



# ANEXOS



**ANEXO 1:** Secuencias de la Mioglobina bovina: gen (NC 007303), el ARNm (NM 173881) y la proteína (NP 776303.1), tomadas de GeneBank (<http://www.ncbi.nlm.nih.gov/>). En cada caso, en amarillo se resalta la zona amplificada. En la secuencia del gen, el resto del ARNm en azul y los primers en rojo. En la secuencia de mRNA, el resto de la zona transcrita en azul.

**Nombre:** myoglobina [*Bos taurus*]

**Cromosoma:** 5

**GenID:** 280695

**Locus:** NC\_007303

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**ANEXO 2:** Secuencias del gen Glutation S-Transferasa Pi 1 (GSTP1) bovina (NC 007330), tomada de GeneBank (<http://www.ncbi.nlm.nih.gov/>). En amarillo se resalta la zona amplificada, el ARNm en azul y los SNPs encontrados en verde.

**Nombre:** Glutation S-Transferasa Pi 1 (GSTP1) [*Bos taurus*]

**Cromosoma:** 29

**GenID:** 280695

**Locus:** NC\_007330

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841 cgggagacct acgctgtacc agtccaatgc catcctgctg cacctgggcc gcaccctcgg
901 tgagtctctg cactacaagt ggctcagccc aggctggggc ggcaggcatc agccagcctt
961 cctgagcacc tgctgagcct cctccatgtc aatcaaatcg cccagccacc ctgtggaatg
1021 gaggcgtgtg gaggttatct agggcttggc tggtagctca gttggtaaag aatctacctg
1081 caatgcagga gaccccgggt ccattcctgg gtcaggaaga taccctggcg aagggatagg
1141 ctaccactc tagtattctt gggcttccct tgtggctcag ctggtaaaga atccacctgc
1201 agtgctggag acctgggttc gatccctgag ttgggaagat ccctgcctta gagtggggcc
1261 acctgccctg aattccgggc gcggactcag cccctttctt cctgcgcata ctccctcctc
1321 ctgcctggcc caggggacag ggcagccaca tggcctggct gcagggcgct ggggggtcat
1381 gttgccgtgg ctttcaggct cccactcatg cctctgctc tcccgccacc ccagggctgt
1441 atgggaagga ccagcaggag gcggccctgg tggacatggt gaatgacggt gtagaggacc
1501 ttcgctgcaa atacgtctcc ctcatttaca ccaactacgt aagcgcaggc gtcgggggtg
1561 acacggagga caaagaaaga aaggggcttt ttccttctca cctatactg cccccctctt
1621 gtggctctgg ctgatccccg cctggggctg cttctgggtc tgggtggggg ggtgggaatc
1681 aagagccact gtagaccaga cacaccttc tgcctccctg cctgggggag gtaggttca
1741 ggtagcagtg cactgcagaa cggctagag acaggagacg accagcaga ggtggttccc
1801 tgatcctcag cccggggagg tcaggagggc tccttgagc aggtgcagaa ggaggagctt
1861 ctggaagggg tgctggtaact ttcggatgca cgaagtgtgc aggcgcaggg cacatctggg
1921 cacttgggag cagtttcgca gaggcagggg gtgctctgtg gtgcgagcaa atgagagtgt
1981 caggagatga atggagctgg agggacagca ggcccgtctc tgaaggctc ggccagctgg
2041 cttggagatg cgctttgggg ggtctaagca gggcgggtgc tgtgcgatct ggaaagatcc
2101 tgtgaggctt ttgcaaggct ggggagcgat catgacaaga ctggacaaga ggagactcag
2161 cctctgaaat ggacaggatg tggcaatagc ctggggggag gtgaggagag cagggcaggg
2221 ctgggagcagt ggccatcctc tcatccccgg gggcggggac gggacgcgac gggatggcag
2281 catgccaggg ccaggaggat gatacccagc ggcctctctc tggcaggagg caggcaagga
2341 ggactatgtg aaggcgtgct cccagcacct gaagcctttc gagaccctgc tgtcccagaa
2401 caagggtggc caggccttca tegtgggaga ccagggtgagc tggccccacc ccgccccttc
2461 tgacccccgc tctgtccaga tggcacagcc gtgcagagac agcacgggag tcatgggttc
2521 agcaaagctg gggactgcct tgggcgcctt gcccccaac tcccagccc cctgagtccc
2581 atcctgctct gccctgcaga tctcctttgc ggactacaac ctgctggacc tgcttcggat
2641 tcaccagctc ctggcccccga gctgtatgga ctcctccc ctgctctcag cctacgtggc
2701 ccgtctcaac tcccggccca agctcaaggc cttcctggcc tcccctgagc acatgaaccg
2761 gcccatcaac ggcaatggga aacagtga ggccttggca cttctgtggc ctctctgctc gaggcagggg
2821 gctgcctggt cttcctttcc ccaggaccaa taaaacttcc aagagagaa

```

**ANEXO 3: Alineamiento del exón II (zona amplificada) del gen de la mioglobina bovina con los de otras especies (BLAST), en verde se marca la posición polimórfica encontrada.**

**Ovino**

ref|NM\_001078658.1| Ovis aries myoglobin (LOC780509), mRNA  
 gb|DQ995220.1| Ovis aries myoglobin mRNA, complete cds  
 Length=590  
 GENE ID: 780509 LOC780509 | myoglobin [Ovis aries] (10 or fewer PubMed links)  
 Score = 370 bits (200), Expect = 2e-99  
 Identities = 217/225 (97%), Gaps = 2/225 (0%)  
 Strand=Plus/Plus

