Figure 1: STEAP-1 SSH sequence of 436 nucleotides. (SEQ ID NO: 1)

```
  1 GTACAGCAAA AAAGAAACTG AGAAGCCCAA ACTGCTTTCT TGTTAACATC CACTTATCCA
 61 ACCAATGTGG AAACTTCTTA TACTTGGTTC CATTATGAAG TTGGACAATT GCTGCTATCA
121 CACCTGGCAG GTAAACCAAT GCCAAGAGAG TGATGGAAAC CATTGGCAAG ACTTTGTTGA
181 TGACCAGGAT TGGAATTTTA TAAAAATATT GTTGATGGGA AGTTGCTAAA GGGTGAATTA
241 CTTCCCTCAG AAGAGTGTAA AGAAAAGTCA GAGATGCTAT AATAGCAGCT ATTTTAATTG
301 GCAAGTGCCA CTGTGGAAAG AGTTCCTGTG TGTGCTGAAG TTCTGAAGGG CAGTCAAATT
361 CATCAGCATG GGCTATTTGG TGCAAATGCA AAAGCACAGG TCTTTTTAGC ATGCTGGTCT
421 CTCCCGTGTC CTTATG
```

Figure 2:

Figure 2A. The cDNA (SEQ ID NO: 2) and amino acid sequence (SEQ ID NO: 3) of STEAP-1 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 66-1085 including the stop codon.

```
   1 ccgagactcacggtcaagctaaggcgaagagtgggtggctgaagccatactattttatag
   1      M  E  S  R  K  D  I  T  N  Q  E  E  L  W  K  M  K  P  R
  61 aattaATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA
  20   R  N  L  E  E  D  D  Y  L  H  K  D  T  G  E  T  S  M  L  K
 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
  40   R  P  V  L  L  H  L  H  Q  T  A  H  A  D  E  F  D  C  P  S
 181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
  60   E  L  Q  H  T  Q  E  L  F  P  Q  W  H  L  P  I  K  I  A  A
 241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
  80   I  I  A  S  L  T  F  L  Y  T  L  L  R  E  V  I  H  P  L  A
 301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
 100   T  S  H  Q  Q  Y  F  Y  K  I  P  I  L  V  I  N  K  V  L  P
 361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
 120   M  V  S  I  T  L  L  A  L  V  Y  L  P  G  V  I  A  A  I  V
 421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
 140   Q  L  H  N  G  T  K  Y  K  K  F  P  H  W  L  D  K  W  M  L
 481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT
 160   T  R  K  Q  F  G  L  L  S  F  F  F  A  V  L  H  A  I  Y  S
 541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA
 180   L  S  Y  P  M  R  R  S  Y  R  Y  K  L  L  N  W  A  Y  Q  Q
 601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
 200   V  Q  Q  N  K  E  D  A  W  I  E  H  D  V  W  R  M  E  I  Y
 661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
 220   V  S  L  G  I  V  G  L  A  I  L  A  L  L  A  V  T  S  I  P
 721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
 240   S  V  S  D  S  L  T  W  R  E  F  H  Y  I  Q  S  K  L  G  I
 781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
 260   V  S  L  L  L  G  T  I  H  A  L  I  F  A  W  N  K  W  I  D
 841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
 280   I  K  Q  F  V  W  Y  T  P  P  T  F  M  I  A  V  F  L  P  I
 901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA
 300   V  V  L  I  F  K  S  I  L  F  L  P  C  L  R  K  K  I  L  K
 961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA
 320   I  R  H  G  W  E  D  V  T  K  I  N  K  T  E  I  C  S  Q  L
1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT
 340   *
1081 TGTAGaattactgtttacacacatttttgttcaatattgatatattttatcaccaacatt
1141 tcaagtttgtatttgttaataaaatgattacaaggaaaaaaaaaaaaaaaaa
```

Figure 2B. The cDNA (SEQ ID NO: 4) and amino acid sequence (SEQ ID NO: 5) of STEAP-1 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                       M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250   F  H  Y  I  Q  V  N  N  I  *
 841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
 901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
 961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattctttacctgtcacctgaatttagtaatgccttttatgttacacaact
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```
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgctttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
```

Figure 2C. The cDNA (SEQ ID NO: 6) and amino acid sequence (SEQ ID NO: 7) of STEAP-1 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 96-944 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                       M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
```

```
121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
 30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
 50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
 70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
 90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
361 CTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAA
110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
601 TCTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250   F  H  Y  I  Q  I  I  H  K  K  S  D  V  P  E  S  L  W  D  P
841 AATTTCACTATATTCAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATC
270   C  L  T  R  F  K  G  L  N  L  I  Q  S  *
901 CTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAGTCATGAacactgccaattaccg
961 tttatgggtagacatctttggaaatttccacaagagcaagctaggaattgtttcccttct
1021 actgggcacaatacacgcattgatttttgcctggaataagtggatagatataaaacaatt
1081 tgtatggtatacacctccaacttttatgatagctgttttccttccaattgttgtcctgat
1141 atttaaaagcatactattcctgccatgcttgaggaagaagatactgaagattagacatgg
1201 ttgggaagacgtcaccaaaattaacaaaactgagatatgttcccagttgtagaattactg
1261 tttacacacatttttgttcaatattgatatattttatcaccaacatttcaagtttgtatt
1321 tgttaataaaatgattattcaaggaaaaaaaaaaaaaaaaaaa
```

Figure 2D. The cDNA (SEQ ID NO: 8) and amino acid sequence (SEQ ID NO: 9) of STEAP-1 v.4. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
  1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
  1                                       M  E  S  R  K  D  I  T  N
 61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
 10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
```

```
121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
 30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
 50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
 70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
 90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  L
541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
601 TGTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250   F  H  Y  I  Q  V  N  N  I  *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
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1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
```

Figure 2E. The cDNA (SEQ ID NO: 10) and amino acid sequence (SEQ ID NO: 11) of STEAP-1 v.5. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                    M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
```

```
301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
 90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
361 CTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAA
110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250   F  H  Y  I  Q  V  N  N  I  *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatatttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaatttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtattttcaact
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2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctattttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
```

Figure 2F. The cDNA (SEQ ID. NO.: 12) and amino acid sequence (SEQ ID NO: 13) of STEAP-1 v.6. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                       M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10    Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30    K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50    A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70    Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90    L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110    P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130    Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
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481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
150 F P H W L D K W M L T R K Q F G L L S F
541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
170 F F A V L H A I Y S L S Y P M R R S Y R
601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
190 Y K L L N W A Y Q Q V Q Q N K E D A W I
661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210 E H D V W R M E I Y V S L G I V G L A I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230 L A L L A V T S I P S V S D S L T W R E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250 F H Y I Q V N N I *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttgttttgtttgtttgttttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctattttgtgcagacattgaaaaaattgtt

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2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttctttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
```

Figure 2G. The cDNA (SEQ ID NO: 14) and amino acid sequence (SEQ ID NO: 15) of STEAP-1 v.7. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                          M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
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661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210 E H D V W R M E I Y V S L G I V G L A I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230 L A L L A V T S I P S V S D S L T W R E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250 F H Y I Q V N N I *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgccacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag

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3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatatttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaa
```

Figure 2H. The cDNA (SEQ ID NO: 16) and amino acid sequence (SEQ ID NO: 17) of STEAP-1 v.8. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                   M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250   F  H  Y  I  Q  V  N  N  I  *
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841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 ttatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctattttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgatttttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc

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3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
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Figure 2I. The cDNA (SEQ ID NO: 18) and amino acid sequence (SEQ ID NO: 19) of STEAP-1 v.9. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                       M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10    Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30    K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50    A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70    Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90    L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110    P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130    Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150    F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170    F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190    Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210    E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230    L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250    F  H  Y  I  Q  V  N  N  I  *
 841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
 901 tgtgtttatgatatagaatatgttgactttacccca taaaaaataacaaatgtttttcaa
 961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
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1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atattctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa

Figure 2J. The cDNA (SEQ ID NO: 20) and amino acid sequence (SEQ ID NO.: 21) of STEAP-1 v.10. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                   M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250   F  H  Y  I  Q  V  N  N  I  *
 841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
 901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
 961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
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1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgctttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaaatatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctattttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttctttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
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Figure 2K. The cDNA (SEQ ID NO: 22) and amino acid sequence (SEQ ID NO: 23) of STEAP-1 v.11. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
  1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
  1                                   M  E  S  R  K  D  I  T  N
 61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
 10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
```

```
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250   F  H  Y  I  Q  V  N  N  I  *
 841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
 901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
 961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacatttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
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1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaatgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
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Figure 2L. The cDNA (SEQ ID NO: 24) and amino acid sequence (SEQ ID NO: 25) of STEAP-1 v.12. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                   M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10    Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30    K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50    A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70    Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
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301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
 90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250   F  H  Y  I  Q  V  N  N  I  *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgttttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgctttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatccctttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
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2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttttgtgcagacattgaaaaaattgtt
2641 catatgatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
```

Figure 2M. The cDNA (SEQ ID NO: 26) and amino acid sequence (SEQ ID NO: 27) of STEAP-1 v.13. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                          M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactatttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10    Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30    K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50    A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70    Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90    L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110    P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130    Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
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```
481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250   F  H  Y  I  Q  V  N  N  I  *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgttttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgctttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgctttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctattttgtgcagacattgaaaaaattgtt
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2641 catattatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagggatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaaa
```

Figure 2N. The cDNA (SEQ ID NO: 28) and amino acid sequence (SEQ ID NO: 29) of STEAP-1 v.14. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                          M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10    Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30    K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50    A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70    Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90    L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110    P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130    Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150    F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170    F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190    Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
```

661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
210 E H D V W R M E I Y V S L G I V G L A I
721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
230 L A L L A V T S I P S V S D S L T W R E
781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
250 F H Y I Q V N N I *
841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgctttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgataagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag

```
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttctttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatatttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
```

Figure 2 (O). The cDNA (SEQ ID NO: 30) and amino acid sequence (SEQ ID NO: 31) of STEAP-1 v.15. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                   M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10    Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30    K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50    A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70    Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90    L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110    P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130    Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150    F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170    F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190    Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210    E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230    L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250    F  H  Y  I  Q  V  N  N  I  *
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841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctattttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttcatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttcttttgcagagcaagctaggaattgtttccccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc

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3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa
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Figure 2P. The cDNA (SEQ ID NO: 32) and amino acid sequence (SEQ ID NO: 33) of STEAP-1 v.16. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                          M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaatta ATG GAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250   F  H  Y  I  Q  V  N  N  I  *
 841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
 901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
 961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgtttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
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1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggttttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgcttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
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2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
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2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
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2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagtagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaaca
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttctttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa

Figure 2Q. The cDNA (SEQ ID NO: 34) and amino acid sequence (SEQ ID NO: 35) of STEAP-1 v.17. The start methionine is underlined. The open reading frame extends from nucleic acid 96-872 including the stop codon.

```
   1 ggggcccgcacctctgggcagcagcggcagccgagactcacggtcaagctaaggcgaaga
   1                                   M  E  S  R  K  D  I  T  N
  61 gtgggtggctgaagccatactattttatagaattaATGGAAAGCAGAAAAGACATCACAA
  10   Q  E  E  L  W  K  M  K  P  R  R  N  L  E  E  D  D  Y  L  H
 121 ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGC
  30   K  D  T  G  E  T  S  M  L  K  R  P  V  L  L  H  L  H  Q  T
 181 ATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAA
  50   A  H  A  D  E  F  D  C  P  S  E  L  Q  H  T  Q  E  L  F  P
 241 CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTC
  70   Q  W  H  L  P  I  K  I  A  A  I  I  A  S  L  T  F  L  Y  T
 301 CACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACA
  90   L  L  R  E  V  I  H  P  L  A  T  S  H  Q  Q  Y  F  Y  K  I
 361 CTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAA
 110   P  I  L  V  I  N  K  V  L  P  M  V  S  I  T  L  L  A  L  V
 421 TTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGG
 130   Y  L  P  G  V  I  A  A  I  V  Q  L  H  N  G  T  K  Y  K  K
 481 TTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGA
 150   F  P  H  W  L  D  K  W  M  L  T  R  K  Q  F  G  L  L  S  F
 541 AGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTT
 170   F  F  A  V  L  H  A  I  Y  S  L  S  Y  P  M  R  R  S  Y  R
 601 TCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACA
 190   Y  K  L  L  N  W  A  Y  Q  Q  V  Q  Q  N  K  E  D  A  W  I
 661 GATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGA
 210   E  H  D  V  W  R  M  E  I  Y  V  S  L  G  I  V  G  L  A  I
 721 TTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAA
 230   L  A  L  L  A  V  T  S  I  P  S  V  S  D  S  L  T  W  R  E
 781 TACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAG
 250   F  H  Y  I  Q  V  N  N  I  *
 841 AATTTCACTATATTCAGGTAAATAATATATAAaataaccctaagaggtaaatcttctttt
 901 tgtgtttatgatatagaatatgttgactttaccccataaaaaataacaaatgtttttcaa
 961 cagcaaagatcttatacttgttccaattaataatgtgctctcctgttgttttccctattg
1021 cttctaattaggacaagtgtttcctagacataaataaaggcattaaaatattctttgtt
1081 ttttttttttgtttgtttgttttttgtttgtttgtttgtttttttgagatgaagtctcg
1141 ctctgttgcccatgctggagtacagtggcacgatctcggctcactgcaacctgcgcctcc
1201 tgggttcaggcgattctcttgcctcagcctcctgagtagctgggattacaggcacccatc
1261 accatgtccagctaatttttgtatttttagtagagacagggtttcccatgttggccagg
1321 ctggtctcgatctcctgacctcaaatgatccgcccacctcggcctcccaaagtgctggga
1381 tgacagttgtgagccaccacactcagcctgctctttctaatatttgaaacttgttagaca
1441 atttgctacccatctaatgtgatattttaggaatccaatatgcatggtttattatttctt
1501 aaaaaaaatattcttttacctgtcacctgaatttagtaatgccttttatgttacacaact
```

1561 tagcactttccagaaacaaaaactctctccttgaaataatagagtttttatctaccaaag
1621 atatgctagtgtctcatttcaaaggctgctttttccagcttacattttatatacttactc
1681 acttgaagtttctaaatattcttgtaattttaaaactatctcagatttactgaggtttat
1741 cttctggtggtagattatccataagaagagtgatgtgccagaatcactctgggatccttg
1801 tctgacaagattcaaaggactaaatttaattcagtcatgaacactgccaattaccgttta
1861 tgggtagacatctttggaaatttccacaaggtcagacattcgcaactatcccttctacat
1921 gtccacacgtatactccaacactttattaggcatctgattagtttggaaagtatgcctcc
1981 atctgaattagtccagtgtggcttagagttggtacaacattctcacagaatttcctaatt
2041 ttgtaggttcagcctgataaccactggagttctttggtcctcattaaatagctttcttca
2101 cacattgctctgcctgttacacatatgatgaacactgcttttagacttcattaggaatt
2161 taggactgcatcttgacaactgagcctattctactatatgtacaatacctagcccataat
2221 aggtatacaatacacatttggtaaaactaattttcaaccaatgacatgtatttttcaact
2281 agtaacctagaaatgtttcacttaaaatctgagaactggttacactacaagttaccttgg
2341 agattcatatatgaaaacgcaaacttagctatttgattgtattcactgggacttaagaat
2401 gcgcctgaataattgtgagttcgatttgttctggcaggctaatgaccatttccagtaaag
2461 tgaatagaggtcagaagtcgtataaaagaggtgttgtcagaacaccgttgagattacata
2521 ggtgaacaactatttttaagcaactttatttgtgtagtgacaaagcatcccaatgcaggc
2581 tgaaatgtttcatcacatctctggatctctctatttgtgcagacattgaaaaaattgtt
2641 catattatttccatgttatcagaatatttgatttttaaaaacataggccaagttcattc
2701 acttcattattcatttatcaaaatcagagtgaatcacattagtcgccttcacaactgata
2761 aagatcactgaagtcaaattgatttttgctataatcttcaatctacctatatttaattga
2821 gaatctaaaatgtacaaatcattgtgttgattctgcagtgatcctgctataagtaagact
2881 cagtccctgattttaggtatcctgtgaaaagcagaattaagacaaatacacaagagacaa
2941 agcacaaaaaataaatatcataaggggatgaacaaaatggtggagaaagagtagacaaag
3001 tttttgatcacctgccttcaaagaaaggctgtgaattttgttcacttagacagcttggag
3061 acaagaaattacccaaaagtaaggtgaggaggataggcaaaaagagcagaaagatgtgaa
3121 tggacattgttgagaaatgtgataggaaaacaatcatagataaaggatttccaagcaact
3181 gagcatatccagatgaggtaggatgggataaactcttattgaaccaatcttcaccaattt
3241 tgtttttctttgcagagcaagctaggaattgtttcccttctactgggcacaatacacgc
3301 attgatttttgcctggaataagtggatagatataaaacaatttgtatggtatacacctcc
3361 aacttttatgatagctgttttccttccaattgttgtcctgatatttaaaagcatactatt
3421 cctgccatgcttgaggaagaagatactgaagattagacatggttgggaagacgtcaccaa
3481 aattaacaaaactgagatatgttcccagttgtagaattactgtttacacacatttttgtt
3541 caatattgatatattttatcaccaacatttcaagtttgtatttgttaataaaatgattat
3601 tcaaggaaaaaaaaaaaaaaaaaaaa

Figure 3:

Figure 3A. Amino acid sequence of STEAP-1 v.1 (SEQ ID NO: 36). The STEAP-1 v.1 protein has 339 amino acids.

```
  1 MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE
 61 LQHTQELFPQ WHLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM
121 VSITLLALVY LPGVIAAIVQ LHNGTKYKKF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL
181 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS
241 VSDSLTWREF HYIQSKLGIV SLLLGTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV
301 VLIFKSILFL PCLRKKILKI RHGWEDVTKI NKTEICSQL
```

Figure 3B. Amino acid sequence of STEAP-1 v.2 (SEQ ID NO: 37). The STEAP-1 v.2 protein has 258 amino acids.

```
  1 MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE
 61 LQHTQELFPQ WHLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM
121 VSITLLALVY LPGVIAAIVQ LHNGTKYKKF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL
181 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS
241 VSDSLTWREF HYIQVNNI
```

Figure 3C. Amino acid sequence of STEAP-1 v.3 (SEQ ID NO: 38). The STEAP-1 v.3 protein has 282 amino acids.

