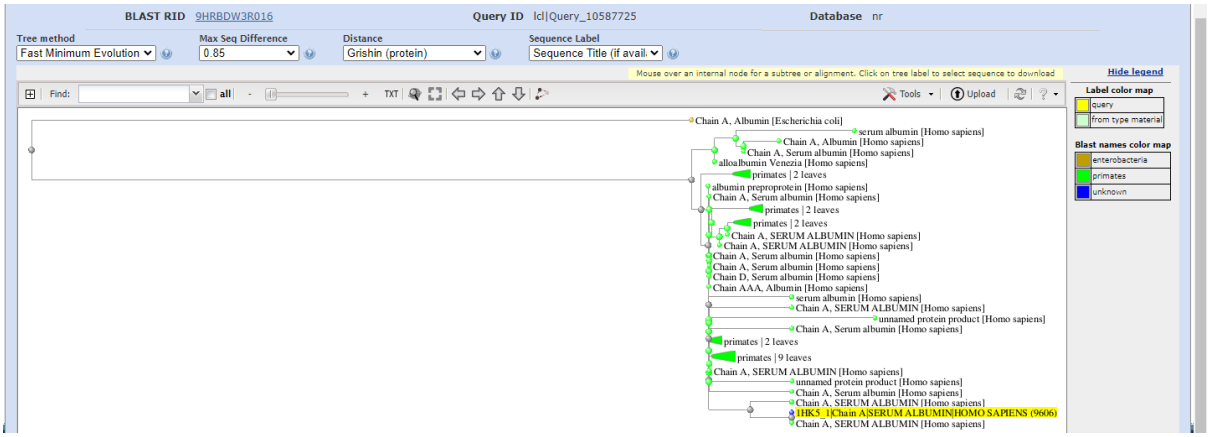
Experiment no:2
21BBT050

BLAST

OXYTOCIN

DISTANCE TREE OF OXYTOCIN:



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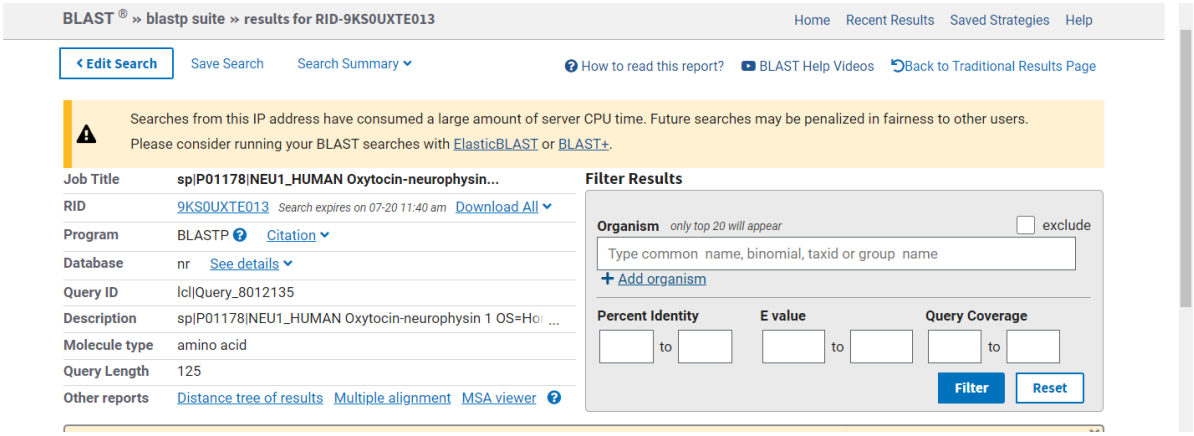
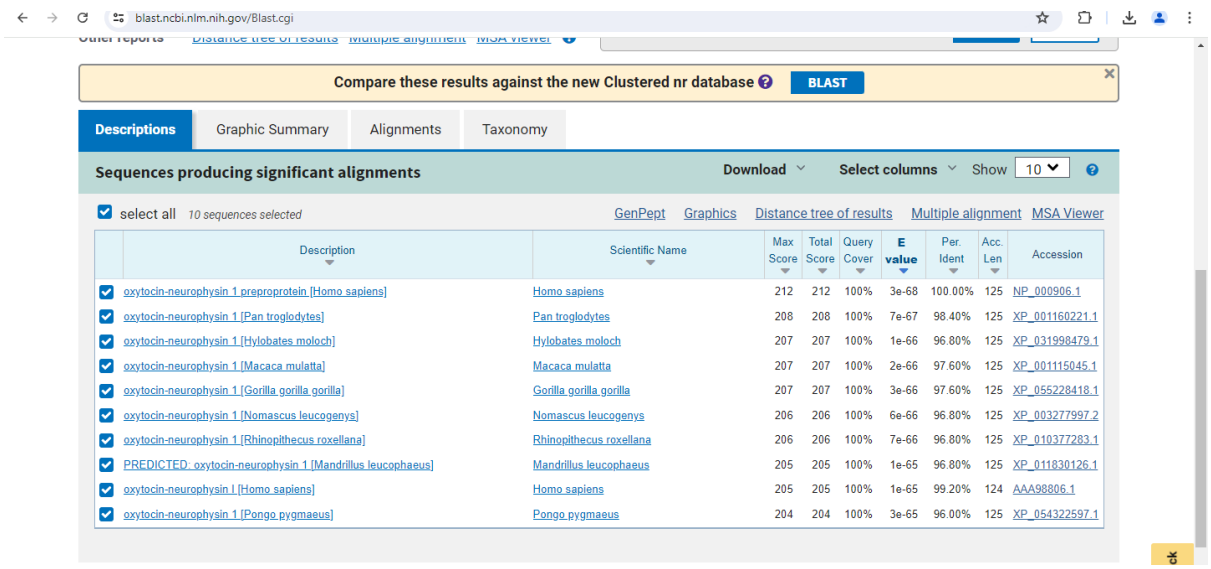


