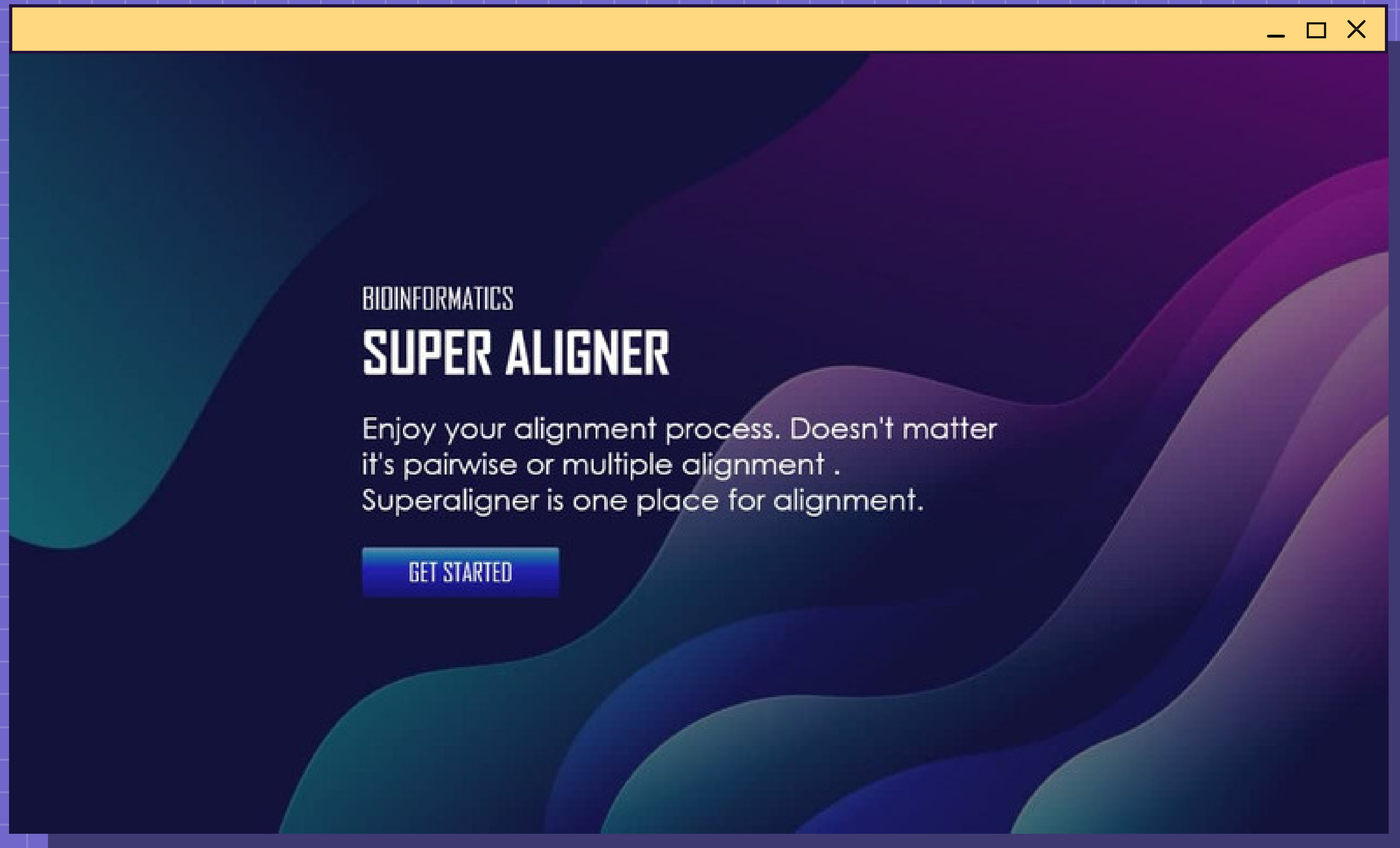


SuperAligner GUI

Genomics Project 2021





BIOINFORMATICS

SUPER ALIGNER

Enjoy your alignment process. Doesn't matter
it's pairwise or multiple alignment .
Superaligner is one place for alignment.

GET STARTED

CHOOSE YOUR ALIGNMENT :

PAIRWISE

- ☒ NEEDLEMAN WUNSCH
(GLOBAL)
- ☐ SMITH WATERMAN
(LOCAL)

MULTIPLE

- ☐ PROGRESSIVE

Write Your Sequences ...



