A

>R2_Bg_Ribo

GTGCTGACGCAATGTGATTTCTGCCCAGTGCTCTGAATGTCAAAGTGAAGAAATTCAAGCAAGCGCGGGTAAACGGCGGGAGTAACTATGACTCTCT
TACGGGCACCCTGCCTGTAGGACACGACTGCAGTCTCCCTTCTGCAGACCTCGTCGGAAGATGAGGTGGATGTCGTGATGTCAGCTGGCTCCGGGAT
AATTTCCAGCCAGGGTTGGTAAGGGGGGAGGAAGTCTAGTGATGCCTTGGGAAAGTTGAAGGCTCCTCTCTCGACCAAAGCTGACACAGGGGAATG
GGTATGGGTTGACCCCCCATACTCATGAACTCTGGTCTTCGATAACGGTATCAGGCCTCGGACTTGGGGGGGGTATGGTTCCGCCTCCCCCTCGACC
TCCAGGGAACCACTTGTTGACGGACTCTGCGTGTCTATGGACGATTCTGGTTCTAACTCTGCCGTGCGCGTCTTGGTAGTTCTACCCTTCGAGCCTG
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TGTGGTGGCATTTCAGTGCAGGAAATGCAAACGGGTGAATTCCAAGAAGCACAGTATTTTTGTGCATATTAGTAAATGTAGGGGTGAAACTGAAGCA
CCAACTGCTGCGCCATACCCTTGCAGGGTATGCGGGGAAGGCTTCAGTAGCAAGATCGGCCTCGGTCAGCACGAGAGGCACCGGCACCCTGTACAGA
GAAATGAGGCGCGAGCACCCACTCCCAAAACCCCACAGCGTGGGGCACCACCTGATGAgGGTCTCGCTCGATTGGCAATGCTCGAGGTGGAACTCGA
GTCCCGGGGGGGAGTTAAGTTCATCAATAAGGAGCTGGCTTGTAGGTTTGGGAGTCTTACGCCAAAGCAGATTAGCGACCGACGGAGGTCGGCCGCT
TACCGTGACCTTCTTTTGAAGGCTCGTGGTGGAGCGGTCGAAACCCCCCCTCCTGGGGGGCAAGGGGATGTTCTGCCTACATCCCAGGACGCGTCAC
GCGAGGAGCAGTGTGGCGTGTACCCAGATGCTGCAGTCCGTGACTCCAAAGTGGAGGAGACTACCGCTTCGATGGCGCCGCAGACCTGTGAATCCGA
TTCGGATGAGGTTGAGTGGCGCGAGGAAGCTCTCAATGCCTTTGTGGGAGCTCTGCCCACGGGACTTCCTCCCGAAGCGGAGGCCCTGGTACAAGCT
TGTCGAGAGGCTGCTGTGAATCAGGGGTCAAACCCTGACAAACAGGGCGTTATTGACGGCTTGTATGACTTAGTCATCCGGTTCTTGGCTCAAGCGT
CCCCCGCATGTGCTGGACCAGGTCCTCAGCGTCAACCTCGCCGAAAGGGCAAGGGCAAGAAAGCTCTTAAAAGGTTCAAGTTCGGAAGAGTCCAGGA
