

Bio-Silicon Labs

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Bio-Silicon Valley



BSLV Exam 2026 – Official Prospectus

Bio-Silicon Labs Vision (BSLV) Exam

Organized by *Bio-Silicon Labs & DRY eWorks*
(An Autonomous Research & Innovation Organization under Bio-Silicon Valley Initiative)

05 November 2025

Inviting Online Applications for Bio-Silicon Labs Vision (BSLV) Exam – 2026

The **Bio-Silicon Labs Vision (BSLV) Exam** is an International **Bioinformatics** Competitive examination for pursuing research in biotechnology to NGS, AI-driven genomics, BigData handling, Quantum algorithms, Molecular simulation, XR, and advanced workflows. Apply here : www.biosiliconlabs.com/BSLV

Important Dates, Fee & Application Procedure

Online Registration & Submission of Application Form	05 November – 07 January
Last Date of Fee Payment (Card / Net Banking)	31 Jan 2026 (up to 11:50 PM UTC)
Date of Examination (BSLV 2026)	01 November 2026 (Sunday)
Duration of Examination	180 minutes (03 hours)
Exam Timing	10AM - 13 PM others & U.S 17 - 20 (UTC)
Mode of Examination	CLI-Based Bioinformatics Test (Remote BSLV-Machine via Terminal)
Syllabus	Given in Information Bulletin Below

Fee payable for BSLV– 2026:

Examination	Developing Countries	Developed Countries
BSLV	₹1000 / EWS- ₹500	\$100 / EWS- \$50

Sci. Abhinandan Yadav
(Bioinformatics AI Scientist)
Founder Bio-Silicon Labs

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About the BSLV Exam

The Bio-Silicon Labs Vision (BSLV == Bio-Silicon Valley) Exam is a pioneering bioinformatics-specific competitive exam designed to identify and empower real-world talent on an international and global level. It is a unique initiative to:

- Fully reward top scorer with crowd funded amount of this exam.
- Evaluate candidates through CLI-based real-time secure testing.
- Offer direct access to internships, R&D fellowships, and startup incubation.

Exam Details

Name: [BSLV Exam 2026](#)

Organizers: Bio-Silicon Labs, DRY eWorks & Vision@EnterprizeNX-01

ELIGIBILITY CRITERIA

Academic Qualification: Bachelors (B.Sc/ B.E./ B.Tech./ M.B.B.S.), Masters (M.Sc./ M.Tech./ M.VSc./ M.Pharm./ Integrated M.Sc./M.Tech.) and PhD in any discipline of Biotechnology, Life-Sciences or any other allied areas of Bioinformatics. Those who are yet to appear in the final semester examination or awaiting result of final semester examination are also eligible to apply.

Marks: Minimum 60% of marks for all aspirants (or equivalent grades).

Application Fee: • Developing Countries (eg. India): ₹1000 (Standard), ₹500 (Weaker Sections))
• Developed Countries (eg. US, Europe: \$100 (Standard), \$50 (Weaker Sections))

Fellowships: for Direct PhD / Scientist position

- ~*1000 applicants from Developing Countries(**₹10,00,000 Fellowship**)
- ~*350 applicants from Developed Countries(**\$35,000 Fellowship**)

Mode: CLI-based Online Exam

Top 100 Candidates will be called for the Interview Round at Bio-Silicon Labs.

Topper: Receives 100% of applicant pool fee as annual salary (e.g., 10,00,000 for *1000 developing country applicants and \$35000 for developed country)

Next Top 10: Offered full-time R&D Internship

Next Top 50: Offered bootcamps, and courses

Exam Format

Practice Phase – System Setup & Terminal access Challenge

ssh candidateid@biosiliconvalley

BSLV-Machine: Virtual Machine Installation and testing for actual exam.

VM locks to full screen; only one-time ID login. Timed challenges (5–7 seconds per question). Application-based coding + reasoning - **human touch required*. If you know it, you make it. No questions repeated, No going back.

