# Jacek Radajewski
## Student number: 43612772
## BIOL3014 – Advanced Bioinformatics
## Practical 2

## Table of Contents

# Exercise 1B

HPRD background distribution has been created from the set of sequences found the HPRD.fa FASTA file.  Distribution was created by the get_distrib_from_fasta function shown in code listing below.


First graph shows both, HPRD and BLOSUM62 derived distributions.  L (Leucine) is the most frequent amino acid in both distributions with the frequency of 0.1 and W (Tryptophan) is the least frequent amino acid with a frequency of about 0.01.

### HPRD & BLOSUM62 Distributions
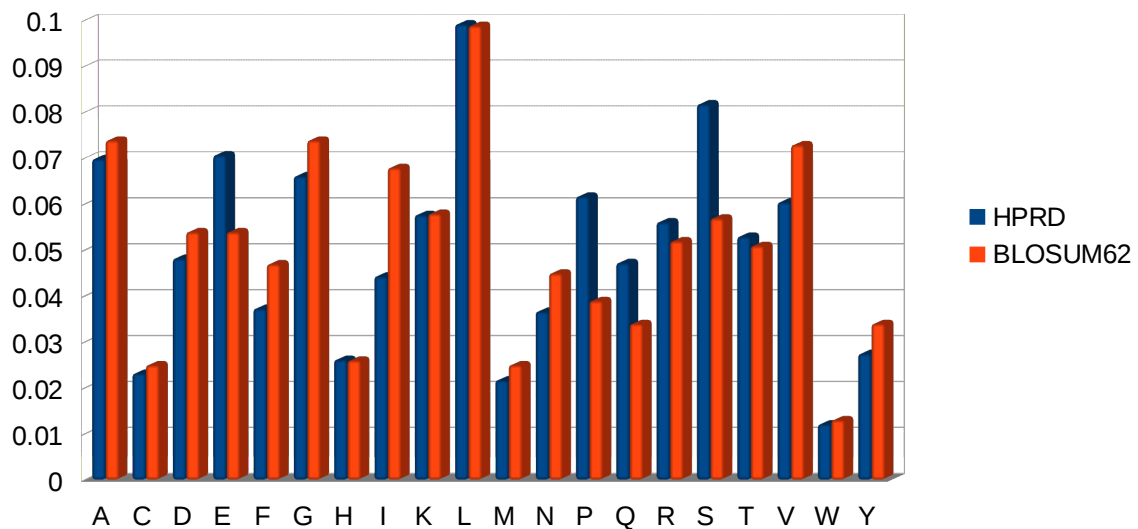


The following bar graph shows deltas between the HPRD and BLOSUM62 distributions with positive value representing higher frequencies in HPRD and negative values representing higher frequencies in the BLOSUM62 background distributiobns.

### BLOSUM62 & HPRD Background Distribution Deltas
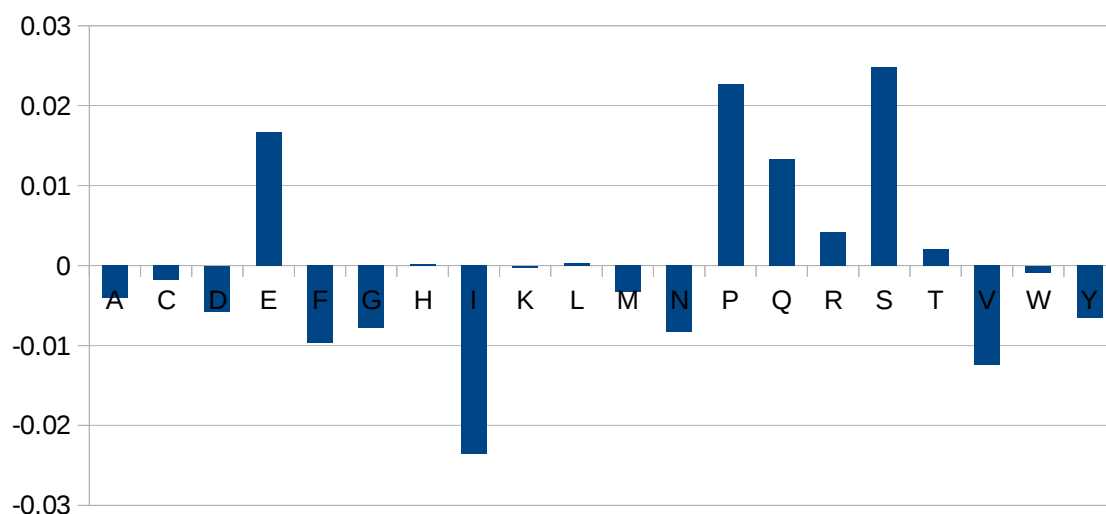
## Code

```python
'''
Created on 05/08/2014

@author: jacekrad
'''
from sequence import *
from prob import *
from symbol import *
from webservice import *
from sys import stderr

blosum62_background = readDistrib("blosum62.distrib")


def get_distrib_from_fasta(fasta_filename):
    '''
    This function creates a distribution from a set sequences
    read from a FASTA file.  All sequences are read and every
    residue is used to construct the distribution.  This
    function assumes that the FASTA file contains protein alphabet
    sequence.  The function returns a Distrib object containing the
    generated distribution.
    '''
    protein_counts = {}
    # initilise the dictionary with zeros
    for residue in Protein_Alphabet.symbols:
        protein_counts[residue] = 0

    sequences = readFastaFile(fasta_filename)
    for sequence in sequences:
        for letter in sequence:
            protein_counts[letter] += 1

    return Distrib(Protein_Alphabet, protein_counts)

hprd_background = get_distrib_from_fasta("HPRD.fa")

hprd_background.writeDistrib("HPRD.distrib")

print hprd_background
print blosum62_background

# compare the two distributions by calculating deltas for each amino acid
for amino_acid in hprd_background.alpha:
    delta = hprd_background[amino_acid] - blosum62_background[amino_acid]
    sys.stderr.write(amino_acid + "," + str(delta) + "\n")
```

## Raw Results

| AA | HPRD | BLOSUM62 | DELTA |
|----|------|----------|-------|
| A | 0.0698457839 | 0.0738522954 | -0.0040065115 |
| C | 0.0231226168 | 0.0249500998 | -0.001827483 |
| D | 0.0481476988 | 0.0538922156 | -0.0057445168 |
| E | 0.070644439 | 0.0538922156 | 0.0167522234 |
| F | 0.0372439945 | 0.0469061876 | -0.0096621931 |
| G | 0.0660838698 | 0.0738522954 | -0.0077684256 |
| H | 0.0261162961 | 0.0259481038 | 0.0001681923 |
| I | 0.044277412 | 0.0678642715 | -0.0235868595 |
| K | 0.0576285349 | 0.0578842315 | -0.0002556966 |
| L | 0.0991363806 | 0.0988023952 | 0.0003339854 |
| M | 0.0216587524 | 0.0249500998 | -0.0032913474 |
| N | 0.0366184744 | 0.0449101796 | -0.0082917052 |
| P | 0.0616506862 | 0.0389221557 | 0.0227285305 |
| Q | 0.0471915942 | 0.0339321357 | 0.0132594584 |
| R | 0.0560535647 | 0.0518962076 | 0.0041573571 |
| S | 0.0817464702 | 0.0568862275 | 0.0248602426 |
| T | 0.0529277466 | 0.0508982036 | 0.002029543 |
| V | 0.0604048745 | 0.0728542914 | -0.0124494169 |
| W | 0.0120893881 | 0.0129740519 | -0.0008846638 |
| Y | 0.0274114222 | 0.0339321357 | -0.0065207135 |

## Execution Output

# Exercise 1C

HTH protein chosen was P56179 (http://www.uniprot.org/uniprot/P56179) whose sequence is:

```
MSHSQHSPYLQSYHNSSAAAQTRGDDTDQQKTTVIENGEIRFNGKGKKIRKPRTIYSSLQ
LQALNHRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLLKQGSNPHESDPL
QGSAALSPRSPALPPVWDVSASAKGVSMPPNSYMPGYSHWYSSPHQDTMQRPQMM
```

Homeobox protein DLX-6 is is located between positions 1 and 175 and the DNA binding Homeobox is between positions 49 and 108.

The homeobox is highlighted in the jpred output below with alpha helix predictions shown as well.

## Exercise 1D

Document code is shown below.

```python
'''
Created on 06/08/2014

@author: jacekrad
'''
from gibbs import *
from sequence import *

seqs = readFastaFile("hth_40.fa", Protein_Alphabet)

W = 10 # the width of the motif sought

# create a GibbsMotif object from a list of sequences
# and of length W
g = GibbsMotif(seqs, W)

# execute the core Gibbs Sampling algorithm to discover
# the motif
q = g.discover()

# get the probability distribution for the background used
# in the discovery calculated above
p = g.getBackground()

# getAlignments is called and alignment for sequences seq
# is calculated from the foreground q and background p
# the resulting alignment is assigned to a
a = getAlignment(seqs, q, p)

k = 0
for seq in seqs:
    print "%s \t%s" % (seq.name, seq[a[k]:a[k]+W])
    k += 1
```

# Exercise 1E

## *Code*

## Small change to gibbs.py

```python
                #print "LL @ %5d=\t%5.2f" % (round, LL)

                if LL > self.maxLL:
                    self.maxLL = LL
```

## exercise1f.py

```python
'''
Created on 07/08/2014

@author: jacekrad
'''
from gibbs import *
from sequence import *
import sys

seqs = readFastaFile("hth_40.fa", Protein_Alphabet)
width_values = [10, 24, 30]

# list of the files where we dump the results
# these will go to stderr for logo post processing
alignment_filenames = []

# maximum values for saving
maxLL = 0.0
max_p = None
max_q = None
p_filename = None
q_filename = None

for W in width_values:
    for i in range(1,4): # create 3 sets of results
        g = GibbsMotif(seqs, W)
        q = g.discover()
        p = g.getBackground()
        a = getAlignment(seqs, q, p)
        k = 0
        results_filename = "ex1e-W" + str(W) + "-iteration" + str(i) +
".aln"
        if g.maxLL > maxLL:
            maxLL = g.maxLL
            max_p = p
            max_q = q
            p_filename = "ex1e-W" + str(W) + "-iteration" + str(i) + "-p-
max.distrib"
            q_filename = "ex1e-W" + str(W) + "-iteration" + str(i) + "-q-
max.distrib"
            print "New maxLL distribution is ", q_filename
        sys.stderr.write(results_filename + "\n")
        results_file = open(results_filename, 'w')
```

```python
        for seq in seqs:
            results_file.write("%s \t%s\n" % (seq.name, seq[a[k]:a[k]+W]))
            k += 1
        results_file.close()

# save distributions with highest log odds
print "Writing best distributions to ", p_filename, " and ", q_filename
max_p.writeDistrib(p_filename)
writeDistribs(max_q, q_filename)
```

## BASH
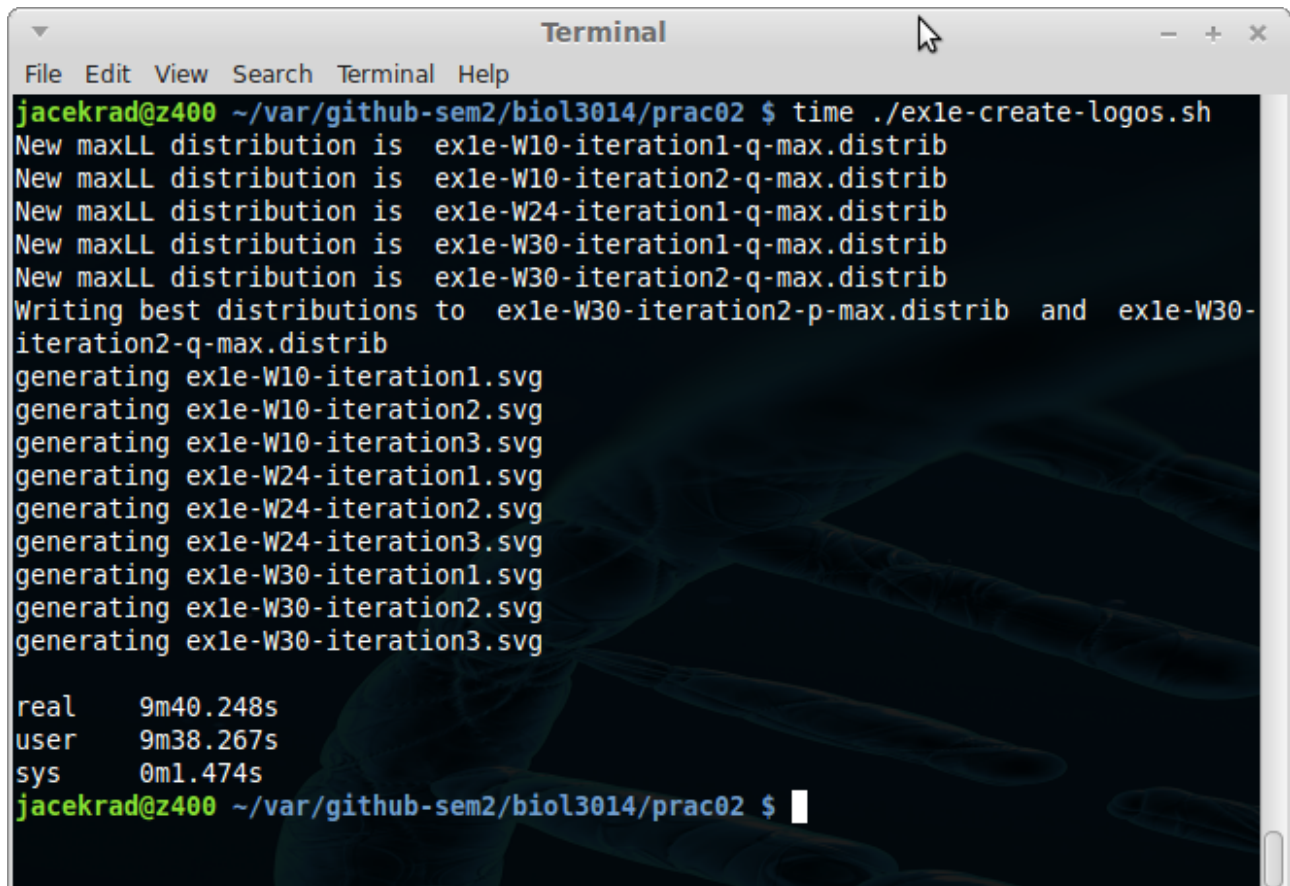
```bash
#!/bin/bash

python exercise1e.py 2>alignment_filenames.txt

for alignment_filename in `cat alignment_filenames.txt`; do
    export logo_filename=`echo ${alignment_filename} | cut -f 1 -d "."`.svg
    echo "generating ${logo_filename}"
    weblogo --format=svg < ${alignment_filename} > ${logo_filename}
done
```

## *Execution*

```
jacekrad@z400 ~/var/github-sem2/biol3014/prac02 $ time ./ex1e-create-logos.sh
New maxLL distribution is  ex1e-W10-iteration1-q-max.distrib
New maxLL distribution is  ex1e-W10-iteration2-q-max.distrib
New maxLL distribution is  ex1e-W24-iteration1-q-max.distrib
New maxLL distribution is  ex1e-W30-iteration1-q-max.distrib
New maxLL distribution is  ex1e-W30-iteration2-q-max.distrib
Writing best distributions to  ex1e-W30-iteration2-p-max.distrib  and  ex1e-W30-
iteration2-q-max.distrib
generating ex1e-W10-iteration1.svg
generating ex1e-W10-iteration2.svg
generating ex1e-W10-iteration3.svg
generating ex1e-W24-iteration1.svg
generating ex1e-W24-iteration2.svg
generating ex1e-W24-iteration3.svg
generating ex1e-W30-iteration1.svg
generating ex1e-W30-iteration2.svg
generating ex1e-W30-iteration3.svg

real    9m40.248s
user    9m38.267s
sys     0m1.474s
jacekrad@z400 ~/var/github-sem2/biol3014/prac02 $
```

## *Logos*

Inspecting motifs of different widths we can see a pattern of highly conserved region WFQNRR (and slightly less conserved surrounding resides) appearing in most logos. The exceptions are two of the W=10 and one of the W=30 logos. Inspecting the original amino acid sequence we can find this region starting at position 96 which is between the second and third alpha helices.

