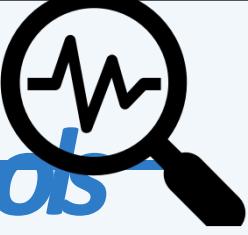


Computational Analysis of Unknown DNA

Sequences Using Integrated Bioinformatics Tools



Organism: Homo Sapien

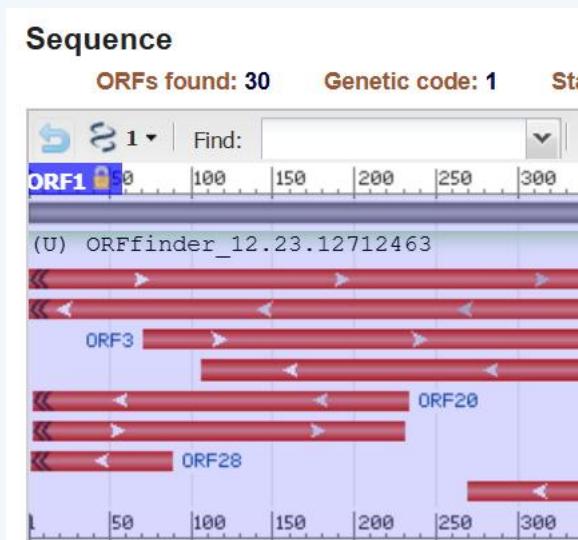
Gene: KRT17

Protein : Keratin

DNA ANALYSIS

Score 2802 bits(1517)	Expect 0.1517(100%)	Identities 0/1517(0%)	Gaps 0	Strand Plus/Plus
Query 1 ACACAACTTGGGGCCCTCTCTCTCAGCCCTCTCTCTGTCGCTGCCCTCTGGCC	60			
Sbjct 1 ACACAACTTGGGGCCCTCTCTCAGCCCTCTCTCTGTCGCTGCCCTCTGGCC	60			
Query 61 GCGACCATGACACTCCATGCCAGTGTCACCTCCCAEGCTCCATCAAAGGGCTCTCC	120			
Sbjct 61 GCGACCATGACACTCCATGCCAGTGTCACCTCCCAEGCTCCATCAAAGGGCTCTCC	120			
Query 121 GGCTTGGGGGCTGGCTGGCCGACCTCTCTGGGGCTGTCTGGGGCTGGCTGGGG	180			
Sbjct 121 GGCTTGGGGGCTGGCTGGCCGACCTCTCTGGGGCTGTCTGGGGCTGGCTGGGG	180			
Query 181 TCTCTGCAGGGCTGGGAATCTCTGGGGCTGGGGAGACCCCTGGGGTAGAGCTACTCC	240			
Sbjct 181 TCTCTGCAGGGCTGGGAATCTCTGGGGCTGGGGAGACCCCTGGGGTAGAGCTACTCC	240			
Query 241 AGCTGCTCACAGCTTGGCTCTGGGGCTGGGGAGACCCCTGGGGTAGAGCTACTCC	300			
Sbjct 241 AGCTGCTCACAGCTTGGCTCTGGGGCTGGGGAGACCCCTGGGGTAGAGCTACTCC	300			
Query 301 CTGCTGGGGGGGGAGAACCCATGGAGAACCTCAATGGGGCTGGCTCTTAC	360			

Homo sapiens	2765	2765	99%	0.0	100.00%	1514
Homo sapiens	2761	2761	99%	0.0	99.93%	1512
Pan troglodytes...	2730	2730	100%	0.0	99.14%	1591

