## FORM BIO

# Built to work with PacBio.

GET FROM HIFI READS TO BREAKTHROUGH INSIGHTS WITH A FRACTION OF THE EFFORT, TIME AND COST.

# N **Our Platform**

Your complete operating system for end to end PacBio sequencing data analysis:

### DATA MANAGEMENT

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Form makes uploading and organizing your data a breeze.

### DATA VISUALIZATION

Build interactive charts and graphs to visualize and share results.

### 👯 WORKFLOW EXECUTION

Dozens of verified workflows for genomics, proteomics and more.

### 🙅 RESEARCH COLLABORATION

Invite internal and external colleagues to work on research together.

# **Services and Solutions**

Get even more from your PacBio investment.

### Biomatic Bioinformatics as a service

Let Form Bio handle your bioinformatics needs to augment your existing programs or start from scratch.

✓ Full service bioinformatics with available SLAs

Use your existing cloud infrastructure or rely on us

 Dedicated account manager and direct access to our expert team

	Workflows		Q. Search
y Mammoth 🛛 👻		avourite	a veren
lome	Category	RNA Seq	
lle Manager	Q Eukaryotes	RNA Sea Genome Editing Genomics	RNA Seg Genome Editing Cancer
Vorkflows	Gene Alignment	Expression Analysis	Expression Analysis (SRA)
Aembers	& Gene Finding	FormBio® certified This pipeline can bu used to determine cane abundances.	Formitie® certified This pipeline can bu used to determine cene abundan
	Gene Regulation	splice variants and differential expression analysis of project data	splice variants and differential expression analysis of S data.
	G Genome Editing		
	X Genomics		
	RE NGS	RNA Seq (Blast Search) Cancer Expression Analysis and Fusion Detection in	RNA Seq Genomics (NGS) Differential Expression Analysis from Gene
	O Oglio Design	Human Tumors FormBioS certified	Abundance Tables FormBiels certified
	∿ Protein	This pipeline can bu used to determine gene abundances, splice variants, gene fusion events, skipped exons and	This pipeline can bu used to re-calculate differential g expression from samples previously analyzed by the
	O Prokaryotes	differential expression analysis using project data	expression detection workflows
	🖍 RNA		
	☆ Label	(RNA Seq) Genome Editing (Blast Search) Recount3 Data Download	
VID	& Structure	Formilie's certified	
	# Trait Association	This pipeline can bu used to download count and FPKM data from recount3	

# **PacBi**

With a few clicks, run PacBio optimized workflows including:

### **AAV PacBio QC**

Characterize the quality of AAV vector manufacturing

### Long Read Assembly

Generate reference-quality de novo assemblies

### Metagenomics

Analyze how microbial communities function and interact with their environments

### AND MUCH MORE

### **More services**

### ADUANCED SOLUTIONS

Premium, Al-based solutions tailored to specific R&D and manufacturing challenges

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### CUSTOM WORKFLOWS

Bespoke development of workflows that can be run on our platform with PacBio output data

### BIOINFORMATICS TRAINING & CONSULTING

Expert guidance for architecting and operating your ideal computational life science program

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