PGT11-S-A-P Blast 70911J

>ens|ENSRNOP00000012162 pep:known
chromosome:RGSC3.4:8:108012829:108098561:1
gene:ENSRNOG00000009005 transcript:ENSRNOT00000012162
Length = 641

Score = 49.9 bits (105), Expect = 3e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 SWRMKKNREYSLQENTSGLI 20
SWRMKKNREYSLQENTSGLI
Sbjct: 622 SWRMKKNREYSLQENTSGLI 641

>sp|Q00910|SO2A1_RAT (Slco2a1)Solute carrier organic anion
transporter family member 2A1 (Solute carrier family 21
member 2) (Prostaglandin transporter) (PGT) (Matrin F/G
1).[Rattus norvegicus]
Length = 643

Score = 49.9 bits (105), Expect = 3e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 SWRMKKNREYSLQENTSGLI 20
SWRMKKNREYSLQENTSGLI
Sbjct: 624 SWRMKKNREYSLQENTSGLI 643

>sp|Q9EPT5|SO2A1_MOUSE (Slco2a1)Solute carrier organic anion
transporter family member 2A1 (Solute carrier family 21
member 2) (Prostaglandin transporter) (PGT).[Mus
musculus]
Length = 643

Score = 45.8 bits (96), Expect = 5e-04
Identities = 18/20 (90%), Positives = 19/20 (95%)

Query: 1 SWRMKKNREYSLQENTSGLI 20
SWR+KKNREYSLQEN SGLI
Sbjct: 624 SWRVKKNREYSLQENASGLI 643

>ens|ENSMODP00000023067 pep:novel
chromosome:BROADO5:4:94500271:94581752:-1
gene:ENSMODG00000018498 transcript:ENSMODT00000023479
Length = 606

Score = 38.3 bits (79), Expect = 0.100
Identities = 14/19 (73%), Positives = 16/19 (84%)

Query: 2 WRMKKNREYSLQENTSGLI 20
WR+KKN+EY LQE SGLI
Sbjct: 588 WRVKKNKEYDLQEKASGLI 606

>ens|ENSMODP00000023065 pep:novel
chromosome:BROADO5:4:94500271:94581752:-1
gene:ENSMODG00000018498 transcript:ENSMODT00000023477
Length = 609

Score = 38.3 bits (79), Expect = 0.100

```
 Identities = 14/19 (73%), Positives = 16/19 (84%)

Query: 2   WRMKKNREYSLQENTSGLI 20
           WR+KKN+EY LQE  SGLI
Sbjct: 591 WRVKKNKEYDLQEKASGLI 609


>ens|ENSMODP00000036628 pep:novel
           chromosome:BROADO5:4:94500271:94581752:-1
           gene:ENSMODG00000018498 transcript:ENSMODT00000038221
          Length = 610

 Score = 38.3 bits (79), Expect = 0.100
 Identities = 14/19 (73%), Positives = 16/19 (84%)

Query: 2   WRMKKNREYSLQENTSGLI 20
           WR+KKN+EY LQE  SGLI
Sbjct: 592 WRVKKNKEYDLQEKASGLI 610


>ens|ENSLAFP00000008303 pep:novel
           genescaffold:BROADE1:GeneScaffold_4575:126570:173558:-1
           gene:ENSLAFG00000009909 transcript:ENSLAFT00000009909
          Length = 612

 Score = 37.8 bits (78), Expect = 0.14
 Identities = 13/20 (65%), Positives = 18/20 (90%)

Query: 1   SWRMKKNREYSLQENTSGLI 20
           SWR+KKN+EY++QE  +GLI
Sbjct: 593 SWRVKKNKEYNVQEKATGLI 612


>tr|Q8HZ68|Q8HZ68_BOVIN Prostaglandin transporter.[Bos taurus]
          Length = 644

 Score = 37.8 bits (78), Expect = 0.14
 Identities = 13/20 (65%), Positives = 18/20 (90%)

Query: 1   SWRMKKNREYSLQENTSGLI 20
           SWR+KKN+EY++QE  +GLI
Sbjct: 625 SWRVKKNKEYNVQEKAAGLI 644


>ens|ENSCAFP00000009991 pep:known
           chromosome:BROADD2:23:33851690:33931074:-1
           gene:ENSCAFG00000006695 transcript:ENSCAFT00000010783
          Length = 644

 Score = 35.6 bits (73), Expect = 0.64
 Identities = 12/20 (60%), Positives = 18/20 (90%)

Query: 1   SWRMKKNREYSLQENTSGLI 20
           SWR+KK++EY++QE  +GLI
Sbjct: 625 SWRVKKSKEYNVQEKAAGLI 644


>tr|Q5FX75|Q5FX75_CANFA Prostaglandin transporter.[Canis familiaris]
          Length = 644

 Score = 35.6 bits (73), Expect = 0.64
 Identities = 12/20 (60%), Positives = 18/20 (90%)
```

```
Query: 1   SWRMKKNREYSLQENTSGLI 20
           SWR+KK++EY++QE  +GLI
Sbjct: 625 SWRVKKSKEYNVQEKAAGLI 644


>ens|ENSBTAP00000001747 pep:known
           chromosome:Btau_3.1:1:125478811:125566321:1
           gene:ENSBTAG00000001324 transcript:ENSBTAT00000001747
          Length = 644

 Score = 35.1 bits (72), Expect = 0.87
 Identities = 12/20 (60%), Positives = 17/20 (85%)

Query: 1   SWRMKKNREYSLQENTSGLI 20
           SWR+KKN+EY++QE  + LI
Sbjct: 625 SWRVKKNKEYNVQEKAASLI 644


>tr|Q2VLH9|Q2VLH9_SHEEP Prostaglandin transporter.[Ovis aries]
          Length = 644

 Score = 35.1 bits (72), Expect = 0.87
 Identities = 12/20 (60%), Positives = 17/20 (85%)

Query: 1   SWRMKKNREYSLQENTSGLI 20
           SWR+KKN+EY++QE  + LI
Sbjct: 625 SWRVKKNKEYNVQEKAASLI 644
```