GCTCTTCAAACGTGATCCGCGTGTATTGGCAAAGCGCGTGTTGCAGGGACTTGAACCGTCTGGACTGAGGGACGGGGAACGAGATCTCCTCGAGCCC
TGTGATGTTCGAAGGTGCTACCAGGATCTCTGGGGAGAAAGACACCTTCAGACAAATCTTGACTGCACAGGCATGCCGAAGGCGGATGAGATCCCTA
TTGATCGAATCTGCTGCCGAATTGCCTGCGACGAGGTTGGGCGTCGCGTGCGCAAGATTAAGAGCACGACGGCTCCAGGGCCAGACGGAATTAACAT
CCAGGCAGTCCGTTCTGCGCCCGCCCAGGCTGTATTATCCACCTTTTACAGCCTTATCCTTCTCCTGGGACGGCCCCCGGCAGCCTGGCGGGAAAAC
CGATCTGTGTTAATACCGAAAGAGGGGTACGATGTTCGATTAATTTCGAATTATCGCCCTCTGACCATCGGATCGATTCTCAGTCGGATCTTTTGGG
GGATCATCGATCGACGGCTGAGGGAACTGTTAAAGATCCACCGGTATCAGAAAGGTTTTACTACGGAGCCAGGCTGCTATCAAAATGTGCGCATCTT
CTCGGAGGTACTGAGGCAGGCTAAGTCTGCACGCGGGCTCGTAGCGGTGCAGCTTGACATTTCAAAGGCCTTTGACACTGTACCACATGCTGCGATT
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ACCGCATTCAACTGGAACTCAAGCGAGGGGTGAAGCAGGGGGACCCGATCTCACCTCTGCTTTTCAACATGATAATGGAACCGCTCCTCAACAAGCT
TGAGTCTCTGGGCGGTGTTACTTTGGCTGACGGCTCCCAGCTTGCTTGCCTTGCTTTTGCTGATGACTTGATACTCCTCGCCGACAATCGAGAGAGA
GCACGGGAGTTGCTTGAGACCGTGGAGGAGTTCCTGGATGGTTTGGGCATGAAGATCTGGGCGCCCAAAAGCGTCGCATTCGAGATCGTGCCAACCA
AGGACTCCTGGTGTGTCGTGGATCCGGGTCTTCGCCTGCGGCAGGGCGGCGCGATCACCTATGCAGGCCCGGATCACTCATTGAAGTACTTGGGTGT
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CAGAAGCTACATCTTTTGAAGACGTATCTCATCCCTCACTTCACGCACCGGCTGGTCTCTAGTCTGCCATCGATCGCAGAGCTGAGGGCTCTCGATC
TGGAGATCAGAGGATGCGTGAAGCAAATCCTTCATTTGCATCCGTCGACCGCGGATGGCATGCTTTATTCAAAGCCGAAGGATGGAGGGTTGGGAAT
ACCGTGTCTTGAGGTGGGTATAGTGTGCTCTGCACTCAAGATGGCCATAAAGACACGGCAGAGCGATGACCCAACTCTCCAAGCACTAGACCCCAAC