Genomic ID: P01178

DESCRIPTION OF OXYTOCIN:



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Compare these results against the new Clustered nr database BLAST

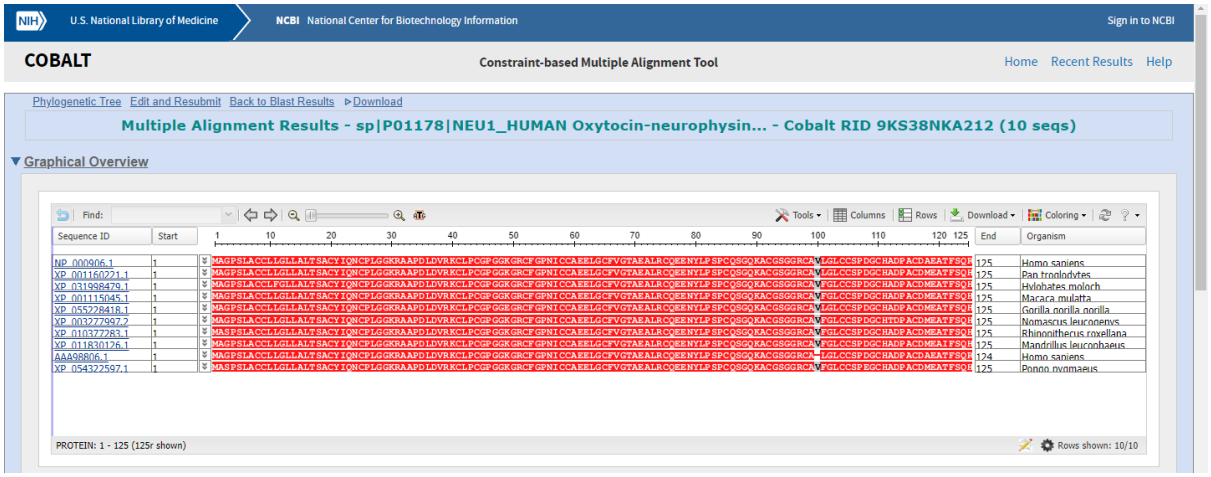
Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments — Download — Select columns — Show 10

select all 10 sequences selected — GenPept | Graphics | Distance tree of results | Multiple alignment | MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
oxytocin-neurophysin 1 preproprotein [Homo sapiens]	Homo sapiens	212	212	100%	3e-68	100.00%	125	NP_000906.1
oxytocin-neurophysin 1 [Pan troglodytes]	Pan troglodytes	208	208	100%	7e-67	98.40%	125	XP_001160221.1
oxytocin-neurophysin 1 [Hylobates moloch]	Hylobates moloch	207	207	100%	1e-66	96.80%	125	XP_031998479.1
oxytocin-neurophysin 1 [Macaca mulatta]	Macaca mulatta	207	207	100%	2e-66	97.60%	125	XP_001115045.1
oxytocin-neurophysin 1 [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	207	207	100%	3e-66	97.60%	125	XP_055228418.1
oxytocin-neurophysin 1 [Nomascus leucogenys]	Nomascus leucogenys	206	206	100%	6e-66	96.80%	125	XP_003277997.2
oxytocin-neurophysin 1 [Rhinopithecus roxellana]	Rhinopithecus roxellana	206	206	100%	7e-66	96.80%	125	XP_010377283.1
PREDICTED: oxytocin-neurophysin 1 [Mandrillus leucophaeus]	Mandrillus leucophaeus	205	205	100%	1e-65	96.80%	125	XP_011830126.1
oxytocin-neurophysin I [Homo sapiens]	Homo sapiens	205	205	100%	1e-65	99.20%	124	AAA98806.1
oxytocin-neurophysin 1 [Pongo pygmaeus]	Pongo pygmaeus	204	204	100%	3e-65	96.00%	125	XP_054322597.1

MULTIPLE ALLIGNMENT OF OXYTOCIN:



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Phylogenetic Tree | Edit and Resubmit | Back to Blast Results | Download

