



sequence + structure  
profile (CM): 17 bits

consensus  
secondary  
structure

individual secondary structures

Ecoli	Bsubt	Hpylo	Spneu
U C	U C	U C	U C
U G	U G	U G	U G
G·C	C·G	A·U	U·A
U·A <sup>U</sup>	C·G <sup>C</sup>	C·G <sup>A</sup>	U·A <sup>U</sup>
G·C	G·C	G·C	G·C
Nequi	Tcele	Mther	Ssulf
U C	U C	U C	U C
U G	U G	U G	U G
C·G	G·C	U·A	A·U
U·A <sup>A</sup>	C·G <sup>G</sup>	C·G <sup>G</sup>	U·A <sup>C</sup>
G·C	G·C	G·C	G·C

struct

<<<---->->>

struct

Ecoli	GUGUUCGCUAC
Bsubt	GCCUUCGGCGC
Hpylo	GCAUUCGUAGC
Spneu	GUUUUCGAUAC
Nequi	GUCUUCGGAAC
Tcele	GCGUUCGCGGC
Mther	GCUUUCGAGGC
Ssulf	GUAUUCGUCAC



1 2 3 4 5 6 7 8 9 10 11

sequence profile  
(profile HMM) :14 bits