CTGATGGAACGAATGGAGAGGTACATCCGGAGCATACGCATTAGTGAGCTGACTGTGAAAGCAGTCAACTCCTATGCGCGAAGGGTGTACTCTGCTA
GGGTGGGTCAATGGTCTAACCTCCCGGTACAGGGTCGCGCGGTTAAGTCTCTGACCGGAGATAGAATTGGGAATTCTATTTTCTACGACCCGAGCCT
ATTAAAGCCATGTAGATTTATAACGGCTTTAAGGCTCCGTTCGAACACCGGGGGGAATAGGACAAATTTGTCAAAGATTAGACCACTCCAATCCGTG
CAATGTCGCCGCTGTGGTTTCCAGAGAGAGACACTGGGACACATACTTGGGCAATGTCTGCACACCAAGGCTGCACGGATACGGAGACACGACGCTA
TTAAAGACTTCATCTGCGATAGCGTCACTCGCGAAGGAGACAAAACGGCGACAGTTACTAGGGAGCCTGAGCTTCTCTTGAGTGGCGACTCGGGTAA
ACTGAAACCGGACCTGGTGATAACCCGCCAGGGAAGGGTCTTTGTGGTCGACGTAACAGTCCGCCATGAGGATTCAGATTACCTCGAGCGCGCTCGA
CGAGAGAAGATAGACAAGTACCAGGCGCTGTTGCCGTCGCTCATCGCCCAGTTTGGGGCAACTGGGGGTGAGGTGTTGCCCATTGTTGTGGGCACAC
GTGGAGCGATGCCCAAGCTTACCATGGAAGCTTTAGCTCAGTTGGGGATTACTGAGCGTGGAAGGTTGAAGACCATTAGCCTTATGAGTCTAAGAAG
TTCGATTGAGATCTACCATGGTTTCTTAGACTACGATGCATCGCTCCTATAATTTTGTTGTGGAAGGAACTACCGGCAAGCAGATTGTGAACCAGGA
GATTGATTGTCCTTACTCTATAGGCCCTTTTTAAGTAGGTATCCCATCTACAGGTACCTACCCTTCTTTTGACCGGGGATTAAAGTAAATTTAAGGC
TTCAGATTCGAGGGCAGCTGAGGCCTACTGGTTGCCTATTGCAACGGGCGCAATCTGCGAGTCTTCAGCTGAGTATCAAGCTTTTGATAGTAATTGC
AGCTGGGGGCGGCGAGTCTGCATTGCAGAGTGGACACCTACGCGAGGTTTTCCCTGTTAAGGTTTTCTTGCACCATAATGGTGGGGGACCGAACTAA
GTTCCATCCTCCTTCGGGGGGCTCGCTTGCCTGATTCTCCAAGCCCTTTTTGGCGCAAGAAAAGACCGTCTAAATTAATATAAAGGAACCTTCCCGG
CAGTGGTTGGGCCGGCGCTAGACTCGTTAATCTGTTTGAGAGGGGCAGATAATGGAGGGTCCTCGGTGGCCCTGCTCTCTGCACTTCTGCTTCCCAG
CTAAGGGTATGAGGTTACTATGCCTTCCAAAAAGATAGTAAGTTGCACTCGGTGGGGTGTTAGTAAGTAGCCAAATGCCTCGTCATCTAATTAGTGA
CGCGCATGAATGGATTAACG

