

Table S7. BlastX results with the list of genes associated with RNAi mechanism identified in the *T. absoluta* assembled transcriptome at $E\text{-value} < e^{-30}$ using homologues, particularly from *Bombyx mori*.

BLASTX 2.2.29+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Database: herai/heraiprot.txt
93,476 sequences; 49,077,216 total letters

Query= gi|164448645:280-2625 *Bombyx mori* sid-1-related gene1 (Sir-1), mRNA

Length=2346

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript74094_1	407	9e-127
ta_transcript44271_1	131	3e-33
ta_transcript44268_1	132	4e-32
ta_transcript44264_1	134	1e-31

> ta_transcript74094_1
Length=937

Score = 407 bits (1045), Expect = 9e-127, Method: Compositional matrix adjust.
Identities = 215/425 (51%), Positives = 289/425 (68%), Gaps = 7/425 (2%)
Frame = +1

Query	1078	RED-SAETDTQPILEAGAADESWSREHA--LTVGKLTRAPDPTLARRSDRYFWGALT LAV	1248
		RED S+ +DT+ + + +A L V L+R P L RS Y W LT+AV	
Sbjct	503	REDCSSPSDTESEISTVVEPDPKTTYAGRLCVANLSRCRPRVLQARSKMYLWNILTVAV	562
Query	1249	VYALPVVQLLLTYQRMVFQTDGQDLCYNNFLCAHPLGTLSDFNHVFVSNVGYVLLGAVFAG	1428
		Y LPV+QL++TYQR++ Q+G+QDLCY+NFLCAHPL LSDFNHV+SN+GYV+LG++F	
Sbjct	563	FYTLPLVIQLVVTYQRLNQSNGQDLCYFNFLCAHPLMVLSDFNHVSNLGYVILGSLFLF	622
Query	1429	QVRFRQVKSQRQP---ENLGIPQHYGLLYSMGLALSMEGLLSACYHLCPNKMNQFDSSSF	1599
		QV R P + LGIPQH+GLLY+MG+AL EGLLSA YH+CPN MNFQFD+SF	
Sbjct	623	QVWRRHSYHTIMPAHRKELGIPQHFGLLYAMGIALVSEGLLSAAYHVCPSNMNFQFDTSF	682
Query	1600	MYVIAVLVTLKLYQNRHSDIIPSAHSTFMILAVIMTIGLFGILHPSAGFAASFTLLHLGA	1779
		MYV +VL +K+YQ+RH DI AH+TF +LA+I+ IGL G+L+ + F FT+LHL	
Sbjct	683	MYVTSVLCMVKIYQSRHPDINARAHATFGVLALIIIFGLVGVNLNANFYFWIMFTVLHLLT	742
Query	1780	CLVLTCLKIYYAGRFKMDRRVLLRAYAHVAARGWRSLLPAHPYRagllgJanlanwslagY	1959
		CLV+T +IYY GRF++D V+ RA + R ++ P H R +L LANL+NW++A Y	
Sbjct	743	CLVMTFQIYYLGRFRLDGGVVYRAARELIRPLAAITPTHCGRCVMLLLANLSNWAIAAY	802
Query	1960	SVYSHHNTDLARQLLAILMGNAILYTMFYVMVKLVNRERILARTWMYCILAHVAWFLALR	2139
		V S H+ D A LL +LM N LYT+FY+VMKL++RE I +W++ L + WF +	
Sbjct	803	GV-SQHSRDFASHLLLVLMNSNLFYTLFYIVMKLLHRETIGWYSWVFIALTYSVWFSSSY	861
Query	2140	LFLDSKTKWSETPAQSRQHNA PCSSLSFYDTHDLWHGVSAALFLSFNMLLTMDALRDT	2319
		+LD T W+ +PA+SRQ N CS L YD+HD+WH +S+ A+F SFNM LT+DD L +	
Sbjct	862	FYLDQSTNWALSPAESRQSNRQCSSLQLYDSHDIWHFMSSIAMFFSFNMYLTIDDGLLN	921
Query	2320	PRDQI 2334	
		RD+I	
Sbjct	922	GRDEI 926	

Score = 223 bits (569), Expect = 1e-60, Method: Compositional matrix adjust.
Identities = 135/330 (41%), Positives = 181/330 (55%), Gaps = 48/330 (15%)
Frame = +1

Query	91	FQYN-IYNYDTWINLQVNNTIEQILDFTEDSDKLLGFPTRVHVTTNSTLTSDHPLFITAT	267
		F YN Y Y+ + V+ E I++F D +K P RV V ++ +PLFITAT	
Sbjct	83	FHYNNYKYKNVEYVVDVDKHTEYIMEFAGD-EKAYDTPARVTVASDFA-NRTYPLFITAR	140

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Query 268 QQKGVSWSWELPLVLQTDYFLMLNDMGRITLCPH-----DAGSDIRRESPPTVQLTTSS 426
          QQKGV SW+LP+++QT      N++ RTLCPH      + D+ + P V LT++S
Sbjct 141 QQKGVFSWQLPLMLIQTPMSLEQFNNISRTLCPHNNLYNEDEESCDVTTINTPIVHLTSAS 200

Query 427 SANVSVDIKLRVEDFYIELGKVNIVNPSSPRYYYYFSFDQNPW----- 561
          + V I ++ V DFYI K + V PS P+YY++ F QNP
Sbjct 201 PEPIRVTIVVESVLDFYIVTNKTTNMTVTPSQPKYFYFYPFKQNPDLHTQKIKKKYKCN 260

Query 562 -NVSHAAGGPLDG-----TQRYNY-NIPKSVILVIESDDEICATVSIQNNSCPVFND 711
          + H LD      ++Y++ PKSVI++IESDD+ICA VSIQN SCPVFND
Sbjct 261 EELDHKELISLDRYFLKSNALKRQYSWLTRPKSVIVMIESDDDICAVVSIQNFSCPVFND 320

Query 712 EREVKYKGYHLTMSSQGGITLTQAMFPGFYVVLIVRQSDADCT--GASETE----- 861
          ER++ Y GY+LTM+ +GGITLTQ MFP GFY+V IV+ SD DC G S+
Sbjct 321 ERDILYDGYLLTMTRRGGITLTQDMFPLGFYIVFIVKSSDDDCVMGGVSDVNVSRITVRW 380

Query 862 ---DAPKSFPAKRSKTFRLKIIATISYQEY 942
          A + R KTF +II TISY+EY
Sbjct 381 QHGKATATSDDGRVKTFSFRIIETISYREY 410

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> ta_transcript44271_1
Length=224

Score = 131 bits (329), Expect = 3e-33, Method: Compositional matrix adjust.
Identities = 87/175 (50%), Positives = 105/175 (60%), Gaps = 2/175 (1%)
Frame = -2

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Query 1712 PIVMMTARIMKVECALGMMSECLFWYSLSVTSTAITYMNDESNNWKFILLGQRW*QADRRP 1533
          P+ M TA KV CA +MS C WY ++ STA TYMN SNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKACARALMSGCRDWYIFTMLSTASTYMNNAVSNWKLRLGQMW*VAESSA 79

Query 1532 SMLRARPIEYSSP*CWGMPKFS--GRCLLLTCLKRTWPANTAPSS*PTLENTWLKSESV 1359
          + + P SSP*C GMP S G L +RT N+APSS *P LENTWLKSE+
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIIRRRRTCSMNSAPSSK*PRLENTWLKSETP 139

Query 1358 PSGWAHRKL**HRSWSPVWNTMRWYVSSSCTTGSAYTASVRAPQKYLSDLLASV 1194
          P G AHRKL**HRS P + W V+++C TGSA T +V + +YLS+ SV
Sbjct 140 PHGCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVCRLSERADSV 194

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> ta_transcript44268_1
Length=404

Score = 132 bits (331), Expect = 4e-32, Method: Compositional matrix adjust.
Identities = 87/175 (50%), Positives = 105/175 (60%), Gaps = 2/175 (1%)
Frame = -2

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Query 1712 PIVMMTARIMKVECALGMMSECLFWYSLSVTSTAITYMNDESNNWKFILLGQRW*QADRRP 1533
          P+ M TA KV CA +MS C WY ++ STA TYMN SNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKACARALMSGCRDWYIFTMLSTASTYMNNAVSNWKLRLGQMW*VAESSA 79

Query 1532 SMLRARPIEYSSP*CWGMPKFS--GRCLLLTCLKRTWPANTAPSS*PTLENTWLKSESV 1359
          + + P SSP*C GMP S G L +RT N+APSS *P LENTWLKSE+
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIIRRRRTCSMNSAPSSK*PRLENTWLKSETP 139

Query 1358 PSGWAHRKL**HRSWSPVWNTMRWYVSSSCTTGSAYTASVRAPQKYLSDLLASV 1194
          P G AHRKL**HRS P + W V+++C TGSA T +V + +YLS+ SV
Sbjct 140 PHGCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVCRLSERADSV 194

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> ta_transcript44264_1
Length=747

Score = 134 bits (337), Expect = 1e-31, Method: Compositional matrix adjust.
Identities = 87/175 (50%), Positives = 105/175 (60%), Gaps = 2/175 (1%)
Frame = -2

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Query 1712 PIVMMTARIMKVECALGMMSECLFWYSLSVTSTAITYMNDESNNWKFILLGQRW*QADRRP 1533
          P+ M TA KV CA +MS C WY ++ STA TYMN SNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKACARALMSGCRDWYIFTMLSTASTYMNNAVSNWKLRLGQMW*VAESSA 79

Query 1532 SMLRARPIEYSSP*CWGMPKFS--GRCLLLTCLKRTWPANTAPSS*PTLENTWLKSESV 1359
          + + P SSP*C GMP S G L +RT N+APSS *P LENTWLKSE+
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIIRRRRTCSMNSAPSSK*PRLENTWLKSETP 139

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Query 1358  PSGWAHRKL**HRSWSPVWNTMRWYVSSSCTTGSAYTTASVRAPQKYLSDLLASV 1194
           P G AHRKL**HRS   P   + W V+++C TGSA  T +V +  +YLS+   SV
Sbjct 140   PHGCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVCRYLSERADSV 194

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Query= gi|512925015:122-4090 PREDICTED: Bombyx mori sid-1-related gene2 (Sir-2), mRNA

Length=3969

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript74094_1	1033	0.0
ta_transcript84451_1	709	0.0
ta_transcript84449_1	714	0.0
ta_transcript84450_1	712	0.0
ta_transcript84448_1	713	0.0
ta_transcript84453_1	464	3e-150
ta_transcript44271_1	156	2e-41
ta_transcript44268_1	156	9e-40
ta_transcript44264_1	158	7e-39
ta_transcript44270_1	135	5e-34

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> ta_transcript74094_1
Length=937

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Score = 1033 bits (2672), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 519/821 (63%), Positives = 609/821 (74%), Gaps = 58/821 (7%)
Frame = +1

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Query 1651  YDVPARVTVACDSANRTYPLFVTARQQKGVFSWQLPMLVQTPVTTEQFTSISRTLCPHNN 1830
           YD PARVTVA D ANRTYPLF+TARQQKGVFSWQLPML+QTP++ EQF +ISRTLCPHNN
Sbjct 116   YDTPARVTVASDFANRTYPLFITARQQKGVFSWQLPMLIQTPMSLEQFNNISRTLCPHNN 175

Query 1831  MFDEDAEACDAPSLNTPIVHLTSSSSSEQLKVTLVEKVQDFYIKINQNTINITVSPSQPKY 2010
           +++ED E+CD ++NTPIVHLTS+S E ++VTI+VE V DFYI N+T N+TV+PSQPKY
Sbjct 176   LYNEDEESCDVTINTPIVHLTSASPEPIRVTVIVESVLDFYIVTNKTTNMTVTPSQPKY 235

Query 2011  YFYFPFKKGSGKTVDFDEQKMRKEYICGASGGRGHGEV-----QRNEVG--YGWLSRP 2160
           YFYFPK+   +D QK++K+Y C   H E+   + N +   Y WL+RP
Sbjct 236   YFYFPKQN--PELDLHTQKIKKKYKCNEE--LDHKELISLDRYFLKSNALKRQYSWLTRP 291

Query 2161  ENVIFMIESDDELCAVVSIGNFSCPVFDNERDILYDGYLTMTRRGGITLTQDTFPIGFY 2340
           ++VI MIESDD++CAVVSIGNFSCPVFDNERDILYDGYLTMTRRGGITLTQD FP+GFY
Sbjct 292   KSVIVMIESDDDICAVVSIGNFSCPVFDNERDILYDGYLTMTRRGGITLTQDMFPLGFY 351

Query 2341  IVFIVKTSDEDCKEPGTNGSVPAVARLLGWGDNIQVSSSTEGRVKNFRFKIVETISYREYL 2520
           IVFIVK+SD+DC G +   +   +   +S +GRVK F F+I+ETISYREYL
Sbjct 352   IVFIVKSSDDDCVMGGVSDVNVSRITVRWQHKGATATSDDGRVKTFSFRIETISYREYL 411

Query 2521  IAAGATVLFYASFYLAFFVFVLYQSRKSTGVEHQDQET----- 2634
           IAAGA + F+ SFY F + V+YQ + G+ D +T
Sbjct 412   IAAGAVLGGFFMSFYAGFAIVVYQ--RVQGLRRSDSDTLDSSEEGRSTPPTASYDDTATQ 469

Query 2635  -----IVRsshgsegqssgeggsLPRPT-DGSSVD---SQDTESEYSTLDDVTDKELY 2787
           +V +   S +S +   R DG + +   S SDTESE ST+ V D +
Sbjct 470   TTRRRVVNAMSASVESTSRQSDLQQRLVGDGDAREDCSSPSDTESEISTV--VEPDPKT 527

Query 2788  RYGTKLCLADLSRCRARVLATRSNRYLWTVLTVSVFYTLPLVLQLVVTYQRLLNQSGNQDL 2967
           Y +LC+A+LSRCR RVL RS YLW +LTV+VFYTLPV+QLVVTYQRLLNQSGNQDL
Sbjct 528   TYAGRLCVANLSRCRPRVLQARSKMYLWNILTVAVFYTLPLVLQLVVTYQRLLNQSGNQDL 587

Query 2968  CYFNFFCAHPLMMLSDFNHVFNLGYVVLGALFLLQVWRRQRIMRNEPEEKKQKQIPQHF 3147
           CYFNF CAHPLM+LSDFNHV+NLGYV+LG+LFL QVWRR   P +K+ GIPQHF
Sbjct 588   CYFNFLCAHPLMVLSDFNHVYNLGYVILGSLFLFQVWRRHSYHTIMPAHRKELGIPQHF 647

Query 3148  GLLYAMGVALISEGFLSAAYHVCPNSMNFQFDTSFMYVTSALCMVKIYQSRHPDINARAH 3327
           GLLYAMG+AL+SEG LSAAYHVCPNSMNFQFDTSFMYVTS LCMVKIYQSRHPDINARAH
Sbjct 648   GLLYAMGIALVSEGLLSAAYHVCPNSMNFQFDTSFMYVTSVLCMVKIYQSRHPDINARAH 707

Query 3328  ATFGVLALIIIFIGLVGVNLNANVYFWVAFTALHLLTCFFITFQIYYLGRFKLDMGWVRAAS 3507
           ATFGVLALIIIFIGLVGVNLNAN YFW+ FT LHLLTC +TFQIYYLGRF+LD G V A+
Sbjct 708   ATFGVLALIIIFIGLVGVNLNANFYFWIMFTVLHLLTCLVMTFQIYYLGRFRLDGGVVYRAA 767

Query 3508  RGAALRP-----SRGLMLLLANLINWGLAGYGVAGHSRDFASHLLLVLMTNLFlyT 3660
           R   RP   R +MLLLANL NW +A YGV+QHSRDFASHLLLVLMTNLFlyT

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Sbjct 768 RELIRRPLAAITPTHCGRCVMLLLANLSNWAIAAYGVSQHSRDFASHLLLVLMSNLFlyT 827
Query 3661 LFYIVMKLLHRETITCYTWVFIVLTYSWAGSSYFYLDQNTNWALSPAQSRERNAACSVL 3840
LFYIVMKLLHRETI Y+WVFI LTYS W SSYFYLDQ+TNWALSPA+SR+ N CS+L
Sbjct 828 LFYIVMKLLHRETIGWYSWVFIALTYSVWVSSSYFYLDQSTNWALSPAESRQSNRQCSLL 887
Query 3841 RLFDADAWHAMSAMVAMFLSFNMYLTLDGLAGADRARPV 3963
+L+D+HD WH MS++AMF SFNMYLT+DDGL R + V
Sbjct 888 QLYDSHDIWHFMSSIAMFFSFNMYLTIDGLNVGRDEIAV 928

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> ta_transcript84451_1
Length=645

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Score = 709 bits (1831), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 402/606 (66%), Positives = 455/606 (75%), Gaps = 56/606 (9%)
Frame = +1

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Query 1 MTEWYRMKTGLNNKHNSSELSVETSCDMSDPFNIFSDNLSPIPASIVPRKLDfSNLDDDD 180
M E YRMK G N+KHNSSELSVETSCD SDPFN+FSDNLSPIPASIVPRKLDf+N+DD+D
Sbjct 34 MAETYRMKDGYNHKNHNSSELSVETSCDTSDFPNMFSDNLSPIPASIVPRKLDfTNVDDDED 93
Query 181 GIRDESQAPVSHSPPYKRVRLRLFDSPHTPKTLLEKCSPTPHHPPTRLFPKINVQTg 360
++D S AP+S SPPYKRVRLRLFDSPHTPKTLLEKCSPTPH+ RTRLFPK++V T
Sbjct 94 PMKDASMAPMSLSPPYKRVRLRLFDSPHTPKTLLEKCSPTPHNNTRTLFPKLSV-TN 152
Query 361 mpsgsshhhlhpsgdddsALGSLPPDELDESRLTVRRPIANINPFTPDGQALNKKKRALS 540
S H P DDDASALGSL PD+ S L +RR +ANINPFTP GQALNKKKRALS
Sbjct 153 GIPSGSSHHHLHPPSDDASALGSLLPDD---SGLAIRRSVANINPFTPDGQALNKKKRALS 209
Query 541 KTPTWDGTPEQPAKRLRESNISRYNVEFIELGVIGRGQFGRVTRCVNKLDGCVYALKRSL 720
KTPTWD +PE PAKRLRESNISRY VEF+EL VIGRG+FG VT+CVNKLDGCVYA+KRS+
Sbjct 210 KTPTWDASPELPAKRLRESNISRYTVEFVELEVIGRGEFGLVTKCVNKLDGCVYAIKRSI 269
Query 721 R PVAGSAAERAAALTEVYAHAAALGKHPHVVRYSAWAEDDHMI IQNEYCDGGS LQ LK MED- 897
+PVAGSAAERAAALTEVYAHAAALGKHPHVVRYSAWAEDDHMI IQNEYCDGGS LQ + D
Sbjct 270 KPVAGSAAERAAALTEVYAHAAALGKHPHVVRYSAWAEDDHMI IQNEYCDGGS LQ QYVTDN 329
Query 898 GplpesellilshiaaGLAYIHSQQLVHMDVKPGNIFICSGD VDACRESDDGYDDEEPA 1077
GPLPESELL+LL+HIA GLAYIHS QLVHMDVKPGNIFI D S D DDE P
Sbjct 330 GPLPESELLVLLAHIAHGLAYIHS LQVLVHMDVKPGNIFISRSDTPPPGNSDSEDDEAPQ 389
Query 1078 PNHKYKIGDLGHVTCVSSPAVEEGDCRYLPKEVLHEDFSQLPKADIFAFGLTLFEAAGGG 1257
P HKYKIGDLGHVTC +P VEEGDCRYLP+EV L EDF+ L KADIFAFGLTL+EAAGGG
Sbjct 390 PKHKYKIGDLGHVTCAWAPTVEEGDCRYLPREVLQEDFTHLAKADIFAFGLTLFEAAGGG 449
Query 1258 PLPKNGQKWHYDRDGKLPDLNLSREFNDLLKSMVDpspsarpsarrrmawrggawrg 1437
PLP+NGQ WHD RDGKLP+L NLSREFN LLK MV P PS RPS+R
Sbjct 450 PLPQNGQDWHDIRDGKLPDLNLSREFNQLLKQMVHPDPSQRPSSRG----- 496
Query 1438 vaaPIKSRAQLRRELA---NMKNELLARKLHDAKCIKSLTPS 1563
++ + LRR +A+ NMKNELL R+L +A++CIKSLTP+
Sbjct 497 ----LRKHSILRRGVASGSDTRRASRAALARELAATNMKNELLTRQLQEASRCIKSLTPN 552
Query 1564 L----ESSKFRTRSAA-----KRTQKPRIDTCLSD*IKYDVPARVTVACDSAN 1695
+ ES+KFRTRSA +R+ KP+ D L+D ++ R +++
Sbjct 553 IQINQESAKFRTRSARLQPTSTHRSRRSTKPKADAQLADMLQAVTSPRRIDRRNNSR 612
Query 1696 RTYPLF 1713
RT L
Sbjct 613 RTKSLI 618

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> ta_transcript84449_1
Length=896

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```

Score = 714 bits (1844), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 398/582 (68%), Positives = 446/582 (77%), Gaps = 56/582 (10%)
Frame = +1

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Query 1 MTEWYRMKTGLNNKHNSSELSVETSCDMSDPFNIFSDNLSPIPASIVPRKLDfSNLDDDD 180
M E YRMK G N+KHNSSELSVETSCD SDPFN+FSDNLSPIPASIVPRKLDf+N+DD+D
Sbjct 34 MAETYRMKDGYNHKNHNSSELSVETSCDTSDFPNMFSDNLSPIPASIVPRKLDfTNVDDDED 93
Query 181 GIRDESQAPVSHSPPYKRVRLRLFDSPHTPKTLLEKCSPTPHHPPTRLFPKINVQTg 360
++D S AP+S SPPYKRVRLRLFDSPHTPKTLLEKCSPTPH+ RTRLFPK++V T
Sbjct 94 PMKDASMAPMSLSPPYKRVRLRLFDSPHTPKTLLEKCSPTPHNNTRTLFPKLSV-TN 152

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Query	361	mpsgssshhlhppsghdddsALGSLPPDELDESRLTVRRPIANINPFTPDGQALNKKKRALS	540
		S H P DDDALGSL PD+ S L +RR +ANINPFTP GQALNKKKRALS	
Sbjct	153	GIPSGSSSHLHPPSDDDSALGSLLPDD---SGLAIRSVANINPFTPQGQALNKKKRALS	209
Query	541	KTPTWDGTPEQPAKRLRESNISRYNVEFIELGVIGRGQFGRVTRCVNKL DGC VYAL KRS L	720
Sbjct	210	KTPTWD +PE PAKRLRESNISRY VEF+EL VIGRG+FG VT+CVNKL DGC VYA+KRS+	269
		KTPTWDASPELPAKRLRESNISRYTVEFVELEVIGRGEFGLVTKCVNKL DGC VYAIKRSI	
Query	721	RPVAGSAAERAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGS LQLK MED-	897
Sbjct	270	+PVAGSAAERAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGS LQ + D	329
		KPVAGSAAERAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGS LQQYVTDN	
Query	898	GplpesellillshiaaGLAYIHSQQLVHMDVKPGNIFICSGD VDACRESDDGYDDEEPA	1077
		GPLPESELL+LL+HIA GLAYIHS QLVHMDVKPGNIFI D S D DDE P	
Sbjct	330	GPLPESELLVLLAHIAHGLAYIHS LQLVHMDVKPGNIFISRSDTPPPGNSSDSEDDEAPQ	389
Query	1078	PNHKYKIGDLGHVTCVSSPAVEEGDCRYLPKEVLHEDFSQLPKADIFAFGLTLFEAAGGG	1257
Sbjct	390	P HKYKIGDLGHVTC +P VEEGDCRYLP+EVL EDF+ L KADIFAFGLTL+EAAGGG	449
		PKHKYKIGDLGHVTCAWAPTVEEGDCRYLPREVLQEDFTHLAKADIFAFGLTLFEAAGGG	
Query	1258	PLPKNGQKWHDYRDGKLPDLNLSREFNDLLKSMVDpspsarpsarrlrmawrggawrg	1437
Sbjct	450	PLP+NGQ WHD RDGKLP+L NLSREFN LLK MV P PS RPS+R	496
		PLPQNGQDWHDIRDGKLPDLNLSREFNQLLKQMVHPDPSQRPSSRG-----	
Query	1438	vaaPIKSRAQLRRELA---NMKNELLARKLHDAAKCIKSLTPS	1563
		++ + LRR +A+ NMKNELL R+L +A++CIKSLTP+	
Sbjct	497	----LRKHSILRRGVASGSDTRRASRAALARELAATNMKNELLTRQLQEASRCIKSLTPN	552
Query	1564	L----ESSKFRTSAA-----KRTQKPRIDTCLSD 1641	
		+ ES+KFRTRSA +R+ KP+ D L+D	
Sbjct	553	IQINQESAKFRTSARLQPTESHRSDRRSTKPKADAQLAD 594	

> ta_transcript84450_1
Length=858

Score = 712 bits (1839), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 398/582 (68%), Positives = 446/582 (77%), Gaps = 56/582 (10%)
Frame = +1

Query	1	MTEWYRMKTGLNNKHNSSELSVETSCDMSDPFNIFSDNLSPIPASIVPRKLDFS NLDDDD	180
Sbjct	34	M E YRMK G N+KHNSSELSVETSCD SDPFN+FSDNLSPIPASIVPRKLDF+N+DD+D	93
		MAETYRMKDGYNHKNNSSELSVETSCDSDPFNMFSNLSPIPASIVPRKLDFTNVDD	
Query	181	GIRDESQAPVSHSPPYKRVRLRLFDSPHTPKTLLEKCSPTTHHPPRTRLFPFKINVQTg	360
Sbjct	94	++D S AP+S SPPYKRVRLRLFDSPHTPKTLLEKCSPTTH+ RTRLFPFK++V T	152
		PMKDASAMPMSLSPPYKRVRLRLFDSPHTPKTLLEKCSPTTHNNTRTRLFPFKLSV-TN	
Query	361	mpsgssshhlhppsghdddsALGSLPPDELDESRLTVRRPIANINPFTPDGQALNKKKRALS	540
		S H P DDDALGSL PD+ S L +RR +ANINPFTP GQALNKKKRALS	
Sbjct	153	GIPSGSSSHLHPPSDDDSALGSLLPDD---SGLAIRSVANINPFTPQGQALNKKKRALS	209
Query	541	KTPTWDGTPEQPAKRLRESNISRYNVEFIELGVIGRGQFGRVTRCVNKL DGC VYAL KRS L	720
Sbjct	210	KTPTWD +PE PAKRLRESNISRY VEF+EL VIGRG+FG VT+CVNKL DGC VYA+KRS+	269
		KTPTWDASPELPAKRLRESNISRYTVEFVELEVIGRGEFGLVTKCVNKL DGC VYAIKRSI	
Query	721	RPVAGSAAERAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGS LQLK MED-	897
Sbjct	270	+PVAGSAAERAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGS LQ + D	329
		KPVAGSAAERAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGS LQQYVTDN	
Query	898	GplpesellillshiaaGLAYIHSQQLVHMDVKPGNIFICSGD VDACRESDDGYDDEEPA	1077
		GPLPESELL+LL+HIA GLAYIHS QLVHMDVKPGNIFI D S D DDE P	
Sbjct	330	GPLPESELLVLLAHIAHGLAYIHS LQLVHMDVKPGNIFISRSDTPPPGNSSDSEDDEAPQ	389
Query	1078	PNHKYKIGDLGHVTCVSSPAVEEGDCRYLPKEVLHEDFSQLPKADIFAFGLTLFEAAGGG	1257
Sbjct	390	P HKYKIGDLGHVTC +P VEEGDCRYLP+EVL EDF+ L KADIFAFGLTL+EAAGGG	449
		PKHKYKIGDLGHVTCAWAPTVEEGDCRYLPREVLQEDFTHLAKADIFAFGLTLFEAAGGG	
Query	1258	PLPKNGQKWHDYRDGKLPDLNLSREFNDLLKSMVDpspsarpsarrlrmawrggawrg	1437
Sbjct	450	PLP+NGQ WHD RDGKLP+L NLSREFN LLK MV P PS RPS+R	496
		PLPQNGQDWHDIRDGKLPDLNLSREFNQLLKQMVHPDPSQRPSSRG-----	
Query	1438	vaaPIKSRAQLRRELA---NMKNELLARKLHDAAKCIKSLTPS	1563
		++ + LRR +A+ NMKNELL R+L +A++CIKSLTP+	
Sbjct	497	----LRKHSILRRGVASGSDTRRASRAALARELAATNMKNELLTRQLQEASRCIKSLTPN	552

```

Query 1564 L----ESSKFRTRSAA-----KRTQKPRIDTCLSD 1641
+      ES+KFRTRS      +R+ KP+ D  L+D
Sbjct 553 IQINQESAKFRTRSARLQPTTESTHRSDRRSTKPKADAQLAD 594

```

```

> ta_transcript84448_1
Length=975

```

```

Score = 713 bits (1840), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 398/582 (68%), Positives = 446/582 (77%), Gaps = 56/582 (10%)
Frame = +1

```

```

Query 1      MTEWYRMKTGLNNKHNSSELSVETSCDMSDPFNIFSDNLSPIPASIVPRKLDFSNLDDDD 180
M E YRMK G N+KHNSSELSVETSCD SDPFN+FSDNLSPIPASIVPRKLDF+N+DD+D
Sbjct 34      MAETYRMKDGYNHKNHNSSELSVETSCDTSDFNMFSDNLSPIPASIVPRKLDFTNVDDDED 93

Query 181     GIRDESQAPVSHSPPYKRVRLRLFDSPHTPKTLLEKCSTPTHHPPTRLFPFKINVQTg 360
++D S AP+S SPPYKRVRLRLFDSPHTPKTLLEKCSTPTH+ RTRLFPFK++V T
Sbjct 94      PMKDASMAPMSLSPPYKRVRLRLFDSPHTPKTLLEKCSTPTHNNTRTRLFPFKLSV-TN 152

Query 361     mpsgsshhhlhpsgdddsALGSLPPDELDESRLTVRRPIANINPFTPDGQALNKKKRAL 540
S H P DDDALGSL PD+ S L +RR +ANINPFTP GQALNKKKRAL
Sbjct 153     GIPSGSSHHLHPPSDDDSALGSLLPDD---SGLAIRRSVANINPFTPQGQALNKKKRAL 209

Query 541     KTPTWDGTPEQPAKRLRESNISRYNVEFIELGVIGRGQFGRVTRCVNKL DGC VYALKRSL 720
KTPTWD +PE PAKRLRESNISRY VEF+EL VIGRG+FG VT+CVNKL DGC VYA+KRS+
Sbjct 210     KTPTWDASPELPAKRLRESNISRYTVEFVELEVIGRGEFGLVTKCVNKL DGC VYAIKRSI 269

Query 721     R PVAGSAAERAAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGSLQLKMED- 897
+PVAGSAAERAAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGSLQ + D
Sbjct 270     KPVAGSAAERAAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGSLQQYVTDN 329

Query 898     GplpesellillshiaaGLAYIHSQQLVHMDVKPGNIFICSGD VDACRESDDGYDDEEPA 1077
GPLPESELL+LL+HIA GLAYIHS QLVHMDVKPGNIFI D S D DDE P
Sbjct 330     GPLPESELLVLLAHIAHGLAYIHS LQVLVHMDVKPGNIFISRSDTPPPGNSSDSEDDEAPQ 389

Query 1078    PNHKYKIGDLGHVTCVSSPAVEEGDCRYLPKEVLHEDFSQLPKADIFAFGLTLFEAAGGG 1257
P HKYKIGDLGHVTC +P VEEGDCRYLP+EVL EDF+ L KADIFAFGLTL+EAAGGG
Sbjct 390     PKHKYKIGDLGHVTC AWAPTVEEGDCRYLPREVLQEDFTHLAKADIFAFGLTLFEAAGGG 449

Query 1258    PLPKNGQKWHYDRDGKLPDLNLSREFNDLLKSMVDpspsarpsarrrrmawrggawrg 1437
PLP+NGQ WHD RDGKLP+L NLSREFN LLK MV P PS RPS+R
Sbjct 450     PLPQNGQDWHDIRDGKLPDLNLSREFNQLLKQMVHPDPSQRPSSRG----- 496

Query 1438    vaaPIKSRAQLRRELAAA-----NMKNELLARKLHDAAKCIKSLTPS 1563
++ + LRR +A+ NMKNELL R+L +A++CIKSLTP+
Sbjct 497     ----LRKHSILRRGVASGSDTRRASRAALARELAATNMKNELLTRQLQEASRCIKSLTPN 552

Query 1564 L----ESSKFRTRSAA-----KRTQKPRIDTCLSD 1641
+      ES+KFRTRS      +R+ KP+ D  L+D
Sbjct 553 IQINQESAKFRTRSARLQPTTESTHRSDRRSTKPKADAQLAD 594

```

```

> ta_transcript84453_1
Length=385

```

```

Score = 464 bits (1195), Expect = 3e-150, Method: Compositional matrix adjust.
Identities = 236/299 (79%), Positives = 259/299 (87%), Gaps = 4/299 (1%)
Frame = +1

```

```

Query 1      MTEWYRMKTGLNNKHNSSELSVETSCDMSDPFNIFSDNLSPIPASIVPRKLDFSNLDDDD 180
M E YRMK G N+KHNSSELSVETSCD SDPFN+FSDNLSPIPASIVPRKLDF+N+DD+D
Sbjct 34      MAETYRMKDGYNHKNHNSSELSVETSCDTSDFNMFSDNLSPIPASIVPRKLDFTNVDDDED 93

Query 181     GIRDESQAPVSHSPPYKRVRLRLFDSPHTPKTLLEKCSTPTHHPPTRLFPFKINVQTg 360
++D S AP+S SPPYKRVRLRLFDSPHTPKTLLEKCSTPTH+ RTRLFPFK++V T
Sbjct 94      PMKDASMAPMSLSPPYKRVRLRLFDSPHTPKTLLEKCSTPTHNNTRTRLFPFKLSV-TN 152

Query 361     mpsgsshhhlhpsgdddsALGSLPPDELDESRLTVRRPIANINPFTPDGQALNKKKRAL 540
S H P DDDALGSL PD+ S L +RR +ANINPFTP GQALNKKKRAL
Sbjct 153     GIPSGSSHHLHPPSDDDSALGSLLPDD---SGLAIRRSVANINPFTPQGQALNKKKRAL 209

Query 541     KTPTWDGTPEQPAKRLRESNISRYNVEFIELGVIGRGQFGRVTRCVNKL DGC VYALKRSL 720
KTPTWD +PE PAKRLRESNISRY VEF+EL VIGRG+FG VT+CVNKL DGC VYA+KRS+
Sbjct 210     KTPTWDASPELPAKRLRESNISRYTVEFVELEVIGRGEFGLVTKCVNKL DGC VYAIKRSI 269

Query 721     R PVAGSAAERAAALTEVYAHAAALGKHPHVVRYYSAWAEDDHMI IQNEYCDGGSLQLKMED 897

```

```

+PVAGSAAERAAALTEVYAAALGKHPHVVRYYSAWAEDDHM+IQNEYCDGGSLQ + D
Sbjct 270 KPVAGSAAERAAALTEVYAAALGKHPHVVRYYSAWAEDDHMVIQNEYCDGGSLQQYVTD 328

```

```

> ta_transcript44271_1
Length=224

```

```

Score = 156 bits (395), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 101/188 (54%), Positives = 117/188 (62%), Gaps = 1/188 (1%)
Frame = -2

```

```

Query 3365 PINMSARTPKVACALALMSGCRDW*IFTMQSADVTYMNVDVSNWKFMLLGQW*AADRKP 3186
          P+ M +A KVACA ALMSGCRDW IFTM S TYMN VSNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNAVSNWKLRLGQMW*VAESSA 79

Query 3185 SLIRATPIAYSSPKCWGMPFCFFSSGSFLMILCLLQTCNRAPSTT*PRFENTWLKSDS 3006
          + I P A SSP C GMP+C + I +TCS N APS+ *PR ENTWLKS++
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIR-RRRTCSMNSAPSSK*PRLENTWLKSET 138

Query 3005 IISGCAQKKLK*HRSWFPDWFRSRW*vttscstgsv*NTETVSTVHRYRLERVASTRARH 2826
          GCA +KL *HRS PD F W V T+C TGS *NT+TV +V RY ER S R+
Sbjct 139 PPHGCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVCRYLSEADSVRSVR 198

Query 2825 LDRSARHS 2802
          DR+A S
Sbjct 199 RDRAATFS 206

```

```

> ta_transcript44268_1
Length=404

```

```

Score = 156 bits (395), Expect = 9e-40, Method: Compositional matrix adjust.
Identities = 101/188 (54%), Positives = 117/188 (62%), Gaps = 1/188 (1%)
Frame = -2

```

```

Query 3365 PINMSARTPKVACALALMSGCRDW*IFTMQSADVTYMNVDVSNWKFMLLGQW*AADRKP 3186
          P+ M +A KVACA ALMSGCRDW IFTM S TYMN VSNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNAVSNWKLRLGQMW*VAESSA 79

Query 3185 SLIRATPIAYSSPKCWGMPFCFFSSGSFLMILCLLQTCNRAPSTT*PRFENTWLKSDS 3006
          + I P A SSP C GMP+C + I +TCS N APS+ *PR ENTWLKS++
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIR-RRRTCSMNSAPSSK*PRLENTWLKSET 138

Query 3005 IISGCAQKKLK*HRSWFPDWFRSRW*vttscstgsv*NTETVSTVHRYRLERVASTRARH 2826
          GCA +KL *HRS PD F W V T+C TGS *NT+TV +V RY ER S R+
Sbjct 139 PPHGCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVCRYLSEADSVRSVR 198

Query 2825 LDRSARHS 2802
          DR+A S
Sbjct 199 RDRAATFS 206

```

```

> ta_transcript44264_1
Length=747

```

```

Score = 158 bits (399), Expect = 7e-39, Method: Compositional matrix adjust.
Identities = 101/188 (54%), Positives = 117/188 (62%), Gaps = 1/188 (1%)
Frame = -2

```

```

Query 3365 PINMSARTPKVACALALMSGCRDW*IFTMQSADVTYMNVDVSNWKFMLLGQW*AADRKP 3186
          P+ M +A KVACA ALMSGCRDW IFTM S TYMN VSNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNAVSNWKLRLGQMW*VAESSA 79

Query 3185 SLIRATPIAYSSPKCWGMPFCFFSSGSFLMILCLLQTCNRAPSTT*PRFENTWLKSDS 3006
          + I P A SSP C GMP+C + I +TCS N APS+ *PR ENTWLKS++
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIR-RRRTCSMNSAPSSK*PRLENTWLKSET 138

Query 3005 IISGCAQKKLK*HRSWFPDWFRSRW*vttscstgsv*NTETVSTVHRYRLERVASTRARH 2826
          GCA +KL *HRS PD F W V T+C TGS *NT+TV +V RY ER S R+
Sbjct 139 PPHGCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVCRYLSEADSVRSVR 198

Query 2825 LDRSARHS 2802
          DR+A S
Sbjct 199 RDRAATFS 206

```

```

> ta_transcript44270_1

```

Length=226

Score = 135 bits (339), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 78/142 (55%), Positives = 89/142 (63%), Gaps = 1/142 (1%)
Frame = -2

```
Query 3365 PINMMSARTPKVACALALMSGCRDW*IFTMQSADVTYMNDVSNWKFMLLGQTW*AADRKP 3186
          P+ M +A KVACA ALMSGCRDW IFTM S TYMN VSNWK LGQ W* A+
Sbjct 20 PMAMSTASAAKACARALMSGCRDWYIFTMLSTASTYMNNAVSNWKLRLGQMW*VAESSA 79

Query 3185 SLIRATPIAYSSPKCWGMPFCFFSSGSFLMILCLLQTCNRAPSTT*PRFENTWLKSDS 3006
          + I P A SSP C GMP+C + I +TCS N APS+ *PR ENTWLKS++
Sbjct 80 TTIMLAPSAVSSP*CAGMPYCSWRGLRLRRIR-RRRTCSMNSAPSSK*PRLENTWLKSET 138

Query 3005 IISGCAQKKLK*HRSWFPDWER 2940
          GCA +KL *HRS PD F
Sbjct 139 PPHGCAHRKL**HRSSEPDTFN 160
```


Query= gi|164448647:159-2792 Bombyx mori sid-1-related gene3 (Sir-3), mRNA

Length=2634

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript74094_1	369	1e-111
ta_transcript44271_1	219	2e-64
ta_transcript44268_1	218	8e-62
ta_transcript44264_1	220	8e-60
ta_transcript44270_1	187	7e-53
ta_transcript44272_1	125	4e-32