```
  1 MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE
 61 LQHTQELFPQ WHLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM
121 VSITLLALVY LPGVIAAIVQ LHNGTKYKKF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL
181 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS
241 VSDSLTWREF HYIQIIHKKS DVPESLWDPC LTRFKGLNLI QS
```

Figure 3D. Amino acid sequence of STEAP-1 v.4 (SEQ ID NO: 39). The STEAP-1 v.4 protein has 258 amino acids.

```
  1 MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE
 61 LQHTQELFPQ WHLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM
121 VSITLLALVY LPGVIAAIVQ LHNGTKYKKF PHWLDKWMLT RKQFGLLSLF FAVLHAIYSL
181 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS
241 VSDSLTWREF HYIQVNNI
```

Figure 4:

Figure 4A-Homology of STEAP-1 (SEQ ID NO: 40) to mouse TNFα-induced adipose-related protein (gi|16905133|). (SEQ ID NO: 41)

```
 Score =  224 bits (570), Expect = 2e-57
 Identities = 110/270 (40%), Positives = 174/270 (63%)

Query: 66  ELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITL 125
           +LFP W  P  +++++     F+Y  +REVI+P          Y++ I + N+V P+ ++ L
Sbjct: 195 QLFPMWRFPFYLSSVLCIFFFVYCAIREVIYPYVNGKTDATYRLAISIPNRVFPITALIL 254

Query: 126 LALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMR 185
           LALVYLPG++AAI+QL+ GTKY++FP+WLD WML RKQ GL++  FA LH IY+L  P+R
Sbjct: 255 LALVYLPGILAAILQLYRGTKYRRFPNWLDHWMLCRKQLGLVALGFAFLHVIYTLVIPIR 314

Query: 186 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSL 245
              R++L N    Q   NK+  +I    W  + Y++LGI+G  +  LL +TS+PSVS+ +
Sbjct: 315 YYVRWRLRNATITQALTNKDSPFITSYAWINDSYLALGILGFFLFLLLGITSLPSVSNMV 374

Query: 246 TWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFK 305
            WREF ++QSKLG ++L+L T H L++   +++      W  P  +++A+ +P  VL+ K
Sbjct: 375 NWREFRFVQSKLGYLTLVLCTAHTLVYGGKRFLSPSILRWSLPSAYILALIIPCAVLVLK 434

Query: 306 SILFLPCLRKKILKIRHGWEDVTKINKTEI 335
           IL +PC+ K + +IR GWE  +K  ++ +
Sbjct: 435 CILIMPCIDKTLTRIRQGWERNSKYTQSAL 464
```

Figure 4B-Homology of STEAP-1 (SEQ ID NO: 42) to rat pHyde protein (gi|21717655|). (SEQ ID NO: 43)

```
 Score =  283 bits (724), Expect = 2e-75
 Identities = 127/259 (49%), Positives = 184/259 (71%)

Query: 67  LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLL 126
           L P W +P  +A  +++ ++ Y  +R+V+ P     +  FYK+P+ V+N  +P V+  LL
Sbjct: 208 LLPSWKVPTLLALGLSTQSYAYNFIRDVLQPYIRKDENKFYKMPLSVVNTTIPCVAYVLL 267

Query: 127 ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRR 186
           +LVYLPGV+AA +QL  GTKY++FP WLD W+  RKQ GLLSFFFA+LHA+YS   P+RR
Sbjct: 268 SLVYLPGVLAAALQLRRGTKYQRFPDWLDHWLQHRKQIGLLSFFFAMLHALYSFCLPLRR 327

Query: 187 SYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLT 246
           S+RY L+N A +QV  NK   W+E +VWRMEIY+SLG++ L +L+LLAVTSIPS+++SL
Sbjct: 328 SHRYDLVNLAVKQVLANKSRLWVEEEVWRMEIYLSLGVLALGMLSLLAVTSIPSIANSLN 387

Query: 247 WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIFKS 306
           W+EF ++QS LG V+L+L T+H L + W +   +  + +Y PPTF + + LP V+++ K
Sbjct: 388 WKEFSFVQSTLGFVALMLSTMHTLTYGWTRAFEENHYKFYLPPTFTLTLLLPCVIILAKG 447

Query: 307 ILFLPCLRKKILKIRHGWE 325
           +  LPCL  ++ KIR GWE
Sbjct: 448 LFLLPCLSHRLTKIRRGWE 466
```

Figure 4C-Homology of STEAP-1 (SEQ ID NO: 44) to mouse six transmembrane epithelial antigen of the prostate (gi|20820492|). (SEQ ID NO: 45)

```
Score =  488 bits (1256), Expect = e-137
Identities = 255/303 (84%), Positives = 277/303 (91%)
```

```
Query: 1   MLKRPVLLHLHQTAHADEFDCPSELQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIH 60
           MLKRP L HL     H D FDCPSELQHTQE FP W LP+K+AAII+SLTFLYTLLRE+I+
Sbjct: 37  MLKRPGLSHLQHAVHVDAFDCPSELQHTQEFFPNWRLPVKVAAIISSLTFLYTLLREIIY 96

Query: 61  PLATSHQQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDK 120
           PL TS +QYFYKIPILVINKVLPMV+ITLLALVYLPG +AA+VQL NGTKYKKFP WLD+
Sbjct: 97  PLVTSREQYFYKIPILVINKVLPMVAITLLALVYLPGELAAVVQLRNGTKYKKFPPWLDR 156

Query: 121 WMLTRKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRM 180
           WML RKQFGLLSFFFAVLHA+YSLSYPMRRSYRYKLLNWAY+QVQQNKEDAW+EHDVWRM
Sbjct: 157 WMLARKQFGLLSFFFAVLHAVYSLSYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRM 216

Query: 181 EIYVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK 240
           EIYVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGT+HAL+FAWNK
Sbjct: 217 EIYVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK 276

Query: 241 WIDIKQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTEIC 300
           W+D+ QFVWY PPTFMIAVFLP +VLI K  L LPCLRKKILKIR GWEDV+KIN+TE+
Sbjct: 277 WVDVSQFVWYMPPTFMIAVFLPTLVLICKIALCLPCLRKKILKIRCGWEDVSKINRTEMA 336

