

H2_phylogenetics

October 11, 2019

[15]:

```
import sys
import pylab
from Bio import Phylo
import matplotlib
import matplotlib.pyplot as plt
from io import StringIO
```

[16]:

```
#import urllib.request, urllib.parse, urllib.error
#import xml.etree.ElementTree as ET

#url = 'https://www.jasondavies.com/tree-of-life/life.txt'
#uh = urllib.request.urlopen(url)
#tree = uh.read()
#print (tree)

tree = Phylo.read("/home/sedreh/Desktop/life_tree", "newick")

#draw this tree with pseudographics (draw_ascii)
Phylo.draw_ascii(tree)
```

```
, Escherichia_coli_EDL933
|
| Escherichia_coli_O157_H7
|
, Escherichia_coli_06
|
| Escherichia_coli_K12
|
, Shigella_flexneri_2a_2457T
|
| Shigella_flexneri_2a_301
|
, Salmonella_enterica
|
| Salmonella_typhi
|
```

```
|  | Salmonella_typhimurium
|  |
|  , Yersinia_pestis_Medievalis
|
|  , Yersinia_pestis_KIM
|
|  ,| Yersinia_pestis_C092
|||
||| Photorhabdus_luminescens
|||
|||   ___ Blochmannia_floridanus
||| ,|
||| ||____ Wigglesworthia_brevipalpis
|||_|
||| |___ Buchnera_aphidicola_Bp
||| |
||| | , Buchnera_aphidicolaAPS
||| |_|
||| | Buchnera_aphidicola_Sg
|
|, Pasteurella_multocida
|||
||| Haemophilus_influenzae
,||
||| Haemophilus_ducreyi
|||
||| Vibrio_vulnificus_YJ016
|||
||| Vibrio_vulnificus_CMCP6
,|||
|||_| Vibrio_parahaemolyticus
|||||
||||| Vibrio_cholerae
|||||
,||| Photobacterium_profundum
|||
|||_| Shewanella_oneidensis
|||
||| , Pseudomonas_putida
|||,|
||||| Pseudomonas_syringae
|||
||| | Pseudomonas_aeruginosa
|
||| , Xylella_fastidiosa_700964
|||_|
,||| | Xylella_fastidiosa_9a5c
|||_|
```

```
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    ||  ||
    ||  | Xanthomonas_campesiris
    ||
    ||___ Coxiella_burnetii
    |
    -|  , Neisseria_meningitidis_A
    | |  ,
    | |  || Neisseria_meningitidis_B
    | |  ||
    | |  || Chromobacterium_violaceum
    | |  ,
    | |  || , Bordetella_pertussis
    | |  ||_
    | |  ||| , Bordetella_parapertussis
    | |  |||
    | |  ||| Bordetella_bronchiseptica
    | |  ||
    | |  ||_ Ralstonia_solanacearum
    | |
    | |__ Nitrosomonas_europaea
    ,
    ||  , Agrobacterium_tumefaciens_Cereon
    ||  ,
    ||  || Agrobacterium_tumefaciens_WashU
    ||  ||
    ||  || Rhizobium_meliloti
    ||  ,
    ||  || Brucella_suis
    ||  ||
    ||  ||| Brucella_melitensis
    ||  ||
    ||  |||_ Rhizobium_loti
    ||  ||
    ||  ||| , Rhodopseudomonas_palustris
    ||  |||_
    ,||  ||| Bradyrhizobium_japonicum
    ||  ||
    ||  |||__ Caulobacter_crescentus
    ||  |
    ||  |||----- Wolbachia_sp._wMel
    ||  |||_
    ||  |||  , Rickettsia_prowazekii
    ||  |||_____
    ||  |||  | Rickettsia_conorii
    ||
    ||  , Helicobacter_pylori_J99
    ||  _|
```

```
||      ,| | Helicobacter_pylori_26695
||      ||
||      ,|| Helicobacter_hepaticus
||      ||
|| ____|| Wolinella_succinogenes
||      |
||      |_ Campylobacter_jejuni
|
| ____ Desulfovibrio_vulgaris
|
|| __ Geobacter_sulfurreducens
|||
||| ____ Bdellovibrio_bacteriovorus
,||
||| __ Acidobacterium_capsulatum
|||-|
||| |__ Solibacter_usitatus
|
||| ____ Fusobacterium_nucleatum
|
||| ____ Aquifex_aeolicus
|||-|
||| |__ Thermotoga_maritima
|
||| __ Thermus_thermophilus
|||-|
||| |__ Deinococcus_radiodurans
|
||| ____ Dehalococcoides_ethenogenes
|||
||| |__ Nostoc_sp._PCC_7120
||| |
||| ,|_ Synechocystis_sp._PCC6803
||| ||
||| |__ Synechococcus_elongatus
||| |
||| ,| , Synechococcus_sp._WH8102
||| || ,|
||| ||| Prochlorococcus_marinus_MIT9313
||| |||
||| __|__|_ Prochlorococcus_marinus_SS120
||| |
||| |__ Prochlorococcus_marinus_CCMP1378
|
||| |__ Gloeobacter_violaceus
|
| ____ Gemmata_obscuriglobus
|_-|
```

```
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|,|     , Leptospira_interrogans_L1-130
||| ____|
||||  | Leptospira_interrogans_56601
|||
|||   ___ Treponema_pallidum
|||   _|
|||__|_|_ Treponema_denticola
|||
|||____ Borrelia_burgdorferi
|||
|||      , Tropheryma_whipplei_TW08/27
|||      ____|
|||      _|_ Tropheryma_whipplei_Twist
|||
|||____ Bifidobacterium_longum
|||
|||      , Corynebacterium_glutamicum_13032
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|||      || Corynebacterium_glutamicum
|||
|||____ _| Corynebacterium_efficiens
|||      |
|||      || Corynebacterium_diphtheriae
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|||____ ,| Mycobacterium_bovis
|||      |
|||      ||, Mycobacterium_tuberculosis_CDC1551
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|||      ||| Mycobacterium_tuberculosis_H37Rv
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|||      |||_ Mycobacterium_leprae
|||
|||      ||| Mycobacterium_paratuberculosis
|||
|||      ||, Streptomyces_avermitilis
|||      |
|||      ||| Streptomyces_coelicolor
|||
-----|____ Fibrobacter_succinogenes
|,|____ Chlorobium_tepidum
|||
|||____ , Porphyromonas_gingivalis
|||____ |
|||      ||_ Bacteroides_thetaiotaomicron
|||
```

```
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|| |, Chlamydia_pneumoniae_J138
|| ||
|| |, Chlamydia_pneumoniae_CWL029
|| ||
|| ||| Chlamydia_pneumoniae_AR39
|| -----
|| | Chlamydophila_caviae
|| |
|| |, Chlamydia_muridarum
|| |
|| | Chlamydia_trachomatis
|
| _ Thermoanaerobacter_tengcongensis
|
|_| _ Clostridium_tetani
| |
|_|_ Clostridium_perfringens
| |
|_|_ Clostridium_acetobutylicum
|
|     ___ Mycoplasma_mobile
|     --|
|     |___ Mycoplasma_pulmonis
|
|     |     ___ Mycoplasma_pneumoniae
|     ,|     ___|
|     ||     |_ Mycoplasma_genitalium
|     || |
|     || ,| |__ Mycoplasma_gallisepticum
|     -|| |
|     || ||| ___ Mycoplasma_penetrans
|     || |
|     ,| | |___ Ureaplasma_parvum
|     || |
|     || |___ Mycoplasma_mycooides
|     ||
|     ||____ Phytoplasma_Onion_yellows
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|     | , Listeria_monocytogenes_F2365
|     ,|
|     | | Listeria_monocytogenes_EGD
|     || |
|     || | Listeria_innocua
|     ||
|     | | |, Oceanobacillus_iheyensis
|     || |
```

```
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|   |   | , Bacillus_cereus_ATCC_14579
|   |   |
|   |   |||_|| Bacillus_cereus_ATCC_10987
|   |   ||
|   |   |||_|| Bacillus_anthracis
|   |   ||
|   |   |||_|| Bacillus_subtilis
|   |   ||
|   |   ||| , Staphylococcus_aureus_MW2
|   |   ||
|   |   ||| , Staphylococcus_aureus_N315
|   |   ||
|   |   |||_|| Staphylococcus_aureus_Mu50
|   |   ||
|   |   |||_|| Staphylococcus_epidermidis
|   |   ||
|   |   ||| , Streptococcus_agalactiae_III
|   |   ||
|   |   |||_|| Streptococcus_agalactiae_V
|   |   ||
|   |   | , Streptococcus_pyogenes_M1
|   |   ||
|   |   | , Streptococcus_pyogenes_MGAS8232
|   |   ||
|   |   | , Streptococcus_pyogenes_MGAS315
|   |   ||
|   |   | | Streptococcus_pyogenes_SSI-1
|   |   | ,
|   |   | | Streptococcus_mutans
|   |   ||
|   |   | | , Streptococcus_pneumoniae_R6
|   |   ||
|   |   | ||| Streptococcus_pneumoniae_TIGR4
|   |   ||
|   |   |||| Lactococcus_lactis
|   |   ||
|   |   |||| Enterococcus_faecalis
|   |   ||
|   |   | __ Lactobacillus_johnsonii
|   |   ||
|   |   | |_ Lactobacillus_planatarum
|
|   |   ---- Thalassiosira_pseudonana
|   |
|   |   | __ Cryptosporidium_hominis
|   |   |
```

```

|   | ___ Plasmodium_falciparum
|   |
|   |   , Oryza_sativa
|   | _|
|   | | | Arabidopsis_thaliana
|   | |
|   | | ___ Cyanidioschyzon_merolae
|   | |
|   | | ___ Dictyostelium_discoideum
|   | |
|   | |   , Eremothecium_gossypii
|   | | _|
|   | | | | Saccharomyces_cerevisiae
|   | | |
|   | | | __ Schizosaccharomyces_pombe
|   | | |
|   | | |   , Anopheles_gambiae
|   | | |
|   | | | ___ Drosophila_melanogaster
|   | | |
|   | | |   , Takifugu_rubripes
|   | | |
|   | | | | | Danio rerio
|   | | |
|   | | | | | Rattus_norvegicus
|   | | |
|   | | | | | Mus_musculus
|   | | |
|   | | | | |   , Homo_sapiens
|   | | |
|   | | | | | | | Pan_troglodytes
|   | | |
|   | | | | | | | Gallus_gallus
|   | | |
|   | | | | | | |   , Caenorhabditis_elegans
|   | | |
|   | | | | | | | | | Caenorhabditis briggsae
|   | |
|   | | | | | | | | | Leishmania_major
|   | |
|   | | | | | | | | | Giardia_lamblia
|   | |
|   | | | | | | | | | | Nanoarchaeum_equitans
|   | | |
|   | | | | | | | | | | | Sulfolobus_tokodaii
|   | | |
|   | | | | | | | | | | | | | | | Sulfolobus_solfataricus
|   | | |

```

```

|   |   |_||____ Aeropyrum_pernix
|   |   |
|   |   |____ Pyrobaculum_aerophilum
|
|___|       , Thermoplasma_volcanium
|   |   |
|   |   |____ Thermoplasma_acidophilum
|
|   |   ____ Methanobacterium_thermautotrophicum
|   |   |
|   |   |____ Methanopyrus_kandleri
|
|   |   |
|   |   |____ Methanococcus_maripaludis
|   |   |
|   |   |____ Methanococcus_jannaschii
|
|   |   |
|   |   |____ Pyrococcus_horikoshii
|   |   |
|   |   |____ Pyrococcus_abyssi
|
|   |   |
|   |   |____ Pyrococcus_furiosus
|
|   |   ____ Archaeoglobus_fulgidus
|
|   |   |
|   |   |____ Halobacterium_sp._NRC-1
|
|   |   |
|   |   |____ , Methanosaeca_acetivorans
|
|   |   |
|   |   |____ Methanosaeca_mazei

```

[20]: `#draw a tree with draw and save as png`

```

matplotlib.rc('font', size=6) # set the size of the figure
fig = plt.figure(figsize=(20, 30), dpi=400)
axes = fig.add_subplot(1, 1, 1)
Phylo.draw(tree, axes=axes)
pylab.savefig('phylo-draw.png', dpi=300, facecolor='w', edgecolor='w',
              orientation='portrait', papertype=None, format=None,
              transparent=True, bbox_inches='tight', pad_inches=0.1,
              frameon=None, metadata=None)

```



```
/home/sedreh/anaconda3/lib/python3.6/site-packages/ipykernel_launcher.py:10:  
MatplotlibDeprecationWarning:  
The frameon kwarg was deprecated in Matplotlib 3.1 and will be removed in 3.3.  
Use facecolor instead.  
# Remove the CWD from sys.path while we load stuff.
```