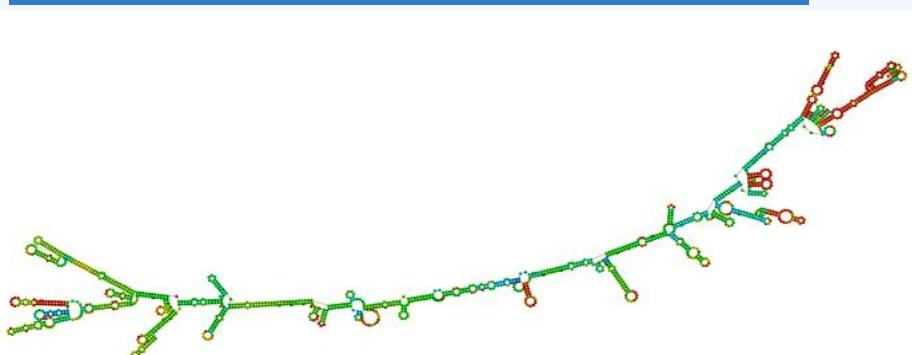


5' Frame 1:
 TOLGAPLLSSPSPVCLPPAAATMTSIRQFTSSSSIKGGSSRTSCLRSGLGGAGSCRLGSAGGLGSTLGSSYSSCSYFGS
 GGGYSSFGGVGDLLLAGGEKATMQNINDRLASLYLDKVRALLEANTELEVIRDWYQRQAFGPARDYSQQYRTIEELQNKNIATVDN
 ANILQLIDNARIAADDFTKPETEQALRLSVEADINGLRLRVLDELTILARADLEMOIENILKEELAYLKKNNHEEMNALRGQVGEINV
 EMDAAPGVDSLRLNEMRDQYEMKAENRKAEDWFSSKTEELNRREVATNSELVQSGKSEISELRRTMQALEIELQSQLSMASLEG
 NLAETENRYCVQLSQIQLIGSVEEQLAQLRCMEQQNQYEYKILLDVKTRLEQEIA TYRRLLEGEDAHLTYKKEPVTRQVRTIVE
 EVQDGKVISSREQVHQTRR-GLSYPGRPPRRQGSRPICPTVSGLSSLSPLIQSLPHASLPDDNKAC-LS

3'5' Frame 2:
 S-VNKLYCHARKHGECETEAGG-GWGRRLWGRWGCLPASWAGRGS-VLSGWSGGPAGR-R-PCHCPPLPQWYAPDGNPSVPLSCT
 ESGGHPLPPAGGGWRWQSPPAASSHAGFCIPGSAPRQCSAPGSGTAARSGLSLSPFGCPGPMMISG-ATAALSP
 PRAWCAGAPRSHSCHSAPAHCHWPWRGSVPLSC-RUNPRHPGSSLPSHTCHASR-CGGSGPRLQQRSPH-SHIPPGLAGRSSPP
 RGSSSGRAPP-GQSASPGRWLPGSAHAPCAGH-CRPHSGAGPALSQTWCQSHQQPDPGHQCQSVAGCWHCPRWL-GSCSAAPQLS
 CSTGCSHGRAPGPASGSTHGSPPAOCWPPGAPCPCGRPGRGH-GSAWWPSHQLPAAHQHPSQCSCHSHQSQCSQSSWSSCYPRCC
 PGRQQIIPACSRSHRPGQTAGRRCGTSRPGRRSP-WSWR-TGCRNWSWWRRQEAQTOEKGRGEQPV

ORF1 was selected because it is among the longest predicted ORFs with a start and stop codon, makes it a reliable candidate for analysis.

RNA ANALYSIS

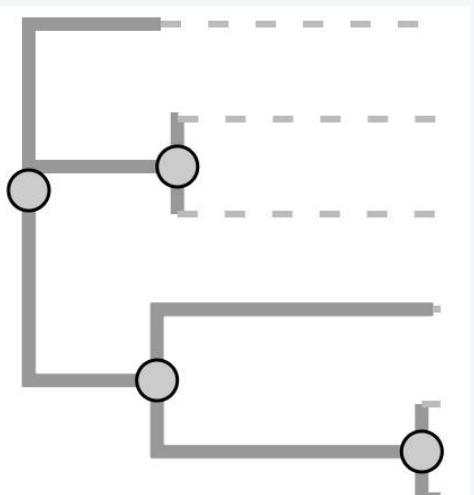


The stability of the keratin-encoding messenger RNA (mRNA) is a separate biological process.

PHYLOGENETIC ANALYSIS

CLUSTAL 0(1.2.4) multiple sequence alignment

```
GGTCAGGAGATTGAGACCA CGGTAAACCCCGTCTCTACTAAAAATAACAAAAATTAGCCGGCGTGGT
GGCGGGCGCTGTAGTCCCAGCTACTCGGAGAGGCTGAGCAGGAGAATGGTGTAACCC 60
ACACAATTTGGGGCCCTCTCTCCAGCCCTTCTCTGCTGCTGCCCTCTGCTGCTCTGCCGCCACCATG
----- 0
CTCTCTCTCCAGCCCTCTCTCTGCTGCTGCTGCTGCCCTCTGCTGCTGCTGCCCTCTGCTGCTGCTGCC
----- 0
TCCTCTAGAGCCACTCTCTCTGCTGCTGCTGCTGCTGCCCTCTGCTGCTGCTGCCCTCTGCTGCTGCTGCC
----- 0
CGCACCTCGGACCTCTCTCTGCTGCTGCTGCTGCTGCCCTCTGCTGCTGCTGCCCTCTGCTGCTGCTGCC
----- 0
ATGACCACCATCCGCCAGTTCACCTCTCCAGCTCATCAAGGCTCTCTGGCTGGGGGGCGCT
```



