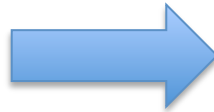


```

>sequence1
PPGVKSDCAS
>sequence2
PADGVKDCAS
>sequence3
PPDGKSDS
>sequence4
GADGKDCCS
>sequence5
GADGKDCAS

```



SeqA ♦	Name ♦	Length ♦	SeqB ♦	Name ♦	Length ♦	Score ♦
1	sequence1	10	2	sequence2	10	50.0
1	sequence1	10	3	sequence3	8	62.5
1	sequence1	10	4	sequence4	9	33.33
1	sequence1	10	5	sequence5	9	44.44
2	sequence2	10	3	sequence3	8	50.0
2	sequence2	10	4	sequence4	9	44.44
2	sequence2	10	5	sequence5	9	55.56
3	sequence3	8	4	sequence4	9	37.5
3	sequence3	8	5	sequence5	9	37.5
4	sequence4	9	5	sequence5	9	88.89



CLUSTAL 2.1 multiple sequence alignment

```

sequence1      PPGVKSDCAS 10
sequence3      PPDGKSD--S 8
sequence2      PADGVKDCAS 10
sequence4      GADGK-DCCS 9
sequence5      GADGK-DCAS 9
               ..  *  *

```