Phase 1 – Interactive CLI-Based Exam

Real-world questions on NGS, AI, Genomics & allied fields, with responses stored and shared as soon as the exam gets over, a copy stored in VM for authenticity.

PATTERN OF EXAMINATION

Type	Questions	Time / Q	Total Time
Ultra-short	400	5 sec	33 min 20 sec
Short MCQ	70	20 sec	23 min 20 sec
Medium reasoning	20	1 min	20 min
Long analytical	10	5 min	50 min
Active test time	500	—	2 h 6 min 40 sec

Breaks: 10-15 minutes after every 100 questions (4 breaks = 55 min).

Total Exam Time including breaks: **3hrs**.

Block-wise Structure

Block	Range	U/S/M/L	Block Time	Break	Cumulative Time
1	1–100	80/14/4/2	25:20	10:00	35:20
2	101–200	80/14/4/2	25:20	10:00	1:10:40
3	201–300	80/14/4/2	25:20	10:00	1:46:00
4	301–400	80/14/4/2	25:20	10:00	2:21:20
5	401–500	80/14/4/2	25:20	+15min(Review)	3:00:00 (END)

Post-Exam Feedback

Candidates receive a score sheet with score, percentile, and hash ID.

Phase 2 – *Top 100 Candidates will be called for the Interview Round at Bio-Silicon Labs. *Final selected Fellows(3-5) can choose* a 3-year **PhD** program or 1-year **Scientist** position. Other **Top 60 Candidates** receive full-time R&D Internship, Offered bootcamps, and courses.

Benefits

For **Top 60-70 Candidates**. *Final selected Fellows(3-5) can choose* a 3-year **PhD** program or 1-year **Scientist**, *receiving the entire collected exam fee as a reward*. Next Top 10: Offered full-time R&D Internship, Next Top 50: Offered bootcamps, and courses.

Region	Top Performer Reward
Developing Countries	₹10,00,000
Developed Countries	\$35,000

- Entry into the Bio-Silicon Valley innovation ecosystem
- Work with real-time data, Quantum -AI models, and biotech systems
- Our current work on Space Biotechnology, which is an interesting one and you can join us in that too.
- Direct collaboration opportunities with NGS and precision medicine pipeline dev work i.e for PRS.

[Apply Now](#)

Website: www.biosiliconlabs.com/BSLV

Contact: abhinandan@biosiliconlabs.com or +91 8802273055

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BSLV Exam Syllabus (Detailed Guide)

1. Core Bioinformatics with NGS

- **Sequence Analysis:** DNA, RNA, and Protein sequence alignment (global vs local, multiple sequence alignment).
- **File Formats:** FASTA, FASTQ, SAM/BAM, GFF, VCF - structure, usage, and parsing.
- **Reference Genome & Indexing:** Bowtie2, BWA, STAR - how reference indexing works.
- **NGS Pipeline Concepts:**
 - Quality control (FastQC, MultiQC)
 - Adapter trimming (Trimmomatic, Cutadapt)
 - Mapping and alignment
 - Variant calling (GATK, FreeBayes, bcftools)
 - Expression quantification (featureCounts, HTSeq)
 - Differential expression (DESeq2, edgeR)
 - Annotations to gene functions
 - Conclusive flowcharts
- **Transcriptomics:** RNA-seq pipeline overview; normalization (TPM, FPKM, RPKM).
- **Metagenomics:** Assembly vs binning; taxonomic profiling. Binning vs Mapping.
- **Epigenomics:** DNA methylation, ATAC-seq, and histone modification basics.
- **Data Integration:** Combining omics datasets (multi-omics approaches).

Points to Look For:

- Logic behind read alignment algorithms.
- Interpreting sequencing errors.
- Real-world applications (e.g., precision medicine, rare disease discovery).

