The inferred HIM-5 amino acid sequence

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MSRIRSNNDN IIILTDEQRK TVGRIAGRSQ NRNTSKKIAD GPYFLPRYRI
RDNAERSVGA RFKSLPQKEQ DEVVNEAFSN LREYLKKREP FYAKLRKANS
KYSSKPKERE KSVDSNDEAD RRNKGNKKTQ KNASKNCQIE KSSNNSGILK
KSGSGISVAS KPKKSVAFAP GVYEDLSTDD DLEFLNSVIV NSDRPTSQCD
NPARRMCGRP PTKHRDTEQS QEITGSKKQK IFPTPHEKPA WWSFRIPKKR
AQ
```

Results from using LALIGN to compare him-5 with hsp83 from *Drosophila melanogaster*.

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Waterman-Eggert score: 72;  21.6 bits; E(1) <  0.054
24.0% identity (53.8% similar) in 104 aa overlap (48-151:158-255)
        50        60        70        80        90       100       110       120
him-5  YRIRDNAERSVGARFKSLPQKEQDEVVNEAFSNLREYLKKREPFYAKLRKANSKYSSKPKEREKSVDSNDEADRRNKGNK
       . .: .  .. :   : .   ..:..     :...: ..:.  : .   :   .     ::::: : :.:::: ..: .
HSP83  FTVRADNSEPLGRGTKIVLYIKEDQTDYLEESKIKEIVNKHSQFIGYPIKLLVE-----KEREKEV-SDDEADDEKKEGD
       160       170       180       190       200       210             220       230

       130       140       150
him-5  KTQKNASKNCQIEKSSNNSGILKK
       . ..  . . .::  ...    ::
HSP83  EKKEMETDEPKIEDVGEDEDADKK
             240       250
```

Figure S1 The inferred amino acid sequence of HIM-5 is highly basic and novel.The region of optimal alignment with HSP83 from Drosophila melanogaster is highlighted in red and the alignment is shown at the bottom. The E value is 0.05, as shown. The sequence KEREKxVxSxxDEAD is not identical in the HSP83 proteins from other species so its function is not known.