Query: 301 SQL 303
           S+L
Sbjct: 337 SRL 339
```

Figure 5a STEAP-1 variant 1 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

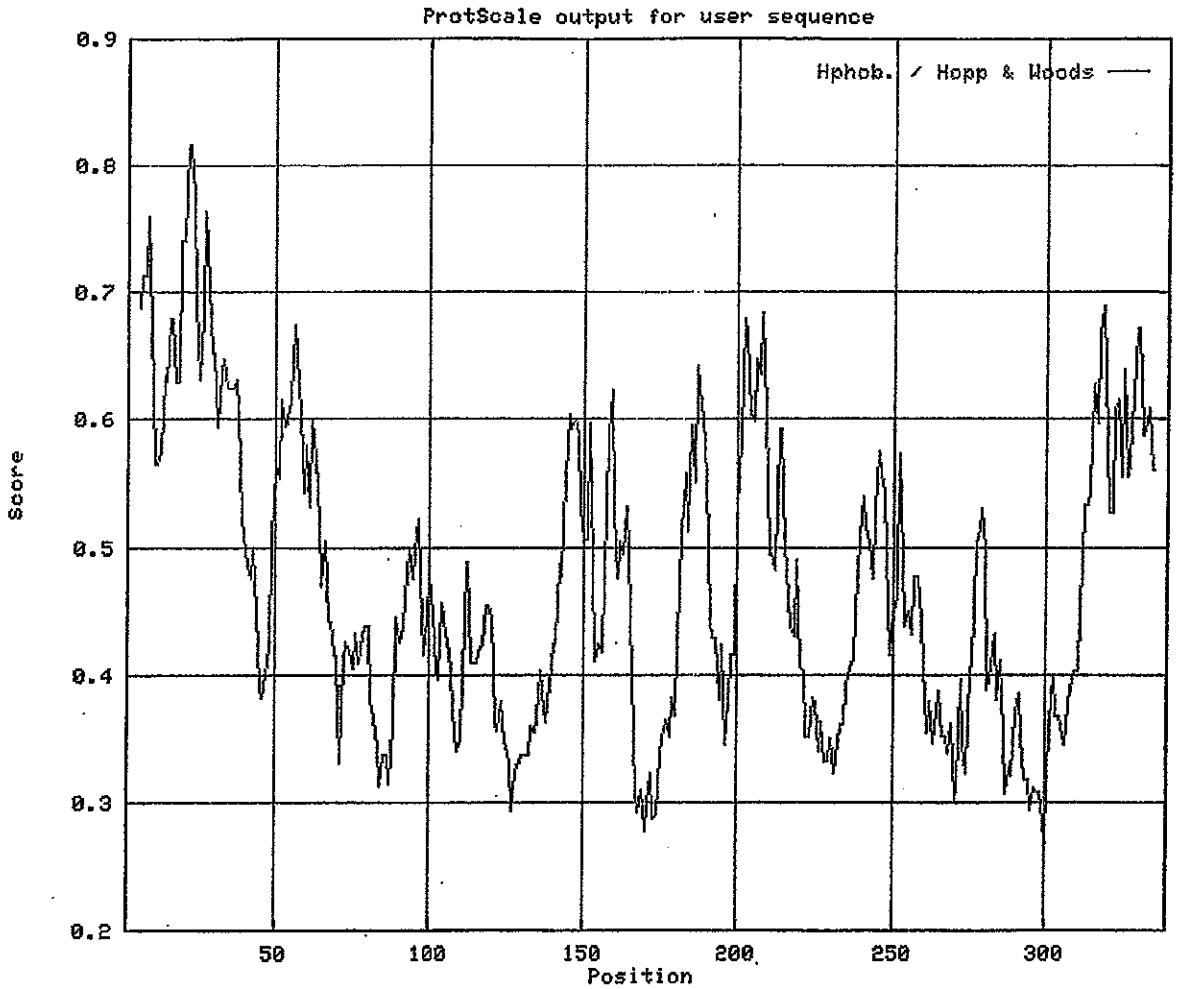


Figure 5b STEAP-1 variant 3 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

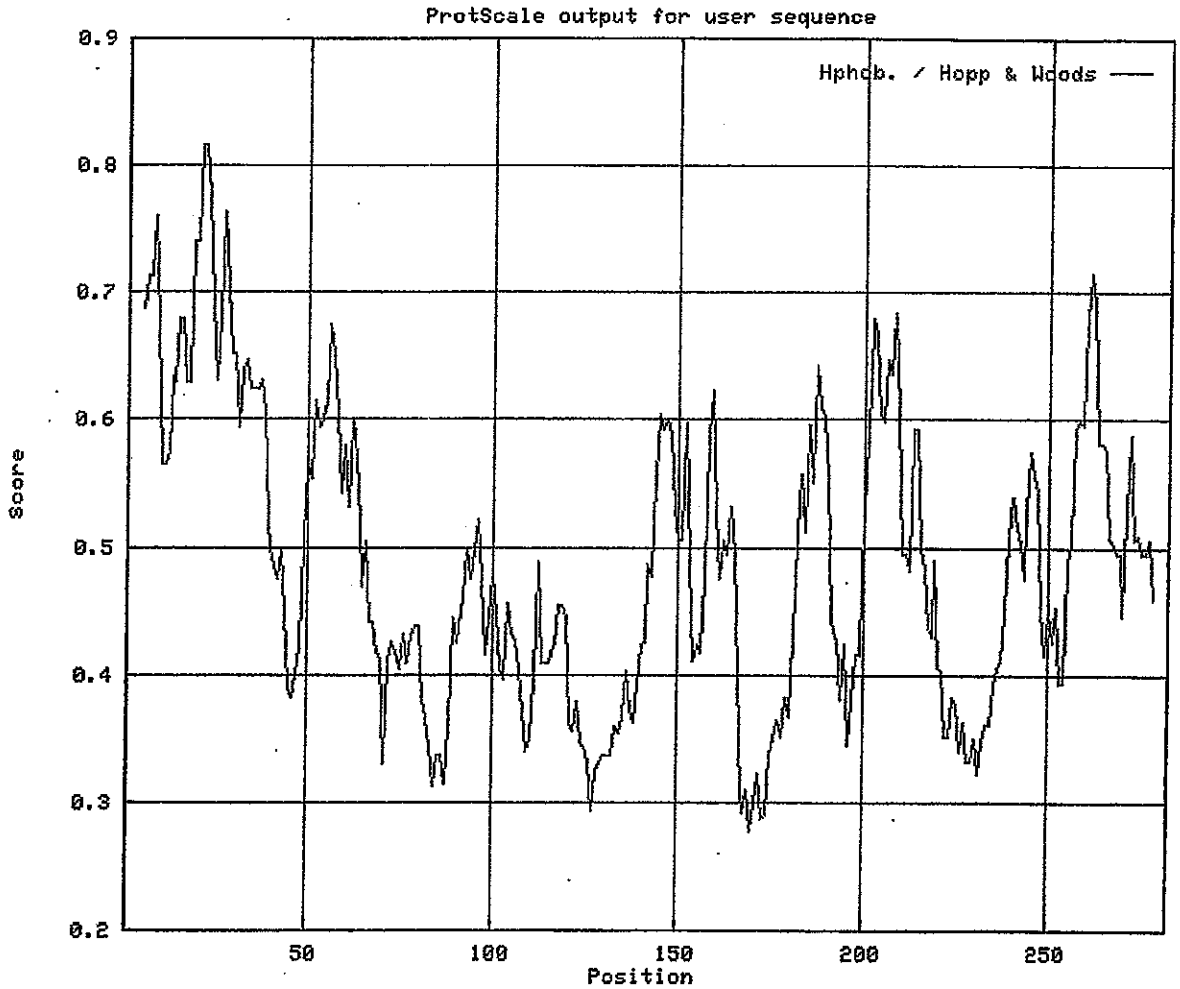


Figure 6a STEAP-1 variant 1 Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

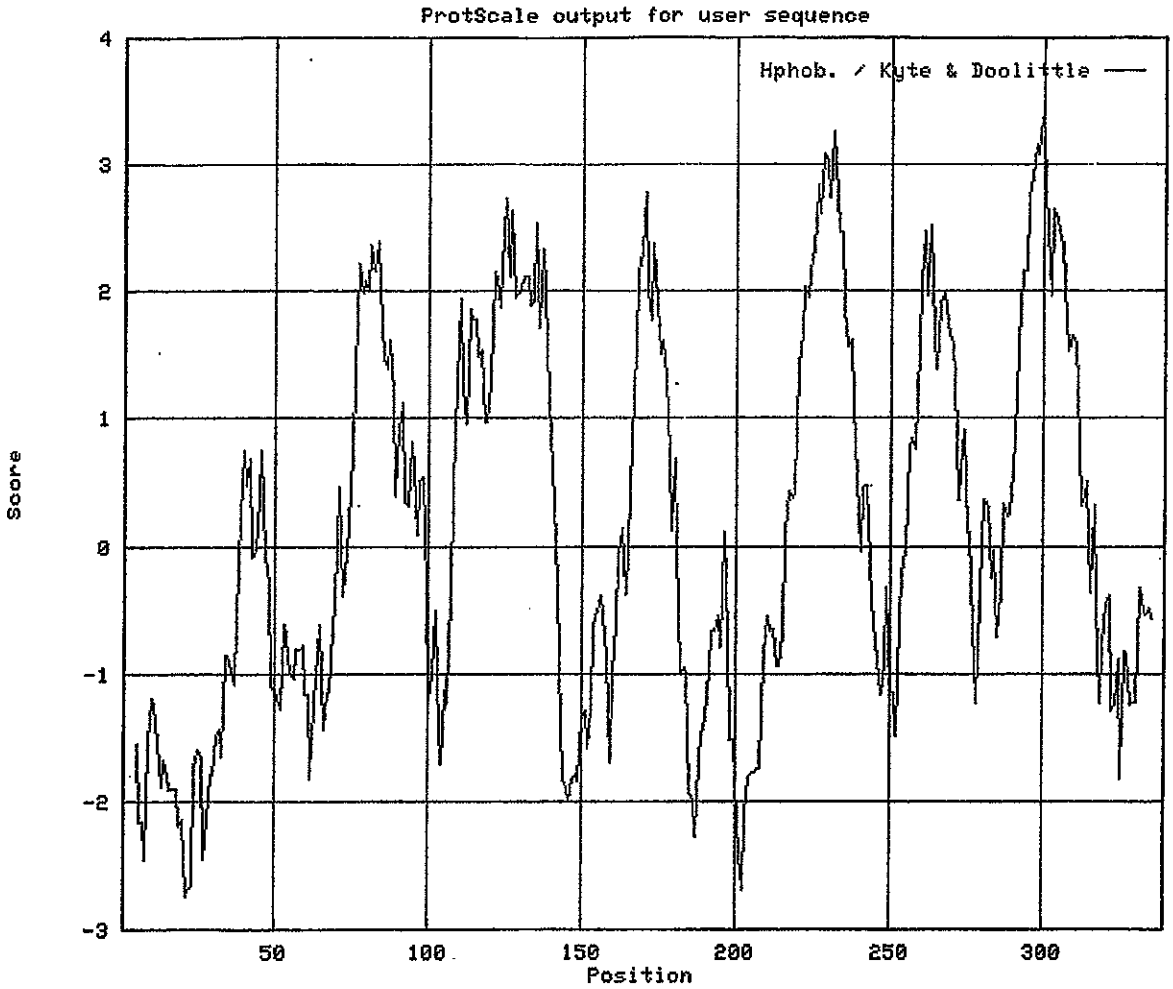


Figure 6b STEAP-1 variant 3 Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

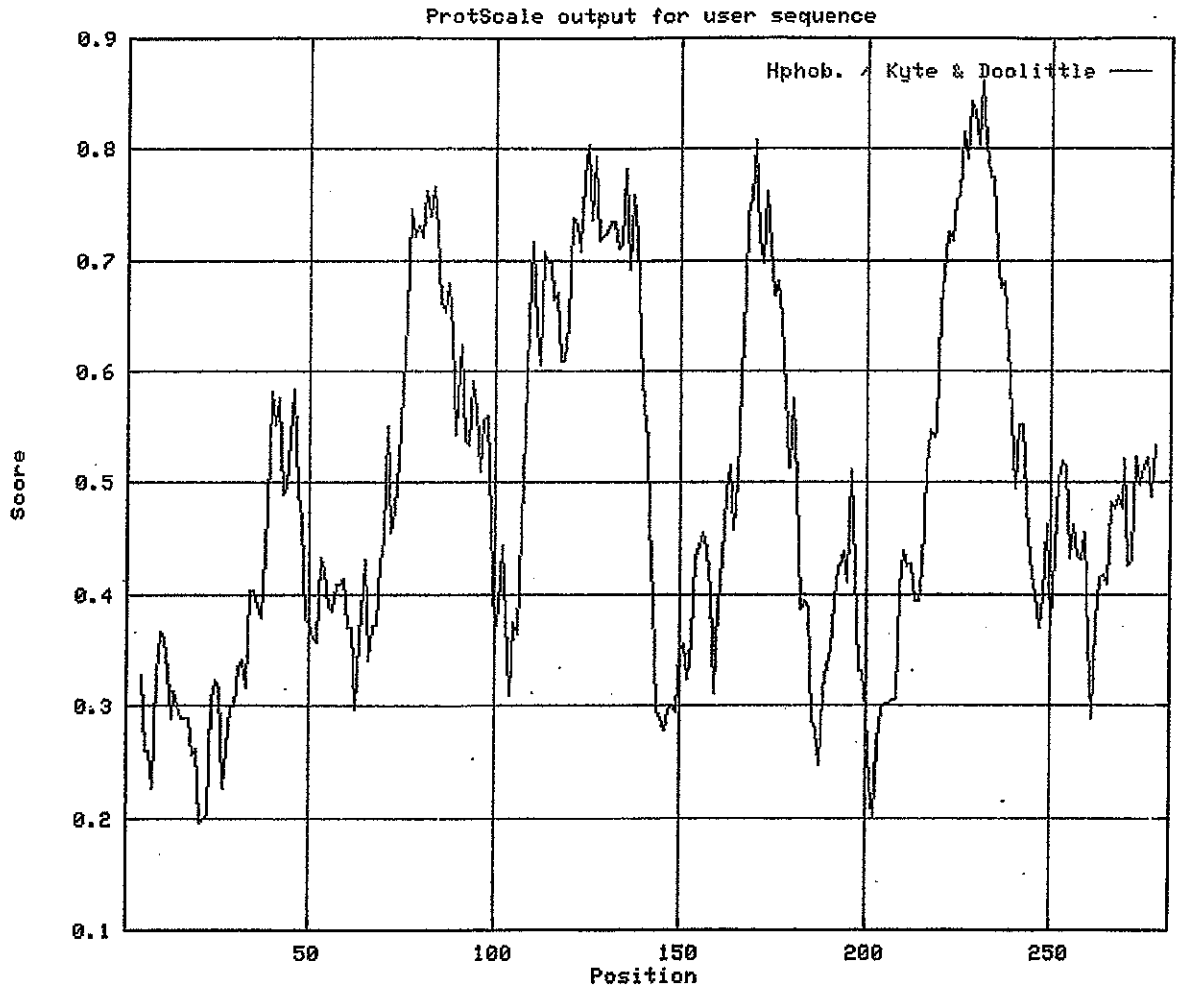


Figure 7a STEAP-1 variant 1 % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)

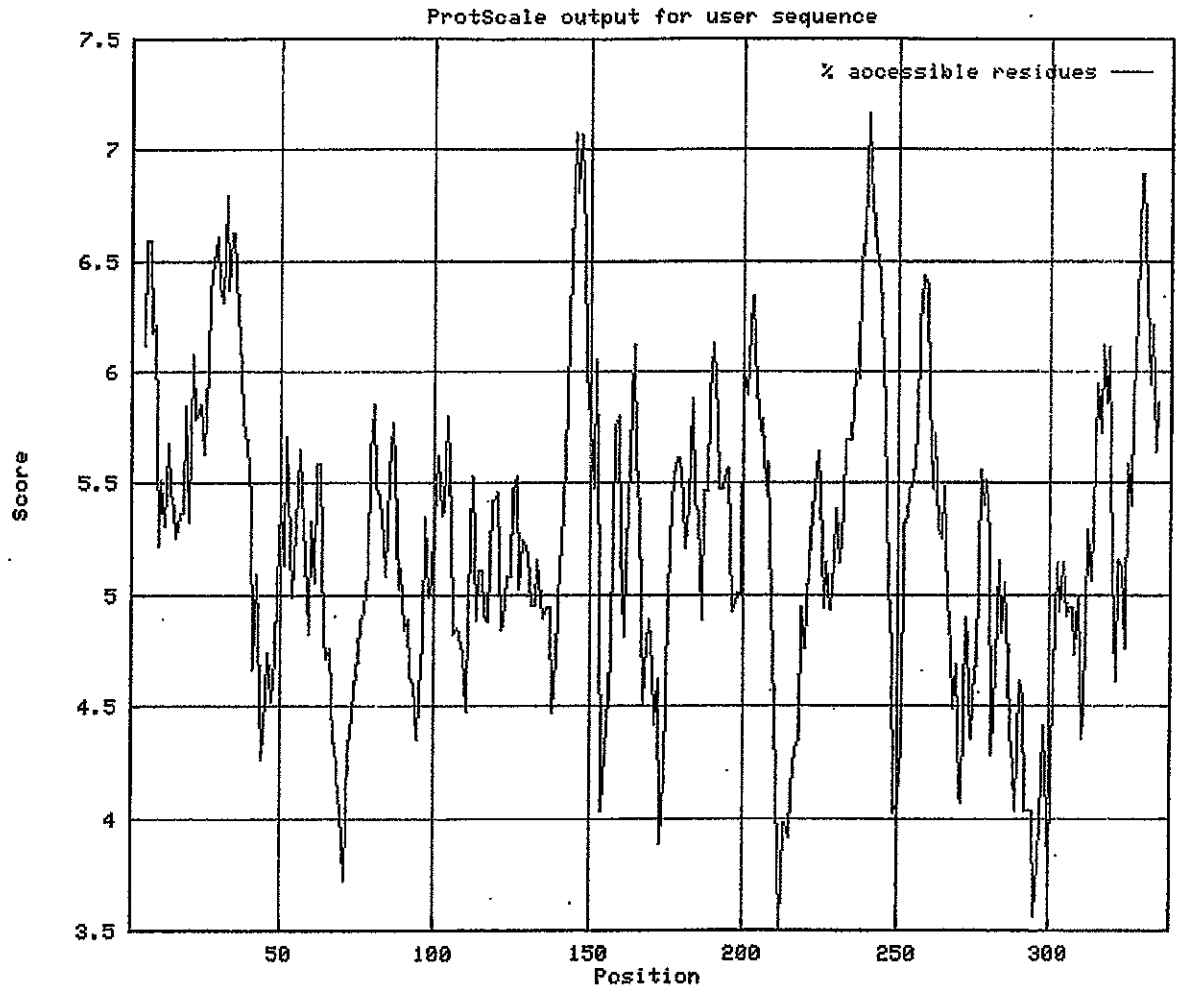


Figure 7b STEAP-1 variant 3 % Accessible Residues Profile

(Janin J., 1979. Nature 277:491-492)

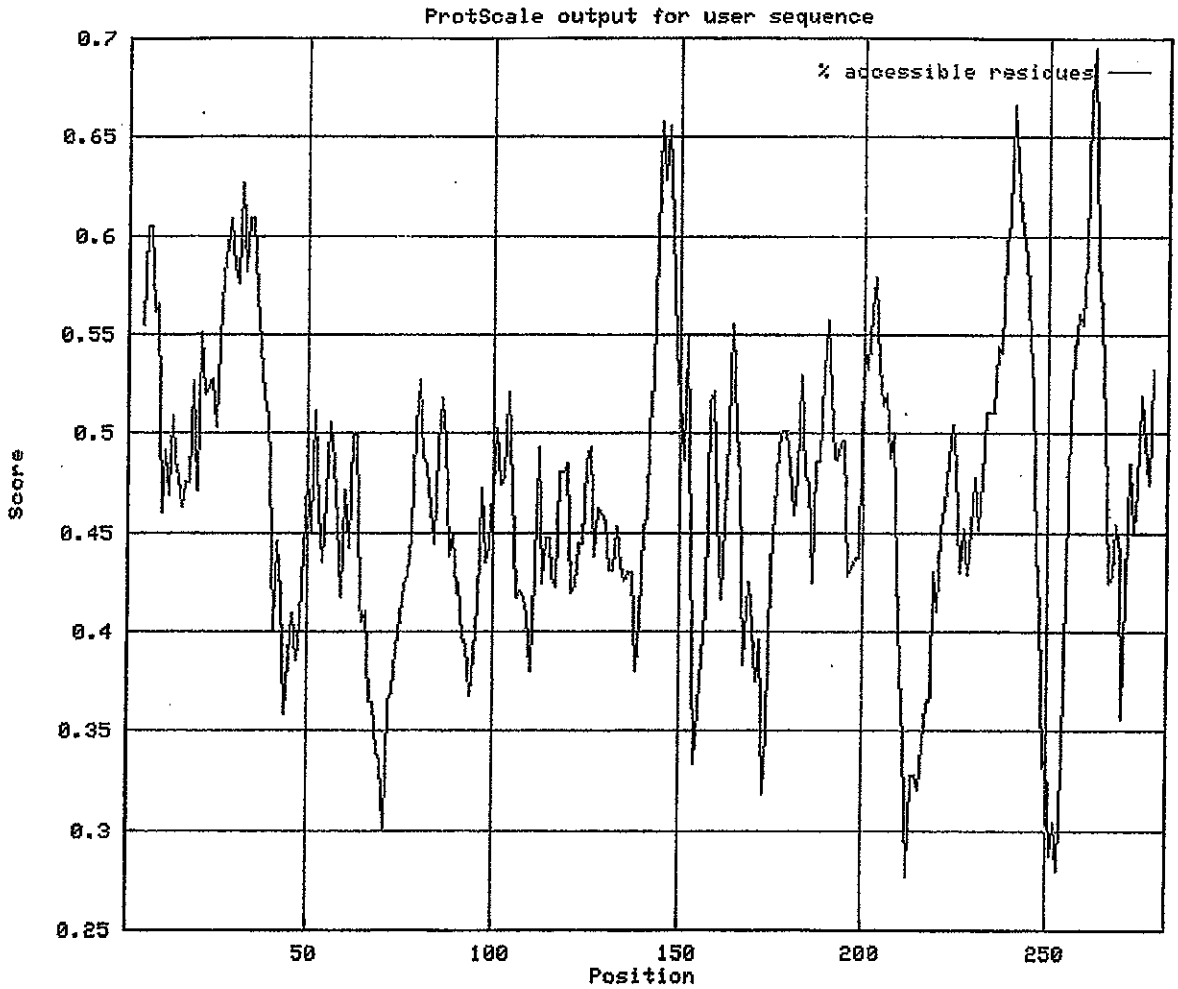


Figure 8a STEAP-1 variant 1
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

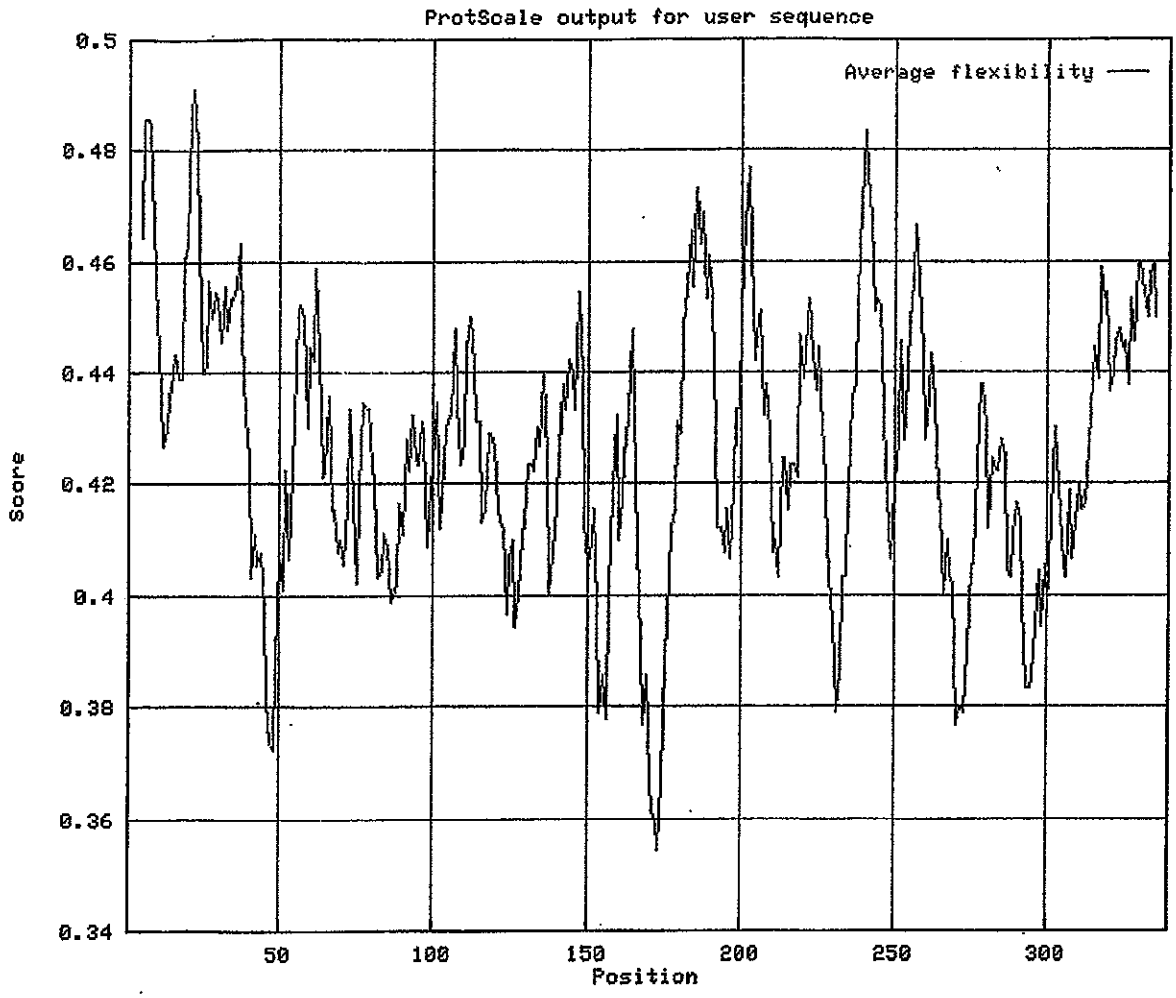


Figure 8b STEAP-1 variant 3
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

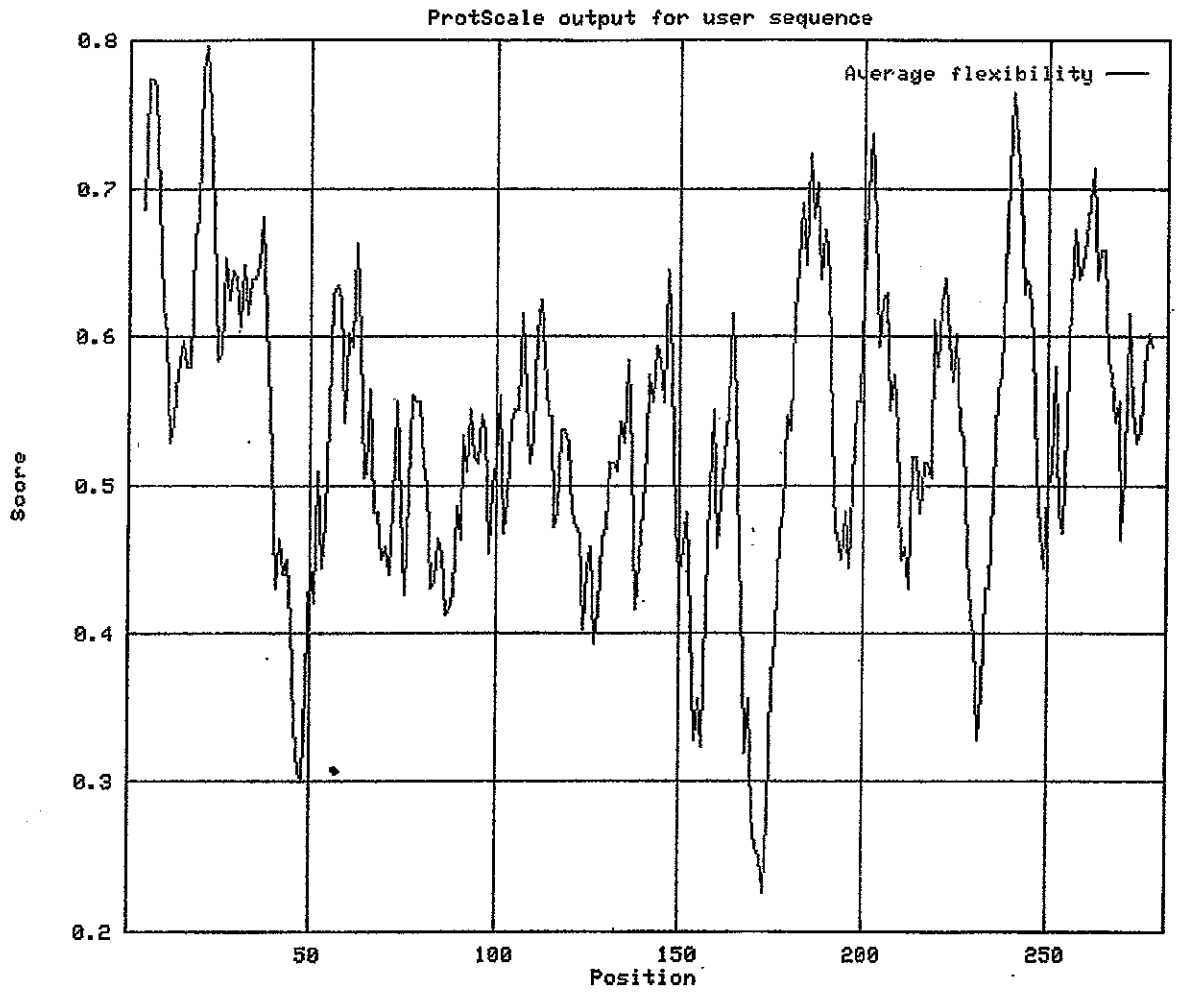


