

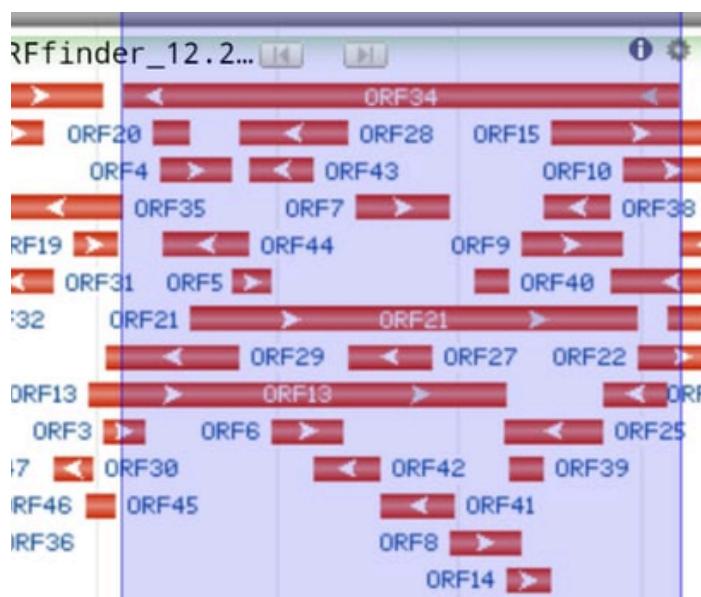
Computational Analysis of Unknown DNA Sequences Using Integrated Bioinformatics Tools

AOA1H6JFX1_9GAMM
Hydrogenase (acceptor)
BAZSYMB_SCAFFOLD00037_1
Bathymodiolus azoricus
409AA

DNA ANALYSIS

Sequence ID: XM_030474951.1 Length: 2250 Number of Matches: 1							
Range 1: 1 to 2250 GenBank Graphics		Next Match & Previous Match					
Score 4156 bits(2250)	Expect 0.0	Identities 2250/2250(100%)	Gaps 0/2250(0%)	E value	Per. Ident.	Acc. Len	Accession
Query 1 GCGCCGGCTGGCGCTCCAGAGAGGGCGGAAAGTGACGTC/	- <i>Strigopsgenotricha</i>	4156 4156 100%	0.0 100.00% 2250	XM_03047491			
Sbjct 1 GCGCCGGCTGGCGCTCCAGAGAGGGCGGAAAGTGACGTC/	- <i>Pezopora</i>	1271 1271 44%	0.0 89.61% 1381	XM_0614444			
Query 61 TCGCTCTGGCTGGGGCTCTGTCCCCCTATAAACGCTCCAT/	- <i>Ciona</i>	1264 1264 44%	0.0 89.63% 1723	XM_0728481			
Sbjct 61 TCGCTCTGGCTGGGGCTCTGTCCCCCTATAAACGCTCCAT/	- <i>Calanoida</i>	1199 1199 44%	0.0 88.52% 1753	XM_0751350			
Query 121 CTATGGGGCCTATAAGACCTCCGCTGccccctatagacact/	-						
Sbjct 121 CTATGGGGCCTATAAGACCTCCGCTGccccctatagacact/	-						
Query 181 ttccacggcccccgttttacccctatacgcccttcgcgtt/	-						
Sbjct 181 tccacggcccccgttttacccctatacgcccttcgcgtt/	-						
Query 245	-						