> ta_transcript74094_1
Length=937

Score = 369 bits (947), Expect = 1e-111, Method: Compositional matrix adjust.
Identities = 213/379 (56%), Positives = 274/379 (72%), Gaps = 7/379 (2%)
Frame = +1

```
Query 1504 SDRYLHTLYTVAVFYALPVLQFVAQVMLNISGSLDMCYNFLCAHPAGGLSDFNHVFS 1683
          S YL + TVAVFY LPV+Q V +Q +LN SG+ D+CY+NFLCAHP LSDFNHV+S
Sbjct 550 SKMYLWNILTVAVFYTLFVIQLVVVYQRLNQSGNQDLCYFNFLCAHPLMVLSDFNHVVS 609

Query 1684 NLgylllgalfmlqlqrkrnrkrAPRH-EEYGIPAHYGLLSSLGAAMMVVALLSASYHV 1860
          NLGY++LG+LF+ Q+ RR P H +E GIP H+GLL ++G A++ LLSA+YHV
Sbjct 610 NLGYVILGSLFLFQVWRHSHYHTIMPAHRKELGIPQHFGLLYAMGIALVSEGLLSAAYHV 669

Query 1861 CPNSLNQFQDFTAFMYVLAVLCMVKIYQSRHPDINARAHATFGVLAVFIALvvgvlgggp 2040
          CPNS+NFQFDT+FMVY +VLCMVKIYQSRHPDINARAHATFGVLA+ I + + GVL
Sbjct 670 CPNSMNFQFDTSMYVTVSVMCMVKIYQSRHPDINARAHATFGVLALIIIFIGLVGVNLNANF 729

Query 2041 lFWsvftvlhvftfllllslRIYYVGQFRLEKSSLAVAARGLRARPL--YTP---RLVML 2202
          FW +FTVLH+ T L+++ +IYY+G+FRL+ + AAR L RPL TP R VML
Sbjct 730 YFWIMFTVLHLLTCLVMTFQIYYLGRFRLDGGVVYRAARELIRPLAAITPTHCGRCVML 789

Query 2203 LIANAANWGFAYIGLLTHAGDIATHllnvllcntllYIVFYVLMKLLHGERIRWYSWCFL 2382
          L+AN +NW A YG+ H+ D A+HLL VL+ N LY +FY++MKLLH E I WYSW F+
Sbjct 790 LLANLSNWAIAAYGVSQHSRDFASHLLLVMSNLFLYTLFYIVMKLLHRETIGWYSWVFI 849

Query 2383 aaaaaCWVPALYFFTSSTDWSATPARSRHRNHECRVLQFYDSDHLWHMLSAAALYFTFN 2562
          A + W + YF+ ST+W+ +PA SR N +C +LQ YDSDH+WH +S+ A++F+FN
Sbjct 850 ALTYSVWFSSSYFYLDQSTNWALSPAESRQSNRQCSLLQLYDSDHIWHFMSSIAMFFSFN 909

Query 2563 VMLTWDDGLSAVKRTEIAV 2619
          + LT DDGL V R EIAV
Sbjct 910 MYLTIDDGLLNVRDEIAV 928
```

Score = 135 bits (340), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 92/382 (24%), Positives = 163/382 (43%), Gaps = 60/382 (16%)
Frame = +1

```
Query 19 LALCVSVVLASNITVEQRILNLEE-----EYTLVVTPSIEFILQFVPNEDQAEFPSRLW 180
          L +C+ V A + ++ + + EY + V E+I++F +E + P+R+
```



```

Sbjct 64 L FVCLHVSYAQKLKRDEIVFHYNNYKYNVEYVVDVDKHTEYIMEFAGDEKAYDTPARVT 123
Query 181 VRSVGGDTSRPLLLTARTKTGATTWQLPY--QSGSML--MSELERTLCDWDGSPDVAVGAP 348
V S + + PL +TAR + G +WQLP Q+ L + + RTLC +
Sbjct 124 VASDFANRTYPLFITARQQKGVFSWQLPMLIQTPMSLEQFNNISRTLCT---PHNNLYNED 180
Query 349 SECEGAGSQRGFTLHLASACAAPLTVTLRAAPARDWLLGFQARTTVTATQTGPVNYDF 528
E + +HL SA P+ VT+ D+ + T +T T + P +Y F
Sbjct 181 EESCDVTINTPIVHLTSASPEPIRVTVVSVLDYFIVTNKTNTMTVTPSQPKYYFYPF 240
Query 529 -----IPGQNSVRLIVES 567
+ SV +++ES
Sbjct 241 KQNPDLHTQKIKKKYKCNEELDHKELISLDYFLKSNALKRQYSWLTRPKSVIVMIES 300
Query 568 EDEVCATISVQRYTCPLAETIEDIDLTLRMTVMRSGAVQLSRSLYPMGFYVVSILVRPDD 747
+D++CA +S+Q ++CP+ + DI +T+ R G + L++ ++P+GFY+V +V+ D
Sbjct 301 DDDICAVVSIQNFSCPVFDNERDILYDGYLTMTRRGGITLTQDMFPLGFYIVFIVKSSD 360
Query 748 AACSGEPAPEDDWLLEAALWAHTDRSPPATLRQKTFTLTVRASLSRAQYMGAGVTVAV 927
C + + W H + R KTF+ + ++S +Y++ AG +
Sbjct 361 DDCVMGVSDVNVSRITVRWQH GKATATSDDGRVKTFSFRIIETISYREYLIAAGAVLGF 420
Query 928 FLLFYAGFAALVLAQRWPACAR 993
F+ FYAGFA +V+ QR R
Sbjct 421 FMSFYAGFAIVVYQRVQGLRR 442

```

> ta_transcript44271_1
Length=224

Score = 219 bits (558), Expect = 2e-64, Method: Compositional matrix adjust.
Identities = 121/163 (74%), Positives = 130/163 (80%), Gaps = 0/163 (0%)
Frame = -2

```

Query 2006 AMKTASTPKVACARALMSGCRDW*IFTMHSTASTYMKAVSNWKLRLLGQTW*LAESSATT 1827
AM TAS KVACARALMSGCRDW IFTM STASTYM AVSNWKL LGQ W*+AESSATT
Sbjct 22 AMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNVAWSNWKLSRLGQMW*VAESSATT 81
Query 1826 IMAAPRDDSSP*CAGIPYSSCRGARFLFRFLRCSCSMKSAPSSR*PRFENTWLKSDSPPA 1647
IM AP SSP*CAG+PY S RG R R +CSM SAPSS*+PR ENTWLKS++PP
Sbjct 82 IMLAPSAVSSP*CAGMPYCSWRGLRLRRIRRRRTCSMNSAPSSK*PRLENTWLKSETPPH 141
Query 1646 GCAHRKL**HMSSDPDMFSITWKAATNCSTGSA*NTATV*SVC 1518
GCAHRKL**H SS+PD F+I+WK TNC TGSA*NT TV SVC
Sbjct 142 GCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVC 184

```

> ta_transcript44268_1
Length=404

Score = 218 bits (555), Expect = 8e-62, Method: Compositional matrix adjust.
Identities = 121/163 (74%), Positives = 130/163 (80%), Gaps = 0/163 (0%)
Frame = -2

```

Query 2006 AMKTASTPKVACARALMSGCRDW*IFTMHSTASTYMKAVSNWKLRLLGQTW*LAESSATT 1827
AM TAS KVACARALMSGCRDW IFTM STASTYM AVSNWKL LGQ W*+AESSATT
Sbjct 22 AMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNVAWSNWKLSRLGQMW*VAESSATT 81
Query 1826 IMAAPRDDSSP*CAGIPYSSCRGARFLFRFLRCSCSMKSAPSSR*PRFENTWLKSDSPPA 1647
IM AP SSP*CAG+PY S RG R R +CSM SAPSS*+PR ENTWLKS++PP
Sbjct 82 IMLAPSAVSSP*CAGMPYCSWRGLRLRRIRRRRTCSMNSAPSSK*PRLENTWLKSETPPH 141
Query 1646 GCAHRKL**HMSSDPDMFSITWKAATNCSTGSA*NTATV*SVC 1518
GCAHRKL**H SS+PD F+I+WK TNC TGSA*NT TV SVC
Sbjct 142 GCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVC 184

```

> ta_transcript44264_1
Length=747

Score = 220 bits (560), Expect = 8e-60, Method: Compositional matrix adjust.
Identities = 121/163 (74%), Positives = 130/163 (80%), Gaps = 0/163 (0%)
Frame = -2

```

Query 2006 AMKTASTPKVACARALMSGCRDW*IFTMHSTASTYMKAVSNWKLRLLGQTW*LAESSATT 1827
AM TAS KVACARALMSGCRDW IFTM STASTYM AVSNWKL LGQ W*+AESSATT
Sbjct 22 AMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNVAWSNWKLSRLGQMW*VAESSATT 81

```

```

Query 1826  IMAAPRDDSSP*CAGIPYSSCRGARFLFRFLRCSCSMKSAPSSR*PRFENTWLKSDSPPA 1647
IM AP  SSP*CAG+PY S RG R      R +CSM SAPSS+*PR ENTWLKS++PP
Sbjct 82    IMLAPSAVSSP*CAGMPYCSWRGLRLRRIRRRRTCSMNSAPSSK*PRLENTWLKSETPPH 141

Query 1646  GCAHRKL**HMSSDPDMFSITWKAATNCSTGSA*NTATV*SVC 1518
GCAHRKL**H SS+PD F+I+WK  TNC TGSA*NT TV SVC
Sbjct 142   GCAHRKL**HRSSEPDTFNISWKVNTNCMTGSA*NTDTVYSVC 184

```

Score = 88.6 bits (218), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 119/300 (40%), Positives = 144/300 (48%), Gaps = 21/300 (7%)
 Frame = -2

```

Query 917  VTPAPTMYCARDSDALTVSVKVFCCRVRAGGEG-----RSVWagraasssqsssgagSPE 756
VT  T YCARDS      V V  ++GG G      R      AA  SQS++  SP
Sbjct 369  VTAHATTYCARDSAGFRSMVSVLA--LSGGAGVVVVVVRPSLPTAAAWYSQSAARGCSPA 426

Query 755  HAASSGRSDT*T*NPIGYRLRESECTAPERMTV--ILrvvrsmssmvSANGHVYLCTEMVA 582
H +S  T+  T  P G  LR+ C  PER TV  I      R  +  VSA GH
Sbjct 427  HGSSDDSTTTDTKKPRGNSLRDICAPPERSTVMNIPSAGRVTACCVSATGHE*SRMATTE 486

Query 581  HTSSSDSTISRTLFCPGMKS**FTAGPVCVAVTVVRWKPSSQSLAGAARSVTVRGAAQA 402
HTSSSD+T SRT  C   K **+T  +CV  T + A K S QS AG+ R+VTV  A  A
Sbjct 487  HTSSSDATTSRTSCCSAEKL**YTRDDICVTRTFLVAPKLSIQSRAGSTRAVTVTDALLA 546

Query 401  DARCRVKPRCEPAPSHSDGAPTASVGEPSQHSVRSSSDISIDPDWY--GSCHv vapvlvl 228
D  C V      P  SD      +H+VR SS      P      GSCHV APV+
Sbjct 547  DDTCSVNRSVLEPPPFSDT-----RKHNVRWSSYNCSSPAAM*GSCHV*APVVCR 597

Query 227  avssSGREVSPPTLRTHNRLGNSA*SSFGTNCKMNSMDGVTTNVYSSSRFNILCSTVMLL 48
AVSS+GR  SP +      R G++A S+ G+N KM SM  T  V S S  +  ST+  L
Sbjct 598  AVSSTGRATSPASAVRRMRAGHAACSAVGSNSKMYSMVPSTVIVCSLNGTVYLSLTAL 657

```

> ta_transcript44270_1
 Length=226

Score = 187 bits (474), Expect = 7e-53, Method: Compositional matrix adjust.
 Identities = 104/140 (74%), Positives = 112/140 (80%), Gaps = 0/140 (0%)
 Frame = -2

```

Query 2006  AMKTASTPKVACARALMSGCRDW*IFTMHSTASTYMKAVSNWKLRLLLGQTW*LAESSATT 1827
AM TAS  KVACARALMSGCRDW IFTM STASTYM AVSNWKL  LGQ W*+AESSATT
Sbjct 22    AMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNVAVSNWKLRLGQMW*VAESSATT 81

Query 1826  IMAAPRDDSSP*CAGIPYSSCRGARFLFRFLRCSCSMKSAPSSR*PRFENTWLKSDSPPA 1647
IM AP  SSP*CAG+PY S RG R      R +CSM SAPSS+*PR ENTWLKS++PP
Sbjct 82    IMLAPSAVSSP*CAGMPYCSWRGLRLRRIRRRRTCSMNSAPSSK*PRLENTWLKSETPPH 141

Query 1646  GCAHRKL**HMSSDPDMFSI 1587
GCAHRKL**H SS+PD F+I
Sbjct 142   GCAHRKL**HRSSEPDTFNI 161

```

> ta_transcript44272_1
 Length=119

Score = 125 bits (313), Expect = 4e-32, Method: Compositional matrix adjust.
 Identities = 67/86 (78%), Positives = 69/86 (80%), Gaps = 0/86 (0%)
 Frame = -2

```

Query 2006  AMKTASTPKVACARALMSGCRDW*IFTMHSTASTYMKAVSNWKLRLLLGQTW*LAESSATT 1827
AM TAS  KVACARALMSGCRDW IFTM STASTYM AVSNWKL  LGQ W*+AESSATT
Sbjct 22    AMSTASAAKVACARALMSGCRDWYIFTMLSTASTYMNVAVSNWKLRLGQMW*VAESSATT 81

Query 1826  IMAAPRDDSSP*CAGIPYSSCRGARF 1749
IM AP  SSP*CAG+PY S RG R
Sbjct 82    IMLAPSAVSSP*CAGMPYCSWRGLRL 107

```


 Query= gi|392897213|ref|NM_067422.6| Caenorhabditis elegans Protein SID-2
 (sid-2) mRNA, complete cds
 Length=936

***** No hits found *****

Query= gi|442620537|ref|NM_079729.3| Drosophila melanogaster Dicer-1 (Dcr-1), mRNA

Length=6913

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript89347_1	160	1e-38
ta_transcript89348_1	160	2e-38

> ta_transcript89347_1
Length=1497

Score = 160 bits (406), Expect = 1e-38, Method: Compositional matrix adjust.
Identities = 98/210 (47%), Positives = 127/210 (60%), Gaps = 21/210 (10%)
Frame = +2

Query	4865	QVAKVSM---MELLKQLLPYVNEDVLAKKLGDRRELLSDDLVELN----ADWVARHEQ	5017
		Q++K+++ +LL ++ PY N D+ KL D + +++E N A+ +	
Sbjct	1291	QMSKLAIKDNTTDLLEIFPYGNTDL---KLTDENGQISLEIIEKNKRVLAEKKSLE	1347
Query	5018	ETYNVMGCGDSFD-----NYNDHHRNLNDEKQLKLQYERIE-IEPPTSTKA--ITSAIL	5170
		E + C D NY + +N+ + E++E P K + S +	
Sbjct	1348	EEVKKLHCFSMIDVDIDAPNYVNEKVVNVGFDNIDSYKEKVEKWRHPDEYKPYMESKVG	1407
Query	5171	PAGFSFDRQPDVLVGHGPGSPSIIQALTMSNANDGINLERLETIGDSFLKYAITTYLYIT	5350
		F FD QPDL GHPGSPS+ILQALTMSNANDGINLERLETIGDSFLK+AIT YLY	
Sbjct	1408	GKEFDYQPDLEGHGPGSPSVILQALTMSNANDGINLERLETIGDSFLKFAITAYLYCA	1467
Query	5351	YENVHEGKLSHLRSKQVANLNLYRLGRKR	5440
		+ VHEGKLSH+RSKQV+NLNLYRLGR KR	
Sbjct	1468	HPTVHEGKLSHMRKQVSNLNLYRLGRNKR	1497

Score = 37.7 bits (86), Expect = 0.54, Method: Compositional matrix adjust.
Identities = 23/50 (46%), Positives = 28/50 (56%), Gaps = 9/50 (18%)
Frame = +2

Query	4166	LQEADDF---IEIGTWSNDMADDIASFNQEDDDEDDAFHLPVLPANVKFC	4306
		LQE + + EIGTWSN+MA I DDE D + P LP N+ FC	
Sbjct	1010	LQEKECYENAFEIGTWSNEMASSIPL-----DDEYDDYTQP-LPPNLTFC	1053

Score = 37.0 bits (84), Expect = 0.91, Method: Compositional matrix adjust.
Identities = 21/40 (53%), Positives = 24/40 (60%), Gaps = 0/40 (0%)
Frame = +3

Query	3417	RSARRSLIRNASRMPSLCRGIATRINRSISMWRRYVHIY	3536
		R +R L+R + PS RGI TRINRS S RRYV Y	
Sbjct	764	RLEKRLFLMRTNTERPSSHRGIGTRINRSFS**RRYVGNV	803

> ta_transcript89348_1
Length=1490

Score = 160 bits (406), Expect = 2e-38, Method: Compositional matrix adjust.
Identities = 98/210 (47%), Positives = 127/210 (60%), Gaps = 21/210 (10%)
Frame = +2

Query	4865	QVAKVSM---MELLKQLLPYVNEDVLAKKLGDRRELLSDDLVELN----ADWVARHEQ	5017
		Q++K+++ +LL ++ PY N D+ KL D + +++E N A+ +	
Sbjct	1284	QMSKLAIKDNTTDLLEIFPYGNTDL---KLTDENGQISLEIIEKNKRVLAEKKSLE	1340
Query	5018	ETYNVMGCGDSFD-----NYNDHHRNLNDEKQLKLQYERIE-IEPPTSTKA--ITSAIL	5170
		E + C D NY + +N+ + E++E P K + S +	
Sbjct	1341	EEVKKLHCFSMIDVDIDAPNYVNEKVVNVGFDNIDSYKEKVEKWRHPDEYKPYMESKVG	1400
Query	5171	PAGFSFDRQPDVLVGHGPGSPSIIQALTMSNANDGINLERLETIGDSFLKYAITTYLYIT	5350
		F FD QPDL GHPGSPS+ILQALTMSNANDGINLERLETIGDSFLK+AIT YLY	
Sbjct	1401	GKEFDYQPDLEGHGPGSPSVILQALTMSNANDGINLERLETIGDSFLKFAITAYLYCA	1460
Query	5351	YENVHEGKLSHLRSKQVANLNLYRLGRKR	5440

Sbjct 1461 + VHEGKLSH+RSKQV+NLNLYRLGR KR
HPTVHEGKLSHMRSKQVSNLNLRYRLGRNKR 1490

Score = 37.4 bits (85), Expect = 0.58, Method: Compositional matrix adjust.
Identities = 23/50 (46%), Positives = 28/50 (56%), Gaps = 9/50 (18%)
Frame = +2

Query 4166 LQEADDF---IEIGTWSNDMADDIASFNQEDDEDDAFHLPVLPANVKFC 4306
LQE + + EIGTWSN+MA I DDE D + P LP N+ FC
Sbjct 1010 LQEKECYENAFEIGTWSNEMASSIPL-----DDEYDDYTQP-LPPNLTFC 1053

Score = 37.0 bits (84), Expect = 0.84, Method: Compositional matrix adjust.
Identities = 21/40 (53%), Positives = 24/40 (60%), Gaps = 0/40 (0%)
Frame = +3

Query 3417 RSARRSLIRNASRMPSLCRGIATRINRSISMWRRYVHIY 3536
R +R L+R + PS RGI TRINRS S RRYV Y
Sbjct 764 RLEKRLFLMRTNTERPSSHRGIGTRINRSFS**RRYVGNV 803

Query= gi|300669732|dbj|AB566386.1| Bombyx mori Dicer-2 mRNA for DICER-2,complete cds

Length=5034

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript86357_1	288	4e-79
ta_transcript86358_1	280	3e-77
ta_transcript86359_1	150	2e-36

> ta_transcript86357_1
Length=1072

Score = 288 bits (736), Expect = 4e-79, Method: Compositional matrix adjust.
Identities = 337/1061 (32%), Positives = 498/1061 (47%), Gaps = 34/1061 (3%)
Frame = -1

Query 4977 VDADSVGGETLVVLRERNRHHYLRDVRIDDYLFENRTSVYHFV*NFDGLLRVAFRERID 4798
V +V G L RHH+L +V + + F RT VY + L ER++
Sbjct 1 VGPAAVHGVLFALGHGCHYRHHHLLEVIVGEPGFAYLRTGVYILIQQSHWLFQDVSV*ERVN 60

Query 4797 LDVHYLVQNRPHRLQIPARVQVHGAD*CFENVAQHLRHINIFSDLTIDFADK*QNVELNL 4618
L H V++ P+ L + A VQV+ A * FE +A++L H ++FSD TI ++ Q++ L +
Sbjct 61 LVAHDSVEDCPNSL*VSAAVQVYSAG*RFEYIAENLGHFHVFSDDHTILLVNVQIQHIFLYI 120

Query 4617 VISFYLMFDEFHYRLLQRRVQLRAEVLVQSKFDGVGRERDVIDEGGSQVSHFAGLQFATV 4438
++ L+ E HY L VQL A V VQ+ FD + E DV+DE S + +G+Q T
Sbjct 121 MLPSLLVLVYERHYSRL*AGVQIVA*VFVQAHFDNIRGESDVVDESRS*IR*VSGIQRGTA 180

Query 4437 LEDV*RHQEIDYGVPEELEALVrarqpvpdvrrvrqsv*QEG*IFERVV*DLDISSRIV 4258
+DV + +I GV E+L + V Q V DVRRV + + I E ++ LF+I +V
Sbjct 181 FKDVRSY*KIQNGVAEKL*SFVGTGQSVADVRRVGKRFK*KRWILEFIEYLFNIPAVV 240

Query 4257 **KVNISFGS*ILR*RCLHRLVEHVCKVILWRKHLHPFK*FYSC*YPSTK*ICADQSFHG 4078
V+ G IL + E K++LW K+ PF F + +*I + FH
Sbjct 241 HYSVHFGRGGLILGKNRWNLPG*RLKIVLWKNFEPF*HFDTAQDSIAE*ISSH**FHA 300

Query 4077 IGYRFVRNCL*MYIALHRILGTAFGFLSDAIL--EIIHHRFPFFT*FTGHYFLFGEL 3907
+ RFVR+ L Y+ LH L T ++ +++ ++ A F +F + E
Sbjct 301 VRQRFVRHSLRSYVTLHCNLHTVERLLFQRRLIIS*QLTYQLKALFGEVPT*HFFWREF 360

Query 3906 YAD*ECWTNLSLFNKKFQFRGRKETWDEEVTSAELLHLHASTQVEFRTSVI*IPVTDQL 3727
AD C +L +FN R++ +E V+SR+EL H H +T+++F T V +PV+++
Sbjct 361 *ADETCRDPDLFIFNHLHLFRREKPGNEVVSSRSELFHFTTTELDFGTCVEQVPVSNE 420

Query 3726 ALDVR*LTLVHVVRKLVVQVQAGGELQERVPQCLRSIQIEGVV*VDRGERGEHVSQFRTSP 3547
+LDV L+ +H +LV+Q+ +LQE + S Q+E +V V +V+QFR S
Sbjct 421 SLDVGKLSFIHRWELWQI*RSSKLQEGIS*RFGSFQVESIVRVYCSNCC*YVAQFRPSG 480

Query 3546 GRRL*YFDFINVLDRRCYSWGLRNDSSrrgrtrvrrcrrysRHKLVTTFYVH*RDGRQV 3367

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      L *YFDF  L RR Y  L          V  R+RSR + VV FYVH  R V
Sbjct  481  RHFLF*YFDFHEFLYRRRQYGCGLPRRAVRRGSVGRDRHRSRDEFVVAFYVHHGYRRYV  540

Query  3366  TLYVDGFDLSLIPGVLFVDFLSLQFI*ALF*RYNFLQTIICAF---VYSVNSVDMKW-FF  3202
      L V      LIP +LF  L LQ I AL  YN +    C F      VYSVN V M++ +
Sbjct  541  ALDVQRLGLFLIPVILFAYLLFLQLIQALLHGYN-VHRPRCVFVNRVVSVNIVRMRFIWL  599

Query  3201  NLGQ**IYGYIPVHLYRLK*FRFFQNWLVPVFSGV*YFHEQFMCH*QHVNSVNNTGQ*RCL  3022
      + Q ++ + +H YRL      Q      F      F Q +CH*QH + V++T Q
Sbjct  600  DERQKGLHSHFNIHFYRLPLLSCRQMHD TDFCLPRDFS AQLICH*QHGHVPVHDTRQHTRF  659

Query  3021  IPQYSWVIVFNAEFKYKYLCKSLRFIVAERNRYHLQLLVCERFE-RCCSG*EAVHPRAYV  2845
      +PQ +  IV + E  Y+ L K  ++ + A R  H L  +  + R C  *      R
Sbjct  660  VPQSAREIVADTELWYENLWKPFKLVA*RQGNHFLFF*KSLDGRGCRQ*TVESTRG*P  719

Query  2844  TYLQQWLTFTS*YiqviviicirfiavsIELRFRRHVFENLRHDPFR*NSPAIPGR  2665
      L+Q L  S Y  V+ + I++ +R  +  +LR  HV +N+ + VP R N  +IP
Sbjct  720  LDLKQGLVLVSHYF*VVFIRIVVGVSF*IRKRLRLGSHVLQNI*YVPRRKNDS SIPRG  779

Query  2664  YNAIRVVFCDYQRFSFLN*RRGDRWHRVSLHCCPVNVVSIMFQY-----RDNVHAVF  2503
      + AI V F  D R SFL      R +  V LH  PV++V  +      R +V  V
Sbjct  780  HYAISVAFLRDT*RPSFLKRGHLHRRPYLCVRLHNFPVDIVVQCACHVGSRSRHSVKRVI  839

Query  2502  SSLEYQKLLIDRQDLVE*KIMELLH*LEYNRGQFYNCVIDFY*R-----GDFSNGRER  2344
      ++EY KLL+DR  LVE + +E  H      QF + VI F R      D +
Sbjct  840  ETVEYGKLLDR*HLVEYEPVEAFH-----QFKSLVIQFDCRIVHEQLGVDLAFSHAY  892

Query  2343  WELAQFRQRLLRQKPVAFVS LYKIVQSLFTIIVGFLECLRHFFYVKIEYRTI--WYCV*V  2170
      ELA RQ L  ++  F L  VQ  + I F  R+  +V++E+      W  V
Sbjct  893  GELANPRQSLHCKQSETFPFLQ*SVQGSRSGIAWFGISRV*CDHVEVEFARFAHW*AFEV  952

Query  2169  *RELYFMLSFSFLGTRLGYILFDLGLAIFSPVRKAATYVISFVINFRVVFRE*C*RMKFA  1990
      RE + +  SFLG  G+++      I PV +A      +  V R *  +  +
Sbjct  953  LREHFLVFPHSFLGA--GFLVAVAFFLIRRPVGEAGHQFWLLEVYRSVIFR**SQIV*LS  1010

Query  1989  QFM*LNARLQCSGAFSGFRI*VRVTLNFFFDGGSYGKYDGD  1867
      FM* +A +Q  A  ++ +R T  FD      D D
Sbjct  1011  SFM*RDAGVQSCRALRSLQLGLRFTGYQIFDRAGDRHVDLD  1051

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> ta_transcript86358_1
Length=918

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```

Score = 280 bits (716), Expect = 3e-77, Method: Compositional matrix adjust.
Identities = 305/926 (33%), Positives = 446/926 (48%), Gaps = 30/926 (3%)
Frame = -1

```

```

Query  4977  VDADS VGGETLVVLRERNRHHYLRDVRIDDYLFENRTSVYHFV*NFDGLLRYAFRERID  4798
      V  +V G  L  RHH+L +V + + F  RT VY  +  L      ER++
Sbjct  1      VGPAAVHGVLFALGHGCHYRHHHLLEVLVGEPEGFAYLRTGVYILIQQSHWLF GDVS*ERVN  60

Query  4797  LDVHYLVQNRPHRLQIPARVQVHGAD*CFENVAQHRLRHINIFSDLTIDFADK*QNVELNL  4618
      L  H  V++ P+ L + A VQV+ A * FE +A++L H ++FSD TI  ++ Q++ L +
Sbjct  61      LVAHDSVEDCPNSL*VSAAVQVYSAG*RFEYIAENLGHFHVFS DHTILLVNQIQHIFLYI  120

Query  4617  VISFYLMFDEFHYRLLQRRVQLRAEVLVQSKFDGVGRERDVIDEGGSQVSHFAGLQFATV  4438
      ++  L+  E HY  L  VQL A V VQ+ FD +  E DV+DE  S +  +G+Q  T
Sbjct  121  MLPSLLVLVYERHYSRL*AGVQLVA*VVFQAHFDNIRGESDVVDESRS*IR*VSGIQRGTA  180

Query  4437  LEDV*RHQEIDYGVPEELEALvrarqpvpdvrrvrqsv*QEG*IFERVV*DLFDISSRIV  4258
      +DV  + +I  GV E+L + V  Q V DVRRV +  +  I E ++  LF+I  +V
Sbjct  181  FKDVRSY*KIQNGVAEKL*SFVGTGQSVADVRRVGKREK*KRWILEFIIEYLFNIPAVV  240

Query  4257  **KVNISFGS*ILR*RCLHRLVEHVCKVILWRKHLHPFK*FYSC*YPSTK*ICADQSFHG  4078
      V+  G  IL  +  E  K++LW K+  PF  F +  ++I +  FH
Sbjct  241  HYSVHFRGGGLILGKNRWNLPG*RLKIVLWKNFEPF*HFDTAQDSIAE*ISSH**FHA  300

Query  4077  IGYRFVRNCL*MYIALHRILGTAFGFCLSDAIL---EIIHHRFPAFFT*FTGHYFLFGEL  3907
      +  RFVR+ L  Y+ LH  L T      ++  +++ ++  A F      +F + E
Sbjct  301  VRQRFVRHSLRSYVTLHCNLHTVERLLFQORLIIS*QLLTYQLKALFGEVPT*HFFWREF  360

Query  3906  YAD*ECWTNLSLFNKKFFQFRGRKETWDEEVTSSRAELLHLHASTQVEFRTSVI*IPVTDQL  3727
      AD  C  +L +FN      R++  +E V+SR+EL H H +T+++F T V  +PV+++
Sbjct  361  *ADETCRPDLFIFNHLHLFRREKPGNEVVSSRSELFHFTTTELDFGTCVEQVPVSNES  420

Query  3726  ALDVR*LTLVHVRKLVVQVQAGGELQERVPQCLRSLQIEGVV*VDRGERGEHVSQFRTSP  3547
      +LDV  L+ +H  +LV+Q+  +LQE +  S  Q+E +V V      +V+QFR S

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```

Sbjct 421 SLDVGKLSFIHRWELVMI*RSSKLQEGIS*RFGSFQVESIVRVYCSNCC*YVAQFRPSG 480

Query 3546 GRRLL*YFDFINVLGRRRCYSWGLRNDSSrgtrvvrccrryrsRHKLVTTFYVH*RDGRQV 3367
          L *YFDF L RR Y L V R+RSR + VV FYVH R V
Sbjct 481 RHFLF*YFDFHEFLYRRRQYGCELPRRRRAVRRGSGVGRDRHRSRDEFVVAFYVHHGYRRYV 540

Query 3366 TLYVDGFDSLIPGVLFVDFLSLQFI*ALF*RYNFLQTIICAF---VYSVNSVDMKW-FF 3202
          L V LIP +LF L LQ I AL YN + C F VYSVN V M++ +
Sbjct 541 ALDVQRLGLFIPVILFAYLLFLQLIQALLHGYN-VHRPRCVFVNRVVYSVNIVRMRFIWL 599

Query 3201 NLGQ**IYGYIPVHLYRLK*FRFFQNWLPVFSGV*YFHEQFMCH*QHVNSVNNTGQ*RCL 3022
          + Q ++ + +H YRL Q F F Q +CH*QH + V++T Q
Sbjct 600 DERQKGLHSHFNIHFYRLPLLSCRQMHDTDFCLPRDFSAQLICH*QHGHVPVHDTRQHTRF 659

Query 3021 IPQYSWVIVFNAEFRYKYLCKSLRFIVAERNRYHLQLLVCERFE-RCCSG*EAVHPRAYV 2845
          +PQ + IV + E Y+ L K ++ + A R H L + + R C * R
Sbjct 660 VPQSAREIVADTELWYENLWKPFKLVA*RQGNHFHLFF*KSLDGRGCRQ*TVESTRG*P 719

Query 2844 TYLQQWLTFTS*YiqvivvcciicirfiavsiELRFRRHVFENLRHDPVFR*NSPAIPGR 2665
          L+Q L S Y V+ + I++ +R + +LR HV +N+ + VP R N +IP
Sbjct 720 LDLKQGLVLVSHYF*VVFIRIVVGVRSF*IRKRLRLGSHVLQNI*YYVPRRKNDSSIPRG 779

Query 2664 YNAIRVVFCDYQRFSLN*RRGDRWHRVVSLHCCPVNVVSIMFQY-----RDNVHAVF 2503
          + AI V F D R SFL R + V LH PV++V + R +V V
Sbjct 780 HYAISVAFLRDT*RPSTLKRGLHHRPYLCVRLHNFVDIVVQCACHVGSRSRHSVSKRVI 839

Query 2502 SSLEYQKLLIDRQDLVE*KIMELLH*LEYNRGQFYNCVIDFY*R-----GDFSNGRER 2344
          ++EY KLL+DR LVE + +E H QF + VI F R D +
Sbjct 840 ETVEYGKLLDR*HLVEYEPVEAFH-----QFKSLVIQFDCRIVHEQLGVDLAFSHAY 892

Query 2343 WELAQFRQRLLRQKPVAFVSLYKIVQ 2266
          ELA RQ L Q+ F L + VQ
Sbjct 893 GELANPRQSLHCQQSETFPFLQESVQ 918

> ta_transcript86359_1
Length=683

Score = 150 bits (379), Expect = 2e-36, Method: Compositional matrix adjust.
Identities = 153/528 (29%), Positives = 254/528 (48%), Gaps = 1/528 (0%)
Frame = -1

Query 1809 ELIVW*NRAIPA**TNC*YGI*YIAIRRFVWGNLVVLIQVLMNVLSGSGAAV-IADYEI 1633
          ELIVW*+R +P +G + V + V+++Q + ++L C S A + +A+ +
Sbjct 3 ELIVW*HRTVPVEEAYSLHG*QAGTVLCDVRRDFVLVVQRIQFIDILLCWSVAVLSVANQHL 62

Query 1632 TNTFFGFLERVVFY*ERLFVFNINEYNETGFRTSCTTFALDIRSIFGWRIVSDN*RTLRY 1453
          N FG+LE + + E + V I++ +E T CTTFALDIRS+F R+VS + LR
Sbjct 63 INIMFGYLEALELFHEFVSVTLIDQQDEC*I*TPCTTFALDIRSVFERRVVSQHEHALRD 122

Query 1452 VQAFDDARRYQTVQSVIKSQNGflg*ff*imffPCTFKGIDTEADNKIMFQKFKLVRS 1273
          V F A YQTVQ V + Q G L F I FP F + E +++++FQK + R
Sbjct 123 VHTFLYHAC*YQTVQFLVRELQQGSLARFLRIKLPGRFVRVYIEPNDEVVFQKAEFFRV 182

Query 1272 SFFQVH*DIIQNL*SKPLFRENYSTERFS*VVYFQQFSRLFYQRVIFLQQVNQL*NLFR 1093
          SFF + I+ + + LFRE S +VY + R RV LQ + Q *N F
Sbjct 183 SFFDILEKIVNDFSCESLFREYDSG*WFLSLVYSEMS*RFVVIFRVELLQNIQKQ*NFF* 242

Query 1092 *MFYYFIVPSLVFHGVQEYHASFCGMGDDS*IQQiflfc*cftf*sF*QDNVRQNTQRST 913
          M + + H +YH+ M + + +Q FL F F S *+ +R T +
Sbjct 243 RMSDDSFITLVAIH*S*KYHSCHSNMNCNFVQMFFLRNNGFAFQSL*EY*IRDTT*LAA 302

Query 912 IQTHLFEICYHSYYKIFYRLHNLVRVVRNISLAWCLFKIF*WQRDRQLNTHHKIL*RIK* 733
          +++ LF Y + + L++ + V ++ L + H L* +
Sbjct 303 VRSQLFNEHYQ**HHFTHFLYDFLWVSADVPLPPFQLNVRVASHGG*SYFHDDHL*FL*Y 362

Query 732 TYRFLSCFRHLRLPEVLYKLLGVGRVSHNFTKIINSCDGCМКRVFQLLKCFDLDRY*YIP 553
          F S R + L+ V RV+ T+ I+S +G MKR Q FL ++
Sbjct 363 ADGFPSRRSRWRAAV*FHALIRVRRVAQYLTEFIDSGNGGMRGLQFA*RFLHSIDIHVG 422

Query 552 IQ*CRR*T*NSGLFVSFTIQKVLHYNSHWMVFHSMMTFIKYNQINILDSYICMCKHVT*Y 373
          +Q C R + N LF + K+ H SH MV +M FI+ +++++ I + +HV+
Sbjct 423 VQKCCRQSQNPRLFFNRNTLKMFDKSHGMVDDRVMAFIEDQKVDVMPDIRVGQHVSQD 482

Query 372 LRGHYNYLVSCQFRVPIGFLPIVYPIFATIGTNTVDGTHHFNYIFLLI 229
          L H+++L+ + +P +P+++ + + + T+ GTH + F ++
Sbjct 483 LTRHHDHLMF*ELGIPFILVPIHAVLSAVSGYTLHGTHFLYHFFSVV 530

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Query= gi|665399372|ref|NM_058088.4| *Drosophila melanogaster* drosha (drosha), mRNA

Length=4290

Sequences producing significant alignments: Score E
(Bits) Value

ta_transcript89214_1 1231 0.0

> ta_transcript89214_1
Length=1538

Score = 1231 bits (3185), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 670/1139 (59%), Positives = 822/1139 (72%), Gaps = 62/1139 (5%)
Frame = +1