```

Query 1      GGCTCTTCACAGGTCATCCCAGACCCTGGAGAAATTTGACAAGTTCAAGCACCTGAAGA 60
             |||
Sbjct 95      GGCTCTTCACAGGTCATCCCAGACCCTGGAGAAATTTGACAAGTTCAAGCACCTGAAGA 154

Query 61     CAGAGGCTGAGATGAAGGCCTCCGAGGACCTGAAGAAGCATGGCAACACGGTGCTCACGG 120
             |||
Sbjct 155     CAGAGGCTGAGATGAAGGCCTCCGAGGACCTGAAGAAGCATGGCAACACCGTGCTCACGG 214

Query 121    CCCTGGGGGGTATCCTGAAGAAA-AAGGGTCACCATGAGGCCAGAGGTGAAGCACCTGGCC 179
             |||
Sbjct 215     CCCTAGGGGGTATCCTGGA-AAAGAAGGGTCACCACGAGGCCAGAGGTGAAGCACCTGGCC 273

Query 180    GAGTCACATGCCAACCAAGCACAAGATCCCTGTCAAGTACCTGGAG 224
             |||
Sbjct 274    GAGTCACACGCCAACCAAGCACAAGATCCCTGTCAAGTACCTGGAG 318
  
```

**Porcino**

ref|NM\_214236.1| Sus scrofa myoglobin (MB), mRNA  
 gb|M14433.1|PIGGM Porcine myoglobin mRNA, complete cds  
 Length=1111  
 Score = 287 bits (155), Expect = 1e-74  
 Identities = 202/225 (89%), Gaps = 2/225 (0%)  
 Strand=Plus/Plus

```

Query 1      GGCTCTTCACAGGTCATCCCAGACCCTGGAGAAATTTGACAAGTTCAAGCACCTGAAG 59
             |||
Sbjct 154     GGCTCTTTAAGGGTCACCCCGAGACCCTGGAGAAATTTGACAAGTTTAAGCACCTGAAG 212

Query 60     ACAGAGGCTGAGATGAAGGCCTCCGAGGACCTGAAGAAGCATGGCAACACGGTGCTCACG 119
             |||
Sbjct 213     TCAGAGGATGAGATGAAGGCCTCTGAGGACCTGAAGAAGCACGGCAACACGGTGCTGACT 272

