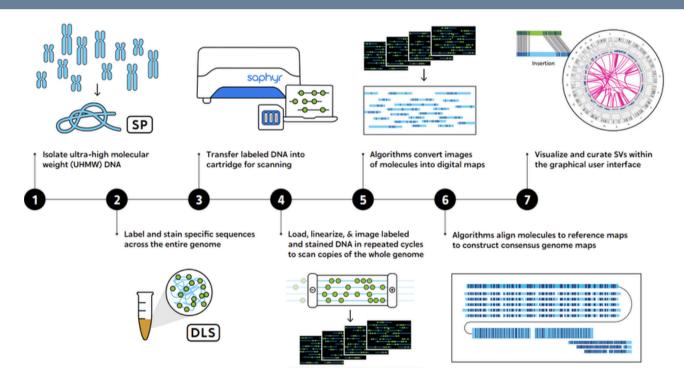


Bionano Compute Solutions: Flexible and Scalable On-premise and Cloud Computing Options

Bionano compute solutions include a complete suite of hardware, software, and cloud-based solutions for end-to-end experiment management and bioinformatics processing of OGM data. The Saphyr[®] Compute Server and Bionano™ Compute Server offer on-site cluster-like performance in an affordable, compact solution, capable of performing multiple simultaneous analyses and sustaining continuous throughput. 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.

SAPHYR® WORKFLOW



OVERVIEW OF COMPUTE OPTIONS



COMPUTE SERVER

- Control compute costs with on premise solution
- · Execute consistent workloads
- · Internet access not required
- · Reliable access to compute resources



COMPUTE ON DEMAND

- · Execute variable workloads
- · No upfront server costs required
- Data centers compliant with IPAA, CSA, SOC2, ITAR regulations
- Work on large genomes up to 24 Gbp genome size



Typical Ranges for Bionano Solve Processes								
HUMAN	North America Tokens		Germany Tokens		Europe Tokens		Typical Job Processing Time**	
Compute On Demand	typical	min/max	typical	min/max	typical	min/ max		
De novo assembly*, 400 Gbp	9	1/22	22	1/38	10	1/29	12-24 hours	
De novo assembly*, 800 Gbp	12	1/25	25	1/45	11	1/31	18-50 hours	
Rare Variant Analysis, 1500 Gbp	8	3/38	24	3/38	8	3/38	10-12 hours	
Rare Variant Analysis, 5Tbp	30	5/75	95	5/125	30	5/75	15-30 hours	
EnFocus™ FSHD/Fragile X	4	1/8	7	3/8	4	1/8	2-4 hours	
Guided Assembly, Constitutional 800Gbp	10	3/38	17	3/64	10	3/38	8-20 hours	
Guided Assembly, Low Allele Frequency 1500Gbp	11	3/38	12	3/64	11	3/38	10-20 hours	
Compute Server, Gen4	Typical	Typical Time to Complete† Typi				pical Sample Throughput††		
				ONE SERVER		TWO SERVERS		
De novo assembly*, 400 Gbp	10-16 hours			10-16 per week		20-30 per week		
De novo assembly*, 800 Gbp	13-20 hours			8-12 per week		20-30 per week		
Rare Variant Analysis, 1500 Gbp	5-8 hours			20-30 per week		40-60 per week		
EnFocus™ FSHD/Fragile X	1-2 hours			Up to 60 a week		N/A		

Token ranges provided here are typical for good quality data, defined as having Map Rate > 80%, molecule N50 (>20kbp) > 180kbp. Actual min/max ranges are calculated for each submitted compute job based on data quantity and quality.

[#]Estimated sample throughput based on typical processing time of good quality data with network access to compute resources spanning 7 days per week.

	Part No.	Product			
Computing Hardware	80083	Saphyr Compute Server, Gen4			
	80084	Bionano Compute Server, Gen4			
Cloud Computing	90047	Bionano Compute On Demand, US			
	90052	Bionano Compute On Demand, Germany			
	90060	Bionano Compute On Demand, Europe			
	90128	Bionano Compute On Demand, Canada			

Contact your Bionano Regional Business Manager to get started. 858.888.7600 | orders@bionano.com

^{*}de novo assembly runs without a reference will require more processing to first generate an automatic rough assembly. The "max" may 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. Queue time to initate processing with

cloud resources can vary significantly.
†Typical time to complete hours are estimated based on internal tests processing good quality data using the current version of Bionano Access.