Query	559	YEQRHDQEHRQIQDSRYAHEPRHGHYAHRQAKGSQHGYGSAARNQVSDDYSP----	RGH	726
		YE+RH HR+ + ++PR HR S YSP R H		
Sbjct	324	YERRHSL-HREHRSHSRVYDPRDERKYHRSP-----	SRKYSPGRDSRSH	366
Query	727	--HERERNETLEKTRAKPKVETERDRLLRQWCSNFCEKPEDYVKKMNALS-EADAPVES-		894
		H R T ++ +K + T+R+++L ++ N+C +D ++KM + E D+ E		
Sbjct	367	SRHPSVRPSTRHESVSKRPL-TDREKILEEYRKNYCRSDDIIEKMEQWTKEHDSDEEET		425
Query	895	--WVRSSPAELYERTKSENEVRGRARLQKLCTLFDEELLQRAKRVREKLPVYVPPPRKA		1068
		W RSSPAELY+ + V A+LQ+LC F + L+ R ++ R ++ +PP +		
Sbjct	426	KIWYRSSPAELYKPEVGAGVAQTAKLQRLCDAFQKHLIDRGRKARPEVDE-LPPLKPP		484
Query	1069	RRRVCKHKHKSEACssssssdddsdEDAFKIEQDCCMEELSRKVQHPQRVHADLWHNDAG		1248
		+ ++CKH+ + + SSS S D+ DED + D M EL RK HP+R+H ++W N+ G		
Sbjct	485	KSKLCKHRLEEGSSSSSESEDECLDEGLQGYTDRIMLELQKQSHPRRLHPMWFNNTG		544
Query	1249	EMNDGPLCRCSAKSRRIGIRHGIYPGETGYKLCDPNSNAGKLFHYRISISPTNFLT	TKT	1428
		EMN GPLCRCSA+++R G+RHG+Y GE + C P +N KL+HYRI++SPNTN	FL K+	
Sbjct	545	EMNGGPLCRCSARAKRHGMRHGVYAGEQTFPKCVPTQSNVDKLYHYRITVSPNTN	FLIKS	604
Query	1429	PTIIKHDEHEFLFEGFSLLSHVRLSDLPVCKVIRFNIEYTIIEYEEKMPENFTI	HELDIF	1608
		PTII+HDEHEFLF GFS+ SH +L+ LP CKVIRFNIEYTI Y EE P+NF+I	ELD+ F	
Sbjct	605	PTIIRHDEHEFLFSGFSMFHYKLARLPTCKVIRFNIEYTILYIEEPPPQNFSI	RELDLF	664
Query	1609	FKYLFHELLELVDFNLMFNLPSGNVEESCPAFHFFPRFVRDLDPNGKEVLAM	VEVLRYLL	1788
		++LF ELLEL+D +L + + +C FHF PRFVR LP+ G EVL+M EVL+YLL		
Sbjct	665	EEFLFTELLELDLIDL-----GKSTDACSQFHFIPRFVRSLEGGCEVLSMCE	VLYLL	719
Query	1789	DNSAQLVERQQLHLNLQISQSEWQNYVDFIKGMLVTKPGYKPCSLRVDQLDRN	---NSDL	1959
		D S LV L ++ + WQ +VD IKGM+VT PG KPCS+RVDQLDR+ N D		
Sbjct	720	DESGLLVPPASLADIHMDHYTWQKFVDRIKGMIVTYPGKKPCSVRVQDLDRS	PPANEDG	779
Query	1960	PECVDRETGISHPAIVHFGICHQPQLSYAGNPEYQKAWREYVKYRHLMANMSK	PSFKDKRK	2139
		D+ +P IVHFGI PQLSYAGNPEYQKAWR YVKYRHL+ANM+KPSFK+++		
Sbjct	780	RVPKDKNF---YPEIVHFGIRPPQLSYAGNPEYQKAWRYVVKYRHLIANMAK	PSFKERQR	836
Query	2140	LEEKEQRLQEMRTQGRMKRNITVAISSEGFYRTGIMCDVVQHAMLIPVLTGHL	RFHKSLE	2319
		L K+ +LQEMRTQ +MKR++TVAISS+GF+ TG+MCDVVQHAMLIPVL	HLRFHKSLE	
Sbjct	837	LAACKQAKLQEMRTQTKMKRDVTVAISSQGFTTGLMCDVVQHAMLIPVLVRH	LRHFKSLE	896
Query	2320	LLEESIGYRFKNRYLLQLALTHPSYKENYGTNPDHARNSLTNCGIRQPEYGDR	KIHYMNT	2499
		LE +GY F+ R LLQ ALTHPSY+EN+GTNPDHARNSLTNCGIRQPEYGDR+I	HY T	
Sbjct	897	SLERKVGYTFRQLLLQTALTHPSYRENFGTNPDHARNSLTNCGIRQPEYGDR	RIHY--T	954
Query	2500	RKRGINTLVSIMSRFGKEHETVSNITHNERLEFLGDVVEFLSSIHLFFMFPE	LEEGLA	2679
		RK+GI TL++IMSRFGK ET S I HNERLEFLGDVVEFLSSIHLF MFP L	EEGLA	
Sbjct	955	RKKGIVTLINIMSRFGKLSETESEIKHNERLEFLGDVVEFLSSIHLFRMF	PLAEEGLA	1014
Query	2680	TYRAAIVQNqhlallakklqleeFMLYAHGSDLCHELELRHAMANCFEALMG	ALLLDGGI	2859
		TYRA+IVQNQH LA LAK +QLE++MLYAHGSDLC E+ +RHAMANCFEALMG	AL LD G+	
Sbjct	1015	TYRASIVQNQH LAQLAKNIQLEQYMLYAHGSDLCREVVMRHAMANCFEALMG	ALFLDAGL	1074
Query	2860	KVADEVFTDALFRQDEKLLSIWKNLPEHPLQEQEPLGDRSCIDSYRVLKELT	KFEDSIGI	3039
		KVAD VF+ AL+ + +LL +W HPLQEQEPLGDR I + L++LT+FE+SIG+		
Sbjct	1075	KVADRVFSLALWYNEPELLHVWTKERSHPLQEQEPLGDRKYIKDFEFLQKL	TEFEESIGV	1134
Query	3040	KFKHIRLLARAFTDRSIGFTHLTLGNSQRLEFLGDTVLQLICSEYLYRHFP	EHHEGHLs1	3219
		+FKHIRLLARAFTDRS+GFTHLTGNSQRLEFLGDTVLQL+ S+ LYRHFP+H	HEGHLSL	
Sbjct	1135	QFKHIRLLARAFTDRSVGFTHLTGNSQRLEFLGDTVLQLVVS	DRLYRHFPDHEGHLSL	1194


```

Query 3220 lrsslVNNRTQAVVCDDLGMPPKYAVYANPKADLKTCD-RADLLEAFLGALYVDKGLLYCE 3396
Sbjct 1195 LRSSLVNNRTQ++VCDDL M YA+Y NPKA TK +ADLLEAFLGALYVDK L YC+ 1254

Query 3397 QFCHVCLFPRQLQFIMNQDWNDFKSKLQQCCCLTLRTMDGGEPDIPYYKVVEASGPTNTRV 3576
Sbjct 1255 FC+ CLFPRQLQ FIMNQDWNDFKSKLQQCCCLTLR+M+GGEPDIP YKV+E GPTNTRV 1314

Query 3577 YKVAVYFRSKRLATSSGSSIQQAEMNAAQALENSRDLFPQLDHQKRVIKSIKKQTGNE 3756
Sbjct 1315 Y V VYFR RLA + G SIQ+AE MNAA+ AL + +LFPQLDHQKRVIK +KK+ 1374

Query 3757 LDNDSRQHQEIKIRPKYATPLQDESHLPKQYRMHENISSDELPEDEDFESTAPKSPT 3933
Sbjct 1375 D +D+ Q E +PK YR+ D P D E++ P+ 1414
-DDTADKTKQNTL-----EDRVPKAYRL-----DNQPSDSSDETSHSNPPS

```


Query= gi|304307736|ref|NM_001195079.1| Bombyx mori loquacious (Logs), mRNA
Length=1149

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript67781_1	609	0.0
ta_transcript67777_1	612	0.0
ta_transcript67782_1	506	2e-170
ta_transcript67778_1	508	7e-167
ta_transcript67779_1	163	8e-43
ta_transcript67775_1	159	3e-41

> ta_transcript67781_1
Length=971

Score = 609 bits (1571), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 318/388 (82%), Positives = 343/388 (88%), Gaps = 13/388 (3%)
Frame = +1

```

Query 1 MEGNTVHPHPSPVPPGLPPGVHGMTVHSGPNGEHFPHGPRRRYQTRPKP-NNLQRLPLD 177
Sbjct 55 M+G VHPHP VV G PGV+HGM VHG+GP+GEH PHGPRRRYQ RPKP NN++RLPLD 114
MDGGVVHHPHGVVHGSVPGVVHGMPVHAGPDGEHAPHGPRRRYQNRPKPPNNVERLPLD

Query 178 EAAKRKMETLPTKTPVSVLQELLARRETVPKYELLQIEGMIHEPTFRYRVTVADLFAMGT 357
Sbjct 115 EAAKR+ME+LP KTPVSVLQELLARR TVPKYEL+QIEGMIHEPTFRYRVTVADL AMGT 174
EAAKREMESLPMKTPVSVLQELLARRGTVPKYELVQIEGMIHEPTFRYRVTVADLVAMGT

Query 358 GRskkeakhsaakaLLDKLTGATPSDQTNGSVPETGAVVPTFEDKLMGNPVGWLRSCVC 537
Sbjct 175 GRSKKEAKHSAAKALLDKLTGATP+DQ TNG+VPETGAVV +FEDKLMGNPVGWL+ +C 233
GRSKKEAKHSAAKALLDKLTGATPADQTNGNVPETGAVVTSFEDKLMGNPVGWLQE-LC

Query 538 HD SGH----HHLTMLKTMTMLIDQFQVCPHERQFTI ICTLLKRREVGTGKSKKLAKRQAA 705
Sbjct 234 +H + + PHERQFTI+CTLLKRRE+GTGKSKKLAKRQAA 287
MSRFWPPPSYHAENDDNVNRRL-----PHERQFTIVCTLLKRREIGTGKSKKLAKRQAA

Query 706 YKMWQALQDNPPESFQNDDEGGVAARYADLKDSKISTLTSSHSHKVSQFHKHLKQSVGPN 885
Sbjct 288 YKMWQALQDNPPESFQ D+EG +AARYADLKDSKISTLTSSHSHKVSQFHKHLKQSVGPN 346
YKMWQALQDNPPESFQDDEEG-MAARYADLKDSKISTLTSSHSHKVSQFHKHLKQSVGPN

Query 886 LAKLQVTPLNKDFNFVQFLQEIASQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVCH 1065
Sbjct 347 LAKLQVTPLNKDFNFVQFLQEIASQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVC+ 406
LAKLQVTPLNKDFNFVQFLQEIASQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVCY

Query 1066 GAGLTSKDAQSSAAQNALEYLKIMTKK* 1149
Sbjct 407 GAGL+SKDAQ+SAAQNALEYLKIMTKK* 434
GAGLSSKDAQSAAQNALEYLKIMTKK*

```

> ta_transcript67777_1
Length=1407

Score = 612 bits (1579), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 318/388 (82%), Positives = 343/388 (88%), Gaps = 13/388 (3%)
Frame = +1

```

Query 1 MEGNTVHPHPSPVPPGLPPGVHGMTVHSGPNGEHFPHGPRRRYQTRPKP-NNLQRLPLD 177
M+G VHPHP VV G PGV+HGM VHG+GP+GEH PHGPRRRYQ RPKP NN++RLPLD

```

```

Sbjct 55 MDGGVVHPHPGVVHGSVPGVVHGMFVHGAGPDGEHAPHGPRRRYQNRPKPPNNVERLPLD 114
Query 178 EAAKRKMETLPTKTPVSVLQELLARRETVPKYELLQIEGMIHEPTFRYRVTVADLFAMGT 357
EAAKR+ME+LP KTPVSVLQELLARR TVPKYEL+QIEGMIHEPTFRYRVTVADL AMGT
Sbjct 115 EAAKREMESLPMKTPVSVLQELLARRGTVPKYELVQIEGMIHEPTFRYRVTVADLVAMGT 174
Query 358 GRskkeakhsaakaLLDKLTGATPSDQTNGSVPETGAVVPTFEDKLMGNPVGWLRSCVC 537
GRSKKEAKHSAAKALLDKLTGATP+DQ TNG+VPETGAVV +FEDKLMGNPVGWL+ +C
Sbjct 175 GRSKKEAKHSAAKALLDKLTGATPADQGTNGNVPETGAVVTSFEDKLMGNPVGWLQE-LC 233
Query 538 HD SGH----HHLTMLKTMTMLIDQFQVCPHERQFTI ICTLLKRREVGTGKSKKLAKRQAA 705
+H + + PHERQFTI+CTLLKRRE+GTGKSKKLAKRQAA
Sbjct 234 MSRFWPPPSYHAENDDNVNRRL-----PHERQFTIVCTLLKRREIGTGKSKKLAKRQAA 287
Query 706 YKMWQALQDNPPESFQNDDEGGVAARYADLKDSKISTLTTS SHHKVSQFHKLKQSVGPN 885
YKMWQALQDNPPESFQ D+EG +AARYADLKDSKISTLTTS SHHKVSQFHKLKQSVGPN
Sbjct 288 YKMWQALQDNPPESFQPDDEG-MAARYADLKDSKISTLTTS SHHKVSQFHKLKQSVGPN 346
Query 886 LAKLQVTPLNNKDFNFVQFLQEIASEQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVCH 1065
LAKLQVTPLNNKDFNFVQFLQEIASEQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVC+
Sbjct 347 LAKLQVTPLNNKDFNFVQFLQEIASEQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVCY 406
Query 1066 GAGLTSKDAQSSAAQNALEYLKIMTKK* 1149
GAGL+SKDAQ+SAAQNALEYLKIMTKK*
Sbjct 407 GAGLSSKDAQSAAQNALEYLKIMTKK* 434

```

```

> ta_transcript67782_1
Length=927

```

```

Score = 506 bits (1302), Expect = 2e-170, Method: Compositional matrix adjust.
Identities = 275/388 (71%), Positives = 299/388 (77%), Gaps = 57/388 (15%)
Frame = +1

```

```

Query 1 MEGNTVHPHPSVVPGLPPGVIHGMTVHSGSPNGEHFPHGPRRRYQTRPKP-NNLQRLPLD 177
M+G VHPHP VV G PGV+HGM VHG+GP+GEH PHGPRRRYQ RPKP NN++RLPLD
Sbjct 55 MDGGVVHPHPGVVHGSVPGVVHGMFVHGAGPDGEHAPHGPRRRYQNRPKPPNNVERLPLD 114
Query 178 EAAKRKMETLPTKTPVSVLQELLARRETVPKYELLQIEGMIHEPTFRYRVTVADLFAMGT 357
EAAKR+ME+LP KTPVSVLQELLARR TVPKYEL+QIEGMIHEPTFRYRVTVADL AMGT
Sbjct 115 EAAKREMESLPMKTPVSVLQELLARRGTVPKYELVQIEGMIHEPTFRYRVTVADLVAMGT 174
Query 358 GRskkeakhsaakaLLDKLTGATPSDQTNGSVPETGAVVPTFEDKLMGNPVGWLRSCVC 537
GRSKKEAKHSAAKALLDKLTGATP+DQ TNG+VPETGAVV +FEDKLMGNPVGWL+ +C
Sbjct 175 GRSKKEAKHSAAKALLDKLTGATPADQGTNGNVPETGAVVTSFEDKLMGNPVGWLQE-LC 233
Query 538 HD SGH----HHLTMLKTMTMLIDQFQVCPHERQFTI ICTLLKRREVGTGKSKKLAKRQAA 705
+H + + PHERQFTI+CTLLKRRE+GTGKSKKLAKRQAA
Sbjct 234 MSRFWPPPSYHAENDDNVNRRL-----PHERQFTIVCTLLKRREIGTGKSKKLAKRQAA 287
Query 706 YKMWQALQDNPPESFQNDDEGGVAARYADLKDSKISTLTTS SHHKVSQFHKLKQSVGPN 885
YKMWQALQDNPPESFQ D+E
Sbjct 288 YKMWQALQDNPPESFQPDDE----- 307
Query 886 LAKLQVTPLNNKDFNFVQFLQEIASEQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVCH 1065
VTPLNNKDFNFVQFLQEIASEQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVC+
Sbjct 308 -----VTPLNNKDFNFVQFLQEIASEQSFEVTVVDIEEKSMTGLCQCLVQLSTLPVAVCY 362
Query 1066 GAGLTSKDAQSSAAQNALEYLKIMTKK* 1149
GAGL+SKDAQ+SAAQNALEYLKIMTKK*
Sbjct 363 GAGLSSKDAQSAAQNALEYLKIMTKK* 390

```

```

> ta_transcript67778_1
Length=1363

```

```

Score = 508 bits (1307), Expect = 7e-167, Method: Compositional matrix adjust.
Identities = 275/388 (71%), Positives = 299/388 (77%), Gaps = 57/388 (15%)
Frame = +1

```

```

Query 1 MEGNTVHPHPSVVPGLPPGVIHGMTVHSGSPNGEHFPHGPRRRYQTRPKP-NNLQRLPLD 177
M+G VHPHP VV G PGV+HGM VHG+GP+GEH PHGPRRRYQ RPKP NN++RLPLD
Sbjct 55 MDGGVVHPHPGVVHGSVPGVVHGMFVHGAGPDGEHAPHGPRRRYQNRPKPPNNVERLPLD 114
Query 178 EAAKRKMETLPTKTPVSVLQELLARRETVPKYELLQIEGMIHEPTFRYRVTVADLFAMGT 357
EAAKR+ME+LP KTPVSVLQELLARR TVPKYEL+QIEGMIHEPTFRYRVTVADL AMGT
Sbjct 115 EAAKREMESLPMKTPVSVLQELLARRGTVPKYELVQIEGMIHEPTFRYRVTVADLVAMGT 174

```

```

Query 358  GRskkeakhsaakaLLDKLTGATPSDQTTNGSVPETGAVVPTFEDKLMGNPVGWLRSCVC 537
Sbjct 175  GRSKKEAKHSAAKALLDKLTGATP+DQ TNG+VPETGAVV +FEDKLMGNPVGWL+ +C 233

Query 538  HDSGH---HHLTMLKTMMLIDQFQVCPHERQFTIICTLLKRREVGTKSKKLAKRQAA 705
          +H      +      +      PHERQFTI+CTLLKRRE+GTGSKKLAKRQAA
Sbjct 234  MSRFWPPPSYHAENDDNVNRRL-----PHERQFTIVCTLLKRREIGTKSKKLAKRQAA 287

Query 706  YKMWQALQDNPPESFQNDDEGGVAARYADLKDSKISTLTTS SHSHKVSQFHKLKQSVGPN 885
          YKMWQALQDNPPESFQ D+E
Sbjct 288  YKMWQALQDNPPESFQPDEE----- 307

Query 886  LAKLQVTPLNKDFNFVQFLQEIASQSFEVTVVDIEEKSM TGLCQCLVQLSTLPVAVCH 1065
          VTPLNKDFNFVQFLQEIASQSFEVTVVDIEEKSM+G QCLVQLSTLPVAVC+
Sbjct 308  -----VTPLNKDFNFVQFLQEIASQSFEVTVVDIEEKSMGRSQCLVQLSTLPVAVCY 362

Query 1066 GAGLTSKDAQSSAAQNALEYLKIMTKK* 1149
          GAGL+SKDAQ+SAAQNALEYLKIMTKK*
Sbjct 363  GAGLSSKDAQSAAQNALEYLKIMTKK* 390

```

```

> ta_transcript67779_1
Length=1051

```

```

Score = 163 bits (412), Expect = 8e-43, Method: Compositional matrix adjust.
Identities = 132/326 (40%), Positives = 181/326 (56%), Gaps = 14/326 (4%)
Frame = +3

```

```

Query 186  QKENGNTSYKDSCLCFARAVGTSGNCS*I*ttppdrhdt*thFPVQSNCG*FICNGHWSL 365
          Q+ NG ++ +DS + AR G + + + T DR HD+* HFP+Q + * C GHW+
Sbjct 198  QEGNGISTNEDSGVSTARTAGETWYRAQVRTGADRGHDS*AHFPLQGHSC*SCCYGHWTF 257

Query 366  KKR GKALCSQGFTGQVNWCPYI*SDYQWQCP*NWCCSTYI*R*TNG*SCWMASE-----L 530
          K+RG+AL G GQ +WCY *S + +C NWC I*R +G +A+ L
Sbjct 258  KER GQALGC*GSPGQTDWCYSC*SRNKRKCTRNWCSGYVI*RQADGQPGGLAARAVHVSL 317

Query 531  CMSRFWPPPSYHAENDDNVNRPVSGLP*TSIYDHLHIAQAP*SWYRQVKEIS*TASCLQ 710
          S F P + +R ++ +H A+A +RQV+E S LQ
Sbjct 318  LASSFIPC*KRRQRQPSSASR-----APVHHCVHSAEAAGDRHRQVQEACQAPSRLQ 369

Query 711  DVAGLTGQPTRILPE***GRCCGPLCRFER**NLHIDHEP*P*SVAVPQTSQTVCPWPQPG 890
          DVA GQP+ ILP ** G G LCR ER**NLH D++ P S+AVPQT QT+ PQPG
Sbjct 370  DVASSAGQPSGILPA**RGNG-GSLCRPER**NLHTDYQSQPQSLAVPQTPQTIRGPQPG 428

Query 891  QVAGDTTKQ*GF*LRSVLARN SIRAI*FDLCRHRKRYVDWSMSVSCPAFHIASSCMPRS 1070
          QVAGD+ +Q LR+V A + + A+ GD+ HR +V +++V A H A + R
Sbjct 429  QVAGDSAEQQGLQLRAVPAGDRVGAVVRGHRGEVDVGALAVPRAAVHAARGVRLRR 488

Query 1071 RPHQQGCPVICC SERLGVSQDYDQKV 1148
          RP QQG + +ER V QD+DQ+V
Sbjct 489  RPLQQGRAGLRRARARVPQDHDQEV 514

```

```

> ta_transcript67775_1
Length=1487

```

```

Score = 159 bits (402), Expect = 3e-41, Method: Compositional matrix adjust.
Identities = 132/326 (40%), Positives = 181/326 (56%), Gaps = 14/326 (4%)
Frame = +3

```

```

Query 186  QKENGNTSYKDSCLCFARAVGTSGNCS*I*ttppdrhdt*thFPVQSNCG*FICNGHWSL 365
          Q+ NG ++ +DS + AR G + + + T DR HD+* HFP+Q + * C GHW+
Sbjct 198  QEGNGISTNEDSGVSTARTAGETWYRAQVRTGADRGHDS*AHFPLQGHSC*SCCYGHWTF 257

Query 366  KKR GKALCSQGFTGQVNWCPYI*SDYQWQCP*NWCCSTYI*R*TNG*SCWMASE-----L 530
          K+RG+AL G GQ +WCY *S + +C NWC I*R +G +A+ L
Sbjct 258  KER GQALGC*GSPGQTDWCYSC*SRNKRKCTRNWCSGYVI*RQADGQPGGLAARAVHVSL 317

Query 531  CMSRFWPPPSYHAENDDNVNRPVSGLP*TSIYDHLHIAQAP*SWYRQVKEIS*TASCLQ 710
          S F P + +R ++ +H A+A +RQV+E S LQ
Sbjct 318  LASSFIPC*KRRQRQPSSASR-----APVHHCVHSAEAAGDRHRQVQEACQAPSRLQ 369

Query 711  DVAGLTGQPTRILPE***GRCCGPLCRFER**NLHIDHEP*P*SVAVPQTSQTVCPWPQPG 890
          DVA GQP+ ILP ** G G LCR ER**NLH D++ P S+AVPQT QT+ PQPG
Sbjct 370  DVASSAGQPSGILPA**RGNG-GSLCRPER**NLHTDYQSQPQSLAVPQTPQTIRGPQPG 428

```

```

Query   891   QVAGDTTKQ*GF*LRSVLARNISIRAI*F*GDLCHRRKVDWMSVSCPAFHIASSCMPRS 1070
          QVAGD+ +Q G LR+V A + + A+ GD+ HR +V +++V A H A + R
Sbjct   429   QVAGDSAEQQGLQLRAVPAGDRVGAVVRGDVGRHGEVDVGALAVPRAAVHAARGRVLRR 488

Query   1071  RPHQQGCPVICCSERLGVSQDYDQKV 1148
          RP QQG + +ER V QD+DQ+V
Sbjct   489   RPLQQGRAGLRRARARVPQDHDQEV 514

```


Query= gi|300669730|dbj|AB566385.1| Bombyx mori R2D2 mRNA for R2D2,complete cds

Length=1023

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript64766_1	276	4e-87
ta_transcript64768_1	275	6e-87
ta_transcript64758_1	276	7e-87
ta_transcript64763_1	275	9e-87
ta_transcript64759_1	276	1e-86
ta_transcript64764_1	275	1e-86
ta_transcript64762_1	275	2e-86
ta_transcript64751_1	283	2e-84
ta_transcript64749_1	283	2e-84
ta_transcript64767_1	268	3e-84
ta_transcript64769_1	267	4e-84
ta_transcript64761_1	269	4e-84
ta_transcript64760_1	269	6e-84
ta_transcript64765_1	268	7e-84
ta_transcript64753_1	280	2e-83
ta_transcript64755_1	276	6e-82
ta_transcript64752_1	276	7e-82
ta_transcript64750_1	276	7e-82
ta_transcript64747_1	273	4e-81
ta_transcript64757_1	273	6e-81
ta_transcript64756_1	273	6e-81
ta_transcript64754_1	273	8e-81
ta_transcript64748_1	266	1e-78

> ta_transcript64766_1
Length=505

Score = 276 bits (705), Expect = 4e-87, Method: Compositional matrix adjust.
Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
Frame = +1

```

Query   4      KTPITVLQEMMKLGIPEYECVAQSGPQHQTATFEFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct   77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query   184     RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEGKAPTVDRSYVALLKELCEEY 360
          + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct   137     KLMLFQLARRGHRVPPPYNS---GPQLSTQQSSASKKEAEPISIVGSHSYVLLKDLCEEY 193

Query   361     KLPGVEYALVADTGPAHMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct   194     HLPGVEYTLIGDTGPPHMREFITIRVIRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query   541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct   254     VTKDFTEEEALVRAHERAMDREYVEMRDELPVWRPDLGQKIADYPIGLKTH----- 303

Query   715     RLPVVLQCLRRAMVDTDPEKRMARAVLSETDDIeea-----aeraaaalelQTCW 870
          DPEK AR VLS D+I+ + AAAL L W
Sbjct   304     -----IDPEKCLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query   871     ETLD----PLHVLKLD-AAPALAFSGHS 939
          L L +L+L +PALAF+G +
Sbjct   348     SELQAERGKQLQMLELTPSPALAFAGEN 375

```

> ta_transcript64768_1
Length=485

Score = 275 bits (702), Expect = 6e-87, Method: Compositional matrix adjust.
 Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
 Frame = +1

```

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVSASARSKREAKQEAA 183
Sbjct 77     KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184    RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEGKAPTVD SRSYVALLKELCEEY 360
Sbjct 137    KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVLLKDLCEEY 193

Query 361    KLPGVEYALVADTGP AHMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
Sbjct 194    HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541    LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
Sbjct 254    +T DF EE+ALVRAHERAM+R VE W+PD LGQ++++Y GL +H
VTKDFTEEEALVRAHERAMDRYVEMRDP ELVWRPDLGQKIADYPIGLKTH----- 303

Query 715    RLPVVLDQCLRRAMVDT DPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
Sbjct 304    DPEK AR VLS D+I+ + AAAL L W
-----IDPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871    ETLD----PLHVLKLD-AAPALAFSGHS 939
Sbjct 348    L L +L+L +PALAF+G +
SELQAERGKLMLELTPTSPALAFAGEN 375

```

> ta_transcript64758_1
 Length=540

Score = 276 bits (706), Expect = 7e-87, Method: Compositional matrix adjust.
 Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
 Frame = +1

```

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVSASARSKREAKQEAA 183
Sbjct 77     KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184    RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEGKAPTVD SRSYVALLKELCEEY 360
Sbjct 137    KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVLLKDLCEEY 193

Query 361    KLPGVEYALVADTGP AHMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
Sbjct 194    HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541    LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
Sbjct 254    +T DF EE+ALVRAHERAM+R VE W+PD LGQ++++Y GL +H
VTKDFTEEEALVRAHERAMDRYVEMRDP ELVWRPDLGQKIADYPIGLKTH----- 303

Query 715    RLPVVLDQCLRRAMVDT DPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
Sbjct 304    DPEK AR VLS D+I+ + AAAL L W
-----IDPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871    ETLD----PLHVLKLD-AAPALAFSGHS 939
Sbjct 348    L L +L+L +PALAF+G +
SELQAERGKLMLELTPTSPALAFAGEN 375

```

> ta_transcript64763_1
 Length=520

Score = 275 bits (704), Expect = 9e-87, Method: Compositional matrix adjust.
 Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
 Frame = +1

```

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVSASARSKREAKQEAA 183
Sbjct 77     KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184    RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEGKAPTVD SRSYVALLKELCEEY 360
Sbjct 137    KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVLLKDLCEEY 193

Query 361    KLPGVEYALVADTGP AHMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540

```

```

          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 254 VTKDFTEEEEALVRAHERAMDREYVEMRDPELVWRPDLGQKIADYPIGLKTH----- 303

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeea-----aeraaaalelQTCW 870
          DPEK AR VLS D+I+ + AAAL L W
Sbjct 304 -----IDPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
          L L +L+L +PALAF+G +
Sbjct 348 SELQAERGKQLMLELTPSPALAFAGEN 375

```

> ta_transcript64759_1
Length=539

Score = 276 bits (705), Expect = 1e-86, Method: Compositional matrix adjust.
Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
Frame = +1

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEKAPTVDERSYVALLKELCEEY 360
          + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query 361 KLPGVEYALVADTGAHMRFLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 254 VTKDFTEEEEALVRAHERAMDREYVEMRDPELVWRPDLGQKIADYPIGLKTH----- 303

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeea-----aeraaaalelQTCW 870
          DPEK AR VLS D+I+ + AAAL L W
Sbjct 304 -----IDPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
          L L +L+L +PALAF+G +
Sbjct 348 SELQAERGKQLMLELTPSPALAFAGEN 375

```

> ta_transcript64764_1
Length=519

Score = 275 bits (703), Expect = 1e-86, Method: Compositional matrix adjust.
Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
Frame = +1

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEKAPTVDERSYVALLKELCEEY 360
          + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query 361 KLPGVEYALVADTGAHMRFLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 254 VTKDFTEEEEALVRAHERAMDREYVEMRDPELVWRPDLGQKIADYPIGLKTH----- 303

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeea-----aeraaaalelQTCW 870
          DPEK AR VLS D+I+ + AAAL L W
Sbjct 304 -----IDPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
          L L +L+L +PALAF+G +

```

Sbjct 348 SELQAERGKQLQMLELTPPTSPALAFAGEN 375

> ta_transcript64762_1
Length=523

Score = 275 bits (703), Expect = 2e-86, Method: Compositional matrix adjust.
Identities = 160/328 (49%), Positives = 203/328 (62%), Gaps = 45/328 (14%)
Frame = +1

```

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVVSASARSKREAKQEAA 183
              KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184     RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSE GKAPTVD SRSYVALLKELCEEY 360
              + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137     KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVVLKDLCEEY 193

Query 361     KLPGVEYALVADTGPAHMLRFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
              LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194     HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
              +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 254     VTKDFTEEEALVRAHERAMD RYVEMRDP ELVWRPDLGQKIADYPIGLKTH----- 303

Query 715     RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
              DPEK AR VLS D+I+ + AAAL L W
Sbjct 304     -----IDPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871     ETLD----PLHVLKLD-AAPALAFSGHS 939
              L L +L+L +PALAF+G +
Sbjct 348     SELQAERGKQLQMLELTPPTSPALAFAGEN 375

```

> ta_transcript64751_1
Length=1749

Score = 283 bits (723), Expect = 2e-84, Method: Composition-based stats.
Identities = 157/328 (48%), Positives = 201/328 (61%), Gaps = 45/328 (14%)
Frame = +1

```

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVVSASARSKREAKQEAA 183
              KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184     RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSE GKAPTVD SRSYVALLKELCEEY 360
              + ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137     KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVVLKDLCEEY 193

Query 361     KLPGVEYALVADTGPAHMLRFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
              LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194     HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
              +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 254     VTKDFTEEEALVRAHERAMD RYVEMRDP ELVWRPDLGQKIADYPIGLKTH----- 303

Query 715     RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeeaaeraaaalelQTC-----W 870
              DPEK AR VLS D+I+ + + A T W
Sbjct 304     -----IDPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871     ETLDP----LHVLKLD-AAPALAFSGHS 939
              L L +L+L +PALAF+G +
Sbjct 348     SELQAERGKQLQMLELTPPTSPALAFAGEN 375

```

> ta_transcript64749_1
Length=1762

Score = 283 bits (723), Expect = 2e-84, Method: Composition-based stats.
Identities = 157/328 (48%), Positives = 201/328 (61%), Gaps = 45/328 (14%)
Frame = +1

```

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTATFEFRCKALGESVVSASARSKREAKQEAA 183
              KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSTFEYRCQALGELVTATARSKKEAKQEVA 136

```

```

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSE GKAPTVD SRSYVALLKELCEEY 360
+ ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVLLKDLCEEY 193

Query 361 KLP GVEYALVADTGP AHMRLFSVRASIGLH SRDASGTTKRQARQKAAADLYLFLRXNLSR 540
LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLP GVEYTLIGDTGPPHMREF TIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
+T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 254 VTKDFTEEEALVRAHERAMDRYVEMRDP ELVWRPDLGQKIADYPIGLKTH----- 303

Query 715 RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeeaaeraaaalelQTC-----W 870
DPEK AR VLS D+I+ + + A T W
Sbjct 304 -----IDPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query 871 ETLDP----LHVLKLD-AAPALAFSGHS 939
L L +L+L +PALAF+G +
Sbjct 348 SELQAERGKQLMLELTP TSPALAFAGEN 375

```

```

> ta_transcript64767_1
Length=499

```

```

Score = 268 bits (686), Expect = 3e-84, Method: Compositional matrix adjust.
Identities = 158/328 (48%), Positives = 201/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQH QATFEFRCKALGESVSASARSKREAKQEAA 183
KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTA VTVLQELMVKMGHTPEYDCVSQSGPQHLS TFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSE GKAPTVD SRSYVALLKELCEEY 360
+ ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVLLKDLCEEY 193

Query 361 KLP GVEYALVADTGP AHMRLFSVRASIGLH SRDASGTTKRQARQKAAADLYLFLRXNLSR 540
LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLP GVEYTLIGDTGPPHMREF TIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
+T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDRYVEMRDP ELVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
P+ DPEK AR VLS D+I+ + AAAL L W
Sbjct 297 --PI-----DPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
L L +L+L +PALAF+G +
Sbjct 342 SELQAERGKQLMLELTP TSPALAFAGEN 369

```

```

> ta_transcript64769_1
Length=479

```

```

Score = 267 bits (683), Expect = 4e-84, Method: Compositional matrix adjust.
Identities = 158/328 (48%), Positives = 201/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQH QATFEFRCKALGESVSASARSKREAKQEAA 183
KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTA VTVLQELMVKMGHTPEYDCVSQSGPQHLS TFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSE GKAPTVD SRSYVALLKELCEEY 360
+ ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEP SIVGSHSYVLLKDLCEEY 193

Query 361 KLP GVEYALVADTGP AHMRLFSVRASIGLH SRDASGTTKRQARQKAAADLYLFLRXNLSR 540
LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLP GVEYTLIGDTGPPHMREF TIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
+T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDRYVEMRDP ELVWRPDLGQKIADY----- 296

```



```

Query 715 RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
          P+                DPEK  AR VLS  D+I+ +                AAAL L  W
Sbjct 297 --PI-----DPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
          L      L +L+L  +PALAF+G +
Sbjct 342 SELQAERGKQLMLELTPTSPALAFAGEN 369

> ta_transcript64761_1
Length=534

Score = 269 bits (687), Expect = 4e-84, Method: Compositional matrix adjust.
Identities = 158/328 (48%), Positives = 201/328 (61%), Gaps = 51/328 (16%)
Frame = +1

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQATFEFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184     RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEKAPTVD SRSYVALLKELCEEY 360
          + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137     KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPSIVGSHSYVLLKDLCEEY 193

Query 361     KLPGVEYALVADTGP AHMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194     HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PD LGQ++++Y
Sbjct 254     VTKDFTEEEALVRAHERAMDRYVEMRDP ELPVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
          P+                DPEK  AR VLS  D+I+ +                AAAL L  W
Sbjct 297 --PI-----DPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
          L      L +L+L  +PALAF+G +
Sbjct 342 SELQAERGKQLMLELTPTSPALAFAGEN 369

> ta_transcript64760_1
Length=537

Score = 269 bits (687), Expect = 6e-84, Method: Compositional matrix adjust.
Identities = 158/328 (48%), Positives = 201/328 (61%), Gaps = 51/328 (16%)
Frame = +1

Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQATFEFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184     RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEKAPTVD SRSYVALLKELCEEY 360
          + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct 137     KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPSIVGSHSYVLLKDLCEEY 193

Query 361     KLPGVEYALVADTGP AHMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194     HLPGVEYTLIGDTGPPHMREFTIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPD LGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PD LGQ++++Y
Sbjct 254     VTKDFTEEEALVRAHERAMDRYVEMRDP ELPVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeea-----aeraaaalelQTCW 870
          P+                DPEK  AR VLS  D+I+ +                AAAL L  W
Sbjct 297 --PI-----DPEKCQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLD----PLHVLKLD-AAPALAFSGHS 939
          L      L +L+L  +PALAF+G +
Sbjct 342 SELQAERGKQLMLELTPTSPALAFAGEN 369

> ta_transcript64765_1
Length=514

Score = 268 bits (684), Expect = 7e-84, Method: Compositional matrix adjust.