Figure 9a STEAP-1 variant 1
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

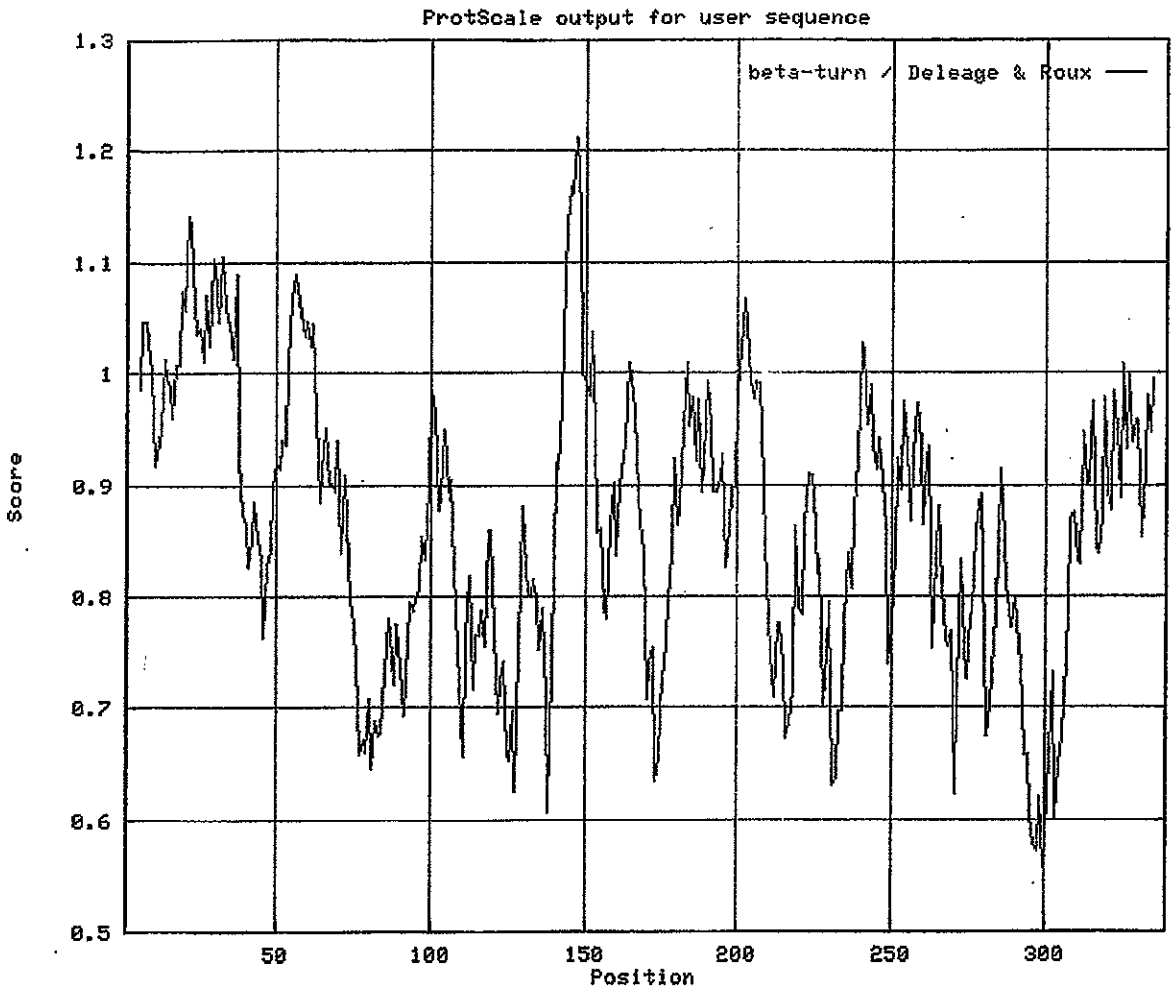


Figure 9b STEAP-1 variant 3
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

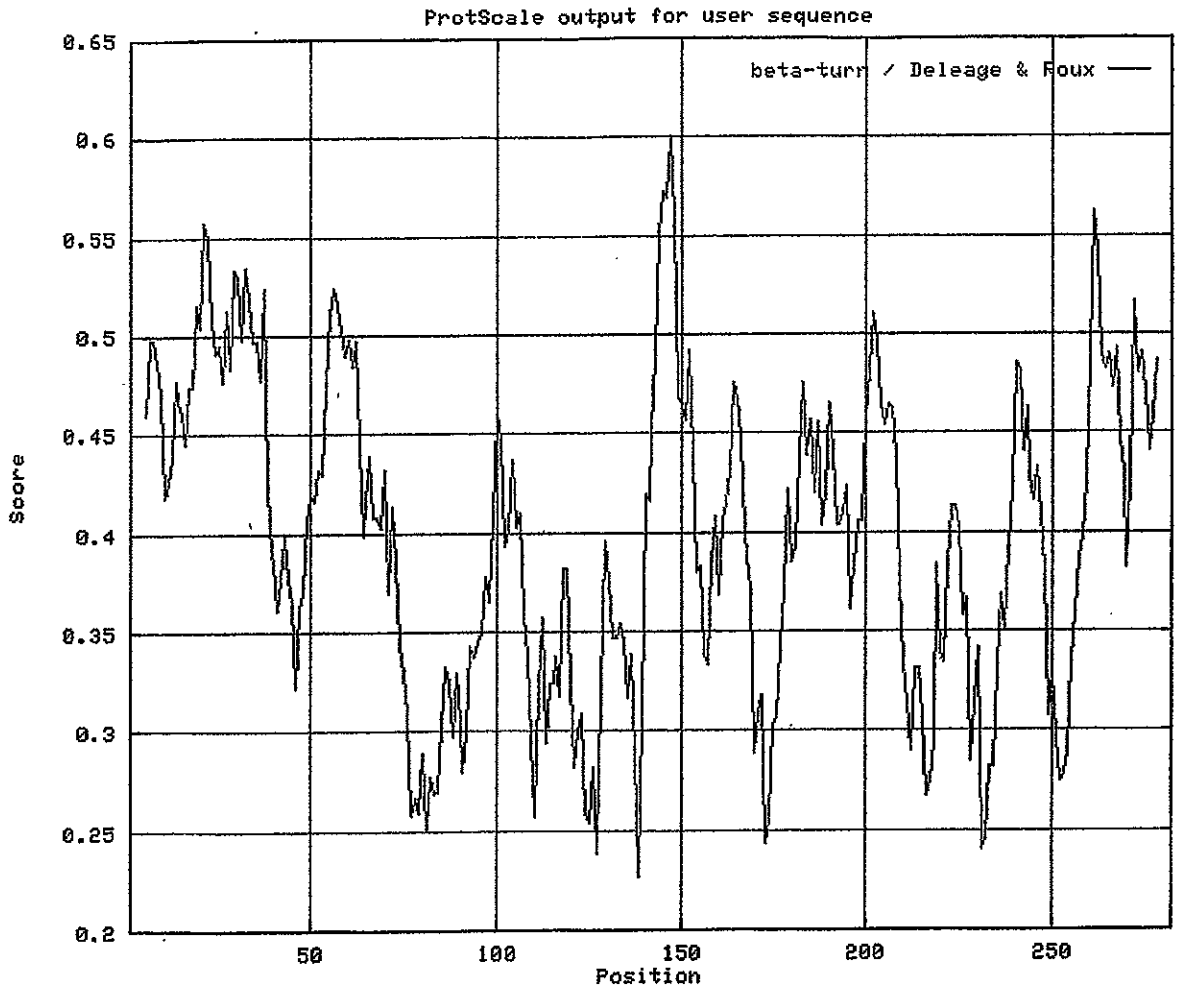


Figure 10

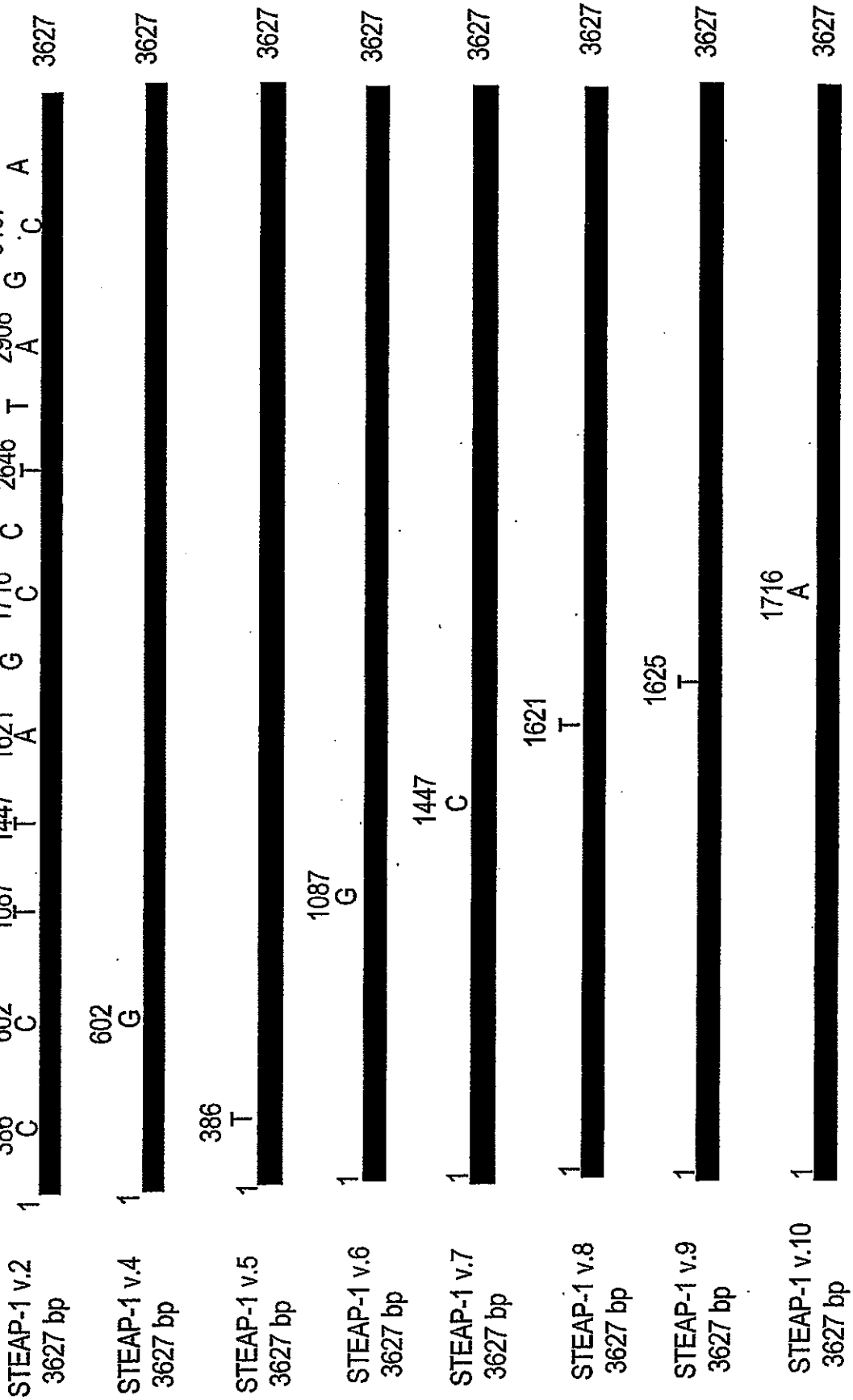

STEAP-1 v.2
3627 bp
STEAP-1 v.4
3627 bp
STEAP-1 v.5
3627 bp
STEAP-1 v.6
3627 bp
STEAP-1 v.7
3627 bp
STEAP-1 v.8
3627 bp
STEAP-1 v.9
3627 bp
STEAP-1 v.10
3627 bp
1
3627
386 C
602 C
1087 T
1447 T
1621 A
1625 G
1716 C
2358 C
2646 T
2859 T
2908 A
3006 G
3107 C
3180 A
602 G
386 T
1087 G
1447 C
1621 T
1625 T
1716 A

Figure 10 (con'd)

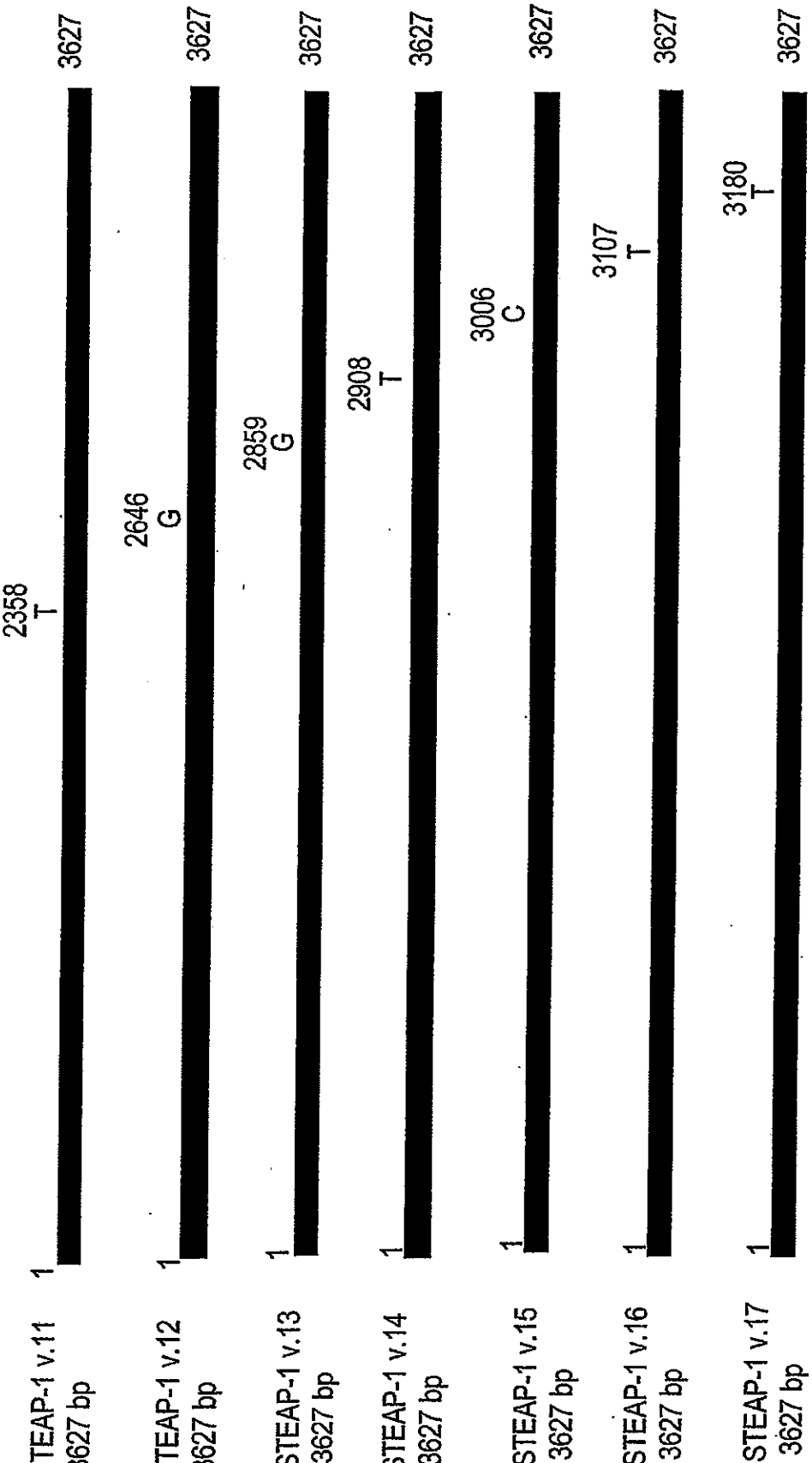


Figure 11

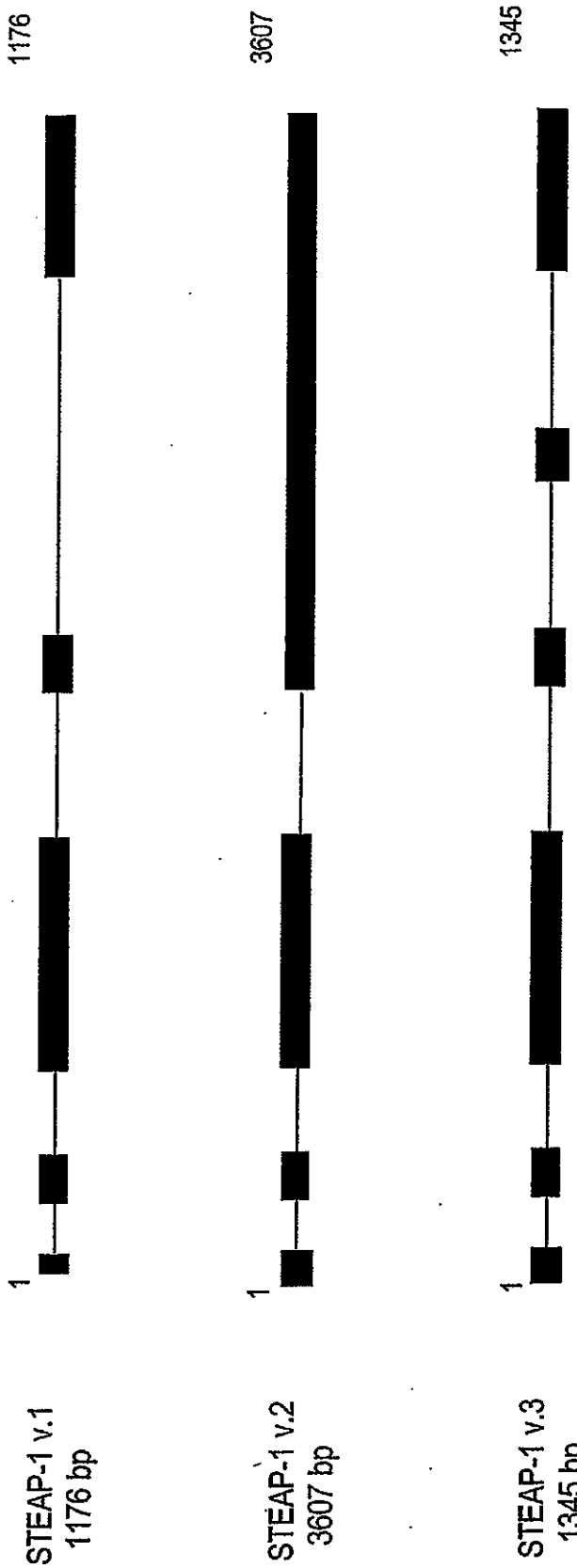

1176
3607
1345
1
1
1
STEAP-1 v.1
1176 bp
STEAP-1 v.2
3607 bp
STEAP-1 v.3
1345 bp

Figure 12


STEAP-1 v.1
339 aa
1
339
STEAP-1 v.2
258 aa
1
169
F
254
255
258
(1)
(254)
STEAP-1 v.3
282 aa
1
254
255
282
(1)
(254)
STEAP-1 v.4
2585 aa
1
169
L
254
255
258
(1)
(254)

Figure 13A Secondary structure prediction of STEAP-1 variant 1