Query 120    GCCCTGGGGGGTATCCTGAAGAAAAAGGGTCACCATGAGGCCAGAGGTGAAGCACCTGGCC 179
             |||
Sbjct 273     GCCCTGGGGGGCATCCTTAAGAAGAAGGGGCATCATGAGGCCAGAGCTGACGCCCTGGCC 332

Query 180    GAGTCACATGCCAACCAAGCACAAGATCCCTGTCAAGTACCTGGAG 224
             |||
Sbjct 333     CAATCGCATGCCACCAAGCACAAGATCCCTGTCAAGTACCTGGAG 377
  
```



**Humano**

ref|NM\_005368.2| Homo sapiens myoglobin (MB), transcript variant 1, mRNA  
 Length=1078  
 Score = 251 bits (278), Expect = 2e-64  
 Identities = 190/224 (84%), Gaps = 0/224 (0%)  
 Strand=Plus/Plus

```

Query 1   GGCTCTTCACAGGTCATCCCAGACCCCTGGAGAAATTTGACAAGTTCAAGCACCTGAAGA 60
          ||||| | | |||| | | |||| | ||||| | ||||| | ||||| | ||||| |
Sbjct 175  GGCTCTTTAAGGGTCACCCAGAGACTCTGGAGAAGTTTGAACAAGTTCAAGCACCTGAAGT 234

Query 61  CAGAGGCTGAGATGAAGGCCTCCGAGGACCTGAAGAAGCATGGCAACACGGTGCTCACGG 120
          ||||| | ||||| | || |||| | | ||||| | || | ||||| | |
Sbjct 235  CAGAGGACGAGATGAAGGCGTCTGAGGACTTAAAGAAGCATGGTGCCACCCTGCTCACCG 294

Query 121  CCCTGGGGGGTATCCTGAAGAAAAGGGTCACCATGAGGCAAGAGGTGAAGCACCTGGCCG 180
          ||||| | | |||| | |||| | |||| | | ||||| | || | |||| |
Sbjct 295  CCCTGGGTGGCATCCTTAAGAAGAAGGGGCATCATGAGGCAAGAGATTAAGCCCCTGGCAC 354

Query 181  AGTCACATGCCAACCAAGCACAAAGATCCCTGTCAAGTACCTGGAG 224
          ||| | |||| | ||||| | |||| | | ||||| | ||
Sbjct 355  AGTCGCATGCCACCAAGCACAAAGATCCCCGTGAAGTACCTGGAG 398

```

**Ratón**

>ref|NM\_013593.2| Mus musculus myoglobin (Mb), mRNA  
 Length=1100  
 Score = 210 bits (232), Expect = 4e-52  
 Identities = 173/211 (81%), Gaps = 0/211 (0%)  
 Strand=Plus/Plus

```

Query 14  TCATCCCGAGACCCTGGAGAAATTTGACAAGTTCAAGCACCTGAAGACAGAGGCTGAGAT 73
          ||| | | ||||| | || ||||| | || |||| | |||| | || ||
Sbjct 272  TCACCCTGAGACCCTGGATAAGTTTGAACAAGTTCAAGAAGTTGAAGTCAGAGGAAGATAT 331

Query 74  GAAGGCCTCCGAGGACCTGAAGAAGCATGGCAACACGGTGCTCACGGCCCTGGGGGGTAT 133
          ||||| | | ||||| | ||||| | || | ||||| | ||||| | ||
Sbjct 332  GAAGGGCTCAGAGGACCTGAAGAAGCATGGTTGCACCCTGCTCACAGCCCTGGGTACCAT 391

Query 134  CCTGAAGAAAAGGGTCACCATGAGGCAAGAGGTGAAGCACCTGGCCGAGTCACATGCCAA 193
          ||||| | |||| | || || | || | || | || | || || | || ||
Sbjct 392  CCTGAAGAAGAAGGGACAACATGCTGCAGATCCAGCCTCTAGCCCAATCACACGCCAC 451

