



## Naming Scheme:

Search Method:  
SBH = Specific Best Blast Hit,  
BBH = Best Blast Hit,  
HMM = HMM profile search

Completeness of the sequence  
in the trimmed alignment

Unique ID

Paralog ID

Trepomonas sp. PPS6 DAR\_BBH\_q1c\_0.82@TrepoPPS6DAR..p2345435

Long Name

Order of hit

Starting Database BLAST:

c = corresponding ortholog alignment IS best hit

n = corresponding ortholog alignment IS NOT best hit