

profile HMM

For each sequence

Hmsearch

MSA

Profile CEVEAPTAGPTTPNGNPVDECDQANCHSGTGDDFQLTG...GTTVLTEKP

ceveaptag+ p+g +++ + +++ t + + t tvlttekp

Sequence A CEVEAPTAGQPLPMGTWWM - - NVMMTRPTATAEQVM - TSSSQVVPTVLTEKP

.	.	.
.	.	.
7	t	1
8	a	1
9	g	1
10	+	0.92
11		0.77
12		0.62
13	p	0.77
14	+	0.69
15	g	0.84
16		0.69
17	+	0.61
18	+	0.53
19	+	0.45
20		0.3
21		0.15
22		0
23	+	0
.	.	.
.	.	.
.	.	.

Score

Low Similarity Segment

1.00

0.75

0.50

0.25

0.00

0 20 40

Position