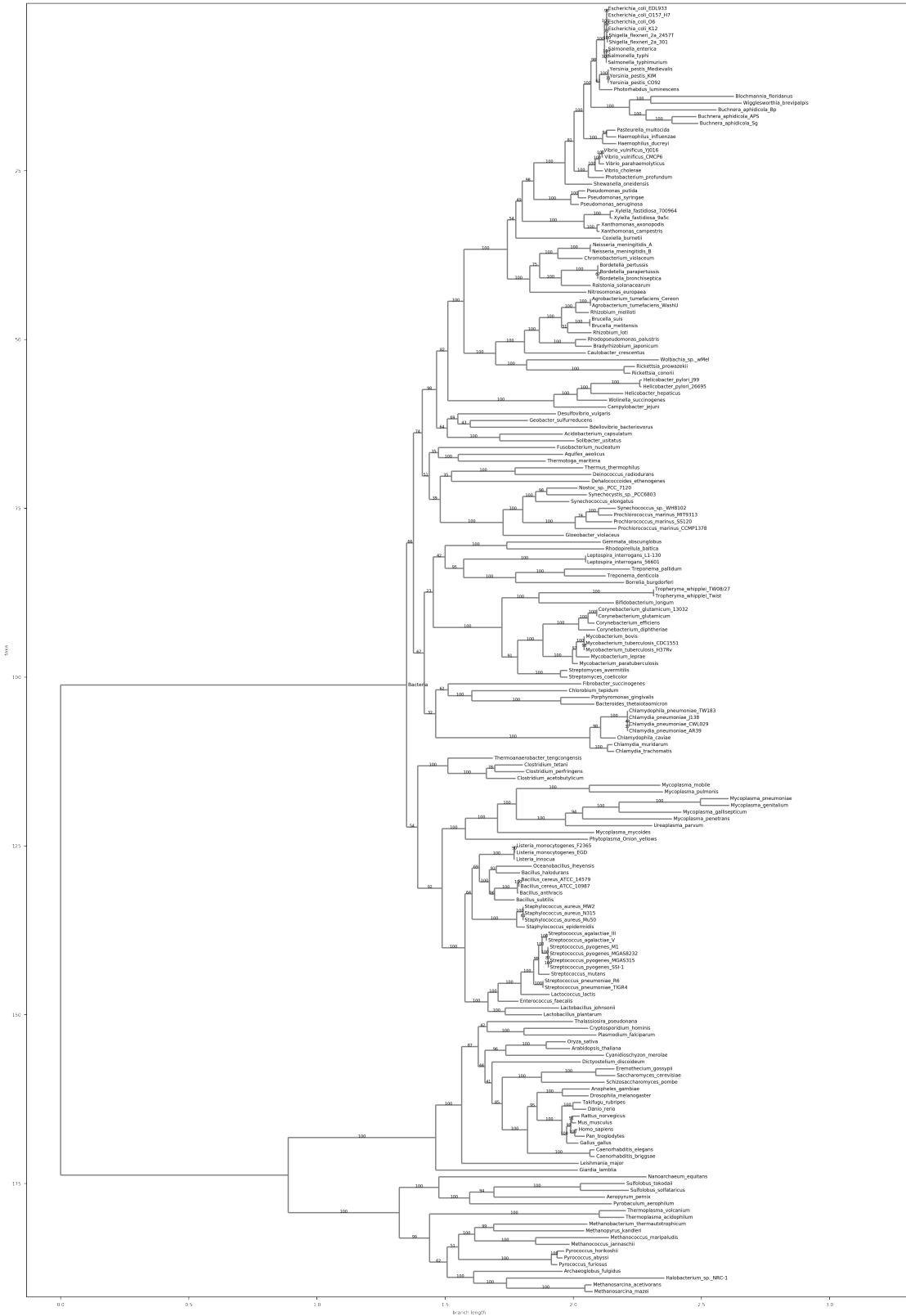
```
<Figure size 432x288 with 0 Axes>
```

```
[27]: #save as pdf  
matplotlib.rc('font', size=6)  
fig = plt.figure(figsize=(20, 30), dpi=400)  
axes = fig.add_subplot(1, 1, 1)  
Phylo.draw(tree, axes=axes)  
  
plt.savefig("phylo-draw.svg", format="svg")
```



<Figure size 432x288 with 0 Axes>

```
[29]: #colorize the root here
from Bio.Phylo.PhyloXML import Phylogeny
tree = Phylogeny.from_tree(tree)
tree.root.color = "#808080"
matplotlib.rcParams['font', size=6]
fig = plt.figure(figsize=(20, 30), dpi=400)
axes = fig.add_subplot(1, 1, 1)
Phylo.draw(tree, axes=axes)
```



```
[30]: tree.ladderize()    # Flip branches so deeper clades are displayed at top
matplotlib.rc('font', size=6)
fig = plt.figure(figsize=(20, 30), dpi=400)
axes = fig.add_subplot(1, 1, 1)
Phylo.draw(tree, axes=axes)
pylab.savefig('phylo-dot.png')

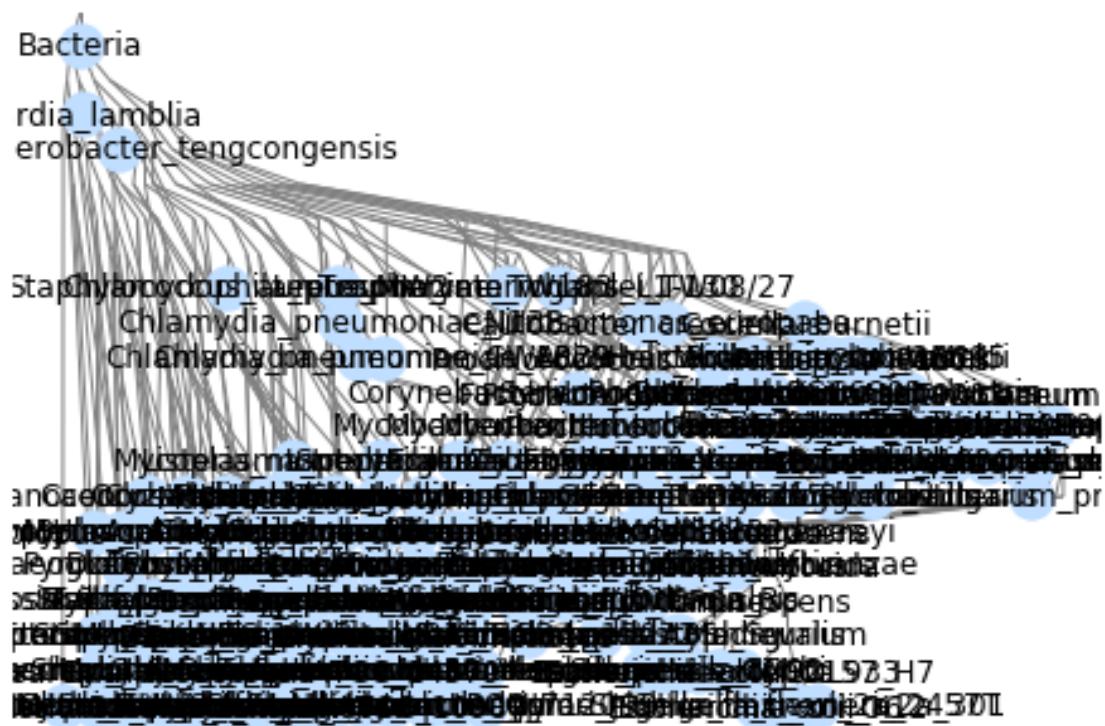
#fig.savefig(f'{output_file}.png', dpi=100) # save png
#fig.savefig(f'{output_file}.pdf', dpi=100) # save pdf
```



<Figure size 432x288 with 0 Axes>

```
[31]: #Using graphviz and save the tree as png  
Phylo.draw_graphviz(tree, prog='dot')  
pylab.show() # Displays the tree  
pylab.savefig('phylo-dot.png') # Creates a PNG file of the same graphic
```

```
/home/sedreh/.local/lib/python3.6/site-packages/Bio/Phylo/_utils.py:135:  
BiopythonDeprecationWarning: draw_graphviz is deprecated; use Bio.Phylo.draw  
instead  
    BiopythonDeprecationWarning)  
/home/sedreh/anaconda3/lib/python3.6/site-  
packages/networkx/drawing/nx_pylab.py:579: MatplotlibDeprecationWarning:  
The iterable function was deprecated in Matplotlib 3.1 and will be removed in  
3.3. Use np.iterable instead.  
    if not cb.iterable(width):  
/home/sedreh/anaconda3/lib/python3.6/site-  
packages/networkx/drawing/nx_pylab.py:585: MatplotlibDeprecationWarning:  
The iterable function was deprecated in Matplotlib 3.1 and will be removed in  
3.3. Use np.iterable instead.  
    and cb.iterable(edge_color) \
```





```
<Figure size 432x288 with 0 Axes>
```

```
[10]: #Convert files between any of the supported formats
Phylo.convert('/home/sedreh/Desktop/life.txt', 'newick', 'life.xml', 'phyloxml')
Phylo.write(tree, 'convert_tree.xml', 'phyloxml')

[10]: 1

[11]: #converting the tree to a subclass of the basic tree object called Phylogeny, ↴
      from the Bio.Phylo.PhyloXML module
from Bio.Phylo.PhyloXML import Phylogeny
tree1 = Phylogeny.from_tree(tree)

[12]: Phylo.write(tree, sys.stdout, "phyloxml")
```

```
<phyloxml xmlns="http://www.phyloxml.org"
xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.phyloxml.org
http://www.phyloxml.org/1.10/phyloxml.xsd">
  <phylogeny rooted="false">
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```

```

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```

```

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```

```

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```

```

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```

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```

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[12]: 1

[15]: #ETE toolkit

[36]: #Read the same tree
from ete3 import Tree
tree_ete = Tree('/home/sedreh/Desktop/life_tree', format = 1)
tree_ete.show()

[37]: # We can also write into a file
tree_ete.write(format=1, outfile="new_tree_ete.nw")

[38]: #To generate pdf/ SVG or png file
tree_ete.render("tree_ete.png", w=183, units="mm")
tree_ete.render("tree_ete.pdf", w=183, units="mm")

[38]: {'nodes': [[0.7938913507200315,
3260.095588927692,
7.145022156480283,
3266.4467197334525,
0,
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[150.74208013639762,
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1900.9071097082187,
2,
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1360.2373725519797,

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695.8674768727288,
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560.1771797994672,
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276.770372144771,
296.3624462940096,
283.12150295053124,
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194.90032660176772,
303.47420026386976,
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311.6057841744224,
126.82414327752502,
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64.30519940832255,
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322.0544152556087,
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18,
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21,  
None],  
[320.44296561461675,  
69.86243886336277,  
326.794096420377,  
76.21356966912302,  
22,  
None]
```

[26]: #cut from a tree a non-random set leaves. Use prune function. I tried this with → 4 leaves.

```
tree_ete.prune(['Shigella_flexneri_2a_2457T', 'Shewanella_oneidensis',  
→ 'Caulobacter_crescentus', 'Desulfovibrio_vulgaris'])  
print(tree_ete)  
None],  
[325.2299806584889,  
81.77080912416324  
| Shewanella_oneidensis  
| 331.58111146424915,  
| 88.1219389299235  
| | Shigella_flexneri_2a_2457T  
| | 24,  
| | None]  
| | Caulobacter_crescentus  
| | [320.7054534896473,  
| | 117.49591990656465  
| | | Desulfovibrio_vulgaris  
| | | 327.05658429540756,
```

[43]: #cut from a tree a random (or non-random, up to you) set of 42 (or other → number) leaves. Use prune function.

```
import random  
species = []  
for node in tree_ete.get_leaf_names():  
    species.append(node)  
  
random_nodes = []  
  
i = 0  
for i in range(0, 42):  
    random_nodes.append(str(random.choice(species)))  
    i = i + 1  
tree_ete.prune(random_nodes)  
print(tree_ete)
```

```
182.99195634096725,  
317.12432280444534,  
189.3430871467275,  
28,  
None],  
[315.69360252003173,
```

```

                /-Xylella_fastidiosa_9a5c
                /-|
                |   |   /-Haemophilus_influenzae
                /-|   \-|
                |   |       \-Yersinia pestis_Medievalis
                /-|   |
                |   |       \-Nitrosomonas_europaea
                /-|   |
                |   |       \-Caulobacter_crescentus
                |   |
                /-|       \-Helicobacter_hepaticus
                |   |
                |   |       /-Bdellovibrio_bacteriovorus
                |   \-|
                /-|       \-Acidobacterium_capsulatum
                |   |
                |   |       /-Deinococcus_radiodurans
                |   |       /-|
                |   |       |   |   /-Synechocystis_sp._PCC6803
                /-|   \-|   \-|
                |   |       |   \-Synechococcus_sp._WH8102
                |   |
                |   |       \-Aquifex_aeolicus
                |   |
                |   |       /-Chlamydia_pneumoniae_AR39
                |   \-|
                /-|       \-Mycobacterium_paratuberculosis
                |   |
                |   |       /-Thermoanaerobacter_tengcongensis
                |   /-|
                |   |       |   |   /-Clostridium_acetobutylicum
                |   |       \-|
                |   |       \-Clostridium_tetani
                \-|
                |   |       /-Mycoplasma_mycooides
                |   |       /-|
                |   |       \-Mycoplasma_mobile
                |   |
                --|   \-|       /-Streptococcus_mutans
                |   |       /-|
                |   |       /-|       \-Streptococcus_agalactiae_III
                |   |       |   |
                |   |       \-|       \-Streptococcus_pneumoniae_R6
                |   |
                |       \-Lactococcus_lactis
                |
                |       /-Nanoarchaeum_equitans

```

```

|   /-
|   \-Pyrococcus_horikoshii
|
\-|   /-Arabidopsis_thaliana
|   /-
|   |   /-Eremothecium_gossypii
\-|   \-
|       \-Rattus_norvegicus
|
\-Thalassiosira_pseudonana

```

[45]: *#draws the pruned tree with additional aesthetic processing(I used TreeStyle to make beautiful changes in tree)*

#The TreeStyle class can be used to create a custom set of options that control the general aspect of the tree image.

```

from ete3 import Tree, TreeStyle

circular_style = TreeStyle()
circular_style.mode = "c" # draw tree in circular mode
circular_style.scale = 20
tree_ete.render("tree_ete_pruned.png", w=183, units="mm",
                tree_style=circular_style)

```

[45]: {'nodes': [[320.25457330366345,
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```
[46]: #Increases the separation between leaf branches
ts = TreeStyle()
ts.show_leaf_name = True
ts.branch_vertical_margin = 20 # 10 pixels between adjacent branches
tree_ete.show(tree_style=ts)
```

```
[ ]: #change Node style
# Basic tree style

from ete3 import Tree, TreeStyle, NodeStyle
ts = TreeStyle()
ts.show_leaf_name = True

# Draws nodes as small red spheres of diameter equal to 10 pixels
nstyle = NodeStyle()
nstyle["shape"] = "sphere"
nstyle["size"] = 10
nstyle["fgcolor"] = "darkred"

# Gray dashed branch lines
nstyle["hz_line_type"] = 1
nstyle["hz_line_color"] = "#cccccc"

# Applies the same static style to all nodes in the tree
for n in tree_ete.traverse():
    n.set_style(nstyle)

tree_ete.show(tree_style=ts)
```

```
[ ]: ##### Part 2
→ #####
```

```
[1]: #Entrez is a data retrieval system that provides users access to NCBI's databases
      # Tell NCBI who i AM
from Bio import Entrez
Entrez.email = "snassirnia@outlook.com"      # Tell NCBI who i AM
#Using EInfo to obtain a list of all NCBI's database names
handle = Entrez.einfo()
record = Entrez.read(handle)
record.keys()
record["DbList"]

[1]: ['pubmed', 'protein', 'nuccore', 'ipg', 'nucleotide', 'structure', 'sparcle',
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'biosystems', 'pccompound', 'pcsubstance', 'seqannot', 'snp', 'sra', 'taxonomy',
'biocollections', 'gtr']

[10]: #choosing "nuccore" database and get information about it
      from Bio import Entrez
      handle = Entrez.einfo(db="nuccore")
      record = Entrez.read(handle)
      record["DbInfo"]["Description"]