Query 194  CAAGCACAAAGATCCCTGTCAAGTACCTGGAG 224
          ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
Sbjct 452  CAAGCACAAAGATCCCGGTCAAGTACCTGGAG 482

```

**ANEXO 4:** Alineamiento de la secuencia proteica de la mioglobina bovina con los de otras especies (BLAST), en amarillo se marca la sección de la proteína codificada por el segmento amplificado.

### Búfalo

[sp|P84997.2|MYG\\_BUBBU](#) RecName: Full=Myoglobin Length=154  
 Score = 303 bits (777), Expect = 3e-81, Method: Compositional matrix adjust.  
 Identities = 151/154 (99%), Positives = 152/154 (99%), Gaps = 0/154 (0%)

```

Query 1  MGLSDGEWQLVLNAWGKVEADVAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE 60
          MGLSDGEWQLVLNAWGKVE DVAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE
Sbjct 1  MGLSDGEWQLVLNAWGKVEDVAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE 60

Query 61 DLKKGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLHAKH 120
          DLKKGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLH KH
Sbjct 61 DLKKGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLHDKH 120

Query 121 PSDFGADAQAAMSKALELFRNDMAAQYKVLGFHG 154
          PSDFGADAQAAMSKALELFRN+MAAQYKVLGFHG
Sbjct 121 PSDFGADAQAAMSKALELFRNEMAAQYKVLGFHG 154
  
```

### Ovino

[ref|NP\\_001072126.1|](#) myoglobin [Ovis aries]  
[gb|ABJ97274.1|](#) myoglobin [Ovis aries] Length=154  
[GENE ID: 780509 LOC780509](#) | myoglobin [Ovis aries] (10 or fewer PubMed links)  
 Score = 301 bits (771), Expect = 1e-80, Method: Compositional matrix adjust.  
 Identities = 150/154 (98%), Positives = 151/154 (99%), Gaps = 0/154 (0%)

```

Query 1  MGLSDGEWQLVLNAWGKVEADVAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE 60
          MGLSDGEWQLVLNAWGKVEA VAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE
Sbjct 1  MGLSDGEWQLVLNAWGKVEAGVAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE 60

Query 61 DLKKGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLHAKH 120
          DLKKGNTVLTALGGIL+KKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLHAKH
Sbjct 61 DLKKGNTVLTALGGILEKKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLHAKH 120

Query 121 PSDFGADAQAAMSKALELFRNDMAAQYKVLGFHG 154
          PSDFGADAQ AMSKALELFRNDMAAQYKVLGF G
Sbjct 121 PSDFGADAQGAMSKALELFRNDMAAQYKVLGFQG 154
  
```

### Equino

[ref|NP\\_001157488.1|](#) myoglobin [Equus caballus]  
[sp|P68083.2|MYG\\_EQUBU](#) RecName: Full=Myoglobin  
[sp|P68082.2|MYG\\_HORSE](#) RecName: Full=Myoglobin  
 Length=154  
[GENE ID: 100054434 MB](#) | myoglobin [Equus caballus] (10 or fewer PubMed links)  
 Score = 279 bits (713), Expect = 9e-74, Method: Compositional matrix adjust.  
 Identities = 136/154 (89%), Positives = 144/154 (94%), Gaps = 0/154 (0%)

```

Query 1  MGLSDGEWQLVLNAWGKVEADVAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE 60
          MGLSDGEWQ VLN WGKVEAD+AGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE
Sbjct 1  MGLSDGEWQVLNVWGKVEADIAGHGQEVLI R LFTGHPETLEKFDKFKHLKTEAEMKASE 60

Query 61 DLKKGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKI PVKYLEFISDAIIHVLHAKH 120
  
```

```

Sbjct 61 DLKKHG VLTALGGILKKKGHHEAE+K LA+SHA KHKIP+KYLEFISDAIIHVLH+KH 120
          DLKKHGTVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISDAIIHVLHSHK 120
Query 121 PSDFGADAQAAMSKALELFRNDMAAQYKVLGFHG 154
          P DFGADAQ AM+KALELFRND+AA+YK LGF G
Sbjct 121 PGDFGADAQGAMTKALELFRNDIAAKYKELGFQG 154

```

### Porcino

[ref|NP\\_999401.1|](#) myoglobin [Sus scrofa]  
[sp|P02189.2|MYG\\_PIG](#) RecName: Full=Myoglobin  
[gb|AAA31073.1|](#) myoglobin [Sus scrofa]  
 Length=154  
[GENE ID: 397467 MB](#) | myoglobin [Sus scrofa] (10 or fewer PubMed links)  
 Score = 276 bits (705), Expect = 7e-73, Method: Compositional matrix adjust.  
 Identities = 136/154 (89%), Positives = 142/154 (93%), Gaps = 0/154 (0%)

