

Homo_sapiens_ KFKPQSLPDHKWEMCTSIDKFSWGYRRDMALSDVTEESEI I SELVQTVSL
 Thermotoga_maritima_MSB8 --YPGDLPGYKWEFTRGIG-LSFGYNRNEGPEHMLSVEQLVYTLVDVVS
 * .**.:***: .*. :*:**.*: :*:**

Homo_sapiens_ GGNLLNIGPTKDGLIVPIFQERLLAVGKWL SINGEAIYASKPWR--VQW
 Thermotoga_maritima_MSB8 GGNLLNVGPKGDGTIPDLQKERLLGLGEWLRKYGDAIYGTSVWERCCA
 *** ***:** . ** * : :****.:** *:**.:. *

Homo_sapiens_ EKNTTSVWYTSKGSAVYAI FLHWPENGLNLESPITTSTTKITMLGIQGD
 Thermotoga_maritima_MSB8 TEDGTEIRFTRKCNRI FVIFLGIPTGEKIVIEDNLSAGTVRHFL--TGE
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Homo_sapiens_ LKWSTRDPDKGLFISLPQLPPSAVPAEFAWTIKLTGVK
 Thermotoga_maritima_MSB8 RLSFKNVGKNLEITVPKKLLETDSITLVLEAVEE---
 .: .*. * ***: : .: . . .

Sequence type explicitly set to Protein
 Sequence format is Pearson
 Sequence 1: Homo_sapiens_ 461 aa
 Sequence 2: Thermotoga_maritima_MSB8 449 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 31

