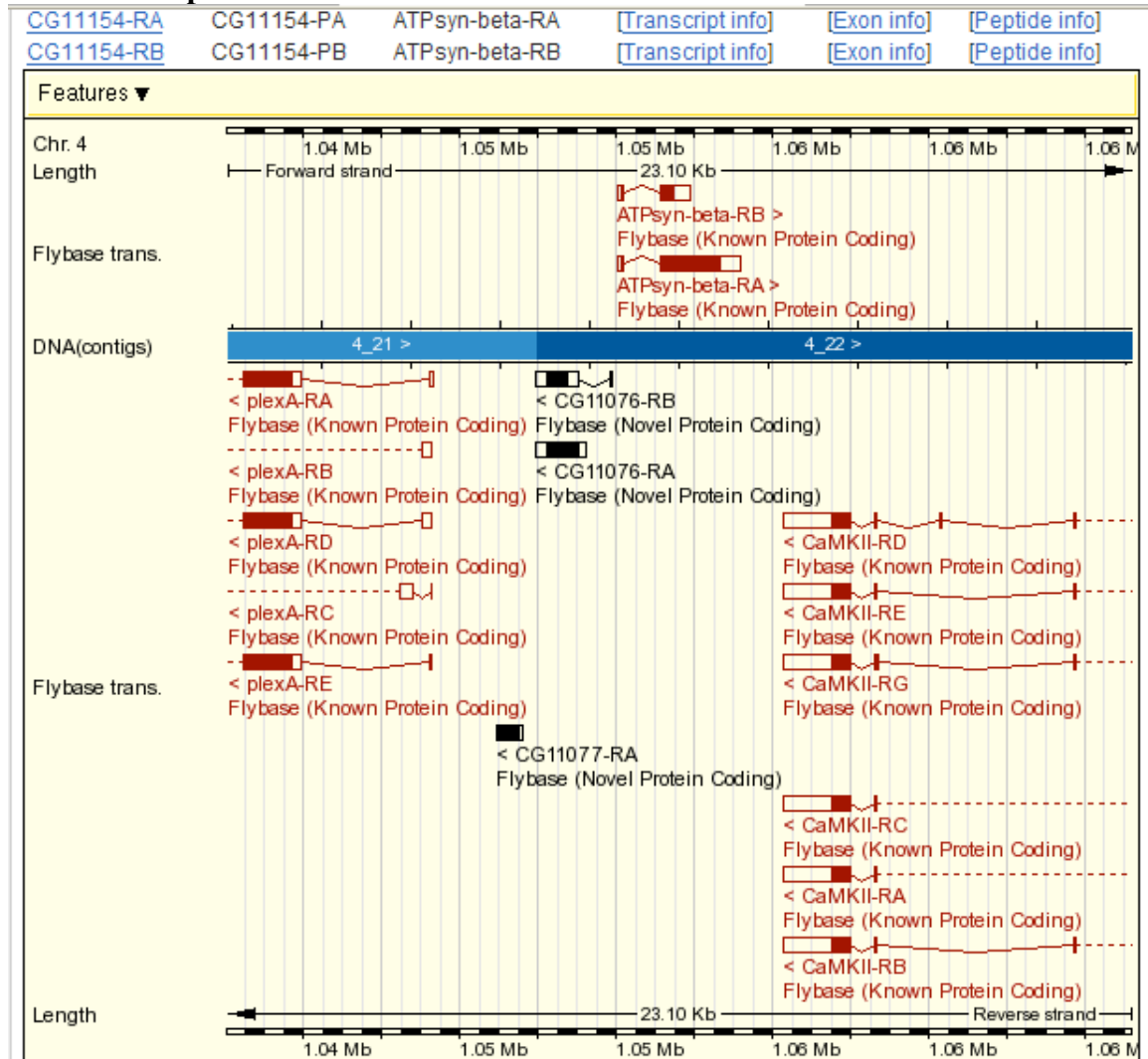


Annotation Documentation Sample for Contig 7.2A

Fly base gene ID=CG11154

```
>contig7.2 Predicted Protein
MFALRAASKADKNLLPFLGQLSRSHAAKAAKAAAAANGKIVAVIGAVVDV
QFDDNLPPIILNALEVNDNRSPRLVLEVAQHLGENTVRTIAMDGTEGLVRGQ
KVLDTGYPPIRIPVGAETLGRIINVIGEPIDERGPIDTDKTAIIHAEPEF
VQMSVEQEILVTGIKVVDDLAPYAKGGKIGLFGGAGVGKTVLIMELINNV
AKAHGGYSVFAGVGERTRENDLYNEMIEGGVILSKDKTSKVALVYGQMN
EPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLG
RIPSAVGYQPTLATDMGSMQERITTTKKSITSVQAIYVPADDLTPAPA
TTFAHLDAATTVLSRAIAELGIYPAVDPLDSTSRIMDPNIIGQEHYVARG
