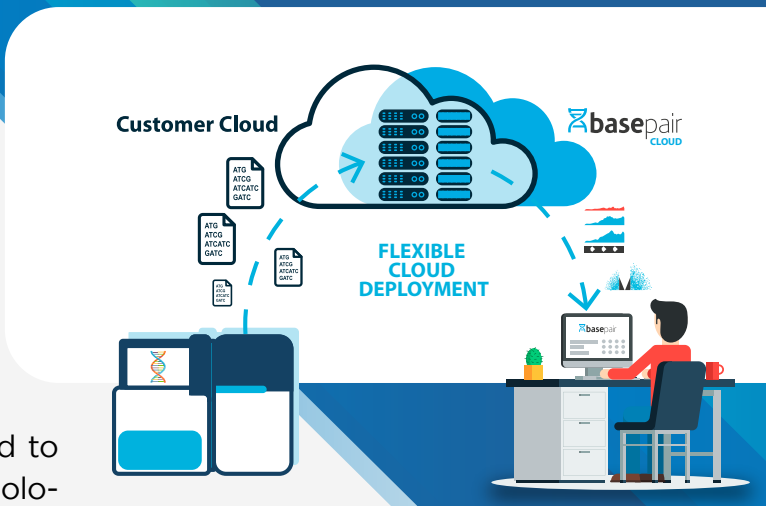
basepair

NGS Analysis, Delivered



Transform the way you analyze NGS data

BasePair is a second-generation SaaS platform designed to democratize the analysis of NGS data. Computational biologists can interact from the command line or using APIs and quickly deploy their approved workflows to biologists. The point-and-click GUI then allows the bench scientist to visually explore the data themselves in a controlled and interactive setting, collaborating with the bioinformatics team when they have an informed question.

Connected Cloud

- Flexibility to plug and play using the BasePair cloud or simply connect the platform to the storage and compute resources in your own cloud account
- Easily serve a global audience. Existing multi-region availability with low activation levels for new regions

Cost Effective

- Benefit from economies of scale offered by your cloud provider
- Use your own cloud resources - no expensive mark up on compute and storage
- Flexible pricing models including PAYG or annual licenses with a variety of usage bands

Automation and Integration

- Use REST, Python API or CLI to automate workflows, data ingestion, and more
- Integrate with upstream and downstream third party applications (e.g. instruments, LIMS, data lakes, etc)

Security

- BasePair has all the necessary certifications you would expect of a genomic analysis platform and all data is encrypted during rest and transfer
- For added security, connecting it to your own cloud account means no data or compute ever has to happen outside your IT approved environment

Provide more NGS analysis solutions without additional hires or infrastructure

As an R&D team you pride yourself on the use of advanced methodologies to generate high quality data and perform cutting edge science. Yet the value of the data generated is only as good as the capacity to make sense of it. Limiting this work to a select few, often because of technology limitations, especially for routine analyses, leads to increased data analysis turnaround times and ultimately reduced efficiency in R&D teams. What if you could combine easy deployment of validated workflows with the dev ops management of a bioinformatics platform, all whilst leveraging the compute and storage resources in your own cloud account? Introducing BasePair.... Analysis, Delivered.

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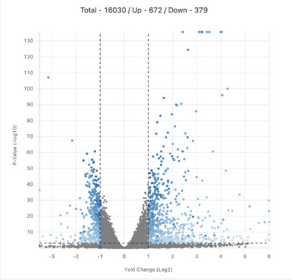
basepair

Meaningful results with beautiful visuals and interactive reports

Use Basepair's user-friendly interface to give the colleagues you work with easy to understand results. Our out-of-the-box pipelines support the more common NGS data types, including bulk single cell RNA-seq, ChIP-seq, ATAC-seq, WES, and WGS, but if you can't find what you need its quick and easy to bring your own to the platform as a dockerized container.

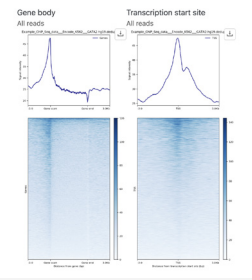
03 TRANSCRIPTOMICS

Use tools like STAR, DESeq2, and Seurat to perform alignment, gene quantification, and differential expression analyses or run the 10x cellranger pipelines directly in Basepair



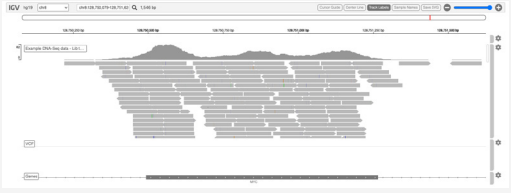
02 EPIGENETICS

Run peak calling and motif analysis on your Epigenetics data like ChIP-seq and ATAC-seq using tools like MACS2, SEACR, and Homer



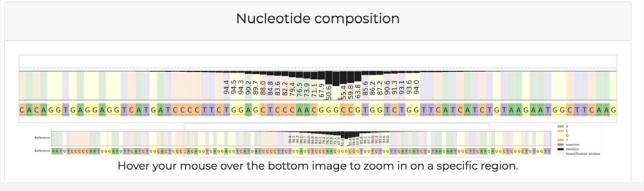
01 WGS & WES

Use tools like BWA, GATK4, Mutect, and Sentieon to perform alignment and variant calling on your Whole Genome, Whole Exome, or Panel data and visualize the results in an integrated genome browser.



04 CRISPR

Analyze CRISPR data using Crispresso for NGS data or TIDE for Sanger sequencing data



Flexible Pricing

Option to pay-as-you-go with per sample pricing and no up front commitment, or alternatively take advantage of annual licenses with a variety of usage bands to benefit from volume discounting.

Some of our Customers

HARVARD MEDICAL SCHOOL · Memorial Sloan Kettering Cancer Center · ACTIVE MOTIF · NEW YORK UNIVERSITY · Stanford University · YOUSEQ · nkarta THERAPEUTICS · Vitrolife

Basepair is trusted by top companies and hospitals, and Basepair-powered research is consistently published in high impact journals like Cell, Nature, Cancer Cell, and more.

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