Furthermore, even for the logos of the same width motif is shifted, that starts and ends in different positions.

For the short width of W=10 two of the three motifs do not show the highly conserved region WFQNRR. The first of the logos does not seem to overlap either of the other two and there is an overlap of three positions between logo 2 and logo 3.

When W=30, two of the three logos provide a significant overlap of 28 positions. The overlap is from position 69 to 97 of the original sequence and covers 2 helices as highlighted in a blue box below.



**W=10**







**W=24**

W=30
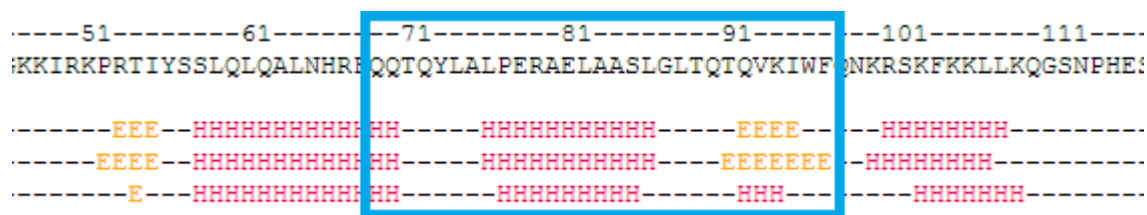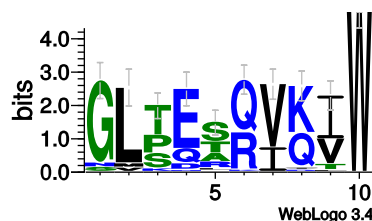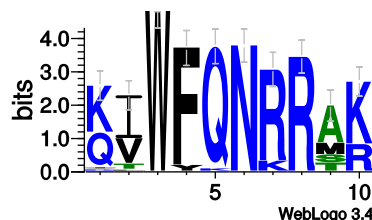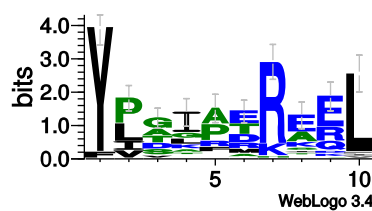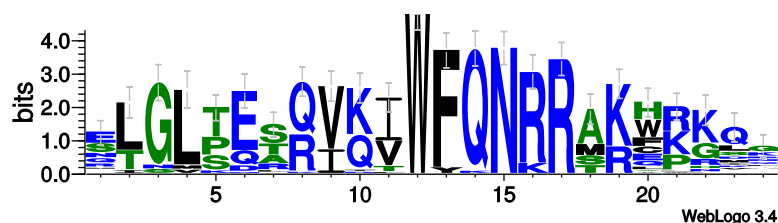
# Exercise 1f

To construct the two PWMs I have used the foreground saved in previous questions.  For the backgrounds I've used the HPRD background from question 1B (PWM2) and background saved in last exercise 1e (PWM1).

PWM1 returned 143 proteins with a total of 151 hits. PWM2 returned 138 proteins with a total of 143 hits. PWM1 returned more hits than PWM2 as it used background generated from the hth_40.fa so we can expect for it to be more highly tuned to the HTH motif.

I chose Q92826  as one of the proteins and checked in uniprot (http://www.uniprot.org/uniprot/Q92826).   It is a *Homeobox protein Hox-B13* and contains one DNA binding domain hence it most likely is a Helix Turn Helix.  Protein 3D structure is shown below.
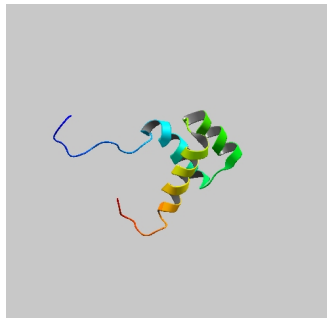


Examining the top GO Terms below we can see that the motif is for a nucleus, DNA-binding protein and takes part in regulation of transcription which is consistent with HTH proteins.  This motif seems to be some sort of transcription factor.

```
GO:0003677  143    DNA binding
GO:0005634  143    nucleus
GO:0006355  140    regulation of transcription, DNA-templated
GO:0043565  135    sequence-specific DNA binding
GO:0006351  107    transcription, DNA-templated
GO:0007275  106    multicellular organismal development
GO:0003700  70     sequence-specific DNA binding transcription factor activity
GO:0045944  64     positive regulation of transcription from RNA polymerase II promoter
GO:0009952  40     anterior/posterior pattern specification
GO:0005515  34     protein binding
GO:0000122  30     negative regulation of transcription from RNA polymerase II promoter
GO:0005737  29     cytoplasm
GO:0048704  27     embryonic skeletal system morphogenesis
GO:0006366  26     transcription from RNA polymerase II promoter
GO:0003682  23     chromatin binding
GO:0005667  23     transcription factor complex
GO:0045893  20     positive regulation of transcription, DNA-templated
GO:0006357  20     regulation of transcription from RNA polymerase II promoter
```

## Code

```
'''
Created on 06/08/2014

@author: s4361277
'''
from sequence import *
from reportlab.lib.set_ops import intersect

foreground = readDistribs("ex1e-W30-iteration2-q-max.distrib")
q1e_background = readDistrib("ex1e-W30-iteration2-p-max.distrib")
hprd_background = readDistrib("HPRD.distrib")

# create two Position Wighted Matrices.  First used the background
# saved in question 1e and the second PWM is created using the
# background from question 1b, ie from the HPRD sequence data
pwm1 = PWM(foreground, q1e_background)
pwm2 = PWM(foreground, hprd_background)

print "PWM1\n", pwm1, "\nPWM2\n", pwm2
ids1 = [] # ids with hits from PWM1 search
ids2 = [] # ids with hits from PWM2 search

hprd_sequences = readFastaFile('HPRD.fa', Protein_Alphabet)
hth_sequences = readFastaFile('hth_40.fa', Protein_Alphabet)
hth_ids = [seq.name for seq in hth_sequences]

# these are the sequences we are going to search.  These are the
# HPRD sequences that do not have an entry in our hth_40.fa FASTA
# file, which was our training set
search_sequences = [seq for seq in hprd_sequences if not(seq.name in hth_ids)]

print "will search", len(search_sequences), "sequences out of a total of", \
    len(hprd_sequences), "entries found."

# because each sequence is a match we'll count the total number of hits
# for the two different sequences.  hits is not the same as the number of
# sequences matched as a sequence can be matched in more than one place
pwm1_hit_count = 0
pwm2_hit_count = 0

for sequence in search_sequences:
    hits1 = pwm1.search(sequence) # search using first PWM
    hits2 = pwm2.search(sequence) # search using second PWM
    pwm1_hit_count += len(hits1)
    pwm2_hit_count += len(hits2)
    # for both pwm1 and pwm2 search hits we only print the first of the hits
    # for each sequence as we were not asked to print them all.  There will
    # be sequences where the motif provides hits in more than one location
    if len(hits1) > 0:
        print "PWM1 hit: %s \t%d \t%s \t%5.3f" % (sequence.name, \
                                                  hits1[0][0], hits1[0][1], \
                                                  hits1[0][2])
        ids1.append(sequence.name)
    if len(hits2) > 0:
        print "PWM2 hit: %s \t%d \t%s \t%5.3f" % (sequence.name, \
                                                  hits2[0][0], hits2[0][1], \
                                                  hits2[0][2])
        ids2.append(sequence.name)

print "number of sequences matched by pwm1 and pwm2, and total unique", \
    len(ids1), len(ids2), len(intersect(ids1, ids2))
print "total hits by pwm1 and pwm2", pwm1_hit_count, pwm2_hit_count
print ids1
print "getting report"
report = getGOReport(ids1)
print "report rows"
for row in report:
    print "%s \t%d \t%s" % row
```

# Full Output

Font size and colour have been used to highlight relevant parts of the output.

```
PWM1
A    -4.59  -1.55  -4.59  -4.59  -4.59  +0.36  -0.48  +0.97  -0.48  -4.59  +0.61  -4.59  -4.59  +1.93  +0.81  +0.49  -4.59  -4.59  -4.59  -4.59  -4.59  +0.36  -4.59  -4.59  -4.59  -4.59  -4.59  -4.59  -4.59  -4.59
C    +0.76  +1.42  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29  -2.29
D    -3.17  +0.54  -3.17  -3.17  -3.17  +1.44  -3.17  -0.13  +1.77  -3.17  -0.13  +0.54  -3.17  -3.17  -3.17  -0.13  -3.17  -0.13  -3.17  -3.17  +0.94  -3.17  -3.17  -3.17  -3.17  -3.17  -3.17  -3.17  -3.17  -3.17
E    +0.27  -3.85  -3.85  -3.85  -3.85  -3.85  -3.85  -3.85  +1.55  -3.85  +1.93  +2.10  -3.85  -3.85  -0.80  +0.27  -3.85  -3.85  -3.85  -3.85  +2.48  -3.85  -3.85  -3.85  -3.85  -3.85  -3.85  -3.85  -3.85  -3.85
F    -0.03  -3.07  -3.07  +0.64  -3.07  -3.07  -3.07  +1.32  -3.07  -3.07  -3.07  -3.07  -0.03  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  +3.54  -3.07  -3.07
G    -4.30  -4.30  -4.30  -4.30  -4.30  +1.09  +0.31  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -1.26  -4.30  +2.22  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30  -4.30
H    -0.03  -3.07  +1.54  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -0.03  -3.07  -3.07  -3.07  -3.07  +0.64  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07  -3.07
I    +1.19  -2.52  -2.52  -2.52  +2.28  -2.52  +3.37  -2.52  -2.52  -2.52  +1.19  -2.52  +0.52  -2.52  +0.52  -2.52  +2.78  -2.52  +2.56  -2.52  -2.52  -2.52  -2.52  +1.59  +0.52  +3.66  -2.52  -2.52  -2.52  -2.52
K    +1.93  -0.43  +1.73  -3.47  -3.47  +0.92  -0.43  -3.47  +1.14  +1.14  +0.24  -3.47  -3.47  -0.43  -0.43  -3.47  -3.47  +0.24  -3.47  -3.47  -3.47  -3.47  +2.62  -3.47  -3.47  -3.47  -3.47  -3.47  -3.47  -3.47
L    -4.21  -4.21  -1.17  -4.21  +1.27  -4.21  +0.41  -4.21  -4.21  -4.21  -1.17  -4.21  +2.37  -4.21  -1.17  -4.21  +2.05  -4.21  +2.12  -4.21  -4.21  -0.50  -4.21  -4.21  -4.21  -4.21  -4.21  -4.21  -4.21  -4.21
M    -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  +1.95  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  +1.27  -2.44  -2.44  +1.27  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44  -2.44
N    -2.70  +2.86  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  +1.69  -2.70  +1.01  -2.70  -2.70  +0.34  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  -2.70  +3.96
P    -4.57  -4.57  +0.63  -4.57  +1.21  -4.57  -1.52  +0.92  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  +0.83  -4.57  -4.57  +0.52  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57  -4.57
Q    +0.81  +1.14  +1.39  -3.81  -3.81  -3.81  -3.81  -0.76  -3.81  -3.81  +0.99  -3.81  -3.81  +1.76  +0.81  -3.81  -3.81  -3.81  -3.81  +1.14  -3.81  +2.33  -3.81  +1.97  -3.81  -3.81  -3.81  +2.85  -3.81
R    +1.30  -4.10  +0.70  -4.10  -4.10  -4.10  -1.05  +0.52  +0.52  +2.40  -4.10  +1.10  -4.10  -4.10  +0.52  +0.30  -4.10  -4.10  -4.10  -4.10  -4.10  +0.52  +1.67  -4.10  -4.10  -4.10  -4.10  -4.10  -4.10  -4.10
S    -4.37  -0.26  -4.37  -4.37  -4.37  +0.43  -4.37  -4.37  -1.32  -4.37  -0.26  -1.32  -4.37  +0.25  -1.32  +0.83  -4.37  -0.65  -4.37  +0.83  -4.37  +0.71  -4.37  -4.37  -4.37  -4.37  -4.37  -4.37  -4.37  -4.37
T    -3.53  +1.77  -3.53  -3.53  -3.53  +1.41  +0.18  -0.49  +1.55  -3.53  +0.18  -3.53  -3.53  -3.53  -0.49  +0.58  -3.53  -3.53  +2.30  -3.53  +1.66  -3.53  -3.53  -3.53  +0.58  -3.53  -3.53  -3.53  -3.53  -3.53
V    -3.24  -3.24  -3.24  -3.24  +1.37  +0.87  -3.24  -3.24  -3.24  -3.24  -3.24  -3.24  -0.20  -3.24  -0.20  -3.24  -3.24  -3.24  -0.20  -3.24  -3.24  -3.24  -3.24  +3.34  -3.24  +2.24  -3.24  -3.24  -3.24  -3.24
W    -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  +0.68  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  -2.37  +4.30  -2.37  -2.37  -2.37
Y    +1.71  -2.69  -2.69  +3.92  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  +1.03  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  -2.69  +1.03  -2.69  -2.69
```

```
PWM2
A    -4.02  -0.98  -4.02  -4.02  -4.02  +0.93  +0.09  +1.54  +0.09  -4.02  +1.18  -4.02  -4.02  +2.50  +1.38  +1.06  -4.02  -4.02  -4.02  -4.02  -4.02  +0.93  -4.02  -4.02  -4.02  -4.02  -4.02  -4.02  -4.02  -4.02
C    +0.13  +0.80  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92  -2.92
D    -3.65  +0.06  -3.65  -3.65  -3.65  +0.96  -3.65  -0.61  +1.30  -3.65  -0.61  +0.06  -3.65  -3.65  -3.65  -0.61  -3.65  -0.61  -3.65  -3.65  +0.46  -3.65  -3.65  -3.65  -3.65  -3.65  -3.65  -3.65  -3.65  -3.65
E    +0.08  -4.03  -4.03  -4.03  -4.03  -4.03  -4.03  -4.03  +1.36  -4.03  +1.74  +1.91  -4.03  -4.03  -0.99  +0.08  -4.03  -4.03  -4.03  -4.03  +2.30  -4.03  -4.03  -4.03  -4.03  -4.03  -4.03  -4.03  -4.03  -4.03
F    -0.35  -3.39  -3.39  +0.32  -3.39  -3.39  -3.39  +1.00  -3.39  -3.39  -3.39  -3.39  -0.35  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  -3.39  +3.21  -3.39  -3.39
G    -3.97  -3.97  -3.97  -3.97  -3.97  +1.43  +0.65  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -0.92  -3.97  +2.56  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97  -3.97
H    +0.01  -3.04  +1.58  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  +0.01  -3.04  -3.04  -3.04  -3.04  +0.67  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04  -3.04
I    +0.15  -3.57  -3.57  -3.57  +1.23  -3.57  +2.32  -3.57  -3.57  -3.57  +0.15  -3.57  -0.52  -3.57  -0.52  -3.57  +1.74  -3.57  +1.51  -3.57  -3.57  -3.57  -3.57  +0.54  -0.52  +2.61  -3.57  -3.57  -3.57  -3.57
K    +1.57  -0.79  +1.37  -3.83  -3.83  +0.56  -0.79  -3.83  +0.78  +0.78  -0.12  -3.83  -3.83  -0.79  -0.79  -3.83  -3.83  -0.12  -3.83  -3.83  -3.83  -3.83  +2.26  -3.83  -3.83  -3.83  -3.83  -3.83  -3.83  -3.83
L    -4.37  -4.37  -1.33  -4.37  +1.11  -4.37  +0.24  -4.37  -4.37  -4.37  -1.33  -4.37  +2.21  -4.37  -1.33  -4.37  +1.88  -4.37  +1.96  -4.37  -4.37  -0.66  -4.37  -4.37  -4.37  -4.37  -4.37  -4.37  -4.37  -4.37
M    -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  +1.54  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  +0.86  -2.85  -2.85  +0.86  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85  -2.85
N    -3.38  +2.19  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  +1.02  -3.38  +0.34  -3.38  -3.38  -0.33  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  -3.38  +3.28
P    -3.90  -3.90  +1.30  -3.90  +1.87  -3.90  -0.85  +1.59  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  +1.50  -3.90  -3.90  +1.18  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90  -3.90
Q    +0.98  +1.32  +1.57  -3.63  -3.63  -3.63  -3.63  -0.59  -3.63  -3.63  +1.16  -3.63  -3.63  +1.93  +0.98  -3.63  -3.63  -3.63  -3.63  +1.32  -3.63  +2.50  -3.63  +2.14  -3.63  -3.63  -3.63  +3.03  -3.63
R    +1.59  -3.80  +0.99  -3.80  -3.80  -3.80  -0.76  +0.81  +0.81  +2.69  -3.80  +1.40  -3.80  -3.80  +0.81  +0.59  -3.80  -3.80  -3.80  -3.80  -3.80  +0.81  +1.97  -3.80  -3.80  -3.80  -3.80  -3.80  -3.80  -3.80
S    -4.18  -0.07  -4.18  -4.18  -4.18  +0.62  -4.18  -4.18  -1.14  -4.18  -0.07  -1.14  -4.18  +0.43  -1.14  +1.02  -4.18  -0.47  -4.18  +1.02  -4.18  +0.90  -4.18  -4.18  -4.18  -4.18  -4.18  -4.18  -4.18  -4.18
T    -3.75  +1.56  -3.75  -3.75  -3.75  +1.20  -0.03  -0.70  +1.34  -3.75  -0.03  -3.75  -3.75  -3.75  -0.70  +0.37  -3.75  -3.75  +2.09  -3.75  +1.45  -3.75  -3.75  -3.75  +0.37  -3.75  -3.75  -3.75  -3.75  -3.75
V    -3.88  -3.88  -3.88  -3.88  +0.74  +0.23  -3.88  -3.88  -3.88  -3.88  -3.88  -3.88  -0.83  -3.88  -0.83  -3.88  -3.88  -3.88  -0.83  -3.88  -3.88  -3.88  -3.88  +2.70  -3.88  +1.61  -3.88  -3.88  -3.88  -3.88
W    -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  +0.78  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  -2.27  +4.39  -2.27  -2.27  -2.27
Y    +1.31  -3.09  -3.09  +3.52  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  +0.63  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  -3.09  +0.63  -3.09  -3.09
```

