

Übung 2. Bioinformatik

Aufgabe 2.1

2.1.1

A A K H W V
A S K M V V

$$I = 100 \times \frac{M}{L}$$

$$= 100 \times \frac{4}{6} \approx 67\%$$

$I > 30\%$ Wahrscheinlich zwei homologe Proteine

2.1.2

$$\text{Score: } 4 + 1 + 5 + 5 - 3 + 4 = 16$$

Aufgabe 2.4

$$\sigma = 0$$

	-	G	C	A	T	G
-	0	0	0	0	0	0
G	0	1	1	1	1	1
A	0	1	1	2	2	2
T	0	1	1	2	3	3
T	0	1	1	2	3	3
A	0	1	1	2	3	3

G C A T - G
: : :
G - A T T A

$$\sigma = -1$$

	-	G	C	A	T	G
-	0	-1	-2	-3	-4	-5
G	-1	1	0	-1	-2	-3
A	-2	0	1	1	0	-1
T	-3	-1	0	1	2	1
T	-4	-2	-1	0	2	2
A	-5	-3	-2	0	1	2

G C A T G
: : :
G A T T A

Aufgabe 2.5

2.5.1

- Wir nutzen BLASTp, weil query sequence, database sequence und Alignment für Proteine sind.

BLAST Program	Query Sequence	Database Sequence	Alignment
blastn	Nucleotide	Nucleotide	Nucleotide
blastp	Protein	Protein	Protein

- Wahrscheinlich gehört diese Sequenz zu den Hexokinasen
- Wahrscheinlich gehört diese Sequenz zu den Hexokinasen 1.
- die Percentage Identity ist $\sim 99\%$
- Der E. Score ist 0.0. E-value $< 10^{-6}$: Bestimmt homologe Sequenzen
E-value $< 0,01$: Wahrscheinlich homologe Sequenzen
Hier wissen wir nicht ob $E < 10^{-6}$ oder $E < 0,01$ ist. Aber wir können sagen, dass diese Sequenz wahrscheinlich ~~zu~~ Hexokinasen 1 ist. gehört.
zu den

☒ select all 100 sequences selected

GenPeptGraphicsDistance tree of resultsMultiple alignmentMSA View

Description		Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	hexokinase 1 [Saccharomyces cerevisiae S288C]	Saccharomyces ...	953	953	100%	0.0	99.79%	485	NP_116711.3
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	953	953	100%	0.0	99.59%	485	AEP68292.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM693]	Saccharomyces ...	951	951	100%	0.0	99.38%	485	AJU37745.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM1129]	Saccharomyces ...	951	951	100%	0.0	99.38%	485	AJU38858.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM1386]	Saccharomyces ...	951	951	100%	0.0	99.38%	485	AJV23225.1
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	950	950	100%	0.0	99.38%	485	AEP68272.1
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	950	950	100%	0.0	99.38%	485	AEP68293.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae FostersB]	Saccharomyces ...	949	949	100%	0.0	99.18%	485	EGA58845.1
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	949	949	100%	0.0	99.18%	485	AEP68270.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM195]	Saccharomyces ...	949	949	100%	0.0	98.97%	485	AJU35571.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM1336]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	AJV22291.1
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	AEP68295.1
<input checked="" type="checkbox"/>	hexokinase 1 [Saccharomyces cerevisiae]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	PTN13393.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae EC1118]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	CAY79505.1
<input checked="" type="checkbox"/>	hexokinase 1 [Saccharomyces cerevisiae]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	PTN32081.1
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	AEP68300.1
<input checked="" type="checkbox"/>	hexokinase isoenzyme 1 [Saccharomyces cerevisiae]	Saccharomyces ...	948	948	100%	0.0	98.97%	485	AEP68277.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM428]	Saccharomyces ...	948	948	100%	0.0	98.97%	485	AJU36282.1
<input checked="" type="checkbox"/>	Hxk1p [Saccharomyces cerevisiae YJM1463]	Saccharomyces ...	948	948	100%	0.0	99.18%	485	AJV25280.1

verschiedene varianten für verschiedene sequenzen