcription factor binding sites.

HumanPSD[™] + **TRANSPATH**[®] – a unified resource, granting access to TRANSPATH[®] database of mammalian signal transduction and metabolic pathways, and HumanPSD[™] (Human Proteome Survey Database) containing information on diseases, their biomarkers, associated drugs and clinical trials.

BRENDA – world's largest manually curated database on enzymes and enzyme ligand data, all cross-linked to other major databases like KEGG, UniProt, MetaCyc, EMBL, NCBI. All enzymes in BRENDA are classified according to the biochemical reaction catalyzed, reaction kinetics are described in detail.

OUR SOFTWARE

geneXplain® platform

Comprehensive system for a broad range of bioinformatics applications. Includes Upstream Analysis (integrated promoter and pathway analysis) for identification of master regulators governing the studied pathological processes.

Genome Enhancer

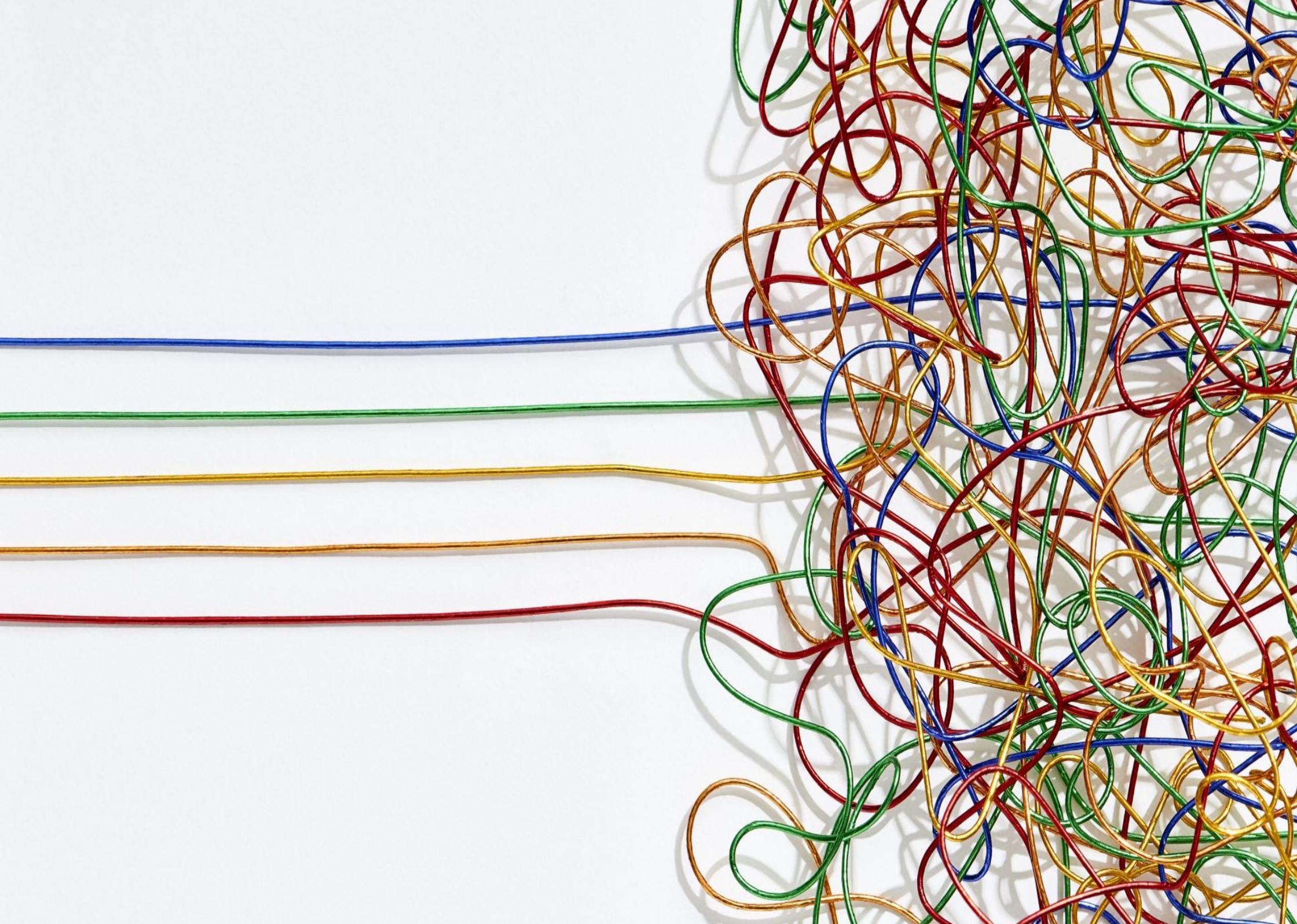
Fully automatized pipeline for patient multi-omics data analysis. Identifies prospective drug targets and corresponding treatments by full reconstruction of the pathology molecular mechanism.