**will search 14989 sequences out of a total of 15007 entries found.**

```
PWM1 hit: P20719   215      FNRYLTRRRRIEIAHALCLSERQIKIWFQN    49.944
PWM2 hit: P20719   215      FNRYLTRRRRIEIAHALCLSERQIKIWFQN    44.862
PWM1 hit: P78415   150      KNPYPTKGEKIMLAIITKMTLTQVSTWFAN    19.542
PWM2 hit: P78415   150      KNPYPTKGEKIMLAIITKMTLTQVSTWFAN    13.122
PWM1 hit: Q99453   118      ETHYPDIYTREELALKIDLTEARVQVWFQN    55.278
PWM2 hit: Q99453   118      ETHYPDIYTREELALKIDLTEARVQVWFQN    49.793
PWM1 hit: P43699   181      QQKYLSAPEREHLASMIHLTPTQVKIWFQN    44.607
PWM2 hit: P43699   181      QQKYLSAPEREHLASMIHLTPTQVKIWFQN    42.058
PWM1 hit: P14652   163      FNKYLCRPRRVEIAALLDLTERQVKVWFQN    42.657
PWM2 hit: P14652   163      FNKYLCRPRRVEIAALLDLTERQVKVWFQN    37.672
PWM1 hit: Q96KN3   311      MHPYPTEDEKRQIAAQTNLTLLQVNNWFIN    12.173
PWM2 hit: Q96KN3   311      MHPYPTEDEKRQIAAQTNLTLLQVNNWFIN    6.691
PWM1 hit: O00470   295      THPYPSEEQKKQLAQDTGLTILQVNNWFIN    11.023
PWM2 hit: O00470   295      THPYPSEEQKKQLAQDTGLTILQVNNWFIN    6.099
PWM1 hit: Q05925   323      ANRYITEQRRQTLAQELSLNESQIKIWFQN    32.719
PWM2 hit: Q05925   323      ANRYITEQRRQTLAQELSLNESQIKIWFQN    28.351
PWM1 hit: Q9GZN2   41       YNAYPSEQEKLSLSGQTNLSVLQICNWFIN    9.258
PWM2 hit: Q9GZN2   41       YNAYPSEQEKLSLSGQTNLSVLQICNWFIN    3.409
PWM1 hit: Q07687   172      KTQYLALPERAELAASLGLTQTQVKIWFQN    62.633
```

```
PWM2 hit: Q07687    172     KTQYLALPERAELAASLGLTQTQVKIWFQN     61.557
PWM1 hit: Q9NP08    223     LKRYLSSAERAGLAASLQLTETQVKIWFQN     37.874
PWM2 hit: Q9NP08    223     LKRYLSSAERAGLAASLQLTETQVKIWFQN     36.835
PWM1 hit: O95076    173     KTHYPDVYAREQLALRTDLTEARVQVWFQN     45.707
PWM2 hit: O95076    173     KTHYPDVYAREQLALRTDLTEARVQVWFQN     43.100
PWM1 hit: P40424    256     SNPYPSEEAKEELAKKCGITVSQVSNWFGN     13.475
PWM2 hit: P40424    256     SNPYPSEEAKEELAKKCGITVSQVSNWFGN     9.727
PWM1 hit: P31267    175     FNRYLTRRRRIEIANALCLTERQIKIWFQN     48.067
PWM2 hit: P31267    175     FNRYLTRRRRIEIANALCLTERQIKIWFQN     41.878
PWM1 hit: O95343    226     QDPYPNPSKKRELAQATGLTPTQVGNWFKN     12.033
PWM2 hit: O95343    226     QDPYPNPSKKRELAQATGLTPTQVGNWFKN     11.521
PWM1 hit: P17481    166     FNPYLTRKRRIEVSHALGLTERQVKIWFQN     54.251
PWM2 hit: P17481    166     FNPYLTRKRRIEVSHALGLTERQVKIWFQN     49.895
PWM1 hit: P50458    286     INHNPDAKDLKQLAQKTGLTKRVLQVWFQN     25.625
PWM2 hit: P50458    286     INHNPDAKDLKQLAQKTGLTKRVLQVWFQN     20.756
PWM1 hit: Q15911    2262    ANAYPKDDEFEQLSNLLNLPTRVIVVWFQN     4.113
PWM1 hit: Q00056    235     FNRYLTRRRRIEIAHTLCLSERQVKIWFQN     50.712
PWM2 hit: Q00056    235     FNRYLTRRRRIEIAHTLCLSERQVKIWFQN     45.261
PWM1 hit: Q9UPM6    268     QDNNPDAQTLQKLADMTGLSRRVIQVWFQN     12.884
PWM2 hit: Q9UPM6    268     QDNNPDAQTLQKLADMTGLSRRVIQVWFQN     8.996
PWM1 hit: Q8IYA7    93      DNPYPTKTEKILLALGSQMTLVQVSNWFAN     2.591
PWM1 hit: P17509    166     YNRYLTRRRRIEIAHALCLTERQIKIWFQN     53.146
PWM2 hit: P17509    166     YNRYLTRRRRIEIAHALCLTERQIKIWFQN     47.586
PWM1 hit: P78411    136     KNPYPTKGEKIMLAIITKMTLTQVSTWFAN     19.542
PWM2 hit: P78411    136     KNPYPTKGEKIMLAIITKMTLTQVSTWFAN     13.122
PWM1 hit: P50219    261     LNKYLSRPKRFEVATSLMLTETQVKIWFQN     37.605
PWM2 hit: P50219    261     LNKYLSRPKRFEVATSLMLTETQVKIWFQN     32.379
PWM1 hit: Q8N693    159     ESQYPDVVARERLAARLNLTEDRVQVWFQN     42.474
PWM2 hit: Q8N693    159     ESQYPDVVARERLAARLNLTEDRVQVWFQN     40.001
PWM1 hit: P32243    66      KTRYPDIFMREEVALKINLPESRVQVWFKN     51.648
PWM2 hit: P32243    66      KTRYPDIFMREEVALKINLPESRVQVWFKN     45.426
PWM1 hit: Q9Y2V3    156     KSHYPDVYSREELAGKVNLPEVRVQVWFQN     32.343
PWM2 hit: Q9Y2V3    156     KSHYPDVYSREELAGKVNLPEVRVQVWFQN     28.286
PWM1 hit: Q8NFW5    91      KTHYPDVVMRERLAMCTNLPEARVQVWFKN     37.182
PWM2 hit: Q8NFW5    91      KTHYPDVVMRERLAMCTNLPEARVQVWFKN     32.459
PWM1 hit: P31274    212     FNMYLTRDRRYEVARVLNLTERQVKIWFQN     44.208
PWM2 hit: P31274    212     FNMYLTRDRRYEVARVLNLTERQVKIWFQN     37.736
PWM1 hit: P48742    200     ATPKPTRHIREQLAQETGLNMRVIQVWFQN     19.440
PWM2 hit: P48742    200     ATPKPTRHIREQLAQETGLNMRVIQVWFQN     16.814
PWM1 hit: P35548    162     QKQYLSIAERAEFSSSLNLTETQVKIWFQN     56.332
PWM2 hit: P35548    162     QKQYLSIAERAEFSSSLNLTETQVKIWFQN     51.978
PWM1 hit: Q9BYU1    233     NNPYPSEEAKEELARKGGLTISQVSNWFGN     14.351
PWM2 hit: Q9BYU1    233     NNPYPSEEAKEELARKGGLTISQVSNWFGN     11.832
PWM1 hit: P52952    158     QQRYLSAPERDQLASVLKLTSTQVKIWFQN     40.131
PWM2 hit: P52952    158     QQRYLSAPERDQLASVLKLTSTQVKIWFQN     37.877
PWM1 hit: Q9UBX0    128     VNCYPGIDIREDLAQKLNLEEDRIQIWFQN     38.935
PWM2 hit: Q9UBX0    128     VNCYPGIDIREDLAQKLNLEEDRIQIWFQN     30.671
PWM1 hit: Q8TE12    215     VSSKPCRKVRETLAAETGLSVRVVQVWFQN     10.985
PWM2 hit: Q8TE12    215     VSSKPCRKVRETLAAETGLSVRVVQVWFQN     7.733
PWM1 hit: O75364    82      RNRYPDMSTREEIAVWTNLTEARVRVWFKN     32.798
PWM2 hit: O75364    82      RNRYPDMSTREEIAVWTNLTEARVRVWFKN     28.142
PWM1 hit: P31270    261     FSVYINKEKRLQLSRMLNLTDRQVKIWFQN     35.714
PWM2 hit: P31270    261     FSVYINKEKRLQLSRMLNLTDRQVKIWFQN     28.136
PWM1 hit: Q9NY43    252     RQKYLSVQDRMDLAAALNLTDTQVKTWYQN     44.724
PWM2 hit: Q9NY43    252     RQKYLSVQDRMDLAAALNLTDTQVKTWYQN     40.734
PWM1 hit: Q00444    175     FNRYLTRRRRIEIANNLCLNERQIKIWFQN     44.269
PWM2 hit: Q00444    175     FNRYLTRRRRIEIANNLCLNERQIKIWFQN     36.373
PWM1 hit: Q9H161    234     KTHYPDVYAREQLAMRTDLTEARVQVWFQN     44.430
PWM2 hit: Q9H161    234     KTHYPDVYAREQLAMRTDLTEARVQVWFQN     41.576
PWM1 hit: P28360    192     QKQYLSIAERAEFSSSLSLTETQVKIWFQN     54.668
PWM2 hit: P28360    192     QKQYLSIAERAEFSSSLSLTETQVKIWFQN     51.175
PWM1 hit: Q96A47    211     ANPRPDALMKEQLVEMTGLSPRVIRVWFQN     11.206
PWM2 hit: Q96A47    211     ANPRPDALMKEQLVEMTGLSPRVIRVWFQN     8.837
PWM1 hit: P14653    223     FNKYLSRARRVEIAATLELNETQVKIWFQN     42.995
PWM2 hit: P14653    223     FNKYLSRARRVEIAATLELNETQVKIWFQN     37.583
PWM1 hit: O43812    39      RNLYPGIATKEELAQGIDIPEPRVQIWFQN     59.401
PWM2 hit: O43812    39      RNLYPGIATKEELAQGIDIPEPRVQIWFQN     55.582
PWM1 hit: P17482    205     FNMYLTRDRRHEVARLLNLSERQVKIWFQN     41.390
PWM2 hit: P17482    205     FNMYLTRDRRHEVARLLNLSERQVKIWFQN     36.221
PWM1 hit: O43763    177     RQKYLASAERAALAKALRMTDAQVKTWFQN     36.970
PWM2 hit: O43763    177     RQKYLASAERAALAKALRMTDAQVKTWFQN     37.542
PWM1 hit: P39880    1264    QKPYPSPKTIEDLATQLNLKTSTVINWFHN     16.638
PWM2 hit: P39880    1264    QKPYPSPKTIEDLATQLNLKTSTVINWFHN     11.498
PWM1 hit: Q9BZI1    137     KNPYPTKGEKIMLAIITKMTLTQVSTWFAN     19.542
PWM2 hit: Q9BZI1    137     KNPYPTKGEKIMLAIITKMTLTQVSTWFAN     13.122
PWM1 hit: P50221    191     HHNYLTRLRRYEIAVNLDLSERQVKVWFQN     34.854
PWM2 hit: P50221    191     HHNYLTRLRRYEIAVNLDLSERQVKVWFQN     29.120
PWM1 hit: P09629    157     YNRYLTRRRRIEIAHTLCLTERQIKIWFQN     52.168
```

```
PWM2 hit: P09629   157      YNRYLTRRRRIEIAHTLCLTERQIKIWFQN      45.827
PWM1 hit: Q99697   112      RNRYPDMSTREEIAVWTNLTEARVRVWFKN      32.798
PWM2 hit: Q99697   112      RNRYPDMSTREEIAVWTNLTEARVRVWFKN      28.142
PWM1 hit: P40425   267      SNPYPSEEAKEELAKKCGITVSQVSNWFGN      13.475
PWM2 hit: P40425   267      SNPYPSEEAKEELAKKCGITVSQVSNWFGN       9.727
PWM1 hit: Q96QS3   348      KTHYPDVFTREELAMRLDLTEARVQVWFQN      53.044
PWM2 hit: Q96QS3   348      KTHYPDVFTREELAMRLDLTEARVQVWFQN      49.173
PWM1 hit: O15499   146      QNQYPDVSTRERLAGRIRLREERVEVWFKN      18.359
PWM2 hit: O15499   146      QNQYPDVSTRERLAGRIRLREERVEVWFKN      15.175
PWM1 hit: P09017   176      YNRYLTRRRRIEIAHSLCLSERQIKIWFQN      52.023
PWM2 hit: P09017   176      YNRYLTRRRRIEIAHSLCLSERQIKIWFQN      46.478
PWM1 hit: P78414   150      KNPYPTKGEKIMLAIITKMTLTQVSTWFAN      19.542
PWM2 hit: P78414   150      KNPYPTKGEKIMLAIITKMTLTQVSTWFAN      13.122
PWM1 hit: O15522   104      QQRYLSAPEREQLASLLRLTPTQVKIWFQN      40.397
PWM2 hit: O15522   104      QQRYLSAPEREQLASLLRLTPTQVKIWFQN      40.035
PWM1 hit: Q04741   212      KNHYVVGAERKQLAGSLSLSETQVKVWFQN      54.351
PWM2 hit: Q04741   212      KNHYVVGAERKQLAGSLSLSETQVKVWFQN      50.896
PWM1 hit: P09630   161      FNRYLTRRRRIEIANALCLTERQIKIWFQN      48.067
PWM2 hit: P09630   161      FNRYLTRRRRIEIANALCLTERQIKIWFQN      41.878
PWM1 hit: O60663   216      VSSKPCRKVRETLAAETGLSVRVVQVWFQN      10.985
PWM2 hit: O60663   216      VSSKPCRKVRETLAAETGLSVRVVQVWFQN       7.733
PWM1 hit: P28356   295      FNMYLTRDRRYEVARILNLTERQVKIWFQN      44.932
PWM2 hit: P28356   295      FNMYLTRDRRYEVARILNLTERQVKIWFQN      38.047
PWM1 hit: P26367   244      RTHYPDVFARERLAAKIDLPEARIQVWFSN      42.222
PWM2 hit: P26367   244      RTHYPDVFARERLAAKIDLPEARIQVWFSN      40.188
PWM1 hit: O43248   252      FNVYINKEKRLQLSRMLNLTDRQVKIWFQN      38.831
PWM2 hit: O43248   252      FNVYINKEKRLQLSRMLNLTDRQVKIWFQN      30.393
PWM1 hit: P31268   150      FNRYLTRRRRIEIAHALCLTERQIKIWFQN      51.410
PWM2 hit: P31268   150      FNRYLTRRRRIEIAHALCLTERQIKIWFQN      45.930
PWM1 hit: Q99811   124      RTHYPDAFVREELARRVNLSEARVQVWFQN      47.734
PWM2 hit: Q99811   124      RTHYPDAFVREELARRVNLSEARVQVWFQN      45.732
PWM1 hit: O43316   182      RGQYPDSVARGKLATATSLPEDTVRVWFSN       4.014
PWM2 hit: O43316   182      RGQYPDSVARGKLATATSLPEDTVRVWFSN       3.674
PWM1 hit: P23759   237      RTHYPDIYTREELAQRTKLTEARVQVWFSN      47.192
PWM2 hit: P23759   237      RTHYPDIYTREELAQRTKLTEARVQVWFSN      44.147
PWM1 hit: P31275   234      VNEFITRQRRRELSDRLNLSDQQVKIWFQN      28.665
PWM2 hit: P31275   234      VNEFITRQRRRELSDRLNLSDQQVKIWFQN      22.881
PWM1 hit: Q9UIU6   243      QNRYPSPAEKRHLAKITGLSLTQVSNWFKN      16.378
PWM2 hit: Q9UIU6   243      QNRYPSPAEKRHLAKITGLSLTQVSNWFKN      14.198
PWM1 hit: Q9NQ69   287      INHNPDAKDLKQLAQKTGLTKRVLQVWFQN      25.625
PWM2 hit: Q9NQ69   287      INHNPDAKDLKQLAQKTGLTKRVLQVWFQN      20.756
PWM1 hit: O95475   148      QDPYPNPSKKRELAQATGLTPTQVGNWFKN      12.033
PWM2 hit: O95475   148      QDPYPNPSKKRELAQATGLTPTQVGNWFKN      11.521
