

a) $S \rightarrow LS \rightarrow LLLLLLLS \rightarrow LLLLLLLL$
 $\rightarrow ssLsssss \rightarrow ssdFdsssss$
 $\rightarrow ssdddFdddsssss$
 $\rightarrow ssdddLSdddsssss$
 $\rightarrow ssdddLLLLdddsssss$
 $\rightarrow ssdddsssssdddsssss$

b)

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

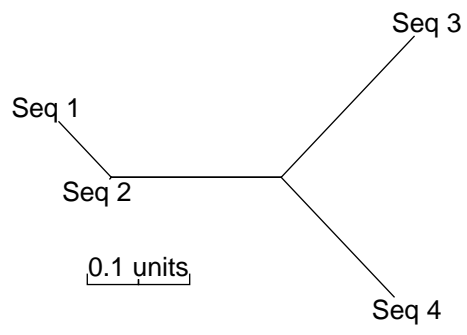
c) $F \rightarrow dFd \rightarrow ddFdd \rightarrow ddLSdd$
 $\rightarrow ddLLdd \rightarrow ddLsdd \rightarrow dddFdsdd$

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%			

$X \backslash Y$	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

$X \backslash Y$	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



Structural alignment

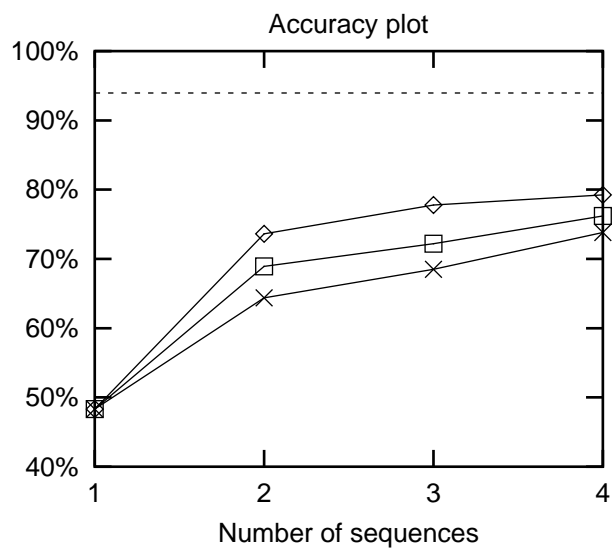
No of sequences	1	2	3	4
Min result	41.2%	65.2%	73.9%	79.2%
Max result	57.7%	82.1%	79.6%	79.2%
Average	48.3%	73.6%	77.8%	79.2%

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%