1b.

* Tool: BALSTP
* Algorithm: blastp (protein-protein BLAST)
* Scoring Matrix: PAM 30
* Gap penalty: Existence: 9, Extension: 1
* Query Length: 380

1c.

Name: cytochrome b

Organism: Homo sapiens neanderthalensis

Accession: YP\_002124314

Version: YP\_002124314.2

1d.

Accession number: YP\_002124314.2

Max score: 789

Total score: 789

Query cover: 100%

E-value: 0

Per identity: 100.00%

Yes, I get an exact match because per identity is 100% and query cover is 100%.

2a.

ORIGIN

1 gatcacaggt ctatcaccct attaaccact cacgggagct ctccatgcat ttggtatttt

61 cgtctggggg gtgtgcacgc gatagcattg cgagacgctg gagccggagc accctatgtc

121 gcagtatctg tctttgattc ctgccccatt ccattattta tcgcacctac gttcaatatt

181 acaggcgagc atacttactg aagtgtgtta attaattaat gcttgtagga cataataata

241 acgactaaat gtctgcacag ctgctttcca cacagacatc ataacaaaaa atttccacca

301 aaccccccct cccccgcttc tggccacagc acttaaacac atctctgcca aaccccaaaa

361 acaaagaacc ctaacaccag cctaaccaga tttcaaattt tatcttttgg cggtatacac

421 ttttaacagt caccccctaa ctaacacatt attttcccct cccactccca tactactaat

481 ctcatcaata caacccccgc ccatcctacc cagcacacac cgctgctaac cccatacccc

541 gagccaacca aaccccaaag acacccccca cagtttatgt agcttacctc ctcaaagcaa

601 tacactgaaa atgtttagac gggctcacat caccccataa acaaataggt ttggtcctag

661 cctttctatt agctcttagt aagattacac atgcaagcat ccccattcca gtgagttcac

721 cctctaaatc accacgatca aaagggacaa gcatcaagca cgcaacaatg cagctcaaaa

781 cgcttagcct agccacaccc ccacgggaaa cagcagtgat aagcctttag caataaacga

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1141 acgagccaca gcttaaaact caaaggacct ggcggtgctt catatccctc tagaggagcc

1201 tgttctgtaa tcgataaacc ccgatcaacc tcaccacctc ttgctcagcc tatataccgc

1261 catcttcagc aaaccctgat gaaggctaca aagtaagcgc aagtacccac gtaaagacgt

1321 taggtcaagg tgtagcccat gaggtggcaa gaaatgggct acattttcta ccccagaaaa

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1441 gagtgcttag ttgaacaggg ccctgaagcg cgtacacacc gcccgtcacc ctcctcaagt

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1561 acatggtaag tgtactggaa agtgcacttg gacgaaccag agtgtagctt aacacaaagc

1621 acccaactta cacttaggag atttcaactt aacttgaccg ctctgagcta aacctagccc

1681 caaacccact ccaccttact accaaacaac cttagccaaa ccatttaccc aaataaagta

1741 taggcgatag aaattgaaac ctggcgcaat agatgtagta ccgcaaggga aagatgaaaa

1801 attataacca agcataatat agcaaggact aacccctata ccttctgcat aatgaattaa

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2401 cattattacc ctcactgtca acccaacaca ggcatgctca taaggaaagg ttaaaaaaag

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2581 gtgcaaaggt agcataatca cttgttcctt aaatagggac ctgtatgaat ggctccacga

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13861 acttaaaata aaaaccccac tatacacatt ttatttctcc aacatactcg ggttctaccc