2. Molecular Docking and Dynamic Simulations

- **Docking Fundamentals:**
 - Types: Rigid, flexible, blind docking.
 - Scoring functions and binding affinity.
 - Docking software: AutoDock, Vina, Schrödinger Glide.
- **Ligand and Receptor Preparation:**
 - Energy minimization.
 - Water molecule role and removal.
 - File formats (PDB, MOL2, PDBQT).

- **Molecular Dynamics (MD):**
 - Force fields (CHARMM, AMBER, GROMOS).
 - Solvation and ionization.
 - Temperature and pressure control.
 - Equilibration and production runs.
- **Post-simulation Analysis:**
 - RMSD, RMSF, radius of gyration, hydrogen bonding.
 - Free energy calculation (MM-PBSA/MM-GBSA).
- **Visualization Tools:** PyMOL, Chimera, VMD, UCSF ChimeraX.

Points to Look For:

- Understand energy landscapes.
- Interpretation of binding affinity and MD plots.
- Quantum docking vs. classical docking concepts.

3. Programming Knowledge

- **Languages:** Python, R, Shell scripting (focus on practical bioinformatics use cases).
- **Key Python Libraries:** Biopython, pandas, numpy, matplotlib, scikit-learn, TensorFlow, PyTorch.
- **Key R Packages:** DESeq2, ggplot2, dplyr, edgeR.
- **Command-Line Tools:** grep, awk, sed, cut, sort, uniq.
- **File I/O Operations:** Parsing FASTA, GFF, and VCF files.
- **Automation:** Snakemake, Nextflow, and workflow pipelines.

Points to Look For:

- Code understanding.
- Handling large biological datasets efficiently. File handling, ETL ways.
- Implementing algorithms for real problems (e.g., motif finding, clustering).

4. Database Development

- **Database Basics:** SQL vs NoSQL; Graph Dbs.
- **Schema Design:** Entity-relationship modeling for biological data.
- **Biological Databases:** GenBank, UniProt, PDB, Ensembl, GEO, KEGG, Reactome.
- **APIs and Integration:** Accessing data programmatically (NCBI Entrez, EBI APIs).
- **Web Development:** Flask/Django-based bioinformatics dashboards.
- **Data Curation:** Cleaning and annotating large-scale biological datasets.

Points to Look For:

- How biological databases are structured and maintained.
- Real-time data retrieval and storage methods.
- Efficient indexing and query optimization.

5. Hardware Details Required for Working

- **Basic Hardware Setup:** CPU, GPU, RAM requirements for NGS pipelines.
- **High-Performance Computing (HPC):** Clusters, SLURM job scheduling.
- **Parallel Computing:** MPI, CUDA, multithreading in genomics.
- **Cloud Platforms:** AWS, GCP, Azure for Bioinformatics workloads.
- **Data Storage and Backup:** SSDs vs HDDs, RAID systems, networked storage.

- **Edge & Quantum Devices:** Bioinformatics on embedded systems or quantum simulators.

Points to Look For:

- How computational resources affect bioinformatics workflows.
- Cost-effective system setups for research labs.
- Concept of quantum hardware for bio-data analysis.

6. Concepts Behind Software (e.g., BLAST, Seq to Structure Prediction, Live graphs ...)

- **BLAST Algorithm:** Word seeding, scoring matrices (BLOSUM, PAM), alignment extension.
- **Algorithm:** Local alignment principle and heuristic search. MSA (ClustalW, MegaN).
- **Hidden Markov Models (HMMER):** Protein domain search.
- **Sequence Assembly:** De Bruijn Graph, Overlap-Layout-Consensus (OLC).
- **Read Mapping:** Smith-Waterman, Needleman-Wunsch, Burrows-Wheeler Transform (BWT).
- **Structural Prediction Tools:** AlphaFold, RoseTTAFold, MODELLER basics.
- **Full Stack Development:** Data fetching and hosting for live interactive graphs.