```

Identities = 158/328 (48%), Positives = 201/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

Query   4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQAATFEFRCKALGESVSASARSKREAKQEAA 183
           KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct   77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query   184     RAMLLCLSTIGHRVPPPFATEFTQPSHSNQ-SAGECSEGKAPTVDSSRSYVALLKELCEEY 360
           + ML L+ GHRVPPP+ + P S Q S+ E + V S SYV LLK+LCEEY
Sbjct   137     KLMLFQLARRGHRVPPPYNS---GPQLSTQQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query   361     KLPGVEYALVADTGAHMRFLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
           LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct   194     HLPGVEYTLIGDTGPPHMREFTIRVRIGHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query   541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
           +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct   254     VTKDFTEEEALVRAHERAMDREYVEMRDPELVWRPDLGQKIADY----- 296

Query   715     RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeea-----aeraaaalelQTCW 870
           P+ DPEK AR VLS D+I+ + AAAL L W
Sbjct   297     --PI-----DPEKQCLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query   871     ETLD---PLHVLKLD-AAPALAFSGHS 939
           L L +L+L +PALAF+G +
Sbjct   342     SELQAERGLQMLELTPTSPALAFAGEN 369

```

> ta_transcript64753_1
Length=1742

Score = 280 bits (716), Expect = 2e-83, Method: Composition-based stats.
Identities = 157/328 (48%), Positives = 201/328 (61%), Gaps = 45/328 (14%)
Frame = +1

```

Query   4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQAATFEFRCKALGESVSASARSKREAKQEAA 183
           KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct   77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query   184     RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEGKAPTVDSSRSYVALLKELCEEY 360
           + ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct   137     KLMLFQLARRGHRVPPPYNS---GPQLSTQQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query   361     KLPGVEYALVADTGAHMRFLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
           LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct   194     HLPGVEYTLIGDTGPPHMREFTIRVRIGHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query   541     LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
           +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct   254     VTKDFTEEEALVRAHERAMDREYVEMRDPELVWRPDLGQKIADYPIGLKT----- 303

Query   715     RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeeaaeraaaalelQTC-----W 870
           DPEK AR VLS D+I+ + + A T W
Sbjct   304     -----IDPEKQCLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 347

Query   871     ETLDP---LHVLKLD-AAPALAFSGHS 939
           L L +L+L +PALAF+G +
Sbjct   348     SELQAERGLQMLELTPTSPALAFAGEN 375

```

> ta_transcript64755_1
Length=1644

Score = 276 bits (705), Expect = 6e-82, Method: Composition-based stats.
Identities = 155/328 (47%), Positives = 199/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

Query   4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQAATFEFRCKALGESVSASARSKREAKQEAA 183
           KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct   77      KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKKEAKQEVA 136

Query   184     RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEGKAPTVDSSRSYVALLKELCEEY 360
           + ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct   137     KLMLFQLARRGHRVPPPYNS---GPQLSTQQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query   361     KLPGVEYALVADTGAHMRFLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
           LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R

```

```

Sbjct 194 HLPGVEYTLIGDTGPPHMREFITIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
+T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDREYVEMRDPDLVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeaaeraaaalelQTC-----W 870
P+ DPEK AR VLS D+I+ + + A T W
Sbjct 297 --PI-----DPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLDP----LHVLKLD-AAPALAFSGHS 939
L L +L+L +PALAF+G +
Sbjct 342 SELQAERGKLMLELTPTSPALAFAGEN 369

```

```

> ta_transcript64752_1
Length=1743

```

```

Score = 276 bits (705), Expect = 7e-82, Method: Composition-based stats.
Identities = 155/328 (47%), Positives = 199/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQHQAATFEFRCKALGESVSASARSKREAKQEAA 183
KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTAFTVLQELMVKMGHTPEYDCVSQSGPQHLSTFEYRCQALGELVTATARSKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEGKAPTVDERSYVALLKELCEEY 360
+ ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query 361 KLPGVEYALVADTGPAMHRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFITIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
+T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDREYVEMRDPDLVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeaaeraaaalelQTC-----W 870
P+ DPEK AR VLS D+I+ + + A T W
Sbjct 297 --PI-----DPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLDP----LHVLKLD-AAPALAFSGHS 939
L L +L+L +PALAF+G +
Sbjct 342 SELQAERGKLMLELTPTSPALAFAGEN 369

```

```

> ta_transcript64750_1
Length=1756

```

```

Score = 276 bits (705), Expect = 7e-82, Method: Composition-based stats.
Identities = 155/328 (47%), Positives = 199/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQHQAATFEFRCKALGESVSASARSKREAKQEAA 183
KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTAFTVLQELMVKMGHTPEYDCVSQSGPQHLSTFEYRCQALGELVTATARSKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEGKAPTVDERSYVALLKELCEEY 360
+ ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPISVGSHSYVLLKDLCEEY 193

Query 361 KLPGVEYALVADTGPAMHRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFITIRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
+T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDREYVEMRDPDLVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeaaeraaaalelQTC-----W 870
P+ DPEK AR VLS D+I+ + + A T W
Sbjct 297 --PI-----DPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLDP----LHVLKLD-AAPALAFSGHS 939
L L +L+L +PALAF+G +
Sbjct 342 SELQAERGKLMLELTPTSPALAFAGEN 369

```

> ta_transcript64747_1
Length=1769

Score = 273 bits (699), Expect = 4e-81, Method: Compositional matrix adjust.
Identities = 144/274 (53%), Positives = 181/274 (66%), Gaps = 30/274 (11%)
Frame = +1

```
Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTFFFRCKALGESVSASARSKREAKQEAA 183
             KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77     KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184    RAMLLCLSTIGHRVPPPFATEFTQPSHSNQSAGECSEKAPTVDSSSYVALLKELCEEYK 363
             + ML L+ GHRVPPP+ + Q S + QS+ E + V S SYV LLK+LCEEY
Sbjct 137    KLMLFQLARRGHRVPPPYNSG-PQLS-TQSSASKKEAEPSIVGSHSYVLLKDLCEEYH 194

Query 364    LPGVEYALVADTGPAMHRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSRL 543
             LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R+
Sbjct 195    LPGVEYTLIGDTGPPHMREFITIRVRIQHERTATSTTKKAARQMAAEQLYKYMRENLHRV 254

Query 544    THDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRRR 717
             T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y GL +H
Sbjct 255    TKDFTTEEEALVRAHERAMDRYVEMRDPELVWRPDLGQKIADYPIGLKTH----- 303

Query 718    LPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDI 819
             DPEK AR VLS D+I
Sbjct 304    -----IDPEKCQLARTVLSLDEI 322
```

> ta_transcript64757_1
Length=1624

Score = 273 bits (697), Expect = 6e-81, Method: Composition-based stats.
Identities = 155/328 (47%), Positives = 199/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```
Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTFFFRCKALGESVSASARSKREAKQEAA 183
             KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77     KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184    RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEKAPTVDSSSYVALLKELCEEY 360
             + ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137    KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPSIVGSHSYVLLKDLCEEY 193

Query 361    KLPGVEYALVADTGPAMHRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
             LPGAUEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194    HLPGVEYTLIGDTGPPHMREFITIRVRIQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541    LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
             +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254    VTKDFTTEEEALVRAHERAMDRYVEMRDPELVWRPDLGQKIADY----- 296

Query 715    RLPVVLDQCLRRAMVDTDPEKRMAARAVLSETDDIeeaaeraaaalelQTC-----W 870
             P+ DPEK AR VLS D+I+ + + A T W
Sbjct 297    --PI-----DPEKCQLARTVLSLDEIQSSDPQVVEAALTATAALGLTINW 341

Query 871    ETLDP----LHVLKLD-AAPALAFSGHS 939
             L L+L+L +PALAF+G +
Sbjct 342    SELQAERGKQLQMLELTPTSPALAFAGEN 369
```

> ta_transcript64756_1
Length=1628

Score = 273 bits (697), Expect = 6e-81, Method: Composition-based stats.
Identities = 155/328 (47%), Positives = 199/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```
Query 4      KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTFFFRCKALGESVSASARSKREAKQEAA 183
             KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77     KTAVTVLQELMVKMGHTPEYDCVSQSGPQHLSFEYRCQALGELVTATARSKKEAKQEVA 136

Query 184    RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEKAPTVDSSSYVALLKELCEEY 360
             + ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137    KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPSIVGSHSYVLLKDLCEEY 193
```

```

Query 361 KLPGVEYALVADTGPAMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFITRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDRYVEMRDPQLVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeaaeraaaalelQTC-----W 870
          P+ DPEK AR VLS D+I+ + + A T W
Sbjct 297 --PI-----DPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLDP----LHVLKLD-AAPALAFSGHS 939
          L L +L+L +PALAF+G +
Sbjct 342 SELQAERKGLQMLELTPTSPALAFAGEN 369

```

```

> ta_transcript64754_1
Length=1736

```

```

Score = 273 bits (697), Expect = 8e-81, Method: Composition-based stats.
Identities = 155/328 (47%), Positives = 199/328 (61%), Gaps = 51/328 (16%)
Frame = +1

```

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTFFFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTAFTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHS-NQSAGECSEGKAPTVDSSRSYVALLKELCEEY 360
          + ML L+ GHRVPPP+ + P S QS+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNS---GPQLSTQSSASKKEAEPSIVGSHSYVLLKDLCEEY 193

Query 361 KLPGVEYALVADTGPAMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSR 540
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R
Sbjct 194 HLPGVEYTLIGDTGPPHMREFITRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHR 253

Query 541 LTHDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRR 714
          +T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 254 VTKDFTEEEALVRAHERAMDRYVEMRDPQLVWRPDLGQKIADY----- 296

Query 715 RLPVVLDQCLRRAMVDTDPEKRMARAVLSETDDIeaaeraaaalelQTC-----W 870
          P+ DPEK AR VLS D+I+ + + A T W
Sbjct 297 --PI-----DPEKQLARTVLSLDEIQSSDPQVVEAALTATAAALGLTINW 341

Query 871 ETLDP----LHVLKLD-AAPALAFSGHS 939
          L L +L+L +PALAF+G +
Sbjct 342 SELQAERKGLQMLELTPTSPALAFAGEN 369

```

```

> ta_transcript64748_1
Length=1763

```

```

Score = 266 bits (681), Expect = 1e-78, Method: Compositional matrix adjust.
Identities = 142/274 (52%), Positives = 179/274 (65%), Gaps = 36/274 (13%)
Frame = +1

```

```

Query 4 KTPITVLQEMMMKLGQIPEYECVAQSGPQHQTFFFRCKALGESVSASARSKREAKQEAA 183
          KT +TVLQE+M+K+G PEY+CV+QSGPQH +TFE+RC+ALGE V+A+ARSK+EAKQE A
Sbjct 77 KTAFTVLQELMVKMGHTPEYDCVSQSGPQHLSSTFEYRCQALGELVTATARSKEAKQEVA 136

Query 184 RAMLLCLSTIGHRVPPPFATEFTQPSHSNQSAGECSEGKAPTVDSSRSYVALLKELCEEYK 363
          + ML L+ GHRVPPP+ + Q S + QS+ E + V S SYV LLK+LCEEY
Sbjct 137 KLMLFQLARRGHRVPPPYNSG-PQLS-TQSSASKKEAEPSIVGSHSYVLLKDLCEEYH 194

Query 364 LPGVEYALVADTGPAMRLFSVRASIGLHSRDASGTTKRQARQKAAADLYLFLRXNLSRL 543
          LPGVEY L+ DTGP HMR F++R IG H R A+ TTK+ ARQ AA LY ++R NL R+
Sbjct 195 LPGVEYTLIGDTGPPHMREFITRVRIGQHERTATSTTKKAARQMAAEQLYKYMRENLHRV 254

Query 544 THDFVEEQALVRAHERAMERLVETTPAP--WKPDLGQRVSEYHYGLISHTGECTARSRRR 717
          T DF EE+ALVRAHERAM+R VE W+PDLGQ++++Y
Sbjct 255 TKDFTEEEALVRAHERAMDRYVEMRDPQLVWRPDLGQKIADY----- 296

Query 718 LPVVLDQCLRRAMVDTDPEKRMARAVLSETDDI 819
          P+ DPEK AR VLS D+I
Sbjct 297 -PI-----DPEKQLARTVLSLDEI 316

```


Query= gi|161579134|gb|EU273921.1| Tribolium castaneum C3PO protein (C3PO)mRNA, partial cds

Length=353

Sequences producing significant alignments:	Score (Bits)	E Value
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ta_transcript67781_1	32.3	0.20
ta_transcript67782_1	32.3	0.20
ta_transcript67778_1	32.0	0.27
ta_transcript67777_1	32.0	0.28
ta_transcript14282_1	29.6	1.3
ta_transcript53466_1	28.9	3.1
ta_transcript53468_1	28.9	3.8
ta_transcript54484_1	27.7	9.4
ta_transcript54486_1	27.3	9.9
ta_transcript54485_1	27.7	9.9

> ta_transcript67781_1
 Length=971

Score = 32.3 bits (72), Expect = 0.20, Method: Composition-based stats.
 Identities = 29/86 (34%), Positives = 37/86 (43%), Gaps = 11/86 (13%)
 Frame = +2

Query	41	SFKCTVKAGGVTACGYGTSKKNAKHESAKNALVKLRREDKS-----PEIKPRAEN--	190
		+F+ V + A G G SKK AKH +AK L KL + PE +	
Sbjct	159	TFRYRVTVADLVAMGTGRSKKEAKHSAKALLDKLTGATPADQGTVGNVPETGAVVTSFE	218
Query	191	NNLFRNFVGGELNEYAASRYGAKYPSY	268
		+ L N VG L E SR+ PSY	
Sbjct	219	DKLMGNPVGWLQELCMSRWFPP-PSY	243

> ta_transcript67782_1
 Length=927

Score = 32.3 bits (72), Expect = 0.20, Method: Composition-based stats.
 Identities = 29/86 (34%), Positives = 37/86 (43%), Gaps = 11/86 (13%)
 Frame = +2

Query	41	SFKCTVKAGGVTACGYGTSKKNAKHESAKNALVKLRREDKS-----PEIKPRAEN--	190
		+F+ V + A G G SKK AKH +AK L KL + PE +	
Sbjct	159	TFRYRVTVADLVAMGTGRSKKEAKHSAKALLDKLTGATPADQGTVGNVPETGAVVTSFE	218
Query	191	NNLFRNFVGGELNEYAASRYGAKYPSY	268
		+ L N VG L E SR+ PSY	
Sbjct	219	DKLMGNPVGWLQELCMSRWFPP-PSY	243

> ta_transcript67778_1
 Length=1363

Score = 32.0 bits (71), Expect = 0.27, Method: Composition-based stats.
 Identities = 29/86 (34%), Positives = 37/86 (43%), Gaps = 11/86 (13%)
 Frame = +2

Query	41	SFKCTVKAGGVTACGYGTSKKNAKHESAKNALVKLRREDKS-----PEIKPRAEN--	190
		+F+ V + A G G SKK AKH +AK L KL + PE +	
Sbjct	159	TFRYRVTVADLVAMGTGRSKKEAKHSAKALLDKLTGATPADQGTVGNVPETGAVVTSFE	218
Query	191	NNLFRNFVGGELNEYAASRYGAKYPSY	268
		+ L N VG L E SR+ PSY	
Sbjct	219	DKLMGNPVGWLQELCMSRWFPP-PSY	243

> ta_transcript67777_1
 Length=1407

Score = 32.0 bits (71), Expect = 0.28, Method: Composition-based stats.
 Identities = 29/86 (34%), Positives = 37/86 (43%), Gaps = 11/86 (13%)
 Frame = +2

Query	41	SFKCTVKAGGVTACGYGTSKKNAKHESAKNALVKLRREDKS-----PEIKPRAEN--	190
		+F+ V + A G G SKK AKH +AK L KL + PE +	

```

Sbjct  159  TFRYRVTVADLVAMGTGRSKKEAKHSAKALLDKLTGATPADQGNGNVPETGAVVTSFE  218

Query  191  NNLFRNFVVGELNEYAASRYGAKYPSY  268
          + L N VG L E SR+ PSY
Sbjct  219  DKLMGNFVGWLQELCMSRFWPP-PSY  243

> ta_transcript14282_1
Length=138

Score = 29.6 bits (65), Expect = 1.3, Method: Compositional matrix adjust.
Identities = 14/39 (36%), Positives = 18/39 (46%), Gaps = 0/39 (0%)
Frame = +2

Query  2     ISLPVYIEEGFGTSFKCTVKAGGVTACGYGTSKKNKHE  118
          + LP+ IE GF + GV CG T N +HE
Sbjct  37     VFLPLPIESGFQMGVHQLPQVQGVPCG*KTQGVNEQHE  75

> ta_transcript53466_1
Length=1278

Score = 28.9 bits (63), Expect = 3.1, Method: Composition-based stats.
Identities = 18/68 (26%), Positives = 30/68 (44%), Gaps = 1/68 (1%)
Frame = +2

Query  47     KCTVKAGGVTACGYGTSKKNKHEHESAK-NALVKLRREDKSPEIKPRAENNNLFRNFVGEL  223
          KC VT GY +K+ K + +K A++K+ R + E++ N F F+
Sbjct  252     KCVFLVNEVTYLGYYVVTKEGIKADKSKIEAILKMSRPENVSELRSFLGLVNFFAKFIKNF  311

Query  224     NEYAASRY  247
          + A Y
Sbjct  312     SSVLAPLY  319

> ta_transcript53468_1
Length=720

Score = 28.9 bits (63), Expect = 3.8, Method: Composition-based stats.
Identities = 18/68 (26%), Positives = 30/68 (44%), Gaps = 1/68 (1%)
Frame = +2

Query  47     KCTVKAGGVTACGYGTSKKNKHEHESAK-NALVKLRREDKSPEIKPRAENNNLFRNFVGEL  223
          KC VT GY +K+ K + +K A++K+ R + E++ N F F+
Sbjct  252     KCVFLVNEVTYLGYYVVTKEGIKADKSKIEAILKMSRPENVSELRSFLGLVNFFAKFIKNF  311

Query  224     NEYAASRY  247
          + A Y
Sbjct  312     SSVLAPLY  319

> ta_transcript54484_1
Length=785

Score = 27.7 bits (60), Expect = 9.4, Method: Composition-based stats.
Identities = 21/63 (33%), Positives = 28/63 (44%), Gaps = 3/63 (5%)
Frame = +2

Query  95     SKKNKHEHESAKNALV--KLRREDKSPEIKPRAENNNLFRNFVGELNEYAASRY-GAKYPS  265
          SK K NAL+ + + K ++ P NLFRNF L Y S+Y G K
Sbjct  382     SKNKIKRMEGPNALLYTDMMVQ*KVVQLTPTIHPVNLFRNFPNILYHYCYSKYLGKKGY  441

Query  266     YDF  274
          Y +
Sbjct  442     YRY  444

> ta_transcript54486_1
Length=486

Score = 27.3 bits (59), Expect = 9.9, Method: Composition-based stats.
Identities = 21/63 (33%), Positives = 28/63 (44%), Gaps = 3/63 (5%)
Frame = +2

Query  95     SKKNKHEHESAKNALV--KLRREDKSPEIKPRAENNNLFRNFVGELNEYAASRY-GAKYPS  265
          SK K NAL+ + + K ++ P NLFRNF L Y S+Y G K
Sbjct  83     SKNKIKRMEGPNALLYTDMMVQ*KVVQLTPTIHPVNLFRNFPNILYHYCYSKYLGKKGY  142

```

```

Query  266  YDF  274
          Y  +
Sbjct  143  YRY  145

```

```

> ta_transcript54485_1
Length=775

```

```

Score = 27.7 bits (60), Expect = 9.9, Method: Composition-based stats.
Identities = 21/63 (33%), Positives = 28/63 (44%), Gaps = 3/63 (5%)
Frame = +2

```

```

Query  95  SKKNAKHESAKNALV--KLRRREDKSPEIKPRAENNNLFRNFVGLNELNEYAASRY-GAKYPS  265
          SK  K      NAL+  +  + K  ++ P      NLFRNF  L  Y  S+Y G K
Sbjct  382  SKNKIKRMEGPNALLYTDMMVQ*KVVQLTPTIHPVNLFRNFPNILYHYCYSKYLGVKKGY  441

```

```

Query  266  YDF  274
          Y  +
Sbjct  442  YRY  444

```

```

*****
*****
Query= gi|21912829|gb|AY071926.1| Caenorhabditis elegans RNA interference promoting factor (rde-
4) mRNA, complete cds

```

```

Length=1222

```

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript67778_1	43.9	6e-04
ta_transcript67777_1	43.9	6e-04
ta_transcript67781_1	38.5	0.037
ta_transcript67782_1	38.1	0.047

```

> ta_transcript67778_1
Length=1363

```

```

Score = 43.9 bits (102), Expect = 6e-04, Method: Composition-based stats.
Identities = 58/243 (24%), Positives = 89/243 (37%), Gaps = 55/243 (23%)
Frame = +1

```

```

Query  40  GSDVPMKPSRSEDN--KTPRN-----RTDLEMFLKKTPLMVLEE-----AAKAVY  168
          G  P  P R  N  K P N      + ++E  KTP+ VL+E      Y
Sbjct  87  GEHAPHGPRRRYQNRPKPPNNVERLPLDEAAKREMESLPMKTPVSVLQELLARRGTVPKY  146

```

```

Query  169  QKTPTWGTVELPEGFEMTLILNEITVKGQATSCKAARQKAAVEYLRKVVEKGKHEIFFIP  348
          +    G +  P  F  + + ++  G  SKK A+  AA  L K+
Sbjct  147  ELVQIEGMIHEPT-FRYRVTVADLVAMGTGRSKKEAKHSAKALLDKLT-----  194

```

```

Query  349  GTTKEEALSNIQISDKAEELKRSTSDAVQDNDND--DSIPTSAEFPPGISPTENWVGKl  522
          G T  +  +N+  A  +  S D +  N      +  S  +PP  EN
Sbjct  195  GATPADQGTNGNVPETGA--VVTSFEDKLMGNPVGWLQELCMSRFWPPPSYHAEN-----  247

```

```

Query  523  qeksqksklqAPIYEDSKNER---TERFLVICTMCNQKTRGIRSKKKDAKNLAAWLMWKA  693
          +D+ N R      +F ++CT+  ++  G  KK AK  AA+ MW+A
Sbjct  248  -----DDNVNRRLPHERQFTIVCTLLKRREIGTGKSKKLAKRQAAYKMWQA  293

```

```

Query  694  LED  702
          L+D
Sbjct  294  LQD  296

```

```

> ta_transcript67777_1
Length=1407

```

```

Score = 43.9 bits (102), Expect = 6e-04, Method: Composition-based stats.
Identities = 58/243 (24%), Positives = 89/243 (37%), Gaps = 55/243 (23%)
Frame = +1

```

```

Query  40  GSDVPMKPSRSEDN--KTPRN-----RTDLEMFLKKTPLMVLEE-----AAKAVY  168
          G  P  P R  N  K P N      + ++E  KTP+ VL+E      Y
Sbjct  87  GEHAPHGPRRRYQNRPKPPNNVERLPLDEAAKREMESLPMKTPVSVLQELLARRGTVPKY  146

```

```

Query  169  QKTPTWGTVELPEGFEMTLILNEITVKGQATSCKAARQKAAVEYLRKVVEKGKHEIFFIP  348
          +    G +  P  F  + + ++  G  SKK A+  AA  L K+

```



```

Sbjct  147  ELVQIEGMIHEPT-FRYRVTVADLVAMGTGRSKKEAKHSAAKALLDKLT----- 194
Query  349  GTTKEEALSNIQISDKAEELKRSTSDAVQDNDND--DSIPTSAEFPPGISPTENWVGk1 522
          G T + +N +      A + S D + N      + S +PP      EN
Sbjct  195  GATPADQGTNGNVPETGA--VVTSFEDKLMGNPVGWLQELCMSRFWPPPSYHAEN----- 247
Query  523  qeksqskslqAPIYEDSKNER---TERFLVICTMCNQKTRGIRSKKKDAKNLAAWLMWKA 693
          +D+ N R      +F ++CT+ ++ G      KK AK AA+ MW+A
Sbjct  248  -----DDNVNRRLPHERQFTIVCTLLKRREIGTGKSKKLAKRQAAYKMWQA 293
Query  694  LED  702
          L+D
Sbjct  294  LQD  296

```

```

> ta_transcript67781_1
Length=971

```

```

Score = 38.5 bits (88), Expect = 0.037, Method: Compositional matrix adjust.
Identities = 60/244 (25%), Positives = 92/244 (38%), Gaps = 57/244 (23%)
Frame = +1

```

```

Query  40  GSDVPMKPSRSEDN--KTPRN-----RTDLEMFLKKTPLMVLEAAKAVYQKTPT 183
          G P P R N K P N      + ++E      KTP+ VL+E A P
Sbjct  87  GEHAPHGPRRRYQNRPKPPNNVERLPLDEAAKREMESLPMKTPVSVLQELL-ARRGTVPK 145
Query  184  WGTVELPEG-----FEMTLILNEITVKQATSCKAARQKAAVEYLRKVVEKGKHEIFFI 345
          + V++ EG      F + + ++ G      SKK A+ AA L K+
Sbjct  146  YELVQI-EGMIHEPTFRYRVTVADLVAMGTGRSKKEAKHSAAKALLDKLT----- 194
Query  346  PGTTEEALSNIQISDKAEELKRSTSDAVQDNDND--DSIPTSAEFPPGISPTENWVGk 519
          G T + +N +      A + S D + N      + S +PP      EN
Sbjct  195  -GATPADQGTNGNVPETGA--VVTSFEDKLMGNPVGWLQELCMSRFWPPPSYHAEN----- 247
Query  520  lqeksqskslqAPIYEDSKNERT---ERFLVICTMCNQKTRGIRSKKKDAKNLAAWLMWK 690
          +D+ N R      +F ++CT+ ++ G      KK AK AA+ MW+
Sbjct  248  -----DDNVNRRLPHERQFTIVCTLLKRREIGTGKSKKLAKRQAAYKMWQ 292
Query  691  ALED  702
          AL+D
Sbjct  293  ALQD  296

```

```

> ta_transcript67782_1
Length=927

```

```

Score = 38.1 bits (87), Expect = 0.047, Method: Compositional matrix adjust.
Identities = 60/244 (25%), Positives = 92/244 (38%), Gaps = 57/244 (23%)
Frame = +1

```

```

Query  40  GSDVPMKPSRSEDN--KTPRN-----RTDLEMFLKKTPLMVLEAAKAVYQKTPT 183
          G P P R N K P N      + ++E      KTP+ VL+E A P
Sbjct  87  GEHAPHGPRRRYQNRPKPPNNVERLPLDEAAKREMESLPMKTPVSVLQELL-ARRGTVPK 145
Query  184  WGTVELPEG-----FEMTLILNEITVKQATSCKAARQKAAVEYLRKVVEKGKHEIFFI 345
          + V++ EG      F + + ++ G      SKK A+ AA L K+
Sbjct  146  YELVQI-EGMIHEPTFRYRVTVADLVAMGTGRSKKEAKHSAAKALLDKLT----- 194
Query  346  PGTTEEALSNIQISDKAEELKRSTSDAVQDNDND--DSIPTSAEFPPGISPTENWVGk 519
          G T + +N +      A + S D + N      + S +PP      EN
Sbjct  195  -GATPADQGTNGNVPETGA--VVTSFEDKLMGNPVGWLQELCMSRFWPPPSYHAEN----- 247
Query  520  lqeksqskslqAPIYEDSKNERT---ERFLVICTMCNQKTRGIRSKKKDAKNLAAWLMWK 690
          +D+ N R      +F ++CT+ ++ G      KK AK AA+ MW+
Sbjct  248  -----DDNVNRRLPHERQFTIVCTLLKRREIGTGKSKKLAKRQAAYKMWQ 292
Query  691  ALED  702
          AL+D
Sbjct  293  ALQD  296

```

```

*****
*****

```

```

Query= gi|442622090|ref|NM_001276221.1| Drosophila melanogaster partner of drosha (pasha),
transcript variant C, mRNA

```

Length=2579

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript34188_1	89.4	2e-17
ta_transcript34186_1	88.6	3e-17
ta_transcript34187_1	88.6	4e-17

> ta_transcript34188_1
Length=760

Score = 89.4 bits (220), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 121/348 (35%), Positives = 169/348 (49%), Gaps = 17/348 (5%)
Frame = -1

Query	1934	QFQHLGFKFVQYGVVGLVDCRl alqhgdllllqllllegLYGVVAVEAQQGTPGLDVRMQ	1755
		QF H + ++YGV+ L+ R L+ DLL LQLLLL L G AV+AQQ P + +R++	
Sbjct	5	QFPHFVSQLLEYGVIRLIVARRVLEQSDLLFLQLLLLAALDGARAVQAQQRAPRVQLRVE	64
Query	1754	NLEDCLRSQLLALPLVFTHHFGSMFAHGHGKLVLVIRGAVDLLADLNI-AAVVALQASQQ	1578
		L LR LL LV T G + AH H +L L++ + L ++ + A V QAS	
Sbjct	65	RL*YSLRGALLRHLLVLTDDGGGVLAHFHRQLDLLVLQLLHLGINVLVPCAEPVEQASA*	124
Query	1577	NGVGRWLRLVAEFGDSGIFDADVIENRQIALRFLRSAALLVLIVARYLVLDIGNEYFQR	1398
		NGV R L AE D+ + DA V+E ++ + LV +A +L + ++R	
Sbjct	125	NGVRRGLTGRRARLDRVLDAAHVVEKAKVGVAGAAGVRALVFQLASHLR---DQDVYRR	181
Query	1397	FPSRL*LGLLFTGAIAARAILEIVHRYGGGVRRGCVLELLELIGGLRFQSMHLVLVQDADE	1218
		LG F GA+ ++L G V RG VL+LLELI GL Q + HVLV+	
Sbjct	182	LGCGR-LGGAFAGAVPHSVLHAADVDRGLVGRGRVLQLELIDGLFLQRPVPHVVEHGGV	240
Query	1217	ALAIGIHDPPLPTARVR*SFASIR*YW--ELNKLSAIRQGRSLNILDVFAVFGELAASIP	1044
		A + +H P+L F SI + + ++L A R IL A G L P	
Sbjct	241	AAPVHVHPILFV-----RFPISFLFVAGDDELGAFR*SW---ILQGLARLGLVLPPISP	292
Query	1043	TPKSQHTNHLEFEFEFLAVGV*LLRCNGFLLGILVDRNFFSSRHKGSYS	900
		T + ++LEFE+ LAV V L L D F SR + YS	
Sbjct	293	TLEMHDVDNLEFEQILAVIVDLFMREMLRLPTCAD--GFHSRRRHDS	338

Score = 41.2 bits (95), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 21/69 (30%), Positives = 36/69 (52%), Gaps = 0/69 (0%)
Frame = -1

Query	740	SPPVVKTGDCSQGHCMAGTSSAEKIGPRCATDASFAMQEERHSTVVGHLPGLG*DFKV	561
		S + +TGDC+ + G + +E++G ++ A+ RH+ V+ H HP +	
Sbjct	639	SSTISETGDCADRDVSPGVAFSEEVGLGERAHSTGAVHIHRHAAMPVHPVQRQHLEC	698
Query	560	VEALFFQHS	534
		V AL FQH+	
Sbjct	699	VHALLFQHN	707

> ta_transcript34186_1
Length=917

Score = 88.6 bits (218), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 121/348 (35%), Positives = 169/348 (49%), Gaps = 17/348 (5%)
Frame = -1

Query	1934	QFQHLGFKFVQYGVVGLVDCRl alqhgdllllqllllegLYGVVAVEAQQGTPGLDVRMQ	1755
		QF H + ++YGV+ L+ R L+ DLL LQLLLL L G AV+AQQ P + +R++	
Sbjct	5	QFPHFVSQLLEYGVIRLIVARRVLEQSDLLFLQLLLLAALDGARAVQAQQRAPRVQLRVE	64
Query	1754	NLEDCLRSQLLALPLVFTHHFGSMFAHGHGKLVLVIRGAVDLLADLNI-AAVVALQASQQ	1578
		L LR LL LV T G + AH H +L L++ + L ++ + A V QAS	
Sbjct	65	RL*YSLRGALLRHLLVLTDDGGGVLAHFHRQLDLLVLQLLHLGINVLVPCAEPVEQASA*	124
Query	1577	NGVGRWLRLVAEFGDSGIFDADVIENRQIALRFLRSAALLVLIVARYLVLDIGNEYFQR	1398
		NGV R L AE D+ + DA V+E ++ + LV +A +L + ++R	
Sbjct	125	NGVRRGLTGRRARLDRVLDAAHVVEKAKVGVAGAAGVRALVFQLASHLR---DQDVYRR	181
Query	1397	FPSRL*LGLLFTGAIAARAILEIVHRYGGGVRRGCVLELLELIGGLRFQSMHLVLVQDADE	1218
		LG F GA+ ++L G V RG VL+LLELI GL Q + HVLV+	
Sbjct	182	LGCGR-LGGAFAGAVPHSVLHAADVDRGLVGRGRVLQLELIDGLFLQRPVPHVVEHGGV	240

```

Query 1217 ALAIGIHDPLLPTARVR*SFASIR*YW--ELNKLSAIRQRGSLNILDVFAVFGELAASIP 1044
          A + +H P+L      F SI + + ++L A R      IL A G L P
Sbjct 241 AAPVHVHHPILFV-----RFPSIFLRFVAGDDELGAFR*SW---ILQGLARLGVLPPISP 292

Query 1043 TPKSQHTNHLEFEEFLAVGV*LLRCNGFLLGILVDRNNFSSRHKGSYS 900
          T + ++LEFE+ LAV V L      L D F SR + YS
Sbjct 293 TLEMHDVDNLEFEQILAVIVDLFMREMLRLPTCAD--GFHSRRRHDYS 338

```

Score = 41.2 bits (95), Expect = 0.013, Method: Compositional matrix adjust.
 Identities = 21/69 (30%), Positives = 36/69 (52%), Gaps = 0/69 (0%)
 Frame = -1

```

Query 740 SPPVVKTGDCSQGHCMLAGTSSAEKIGPRCATDASFAMQEERHSTVVGHLHPSLG*DFKV 561
          S + +TGDC+ + G + +E++G ++ A+ RH+ V+ H HP +
Sbjct 639 SSTISETGDCADRDVSPGVAFSEEVGLGERAHSTGAVHIHRHAAMPVHPVQRQHLEC 698

Query 560 VEALFFQHS 534
          V AL FQH+
Sbjct 699 VHALLFQHN 707

```

> ta_transcript34187_1
 Length=901

Score = 88.6 bits (218), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 121/348 (35%), Positives = 169/348 (49%), Gaps = 17/348 (5%)
 Frame = -1

```

Query 1934 QFQHLGFKFVQYGVVGLVDCRlqlhgdllllqllllegLYGVVAVEAQQGTPGLDVRMQ 1755
          QF H + ++YGV+ L+ R L+ DLL LQLLLL L G AV+AQQ P + +R++
Sbjct 5 QFPHFVSQLLLEYGVIRLIVARRVLEQSDLLFLQLLLAALDGAARVQAQQRAPRVQLRVE 64

Query 1754 NLEDCLRSQLLALPLVFTHHFGSMFAHGHGKLVLVIRGAVDLLADLNI-AAVVALQASQQ 1578
          L LR LL LV T G + AH H +L L++ + L ++ + A V QAS
Sbjct 65 RL*YSLRGALLRHLLVLTDDGGGVLAHFHRQLDLLVLQLLHLGINVLVPCAIEVPEQASA* 124

Query 1577 NGVGRWLRRLVAEFGDSGIFDADVIEENRQIALRFLRSAALLVLIVARYLVLDIGNEYFQR 1398
          NGV R L AE D+ + DA V+E ++ + LV +A +L + +R+
Sbjct 125 NGVRRGLTGRRAELRDARVLDAAHVVEKAKVGVAGAAGVRALVFQLASHLR---DQDVYRR 181

Query 1397 FPSRL*LGLLFTGAIAARAILEIVHRYGGGVRRGCVLELLELIGGLRFQSMHLVIVQDADE 1218
          LG F GA+ ++L G V RG VL+LLELI GL Q + HVLV+
Sbjct 182 LGCGR-LGGAFAAGAVPHSVLHAADVDRGLVGRGRVLQLELIDGLFLQRPVPHVIVEHGQV 240

Query 1217 ALAIGIHDPLLPTARVR*SFASIR*YW--ELNKLSAIRQRGSLNILDVFAVFGELAASIP 1044
          A + +H P+L      F SI + + ++L A R      IL A G L P
Sbjct 241 AAPVHVHHPILFV-----RFPSIFLRFVAGDDELGAFR*SW---ILQGLARLGVLPPISP 292

Query 1043 TPKSQHTNHLEFEEFLAVGV*LLRCNGFLLGILVDRNNFSSRHKGSYS 900
          T + ++LEFE+ LAV V L      L D F SR + YS
Sbjct 293 TLEMHDVDNLEFEQILAVIVDLFMREMLRLPTCAD--GFHSRRRHDYS 338

```

Score = 41.2 bits (95), Expect = 0.012, Method: Compositional matrix adjust.
 Identities = 21/69 (30%), Positives = 36/69 (52%), Gaps = 0/69 (0%)
 Frame = -1

```

Query 740 SPPVVKTGDCSQGHCMLAGTSSAEKIGPRCATDASFAMQEERHSTVVGHLHPSLG*DFKV 561
          S + +TGDC+ + G + +E++G ++ A+ RH+ V+ H HP +
Sbjct 639 SSTISETGDCADRDVSPGVAFSEEVGLGERAHSTGAVHIHRHAAMPVHPVQRQHLEC 698

Query 560 VEALFFQHS 534
          V AL FQH+
Sbjct 699 VHALLFQHN 707

```


 Query= gi|156255205|ref|NM_001102461.1| Bombyx mori argonaute 1 (Ago1), mRNA

Length=2739

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript56183_1	284	2e-80
ta_transcript56182_1	284	3e-80
ta_transcript51551_1	173	2e-43

ta_transcript44491_1

142 6e-37

> ta_transcript56183_1
Length=962

Score = 284 bits (727), Expect = 2e-80, Method: Compositional matrix adjust.
Identities = 169/326 (52%), Positives = 219/326 (67%), Gaps = 0/326 (0%)
Frame = +3

```

Query 231   TKPWPRGQANNAESKPFNSINAKRVCSL*CEYST**MP*EGE*RNS*DNGALL**NIWS 410
            TK P QA A+S +INA + +SL*C+Y+ +P*+G*RN *+ G LL *+IW
Sbjct 118   TKSRP*RQAYYAQS*SLPDINA*GLRTSL*CQYTARQVP*KGK*RNC*NYGTLLQ*DIWC 177

Query 411   PQTSV*WKK*FVHKRPSSHRK**NGIRSNFTW*RKRQSVPCYY*MGSSGFIVCTGRGIGR 590
            PQ V*W K*F+H R S++R*** S+F RK S+PCYY MGSSG VCTGR + R
Sbjct 178   PQACV*W*K*FIH*RSSTNRQ**S*AGSDFAGRRKG*SIPCYQMGSSGITVCTGRSVRR 237

Query 591   SHKTNP*CNLSSGCSDETFTINDVPCWTLIFLFTRGILSSPWWTRSLVWFSSIGETK 770
            +HKT+ L*CN C DET +NDV+ WT++ +R +LSSP LVWF S+ +T
Sbjct 238   AHKTD*SL*CNLSSGCSDETFTINDVPCWTLIFLFTRGILSSPWWTRSLVWFSSIGETK 297

Query 771   PMENDA*Y*CVSNCF*SSARYRVHV*SS*YTRY**PKKTINRLTES*VY*RN*RFENRN 950
            PMENDA Y*C NC L S+A YRV+V*S + Y**PKK +RL ES ++ RN*R ++RN
Sbjct 298   PMENDA*Y*CVSNCF*SSARYRVHV*SS*YTRY**PKKTINRLTES*VY*RN*RFENRN 357

Query 951   HALWY*YEA*IQSVQCDT*ACSNVAFSSSTRKWTNSRMHSS*IFFGQI*DEA*IPSSAMFT 1130
            H LWY E IQSVQCD C+NA+ + WTNSR++ S*IF GQ+ +E IP+ AM T
Sbjct 358   HTLWYDEEKIQSVQCDT*ACSNVAFSSSTRKWTNSRMHSS*IFFGQI*DEA*IPSSAMFT 417

Query 1131  SRPGTQTHIPTS*SL*YCSGTEMYKK 1208
            S GTQT+I S+++ S + +YKK
Sbjct 418   SWAGTQTYILAIGSV*HSSRSALYKK 443

```

Score = 135 bits (341), Expect = 8e-32, Method: Compositional matrix adjust.
Identities = 173/389 (44%), Positives = 207/389 (53%), Gaps = 4/389 (1%)
Frame = +2

```

Query 1148  NTHTYLLKFVIL---FRDRDV*KN*QICKHQP*SKQQHVPLQTGRGKSIISVEQTSILI 1318
            T TY+L + R K+*QICK *SK Q KS WSV +TS
Sbjct 421  GTQTYILAIGSV*HSSRSALYKKS*QICKPLQ*SKPQRGRRIPIESAKSTTWSVARTSTPT 480

Query 1319  RM*KNLG*PYPIT*WRFAAECYLRRSCNMVVCVPHWVDSKHYRIFGTCSEENSFLWESR 1498
            *** G P P T*WR AA C R SC+ P D K +I+ GTC +S W SR
Sbjct 481  CT*RSSGSPSPPT*WRCAAACRRPSCSTAAASPRAD-KRCQIKACGTCGASSSSWASR 539

Query 1499  *EYGR*HVSRRHKEQYERMLSRILLNNFKRYPTTLACQ**GNPVSASTLQGQTKWSLCLNT 1678
            G SR +M R ++ +R TT AC G+ SAST +G+T+ S C +T
Sbjct 540  SACGPPSPASRRNAPSGKMLRTSPSSCRRSRTRACPSGSRASASTRRGRTRSSPCSS 599

Query 1679  *slhlcsysslssscyQEKHLSMPK*KELVTQYWEWQLNVYKRRT*TKLHRRPSVIYV*KL 1858
            S S S + S +* T+ W W+ + + RT*T+ RR S +
Sbjct 600  SSPPSYSCSWWWSCPGRRRSTR*SAWATRCWAWRRSACRPRT*TRPRRRRSPTSASRS 659

Query 1859  MLNWEALILFSFHLFVRRCSstsp*ssWAwT*rtrppvttrslpsrpsAPWTRIRRGTPP 2038
            +W A S RCSTS * SWAWT*RTR P TTRS PSRPSSAPWTR R TTP
Sbjct 660  T*SWAASTPSSCPRCAPRCSTSR*YSWAWT*RTRRPATTRSPSRPSAPWTRTPRATPP 719

Query 2039  PSGYSSTGKR*FTK*AAWSRSCSSCFTRAPADSNPTGSSCIATASPKASSCTSYSMS*LL 2218
            P SSTG+R T+*AAW RSC SC TRA A S+ T SSC ATAS + SS T S S
Sbjct 720  PCACSSSTGRRSCTR*AAWCRSC*SCSTRARAGSSRTASSCTATASARGSSSTCCSTSSPP 779

Query 2219  *GRLVSSWKRSTSRASLSSWYRSDITRGC 2305
            R SSW+R+TSRAS SSW RS TRGC
Sbjct 780  CARPASSWRRNTSRASRSSWCRSATTTRGC 808

```

> ta_transcript56182_1
Length=977

Score = 284 bits (726), Expect = 3e-80, Method: Compositional matrix adjust.
Identities = 169/326 (52%), Positives = 219/326 (67%), Gaps = 0/326 (0%)
Frame = +3

```

Query 231   TKPWPRGQANNAESKPFNSINAKRVCSL*CEYST**MP*EGE*RNS*DNGALL**NIWS 410
            TK P QA A+S +INA + +SL*C+Y+ +P*+G*RN *+ G LL *+IW

```

```

Sbjct 118 TKS RP* RQAYYAQS*SLPDINA*GLRTSL*CQYTARQVP*KGK*RNC*NYGTLLQ*DIWC 177
Query 411 PQTSV*WKK*FVHKRPSSHRK**NGIRSNFTW*RKRQSVPCYY*MGSSGFIVCTGRGIGR 590
PQ V*W K*F+H R S++R*** S+F RK S+PCYY MGSSG VCTGR + R
Sbjct 178 PQACV*W*K*FIH*RSSTNRQ**S*AGSDFAGRRKG*SIPCYQMGSSGITVCTGRSVRR 237
Query 591 SHKTNPL*CNLSSGCSDETFITINDVYPCWTLIFLFTRGILSSPWWTRSLVWFSSIGETK 770
+HKT+ L*CN C DET +NDV+ WT++ +R +LSSP LVWF S+ +T
Sbjct 238 AHKTD SL*CNTGFRCGDETLALNDVHTSWTVLLFVSRLLSSPGRRKGLVWFPSVRQT* 297
Query 771 PMENDA*Y*CVSNCFL*SSARYRVHV*SS*YTRY**PKKTINRLTES*VY*RN*RFENRN 950
PMENDA Y*C NC L S+A YRV+V*S + Y**PKK +RL ES ++ RN*R ++RN
Sbjct 298 PMENDA EY*CFGNCILQSAASYRVYV*SIRH*GY**PKKATDRLPESEIHKRN*RSQDRN 357
Query 951 HALWYIEA*IQSVQCDT*ACSNVFSSTSRKWTNSRMHSS*IFFGQI*DEA*IPSSAMFT 1130
H LWY E IQSVQCD C+NA+ + WTNSR++ S*IF GQ+ +E IP+ AM T
Sbjct 358 HTLWYDEEKIQSVQCD AQTCTNAIIPAA**WTNSRVYGS*IFPGQVQNETKIPTLAML 417
Query 1131 SRPGTQTHIPTS*SL*YCSGTEMYKK 1208
S GTQT+I S+++ S + +YKK
Sbjct 418 SWAGTQTYILAIGSV*HSSRSALYKK 443

```

Score = 123 bits (308), Expect = 8e-28, Method: Compositional matrix adjust.
Identities = 173/404 (43%), Positives = 206/404 (51%), Gaps = 19/404 (5%)
Frame = +2