B

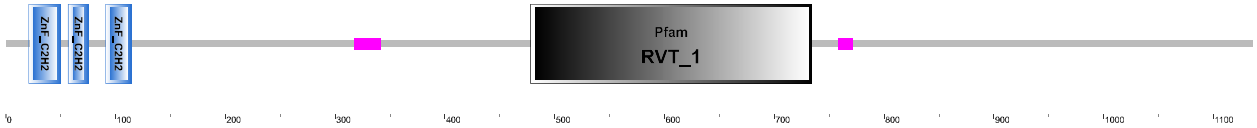
>ORF_R2_Bg_Ribo

MDDSGSNSAVRVLVVLPFEPVL**C**PV**C**LSGRGANYQALSLKDYLD**H**LGRA**H**AAAVVAFQ**C**RK**C**KRVNSKK**H**SIFV**H**ISK**C**RGETEAP
TAAPYP**C**RV**C**GEGFSSKIGLGQ**H**ERHR**H**PVQRNEARAPTPKTPQRGAPPDEGLARLAMLEVELESRGGVKFINKELACRFGSLTPK
QISDRRRSAAYRDLLLKARGGAVETPPPGGQGDVLPTSQDASREEQCGVYPDAAVRDSKVEETTASMAPQTCESDSDEVEWREEAL
NAFVGALPTGLPPEAEALVQACREAAVNQGSNPDKQGVIDGLYDLVIRFLAQASPACAGPGPQRQPRRKGKGKKALKRFKFGRVQE
LFKRDPRVLAKRVLQGLEPSGLRDGERDLLEPCDVRRCYQDLWGERHLQTNLDCTGMPKADEIPIDRICCRIACDEVGRRVRKIKS
TTAPGPDGINIQAVRSAPAQAVLSTFYSLILLLGRPPAAWRENRSVLIPKEGYDVRLISNYRPLTIGSILSRIFWGIIDRRLRELL
KIHRYQKGFTTEPGCYQNVRIFSEVLRQAKSARGLVAVQLDISKAFDTVPHAAIATVLRQKGLPPYFADMVRRSYEGAYTSIRVRD
HRIQLELKRGVKQGDPISPLLFNMIMEPLLNKLESLGGVTLADGSQLACLAFADDLILLADNRERARELLETVEEFLDGLGMKIWA
PKSVAFEIVPTKDSWCVVDPGLRLRQGGAITYAGPDHSLKYLGVKVSPWVGVDVSDLRTHFSKTLEDTRKLPLKPHQKLHLLKTYL
IPHFTHRLVSSLPSIAELRALDLEIRGCVKQILHLHPSTADGMLYSKPKDGGLGIPCLEVGIVCSALKMAIKTRQSDDPTLQALDP
NLMERMERYIRSIRISELTVKAVNSYARRVYSARVGQWSNLPVQGRAVKSLTGDRIGNSIFYDPSLLKPCRFITALRLRSNTGGNR
TNLSKIRPLQSVQ**C**RR**C**GFQRETLG**H**ILGQ**C**LHTKAARIRRHDAIKDFICDSVTREGDKTATVTREPELLLSGDSGKLKPDLVITR
QGRVFVVDVTVRHEDSDYLERARREKIDKYQALLPSLIAQFGATGGEVLPIVVGTRGAMPKLTMEALAQLGITERGRLKTISLMSL
RSSIEIYHGFLDYDASLL

C

Zn finger domains:

#1 YPCRVCGEGFSSKIGLGQHERHRH
#2 FQCRKCKRVNSKKHSIFVH
#3 VLCPVCLSGRGANYQALSLKDYLDHLGRAH



D

C-myb motif:

```
Q ss_pred          CCCHHHHHHHHHHHHHHHHhHHccCchHHHHHHHHHHcCCCCHHHHHHhhhhcHHHHHHHHHHH
Q Q_R2_ORF_Bg      APPDEGLARLAMLEVELESRGGVKFINKELACRFGSLTPKQISDRRRSAAYRDLLLKA
Q Consensus     29 rWs~eE~~~La~lE~~l~~~~~~~~in~~L~~~~p~Rt~eaIk~~Rr~~~yk~~v~~~
                   .||.+|..+|..+-..+    ......-..|+..||+||..+|+.+      |..++..+
T Consensus     35 ~WT~eED~~Ll~~v~~~---G~~~~~W~~Ia~~lpgRT~~q~k~R-----~~~Ll~~~    84 (95)
T 1UG2_A        35 LWTREADRVILTMCQEQ---GAQPHTFSVISQQLGNKTPVEVSHR-----FRELMQLF    84 (95)
T ss_dssp          SSCHHHHHHHHHHCCCC---CSCTTTHHHHHHHHSSCCHHHHHHH-----HHHHHHHH
T ss_pred          CCCHHHHHHHHHHHHHh---CCCcccHHHHHHHHhCCCCHHHHHHH-----HHHHHHHH
```

HHpred alignment with mouse hypothetical gene (2610100B20Rik) product homologous to Myb DNA-binding domain (PDB accession number - 1UG2_A).
Probability: 92.4%, E-value: 0.78, Score: 36.1, Aligned cols: 50, Identities: 20%.

