

Hendrix Top FuzzBuster Bottom Hendrix calls frameshift

unnamed protein product

Sequence ID: Query_37395 Length: 106 Number of Matches: 1

Range 1: 23 to 106 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
57.8 bits(138)	4e-17	Compositional matrix adjust.	34/105(32%)	54/105(51%)	21/105(20%)
Query 20	GVQYLINPPKTSLTMDMADTMGSFTAKKLDENASDAEQQAMKESRKASKKTREALNTWM				79
	G +YL+ PPK+++ + +A GS A D EA+ +W+				
Sbjct 23	GFEYLVTPPKSTIAIALA---GSLKAAGEDPAL-----LMEAMESWI				61
Query 80	LQAFGADGFQEIQRKLDPLDKLDIEHVMELMNAVAEAKTGNPTT				124
	+AFG +++ RL D D LDI+H+++LM +AE TG+PTT				
Sbjct 62	DKAFGKKQAPKVRARLLDEEDPLDIKHIVDLMQQQLAEVTTGDPTT				106

Hendrix
EAKTGNPTT
KP

FuzzBuster
EVTTGDPTT
RP

FuzzBuster Top MementoMori (EI) Bottom EI's don't call frameshift

>MementoMori_30, function unknown, 109
Length = 109

Score = 69.3 bits (168), Expect = 2e-12
Identities = 41/104 (39%), Positives = 63/104 (60%), Gaps = 5/104 (4%)

Query: 6	IVIDLEPAKPVTVGLGEGFEYLVTPPKSTIAIALAGSLKAA---GEDPALLMEAMESWID				62
	I ID +P + VTV L G YL+TPPK+ + I LA AA G+ ++ E M W+				
Sbjct: 4	ITIDAQPREQVTVHL-VGKPYLLTPPKAALGIELAKKATAAQASGDIESIWGEIM-GWLT				61
Query: 63	KAFGKKQAPKVRARLLDEEDPLDIKHIVDLMQQQLAEVTTGDPTT				106
	A G+ QA ++ARL D D LD+ HI+++M+++ E T +P++				
Sbjct: 62	MAVGETQAAAIQARLDDNDDLDVIHIIIEVMEKVIEAVTENPSS				105

EI's Missing Glycine

Start pos

Mouse pos

20230

20240

Q Q L A E V T T G D P T T * S S

A A A R R G H D G R P Y Y V V V R

C S S S P R S R R A T L L R S R P

TG CAGCAGCTCGCCGAGGTCACGACGGGGCGACCCCTACTACG TAG TCGTCC

ACGTCTGTCTGAGCGGCTCC AGTG CTGCCCCTGG GATGAT GCATCAGCAGG

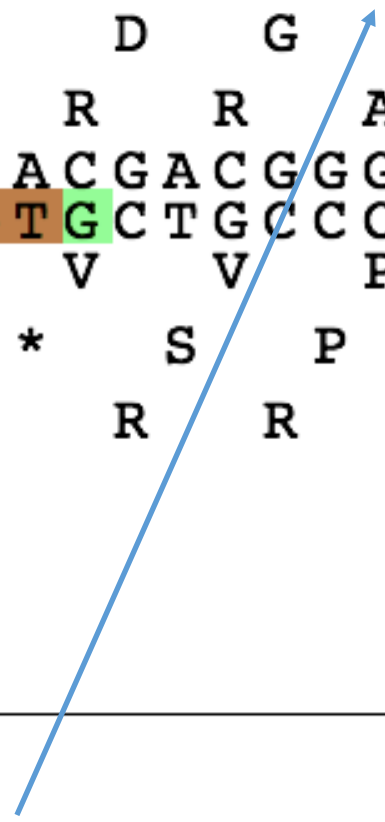
I C C S A S T V V P S G V V Y D D

A A A R R P * S P R G * * T T T

H L L E G L D R R A V R S R L R G

Henrix
EAKTGNPTT
KP

FuzzBuster
EVTGDPPT
RPYY



- >Hendrix gp68
- MELIEIEAKAAELIPIKLVGVQYLINPPKTSLTMDMADTMGSFTAkkLDENASDAEKQQAMKESRKASKKTREALNTWMLQA
FGADGFQEIQRLKDPLDKLDIEHVMELMNAVAEAKTGNPTT
-
- >Hendrix gp69
- MELIEIEAKAAELIPIKLVGVQYLINPPKTSLTMDMADTMGSFTAkkLDENASDAEKQQAMKESRKASKKTREALNTWMLQA
FGADGFQEIQRLKDPLDKLDIEHVMELMNAVAEAKTGKPYVYRYGQIALENWADLDGYAVGHNMPDLRSLPLERFCNW
MWWMLTKNAKNEQEKEKLRAKIWRPPPEQLKKSVPIDKRSPWSAENEMKAFGALKMQLMPSAPPKPSATPEAVS
-
- >FuzzBuster_Draft gp38
- MPKTRIVIDLEPAKPVTVGLGEGFEYLVTPPKSTIAIALAGSLKAAGEDPALLMEAMESWIDKAFGKKQAPKVRARLLDEEDPL
DIKHIVDLMQQLAEVTTGDPTT
-
- >FuzzBuster_Draft gp39
- MEDLRTLSDRFCNYVYWMATRNASATDIEKFRARLWRPPKGEVPDDRSPWSQANETGAFQALKAGLGLGAKTSAS