TERMINAL LAB

BIOINFORMATICS

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Sahiwal Campus

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Introduction to Bioinformatics

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COMPLETED LAB TASKS

1. Task 1

Sequence:

MNSLYTAEGVMDKHSLWQRYVPLVRHEALRLQVRLPASVELDDLLQAGGIGLLNA
VDRYDALQGTAFTTYAVQRIRGAMLDELRSRDWVPRSVRRNAREVAHAMGQLEQE
LGRNATETEVADRLGIAVEEYRQMLLDTNNSQLFSYDEWREEHGDSIELVTDEHQQ
ENPLHHLMEGNLRQRVMEAIEALPEREQLVLTLYYQEELNLKEIGAVLEVGESRVSQ
LHSQAIKRLRTKLGKL

Protein	**RNA polymerase sigma factor FliA**
Gene	**fliA**
Organism	*Salmonella typhi*
Status	Reviewed - Annotation score: ◉◉◉◯◯ - Protein inferred from homology[i]

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

1.1 Biological Process

GO - Biological process[i]

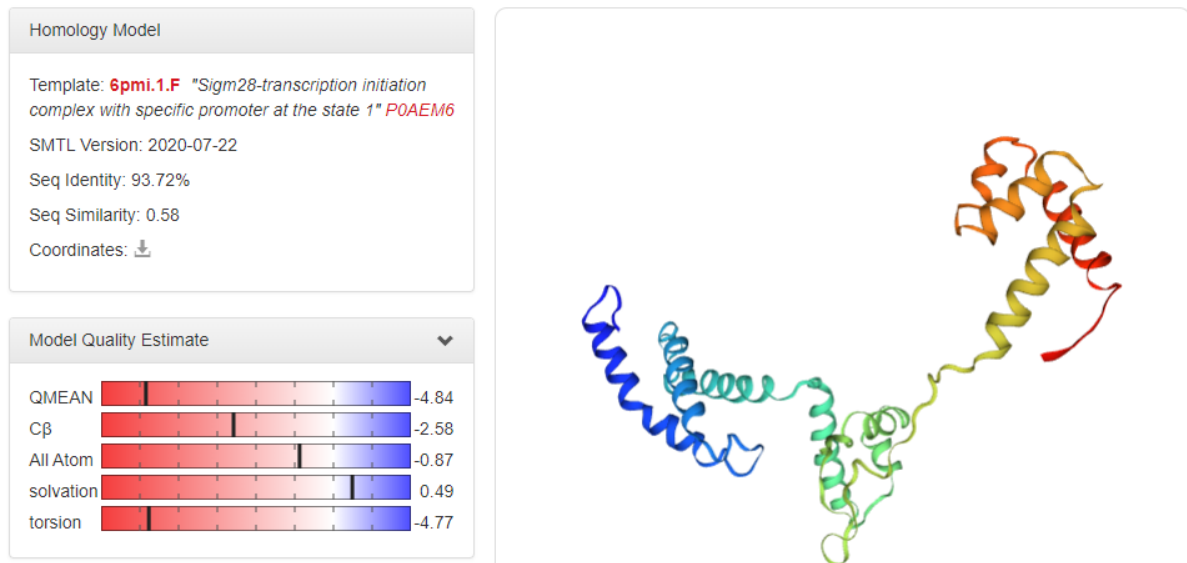- pathogenesis   Source: UniProtKB-KW
- transcription initiation from bacterial-type RNA polymerase promoter   Source: UniProtKB-UniRule

1.2 Molecular Function

GO - Molecular function[i]

- DNA binding   Source: UniProtKB-UniRule
- DNA-binding transcription factor activity   Source: InterPro
- DNA-directed 5'-3' RNA polymerase activity   Source: InterPro
- sigma factor activity   Source: UniProtKB-UniRule

1.3 Protein Structure

Homology Model

Template: **6pmi.1.F** *"Sigm28-transcription initiation complex with specific promoter at the state 1"* *P0AEM6*