PWM1 hit: P31271   342      TNKFITKDKRRRISATTNLSERQVTIWFQN      31.171
PWM2 hit: P31271   342      TNKFITKDKRRRISATTNLSERQVTIWFQN      24.322
PWM1 hit: P32242   58       KTRYPDIFMREEVALKINLPESRVQVWFKN      51.648
PWM2 hit: P32242   58       KTRYPDIFMREEVALKINLPESRVQVWFKN      45.426
PWM1 hit: P61371   201      ANPRPDALMKEQLVEMTGLSPRVIRVWFQN      11.206
PWM2 hit: P61371   201      ANPRPDALMKEQLVEMTGLSPRVIRVWFQN       8.837
PWM1 hit: O14770   299      THPYPSEEQKKQLAQDTGLTILQVNNWFIN      11.023
PWM2 hit: O14770   299      THPYPSEEQKKQLAQDTGLTILQVNNWFIN       6.099
PWM1 hit: Q9C0A1   822      QDSNPTRKMLDCISEEVGLKKRVVQVWFQN       8.310
PWM2 hit: Q9C0A1   822      QDSNPTRKMLDCISEEVGLKKRVVQVWFQN       1.650
PWM1 hit: O43711   186      RQKYLASAERAALAKSLKMTDAQVKTWFQN      37.940
PWM2 hit: O43711   186      RQKYLASAERAALAKSLKMTDAQVKTWFQN      37.475
PWM1 hit: Q99687   331      QHPYPSEEQKKQLAQDTGLTILQVNNWFIN      15.366
PWM2 hit: Q99687   331      QHPYPSEEQKKQLAQDTGLTILQVNNWFIN      10.828
PWM1 hit: P35453   522      INKFINKDKRRISAATNLSERQVTIWFQN      32.759
PWM2 hit: P35453   522      INKFINKDKRRISAATNLSERQVTIWFQN      25.394
PWM1 hit: Q96PT3   39       RNLYPGIATKEELAQGIDIPEPRVQIWFQN      59.401
PWM2 hit: Q96PT3   39       RNLYPGIATKEELAQGIDIPEPRVQIWFQN      55.582
PWM1 hit: O43365   211      FNRYLCRPRRVEMANLLNLTERQIKIWFQN      35.962
PWM2 hit: O43365   211      FNRYLCRPRRVEMANLLNLTERQIKIWFQN      30.000
PWM1 hit: P19622   264      TNRYLTEQRRQSLAQELSLNESQIKIWFQN      34.989
PWM2 hit: P19622   264      TNRYLTEQRRQSLAQELSLNESQIKIWFQN      31.121
PWM1 hit: P31269   226      FNMYLTRDRRYEVARLLNLTERQVKIWFQN      43.242
PWM2 hit: P31269   226      FNMYLTRDRRYEVARLLNLTERQVKIWFQN      37.241
PWM1 hit: P23760   239      RTHYPDIYTREELAQRAKLTEARVQVWFSN      42.023
PWM2 hit: P23760   239      RTHYPDIYTREELAQRAKLTEARVQVWFSN      39.758
PWM1 hit: P56177   148      QTQYLALPERAELAASLGLTQTQVKIWFQN      61.515
PWM2 hit: P56177   148      QTQYLALPERAELAASLGLTQTQVKIWFQN      60.974
PWM1 hit: Q15475   144      HNPYPSPREKRELAEATGLTTTQVSNWFKN      24.969
PWM2 hit: Q15475   144      HNPYPSPREKRELAEATGLTTTQVSNWFKN      23.863
PWM1 hit: Q8N196   221      GNRYPTPDEKRRLATLTGLSLTQVSNWFKN      10.525
PWM2 hit: Q8N196   221      GNRYPTPDEKRRLATLTGLSLTQVSNWFKN       8.356
PWM1 hit: Q9NYD6   288      FNMYLTRERRLEISKTINLTDRQVKIWFQN      42.055
PWM2 hit: Q9NYD6   288      FNMYLTRERRLEISKTINLTDRQVKIWFQN      33.908
PWM1 hit: Q92826   236      ANKFITKDKRRKISAATSLSERQITIWFQN      26.823
```

```
PWM2 hit: Q92826    236    ANKFITKDKRRKISAATSLSERQITIWFQN    21.330
PWM1 hit: O14813    110    ETHYPDIYTREELALKIDLTEARVQVWFQN    55.278
PWM2 hit: O14813    110    ETHYPDIYTREELALKIDLTEARVQVWFQN    49.793
PWM1 hit: P49639    249    FNKYLTRARRVEIAASLQLNETQVKIWFQN    45.341
PWM2 hit: P49639    249    FNKYLTRARRVEIAASLQLNETQVKIWFQN    40.293
PWM1 hit: P50222    207    HHNYLTRLRRYEIAVNLDLTERQVKVWFQN    36.320
PWM2 hit: P50222    207    HHNYLTRLRRYEIAVNLDLTERQVKVWFQN    30.188
PWM1 hit: P17483    182    YNRYLTRRRRVEIAHALCLSERQIKIWFQN    47.243
PWM2 hit: P17483    182    YNRYLTRRRRVEIAHALCLSERQIKIWFQN    42.494
PWM1 hit: P40426    258    SNPYPSEEAKEELAKKCSITVSQVSNWFGN    10.602
PWM2 hit: P40426    258    SNPYPSEEAKEELAKKCSITVSQVSNWFGN    6.705
PWM1 hit: Q03014    157    TQKYLSPPERKRLAKMLQLSERQVKTWFQN    43.400
PWM2 hit: Q03014    157    TQKYLSPPERKRLAKMLQLSERQVKTWFQN    42.014
PWM1 hit: Q86UP3    2201   TNAYPKDDEIEQLSTVLNLPTRVIVVWFQN    5.859
PWM2 hit: Q86UP3    2580   LDSNPTRKMLDHIAREVGLKKRVVQVWFQN    0.039
PWM1 hit: P49640    203    RENYVSRPRRCELAAALNLPETTIKVWFQN    36.379
PWM2 hit: P49640    203    RENYVSRPRRCELAAALNLPETTIKVWFQN    33.521
PWM1 hit: P78367    226    HQRYLSGPERADLAASLKLTETQVKIWFQN    53.428
PWM2 hit: P78367    226    HQRYLSGPERADLAASLKLTETQVKIWFQN    52.020
PWM1 hit: P09016    174    FNRYLTRRRRIEIAHTLCLSERQIKIWFQN    48.966
PWM2 hit: P09016    174    FNRYLTRRRRIEIAHTLCLSERQIKIWFQN    43.102
PWM1 hit: Q8N5B7    98     ITKYPDKKRLEGLSKQLDWNVRKIQCWFRH    1.267
PWM1 hit: Q14549    281    CKKYLSLTERSQIAHALKLSEVQVKIWFQN    43.217
PWM2 hit: Q14549    281    CKKYLSLTERSQIAHALKLSEVQVKIWFQN    37.788
PWM1 hit: P31276    280    ASKFITKEKRRRISATTNLSERQVTIWFQN    23.280
PWM2 hit: P31276    280    ASKFITKEKRRRISATTNLSERQVTIWFQN    18.360
PWM1 hit: Q9BZE3    198    RQKYLSVQDRMELAASLNLTDTQVKTWYQN    46.626
PWM2 hit: Q9BZE3    198    RQKYLSVQDRMELAASLNLTDTQVKTWYQN    42.539
PWM1 hit: Q9GZZ0    249    FNKYLTRARRIEIANCLHLNDTQVKIWFQN    42.334
PWM2 hit: Q9GZZ0    249    FNKYLTRARRIEIANCLHLNDTQVKIWFQN    34.386
PWM1 hit: P52951    267    CKKYLSLTERSQIAHALKLSEVQVKIWFQN    43.217
PWM2 hit: P52951    267    CKKYLSLTERSQIAHALKLSEVQVKIWFQN    37.788
PWM1 hit: P78413    165    KNPYPTKGEKIMLAIITKMTLTQVSTWFAN    19.542
PWM2 hit: P78413    165    KNPYPTKGEKIMLAIITKMTLTQVSTWFAN    13.122
PWM1 hit: Q9H4S2    167    SNMYLSRLRRIEIATYLNLSEKQVKIWFQN    30.460
PWM2 hit: Q9H4S2    167    SNMYLSRLRRIEIATYLNLSEKQVKIWFQN    23.617
PWM1 hit: Q14863    254    KNPLPTGQEITEIAKELNYDREVVRVWFCN    3.978
PWM1 hit: P54821    114    RTHYPDAFVREDLARRVNLTEARVQVWFQN    47.641
PWM2 hit: P54821    114    RTHYPDAFVREDLARRVNLTEARVQVWFQN    44.954
PWM1 hit: O95096    148    QQRYLSAPEREHLASLIRLTPTQVKIWFQN    37.071
PWM2 hit: O95096    148    QQRYLSAPEREHLASLIRLTPTQVKIWFQN    35.685
PWM1 hit: P14651    208    FNRYLCRPRRVEMANLLNLSERQIKIWFQN    34.496
PWM2 hit: P14651    208    FNRYLCRPRRVEMANLLNLSERQIKIWFQN    28.932
PWM1 hit: P56915    180    ETKYPDVGTREQLARKVHLREEKVEVWFKN    10.962
PWM2 hit: P56915    180    ETKYPDVGTREQLARKVHLREEKVEVWFKN    6.172
PWM1 hit: P35452    231    VNEFINRQKRKELSNRLNLSDQQVKIWFQN    26.274
PWM2 hit: P35452    231    VNEFINRQKRKELSNRLNLSDQQVKIWFQN    18.519
PWM1 hit: Q969G2    177    NSPKPARHVREQLSSETGLDMRVVQVWFQN    14.033
PWM2 hit: Q969G2    177    NSPKPARHVREQLSSETGLDMRVVQVWFQN    11.995
PWM1 hit: Q15583    58     YNAYPSEQEKALLSQQTHLSTLQVCNWFIN    11.576
PWM2 hit: Q15583    58     YNAYPSEQEKALLSQQTHLSTLQVCNWFIN    7.493
PWM1 hit: P56178    157    KTQYLALPERAELAASLGLTQTQVKIWFQN    62.633
PWM2 hit: P56178    157    KTQYLALPERAELAASLGLTQTQVKIWFQN    61.557
PWM1 hit: O43186    59     KTQYPDVYAREEVALKINLPESRVQVWFKN    39.287
PWM2 hit: O43186    59     KTQYPDVYAREEVALKINLPESRVQVWFKN    34.259
PWM1 hit: Q8TAU0    168    QQRYLSAPEREHLASSLKLTSTQVKIWFQN    42.202
PWM2 hit: Q8TAU0    168    QQRYLSAPEREHLASSLKLTSTQVKIWFQN    40.913
PWM1 hit: O43364    163    FNKYLCRPRRVEIAALLDLTERQVKVWFQN    42.657
PWM2 hit: O43364    163    FNKYLCRPRRVEIAALLDLTERQVKVWFQN    37.672
PWM1 hit: P78337    109    RNRYPDMSMREEIAVWTNLTEPRVRVWFKN    33.362
PWM2 hit: P78337    109    RNRYPDMSMREEIAVWTNLTEPRVRVWFKN    28.606
PWM1 hit: P55347    282    GHPYPTEDEKKQIAAQTNLTLLQVNNWFIN    15.554
PWM2 hit: P55347    282    GHPYPTEDEKKQIAAQTNLTLLQVNNWFIN    10.163
PWM1 hit: Q9UBX2    39     RNPYPGIATRERLAQAIGIPEPRVQIWFQN    65.553
PWM2 hit: Q9UBX2    39     RNPYPGIATRERLAQAIGIPEPRVQIWFQN    64.748
PWM1 hit: P31314    221    RQKYLASAERAALAKALKMTDAQVKTWFQN    37.597
PWM2 hit: P31314    221    RQKYLASAERAALAKALKMTDAQVKTWFQN    37.515
PWM1 hit: Q01860    250    QCPKPTLQQISHIAQQLGLEKDVVRVWFCN    0.660
PWM1 hit: P28358    286    FNMYLTRERRLEISKSVNLTDRQVKIWFQN    37.350
PWM2 hit: P28358    286    FNMYLTRERRLEISKSVNLTDRQVKIWFQN    30.014
PWM1 hit: Q9H9S0    115    RQKYLSLQQMQELSNILNLSYKQVKTWFQN    22.235
PWM2 hit: Q9H9S0    115    RQKYLSLQQMQELSNILNLSYKQVKTWFQN    16.694
PWM1 hit: Q9H2P0    776    KQPYPTRREIEKLAASLWLWKSDIASHFSN    3.044
PWM2 hit: Q9H2P0    776    KQPYPTRREIEKLAASLWLWKSDIASHFSN    1.688
PWM1 hit: P52945    166    FNKYISRPRRVELAVMLNLTERHIKIWFQN    48.109
PWM2 hit: P52945    166    FNKYISRPRRVELAVMLNLTERHIKIWFQN    41.322
PWM1 hit: Q99801    144    HQKYLSAPERAHLAKNLKLTETQVKIWFQN    49.681
PWM2 hit: Q99801    144    HQKYLSAPERAHLAKNLKLTETQVKIWFQN    46.572
```

```
PWM1 hit: Q03828    208        RENYVSRPRRCELAAALNLPETTIKVWFQN        36.379
PWM2 hit: Q03828    208        RENYVSRPRRCELAAALNLPETTIKVWFQN        33.521
PWM1 hit: P31277    286        FNVYINKEKRLQLSRMLNLTDRQVKIWFQN        38.831
PWM2 hit: P31277    286        FNVYINKEKRLQLSRMLNLTDRQVKIWFQN        30.393
PWM1 hit: P13378    217        FNPYLTRKRRIEVSHALALTERQVKIWFQN        47.439
PWM2 hit: P13378    217        FNPYLTRKRRIEVSHALALTERQVKIWFQN        43.316
PWM1 hit: Q15699    152        KTHYPDVYVREQLALRTELTEARVQVWFQN        39.230
PWM2 hit: Q15699    152        KTHYPDVYVREQLALRTELTEARVQVWFQN        35.706
PWM1 hit: Q9H2C1    200        ATPKPTRHIREQLAQETGLNMRVIQVWFQN        19.440
PWM2 hit: Q9H2C1    200        ATPKPTRHIREQLAQETGLNMRVIQVWFQN        16.814
PWM1 hit: P09067    214        FNRYLTRRRRIEIAHALCLSERQIKIWFQN        49.944
PWM2 hit: P09067    214        FNRYLTRRRRIEIAHALCLSERQIKIWFQN        44.862
PWM1 hit: P31249    214        FNRYLCRPRRVEMANLLNLTERQIKIWFQN        35.962
PWM2 hit: P31249    214        FNRYLCRPRRVEMANLLNLTERQIKIWFQN        30.000
PWM1 hit: P58304    168        EAHYPDVYAREMLAMKTELPEDRIQVWFQN        24.839
PWM2 hit: P58304    168        EAHYPDVYAREMLAMKTELPEDRIQVWFQN        21.405
PWM1 hit: P31260    339        FNMYLTRERRLEISRSVHLTDRQVKIWFQN        34.210
PWM2 hit: P31260    339        FNMYLTRERRLEISRSVHLTDRQVKIWFQN        28.237
PWM1 hit: P78412    169        KNPYPTKGEKIMLAIITKMTLTQVSTWFAN        19.542
PWM2 hit: P78412    169        KNPYPTKGEKIMLAIITKMTLTQVSTWFAN        13.122
PWM1 hit: Q9NZR4    184        EAHYPDVYAREMLAVKTELPEDRIQVWFQN        27.082
PWM2 hit: Q9NZR4    184        EAHYPDVYAREMLAVKTELPEDRIQVWFQN        23.424
PWM1 hit: O15266    137        ETHYPDAFMREELSQRLGLSEARVQVWFQN        57.953
PWM2 hit: O15266    137        ETHYPDAFMREELSQRLGLSEARVQVWFQN        56.669
PWM1 hit: Q9UBR4    182        TSPKPARHVREQLSSETGLDMRVVQVWFQN        13.202
PWM2 hit: Q9UBR4    182        TSPKPARHVREQLSSETGLDMRVVQVWFQN        11.627
PWM1 hit: Q9NPC8    144        HNPYPSPREKRELTEATGLTTTQVSNWFKN        19.504
PWM2 hit: Q9NPC8    144        HNPYPSPREKRELTEATGLTTTQVSNWFKN        17.617
```