```
          10        20        30        40        50        60        70
          |         |         |         |         |         |         |
MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAHADEFDCPSELQHTQELFPQ
ccccccccchhhhhhhccccccccccccccccchhhhhhhhhheccccccccccccccccchhhccc
WHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQ
chcchhhhhhhhhhhhhhhhhhhhcchhhhhhhhhheccceeehcchhchhhhhhhhhhhhchhhhhhhh
LHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIE
hccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhcccchheh
HDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDI
hhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhchhhhhhhhhhhhhhhhhhheee
KQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTEICSQL
eeeeeccccchhhhhhhhhhhhhhhhhhhhhhhhhhhheccccccchhhccchcehhcc
```

Alpha helix	(h)	: 64.60%
Extended strand	(e)	: 4.72%
Random coil	(c)	: 30.68%

Figure 13B Secondary structure prediction of STEAP-1 variant 2

```
          10        20        30        40        50        60        70
          |         |         |         |         |         |         |
MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAHADEFDCPSELQHTQELFPQ
ccccccccchhhhhhhccccccccccccccccchhhhhhhhhheccccccccccccccccchhhccc
WHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQ
chcchhhhhhhhhhhhhhhhhhhhcchhhhhhhhhheccceeehcchhchhhhhhhhhhhhchhhhhhhh
LHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIE
hccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhcccchheh
HDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQVNNI
hhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccchhhhhhhheehccc
```

Alpha helix (h) : 62.79%
Extended strand (e) : 3.10%
Random coil (c) : 34.11%

Figure 13C Secondary structure prediction of STEAP-1 variant 3