13921 tagcatcaca caccgcacaa tcccctatct aggccttctt acgagccaaa acctgcccct

13981 actcctccta gacctaacct gactagaaaa gctattacct aaaacaattt cacagcacca

14041 aatctccgcc tccatcacca cctcaaccca aaaaggcata attaaacttt acttcctctc

14101 tttcttcttc ccactcatcc taaccctact cctaatcata taacctattc ccccgagcaa

14161 tctcaattac aacatataca ccaacaaaca atgttcaacc agtaactact actaatcaac

14221 gcccataatc atacaaagcc cccgcaccaa taggatcctc ccgaatcaac cctgacccct

14281 ctccttcata gattattcag cttcctacac tattaaagtt taccacaacc accaccccat

14341 catactcttt cacccacagc accaatccta cctccatcgc taaccccact aaaacactca

14401 ccaagacctc aacccctgac ccccatgcct caggatactc ctcaatagcc atcgctgtag

14461 tatatccaaa gacaaccatc attcccccta aataaattaa aaaaactatt aaacccatat

14521 aacctccccc aaaattcaga ataataacac acccaaccac accgctaaca atcaatacta

14581 aacccccata aataggagaa ggcttagaag aaaaccccac aaaccccatt actaaaccca

14641 cactcaacag aaacaaagca tacatcatta ttctcgcacg gactacaacc acgaccaatg

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14761 ttaaccccct aataaaatta attaaccact cattcatcga cctccccacc ccatccaaca

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14881 caggactatt cctagccatg cactactcac cagacgcctc gaccgccttt tcatcaatcg

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15061 ttctctactc aaaaacctga aacatcggca ttatcctcct gcttgcaact atagcaacag

15121 ccttcatagg ctatgtcctc ccatgaggcc aaatatcatt ctgaggggcc acagtaatta

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15361 accccctagg aatcacctcc cattccgata aaatcacctt ccacccttac tacacaatca

15421 aagacgccct cggcttattt ctcttccttc tctccttaat gacattaaca ctactctcac

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15661 ttcatgtatc caaacaacaa agcataatat ttcgcccact aagccaatca ctttattgac

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15781 ttatcatcat tggacaagta gcatccgtac tatacttcac aacaatccta atcctaatac

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15961 agtctttaac tccaccatta gcacccaaag ctaagattct aatttaaact attctctgtt

16021 ctttcatggg ggagcagatt tgggtaccac ccaagtattg actcacccat cagcaaccgc

16081 tatgtatttc gtacattact gccagccacc atgaatattg tacagtacca taattacttg

16141 actacctgca gtacataaaa acctaatcca catcaacccc ccccccccat gcttacaagc

16201 aagcacagca atcaaccttc aactgtcata catcaactac aactccaaag acgcccttac

16261 acccactagg atatcaacaa acctacccac ccttgacagt acatagcaca taaagtcatt

16321 taccgtacat agcacattac agtcaaatcc cttctcgccc ccatggatga cccccctcag

16381 ataggggtcc cttgatcacc atcctccgtg aaatcaatat cccgcacaag agtgctactc

16441 tcctcgctcc gggcccataa cacttggggg tagctaaagt gaactgtatc cgacatctgg

16501 ttcctacttc agggccataa agcctaaata gcccacacgt tccccttaaa taagacatca

16561 cgatg

2b.