number of sequences matched by pwm1 and pwm2, and total unique 143 138 138
total hits by pwm1 and pwm2 151 143
['P20719', 'P78415', 'Q99453', 'P43699', 'P14652', 'Q96KN3', 'O00470', 'Q05925', 'Q9GZN2', 'Q07687', 'Q9NP08', 'O95076', 'P40424', 'P31267',
'O95343', 'P17481', 'P50458', 'Q15911', 'Q00056', 'Q9UPM6', 'Q8IYA7', 'P17509', 'P78411', 'P50219', 'Q8N693', 'P32243', 'Q9Y2V3', 'Q8NFW5',
'P31274', 'P48742', 'P35548', 'Q9BYU1', 'P52952', 'Q9UBX0', 'Q8TE12', 'O75364', 'P31270', 'Q9NY43', 'Q00444', 'Q9H161', 'P28360', 'Q96A47',
'P14653', 'O43812', 'P17482', 'O43763', 'P39880', 'Q9BZI1', 'P50221', 'P09629', 'Q99697', 'P40425', 'Q96QS3', 'O15499', 'P09017', 'P78414',
'O15522', 'Q04741', 'P09630', 'O60663', 'P28356', 'P26367', 'O43248', 'P31268', 'Q99811', 'O43316', 'P23759', 'P31275', 'Q9UIU6', 'Q9NQ69',
'O95475', 'P31271', 'P32242', 'P61371', 'O14770', 'Q9C0A1', 'O43711', 'Q99687', 'P35453', 'Q96PT3', 'O43365', 'P19622', 'P31269', 'P23760',
'P56177', 'Q15475', 'Q8N196', 'Q9NYD6', 'Q92826', 'O14813', 'P49639', 'P50222', 'P17483', 'P40426', 'Q03014', 'Q86UP3', 'P49640', 'P78367',
'P09016', 'Q8N5B7', 'Q14549', 'P31276', 'Q9BZE3', 'Q9GZZ0', 'P52951', 'P78413', 'Q9H4S2', 'Q14863', 'P54821', 'O95096', 'P14651', 'P56915',
'P35452', 'Q969G2', 'Q15583', 'P56178', 'O43186', 'Q8TAU0', 'O43364', 'P78337', 'P55347', 'Q9UBX2', 'P31314', 'Q01860', 'P28358', 'Q9H9S0',
'Q9H2P0', 'P52945', 'Q99801', 'Q03828', 'P31277', 'P13378', 'Q15699', 'Q9H2C1', 'P09067', 'P31249', 'P58304', 'P31260', 'P78412', 'Q9NZR4',
'O15266', 'Q9UBR4', 'Q9NPC8']
getting report
report rows
GO:0003677   143     DNA binding
GO:0005634   143     nucleus
GO:0006355   140     regulation of transcription, DNA-templated
GO:0043565   135     sequence-specific DNA binding
GO:0006351   107     transcription, DNA-templated
GO:0007275   106     multicellular organismal development
GO:0003700   70      sequence-specific DNA binding transcription factor activity
GO:0045944   64      positive regulation of transcription from RNA polymerase II promoter
GO:0009952   40      anterior/posterior pattern specification
GO:0005515   34      protein binding
GO:0000122   30      negative regulation of transcription from RNA polymerase II promoter
GO:0005737   29      cytoplasm
GO:0048704   27      embryonic skeletal system morphogenesis
GO:0006366   26      transcription from RNA polymerase II promoter
GO:0003682   23      chromatin binding
GO:0005667   23      transcription factor complex
GO:0045893   20      positive regulation of transcription, DNA-templated

```
GO:0006357  20    regulation of transcription from RNA polymerase II promoter
GO:0005730  18    nucleolus
GO:0009653  18    anatomical structure morphogenesis
GO:0045892  17    negative regulation of transcription, DNA-templated
GO:0009887  17    organ morphogenesis
GO:0001501  16    skeletal system development
GO:0048706  16    embryonic skeletal system development
GO:0001077  16    RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in
positive regulation of transcription
GO:0030154  16    cell differentiation
GO:0046872  15    metal ion binding
GO:0030326  15    embryonic limb morphogenesis
GO:0030182  15    neuron differentiation
GO:0007420  15    brain development
GO:0000978  14    RNA polymerase II core promoter proximal region sequence-specific DNA binding
GO:0008270  14    zinc ion binding
GO:0010468  14    regulation of gene expression
GO:0008134  13    transcription factor binding
GO:0044212  12    transcription regulatory region DNA binding
GO:0007389  12    pattern specification process
GO:0009954  12    proximal/distal pattern formation
GO:0009953  12    dorsal/ventral pattern formation
GO:0008284  11    positive regulation of cell proliferation
GO:0005622  11    intracellular
GO:0007399  11    nervous system development
GO:0008285  10    negative regulation of cell proliferation
GO:0045665  10    negative regulation of neuron differentiation
GO:0001764  10    neuron migration
GO:0051216  10    cartilage development
GO:0030901  10    midbrain development
GO:0001656  9     metanephros development
GO:0008283  9     cell proliferation
GO:0046982  9     protein heterodimerization activity
GO:0035115  9     embryonic forelimb morphogenesis
GO:0042472  9     inner ear morphogenesis
GO:0043066  8     negative regulation of apoptotic process
GO:0071837  8     HMG box domain binding
GO:0007411  8     axon guidance
GO:0007507  8     heart development
GO:0005654  8     nucleoplasm
GO:0042127  8     regulation of cell proliferation
GO:0007601  8     visual perception
GO:0030878  8     thyroid gland development
GO:0030900  8     forebrain development
GO:0042733  8     embryonic digit morphogenesis
GO:0042474  8     middle ear morphogenesis
GO:0048663  8     neuron fate commitment
GO:0048705  7     skeletal system morphogenesis
```

```
GO:0048701  7        embryonic cranial skeleton morphogenesis
GO:0043010  7        camera-type eye development
GO:0008045  7        motor neuron axon guidance
GO:0007519  7        skeletal muscle tissue development
GO:0021983  7        pituitary gland development
GO:0007517  7        muscle organ development
GO:0003714  7        transcription corepressor activity
GO:0007417  7        central nervous system development
GO:0048536  7        spleen development
GO:0031016  6        pancreas development
GO:0060021  6        palate development
GO:0043524  6        negative regulation of neuron apoptotic process
GO:0045666  6        positive regulation of neuron differentiation
GO:0010628  6        positive regulation of gene expression
GO:0030324  6        lung development
GO:0035116  6        embryonic hindlimb morphogenesis
GO:0003705  6        RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity
GO:0048646  6        anatomical structure formation involved in morphogenesis
GO:0001525  6        angiogenesis
GO:0021520  6        spinal cord motor neuron cell fate specification
GO:0021527  6        spinal cord association neuron differentiation
GO:0045165  6        cell fate commitment
GO:0048666  6        neuron development
GO:0048839  5        inner ear development
GO:0048863  5        stem cell differentiation
GO:0000977  5        RNA polymerase II regulatory region sequence-specific DNA binding
GO:0021766  5        hippocampus development
GO:0001658  5        branching involved in ureteric bud morphogenesis
GO:0071542  5        dopaminergic neuron differentiation
GO:0008344  5        adult locomotory behavior
GO:0030902  5        hindbrain development
GO:0009611  5        response to wounding
GO:0009791  5        post-embryonic development
GO:0042475  5        odontogenesis of dentin-containing tooth
GO:0003151  4        outflow tract morphogenesis
GO:0001759  4        organ induction
GO:0021537  4        telencephalon development
GO:0048565  4        digestive tract development
GO:0090190  4        positive regulation of branching involved in ureteric bud morphogenesis
GO:0021549  4        cerebellum development
GO:0048844  4        artery morphogenesis
GO:0000790  4        nuclear chromatin
GO:0050896  4        response to stimulus
GO:0042493  4        response to drug
GO:0030509  4        BMP signaling pathway
GO:0001822  4        kidney development
GO:0007605  4        sensory perception of sound
GO:0060041  4        retina development in camera-type eye
GO:0001701  4        in utero embryonic development
GO:0042803  4        protein homodimerization activity
GO:0001570  4        vasculogenesis
GO:0035108  4        limb morphogenesis
GO:0007492  4        endoderm development
GO:0023019  4        signal transduction involved in regulation of gene expression
GO:0048665  4        neuron fate specification
GO:0031018  4        endocrine pancreas development
GO:0048538  4        thymus development
GO:0021879  4        forebrain neuron differentiation
GO:0001843  4        neural tube closure
GO:0060037  4        pharyngeal system development
GO:0000981  4        sequence-specific DNA binding RNA polymerase II transcription factor activity
GO:0008150  4        biological_process
GO:0045638  4        negative regulation of myeloid cell differentiation
GO:0030097  4        hemopoiesis
GO:0005575  4        cellular_component
GO:0048589  3        developmental growth
GO:0001755  3        neural crest cell migration
GO:0048935  3        peripheral nervous system neuron development
GO:0021895  3        cerebral cortex neuron differentiation
GO:0021892  3        cerebral cortex GABAergic interneuron differentiation
GO:0001655  3        urogenital system development
GO:0007409  3        axonogenesis
GO:0007224  3        smoothened signaling pathway
GO:0002087  3        regulation of respiratory gaseous exchange by neurological system process
GO:0060349  3        bone morphogenesis
GO:0001889  3        liver development
```

```
GO:0050905    3    neuromuscular process
GO:0090009    3    primitive streak formation
GO:0007368    3    determination of left/right symmetry
GO:0016020    3    membrane
GO:0045664    3    regulation of neuron differentiation
GO:0043234    3    protein complex
GO:0005829    3    cytosol
GO:0001085    3    RNA polymerase II transcription factor binding
GO:0019899    3    enzyme binding
GO:0021953    3    central nervous system neuron differentiation
GO:0021772    3    olfactory bulb development
GO:0072086    3    specification of loop of Henle identity
GO:0002088    3    lens development in camera-type eye
GO:0048468    3    cell development
GO:0008584    3    male gonad development
GO:0048645    3    organ formation
GO:0003674    3    molecular_function
GO:0003676    3    nucleic acid binding
GO:0043388    3    positive regulation of DNA binding
GO:0042981    3    regulation of apoptotic process
GO:0060040    3    retinal bipolar neuron differentiation
GO:0060272    3    embryonic skeletal joint morphogenesis
GO:0003690    3    double-stranded DNA binding
GO:0021569    3    rhombomere 3 development
GO:2000678    3    negative regulation of transcription regulatory region DNA binding
GO:0034504    3    protein localization to nucleus
GO:2001055    3    positive regulation of mesenchymal cell apoptotic process
GO:0000976    3    transcription regulatory region sequence-specific DNA binding
GO:0006915    3    apoptotic process
GO:0003148    3    outflow tract septum morphogenesis
GO:0021522    3    spinal cord motor neuron differentiation
GO:0050680    3    negative regulation of epithelial cell proliferation
GO:0048856    3    anatomical structure development
GO:0003007    3    heart morphogenesis
GO:0021612    3    facial nerve structural organization
GO:0001709    3    cell fate determination
GO:0045595    3    regulation of cell differentiation
GO:0035137    3    hindlimb morphogenesis
GO:0007585    3    respiratory gaseous exchange
GO:0021904    3    dorsal/ventral neural tube patterning
GO:0021570    3    rhombomere 4 development
GO:0002009    3    morphogenesis of an epithelium
GO:0021615    3    glossopharyngeal nerve morphogenesis
GO:0042476    3    odontogenesis
GO:0001654    3    eye development
GO:0001503    2    ossification
GO:0072001    2    renal system development
GO:0071363    2    cellular response to growth factor stimulus
GO:0070410    2    co-SMAD binding
GO:0030917    2    midbrain-hindbrain boundary development
GO:0030855    2    epithelial cell differentiation
GO:0021516    2    dorsal spinal cord development
GO:0019233    2    sensory perception of pain
GO:0001757    2    somite specification
GO:0000983    2    RNA polymerase II core promoter sequence-specific DNA binding transcription factor activity
GO:0000982    2    RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity
GO:0060322    2    head development
GO:0000980    2    RNA polymerase II distal enhancer sequence-specific DNA binding
GO:0048568    2    embryonic organ development
GO:0030178    2    negative regulation of Wnt signaling pathway
GO:0032332    2    positive regulation of chondrocyte differentiation
GO:0042551    2    neuron maturation
GO:0042826    2    histone deacetylase binding
GO:0048703    2    embryonic viscerocranium morphogenesis
GO:0021546    2    rhombomere development
GO:0021544    2    subpallium development
GO:0021893    2    cerebral cortex GABAergic interneuron fate commitment
GO:0033574    2    response to testosterone
GO:0000979    2    RNA polymerase II core promoter sequence-specific DNA binding
GO:0007498    2    mesoderm development
GO:0051451    2    myoblast migration
GO:0045746    2    negative regulation of Notch signaling pathway
GO:0021798    2    forebrain dorsal/ventral pattern formation
GO:0072095    2    regulation of branch elongation involved in ureteric bud branching
GO:0021797    2    forebrain anterior/posterior pattern specification
GO:0001657    2    ureteric bud development
GO:0016525    2    negative regulation of angiogenesis
GO:0042593    2    glucose homeostasis
```

```
GO:0045880    2    positive regulation of smoothened signaling pathway
GO:0043065    2    positive regulation of apoptotic process
GO:0090090    2    negative regulation of canonical Wnt signaling pathway
GO:0032525    2    somite rostral/caudal axis specification
GO:0006606    2    protein import into nucleus
GO:0001205    2    RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription
GO:0040019    2    positive regulation of embryonic development
GO:0030539    2    male genitalia development
GO:0002011    2    morphogenesis of an epithelial sheet
GO:0048852    2    diencephalon morphogenesis
GO:0007179    2    transforming growth factor beta receptor signaling pathway
GO:0045662    2    negative regulation of myoblast differentiation
GO:0031290    2    retinal ganglion cell axon guidance
GO:0045669    2    positive regulation of osteoblast differentiation
GO:0032330    2    regulation of chondrocyte differentiation
GO:0021913    2    regulation of transcription from RNA polymerase II promoter involved in ventral spinal cord interneuron specification
GO:0010629    2    negative regulation of gene expression
GO:0001568    2    blood vessel development
GO:0001569    2    patterning of blood vessels
GO:0006367    2    transcription initiation from RNA polymerase II promoter
GO:0061312    2    BMP signaling pathway involved in heart development
GO:0009880    2    embryonic pattern specification
GO:0060070    2    canonical Wnt signaling pathway
GO:0061072    2    iris morphogenesis
GO:0060541    2    respiratory system development
GO:0055123    2    digestive system development
GO:0021882    2    regulation of transcription from RNA polymerase II promoter involved in forebrain neuron fate commitment
GO:0021884    2    forebrain neuron development
GO:0032880    2    regulation of protein localization
GO:0050767    2    regulation of neurogenesis
GO:0003309    2    type B pancreatic cell differentiation
GO:0001942    2    hair follicle development
GO:0032403    2    protein complex binding