```
          10        20        30        40        50        60        70
          |         |         |         |         |         |         |
MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAHADEFDCPSELQHTQELFPQ
ccccccccchhhhhhhccccccccccccccccccchhhhhhhhhheccccccccccccccccchhhccc
WHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQ
chcchhhhhhhhhhhhhhhhhhhhcchhhhhhhhheccceeehcchhchhhhhhhhhhhhchhhhhhhh
LHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIE
hccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhcccchheh
HDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQIIHKKSDVPESLWDPCLTRFKGLNLI
hhhhhhhhhhhhhhhhhhhhhhhhhhcccccccchhhhhheeeeeeccccccccchhhhchhccccceee
QS
cc
```

Alpha helix (h) : 58.87%

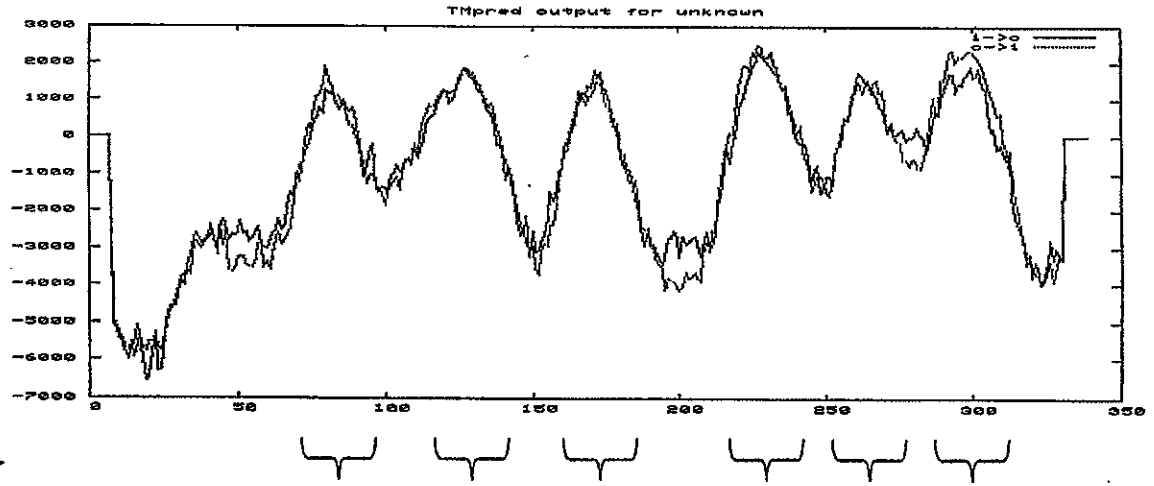
Extended strand (e) : 5.32%

Random coil (c) : 35.82%

Transmembrane prediction for STEAP-1 variant 1

Figure 13D

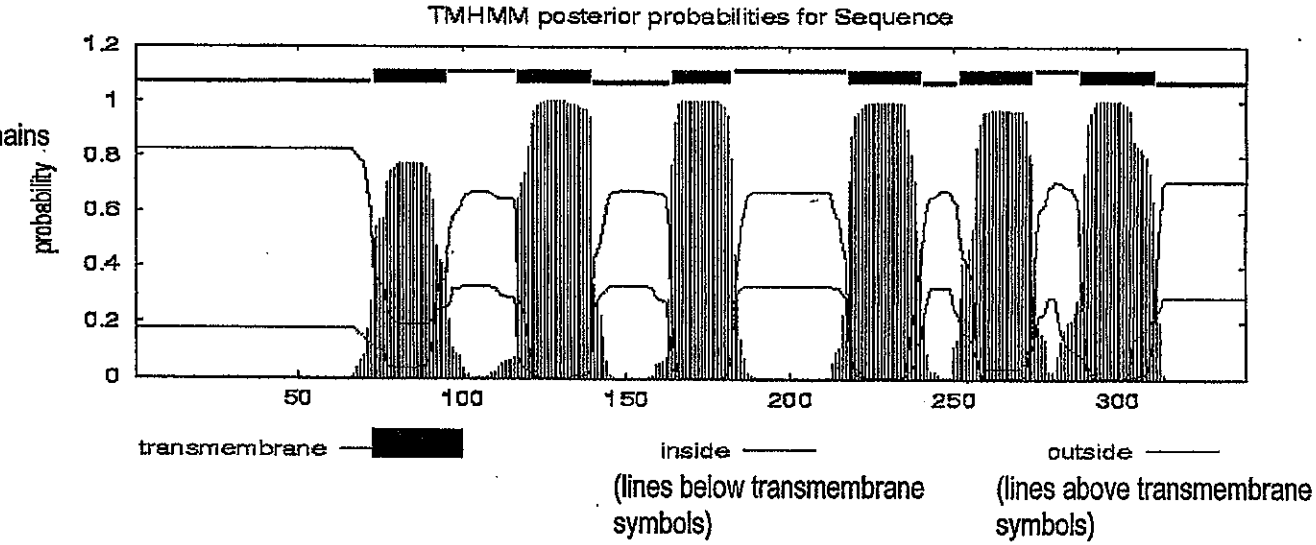
6 transmembrane domains predicted



Transmembrane domains →

Figure 13E

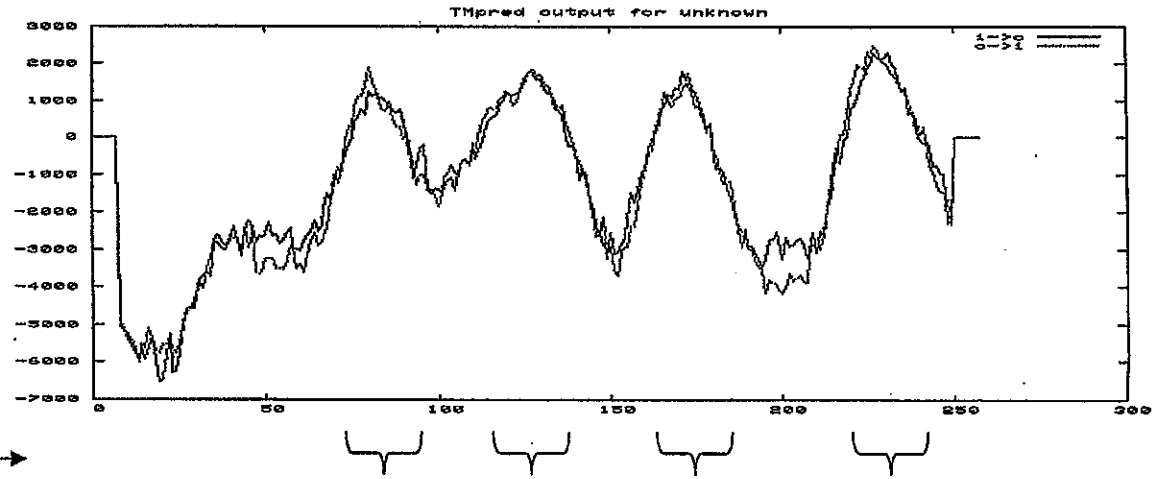
6 transmembrane domains predicted



Transmembrane prediction for STEAP-1 variant 2

Figure 13F

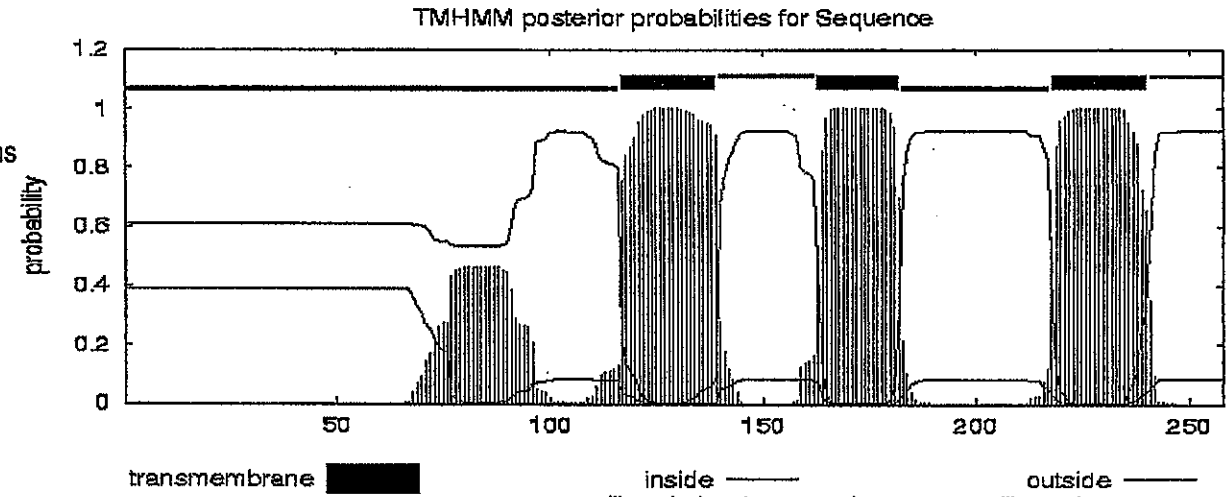
4 transmembrane domains predicted



Transmembrane domains →

Figure 13G

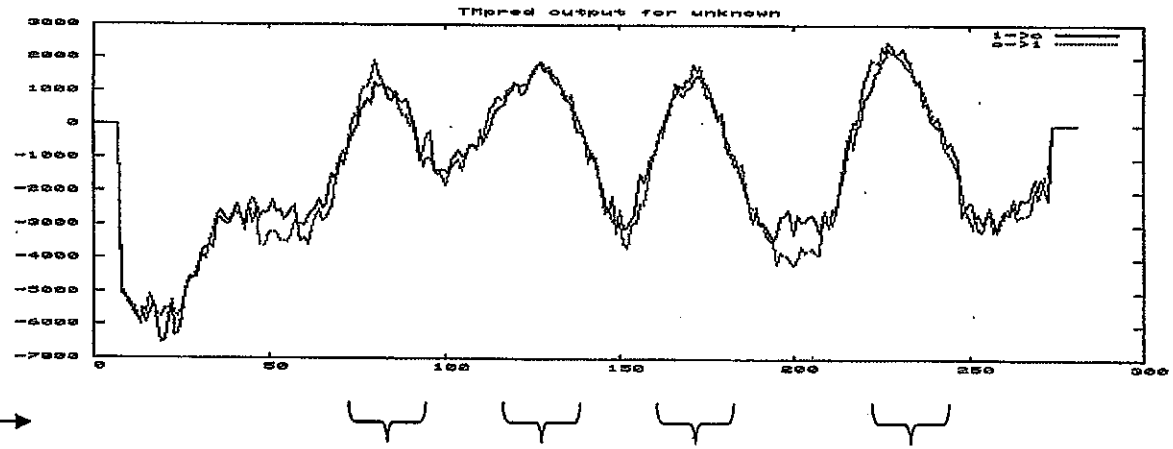
3 transmembrane domains predicted



Transmembrane prediction for STEAP-1 variant 3

Figure 13H

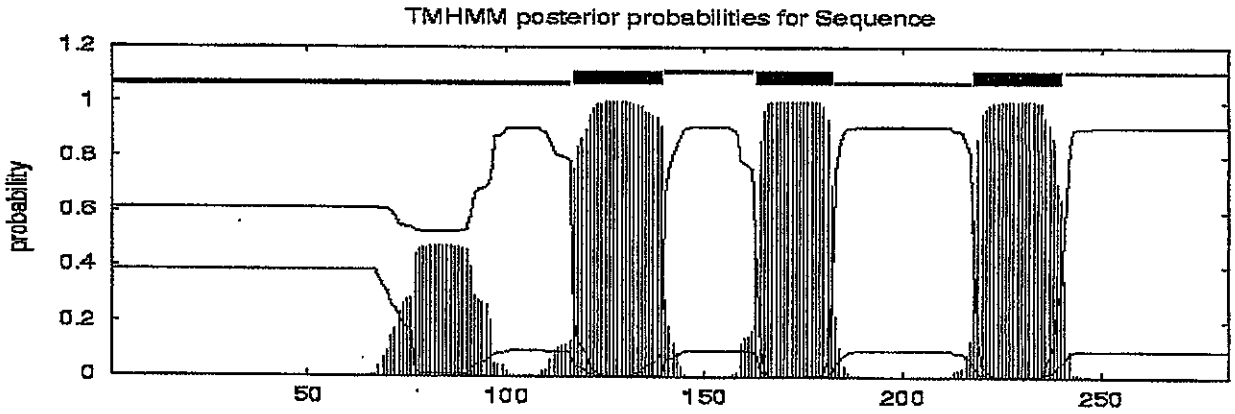
4 transmembrane domains predicted



Transmembrane domains →

Figure 13I

3 transmembrane domains predicted



(lines below transmembrane symbols)

(lines above transmembrane symbols)

Figure 14a: STEAP-1 Expression in Stomach Cancer Patient Specimens

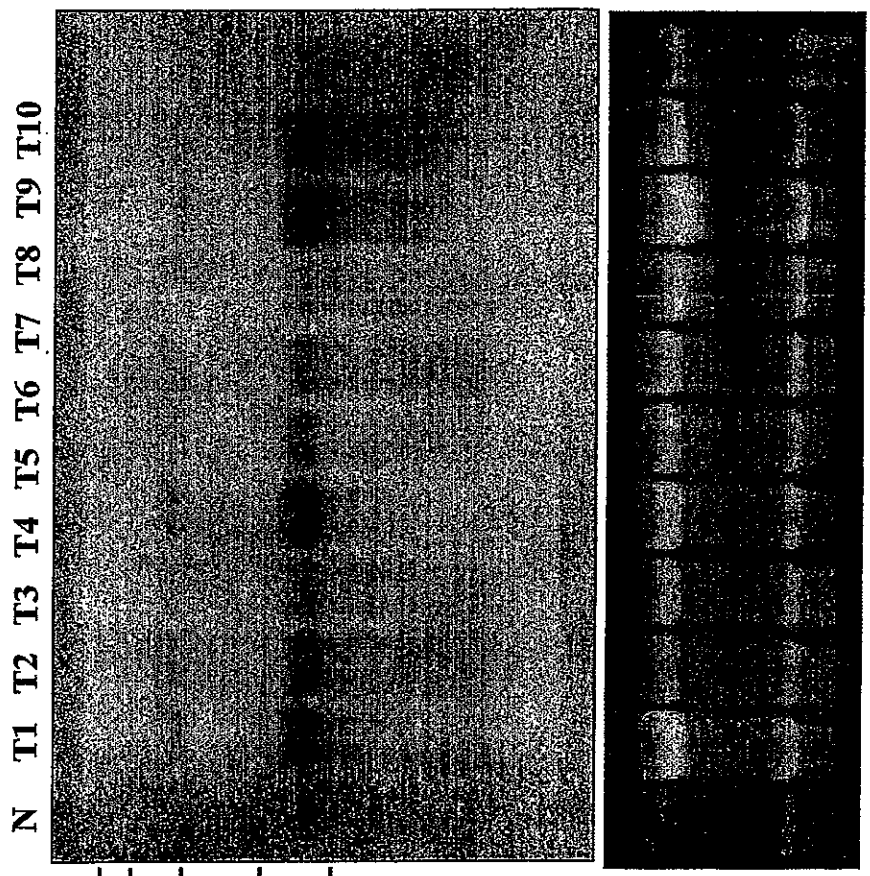


Figure 14b: STEAP-1 Expression in Rectum Cancer Patient Specimens

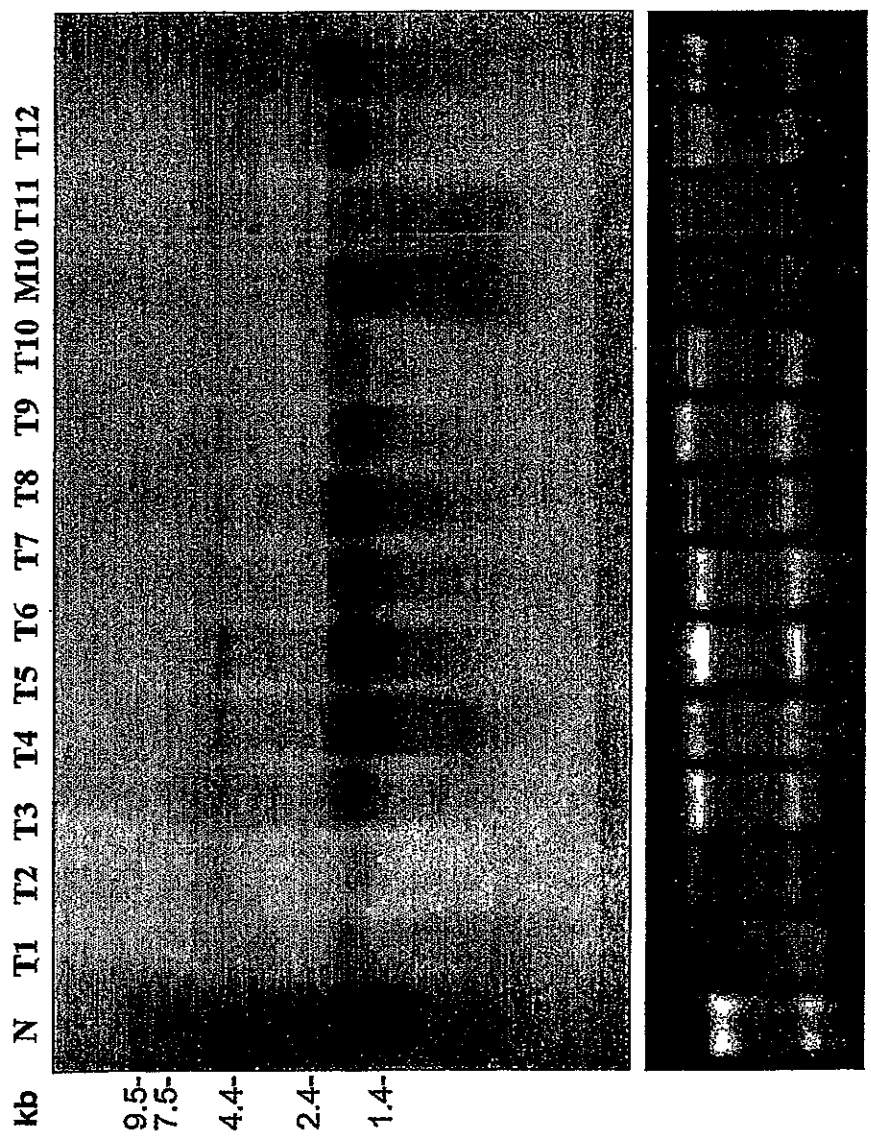


Figure 14c: STEAP-1 Expression in HUVEC by RT-PCR

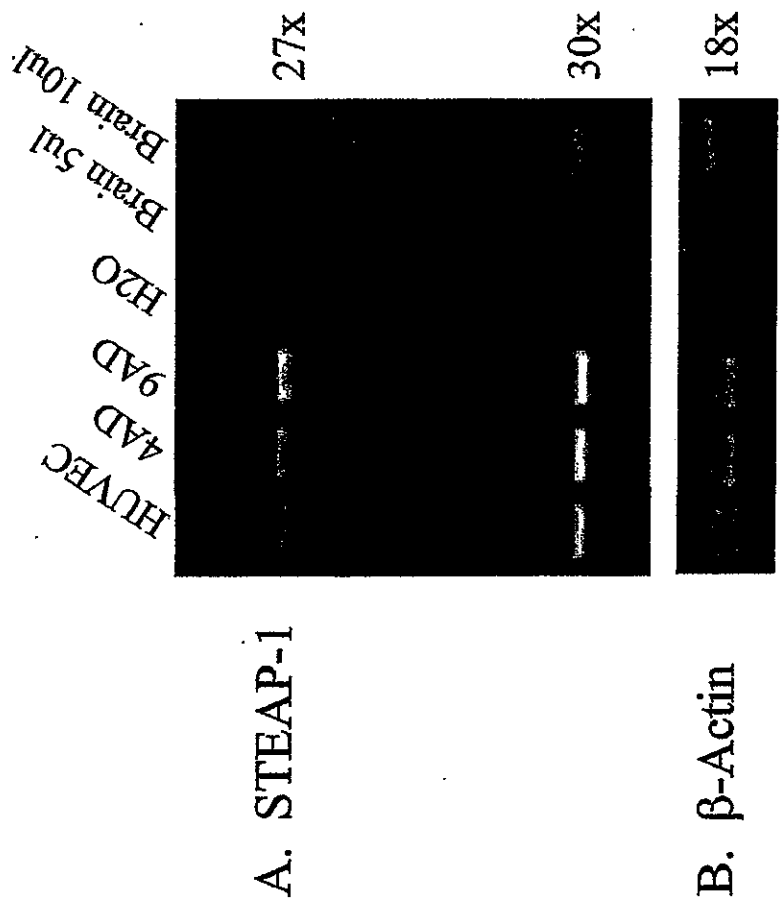
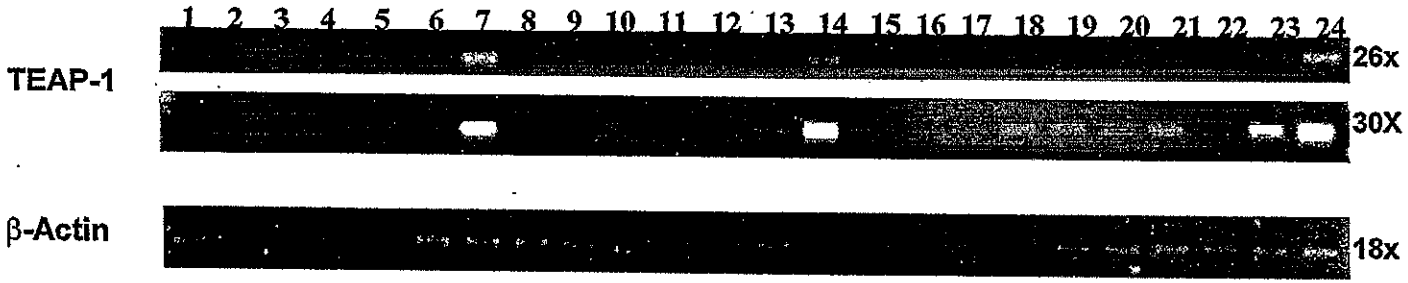
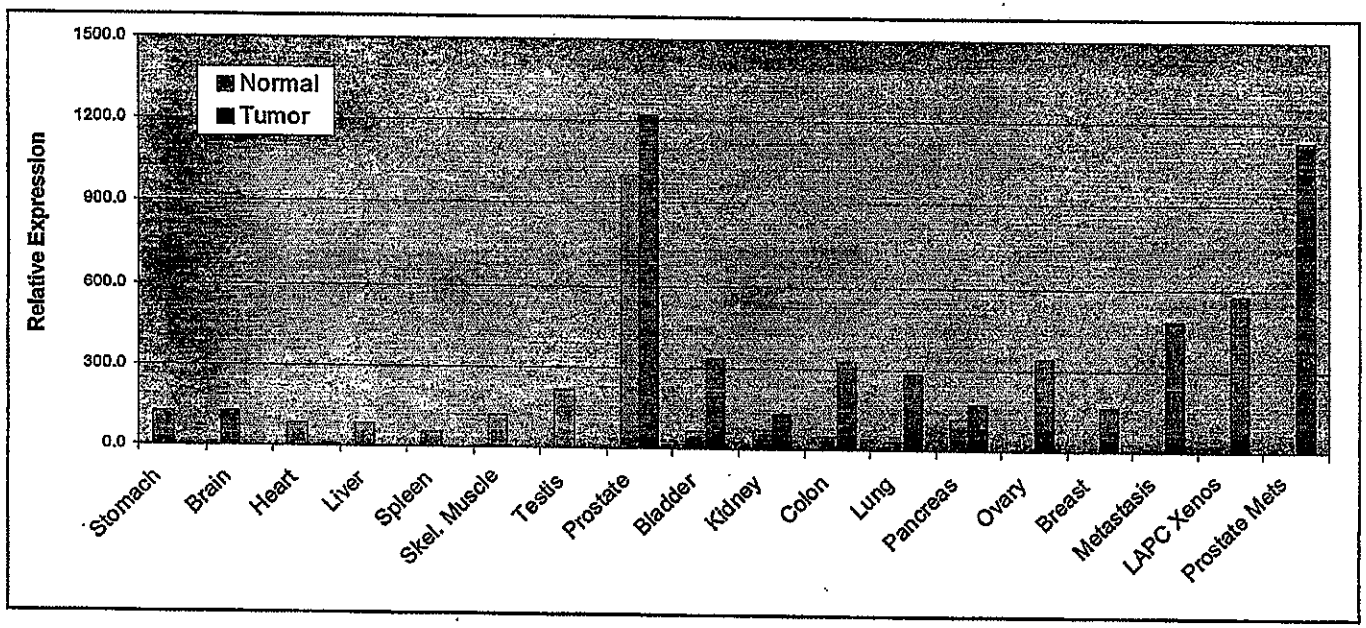


Figure 14(d) and 14(e): STEAP-1 Expression in Normal and Cancer Tissues

14d.



14e.



1. Bladder
2. Brain
3. Heart
4. Kidney
5. Liver
6. Lung
7. Prostate
8. Spleen
9. Skel. Muscle
10. Testis
11 .Pancreas
12. Colon
13. Stomach
14. Prostate Cancer Pool
15. Bladder Cancer Pool
16. Kidney Cancer Pool
17. Colon Cancer Pool
18. Lung Cancer Pool
19. Ovarian Cancer Pool
20. Breast Cancer Pool
21. Metastasis Pool
22. Pancreas Cancer Pool
23. LAPC Xenograft Pool
24. Prostate Met to Lymph Node

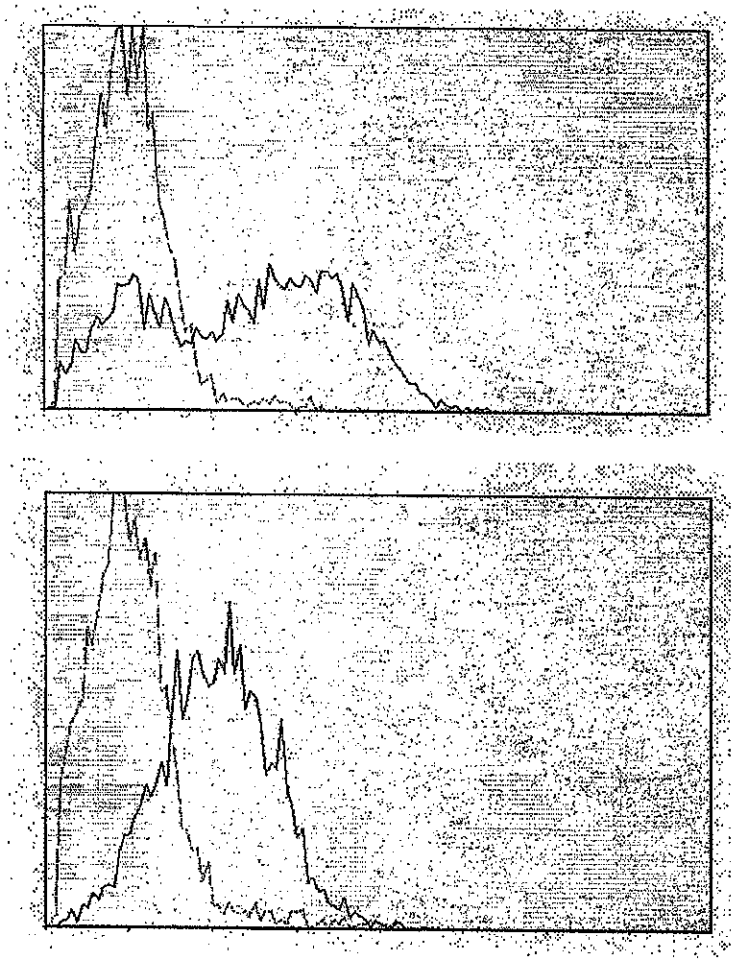
Figure 14(f): STEAP-1 Expression in Lymphoma Patient Specimens

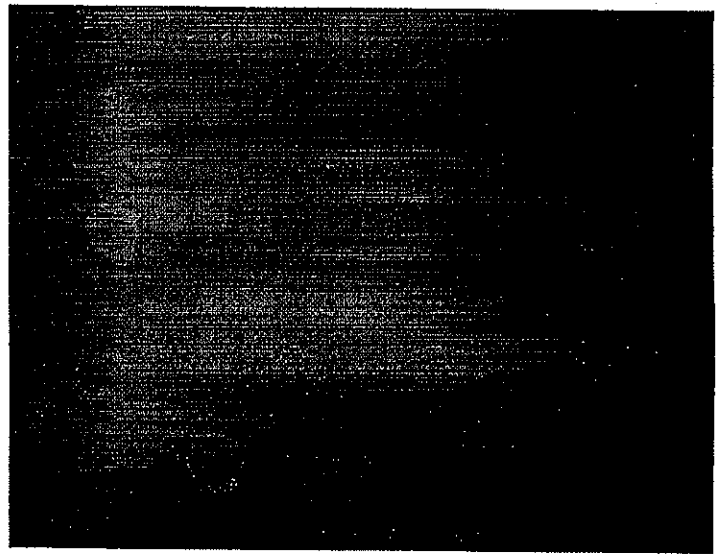
Patient #	Diagnosis	STEAP-1 expression
1	Spleen follicular lymphoma Atypical B-cell type	
2	LCA+,CD20+,Ki+,CD3-,keratin-	
3	Diffuse large B-cell type	
4	Hodgkin's, mixed cellularity	
5	Mantle-cell Lymphoma	
6	Large cell B-cell type	
7	Diffuse mixed large & small cell lymphoma-Stage II	
8	Diffuse large cell lymphoma-Stage I	
9	CD20+,CD10+,CD22+, CD14-,CD38-,CD5-,CD3-	
10	B-Cell lymphoma (CD5-&CD10-)	
11	Small B lymphocytic type (CLL)	
Percentage		**72.7%**

	Strong expressin
	Medium expression
	No expression

Figure 15: Cell Surface STEAP-1 – Specific MAbs

STEAP1/92.30 MAb





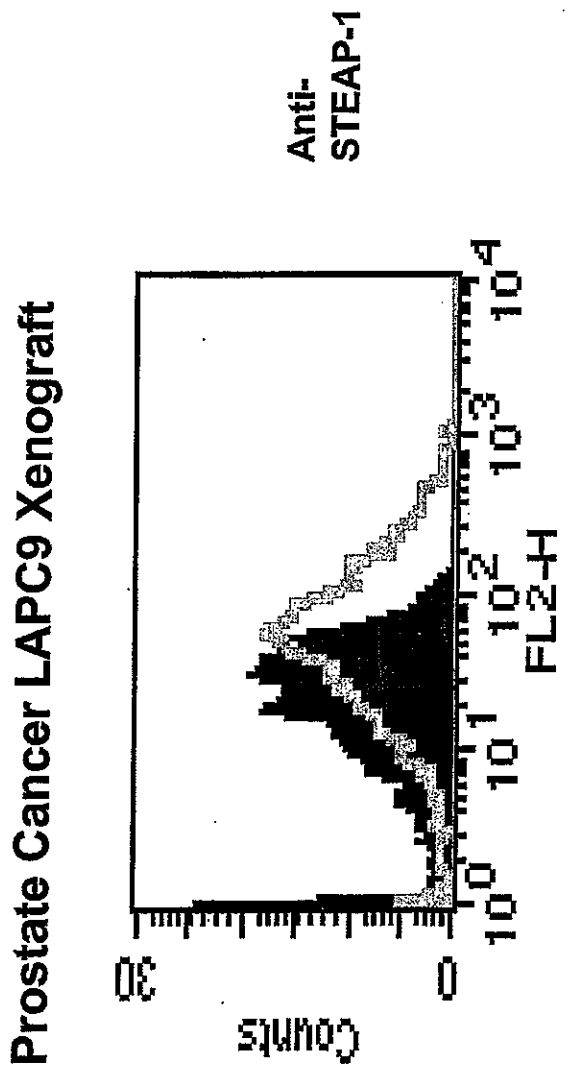


Figure 16: STEAP1/92.30 MAb Recognizes Cell-Surface STEAP-1 on Human Prostate Cancer Xenografts

Figure 17: STEAP1/92.30 MAb Recognizes Mouse STEAP-1

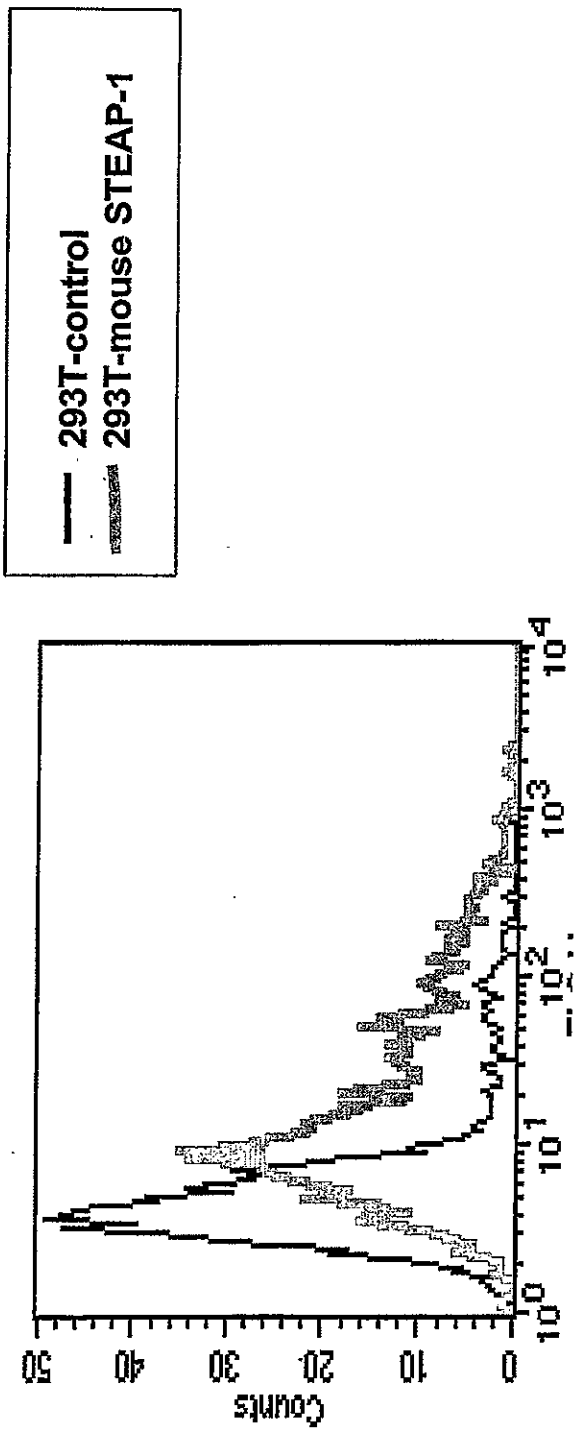
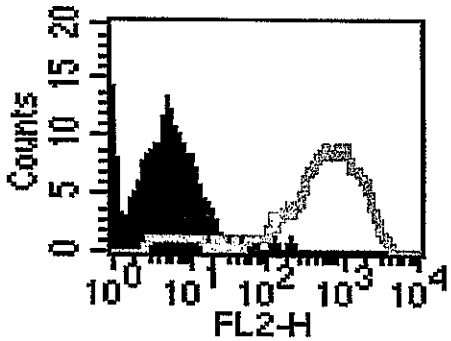
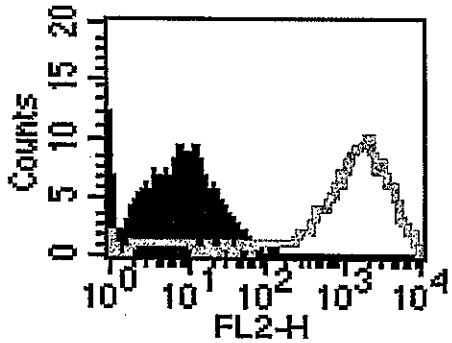


Figure 18: STEAP1/120.545 MAb Recognizes Cell Surface STEAP-1

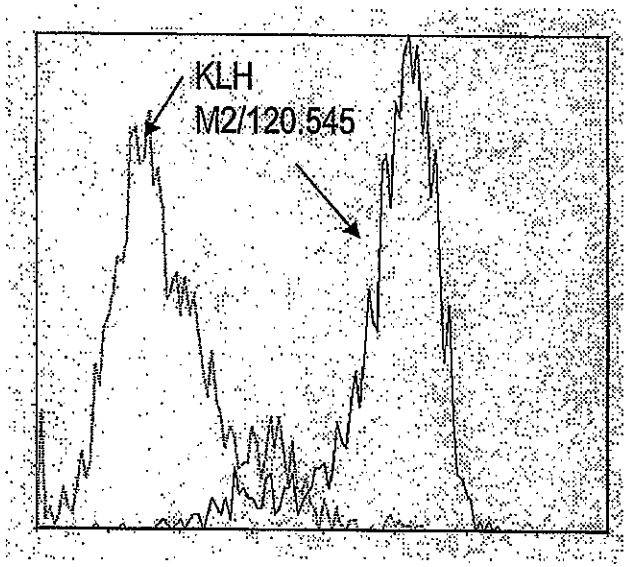
Panel A.
3T3-STEAP1 cells





Panel B.
RAT1-STEAP1 cells

Panel C.
LNCaP cells



Panel D. Fluorescence microscopy

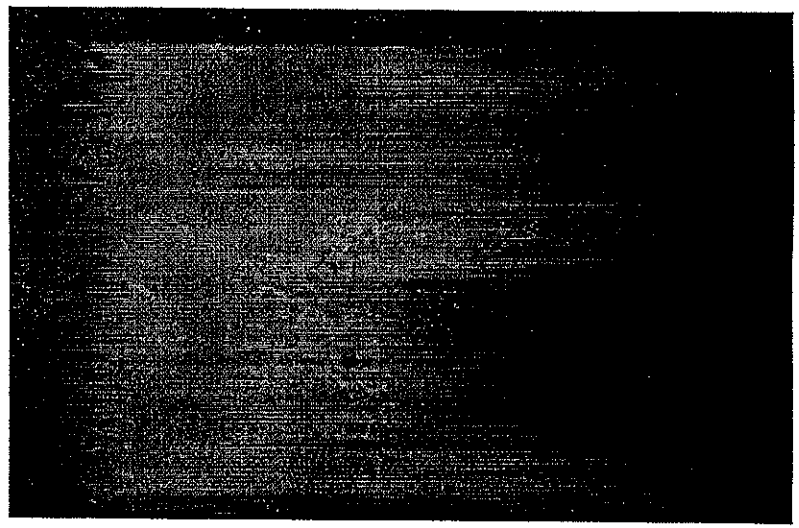


Figure 19:

Figure 19a. The cDNA and amino acid sequence of M2/X92.30 VH clone #2.