```

Query 1148 NTHTYLLKFVIL---FRDRDV*KN*QICKHQP*SKQQHVPLQTGRGKSIWSVEQTSILI 1318
T TY+L + R K+*QICK *SK Q KS WSV +TS
Sbjct 421 GTQTYILAIGSV*HSSRSALYKKS*QICKPLQ*SKPQRGRPIESAKSTTWSVARTSTPT 480
Query 1319 RM*KNLG*PYPIT*WRFAAECYLRRSCNMVVC PHWVDSKHYRIFEGTCEENSFLWESR 1498
+++ G P P T*WR AA C R SC+ P D K +I+ GTC +S W SR
Sbjct 481 CT*RSSGSPSPPT*WRCAAACRRPSCSTAAASPRAD-KRCQIKACGTCGASSSSWASR 539
Query 1499 *EYGR*HVS RHKEQYERMLSRILLNNFKRYPTTLACQ**GNPVSASTLQGQTKWSLCLNT 1678
G SR +M R ++ +R TT AC G+ SAST +G+T+ S C +T
Sbjct 540 SACGPSPASRRNAPSGKMLRTSPSSCRRSRTRACPSGSRASASTRRGRTRSSPCSSST 599
Query 1679 *slhlcsysslsscyQEKLHSMKP*KELVTQYWEWQLNVYKRRT*TKLHRRPSVIYV*KL 1858
S S S + S +* T+ W W+ + + RT*T+ RR S +
Sbjct 600 SSPPSYSCSWWWWSCPGRRRSTR*SAWATRCWAWRRSACRPRT*TRPRRRRSPTSASRS 659
Query 1859 MLNWEALILFSFHLFVRRCstsp*ssAWAtrtrppvttrslpsrpssAPWTRIRRGTPP 2038
+W A S RCSTS * SWAWT*RTR P TTRS PSRPSSAPWTR R TTP
Sbjct 660 T*SWAASTPSSCPRCAPRCSTSR*YSAWT*RTRRPATTRSPSRPSSAPWTRTPRATPP 719
Query 2039 PSGYSSTGK-----R*FTK*AAWSRSCSCFTRAPADSNTGSSCIATAS 2173
P SST K R T+*AAW RSC SC TRA A S+ T SSC ATAS
Sbjct 720 PCACSTEKTSYPIGWIIIPFKSSRRSCTR*AAWCRSC*SCSTRARAGSSRTASSCTATAS 779
Query 2174 PKASSCTSYSMS*LL*GRLVSSWKRSTSRASLSSWYRSDITRGC 2305
+ SS T S S R SSW+R+TSRAS SSW RS TRGC
Sbjct 780 ARGSSSTCCSTSSPPCARPASSWRRNTSRASRSSWCRSATTRGC 823

```

> ta_transcript51551_1
Length=1362

Score = 173 bits (438), Expect = 2e-43, Method: Compositional matrix adjust.
Identities = 210/825 (25%), Positives = 362/825 (44%), Gaps = 110/825 (13%)
Frame = +1

```

Query 241 GHEGRPIMLRANHFQI-SMPRGFVHHYDVNIQPDKCPKVNREIVETMVHHCYNKIFGALK 417
G G P+ + AN+F + + P+ ++ Y V+ QP++ + + ++ VH N + G L
Sbjct 32 GSTGDLPLDVCANYFTVETTPQWCLYQYHVDFQPEEDSTGLRKALLR--VHA-NTLGGYL- 87
Query 418 PVFDGRNNLYTR----DLP LIGNDRMELEVLPGEGKDRVFRVTIKWVAQVSLFALEEA 582
FDG LYT DP+ + +DR GE R+ IK VS
Sbjct 88 --FDG-AILYTVKRLHPDPMELYSDRKH-----DGER---MRILIKLTCDVS----- 128
Query 583 LEGRTRQIPYDAILALDVVMRHLPSMM-YTPVGRSFFSSPEGYYHPLGGGREVWFGFHQS 759
G Y I ++++R +++ VGR +F P ++W G+ +
Sbjct 129 -PG-----DYHYIQVFNI IIRKCFNLNLQLVGRDYFD-PIAKVDIPEHKLQIWPYKTT 181
Query 760 VRPSQWKMLNIDVSATAFYKAQPVIEFMCEVLDIRDINDQRKPLTDSQRVKFTKEIKGL 939
+ + +++++ ++ A + V++ + E + N ++ F +++ G

```

```

Sbjct 182 INQYEDRLLMVTEI-AHKVLRMDNVLQMLNEYAATKGSNYKKI-----FLEDVVG- 230
Query 940 KIEITHCGTMKRKYRVNCVTRRPAQMQSFPQLQLENGQTVECTVAKYFLDKYKMKLRYPHL 1119
KI +T KR YRV +V + +F ++ E ++ Y+ KY ++++ P+
Sbjct 231 KIVMTDYN--KRTYRVDDVHWETSPRSTFKMKDETVCYMD-----YYQKKYNIRIQDPNQ 283
Query 1120 PCLQVGQEHKH-----TYLPLEVCNIVPGQRCIKKLTDMQTSTMIKATARSAPD-RE 1272
P L + + YL E+C + L + Q + + + PD R
Sbjct 284 PLLVYRAKAREIRSGMPELVYLVPELCRQTGLSD--EMLANFQILMSALGRHTKIGPDLRI 341
Query 1273 REINNLRANFNTDSYVKE---FGLTISNNMEVRGRVLPPEKLQYGGRVSSLGGQQAL 1443
+++ RR T V+E + L +SN+++ +GR LPP + V G
Sbjct 342 QKLLQFNRRLT-QTKEVVQELASWSLKLNDLVRFKGRQLPPEAIIQANNVYAAGDIT- 399
Query 1444 PNQGVW--DMRGKQFFMGVEIRVWAIACFAPQRTVREDALKNFQQLQKISNDAG--MPI 1611
+G W DMR K + W + P+R R DA ++F + K N G MP
Sbjct 400 --EG-WTRDMRSKPLLTIAPVGSVWV--ITPERQ-RRDA-ESFVDLIMKTGNGVGFMRP- 451
Query 1612 IGQPCFCKYA-TGPDQVEPMFKYLKSTFvqlqlvvvvlPGKTPVYAEVKRVGDTVLMGAT 1788
+P C A G M + + + ++ V+ Y +K+ M T
Sbjct 452 --KPEICPIARDGHMDYANMCENVIAKNPSFILCVLRQKSADRYEAIKKKCTVDRAMPT 509
Query 1789 QCVQAKNVNKTSPQTLN-LCLKINVLGGIN-SILVPSLRPKVFNEPVIFLGVDVTHPP 1962
QCV +N+ S +++ + ++IN KLGG S+ VP ++ +G DV H
Sbjct 510 QCVVGRNMTSKSAMSIAIKIAIQTINCKLGGAPWSVEVPL-----PTLMVIGYDVCHDT 562
Query 1963 AGDNKKPSIAAVVGSMDAHPSPRYAATVRVQQRQEIIVHEMSSMVQELLIMFYKSTGGFKP 2142
+K S A V ++D + Y +TV +E+ M + + Y+ P
Sbjct 563 RAKDK--SFGAFVATLDKQMTHTYSTVNAHTSGEELSAHMGINIATA-VRKYRERNNVLP 619
Query 2143 HRIIMYRDGISEGQFLHVLQHELTAVREACIKLEAEYK---PGITFIVVQKRHHTRLFCA 2313
RI +YRDG+ +GQ +V HE+ +++ +LE Y+ + FI+V KR +TR+F
Sbjct 620 GRIFIYRDGVGDGQIPYVHSHEVEEIKK---QLETLYQGEPVKLAFIIVSKRINTRIFV- 675
Query 2314 DKKEQSGKSGNIP-AGTTVDLGITHPTFEFDYLCSHQGIQGTSRPSHYHVLWDDNHFGSD 2490
G+SG+ P GT +D IT P +DFYL S +GT P+ Y+V++D D
Sbjct 676 ----DRGRSGDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPTSYNVIYDTTSLHPD 731
Query 2491 ELQCLTYQLCHTYVRCTRSVSIPAPAYYAHLVAFRARYHLVEKEH 2625
+Q LTY+L H Y + +V +P+ YAH +AF A L + H
Sbjct 732 RIQRLTYKLTHMYFNNSCAVRVPSVCQYAHKLAFLAANSLHNQPH 776

> ta_transcript44491_1
Length=234

Score = 142 bits (359), Expect = 6e-37, Method: Compositional matrix adjust.
Identities = 89/245 (36%), Positives = 137/245 (56%), Gaps = 15/245 (6%)
Frame = +1

Query 1849 LKINVKLGG-INSILVPSLRPKVFNEPVIFLGVDVTHPPAGDNKKPSIAAVVGSMDAHP 2025
L++N KLGG + SI +P F +I +G+D H A K S+ + + S + +
Sbjct 2 LQMNCGLGGTLWSIAIP-----FKTAMI-VGIDSYHDAA--RKSRVCSFIASYNQSM 52
Query 2026 RYAATVRVQQRQEIIVHEMSSMVQELLIMFYKSTGGFKPHRIIMYRDGISEGQFLHVLQH 2205
++ + Q+ QE+V + S + + L + ++ G P R+IMYRDG+ +GQ + Q+
Sbjct 53 QWYSRAIFQERGQEVVDGLKSLVDALHTYLRTNGKL-PDRVIMYRDGVGDGQLNTIKQY 111
Query 2206 ELTAVREACIKLEAEYKPGITFIVVQKRHHTRLFCADKKEQSGKSGNIPAGTTVDLGITH 2385
E+ ++ +EA YKP +T++VVQKR +TR+F K Q G P GT VD IT
Sbjct 112 EIPQMVCFSLMEATYKPTLTYYVVVQKRINTRIF--MKVQGGFENPHP-GTVVDHDITR 167
Query 2386 PTEFDYLCSHQGIQGTSRPSHYHVLWDDNHFGSDELQCLTYQLCHTYVRCTRSVSIPAP 2565
+DF + S + QGT P+HY V+ DD+ +D+ Q LTY+LCH Y +V +PAP
Sbjct 168 RDWYDFLIASQKVNQGTVTPTHYVVVHDDSAMTADQCQRLTYKLCHLYYNWPGTVRVPAP 227
Query 2566 AYYAH 2580
YAH
Sbjct 228 CQYAH 232
*****
*****

```

Query= gi|166706853|ref|NM_001043530.2| Bombyx mori argonaute 2 (Ago2), mRNA

Length=4863

Sequences producing significant alignments:

Score E
(Bits) Value

```

ta_transcript85453_1      370    6e-105
ta_transcript85452_1      370    6e-105
ta_transcript51551_1      143    2e-33

```

```

> ta_transcript85453_1
Length=1417

```

```

Score = 370 bits (950), Expect = 6e-105, Method: Compositional matrix adjust.
Identities = 279/761 (37%), Positives = 421/761 (55%), Gaps = 6/761 (1%)
Frame = -3

```

```

Query 3472 DEEHTALFQHAVEDPETFGILLEIIVIEYLAIGERASPqtgqvrvvgrrgv*ngahttRV 3293
          ++EH+A QH V+ PE ILL+++I+E L I ERA QT Q+RVV RR V G HT RV
Sbjct 226 NKEHSAEVQHVFQHPPEPSWILLQVLIVELLPICERARAQTRQMRVVSRRRVGDGPHTARV 285

Query 3292 QMAQVVREVLHFVLRDPAVVADGVVARRTSRALDRLVRHQIEVQFTWYYITVDHCPRID 3113
          Q+ QVV ++ H V+RD AVVA GVVA R SRAL V +QIEV+ + + VD +
Sbjct 286 QVTQVVSQQLFHLVVRDLAVVAHGVVASRASRALYSCVGYQIEVELLRVNDVCVDDGAGLH 345

Query 3112 VETGVVPGQ-EESRVMFLYKNEQYFWFSVQSRDTLVGAMQSSQFTLHYLSKLTLRNPVT 2936
          V G + + EESRVM+FL++ E+ V S L+ ++ QFTLHYLS+L+L N ++
Sbjct 346 VLIGDLRVRVEESRVMsFLHQ*EENLRGLGVVSLHPLIRSVHRLQFTLHYLSLSELGNAIS 405

Query 2935 EHEHLLRQNPLTFLESMEMIHYYVLKLNHDLFLRCLYTQFDVVYVAFRIHRGGYGGDTRY 2756
          EHE L RQ L ++ H++VL+L DHLFL L + DVV+ AF I+R + +
Sbjct 406 EHEDLPQRALLLFVHHQVFHYHVLELYDHLFLWSLNAELDVVHEAFLIYRRRHRCNAGQ 465

Query 2755 ITLIWRWMRDVSADHDNSPTL*ALRNGTILQCLIIYSHKLRVHL**NVPSCLIWHSARGGV 2576
          L+ R MR VSA H++ A R + L+ H+LR+HL* + L +H R
Sbjct 466 RGLLGRGMRHVSADHHHAAGRQAARQAAPV*SLVNPQLRIHL*KYIFCRLRVHFTRCSE 525

Query 2575 FFEYMRQYTHFEFGNLFQLVIIIAAPSRNDHDEIDLFF*SVQHTLVQVIYTDVEASHLW 2396
          F + + QYT+F L +II+ + R+D D+E DL ++ L+ ++ DV
Sbjct 526 FLDALCQYTNFPLCKLLHPMIIVVSSCRDDDEETDLILQCIEHLL*FLHLDVVVPLSR 585

Query 2395 LGHVHAHLSTGIH*LRHDVFIITSTWIFYGNEAP*IQSFRFQKTGVLPSYLLWYSKLPW 2216
          L + HAH L + * D+ +T I+ YG++ P +Q RFQ+ V LP S W+ LP
Sbjct 586 LRYPHAHLISLAF**LDDILAVTPVDIRLYGDDCPRLQGLRFQQLVCLPSSTEWFDGLPV 645

Query 2215 THF*CGRFENFRFNLIKILIGYLQAVCFEELILRVIHLLNHFLDLTFPYIRWGCSLSSHCR 2036
          H G + F + KL+ L A E LI RVIH+ FL+ T +R L HHCR
Sbjct 646 AHVKVGWLQYFGLHADKLVLDLHAERLEILIRVIHVSYDFLNF TLAVVRRRRGLPHHCR 705

Query 2035 QLSVI*LLVTGLAICNFD*FHR*IDVLVFRADPQTQVQRILNPVFFLFHKIFVYGHPNRR 1856
          QL + LLV L+I +F * R +D+LV R+ P TVQ+R+L F F ++ H
Sbjct 706 QLVFVQLLVQSLSIRDFO*LKRVDLILVARSHPHTVQIRVLQSDFLDFCEVVCDSHLYLL 765

Query 1855 SFVVLQRKCLT*RWVDNPVAVVLA*LSRRRSGTKYLRVLDKPSNEFIESFS-STAWLPIH 1679
          +FV+ R+ W+D V L+RRR+ + + + N+ E F+ W +
Sbjct 766 AFVIGHREYDLVWVIDQLVTDKFPFLARRRAISTDICHYP*ILNKHFEFHAHKPVW---Y 822

Query 1678 WTIGVQTKITRESINHRILILWETFVCNINVDEGFRCKYSRLE*TSPLHLEPVAQVNRRCRT 1499
          WT+ V+ ++ S++H L+LWE V +INVD C+ RLE + PHL+ V++V+ T
Sbjct 823 WTV*VKLEVIS*SVDHPLLLWEPLVRHINVDVRTICEDRRLEQSRPHLQAVSKVDGSLWT 882

Query 1498 HEVLSACFHI*FQCSLF*HYVNTLYGVSWCIG*STRCHMLQNIIVVYTTTSFE*HFKRH 1319
          E+L ++ F+ L * VN LY SW ++G ++ +++ + + +++ F+ +F+ H
Sbjct 883 FEILPPRLYVTFKSPLP*DDVNALYCSWRVQGTASILYVI*DRTQIDHSSRFGYFEIH 942

Query 1318 VFAVHIFDHHFYTISLSGDFWQRR-Q*ITIFCLIKGKDFFR 1199
          + + + + + ++R Q ITI L+KG D FR
Sbjct 943 FPPIVQKFNRCSPFIACYIRKRLQRITILHLVKGDDIFR 983

```

```

> ta_transcript85452_1
Length=1460

```

```

Score = 370 bits (951), Expect = 6e-105, Method: Compositional matrix adjust.
Identities = 279/761 (37%), Positives = 421/761 (55%), Gaps = 6/761 (1%)
Frame = -3

```

```

Query 3472 DEEHTALFQHAVEDPETFGILLEIIVIEYLAIGERASPqtgqvrvvgrrgv*ngahttRV 3293
          ++EH+A QH V+ PE ILL+++I+E L I ERA QT Q+RVV RR V G HT RV
Sbjct 269 NKEHSAEVQHVFQHPPEPSWILLQVLIVELLPICERARAQTRQMRVVSRRRVGDGPHTARV 328

Query 3292 QMAQVVREVLHFVLRDPAVVADGVVARRTSRALDRLVRHQIEVQFTWYYITVDHCPRID 3113

```

```

Sbjct 329 Q+ QVV ++ H V+RD AVVA GVVA R SRAL V +QIEV+ + + VD +
QVTQVVSQFLFHLVVRDLAVVAHGVVASRASRALYSCVGYQIEVELLRVNDVCVDDGAGLH 388

Query 3112 VETGVVPGQ-EESRVMFLYKNEQYFWSVQSRDTLVGAMQSSQFTLHYLSKLTLRNPVT 2936
V G + + EESRVM+FL++ E+ V S L+ ++ QFTLHYLS+L+L N ++
Sbjct 389 VLIGDLRVRVEESRVSFLHQ*EENLRLGVVSLHPLIRSVHRLQFTLHYLSELSLGNALS 448

Query 2935 EHEHLLRQNPLTFLESMEMIHYYVLKLNHDLFLRCLYTQFDVVYVAFRIHRGGYGGDTRY 2756
EHE L RQ L ++ H++VL+L DHLFL L + DVV+ AF I+R + +
Sbjct 449 EHEDLPRQRALLLFVHHQVFHYHVLELYDHLFLWSLNAELDVVHEAFLIYRRRHRCNAGQ 508

Query 2755 ITLIWRWMRDVSADHNSPTL*ALRNGTILQCLIYSHKLRVHL**NVPSCLWIHSARGGV 2576
L+ R MR VSA H++ A R + L+ H+LR+HL* + L +H R
Sbjct 509 RGLLGRGMRHVSADHHAAGRQAARQAAPV*SLVNPQLRIHL*KYIFCRLRVHFTRCSE 568

Query 2575 FFEYMRQYTHFEFGNLFQLVIIIAAPSRNDHDQEIIDLFF*SVQHTLVQVIYTDVEASHLW 2396
F + + QYT+F L +II+ + R+D D+E DL ++ L+ ++ DV
Sbjct 569 FLDALCQYTNFPLCKLLHPMIIVVSSCRDDDEETDLILQCIEHLL*FLHLDVVVPLSR 628

Query 2395 LGHVHAHLSTGIH*LRHDVFIITSTWIFYGNEAP*IQSFRQKTVGLPYSLLWYSKLPW 2216
L + HAH L + * D+ +T I+ YG++ P +Q RFQ+ V LP S W+ LP
Sbjct 629 LRYPHAHLISLAF**LDDILAVTPVDIRLYGDDCPRLQGLRFQQLVCLPSSTEWFDGLPV 688

Query 2215 THF*CGRFENFRFNLIKIGYLQAVCFEELILRVIHLLNHFLDLTFPYIRWGCSLSHHCR 2036
H G + F + KL+ L A E LI RVIH+ FL+ T +R L HHCR
Sbjct 689 AHVKVGWLQYFGLHADKLVLDLHAERLEILIRVIHVSDFLNFTLAVVRRRGLPHHCR 748

Query 2035 QLSVI*LLVTGLAICNFD*FHR*IDVLVFRADPQTVQVRILNPVFFLFHKIFVYGHPNRR 1856
QL + LLV L+I +F * R +D+LV R+ P TVQ+R+L F F ++ H
Sbjct 749 QLVFVQLLVQSLSIRDFQ*LKRVDLLVARSHPHTVQIRVLQSDFLDFCEVVCDSHLYLL 808

Query 1855 SFVVLQRKCLT*RWVDNPVAYVLA*LSRRRSGTKYLRVLDKPSNEFIESFS-STAWLPIH 1679
+FV+ R+ W+D V L+RRR+ + + + N+ E F+ W +
Sbjct 809 AFVIGHREYDLVWVIDQLVTDKFPFLARRRAISTDICHYP*ILNKHFEFHAHKPVW---Y 865

Query 1678 WTIGVQTKITRESINHRILWETFCVNCINVDGFRCKYSRLE*TSPHLEPVAQVNRRCRT 1499
WT+ V+ ++ S++H L+LWE V +INVD C+ RLE + PHL+ V++V+ T
Sbjct 866 WTV*VKLEVIS*SVDHPLLLWEPLVRHINVDVRTICEDRRLEQSRPHLQAVSKVDGSLWT 925

Query 1498 HEVLSACFHI*FQCSLF*HYVNTLYGVSWCIKG*STRCHMLQNIIVVYTTTSE*HFKRH 1319
E+L ++ F+ L * VN LY SW ++G ++ +++ + + +++ F+ +F+ H
Sbjct 926 FEILPPRLYVTFKSPLP*DDVNALYCFSWRQGTASILYVI*DRTQIDHSSRFKGYFEIH 985

Query 1318 VFAVHIFDHHFYTISLSGDFWQRR-Q*ITIFCLIKGKDFFR 1199
+ + + + + ++R Q ITI L+KG D FR
Sbjct 986 FPPIVVQKFNRCSPFIACYIRKRLQRITILHLVKGDDIFR 1026

```

```

> ta_transcript51551_1
Length=1362

```

```

Score = 143 bits (361), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 161/676 (24%), Positives = 298/676 (44%), Gaps = 65/676 (10%)
Frame = +2

```

```

Query 1424 IQCIDIVLKQG-TLESYVKAGRQYFMRPASPIDLGD-GLEMWTGLFQSAI--FTSKAFIN 1591
IQ +I++++ L + GR YF P + +D+ + L++W G +++ I + + +
Sbjct 135 IQVFNIIRKCFNLLNLQLVGRDYF-DPIAKVDIPEHKLQIWPQ-YKTINQYEDRLLMV 192

Query 1592 VDVAHKGFPKNQPMIDAFTRDFRLDPNRPVDRQPGRAAEAFNEFIRGLKVVSKILGTGPS 1771
++AHK R+D + + + + I VV KI+ T +
Sbjct 193 TEIAHKVL-----RMDNVLQMLNEYAATKGSNYKKIFLEDVVGKIVMTDYN 238

Query 1772 SGQLREHICNGVVDPPSRQTFTELENDKGPPVRMTVYEFYFMKEKKYRIKYPDLNCLWVGPK 1951
R + P R TF +++ + +Y+ K+ RI+ P+ L K
Sbjct 239 KRTYRVDVHWETSP--RSTFKMKDET-----VCYMDYYQKKYNIRIQDPNQPLLRYRAK 291

Query 1952 DKNIYLP-ELVEVAYQARNKQLNDRQL-----STMVREAAATPPDVRKRKIEEVIQKM 2110
+ I M ELV + R L+D L S + R PD+R +K+ + +++
Sbjct 292 AREIRSGMPELVYLVPELCRQTGLSDEMLANFQLMSALGRHTKIGPDLRIQKLLQFNRR 351

Query 2111 NYSKN--QFFKTYGLEIANEFYQVEAK-----ILEAPTLEVGPQFTVPKKGWVQANCL 2266
+K Q ++ L+++N+ + + + I++A ++ T ++ L
Sbjct 352 TQTKEVVQELASWSLKLNDLVRFKGRQLPPEAIIQANNVKAAGDTTEGWTRDMRSKPL 411

Query 2267 LKPEALNSWGFI AIELDPRGCNYEDIVSKLMNTGRQMGMNVTQPKMACFNIRINDLHKSM 2446
L + SW I E R + E V +M TG +G + +P++ C R D H

```



```

Sbjct  412  LTIAPVGSWVITPERQRR--DAESFVDLIMKTGNVGFMRMPKPEI-CPIAR--DGHMDY  466

Query  2447  LHALE-----KQVNFLVVVSGRGRDYHKLKQIAELKVGILTHVFKEDTATRRMNPQTA  2611
          + E      K  +F++ V+  + D Y  +K+  +  + T      T +      A
Sbjct  467  ANMCENVIARKNPSFILCVLRQKSADRYEAIKKKCTVDRAMPTQCVVGRNMTSKSAMSIA  526

Query  2612  RNILLKVNKLMGINQALENRSIPQCLKGGAVMIVGADVTHPSPDQSNIPSTAAVTASMD  2791
          I +++N KL G  ++E  +P      +M++G DV H +  ++  S  A  A++D
Sbjct  527  TKIAIQINCKLGGAPWSVE---VPL----PTLMVIGYDVCHDT--RAKDKSFGAFVATLD  577

Query  2792  TKCYIYNIELSIQTPKKEMIVQFEDIMVDHFHAFKKSQGILPKKVVFVRDGVSEGQFAEV  2971
          + Y  ++  T  +E+      +      +++  +LP ++F++RDGV +GQ  V
Sbjct  578  KQMTHYYSTVNAHTSGEELSAHMGINIATAVRKYRERNNVLPGRIFIYRDGVGDGQIPYV  637

Query  2972  MKSELTGLHRAYQRVAGLNAKP-EVLFILVQKRHHTREFFLPGNNAFNVDPGTVVDRDIV  3148
          E+  + +  + +      +P ++ FI+V KR +TR F+  + N  PGT++D  I
Sbjct  638  HSHEVEEIKKQLETL--YQGEFVKLAFIIVSKRINTRIFVDRGRSGDNPRPGTIIDDVIT  695

Query  3149  HPRELDIFYLVSHQAIKGTARPTRYHAVCNDGRIPENEVEHLAYYLCHLYARCMRAVSYP  3328
          P  DFYLV  +GT  PT Y+ + +  +  + ++ L Y L H+Y      AV  P+
Sbjct  696  LPERYDFYLVSNVREGTIAPTSYNVIYDTTSLHPDRIQRLTYKLTHMYFNNSCAVRVPS  755

Query  3329  PTYYAH-LACLRARSL  3373
          YAH LA L A SL
Sbjct  756  VCQYAHKLAFLAANSL  771

```


Query= gi|166706857|ref|NM_001104597.2| Bombyx mori argonaute 3 (Ago3),mRNA

Length=2781

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript51551_1	498	1e-155
ta_transcript44491_1	425	4e-141

> ta_transcript51551_1
Length=1362

Score = 498 bits (1282), Expect = 1e-155, Method: Compositional matrix adjust.
Identities = 270/767 (35%), Positives = 421/767 (55%), Gaps = 16/767 (2%)
Frame = +1

```

Query  502  KKGETGVPIEVTCTNYIYNLFKEN-IVFEYEVKFEPDQDYKHLRFKLLNEHIEHFKEKTFD  678
          KKG TG P++V NY  +      +++Y V F+P++D  LR  LL  H      FD
Sbjct  30  KKGSTGDPDVCANYFTVETTPQWCYQYHVDVQPEEDSTGLRKALLRVHANTLGGYLF  89

Query  679  GTTLYVPHELPAVRNLVSTNPYDQSKVNVSIIFRRTRRLS----EMIHIYNVMFKCIMK  846
          G  LY  L      L S  +D  ++  I+ + T  +S      I ++N++ +
Sbjct  90  GAILYTVKRLHPDPMELYSRKHGGERMR--ILIKLTCDVSPGDYHYIQVFNIIRKCFN  147

Query  847  DLKLIRFGRQHYNEHAAIQIPQHKLEVWPGYVTAVDEYEGGLMLTLDSTHRVLRQTQTVLS  1026
          L L  GR +++  A + IP+HKL++WPGY T +++YE  L++  +  H+VLR  VL
Sbjct  148  LLNLQLVGRDYDFPIAKVDIPEHKLQIWPGYKTINQYEDRLLMVTEIAHKVLRMDNVLQ  207

Query  1027  LIKEVVQTEGANWKRKMTDILIGASVMTTYNKKLFRVDTIDDKMSPRSTFEKTEKGETVQ  1206
          ++ E  T+G+N+K+  + ++G  VMT YNK+ +RVD +  + SPRSTF+  K  ETV
Sbjct  208  MLNEYAATKGSNYKKIFLEDVVGKIVMTDYNKRTYRVDDVHWETS PRSTFKM--KDET-  264

Query  1207  ISFIDYYKKNYGIEIMDWDQPLLISRDTKRMPGSDTPTDFMICLIPELCQLTGLTDDQRS  1386
          ++DYY+K Y I I D +QPLL+ R  R  S  P  ++ L+PELC+ TGL+D+  +
Sbjct  265  -CYMDYYQKKYNIRIQDPNQPLLVRARAREIRSGMPE--LVYLVPELCRQTGLSDEMLA  321

Query  1387  NFRLMKDVATYTRITPNQRHAAFKKYIESVMKNETAKSRLAGWGLSIAPETVNLARTLP  1566
          NF+LM  +  +T+I P+ R  ++  + + +  LA W L ++ + V  R  LP
Sbjct  322  NFQLMSALGRHTKIGPDLRIQKLLQFNRLTQTKEVVQELASWSLKLSDNLVRFKGRQLP  381

Query  1567  PETLYFGDNVRVPGKPNAE-WNSEVTKHSVMQAVDIMRWVLLFTQRDKQVAMDFLSTLKR  1743
          PE +  +NV+      E W  ++  ++  +  WV++  +R ++ A  F+  + +
Sbjct  382  PEAIQANNVYAAGDTTEGWRDMRSKPLLTAPVGSWVITPERQRRDAESFVDLIMK  441

Query  1744  NCRPMGIMVSDAELVPLANDRTDTYVLALKKCIT-SSVQLVVAICSTKRDDRYAAIKKVC  1920
          +G  +  E+ P+A D  Y  +  I  +  ++ +  K  DRY AIKK C
Sbjct  442  TGNVGFMRMPKPEICPIARDGHMDYANMCENVIARKNPSFILCVLRQKSADRYEAIKKK  501

```

```

Query 1921 CADNPVPSQVINARTLMNTNKIRSITQKILLQLNCKLGGTLWSISIPFKSAMIVGIDSYH 2100
          D ++P+Q + R M + SI KI +Q+NCKLGG WS+ +P + M++G D H
Sbjct 502 TVDRAMPTQCVVGRN-MTSKSAMSIATKIAIQINCKLGGAPWSVEVPLPTLMVIGYDVCH 560

Query 2101 DPSRRNRSVCSFVASYNQSMTLWYSKVIFQEKGQEIVDGLKCCLVDALTHYLRNSNGQLPD 2280
          D +++S +EVA+ ++ MT +YS V G+E+ + + A+ Y N LP
Sbjct 561 DTRAKDKSFGAFVATLDKQMTHTYYSTVNAHTSGEELSAHMGINIATAVRKYRERNNVLP 620

Query 2281 RIIYRDGVGDGQLKLLQQYEIPQMKICFTILGSNYQPTLTYYVVQKRINTRIFLKS RDG 2460
          RI IYRDGVGDGQ+ + +E+ ++K L L +++V KRINTRIF+
Sbjct 621 RIFIYRDGVGDGQIPYVHSHEVEEIKKQLETLYQGEVVKLAFIIVSKRINTRIFVDRGRS 680

Query 2461 YDNPNGPTVVDHCITRRDWYDFLIVSQKVTQGTVTPTHYVVVYDDSGITPDQCQRLTYKM 2640
          DNP PGT++D IT + YDF +VSQ V +GT+ PT Y V+YD + + PD+ QRLTYK+
Sbjct 681 GDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPTSYNVIYDTTSLHPDRIQRLTYKL 740

Query 2641 CHLYYNWPGTVRVVPAPCQYAHKLSYLVGQCVHAQPSDVLVDKFLFL* 2781
          H+Y+N VRVP+ CQYAHKL++L +H QP L + L+FL*
Sbjct 741 THMYFNNSCAVRVPSVCQYAHKLAFLAANSLHNQPHYTLNETLYFL* 787

```

```

> ta_transcript44491_1
Length=234

```

```

Score = 425 bits (1092), Expect = 4e-141, Method: Compositional matrix adjust.
Identities = 188/234 (80%), Positives = 219/234 (94%), Gaps = 0/234 (0%)
Frame = +1

```

```

Query 2008 LLQLNCKLGGTLWSISIPFKSAMIVGIDSYHDPSSRRNRSVCSFVASYNQSMTLWYSKVIF 2187
          LLQ+NCKLGGTLWSI+IPFK+AMIVGIDSYHD +R++RSVCSF+ASYNQSMT WYS+ IF
Sbjct 1 LLQMCKLGGTLWSIAIPFKTAMIVGIDSYHDAARKSRVCSFASYNQSMTQWYSRAIF 60

Query 2188 QEKGQEIVDGLKCCLVDALTHYLRNSNGQLPDRIIYRDGVGDGQLKLLQQYEIPQMKICF 2367
          QE+GQE+VDGLK CLVDALTHYLR+NG+LPDR+I+YRDGVGDGQL ++QYEIPQM++CF
Sbjct 61 QERGQEVVDGLKSCLDALTHYLRNKGKLPDRVIMYRDGVGDGQLNTIKQYEIPQMVCVF 120

Query 2368 TILGSNYQPTLTYYVVQKRINTRIFLKS RDGYDNPNGPTVVDHCITRRDWYDFLIVSQKV 2547
          +++ + Y+PTLTYYVVQKRINTRIF+K + G++NP+PGTVVDH ITRRDWYDFLI SQKV
Sbjct 121 SLMEATYKPTLTYYVVQKRINTRIFMKVQGGFENPHPGTVVDHITRRDWYDFLIASQKV 180

Query 2548 TQGTVTPTHYVVVYDDSGITPDQCQRLTYKMCHLYYNWPGTVRVVPAPCQYAHKL 2709
          QGTVTPTHYVVV+DDS +T DQCQRLTYK+CHLYYNWPGTVRVVPAPCQYAHKL
Sbjct 181 NQGTVTPTHYVVVHDDSAMTADQCQRLTYKLCHLYYNWPGTVRVVPAPCQYAHKL 234

```

```

*****
*****
Query= gi|577028025|gb|KF579958.1| Caenorhabditis japonica strain VX0158
ALG-1 (alg-1) gene, partial cds

```

```

Length=624

```

```

***** No hits found *****

```

```

*****
*****
Query= gi|114051845|ref|NM_001046722.1| Bombyx mori apoptosis-linked protein 2 (Alg-2), mRNA

```

```

Length=631

```

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript79570_1	171	2e-47
ta_transcript79596_1	123	5e-32
ta_transcript79595_1	122	2e-31
ta_transcript79592_1	122	2e-31
ta_transcript79591_1	122	2e-31

```

> ta_transcript79570_1
Length=1270

```

```

Score = 171 bits (432), Expect = 2e-47, Method: Compositional matrix adjust.
Identities = 95/176 (54%), Positives = 129/176 (73%), Gaps = 0/176 (0%)
Frame = -2

```

```

Query 585 LYL*SKTHFKELLIMYRDDTILVRVLAEC*CKSIKDAALYEIIKQYCPSTESIKFLHH 406
          YL SK HF++LLI+Y D TIL+RVVLA+ *C IKCD L +IIK C +++SI+FL+H
Sbjct 1028 FYLESKDHFQKLLIVYGDHTILIRVVLAGK*C*HIKCDTTLNKIIK*DCATSKSIEFLNH 1087

Query 405 YTNNIIRQSVSKGCKCILQFHSIYIPRIITVK*SETILPIRNIFPKCTKVLK*YDTPILF 226
          + +N IRQSVS+ K L F I IPR+I V+ ET+LPIR+IFP+ ++V+K*Y+T L
Sbjct 1088 HLHNFIRQSVSECRKGT*FTLINIPRVIPVEGPETVLPIRDIFPQRSEVIK*YNTSALL 1147

Query 225 VKHTNHQTYSFRIKWIPCSIGQSLQFISRYVTTSIFVNTSKNVP*EISAWHWRLE 58
          VKH H++ F ++ IPCSI +SLL ISR V TS+ VN+S+ +P ++SAWH LE
Sbjct 1148 VKHAYHESNCFWVERIPCSIRKSL*LI SRNVATSVLVNSSEYIPKKLSAWHG*LE 1203

```

```

> ta_transcript79596_1
Length=470

```

```

Score = 123 bits (309), Expect = 5e-32, Method: Compositional matrix adjust.
Identities = 86/176 (49%), Positives = 99/176 (56%), Gaps = 0/176 (0%)
Frame = -1

```

```

Query 586 FIPLIQNPFF*GIAHNVS**HHLGPSRTGGMLM*EYKV*RSTV*NHQTILSLYRIYQISAP 407
          +P +Q PF IAH+V * HHL P RTG LM YKV* +T *NHQ L +I +IS P
Sbjct 228 LLP+VQRPFSEIAHSVW*SHHLDPCRTGERLMLTYKV*HNTE*NHQIGLCHVQIDRISEP 287

Query 406 LYQQHHQTICIQRL*VHSSIPLYLYSQNYHGMIGNNFANQKHISKVHQSPQMI*HPYFV 227
          Q H TICI+ * HS + Y YSQ+Y + GN+FAN HIS +S QMI*H
Sbjct 288 SSAQFHPTICIRMP*GHSLVHSYQYSQSYPCRRGTGNSFANP*HISTKIRSHQMI*HLCLA 347

Query 226 CQTYQSSDVQFQD*MDSMFHWTEPVAHVHQQICNHFYLCQHF*KCSIRNLCCLALAIG 59
          CQT S F * DSMFH E HQQ C+HF CQ F LCLA G
Sbjct 348 CQTCLS*VELFLG*KDSMFH*KELAVTHQQKCSHFPCQLFGIYPKETLCLAWVTG 403

```

```

> ta_transcript79595_1
Length=500

```

```

Score = 122 bits (305), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 85/172 (49%), Positives = 97/172 (56%), Gaps = 0/172 (0%)
Frame = -1

```

```

Query 574 IQNPFF*GIAHNVS**HHLGPSRTGGMLM*EYKV*RSTV*NHQTILSLYRIYQISAPLYQQ 395
          +Q PF IAH+V * HHL P RTG LM YKV* +T *NHQ L +I +IS P Q
Sbjct 262 VQRPFSEIAHSVW*SHHLDPCRTGERLMLTYKV*HNTE*NHQIGLCHVQIDRISEPSSAQ 321

Query 394 HHQTICIQRL*VHSSIPLYLYSQNYHGMIGNNFANQKHISKVHQSPQMI*HPYFVCQTY 215
          H TICI+ * HS + Y YSQ+Y + GN+FAN HIS +S QMI*H CQT
Sbjct 322 FHPTICIRMP*GHSLVHSYQYSQSYPCRRGTGNSFANP*HISTKIRSHQMI*HLCLACQTC 381

Query 214 QSSDVQFQD*MDSMFHWTEPVAHVHQQICNHFYLCQHF*KCSIRNLCCLALAIG 59
          S F * DSMFH E HQQ C+HF CQ F LCLA G
Sbjct 382 LS*VELFLG*KDSMFH*KELAVTHQQKCSHFPCQLFGIYPKETLCLAWVTG 433

```

```

> ta_transcript79592_1
Length=554

```

```

Score = 122 bits (306), Expect = 2e-31, Method: Compositional matrix adjust.
Identities = 85/172 (49%), Positives = 97/172 (56%), Gaps = 0/172 (0%)
Frame = -1

```

```

Query 574 IQNPFF*GIAHNVS**HHLGPSRTGGMLM*EYKV*RSTV*NHQTILSLYRIYQISAPLYQQ 395
          +Q PF IAH+V * HHL P RTG LM YKV* +T *NHQ L +I +IS P Q
Sbjct 316 VQRPFSEIAHSVW*SHHLDPCRTGERLMLTYKV*HNTE*NHQIGLCHVQIDRISEPSSAQ 375

Query 394 HHQTICIQRL*VHSSIPLYLYSQNYHGMIGNNFANQKHISKVHQSPQMI*HPYFVCQTY 215
          H TICI+ * HS + Y YSQ+Y + GN+FAN HIS +S QMI*H CQT
Sbjct 376 FHPTICIRMP*GHSLVHSYQYSQSYPCRRGTGNSFANP*HISTKIRSHQMI*HLCLACQTC 435

Query 214 QSSDVQFQD*MDSMFHWTEPVAHVHQQICNHFYLCQHF*KCSIRNLCCLALAIG 59
          S F * DSMFH E HQQ C+HF CQ F LCLA G
Sbjct 436 LS*VELFLG*KDSMFH*KELAVTHQQKCSHFPCQLFGIYPKETLCLAWVTG 487

```

```

> ta_transcript79591_1
Length=555

```

Score = 122 bits (306), Expect = 2e-31, Method: Compositional matrix adjust.
 Identities = 85/172 (49%), Positives = 97/172 (56%), Gaps = 0/172 (0%)
 Frame = -1

```

Query  574  IQNPF*GIAHNVS**HHLGPSRTGGMLM*EYKV*RSTV*NHQ TILSLYRIYQISAPLYQQ 395
          +Q PF IAH+V * HHL P RTG LM YKV* +T *NHQ L +I +IS P Q
Sbjct  317  VQRPFSEIAHSVW*SHHLDP CRTGERLMLTYKV*HNTE*NHQ IGLCHVQIDRISEPSSAQ 376

Query  394  HHQTICIQRL*VHSSIPLYLYSQNYHGMIGNNFANQKHISKVHQSPQMI*HPYFVCQTY 215
          H TICI+ * HS + Y YSQ+Y + GN+FAN HIS +S QMI*H CQT
Sbjct  377  FHPTICIRMP*GHSLVHSYQYSQSYPCRRTGNSFANP*HISTKIRSHQMI*HLCLACQTC 436