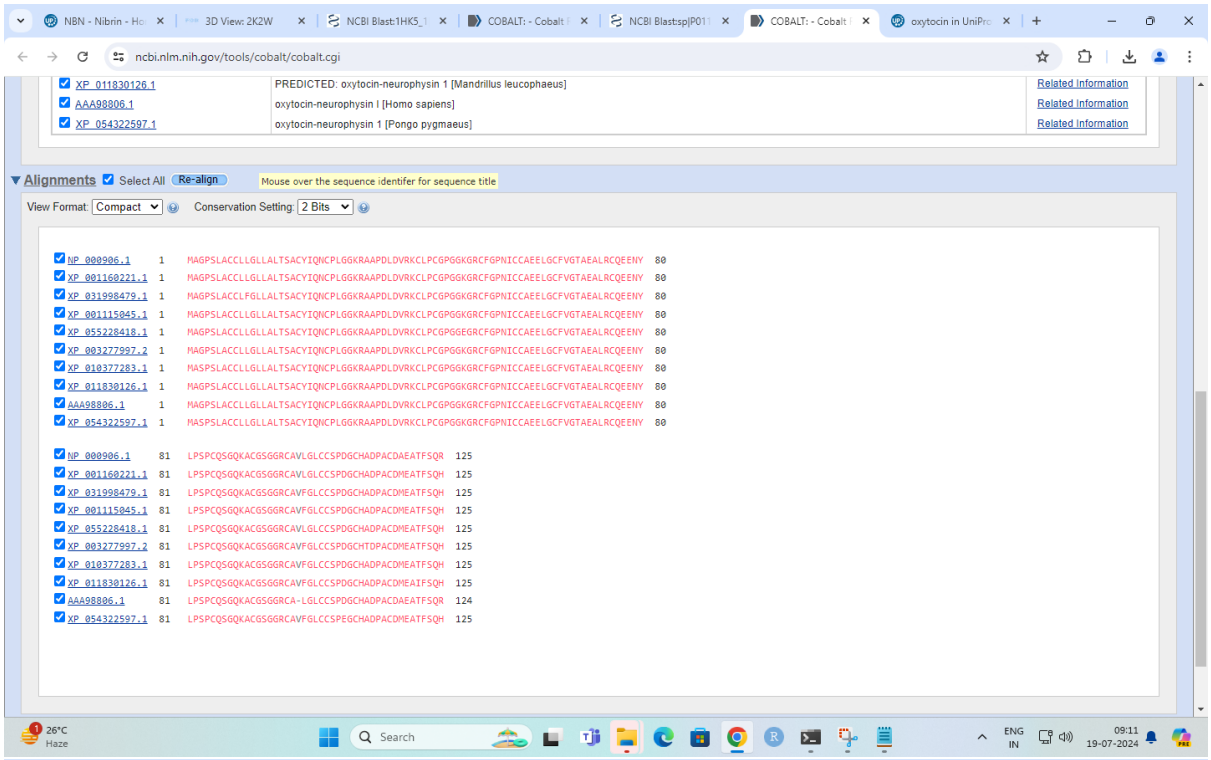
Multiple Alignment Results - sp|P01178|NEU1_HUMAN Oxytocin-neurophysin... - Cobalt RID 9KS38NKA212 (10 seqs)

Graphical Overview

Find: — Tools | Columns | Rows | Download | Coloring

Sequence ID	Start	1 10 20 30 40 50 60 70 80 90 100 110 120 125	End	Organism
NP_000906.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Homo sapiens
XP_001160221.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Pan troglodytes
XP_031998479.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Hylobates moloch
XP_001115045.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Macaca mulatta
XP_055228418.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Gorilla gorilla gorilla
XP_003277997.2	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Nomascus leucogenys
XP_010377283.1	1	MASPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Rhinopithecus roxellana
XP_011830126.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Mandrillus leucophaeus
AAA98806.1	1	MAGPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	124	Homo sapiens
XP_054322597.1	1	MASPSLACCLGLLALTSACYIQNCPLGGKRAAPDLDVRKCLPCGPGGKGRCFGPNICCAEELGCFVGTAEALRCQEENYLPSPCQSGQKACGSGGRCA	125	Pongo pygmaeus

