Biyoinformatiğe Giriş Proje 4:

Derya Öztürk

Her örnek için yazdığım kodları ve aldığım çıktıları sırasıyla aşağıya ekledim.


```python
from Bio import AlignIO
align = AlignIO.read("clustalw.aln", "clustal")

print(align)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 7 rows and 30 columns
gi|6273285|gb|AF191659.1|AF191 TATACATTAAAGAAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273284|gb|AF191658.1|AF191 TATACATTAAAGAAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273287|gb|AF191661.1|AF191 TATACATTAAAGAAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273286|gb|AF191660.1|AF191 TATACATAAAAGAAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273290|gb|AF191664.1|AF191 TATACATTAAAGGAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273289|gb|AF191663.1|AF191 TATACATTAAAGGAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273291|gb|AF191665.1|AF191 TATACATTAAAGGAGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
```

```python
from Bio import AlignIO
align = AlignIO.read("clustalw.aln", "clustal")
#print(align)
print(len(align))
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
7
```

```python
for record in align:
    print("%s %i" % (record.seq, len(record)))
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
gi|6273285|gb|AF191659.1|AF191 30
gi|6273284|gb|AF191658.1|AF191 30
gi|6273287|gb|AF191661.1|AF191 30
gi|6273286|gb|AF191660.1|AF191 30
gi|6273290|gb|AF191664.1|AF191 30
gi|6273289|gb|AF191663.1|AF191 30
gi|6273291|gb|AF191665.1|AF191 30
```

```python
print(align[0].seq)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
gi|6273285|gb|AF191659.1|AF191
```

```python
print(align[-1].seq)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
gi|6273291|gb|AF191665.1|AF191
```

```python
for row in align:
    print(row.id[1], end='')
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
AAAAAAA
```

```python
for row in align:
    print(row.id[ :10],row.seq[:])
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
TATACATTAA gi|6273285|gb|AF191659.1|AF191
TATACATTAA gi|6273284|gb|AF191658.1|AF191
TATACATTAA gi|6273287|gb|AF191661.1|AF191
TATACATAAA gi|6273286|gb|AF191660.1|AF191
TATACATTAA gi|6273290|gb|AF191664.1|AF191
TATACATTAA gi|6273289|gb|AF191663.1|AF191
TATACATTAA gi|6273291|gb|AF191665.1|AF191
```

```python
for row in align:
    print(row.id[:10]  + row.id[-10:])
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
TATACATTAAAAAAG...AGA
TATACATTAAAAAAG...AGA
TATACATTAAAAAAG...AGA
TATACATAAAAAAG...AGA
TATACATTAAAAAAG...AGA
TATACATTAAAAAAG...AGA
TATACATTAAAAAAG...AGA
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

a = SeqRecord(Seq("AAAACGT"), id="Alpha", description="", name="", dbxrefs=[], features=[], annotations={"molecule_type": "DNA"})
b = SeqRecord(Seq("AAA-CGT"), id="Beta", description="", name="", dbxrefs=[], features=[], annotations={"molecule_type": "DNA"})
c = SeqRecord(Seq("AAAAGGT"), id="Gamma", description="", name="", dbxrefs=[], features=[], annotations={"molecule_type": "DNA"})

align = MultipleSeqAlignment([a, b, c],
                            annotations={"tool": "demo"},
                            column_annotations={"stats": "CCCXCCC"})
print(align)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 7 columns
AAAACGT Alpha
AAA-CGT Beta
AAAAGGT Gamma
```

```python
from Bio.Align import MultipleSeqAlignment
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord

seq_alpha = SeqRecord(Seq("ACTGCTAGCTAG"), id="Alpha", description="")
seq_beta = SeqRecord(Seq("ACT-CTAGCTAG"), id="Beta", description="")
seq_gamma = SeqRecord(Seq("ACTGCTAGATAG"), id="Gamma", description="")
align = MultipleSeqAlignment([seq_alpha, seq_beta, seq_gamma])
print(align)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 12 columns
ACTGCTAGCTAG Alpha
ACT-CTAGCTAG Beta
ACTGCTAGATAG Gamma
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

seq_alpha = Seq("ACTGCTAGCTAG")
seq_beta = Seq("ACT-CTAGCTAG")
seq_gamma = Seq("ACTGCTAGATAG")

record_alpha = SeqRecord(seq_alpha, id="Alpha", description="")