Accession: NC\_011137

Max score: 502

Total score: 502

Query cover: 100%

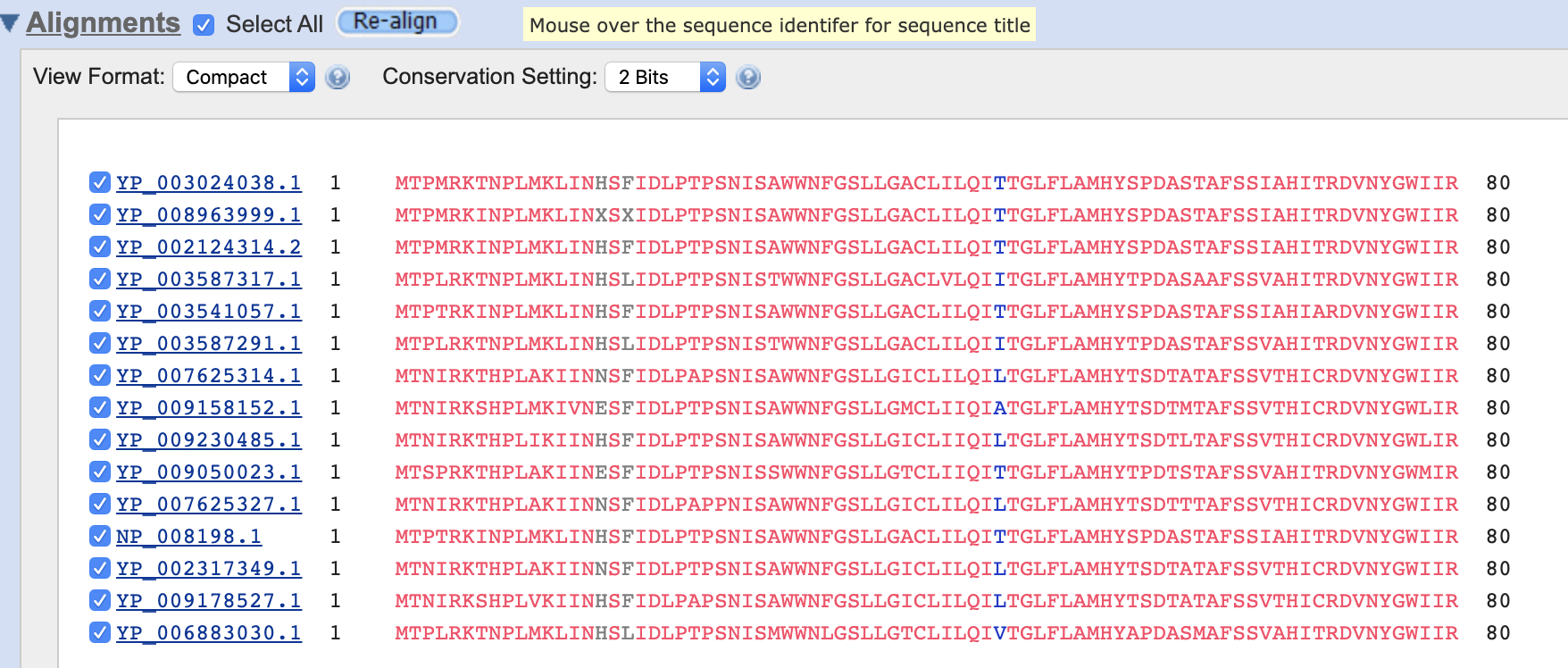
E-value: 4e-149

Per identity: 73.77%

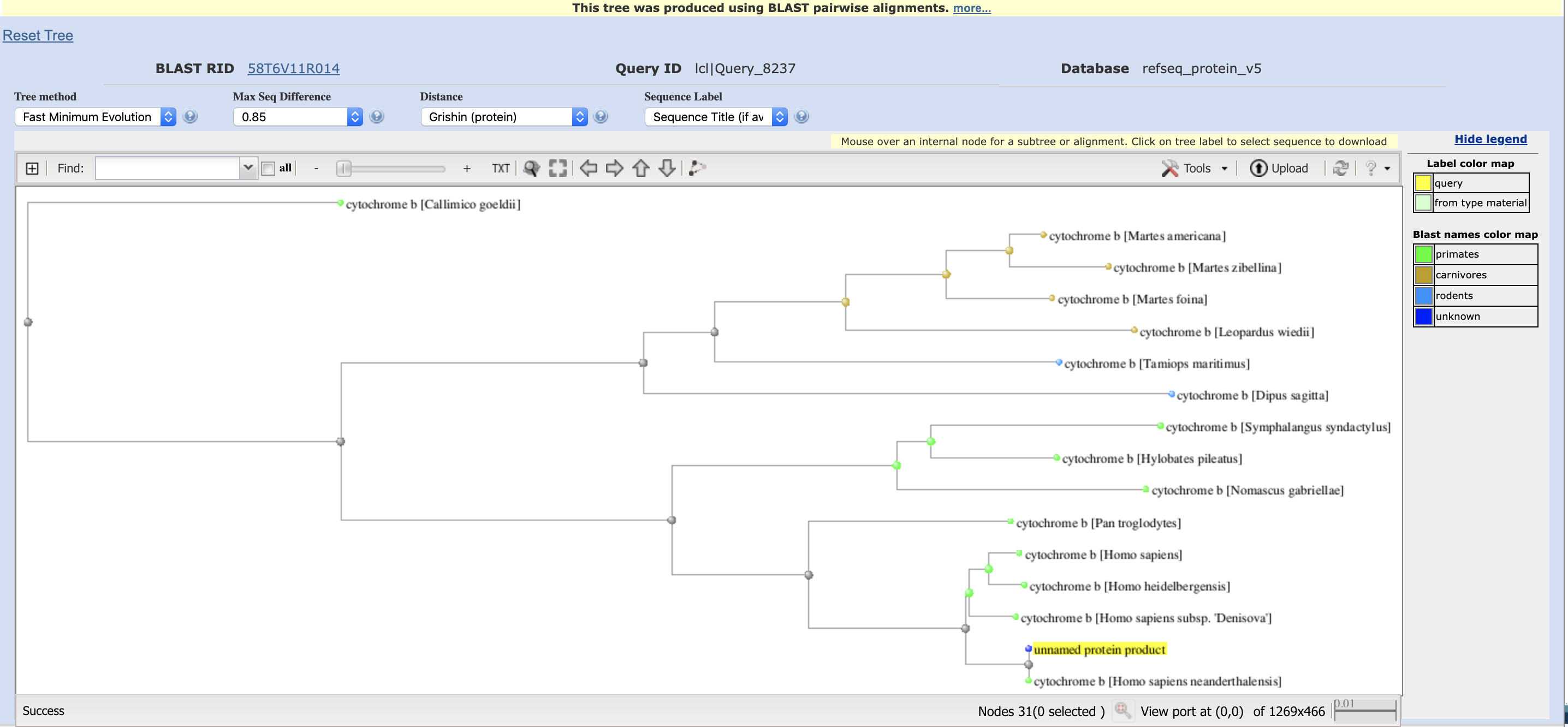
Gap penalty: Existence 9, extension 1

4a.

* Tool: BALSTP
* blastp (protein-protein BLAST)
