**TERMINAL LAB**

BIOINFORMATICS

**COMSATS University Islamabad**

Sahiwal Campus



**Usama Sarwar**

FA17-BS(CS)-090-B

**Dr Ibrahim**

Introduction to Bioinformatics

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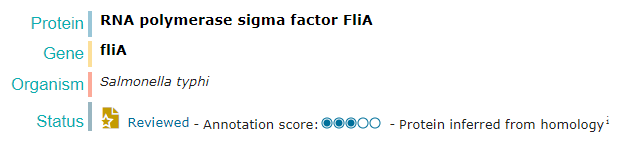
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COMPLETED LAB TASKS

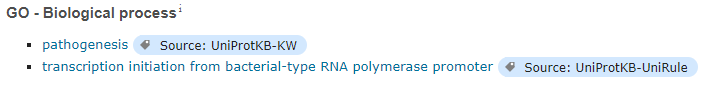
# Task 1

Sequence: MNSLYTAEGVMDKHSLWQRYVPLVRHEALRLQVRLPASVELDDLLQAGGIGLLNAVDRYDALQGTAFTTYAVQRIRGAMLDELRSRDWVPRSVRRNAREVAHAMGQLEQELGRNATETEVADRLGIAVEEYRQMLLDTNNSQLFSYDEWREEHGDSIELVTDEHQQENPLHHLMEGNLRQRVMEAIEALPEREQLVLTLYYQEELNLKEIGAVLEVGESRVSQLHSQAIKRLRTKLGKL

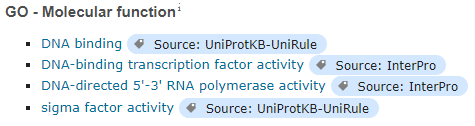


Source: <https://www.uniprot.org/uniprot/P0A2E9>

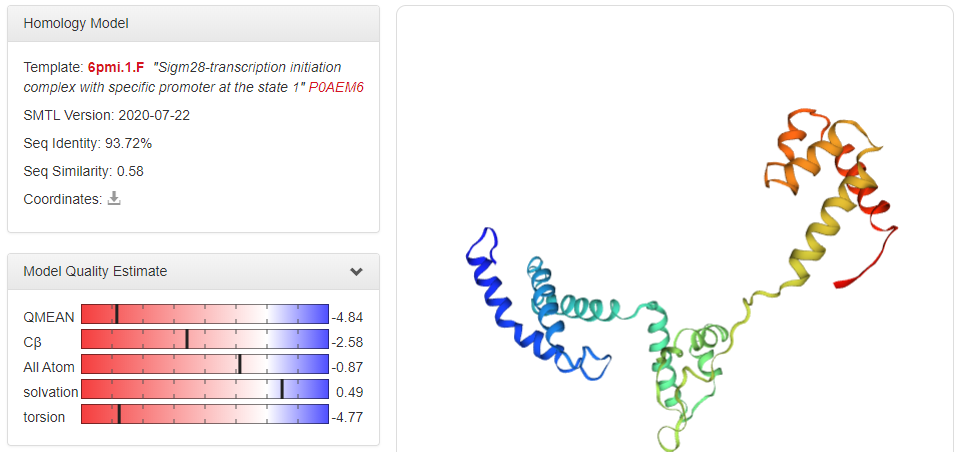
## Biological Process



## Molecular Function

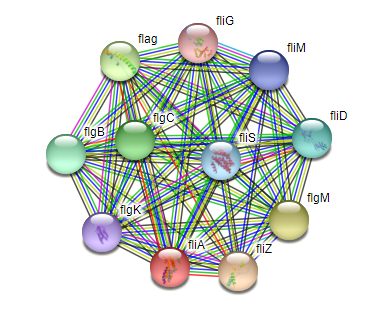


## Protein Structure



Source: [P0A2E9](https://swissmodel.expasy.org/repository/uniprot/P0A2E9?csm=1667E11EA4251F72)

## Protein-Protein Interaction



Source: [220341.16503199](https://string-db.org/network/220341.16503199)

