**UCSC Genome Browser**

**Looking for a gene and displaying different features**

For human NR4A2 gene:

1. Locate the gene in the human genome

<https://genome.ucsc.edu/cgi-bin/hgGateway>

Select human. Human Assembly Dec 2013 NR4A2

2. Hide all tracks and display the RefSeq gene (compact)in the genome browser

Hide all. RefSeq gene. Pack.Refresh.

3. Indicate the coordinates of the gene in the genome

[chr2:156324437-156332721](https://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=304480531_uACX9UJLLcWzk3AsAfjmYRsEaYv3&db=hg38&position=chr2%3A156324437-156332721)

4. What’s the lenght of the gene?

8285

5. Is the gene transcribed in the main strand or in the complementary strand?

Complementary strand

6. Obtain main infomation and links of human NR4A2 gene (OMIM, PubMed)

<http://omim.org/entry/601828>

7. Download gene sequence, with the introns in lower case and the exons in upper case

>hg38\_ncbiRefSeqCurated\_NM\_006186.4 range=chr2:156324437-156332721 5'pad=0 3'pad=0 strand=- repeatMasking=none

AAGCCACATAAACAAAGGCACATTGGCGGCCAGGGCCAGTCCGCCCGGCG

GCTCGCGCACGGCTCCGCGGTCCCTTTTGCCTGTCCAGCCGGCCGCCTGT

CCCTGCTCCCTCCCTCCGTGAGGTGTCCGGGTTCCCTTCGCCCAGCTCTC

CCACCCCTACCCGACCCCGGCGCCCGGGCTCCCAGAGGGAACTGCACTTC

GGCAGAGTTGAATGAATGAAGACAGACGCGGAGAACTCCTAAgtgagtag

atgcagcccatgcagttcgccttcttttatgctttttccttcttttgcac

gtctcttctttccacttgtgtgggacaggttctctggaagtgggagccag

aggcttctagtgagagtgggaccgaaggatggggagtgcgtgcgcgcagt

taccggggggcatttgttcgaactccggctttggcactagtggggagttg

gctctcgacagaggtttccaggctcctcattggtggacgtggaagggaga

ctccacagtttgggagctgaggactagcccgcggaaatgtgcgcaaagtt

tgctgttagtgaggaattgattgtggcctgtgaacacggagactccaagt

cctatgtatacgagggaagctgcccacaaactgacagggagaggaagttc

ttcagtttatgcgttgcttgggaactgtgtctccgcggctggccagcgcg

cgatgtttcccgggtattgttgagtaagggtggtgttggtagcgtgtcct

gttactaagttgcctgaaatttctggttttgacatatgctgtccttgggt

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ccacccccaccaccactatgaagcaagattgtgggggaggggaaagaata

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cctaagatggaaatgacctctccacctacactgtagcaaaggggccagtt

cattacatcataaatgttaaatgagttcatggactagctttcctcttgca

ggatcttctctctgcaaggatttacacagtgcaatgggtggtattttctg

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TTACGACACTGTCCACCTTTAATTTCCTCGAAAACGCCTGTAACTCGGCT

GAAGgttagtgcaacttcatttctttcctttactctccagagctccccaa

acatcaagaaacaggacaaggcaaaccctgtaacttaaggtttgcccgac

ccatcgccttcgggaacaactttctcattgtgaaattcaacttcatttct

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gttagtctttccacgccctaaactgttgttctgcagcattctctctctcc

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gctgagtgtgttatcaccctgtttcatttccagCCATGCCTTGTGTTCAG