* Database: refseq\_protein
* Scoring matrix: pam 250
* Gap penalty: Existence 14 Extension 2

4b.

4c.

The tree shows an evolutionary relationship because all the sub-branches are developed from the root node, indicating that they shared an ancestor before.

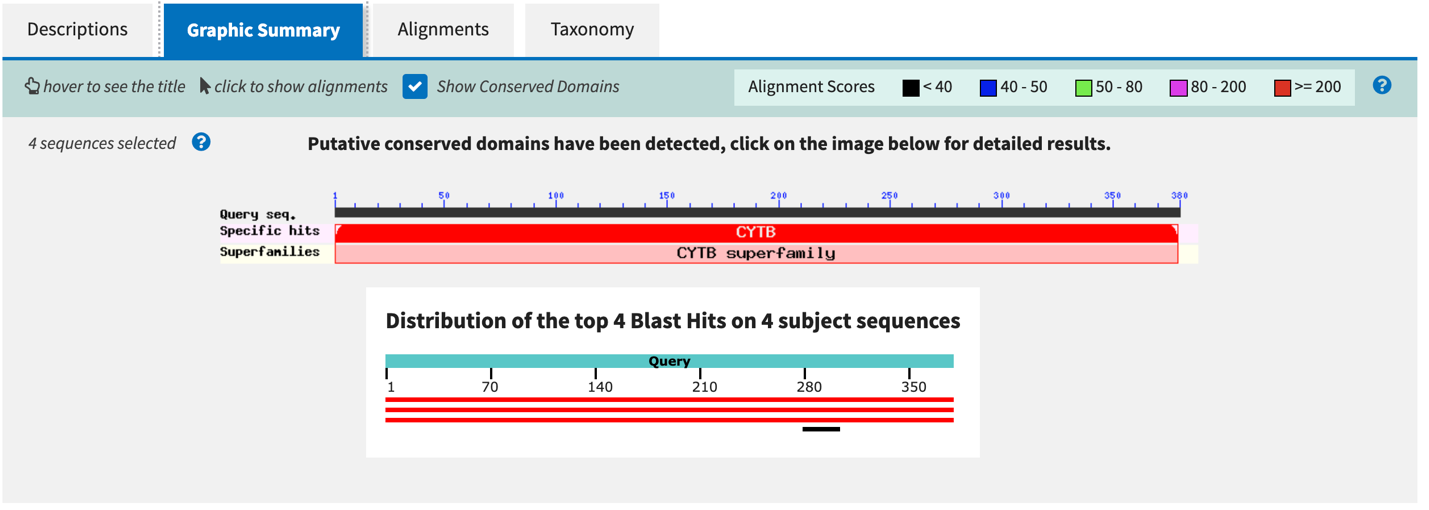
5a.