SMTL Version: 2020-07-22

Seq Identity: 93.72%

Seq Similarity: 0.58

Coordinates: ⬇

Model Quality Estimate

QMEAN	-4.84
Cβ	-2.58
All Atom	-0.87
solvation	0.49
torsion	-4.77

Source: P0A2E9

1.4 Protein-Protein Interaction
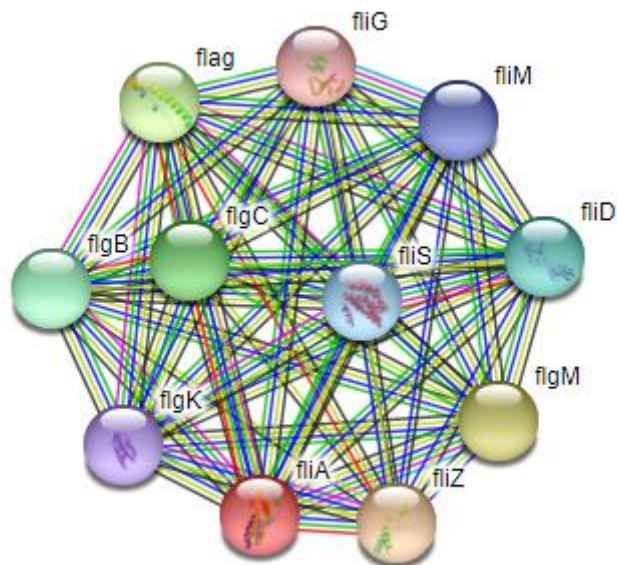
Source: 220341.16503199

1.5   Family and Domain

HAMAP[i]	MF_00962, Sigma70_FliA, 1 hit
InterPro[i]	View protein in InterPro IPR014284, RNA_pol_sigma-70_dom IPR000943, RNA_pol_sigma70 IPR007627, RNA_pol_sigma70_r2 IPR007624, RNA_pol_sigma70_r3 IPR007630, RNA_pol_sigma70_r4 IPR012845, RNA_pol_sigma_FliA_WhiG IPR013325, RNA_pol_sigma_r2 IPR013324, RNA_pol_sigma_r3/r4-like IPR028617, Sigma70_FliA
Pfam[i]	View protein in Pfam PF04542, Sigma70_r2, 1 hit PF04539, Sigma70_r3, 1 hit PF04545, Sigma70_r4, 1 hit
PIRSF[i]	PIRSF000770, RNA_pol_sigma-SigE/K, 1 hit
PRINTS[i]	PR00046, SIGMA70FCT
SUPFAM[i]	SSF88659, SSF88659, 2 hits SSF88946, SSF88946, 1 hit
TIGRFAMs[i]	TIGR02479, FliA_WhiG, 1 hit TIGR02937, sigma70-ECF, 1 hit
PROSITE[i]	View protein in PROSITE PS00715, SIGMA70_1, 1 hit PS00716, SIGMA70_2, 1 hit

2. Task 2

2.1 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
wsncarytntttywsntaygaygartggmgngargarcayggngaywsnathgarytngtn
acngaygarcaycarcargaraayccnytncaycayytnatggarggnaayytnmgncar
mgngtnatggargcnathgargcnytnccngarmgngarcarytngtnytnacnytntay
taycargargarytnaayytnaargarathggngcngtnytngargtnggngarwsnmgn
gtnwsncarytncaywsncargcnathaarmgnytnmgnacnaarytnggnaarytn

2.2 Size

==239 x 3 = 717 Base Sequence==

References

1. UniProtKB - P0A2E9 (FLIA_SALTI)

    a. Source: https://www.uniprot.org/uniprot/P0A2E9

2. Sequence Manipulation Suite: Reverse Translate

    a. Source: https://www.bioinformatics.org/sms2/rev_trans.html