

NTHRYS

OPC PVT LTD

CATALOGUE 02 • NBSQ

Sequence Alignment & Similarity Search

A complete industrial catalogue of hands-on training modules in sequence comparison — from substitution matrices and dynamic-programming alignment to BLAST+ deployment, profile-based remote homology detection, whole-genome alignment and automated search pipelines. Every module is issued against its own controlled protocol, contact-hour allocation and published fee.

59 PROTOCOL-BACKED MODULES • 10 CATEGORY STREAMS

1634 CONTACT HOURS • 2026 EDITION

59

MODULES

10

STREAMS

1634

HOURS

59

PROTOCOLS

Program Categories at a Glance

This catalogue lists every alignment and similarity-search method our training programs are equipped to operate and teach, organised into 10 technology streams. Each module carries a unique product code, a controlled protocol document, an individually assessed contact-hour allocation and its own published fee. No two protocols are priced alike — duration and fee follow the algorithmic depth, compute load and assessment weight of that specific module.

STREAM	CATEGORY	FOCUS DESCRIPTION	MODULES	HOURS	DAYS	BUNDLE (INR)
NBSQ-FD	Alignment Foundations & Scoring Systems	Homology concepts, matrices, gaps & statistics	6	126	23	37,100
NBSQ-PW	Pairwise Alignment Algorithms	Dot plots & dynamic-programming alignment	6	160	28	48,400
NBSQ-BL	BLAST Family & Web Search	Seeding, extension & the five BLAST programs	6	150	27	45,000
NBSQ-CL	Command-Line BLAST & Local Databases	BLAST+ deployment, custom databases & batching	6	162	28	50,100
NBSQ-SN	Sensitive & Profile-Based Search	Iterative, pattern & HMM-driven homology detection	6	196	35	61,700
NBSQ-FA	Fast Heuristic & High-Throughput Aligners	FASTA, DIAMOND, MMseqs2 & benchmarking	6	174	31	53,900
NBSQ-GN	Genomic & Long-Sequence Alignment	Whole-genome comparison, anchoring & synteny	6	190	33	59,100
NBSQ-SP	Specialised Alignment Problems	Spliced, protein-to-genome & constrained alignment	5	140	25	43,800
NBSQ-AU	Automation, Parsing & Search Pipelines	Scripted alignment, output parsing & reporting	6	184	32	57,300
NBSQ-AP	Applied Similarity Analysis	Orthology, annotation transfer & screening	6	152	28	46,600
Complete NBSQ catalogue			59	1634	290	384,600

HOW TO READ A MODULE CODE

NBSQ – FD – 01

NBSQ
Nthrys Bioinformatics catalogue — Sequence Alignment & Similarity Search

FD
Category stream code

01
Module number within the stream

HOW TO READ A PROTOCOL REFERENCE

PRT/NBSQ/FD/01

PRT
Controlled protocol held in the training SOP register

NBSQ/FD/01
Maps one-to-one to the module code alongside

Bundle figures are the discounted price for enrolling in every module of that stream together. Individual module hours and fees are printed on each category page. All fees exclude applicable GST.

Every Module Is a Controlled Protocol

There is no flat course fee in this catalogue. Each module is written up as its own protocol document, timed against the work it actually contains, and priced on that basis — contact hours, algorithmic and compute load, number of tools operated and the depth of the assessment task.

CONTENTS OF EVERY PRT DOCUMENT

01

Scope & competency statement

What the trainee will be able to do on completion, mapped to the module code.

02

Resource inventory

Tools, versions, reference databases and datasets recorded before start.

03

Stepwise procedure

Numbered operations with decision points, parameters and expected intermediates.

04

Worked reference exercise

A supplied query and subject set with the correct output for self-verification.

05

Acceptance criteria

The result a trainee must reproduce for the protocol to be signed as complete.

06

Failure modes & troubleshooting

Known error states, misleading hits and how each is resolved.

07

Assessment task & marking

The independent task, its weighting and the pass threshold.

08

Completion record

Trainer sign-off, date, hours logged and certificate serial entry.

MODULE DURATION RANGE

16 – 44 hours

Allocated per protocol, not per tier. A scoring-concepts module runs 16 hours; profile-profile remote homology detection runs 44.