```
   1 V  K  L  Q  E  S  G  P  E  L  K  K  P  G  E  T  V  K  I  S
   1 gtcaagctgcaggagtctggacctgagctgaagaagcctggagagacagtcaagatctcc
  21 C  K  A  S  G  Y  T  F  T  N  Y  G  M  N  W  V  K  Q  A  P
  61 tgcaaggcttctgggtatacgttcacaaactatggaatgaactgggtgaagcaggctcca
  41 G  K  G  L  K  W  M  G  W  I  N  T  Y  T  G  E  P  T  Y  A
 121 ggaaagggtttaaagtggatgggctggataaacacctacactggagagccaacatatgct
  61 D  D  F  K  G  R  F  A  F  S  L  E  T  S  A  S  T  A  Y  L
 181 gatgacttcaagggacggtttgccttctctttggaaacctctgccagcactgcctatttg
  81 Q  I  N  N  L  K  N  E  D  T  A  T  Y  F  C  A  R  P  W  F
 241 cagatcaacaacctcaaaaatgaggacacggctacatatttctgtgcaagaccctggttt
 101 A  Y  W  G  Q  G  T  T  V  T  V  S  S
 301 gcttactggggccaagggaccacggtcaccgtctcctca
```

Figure 19b. The cDNA and amino acid sequence of M2/X92.30 VL clone #2.

```
   1 G  L  F  E  A  A  T  M  K  L  P  V  R  L  L  V  L  W  I  R
   1 ggactgttcgaagccgccaccatgaagttgcctgttaggctgttggtgctctggattcgg
  21 E  T  N  G  D  V  V  M  T  Q  T  P  L  T  L  S  V  T  I  G
  61 gaaaccaacggtgatgttgtgatgacccagactccactcactttgtcggttaccattgga
  41 Q  P  A  S  I  S  C  K  S  S  Q  S  L  L  D  S  D  G  K  T
 121 caaccagcctccatctcttgcaagtcaagtcagagcctcttagatagtgatggaaagaca
  61 Y  L  N  W  L  L  Q  R  P  G  Q  S  P  K  R  L  I  Y  L  V
 181 tatttgaattggttgttacagaggccaggccagtctccaaagcgcctaatctatctggtg
  81 S  K  L  D  S  G  V  P  D  R  F  T  G  S  G  S  G  T  D  F
 241 tctaaactggactctggagtccctgacaggttcactggcagtggatcagggacagatttc
 101 T  L  K  I  S  R  V  E  A  E  D  L  G  V  Y  Y  C  W  Q  G
 301 acactgaaaatcagcagagtggaggctgaggatttgggagtttattattgctggcaaggt
 121 T  H  F  P  F  T  F  G  S  G  T  K  L  E  I  K  R  T  D  A
 361 acacattttccattcacgttcggctcggggacaaagttggaaataaaacgtacggatgct
 141 A  P  T  V  S
 421 gcaccaactgtatcc
```

Figure 19c. The cDNA and amino acid sequence of M2/X92.30 VL clone #6.

```
   1 G  L  F  E  A  A  T  M  E  A  P  A  Q  L  T  L  S  V  T  I
   1 ggactgttcgaagccgccaccatggaagccccagctcagctcactttgtcggttaccatt
  21 G  Q  P  A  S  I  S  C  K  S  S  Q  S  L  L  D  S  D  G  K
  61 ggacaaccagcctccatctcttgcaagtcaagtcagagcctcttagatagtgatggaaag
  41 T  Y  L  N  W  L  L  Q  R  P  G  Q  S  P  K  R  L  I  Y  L
 121 acatatttgaattggttgttacagaggccaggccagtctccaaagcgcctaatctatctg
  61 V  S  K  L  D  S  G  V  P  D  R  F  T  G  S  G  S  G  T  D
 181 gtgtctaaactggactctggagtccctgacaggttcactggcagtggatcagggacagat
  81 F  T  L  K  I  S  R  V  E  A  E  D  L  G  V  Y  Y  C  W  Q
 241 ttcacactgaaaatcagcagagtggaggctgaggatttgggagtttattattgctggcaa
 101 G  T  H  F  P  F  T  F  G  S  G  T  K  L  E  I  K  R  T  D
 301 ggtacacattttccattcacgttcggctcggggacaaagttggaaataaaacgtacggat
 121 A  A  P  T  V  S
 361 gctgcaccaactgtatcc
```

Figure 19D. The cDNA and amino acid sequence of M2/X120.545 VL clone #8.

```
   1 M  G  F  K  M  E  S  Q  A  Q  V  L  M  L  L  L  L  W  V  S
   1 atgggcttcaagatggagtcacaggcccaggttcttatgttactgctgctatgggtatct
  21 G  T  C  G  D  I  V  M  S  Q  S  P  S  S  L  A  V  S  V  G
  61 ggtacctgtggggacattgtgatgtcacagtctccatcctccctagctgtgtcagttgga
  41 E  K  V  T  M  S  C  K  S  S  Q  S  L  L  Y  R  S  N  Q  K
 121 gagaaggttaccatgagctgcaagtccagtcagagccttttatataggagcaatcaaaag
  61 N  Y  L  A  W  Y  Q  Q  K  P  G  Q  S  P  K  L  L  I  Y  W
 181 aactacttggcctggtaccagcagaaaccagggcagtctcctaaactgctgatttattgg
  81 A  S  T  R  E  S  G  V  P  D  R  F  T  G  S  G  S  G  T  D
 241 gcctccactagggaatctggggtccctgatcgcttcacaggcagtggatctgggacagat
 101 F  T  L  T  I  S  S  V  K  A  E  D  L  A  V  Y  Y  C  Q  Q
 301 ttcactctcaccatcagcagtgtgaaggctgaagacctggcagtttattactgtcagcaa
 121 Y  Y  N  Y  P  R  T  F  G  G  G  T  K  L  E  I  K  R  T  D
 361 tattataactatcctcggacgttcggtggaggcaccaagctggaaatcaaacgtacggat
 141 A  A  P  T  V  S
 421 gctgcaccaactgtatcc
```

Figure 20:

Figure 20a. The amino acid sequence of M2/X92.30 VH clone #2.

```
  1 VKLQESGPEL KKPGETVKIS CKASGYTFTN YGMNWVKQAP GKGLKWMGWI NTYTGEPTYA
 61 DDFKGRFAFS LETSASTAYL QINNLKNEDT ATYFCARPWF AYWGQGTTVT VSS
```

Figure 20b. The amino acid sequence of M2/X92.30 VL clone #2.

```
  1 GLFEAATMKL PVRLLVLWIR ETNGDVVMTQ TPLTLSVTIG QPASISCKSS QSLLDSDGKT
 61 YLNWLLQRPG QSPKRLIYLV SKLDSGVPDR FTGSGSGTDF TLKISRVEAE DLGVYYCWQG
121 THFPFTFGSG TKLEIKRTDA APTVS
```

Figure 20c. The cDNA and amino acid sequence of M2/X92.30 VL clone #6.

```
1 G  L  F  E  A  A  T  M  E  A  P  A  Q  L  T  L  S  V  T  I
1 ggactgttcgaagccgccaccatggaagccccagctcagctcactttgtcggttaccatt
21 G  Q  P  A  S  I  S  C  K  S  S  Q  S  L  L  D  S  D  G  K
61 ggacaaccagcctccatctcttgcaagtcaagtcagagcctcttagatagtgatggaaag
41 T  Y  L  N  W  L  L  Q  R  P  G  Q  S  P  K  R  L  I  Y  L
121 acatatttgaattggttgttacagaggccaggccagtctccaaagcgcctaatctatctg
61 V  S  K  L  D  S  G  V  P  D  R  F  T  G  S  G  S  G  T  D
181 gtgtctaaactggactctggagtccctgacaggttcactggcagtggatcagggacagat
81 F  T  L  K  I  S  R  V  E  A  E  D  L  G  V  Y  Y  C  W  Q
241 ttcacactgaaaatcagcagagtggaggctgaggatttgggagtttattattgctggcaa
101 G  T  H  F  P  F  T  F  G  S  G  T  K  L  E  I  K  R  T  D
301 ggtacacattttccattcacgttcggctcggggacaaagttggaaataaaacgtacggat
121 A  A  P  T  V  S
361 gctgcaccaactgtatcc
```

Figure 20d. Amino acid alignment of M2/X92.30 VL clone #2 and M2/M92.30 VL clone #6.

```
Clone 2: 1   GLFEAATMKLPVRLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKT 60
             GLFEAATM+ P +L                    TLSVTIGQPASISCKSSQSLLDSDGKT
Clone 6: 1   GLFEAATMEAPAQL-------------------TLSVTIGQPASISCKSSQSLLDSDGKT 41

Clone 2: 61  YLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQG 120
             YLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQG
Clone 6: 42  YLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQG 101

Clone 2: 121 THFPFTFGSGTKLEIKRTDAAPTVS 145
             THFPFTFGSGTKLEIKRTDAAPTVS
Clone 6: 102 THFPFTFGSGTKLEIKRTDAAPTVS 126
```

Figure 20e. The amino acid sequence of M2/X120.545 VL clone #8. The sequence of the signal peptide is underlined.

