Bioinformatics project

Submitted to: Dr. Samina Shakeel

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Department: Biochemistry Bs 7th Morning

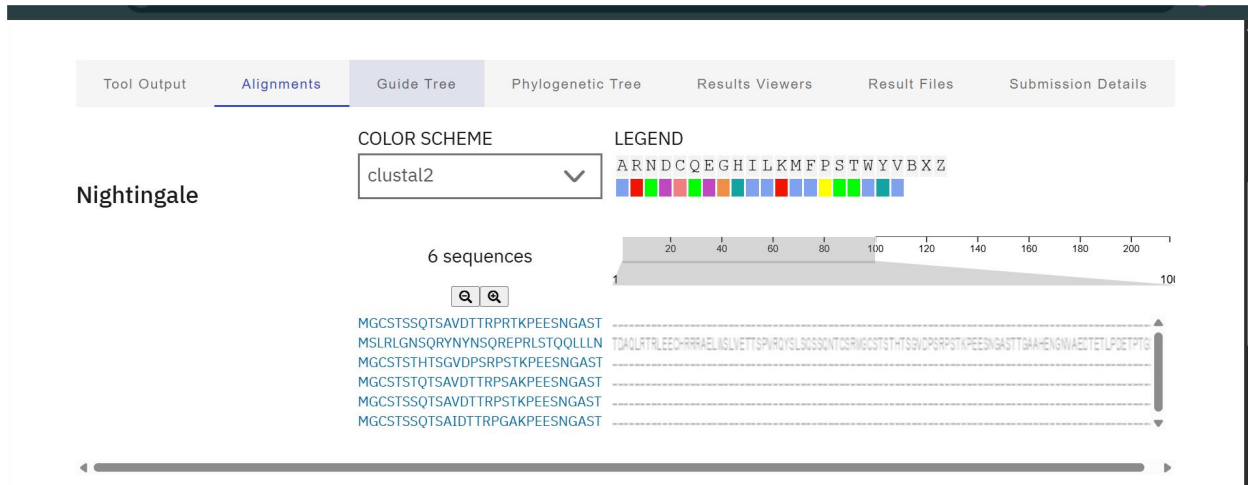## Task No: 5

Polygenetic Analysis:

NCBI BLASTp:

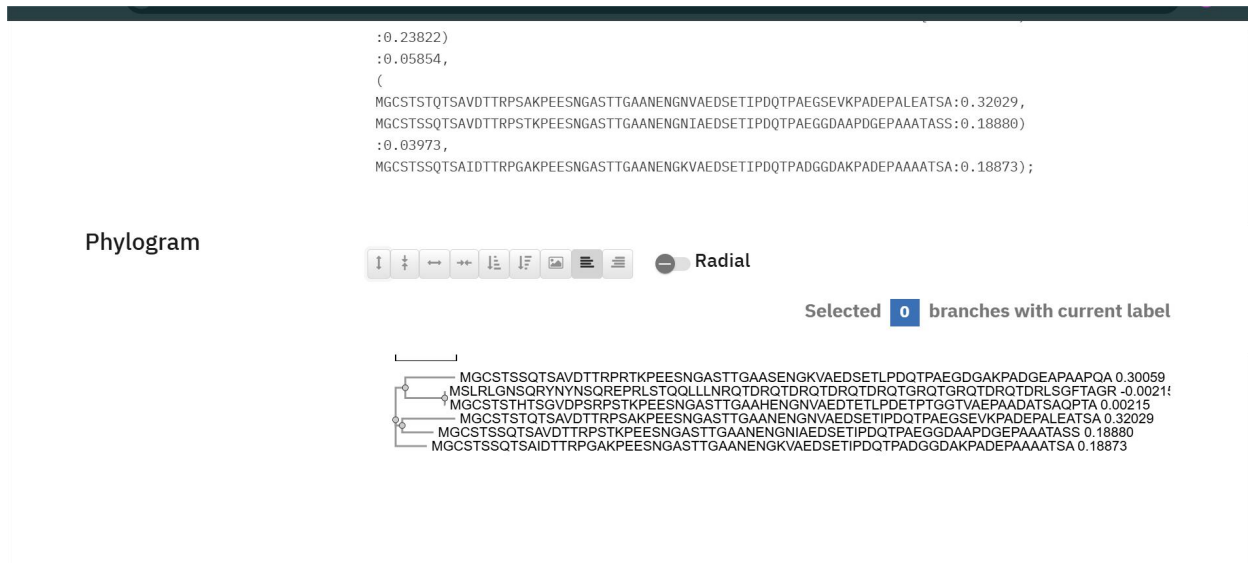| Cluster Composition	Cluster Ancestor	Cluster Representative Sequence	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Acc
☑ ⊞1 member(s), 1 organism(s)	blunt-snouted clingfish	tropomyosin-1, isoforms 33/34 isoform X1 [Gouania willden…	281	281	100%	4e-93	100.00%	272	XP_02
☑ ⊞1 member(s), 1 organism(s)	blunt-snouted clingfish	tropomyosin-1, isoforms 33/34 isoform X2 [Gouania willden…	271	271	100%	7e-91	100.00%	158	XP_02
☑ ⊞2 member(s), 1 organism(s)	flier cichlid	uncharacterized protein LOC115788063 isoform X2 [Archoc…	99.4	99.4	58%	2e-23	60.40%	131	XP_03
☑ ⊞1 member(s), 1 organism(s)	mandarinfish	nematocyst expressed protein 3-like [Synchiropus splendidus]	98.6	98.6	70%	9e-23	62.28%	162	XP_05
☑ ⊞1 member(s), 1 organism(s)	mangrove rivulus	skin secretory protein xP2 [Kryptolebias marmoratus]	95.9	95.9	49%	6e-22	65.91%	138	XP_01
☑ ⊞1 member(s), 1 organism(s)	banded archerfish	outer membrane protein H.8 [Toxotes jaculatrix]	92.8	92.8	49%	7e-21	67.07%	130	XP_04
☑ ⊞2 member(s), 2 organism(s)	ray-finned fishes	uncharacterized protein [Chaetodon trifascialis]	93.2	93.2	47%	8e-21	62.65%	143	XP_07
☑ ⊞2 member(s), 2 organism(s)	bony fishes	uncharacterized protein si:dkey-284p5.3 [Solea solea]	92.0	92.0	38%	4e-20	73.33%	174	XP_05
☑ ⊞1 member(s), 1 organism(s)	orbiculate cardinalfish	skin secretory protein xP2 [Sphaeramia orbicularis]	91.7	91.7	34%	4e-20	79.63%	151	XP_03
☑ ⊞2 member(s), 1 organism(s)	pikeperch	cytochrome c1 isoform X2 [Sander lucioperca]	89.7	89.7	54%	1e-19	62.79%	124	XP_03
☑ ⊞1 member(s), 1 organism(s)	black rockcod	skin secretory protein xP2 [Notothenia coriiceps]	90.9	90.9	38%	2e-19	71.67%	179	XP_01
☑ ⊞1 member(s), 1 organism(s)	monkeyface prickleback	brain acid soluble protein 1 [Cebidichthys violaceus]	90.1	90.1	47%	2e-19	62.65%	154	XP_06
☑ ⊞1 member(s), 1 organism(s)	swordfish	predicted GPI-anchored protein 58 [Xiphias gladius]	90.1	90.1	47%	2e-19	67.09%	164	XP_03
☑ ⊞1 member(s), 1 organism(s)	Patagonian blennie	nematocyst expressed protein 3-like [Eleginops maclovinus]	89.4	89.4	34%	3e-19	75.93%	158	XP_06
☑ ⊞1 member(s), 1 organism(s)	leopard coralgrouper	cytochrome c1 [Plectropomus leopardus]	88.6	88.6	34%	4e-19	75.93%	137	XP_04
☑ ⊞4 member(s), 4 organism(s)	bony fishes	cytochrome c1 [Epinephelus fuscoguttatus]	89.0	89.0	35%	5e-19	76.36%	148	XP_04
⊞1 member(s), 1 organism(s)	Acadian redfish	uncharacterized protein LOC141754504 [Sebastes fasciatus]	88.2	88.2	41%	5e-19	68.57%	134	XP_07