MODULE FEE RANGE

INR 5,400 – 16,600

Set individually against each protocol. Iterative profile search, genome-scale alignment and pipeline construction carry the highest compute and supervision load.

1634

290

59

TOTAL HOURS

TOTAL DAYS

PROTOCOLS

ENROLMENT OPTION	SCOPE	HOURS	FEE (INR)	SAVING
Single Module	Any one module code, priced as printed on its category page	16 – 44	5,400 – 16,600	—
Stream Bundle	Every module within one category stream	126 – 196	37,100 – 61,700	15%
Core Alignment Track	Streams FD, PW, BL, CL, SN — 30 modules	794	222,400	22%
Professional Track	Streams FD through SP — 47 modules	1298	338,000	28%
Complete NBSQ Catalogue	All 10 streams — 59 modules, 59 protocols	1634	384,600	35%

WHAT THE MODULE FEE INCLUDES

— Workstation access — dedicated Linux workstation for the logged hours of the module

— Issued protocol — the controlled PRT document, retained by the candidate

— Reference datasets — query sets, subject databases and verified reference outputs

— Certification — serially numbered certificate quoting module code, protocol reference and hours

— Post-training support — 60 days of query support by email

ENROLMENT & PAYMENT TERMS

— Registration — INR 1,000 per candidate, adjusted against the module fee

— Taxes — GST applicable at prevailing rates over and above listed fees

— Live-online mode — 80% of the listed on-campus fee for eligible modules

— Concessions — 10% for groups of three or more; 15% against a valid institutional identity card

— Scheduling — rolling monthly intakes; custom dates for institutional groups

— Validity — fees quoted for the 2026 edition, confirmed at the time of enrolment

01

CATEGORY • NBSQ-FD

Alignment Foundations & Scoring Systems

Homology concepts, matrices, gaps & statistics

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-FD-01	Similarity, Homology & Identity Concepts Orthology, paralogy & the limits of percent identity.	PRT/NBSQ/FD/01	16 HOURS	03 DAYS	5,400
NBSQ-FD-02	PAM Substitution Matrix Series Derivation, evolutionary distance & correct application.	PRT/NBSQ/FD/02	20 HOURS	04 DAYS	6,900
NBSQ-FD-03	BLOSUM Matrices & Matrix Selection Block-derived matrices & choosing by divergence.	PRT/NBSQ/FD/03	22 HOURS	04 DAYS	7,600
NBSQ-FD-04	Gap Penalty Models & Affine Gaps Open/extend costs & their effect on alignment shape.	PRT/NBSQ/FD/04	18 HOURS	03 DAYS	6,200
NBSQ-FD-05	Alignment Statistics: E-value & Bit Score Karlin-Altschul framework, P-values & search space.	PRT/NBSQ/FD/05	26 HOURS	05 DAYS	9,200
NBSQ-FD-06	Alignment Quality Assessment & Artefacts Spurious hits, coverage checks & over-alignment.	PRT/NBSQ/FD/06	24 HOURS	04 DAYS	8,400

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 126 HOURS • 23 DAYS

~~43,700~~ 37,100 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

02

CATEGORY • NBSQ-PW

Pairwise Alignment Algorithms

Dot plots & dynamic-programming alignment

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-PW-01	Dot-Matrix & Dot-Plot Analysis Window/threshold settings, repeats & inversions.	PRT/NBSQ/PW/01	18 HOURS	03 DAYS	6,300
NBSQ-PW-02	Needleman-Wunsch Global Alignment Matrix fill, traceback & hand-worked derivation.	PRT/NBSQ/PW/02	30 HOURS	05 DAYS	10,600
NBSQ-PW-03	Smith-Waterman Local Alignment Local scoring, zero-floor & optimal subalignment.	PRT/NBSQ/PW/03	32 HOURS	06 DAYS	11,400
NBSQ-PW-04	Gotoh Affine-Gap Implementation Three-matrix formulation & complexity handling.	PRT/NBSQ/PW/04	34 HOURS	06 DAYS	12,400
NBSQ-PW-05	Semi-Global, Overlap & Glocal Alignment End-gap-free variants for reads & contigs.	PRT/NBSQ/PW/05	24 HOURS	04 DAYS	8,600
NBSQ-PW-06	EMBOSS Pairwise Suite Operation needle, water, stretcher & matcher in practice.	PRT/NBSQ/PW/06	22 HOURS	04 DAYS	7,700

