

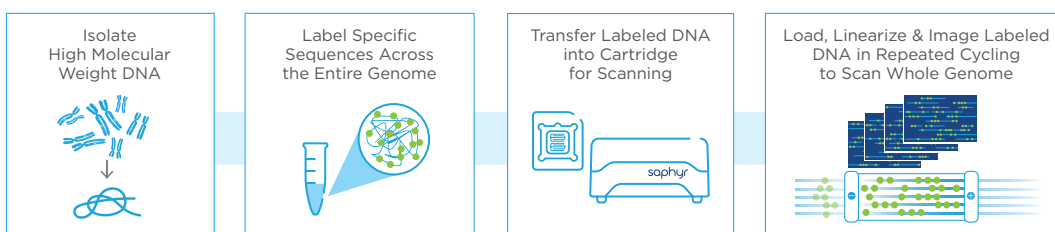
## Increase Scalability and Flexibility with Bionano Compute On Demand

Bionano Compute On Demand is a pay-per-use solution accessible through Bionano Access web server for your Bionano Solve operations. Compute On Demand simplifies the way you perform genome assembly, hybrid scaffolding and structural variant analysis, without the need of any additional infrastructure, giving you the flexibility and scalability your experiment deserves.

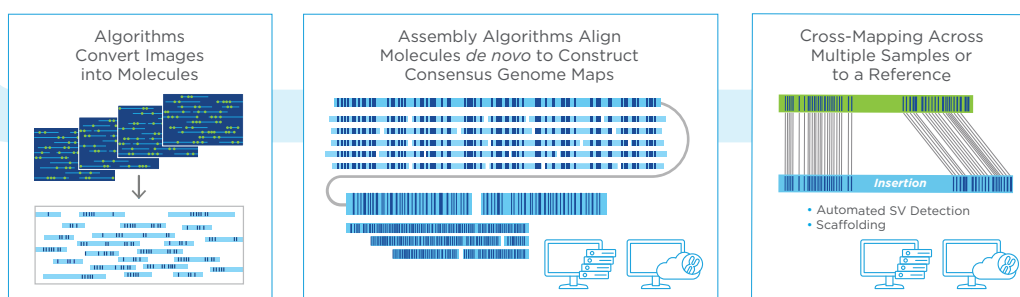
### Advantages include:

- Analyze large genomes and high number of samples simultaneously
- Perform pipeline analysis operations without worrying about server capacity
- Data encrypted for secure operations
- Data centers compliant with HIPAA, CSA, SOC2, HDS, ITAR regulations
- Genomic data accessible only to end users and deleted post-processing

### SAPHYR® WORKFLOW



### High-throughput, High-resolution Imaging of Megabase Length Molecules



### OVERVIEW OF COMPUTE OPTIONS

Choose the right option or a combination for your computing needs



#### COMPUTE SERVER

- Expect to run servers for >25% of the time
- Execute consistent loads
- Internet access not permitted
- Optimized for human-sized genomes



#### COMPUTE ON DEMAND

- Execute variable workloads
- No upfront server costs required
- Receive data from service providers
- Optimized for human and non-human genomes up to 24 Gpb genome size

Learn more at [bionanogenomics.com/computeondemand](https://bionanogenomics.com/computeondemand)

## TYPICAL RANGES FOR BIONANO SOLVE PROCESSES

	US Tokens		Canada Tokens		Europe Tokens		Typical Time to Complete**
	typical	min / max	typical	min / max	typical	min / max	
<b>Human</b>							
<i>De novo</i> assembly*, 400 Gbp	10	1/15	44	1/51	12	1/24	12-24 hours
<i>De novo</i> assembly*, 800 Gbp	12	1/17	46	1/57	16	1/26	25-50 hours
Rare Variant Analysis*, 1500 Gbp	5	3/25	9	3/25	6	3/25	10-20 hours
EnFocus™ FHSD/Fragile X	2	1/5	3	3/5	2	1/5	2-4 hours
<b>Non-Human</b>							
Emmer wheat, 880 Gbp ( <i>de novo</i> assembly)	48	20/250	61	20/250	50	20/250	22-44 hours
Maize, 250Gbp ( <i>de novo</i> assembly)	10	1/50	13	1/50	10	1/50	5-10 hours
Hummingbird, 95 Gbp ( <i>de novo</i> assembly)	4	1/50	7	1/50	4	1/50	3-6 hours

Assembly runs may vary based on quantity and quality of the input data.

Good quality data as defined as having Map Rate > 80%, molecule N50 (>20kbp) > 180kbp.

\**de novo* assemblies without a reference will require more processing to first generate an automatic rough assembly. The "max" may also vary based on quality of input data.

\*\*Time to complete hours are estimated based on the users of the current version of Bionano Access and availability of cloud resources

To get started, contact your sales representative or email [orders@bionanogenomics.com](mailto:orders@bionanogenomics.com)

CATEGORY	Part No.	Product
COMPUTING HARDWARE	80013	Saphyr Compute Server
	80014	Bionano Compute Server
COMPUTING CLOUD	90047	Bionano Compute On Demand, US
	90128	Bionano Compute on Demand, Canada
	90052	Bionano Compute On Demand, Germany
	90060	Bionano Compute On Demand, Europe

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