VQKILQDYKSLQDIIAILGMDLSEEDKLTVARARKIQRFLSQPFQVAEV
FTGHAGKLVPLEQTIKGFSAIAGDYDHLPEVAFYMVGPIIEEVVEKADRL
AKEAA
```

There are 2 splice variants



Gene: ATPsyn-beta (FlyBaseName gene)

Flybase Gene ID: **CG11154**

Genomic Location: This gene can be found on Chromosome 4 at location 1,052,064-1,055,167.

The start of this gene is located in Chunk 4_22.

Description: ATP synthase beta chain, mitochondrial precursor ([EC 3.6.3.14](#)). Source: Uniprot/SWISSPROT Q05825

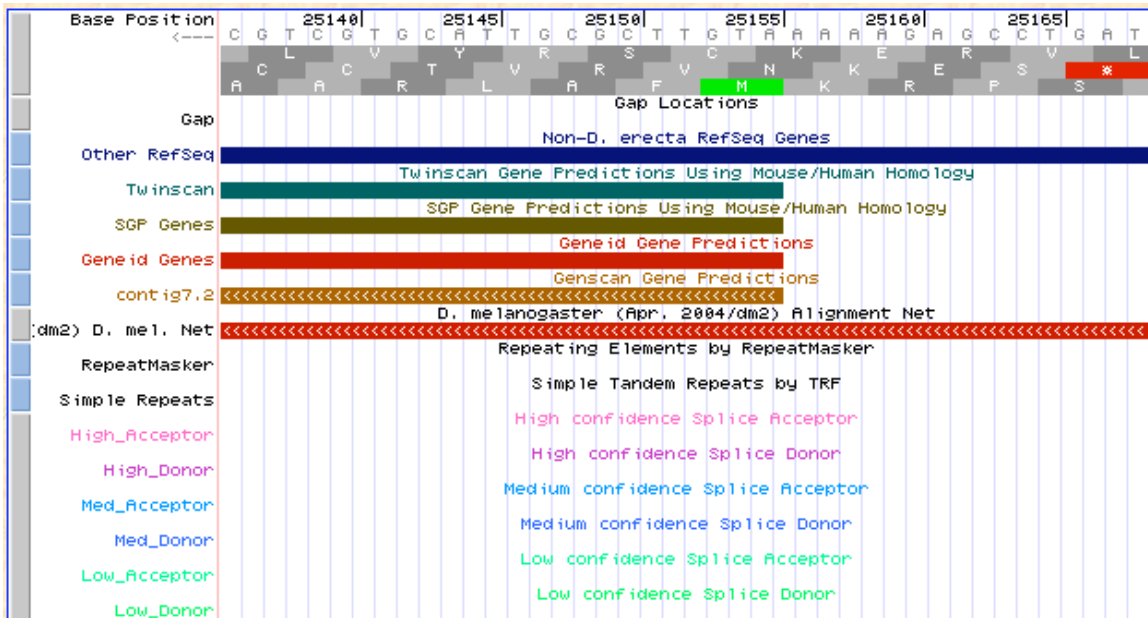
contig 7.2 Splice variant A *D. melanogaster* orthologue