```

Query 1 MGLSDGEWQLVLNNAWGKVEADVAGHGQEVLI RLF GHPETLEKFDKFKHLKTEAEMKASE 60
          MGLSDGEWQLVLN WGKVEADVAGHGQEVLI RLF GHPETLEKFDKFKHLK+E EMKASE
Sbjct 1 MGLSDGEWQLVLNVWGKVEADVAGHGQEVLI RLF KHPETLEKFDKFKHLKSEDEMASE 60

Query 61 DLKKHGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKIPVKYLEFISDAIIHVLHAKH 120
          DLKKHGNTVLTALGGILKKKGHHEAE+ LA+SHA KHKIPVKYLEFIS+AII VL +KH
Sbjct 61 DLKKHGNTVLTALGGILKKKGHHEAELTPLAQSHATKHKIPVKYLEFISEAIIQVLQSKH 120

Query 121 PSDFGADAQAAMSKALELFRNDMAAQYKVLGFHG 154
          P DFGADAQ AMSKALELFRNDMAA+YK LGF G
Sbjct 121 PGDFGADAQGAMSKALELFRNDMAAKYKELGFQG 154

```

### Conejo

[sp|P02170.2|MYG\\_RABIT](#) RecName: Full=Myoglobin  
 Length=154  
 Score = 275 bits (703), Expect = 1e-72, Method: Compositional matrix adjust.  
 Identities = 136/154 (89%), Positives = 143/154 (93%), Gaps = 0/154 (0%)

```

Query 1 MGLSDGEWQLVLNNAWGKVEADVAGHGQEVLI RLF HPETLEKFDKFKHLK+E EMKASE 60
          MGLSD EWQLVLN WGKVEAD+AGHGQEVLI RLF HPETLEKFDKFKHLK+E EMKASE
Sbjct 1 MGLSDAEWQLVLNVWGKVEADLAGHGQEVLI RLF HTHPETLEKFDKFKHLKSEDEMASE 60

Query 61 DLKKHGNTVLTALGGILKKKGHHEAEVKHLAESHANKHKIPVKYLEFISDAIIHVLHAKH 120
          DLKKHGNTVLTALG ILKKKGHHEAE+K LA+SHA KHKIPVKYLEFIS+AIIHVLH+KH
Sbjct 61 DLKKHGNTVLTALGAILKKKGHHEAEIKPLAQSHATKHKIPVKYLEFISEAIIHVLHSHK 120