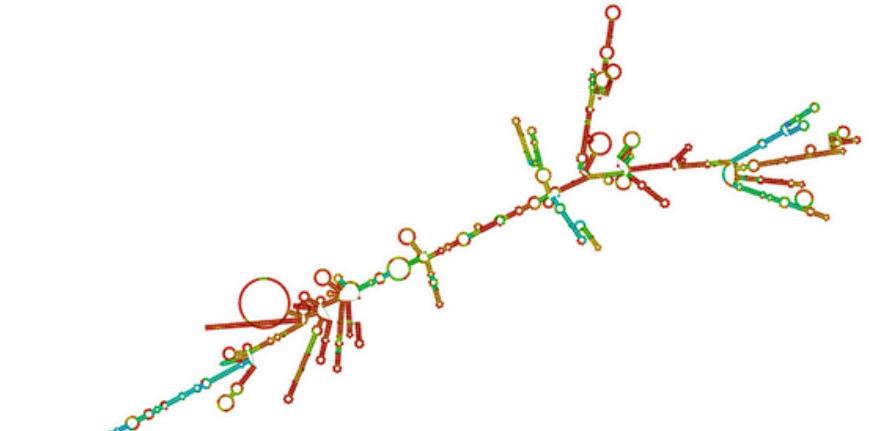
NCBI BLAST



ORF FINDER

EXPASY TRANSLATE

RNA ANALYSIS



The stability of Scaffold00037_1 is measured by its MFE, where a more negative value indicates a more stable, functional fold. This stability depends on strong G-C base pairs.

LLDHЛИNNDRKLKPPEYGLPHTYIEMQSLQIAAFLTVCHVVLLVQDWFTDLGLYRFL
LLDHЛИNNDRKLKPPEYGLPHTYIEMQSLQIAAFLTVCHVVLLVQDWFTDLGLYRFL
-----DRKLKPPEYGLPHTYIEMQSLQIAAFLTVCHVVLLVQDWFTDLGLYRFL

EMVKPSTPSGPHEPSAGAEPEPSEYYPHLGETHSATHGAAPLFPLLGAFRGHGSFAA
EMVKPSTPSGPHEPSAGAEPEPSEYYPHLGETHSATHGAAPLFPLLGAFRGHGSFAA
EMVKPSTPSGPHEPSAGAEPEPSEYYPHLGETHSATHGAAPLFPLLGAFRGHGSFAA

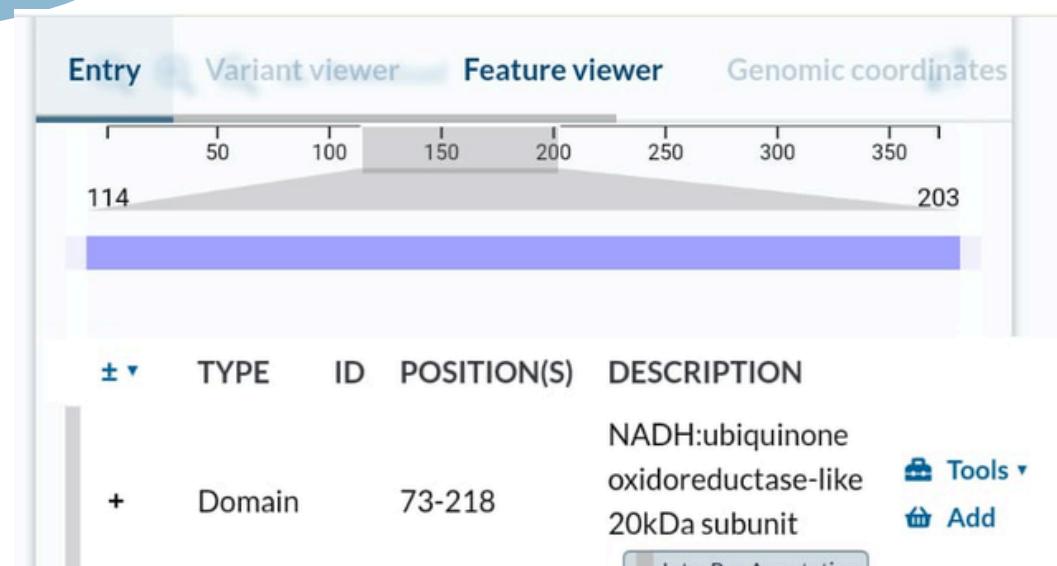
R-----TERSWFHYAARIWDGVKKSSALAEYGRLLG
RLRGRVLAAARAQLSHSLLTERSWFHYAARIWDGVKKSSALAEYGRLLG
RLRGRVLAAARAQLSHSLLTERSWFHYAARIWDGVKKSSALAEYGRLLG
*-----*****