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 160 HOURS • 28 DAYS

~~57,000~~ 48,400 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

03

CATEGORY • NBSQ-BL

BLAST Family & Web Search

Seeding, extension & the five BLAST programs

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-BL-01	BLAST Architecture: Seeding, Extension & HSPs Word hits, ungapped/gapped extension & HSP assembly.	PRT/NBSQ/BL/01	28 HOURS	05 DAYS	9,900
NBSQ-BL-02	Nucleotide Searching with blastn & megablast Task selection, word size & discontinuous megablast.	PRT/NBSQ/BL/02	26 HOURS	05 DAYS	9,100
NBSQ-BL-03	Protein Searching with blastp Matrix choice, composition adjustment & hit ranking.	PRT/NBSQ/BL/03	24 HOURS	04 DAYS	8,400
NBSQ-BL-04	Translated Searches: blastx, tblastn, tblastx Frame handling, genetic codes & use cases.	PRT/NBSQ/BL/04	30 HOURS	05 DAYS	10,700
NBSQ-BL-05	Database Selection, Filters & Organism Limits nr, nt, RefSeq sets, entrez limits & masking.	PRT/NBSQ/BL/05	20 HOURS	04 DAYS	7,000
NBSQ-BL-06	Result Interpretation, Taxonomy & Reporting Graphic summary, taxonomy views & export.	PRT/NBSQ/BL/06	22 HOURS	04 DAYS	7,800

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 150 HOURS • 27 DAYS

~~52,900~~ 45,000 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

04

CATEGORY • NBSQ-CL

Command-Line BLAST & Local Databases

BLAST+ deployment, custom databases & batching

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-CL-01	BLAST+ Installation & Environment Setup Binaries, BLASTDB paths & version control.	PRT/NBSQ/CL/01	18 HOURS	03 DAYS	6,400
NBSQ-CL-02	makeblastdb & Custom Database Construction Parse-seqids, taxid mapping & database QC.	PRT/NBSQ/CL/02	28 HOURS	05 DAYS	10,100
NBSQ-CL-03	Tabular Output Formats & Custom Fields outfmt 6/7/17, field selection & downstream use.	PRT/NBSQ/CL/03	24 HOURS	04 DAYS	8,700
NBSQ-CL-04	Parameter Tuning: Word Size, Masking, Thresholds Sensitivity/speed trade-offs & dust/seg control.	PRT/NBSQ/CL/04	30 HOURS	05 DAYS	10,900
NBSQ-CL-05	Batch, Chunked & Parallel BLAST Execution Query splitting, thread control & job arrays.	PRT/NBSQ/CL/05	36 HOURS	06 DAYS	13,300
NBSQ-CL-06	Remote BLAST & URL API Automation -remote searching & scripted NCBI URL API use.	PRT/NBSQ/CL/06	26 HOURS	05 DAYS	9,500

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 162 HOURS • 28 DAYS

~~58,700~~ 50,100 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

05

CATEGORY • NBSQ-SN

Sensitive & Profile-Based Search

Iterative, pattern & HMM-driven homology detection

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-SN-01	PSI-BLAST Iterative Profile Searching PSSM construction, inclusion threshold & drift control.	PRT/NBSQ/SN/01	34 HOURS	06 DAYS	12,500
NBSQ-SN-02	PHI-BLAST Pattern-Constrained Search Pattern syntax & motif-anchored searching.	PRT/NBSQ/SN/02	22 HOURS	04 DAYS	8,000
NBSQ-SN-03	DELTA-BLAST & Domain-Enhanced Search CDD-seeded profiles for distant relationships.	PRT/NBSQ/SN/03	24 HOURS	04 DAYS	8,800
NBSQ-SN-04	HMMER Profile Construction & Search hmmbuild, hmmsearch, hmmscan & alignment inputs.	PRT/NBSQ/SN/04	40 HOURS	07 DAYS	14,800
NBSQ-SN-05	jackhmmer & phmmer Iterative Search Single-sequence entry to iterative profile search.	PRT/NBSQ/SN/05	32 HOURS	06 DAYS	11,900
NBSQ-SN-06	Profile-Profile Comparison & Remote Homology Profile HMM comparison for twilight-zone detection.	PRT/NBSQ/SN/06	44 HOURS	08 DAYS	16,600