E

Reverse transcriptase domain:

```
Q ss_pred          HHHccCCCCHHHHHHHHhCCCCC-CCCCCCCCHHHHHcCcHHHHHHHHHHHHHHCCCChHHHcceEEEEeCCCCCccch
Q Q_R2_ORF_Bg      IDRICCRIACDEVGRRVRKIKSTT-APGPDGINIQAVRSAPAQAVLSTFYSLILLLGRPPAAWRENRSVLIPKEGYDVRL
Q Consensus        ~~~l~~~it~~Ev~~ai~~~~~~~-ApGpDgi~~~~lk~~~~~~~l~~l~n~~l~~~~~P~~~k~~~~vlipK~~~~~~~
                   .+.|..+++.+||.++++.++.++ ||||||++.+.++.. ....+..+++.++..+..|..|+. ++|||++
T Consensus     1  ~~~l~~~~~~~ei~~a~~~~~~~~apG~dg~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~k~~~~~~   71 (428)
T 6AR1_D        1  MALLERILARDNLITALKRVEANQGAPGIDGVSTDQLRDY-IRAHWSTIHAQLLAGTYRPAPVRR---VEIPKPG-----   71 (428)
T ss_dssp          -CHHHHHSCHHHHHHHHHHHHHTCCCCTTCCCGGGHHHH-HHHHHHHHHHHHHHTCCCCCCBEE---EEEECTT-----
T ss_pred          CcHHHHHcCHHHHHHHHHHHHCCCCCCCCCCCHHHHHHH-HHHHHHHHHHHHHcCCCccCCceE---EEEeCCC-----
Q ss_pred          hhhcCchHHHHHHHHHHHHHHHHHHHHHHc--ccCCCCCCCCCchHHHHHHHHHHHHHHHHHcCCEEEEEEeehhccCCC
Q Q_R2_ORF_Bg      ISNYRPLTIGSILSRIFWGIIDRRLRELLK--IHRYQKGFTTEPGCYQNVRIFSEVLRQAKSARGLVAVQLDISKAFDTV
Q Consensus        ~~n~RPItl~s~~~Ki~~kil~~Rl~~~~~~~~~~Q~gf~~~~g~~~~~~~l~~~~~~~~~~~~~~~~~lD~~kAFDsV
                   ++||||++.+..+|++.+++..+|...+.   ..+.|.||++++++.+++..+...+.    .....++.+|+++|||+|
T Consensus    72  -~~~R~i~~~~~~~k~~~~~l~~~l~~~~~~~~~~q~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~D~~~afd~i   146 (428)
T 6AR1_D       72  -GGTRQLGIPTVVDRLIQQAILQELTPIFDPDFSSSSFGFRPGRNAHDAVRQAQGYIQ----EGYRYVVDMDLEKFFDRV   146 (428)
T ss_dssp          -SSEEEEEECCHHHHHHHHHHHHHHHHHGGGSCTTBCSSCTTCCHHHHHHHHHHHH----HTCCEEEEECBTTTTTTC
T ss_pred          -CCeecCCCCCHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCHHHHHHHHHHHH----cCCCEEEEechHHHccCC
Q ss_pred          CHHHHHHHHHCCCCHHHHHHHHHHHCCcEEEEECCeeeEEEeCCCCCCCCCCchHHHHHHHHHHHHHHHHCCCcccCC
Q Q_R2_ORF_Bg      PHAAIATVLRQKGLPPYFADMVRRSYEGAYTSIRVRDHRIQLELKRGVKQGDPISPLLFNMIMEPLLNKLESLGGVTLAD
Q Consensus        ~h~~l~~~L~~~g~~~~~~~~i~~~~~~~~~~i~~~~~~~~~~~~~~Gv~QGdpLSPlLF~l~~~~l~~~l~~~~~~~~~
                   +|+.+...|...++++.+..++..++.........     +...+|++||+|+|+|+||+++++.+...+..
T Consensus   147 ~~~~l~~~l~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~Gl~qG~~lsp~l~~~~~~~~~~l~~~~~~~~   213 (428)
T 6AR1_D      147 NHDILMSRVARKVKDKRVLKLIRAYLQAGVMIEGVK-----VQTEEGTPQGGPLSPLLANILLDDLDKELEK--------   213 (428)
T ss_dssp          BHHHHHHHHHTTCCCHHHHHHHHHHHCCEESSSCE-----ECCSBCCCTTCTTHHHHHHHHHHHHHHHHH--------