GO:0055015    2    ventricular cardiac muscle cell development
GO:0031625    2    ubiquitin protein ligase binding
GO:0048738    2    cardiac muscle tissue development
GO:0045617    2    negative regulation of keratinocyte differentiation
GO:0001649    2    osteoblast differentiation
GO:0022612    2    gland morphogenesis
GO:0043583    2    ear development
GO:0044822    2    poly(A) RNA binding
GO:0045931    2    positive regulation of mitotic cell cycle
GO:0032024    2    positive regulation of insulin secretion
GO:0030183    2    B cell differentiation
GO:0001047    2    core promoter binding
GO:0007501    2    mesodermal cell fate specification
GO:0009749    2    response to glucose
GO:0007267    2    cell-cell signaling
GO:0060536    2    cartilage morphogenesis
GO:0035136    2    forelimb morphogenesis
GO:0060325    2    face morphogenesis
GO:0010720    2    positive regulation of cell development
GO:0016477    2    cell migration
GO:0016055    2    Wnt signaling pathway
GO:0002076    2    osteoblast development
GO:0007626    2    locomotory behavior
GO:0014070    2    response to organic cyclic compound
GO:0007623    2    circadian rhythm
GO:0021702    2    cerebellar Purkinje cell differentiation
GO:0090103    2    cochlea morphogenesis
GO:0030879    2    mammary gland development
GO:0021854    2    hypothalamus development
GO:0048708    2    astrocyte differentiation
GO:0021877    2    forebrain neuron fate commitment
GO:0072272    2    proximal/distal pattern formation involved in metanephric nephron development
GO:0045596    2    negative regulation of cell differentiation
GO:0001708    2    cell fate specification
GO:0005739    2    mitochondrion
GO:0060441    2    epithelial tube branching involved in lung morphogenesis
GO:0035019    2    somatic stem cell maintenance
GO:0060216    2    definitive hemopoiesis
GO:0021568    2    rhombomere 2 development
GO:0035880    2    embryonic nail plate morphogenesis
GO:2000288    2    positive regulation of myoblast proliferation
GO:0001228    2    RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription
GO:0032993    2    protein-DNA complex
GO:0021800    2    cerebral cortex tangential migration
GO:0010942    2    positive regulation of cell death
```

```
GO:0021987    2    cerebral cortex development
GO:0002053    2    positive regulation of mesenchymal cell proliferation
GO:0030334    2    regulation of cell migration
GO:0030331    2    estrogen receptor binding
GO:0008190    2    eukaryotic initiation factor 4E binding
GO:0008582    2    regulation of synaptic growth at neuromuscular junction
GO:0008585    2    female gonad development
GO:0001076    2    RNA polymerase II transcription factor binding transcription factor activity
GO:0035264    2    multicellular organism growth
GO:0001078    2    RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription
GO:0003713    2    transcription coactivator activity
GO:0003712    2    transcription cofactor activity
GO:0060527    2    prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis
GO:0021524    2    visceral motor neuron differentiation
GO:0021526    2    medial motor column neuron differentiation
GO:0031965    2    nuclear membrane
GO:0010971    2    positive regulation of G2/M transition of mitotic cell cycle
GO:0003357    2    noradrenergic neuron differentiation
GO:0030513    2    positive regulation of BMP signaling pathway
GO:0003350    2    pulmonary myocardium development
GO:0055007    2    cardiac muscle cell differentiation
GO:0090427    2    activation of meiosis
GO:0060913    2    cardiac cell fate determination
GO:0021846    2    cell proliferation in forebrain
GO:0030199    2    collagen fibril organization
GO:0060413    2    atrial septum morphogenesis
GO:0060412    2    ventricular septum morphogenesis
GO:0048715    2    negative regulation of oligodendrocyte differentiation
GO:2000543    2    positive regulation of gastrulation
GO:0060173    2    limb development
GO:0048486    2    parasympathetic nervous system development
GO:0048484    2    enteric nervous system development
GO:0048485    2    sympathetic nervous system development
GO:0048483    2    autonomic nervous system development
GO:0021853    2    cerebral cortex GABAergic interneuron migration
GO:0008406    2    gonad development
GO:0021937    2    cerebellar Purkinje cell-granule cell precursor cell signaling involved in regulation of granule cell precursor cell proliferation
GO:0008015    2    blood circulation
GO:0035050    2    embryonic heart tube development
GO:0071773    2    cellular response to BMP stimulus
GO:0060442    2    branching involved in prostate gland morphogenesis
GO:0061180    2    mammary gland epithelium development
GO:0048853    2    forebrain morphogenesis
GO:0003198    2    epithelial to mesenchymal transition involved in endocardial cushion formation
GO:0060351    2    cartilage development involved in endochondral bone morphogenesis
GO:0022037    2    metencephalon development
GO:0048699    2    generation of neurons
GO:0045597    2    positive regulation of cell differentiation
GO:0001105    2    RNA polymerase II transcription coactivator activity
GO:0001102    2    RNA polymerase II activating transcription factor binding
GO:0001158    2    enhancer sequence-specific DNA binding
GO:0001890    2    placenta development
GO:0001714    2    endodermal cell fate specification
GO:0009725    2    response to hormone
GO:0021796    2    cerebral cortex regionalization
GO:0021571    2    rhombomere 5 development
GO:0072075    2    metanephric mesenchyme development
GO:0001190    2    RNA polymerase II transcription factor binding transcription factor activity involved in positive regulation of transcription
GO:0010467    2    gene expression
GO:0021759    2    globus pallidus development
GO:0021754    2    facial nucleus development
GO:0072107    2    positive regulation of ureteric bud formation
GO:0061303    1    cornea development in camera-type eye
GO:0030225    1    macrophage differentiation
GO:0003326    1    pancreatic A cell fate commitment
GO:0048066    1    developmental pigmentation
GO:0048103    1    somatic stem cell division
GO:0001502    1    cartilage condensation
GO:0044281    1    small molecule metabolic process
GO:0021723    1    medullary reticular formation development
GO:0010040    1    response to iron(II) ion
GO:2000836    1    positive regulation of androgen secretion
GO:0014031    1    mesenchymal cell development
GO:0014036    1    neural crest cell fate specification
GO:0030916    1    otic vesicle formation
GO:0030850    1    prostate gland development
GO:0072193    1    ureter smooth muscle cell differentiation
GO:0021517    1    ventral spinal cord development
```

```
GO:0060017    1    parathyroid gland development
GO:0031103    1    axon regeneration
GO:0031100    1    organ regeneration
GO:0061010    1    gall bladder development
GO:0061011    1    hepatic duct development
GO:0035852    1    horizontal cell localization
GO:0061017    1    hepatoblast differentiation
GO:0007283    1    spermatogenesis
GO:0022027    1    interkinetic nuclear migration
GO:0007286    1    spermatid development
GO:0050678    1    regulation of epithelial cell proliferation
GO:0001756    1    somitogenesis
GO:0022029    1    telencephalon cell migration
GO:0019230    1    proprioception
GO:0072513    1    positive regulation of secondary heart field cardioblast proliferation
GO:0040036    1    regulation of fibroblast growth factor receptor signaling pathway
GO:0070986    1    left/right axis specification
GO:0051781    1    positive regulation of cell division
GO:0045823    1    positive regulation of heart contraction
GO:0070542    1    response to fatty acid
GO:0042696    1    menarche
GO:0060261    1    positive regulation of transcription initiation from RNA polymerase II promoter
GO:0021530    1    spinal cord oligodendrocyte cell fate specification
GO:0090263    1    positive regulation of canonical Wnt signaling pathway
GO:0000301    1    retrograde transport, vesicle recycling within Golgi
GO:0031076    1    embryonic camera-type eye development
GO:0014813    1    skeletal muscle satellite cell commitment
GO:0030177    1    positive regulation of Wnt signaling pathway
GO:0060066    1    oviduct development
GO:0060067    1    cervix development
GO:0035413    1    positive regulation of catenin import into nucleus
GO:0060065    1    uterus development
GO:0060068    1    vagina development
GO:0030073    1    insulin secretion
GO:0016607    1    nuclear speck
GO:0016973    1    poly(A)+ mRNA export from nucleus
GO:0035990    1    tendon cell differentiation
GO:0000902    1    cell morphogenesis
GO:0035992    1    tendon formation
GO:0009948    1    anterior/posterior axis specification
GO:0003208    1    cardiac ventricle morphogenesis
GO:0002686    1    negative regulation of leukocyte migration
GO:0007388    1    posterior compartment specification
GO:0043021    1    ribonucleoprotein complex binding
GO:0050291    1    sphingosine N-acyltransferase activity
GO:0060460    1    left lung morphogenesis
GO:0007625    1    grooming behavior
GO:0006629    1    lipid metabolic process
GO:0048702    1    embryonic neurocranium morphogenesis
GO:0060166    1    olfactory pit development
GO:0090191    1    negative regulation of branching involved in ureteric bud morphogenesis
GO:0007628    1    adult walking behavior
GO:0021542    1    dentate gyrus development
GO:0021543    1    pallium development
GO:0042060    1    wound healing
GO:0004842    1    ubiquitin-protein transferase activity
GO:0060764    1    cell-cell signaling involved in mammary gland development
GO:0030674    1    protein binding, bridging
GO:0010260    1    organ senescence
GO:0071347    1    cellular response to interleukin-1
GO:0048793    1    pronephros development
GO:0003337    1    mesenchymal to epithelial transition involved in metanephros morphogenesis
GO:0001974    1    blood vessel remodeling
GO:0048812    1    neuron projection morphogenesis
GO:0035907    1    dorsal aorta development
GO:0043393    1    regulation of protein binding
GO:0035909    1    aorta morphogenesis
GO:0051384    1    response to glucocorticoid
GO:0060431    1    primary lung bud formation
GO:0008022    1    protein C-terminus binding
GO:0060346    1    bone trabecula formation
GO:0048146    1    positive regulation of fibroblast proliferation
GO:0031490    1    chromatin DNA binding
GO:0021763    1    subthalamic nucleus development
GO:0010001    1    glial cell differentiation
GO:0021642    1    trochlear nerve formation
GO:0048387    1    negative regulation of retinoic acid receptor signaling pathway
GO:0042481    1    regulation of odontogenesis
```

```
GO:0043569    1    negative regulation of insulin-like growth factor receptor signaling pathway
GO:0021799    1    cerebral cortex radially oriented cell migration
GO:0033273    1    response to vitamin
GO:0070365    1    hepatocyte differentiation
GO:0021795    1    cerebral cortex cell migration
GO:0021794    1    thalamus development
GO:0035239    1    tube morphogenesis
GO:0055005    1    ventricular cardiac myofibril assembly
GO:0055008    1    cardiac muscle tissue morphogenesis
GO:0055009    1    atrial cardiac muscle tissue morphogenesis
GO:0051015    1    actin filament binding
GO:0001558    1    regulation of cell growth
GO:0045214    1    sarcomere organization
GO:0048755    1    branching morphogenesis of a nerve
GO:1901166    1    neural crest cell migration involved in autonomic nervous system development
GO:0048619    1    embryonic hindgut morphogenesis
GO:0035849    1    nephric duct elongation
GO:0006338    1    chromatin remodeling
GO:0060971    1    embryonic heart tube left/right pattern formation
GO:0030948    1    negative regulation of vascular endothelial growth factor receptor signaling pathway
GO:0043491    1    protein kinase B signaling
GO:0060347    1    heart trabecula formation
GO:0060430    1    lung saccule development
GO:0060435    1    bronchiole development
GO:0060439    1    trachea morphogenesis
GO:0050900    1    leukocyte migration
GO:0035690    1    cellular response to drug
GO:0032760    1    positive regulation of tumor necrosis factor production
GO:0002089    1    lens morphogenesis in camera-type eye
GO:0008219    1    cell death
GO:0045446    1    endothelial cell differentiation
GO:0035284    1    brain segmentation
GO:0006091    1    generation of precursor metabolites and energy
GO:0070491    1    repressing transcription factor binding
GO:0001104    1    RNA polymerase II transcription cofactor activity
GO:0001886    1    endothelial cell morphogenesis
GO:0005615    1    extracellular space
GO:0033993    1    response to lipid
GO:0061549    1    sympathetic ganglion development
GO:0021984    1    adenohypophysis development
GO:0032526    1    response to retinoic acid
GO:0021912    1    regulation of transcription from RNA polymerase II promoter involved in spinal cord motor neuron fate specification
GO:0021915    1    neural tube development
GO:0006461    1    protein complex assembly
GO:0048596    1    embryonic camera-type eye morphogenesis
GO:0060484    1    lung-associated mesenchyme development
GO:0060481    1    lobar bronchus epithelium development
GO:0030534    1    adult behavior
GO:0003278    1    apoptotic process involved in heart morphogenesis
GO:0048857    1    neural nucleus development
GO:0010453    1    regulation of cell fate commitment
GO:0032755    1    positive regulation of interleukin-6 production
GO:0033327    1    Leydig cell differentiation
GO:0007160    1    cell-matrix adhesion
GO:0007520    1    myoblast fusion
GO:0043522    1    leucine zipper domain binding
GO:0007165    1    signal transduction
GO:0007387    1    anterior compartment pattern formation
GO:0050728    1    negative regulation of inflammatory response
GO:0021599    1    abducens nerve formation
GO:0070848    1    response to growth factor
GO:0030295    1    protein kinase activator activity
GO:0016740    1    transferase activity
GO:0045663    1    positive regulation of myoblast differentiation
GO:0002062    1    chondrocyte differentiation
GO:0002063    1    chondrocyte development
GO:0006665    1    sphingolipid metabolic process
GO:0033147    1    negative regulation of intracellular estrogen receptor signaling pathway
GO:0030216    1    keratinocyte differentiation
GO:0030217    1    T cell differentiation
GO:0030218    1    erythrocyte differentiation
GO:0048754    1    branching morphogenesis of an epithelial tube
GO:2001022    1    positive regulation of response to DNA damage stimulus
GO:0010033    1    response to organic substance
GO:0019827    1    stem cell maintenance
GO:0003166    1    bundle of His development
GO:0003161    1    cardiac conduction system development
GO:0003162    1    atrioventricular node development
```