Query  214  QSSDVQFQD*MDSMFHWTEPVAHVHQQICNHFYLCQHF*KCSIRNLCLALAIG 59
          S F * DSMFH E HQQ C+HF CQ F LCLA G
Sbjct  437  LS*VELFLG*KDSMFH*KELAVTHQKCSHFPCQLFGIYPKETLCLAWVTG 488

```


Query= gi|392920128|ref|NM_171525.4| Caenorhabditis elegans Protein RDE-1 (rde-1) mRNA, complete cds

Length=3063

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript44491_1	94.7	2e-20
ta_transcript51551_1	94.7	7e-19

> ta_transcript44491_1
 Length=234

Score = 94.7 bits (234), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 79/300 (26%), Positives = 123/300 (41%), Gaps = 71/300 (24%)
 Frame = +1

```

Query  2029  LKINAKLGGINQELDWSEIAEISPEEKERRKT MPL--TMYVGIDVTHPTSYSYSGIDYSIAA 2202
          L++N KLGG WS IA +P M VGID H + S+ +
Sbjct  2      LQMCKLGGTL----WS-IA-----IPFKTAMIVGIDSYHDAARKS--RSVCS 42

Query  2203  VVASINPGGTIYRNMIQTQEECRPGERAVAHGRERTDILEAKFVKLLREFAENNDNRAPA 2382
          +AS N T + + + QE G+E D L++ V L + N + P
Sbjct  43      FIASYNQSMQTQWYSRAIFQER-----GQEVVDGLKSLVDALTHYLRTN-GKLPD 91

Query  2383  HIVVYRDGVSDSEMLRVSHDELRLSLKSEVKQFMSERDGEDPEPKYTFIVIQKRHNTRLR 2562
          +++YRDGV D ++ + E+ ++ + +P T++V+QKR NTR+
Sbjct  92      RVIMYRDGVGDGQLNTIKQYEIPQMVCVCSLMEATY----KPTLTYYVVVQKRINTRIFM 146

Query  2563  RMEKDKPVVNKDLTPAETDVAVAAVKQWEEDMKESKETGIVNPSSGTTVDKLIVSKYKFD 2742
          +++ G NP GT VD I + +D
Sbjct  147     KVQG-----GFENPHPGTVVDHDITRDWYD 172

Query  2743  FFLASHHGVLTGSRPGHYTVMYDDKGMSQDEVYKMTYGLAFLSARCRKPISLPVPVHYAH 2922
          F +AS GT P HY V++DD M+ D+ ++TY L L + +P P YAH
Sbjct  173     FLIASQKVNQGTVTPTHYVVVHDDSAMTADQCQRLTYKLCHLYYNWPGTVRVPAPCQYAH 232

```

> ta_transcript51551_1
 Length=1362

Score = 94.7 bits (234), Expect = 7e-19, Method: Compositional matrix adjust.
 Identities = 93/369 (25%), Positives = 146/369 (40%), Gaps = 75/369 (20%)
 Frame = +1

```

Query  1816  NMFERLPDKEQKVLFIISKRLNAYGFVKHYCDHTIGVANQHITSETVTKALASLRHE 1995
          NM E + ++ + ++ ++ + Y +K C + Q + +T
Sbjct  468     NMCENVIARKNPFSILCVLRQKSADRYEAIKKKCTVDRAMPTQCVVGRNMT-----S 519

Query  1996  KGSKRIFYQIALKINAKLGGINQELDWSEIAEISPEEKERRKT MPLTMYVGIDVTHPTSYS 2175
          K + I +IA++IN KLGG WS E+ +P M +G DV H T
Sbjct  520     KSAMSIATKIAIQINCKLGA----PWS--VEVP-----LPTLMVIGYDVCHDTR- 563

Query  2176  SGIDYSIAAVVASINPGGTIYRNMIQTQEECRPGERAVAHGRERTDILEAKFVKLLREFA 2355
          D S A VA+++ T Y + + GE AH + +R++
Sbjct  564     -AKDKSFGAFVATLDKQMTYHYSTVNAHTS---GEELSAH-----MGINIATAVRKYR 612

```

```

Query 2356 ENNDNRAPAHIVVYRDGVSDSEMLRVSHDELRLSLKSEVKQFMSERDGEDPEPKYTFIVIQ 2535
          E N N P I +YRDGV D ++ V E+ +K KQ + GE K FI++
Sbjct 613 ERN-NVLPGRIFIFYRDGVGDGQIPYVHSHEVEEIK---KQLETLYQGE--PVKLAIFIIVS 666

Query 2536 KRHNTRLLRRMEKDKPVVNKDLTPAETDVAVAAVKQWEEDMKESKETGIVNPSSGTTVDK 2715
          KR NTR+ D S + NP GT +D
Sbjct 667 KRINTRIF-----VDRGRSGD----NPRPGTIIDD 692

Query 2716 LIVSKYKFDFFLASHHGVLGTSRPGHYTMVYDDKGMSQDEVYKMTYGLAFLSARCRKPIS 2895
          +I ++DF+L S + GT P Y V+YD + D + ++TY L + +
Sbjct 693 VITLPERYDFYLVSQNVREGTIAPTSYNVIYDTTSLHPDRIQLTYKLTHMYFNNSCAVR 752

Query 2896 LPVPVHYAH 2922
          +P YAH
Sbjct 753 VPSVCQYAH 761

```


Query= gi|392918268|ref|NM_070961.7| *Caenorhabditis elegans* Protein ERGO-1 (ergo-1) mRNA, complete cds

Length=3366

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript44491_1	103	3e-23
ta_transcript51551_1	94.4	1e-18

> ta_transcript44491_1
 Length=234

Score = 103 bits (257), Expect = 3e-23, Method: Compositional matrix adjust.
 Identities = 67/243 (28%), Positives = 121/243 (50%), Gaps = 31/243 (13%)
 Frame = +1

```

Query 2506 WTIFTDPAKPTLVLGIDVSHPSTRDRETGNVLQKMSAATVVGNIIDLVDTEFRASSRIQDT 2685
          W+I P K +++GID H + R + S + + + + +T++ + + Q+
Sbjct 13 WSI AI-PFKTAMIVGIDSYHDAAR-----KSRVCSFIASYNQSM TQWYSRAIFQER 63

Query 2686 GVECLIDFSKEIDERIGEFIDHTGKRPAHIVVYRDGLSEGDF---QKYLFEERVCI EER 2853
          G E + + + + + GK P +++YRDG+ +G Q + + +VC
Sbjct 64 GQEVVDGLKSLVDALTHYLRTNGKLPDRVIMYRDGVGDGQLNTIKQYEIPQM QVCFS-- 121

Query 2854 CLKIDTSFQPSITYIVVTKRHHTQFFLEDPSQGYESQGYNVLPGLTIEDAVTTNKYYDFF 3033
          ++ +++P+++TY+VV KR +T+ F++ G+E N PGT+++ +T +YDF
Sbjct 122 --LMEATYKPTLT YVVVQKRINTRIFMK-VQGGFE----NPHPGTVDHDITRRDWYDFL 174

Query 3034 LSTQIGNEGCFRPTHYVVLHDTWTGKPDSEFWPTVTHALTYNFCR---STTTVALPAPVL 3201
          +++Q N+G PTHY V+HD D LTY C TV +PAP
Sbjct 175 IASQKVNQGTVP TPHYVVVHDDSAMTADQ-----CQRLTYKLCHLYYNWPGTVRV P APCQ 229

Query 3202 YAH 3210
          YAH
Sbjct 230 YAH 232

```

> ta_transcript51551_1
 Length=1362

Score = 94.4 bits (233), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 81/295 (27%), Positives = 137/295 (46%), Gaps = 26/295 (9%)
 Frame = +1

```

Query 2374 LEKSLGVVGPSPKNCALTRLMV EKVLGKVG T---THRKL ERGGAHK TWTIFTDPAKPTLV 2544
          ++K V P C + R M K + T + GGA W++ P +V
Sbjct 497 IKKKCTVDRAMPTQCVVGRNMTSKSAMSIA TKIAIQINCKLGGA--PWSVEV-PLPTLMV 553

Query 2545 LGIDVSHPSTRDRETGNVLQKMSAATVVGNIIDLVDTEFRASSRIQDTGVECLIDFSKEID 2724
          +G DV H TR ++ S V +D +T + ++ +G E I
Sbjct 554 IGYDVCH-DTRAKDK-----SFGAFVATLDKQ MTHYYSTVNAHTSGEELSAHMGINIA 605

Query 2725 ERIGEFIDHTGKRPAHIVVYRDGLSEGDFQKYLFEERVCI EERCLKIDTSFQ---PSITY 2895
          + ++ + P I +YRDG+ +G Y+ V EE +++T +Q + +
Sbjct 606 TAVRK YRERNNVLPGRIFIFYRDGVGDGQI-PYVHSHEV--E EIKKQLETLYQGE PVKLAF 662

```

```

Query 2896  IVVTKRHHTQFFLEDPSQGYESQGYNVLPGLTIEDAVTTNKYYDFFLSTQIGNEGCFRPT 3075
            I+V+KR +T+ F++ +G G N PGT+I+D +T + YDF+L +Q EG PT
Sbjct 663  IIVSKRINTRIFVD---RG--RSGDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPT 717

Query 3076  HYYVLHDTWTGKPDSEFWPTVTHALTYNFCRSTTTVALPAPVLYAHLAAKRAKETL 3240
            Y V++DT + PD +T+ LT+ + ++ V +P+ YAH A A +L
Sbjct 718  SYNVIYDTSLHPDRI-QRLTYKLTHMYFNNSCAVRVPSVCQYAHKLAFLAANSL 771

```


Query= gi|157674347|gb|EU143547.1| Bombyx mori PIWI mRNA, complete cds

Length=3533

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript51551_1	1340	0.0
ta_transcript44491_1	213	2e-61

> ta_transcript51551_1
Length=1362

Score = 1340 bits (3468), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 625/777 (80%), Positives = 694/777 (89%), Gaps = 0/777 (0%)
Frame = +1

```

Query 511  LPETISILRTRPEAVTSKKGTSGLDLLANYFTVETTPKWGLYQYHVDISPEEDSTGVR 690
            LPE ++ILRTRP V SKKG++G PLD+ ANYFTVETTP+W LYQYHVD PEEDSTG+R
Sbjct 13  LPEQMTILRTRPATVESKKGSTGDPLDVCANYFTVETTPQWCYLYQYHVDVFQPEEDSTGLR 72

Query 691  KALMRVHSKTLLGGYLFDTGLVLYTVNRLHPDPMELYSRKTNDNERMRILIKLTCEVSPGDY 870
            KAL+RVH+ TLGGYLFDTG +LYTV RLHPDPMELYSRKT D ERMRLIKLTC+VSPGDY
Sbjct 73  KALLRVHANTLGGYLFDTGAILYTVKRLHPDPMELYSRKTNDGERMRILIKLTCVSPGDY 132

Query 871  HYIQIFNIIIRKCFNLLKQLMGRDYFDPEAKIDIPEFKLQIWPQYKTTINQYEDRLLLV 1050
            HYIQ+FNIIIRKCFNLL LQL+GRDYFDP AK+DIPE KLQIWPQYKTTINQYEDRLL+V
Sbjct 133  HYIQVFNIIIRKCFNLLNLQLVGRDYFDPIAKVDIPEHKLQIWPQYKTTINQYEDRLLMV 192

Query 1051  TEIAHKVLRMDTVLQMLSEYAATKGNNYKKIFLEDVVGKIVMTDYNKRTYRVDDVAWNVS 1230
            TEIAHKVLRMD VLQML+EYAATKG+NYKKIFLEDVVGKIVMTDYNKRTYRVDDV W S
Sbjct 193  TEIAHKVLRMDNVLQMLNEYAATKGSNYKKIFLEDVVGKIVMTDYNKRTYRVDDVHWETS 252

Query 1231  PKSTFKMRDENITYIEYYYKKYNLRIQDPGQPLLISRSKPREIRAGLPPELIYLVPELCRQ 1410
            P+STFKM+DE + Y++YY KYN+RIQDP QPLL+ R+K REIR+G+PEL+YLVPELCRQ
Sbjct 253  PRSTFKMKDETVCYMDYYQKKYNIRIQDPNQPLLVRKAREIRSGMPELVYLVPELCRQ 312

Query 1411  TGLSDEMFRANFKLMRSLDVHTKIGPDKRIEKLNNFNRRFTSTPEVVEELATWSLKLSKEL 1590
            TGLSDEM ANF+LM +L HTKIGPD RI+KL FNRR T T EVV+ELA+WSLKLS +L
Sbjct 313  TGLSDEMLANFQLMSALGRHTKIGPDLRIQKLLQFNRRLTQTKEVVQELASWSLKLSNDL 372

Query 1591  VKIKGRQLPPENIIQANNVKYPAGDTTEGWTRDMRSKHLAIAQLNSWVVITPERQRRDT 1770
            V+ KGRQLPPE IIQANNVKY AGDTTEGWTRDMRSK LL IA + SWVVITPERQRRD
Sbjct 373  VRFKGRQLPPEAIIQANNVKYAAGDTTEGWTRDMRSKPLLTIAVPGSWVVITPERQRDA 432

Query 1771  ESFIDLIKTGGGVGFRMRSPDLVIRHDGPIEYANMCEEVIARKNPALILCVLARNYAD 1950
            ESF+DLI+KTG GVGFRM P++ I DG ++YANMCE VIARKNP+ ILCVL + AD
Sbjct 433  ESFVDLIMKTGNVGFRMPKPEICPIARDGHMDYANMCENVIARKNPFIILCVLRQKSAD 492

Query 1951  RYEAIKKKCTVDRAPTQVVCARNMSSKSAMSIATKVAIQINCKLGGSPWTVDIPLPSLM 2130
            RYEAIKKKCTVDRA+PTQ V RNM+SKSAMSIATK+AIQINCKLGG+PW+V++PLP+LM
Sbjct 493  RYEAIKKKCTVDRAMPTQCVVGRNMTSKSAMSIATKIAIQINCKLGGAPWSVEVPLPTLM 552

Query 2131  VVGVDVCHDTRSKEKSFGAFVATLDKQMTQYYSIVNAHTSGEELSSHMGFNIAAVKKFR 2310
            V+GYDVCHDTR+K+KSFGAFVATLDKQMT YYS VNAHTSGEELS+HMG NIA+AV+K+R
Sbjct 553  VIGYDVCHDTRAKDKSFGAFVATLDKQMTTHYYSTVNAHTSGEELSAHMGINIATAVRKYR 612

Query 2311  EKNGTYPARIFIYRDGVGDGQIPYVHSHEVAEIKKKLAEIYAGVEIKLAFIIVSKRINTR 2490
            E+N P RIFIYRDGVGDGQIPYVHSHEV EIKK+L +Y G +KLAFIIVSKRINTR
Sbjct 613  ERNNVLPGRIFIYRDGVGDGQIPYVHSHEVEEIKKQLETLYQGEPVKLAFIIVSKRINTR 672

Query 2491  IFVQRGRSGENPRPGTVIDDVITLPERYDFYLVSNVREGTIAPTSYNVIEDTTGLNPDR 2670
            IFV RGRSG+NPRPGT+IDDV+TLPERYDFYLVSNVREGTIAPTSYNVI DTT L+PDR
Sbjct 673  IFVDRGRSGDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPTSYNVYDTSLHPDR 732

```

```

Query  2671  IQRLTYKLTHLYFNCSSQVRVPSVCQYAHKLAFLAANSLHNQPHYSLNETLYFL*VF  2841
          IQRLTYKLTH+YFN S  VRVPSVCQYAHKLAFLAANSLHNQPHY+LNETLYFL*
Sbjct  733   IQRLTYKLTHMYFNNSCAVRVPSVCQYAHKLAFLAANSLHNQPHYTLNETLYFL*AL  789

```

```

> ta_transcript44491_1
Length=234

```

```

Score = 213 bits (543), Expect = 2e-61, Method: Compositional matrix adjust.
Identities = 98/233 (42%), Positives = 147/233 (63%), Gaps = 0/233 (0%)
Frame = +1

```

```

Query  2065  IQINCKLGGSPWTVDIPLPSLMVVGVDVCHDTRSKEKSFQAFVATLDKQMTQYYSIVNAH  2244
          +Q+NCKLGG+ W++ IP + M+VG D HD K +S +F+A+ ++ MTQ+YS
Sbjct  2      LQMNCCKLGGTLWSIAIPFKTAMIVGIDSYHDAARKSRVCSFIASYNQSMQWYSRAIFQ  61

Query  2245  TSGEELSSHMGFNIASAVKKFREKNGTYPARIFIYRDGVGDGQIPYVHSHEVAEIKKKLA  2424
          G+E+ + + A+ + NG P R+ +YRDGVGDGQ+ + +E+ +++ +
Sbjct  62     ERGQEVVDGLKSLVDALTHYLRTNGKLPDRVIMYRDGVGDGQLNTIKQYEIPQMVCFCFS  121

Query  2425  EIYAGVEIKLAFIIVSKRINTRIFVQRGRSGENPRPGTVIDDVVTLPERYDFYLVSNVR  2604
          + A + L +++V KRINTRIF++ ENP PGTVD +T + YDF + SQ V
Sbjct  122    LMEATYKPTLTLYVVVQKRINTRIFMKVQGGFENPHPGTVVDHDITRRDWYDFLIASQKVN  181

Query  2605  EGTIAPTSYNVIEDTTGLNPDRIQRLTYKLTHLYFNCSSQVRVPSVCQYAHKL  2763
          +GT+ PT Y V+ D + + D+ QRLTYKL HLY+N VRV+ CQYAHKL
Sbjct  182    QGTVPPTHYVVVHDDSAMTADQCQRLTYKLCHLYYNWPGTVRVVPAPCQYAHKL  234

```

```

*****
*****

```

```

Query= gi|392919217|ref|NM_072209.3| Caenorhabditis elegans Protein SAGO-1 (sago-1) mRNA,
complete cds

```

```

Length=2646

```

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript44491_1	63.5	2e-10
ta_transcript51551_1	53.5	2e-06

```

> ta_transcript44491_1
Length=234

```

```

Score = 63.5 bits (153), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 57/225 (25%), Positives = 99/225 (44%), Gaps = 20/225 (9%)
Frame = +1

```

```

Query  1795  KTNMKLGGLNYELRSGVFSNSKRLIIGFETSQRGGLGDAPIAIGFAANMMSHSQQFAGGY  1974
          + N KLGG L S +I+G ++ + A+ S +Q ++
Sbjct  3      QMNCKLGG---TLWSIAIPFKTAMIVGIDSYHDAARKSRVCSFIASYNQSMQWYSRA-  58

Query  1975  MFVKKASADNYGPVPIEILLTILKQAKAN--RPNDR-PDELLIYFSGVSEGQHALVNEYA  2145
          +F ++ G + + L + L A + R N + PD +++Y GV +GQ + +Y
Sbjct  59     IFQER-----GQEVVDGLKSLVDALTHYLRTNGKLPDRVIMYRDGVGDGQLNTIKQYEI  113

Query  2146  NQVKAACGLFNESFRPHITLILASKVHNTRVYKSENGGGVCNVEPGTVIDHTIVSPVLSE  2325
          Q++ L +++P +T ++ K NTR++ GG N PGTVDH I +
Sbjct  114    PQMQVCFSLMEATYKPTLTLYVVVQKRINTRIFMKVQ-GGFENPHPGTVVDHDITR---RD  169

Query  2326  WYH---AGSLARQGTSLVKYSLIFNTKKNEKLSVYERLTNELCY  2451
          WY A QGT Y ++ + +RLT +LC+
Sbjct  170    WYDFLIASQKVNQGTVPPTHYVVVHDDSAMTADQC-QRLTYKLCH  213

```

```

> ta_transcript51551_1
Length=1362

```

```

Score = 53.5 bits (127), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 37/129 (29%), Positives = 59/129 (46%), Gaps = 2/129 (2%)
Frame = +1

```

```

Query  2059  RPNDRPDELLIYFSGVSEGQHALVNEYANQVKAACGLFNESFRPHITLILASKVHNTRV  2238
          R N P + IY GV +GQ V+ + ++K + + I+ SK NTR+

```

```

Sbjct  614  RNNVLPGRIFIYRDGVGDGQIPYVHSHEVEEIKKQLETLYQGEFVKLAFIIVSKRINTRI  673

Query  2239  YKSENGGGVCNVEPGTVIDHTIVSPVLSEWYHAGSLARQGTSLVKYSLIFNTKKNEKLS  2418
+      G  N  PGT+ID  I  P  ++Y      R+GT      Y++I++T
Sbjct  674  FVDRGRSGD-NPRPGTIIDDVITLPERYDFYLVSQNVREGTIAPTSYNVIYDTSLHPDR  732

Query  2419  VYERLTNEL  2445
+ +RLT +L
Sbjct  733  I-QRLTYKL  740
*****
*****
Query= gi|392884665|ref|NM_058357.3| Caenorhabditis elegans Protein SAGO-2, isoform a (sago-2)
mRNA, complete cds

Length=2664

Sequences producing significant alignments:

      ta_transcript44491_1      60.5      3e-09
      ta_transcript51551_1      47.0      2e-04
      ta_transcript27100_1      32.3      6.9

> ta_transcript44491_1
Length=234

Score = 60.5 bits (145), Expect = 3e-09, Method: Compositional matrix adjust.
Identities = 59/245 (24%), Positives = 106/245 (43%), Gaps = 15/245 (6%)
Frame = +1

Query  1795  KTNMKGGLNYAIGSEAFNKPRLIVGFVTSQVRGGNPDYPISVGFAANMLKHHQKFAGG  1974
+ N KLGG ++I  A      +IVG +      S  F A+ +  ++
Sbjct  3      QMNCKLGGTLWSI---AIPFKTAMIVGIDSYHDAARKSRSVCS--FIASYNQSMQTQWYSR  57

Query  1975  YVYVHRDRDVFSGSIKDTLLTIFKTCTEQRGR-PDDILLYFNGVSEGQFSMINEEFSARV  2151
++ R ++V  + K  L+      G+ PD +++Y +GV +GQ + I +++
Sbjct  58  AIFQERGQEVVDGL-KSCLVDALTHYLRTNGKLPDRVIMYRDGVGDGQLNTI-KQYEIPQ  115

Query  2152  KEACMAFQKEGTTPPFRPHITIIASSKAHNERLYKSDKGRIVNLEPGTVVDHTIVSNVYTE  2331
+ C +  E T  ++P +T +  K  N R++ +G  N  PGTVVDH I  + +
Sbjct  116  MQVCFSLM-EAT--YKPTLTLYVVVQKRINTRIFMKVQGGFENPHPGTVVDHDITRRDWYD  172

Query  2332  WYHASAVARQGTAKATKFTLIFTTKAGPQAEPLWHLEQLTNDLCYDHQIVFHPVGLPVPL  2511
+ AS  QGT  T + ++  A  +  ++LT  LC+ +  V +P P
Sbjct  173  FLIASQKVNQGTVTPTHYVVVHDDSAMTADQ----CQRLTYKLCHLYNWPPTVRVPAPC  228

Query  2512  YIADR  2526
A +
Sbjct  229  QYAHK  233

> ta_transcript51551_1
Length=1362

Score = 47.0 bits (110), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 107/486 (22%), Positives = 192/486 (40%), Gaps = 60/486 (12%)
Frame = +1

Query  1054  DYFKKKYGITLKYPD--LFTIEAKGKQGKIHFPAEVL---LCPNQTVTNDQMINNEQA-  1215
DY++KKY I ++ P+  L  AK ++ +  P  V  L  LC  QT  +D+M+ N  Q
Sbjct  268  DYYQKKYNIRIQDPNQPLLVRARAREIRSGMPELVYLVPCLC-RQTGLSDEMLANFQLM  326

Query  1216  -----DMIKMSAAQPHIRKTTTDTIVRNVGLASNNIYGFIVKVEDPVNLEGMVLP  1362
D+      Q + R T T  +V+ +  S  +      D V  +G  LP
Sbjct  327  SALGRHTKIGPDLRIQKLLQFNRLTQTKEVVQELASWSLKLNS----DLVRFKGRQLP  381

Query  1363  KPPIAFAGNRLADLANPKSRFPPTDFNRAGQYYDAKELTKWELVFVQNEEVQGLAKQLADE  1542
P+      N +  A  +  T  R+      +  W ++ + +  ++ A+
Sbjct  382  -PEAIIQANNVKYAAGDTTEGWTRDMRSKPLLTIAVGSWVVTIPERQ-----RRDAES  434

Query  1543  MVNNGMKCSNPTMSFIIRGDLEPIFKKAKAAGTQLLFFVVKSRVNYHQQIKALEQK----  1710
V+  +  MK  N  + + ++ PI +      +  V+ +R N  +  L  QK
Sbjct  435  FVDLIMKTGNVGFRMPKPEICPIARDGHMDYANMCENVI-ARKNPSFILCVLRQKSADR  493

Query  1711  YDVLTEQEI---RAETAEKVFRQPQTR---LNIINKT---NMKLGGLNYAIGSEAFNKP  1860
Y+ + ++  RA  + V +  T  ++I  K  N  KLGG  +++  P
Sbjct  494  YEAIKKKCTVDRAMPTQCVVGRNMTSKSAMSIAIKIAIQINCKLGAPWSVEVPL---PT  550

```



```

Query 1861 RLIVGFVTSQRVGGNPDYPISVG-FAANMLKHHQKFAGGYVYVHRDRDVFSGSIKDTLLT 2037
      +++G+          S G F A + K + V H + + + + T
Sbjct 551 LMVIGYDVCHDTRAKDK--SFGAFVATLDKQMTHYYST-VNAHTSGEELSAHMGINIAT 606

Query 2038 IFKTCTEQRG-RPDDILLYFNGVSEGGQFSMINEEFSARVKEACMAFQKEGTPPFRPHITI 2214
      + E+ P I +Y +GV +GQ ++ +K+ + +G P +
Sbjct 607 AVRKYRERNNVLPGRIFIYRDGVGDGQIPYVHSHEVEEIKKQ-LETLYQGEPV--KLAF 662

Query 2215 IASSKAHNERLYKSDKGRI-VNLEPGTVVDHTIVSNVYTEWYHASAVARQGTAKATKFTL 2391
      I SK N R++ D+GR N PGT++D I ++Y S R+GT T + +
Sbjct 663 IIVSKRINTRIF-VDRGRSGDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPTSYNV 721

Query 2392 IFTTKA 2409
      I+ T +
Sbjct 722 IYDTTS 727

```

```

> ta_transcript27100_1
Length=877

```

```

Score = 32.3 bits (72), Expect = 6.9, Method: Compositional matrix adjust.
Identities = 18/50 (36%), Positives = 26/50 (52%), Gaps = 0/50 (0%)
Frame = +3

```

```

Query 2061 ARKTR*YPFVFQWSFRRSILNDQRGIQCPSEGGVHGIPKGGNPAIQTHH 2210
      +R+ R PEFV+ + + N Q+ Q P G VHG P+ G + HH
Sbjct 679 SRRHRA*PFVFRQFNQLRVFNYYQAAQQPDVGAVHGGPRPGADHVLREHH 728

```

```

*****
*****
Query= gi|392885315|ref|NM_170850.3| Caenorhabditis elegans Protein PPW-1, isoform b (ppw-1)
mRNA, complete cds

```

```

Length=165

```

	Score (Bits)	E Value
Sequences producing significant alignments:		
ta_transcript72377_1	27.7	1.6
ta_transcript72378_1	27.7	1.8
ta_transcript42528_1	26.6	3.6
ta_transcript60738_1	26.6	4.4
ta_transcript74966_1	25.4	8.7

```

> ta_transcript72377_1
Length=1495

```

```

Score = 27.7 bits (60), Expect = 1.6, Method: Composition-based stats.
Identities = 13/26 (50%), Positives = 18/26 (69%), Gaps = 5/26 (19%)
Frame = +3

```

```

Query 3 GKTTRSIVRLGQTCCPSCPKAWYRSA 80
      G++TR L QTCCP C AWY+++
Sbjct 1173 GRSTRC---LEQTCCPRC--AWYQTS 1193

```

```

> ta_transcript72378_1
Length=1465

```

```

Score = 27.7 bits (60), Expect = 1.8, Method: Composition-based stats.
Identities = 13/26 (50%), Positives = 18/26 (69%), Gaps = 5/26 (19%)
Frame = +3

```

```

Query 3 GKTTRSIVRLGQTCCPSCPKAWYRSA 80
      G++TR L QTCCP C AWY+++
Sbjct 1143 GRSTRC---LEQTCCPRC--AWYQTS 1163

```

```

> ta_transcript42528_1
Length=450

```

```

Score = 26.6 bits (57), Expect = 3.6, Method: Compositional matrix adjust.
Identities = 13/22 (59%), Positives = 16/22 (73%), Gaps = 1/22 (5%)
Frame = +2

```

```

Query 56 PKSLVPLRSLQKRREMW-RGEP 118

```

```

          P SLVP R+L+  R MW +GEP
Sbjct  294  PSSLVPERNLRGVRMMWNKGEP  315

```

```

> ta_transcript60738_1
Length=610

```

```

Score = 26.6 bits (57), Expect = 4.4, Method: Composition-based stats.
Identities = 12/33 (36%), Positives = 20/33 (61%), Gaps = 2/33 (6%)
Frame = -2

```

```

Query  110  LSTFLVF--FAASGAVPSFWAAGAAGLSETNIA  18
          L+T+ +F  F A G + SFW+      GL  ++I+
Sbjct  198  LNTYYIFQLFYAQGLIVSFWSIAQCGLRNSSIS  230

```

```

> ta_transcript74966_1
Length=528

```

```

Score = 25.4 bits (54), Expect = 8.7, Method: Composition-based stats.
Identities = 8/19 (42%), Positives = 12/19 (63%), Gaps = 0/19 (0%)
Frame = +3

```

```

Query  36  QTCPCSPKAWYRSARCKK  92
          Q  CPS P+ W+ S+ C +
Sbjct  213  QPTCPSKPRGWWTSSLCSR  231

```

```

*****
*****
Query= gi|392885541|ref|NM_059134.5| Caenorhabditis elegans Protein PPW-2 (ppw-2) mRNA, complete
cds

```

```

Length=2928

```

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript44491_1	63.2	3e-10
ta_transcript51551_1	57.4	2e-07

```

> ta_transcript44491_1
Length=234

```

```

Score = 63.2 bits (152), Expect = 3e-10, Method: Compositional matrix adjust.
Identities = 53/215 (25%), Positives = 86/215 (40%), Gaps = 29/215 (13%)
Frame = +1

```

```

Query  2134  AYNGNGKQEFSGDFVLNAAGQETIAPIEDIVSYSIKGYKKFHDGKAPKRITIYRSGSSEG  2313
          +YN +  Q +S  +  GQE +  ++  +  ++  Y +  +GK P R+ +YR G  +G
Sbjct  46  SYNQSMTQWYSRA-IFQERGQEVVDGLKSCLDLTHYLRT-NGKLPDRVIMYRDGVGDG  103

Query  2314  NHGPIISYEVLARV--AMRNFSPDTQLLYIVVSKEHTYRFFKKESggsgssggsnsagas  2487
          I  YE+P +V ++  +  L Y+VV K  R F K  GG
Sbjct  104  QLNTIKQYEIPQMVCFSLMPEATYKPTLTYYVVVQKRINTRIFMKVQGGFE-----  153

Query  2488  nsgTLTSAPPKPWELNIGPGLTVDYGVTNPACQFFLNSHMTLQSAKTPLYTVLADDRN  2667
          N  PG  VD+ +T  F + S  QG+  Y V+ DD
Sbjct  154  -----NPHPGTVVDHDITRRDWYDFLIASQKVNQGTVTPTHYVVVHDDSA  198

Query  2668  IGMSALEEFTFNLCHLHQIVGLPTSIPPLYVANE  2772
          +  +  T+ LCHL+  +P P  A++
Sbjct  199  MTADQCQLRITYKLCHLYYNWPGTVRVPAPCQYAHK  233

```

```

> ta_transcript51551_1
Length=1362

```

```

Score = 57.4 bits (137), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 129/608 (21%), Positives = 238/608 (39%), Gaps = 113/608 (19%)
Frame = +1

```

```

Query  1090  SNYRGRTRHHKIESIHHEGAATARFELEGGGTCTVATYFKDKYKIQLRYPNANLIV--CK  1263
          ++Y RT  ++++ +H E +  + F+++  C +  Y++ KY I+++ PN  L+V  K
Sbjct  235  TDYNKRT--YRVDVHWETSPRSTFKMKDETVCYM-DYYQKKYNIRIQDPNQPLLVRK  291

Query  1264  ERGALNFYPMELITISPnqrvi-----tqqtssqsqrattKESAVLPDIR-QRLIMTGKI  1425

```

```

Sbjct 292      R  + P EL+ + P      +          + + + PD+R Q+L+      +
AREIRSGMP-ELVYLVPCLCRQTGLSDEMLANFQLMSALGRHTKIGPDLRIQKLLQFNR- 349

Query 1426  AAKITAENEV---LGKMGVTVCEPLVVKGRNLPA-----IRLASFETGEHLINPRD 1572
++T EV L + + ++ + KGR LP ++ A+ +T E RD

Sbjct 350  --RLTQTKEVVQELASWSLKLSDNLVRFKGRQLPPEAIQANNVKYAAGDTTEGWT--RD 405

Query 1573  CKWRPQRYNRSAPVAPK-VWALYGVGSPGSQMNRDVMRRFCDEFMMSRSKGI LFPFPGDV 1749
+ +P +AP W V +P Q RD F D M G P P

Sbjct 406  MRSKPLL---TIAPVGSWV---VITPERQ-RRDA-ESFVDLIMKTGNGVGFMRPKPE-- 454

Query 1750  NLLTPDAIENRLREA-----ANAGCTFVLCITEDNITCLHQKYKFIEHH-----T 1884
+ P A + + A A +F+LC+ +Y+ I+ T

Sbjct 455  --ICPIARDGHMDYANMCENVIAKKNPSFILCVLRQKSA---DRYEAIKKKCTVDRAMPT 509

Query 1885  QMIV-QDMKLSKALSVDNASKKLTLENVINKTNVKLGGSNYVYLDTKNFLQEHLIIGVGI 2061
Q +V ++M A+S+ + K+ ++ N KLGG+ + + L ++IG +

Sbjct 510  QCVVGRNMTSKSAMSI---ATKIAIQ-----INCKLGGAPW---SVEVPLPTLMVIGYDV 558

Query 2062  SSPPPGTKYIMESRGILNPTIVGFAYNGNGKQEFSGDFVLNA--AGQETIAPIEDIVSYS 2235
T+ +S G T+ KQ +NA +G+E A + ++ +

Sbjct 559  CH---DTRAKDKSFGAFVATL-----DKQMTHYYSTVNAHTSGEELSAHMGINIATA 607

Query 2236  IKGYKKFHDGKAPKRITIRSGSSEGNHGPIISYEVPLARVAMRNF--SPDTQLLYIVVS 2409
++ Y++ + P RI IYR G +G + S+EV + + +L +I+VS

Sbjct 608  VRKYRE-RNNVLPGRIFIYRDGVGDGQIPYVHSHEVEEIKKQLETLYQGEVPVKLAFIIVS 666

Query 2410  KEHTYRFFKKEsggsssggsnsagasnsGTLTSAPPKPWELNIGPGLTVDYGVTNPCKQ 2589
K R F N PG +D +T P

Sbjct 667  KRINTRIFVDRGRSGD-----NPRPGTIIDDVITLPERYD 701

Query 2590  FFLNSHMTLQGSAKTPLYTVLADDRNIGMSALEEFTFNLCHLHQIVGLPTSIPTPLYVAN 2769
F+L S +G+ Y V+ D ++ ++ T+ L H++ +P+ A+

Sbjct 702  FYLVSQNVREGTIAPTSYNVIYDTSLSHPDRIQRLTYKLTHMYFNNSCAVRVPSVCQYAH 761

Query 2770  EYAKRGRN 2793
+ A N

Sbjct 762  KLAFLAAN 769

*****
*****
Query= gi|429892795|gb|KC116214.1| Drosophila melanogaster isolate 3893 aubergine (Aub) gene,
complete cds

Length=3434

Sequences producing significant alignments:

      ta_transcript51551_1          320 3e-90
      ta_transcript44491_1          184 5e-51

> ta_transcript51551_1
Length=1362

Score = 320 bits (821), Expect = 3e-90, Method: Compositional matrix adjust.
Identities = 161/304 (53%), Positives = 208/304 (68%), Gaps = 14/304 (5%)
Frame = +3

Query 2535  YSICKKRTCVDPRVPVSVVTLKVIAPRQKPTGLMSIATKVVVIQMNAKLMGAPWQVVIPL 2714
Y IKK+ VDR +P+Q V R MSIATK+ IQ+N KL GAPW V +PL

Sbjct 494  YEAIAKKCTVDRAMPTQCV-----VGRNMTSKSAMSIATKIAIQINCKLGGAPWSVEVPL 548

Query 2715  HGLMTVGFVDVCHSPKNKNKSYGAFVATMDQKESFRYFSTVNEHIKGQELSEQMSVNMACA 2894
LM +G+DVCH + K+KS+GAFVAT+D K+ Y+STVN H G+ELS M +N+A A

Sbjct 549  PTLMVIGYDVCHDTRAKDKSFGAFVATLD-KQMTHYYSTVNAHTSGEELSAHMGINIATA 607

Query 2895  LRSYQEQHRS LPERILFFRDGVGDGQLYQVVNSEVNTLKDRLDEIYKSAGKQEGCRMTFI 3074
+R Y+E++ LP RI +RDGVGDGQ+ V + EV +K +L+ +Y+ E ++ FI

Sbjct 608  VRKYRE-RNNVLPGRIFIYRDGVGDGQIPYVHSHEVEEIKKQLETLYQG----EPVKLAFI 663

Query 3075  IVSKRINSRYFTGH----RNPVPGTVDDVITLPERYDFFLVSAVRIGHTVSPSYNVIS 3242
IVSKRIN+R F NP PGT++DDVITLPERYDF+LVSQ VR GT++PTSYNVI

Sbjct 664  IVSKRINTRIFVDRGRSGDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPTSYNVIY 723