record_beta = SeqRecord(seq_beta, id="Beta", description="")
record_gamma = SeqRecord(seq_gamma, id="Gamma", description="")

align = MultipleSeqAlignment([record_alpha, record_beta, record_gamma])

with open("output.fasta", "w") as output_handle:
    for record in align:
        output_handle.write(">%s\n%s\n" % (record.id, record.seq))

with open("output.fasta", "r") as output_handle:
    for line in output_handle:
        if line.startswith(">"):
            print(line.strip())
        else:
            print(line.strip().upper())
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
>Alpha
ACTGCTAGCTAG
>Beta
ACT-CTAGCTAG
>Gamma
ACTGCTAGATAG
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment
from Bio import AlignIO

seq_alpha = Seq("ACTGCTAGCTAG")
seq_beta = Seq("ACT-CTAGCTAG")
seq_gamma = Seq("ACTGCTAGATAG")

record_alpha = SeqRecord(seq_alpha, id="Alpha", description="")
record_beta = SeqRecord(seq_beta, id="Beta", description="")
record_gamma = SeqRecord(seq_gamma, id="Gamma", description="")

align = MultipleSeqAlignment([record_alpha, record_beta, record_gamma])

with open("output.phy", "w") as output_handle:
    AlignIO.write(align, output_handle, "phylip-relaxed")

with open("output.phy", "r") as output_handle:
    print(output_handle.read())
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
 3 12
 Alpha    ACTGCTAGCT AG
 Beta     ACT-CTAGCT AG
 Gamma    ACTGCTAGAT AG
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

seq_alpha = Seq("ACTGCTAGCTAG")
seq_beta = Seq("ACT-CTAGCTAG")
seq_gamma = Seq("ACTGCTAGATAG")

record_alpha = SeqRecord(seq_alpha, id="Alpha", description="")
record_beta = SeqRecord(seq_beta, id="Beta", description="")
record_gamma = SeqRecord(seq_gamma, id="Gamma", description="")

align = MultipleSeqAlignment([record_alpha, record_beta, record_gamma])
for record in align:
    print(record.id)
    print(record.seq)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
 Alpha
 ACTGCTAGCTAG
 Beta
 ACT-CTAGCTAG
 Gamma
 ACTGCTAGATAG
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

seq_alpha = Seq("ACTGCTAGCTAG")
seq_beta = Seq("ACT-CTAGCTAG")
seq_gamma = Seq("ACTGCTAGATAG")

record_alpha = SeqRecord(seq_alpha, id="Alpha")
record_beta = SeqRecord(seq_beta, id="Beta")
record_gamma = SeqRecord(seq_gamma, id="Gamma")

align = MultipleSeqAlignment([record_alpha, record_beta, record_gamma])


print("Alignment length:", align.get_alignment_length())
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
 Alignment length: 12
```

```python
print(len(align))
```

```
3
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

a = SeqRecord(Seq("AAAACGT"), id="Alpha")
b = SeqRecord(Seq("AAA-CGT"), id="Beta")
c = SeqRecord(Seq("AAAAGGT"), id="Gamma")
d = SeqRecord(Seq("AAAACGT"), id="Delta")
e = SeqRecord(Seq("AAA-GGT"), id="Epsilon")

align = MultipleSeqAlignment([a, b, c, d, e])
align = MultipleSeqAlignment([a, b, c])
print(align)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 7 columns
AAAACGT Alpha
AAA-CGT Beta
AAAAGGT Gamma
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

a = SeqRecord(Seq("AAAACGT"), id="Alpha")
b = SeqRecord(Seq("AAA-CGT"), id="Beta")
c = SeqRecord(Seq("AAAAGGT"), id="Gamma")
d = SeqRecord(Seq("AAAACGT"), id="Delta")
e = SeqRecord(Seq("AAA-GGT"), id="Epsilon")

align = MultipleSeqAlignment([a, b, c, d, e])
align.extend([d, e])
print(align)
```

```
Alignment with 7 rows and 7 columns
AAAACGT Alpha
AAA-CGT Beta
AAAAGGT Gamma
AAAACGT Delta
AAA-GGT Epsilon
AAAACGT Delta
AAA-GGT Epsilon
PS C:\Users\MONSTER\Desktop\AlignIO>
```

```python
from Bio import AlignIO
align = AlignIO.read("clustalw.aln", "clustal")
print(align)
print(len(align))
```

```
Alignment with 7 rows and 30 columns
