

a)  $S \rightarrow LS \rightarrow LLLLLLS \rightarrow LLLLLLL$   
 $\rightarrow ssLssss \rightarrow ssdFdssss$   
 $\rightarrow ssdddFdddsssss$   
 $\rightarrow ssdddLSdddsssss$   
 $\rightarrow ssdddLLLdddsssss$   
 $\rightarrow ssdddssssdddsssss$

b)

$$\begin{array}{c} s \quad ss \quad s \\ d-d \\ d-d \\ ss \quad d-d \quad sssss \end{array}$$

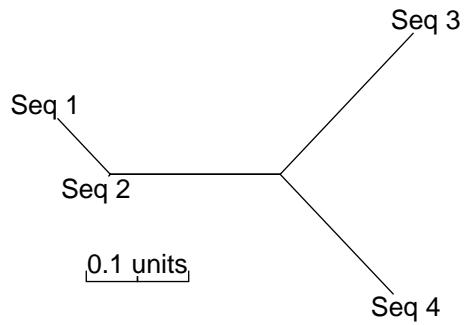
c)  $F \rightarrow dFd \rightarrow ddFdd \rightarrow ddLSdd$   
 $\rightarrow ddLLdd \rightarrow ddLsdd \rightarrow dddFdssdd$

	Stem		Loop		Overall
<i>AU/UA</i>	35.6%	<i>A</i>	36.4%	<i>A</i>	26.8%
<i>GC/CG</i>	53.4%	<i>C</i>	15.1%	<i>C</i>	21.4%
<i>UG/GU</i>	9.8%	<i>G</i>	21.2%	<i>G</i>	26.7%
Other	1.2%	<i>U</i>	27.3%	<i>U</i>	25.1%
	Total: 52.6%		Total: 47.4%		

$X \setminus Y$	$A$	$C$	$G$	$U$
$A$	-0.75	0.16	0.32	0.26
$C$	0.40	-1.57	0.24	0.93
$G$	0.55	0.17	-0.96	0.24
$U$	0.35	0.51	0.19	-1.05

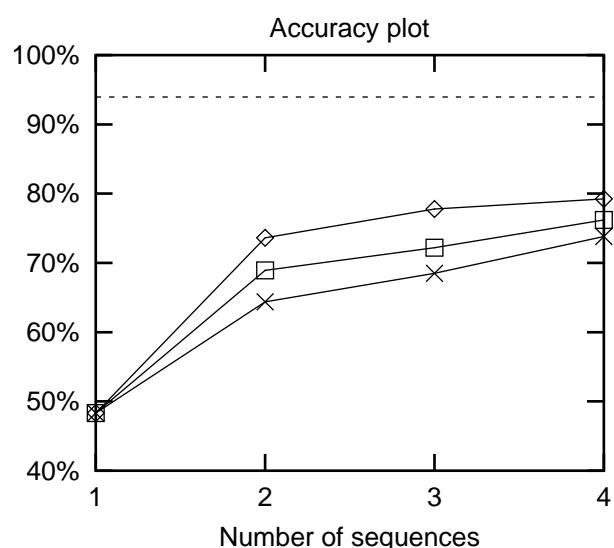
$X \setminus Y$	$AU$	$UA$	$GC$	$CG$	$UG$	$GU$
$AU$	-1.16	0.18	0.50	0.12	0.02	0.27
$UA$	0.18	-1.16	0.12	0.50	0.27	0.02
$GC$	0.33	0.08	-0.82	0.13	0.02	0.23
$CG$	0.08	0.33	0.13	-0.82	0.23	0.02
$UG$	0.08	1.00	0.10	1.26	-2.56	0.04
$GU$	1.00	0.08	1.26	0.10	0.04	-2.56

$X \setminus Y$	$A$	$C$	$G$	$U$
$A$	-1.15	0.13	0.79	0.23
$C$	0.09	-0.84	0.16	0.59
$G$	0.45	0.13	-0.70	0.11
$U$	0.18	0.70	0.16	-1.03



1 100  
 1: GAAGCUGACC AGACAGUCGC CGCUUCGUCG UCGUCCUCCU UCAGGGGGAG ACGGGCGGAG GGGAGGAAG UCCGGGCUCC AUAGGGCAAG GUGCCAGGUA  
 2: GGAGUUGACC AGACAGUCGC CGCUUCAUUG CCGUCCUC-U UCG-GGGGAG ACAGAUGGAG GGGAGGAAG UCCGGGCUCC AUAGGGCAGG GUGCCAGGUA  
 3: AGAGUCCAUU GGACAGUCGC UGCCUCUUAU -----G AAA----- -AUUAGGGG GGGAGGAAG UCCGGGCUCC AUAGGGCAAG GUGCCAGGUA  
 4: GGAGUGGGC AGGCGACCGC CGCGGA-----G CAA----- -----UCCG GGGAGGAAG UCCGGGCUCC AUAGGGCAAG GCGCCGGUA  
 s: (((((((((( ((((((((.((.(((((( {(.((((((. ....))))))) }))).))).))).)...[[[.[[[[[((( ...[[[.{{(( (((((..  
 p: (((((((((( .(((((((.((.(((((( (((((((((. ....))))))) )).))).))).)...(((...))).)..((((. ....)(( (((((..  
  