Multiple Sequence Alignment:

I performed a Multiple Sequence Alignment (MSA) using the Clustal Omega tool to compare the Tropomyosin 1 protein sequence of Gouania willdenowi with five other homologous sequences from different fish species identified through BLASTp. This step is crucial to identify conserved regions that are essential for the protein's function.

MSA:

Nightingale

| Tool Output | Alignments | Guide Tree | Phylogenetic Tree | Results Viewers | Result Files | Submission Details |

COLOR SCHEME

clustal2

LEGEND

A R N D C Q E G H I L K M F P S T W Y V B X Z

6 sequences

20 40 60 80 100 120 140 160 180 200

1   100

MGCSTSSQTSAVDTTRPRTKPEESNGAST ------------------------------
MSLRLGNSQRYNYNSQREPRLSTQQLLLN TDAQLRTRLEECHRRAELNSLVETTSPIRDYSLSQSSQNTQSRWGCSTSTHTSGVDPSRPSTKPEESNGASTTGAAHENGNVAEDTETLPDETPTG
MGCSTSTHTSGVDPSRPSTKPEESNGAST ------------------------------
MGCSTSTQTSAVDTTRPSAKPEESNGAST ------------------------------
MGCSTSSQTSAVDTTRPSTKPEESNGAST ------------------------------
MGCSTSSQTSAIDTTRPGAKPEESNGAST ------------------------------

Polygenetic Tree:

Phylogram

```
:0.23822)
:0.05854,
(
MGCSTSTQTSAVDTTRPSAKPEESNGASTTGAANENGNVAEDSETIPDQTPAEGSEVKPADEPALEATSA:0.32029,
MGCSTSSQTSAVDTTRPSTKPEESNGASTTGAANENGNIAEDSETIPDQTPAEGGDAAPDGEPAAATASS:0.18880)
:0.03973,
MGCSTSSQTSAIDTTRPGAKPEESNGASTTGAANENGKVAEDSETIPDQTPADGGDAKPADEPAAAATSA:0.18873);
```

Radial

Selected **0** branches with current label

```
MGCSTSSQTSAVDTTRPRTKPEESNGASTTGAASENGKVAEDSETLPDQTPAEGDGAKPADGEAPAAPQA 0.30059
MSLRLGNSQRYNYNSQREPRLSTQQLLLNRQTDRQTDRQTDRQTDRQTGRQTGRQTDRQTDRLSGFTAGR -0.0021!
MGCSTSTHTSGVDPSRPSTKPEESNGASTTGAAHENGNVAEDTETLPDETPTGGTVAEPAADATSAQPTA 0.00215
MGCSTSTQTSAVDTTRPSAKPEESNGASTTGAANENGNVAEDSETIPDQTPAEGSEVKPADEPALEATSA 0.32029
MGCSTSSQTSAVDTTRPSTKPEESNGASTTGAANENGNIAEDSETIPDQTPAEGGDAAPDGEPAAATASS 0.18880
MGCSTSSQTSAIDTTRPGAKPEESNGASTTGAANENGKVAEDSETIPDQTPADGGDAKPADEPAAAATSA 0.18873
```

Phylogenetic Tree Discussion:

The phylogenetic tree illustrates the evolutionary distance between the Tropomyosin 1 protein of Gouania willdenowi and its homologs in other species. The branching pattern shows that my

target protein is most closely related to other ray-finned fishes (Actinopterygii). This indicates that the gene has evolved from a common ancestor shared by these aquatic organisms.