Points to Look For:

- Logic behind algorithmic design, not just tool usage.
- Complexity trade-offs (speed vs accuracy).
- Understanding the evolution of bioinformatics algorithms.

7. Algorithms / Concept to Code

- **Basic Algorithms:**
- Sorting, searching, graph traversal.
 - Dynamic programming (alignment algorithms).
- **Bioinformatics-Specific:**
- Sequence alignment, clustering, motif search, gene prediction.
 - Assembly algorithms (Contigs, Scaffold - SPAdes, Velvet).
- **Optimization Techniques:**
- Gradient descent, simulated annealing, genetic algorithms.
- **Complexity Analysis:** Big O notation and efficiency optimization.

Points to Look For:

- Convert theory to working code.
- Algorithmic thinking for biological data problems.
- Writing basic scripts for test datasets.

8. ML, DL, AI, GenAI, Agentic AI

- **Machine Learning:** Regression, classification, clustering, PCA.
- **Deep Learning:** CNNs, RNNs, Transformers in genomics and proteomics.
- **Generative AI:** Text-to-protein models, structure prediction using LLMs.
- **Agentic AI:** Autonomous agents in bioinformatics pipelines (AI-driven workflow automation).
- **Reinforcement Learning:** Applications in drug design and molecule optimization.
- **Explainable AI (XAI):** Feature interpretation for biological models.

Points to Look For:

- Practical examples of ML/DL in NGS and drug discovery.
- Training vs inference trade-offs.
- Integration of AI models with biological databases.

9. Latest Bioinformatics Trends

- **Quantum Bioinformatics:** Quantum computing for NGS, structure prediction, and molecular docking.
- **Multi-Omics Integration:** Genomics, Transcriptomics, proteomics, metabolomics, epigenomics.
- **Single-Cell Analysis:** scRNA-seq pipelines, trajectory inference.
- **Synthetic Biology & Digital Twins:** In-silico simulation of biological systems.
- **Space Bioinformatics:** Radiation effects/Biomarkers evolution in DNA, bioreactor simulations for space.
- **XR in Bioinformatics:** AR/VR-based molecular visualization and education.
- **Bioinformatics for Personalized Medicine:** PRS, genotype-to-phenotype prediction.

Points to Look For:

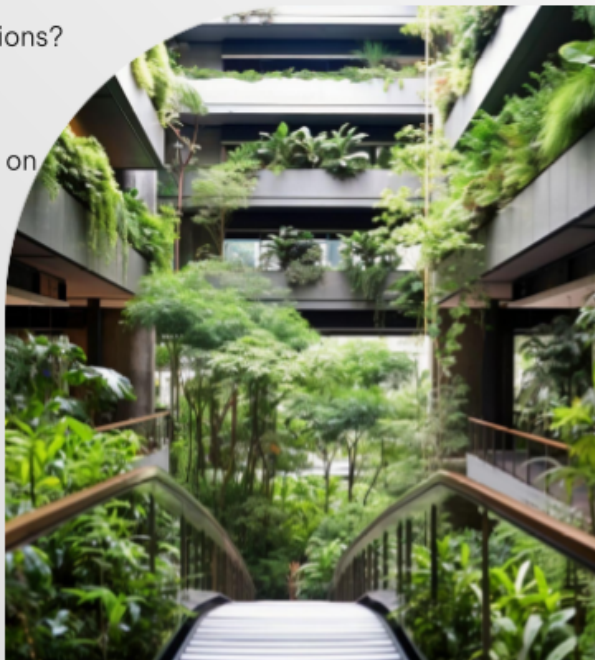
- Awareness of cutting-edge technologies.
- Interdisciplinary integration mindset.
- Translational impact - from computation to real biology.

ALL the Best! @ Bio-Silicon Labs Vision

THANK YOU!

Do you have any questions?

Explore our research work on



CONTACT US!

Welcome(Abhinandan) to Bio-Silicon Labs
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