START ALIGNMENT

Alignment | Basic Statistics | Quality | Protein Transformation

THE RESULT OF USING SMITH WATERMAN :

File Name : -----

File Type : -----

RE-ALIGNMENT

Seq 1 ACTGCTACG**ATATCGAT*****ACGGGAT**CGATTGCTACGGGA

Seq 2 AC*GCTACGGGATATCG*T*GCTACGGGATATCGATTGCTA****A

Alignment | Basic Statistics | Quality | Protein Transformation

No.Match : 37

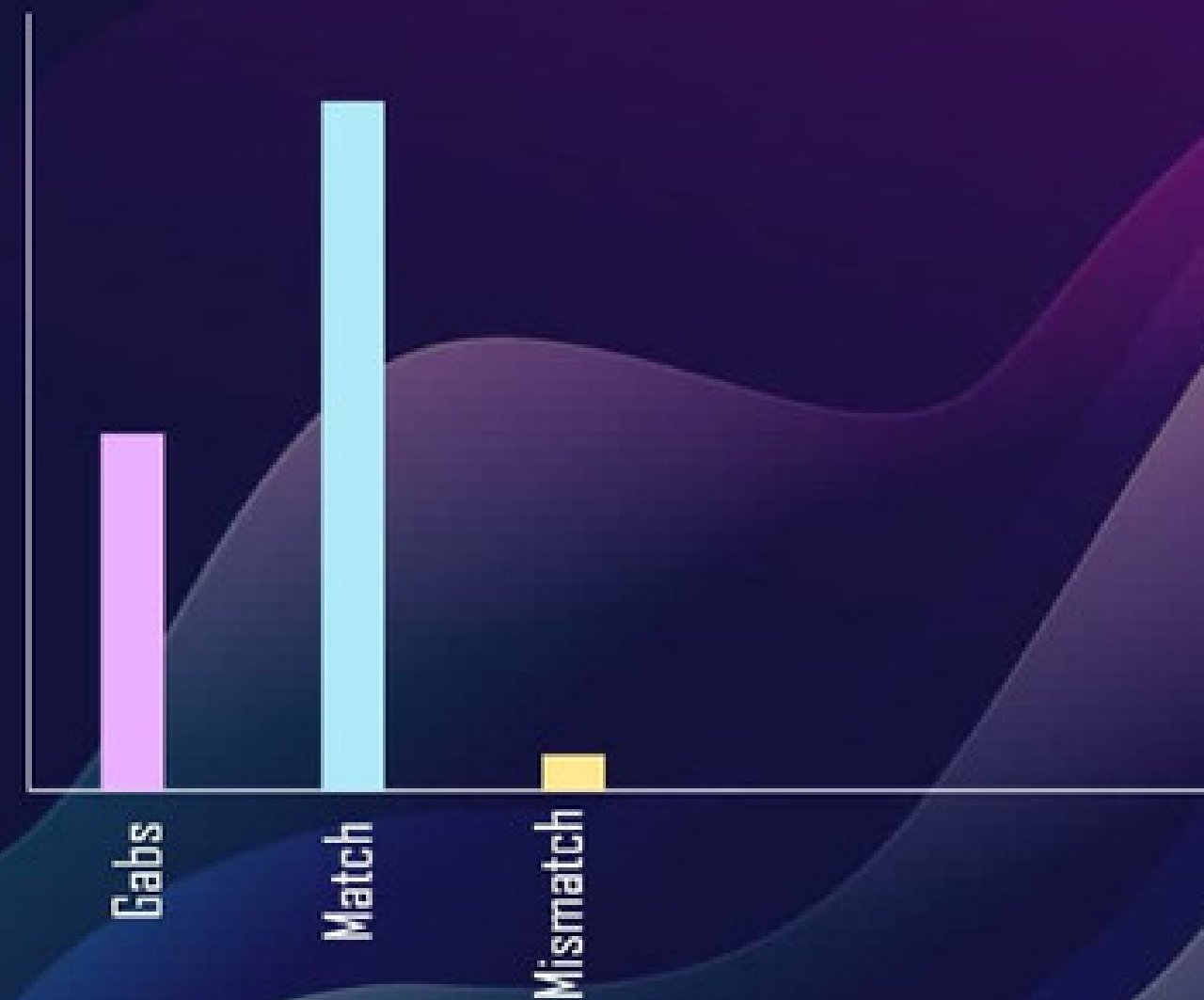
No.Mismatch : 0

No. Gaps : 15

No.Sequences : 2

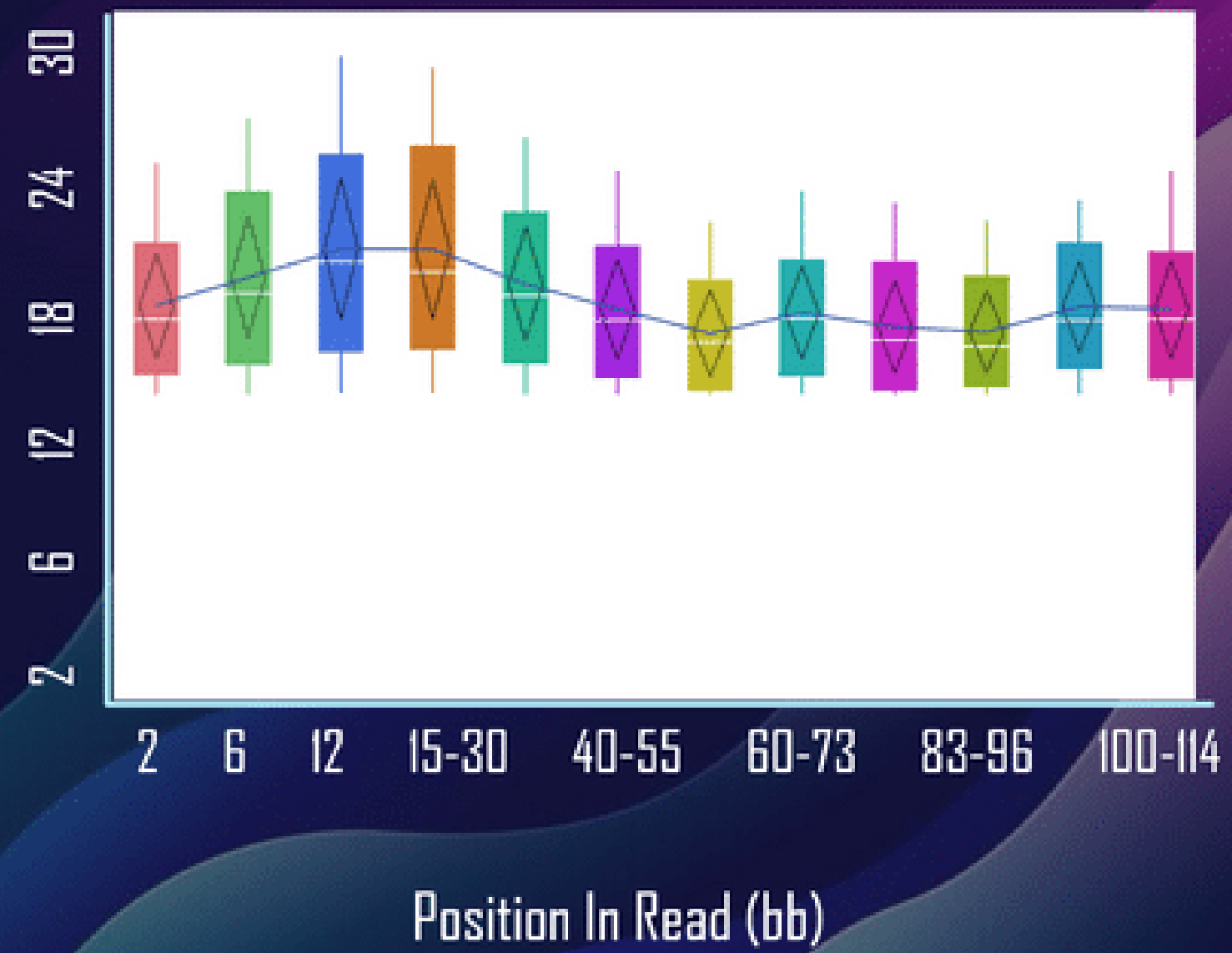
Sequences Length : 46

GC% : 40



Alignment | Basic Statistics | **Quality** | Protein Transformation

Quality Scores Across All Bases



Alignment | Basic Statistics | Quality | Protein Transformation

THE AMINO ACIDS SEQUENCES :

File Name : -----

File Type : -----

RE-ALIGNMENT

Seq 1 Ser Arg Cys Tyr Cys Tyr Ala Leu Ala Asn Asp Ala

Seq 2 Cys Asp Ala Leu Ser Arg Tyr Ala Leu Tyr Leu Thr Ile

For interactive GUI :

<https://assets.adobe.com/id/urn:aaid:sc:EU:84ae86e8-a280-4e09-b6d1-901d72af13b6?view=difile>