gi|6273285|gb|AF191659.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273284|gb|AF191658.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273287|gb|AF191661.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273286|gb|AF191660.1|AF191 TATACATAAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273290|gb|AF191664.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273289|gb|AF191663.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273291|gb|AF191665.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273285|gb|AF191659.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273284|gb|AF191658.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273287|gb|AF191661.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273286|gb|AF191660.1|AF191 TATACATAAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273290|gb|AF191664.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273289|gb|AF191663.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273291|gb|AF191665.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
7
PS C:\Users\MONSTER\Desktop\AlignIO> []
```

```python
from Bio import AlignIO
align = AlignIO.read("clustalw.aln", "clustal")
#print(align)
#print(len(align))

from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
dummy = SeqRecord(Seq("N"*30), id="dummy")
align.append(dummy)
print(align)
print(len(align))
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 8 rows and 30 columns
gi|6273285|gb|AF191659.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273284|gb|AF191658.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273287|gb|AF191661.1|AF191 TATACATTAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273286|gb|AF191660.1|AF191 TATACATAAAAGAAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273290|gb|AF191664.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273289|gb|AF191663.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
gi|6273291|gb|AF191665.1|AF191 TATACATTAAAGGAGGGGGGATGCGGATAAATGGAAAGGCGAAAG...AGA
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNN dummy
8
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment

a1 = SeqRecord(Seq("AAAAC"), id="Alpha")
b1 = SeqRecord(Seq("AAA-C"), id="Beta")
c1 = SeqRecord(Seq("AAAAG"), id="Gamma")
a2 = SeqRecord(Seq("GT"), id="Alpha")
b2 = SeqRecord(Seq("GT"), id="Beta")
c2 = SeqRecord(Seq("GT"), id="Gamma")

left = MultipleSeqAlignment([a1, b1, c1],
                            annotations={"tool": "demo", "name": "start"},
                            column_annotations={"stats": "CCCXC"})
right = MultipleSeqAlignment([a2, b2, c2],
                             annotations={"tool": "demo", "name": "end"},
                             column_annotations={"stats": "CC"})
print(left)
print(right)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 5 columns
AAAAC Alpha
AAAAC Alpha
AAA-C Beta
AAAAG Gamma
Alignment with 3 rows and 2 columns
GT Alpha
GT Beta
GT Gamma
```

```
Alignment with 3 rows and 7 columns
AAAACGT Alpha
AAA-CGT Beta
AAAAGGT Gamma
```

```
Alignment with 3 rows and 7 columns
AAAACGT Alpha
AAA-CGT Beta
AAAAGGT Gamma
3
3
3
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment
a = SeqRecord(Seq("AAAACGT"), id="Alpha")
b = SeqRecord(Seq("AAA-CGT"), id="Beta")
c = SeqRecord(Seq("AAAAGGT"), id="Gamma")
d = SeqRecord(Seq("AAAACGT"), id="Delta")
e = SeqRecord(Seq("AAA-GGT"), id="Epsilon")
align = MultipleSeqAlignment([a, b, c, d, e])
#first_record = align[0]
#print("%s %s" % (first_record.id, first_record.seq))

#last_record = align[-1]
#print("%s %s" % (last_record.id, last_record.seq))

#sub_alignment = align[2:5]
#print(sub_alignment)

#sub_alignment = align[::2]
#print(sub_alignment)

#rev_alignment = align[::-1]
#print(rev_alignment)

print(align[3, 4])
print(align[3][4])
print(align[3].seq[4])
print(align[:, 4])
print(align[1:3, 4])
print(align[1:5, 3:6])
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alpha AAAACGT
```

```
PS C:\Users\MONSTER\Desktop\Align
Epsilon AAA-GGT
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 7 columns
AAAAGGT Gamma
AAAACGT Delta
AAA-GGT Epsilon
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 7 columns
AAAACGT Alpha
AAAAGGT Gamma
AAA-GGT Epsilon
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 5 rows and 7 columns
AAA-GGT Epsilon