## Family and Domain

|  |  |
| --- | --- |
| HAMAPi | [MF\_00962](https://hamap.expasy.org/signature/MF_00962)﻿, Sigma70\_FliA﻿, 1 hit |
| InterProi | [View protein in InterPro](https://www.ebi.ac.uk/interpro/protein/P0A2E9) [IPR014284](https://www.ebi.ac.uk/interpro/entry/IPR014284)﻿, RNA\_pol\_sigma-70\_dom [IPR000943](https://www.ebi.ac.uk/interpro/entry/IPR000943)﻿, RNA\_pol\_sigma70 [IPR007627](https://www.ebi.ac.uk/interpro/entry/IPR007627)﻿, RNA\_pol\_sigma70\_r2 [IPR007624](https://www.ebi.ac.uk/interpro/entry/IPR007624)﻿, RNA\_pol\_sigma70\_r3 [IPR007630](https://www.ebi.ac.uk/interpro/entry/IPR007630)﻿, RNA\_pol\_sigma70\_r4 [IPR012845](https://www.ebi.ac.uk/interpro/entry/IPR012845)﻿, RNA\_pol\_sigma\_FliA\_WhiG [IPR013325](https://www.ebi.ac.uk/interpro/entry/IPR013325)﻿, RNA\_pol\_sigma\_r2 [IPR013324](https://www.ebi.ac.uk/interpro/entry/IPR013324)﻿, RNA\_pol\_sigma\_r3/r4-like [IPR028617](https://www.ebi.ac.uk/interpro/entry/IPR028617)﻿, Sigma70\_FliA |
| Pfami | [View protein in Pfam](http://pfam.xfam.org/protein/P0A2E9) [PF04542](http://pfam.xfam.org/family/PF04542)﻿, Sigma70\_r2﻿, 1 hit [PF04539](http://pfam.xfam.org/family/PF04539)﻿, Sigma70\_r3﻿, 1 hit [PF04545](http://pfam.xfam.org/family/PF04545)﻿, Sigma70\_r4﻿, 1 hit |
| PIRSFi | [PIRSF000770](https://proteininformationresource.org/cgi-bin/ipcSF?id=PIRSF000770)﻿, RNA\_pol\_sigma-SigE/K﻿, 1 hit |
| PRINTSi | [PR00046](http://umber.sbs.man.ac.uk/cgi-bin/dbbrowser/sprint/searchprintss.cgi?display_opts=Prints&category=None&queryform=false&prints_accn=PR00046)﻿, SIGMA70FCT |
| SUPFAMi | [SSF88659](http://supfam.org/SUPERFAMILY/cgi-bin/scop.cgi?ipid=SSF88659)﻿, SSF88659﻿, 2 hits [SSF88946](http://supfam.org/SUPERFAMILY/cgi-bin/scop.cgi?ipid=SSF88946)﻿, SSF88946﻿, 1 hit |
| TIGRFAMsi | [TIGR02479](http://tigrfams.jcvi.org/cgi-bin/HmmReportPage.cgi?acc=TIGR02479)﻿, FliA\_WhiG﻿, 1 hit [TIGR02937](http://tigrfams.jcvi.org/cgi-bin/HmmReportPage.cgi?acc=TIGR02937)﻿, sigma70-ECF﻿, 1 hit |
| PROSITEi | [View protein in PROSITE](https://prosite.expasy.org/cgi-bin/prosite/PSScan.cgi?seq=P0A2E9&output=nice) [PS00715](https://prosite.expasy.org/doc/PS00715)﻿, SIGMA70\_1﻿, 1 hit [PS00716](https://prosite.expasy.org/doc/PS00716)﻿, SIGMA70\_2﻿, 1 hit |

# Task 2

## Reverse Translate results

**Results for 239 residue sequence "Untitled" starting "MNSLYTAEGV"**

>reverse translation of Untitled to a 717 base sequence of most likely codons.

atgaacagcctgtataccgcggaaggcgtgatggataaacatagcctgtggcagcgctat

gtgccgctggtgcgccatgaagcgctgcgcctgcaggtgcgcctgccggcgagcgtggaa

ctggatgatctgctgcaggcgggcggcattggcctgctgaacgcggtggatcgctatgat

gcgctgcagggcaccgcgtttaccacctatgcggtgcagcgcattcgcggcgcgatgctg

gatgaactgcgcagccgcgattgggtgccgcgcagcgtgcgccgcaacgcgcgcgaagtg

gcgcatgcgatgggccagctggaacaggaactgggccgcaacgcgaccgaaaccgaagtg

gcggatcgcctgggcattgcggtggaagaatatcgccagatgctgctggataccaacaac

agccagctgtttagctatgatgaatggcgcgaagaacatggcgatagcattgaactggtg

accgatgaacatcagcaggaaaacccgctgcatcatctgatggaaggcaacctgcgccag

cgcgtgatggaagcgattgaagcgctgccggaacgcgaacagctggtgctgaccctgtat

tatcaggaagaactgaacctgaaagaaattggcgcggtgctggaagtgggcgaaagccgc

gtgagccagctgcatagccaggcgattaaacgcctgcgcaccaaactgggcaaactg

>reverse translation of Untitled to a 717 base sequence of consensus codons.

atgaaywsnytntayacngcngarggngtnatggayaarcaywsnytntggcarmgntay

gtnccnytngtnmgncaygargcnytnmgnytncargtnmgnytnccngcnwsngtngar

ytngaygayytnytncargcnggnggnathggnytnytnaaygcngtngaymgntaygay

gcnytncarggnacngcnttyacnacntaygcngtncarmgnathmgnggngcnatgytn

gaygarytnmgnwsnmgngaytgggtnccnmgnwsngtnmgnmgnaaygcnmgngargtn

gcncaygcnatgggncarytngarcargarytnggnmgnaaygcnacngaracngargtn

gcngaymgnytnggnathgcngtngargartaymgncaratgytnytngayacnaayaay

wsncarytnttywsntaygaygartggmgngargarcayggngaywsnathgarytngtn

acngaygarcaycarcargaraayccnytncaycayytnatggarggnaayytnmgncar

mgngtnatggargcnathgargcnytnccngarmgngarcarytngtnytnacnytntay

taycargargarytnaayytnaargarathggngcngtnytngargtnggngarwsnmgn

gtnwsncarytncaywsncargcnathaarmgnytnmgnacnaarytnggnaarytn

## Size

239 x 3 = 717 Base Sequence

References

1. UniProtKB - P0A2E9 (FLIA\_SALTI)
   1. Source: <https://www.uniprot.org/uniprot/P0A2E9>
2. Sequence Manipulation Suite: Reverse Translate
   1. Source: <https://www.bioinformatics.org/sms2/rev_trans.html>