Query 3243  DNMGLNADKLQMLS YKMTMYNYS GTIRVPAVCHYAHKLAFLVAESINRAPSAGLQNQL 3422
D L+ D++Q L+YK+THMY+N S +RVP+VC YAHKLAFL A S++ P L L

```

Sbjct 724 DTTSLHPDRIQRLTYKLTHMYFNNSCAVRVPSVCQYAHKLAFLAANSLHNQPHYTLNETL 783

Query 3423 YFL* 3434
YFL*

Sbjct 784 YFL* 787

Score = 111 bits (278), Expect(4) = 4e-74, Method: Compositional matrix adjust.
Identities = 59/148 (40%), Positives = 83/148 (56%), Gaps = 6/148 (4%)
Frame = +2

Query 761 SRPPGMTSKKGVVGTHITVQANYFKVLKRPNWITIYQYRVDFTPDVEATRLRRSFLYEHKG 940
+RP + SKKG G + V ANYF V P W +YQY VDF P+ ++T LR++ L H

Sbjct 22 TRPATVESKKGSTGDPDVCANYFTVETTPQWCLYQYHVDFQPEEDSTGLRKALLRVHAN 81

Query 941 ILGGYIFDGTNMFQINQFKAVQDSPYVLELVT-KSRAGENIEIKIKAVGSVQSTDAEQFQ 1117
LGGY+FDG ++ + + P +EL + + GE + I IK V D Q

Sbjct 82 TLGGYLFQDGAIIYTVKRLH-----PDPMELYSDRKHDGERMRILIKLTCDVSPGDYHYIQ 136

Query 1118 VLNILRRAMEGLDLKLVSRYYYDPQAK 1201
V N+I+R+ L+L+LV R Y+DP AK

Sbjct 137 VFNIIRKCFNLLNLQLVGRDYDFPIAK 164

Score = 90.9 bits (224), Expect(4) = 4e-74, Method: Compositional matrix adjust.
Identities = 43/128 (34%), Positives = 69/128 (54%), Gaps = 1/128 (1%)
Frame = +3

Query 1920 LRAMSEHTRLNPDRRIERLRMFNKRKLSCKQSVETLKSWNIELDSALVEIPARVLPPEKI 2099
+ A+ HT++ PD RI++L FN+RL K+ V+ L SW++L + LV R LPPE I

Sbjct 326 MSALGRHTKIGPDLRIQKLLQFNRRLTQTKEVVQELASWSLKLSDNLRVFKRQLPPEAI 385

Query 2100 LFGNQ-KIFVCDARADWTNEFRTCSMFKNVHINRWYVITPSRNLRETQEFVQMCIRTASS 2276
+ N K D WT + R+ + + W VITP R R+ + FV + ++T +

Sbjct 386 IQANNVKYAAGDTTEGWTRDMRSKPLLTIAVGSWVITPERQRRDAESFVDLIMKTGNG 445

Query 2277 MKMNICNP 2300
+ + P

Sbjct 446 VGFRMPKP 453

Score = 88.6 bits (218), Expect(4) = 4e-74, Method: Compositional matrix adjust.
Identities = 41/110 (37%), Positives = 65/110 (59%), Gaps = 18/110 (16%)
Frame = +2

Query 1517 VILTDYNNKTYRIDVDVFQSTPLCKFKTNDGEISYVDYKXXXXXXXXXXXXXXXXXXXXXR 1696
+++TDYN +TYR+DDV +++P FK D + Y+DYY+K +

Sbjct 232 IVMTDYNKRTYRVDDVHWETSPRSTFKMKDETVCYMDYYQK-----K 273

Query 1697 YNIIIRDQLKPLVMSRPTDKNIRGGNDQAIMIPELARATGMTDAMRADF 1846
YNI I+D QPL++ R + IR G + + ++PEL R TG++D M A+F

Sbjct 274 YNIRIQDPNQPLLVYRAKAREIRSGMPELVYLPPELCRQTGLSDEMLANF 323

Score = 52.4 bits (124), Expect(4) = 4e-74, Method: Compositional matrix adjust.
Identities = 21/65 (32%), Positives = 43/65 (66%), Gaps = 1/65 (2%)
Frame = +3

Query 1260 INLENFRMQLWPGYQTSIRQHENDILLCSEICHKVMRTETLYNILSD-AIRDSDDYQSTF 1436
+++ ++Q+WPGY+T+I Q+E+ +L+ +EI HKV+R + + +L++ A +Y+ F

Sbjct 165 VDIPEHKLQIWPGYKTTINQYEDRLLMVTEIAHKVLRMDNVLQMLNEYAATKGSNYKKIF 224

Query 1437 KRAVM 1451
V+

Sbjct 225 LEDVV 229

> ta_transcript44491_1
Length=234

Score = 184 bits (466), Expect = 5e-51, Method: Compositional matrix adjust.
Identities = 96/242 (40%), Positives = 142/242 (59%), Gaps = 15/242 (6%)
Frame = +3

Query 2658 VIQMNAKLMGAPWQVVIPLHGLMTVGFVCHSPKNKNKSYGAFVATMDQKESFRYFSTVN 2837
++QMN KL G W + IP M VG D H K++S +F+A+ +Q + +++S

Sbjct 1 LLQMNCKLGGTLWSIAIPFKTAMIVGIDSYHDAARKSRVCSFIASYNQSM-T-QWYSRAI 59

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Query 2838 EHIKGQELSEQMSVNMALRSYQEQHRSRSLPERILFFRDGVGDGQLYQVVNSEVNTLK-- 3011
          +GQE+ + + + AL Y + LP+R++ +RDGVGDGQL + E+ ++
Sbjct 60 FQERGQEVVDGLKSLVDALTHYLRTNGKLPDRVIMYRDGVGDGQLNTIKQYEIPQMQVC 119

Query 3012 -DRLDEIYKSAGKQEGCRMTFIIVSKRINSRYFT----GHRNPVPGTVVDDVITLPERYD 3176
          ++ YK +T+++V KRIN+R F G NP PGTVVD IT + YD
Sbjct 120 FSLMEATYKPT-----LTYVVVQKRINTRIFMKVQGGFENPHPGTVVDHDITRRDWYD 172

Query 3177 FFLVSQAVRIGTVSPTSYNVISDNMGLNADKLQMLSYKMTMYYNYSGTIRVPAVCHYAH 3356
          F + SQ V GTV+PT Y V+ D+ + AD+ Q L+YK+ H+YYN+ GT+RVPA C YAH
Sbjct 173 FLIASQKVNQGTVTPTHYVVVHDDSAMTADQCQRLTYKLCHLYYNWPGTVRVPAQCQYAH 232

Query 3357 KL 3362
          KL
Sbjct 233 KL 234
*****
*****
Query= gi|166706855|ref|NM_001104596.2| Bombyx mori aubergine protein (Aubergine), mRNA

Length=2700

Sequences producing significant alignments:

          ta_transcript51551_1          1340 0.0
          ta_transcript44491_1          213 3e-62

> ta_transcript51551_1
Length=1362

Score = 1340 bits (3468), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 625/775 (81%), Positives = 694/775 (90%), Gaps = 0/775 (0%)
Frame = +1

Query 376 LPETISILRTRPEAVTSKKGTSGLDPLDLLANYFTVETTPKWGLYQYHVDISPEEDSTGVR 555
          LPE ++ILRTRP V SKKG++G PLD+ ANYFTVETTP+W LYQYHVD PEEDSTG+R
Sbjct 13 LPEQMTILRTRPATVESKKGSTGDPLDVCANYFTVETTPQWCYLYQYHVDQPEEDSTGLR 72

Query 556 KALMRVHSKTLLGGYLFDGTVLYTVNRLHPDPMELYSDRKTDNERMRIKLKTCVSPGDY 735
          KAL+RVH+ TLGGYLFDG +LYTV RLHPDPMELYSDRK D ERMRIKLKTC+VSPGDY
Sbjct 73 KALLRVHANTLGGYLFDGAILYTVKRLHPDPMELYSDRKHDGERMRIKLKTCVSPGDY 132

Query 736 HYIQIFNIIIRKCFNLLKQLMGRDYFDPEAKIDIPEFKLQIWPQYKTTINQYEDRLLLV 915
          HYIQ+FNIIIRKCFNLL LQL+GRDYFDP AK+DIPE KLQIWPQYKTTINQYEDRLL+V
Sbjct 133 HYIQVFNIIIRKCFNLLNLQLVGRDYFDPIAKVDIPEHKLQIWPQYKTTINQYEDRLLMV 192

Query 916 TEIAHKVLRMDTVLQMLSEYAATKGNYYKKIFLEDVVGKIVMTDYNKRTYRVDDVAWNVS 1095
          TEIAHKVLRMD VLQML+EYAATKG+NYKKIFLEDVVGKIVMTDYNKRTYRVDDV W S
Sbjct 193 TEIAHKVLRMDNVLQMLNEYAATKGSNYKKIFLEDVVGKIVMTDYNKRTYRVDDVHWETS 252

Query 1096 PKSTFKMRDENITYIEYYYKKYNLRIQDPGQPLLISRSKPREIRAGLPELIYLVPELCRQ 1275
          P+STFKM+DE + Y++YY KKN+RIQDP QPLL+ R+K REIR+G+PEL+YLVPELCRQ
Sbjct 253 PRSTFKMKDETVCYMDYYQKKYNIRIQDPNQPLLVRKAREIRSGMPELVYLVPELCRQ 312

Query 1276 TGLSDEMFRANFKLMRSLDVHTKIGPDKRIEKLNNFNRRFTSTPEVVEELATWSLKLSKEL 1455
          TGLSDEM ANF+LM +L HTKIGPD RI+KL FNRR T T EVV+ELA+WSLKLS +L
Sbjct 313 TGLSDEMLANFQLMSALGRHTKIGPDLRIQKLLQFNRRLTQTKEVVQELASWSLKLSNDL 372

Query 1456 VKIKGRQLPPENIIQANNVKYPAGDTTEGWTRDMRSKHLAIAQLNSWVVITPERQRRDT 1635
          V+ KGRQLPPE IIQANNVKY AGDTTEGWTRDMRSK LL IA + SWVVITPERQRRD
Sbjct 373 VRFKGRQLPPEAIIQANNVKYAAGDTTEGWTRDMRSKPLLTIAVPGSWVVITPERQRRDA 432

Query 1636 ESFIDLIKTGGGVGFRMRSPDLVIRHDGPIEYANMCEEVIARKNPALILCVLARNYAD 1815
          ESF+DLI+KTG GVGFRM P++ I DG ++YANMCE VIARKNP+ ILCVL + AD
Sbjct 433 ESFVDLIMKTGNVGFRMPKPEICPIARDGHMDYANMCENVIAKNPSPILCVLRQKSAD 492

Query 1816 RYEAIKKKCTVDRAPTQVVCARNMSSKSAMSIATKVAIQINCKLGGSPWTVDIPLPSLM 1995
          RYEAIKKKCTVDRA+PTQ V RNM+SKSAMSIATK+AIQINCKLGG+PW+V++PLP+LM
Sbjct 493 RYEAIKKKCTVDRAMPTQCVVGRNMTSKSAMSIATKIAIQINCKLGGAPWSVEVPLPTLM 552

Query 1996 VVGVDVCHDTRSKEKSFGAFVATLDKQMTQYYSIVNAHTSGEELSSHMGFNIA SAVKKFR 2175
          V+GYDVCHDTR+K+KSFGAFVATLDKQMT YYS VNAHTSGEELS+HMG NIA+AV+K+R
Sbjct 553 VIGYDVCHDTRAKDKSFGAFVATLDKQMTTHYYSTVNAHTSGEELSAHMGINIATAVRKYR 612

Query 2176 EKNGTYPARIFIYRDGVGDGQIPYVHSHEVAEIKKKLAEIYAGVEIKLAFIIVSKRINTR 2355
          E+N P RIFIYRDGVGDGQIPYVHSHEV EIKK+L +Y G +KLAFIIVSKRINTR
Sbjct 613 ERNNVLPGRIFIYRDGVGDGQIPYVHSHEVEEIKKQLETLYQGEVVKLAFIIVSKRINTR 672

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Query 2356 IFVQGRSGENPRPGTVIDDVVTLPERYDFYLVSNVREGTIAPTSYNVIEDTTGLNPDR 2535
          IFV RGRSG+NPRPGT+IDDV+TLPERYDFYLVSNVREGTIAPTSYNVI DTT L+PDR
Sbjct 673 IFVDRGRSGDNPRPGTIIDDVITLPERYDFYLVSNVREGTIAPTSYNVIYDTTSLHPDR 732

Query 2536 IQRLTYKLTHLYFNCSSQVRVPSVCQYAHKLAFLAANSLHNQPHYSLNETLYFL* 2700
          IQRLTYKLTH+YFN S VRVPSVCQYAHKLAFLAANSLHNQPHY+LNETLYFL*
Sbjct 733 IQRLTYKLTHMYFNNSCAVRVPSVCQYAHKLAFLAANSLHNQPHYTLNETLYFL* 787

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> ta_transcript44491_1
Length=234

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```

Score = 213 bits (543), Expect = 3e-62, Method: Compositional matrix adjust.
Identities = 98/233 (42%), Positives = 147/233 (63%), Gaps = 0/233 (0%)
Frame = +1

```

```

Query 1930 IQINCKLGGSPWTVDIPLPSLMVVGVDVCHDTRSKEKSFGAFVATLDKQMTQYYSIVNAH 2109
          +Q+NCKLGG+ W++ IP + M+VG D HD K +S +F+A+ ++ MTQ+YS
Sbjct 2 IQMNCKLGGTLWSIAIPFKTAMIVGIDSYHDAARKSRSVCSFIASYNQSMTQWYSRAIFQ 61

Query 2110 TSGEELSSHMGNFIASAVKKFREKNGTYPARIFIYRDGVGDGQIPYVHSHEVAEIKKKLA 2289
          G+E+ + + A+ + NG P R+ +YRDGVGDGQ+ + +E+ +++ +
Sbjct 62 ERGQEVVDGLKSLVDALTHYLRTNGKLPDRVIMYRDGVGDGQLNTIKQYEIPQMVCFCFS 121

Query 2290 EIYAGVEIKLAFIIVSKRINTRIFVQGRSGENPRPGTVIDDVVTLPERYDFYLVSNVR 2469
          + A + L +++V KRINTRIF++ ENP PGTVD +T + YDF + SQ V
Sbjct 122 LMEATYKPTLTYVVVVQKRINTRIFMKVQGGFENPHPGTVVDHDITRRDWYDFLIASQKVN 181

Query 2470 EGTIAPTSYNVIEDTTGLNPDRIQRLTYKLTHLYFNCSSQVRVPSVCQYAHKL 2628
          +GT+ PT Y V+ D + + D+ QRLTYKL HLY+N V RVP+ CQYAHKL
Sbjct 182 QGTVTPTHYVVVHDDSAMTADQCRLTYKLCHLYYNWPGTVRVPAPCQYAHKL 234

```

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*****
*****
Query= gi|665409862|ref|NM_139559.4| Drosophila melanogaster armitage (armi), transcript variant
D, mRNA

```

```
Length=4151
```

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript31548_1	67.4	2e-10
ta_transcript31554_1	52.8	6e-07
ta_transcript55901_1	43.9	0.003
ta_transcript55900_1	43.9	0.004
ta_transcript31550_1	40.0	0.033

```

> ta_transcript31548_1
Length=534

```

```

Score = 67.4 bits (163), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 69/248 (28%), Positives = 115/248 (46%), Gaps = 42/248 (17%)
Frame = +1

```

```

Query 2020 TSERRQEMIKAEQHYSF-LTEPLSIKTYMHRFRLLHLEEIECFVNFRNYDRDRAHFLR 2196
          S++ QE+ K I+ ++ +TE + Y+ F LL EE +N +NY+ +R
Sbjct 307 ASKQEQLTKDIKDIFAVGVTE----ENYVRFHNLWYEETIVRINLKNYNMSSVPLVR 362

Query 2197 DGE-FLT-----LQIENLAERRPSLVIGDTLRVINPWSDPDSQTTKSYEGI 2331
          + F+T L + LAE+RPSL++GD L + P YE I
Sbjct 363 RVDAFVTVPGTVKKGTSYSYALVVPGLAEKRPSMLGDLL----FVKPVESDEVMYEAI 417

Query 2332 IHKVLFDRIILK-FHSSFQEKYN-GEDYRL--FYFSRYSFRKQHHAIKIV-GVMGEDF 2496
          I ++ + + LK FH F++ + G + R + F+ SR + H A+ V G +
Sbjct 418 ITEMEDNVVNLKGFHPEFEKHFKPGHEQRFVDFRFFMSRMLERMHRAVQAAGVQSSEQRR 477

Query 2497 LFPSKVTKRENPLQDVMKDDMYLYDSKLEWYNQSLNSIQKRAVFNILRGEAENIPYVL 2676
          +EP+ + +P ++ +L+ E Q+ AV +I+ G A PY+L
Sbjct 478 VFPAASS---DPPAQYQVQSFFNHLVEENPE-----QRSABEHIVGGTAGAAPYLL 525

Query 2677 FGPPGSGK 2700
          GPPG+GK
Sbjct 526 HGPPGTGK 533

```

```

> ta_transcript31554_1
Length=123

Score = 52.8 bits (125), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 29/78 (37%), Positives = 43/78 (55%), Gaps = 9/78 (12%)
Frame = +1

Query 3754 QERDIILISTVRSSEEILRMDARFSLGfVRCskRLNVAVSRARAMMIIFGNPHLLAVDEC 3933
          +E+ +I+ISTVRS + +GF+ +R NVA++RA+A I+ GNP L D
Sbjct 1 KEKRVIIISTVRGAQ-----MGFLVDDQRFNVALTRAKAKAIVIGNPLCLQRD LK 51

Query 3934 WRQLILFCVKNNAYFGCD 3987
          WR + C +Y G D
Sbjct 52 WRAYMQLCRAYGSYCGHD 69

> ta_transcript55901_1
Length=1263

Score = 43.9 bits (102), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 39/114 (34%), Positives = 51/114 (45%), Gaps = 0/114 (0%)
Frame = -1

Query 3986 SQPK*ALFLTQNRISWRQHSSTARRWGfPKMIIMARARETATLSRLLQRTNPKEKRASMR 3807
          S PK* + + R S R FP +I +A AR +ATL+ L P AS
Sbjct 328 SWPK*QVLSLHKSM*HRHFLSLMRHAAFPPIIISLALARVSATLNLSSSTRKPSLYLAS*S 387

Query 3806 RISSDERTVDISIMSRSCP*NSSTDPIFGMTTSVPMNILRSIFTCF**GVIPI 3645
          RTVD + S P N ST P S +N R ++TC *G +IP+
Sbjct 388 SRRQLARTVDTRMTLFSLPWNDSVPTSTALYSFCVNQSRILYTCLR*GDMIPM 441

Score = 35.8 bits (81), Expect = 1.0, Method: Compositional matrix adjust.
Identities = 66/219 (30%), Positives = 89/219 (41%), Gaps = 27/219 (12%)
Frame = -1

Query 3257 SRKDMENPIFEAIRLVTIDCSWRGSPERTT*ERFFVSITMG TIVSGSVH*PASS----- 3096
          SR D+ +P+F A R + S GSPE T+ MGT +GS ASS
Sbjct 554 SRSDIPSPLFAASREMHTGPSCLGSPSTSCPVGASRPLMGTSTAGSSACAASSMNRCVM 613

Query 3095 NST*VKWPAGNPCKKFPKVQVEMVMR*VPINLA*QRSFNPDsvTIILS-SQLPTAPTS 2919
          +S + W +P + KVV R+ S+ I L S+ T
Sbjct 614 DSLNLNLWLESDPYLAECskVVT-----IRNMERSLCLDKVSRFAPFDTG 660

Query 2918 LVAQ*LIISGGIKSFST*LYETRRMKSPFWSKALLSM-SLFVTKSAELFDGVPTKIRAPGR 2742
          I SGG+ S RRM LL S+ SA + + V T R G
Sbjct 661 -----ISSGGMILHSRfSELAARMNLLILSCLLYFSSISAMWSAAMLESVHTSTRFFGF 714

Query 2741 FLTNWSSVSISVIVFPLPGGPNST*GMFSASPRsILKTA 2625
          T + S +VIV P+PGGPn+ *G+ +I TA
Sbjct 715 IATICTIASTTVIVLPVPGGPNTM*GLLPDVLETICSTA 753

> ta_transcript55900_1
Length=1269

Score = 43.9 bits (102), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 39/114 (34%), Positives = 51/114 (45%), Gaps = 0/114 (0%)
Frame = -1

Query 3986 SQPK*ALFLTQNRISWRQHSSTARRWGfPKMIIMARARETATLSRLLQRTNPKEKRASMR 3807
          S PK* + + R S R FP +I +A AR +ATL+ L P AS
Sbjct 328 SWPK*QVLSLHKSM*HRHFLSLMRHAAFPPIIISLALARVSATLNLSSSTRKPSLYLAS*S 387

Query 3806 RISSDERTVDISIMSRSCP*NSSTDPIFGMTTSVPMNILRSIFTCF**GVIPI 3645
          RTVD + S P N ST P S +N R ++TC *G +IP+
Sbjct 388 SRRQLARTVDTRMTLFSLPWNDSVPTSTALYSFCVNQSRILYTCLR*GDMIPM 441

Score = 35.8 bits (81), Expect = 1.1, Method: Compositional matrix adjust.
Identities = 66/219 (30%), Positives = 89/219 (41%), Gaps = 27/219 (12%)
Frame = -1

Query 3257 SRKDMENPIFEAIRLVTIDCSWRGSPERTT*ERFFVSITMG TIVSGSVH*PASS----- 3096
          SR D+ +P+F A R + S GSPE T+ MGT +GS ASS
Sbjct 554 SRSDIPSPLFAASREMHTGPSCLGSPSTSCPVGASRPLMGTSTAGSSACAASSMNRCVM 613

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Query 3095 NST*VKWPAGNPCKKFKVQVEMVMR*VPINLA*QRSFNPDSVTIILS-SQLPTAPTS 2919
Sbjct 614 +S + W +P + KVV R+ S+ I L S+ T
DSLNLNLWLESDPYLAECCKVVT-----IRNMERSLCLDLKVSRAFAPFDTG 660

Query 2918 LVAQ*LIISGGIKSFST*LYETRRMKSPWSKALLSM-SLFVTKSAELFDGVPTKIRAPGR 2742
Sbjct 661 I SGG+ S RRM LL S+ SA + + V T R G
-----ISSGGMILHSRFSSELARRMNLILSCLLYFSSISAMWSAAMLESVHTSTRFFGF 714

Query 2741 FLTNWSSVSISVIVFPLPGGPNST*GMFSASPRILKTA 2625
Sbjct 715 T + S +VIV P+PGGPN+ *G+ +I TA
IATICITIASTTVIVLPVPGGPNM*GLLPDVLETICSTA 753

> ta_transcript31550_1
Length=295

Score = 40.0 bits (92), Expect = 0.033, Method: Compositional matrix adjust.
Identities = 50/211 (24%), Positives = 96/211 (45%), Gaps = 32/211 (15%)
Frame = +1

Query 2095 KTYMHRERLLHLEEIECFVNFNRYDRDRAHF---LRDGEFLTQIENLAERRPSLVIGD 2265
Sbjct 107 + Y+ F LL EE ++ YD L+ + L + NL + SL G+
ENYVRPFHNLWYEETTVNIDMMKYDMYNVSLQQNLQQADCYVLVVPNLDQL--SLKRG 164

Query 2266 TL----RVINPWSDPDSQTTKSYEGIIHKVLFDRILLKFHSSFQEKYNGEDYRLEFYFSR 2433
Sbjct 165 + RV W + ++ T + + ++ +L + ++ +S K++ +EF +SR
KVNVRPRVSEAWFE--ARITATDKDVSLLLPYQQFRQYSNSHNMKFD-----VEFMWSR 217

Query 2434 YSFRKQHHAISKIVGVMGEDFLFSPKVTKRENPLDVYMKDDDMYLYDSKLEWYNQSL-- 2607
Sbjct 218 + H A++ + + +FP LD + + Y+ + ++N+ +
TCLERMHCAVAAMQHLSNRTRVFPV-----LDCSV----IAPYNIQ-KYFNKLIKE 263

Query 2608 NSIQKRAVFNLIRGEAENIPYVLFPGPPGSGK 2700
Sbjct 264 N Q+ AV +I+ G A PY+L GPPG+GK
NPEQRSAVEHIVGGTAGAAPYLLHGPPGTGK 294
*****
*****
Query= gi|665394979|ref|NM_079764.3| Drosophila melanogaster abnormal spindle (asp), mRNA

Length=6338

Sequences producing significant alignments:

ta_transcript82361_1 495 2e-141

> ta_transcript82361_1
Length=2641

Score = 495 bits (1274), Expect = 2e-141, Method: Compositional matrix adjust.
Identities = 278/705 (39%), Positives = 444/705 (63%), Gaps = 47/705 (7%)
Frame = +1

Query 1984 FAATTTIDPFLASTMYLDEQAVDRHQADFKKWLNALVSIPADLDADLNNKIDVGKLFNEV 2163
Sbjct 682 ++ ++T+DPFL+ + + DE AV + + +FK+WLN +++ PADL++++ KIDVGK + E
YSQSSTVDPFLLSISYFYDEAAVHKFEFEFKRWLNLYILTPPADLESNIEQKIDVGKAWLEN 741

Query 2164 RNKELVVAPTKEEQSMNYLTKYRLETLRKAARELVFFSEQMRLPCSKVAVYVKNQALRIRS 2343
Sbjct 742 RNKE+ VAPTKE+ Y RLE+LRK+A L S +M K+ + + K+ + IRS
RNKEVPVAPTKEQVCSAYHNSRRLESIRKSARALLMSPEMAQVFQKLNLIQIEKKLIAIRS 801

Query 2344 DRNLHLDVVMQRTILELLLCFNPLWLRGLGVFGEKIQMQSNRDIVGLSTFILNRLFRN 2523
Sbjct 802 DRNLHLDV +Q+ I+ELLL +NPLWLR+GLE ++G + ++SN DI GL+TFI+ R+F+N
DRNLHLDVGLQKIIMELLLSYNPLWLRIGLEAIYGTVLPLKNSDIDGLTTFFIIQRMFKN 861

Query 2524 KCEEQRYSKAYT---LTEEYAEITIKHSLQKilflllflDQAKQKRIVKHNPCLFVKKSP 2694
Sbjct 862 + ++SK+ L Y E IKK +L+K L+ FLDQAKQK+++ H+PCLF + +
PHLKNKHSKSSAPNMLLPAYMEAIAKFTLKKFFMLVFFLDQAKQKKLISHDPCLCRNAV 921

Query 2695 HKETKDILLRFSSELLANIGDITRELRRLGYVLQHRQTFLDEFDYAFNNLAVDLRDGVRL 2874
Sbjct 922 KE+++I++RF+ EL+A IGDIT+ LR +GYV+ H+Q++LDE+ YA N+A+D+RDGVR+
CKESREIIIRFTRELIAGIGDITKHLRPIGYVVSQSYLDEYKYAVQNIALDIRDGVRI 981

Query 2875 TRVMEVILLRDDLTRQLRVPAPISRLQRFNVKLALGALGEANFQLGGDIAAQDIVDGHRE 3054
Sbjct 982 T+VME+ILL++ L QLR PAISRLQ+I NV++AL AL EANF + GDI AQDI DGHRE
TKVMEIILLKNGLLTQLRTPAPISRLQKIHNVQVALNALKEANFSIVGDITAQDIADGHRE 1041

Query 3055 KTLSSLWQLIYKFRSPKFHAAATVLQKWWRRHHLHVVIQRRIRHKELMRRHRAATVIQAV 3234

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Sbjct 1042 KTLSSLWQLI+ R+P F AA V+Q WWR+ + +V +R+ K + + AA+VIQ 1101
 KTLSSLWQLIHVLRAPLFEKAANVIQMWWRKKYEVIVEKRKEEEKLRQKLNTAASVIQCW
 Query 3235 FRGHQMRKYVKLFKTERTOAAIILQKFTRRYLAQKQLYQSYHSIITIQRWWRAQQLGRQH 3414
 +R Q + V+ + A +++QK+ R +L + +L + S+ I+ W+++
 Sbjct 1102 WRRIQYNRLVEWQMKQIVTATVVIQKYCRMWLCRTRLMRQKRSVRKIEEWYKS----- 1154
 Query 3415 RQRFVELREAAIFLQRIWrrrlfakllaaaetarlQRSQKQAAASYIQMQRWSYQLGR 3594
 + +R A + L+ + R QR + +Q +A+ +Q SY
 Sbjct 1155 ---VIMMRNAKVTLEAL-----RKQREELQRSATTLO---SYVRRW 1190
 Query 3595 IQRQQFLRQDLIMFVQRRMRSKWSMLEQRKEFQQLKRAAINIQQRWRAKLSMRKCNADY 3774
 + +++ + I+ +Q +R RK + Q K++ IQ+ ++ KL MR+ +
 Sbjct 1191 LCMKEYSWKVRKIVLIQSLVR---CFLVRKHYIQYKKSVTYIQRLYKGKLVLMREEMKKF 1246
 Query 3775 LALRSSVLKVQAYRKATIOMRIDRNHYSLRKNVICLQQLRAIMKMREQRENYLRLRNA 3954
 R++ + +Q+Y K M R + L+ V +++R A++KMR + + YLRL+ +
 Sbjct 1247 AEARNAAITIQSYK---MFKQRKQFDELKNAVKTIEERYIALLMRNEMKQYLRLKQS 1302
 Query 3955 SILVQKRYMRQMMIQDRNAYLRTKCIINVQRRW-RATLQMRRE 4086
 ++ +Q ++R I+ R YL R I+ +Q++ R+++ RE
 Sbjct 1303 TVRIQSQRW---GIECRKEYLNKRNMIVKLQKKSPRSSVNEERE 1343

Score = 62.8 bits (151), Expect = 1e-08, Method: Compositional matrix adjust.
 Identities = 56/210 (27%), Positives = 108/210 (51%), Gaps = 21/210 (10%)
 Frame = +1

Query 4192 KVTLLVVQKRRRALLQMRKERQEYLHLREVTIK-LQRRFHAQKSMRFMRKYRGTQAAVSC 4368
 K +++ + L +RK+R+E T++ RR+ K + K Q+ V C
 Sbjct 1153 KSVIMMRNAKVTLEALRKQREELQRSATTLOSYVRRWLCMKEYSWKVRKIVLIQSLVRC 1212
 Query 4369 LQMHWNRHLLRKRERNSFLQLRQAAITLQRRYARLNMILKLSYAQLKQAAITIQTRYR 4548
 L+RK ++Q +++ +QR Y+ +L M +++K +A+ + AAITIQ+ Y+
 Sbjct 1213 F-----LVRKH---YIQYKKSVTYIQRLYKGKLVLMREEMKKFAEARNAAITIQSYK 1261
 Query 4549 AKKAMQKQVVLVYQKQREAIKQRRYRGNLEMRKQIEVYQKQRAVIRLQKWWRSIRDNR 4728
 M KQ + + + A+ ++ RY L+MR +++ Y + +Q+ +R+Q WR I
 Sbjct 1262 ---MFKQRKQFDELKNAVKTIEERYIALLMRNEMKQYLRLKQSTVRIQSQRWGIE--- 1314
 Query 4729 LCKAGYrrirlsslsiQRKW-RATVQARRQ 4815
 C+ Y R + +Q+K R++V R+
 Sbjct 1315 -CRKEYLNKRNMIVKLQKKSPRSSVNEERE 1343

Score = 60.8 bits (146), Expect = 4e-08, Method: Compositional matrix adjust.
 Identities = 69/267 (26%), Positives = 117/267 (44%), Gaps = 51/267 (19%)
 Frame = +1

Query 3532 QKQQAASYYIQMQRWSYQLGRIQRQQFLRQDLIMFVQRRMRSKWSMLEQRKEFQQLKRA 3711
 QK AAS IQ WR Q R+ +W M +Q+ A
 Sbjct 1089 QKLNTAASVIQCWRRIQYNRL-----VEWQM-----KQIVTA 1121
 Query 3712 AINIQRWRRAKLSMRKCNADYLALRSSVLKVQAYRKATIOMRIDRNHYSLRK----- 3870
 + IQ+ R M C + + SV K++ + K+ I MR + +LRK
 Sbjct 1122 TVVIQKYCR---MWLCRTRLMRQKRSVRKIEEWYKSVIMMRNAKVTLEALRKQREELRQ 1177
 Query 3871 -NVICLQQLRAIMKMREQRENYLRLRNASILVQKRYMRQMMIQDRNAYLRTKCIINV 4047
 + LQ +R + M+E ++ +L+Q R R Y++ +K + +
 Sbjct 1178 RSATTLOSYVRRWLCMKEYSWKVRKI---VLIQSLVRC---FLVRKHYIQYKKSVTYI 1229
 Query 4048 QRRWRATLQMRERKNYLHLQTTTKRIQIKFRAKREMKKQRAEFLQLKKVTLVVQKRRRA 4227
 QR ++ L MR E K + + IQ ++ M QR +F +LK +++R A
 Sbjct 1230 QRLYKGKLVLMREEMKKFAEARNAAITIQSYK---MFKQRKQFDELKNAVKTIEERYIA 1285
 Query 4228 LLQMRKERQEYLHLREVTIKLQRRFHA 4308
 LL+MR E ++YL L++ T+++Q ++
 Sbjct 1286 LLKMRNEMKQYLRLKQSTVRIQSQRWG 1312

Score = 55.1 bits (131), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 40/145 (28%), Positives = 72/145 (50%), Gaps = 11/145 (8%)
 Frame = +1

Query 202 FEITVTPSRLKQKKRAE-----GREPAVVVMAPFSAKAIVQFEDVPITKTARRQVRVL 360
 FEI TP +++ +R E E +++APFS V FE+V + T R++ V
 Sbjct 53 FEIENTPEHIRRARRTEVVPKKSPEKECPRLILAPFSRPPQVVFENVLLGTTTCERELEV 112

```

Query 361 NPSDDDIIEVKMKAIREEHNL--EWMEHTVTPARDEVSMELVWSPVLEVACKETLQLID 534
          NPS  ++ + KA+   + L  EW+   +   + ++W+P   A +E+++ +
Sbjct 113 NPSKQVQITLKGALPPGLIIQLPGEWL--VLEPETCYCLTMMWTPTQPTALRESIRFTN 170

Query 535 NRNFRKEVMIILKSKSNQPVKNPRK 609
          + R +V+++LKS N  KN K
Sbjct 171 EQRGRYDVIVVLKSTVNLKGKNQAK 195

```

Score = 50.4 bits (119), Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 86/369 (23%), Positives = 155/369 (42%), Gaps = 87/369 (24%)
 Frame = +1

```

Query 4618 RRYRGNLEMRKQIE-VYQKQRQAVIRLQKWWRSIRDMLCKAGYrrirlsslsIQ---RK 4785
          ++Y  +E RK+ E + QK  A  +Q WWR I+  RL +  ++I  +++ IQ  R
Sbjct 1072 KKYEVIVEKRKEEEKLRQKLNTAASVIQCWWRRRIQYNRLVEWQMKQIVTATVVIQKYCRM 1131

Query 4786 WRATVQARRQREIFLSTIRKVRMLQAFIRATLLMRQQRREFE-----MKRRAAVVIQ 4941
          W  +  RQ+   R VR ++ + ++ ++MR  +  E  +++R+A  +Q
Sbjct 1132 WLCRTRLRMQK-----RSVRKIEEWYKSVIMMRNAKVTLALRKQREELRQRSATTLQ 1184

Query 4942 RRFRARCAMLKARQDYQLIQSSVILVQRKFRANRSMKQARQEFVQLRTIAPHVHLQKFRGK 5121
          R  M  ++Y  ++L+Q  R  R+ ++Q +  ++Q+ ++GK
Sbjct 1185 SYVRRWLCM----KEYSWKVRKIVLIQSLVRC---FLVRKHYIQYKKSVTYIQRLYKKG 1236

Query 5122 RLMIEQRNCFQLLRCSMPGFQARARGFMARKRFQAL-----MTPPEMMDL 5253
          +M E+  F  R +  Q+ + F  RK+F  L  M  EM
Sbjct 1237 LVMREEMKKFAEARNAAITIQSYKMFQKQKQFDELKNAVKTIEERYIALLKMRNEMKQY 1296

Query 5254 IRQKRAAKVIQRYWRGYLIRRRQKHQGLLDIRKRIAQLRQEA--KAVNSVRCKVQEAVERF 5427
          +R K++  IQ  WRG  R+  L+ R  I +L++++  +VN  R
Sbjct 1297 LRLKQSTVRIQSQWRGIECRKE-----YLNKRNMIVKLQKKSPRSSVNEER----- 1342

Query 5428 LRGRFIASDA----LAVLSRL-----DRLSRTVPHLLMWC--SEFMS----- 5535
          GRF A +A  +A + ++  D+ S  P  + +C  + F  S
Sbjct 1343 -EGRFPAPAEAVYYHIAAICKVISSNEEDKTSLHTPGPVCYCHTASFPS*AIYENATSIVH 1401

Query 5536 ---TFCYGI 5553
          FCYG+
Sbjct 1402 STEDFCYGL 1410

```


Query= gi|562758882|gb|GABY01018532.1| TSA: Anthonomus grandis A_grandis_454_rep_c7409 mRNA
 sequence

Length=901

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript29552_1	32.3	1.6
ta_transcript39759_1	30.8	4.3
ta_transcript39756_1	30.8	5.1
ta_transcript39757_1	30.8	5.2
ta_transcript39758_1	30.8	5.4

> ta_transcript29552_1
 Length=722

Score = 32.3 bits (72), Expect = 1.6, Method: Compositional matrix adjust.
 Identities = 20/83 (24%), Positives = 33/83 (40%), Gaps = 0/83 (0%)
 Frame = +1

```

Query 208 DQGYADPCSPSFLSKQNHDLRLQIQSSNNPPEEEMLMTVQIVSYTDFDSDPDISGRDCIR 387
          + Y +P S  +RL  S++ P E M+  +  S  ++ R
Sbjct 470 SRWYTEPSSRPITPAPITSMRLGTDFSDSAPVESMICESSNVTPGNGVTSDPVAMRMFFV 529

Query 388 VPLRGPFNPLETKLFGCTIRGCP 456
          + +  PF+P  + L G TI  CP
Sbjct 530 LMVSTPFPSPCTSTLLGATIEPCP 552

```

> ta_transcript39759_1
 Length=585

Score = 30.8 bits (68), Expect = 4.3, Method: Compositional matrix adjust.
 Identities = 27/116 (23%), Positives = 50/116 (43%), Gaps = 3/116 (3%)
 Frame = +1

```
Query 64  PENINRLFQWTDNVVLYIEIYSVVNEVVELELYRSVQKDRSINRYL--LDQGYADPCSP 237
          P + + L + W      Y+ +  ++ +++ L++++ + S +RY+ L      PC P
Sbjct 144  PSSNSSLDRPWPFRRSSRYMSAWRSSSKALKIGLHKKNITESISSSSRYMGPLSSITLVPCDP 203

Query 238  SFLSKQNHDRLRLQIQSQNNPPEEEMLTVDQIVSYTDFDSDPDISGRDCIRVPLRGP 405
          LS +      I S+N      M T+ + + F      IS C R+ L GP
Sbjct 204  RLLSLLSTLAGHLISSSSN-NIVCMHTTLSHVKAILGFLRRRISDTCCFRIRLIGP 258
```

> ta_transcript39756_1
 Length=742

Score = 30.8 bits (68), Expect = 5.1, Method: Compositional matrix adjust.
 Identities = 27/116 (23%), Positives = 50/116 (43%), Gaps = 3/116 (3%)
 Frame = +1

```
Query 64  PENINRLFQWTDNVVLYIEIYSVVNEVVELELYRSVQKDRSINRYL--LDQGYADPCSP 237
          P + + L + W      Y+ +  ++ +++ L++++ + S +RY+ L      PC P
Sbjct 157  PSSNSSLDRPWPFRRSSRYMSAWRSSSKALKIGLHKKNITESISSSSRYMGPLSSITLVPCDP 216

Query 238  SFLSKQNHDRLRLQIQSQNNPPEEEMLTVDQIVSYTDFDSDPDISGRDCIRVPLRGP 405
          LS +      I S+N      M T+ + + F      IS C R+ L GP
Sbjct 217  RLLSLLSTLAGHLISSSSN-NIVCMHTTLSHVKAILGFLRRRISDTCCFRIRLIGP 271
```

> ta_transcript39757_1
 Length=729

Score = 30.8 bits (68), Expect = 5.2, Method: Compositional matrix adjust.
 Identities = 27/116 (23%), Positives = 50/116 (43%), Gaps = 3/116 (3%)
 Frame = +1

```
Query 64  PENINRLFQWTDNVVLYIEIYSVVNEVVELELYRSVQKDRSINRYL--LDQGYADPCSP 237
          P + + L + W      Y+ +  ++ +++ L++++ + S +RY+ L      PC P
Sbjct 144  PSSNSSLDRPWPFRRSSRYMSAWRSSSKALKIGLHKKNITESISSSSRYMGPLSSITLVPCDP 203

Query 238  SFLSKQNHDRLRLQIQSQNNPPEEEMLTVDQIVSYTDFDSDPDISGRDCIRVPLRGP 405
          LS +      I S+N      M T+ + + F      IS C R+ L GP
Sbjct 204  RLLSLLSTLAGHLISSSSN-NIVCMHTTLSHVKAILGFLRRRISDTCCFRIRLIGP 258
```

> ta_transcript39758_1
 Length=598

Score = 30.8 bits (68), Expect = 5.4, Method: Compositional matrix adjust.
 Identities = 27/116 (23%), Positives = 50/116 (43%), Gaps = 3/116 (3%)
 Frame = +1

```
Query 64  PENINRLFQWTDNVVLYIEIYSVVNEVVELELYRSVQKDRSINRYL--LDQGYADPCSP 237
          P + + L + W      Y+ +  ++ +++ L++++ + S +RY+ L      PC P
Sbjct 157  PSSNSSLDRPWPFRRSSRYMSAWRSSSKALKIGLHKKNITESISSSSRYMGPLSSITLVPCDP 216

Query 238  SFLSKQNHDRLRLQIQSQNNPPEEEMLTVDQIVSYTDFDSDPDISGRDCIRVPLRGP 405
          LS +      I S+N      M T+ + + F      IS C R+ L GP
Sbjct 217  RLLSLLSTLAGHLISSSSN-NIVCMHTTLSHVKAILGFLRRRISDTCCFRIRLIGP 271
```


Query= gi|665393316|ref|NM_169121.2| Drosophila melanogaster Rm62 (Rm62),transcript variant F,
 mRNA

Length=2833

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript16727_1	597	0.0
ta_transcript71371_1	190	7e-50
ta_transcript47090_1	189	1e-49
ta_transcript35263_1	190	1e-49
ta_transcript35262_1	190	1e-49
ta_transcript47089_1	188	2e-49

```

ta_transcript65883_1      185    3e-48
ta_transcript35264_1      146    4e-36
ta_transcript16729_1      133    5e-34
ta_transcript20008_1      136    9e-33
ta_transcript20007_1      135    2e-32

```

```

> ta_transcript16727_1
Length=587

```

```

Score = 597 bits (1539), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 284/431 (66%), Positives = 342/431 (79%), Gaps = 3/431 (1%)
Frame = +2