GCGCAGTATGGGTCCTCGCCTCAAGGAGCCAGCCCCGCTTCTCAGAGCTA

CAGTTACCACTCTTCGGGAGAATACAGCTCCGATTTCTTAACTCCAGAGT

TTGTCAAGTTTAGCATGGACCTCACCAACACTGAAATCACTGCCACCACT

TCTCTCCCCAGCTTCAGTACCTTTATGGACAACTACAGCACAGGCTACGA

CGTCAAGCCACCTTGCTTGTACCAAATGCCCCTGTCCGGACAGCAGTCCT

CCATTAAGGTAGAAGACATTCAGATGCACAACTACCAGCAACACAGCCAC

CTGCCCCCCCAGTCTGAGGAGATGATGCCGCACTCCGGGTCGGTTTACTA

CAAGCCCTCCTCGCCCCCGACGCCCACCACCCCGGGCTTCCAGGTGCAGC

ACAGCCCCATGTGGGACGACCCGGGATCTCTCCACAACTTCCACCAGAAC

TACGTGGCCACTACGCACATGATCGAGCAGAGGAAAACGCCAGTCTCCCG

CCTCTCCCTCTTCTCCTTTAAGCAATCGCCCCCTGGCACCCCGGTGTCTA

GTTGCCAGATGCGCTTCGACGGGCCCCTGCACGTCCCCATGAACCCGGAG

CCCGCCGGCAGCCACCACGTGGTGGACGGGCAGACCTTCGCTGTGCCCAA

CCCCATTCGCAAGCCCGCGTCCATGGGCTTCCCGGGCCTGCAGATCGGCC

ACGCGTCTCAGCTGCTCGACACGCAGGTGCCCTCACCGCCGTCGCGGGGC

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CCAACACTACGGCGTGCGCACCTGTGAGGGCTGCAAAGGCTTCTTTAAGg

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gTTCCAGGCGAACCCTGACTATCAAATGAGTGGAGATGACACCCAGCATA

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TGGGCAGAGAAGATCCCTGGCTTCGCAGACCTGCCCAAAGCCGACCAAGA

CCTGCTTTTTGAATCAGCTTTCTTAGAACTGTTTGTCCTTCGATTAGCAT

ACAGgtaataagggagggagggagacaatccagggaggctgtgagagaaa

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GCAATGCGTTCGTGGCTTTGGGGAATGGATTGATTCCATTGTTGAATTCT

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GCTGCCCTGGCTATGGTCACAGgtcagtactgcaggcgcagggcgcttcc

cctccagaactgcctagcaggatttgtcctgagtttcccttgtcacagat

tctccttggttttgccaactagctaactgtcttgtacattcttcttttgt

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GGAAGCTCCCAGAACTTCGTACCCTTTGCACACAGGGGCTACAGCGCATT

TTCTACCTGAAATTGGAAGACTTGGTGCCACCGCCAGCAATAATTGACAA

ACTTTTCCTGGACACTTTACCTTTCTAAGACCTCCTCCCAAGCACTTCAA

AGGAACTGGAATGATAATGGAAACTGTCAAGAGGGGGCAAGTCACATGGG

CAGAGATAGCCGTGTGAGCAGTCTCAGCTCAAGCTGCCCCCCATTTCTGT

AACCCTCCTAGCCCCCTTGATCCCTAAAGAAAACAAACAAACAAACAAAA

ACTGTTGCTATTTCCTAACCTGCAGGCAGAACCTGAAAGGGCATTTTGGC

TCCGGGGCATCCTGGATTTAGAACATGGACTACACACAATACAGTGGTAT

AAACTTTTTATTCTCAGTTTAAAAATCAGTTTGTTGTTCAGAAGAAAGAT

TGCTATAATGTATAATGGGAAATGTTTGGCCATGCTTGGTTGTTGCAGTT

CAGACAAATGTAACACACACACACATACACACACACACACACACACAGAG

ACACATCTTAAGGGGACCCACAAGTATTGCCCTTTAACAAGACTTCAAAG

TTTTCTGCTGTAAAGAAAGCTGTAATATATAGTAAAACTAAATGTTGCGT

GGGTGGCATGAGTTGAAGAAGGCAAAGGCTTGTAAATTTACCCAATGCAG

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TTCAGTAATGTCTATATTATATAAATAGTATTTCAGACACTATGTAGTCT

GTTAGATTTTATAAAGATTGGTAGTTATCTGAGCTTAAACATTTTCTCAA

TTGTAAAATAGGTGGGCACAAGTATTACACATCAGAAAATCCTGACAAAA

GGGACACATAGTGTTTGTAACACCGTCCAACATTCCTTGTTTGTAAGTGT

TGTATGTACCGTTGATGTTGATAAAAAGAAAGTTTATATCTTGATTATTT

TGTTGTCTAAAGCTAAACAAAACTTGCATGCAGCAGCTTTTGACTGTTTC

CAGAGTGCTTATAATATACATAACTCCCTGGAAATAACTGAGCACTTTGA

ATTTTTTTTATGTCTAAAATTGTCAGTTAATTTATTATTTTGTTTGAGTA

AGAATTTTAATATTGCCATATTCTGTAGTATTTTTCTTTGTATATTTCTA

GTATGGCACATGATATGAGTCACTGCCTTTTTTTCTATGGTGTATGACAG

TTAGAGATGCTGATTTTTTTTCTGATAAATTCTTTCTTTGAGAAAGACAA

TTTTAATGTTTACAACAATAAACCATGTAAATGAA

8. Extract the promoting region of the gene (1500 bases upstream)

>hg38\_ncbiRefSeqCurated\_NM\_006186.4 range=chr2:156332722-156334221 5'pad=0 3'pad=0 strand=- repeatMasking=none

acacgagtaggggggcaagttgcaaaagggtcccggctgcctggaaacga

gccacaccgagaaaggaggggcggctgggacgctctgcgcgagtagaaaa

gcgggggcggctccgaactctccctcccaaggcccagccgctggaagccc

cgcgggagaagccctaggaagccctcccagctccggccgggagacgggga

gggggcttgccctccggagctgcggcgtttcctttgctagaaagctccct

gcgctctcggcgtggctaggggaaatgacttgcaaagcagaagcggcggc

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cctctcctggctgggctgtaggctcacaccttacgctttgcggagacgct