| GO:0003168 | 1 | Purkinje myocyte differentiation |
|---|---|---|
| GO:0031667 | 1 | response to nutrient levels |
| GO:0090074 | 1 | negative regulation of protein homodimerization activity |
| GO:0016567 | 1 | protein ubiquitination |
| GO:0046534 | 1 | positive regulation of photoreceptor cell differentiation |
| GO:0043403 | 1 | skeletal muscle tissue regeneration |
| GO:1902255 | 1 | positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator |
| GO:0060574 | 1 | intestinal epithelial cell maturation |
| GO:0045840 | 1 | positive regulation of mitosis |
| GO:0060576 | 1 | intestinal epithelial cell development |
| GO:0060577 | 1 | pulmonary vein morphogenesis |
| GO:0060571 | 1 | morphogenesis of an epithelial fold |
| GO:0061009 | 1 | common bile duct development |
| GO:0003285 | 1 | septum secundum development |
| GO:0060578 | 1 | superior vena cava morphogenesis |
| GO:0001159 | 1 | core promoter proximal region DNA binding |
| GO:0035162 | 1 | embryonic hemopoiesis |
| GO:0050821 | 1 | protein stabilization |
| GO:0010621 | 1 | negative regulation of transcription by transcription factor localization |
| GO:0030284 | 1 | estrogen receptor activity |
| GO:0007435 | 1 | salivary gland morphogenesis |
| GO:0007431 | 1 | salivary gland development |
| GO:0070997 | 1 | neuron death |
| GO:0044344 | 1 | cellular response to fibroblast growth factor stimulus |
| GO:0097162 | 1 | MADS box domain binding |
| GO:0030148 | 1 | sphingolipid biosynthetic process |
| GO:0048557 | 1 | embryonic digestive tract morphogenesis |
| GO:0014807 | 1 | regulation of somitogenesis |
| GO:0060379 | 1 | cardiac muscle cell myoblast differentiation |
| GO:0001741 | 1 | XY body |
| GO:0050795 | 1 | regulation of behavior |
| GO:0060929 | 1 | atrioventricular node cell fate commitment |
| GO:0030858 | 1 | positive regulation of epithelial cell differentiation |
| GO:0060235 | 1 | lens induction in camera-type eye |
| GO:0007548 | 1 | sex differentiation |
| GO:0008656 | 1 | cysteine-type endopeptidase activator activity involved in apoptotic process |
| GO:0010719 | 1 | negative regulation of epithelial to mesenchymal transition |
| GO:0009950 | 1 | dorsal/ventral axis specification |
| GO:0050890 | 1 | cognition |
| GO:0048561 | 1 | establishment of organ orientation |
| GO:0021536 | 1 | diencephalon development |
| GO:0001227 | 1 | RNA polymerase II transcription regulatory region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription |
| GO:0033599 | 1 | regulation of mammary gland epithelial cell proliferation |
| GO:0032967 | 1 | positive regulation of collagen biosynthetic process |
| GO:0021555 | 1 | midbrain-hindbrain boundary morphogenesis |
| GO:0021554 | 1 | optic nerve development |
| GO:0043401 | 1 | steroid hormone mediated signaling pathway |
| GO:0021559 | 1 | trigeminal nerve development |
| GO:0021533 | 1 | cell differentiation in hindbrain |
| GO:0060486 | 1 | Clara cell differentiation |
| GO:0035878 | 1 | nail development |
| GO:0060480 | 1 | lung goblet cell differentiation |
| GO:0050768 | 1 | negative regulation of neurogenesis |
| GO:0001947 | 1 | heart looping |
| GO:0002027 | 1 | regulation of heart rate |
| GO:0060687 | 1 | regulation of branching involved in prostate gland morphogenesis |
| GO:0010765 | 1 | positive regulation of sodium ion transport |
| GO:0006694 | 1 | steroid biosynthetic process |
| GO:0071392 | 1 | cellular response to estradiol stimulus |
| GO:0070306 | 1 | lens fiber cell differentiation |
| GO:0032792 | 1 | negative regulation of CREB transcription factor activity |
| GO:0014068 | 1 | positive regulation of phosphatidylinositol 3-kinase signaling |
| GO:0035198 | 1 | miRNA binding |
| GO:0043576 | 1 | regulation of respiratory gaseous exchange |
| GO:0043473 | 1 | pigmentation |
| GO:0071657 | 1 | positive regulation of granulocyte colony-stimulating factor production |
| GO:0060290 | 1 | transdifferentiation |
| GO:0042491 | 1 | auditory receptor cell differentiation |
| GO:1901522 | 1 | positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus |
| GO:0048854 | 1 | brain morphogenesis |
| GO:0033365 | 1 | protein localization to organelle |
| GO:0060510 | 1 | Type II pneumocyte differentiation |
| GO:1901258 | 1 | positive regulation of macrophage colony-stimulating factor production |
| GO:0016331 | 1 | morphogenesis of embryonic epithelium |
| GO:0055014 | 1 | atrial cardiac muscle cell development |
| GO:0030325 | 1 | adrenal gland development |
| GO:0061325 | 1 | cell proliferation involved in outflow tract morphogenesis |
| GO:0010454 | 1 | negative regulation of cell fate commitment |

```
GO:0010667    1    negative regulation of cardiac muscle cell apoptotic process
GO:0072283    1    metanephric renal vesicle morphogenesis
GO:0014707    1    branchiomeric skeletal muscle development
GO:0072284    1    metanephric S-shaped body morphogenesis
GO:0001837    1    epithelial to mesenchymal transition
GO:0061205    1    paramesonephric duct development
GO:0043587    1    tongue morphogenesis
GO:0043584    1    nose development
GO:0033189    1    response to vitamin A
GO:0042789    1    mRNA transcription from RNA polymerase II promoter
GO:0071157    1    negative regulation of cell cycle arrest
GO:0045930    1    negative regulation of mitotic cell cycle
GO:0031128    1    developmental induction
GO:0046622    1    positive regulation of organ growth
GO:0035502    1    metanephric part of ureteric bud development
GO:0035035    1    histone acetyltransferase binding
GO:0001046    1    core promoter sequence-specific DNA binding
GO:0042220    1    response to cocaine
GO:0008343    1    adult feeding behavior
GO:0007263    1    nitric oxide mediated signal transduction
GO:0043621    1    protein self-association
GO:0003203    1    endocardial cushion morphogenesis
GO:0035993    1    deltoid tuberosity development
GO:0045647    1    negative regulation of erythrocyte differentiation
GO:0060535    1    trachea cartilage morphogenesis
GO:0060580    1    ventral spinal cord interneuron fate determination
GO:2001234    1    negative regulation of apoptotic signaling pathway
GO:2001235    1    positive regulation of apoptotic signaling pathway
GO:0005783    1    endoplasmic reticulum
GO:0090081    1    regulation of heart induction by regulation of canonical Wnt signaling pathway
GO:2000738    1    positive regulation of stem cell differentiation
GO:0060713    1    labyrinthine layer morphogenesis
GO:0021510    1    spinal cord development
GO:0060716    1    labyrinthine layer blood vessel development
GO:0005789    1    endoplasmic reticulum membrane
GO:0072050    1    S-shaped body morphogenesis
GO:0072358    1    cardiovascular system development
GO:0060324    1    face development
GO:0060326    1    cell chemotaxis
GO:0003342    1    proepicardium development
GO:0030054    1    cell junction
GO:0007219    1    Notch signaling pathway
GO:0003266    1    regulation of secondary heart field cardioblast proliferation
GO:0001824    1    blastocyst development
GO:0097374    1    sensory neuron axon guidance
GO:0021778    1    oligodendrocyte cell fate specification
GO:0032331    1    negative regulation of chondrocyte differentiation
GO:0048511    1    rhythmic process
GO:0048512    1    circadian behavior
GO:0048513    1    organ development
GO:0097477    1    lateral motor column neuron migration
GO:0021855    1    hypothalamus cell migration
GO:0032729    1    positive regulation of interferon-gamma production
GO:0003416    1    endochondral bone growth
GO:0032725    1    positive regulation of granulocyte macrophage colony-stimulating factor production
GO:0048762    1    mesenchymal cell differentiation
GO:0043201    1    response to leucine
GO:0048880    1    sensory system development
GO:0030426    1    growth cone
GO:0019901    1    protein kinase binding
GO:0042753    1    positive regulation of circadian rhythm
GO:0019904    1    protein domain specific binding
GO:0019907    1    cyclin-dependent protein kinase activating kinase holoenzyme complex
GO:0060664    1    epithelial cell proliferation involved in salivary gland morphogenesis
GO:0043434    1    response to peptide hormone
GO:0002930    1    trabecular meshwork development
GO:0055117    1    regulation of cardiac muscle contraction
GO:0002932    1    tendon sheath development
GO:0006006    1    glucose metabolic process
GO:0007379    1    segment specification
GO:0060391    1    positive regulation of SMAD protein import into nucleus
GO:0045656    1    negative regulation of monocyte differentiation
GO:0035846    1    oviduct epithelium development
GO:0035847    1    uterine epithelium development
GO:0060038    1    cardiac muscle cell proliferation
GO:0002074    1    extraocular skeletal muscle development
GO:0071103    1    DNA conformation change
GO:0003016    1    respiratory system process
```

```
GO:0003281    1    ventricular septum development
GO:0003171    1    atrioventricular valve development
GO:0021703    1    locus ceruleus development
GO:0071899    1    negative regulation of estrogen receptor binding
GO:0045111    1    intermediate filament cytoskeleton
GO:0090102    1    cochlea development
GO:0051897    1    positive regulation of protein kinase B signaling
GO:0045727    1    positive regulation of translation
GO:0048644    1    muscle organ morphogenesis
GO:0047485    1    protein N-terminus binding
GO:0048709    1    oligodendrocyte differentiation
GO:0035257    1    nuclear hormone receptor binding
GO:0072278    1    metanephric comma-shaped body morphogenesis
GO:0001776    1    leukocyte homeostasis
GO:0009786    1    regulation of asymmetric cell division
GO:0006955    1    immune response
GO:0006959    1    humoral immune response
GO:0048625    1    myoblast fate commitment
GO:0007050    1    cell cycle arrest
GO:0010157    1    response to chlorate
GO:0010159    1    specification of organ position
GO:0007512    1    adult heart development
GO:0008301    1    DNA binding, bending
GO:0016021    1    integral component of membrane
GO:0007369    1    gastrulation
GO:0072148    1    epithelial cell fate commitment
GO:0060364    1    frontal suture morphogenesis
GO:0031017    1    exocrine pancreas development
GO:0061452    1    retrotrapezoid nucleus neuron differentiation
GO:0060363    1    cranial suture morphogenesis
GO:0032808    1    lacrimal gland development
GO:0010842    1    retina layer formation
GO:0060594    1    mammary gland specification
GO:0030323    1    respiratory tube development
GO:0060928    1    atrioventricular node cell development
GO:0060043    1    regulation of cardiac muscle cell proliferation
GO:0008544    1    epidermis development
GO:0060048    1    cardiac muscle contraction
GO:0030278    1    regulation of ossification
GO:0003221    1    right ventricular cardiac muscle tissue morphogenesis
GO:0021918    1    regulation of transcription from RNA polymerase II promoter involved in somatic motor neuron fate commitment
GO:0001706    1    endoderm formation
