Weighted Gene Co-Expression Network Analysis of the Salt-Responsive Transcriptomes Reveals Novel Hub Genes in Green Halophytic Microalgae Dunaliella salina

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Supplementary File S1: Python program to extract the geneID from the blastX result

```python
#!/usr/bin/python

# Usage get_geneID.py <blast output file>

# Python program to extract the geneID from the blastX result


import sys



def get_geneid():

    inFile = open(sys.argv[1], 'r')

    outFile = open("geneID.txt", 'w')


    outer_query = False

    inner_query = False

    first_newline = False

    tophit = False

    dt_name = ''

    for line in inFile.readlines():

        if outer_query == True and inner_query == True:
```

```python
            if first_newline == True:

                if tophit == True:

                    outer_query = False

                    inner_query = False

                    first_newline = False

                    tophit = False

                    continue

                else:

                    geneid = line.split()[0].split('|')[3]

                    outFile.write(dt_name + '\t' + geneid + '\n')

                    tophit = True

            elif line == '\n' and first_newline == False:

                first_newline = True


        elif outer_query == True and 'Sequences producing significant alignments' in line:

            inner_query = True

        elif 'Query=' in line:

            dt_name = line.strip().split()[-1]

            outer_query = True


    inFile.close()

    outFile.close()


if __name__=='__main__':

    if len(sys.argv) < 2:
```

```python
        print 'Invalid arguments!\n'

        sys.exit(0)


get_geneid()

print 'I am DONE. Please check the output. :)'
```