Query 121 PSDFGADAQAAMSKALELFRNDMAAQYKVLGFHG 154
          P DFGADAQAAMSKALELFRND+AAQYK LGF G
Sbjct 121 PGDFGADAQAAMSKALELFRNDIAAQYKELGFQG 154

```

**ANEXO 5:** Alineamiento de la secuencia proteica de la Glutation S-Transferasa Pi 1 (GSTP1) bovina con los de otras especies (BLAST), en amarillo se marca la sección de la proteína codificada por el segmento amplificado.

### Equino

ref|XP\_001498156.1| PREDICTED: similar to glutathione S-transferase, class-pi [Equus caballus]  
 Length=210  
 GENE ID: 100053249 LOC100053249 | similar to glutathione S-transferase, class-pi [Equus caballus]  
 Score = 404 bits (1037), Expect = 4e-111, Method: Compositional matrix adjust.  
 Identities = 192/210 (92%), Positives = 204/210 (98%), Gaps = 0/210 (0%)

Query	1	MPPYTIVYFPVQGRCEAMRMLLADQGQSWKEEVVAMQSWLQGPKASCLYGQLPKFQDGD	60
		MPPYTIVYF V+GRCEAMRMLLADQGQSWKEEVV + +W+QGPKASCLYGQLPKFQDGD	
Sbjct	1	MPPYTIVYFVVRGRCCEAMRMLLADQGQSWKEEVVTVDTWVMQGPLKASCLYGQLPKFQDGD	60
Query	61	LTLYQSNAILRHLGRITLGLYGKDQQAALVDMVNDGVEDLRCKYVSLIYTNYEAGKEDYV	120
		LTLYQSNAILRHLGR+LGLYGKDQ+EAALVDMVNDGVEDLRCKYV+LIYTNYEAGKEDYV	
Sbjct	61	LTLYQSNAILRHLGRSLGLYGKDQREAALVDMVNDGVEDLRCKYVTLIYTNYEAGKEDYV	120
Query	121	KALPQHLKPFETLLSQNKGGQAFIVGDQISFADYNLLDLLRIHQVLAPSCLDSPFLLSAY	180
		KALP HLPKPFETLLSQN+GGQAFIVG+QISFADYNLLDLL IHQVLAPSCLDSPFLLSAY	
Sbjct	121	KALPGHLKPFETLLSQNQGGQAFIVGNQISFADYNLLDLLLIHQVLAPSCLDSPFLLSAY	180
Query	181	VARLNSRPKLKAFLASPEHMNRPINGNGKQ 210	
		VARL++RPKLKAFLASPEH+N PINGNGKQ	
Sbjct	181	VARLSARPKLKAFLASPEHVNLPINGNGKQ 210	

### Perro

ref|XP\_537961.2| PREDICTED: similar to Glutathione S-transferase P (GST 7-7) (Chain 7) (GST class-pi) [Canis familiaris]  
 Length=231  
 GENE ID: 480844 LOC480844 | similar to Glutathione S-transferase P (GST 7-7) (Chain 7) (GST class-pi) [Canis lupus familiaris]  
 Score = 397 bits (1021), Expect = 3e-109, Method: Compositional matrix adjust.  
 Identities = 187/210 (90%), Positives = 203/210 (97%), Gaps = 0/210 (0%)

Query	1	MPPYTIVYFPVQGRCEAMRMLLADQGQSWKEEVVAMQSWLQGPKASCLYGQLPKFQDGD	60
		MPPYTI YFPV+GRCEAMRMLLADQGQSWKEEVV M++W++G LKASCLYGQLPKFQDGD	
Sbjct	22	MPPYTITYFPVRGRCCEAMRMLLADQGQSWKEEVVMTMETWVMKGSGLKASCLYGQLPKFQDGD	81
Query	61	LTLYQSNAILRHLGRITLGLYGKDQQAALVDMVNDGVEDLRCKYVSLIYTNYEAGKEDYV	120
		LTLYQSNAILRHLGR+LGLYGKDQQAAL+D+VNDGVEDLRCKY LIYTNYEAGKE+YV	
Sbjct	82	LTLYQSNAILRHLGRSLGLYGKDQQAALLDVNDGVEDLRCKYALLIYTNYEAGKEEYV	141
Query	121	KALPQHLKPFETLLSQNKGGQAFIVGDQISFADYNLLDLLRIHQVLAPSCLDSPFLLSAY	180