PROTEIN: 1 - 125 (125r shown) — Rows shown: 10/10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COBALT: - Cobalt
NCBI Blast:sp|P01
COBALT: - Cobalt
oxytocin in UniPro
ncbi.nlm.nih.gov/tools/cobalt/cobalt.cgi
XP_011830126.1 PREDICTED: oxytocin-neurophysin 1 [Mandrillus leucophaeus] Related Information
AAA98806.1 oxytocin-neurophysin I [Homo sapiens] Related Information
XP_054322597.1 oxytocin-neurophysin 1 [Pongo pygmaeus] Related Information
Alignments Select All Re-align Mouse over the sequence identifer for sequence title
View Format: Compact Conservation Setting: 2 Bits
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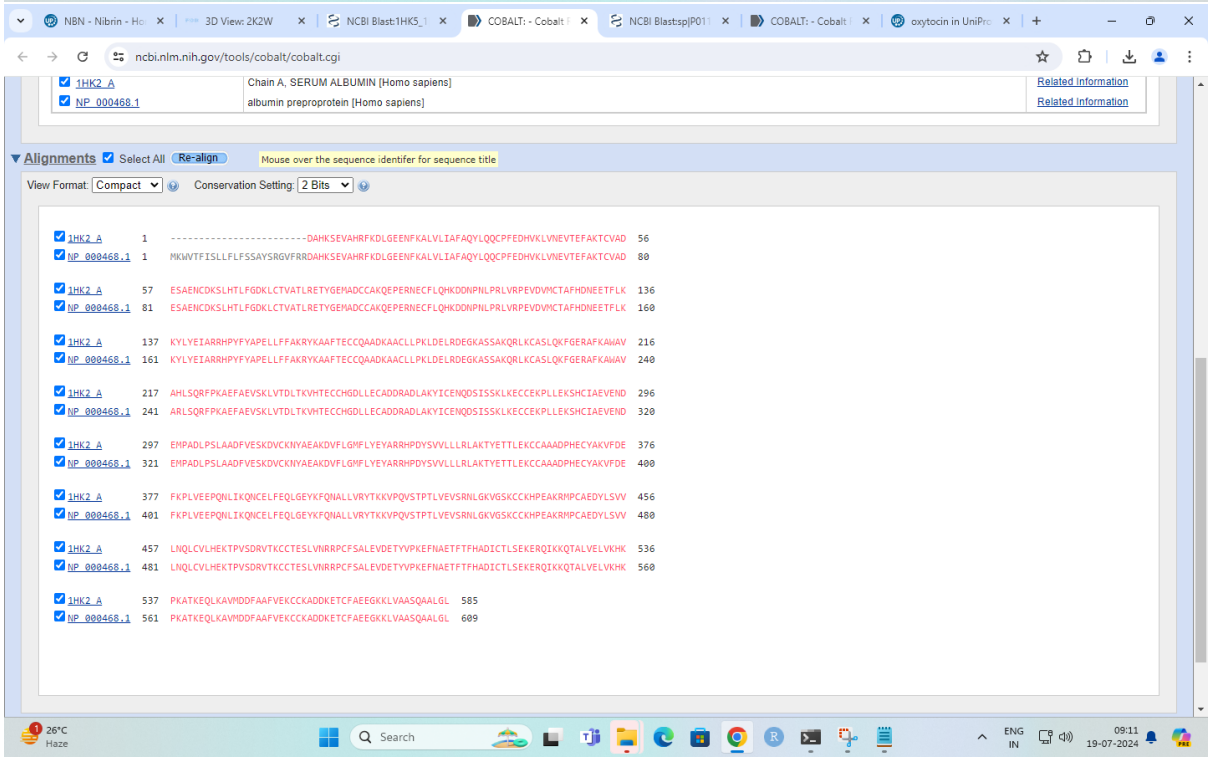
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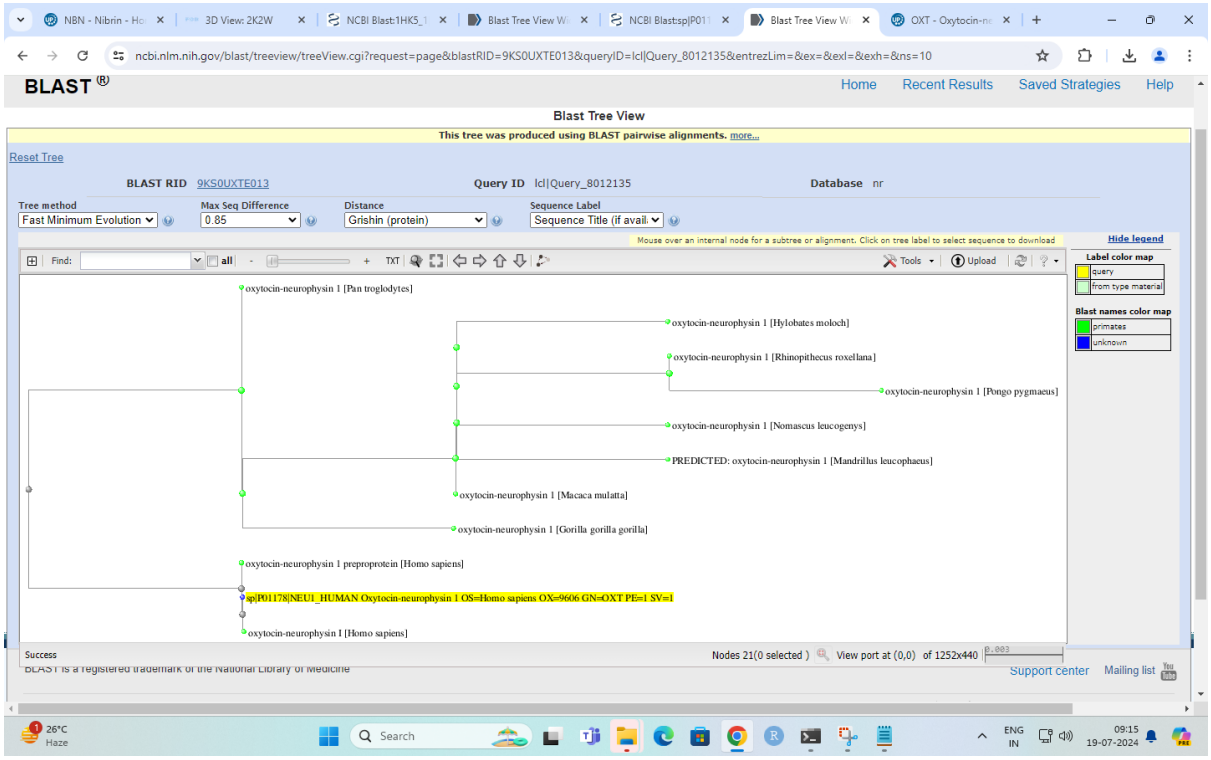
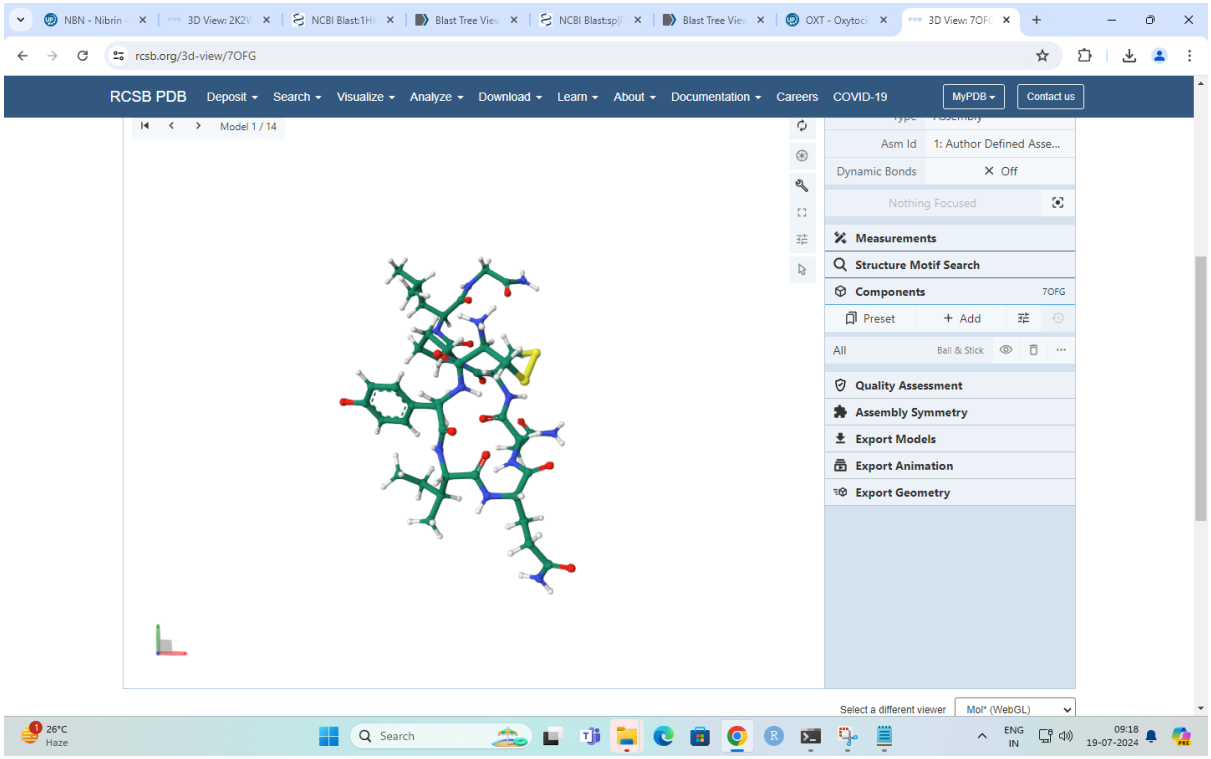
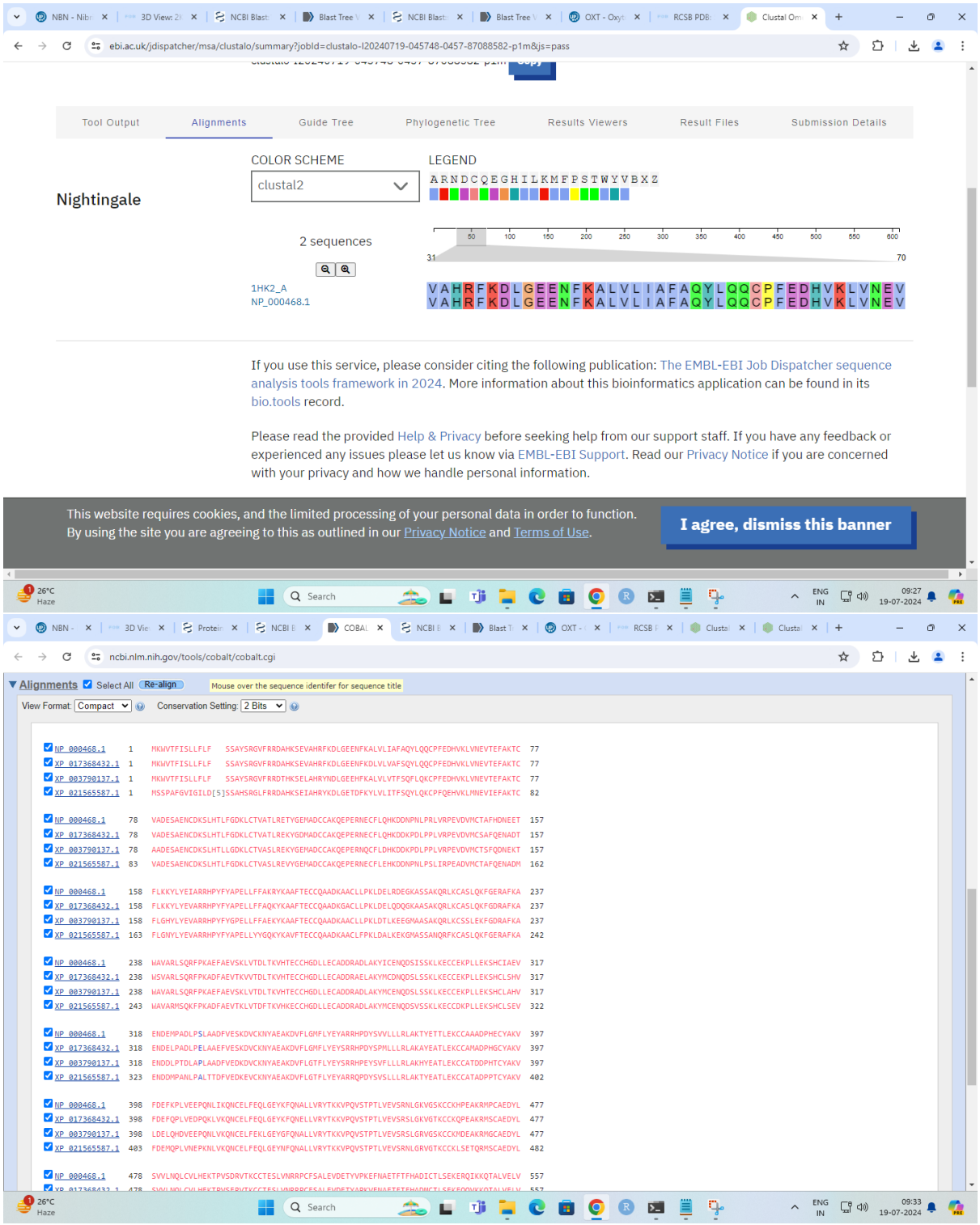
CASE B:

Distance tree view :



UNIOPROT 3 D IMAGE VIEW FROM PDB

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Alignments
Guide Tree
Phylogenetic Tree
Results Viewers
Result Files
Submission Details
Nightingale
COLOR SCHEME
clustal2
LEGEND
A R N D C Q E G H I L K M F P S T W Y V B X Z
2 sequences
1HK2_A
NP_000468.1
If you use this service, please consider citing the following publication: The EMBL-EBI Job Dispatcher sequence analysis tools framework in 2024. More information about this bioinformatics application can be found in its bio.tools record.
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ncbi.nlm.nih.gov/tools/cobalt/cobalt.cgi
Alignments
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Re-align
Mouse over the sequence identifer for sequence title
View Format: Compact
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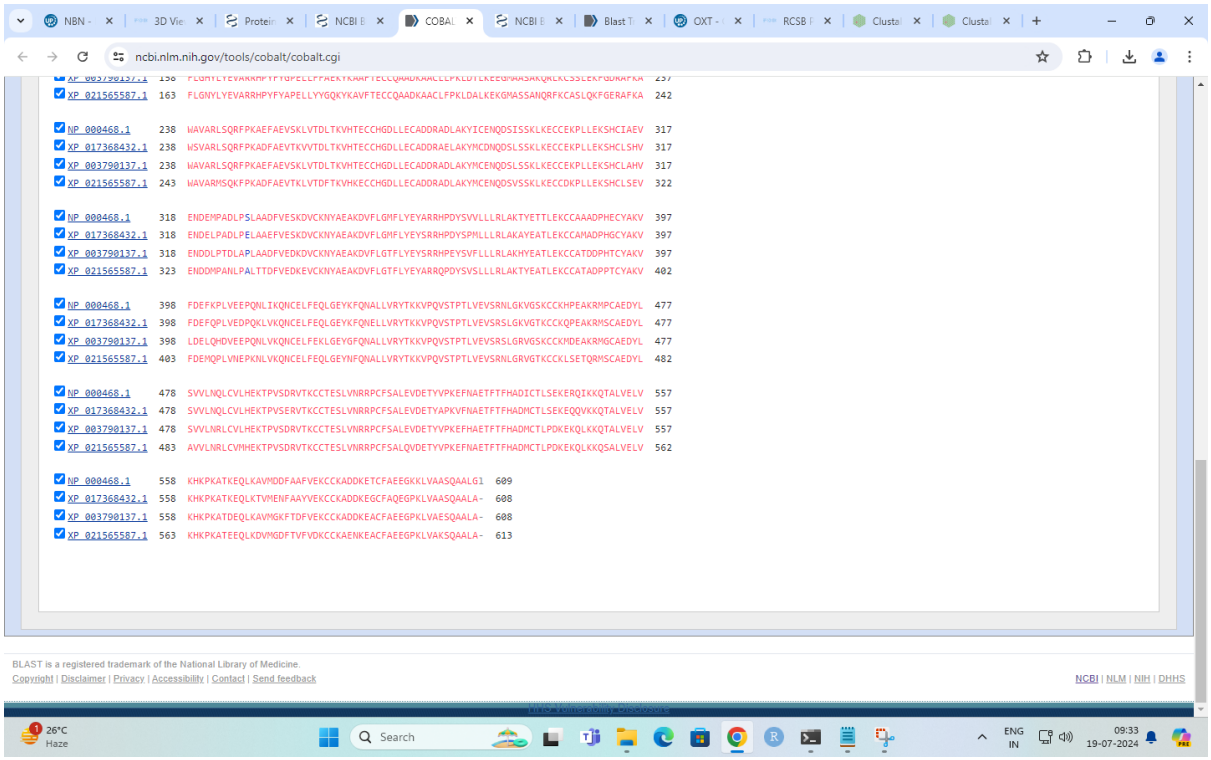
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XP_003790137.1 238 WAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYMCENQDSLSSKLKECCEKPLLEKSHCLAHV 317
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NP_000468.1 318 ENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKV 397