[10]: 'Core Nucleotide db'
```

```
[11]: #Get list of possible search fields for use with ESearch
      from Bio import Entrez
      handle = Entrez.einfo(db="nuccore")
      record = Entrez.read(handle)
      for field in record["DbInfo"]["FieldList"]:
          print("%(Name)s, %(FullName)s, %(Description)s" % field)
```

ALL, All Fields, All terms from all searchable fields
 UID, Unique number assigned to each sequence
 FILT, Filter, Limits the records
 WORD, Text Word, Free text associated with record
 TITL, Title, Words in definition line
 KYWD, Keyword, Nonstandardized terms provided by submitter
 AUTH, Author, Author(s) of publication
 JOUR, Journal, Journal abbreviation of publication
 VOL, Volume, Volume number of publication
 ISS, Issue, Issue number of publication
 PAGE, Page Number, Page number(s) of publication
 ORGN, Organism, Scientific and common names of organism, and all higher levels of taxonomy
 ACCN, Accession, Accession number of sequence
 PACC, Primary Accession, Does not include retired secondary accessions
 GENE, Gene Name, Name of gene associated with sequence

PROT, Protein Name, Name of protein associated with sequence
 ECNO, EC/RN Number, EC number for enzyme or CAS registry number
 PDAT, Publication Date, Date sequence added to GenBank
 MDAT, Modification Date, Date of last update
 SUBS, Substance Name, CAS chemical name or MEDLINE Substance Name
 PROP, Properties, Classification by source qualifiers and molecule type
 SQID, SeqID String, String identifier for sequence
 GPRJ, BioProject, BioProject
 SLEN, Sequence Length, Length of sequence
 FKEY, Feature key, Feature annotated on sequence
 PORG, Primary Organism, Scientific and common names of primary organism, and all higher levels of taxonomy
 COMP, Component Accession, Component accessions for an assembly
 ASSM, Assembly, Assembly
 DIV, Division, Division
 STRN, Strain, Strain
 ISOL, Isolate, Isolate
 CULT, Cultivar, Cultivar
 BRD, Breed, Breed
 BIOS, BioSample, BioSample

```
[125]: #(esearch) query the database of nucleotide sequences for all sequences
       →according to the name of the gene
#esearch Searches and retrieves primary IDs (for use in EFetch, ELink, and
       →ESummary)
from Bio import Entrez
Entrez.email = "snassirnia@outlook.com"
handle = Entrez.esearch(db='nuccore', term="Homo_sapiens[Orgn] AND TNF[Gene]")
record = Entrez.read(handle)
handle.close()
print(record)
#from Bio import SeqIO
#SeqIO.write(my_records, "my_example.faa", "fasta")
```

```
DictElement({'Count': '59', 'RetMax': '20', 'RetStart': '0', 'IdList':
['1519314819', '568815592', '568815569', '568815567', '568815564', '568815561',
'568815551', '568815529', '568815454', '170014716', '236459493', '1387682811',
'1387681679', '1387680719', '1101482042', '226201420', '123996346',
'1015569062', '824328379', '824328378'], 'TranslationSet': [DictElement({'From':
'Homo_sapiens[Orgn]', 'To': '"Homo sapiens"[Organism]'}, attributes={})],
'TranslationStack': [DictElement({'Term': '"Homo sapiens"[Organism]', 'Field':
'Organism', 'Count': '27555217', 'Explode': 'Y'}, attributes={}),
DictElement({'Term': 'TNF[Gene]', 'Field': 'Gene', 'Count': '596', 'Explode':
'N'}, attributes={}), 'AND'], 'QueryTranslation': '"Homo sapiens"[Organism] AND
TNF[Gene]'}, attributes={})
```

```
[126]: #download the list of identifiers
id = record["IdList"]
id
```

[126]: ['1519314819', '568815592', '568815569', '568815567', '568815564', '568815561', '568815551', '568815529', '568815454', '170014716', '236459493', '1387682811', '1387681679', '1387680719', '1101482042', '226201420', '123996346', '1015569062', '824328379', '824328378']

```
[128]: #research + efetch returns the nucleotide sequences in fasta format and writes
       →to the file;*
from Bio import Entrez
Entrez.email = "snassirnia@outlook.com"
id_str = ",".join(id)
handle = Entrez.efetch(db="nuccore", id=id_str, rettype="fasta", ↵
    →retmode="fasta", retmax='100')
record = handle.read()
out_handle = open('esearch_efetch.fasta', 'w')
out_handle.write(record.rstrip('\n'))
```

[128]: 206861610

```
[145]: #research + esummary returns a table with UID (in XML this field is called Id), ↵
       →accession number (in XML this field is called Caption), sequence length ↵
       →(Slen);
Entrez.email = "snassirnia@outlook.com"
handle = Entrez.esummary(db="nuccore", id=id_str, retmode="xml", retmax='100')
record = Entrez.read(handle, validate=False)
#record
records = list(record)
for record in records:
    print("UID:", record.get("Id", "?"))
    print("accession number:", record.get("Caption", "?"))
    print("sequence length:", record.get("slen", "?"))
    print("")
```

↳

| | |
|----------------------------|---|
| <pre>KeyError →last)</pre> | <pre>Traceback (most recent call ↵ ↓ ↓-----</pre> |
|----------------------------|---|

```
<ipython-input-145-d4ea39d9cf9c> in <module>
    7 record = Entrez.read(handle, validate=False)
    8 record
----> 9 info = record[0]["Slen"][0]
```

```
KeyError: 'Slen'
```

```
[1]: #elink + efetch downloads all sequences from the paper with given PMID ... (for  
→example, 12890024)
```

```
from Bio import Entrez  
pmid = "12890024"  
record = Entrez.read(Entrez.elink(dbfrom="pubmed", id=pmid))  
#The "LinkSetDb" key contains the search results, stored as a list consisting  
→of one item for each target database  
for linksetdb in record[0]["LinkSetDb"]:  
    print(linksetdb["DbTo"], linksetdb["LinkName"], len(linksetdb["Link"]))
```

```
/home/sedreh/.local/lib/python3.6/site-packages/Bio/Entrez/__init__.py:580:  
UserWarning:  
Email address is not specified.
```

To make use of NCBI's E-utilities, NCBI requires you to specify your email address with each request. As an example, if your email address is A.N.Other@example.com, you can specify it as follows:

```
from Bio import Entrez  
Entrez.email = 'A.N.Other@example.com'  
In case of excessive usage of the E-utilities, NCBI will attempt to contact a user at the email address provided before blocking access to the E-utilities.  
E-utilities."", UserWarning)
```

```
pubmed pubmed_pubmed 98  
pubmed pubmed_pubmed_citedin 49  
pubmed pubmed_pubmed_combined 6  
pubmed pubmed_pubmed_five 6  
pubmed pubmed_pubmed_reviews 13  
pubmed pubmed_pubmed_reviews_five 6
```

```
[13]: record = Entrez.read(Entrez.elink(dbfrom="pubmed",  
→db="pmc", LinkName="pubmed_pmc_refs", id=pmid))  
linked = [link["Id"] for link in record[0]['LinkSetDb'][0]['Link']]  
handle = Entrez.efetch(db="nucleotide", id=linked, rettype="fasta",  
→retmode="text")  
print(handle.read())
```