MFALRAASKADKNLLPFLGQLSRSHAAKAAKAAAAANGKIVAVIGAVVDVQFDDNLPPIIL
NALEVDNRSRPLVLEVAQHLGENTVRTIAMDGTEGLVRGQKVLDTGYP I R I P V G A E T L G R
I I N V I G E P I D E R G P I D T D K T A A I H A E A P E F V Q M S V E Q E I L V T G I K V V D L L A P Y A K G G K I G
L F G G A G V G K T V L I M E L I N N V A K A H G G Y S V F A G V G E R T R E G N D L Y N E M I E G G V I S L K D K T S
K V A L V Y G Q M N E P P G A R A R V A L T G L T V A E Y F R D Q E G Q D V L L F I D N I F R F T Q A G S E V S A L L G
R I P S A V G Y Q P T L A T D M G S M Q E R I T T T K K S I T S V Q A I Y V P A D D L T D P A P A T T F A H L D A T T
V L S R A I A E L G I Y P A V D P L D S T S R I M D P N I I G Q E H Y N V A R G V Q K I L Q D Y K S L Q D I I A I L G M
D E L S E E D K L T V A R A R K I Q R F L S Q P F Q V A E V F T G H A G K L V P L E Q T I K G F S A I L A G D Y D H L P
E V A F Y M V G P I E E V V E K A D R L A K E A A

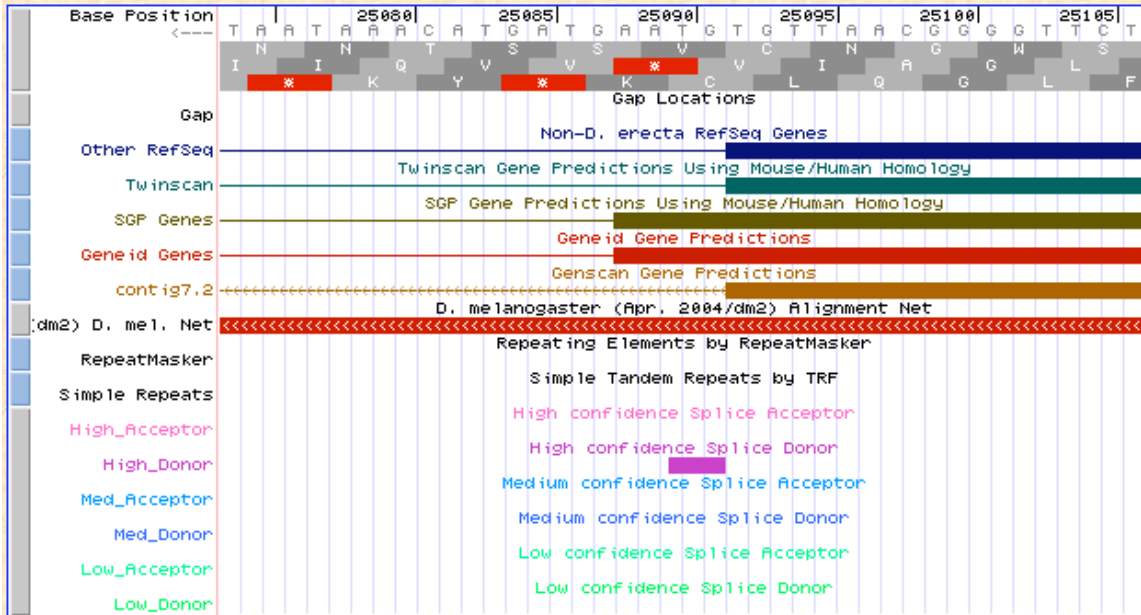
Exon1

Score = 43.9 bits (102), Expect = 0.010
Identities = 21/21 (100%), Positives = 21/21 (100%), Gaps = 0/21 (0%)
Frame = -3

Query 1 MFALRAASKADKNLLPFLGQL 21
MFALRAASKADKNLLPFLGQL
Sbjct 25155 MFALRAASKADKNLLPFLGQL 25093



Exon 1 starts at 25155 with methionine.



Ex1 GT donor at 25090, ends at 25092(1).