T ss_pred          CHHHHHHHHHHhCCCHHHHHHHHHHHcCcEeCCee-----eecCCCcCCCCCcHHHHHHHHhHHHHHHHHH--------

Q ss_pred          CCeEEEEEEccCeEEEecCCHHHHHHHHHHHHHHHH-ccccCCCCCeEEEEEeCCCCceEEeCCCceEeeCccceecCCC
Q Q_R2_ORF_Bg      GSQLACLAFADDLILLADNRERARELLETVEEFLDG-LGMKIWAPKSVAFEIVPTKDSWCVVDPGLRLRQGGAITYAGPD
```

```
Q Consensus          ~~~i~~l~fADD~~l~~~s~~~l~~~l~~l~~~~~~~~GL~iN~~K~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~
                      ..+.++.||||+++++.+.+.++..+..+.+++.. .|+.+|.+||..+ ..
T Consensus      214 -~~~~~~~yaDD~~l~~~~~~~~~~~~~~~~~~~~~~gl~in~~K~~~~-------------------------------~~   264 (428)
T 6AR1_D         214 -RGLKFCRYADDCNIYVKSLRAGQRVKQSIQRFLEKTLKLKVNEEKSAVD---------------------------RP   264 (428)
T ss_dssp            -HTCEEEEETTEEEEEESSHHHHHHHHHHHHHHHHTSCCCBCTTTCBCC----------------------------CG
T ss_pred            -cCCCcccceeCCcEEEEECCHHHHHHHHHHHHHHHHHhCCCcChhhcccC----------------------------Cc
Q ss_pred            CceEEcceeeccc---cCCCHHHHHHHHHHHHHHH--cCCCCHHHHHHHHHHHHHHHHHHHcCCCCHHHHHHHHHHH
Q Q_R2_ORF_Bg        HSLKYLGVKVSPW---VGVDVSDLRTHFSKTLEDTR--KLPLKPHQKLHLLKTYLIPHFTHRLVSSLPSIAELRALDLEI
Q Consensus          ~~~kYLGv~~~~~~~~~~~~~~~~~~~~~~~l~~i~~~~~L~p~qkl~~l~~~~iP~l~y~l~~~~~~~~~l~~lD~~i
                     ..++|||+++...    ...........+...+..+. ...++..+++..++..+.+.+.|.....  ....++++|..+
T Consensus      265 ~~~~~LG~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~i~~~~~~i~~~~~y~~~~~-~~~~~~~~l~~~~   342 (428)
T 6AR1_D         265 WKRAFLGFSFTPERKARIRLAPRSIQRLKQRIRQLTNPNWSISMPERIHRVNQYVMGWIGYFRLVE--TPSVLQTIEGWI   342 (428)
T ss_dssp            GGSCBTTEEECSSSSCCEEECHHHHHHHHHHHHHSCCC--CCHHHHHHHHHHHHHHHHTTCS--CHHHHHHHHHHH
T ss_pred            ccccccccEEEEeccccccccHHHHHHHHHHHHHHhCCCCCCCCHHHHHHHHHHHHHHHHHhhhhcC--CHHHHHHHHHHH
Q ss_pred            HHHHHHHHcCCCcCCCCcceecCHhhCCCCCCCHHHHHHHHHHHHHHHHcCCCHHHHHHcHHHHHH
Q Q_R2_ORF_Bg        RGCVKQILHLHPSTADGMLYSKPKDGGLGIPCLEVGIVCSALKMAIKTRQSDDPTLQALDPNLMER
Q Consensus          r~~vk~~l~lp~~~~~~~ly~~~~~GGLGl~~l~~~~~~~~~k~~~~l~~s~d~~~~~~~~~~~~~
                     +++++.+.........   +.+...||||+++++........+..+++..+.+ ....+.......
T Consensus      343 ~~~l~~~~~~~w~~~~~~~~~~~gglG~~~~~~~~~a~~~k~~w~~~~~~~~~~~~~~~~~   404 (428)
T 6AR1_D         343 RRRLRLCQWLQWKRVR---TRIRELRALGLKETAVMEIANTRKGAWRTTKTPQ-LHQALGKTYWTA   404 (428)
T ss_dssp            HHHHHHHHHHHCCSHH---HHHHHHHHHTCCHHHHHHHHTCCSCHHHHTTSHH-HHHHTSHHHHHH
T ss_pred            HHHHHHHHHHhccChH---HHHHHHHHCCCCHHHHHHHHhcCCChhHhcCCHH-HHHHHCHHHHHH
```