PHYLOGENETIC ANALYSIS

1 0.0140665
Target 0.00378788
2 0.00378788

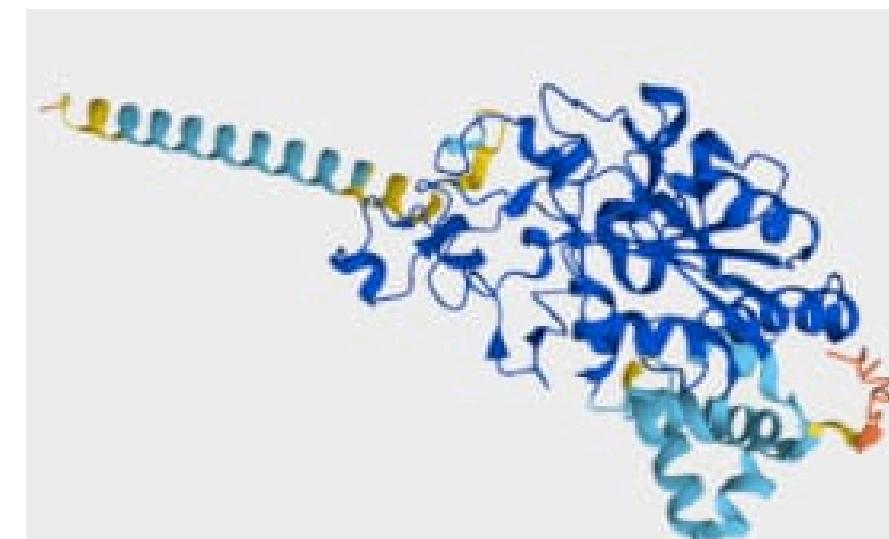
PROTEIN ANALYSIS

AA: 409
PI: 6.48
MW: 4.4K
AI: 75.94
IS: 55.51



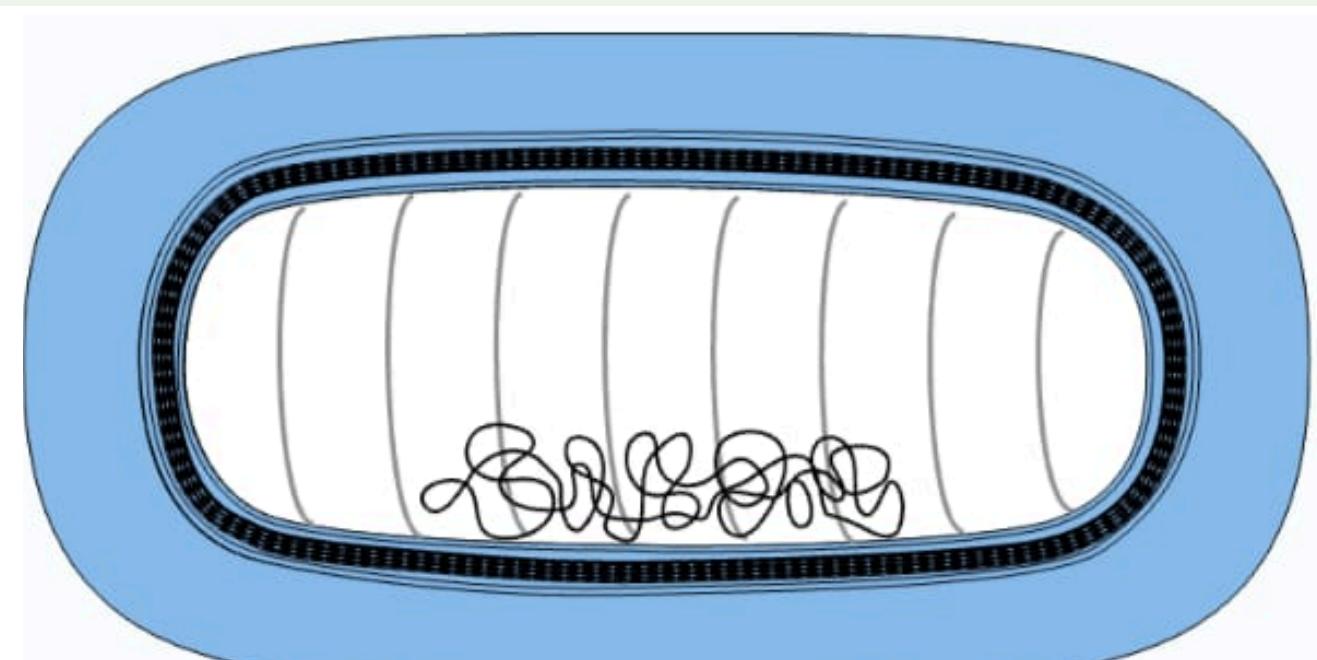
DOMAINS AND FUNCTION

FUNCTION
involves acting as an enzyme (like a cytochrome P450 or a transferase) that helps the organism process nutrients or defend itself against toxins.



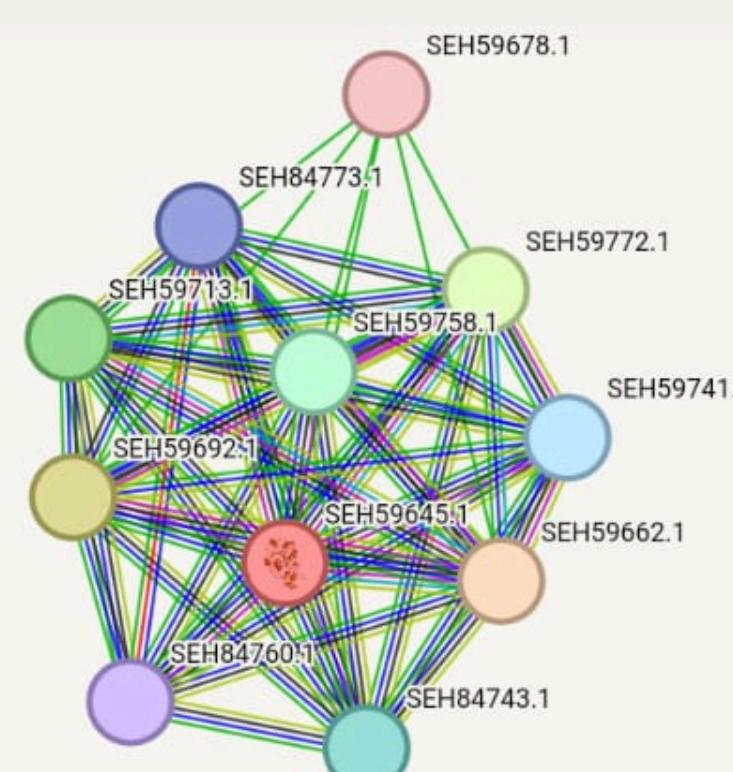
SECONDARY STRUCTURE

SUBCELLULAR LOCALIZATION



As a membrane protein, Scaffold00037_1 is typically localized to the plasma membrane or endomembrane systems (such as the ER or Golgi), where it is anchored via hydrophobic transmembrane domains. (N-terminal signal peptides)

Based on the protein-protein interaction network from the STRING database, the biological importance of Scaffold00037_1 lies in its highly integrated role within a functional protein complex.



PROTEIN INTERACTION

Such dense connectivity typically characterizes essential cellular machinery, such as metabolic pathways or structural complexes, where Scaffold serves as a critical node for maintaining the stability and coordination of the system.