Exon2

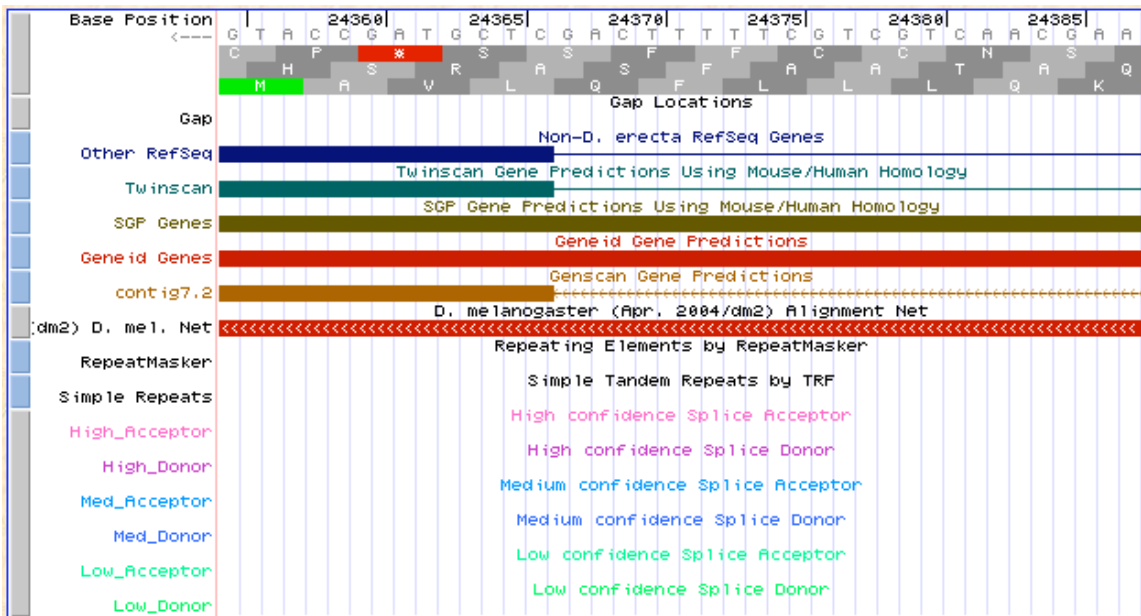
Score = 202 bits (514), Expect = 2e-50

Identities = 104/105 (99%), Positives = 105/105 (100%), Gaps = 0/105 (0%)
 Frame = -2

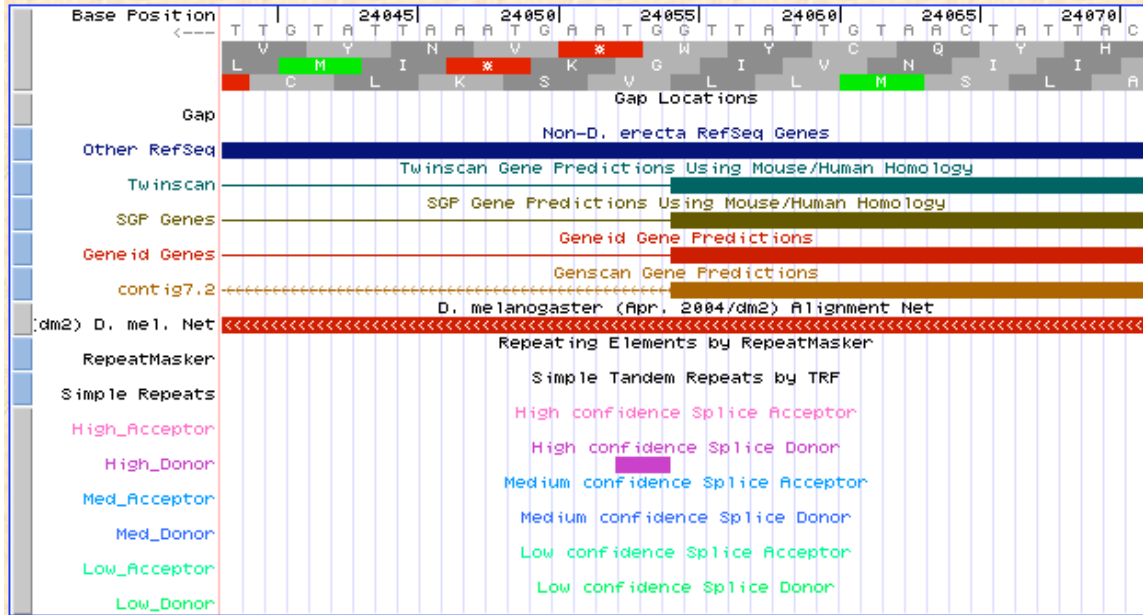
```

Query 1 SRSHAAKAAKAAAANGKIVAVIGAVVDVQFDDNLPPILNALEV DNRSPRLVLEVAQHLG 60
+RSHAAKAAKAAAANGKIVAVIGAVVDVQFDDNLPPILNALEV DNRSPRLVLEVAQHLG
Sbjct 24367 ARSHAAKAAKAAAANGKIVAVIGAVVDVQFDDNLPPILNALEV DNRSPRLVLEVAQHLG 24188

Query 61 ENTVRTIAMDGTEGLVRGQKVLDTGYPIRIPVGAETLGR IINVI G 105
ENTVRTIAMDGTEGLVRGQKVLDTGYPIRIPVGAETLGR IINVI G
Sbjct 24187 ENTVRTIAMDGTEGLVRGQKVLDTGYPIRIPVGAETLGR IINVI G 24053
  
