

Question 11

Partially correct

Mark 1.00 out of 2.00

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Question 11. There are several genomes at the NCBI without annotations. That means none of the genetic elements like CDSs, genes or any other features annotated as "misc_feature", have been indicated in the sequence. Search the records in the NCBI nucleotide database for HIV-1 (Human immunodeficiency virus type 1) complete genomes without any annotation.

How many entries have you found?

22



CORRECT: 23

Indicate here the accession.version number of only one of them.

AY761126.1



Optionally indicate here your search strategy

txid11676[porgn] AND complete genome NOT CDS[key] NOT Gene[key] NC



(no rate)

Option 1.

txid11676[porgn] AND "complete genome"[title] NOT CDS[key] NOT Gene[key] NOT misc_feature[key]

Only 5 entries fulfill these criteria. JN571034.1, AY781127.1, AY781125.1, AY761126.1 and AY761126.1.

UPDATE: now it is 10!

JN571034.1, AY761127.1, AY761125.1, AY761126.1, AY761126.1, ON245430.1, ON245426.1, ON245429.1, ON245427.1, ON245431.1

so both answers are considered right.

However, there is a second option:

txid11676[Primary organism] AND complete genome NOT CDS[key] NOT Gene[key] NOT misc_feature[key]

Here we are not forcing the words "complete" and "genome" neither to the title nor to be together so we can view more results

We use to get 21 good entries (2LDL_A is not a complete genome) with accession numbers:

JX563679.1
M03259.1
M03258.1
JX563677.1
JX563678.1
JX563686.1
JX563673.1
JX563674.1
JX563682.1
JX563671.1
JN571034.1
JX563672.1
JX563675.1
JX563681.1
JX563676.1
JX563683.1
AY781127.1
AY781125.1
AY781128.1
AY781126.1
MK457954.1

UPDATE: now is 26 (again 2LDL_A is not a complete genome).

JX563679.1
M03259.1
M03258.1
JX563677.1
JX563678.1
JX563686.1
JX563673.1
JX563674.1
JX563682.1
JX563671.1
JN571034.1
JX563672.1
JX563675.1
JX563681.1
JX563676.1
JX563683.1
AY781127.1
AY781125.1
AY781128.1
AY781126.1
ON245430.1
ON245428.1
MK457954.1
ON245429.1
ON245427.1
ON245431.1