XP_017368432.1 318 ENDELPADLPELAAEFVESKDVCKNYAEAKDVFLGMFLYEYSRRHPDYSPMLLLRLAKAYEATLEKCCAMADPHGCYAKV 397
XP_003790137.1 318 ENDDLPTDLAPLAADFVEDKDVCKNYAEAKDVFLGTFLYEYSRRHPEYSVFLLLRLAKHYEATLEKCCATDDPHTCYAKV 397
XP_021565587.1 323 ENDDMPANLPALTTDFVEDKEVCKNYAEAKDVFLGTFLYEYARRQPDYSVSLLLRLAKTYEATLEKCCATADPPTCYAKV 402
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NCBI | NLM | NIH | DHHS
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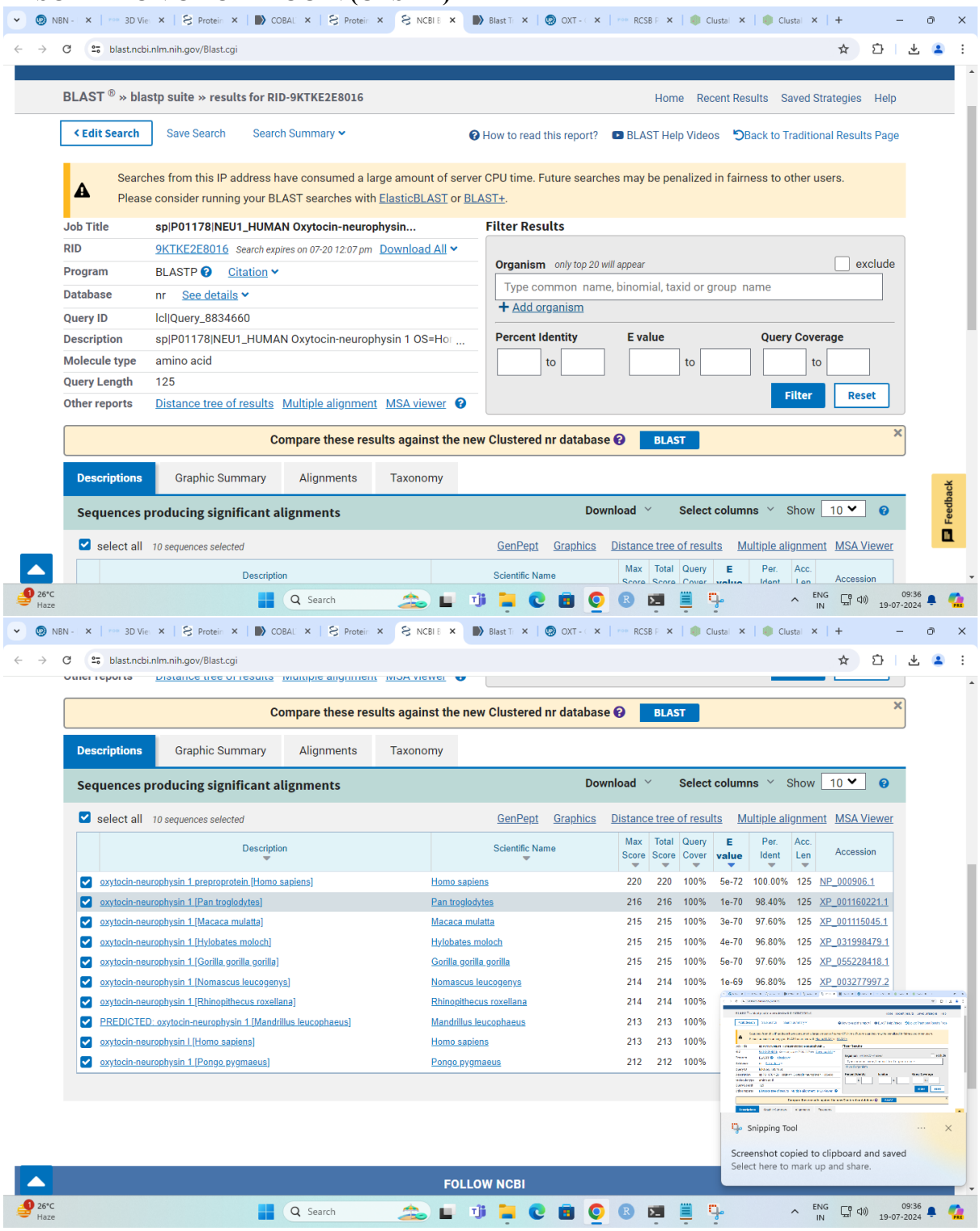
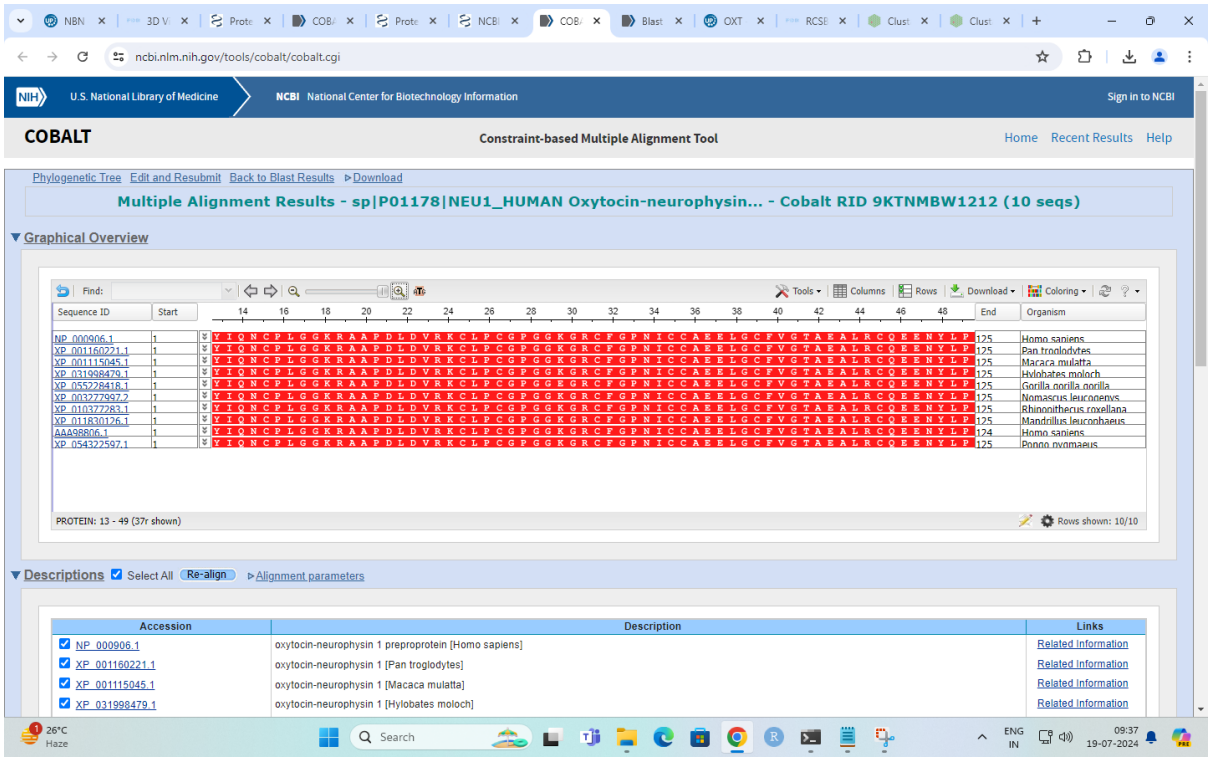
09:33 19-07-2024

DESCRIPTION OF OXYTOCIN (CASE B)





By comparing the case a and case b ,the query length is not changed even after changing threshold value , therefore I conclude there is no presence of mutation.

Inference

BLAST is used to search for "OXYTOCIN" in biological sequences. To use it, access the NCBI BLAST homepage, select the appropriate database, input the sequence, set search parameters, run the search, analyze the results, and interpret the results. This powerful tool helps in comparing biological sequences, identifying homologous sequences, and understanding the structure and function of oxytocin. It is widely used in research to elucidate sequence similarities and biological functions.