```



EX2 AG acceptor at 24368, starts at 24366(2).



Ex2 GT donor at 24053, ends at 24055(1).

Exon3

Score = 739 bits (1907), Expect = 0.0

Identities = 380/380 (100%), Positives = 380/380 (100%), Gaps = 0/380 (0%)

Frame = -1

```

Query 1      GEPIDERGPIDTDKTAAIHAEAEPEFVQMSVEQEILVTGIKVVDDLAPYAKGGKIGLFGGA 60
             GEPIDERGPIDTDKTAAIHAEAEPEFVQMSVEQEILVTGIKVVDDLAPYAKGGKIGLFGGA
Sbjct 24005  GEPIDERGPIDTDKTAAIHAEAEPEFVQMSVEQEILVTGIKVVDDLAPYAKGGKIGLFGGA 23826

Query 61     VVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYNEMIEGGVISLKDKTSKVALV 120
             VVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYNEMIEGGVISLKDKTSKVALV
Sbjct 23825  VVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYNEMIEGGVISLKDKTSKVALV 23646

Query 121    YGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSA 180
             YGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSA
Sbjct 23645  YGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSA 23466

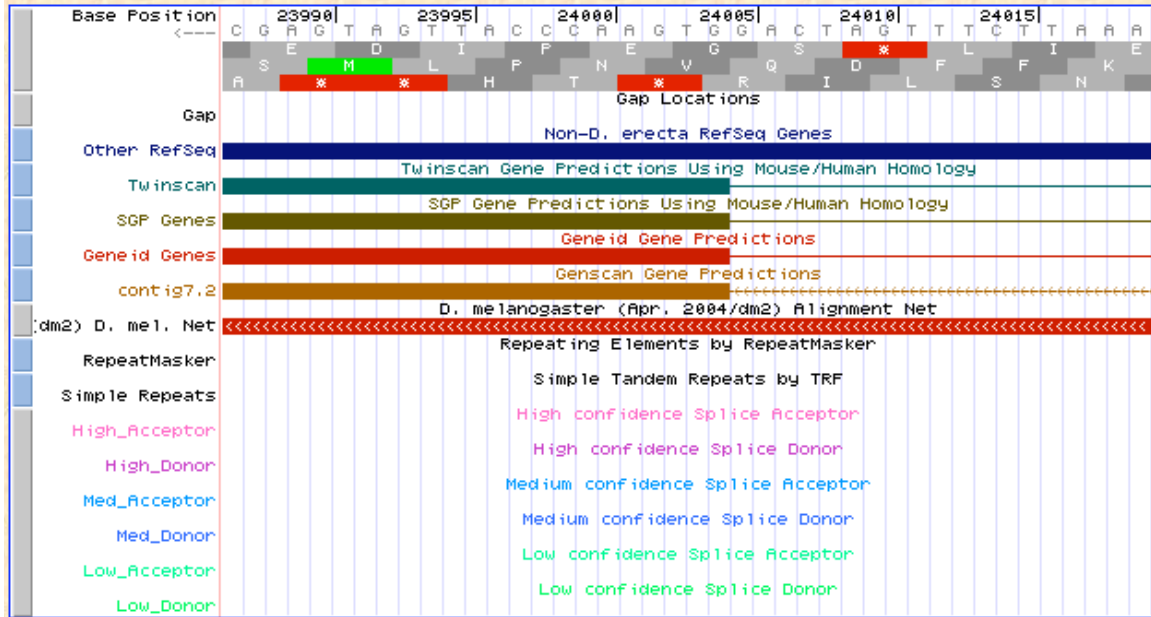
Query 181    VGYQPTLATDMGSMQERITTTKKSITSVQAIYVPADDLTDPAATTF AHLDATTVLSRA 240
             VGYQPTLATDMGSMQERITTTKKSITSVQAIYVPADDLTDPAATTF AHLDATTVLSRA
Sbjct 23465  VGYQPTLATDMGSMQERITTTKKSITSVQAIYVPADDLTDPAATTF AHLDATTVLSRA 23286

Query 241    IAELGIYPAVDPLDSTSRIMDPNIGQEHYNVARGVQKILQDYKSLQDIIAILGMDELSE 300
             IAELGIYPAVDPLDSTSRIMDPNIGQEHYNVARGVQKILQDYKSLQDIIAILGMDELSE
Sbjct 23285  IAELGIYPAVDPLDSTSRIMDPNIGQEHYNVARGVQKILQDYKSLQDIIAILGMDELSE 23106

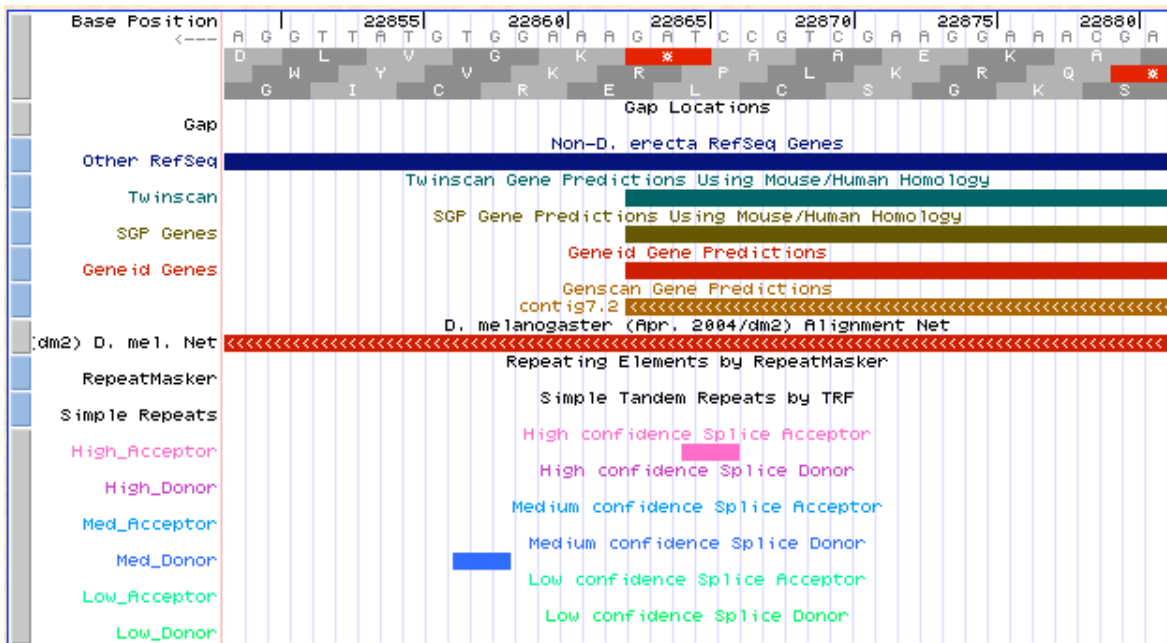
Query 301    EDKLTVARARKIQRFLSQPFQVAEVFTGHAGKLVPLEQTIKGFSAILAGDYDHLPEVAFY 360
             EDKLTVARARKIQRFLSQPFQVAEVFTGHAGKLVPLEQTIKGFSAILAGDYDHLPEVAFY
Sbjct 23105  EDKLTVARARKIQRFLSQPFQVAEVFTGHAGKLVPLEQTIKGFSAILAGDYDHLPEVAFY 22926

Query 361    MVGPIEEVVEKADRLAKEAA 380
             MVGPIEEVVEKADRLAKEAA
Sbjct 22925  MVGPIEEVVEKADRLAKEAA 22866

```



EX3 AG acceptor at 24006, starts 24004(2).



Ex3 ends at 22863 with a stop codon, coding region ends at 22863.