```
>AQ853850.1 nbxb0045C20f CUGI Rice BAC Library Oryza sativa Japonica Group  
genomic clone nbxb0045C20f, genomic survey sequence  
AGCCGGCATTTTCGATNGACATTTGACCAGGAGATCCCTCTAGAGTCTGACCTGCAGGACATGCAACC  
CCTTTAACACGCCAGTTAATTATCACTTTAATCAGCTTCCATGAGTGTATCAGATGNNCGAGG  
ACNNGAGGGCAGGGAGGGNNNTCTGCGANNGCCGGTCAGGCATGCTCTGGCTCTGCNCNNACAATG
```

GCTCNNCGACTGCNGNNACCTCGAGCCCACGGCNGNNCCGCCCNNTCGGCTCNCCTGCNCNNC
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TCCTCTTCGCTCGCTTTCTGGGCTCTCGTCTGTTGCTCGTCTCGTCTCCTGTTGCGTG
TGCCTCTCGTGTGTTCTTGCGCGCTCTCGCGTCCCTCACTCGTCTGTTCCGCTCTCCCT
TCCCGCCTCTCCCTCNCGCCGTTCTGCGCTCGTCNCNTCTCCCTGCTCTCCCTGCCCTCGCTTT
CTCGTCGCTCTCCTCCGGCTCTCTCGTGTGTTGCTCTGCTCTTCCCGCTCTGTCGCCGGGCTGCTTC
TTGGTCCCTTCCTCGNCTGTTGCGTTGCTCTGCTCTTCCCGGCTGTCCTGTCCTGTTGCTGGCTGCTGTG
CGTTTCTCGCTCGTGTGCTCGCTGTCCCTGCCGCGCTNTGCTCTGGCGTCTTCCG
CTGTGTTCTCGTCCGTCTCTTCTGCGGTTGTTCTNNCGTCTGTCGTCCTTGGGTGTCCTTAC
TGCCGCTACATTATAGGGCCGATATGCTGCGTTCTCGTTACCTCCCGTCTCATTCATCGT
TCTATGATTATTCTCAGCTGCTCCTATACTACTTGTGCC

>AI936861.1 wp70c12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467126 3',
mRNA sequence
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ATCATCAGTTATTATGGAAAACTACTAGTTAACCTAGGTTTCCAAAAGAAGCTACTTACTTTGAA
AATAAAACAGAAATCAGATTATCGGGCTGCTACTTAATGCATAATAATTACAAAATGAAGAAGTCAGG
TTAAAAGGCTTGTACAGCTATTGTTCACATTACAGCCTGGCTCAAACCCCTGGTCTCTGACCAAAGAA
AGATCTGCTTATAACCATAATTCCAAGGCTCAGCCCCTTCTATCTTCTTGTGGTAGATTCA
GAGTAAGCAGTGGCAGAACAGCAATTACTAAAGCTACAGCTTGAGTACACTTAAGGTACATGATT
GGCATTGTTCCACCAGACCTGGTAAACAAGTGTGTTCAACATCAA

>AV113267.1 AV113267 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone
2610020F04, mRNA sequence
ACCGTAAAATTAAATTGAGGTAACCTGCATCATAGGCCAGGGCATGGAGACCTTTAGCCATGACCCTTG
ACCTGGGCAGAGCCCTGGGATATTAAAGGGAGGGTATTAGGTATTGGTGGGGAAAGGTACCAAAGA
TCTTTCCAGGGTTTAGTTCATATTCAAGCACCATGGCCACTAATTTCCTCAGGCTGCCTGATGTT
GCTTTGTTTCCCCAGAGAGCACCATGGTTTCTGAGTTTTAGAATCAGAAGTTGGGGGGGGGG
GGGGGGGTTAATT

>AQ580691.1 RPCI-11-43308.TV RPCI-11 Homo sapiens genomic clone RPCI-11-43308,
genomic survey sequence
GTAGAGAACGGATTNGGGNAGTACCAAGCTAACTCTGTGCTATTGGATATTACTTTGTAAGAAAAAC
TTTAAACTTCTTTCCATTCTTCAAAGATTCAAGGAGGTATTAGGTATTGGTGGGGAAAGGTACCAAAGA
TATAGTTTCTTTCTGTGTAGCAGAACATAATGGTAGGGTGAAAGGTAAAGTAGTAGTATACTT
CCTTAGATGGAGTATTGATAACAATTATTAACCCACTTAATGACAATAGAACTTTATTGAATTACAGGA
TCAGGCTACATAAAGGGACAATTAGAGATATCATTCTAGTGATTCAAGGTGAGTATAAGAATATTACT
GAAAAAAATTCTCAAATTCTCTTACCTTACTGTTCAAGCAGATAGCAGTCC
TAAAATTCTATTNTAAATATATNTACTTNTTATTGTATACTTNGTTGGAACAAACTTATATACT
TTGTGGAGAG

>AU068893.1 AU068893 Rice callus Oryza sativa Japonica Group cDNA clone
C50857_12Z, mRNA sequence
CGACGCAGCACCCGACGTCGGAGGAGCTCAGCATGGGAAGATCAAGTTCAAGCCTCGATCTGGCGGC
CACCAGATGCCCGCCCGTCTGGAGGACTACTACGCCAACGGTTGATGCTGTGGTATATTGGTAGATG
CTTATGATAAGGAACGTTTGCTGAGTCAAAAAGGAGCTTGTGACTGCACCTCTATCTGATGATTGATTCATTGGC
AGCTGTCCCGTTCTATCCTGGACAACAGATTGACATCCATATGCTGCTCTGAAGAGGAGCTGCC
TATCATCTAGGCCTTAGCAACTCACAACTGGGAAGGGCAAGGTAGCAGCCTAGGTGAATCCAATGTCCGGC

CCCTCGAAGTGTTCATGTGCAGTGTGTCGCCAAGATGGCTATGGTACGGGTTCAAGTGGGTCTCCCA
GTACATCAAGTAGATCCCTGTCAAGACATACTTGCAACTCTGCCAGCGATTCCCCCTCTCGTT
TGTTCAGTTGGTTGTTCTCACGACAACAATCATGACGGTATGGAGGGTATGAAGAGAAAACAGTG
CTTAAACAATTGGGACATGTTCATGTTGGATATTTAGCCTCAAACCATTGTTATGTCGAGCTCTA
AAATTTTTTGCTTCCATAGGGCGTTACTAAGGACTTGGAAAGATGATGAATTATAAGATTATTGGTT
TCTTAAAAAAAAAAAAAA

>AI659164.1 tu02a12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2249854 3'
similar to contains Alu repetitive element, mRNA sequence
GGTAGAGACAAGGTCTCACTGTATTCAGGCCAGGCTGGTCTCAAATACTTGGCCTCAAGTGATCCTCTGTC
TTGGCCTCCAAAGTGTGGATTACAGGTGTGAGGCCACTGCACCTAGCCTGGTAGGCATTCTTCTAG
CACTGTGCTCAATGATGAGTCTTCAGGGCTAGATATCAAATCTTACACTTCCCACCTAAATGAGTTATA
ACAATCAAAACGTCAAGGAAATTATGTTGGGAATGAACGTGATCCACTAATTCCCTTCCAG
GTAGAAAACATTCAAAGAAGTGAATTATTAATGCAGGTTGCATGTGCTACATGAGTAAATTGAGACC
AACAGGGCTGCAAAGGCCCTGGCTCTGCTGTGGTATTCTGCTGTACACAGACGAGTCATCAT

>AQ503511.1 RPCI-11-297A12.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-297A12,
genomic survey sequence
CTGGCGAACACCGTAAACGTAATTCTATGACTTATAGATCGAGTATTCAATTGGTACGTACGGATC
AATGCCTGTCGAACAGCGCCATATCTCGCGGGAGCTGACTGACCATCAACATTCAACCATGTACCG
TCTGGAAGTGGGTAT

>AI505114.1 vq69b12.x1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:1107551 3' similar to gb:X53176 Mouse integrin alpha-4 mRNA (MOUSE), mRNA
sequence
AGGCAAAGAGCCAGGCTCCTCACTCCAACCTGATGGCCTGACAGTCTACAGTGCTCAGTCATGGAA
TCATTCAATAACACTCCCTCAAGATGGCATAGTAGTCCACCACTGGAGAAGATGCTCTGGTCTTG
AAGATTATATGCCAGTACAGGGGAATGCCAGGGCAGGAAGTGAGAGTGGTTGGGAGCAGGG
TAGGGGGAGGGTACAGGGACTTCAAGGTTGAAATGTAATGAGGAAATATCTAATAAAAAATGCT
CCCTCAAA

>AI383835.1 tc99c08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2074286 3',
mRNA sequence
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GTGGAGGGGGGGGGGGCGGCCGCGCGGGACAGGCAGGGACCGCTATCCGAGGCCAACCGAGGCT
CCGCGCGCTGCCGTATGTTCCGCTGGCGGGATTCTGACTTAGAGGCCTCAGTCATAATCCACAG
ATGGTAGCTCGCCCCATTGGCTCCTCAGCCAAGCACATACACCAAATGTCTGAACGCTGCGGTTCC
CGTACTGAGCAAGGATTACCATGGCAACAACACATCATCA

>U31366.1 Peanut stunt virus RNA 3 complete sequence containing 3a protein and
coat protein mRNA, complete cds
GTTTACCAACCAGGAATCTGACCCGTGCCAGTAGGATTCCACTGTGTTGTAGATAGCAGTACCCACG
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TGAAAGACATGGCAGTAAATGCGTTAGTCGACACCACTGGATGCCGCCATGATGCCGTGTGT
CAGACCCCTCATTCCGGAATCTACGTCCAATAAAGTGACCCGATGGTTAAATCTGGCTATGACCCCGGA
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GGTCAATTACATAACCGAGACCTCCCTGCTCTGGTATCGTCCAGCCCACCTATGATTGCCCTATGGAA
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CGCAGGTAAGACCCTAGTCTACCCCTACAACAGATTATCTGAGTTTCAGAGCCATCAGCTGAACAG
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CACGCCAGGATAGTATTAGTTAACACAGCGTCTGTGGTTAACGGTGTGAACGCTGGACTTGTGAA
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TCCCTTGGTCAATTGGGTTCTTAGTCTAGAATGCTTATCCGAACCTCCGTAGTACTATCGTA
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TCGGTCTTGACTGCTCAACTGAACCGATGGGTGTCTACCATGACTGCCAGATGCCAACCTCGAAC
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GCACTGAAGTCGGTGATATTGGCGATTATGCCATTATCGTCTATTCTAAGGACGACGTTTACAGGCTGA
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CTCGATAACATGTATGCGTTACGCCTGGTACCCCTCATAAAGTAGCTTATGAGGGCCTAAAGGGACCA

>AQ294891.1 HS_3047_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=M, genomic survey sequence
ATTGAAGCCTTGANNNTGANNNCNNTGGNNNNNCCTGAGNGCCTCGACCACCATGGCGAATCTGCGA
AGANAGGATATGTGAGAGACACATTGACTCGATTAGACTTTACGCATTGACACACGACACCGTACTGTG
CCTTAATCCCTGACACACAGAACATCATGTTACATAATGTGTATATACATCTACTGCACAACGAAG
GGTACTATTATGTGTCACTGATTATGAATTAGAGCGCATACGACAGACATCAGGACGATTGTGG
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>AQ294890.1 HS_3047_A1_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=11 Row=M, genomic survey sequence
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GAGTTGAGAACCTAGTAAATGAAGGTAGGAGGCCAGGTTCTCACCCATTGAAGTGGTAGGTAAACAG
CCACACGACCCATCTAAATATTATGAAATTAAAGTCACACACTCCAAAAGATATTATGGCTTATTAGC
CCACTGTCACTATTCCCACACCAAGTTAACACATCCCATCTGCTCTCAATGAGCTTGCTATTCT
GCTTTCTCGAACCTCTTATCCGTGGAATATATCCGATTGCTATTGAAAAGCATGGCTTTAGCAC
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>AQ294885.1 HS_3047_A1_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=E, genomic survey sequence
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GTTGCTATTGCTGCCATAATAGCTGACAATTAACTGTGTGCCAGGACTGCTCTAACGCCCTTCATACA
CTAGCCCACCTATCTGATCAACACCCCTCCTATGTGCGCTCCACCTCCACCCCTAGAACATCTCATATC
TCCTCCCTCCATTCAACCCACTTCATCTCCTCCCTATCCCACCCGCTCTACCCCCCCCCCTTC
ACTCTCCCCTCGATCCCACTCACCCCTCTCCCACGCCCTTCTCCCTCCCCACCCCTCCCTCCTT
ATCCCCCTTACCCCTCCCTCCCTGCC

>AQ290212.1 nbxb0036D03r CUGI Rice BAC Library Oryza sativa Japonica Group
genomic clone nbxb0036D03r, genomic survey sequence
TCCTTTAATAACAAATTCACTCAAATGTTGACCAATGCCCTTCACCTTCAGTATACCAGCAAACG
GTGCTGCACCAATATCCTCAACTGATAAGCCAATATCAGCAAGATGGAGAATACTGATGCCTGATGGCTC
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TGGTGGCTCACTTCCAACCGCTGCCGGTCTACTTGAGGTAACTAGGGCTGTGGTTCTGCCATTGGA
GCAGACCGAGTCGCGGTGAGGATATCACCAGCATTGATCACCTGACGCCATGATTTAGACCCATT
AGCTCGGCATGGCCGTTGTTGACCGGCTATGCTCTTACA

>AQ258624.1 nbxb0020N10r CUGI Rice BAC Library Oryza sativa Japonica Group
genomic clone nbxb0020N10r, genomic survey sequence
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CGTCAATGCTGCCCAACAATCAAACAAGCTTAATGACATAGCCCAAACCTAGATGAACTCAAATT
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>AQ255394.1 mgxb0012J22r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0012J22r, genomic survey sequence
TCGGAGACACCCTGGTTAACGTCGCTACAAGAGACTTGTCTTCCAGCTTGGTGGAGACGCCATGGTGC
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TATCTCCCGATGATACTATTGACTTAACCTCGGCATGGGATTATTCAACATAATCATGACTGTGACG
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>AF085204.1 AF085204 Canis familiaris library (Everts RE) Canis lupus familiaris
genomic clone RE6G3, genomic survey sequence

GGATCTCCAAGTAGTTGAATAACATCTTGAGTCAGGATTCTAGTTCTGTTGGCTTGGTATGAG
AGCCTGCCTTGACGAGAGGACTCTCTCTTGTACGACTGCCTAACTGGATCCATTGTTCTATTAATCC
TTCTTACAGCACACAGAGCTATTTCTTAATGAAAATCACATCATGTCATGCCCTCCCAACCCTG
CTGATCCCCATCATGCCTGAATTCAAGTCCCTTCCATGACTTACAAGGTCTTGTGAGATCC

>AQ104233.1 HS_3110_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=M, genomic survey sequence
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AAAGAATACGGCCAATAAAATACATAAGAAGATGTTCAACATCACTAGTCATAGGGAAAAAGCAAATTGAA
AACACAATGAGTATTTACAACCATAAGATAGTTACAATCGAGATGACAAAGTACGAACAGTTAAGTG
TTTGTGAGAATATGGAGACAATGGAACCTTACACTAGCTGTGGAAATGTAATGGTACAAGCACTTC
AGCCTGGCAGTGCTTCAATTGAATATCCAATATTCCATGACTTACCACTCCTAGTATGTTCAA
AGAAATGATATT

>AI093329.1 qb02d02.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1695075 3' similar to TR:Q15113 Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR. [1], mRNA sequence
TTTTTTTTCTACTGAGAGAACATAGATCTTCAAAGGCAATGGCAGAATACAGCTTAAATGGACACAGT
TCACTGTTAACATTGCTTATTTTAAGGCATCCAGGAGCTCTGATTCTGGTCTTGAACATCATGATA
AAGCTGTTGGCATGATTTGCCTCGCCCATCTCACCTACTTGGCCCATAATAATGTAATTAGACCTC
TTCTGAGGAGAGGGCACTGCTGCAGACAGTCAGCCTGGCACTCATGTTCTGCCGCGCTGCTGAAT
CGCCAAATTCCCTTTGTAGATGTTGATGTCAGACTGTGGCGTGCACACTCCATCGCAGTGATG
GTTGTATAACAGTGCCGGCTAACAAAGTCACTTGAACAATAATTGCCCTCCAGAGTCCCCGTCCGTC
TACACTTTGTTGACACAAGGCCACGGT

>AI079742.1 oy55f07.s1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669765 3' similar to TR:Q92566 Q92566 MYELOBLAST KIAA0279, mRNA sequence
TGAAAAAACTTGTCTGGAGATGTTGGCCCCAGGGTCCAAAGTGCAGTGAGGGGAATGGGGGGGG
GTTGGCACTAGATGGCCTTAGGTGGGTGAGTACCCCTCCGGCAAGGCCCAGGCTCCTCAGATGGACGT
TTCGTCGCTCGAGCCTGACGAGTCCTCATCCACCGTGCCTGCCTGATGCTCATGGCGATGGCATG
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>AQ046679.1 RPCI11-42B3.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-42B3, genomic survey sequence
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>AI020381.1 ub27f05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1378977
5' similar to TR:008973 008973 HYPOTHETICAL 33.5 KD PROTEIN, mRNA sequence
GAAAGAGAAGCCAGAGACAGCCTCACTCTGCCCTTCAGTCAGCTCTGAAAAACAGAAAGCTCTGCTGC
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>AA969381.1 on58e10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560906
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>AA956451 UI-R-E1-fm-a-08-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-
R-E1-fm-a-08-0-UI 3' similar to gi|2938381|gb|AA850841|AA850841 EST193609
Normalized rat ovary, Bento Soares Rattus sp. cDNA 3' end, mRNA sequence
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>AA930960.1 vy79d06.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
clone IMAGE:1312427 5' similar to gb:M10062 Mouse IgE-binding factor mRNA,
complete cds (MOUSE), mRNA sequence
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>AA921844.1 om44c06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543882

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GCTCCCGGGTAGAAGTCACTGATCAGACACACTAGTGTGCCCTGTTGGCTGGAGCTCCTCAGAGGAGG
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>AA887752.1 nr11a10.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161498 3'
similar to contains Alu repetitive element;contains element THR repetitive
element, mRNA sequence
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>AA826485.1 oe66f07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416613 3',
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>AA760837.1 nz10h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287431 3',
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>AA702974.1 zi81c01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
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GCTGGGGATAATTGTTGATGCCACTCATTGCCCTGTTGCATTGGAGAGGACTTGGCTGTATATGCTGAAT
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>AL019795.1 *F.rubripes* GSS sequence, clone 182J23aF2, genomic survey sequence
GAAGATACANCAACCAGCAGCGGCATCCAGACGGAGCGAAAGGAGGCTGCCACACATACTCCACCGTCAC
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>AA678241.1 zi27a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
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>AC003372 *Drosophila melanogaster* chromosome 2 clone P1 DS04106 (D172), ***
SEQUENCING IN PROGRESS ***
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>T43257.1 6520 Lambda-PRL2 Arabidopsis thaliana cDNA clone 119H14T7, mRNA  
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>C40523.1 C40523 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo  
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>D78935.1 HUM527D10B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone  
GEN-527D10 5', mRNA sequence
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[144]: #Additionalpractices  
#Search for citations  
# PMCID or PMC Identifier, assigned to each full-text paper in PubMed Central.  
pmid = "12890024"  
results = Entrez.read(Entrez.elink(dbfrom="pubmed", db="pmc",  
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pmc_ids = [link["Id"] for link in results[0]["LinkSetDb"][0]["Link"]]
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[109]: #we are just getting the raw records
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text = handle.read()
print(text)
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LOCUS NM_000594 1678 bp mRNA linear PRI 27-SEP-2019
 DEFINITION Homo sapiens tumor necrosis factor (TNF), mRNA.
 ACCESSION NM_000594
 VERSION NM_000594.4
 KEYWORDS RefSeq; MANE Select.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1678)
 AUTHORS Ding Y, Feng Q, Chen J and Song J.
 TITLE TLR4/NF-kappaB signaling pathway gene single nucleotide polymorphisms alter gene expression levels and affect ARDS occurrence and prognosis outcomes
 JOURNAL Medicine (Baltimore) 98 (26), e16029 (2019)
 PUBMED 31261506
 REMARK GeneRIF: TNF-[alpha] rs1800629 locus A allele and the IL-6 rs1800796 locus G allele were found to be risk factors for acute respiratory distress syndrome (ARDS); G allele at MyD88 rs7744 locus was a protective factor. Homozygotes for TNF-[alpha] rs1800629, IL-6 rs1800796, and MyD88 rs7744 loci had higher expression levels, of which homozygotes for TNF-[alpha] rs1800629 and IL-6 rs1800796 loci had lower 60-day survival rates.
 REFERENCE 2 (bases 1 to 1678)
 AUTHORS Yuan Y, Piao J and Lu N.
 TITLE Tumor necrosis factor-alpha-308 polymorphism is not associated with Kawasaki disease: A meta-analysis of case-control studies
 JOURNAL Medicine (Baltimore) 98 (26), e15963 (2019)
 PUBMED 31261503
 REMARK GeneRIF: Meta-analysis of 11 studies found no association between tumor necrosis factor-alpha-308 polymorphism and Kawasaki disease.
 REFERENCE 3 (bases 1 to 1678)
 AUTHORS Kang SW, Kim SK, Han YR, Hong D, Chon J, Chung JH, Hong SJ, Park MS and Ban JY.
 TITLE Promoter Polymorphism (-308G/A) of Tumor Necrosis Factor-Alpha (TNF-alpha) Gene and Asthma Risk: An Updated Meta-Analysis
 JOURNAL Genet Test Mol Biomarkers 23 (6), 363-372 (2019)
 PUBMED 31161819
 REMARK GeneRIF: TNF-alpha polymorphism (-308, G/A) was strongly associated with the risk of asthma ($p < 0.05$ in the allelic, dominant, and recessive models, respectively).
 REFERENCE 4 (bases 1 to 1678)
 AUTHORS Aflatoonian M, Moghimi M, Akbarian-Bafghi MJ, Morovati-Sharifabad M, Jarahzadeh MH and Neamatzzadeh H.
 TITLE ASSOCIATION OF TNF- alpha-308G>A POLYMORPHISM WITH SUSCEPTIBILITY TO CELIAC DISEASE: A SYSTEMATIC REVIEW AND META-ANALYSIS
 JOURNAL Arq Gastroenterol 56 (1), 88-94 (2019)

PUBMED 31141070
REMARK GeneRIF: the TNF-alpha -308G>A polymorphism plays an important role in celiac disease susceptibility (Meta-Analysis)
Publication Status: Online-Only
REFERENCE 5 (bases 1 to 1678)
AUTHORS Tabaei S, Mehrad-Majd H, Soori M and Tabaee S.
TITLE The effect of tumor necrosis factor alpha (-308G/a) and interferon gamma (+874T/a) polymorphisms on susceptibility to coronary heart disease
JOURNAL Nucleosides Nucleotides Nucleic Acids 38 (10), 701-712 (2019)
PUBMED 31140911
REMARK GeneRIF: these two cytokine polymorphisms may play a role in predisposition to coronary heart disease.
REFERENCE 6 (bases 1 to 1678)
AUTHORS Buonaguro L, Barillari G, Chang HK, Bohan CA, Kao V, Morgan R, Gallo RC and Ensoli B.
TITLE Effects of the human immunodeficiency virus type 1 Tat protein on the expression of inflammatory cytokines
JOURNAL J. Virol. 66 (12), 7159-7167 (1992)
PUBMED 1279199
REFERENCE 7 (bases 1 to 1678)
AUTHORS Zhang XM, Weber I and Chen MJ.
TITLE Site-directed mutational analysis of human tumor necrosis factor-alpha receptor binding site and structure-functional relationship
JOURNAL J. Biol. Chem. 267 (33), 24069-24075 (1992)
PUBMED 1331108
REFERENCE 8 (bases 1 to 1678)
AUTHORS Stevenson FT, Bursten SL, Locksley RM and Lovett DH.
TITLE Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues
JOURNAL J. Exp. Med. 176 (4), 1053-1062 (1992)
PUBMED 1402651
REFERENCE 9 (bases 1 to 1678)
AUTHORS Stephens JM and Pekala PH.
TITLE Transcriptional repression of the C/EBP-alpha and GLUT4 genes in 3T3-L1 adipocytes by tumor necrosis factor-alpha. Regulation is coordinate and independent of protein synthesis
JOURNAL J. Biol. Chem. 267 (19), 13580-13584 (1992)
PUBMED 1618860
REFERENCE 10 (bases 1 to 1678)
AUTHORS Spriggs DR, Deutsch S and Kufe DW.
TITLE Genomic structure, induction, and production of TNF-alpha
JOURNAL Immunol. Ser. 56, 3-34 (1992)
PUBMED 1550865
REMARK Review article
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AL662801.7, BP215875.1,

BC028148.1 and CA306559.1.

This sequence is a reference standard in the RefSeqGene project.

On Nov 23, 2018 this sequence version replaced NM_000594.3.

Summary: This gene encodes a multifunctional proinflammatory cytokine that belongs to the tumor necrosis factor (TNF) superfamily. This cytokine is mainly secreted by macrophages. It can bind to, and thus functions through its receptors TNFRSF1A/TNFR1 and TNFRSF1B/TNFBR. This cytokine is involved in the regulation of a wide spectrum of biological processes including cell proliferation, differentiation, apoptosis, lipid metabolism, and coagulation. This cytokine has been implicated in a variety of diseases, including autoimmune diseases, insulin resistance, and cancer. Knockout studies in mice also suggested the neuroprotective function of this cytokine. [provided by RefSeq, Jul 2008].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: SRR1163655.92493.1, BC028148.1
[ECO:0000332]
RNaseq introns :: single sample supports all introns
SAMEA1965299, SAMEA1966682
[ECO:0000348]

##Evidence-Data-END##

##RefSeq-Attributes-START##

MANE Ensembl match :: ENST00000449264.3/ ENSP00000398698.2
RefSeq Select criteria :: based on single protein-coding transcript
##RefSeq-Attributes-END##
COMPLETENESS: full length.

| PRIMARY | REFSEQ_SPAN | PRIMARY_IDENTIFIER | PRIMARY_SPAN | COMP |
|---------|-------------|--------------------|--------------|------|
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| | 3-539 | BP215875.1 | 1-537 | |
| | 540-1674 | BC028148.1 | 520-1654 | |
| | 1675-1678 | CA306559.1 | 11-14 | c |

| FEATURES | Location/Qualifiers |
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superfamily member 2; tumor necrosis factor ligand 1F"
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UniProtKB/Swiss-Prot (P01375.1); cleavage site"

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UniProtKB/Swiss-Prot (P01375.1); cleavage site"

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UniProtKB/Swiss-Prot (P01375.1); cleavage site"

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| DEFINITION | Homo sapiens chromosome 6, GRCh38.p13 Primary Assembly. | | | | |
| ACCESSION | NC_000006 | | | | |
| VERSION | NC_000006.12 | | | | |
| DBLINK | BioProject: PRJNA168 Assembly: GCF_000001405.39 | | | | |
| KEYWORDS | RefSeq. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo. | | | | |

REFERENCE 1 (bases 1 to 170805979)
