

Após a preparação de todas as entradas preparadas podemos rodar as análises clicando em Align

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COBALT

Constraint-based Multiple Alignment Tool

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Enter Query Sequences

COBALT computes a multiple protein sequence alignment using conserved domain and local sequence similarity information.

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Enter at least 2 protein accessions, gis, or FASTA sequences

>sp|Q84T65|BRXL4_ORYSJ Protein *Brevis radix*-like 4 OS=Oryza sativa subsp. japonica
QX=39947 GN=BRXL4 PE=3 SV=1
MIQLKDMVMKLSGTSRHGQRRGSGPPRGRITTSVYRSGYRPGMVQDDMAVPPATYLG
GGGTSMSASSTPAMDFAAPGAEGAREWADVQGVQITFVSLAGGGNDLKRTRFSREM
YDKWQAKQWKGNNERIMELTWRRFSQVLPTPPRSDDGGERESFYSGVSGTRGSPAATP
CRAPI TNDPTCTKCAICGRRKASNDNPKCEGRLSDRRKCSNRRCPAWQNNPNDRAQZ

Clear

Or, upload FASTA file

Escolher arquivo

Nenhum arquivo selecionado

Job Title

Align

☐ Show results in a new window

[Advanced parameters](#)

Aqui a sequência FASTA

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PASSO 4 – RESULTADOS

As saídas obtidas