 101 200  
 1: ACGCCUGGGG GGUGUCACGA CCCACGACCA GUGCAACAGA GAGCAAACCG CGCA-UGGCC CGCGCAAGCG GGAUCA-GGU AAGGGUGAAA GGGUGCGGUA  
 2: ACGCCUGGGA GGC-GCAA-G CCUACGACUA GUGCAACAGA GAGCAAACCG CGCA-UGGCC CGCGCAAGCG GGAUCA-GGU AAGGGUGAAA GGGUGCGGUA  
 3: AUGCCUGGG GGC-GUGA-G CCUACCGAAA GUGCCACAGA AAAUA-ACCG CCUAAGCAC- ---UUCG--- -G-UGCAGG AAGGGUGAAA AGGUGCGGUA  
 4: ACGGCCGGGG GGC-GUGA-G CCUACCGAAA GUGCCACAGA AAAUAUACCG CCAA-GCGC- ---GUAA--- -G-CGC-GGU AAGGGUGAAA AGGUGCGGUA  
 s: .....))(( ((. ....))) .((. ....) .((. ....) ..((. ....) ((((( ((. ....))) )).))).)...((. ....) .((. ....) ..((. ....)  
 p: .....))(( ((. ....))) .((. ....) ))..... ....((. ....) ((((( ((. ....))) )).))).))...((. ....) .((. ....) ..((. ....)  
  
 201 300  
 1: AGAGCGCACCG GCGCGCCUGG UAACAGUCCG CGGCACGGUA AACUCCACCC GGAGCAAGGC CAAAUAGGG UUCAUAGGU ACGGCCGUA CUGAACCGGG  
 2: AGAGCGCACCG GCGCGCCUGG UAACAGUUCG UGGCACGGUA AACUCCACCC GGAGCAAGGC CAAAUAGGG UUCAUAGGU ACGGCCGUA CUGAACCGGG  
 3: AGAGCGCACCG GCAACGACUGG CAACAGUUCG UGGCUAGGU AACCCCACUU GGAGCAAGAC CAAAUAGGG UCCA--AGGC GUUGGCCCGG CUGGAACCGG  
 4: AGAGCGCACCG GCAUUUCCGG UAACGG-AAA UGGCAGGGAA AACCCCACCU GGAGCAAGAC CAAAUAGGG UGCGA-UACC GUUGGCCCGG GUGCACCGG  
 s: .....))(( ((. ....))) .((. ....) .((. ....))) ).... . ....) ..)))))))} ))))...((. ....) ((. ....) ((. ....))) )....  
 p: .....))(( ((. ....))) .((. ....) .((. ....))) ).... . ....) ..)))))))} ))))...((. ....) ((. ....) ((. ....))) )....  
  
 301 385  
 1: GUAGGCUGCU UGAGCCAGUG AGCGAUUGCU GGCCUAGAUG AAUGACUGUC CACGACAGAA CCCGGCUUAU CGGUCAACUC CACCU  
 2: GUAGGCUGCU UGAGCCAGUG AGCGAUUGCU GGCCUAGAGG AAUGACUGUC CACGACAGAA CCCGGCUUAU CGGUCAACUC CUCU-  
 3: GUAGGUUGCU AAAGAUGUCC AGUGAUGGCC AUCGUAGACG AAUGACUGUU CAAGACAGAA CCCGGCUUAU AGAUCCACUC UCCAC  
 4: GUAGGUUGCU GGAGCCUGUG CGUAAGUGCA GGCCUAGAGG AAUGGUCGUC CACGACAGAA CCCGGCUUAU CGGGCCACUC CAAU  
 s: .....))... ....((. ....))) ).... . ....) ..))))))) ..... ]]]]]])..) .))))))) )....  
 p: .....))... ....((. ....))) ).... . ....) ..))))))) ..... . ....) ..))))))) )....

Structural alignment				
No of sequences	1	2	3	4
Min result	41.2%	65.2%	73.9%	79.2%
Max result	57.7%	82.1%	79.6%	79.2%
Average	48.3%	73.6%	77.8%	79.2%
CLUSTAL W alignment				
No of sequences	1	2	3	4
Min result	41.2%	54.9%	60.1%	73.8%
Max result	57.7%	69.1%	76.9%	73.8%
Average	48.3%	64.4%	68.5%	73.8%
Structural alignment, no phylogeny				
No of sequences	1	2	3	4
Min result	41.2%	59.9%	67.7%	76.2%
Max result	57.7%	76.6%	76.6%	76.2%
Average	48.3%	68.9%	72.2%	76.2%



Using a certainty limit

Limit	No of pos	Correct pos	Accuracy
0%	1459	1156	79.2%
50%	1314	1146	87.2%
70%	1150	1064	92.5%
80%	1068	1014	94.9%
90%	932	890	95.5%
95%	825	799	96.8%

Sequence	SCFG method	MFOLD
Seq 1	57.7%	67.1%
Seq 2	48.2%	54.0%
Seq 3	41.2%	35.6%
Seq 4	46.2%	50.3%
Average	48.3%	51.7%