 CONSRM International Human Genome Sequencing Consortium
 TITLE Finishing the euchromatic sequence of the human genome
 JOURNAL Nature 431 (7011), 931-945 (2004)
 PUBMED 15496913
 REFERENCE 2 (bases 1 to 170805979)
 AUTHORS Mungall,A.J., Palmer,S.A., Sims,S.K., Edwards,C.A., Ashurst,J.L.,
 Wilming,L., Jones,M.C., Horton,R., Hunt,S.E., Scott,C.E.,
 Gilbert,J.G., Clamp,M.E., Bethel,G., Milne,S., Ainscough,R.,
 Almeida,J.P., Ambrose,K.D., Andrews,T.D., Ashwell,R.I.,
 Babbage,A.K., Bagguley,C.L., Bailey,J., Banerjee,R., Barker,D.J.,
 Barlow,K.F., Bates,K., Beare,D.M., Beasley,H., Beasley,O.,
 Bird,C.P., Blakey,S., Bray-Allen,S., Brook,J., Brown,A.J.,
 Brown,J.Y., Burford,D.C., Burrill,W., Burton,J., Carder,C.,
 Carter,N.P., Chapman,J.C., Clark,S.Y., Clark,G., Clee,C.M.,
 Clegg,S., Cobley,V., Collier,R.E., Collins,J.E., Colman,L.K.,
 Corby,N.R., Coville,G.J., Culley,K.M., Dhami,P., Davies,J.,
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 Francis,M.D., Frankish,A., Frankland,J., French,L., Garner,P.,
 Garnett,J., Ghori,M.J., Gilby,L.M., Gillson,C.J., Glithero,R.J.,
 Grafham,D.V., Grant,M., Gribble,S., Griffiths,C., Griffiths,M.,
 Hall,R., Halls,K.S., Hammond,S., Harley,J.L., Hart,E.A.,
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 Squares,S.L., Steward,C.A., Sycamore,N., Tamlyn-Hall,G., Tester,J.,
 Theaker,A.J., Thomas,D.W., Thorpe,A., Tracey,A., Tromans,A.,
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 Whitehead,S.L., Whittaker,H., Wild,A., Willey,D.J., Wilmer,T.E.,
 Wood,J.M., Wray,P.W., Wyatt,J.C., Young,L., Younger,R.M.,
 Bentley,D.R., Coulson,A., Durbin,R., Hubbard,T., Sulston,J.E.,
 Dunham,I., Rogers,J. and Beck,S.
 TITLE The DNA sequence and analysis of human chromosome 6
 JOURNAL Nature 425 (6960), 805-811 (2003)
 PUBMED 14574404
 REFERENCE 3 (bases 1 to 170805979)
 AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,
 Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R.,
 Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J.,

LeVine,R., McEwan,P., McKernan,K., Meldrim,J., Mesirov,J.P.,
Miranda,C., Morris,W., Naylor,J., Raymond,C., Rosetti,M.,
Santos,R., Sheridan,A., Sougnez,C., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Wyman,D., Rogers,J., Sulston,J.,
Ainscough,R., Beck,S., Bentley,D., Burton,J., Clee,C., Carter,N.,
Coulson,A., Deadman,R., Deloukas,P., Dunham,A., Dunham,I.,
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Humphray,S., Hunt,A., Jones,M., Lloyd,C., McMurray,A., Matthews,L.,
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McPherson,J.D., Marra,M.A., Mardis,E.R., Fulton,L.A.,
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Delehaunty,K.D., Miner,T.L., Delehaunty,A., Kramer,J.B., Cook,L.L.,
Fulton,R.S., Johnson,D.L., Minx,P.J., Clifton,S.W., Hawkins,T.,
Branscomb,E., Predki,P., Richardson,P., Wenning,S., Slezak,T.,
Doggett,N., Cheng,J.F., Olsen,A., Lucas,S., Elkin,C.,
Uberbacher,E., Frazier,M., Gibbs,R.A., Muzny,D.M., Scherer,S.E.,
Bouck,J.B., Sodergren,E.J., Worley,K.C., Rives,C.M., Gorrell,J.H.,
Metzker,M.L., Naylor,S.L., Kucherlapati,R.S., Nelson,D.L.,
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Abola,A.P., Proctor,M.J., Myers,R.M., Schmutz,J., Dickson,M.,
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Yang,S.P., Yeh,R.F., Collins,F., Guyer,M.S., Peterson,J.,
Felsenfeld,A., Wetterstrand,K.A., Patrinos,A., Morgan,M.J., de
Jong,P., Catanese,J.J., Osoegawa,K., Shizuya,H., Choi,S. and
Chen,Y.J.

CONSRTM International Human Genome Sequencing Consortium
 TITLE Initial sequencing and analysis of the human genome
 JOURNAL Nature 409 (6822), 860-921 (2001)
 PUBMED 11237011
 REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
 COMMENT REFSEQ INFORMATION: The reference sequence is identical to CM000668.2.
 On Feb 3, 2014 this sequence version replaced NC_000006.11.
 Assembly Name: GRCh38.p13 Primary Assembly
 The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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##Genome-Annotation-Data-START##
Annotation Provider      :: NCBI
Annotation Status        :: Updated annotation
Annotation Name          :: Homo sapiens Updated Annotation
                           Release 109.20190905
Annotation Version       :: 109.20190905
Annotation Pipeline      :: NCBI eukaryotic genome annotation
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Annotation Software Version :: 8.2
Annotation Method         :: Best-placed RefSeq; propagated
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Features Annotated       :: Gene; mRNA; CDS; ncRNA
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DEFINITION              Homo sapiens chromosome 6 genomic scaffold, GRCh38.p13 alternate
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ACCESSION               NT_167249
VERSION                 NT_167249.2
DBLINK                  BioProject: PRJNA168
                        Assembly: GCF_000001405.39
KEYWORDS                RefSeq; ALTERNATE_LOCUS.
  
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SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4929269)

AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J., Almeida,J., Forbes,S., Gilbert,J.G., Halls,K., Harrow,J.L., Hart,E., Howe,K., Jackson,D.K., Palmer,S., Roberts,A.N., Sims,S., Stewart,C.A., Traherne,J.A., Trevanion,S., Wilming,L., Rogers,J., de Jong,P.J., Elliott,J.F., Sawcer,S., Todd,J.A., Trowsdale,J. and Beck,S.

TITLE Variation analysis and gene annotation of eight MHC haplotypes: the MHC Haplotype Project

JOURNAL Immunogenetics 60 (1), 1-18 (2008)

PUBMED 18193213

REFERENCE 2 (bases 1 to 4929269)

CONSRTM International Human Genome Sequencing Consortium

TITLE Finishing the euchromatic sequence of the human genome

JOURNAL Nature 431 (7011), 931-945 (2004)

PUBMED 15496913

REFERENCE 3 (bases 1 to 4929269)

AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C., Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R., Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J., LeVine,R., McEwan,P., McKernan,K., Meldrim,J., Mesirov,J.P., Miranda,C., Morris,W., Naylor,J., Raymond,C., Rosetti,M., Santos,R., Sheridan,A., Sougnez,C., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Wyman,D., Rogers,J., Sulston,J., Ainscough,R., Beck,S., Bentley,D., Burton,J., Clee,C., Carter,N., Coulson,A., Deadman,R., Deloukas,P., Dunham,A., Dunham,I., Durbin,R., French,L., Grafham,D., Gregory,S., Hubbard,T., Humphray,S., Hunt,A., Jones,M., Lloyd,C., McMurray,A., Matthews,L., Mercer,S., Milne,S., Mullikin,J.C., Mungall,A., Plumb,R., Ross,M., Showkeen,R., Sims,S., Waterston,R.H., Wilson,R.K., Hillier,L.W., McPherson,J.D., Marra,M.A., Mardis,E.R., Fulton,L.A., Chinwalla,A.T., Pepin,K.H., Gish,W.R., Chissoe,S.L., Wendl,M.C., Delehaunty,K.D., Miner,T.L., Delehaunty,A., Kramer,J.B., Cook,L.L., Fulton,R.S., Johnson,D.L., Minx,P.J., Clifton,S.W., Hawkins,T., Branscomb,E., Predki,P., Richardson,P., Wenning,S., Slezak,T., Doggett,N., Cheng,J.F., Olsen,A., Lucas,S., Elkin,C., Uberbacher,E., Frazier,M., Gibbs,R.A., Muzny,D.M., Scherer,S.E., Bouck,J.B., Sodergren,E.J., Worley,K.C., Rives,C.M., Gorrell,J.H., Metzker,M.L., Naylor,S.L., Kucherlapati,R.S., Nelson,D.L., Weinstock,G.M., Sakaki,Y., Fujiyama,A., Hattori,M., Yada,T., Toyoda,A., Itoh,T., Kawagoe,C., Watanabe,H., Totoki,Y., Taylor,T., Weissenbach,J., Heilig,R., Saurin,W., Artiguenave,F., Brottier,P., Bruls,T., Pelletier,E., Robert,C., Wincker,P., Smith,D.R.,

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Jong,P., Catanese,J.J., Osoegawa,K., Shizuya,H., Choi,S. and
Chen,Y.J.

CONSRM International Human Genome Sequencing Consortium
TITLE Initial sequencing and analysis of the human genome
JOURNAL Nature 409 (6822), 860-921 (2001)
PUBMED 11237011
REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
COMMENT REFSEQ INFORMATION: The reference sequence is identical to
GL000256.2.
On Feb 3, 2014 this sequence version replaced NT_167249.1.
This scaffold is an alternate sequence representation of the MHC
region on reference chromosome 6. It is derived from the SSTO cell
line and represents the A32-B44-DR4 haplotype.
Region: MHC.
Assembly Name: GRCh38.p13 ALT_REF_LOCI_7
The DNA sequence is composed of genomic sequence, primarily
finished clones that were sequenced as part of the Human Genome
Project. PCR products and WGS shotgun sequence have been added
where necessary to fill gaps or correct errors. All such additions
are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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##Genome-Annotation-Data-START##  
Annotation Provider      :: NCBI  
Annotation Status        :: Updated annotation
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Annotation Name :: Homo sapiens Updated Annotation
 Release 109.20190905
 Annotation Version :: 109.20190905
 Annotation Pipeline :: NCBI eukaryotic genome annotation
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 Annotation Software Version :: 8.2
 Annotation Method :: Best-placed RefSeq; propagated
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ACCESSION NT_167248 NT_113892 NT_113893 NT_113894 NT_113895 NT_113896
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VERSION NT_167248.2
DBLINK BioProject: PRJNA168
Assembly: GCF_000001405.39
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4606388)
AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J.,
Almeida,J., Forbes,S., Gilbert,J.G., Halls,K., Harrow,J.L.,
Hart,E., Howe,K., Jackson,D.K., Palmer,S., Roberts,A.N., Sims,S.,
Stewart,C.A., Traherne,J.A., Trevanion,S., Wilming,L., Rogers,J.,
de Jong,P.J., Elliott,J.F., Sawcer,S., Todd,J.A., Trowsdale,J. and
Beck,S.
TITLE Variation analysis and gene annotation of eight MHC haplotypes: the
MHC Haplotype Project
JOURNAL Immunogenetics 60 (1), 1-18 (2008)
PUBMED 18193213
REFERENCE 2 (bases 1 to 4606388)
CONSRM International Human Genome Sequencing Consortium
TITLE Finishing the euchromatic sequence of the human genome
JOURNAL Nature 431 (7011), 931-945 (2004)
PUBMED 15496913
REFERENCE 3 (bases 1 to 4606388)
AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,
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CONSRTM International Human Genome Sequencing Consortium
TITLE Initial sequencing and analysis of the human genome
JOURNAL Nature 409 (6822), 860-921 (2001)
PUBMED 11237011
REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
COMMENT REFSEQ INFORMATION: The reference sequence is identical to

GL000255.2.
 On Feb 3, 2014 this sequence version replaced NT_167248.1.
 This scaffold is an alternate sequence representation of the MHC
 region on reference chromosome 6. It is derived from the QBL cell
 line and represents the A26-B18-DR3 haplotype.
 Region: MHC.
 Assembly Name: GRCh38.p13 ALT_REF_LOCI_6
 The DNA sequence is composed of genomic sequence, primarily
 finished clones that were sequenced as part of the Human Genome
 Project. PCR products and WGS shotgun sequence have been added
 where necessary to fill gaps or correct errors. All such additions
 are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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Annotation Status        :: Updated annotation
Annotation Name          :: Homo sapiens Updated Annotation
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Annotation Version       :: 109.20190905
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Annotation Software Version :: 8.2
Annotation Method         :: Best-placed RefSeq; propagated
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Features Annotated       :: Gene; mRNA; CDS; ncRNA
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LOCUS NT_167247 4827813 bp DNA linear CON 09-SEP-2019
DEFINITION Homo sapiens chromosome 6 genomic scaffold, GRCh38.p13 alternate
 locus group ALT_REF_LOCI_5 HSCHR6_MHC_MCF_CTG1.
ACCESSION NT_167247
VERSION NT_167247.2
DBLINK BioProject: PRJNA168
 Assembly: GCF_000001405.39
KEYWORDS RefSeq; ALTERNATE_LOCUS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4827813)
AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J.,
 Almeida,J., Forbes,S., Gilbert,J.G., Halls,K., Harrow,J.L.,
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 de Jong,P.J., Elliott,J.F., Sawcer,S., Todd,J.A., Trowsdale,J. and
 Beck,S.
TITLE Variation analysis and gene annotation of eight MHC haplotypes: the
 MHC Haplotype Project
JOURNAL Immunogenetics 60 (1), 1-18 (2008)
PUBMED 18193213
REFERENCE 2 (bases 1 to 4827813)
CONSRTM International Human Genome Sequencing Consortium
TITLE Finishing the euchromatic sequence of the human genome
JOURNAL Nature 431 (7011), 931-945 (2004)
PUBMED 15496913
REFERENCE 3 (bases 1 to 4827813)
AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,
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Chen,Y.J.

CONSRTM International Human Genome Sequencing Consortium
 TITLE Initial sequencing and analysis of the human genome
 JOURNAL Nature 409 (6822), 860-921 (2001)
 PUBMED 11237011
 REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
 COMMENT REFSEQ INFORMATION: The reference sequence is identical to GL000254.2.
 On Feb 3, 2014 this sequence version replaced NT_167247.1.
 This scaffold is an alternate sequence representation of the MHC region on reference chromosome 6. It is derived from the MCF cell line and represents the A2-B62-DR4 haplotype.
 Region: MHC.
 Assembly Name: GRCh38.p13 ALT_REF_LOCI_5
 The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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Annotation Name          :: Homo sapiens Updated Annotation
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Annotation Version       :: 109.20190905
Annotation Pipeline      :: NCBI eukaryotic genome annotation
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Annotation Software Version :: 8.2
Annotation Method         :: Best-placed RefSeq; propagated
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Features Annotated       :: Gene; mRNA; CDS; ncRNA
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LOCUS NT_167246 4677643 bp DNA linear CON 09-SEP-2019
DEFINITION Homo sapiens chromosome 6 genomic scaffold, GRCh38.p13 alternate
locus group ALT_REF_LOCI_4 HSCHR6_MHC_MANN_CTG1.
ACCESSION NT_167246
VERSION NT_167246.2
DBLINK BioProject: PRJNA168
Assembly: GCF_000001405.39
KEYWORDS RefSeq; ALTERNATE_LOCUS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4677643)
AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J.,
Almeida,J., Forbes,S., Gilbert,J.G., Halls,K., Harrow,J.L.,
Hart,E., Howe,K., Jackson,D.K., Palmer,S., Roberts,A.N., Sims,S.,
Stewart,C.A., Traherne,J.A., Trevanion,S., Wilming,L., Rogers,J.,
de Jong,P.J., Elliott,J.F., Sawcer,S., Todd,J.A., Trowsdale,J. and
Beck,S.
TITLE Variation analysis and gene annotation of eight MHC haplotypes: the
MHC Haplotype Project
JOURNAL Immunogenetics 60 (1), 1-18 (2008)
PUBMED 18193213
REFERENCE 2 (bases 1 to 4677643)
CONSRTM International Human Genome Sequencing Consortium

TITLE Finishing the euchromatic sequence of the human genome
 JOURNAL Nature 431 (7011), 931–945 (2004)
 PUBMED 15496913
 REFERENCE 3 (bases 1 to 4677643)
 AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,
 Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R.,
 Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J.,
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 Jong,P., Catanese,J.J., Osoegawa,K., Shizuya,H., Choi,S. and
 Chen,Y.J.

CONSRM International Human Genome Sequencing Consortium
TITLE Initial sequencing and analysis of the human genome
JOURNAL Nature 409 (6822), 860-921 (2001)
PUBMED 11237011
REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
COMMENT REFSEQ INFORMATION: The reference sequence is identical to GL000253.2.
 On Feb 3, 2014 this sequence version replaced NT_167246.1.
 This scaffold is an alternate sequence representation of the MHC region on reference chromosome 6. It is derived from the MANN cell line and represents the A29-B44-DR7 haplotype.
 Region: MHC.
 Assembly Name: GRCh38.p13 ALT_REF_LOCI_4
 The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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##Genome-Annotation-Data-START##
Annotation Provider      :: NCBI
Annotation Status        :: Updated annotation
Annotation Name          :: Homo sapiens Updated Annotation
                           Release 109.20190905
Annotation Version       :: 109.20190905
Annotation Pipeline      :: NCBI eukaryotic genome annotation
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Annotation Software Version :: 8.2
Annotation Method         :: Best-placed RefSeq; propagated
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Features Annotated       :: Gene; mRNA; CDS; ncRNA
##Genome-Annotation-Data-END##

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 ACCESSION NT_167245
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 Assembly: GCF_000001405.39
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 4604811)
 AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J.,
 Almeida,J., Forbes,S., Gilbert,J.G., Halls,K., Harrow,J.L.,
 Hart,E., Howe,K., Jackson,D.K., Palmer,S., Roberts,A.N., Sims,S.,

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 Beck,S.
TITLE Variation analysis and gene annotation of eight MHC haplotypes: the
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JOURNAL Immunogenetics 60 (1), 1-18 (2008)
PUBMED 18193213
REFERENCE 2 (bases 1 to 4604811)
CONSRTM International Human Genome Sequencing Consortium
TITLE Finishing the euchromatic sequence of the human genome
JOURNAL Nature 431 (7011), 931-945 (2004)
PUBMED 15496913
REFERENCE 3 (bases 1 to 4604811)
AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,
 Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R.,
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 Chen,Y.J.

CONSRTM International Human Genome Sequencing Consortium
TITLE Initial sequencing and analysis of the human genome
JOURNAL Nature 409 (6822), 860-921 (2001)
PUBMED 11237011
REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
COMMENT REFSEQ INFORMATION: The reference sequence is identical to GL000252.2.
 On Feb 3, 2014 this sequence version replaced NT_167245.1.
 This scaffold is an alternate sequence representation of the MHC region on reference chromosome 6. It is derived from the DBB cell line and represents the A2-B57-DR7 haplotype.
 Region: MHC.
 Assembly Name: GRCh38.p13 ALT_REF_LOCI_3
 The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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Annotation Provider      :: NCBI
Annotation Status        :: Updated annotation
Annotation Name          :: Homo sapiens Updated Annotation
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Annotation Version       :: 109.20190905
Annotation Pipeline      :: NCBI eukaryotic genome annotation
                           pipeline
Annotation Software Version :: 8.2
Annotation Method         :: Best-placed RefSeq; propagated
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Features Annotated       :: Gene; mRNA; CDS; ncRNA
  
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DEFINITION Homo sapiens chromosome 6 genomic scaffold, GRCh38.p13 alternate
ACCESSION  NT_113891
VERSION    NT_113891.3
DBLINK     BioProject: PRJNA168
           Assembly: GCF_000001405.39
KEYWORDS   RefSeq; ALTERNATE_LOCUS.

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SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4795265)

AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J., Almeida,J., Forbes,S., Gilbert,J.G., Halls,K., Harrow,J.L., Hart,E., Howe,K., Jackson,D.K., Palmer,S., Roberts,A.N., Sims,S., Stewart,C.A., Traherne,J.A., Trevanion,S., Wilming,L., Rogers,J., de Jong,P.J., Elliott,J.F., Sawcer,S., Todd,J.A., Trowsdale,J. and Beck,S.

TITLE Variation analysis and gene annotation of eight MHC haplotypes: the MHC Haplotype Project

JOURNAL Immunogenetics 60 (1), 1-18 (2008)

PUBMED 18193213

REFERENCE 2 (bases 1 to 4795265)

CONSRTM International Human Genome Sequencing Consortium

TITLE Finishing the euchromatic sequence of the human genome

JOURNAL Nature 431 (7011), 931-945 (2004)

PUBMED 15496913

REFERENCE 3 (bases 1 to 4795265)

AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C., Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R., Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J., LeVine,R., McEwan,P., McKernan,K., Meldrim,J., Mesirov,J.P., Miranda,C., Morris,W., Naylor,J., Raymond,C., Rosetti,M., Santos,R., Sheridan,A., Sougnez,C., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Wyman,D., Rogers,J., Sulston,J., Ainscough,R., Beck,S., Bentley,D., Burton,J., Clee,C., Carter,N., Coulson,A., Deadman,R., Deloukas,P., Dunham,A., Dunham,I., Durbin,R., French,L., Grafham,D., Gregory,S., Hubbard,T., Humphray,S., Hunt,A., Jones,M., Lloyd,C., McMurray,A., Matthews,L., Mercer,S., Milne,S., Mullikin,J.C., Mungall,A., Plumb,R., Ross,M., Showkeen,R., Sims,S., Waterston,R.H., Wilson,R.K., Hillier,L.W., McPherson,J.D., Marra,M.A., Mardis,E.R., Fulton,L.A., Chinwalla,A.T., Pepin,K.H., Gish,W.R., Chissoe,S.L., Wendl,M.C., Delehaunty,K.D., Miner,T.L., Delehaunty,A., Kramer,J.B., Cook,L.L., Fulton,R.S., Johnson,D.L., Minx,P.J., Clifton,S.W., Hawkins,T., Branscomb,E., Predki,P., Richardson,P., Wenning,S., Slezak,T., Doggett,N., Cheng,J.F., Olsen,A., Lucas,S., Elkin,C., Uberbacher,E., Frazier,M., Gibbs,R.A., Muzny,D.M., Scherer,S.E., Bouck,J.B., Sodergren,E.J., Worley,K.C., Rives,C.M., Gorrell,J.H., Metzker,M.L., Naylor,S.L., Kucherlapati,R.S., Nelson,D.L., Weinstock,G.M., Sakaki,Y., Fujiyama,A., Hattori,M., Yada,T., Toyoda,A., Itoh,T., Kawagoe,C., Watanabe,H., Totoki,Y., Taylor,T., Weissenbach,J., Heilig,R., Saurin,W., Artiguenave,F., Brottier,P., Bruls,T., Pelletier,E., Robert,C., Wincker,P., Smith,D.R.,

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 Chen,Y.J.

CONSRM International Human Genome Sequencing Consortium
TITLE Initial sequencing and analysis of the human genome
JOURNAL Nature 409 (6822), 860-921 (2001)
PUBMED 11237011
REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
COMMENT REFSEQ INFORMATION: The reference sequence is identical to GL000251.2.
 On Feb 3, 2014 this sequence version replaced NT_113891.2.
 This scaffold is an alternate sequence representation of the MHC region on reference chromosome 6. It is derived from the COX cell line and represents the A1-B8-DR3 haplotype.
 Region: MHC.
 Assembly Name: GRCh38.p13 ALT_REF_LOCI_2
 The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see:
<https://genomereference.org>.

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Annotation Provider      :: NCBI
Annotation Status        :: Updated annotation
  
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Annotation Name :: Homo sapiens Updated Annotation
 Release 109.20190905
 Annotation Version :: 109.20190905
 Annotation Pipeline :: NCBI eukaryotic genome annotation
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 Annotation Software Version :: 8.2
 Annotation Method :: Best-placed RefSeq; propagated
 RefSeq model
 Features Annotated :: Gene; mRNA; CDS; ncRNA
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ACCESSION NT_167244 NW_003871063
VERSION NT_167244.2

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SOURCE RefSeq; ALTERNATE_LOCUS.
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Catarrhini; Hominidae; Homo.
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AUTHORS Horton,R., Gibson,R., Coggill,P., Miretti,M., Allcock,R.J.,
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Hart,E., Howe,K., Jackson,D.K., Palmer,S., Roberts,A.N., Sims,S.,
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de Jong,P.J., Elliott,J.F., Sawcer,S., Todd,J.A., Trowsdale,J. and
Beck,S.
TITLE Variation analysis and gene annotation of eight MHC haplotypes: the
MHC Haplotype Project
JOURNAL Immunogenetics 60 (1), 1-18 (2008)
PUBMED 18193213
REFERENCE 2 (bases 1 to 4672374)
CONSRTM International Human Genome Sequencing Consortium
TITLE Finishing the euchromatic sequence of the human genome
JOURNAL Nature 431 (7011), 931-945 (2004)
PUBMED 15496913
REFERENCE 3 (bases 1 to 4672374)
AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C.,
Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R.,
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CONSRM International Human Genome Sequencing Consortium
TITLE Initial sequencing and analysis of the human genome
JOURNAL Nature 409 (6822), 860-921 (2001)
PUBMED 11237011
REMARK Erratum: [Nature 2001 Aug 2;412(6846):565]
COMMENT

REFSEQ INFORMATION: The reference sequence is identical to GL000250.2.

On or before Feb 3, 2014 this sequence version replaced NW_003871063.1, NT_167244.1.

This scaffold is an alternate sequence representation of the MHC region on reference chromosome 6. It is derived from the APD cell line and represents the A1-B60-DR13 haplotype.

Region: MHC.

Assembly Name: GRCh38.p13 ALT_REF_LOCI_1

The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see: <https://genomereference.org>.

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Annotation Status        :: Updated annotation
Annotation Name          :: Homo sapiens Updated Annotation
                           Release 109.20190905
Annotation Version       :: 109.20190905
Annotation Pipeline      :: NCBI eukaryotic genome annotation
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Annotation Software Version :: 8.2
Annotation Method         :: Best-placed RefSeq; propagated
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Features Annotated       :: Gene; mRNA; CDS; ncRNA
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 VERSION NG_007462.1
 KEYWORDS RefSeq; RefSeqGene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AL662801.7.
 This sequence is a reference standard in the RefSeqGene project.

 Summary: This gene encodes a multifunctional proinflammatory cytokine that belongs to the tumor necrosis factor (TNF) superfamily. This cytokine is mainly secreted by macrophages. It can bind to, and thus functions through its receptors TNFRSF1A/TNFR1 and TNFRSF1B/TNFBR. This cytokine is involved in the regulation of a wide spectrum of biological processes including cell proliferation, differentiation, apoptosis, lipid metabolism, and coagulation. This cytokine has been implicated in a variety of diseases, including autoimmune diseases, insulin resistance, and cancer. Knockout studies in mice also suggested the neuroprotective function of this cytokine. [provided by RefSeq, Jul 2008].
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 REFERENCE 1 (bases 1 to 9223)
 AUTHORS Alcais A, Alter A, Antoni G, Orlova M, Nguyen VT, Singh M,
 Vanderborgh PR, Katoch K, Mira MT, Vu HT, Nguyen TH, Nguyen NB,
 Moraes M, Mehra N, Schurr E and Abel L.
 TITLE Stepwise replication identifies a low-producing lymphotoxin-alpha
 allele as a major risk factor for early-onset leprosy
 JOURNAL Nat. Genet. 39 (4), 517-522 (2007)
 PUBMED 17353895
 REFERENCE 2 (bases 1 to 9223)
 AUTHORS Seidemann K, Zimmermann M, Book M, Meyer U, Burkhardt B, Welte K,
 Reiter A and Stanulla M.
 TITLE Tumor necrosis factor and lymphotoxin alfa genetic polymorphisms
 and outcome in pediatric patients with non-Hodgkin's lymphoma:
 results from Berlin-Frankfurt-Munster Trial NHL-BFM 95
 JOURNAL J. Clin. Oncol. 23 (33), 8414-8421 (2005)
 PUBMED 16293872
 REFERENCE 3 (bases 1 to 9223)
 AUTHORS Ozaki K, Ohnishi Y, Iida A, Sekine A, Yamada R, Tsunoda T, Sato H,
 Sato H, Hori M, Nakamura Y and Tanaka T.
 TITLE Functional SNPs in the lymphotoxin-alpha gene that are associated
 with susceptibility to myocardial infarction
 JOURNAL Nat. Genet. 32 (4), 650-654 (2002)
 PUBMED 12426569
 REMARK Erratum: [Nat Genet. 2003 Jan;33(1):107.]
 REFERENCE 4 (bases 1 to 9223)
 AUTHORS Evans AM, Petersen JW, Sekhon GS and DeMars R.
 TITLE Mapping of prolactin and tumor necrosis factor-beta genes on human
 chromosome 6p using lymphoblastoid cell deletion mutants
 JOURNAL Somat. Cell Mol. Genet. 15 (3), 203-213 (1989)
 PUBMED 2567059
 REFERENCE 5 (bases 1 to 9223)
 AUTHORS Gray,P.W., Aggarwal,B.B., Benton,C.V., Bringman,T.S., Henzel,W.J.,
 Jarrett,J.A., Leung,D.W., Moffat,B., Ng,P., Svedersky,L.P. et al.
 TITLE Cloning and expression of cDNA for human lymphotoxin, a lymphokine
 with tumour necrosis activity
 JOURNAL Nature 312 (5996), 721-724 (1984)
 PUBMED 6334807

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AL662801.7.
This sequence is a reference standard in the RefSeqGene project.

Summary: The encoded protein, a member of the tumor necrosis factor family, is a cytokine produced by lymphocytes. The protein is highly inducible, secreted, and forms heterotrimers with lymphotoxin-beta which anchor lymphotoxin-alpha to the cell surface. This protein also mediates a large variety of inflammatory, immunostimulatory, and antiviral responses, is involved in the formation of secondary lymphoid organs during development and plays a role in apoptosis. Genetic variations in this gene are associated with susceptibility to leprosy type 4, myocardial infarction, non-Hodgkin's lymphoma, and psoriatic arthritis. Alternatively spliced transcript variants have been observed for this gene. [provided by RefSeq, Jul 2012].

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 7681 cguttaagaa gatatggcca cacactgggg ccctgagaag tgagagcttc ataaaaaaa
 7741 tcagggaccc cagagttcct tggaaagccaa gactgaaacc agcattatga gtctccgggt
 7801 cagaatgaaa gaagaaggcc tgccccagtg gggctgtga attcccgggg gtgatttcac
 7861 tccccggggc tggcccaggc ttgtccctgc taccccccacc cagccttcc tgaggcctca
 7921 agcctgcccc acggccccc gctccttctc cccgcaggga cccaaacaca ggcctcagga
 7981 ctcaacacag ctttccctc caaccccggtt ttctctccct caaggactca gctttctgaa
 8041 gccccctccca gttctagttc tatcttttc ctgcattcctg tctggaagtt agaaggaaac
 8101 agaccacaga cctgggtcccc aaaagaaatg gaggcaatag gttttgggg gcatggggac
 8161 ggggttcagc ctccagggtc ctacacacaa atcagtcagt gggccagaag accccccctcg
 8221 gaatcgaggc agggaggatg gggagtgtga ggggtatcct tcatgtctgt gtgtcccaa
 8281 ctttccaaat ccccgcccc gcgatggaga agaaaccgag acagaagggt cagggcccac
 8341 taccgctcc tccagatgag ctcatgggt tctccaccaa ggaagtttc cgctgggtga
 8401 atgattctt ccccgccctc ctctgcffff agggacat aaaggcagtt gttggcacac
 8461 ccagccagca gacgctccct cagcaaggac agcagaggac cagctaagag ggagagaagc
 8521 aactacagac ccccccgtaa aacaaccctc agacgccaca tcccctgaca agctgccagg
 8581 caggttctct tccttcaca tactgaccca cggctccacc ctctccccc tggaaaggac
 8641 accatgagca ctgaaagcat gatccggac gtggagctgg ccgaggaggg gctccccaag
 8701 aagacagggg ggccccaggg ctccaggcggt tgcttgcact tcagcctt ctccttcgt
 8761 atcgtggcag gcgccaccac gcttctgc ctgctgcact ttggagtgtat cggcccccag
 8821 agggaaagagg tgagtgcctg gccagccctc atccactctc ccacccaagg gggaaatggag
 8881 acgcaagaga gggagagaga tgggatgggt gaaagatgt cgctgatagg gaggatgg
 8941 gaaaaaaa cgtggagaaa gacggggatg cagaaagaga tggcaaga gatggggaaag
 9001 agagagagag aaagatggag agacaggatg tctggcacat ggaaggtgct cactaagtgt
 9061 gtatggagtg aatgaatgaa tgaatgatg aacaagcaga tatataaata agatatggag
 9121 acagatgtgg ggtgtgagaa gagagatggg ggaagaaaca agtgtatgaa ataaagatgg
 9181 tgagacagaa agagcggaa atatgacagc taaggagaga gat

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LOCUS MH102359 319 bp DNA linear PRI 13-MAY-2018
 DEFINITION Homo sapiens isolate RKAPU01 tumor necrosis factor (TNF) gene,
 promoter region.
 ACCESSION MH102359
 VERSION MH102359.1
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa;

Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata;
 Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;
 Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini;
 Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo.

REFERENCE 1 (bases 1 to 319)
 AUTHORS Aiswarya,P.S., Kesavan,P., Umamaheshwari,V., Akram Husain,R.S.,
 Subramaniyan,K. and Ramakrishnan,V.
 TITLE Genotyping of Tumor necrosis factor-a (TNF-a) gene in Migraine
 patients from South India
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 319)
 AUTHORS Aiswarya,P.S., Kesavan,P., Umamaheshwari,V., Akram Husain,R.S.,
 Subramaniyan,K. and Ramakrishnan,V.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-2018) Faculty of Allied Health Sciences,
 Chettinad Academy of Research and Education, Rajiv Gandhi Salai,
 OMR, Kelambakkam, Tamil Nadu 603103, India
 COMMENT ##Assembly-Data-START##
 Sequencing Technology :: Sanger dideoxy sequencing
 ##Assembly-Data-END##
 FEATURES Location/Qualifiers
 source 1..319
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /isolate="RKAPU01"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.33"
 /tissue_type="blood"
 /country="India"
 /collection_date="2018"
 /collected_by="Aiswarya P.S"
 gene <1..>319
 /gene="TNF"
 /note="tumor necrosis factor; TNF-a"
 regulatory <1..>319
 /regulatory_class="promoter"
 /gene="TNF"
 ORIGIN
 1 agttctagtt ctatctttt cctgcattcgtctggaaagt tagaaggaaa cagaccacag
 61 acctggccc caaaaagaaat ggaggcaata ggttttgagg ggcattggaa cggggttcag
 121 cctccagggt cctacacaca aatcagtccat tggcccgagaa gaccccccgc ggaatcggag
 181 cagggaggat ggggagtggtg aggggtatcc ttgatgcttg tgtgtccccca actttccaaa
 241 tccccgcggcc cgcgatggag aagaaaccga gacagaaggt gcagggccca ctaccgcttc
 301 ctccagatga gctcatggg
 //

LOCUS MH105039 319 bp DNA linear PRI 13-MAY-2018
 DEFINITION Homo sapiens isolate RKPRA02 tumor necrosis factor (TNF) gene, promoter region.
 ACCESSION MH105039
 VERSION MH105039.1
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa;
 Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata;
 Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;
 Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini;
 Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo.
 REFERENCE 1 (bases 1 to 319)
 AUTHORS Kesavan,P., Umamaheshwari,V., Aiswarya,P.S., Akram Husain,R.S., Subramaniyan,K. and Ramakrishnan,V.
 TITLE Genotyping of Tumor necrosis factor-a (TNF-a) gene in Migraine patients from South India
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 319)
 AUTHORS Kesavan,P., Umamaheshwari,V., Aiswarya,P.S., Akram Husain,R.S., Subramaniyan,K. and Ramakrishnan,V.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-2018) Faculty of Allied Health Sciences, Chettinad Academy of Research and Education, Rajiv Gandhi Salai, OMR, Kelambakkam, Tamil Nadu 603103, India
 COMMENT ##Assembly-Data-START##
 Sequencing Technology :: Sanger dideoxy sequencing
 ##Assembly-Data-END##
 FEATURES Location/Qualifiers
 source 1..319
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /isolate="RKPRA02"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.33"
 /tissue_type="blood"
 /country="India"
 /collection_date="2018"
 /collected_by="Pallavi Kesavan"
 gene <1..>319
 /gene="TNF"
 /note="tumor necrosis factor; TNF-a"
 regulatory <1..>319
 /regulatory_class="promoter"
 /gene="TNF"

ORIGIN

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1 agttctagtt ctatctttt cctgcacccct gtctggaagt tagaaggaaa cagaccacag
61 acctggccc caaaaagaaat ggaggcaata gggtttgagg ggcacatgagga cggggttcag
121 cctccagggt cctacacaca aatcagtcag tggcccagaa gaccccccctc ggaatcggag
181 cagggaggat ggggagtggt aggggtatcc ttgatgctt tggtccccca actttccaaa
241 tccccgcccc cgcgatggag aagaaaccga gacagaaggt gcagggccca ctaccgcttc
301 ctccagatga gctcatggg
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LOCUS MH105072 319 bp DNA linear PRI 13-MAY-2018
DEFINITION Homo sapiens isolate Rkuap03 tumor necrosis factor (TNF) gene, promoter region.
ACCESSION MH105072
VERSION MH105072.1
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa;
Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata;
Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;
Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini;
Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo.
REFERENCE 1 (bases 1 to 319)
AUTHORS Umamaheshwari,V., Aiswarya,P.S., Pallavi,K., Akram Husain,R.S., Subramaniyan,K. and Ramakrishnan,V.
TITLE Genotyping of Tumor necrosis factor-a (TNF-a) gene in Migraine patients from South India
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 319)
AUTHORS Umamaheshwari,V., Aiswarya,P.S., Pallavi,K., Akram Husain,R.S., Subramaniyan,K. and Ramakrishnan,V.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-2018) Faculty of Allied Health Sciences, Chettinad Academy of Research and Education, Rajiv Gandhi Salai, OMR, Kelambakkam, Tamil Nadu 603103, India
COMMENT ##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..319
/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="Rkuap03"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.33"
/tissue_type="blood"

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/country="India"
/collection_date="2018"
/collected_by="Umamaheshwari . V"
gene <1..>319
/gene="TNF"
/note="tumor necrosis factor; TNF-a"
regulatory <1..>319
/regulatory_class="promoter"
/gene="TNF"

ORIGIN
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61 acctggtccc caaaaagaaat ggaggcaata ggttttgagg ggcattggga cggggttcag
121 cctccagggt cctacacaca aatcagtcag tggcccgagaa gaccccccctc ggaatcggag
181 cagggaggat ggggagtggt aggggtatcc ttgatgcttg tgtgtccca actttccaaa
241 tccccggccc cgcgatggag aagaaaccga gacagaaggt gcagggccca ctaccgcttc
301 ctccagatga gctcatggg

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LOCUS KX953765 796 bp DNA linear PRI 15-NOV-2016
DEFINITION Homo sapiens tumor necrosis factor (TNF) gene, partial sequence.
ACCESSION KX953765
VERSION KX953765.1
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS Issa,A.H. and Salman,M.S.
TITLE Polymorphism in promoter region of tumor necrosis factor alpha
(TNF) of Iraqi patients with TB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 796)
AUTHORS Issa,A.H. and Salman,M.S.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-2016) Biology, Basrah University, Qarmit Ali,
Basrah 334, Iraq
COMMENT ##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..796
/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="A03"
/db_xref="taxon:9606"
/chromosome="6"

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/cell_type="WBC"
/country="Iraq"
gene <1..>796
/gene="TNF"
/note="tumor necrosis factor"
misc_feature <1..>796
/gene="TNF"
/note="contains promoter and 5'UTR"

ORIGIN
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  61 agccaagact gaaaccagca ttatgagttt ccgggtcaga atgaaagaag aaggcctgcc
  121 ccagtgggtt ctgtgaattt ccgggggtga tttcactccc cggggctgtc ccaggcttgt
  181 ccctgctacc cccacccaac ctttcctgag gcctaagcc tgccaccaag cccccagctc
  241 cttctcccg cagggaccca aacacaggg tcaggactca acacagctt tccctccaac
  301 cccgtttctt ctccctcaag gactcagttt tctgaagccc ctcccaggttc tagttctatc
  361 ttttcctgc atcctgtctg gaagtttagaa ggaaacagac cacagacctg gtcccaaaa
  421 gaaatggagg caatagttt tgagggcat ggggacgggg ttcagcctcc agggcctac
  481 acacaaatca ttcaatggcc cagaagaccc ccctcggaaat cggagcagg aggatgggaa
  541 gtgtgagggg tatccttgat gcttgtgtt ccccaacttt ccaaattcccc gccccccgcga
  601 tggagaagaa accgagacag aagggtcagg gcccactacc gtttccttca gatgagctca
  661 tgggtttctc caccaaggaa gttttccgtt ggttgaatga ttctttcccc gccctcctct
  721 cgccccaggg acatataaag gcagttgtt gcacacccag ccagcagacg ctccctcagc
  781 aaggacagca gaggac

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LOCUS          FJ795028                      701 bp    mRNA     linear   PRI 24-JUL-2016
DEFINITION    Homo sapiens tumor necrosis factor alpha (TNF) mRNA, partial cds.
ACCESSION     FJ795028
VERSION        FJ795028.1
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
               Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 701)
AUTHORS        Guan,W.J., Ma,Y.H., Yu,L.L., Na,R.S. and Liu,S.
TITLE          Direct Submission
JOURNAL        Submitted (28-FEB-2009) Academy of Agricultural Sciences, Institute
               of Animal Science, Quanmingyuan West, Beijing 100193, People's
               Republic of China
FEATURES       Location/Qualifiers
source          1..701
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /chromosome="6"
               /map="6p21.3"

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        /tissue_type="placenta"
        /country="China"
        /collection_date="2008"
gene      <1..701
/gene="TNF"
CDS       <1..701
/gene="TNF"
/note="APC1 protein"
/codon_start=3
/product="tumor necrosis factor alpha"
/protein_id="AC037640.1"
/translation="STESMIRDVELAEEALPKKTGGPQGSRRCLFLSFLIVAGAT
TLFCLLHFGVIGPQREEFPRDLSLISPLAQAVRSSRTPSDKPVAVVANPQAEGQLQ
WLNRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTISRIAV
SYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLD
FAESGQVYFGIIAL"

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ORIGIN

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1 tgagcactga aagcatgatc cgggacgtgg agctggccga ggaggcgctc cccaagaaga
61 caggggggcc ccagggctcc aggccgtgct tggcacttcag cctcttcag ttcctgatcg
121 tggcaggcgc caccacgctc ttctgcctgc tgcactttgg agtgatcgcc ccccagaggg
181 aagagtcccc cagggacctc tctctaataca gcccctggc ccaggcagtc agatcatctt
241 ctgcgaaaccc gagtgacaag cctgtagccc atgtttagc aaaccctcaa gctgaggggc
301 agctccagtg gctgaaccgc cgggccaatg ccctcctggc caatggcggtg gagctgagag
361 ataaccagct ggttgtgcca tcagagggcc tgtacctcat ctactccag gtcctttca
421 agggccaagg ctgcccctcc acccatgtgc tcctcaccca caccatcagc cgcatcgccg
481 tctcctacca gaccaaggta aacccctct ctgcccataa gagccctgc cagagggaga
541 ccccagaggg ggctgaggcc aagccctgtt atgagccat ctatctggaa ggggtcttcc
601 agctggagaa gggtgaccga ctgcgcgtc agatcaatcg gccccactat ctgcactttg
661 ccgagtcgtgg gcaggtctac tttggatca ttggccctgtg a
//
```