GO:0001707    1    mesoderm formation
GO:0055010    1    ventricular cardiac muscle tissue morphogenesis
GO:0060444    1    branching involved in mammary gland duct morphogenesis
GO:0043367    1    CD4-positive, alpha-beta T cell differentiation
GO:0021954    1    central nervous system neuron development
GO:0006644    1    phospholipid metabolic process
GO:0060638    1    mesenchymal-epithelial cell signaling
GO:2001244    1    positive regulation of intrinsic apoptotic signaling pathway
GO:0060743    1    epithelial cell maturation involved in prostate gland development
GO:0072164    1    mesonephric tubule development
GO:0060218    1    hematopoietic stem cell differentiation
GO:0060749    1    mammary gland alveolus development
GO:0050775    1    positive regulation of dendrite morphogenesis
GO:0050774    1    negative regulation of dendrite morphogenesis
GO:0035886    1    vascular smooth muscle cell differentiation
GO:0050679    1    positive regulation of epithelial cell proliferation
GO:0001958    1    endochondral ossification
GO:0003253    1    cardiac neural crest cell migration involved in outflow tract morphogenesis
GO:0010575    1    positive regulation vascular endothelial growth factor production
GO:0001953    1    negative regulation of cell-matrix adhesion
GO:0048936    1    peripheral nervous system neuron axonogenesis
GO:0010470    1    regulation of gastrulation
GO:0032570    1    response to progesterone
GO:0048541    1    Peyer's patch development
GO:0002039    1    p53 binding
GO:0015629    1    actin cytoskeleton
GO:0042118    1    endothelial cell activation
GO:0071383    1    cellular response to steroid hormone stimulus
GO:0071385    1    cellular response to glucocorticoid stimulus
GO:0070317    1    negative regulation of G0 to G1 transition
GO:0035094    1    response to nicotine
GO:0042660    1    positive regulation of cell fate specification
GO:0021831    1    embryonic olfactory bulb interneuron precursor migration
GO:0003130    1    BMP signaling pathway involved in heart induction
GO:0003139    1    secondary heart field specification
GO:0042462    1    eye photoreceptor cell development
```

```
GO:0002052    1    positive regulation of neuroblast proliferation
GO:0045766    1    positive regulation of angiogenesis
GO:0002573    1    myeloid leukocyte differentiation
GO:0071316    1    cellular response to nicotine
GO:0048729    1    tissue morphogenesis
GO:1901387    1    positive regulation of voltage-gated calcium channel activity
GO:0060876    1    semicircular canal formation
GO:0030336    1    negative regulation of cell migration
GO:0006919    1    activation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0003785    1    actin monomer binding
GO:0060602    1    branch elongation of an epithelium
GO:0051726    1    regulation of cell cycle
GO:0004882    1    androgen receptor activity
GO:0046513    1    ceramide biosynthetic process
GO:0008589    1    regulation of smoothened signaling pathway
GO:0031062    1    positive regulation of histone methylation
GO:0005499    1    vitamin D binding
GO:0030424    1    axon
GO:0035262    1    gonad morphogenesis
GO:0035265    1    organ growth
GO:0051891    1    positive regulation of cardioblast differentiation
GO:0072224    1    metanephric glomerulus development
GO:0009612    1    response to mechanical stimulus
GO:0030512    1    negative regulation of transforming growth factor beta receptor signaling pathway
GO:0070166    1    enamel mineralization
GO:0017025    1    TBP-class protein binding
GO:0043280    1    positive regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0030510    1    regulation of BMP signaling pathway
GO:0021521    1    ventral spinal cord interneuron specification
GO:0021523    1    somatic motor neuron differentiation
GO:2000729    1    positive regulation of mesenchymal cell proliferation involved in ureter development
GO:0021529    1    spinal cord oligodendrocyte cell differentiation
GO:0001823    1    mesonephros development
GO:0072047    1    proximal/distal pattern formation involved in nephron development
GO:0051591    1    response to cAMP
GO:0051594    1    detection of glucose
GO:0003358    1    noradrenergic neuron development
GO:0030516    1    regulation of axon extension
GO:0010870    1    positive regulation of receptor biosynthetic process
GO:0030514    1    negative regulation of BMP signaling pathway
GO:0071850    1    mitotic cell cycle arrest
GO:0072049    1    comma-shaped body morphogenesis
GO:0003215    1    cardiac right ventricle morphogenesis
GO:0003211    1    cardiac ventricle formation
GO:2000744    1    positive regulation of anterior head development
GO:0051219    1    phosphoprotein binding
GO:0060847    1    endothelial cell fate specification
GO:0010735    1    positive regulation of transcription via serum response element binding
GO:0060047    1    heart contraction
GO:0060795    1    cell fate commitment involved in formation of primary germ layer
GO:0021871    1    forebrain regionalization
GO:0032730    1    positive regulation of interleukin-1 alpha production
GO:0060415    1    muscle tissue morphogenesis
GO:0048714    1    positive regulation of oligodendrocyte differentiation
GO:0007634    1    optokinetic behavior
GO:0060042    1    retina morphogenesis in camera-type eye
GO:0034101    1    erythrocyte homeostasis
GO:0051795    1    positive regulation of catagen
GO:0021623    1    oculomotor nerve formation
GO:0048894    1    efferent axon development in a lateral line nerve
GO:0043425    1    bHLH transcription factor binding
GO:0035313    1    wound healing, spreading of epidermal cells
GO:0060770    1    negative regulation of epithelial cell proliferation involved in prostate gland development
GO:0035315    1    hair cell differentiation
GO:0003329    1    pancreatic PP cell fate commitment
GO:0051154    1    negative regulation of striated muscle cell differentiation
GO:0060384    1    innervation
GO:0003322    1    pancreatic A cell development
GO:0003323    1    type B pancreatic cell development
GO:0003327    1    type B pancreatic cell fate commitment
GO:0003222    1    ventricular trabecula myocardium morphogenesis
GO:0071599    1    otic vesicle development
GO:0010736    1    serum response element binding
GO:0042640    1    anagen
GO:0000989    1    transcription factor binding transcription factor activity
GO:0071456    1    cellular response to hypoxia
GO:0035914    1    skeletal muscle cell differentiation
GO:0021930    1    cerebellar granule cell precursor proliferation
```

```
GO:0021934    1    hindbrain tangential cell migration
GO:0001702    1    gastrulation with mouth forming second
GO:0048621    1    post-embryonic digestive tract morphogenesis
GO:0021675    1    nerve development
GO:0032735    1    positive regulation of interleukin-12 production
GO:0021658    1    rhombomere 3 morphogenesis
GO:0043392    1    negative regulation of DNA binding
GO:0014003    1    oligodendrocyte development
GO:0038092    1    nodal signaling pathway
GO:0008595    1    anterior/posterior axis specification, embryo
GO:0032731    1    positive regulation of interleukin-1 beta production
GO:0001705    1    ectoderm formation
GO:0048469    1    cell maturation
GO:0060965    1    negative regulation of gene silencing by miRNA
GO:0000139    1    Golgi membrane
GO:0045639    1    positive regulation of myeloid cell differentiation
GO:0045736    1    negative regulation of cyclin-dependent protein serine/threonine kinase activity
GO:0030308    1    negative regulation of cell growth
GO:0061031    1    endodermal digestive tract morphogenesis
GO:0043433    1    negative regulation of sequence-specific DNA binding transcription factor activity
GO:0009790    1    embryo development
GO:0009792    1    embryo development ending in birth or egg hatching
GO:0044241    1    lipid digestion
GO:0022008    1    neurogenesis
GO:0034097    1    response to cytokine
GO:0060126    1    somatotropin secreting cell differentiation
GO:0060059    1    embryonic retina morphogenesis in camera-type eye
GO:0060429    1    epithelium development
GO:0043279    1    response to alkaloid
GO:0010832    1    negative regulation of myotube differentiation
GO:0001103    1    RNA polymerase II repressing transcription factor binding
GO:0001894    1    tissue homeostasis
GO:0016922    1    ligand-dependent nuclear receptor binding
GO:0001710    1    mesodermal cell fate commitment
GO:0051091    1    positive regulation of sequence-specific DNA binding transcription factor activity
GO:0003727    1    single-stranded RNA binding
GO:0030099    1    myeloid cell differentiation
GO:0003680    1    AT DNA binding
GO:0017145    1    stem cell division
GO:0045860    1    positive regulation of protein kinase activity
GO:0021902    1    commitment of neuronal cell to specific neuron type in forebrain
GO:0021905    1    forebrain-midbrain boundary formation
GO:0072177    1    mesonephric duct development
GO:0072172    1    mesonephric tubule formation
GO:0042706    1    eye photoreceptor cell fate commitment
GO:0072077    1    renal vesicle morphogenesis
GO:0090308    1    regulation of methylation-dependent chromatin silencing
GO:0010944    1    negative regulation of transcription by competitive promoter binding
GO:0072178    1    nephric duct morphogenesis
GO:0045599    1    negative regulation of fat cell differentiation
GO:0001191    1    RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription
GO:0003360    1    brainstem development
GO:0030521    1    androgen receptor signaling pathway
GO:0040008    1    regulation of growth
GO:0006641    1    triglyceride metabolic process
GO:0042517    1    positive regulation of tyrosine phosphorylation of Stat3 protein
GO:0070412    1    R-SMAD binding
GO:2000768    1    positive regulation of nephron tubule epithelial cell differentiation
GO:0010463    1    mesenchymal cell proliferation
GO:0048539    1    bone marrow development
GO:0048537    1    mucosal-associated lymphoid tissue development
GO:0048535    1    lymph node development
GO:0006406    1    mRNA export from nucleus
GO:0021978    1    telencephalon regionalization
GO:0048667    1    cell morphogenesis involved in neuron differentiation
GO:0015630    1    microtubule cytoskeleton
GO:0060127    1    prolactin secreting cell differentiation
GO:0048505    1    regulation of timing of cell differentiation
GO:0021610    1    facial nerve morphogenesis
GO:0060539    1    diaphragm development
GO:0043517    1    positive regulation of DNA damage response, signal transduction by p53 class mediator
GO:0060644    1    mammary gland epithelial cell differentiation
GO:0021587    1    cerebellum morphogenesis
GO:0042473    1    outer ear morphogenesis
GO:0071356    1    cellular response to tumor necrosis factor
GO:0048286    1    lung alveolus development
GO:0002317    1    plasma cell differentiation
GO:0060840    1    artery development
```

GO:0001934        1        positive regulation of protein phosphorylation