HHpred alignment with Group II Intron Reverse Transcriptase (PDB accession number - 6AR1).
Probability: 100%, E-value: 1.4e-31, Score: 319.99, Aligned cols: 395, Identities: 20%.

F

Endonuclease-like domains:

Cap snatching endonuclease

```
Q ss_pred            hHHHHHHHHHHHHHHHHHHHcCCCCceEEEeCCceecCCCCCccccceEEEEE-CCEEEEEEEccCCC-hhHHHHHHHHH
Q Q_R2_ORF_Bg        KAARIRRHDAIKDFICDSVTREGDKTATVTREPELLLSGDSGKLKPDLVITR-QGRVFVVDVTVRHED-SDYLERARREK
Q Consensus          ~~~ri~RHn~V~~~l~~~l~~~~~~~~~v~~ep~~~~~~~~~~~rPDlv~~~-~~~~~ViDVtV~~e~-~~~l~~a~~~K
                     ...+.-+||-++..|...-...-...|-+..       ++.+.+-||.|+.. ++..+||+++=.--+ ...+..+++.|
T Consensus       73 ~~~~~f~HDftf~~L~~~TD~~l~~~F~~~~~~~~~~d~~d~lTPD~I~~~~~g~~~VvEftT~r~~~~~~l~~~~~~K   145 (226)
T 6NTV_A          73 SEAYKINHDFTFSGLSKTTDRRLSEVFPITH-------DGSDGMTPDVIHTRLDGTIVVVEFSTTRSHNIGGLEAAYRTK   145 (226)
T ss_dssp            HHHTTHHHHHHTTTTCCCCCCCGGGTSCCCC-------SSCTTCCCSEEEECTTSCEEEEEEECCCCSHHHHHHHHHH
T ss_pred            HHHhhcCCceehhhhhccccCCcHHHhCCCCC-------CCCCCcCCcEEEEeCCCeEEEEEEeCCCCCChHhHHHHHHHH
Q ss_pred            HHHHHHHHHHHHHHHCCCccEEEEEEEccCCCCC
Q Q_R2_ORF_Bg        IDKYQALLPSLIAQFGATGGEVLPIVVGTRGAMP
Q Consensus          ~~KY~~l~~~~~~~~~~~v~v~~ivvgarG~~~
                     +.||...........+..++.+..|+||..|.|.
T Consensus      146 ~~KY~~~l~~r~~~~~~~~i~l~vIvV~~~~V~s   179 (226)
T 6NTV_A         146 IEKYRDPISRRVDIMENPRVFFGVIVVSSGGVLS   179 (226)
T ss_dssp            HHHHHHHHHHHHHTSSSCEEEEEEEECSSEEEE
T ss_pred            HHHcHHHHHHHHHHhcCCcEEEEEEEEeCCcEEe
```

HHpred alignment with Cap snatching endonuclease, Severe fever with thrombocytopenia syndrome virus (SFTSV). PDB accession number 6NTV_A.
Probability: 95.69%, E-value: 0.031, Score: 60.56, Aligned cols: 105, Identities: 24%.