| | | | | | |
|------------|--|--------|-----|--------|-----------------|
| LOCUS | DQ894849 | 742 bp | DNA | linear | SYN 14-JUL-2016 |
| DEFINITION | Synthetic construct Homo sapiens clone IMAGE:100009309; FLH179067.01L; RZPD0839C06129D tumor necrosis factor (TNF superfamily, member 2) (TNF) gene, encodes complete protein. | | | | |
| ACCESSION | DQ894849 | | | | |
| VERSION | DQ894849.2 | | | | |
| KEYWORDS | Human ORF Project; ORFeome collaboration; Gateway cloning system; full-length ORF without stop codon; FLEXGene. | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | synthetic construct other sequences; artificial sequences. | | | | |
| REFERENCE | 1 (bases 1 to 742) | | | | |
| AUTHORS | Rolfs,A., Kelley,F., McCarron,S., Jepson,D., Shen,B., Shi,Z., Hu,Y., Taycher,E., Zuo,D., Ebert,L., Hoerlein,A., Ernst,U., Korn,B. and LaBaer,J. | | | | |
| TITLE | Cloning of human full-length CDS FLEXGene in Gateway(TM) | | | | |

recombinational vector system
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 742)
 AUTHORS Rolfs,A., Kelley,F., McCarron,S., Jepson,D., Shen,B., Shi,Z.,
 Hu,Y., Taycher,E., Zuo,D., Ebert,L., Hoerlein,A., Ernst,U., Korn,B.
 and LaBaer,J.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-2006) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles Street,
 Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 742)
 AUTHORS Rolfs,A., Kelley,F., McCarron,S., Jepson,D., Shen,B., Shi,Z.,
 Hu,Y., Taycher,E., Zuo,D., Ebert,L., Hoerlein,A., Ernst,U., Korn,B.
 and LaBaer,J.
 TITLE Direct Submission
 JOURNAL Submitted (22-JAN-2007) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles Street,
 Cambridge, MA 02141, USA
 REMARK Sequence update by submitter
 COMMENT On Jan 22, 2007 this sequence version replaced DQ894849.1.
 This CDS clone is a part of a collection of human full-length ORF
 clones generated and verified by Harvard Institute of Proteomics
 (HIP) and Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 (RZPD, Heubnerweg 6, D-14059 Berlin, Germany). This ORF clone has
 been cloned without stop-codon (to allow fusion with C-terminal
 tag). AttB recombination sites have been added to either end of the
 ORF and directionally cloned using the Gateway cloning system into
 pDONR221. Additional sequences in the clone: 'ACC' before the 'ATG'
 (corresponding to Kozak consensus sequences). Each clone is
 clonally isolated and full-length sequence-verified. This clone is
 available for distribution at HIP (<http://plasmid.hms.harvard.edu/>)
 and RZPD (<http://www.rzpd.de/products/orfclones/rzpdexpression/>).
 This clone is part of the international ORFeome Collaboration
 (<http://www.orfeomecollaboration.org/>).
 FEATURES Location/Qualifiers
 source 1..742
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 /mol_type="other DNA"
 /db_xref="taxon:32630"
 /clone="IMAGE:100009309; FLH179067.01L; RZPDo839C06129D"
 /clone_lib="HIP_Gateway221_fusion"
 /focus
 /note="Vector: pDONR221; derived from parent clone
 IMAGE:5217636 (accession BC028148.1)"
 source 23..721
 /organism="Homo sapiens"
 /mol_type="other DNA"
 /db_xref="taxon:9606"