```

```

Query 644 DFSNLAPFFKKNFYQEHNPVANRSPYEVQRYREEQEITVRGQ-VPNPIQDFSEVHLPDYVM 820
          D + L PFKK FY HP+V NRS EV+ +R E +IT++G+ +P P F E PDYVM
Sbjct 116 DLNRLKPFKKFEFVPHPDVENRSESEVEAWRSENDITLKGRNIPKPTLTFDEAGFPDYVM 175

Query 821 KEIRRQGYKAPTAIQAQGWPIAMSGSNFVGIAKTGSGKTLGYILPAIVHINNQQPLQRGD 1000
          EI + G+ PT IQAQGWPIA+SG + VGIA TGSCKTL YILPAIVHIN+Q RGD
Sbjct 176 DEIDKMGFSKPTPIQAQGWPIALSGHDMVGIASTGSGKTLGYILPAIVHINHQPCKSSRGD 235

Query 1001 GPIALVLAPTRELAAQQIQVATEFGSSSYVRNTCVFGGAPKGGQMRDLQRCGEIIVATPG 1180
          GPIALVLAPTRELAAQQIQ+V +F ++S + NTC+FGGAPKG Q RDL G EIVATPG
Sbjct 236 GPIALVLAPTRELAAQQIQEVCDKFANTSKIHNCTCLFGGAPKGPQARDLDAGVEIIVATPG 295

Query 1181 RLIDFLSAGSTNLKRCTYLVLEADRMLDMGFEPQIRKIVSQIRPDRQTLMWSATWPKEV 1360
          RL+DFL +G TNLKR TYLVLEADRMLDMGFEPQIRKI+ QIRPDRQTLMWSATWP+EV
Sbjct 296 RLLDFLESGRTNLKRRTYLVLEADRMLDMGFEPQIRKIEQIRPDRQTLMWSATWPREV 355

Query 1361 KQLAEDFLGNYIQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLTLLSDIYDTSESPGKI 1540
          + LA +FL +Y+QIN+GSL+L+ANHNI Q++DVC E+ KE KL TLL +I +E K
Sbjct 356 QSLASEFLKDYLQINVGSLQLAANHNILQIIDVCMYEKETKLTLLKEIM--AEKENKT 413

Query 1541 IIFVETKRRVDNLVRFIRSFVRCGAIHGDKSQSERDFVLREFRSGKSNILVATDVAARG 1720
          IIF+ETKRRVD++ R ++ G IHGDKSQ+ERD+VL++FR+GK+ ILVATDVAARG
Sbjct 414 IIFIETKRRVDDITRKMKRDGWPAVCHGDKSQNERDWVLQDFRTGKAPILVATDVAARG 473

Query 1721 LDVDGIKYVINFDYPQNSEDIHRIGRTGRSNTKGTSAFFFTKNNAKQAKALVDVLREAN 1900
          LDVD +K+VINFDYP NSEDI+HRIGRTGR+N GT++ FFT +NA +A LV VL+EA
Sbjct 474 LDVDDVKFVINFDYPSNSEDYVHRIGRTGRNTKTGTAYTFFTPSNAAKAGDLVAVLKEAK 533

Query 1901 QEINPALENLA 1933
          Q +NP L+ LA
Sbjct 534 QVVNPKLQELA 544

```

```

> ta_transcript71371_1
Length=680

```

```

Score = 190 bits (482), Expect = 7e-50, Method: Compositional matrix adjust.
Identities = 121/408 (30%), Positives = 207/408 (51%), Gaps = 25/408 (6%)
Frame = +2

```

```

Query 719 EVQRYREEQEITVRG-QVPNPIQDFSEV----HLPDYVMKEIRRQGYKAPTAIQAQGWPI 883
          E R+R E I G VP + DFS++ + ++ + + GY PT +Q Q P
Sbjct 149 EQNRFRNEHGKAVGRHVPAALTDVSLVSRYSKYSTSLVDTVTQCQGYTEPTPVQRQALPC 208

Query 884 AMSGSNFVGIAKTGSGKTLGYILPAIVHINNQQPLQRGDGPIALVLAPTRELAAQQIQVA 1063
          + + A TGSCKT ++LP + + Q GP LVL PTRELA QI + A
Sbjct 209 MLEDRQILACAPTGSCKTAAFLPLMLHTLGAPQ-----GGPRGLVLCPTRELAHQIYREA 263

Query 1064 TEFSSSYVRNTCVFGGAPKGGQMRDLQ-RGCEIIVATPGRLIDFLSAGST--NLKRCTY 1234
          + + +R + + + R+ R +I+I TP RL L+ + +L + +
Sbjct 264 IRLSAGTELRVSVLRTVKESKVKEREATIRKSDILICTPNRLCYLLNQDNVGLSLDKVRW 323

Query 1235 LVLDEADRMLD-----MGFEPQIRKIVSQI-RPDRQTLMWSATWPKEVKQLAEDFLGNY 1393
          L++DEAD+M + F Q+ +I S R+ M+SAT V + +
Sbjct 324 LIIDEADKMFEGSSEEQSAFRQQLEQIFSSCSHKQRRVAMFSATHTPVAKWCRHHMRGL 383

Query 1394 IQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLTLLSDIYDTSESPGKIIIFVETKRRVD 1573
          I I +G +A + Q + C S+ KL + + P +++FV++K R
Sbjct 384 INITVGQRN-AATQLVEQELLYCG--SEAGKLVAFRQLVQQGLQPP--VLVFVQSKERAK 438

Query 1574 NLVRFIRSFVRCGAIHGDKSQSERDFVLREFRSGKSNILVATDVAARGLDVGDIKYVIN 1753
          L + + G+ AIH D++Q++RD V+R FR G+ +L+ T++ RG+D G+ V+N
Sbjct 439 QLFKELIYDGINVDIAHADRTQAQRDNVVRVFRVGRVWLICTELMGRGIDFRGVNLVVN 498

```

```

Query 1754 FDYPQNSEDIYHRIGRTGRSNTKGTSAFFFTKNNAKQAKALVDVLREA 1897
          +D+P ++ YIHR+GR GR+ KG + FFT+++ +++ V++++
Sbjct 499 YDFPPSAISYIHRVGRAGRAGQKGKAITFFFTQDDVANLRSIASVMKQS 546

```

```

> ta_transcript47090_1
Length=645

```

```

Score = 189 bits (479), Expect = 1e-49, Method: Compositional matrix adjust.
Identities = 110/338 (33%), Positives = 187/338 (55%), Gaps = 15/338 (4%)
Frame = +2

```

```

Query 815 VMKEIRRQGYKAPTAIQAQGWPIAMSGSNFVGIAKTGSGKTLGYILPAIVHINNQQPLQR 994
          ++ ++ G + P+ IQ + P + + VG AKTGSGKTL +++P + ++ N Q +
Sbjct 126 ILAALKTMGIEKPSRIQIETLPHLLQKQDLVGAAKTGSGKTLAFLIPIVNNLINLQ-FTK 184

Query 995 GDGPIALVLAPTRELAQQIQVATEFGSSSYVRNTCVFGGAPKGGQMRDLQRGCEIVIA 1174
          G ++L+PTRELA Q +V + ++ + + + GG K ++ L++GC IV++T
Sbjct 185 KHGTGCIIILSPRELALQTYEVLKLLANIDLTCSLIVGGEKKAKDLKSLKGCNIVVST 244

Query 1175 PGRLIDFL-SAGSTNLKRCTYLVLDEADRMLDMGFEPQIRKIVSQIRPDRQTLMW SATWP 1351
          PGRL+D L + N LV+DEAD++L+ GFE + I+ + DRQT+++SAT
Sbjct 245 PGRLLDHLQNTGEGFNCNNLKCLVVDKLEAGFEKHVTGIKLLPKDRQTVLFSATMD 304

Query 1352 KEVKQLAEDFL-GNYIQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLSDIYDTS 1528
          +VK LA+ L N + I I S ++Q +C E+++ L + + +
Sbjct 305 DKVKNLAKLALRSNPVTIAIRDNVQSTVEGLQQGYIIC---PVEKRIAWLYKMLKKSRL 361

Query 1529 PGKIIIFVETKRRVDNLVRFIRSFVGRCA----IHGDKSQSERDFVLEFRSGKSNILV 1696
          K+++F + + VD F R V C A IHG ++Q R F + ++ L
Sbjct 362 --KVMVFSSKSVDFHYEFFR---VHCKANVTSIHGKQTQPRRKEAYHSFTNAENGALF 416

Query 1697 ATDVAARGLDVGDIKYVINFDYPQNSEDIYHRIGRTGR 1810
          TD+AARGLD+ + +++ +D P + ++YIHR+GRT R
Sbjct 417 CTDIAARGLDIPCDWIVQYDPPTDPKEYIHRVGRTAR 454

```

```

> ta_transcript35263_1
Length=752

```

```

Score = 190 bits (482), Expect = 1e-49, Method: Compositional matrix adjust.
Identities = 106/227 (47%), Positives = 150/227 (66%), Gaps = 9/227 (4%)
Frame = +2

```

```

Query 1253 DRMLDMGFEPQIRKIV-SQIRP---DRQTLMW SATWPKEVKQLAEDFLGNYIQINIGSLE 1420
          +RMLDMGFEPQIRKIV P +RQTLM+SAT+PK+++ LA+DFL NY+ + +G +
Sbjct 1 ERMLDMGFEPQIRKIVECHTMPKTGERQTLMF SATFPKQIQVLAQDFLSNYVFLAVGRVG 60

Query 1421 LSAHNHNRQVVDVCDEFSKEEKLKTL--SDIYDTS--ESPGKIIIFVETKRRVDNLVRF 1588
          S + NI Q V +E K L LL S++ S E ++FVETK+ D L +
Sbjct 61 -STSENITQKVWVVEESQKRSFLLDLNANLLQRSRPEEDQLTLVFVETKKGADQLEEY 119

Query 1589 IRSFGVRCGAIHGDKSQSERDFVLEFRSGKSNILVATDVAARGLDVGDIKYVINFDYPQ 1768
          + + G +IHGD++Q ER+ LR FR+G++ ILVAT VAARGLD+ +++VINFD P
Sbjct 120 LDTEGPVTSIHGDRQREEREARLRRFRTGQTPILVATAVAARGLDIPHVRHVINFDLPS 179

Query 1769 NSEDIYHRIGRTGRSNTKGTSAFFFTKNNAKQAKALVDVLREANQEI 1909
          + E+Y+HRIGRTGR G + +FF NN ++ LV++L EA Q++
Sbjct 180 DVEEYVHRIGRTGRMGNLGVATSFNDNNRGLSRDLVELLVEAKQDV 226

```

```

> ta_transcript35262_1
Length=758

```

```

Score = 190 bits (482), Expect = 1e-49, Method: Compositional matrix adjust.
Identities = 108/235 (46%), Positives = 152/235 (65%), Gaps = 9/235 (4%)
Frame = +2

```

```

Query 1253 DRMLDMGFEPQIRKIV-SQIRP---DRQTLMW SATWPKEVKQLAEDFLGNYIQINIGSLE 1420
          +RMLDMGFEPQIRKIV P +RQTLM+SAT+PK+++ LA+DFL NY+ + +G +
Sbjct 1 ERMLDMGFEPQIRKIVECHTMPKTGERQTLMF SATFPKQIQVLAQDFLSNYVFLAVGRVG 60

Query 1421 LSAHNHNRQVVDVCDEFSKEEKLKTL--SDIYDTS--ESPGKIIIFVETKRRVDNLVRF 1588
          S + NI Q V +E K L LL S++ S E ++FVETK+ D L +
Sbjct 61 -STSENITQKVWVVEESQKRSFLLDLNANLLQRSRPEEDQLTLVFVETKKGADQLEEY 119

Query 1589 IRSFGVRCGAIHGDKSQSERDFVLEFRSGKSNILVATDVAARGLDVGDIKYVINFDYPQ 1768

```

```

Sbjct 120      + + G      +IHGD++Q ER+  LR FR+G++ ILVAT VAARGLD+  +++VINFD P
LDTEGYPVTSIHGDRTQREEREALRRFRTGQTPILVATAVAARGLDIPHVRHVINFDLPS 179

Query 1769  NSEDIYHRIGRTGRSNTKGTSAFAFFTNNNAKQAKALVDVLRANQEIINPALENLA 1933
+ E+Y+HRIGRTGR      G + +FF NN  ++ LV++L EA Q++  L  A
Sbjct 180  DVEEYVHRIGRTGRMGNLGVATSFNDNNRGLSRDLVELLVEAKQDVPNWLTTETA 234

> ta_transcript47089_1
Length=648

Score = 188 bits (478), Expect = 2e-49, Method: Compositional matrix adjust.
Identities = 119/369 (32%), Positives = 193/369 (52%), Gaps = 20/369 (5%)
Frame = +2

Query 815  VMKEIRRQGYKAPTAIQAQGWPIAMSGSNFVGIAGTSGSKTLGYILPAIVHINNQQPLQR 994
++ ++ G + P+ IQ + P + + VG AKTSGSKTL +++P + ++ N Q +
Sbjct 126  ILAALKTMGIEKPSRIQIETLPHLLQQKDLVGAAKTSGSKTLAFLIPIVNNLINLQ-FTK 184

Query 995  GDGPIALVLAPTRELAQQIQQVATEFGSSSYVRNTCVFGGAPKGGQMRDLQRCGEIVAT 1174
G ++L+PTRELA Q +V + ++ + + + GG K ++ L++GC IV++T
Sbjct 185  KHGTGCIILSPTRELAIQTYEVLKLLANIDLTCSLIVGGEKKAKDLKSLKKGCNIVVST 244

Query 1175  PGRLIDFL-SAGSTNLKRCTYLVLDEADRMLDMGFEPQIRKIVSQIRPDRQTLMW SATWP 1351
PGRL+D L + N LV+DEAD++L+ GFE + I+ + DRQT+++SAT
Sbjct 245  PGRLLDHLQNTTEGFNCNNLKCLVVDDEADKLLGAEKHEKVTGIKLLPKDRQTVLFSATMD 304

Query 1352  KEVKQLAEDFL-GNYIQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLSDIYDTSES 1528
+VK LA+ L N + I I S ++Q +C EK L + S
Sbjct 305  DKVKNLAKLALRSNPVTIAIRDNVQSTVEGLQQGYIICPV----EKRIAWLYKMLKKS RK 360

Query 1529  PGKIIIFVETKRRVDNLVRFIRSFVRCGA----IHGDKSQSERDFVLRFRSGKSNILV 1696
K+++F + + VD F R V C A IHG ++Q R F + ++ L
Sbjct 361  L-KVMVFSSCKSVDFHYEFFR---VHCKANVTSIHGKQTQPRRKEAYHSFTNAENGALF 416

Query 1697  ATDVAARGLDVGDIKYVINFDYPQNSEDIYHRIGRTGRS-NTKGTSAFAFFTNNNAKQAKA 1873
TD+AARGLD+ + +++ +D P + ++YIHR+GRT R N G + K
Sbjct 417  CTDIAARGLDIPCDWIVQYDPPDTPKEYIHRVGRGTARGLNNTGNNAVILLRPEEDK---- 472

Query 1874  LVDVLRAN 1900
V+ LR N
Sbjct 473  FVEFLRNEN 481

> ta_transcript65883_1
Length=668

Score = 185 bits (469), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 111/344 (32%), Positives = 189/344 (55%), Gaps = 12/344 (3%)
Frame = +2

Query 827  IRRQGYKAPTAIQAQGWPIAMSGSNFVGIAGTSGSKTLGYILPAIVHINNQQPLQRGDGP 1006
I+ G+ T IQ++ P + G + VG A+TGSGKTL +++PA+ I + R +G
Sbjct 165  IKDMGFTTMTETQSKAIPPLLEGRDLVGAARTSGSKTLAFLIPAVELIYKLFKFKPR-NGT 223

Query 1007  IALVLAPTRELAQQIQQVATEFGSSSYVRNTCVFGGAPKGGQMRDLQRCGEIVATPGRL 1186
++L+PTREL+ Q V E + V GGA + + + L +G I++ATPGRL
Sbjct 224  GVIIILSPTRELSMQTFGVLMELMKYHHHTYGLVMGGANRSTEAQKLSKGINILVATPGRL 283

Query 1187  IDFLSAGSTNL-KRCTYLVLDEADRMLDMGFEPQIRKIVSQIRPDRQTLMW SATWPKEVK 1363
+D L L K LV+DEADR+L++GFE ++++I+ + RQT+M+SAT K+++
Sbjct 284  LDHLQNTPDFLYKNLQCLVIDEADRILEIGFEEVKQIIKLLPKRRQTMMFSATQTKKIE 343

Query 1364  QLAEDFLGN---YIQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLSDIYDTSESPG 1534
L + + Y+ ++ E + ++ Q VC E++ L + + +
Sbjct 344  ALTALAVKHPEVYVGVD-DHREQATVDSLEQGYIVC---PSEKRFLVLFTFLKKNRKK-- 397

Query 1535  KIIIFVETKRRVDNLVRFIRSFVRCGAIHGDKSQSERDFVLRFRSGKSNILVATDVAA 1714
K+++F+ T V + + +IHG + QS+R +F + ++ IL+ TDVAA
Sbjct 398  KVMVFLSTCMVSKYHHELLNYIDLPMVSIHGKQQSKRTTTFQFCNAETGILLCTDVAA 457

Query 1715  RGLDVGDIKYVINFDYPQNSEDIYHRIGRTGRS-NTKGTSAFAFF 1843
RGLD+ + +++ +D P + ++YIHR+GRT R T G + F
Sbjct 458  RGLDIPAVDWIVQYDPPDDPKEYIHRVGRGTARGLTSGHALLFL 501

> ta_transcript35264_1

```

Length=511

Score = 146 bits (368), Expect = 4e-36, Method: Compositional matrix adjust.
Identities = 75/178 (42%), Positives = 106/178 (60%), Gaps = 7/178 (4%)
Frame = +2

```
Query 764 QVPNPIQDFSEVHLPDYVMKEIRRQGYKAPTAIQAGWPIAMSGSNFVGIAGTSGSKTLG 943
          +VP+ I F +V+L + + + I Y PT +Q PI + + + A+TGSGKT
Sbjct 334 RVPDFITTSFEDVNLTEIMRQNIASARYDKPTPVQKYAIPIVLGHDRVMACAQ+TGSGKTAA 393

Query 944 YILPAIVHINNQQPLQ-----RGDGPIALVLAPTRELAQQIQQVATEFGSSSYVRNTC 1102
          +++P + + P++ R P+ LVLAPTRELA QI A +F S VR
Sbjct 394 FLVPILNQMYEAGPVKHMGPYNRRKQYPLGLVLAPTRELATQIFDEARKFAYRSRVRPCV 453

Query 1103 VFGGAPKGGQMRDLQRGCEIVIATPGRLIDFLSAGSTNLKRCTYLVLDEADRMLDMGF 1276
          V+GG+P Q R+L+RGC +++ATPGRL+D L+ G L C +LVLDEADRMLDMG
Sbjct 454 VYGGSPIHEQFRELERGCHLLVATPGRLVDMLARGRVALDHCRHLVLDEADRMLDMGL 511
```

> ta_transcript16729_1
Length=198

Score = 133 bits (334), Expect = 5e-34, Method: Compositional matrix adjust.
Identities = 61/89 (69%), Positives = 74/89 (83%), Gaps = 0/89 (0%)
Frame = +2

```
Query 1667 FRSGKSNILVATDVAARGLDVGDIKYVINFDYPQNSEDIHHRIGRTGRSNTKGTSFAFFT 1846
          FR+GK+ ILVATDVAARGLDVD +K+VINFDYP NSEDY+HHRIGRTGR+N GT++ FFT
Sbjct 67 FRTGKAPILVATDVAARGLDVDVVKFVINFDYPSNSEDYVHRIGRTGR+TKGTAYTFFT 126

Query 1847 KNNAKQAKALVDVLREANQEINPALENLA 1933
          +NA +A LV VL+EA Q +NP L+ LA
Sbjct 127 PSNAAKAGDLVAVLKEAKQVVNPKLQELA 155
```

> ta_transcript20008_1
Length=567

Score = 136 bits (343), Expect = 9e-33, Method: Compositional matrix adjust.
Identities = 73/200 (37%), Positives = 121/200 (61%), Gaps = 7/200 (4%)
Frame = +2

```
Query 1328 LMWSATWPKEVKQLAEDFLGNYIQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLTSLD 1507
          LM+SAT+P++++ LA FL NY+ + +G + A+ ++ Q+ +F K+ LK L+ +
Sbjct 1 LMFSATFPEDIQHLAFLHNYLFVAVGIVG-GASTDVEQIFLQVAKFDKQNALKQLIEE 59

Query 1508 IYDTSESPGKIIIFVETKRRVDNLVRFIRSFVRCGAIHGDKSQSERDFVLREFRSGKSN 1687
          +I+++FVETKR D + + + +IHGD+ Q ER+ L F++G
Sbjct 60 -----NEKKRILVFVETKRNADFIASILSEQQLTSSIHGDRMQREREALHNFKTGHH 114

Query 1688 ILVATDVAARGLDVGDIKYVINFDYPQNSEDIHHRIGRTGRSNTKGTSFAFFTNNAKQA 1867
          ILVAT VAARGLD+ + V+N+D P++ ++Y+HHRIGRTGR +G + +FF + +
Sbjct 115 ILVATAVAARGLDIKNVDIVVNYDLPKSIDEYVHRIGRTGRVGNRGKAVSFFDDSDQAL 174

Query 1868 KA-LVDVLREANQEINPALE 1924
          A L +LR+A+Q + L+
Sbjct 175 CADLAKILRQADQPVPDFLQ 194
```

> ta_transcript20007_1
Length=569

Score = 135 bits (341), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 73/200 (37%), Positives = 121/200 (61%), Gaps = 7/200 (4%)
Frame = +2

```
Query 1328 LMWSATWPKEVKQLAEDFLGNYIQINIGSLELSANHNIRQVVDVCDEFSKEEKLKTLTSLD 1507
          LM+SAT+P++++ LA FL NY+ + +G + A+ ++ Q+ +F K+ LK L+ +
Sbjct 1 LMFSATFPEDIQHLAFLHNYLFVAVGIVG-GASTDVEQIFLQVAKFDKQNALKQLIEE 59

Query 1508 IYDTSESPGKIIIFVETKRRVDNLVRFIRSFVRCGAIHGDKSQSERDFVLREFRSGKSN 1687
          +I+++FVETKR D + + + +IHGD+ Q ER+ L F++G
Sbjct 60 -----NEKKRILVFVETKRNADFIASILSEQQLTSSIHGDRMQREREALHNFKTGHH 114

Query 1688 ILVATDVAARGLDVGDIKYVINFDYPQNSEDIHHRIGRTGRSNTKGTSFAFFTNNAKQA 1867
          ILVAT VAARGLD+ + V+N+D P++ ++Y+HHRIGRTGR +G + +FF + +
Sbjct 115 ILVATAVAARGLDIKNVDIVVNYDLPKSIDEYVHRIGRTGRVGNRGKAVSFFDDSDQAL 174
```

Query 1868 KA-LVDVLREANQEINPALE 1924

A L +LR+A+Q + L+

Sbjct 175 CADLAKILRQADQPVDFLQ 194

Query= gi|392886220|ref|NM_059731.4| *Caenorhabditis elegans* Protein EGO-1 (ego-1) mRNA, complete cds

Length=4899

***** No hits found *****

Query= gi|392886216:1414-3303 *Caenorhabditis elegans* Protein RRF-1, isoform a

Length=1890

***** No hits found *****

Query= gi|392887358:1372-3231 *Caenorhabditis elegans* Protein RRF-2 (rrf-2) mRNA, complete cds

Length=1860

***** No hits found *****

Query= gi|392890784:2059-3819 *Caenorhabditis elegans* Protein RRF-3 (rrf-3) mRNA, complete cds

Length=1761

***** No hits found *****

Query= gi|195438743|ref|XM_002067256.1| *Drosophila willistoni* GK16260 (Dwil\GK16260) (Rdrp), mRNA

Length=558

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript24699_1	125	3e-34
ta_transcript13924_1	124	1e-32

> ta_transcript24699_1
Length=275

Score = 125 bits (315), Expect = 3e-34, Method: Compositional matrix adjust.
Identities = 67/151 (44%), Positives = 92/151 (61%), Gaps = 12/151 (8%)
Frame = +1

Query 85 LDNPTFCCYLFWSTVLVAKMLLSLLTALQRFYKLLGLIPLALRRKIFPNEEDLFFKNL 264
+ +P ++ S VL K+L M+ LTA QR +++K+F NEED
Sbjct 32 VSDPLAQTFVHSAVLALKVLGMAFLTARQR-----MKKKVFANEEDAVKSGA 79

Query 265 EVKFDDPHVERVRAHRNDMENILPYFIMSLIYISTNPSQAIACNLFRVASVARILHTLV 444
+VKFDDP VERVRAH ND+ENI ++I+ +Y++T PS +A L R + +R+LHTLV
Sbjct 80 KVKFDDPDVERVRAHLNDLENIPAFWIVGGGLYLTGSPVAVATWLIRAFASRVLHTLV 139

Query 445 YAVYPVPQPSRILAFATMLCITFYMAAVVAL 537
YAV P+PQP+R LAF IT YM V +
Sbjct 140 YAVKPMPPARGLAFGIANFITIYMGVKVVM 170

> ta_transcript13924_1
Length=422

Score = 124 bits (311), Expect = 1e-32, Method: Compositional matrix adjust.

Identities = 63/147 (43%), Positives = 92/147 (63%), Gaps = 13/147 (9%)
Frame = +1

```
Query 85 LDNPTFCCYLFWSTVLVAKMLLSLLTALQRFYKLLGLIPLALRRKIFPNEEDLFFK-N 261
          LD+P ++ +S +L K+L+M+ +T + R +R+ +F N ED
Sbjct 80 LDSPAVQSFIYLSAILALKVLVMAPMTGMTR-----MRKGVFANPEDAKLTPK 127

Query 262 LEVKFDDPHVERVRRHRNDMENILPYFIMSLIYISTNPSQAIACNLFRVASVARILHTL 441
          +VKFDDP +ER+RRAH ND+ENI +++++ +Y++T P A A LFRV ++ RILHT+
Sbjct 128 GKVKFDPPDIERIRRAHLNDLENIPAFWVLGALYLTGTPVAAWATLLFRVYAIGRILHTI 187

Query 442 VYAVYPVPQPSRILAFATMLCITFYMA 522
          VY + P+PQPSR LAFA L I FYM
Sbjct 188 VYCIVPLPQPSRALAFAIPLFIKFYMG 214
```


Query= gi|665402677|ref|NM_166503.3| *Drosophila melanogaster* snipper (Snp), transcript variant G, mRNA

Length=1667

***** No hits found *****

Query= gi|392898168|ref|NM_171245.4| *Caenorhabditis elegans* Protein ERI-1, isoform a (eri-1) mRNA, complete cds

Length=1347

***** No hits found *****

Query= gi|392898456|ref|NM_067798.5| *Caenorhabditis elegans* Protein ERI-5 (eri-5) mRNA, complete cds

Length=1596

Sequences producing significant alignments:

	Score (Bits)	E Value
--	-----------------	------------

ta_transcript16301_1	30.8	8.5
ta_transcript64721_1	31.2	8.9
ta_transcript34177_1	31.2	8.9
ta_transcript64718_1	31.2	9.0
ta_transcript64722_1	31.2	9.4
ta_transcript64724_1	31.2	9.6
ta_transcript64720_1	31.2	9.8
ta_transcript64716_1	31.2	9.8
ta_transcript64723_1	31.2	9.9
ta_transcript64717_1	31.2	9.9

> ta_transcript16301_1
Length=242

Score = 30.8 bits (68), Expect = 8.5, Method: Compositional matrix adjust.
Identities = 22/71 (31%), Positives = 32/71 (45%), Gaps = 7/71 (10%)
Frame = -1

```
Query 669 DHKISGKLRDHNILHRNRANL-LDRHFFIDFCS-----IWQSVQVHEKRRRAVRAKIHVT 511
          D +I G LR N R R D D C+ + SV +HE+ R R+ I +
Sbjct 124 DSEILGSLRPQNTSTRVRFFFAFDARCARDLCTHLLSG*LQDSVSIHEQMRLYRSDI*LN 183
```

```
Query 510 LVGGNLKFKCF 478
          +VG + FC +
Sbjct 184 VVGLAIHFCTY 194
```

> ta_transcript64721_1
Length=1104

Score = 31.2 bits (69), Expect = 8.9, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)

```

Frame = -3

Query  1033  SRNRRFFADFPSFLRAARKSNVHYQTSFPVP  941
          S+N + F D PS LR +R +   YQ+S+ +P
Sbjct  513  SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP  543

> ta_transcript34177_1
Length=729

Score = 31.2 bits (69), Expect = 8.9, Method: Compositional matrix adjust.
Identities = 15/41 (37%), Positives = 22/41 (54%), Gaps = 0/41 (0%)
Frame = +1

Query  940  LAPEKMSDNEHWIFEQLVKNSNQKIDDFYSNLKNQRPLE  1062
          LAP   DN+H +F ++V+  E  Q  I      +N K  +P E
Sbjct  662  LAPTFWLDNKHTVFGVVRGMEVVQNIGTVKTNPKTDKPYE  702

> ta_transcript64718_1
Length=1109

Score = 31.2 bits (69), Expect = 9.0, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3

Query  1033  SRNRRFFADFPSFLRAARKSNVHYQTSFPVP  941
          S+N + F D PS LR +R +   YQ+S+ +P
Sbjct  518  SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP  548

> ta_transcript64722_1
Length=1102

Score = 31.2 bits (69), Expect = 9.4, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3

Query  1033  SRNRRFFADFPSFLRAARKSNVHYQTSFPVP  941
          S+N + F D PS LR +R +   YQ+S+ +P
Sbjct  518  SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP  548

> ta_transcript64724_1
Length=1097

Score = 31.2 bits (69), Expect = 9.6, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3

Query  1033  SRNRRFFADFPSFLRAARKSNVHYQTSFPVP  941
          S+N + F D PS LR +R +   YQ+S+ +P
Sbjct  513  SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP  543

> ta_transcript64720_1
Length=1106

Score = 31.2 bits (69), Expect = 9.8, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3

Query  1033  SRNRRFFADFPSFLRAARKSNVHYQTSFPVP  941
          S+N + F D PS LR +R +   YQ+S+ +P
Sbjct  518  SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP  548

> ta_transcript64716_1
Length=1120

Score = 31.2 bits (69), Expect = 9.8, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3

Query  1033  SRNRRFFADFPSFLRAARKSNVHYQTSFPVP  941
          S+N + F D PS LR +R +   YQ+S+ +P
Sbjct  513  SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP  543

```

```
> ta_transcript64723_1
Length=1101
```

```
Score = 31.2 bits (69), Expect = 9.9, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3
```

```
Query 1033 SRNRRFFADFPSFLRAARKSNVHYQTSFPVP 941
          S+N + F D PS LR +R + YQ+S+ +P
Sbjct 513 SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP 543
```

```
> ta_transcript64717_1
Length=1113
```

```
Score = 31.2 bits (69), Expect = 9.9, Method: Compositional matrix adjust.
Identities = 13/31 (42%), Positives = 20/31 (65%), Gaps = 0/31 (0%)
Frame = -3
```

```
Query 1033 SRNRRFFADFPSFLRAARKSNVHYQTSFPVP 941
          S+N + F D PS LR +R + YQ+S+ +P
Sbjct 518 SKNMQVFCDIPSQLRGSRTTRGIYQSSWVMP 548
```

```
*****
*****
Query= gi|392901601|ref|NM_001268821.1| Caenorhabditis elegans Protein RSD-2, isoform c (rsd-2) mRNA, complete cds
```

```
Length=1254
```

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript74877_1	35.0	0.33
ta_transcript74875_1	35.0	0.33

```
> ta_transcript74877_1
Length=624
```

```
Score = 35.0 bits (79), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 20/58 (34%), Positives = 30/58 (52%), Gaps = 8/58 (14%)
Frame = +1
```

```
Query 172 SYIFMYRPIEVHKATHYAPFEITQVVEILNTENHGRVDRSEFSSLFTFDLCNVDQRYV 345
          S+ FMYRP+ + K ++P E+T + LN E ++ D+ NVD RYV
Sbjct 153 SFFFMYRPVFLWKVV*FSPVELTLKIYALN-----*IE*DLIYVDDIANVDSRYV 202
```

```
> ta_transcript74875_1
Length=635
```

```
Score = 35.0 bits (79), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 20/58 (34%), Positives = 30/58 (52%), Gaps = 8/58 (14%)
Frame = +1
```

```
Query 172 SYIFMYRPIEVHKATHYAPFEITQVVEILNTENHGRVDRSEFSSLFTFDLCNVDQRYV 345
          S+ FMYRP+ + K ++P E+T + LN E ++ D+ NVD RYV
Sbjct 153 SFFFMYRPVFLWKVV*FSPVELTLKIYALN-----*IE*DLIYVDDIANVDSRYV 202
```

```
*****
*****
Query= gi|392927450|ref|NM_077572.5| Caenorhabditis elegans Protein RSD-3(rsd-3) mRNA, complete cds
```

```
Length=1452
```

```
**** No hits found ****
```

```
*****
*****
Query= gi|392886390|ref|NM_059868.6| Caenorhabditis elegans Protein RSD-6 (rsd-6) mRNA, complete cds
```

Length=2070

	Score (Bits)	E Value
Sequences producing significant alignments:		
ta_transcript20037_1	30.4	8.0

> ta_transcript20037_1
Length=153

Score = 30.4 bits (67), Expect = 8.0, Method: Compositional matrix adjust.
Identities = 18/37 (49%), Positives = 22/37 (59%), Gaps = 0/37 (0%)
Frame = +2

```
Query 1511 QMHLSSVELFDIKMFKSLQSVLRSI*NHMKR*IKRFK 1621
          QM L VE+F + K LRSI* H+KR*+K F
Sbjct 17 QMALCYVEIFTFES*KHFTF*LRSI*VHLKR*VKNFP 53
*****
Query= gi|304307738|ref|NM_001195080.1| Bombyx mori tudor staphylococcus/micrococcal nuclease
(Tudor-SN), mRNA
```

Length=2667

	Score (Bits)	E Value
Sequences producing significant alignments:		
ta_transcript15886_1	246	3e-99

> ta_transcript15886_1
Length=953

Score = 246 bits (628), Expect(2) = 3e-99, Method: Compositional matrix adjust.
Identities = 174/501 (35%), Positives = 265/501 (53%), Gaps = 2/501 (0%)
Frame = -1

```
Query 2667 LATHPEFYRIVLGDVTVPPQVESRALGVLLSGAILGHQCRQSAVTNLLH*HEPIFDKVL 2488
          LA E R+VLGDV V PQVE RALGVLL A+L H+ RQ V + LH H+ FD+VLA
Sbjct 15 LAARAELSRVVLGDVAVLPPQVEPRALGVLLRRAVLAHERRQPVVAHTLHQHQTFFDQVLA 74

Query 2487 QINVCVRINKGNSSW*STDFYIQEQPLANDIIETGYSFCSVIRVRGEFHTAENILCRKR 2308
          + + + + + ++Q+Q L + E + +V+ VRGE H A+ +L R
Sbjct 75 DVEAGGGLEERDAGRGAHLHVQQQLLVERVDGERAHLRGAVVGVRGELHAAQRVLARVA 134

Query 2307 RIVLSTHRECCQSGYV*RLSISIVDVYNLDLPIVCYFFNLCPVPLVIGCKTSSTDGSLPW 2128
          + L R+ Q L++S+VDV L ++ +F +L PVPLV+ + S +G+
Sbjct 135 GLALRAGRQRQPRAAHHLTVSVVDVEYLGGFVIGHFLDLGPVPLVVEGEASGAEGASSR 194

Query 2127 SIRSQRQWTVSKLSVYSFHKTF*FHT*IDILCVEMTFRSDFSDDHAVFKSTILYSCISL 1948
          + + Q +L VY H+ +D L E DH ++F +L+ ++
Sbjct 195 HV*AGQRRVSELLLVYLLHEALELGAEDALREERAVGRHLRHDHLLIFHHAVLHGRVAF 254

Query 1947 LfdffffdDIVFPYADTLFNCILFSGFYGACKLRRFRVMRRGKAMFD*RNGQILVVNPE 1768
          LF FF V PY D + +L G A +LRR V+ G+ + R+GQ+LVV P+
Sbjct 255 LFRLLFFHLHKVLPYTDAFLDRVLGGLDEARELRRLGGVHAGEPVLHQRHGQVLVVRPQ 314

Query 1767 PTDEVPCFVNLFYAD*DVVL*ALFFRELQSFFSERLCILF-GSSANCRSRTSGTVNAGKQ 1591
          P DEV V+L VVL AL RELQ F+ERL +L ++A+ R+R + +AG+Q
Sbjct 315 PADEVARLVHLLDGHVHVVLQALLLRELQRLFAERLSVLHAAAAADRRARAARAADAGQQ 374

Query 1590 KGY*DGFFRNI*THTRSASNEFHSSSLGFLGTfeeweeffcFRWISTGVLHTVGGHFFLVV 1411
          + ++ H R A +E H L L +E E+ F +S GVLH V G L V
Sbjct 375 ERDHHRLLDGDVDAHARPARHELHGRRLALRPLQEREKLFRLGGVSAGVLHAVRGDVLGV 434

Query 1410 NTNCGLNCFQFGLQ*Fiil*aslviiivsiLHCCQ-PFSHQSFYSVRATAYDSTTCLFWEI 1234
          + + L + GLQ +++ A LV++V + C+ F+H FSYV + +Y+ CLFW +
Sbjct 435 HADGRLLRLELGLQLVVRAPLVVVVPVDDCRVTFAH*RFSYVNSLSYNCGACLFWVV 494

Query 1233 IFCWLNVIYCHINFFPNQFFS 1171
          + L+V+ H++FF Q FS
Sbjct 495 VLRGLDVVDSSHVHFFCQQAFA 515
```

Score = 137 bits (346), Expect(2) = 3e-99, Method: Compositional matrix adjust.
Identities = 173/405 (43%), Positives = 190/405 (47%), Gaps = 10/405 (2%)
Frame = -3

```

Query 1192 FSQPVFVEIHFVPTSMEYHTKV*ILLASV*VYCRRQHCSFHEEA*R*LRIFSVHC-YV 1016
          F Q F * I PRTS E *IL A V CSF A* R S C +
Sbjct 509 FCQQAFS*GIPSPRTSRECRIA*IL*ALVTFSPPHLGCSFRAAA*-CWRGISS*RCRWA 567

Query 1015 F*Qrarlr*llPTRWP*IPCLSPGL*VHCLHNLISICAVL-----LP*LHFQRLSM*THL 854
          *+RAR R* R P* PCL P L C + S A P L+ * +
Sbjct 568 A*RRARRR*PPRARS*TPCLWPRLWARCSRSSSRYAAFDLWRRARPHAASTHLTS*PRV 627

Query 853 IS*HISRTLVLVGPQRCYPAGAVSCPR-YCCY*RTPELLRRLSAAIWPGRSVLLLRKAQ 677
          S HISRTL P+RC P GA PR YCC R LR LS TPGR LL RK
Sbjct 628 TSRHISRTLAAAEPRCCPEGAGWYPRSYCCS-RILGSLRCLSEVAATPGRIGLLPRKVL 686

Query 676 IHRLVLQRDIEFQIASV*WECIQVTNKDVL*NHHAHIQ**PLQAYHCIC*RKLSDFR*TT 497
          IHRLV Q DI F AS * Q T K L +H IQ** A HCIC R L +*
Sbjct 687 IHRLVSQLDI*FLRASK*SGRNQATGKV*LSSHL*RIQ**L*SAVHCICSRMLLCSQ*CP 746

Query 496 *CLVHVYQHQSFLCLAIWLSLRSLPAF*AEVYF*HLEL*RDLPARLQ*HFHLWKDF 317
          *CL + K+LCL I + V F L*+D QP LQ*H W
Sbjct 747 *CL*CDPEDLVPKYLCLEILPDPQFQLISLVGVCFLPPSL*QDPQPEGLQ*HSLTW*GL 806

Query 316 CQPIRRHILYSLNSPVSQQ*R*PPCRLASSLGIHGLPTRMVHPSFLCHCWRSFGERV*VR 137
          C+P H + + VSQQ* *P C S LP +MV F CHC +S G V* R
Sbjct 807 CRPTPGHTPWLQS*VVSQQ*I*PLCLQVFSSDTPLLPKQMVRLLFQCHC*QSSGALV*AR 866

Query 136 *YPKGLSLSLEAARPEAVFLLPPYLPVIVPASLFLFCKQVPVLEHS 2
          * P LS SL A R A LLP PA LF FCKQ VLEHS
Sbjct 867 *CPTALSPSLVAGRLRAASLLPLCPLTTPALLFRFCKQGLVLEHS 911

```


Query= gi|512926474|ref|XM_004931038.1| PREDICTED: Bombyx mori probable exonuclease mut-7
homolog (LOC101745346), mRNA

Length=1521

Sequences producing significant alignments:	Score (Bits)	E Value
ta_transcript44087_1	52.0	3e-06

> ta_transcript44087_1
Length=1591

Score = 52.0 bits (123), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 45/89 (51%), Positives = 57/89 (64%), Gaps = 0/89 (0%)
Frame = +2

```

Query 1238 IVNGNHHLQYNHKWP*SKLLLSIMFT**IH*F*TNKNIPVFGTSLINHLWKTVRLSN*D 1417
          IV+GN LE ++ + * K L IM+T**I F*T++N+ VFG S NH K ++ *
Sbjct 463 IVSGNLLLEPHSPRLH*YK*LHLIMYT**IPSF*TDNRNM*VFGIHSTNHS*KMLK**R*A 522

Query 1418 IGLNRI*KK*KHL*MVWEK*MSKVVDY*I 1504
          L N+I K+*K L* V E * KVKDY*I
Sbjct 523 LAWNKILKR*KVL*QV*ET*K*KVKDY*I 551

```