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 196 HOURS • 35 DAYS

~~72,600~~ 61,700 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

06

CATEGORY • NBSQ-FA

Fast Heuristic & High-Throughput Aligners

FASTA, DIAMOND, MMseqs2 & benchmarking

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-FA-01	FASTA Suite & k-tuple Heuristics ktup effects, ssearch & the FASTA output model.	PRT/NBSQ/FA/01	22 HOURS	04 DAYS	7,700
NBSQ-FA-02	DIAMOND High-Throughput Protein Search Double indexing, sensitivity modes & large runs.	PRT/NBSQ/FA/02	32 HOURS	06 DAYS	11,800
NBSQ-FA-03	MMseqs2 Search & Clustering Workflows Prefilter/align modules, cascaded clustering.	PRT/NBSQ/FA/03	38 HOURS	07 DAYS	14,100
NBSQ-FA-04	VSEARCH & USEARCH Operations Dereplication, clustering & global search modes.	PRT/NBSQ/FA/04	28 HOURS	05 DAYS	10,200
NBSQ-FA-05	BLAT & Short-Query Genome Searching Index-based near-identity search & PSL output.	PRT/NBSQ/FA/05	24 HOURS	04 DAYS	8,600
NBSQ-FA-06	Aligner Benchmarking: Speed vs Sensitivity Reference sets, ROC-style comparison & selection.	PRT/NBSQ/FA/06	30 HOURS	05 DAYS	11,000

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 174 HOURS • 31 DAYS

~~69,400~~ 53,900 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

07

CATEGORY • NBSQ-GN

Genomic & Long-Sequence Alignment

Whole-genome comparison, anchoring & synteny

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-GN-01	Whole-Genome Pairwise Alignment Seed-and-extend at genome scale & output formats.	PRT/NBSQ/GN/01	40 HOURS	07 DAYS	14,600
NBSQ-GN-02	Suffix Arrays, MUMs & Anchor-Based Alignment Exact-match anchoring & index structures.	PRT/NBSQ/GN/02	36 HOURS	06 DAYS	13,200
NBSQ-GN-03	Chaining, Netting & Synteny Blocks Chain/net construction & orthologous region calls.	PRT/NBSQ/GN/03	34 HOURS	06 DAYS	12,600
NBSQ-GN-04	Genome Dot Plots & Rearrangement Detection Inversions, translocations & duplication signals.	PRT/NBSQ/GN/04	26 HOURS	05 DAYS	9,400
NBSQ-GN-05	Cross-Species Conservation & Alignment Nets Conserved element extraction from alignments.	PRT/NBSQ/GN/05	30 HOURS	05 DAYS	11,000
NBSQ-GN-06	Repeat Masking & Its Effect on Alignment Soft/hard masking strategy & false-anchor control.	PRT/NBSQ/GN/06	24 HOURS	04 DAYS	8,700

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 190 HOURS • 33 DAYS

~~69,500~~ 59,100 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

08

CATEGORY • NBSQ-SP

Specialised Alignment Problems

Spliced, protein-to-genome & constrained alignment

5

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-SP-01	Spliced Alignment of cDNA & EST to Genome Splice-site-aware alignment & exon boundary calls.	PRT/NBSQ/SP/01	34 HOURS	06 DAYS	12,500
NBSQ-SP-02	Protein-to-Genome Alignment Frame-aware alignment for annotation transfer.	PRT/NBSQ/SP/02	30 HOURS	05 DAYS	11,100
NBSQ-SP-03	Structure-Informed Sequence Alignment Structure-guided refinement of distant alignments.	PRT/NBSQ/SP/03	32 HOURS	06 DAYS	11,900
NBSQ-SP-04	Circular, Permuted & Tandem-Repeat Alignment Origin handling, permutation & repeat resolution.	PRT/NBSQ/SP/04	24 HOURS	04 DAYS	8,800
NBSQ-SP-05	Low-Complexity & Compositional Bias Handling SEG/DUST strategy & composition-based statistics.	PRT/NBSQ/SP/05	20 HOURS	04 DAYS	7,200