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        /transl_table=11
        /product="tumor necrosis factor (TNF superfamily, member
        2)"
        /protein_id="ABM85775.1"
        /db_xref="GeneID:7124"
        /translation="MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSFLSFLIVAGA
        TTLFCLLHFGVIGPQREEFPRLSLISPLAQAVRSSRTPSDKPVAHVVANPQAEGQL
        QWLNRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTISRIA
        VSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYL
        DFAESGQVYFGIIAL"
    misc_feature 722..725
        /note="linker at the 3' end of the ORF"
    misc_feature 726..742
        /note="attL2 site"

ORIGIN
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    61 cgaggaggcg ctccccaga agacaggggg gccccaggcgc tccaggcggt gcttgttcct
    121 cagcctcttc tccttcctga tcgtggcagg cgccaccacg ctctctgcc tgctgcactt
    181 tggagtgtatc ggccccaga gggaaagagtt ccccaggacat ctctctctaa tcagccctct
    241 ggcccaggca gtcagatcat cttctcgaaac cccgagtgac aagcctgttag cccatgttgt
    301 agcaaaccct caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct
    361 gccaatggc gtggagctga gagataacca gctgggtggc ccatcagagg gcctgtacct
    421 catctactcc caggtcctct tcaagggcca aggctggcc tccacccatg tgctcctcac
    481 ccacaccatc agccgcatcg ccgttccta ccagaccaag gtcaacctcc tctctgccat
    541 caagagcccc tgcagaggg agacccaga gggggcttag gccaagccct ggtatgagcc
    601 catctatctg ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa
    661 tcggcccgac tatctcgact ttgccgagtc tggcaggtc tactttggta tcattgccct
    721 gttggaccca gctttcttgt ac
//
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| | | | | | |
|------------|---|--------|-----|--------|-----------------|
| LOCUS | LT546440 | 801 bp | DNA | linear | PRI 06-APR-2016 |
| DEFINITION | Homo sapiens partial TNF promoter region. | | | | |
| ACCESSION | LT546440 | | | | |
| VERSION | LT546440.1 | | | | |
| KEYWORDS | . | | | | |
| SOURCE | Homo sapiens (human) | | | | |

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Salman,M.S.
 TITLE Tumor necrosis factor alfa gene polymorphism in Iraqi patient with
 TB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 801)
 AUTHORS Salman,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2016) Molecular Immunology Laboratory, College of
 Science, 23 Basra St. Basra, IRAQ
 FEATURES Location/Qualifiers
 source 1..801
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /isolation_source="patient with tuberculosis"
 /db_xref="taxon:9606"
 /cell_type="blood cell"
 /country="Iraq"
 /collection_date="20-May-2015"
 gene <1..801
 /gene="TNF"
 regulatory <1..801
 /regulatory_class="promoter"
 /gene="TNF"
 ORIGIN
 1 cactgggcc ctgagaagtg agagctcgt gaaaaaaatc agggaccaca gagttccttg
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 KEYWORDS .
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 ORGANISM Homo sapiens
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 Catarrhini; Hominidae; Homo.
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 AUTHORS AlRashid,M.H., Geo,J.A., AlBustan,S.A. and AlShammeri,S.
 TITLE Investigation of polymorphism in tumor necrosis factor (TNF-a) and
 ghrelin and the potential risk for Non Hodgkin's lymphoma (NHL)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 941)
 AUTHORS AlRashid,M.H., Geo,J.A., AlBustan,S.A. and AlShammeri,S.
 TITLE Direct Submission
 JOURNAL Submitted (25-DEC-2014) Biological Sciences, Kuwait University,
 Khaldiya 13060, Kuwait
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| VERSION | KP339511.1 | | | | | |
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| SOURCE | Homo sapiens (human) | | | | | |
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| AUTHORS | AlRashid,M.H., Geo,J.A., AlBustan,S.A. and AlShammeri,S. | | | | | |
| TITLE | Investigation of polymorphism in tumor necrosis factor (TNF-a) and ghrelin and the potential risk for Non Hodgkin's lymphoma (NHL) | | | | | |
| JOURNAL | Unpublished | | | | | |
| REFERENCE | 2 (bases 1 to 912) | | | | | |
| AUTHORS | AlRashid,M.H., Geo,J.A., AlBustan,S.A. and AlShammeri,S. | | | | | |
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| JOURNAL | Submitted (25-DEC-2014) Biological Sciences, Kuwait University, Khaldiya 13060, Kuwait | | | | | |
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841 agcagacgct ccctcagcaa ggacagcaga ggaccagcta agagggagag aagcaactac
901 agacccccc tg

//
```

[104]: # Uploading a list of identifiers

```

#To give an example of when this is useful, suppose you have a long list of IDs
→you want to download
#using EFetch (maybe sequences, maybe citations anything). When you make a
→request with EFetch your list of IDs,
#the database etc, are all turned into a long URL sent to the server.
#If your list of IDs is long, this URL gets long, and long URLs can break
#Instead, you can break this up into two steps, first uploading the list of IDs
→using EPost
#(this uses an HTML post internally, rather than an HTML get, getting round the
→long URL problem).
#With the history support, you can then refer to this long list of IDs, and
→download the associated data with EFetch.
from Bio import Entrez
Entrez.email = "snassirnia@outlook.com"      # Always tell NCBI who you are
#id_list = ['1519314819', '568815592', '568815569', '568815567', '568815564',
→'568815561', '568815551', '568815529', '568815454', '170014716',
→'236459493', '1387682811', '1387681679', '1387680719', '1101482042',
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print(Entrez.epost("nuccore", id=".join(id_list)).read())

```

```

<?xml version="1.0" encoding="UTF-8" ?>
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[139]:

```

#from Bio import Entrez
#Entrez.email = "snassirnia@outlook.com" # Always tell NCBI who you are
#handle = Entrez.esearch(db='nuccore', term="Homo_sapiens[Orgn] and TNF[Gene]",
#usehistory="y", idtype="acc")
#record = Entrez.read(handle)
#handle.close()

#fetch_handle = Entrez.efetch(db='nuccore',
#                               rettype="xml", retmode="xml",
#                               retstart=start, retmax=batch_size,
#                               webenv=webenv, query_key=query_key,
#                               idtype="acc")
#data = fetch_handle.read()
#fetch_handle.close()
#out_handle.write(data)
#out_handle.close()

```

[140]:

```
#??Entrez.efetch
```

```
[142]: handle = Entrez.efetch(db="nuccore", id=['1519314819', '568815592',  
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→retmode='xml')  
print(handle.read())
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