		KALP +LKPFPETLLSQN+GGQAFIVG+QISFADYNLLDLL IHQVLAPSCLDSPFLLSAY	
Sbjct	142	KALPGYLKPFETLLSQNEGGQAFIVGNQISFADYNLLDLLLIHQVLAPSCLDSPFLLSAY	201

Query 181 VARLNSRPKLKAFLASPEHMNRPINGNGKQ 210  
 VARL++RPKLKAFL+SPEH+NRPINGNGKQ  
 Sbjct 202 VARLSARPKLKAFLSSPEHVNRPINGNGKQ 231

### Humano

[gb|AAH10915.1](#) | Glutathione S-transferase pi 1 [Homo sapiens]

Length=210

Score = 386 bits (992), Expect = 8e-106, Method: Compositional matrix adjust.

Identities = 182/210 (87%), Positives = 198/210 (95%), Gaps = 0/210 (0%)

Query 1 MPPYTIVYFPVQGRCEAMRMLLADQGQSWKEEVVAMQSWLQGPLKASCLYGQLPKFQDGD 60  
 MPPYT+VYFPV+GRC A+RMLLADQGQSWKEEVV +++W +G LKASCLYGQLPKFQDGD  
 Sbjct 1 MPPYTVVYFPVRGRCAALRMLLADQGQSWKEEVVTVETWQEGSLKASCLYGQLPKFQDGD 60

Query 61 LTLYQSNAILRHLGRTLGLYGKDDQEAALVDMVNDGVEDLRCKYVSLIYTNYEAGKEDYV 120  
 LTLYQSN ILRHLGRTLGLYGKDDQEAALVDMVNDGVEDLRCKYVSLIYTNYEAGK+DYV  
 Sbjct 61 LTLYQSNITILRHLGRTLGLYGKDDQEAALVDMVNDGVEDLRCKYVSLIYTNYEAGKDDYV 120

Query 121 KALPQHLKPFETLLSQNKGGQAFIVGDQISFADYNLLDLLRIHQVLAPSCLDSPILLSAY 180  
 KALP LKPFETLLSQN+GG+ FIVGDQISFADYNLLDLL IH+VLAP CLD+FILLSAY  
 Sbjct 121 KALPGQLKPFETLLSQNQGGKTFIVGDQISFADYNLLDLLLIHEVLAPGCLDAFILLSAY 180

Query 181 VARLNSRPKLKAFLASPEHMNRPINGNGKQ 210  
 V RL++RPKLKAFLASPE++N PINGNGKQ  
 Sbjct 181 VGRLSARPKLKAFLASPEYVNLPIPINGNGKQ 210

### Rata

[ref|NP\\_036709.1](#) | glutathione S-transferase P [Rattus norvegicus]

Length=210

[GENE ID: 24426 Gstp1](#) | glutathione S-transferase pi 1 [Rattus norvegicus]  
 (Over 10 PubMed links)

Score = 387 bits (993), Expect = 6e-106, Method: Compositional matrix adjust.

Identities = 180/210 (86%), Positives = 200/210 (96%), Gaps = 0/210 (0%)

Query 1 MPPYTIVYFPVQGRCEAMRMLLADQGQSWKEEVVAMQSWLQGPLKASCLYGQLPKFQDGD 60  
 MPPYTIVYFPV+GRCEA RMLLADQGQSWKEEVV + WLQG LK++CLYGQLPKF+DGD  
 Sbjct 1 MPPYTIVYFPVRGRCEATRMLLADQGQSWKEEVVTVETWQEGSLKSTCLYGQLPKFEDGD 60

Query 61 LTLYQSNAILRHLGRTLGLYGKDDQEAALVDMVNDGVEDLRCKYVSLIYTNYEAGKEDYV 120  
 LTLYQSNAILRHLGR+LGLYGKDDQ+EAALVDMVNDGVEDLRCKY +LIYTNYE GK+DYV  
 Sbjct 61 LTLYQSNAILRHLGRSLGLYGKDDQEAALVDMVNDGVEDLRCKYGTLIYTNYENGKDDYV 120

Query 121 KALPQHLKPFETLLSQNKGGQAFIVGDQISFADYNLLDLLRIHQVLAPSCLDSPILLSAY 180  
 KALP HLKPFETLLSQN+GG+AFIVG+QISFADYNLLDLL +HQVLAP CLD+FILLSAY  
 Sbjct 121 KALPGHLKPFETLLSQNQGGKAFIVGNQISFADYNLLDLLLVHQVLAPGCLDNFILLSAY 180

Query 181 VARLNSRPKLKAFLASPEHMNRPINGNGKQ 210  
 VARL++RPK+KAFL+SP+H+NRPINGNGKQ  
 Sbjct 181 VARLSARPKIKAFLLSPDHLNRPINGNGKQ 210