AAAACGT Delta
AAAAGGT Gamma
AAA-CGT Beta
AAAACGT Alpha
```

```
C
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
 C
 C
 C
 CCGCG
 CG
 Alignment with 4 rows and 3 columns
 -CG Beta
 AGG Gamma
 ACG Delta
 -GG Epsilon
```

```python
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Align import MultipleSeqAlignment
from Bio.SeqUtils import GC

align1 = MultipleSeqAlignment([
            SeqRecord(Seq("ACGT"), id="Human"),
            SeqRecord(Seq("ACGG"), id="Mouse"),
            SeqRecord(Seq("ACGC"), id="Chicken"),
        ])

align2 = MultipleSeqAlignment([
            SeqRecord(Seq("CGGT"), id="Mouse"),
            SeqRecord(Seq("CGTT"), id="Human"),
            SeqRecord(Seq("CGCT"), id="Chicken"),
        ])
print(align1 + align2)
align1.sort()
align2.sort()
print(align1 + align2)

print(align1)

align1.sort(reverse=True)
print(align1)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Alignment with 3 rows and 8 columns
ACGTCGGT <unknown id>
ACGGCGTT <unknown id>
ACGCCGCT Chicken
Alignment with 3 rows and 8 columns
ACGCCGCT Chicken
ACGTCGTT Human
ACGGCGGT Mouse
Alignment with 3 rows and 4 columns
ACGC Chicken
ACGT Human
ACGG Mouse
Alignment with 3 rows and 4 columns
ACGG Mouse
ACGT Human
ACGC Chicken
```

```python
from Bio import Align
aligner = Align.PairwiseAligner()
alignments = aligner.align("GAACT", "GAT")
alignment = alignments[0]
print(alignment)

alignment = alignments[1]
print(alignment)

aligner.mismatch_score = -10
alignments = aligner.align("AAACAAA", "AAAGAAA")
print(len(alignments))

print(alignments[0])
print(alignments[1])
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
target            0 GAACT 5
                  0 ||--| 5
query             0 GA--T 3
                  0 |-|-| 5
query             0 G-A-T 3

2
target            0 AAAC-AAA 7
                  0 |||--||| 8
query             0 AAA-GAAA 7

target            0 AAA-CAAA 7
                  0 |||--||| 8
query             0 AAAG-AAA 7
```

```python
from Bio import Align
aligner = Align.PairwiseAligner()
alignments = aligner.align("TACCG", "ACG")
for alignment in sorted(alignments):
    print("Score = %.1f:" % alignment.score)
    print(alignment)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Score = 3.0:
target            0 TACCG 5
                  0 -|-|| 5
query             0 -A-CG 3

Score = 3.0:
target            0 TACCG 5
                  0 -||-| 5
query             0 -AC-G 3
```

```
from Bio import Align
aligner = Align.PairwiseAligner()
aligner.mode = 'local'
alignments = aligner.align("TACCG", "ACG")
for alignment in sorted(alignments):
    print("Score = %.1f:" % alignment.score)
    print(alignment)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Score = 3.0:
target            1 ACCG 5
                  0 |-|| 4
query             0 A-CG 3

Score = 3.0:
target            1 ACCG 5
                  0 ||-| 4
query             0 AC-G 3
```

```
from Bio import Align
aligner = Align.PairwiseAligner()
aligner.mode = 'global'
aligner.match_score = 2
aligner.mismatch_score = -1
for alignment in aligner.align("TACCG", "ACG"):
    print("Score = %.1f:" % alignment.score)
    print(alignment)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Score = 6.0:
target            0 TACCG 5
                  0 -||-| 5
query             0 -AC-G 3

Score = 6.0:
target            0 TACCG 5
                  0 -|-|| 5
query             0 -A-CG 3
```

```
from Bio.Align import substitution_matrices, PairwiseAligner
aligner = PairwiseAligner()
aligner.substitution_matrix = substitution_matrices.load("BLOSUM62")
alignments = aligner.align("KEVLA", "EVL")
alignments = list(alignments)
print("Number of alignments: %d" % len(alignments))

alignment = alignments[0]
print("Score = %.1f" % alignment.score)

print(alignment)
```

```
PS C:\Users\MONSTER\Desktop\AlignIO> python -u "c:\Users\MONSTER\Desktop\AlignIO\Clustalw.py"
Number of alignments: 1
Score = 13.0
target            0 KEVLA 5
                  0 -|||- 5
query             0 -EVL- 3
```