* Tool: BALSTP

5b.

* Algorithm: blastp (protein-protein BLAST)
* Scoring Matrix: PAM 30
* Gap penalty: Existence: 9, Extension: 1
* Length: 380

5c.



5d.

Max score: 789

Total score: 789

Query cover: 100%

E-value: 0

Per identity: 100%

Accession: YP\_003024038

All queries are covered because both query cover and per identity are 100%.

5e.

Max score: 37.1

Total score: 37.1

Query cover: 6%

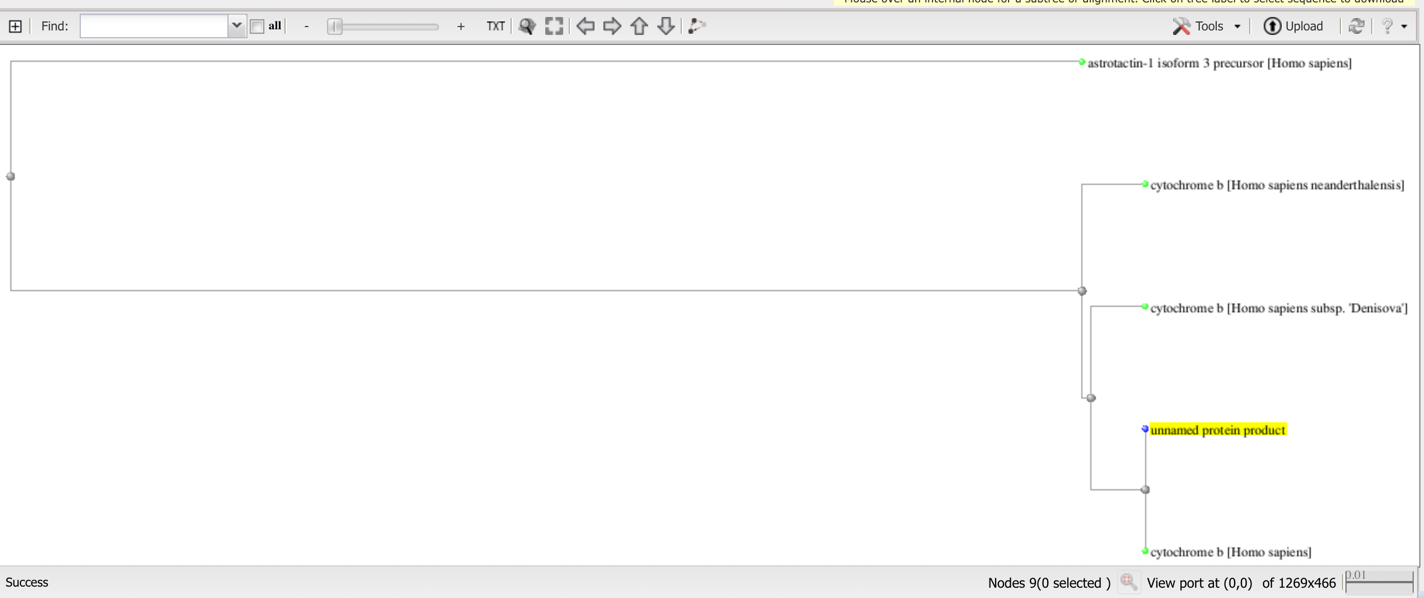
E-value: 0.055

Per identity: 61.54%

Accession: NP\_001273093 XP\_005245252

The best hit covered all query but the worst hit covered the query around 280 to 310.

5f.



The reason some human hits is distantly related to other is that they are not the same protein in one species. Some protein developed then time changes.

6.

The protein is translated from human mitochondrial genome.