PROTEIN ANALYSIS

AA: 503

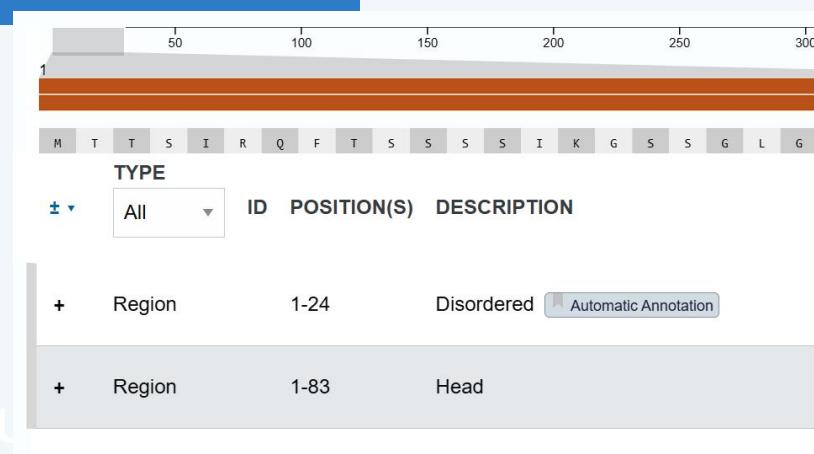
pI: 5.15

MW:

5.5K

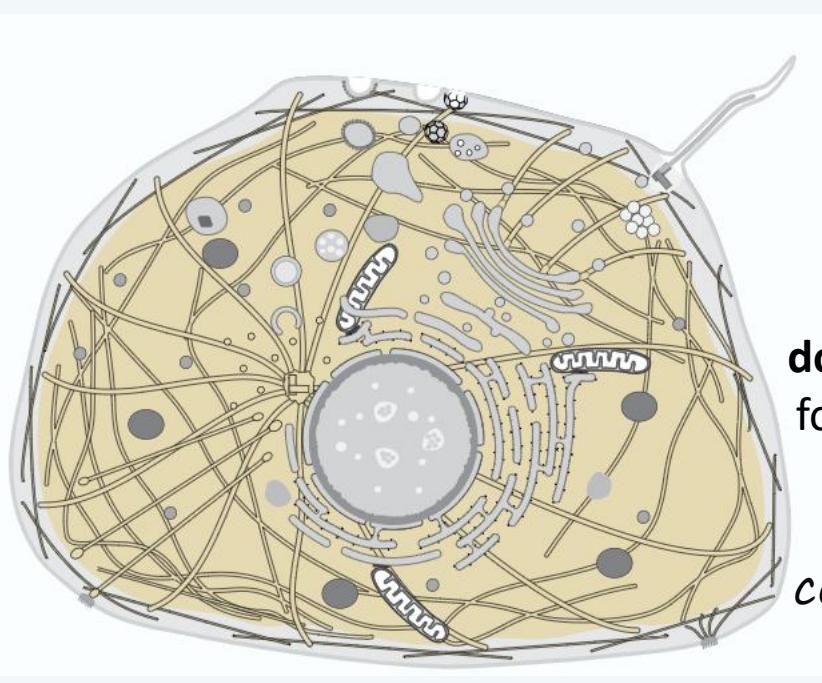
II: 55.97

AI: 82.84



Type I keratin involved in the formation and maintenance of various skin appendages

SUBCELLULAR LOCALIZATION



Keratin protein is localized in **epithelial cells**, forming tough structural components in our body's barriers and appendages like hair, nails, skin's outer layer. **Intermediate filament** interactions **coiled-coil domains** (hydrophobic/hydrophilic interactions), forming dimers, then protofilaments, and finally intermediate filaments, crucial for tissue strength. These filaments anchor to cell structures and interact with other proteins through disulfide bonds, providing mechanical integrity and influencing cell functions like growth, differentiation, and migration.

PROTEIN INTERACTION