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taagattgaggctgtgatagaccttgtgtttcaaacgaagatcgatttat

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aaggcgcacctgttgcctgctgctcggctgcattgtctgcgaaaggaaaa

ggggcgacgcttcactctgacttttggggtttctaaagagctgggtcacg

gtcactgtctaccctctccccttcctctcccccccccccgcaagcaccac

gtcctccatcgaacgtgggcactgcatggaaataaggaaacatagaaaaa

taagccctacccccactcccattccctttcagatgggagtgtggggggtg

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gtcacacctctttcggaaaaaaaaaaagaaaagaaaaaaaacaccaaaaa

ccacccaagctggctaccaaggtgaacgcagagcggttcccaccttaaaa

tcggccctgctcgtgacgtcaggtcggaaatataccaaagcgagcgcggg

ccaggagtccagggagcgcggcagcgcggcgattgggcggcgggccgctg

acgcgcgctgacgcgcggagactttaggtgcatgttggcagcggcagcgc

9. Download the sequence of the predicted protein

>NP\_006177 length=598

MPCVQAQYGSSPQGASPASQSYSYHSSGEYSSDFLTPEFVKFSMDLTNTE

ITATTSLPSFSTFMDNYSTGYDVKPPCLYQMPLSGQQSSIKVEDIQMHNY

QQHSHLPPQSEEMMPHSGSVYYKPSSPPTPTTPGFQVQHSPMWDDPGSLH

NFHQNYVATTHMIEQRKTPVSRLSLFSFKQSPPGTPVSSCQMRFDGPLHV

PMNPEPAGSHHVVDGQTFAVPNPIRKPASMGFPGLQIGHASQLLDTQVPS

PPSRGSPSNEGLCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCL

ANKNCPVDKRRRNRCQYCRFQKCLAVGMVKEVVRTDSLKGRRGRLPSKPK

SPQEPSPPSPPVSLISALVRAHVDSNPAMTSLDYSRFQANPDYQMSGDDT

QHIQQFYDLLTGSMEIIRGWAEKIPGFADLPKADQDLLFESAFLELFVLR

LAYRSNPVEGKLIFCNGVVLHRLQCVRGFGEWIDSIVEFSSNLQNMNIDI

SAFSCIAALAMVTERHGLKEPKRVEELQNKIVNCLKDHVTFNNGGLNRPN

YLSKLLGKLPELRTLCTQGLQRIFYLKLEDLVPPPAIIDKLFLDTLPF

10. Compute and display the conservation ( mammals).

Comparative Genomics. Hide All. Mammals.

11. Display all SNPs in NR4A2 gene. Display only missense SNPs.

Variation. All tracks in this selection. Gnomad. Select Gnomad3. Select missense.

**Using BLAT**

1. Download the sequence of human NR4A2 gene

2. Use BLAT to align NR4A2 gene to the mouse genome, in order to obtain the corresponding orthologous gene. Indicate the coordinates of the orthologous gene in the mouse genome.

Tools<Blat<Genome Mouse

chr2:57106835 57114947

**Using Custom Tracks**

1. Add a custom track for NR4A2 gene. Color the track in pink.

Add custom track.

[chr2](https://genome.ucsc.edu/cgi-bin/hgTracks?hgsid=560166015_BwzBxRpCAzd2AIKdSQz9Iou7aD0S&db=hg38&position=chr2%3A156324432-156332775) 156324437 156332721

Track type=bed Graph name=gene description=text color=200,50,200

2. Add a track with the promoter region of human NR4A2 gene. Color the track in green.

Add custom track.

chr2:chr2:156332722-156333721

Track type=bed Graph name=promoter description=text color=’0,200,0’

3. For human NR4A2 gene, add a custom track for 5’UTR, 3’UTR and CDS.

track type=bed Graph name=cds description=text color=’200,50,200’

chr2:156325744 156330186

track type=bed Graph name=3utr description=text color=’100,50,100’

chr2:156324437 156325743

track type=bed Graph name=5utr description=text color=’100,200,100’

chr2:156330187 156332721

**Using UCSC Table Browser**

1. Download the sequence of all Homo Sapiens RefSeq genes.

Tools<Table Browser

Summay Statistics

Gene and gene prediction. RefSeq Genes. Region: genome. Output file: Sequence

2. Download the coordinates of the CDS for all RefSeq genes.

Tools<Table Browser

Gene and gene prediction. RefSeq Genes. Region: genome. Output file: Select fields. Name and cds start, cds end