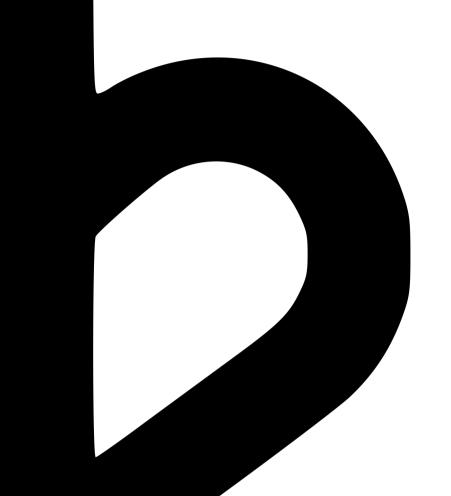


Enter FASTA sequence(s):

>KY106088|k_Fungi;p_Ascomycota;c_Saccharomycetes;o_Saccharomycetales;f_Saccharomyc etaceae;g_Zygotorulaspora;s_Zygotorulaspora_mrakii|SH1312607.09FU GTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATAGAAAAAATGGAAGGGCCATGCGCTTAATTGC GCGGGCCCTCTCTTATTCACACGATGGAGAGACGAATATCTTCCTGCTTAGGGGGCACGAGGCTTGGACCGAGTGGC



You provided 2 valid sequences (max: 100)

Settings

Select embedding model:	MycoAI-BERT		~
Number of top matched results to display:	3	-	+

Run TaxoTagger

Results 💿

For input sequence:

KY106088				
	Family	Genus	Species	
Top 1	Saccharomycetaceae (KY106088;1.000)	Zygotorulaspora (KY106088;1.000)	Zygotorulaspora_mrakii (K	
Top 2	Saccharomycetaceae (KY106087;1.000)	Zygotorulaspora (KY106087;1.000)	Zygotorulaspora_mrakii (K	
Top 3	Saccharomycetaceae (KY106031;1.000)	Zygosaccharomyces (KY106032;0.746)	Zygosaccharomyces_bispc	

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TaxoTagger is an open-source Python library for DNA taxonomy identification, powered by deep learning and semantic search

Conduct efficient semantic searches for precise results
Build vector databases from DNA sequences with ease
Extend support for custom embedding models effortlessly
Interact seamlessly through a user-friendly web app

Try the webapp demo at http://mycoai.org