MATCH Suite

This tool comprehensively addresses the syntax and semantics of gene regulation. It generates a comprehensive report on rigorously filtered transcription factors regulating the gene(s) of your interest in the indicated conditions.

PASS + PharmaExpert + GUSAR

Tools for prediction of potential biological activities of given compounds based on their structural formulas, selection of compounds with predefined biological activities and creation of quantitative structure-activity relationship models. .



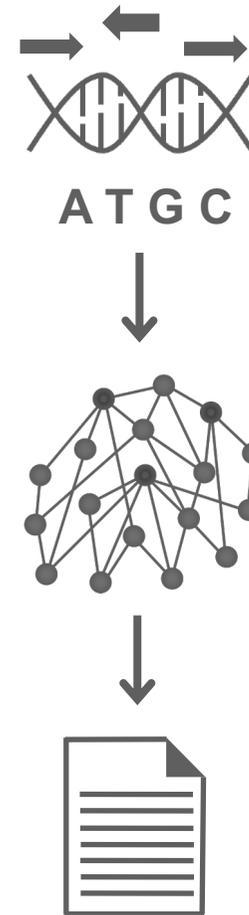
OUR SERVICES

What we offer

As a service provider we are pleased to offer you our excellence in gene regulation studies, as well as our unique approaches towards reconstruction of molecular mechanisms of the studied pathologies.

Our team holds superior expertise in bioinformatics, systems biology, chemistry, biology, artificial intelligence and machine learning – all you need to solve the biomedical research task of any complexity.

If you need to find out how a gene set of your interest is regulated, or process any types of raw omics data, – you know whom to reach out to.



We can provide a customized software pipeline – the fully automatized solution that will automatically process your input and will output the desired result in the form you would request for, including all kinds of graphics, reports, and various file formats.

Find further details on our solutions and offerings at www.genexplain.com





OUR CUSTOMERS

Our clients are located all over the world and each of them has found something special in our products for their particular needs. Big universities, as well as biotech and pharma corporations, tend to subscribe to our databases as to the biggest and most comprehensive information resources on:

- **gene regulation aspects** (including genes and proteins info, promoter and enhancer reports, transcription factors (TF) and their classification, information about individual experimentally validated TF binding sites, comprehensive collection of HTP TFBS data sets, and the most comprehensive library of TF DNA-binding models))
- **metabolic and signal transduction pathways** (including information on all known intercellular reactions, manually collected from scientific literature and documented with all experimental details in a strictly mechanistic way that includes all reaction partners and the taxonomic origin of each molecule as reported in the published experiment; pathway visualization and editing tool is included)
- **gene-drug-disease assignments coupled with the clinical trials info** (drugs targeting human proteins are reported, in addition, information can be retrieved on the molecular functions, biological roles, localization, and modifications of proteins, expression patterns across cells, tissues, organs, and tumors, consequences of gene mutations in mice, and the physical and regulatory interactions between proteins and genes)
- **enzymes and their ligands info** (comprises molecular data from more than 30,000 organisms, all acquired by manual extraction from primary literature, text and data mining, data integration, and prediction algorithms)

OUR CUSTOMERS

We are providing secure cloud solutions, as well as fully autonomous local installations of our tools and databases depending on the customer needs.

Our flexible package selection and pricing policy allow providing the best-fit solution for each particular client request.



Research groups worldwide, both academic and commercial, widely use our tools for solving such tasks as:

- **multi-omics data analysis** (on all levels starting from raw NGS data pre-processing and quality control operations, and ending with complex integration of RNA-seq, microarray, ChIP-seq, genomic variants, DNA methylation, proteomics, and metabolomics data on the studied pathological process into a comprehensive model of its molecular mechanism with master regulators identified)
- **Promoter analysis of target genes** (gene regulation studies with best-in-class database and associated tools)
- **Pathway analysis** (identification of pathways targeting the genes of your interest by building complete networks and pathways from molecules and their reactions)
- **Disease molecular mechanism reconstruction with prospective biomarkers and drug targets identification** (based on integrated promoter and pathway analysis with positive feedback loops identification)
- **Patient stratification** (based on the identified major subtypes of disease molecular mechanisms in respect to the master regulators found to be governing the pathological process under study)
- **Personalized drug target identification** (based on the partifucal master regulators found to be governing the pathology(ies) of the given patient case)
- **Prospective treatment selection** (based on the identified drug targets, prospective treatments are selected from approved drugs, drugs undergoing cinical trials, as well as drug-like compounds based on the cheminformatics analysis)
- **Biological activity profile prediction of drug-like compounds, including compound adverse or toxic effects prediction** (based on the complex cheminformatics analysis of the compound's structural formula in comparison to the compounds from the training set)



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