STREAM BUNDLE • 5 MODULES • 5 PROTOCOLS • 140 HOURS • 25 DAYS

~~54,500~~ 43,800 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

09

CATEGORY • NBSQ-AU

Automation, Parsing & Search Pipelines

Scripted alignment, output parsing & reporting

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-AU-01	Biopython PairwiseAligner & Bio.Align Scoring objects, modes & programmatic alignment.	PRT/NBSQ/AU/01	34 HOURS	06 DAYS	12,400
NBSQ-AU-02	Parsing BLAST XML & Tabular Output Robust parsers, field mapping & error handling.	PRT/NBSQ/AU/02	28 HOURS	05 DAYS	10,200
NBSQ-AU-03	R Biostrings & palign Workflows Alignment objects, scoring & batch operations.	PRT/NBSQ/AU/03	30 HOURS	05 DAYS	11,000
NBSQ-AU-04	Reusable Search Pipelines & Job Control Workflow scripting, restarts & resource control.	PRT/NBSQ/AU/04	42 HOURS	07 DAYS	15,600
NBSQ-AU-05	Hit Filtering, Best-Hit & Reciprocal Best Hits Coverage/identity thresholds & RBH logic.	PRT/NBSQ/AU/05	26 HOURS	05 DAYS	9,500
NBSQ-AU-06	Alignment Visualisation & Result Reporting Hit maps, coverage plots & delivery formats.	PRT/NBSQ/AU/06	24 HOURS	04 DAYS	8,700

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 184 HOURS • 32 DAYS

~~67,400~~ 57,300 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

10

CATEGORY • NBSQ-AP

Applied Similarity Analysis

Orthology, annotation transfer & screening

6

MODULES

CODE	TRAINING MODULE	PROTOCOL REF	DURATION		FEE (INR)
NBSQ-AP-01	Ortholog & Paralog Identification by RBH Reciprocal best hits, thresholds & failure cases.	PRT/NBSQ/AP/01	32 HOURS	06 DAYS	11,700
NBSQ-AP-02	Annotation Transfer & Error Propagation Control Evidence rules & avoiding transitive errors.	PRT/NBSQ/AP/02	28 HOURS	05 DAYS	10,100
NBSQ-AP-03	Species Identification & Barcode Searching Marker searches, reference sets & confidence.	PRT/NBSQ/AP/03	24 HOURS	04 DAYS	8,600
NBSQ-AP-04	Primer & Probe Specificity Verification In-silico specificity & off-target screening.	PRT/NBSQ/AP/04	22 HOURS	04 DAYS	7,900
NBSQ-AP-05	Vector, Adapter & Contamination Screening UniVec-class screening & trimming decisions.	PRT/NBSQ/AP/05	20 HOURS	04 DAYS	7,100
NBSQ-AP-06	Similarity-Based Curation & Submission QC Pre-submission checks & mis-annotation detection.	PRT/NBSQ/AP/06	26 HOURS	05 DAYS	9,400

STREAM BUNDLE • 6 MODULES • 6 PROTOCOLS • 152 HOURS • 28 DAYS

~~54,800~~ 46,600 INR

Each module is enrolled and certified independently against its own protocol reference, or taken together as the discounted stream bundle. Duration is the logged contact-hour allocation for that protocol; days are computed at six contact hours per working day. Fees exclude applicable GST.

Build a Career in Sequence Analysis

Every module in this catalogue is delivered as hands-on training on live sequence data and working search installations, against a controlled protocol issued at the start and signed off at the end — covering scoring systems and alignment statistics, global and local dynamic-programming alignment, the full BLAST family on the web and at the command line, profile and iterative methods for remote homology, high-throughput heuristic aligners, whole-genome and spliced alignment, automated parsing and pipeline construction, and the applied similarity analyses that annotation and curation depend on. Mix and match modules to design a track that fits your goals.

59TRAINING
MODULES

59CONTROLLED
PROTOCOLS

10CATEGORY
STREAMS

1634CONTACT
HOURS

02OF THE NTHRYS
BIOINFORMATICS SERIES**NTHRYS OPC PVT LTD**

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CATALOGUE

NBSQ • 2026 Edition