Holliday junction resolvase

```
                                α1              β1                  β2        β3
Q ss_pred                HHHHHHHHHHHHHHHHCCCCCEEEEECCCCCCCCCCCCCCCCEEEEECCEEEEEEEEEEC
Q R2_ORF_Bg              RRHDAIKDFICDSVTREGDKTATVTREPELLLSGDSGKLKPDLVITRQGRVFVVDVTVRH
Q Consensus              ~RHn~I~~~i~~~l~~~~~k~w~v~~Ep~i~~~~~~~~~kPDLV~~~~~~~~ViDVtV~~
                         +|-..--+.+...|.+   .||-|.     +.|.++.   ||||+.+++..++++|-...
T Consensus            3 rkG~~~ERel~~~L~~~~~Gf~vv-----R~~gSg~---pDiiA~~~~~~~aiEvKst~   51 (120)
T 1gef                 3 RKGAQAERELIKLLEK---HGFAVV-----RSAGSKK---VDLVAGNGKKYLCIEVKVTK   51 (120)
T ss_dssp                HHHHHHHHHHHHHHHH---TTCEEE-----ECGGGSS---CSEEEECSSCEEEEEEEEES
T ss_pred                CCHHHHHHHHHHHHHH---CCCEEE-----EECCCCC---CCEEEEECCEEEEEEEEECC


                                α2                  β4
Q ss_pred                CCCHHHHHHHHHHHHHHHHHHHHHHCCCCCEEEEEEEECCCCCC
Q R2_ORF_Bg              EDSDYLERARREKIDKYQALLPSLIAQFGATGGEVLPIVVGTRGAM
Q Consensus              e~~~~L~~a~~~Kv~KY~~l~~~i~~~~~~~~V~~~~vvigaRG~w
                         ..+-.++..--+|..       +..+.++++.  ++++=+.-+| |
T Consensus           52 ~~~iyi~~eqvekL~~~~~~~~f~~~fg~~p---IAvkf~g~~-W   87 (120)
T 1gef                52 KDHLYVGKRDMGRLI-------EFSRRFGGIP--VLAVKFLNVG-W   87 (120)
T ss_dssp                SSCEEECHHHHHHHH-------HHHHHHTCEE--EEEEEETTTE-E
T ss_pred                CCEEEECHHHHHHHH-------HHHHHCCCCE--EEEEEECCCC-E
```

HHpred alignment with the archaeal Holliday junction resolvase (Hjc) from *Pyrococcus furiosus* (PDB accession number - 1GEF).

Probability: 90.96%, E-value: 2.1, Score: 23.84, Aligned cols: 85, Identities: 20%/

Supplementary Figure 1

Structural and functional characterization of the site-specific R2 retrotransposon of *Blattella germanica*.

A – Nucleotide sequence of the site-specific R2 retrotransposon of *Blattella germanica* with the environment of the integration site. The sequences of the 28S RNA gene are highlighted in gray, the sequence of the open reading frame (ORF) is highlighted in yellow, and the sequences without background highlighting correspond to 5'- and 3'- untranslated regions. The sequences of the primers used to amplify full-length copies of this mobile element are underlined.

B – Domain organization of the protein corresponding to the ORF of the R2 retrotransposon. Zinc finger domains are highlighted in yellow, the c-myb domain in crimson, and the reverse transcriptase domain in blue. The endonuclease-like domain shows significant similarities to Cap-snatching endonucleases (underlined) and Holliday junction resolvases (highlighted in green).

C – Domain organization predicted by SMART (Simple Modular Architecture Research Tool). Blue boxes indicate zinc finger domains, and gray boxes indicate reverse transcriptase domains. The amino acid sequences corresponding to the three zinc finger domains located at the N-terminus of the ORF are shown.

In this study, for the identification of similarity and prediction of the structure of the domains of the R2 retrotransposon, we applied HHpred software, which was used for the detection of HHsearch PDB hits. The maximum similarity was revealed between the analyzed domain of the R2 retrotransposon of *B. germanica* and the following proteins with known structures related to the **D** – c-myb motif, **E** – reverse transcriptase domain, **F** – endonuclease-like domain (Cap-snatching endonucleases and Holliday junction resolvases).