```
  1 MGFKMESQAQ VLMLLLLWVS GTCGDIVMSQ SPSSLAVSVG EKVTMSCKSS QSLLYRSNQK
 61 NYLAWYQQKP GQSPKLLIYW ASTRESGVPD RFTGSGSGTD FTLTISSVKA EDLAVYYCQQ
121 YYNYPRTFGG GTKLEIKRTD AAPTVS
```

Figure 21: STEAP1 M2/92.30 MAb Recognizes Cell-Surface STEAP-1 on Human Prostate and Bladder Cancer Xenografts

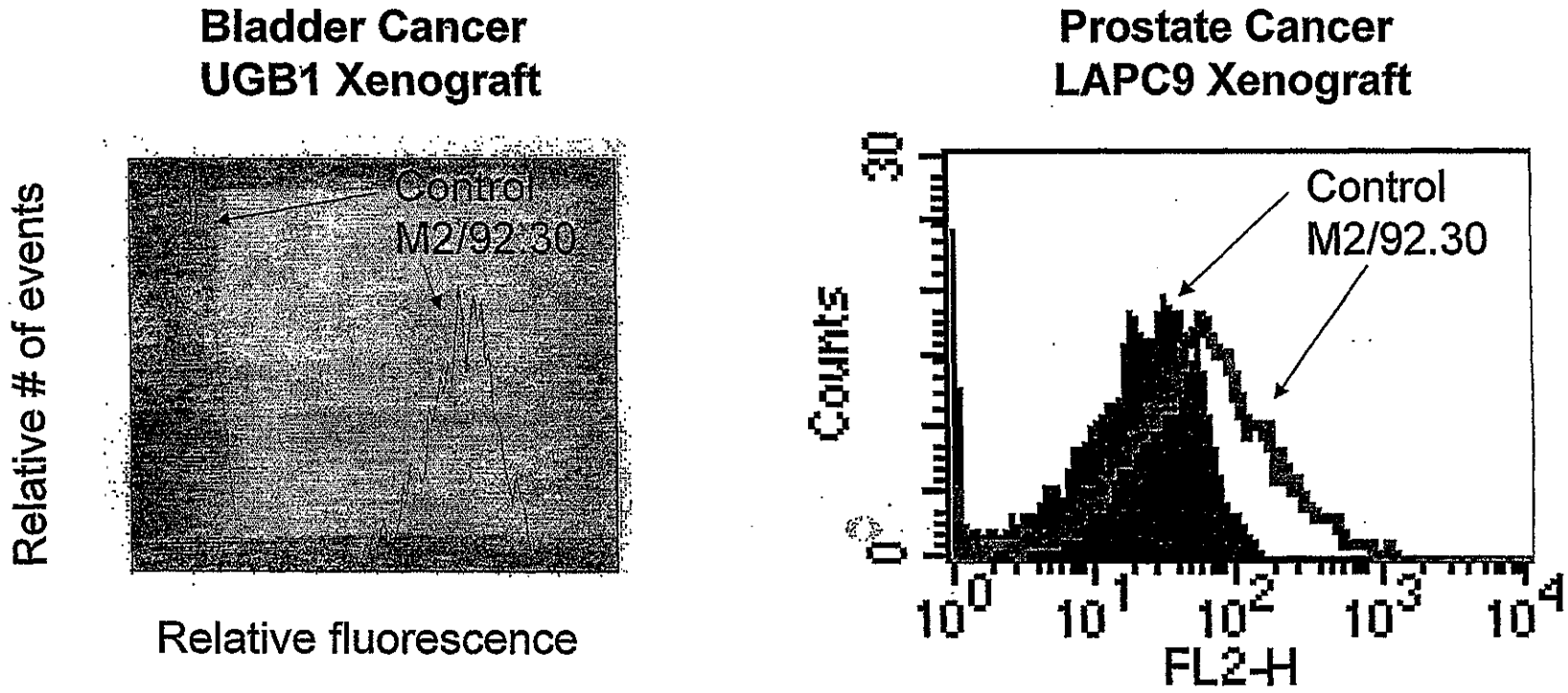
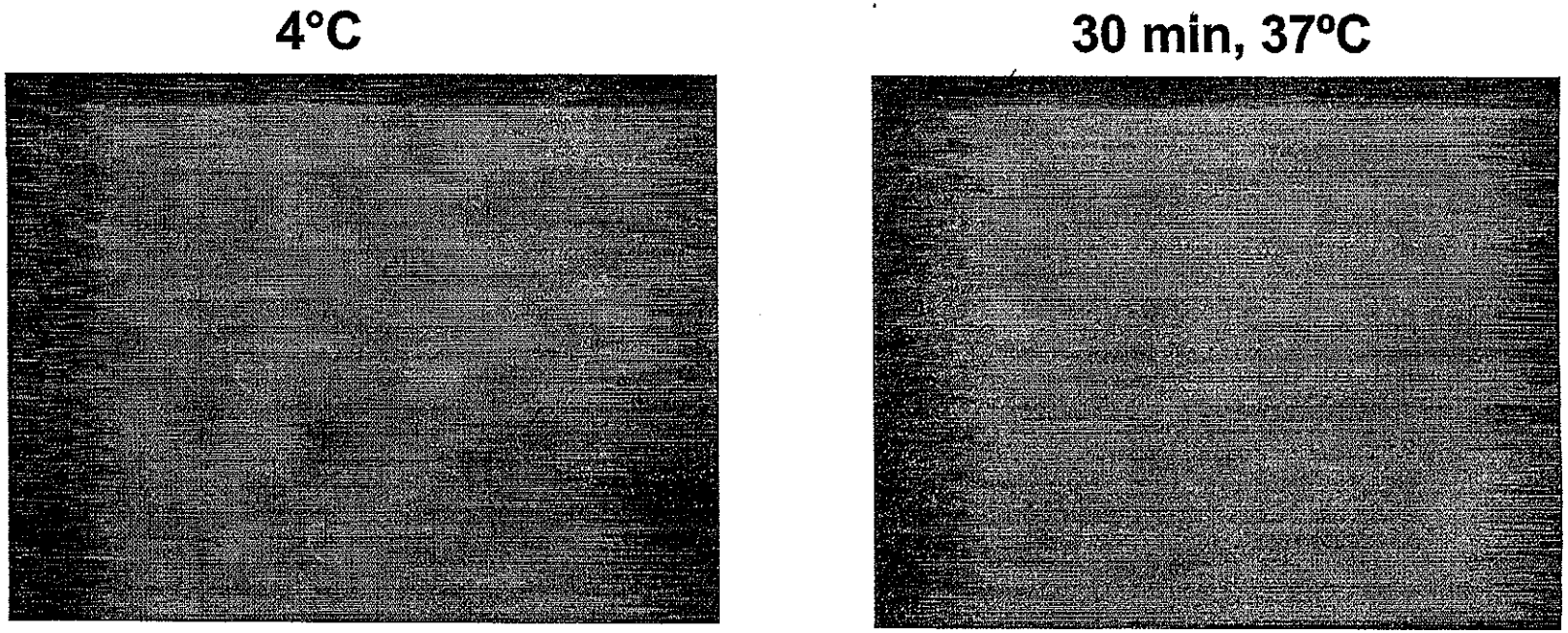


Figure 22: STEAP-1 internalization by STEAP1 M2/92.30 MAb



Fluorescent microscopy

Figure 23: STEAP-1 internalization by STEAP1 M2/120.545 MAb

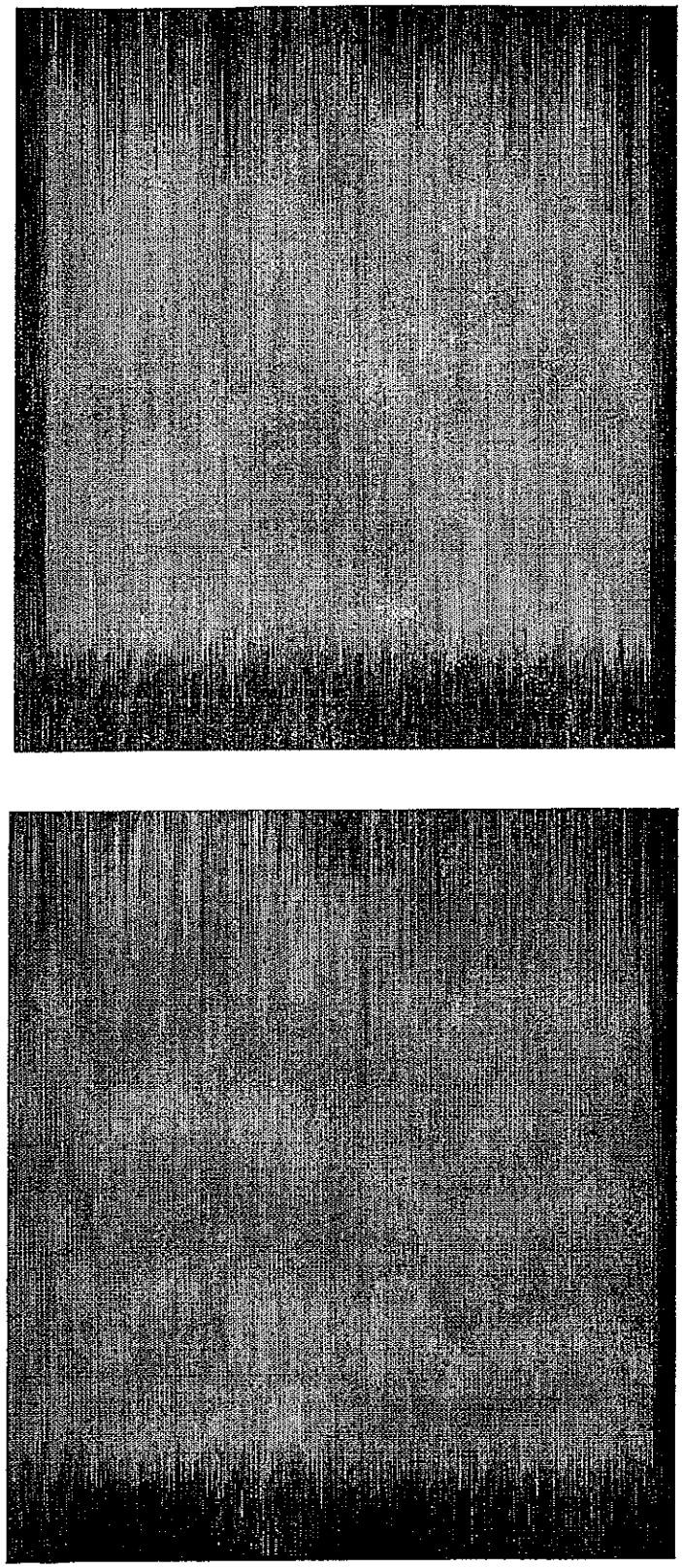


Figure 24: STEAP-1 Internalization

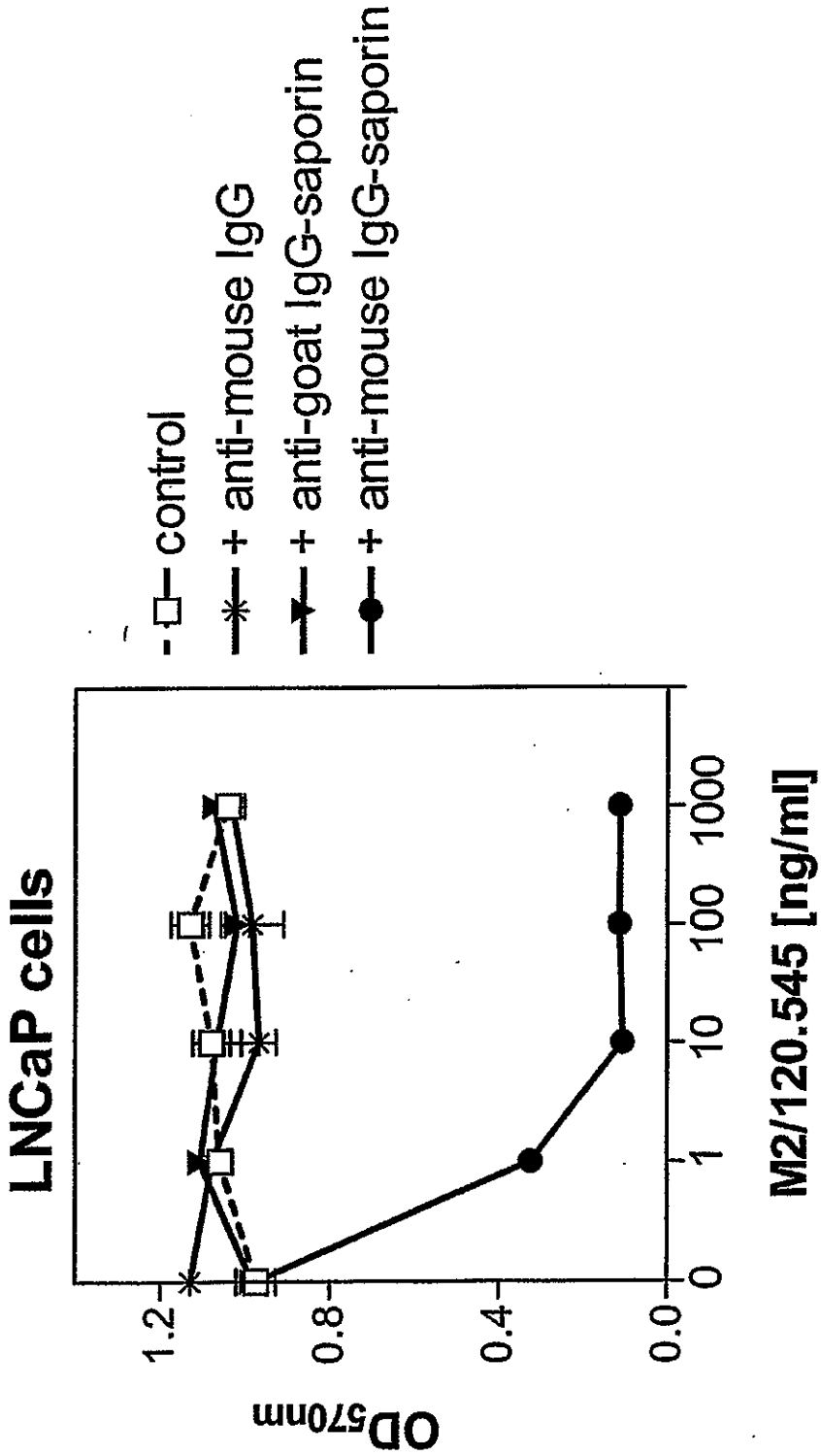


Figure 25 - Immunoprecipitation of STEAP1 by anti-STEAP1 MAbs M2/92.30 and M2/120.545

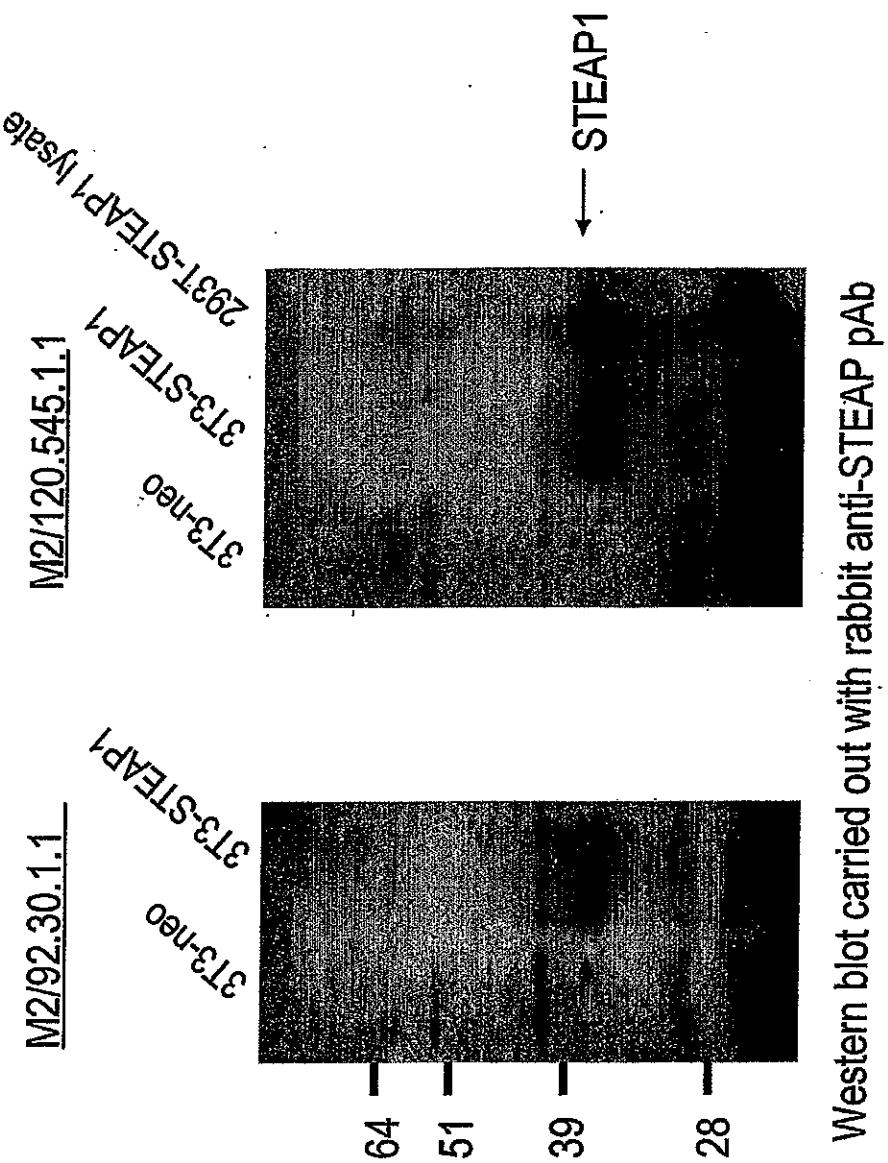


Figure 26: Effect of STEAP-1 MAbs on the Growth of LAPC9 Human Prostate Cancer Xenografts in Mice

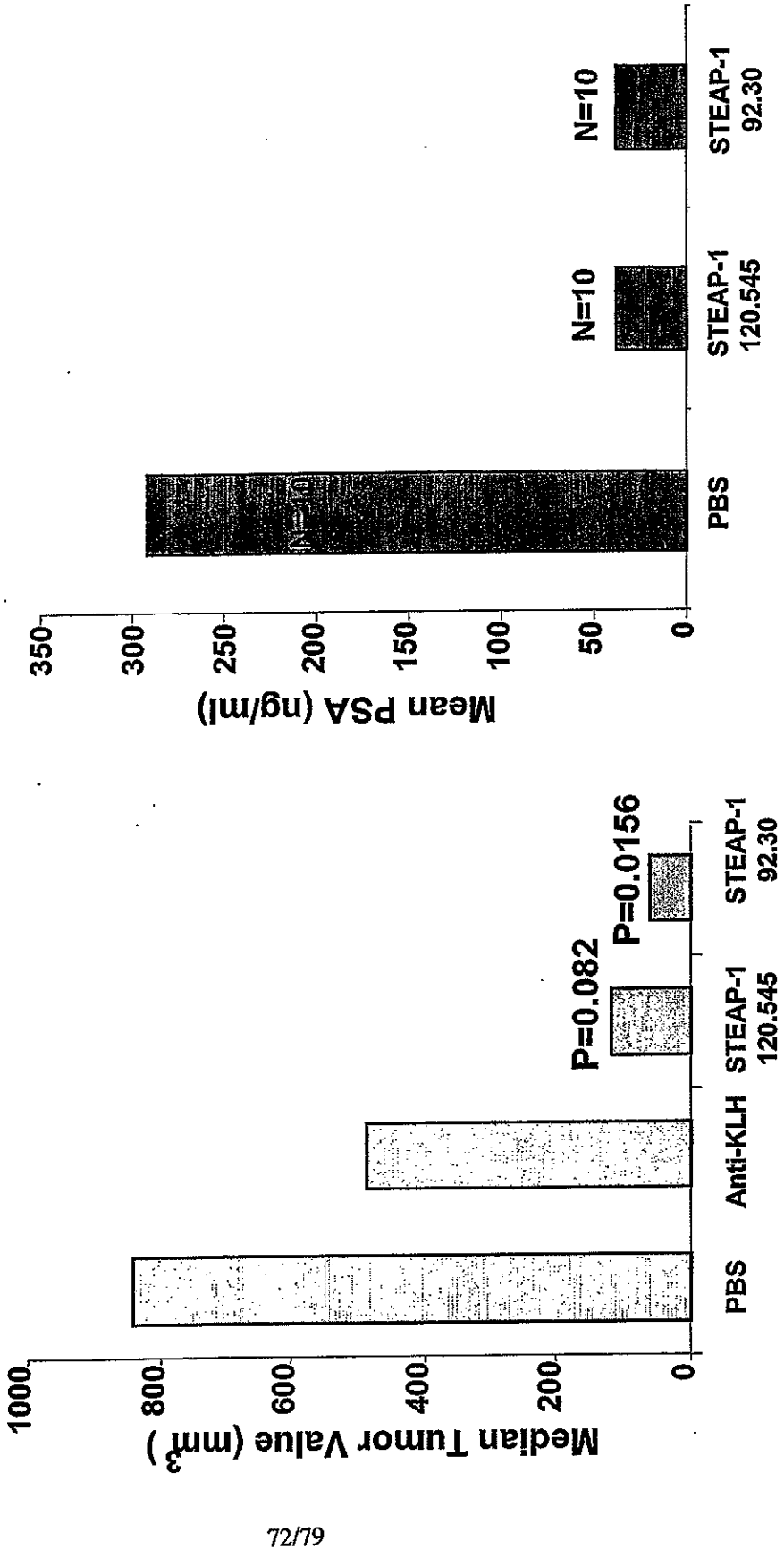
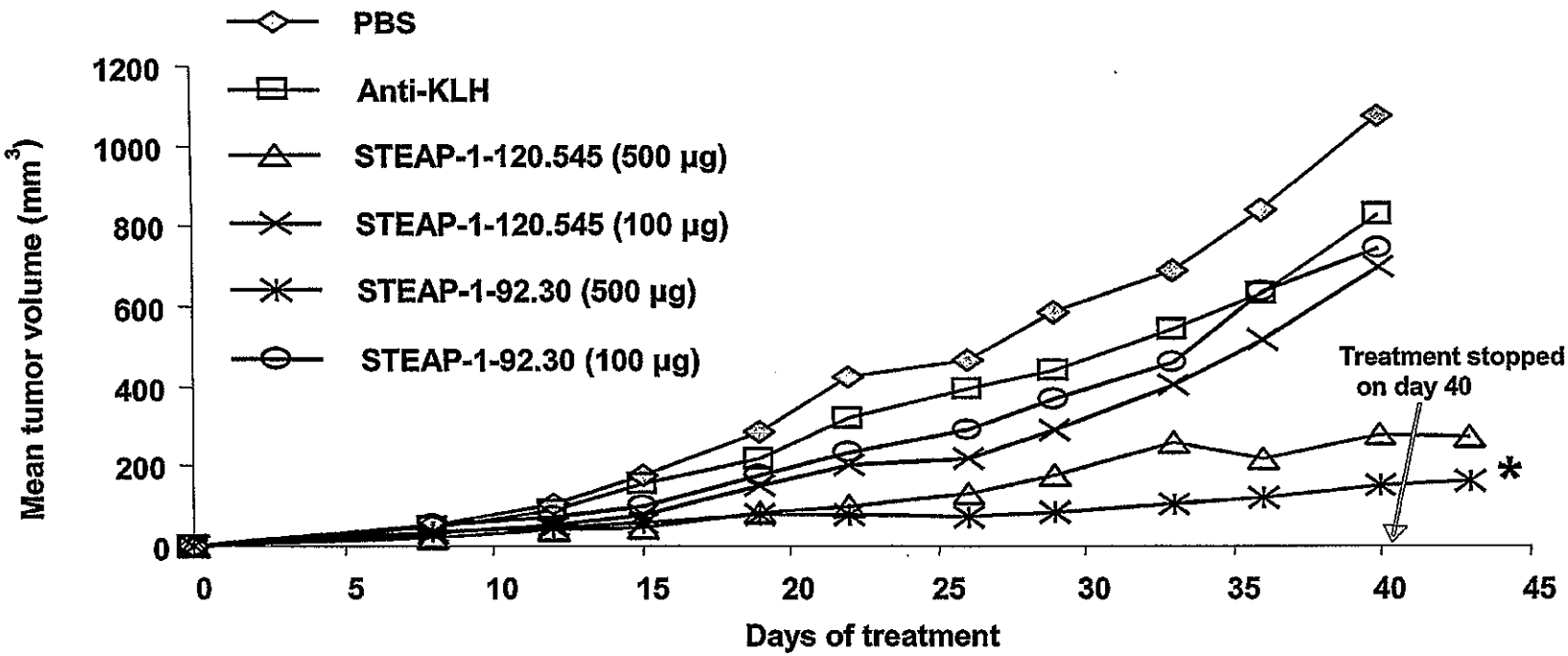


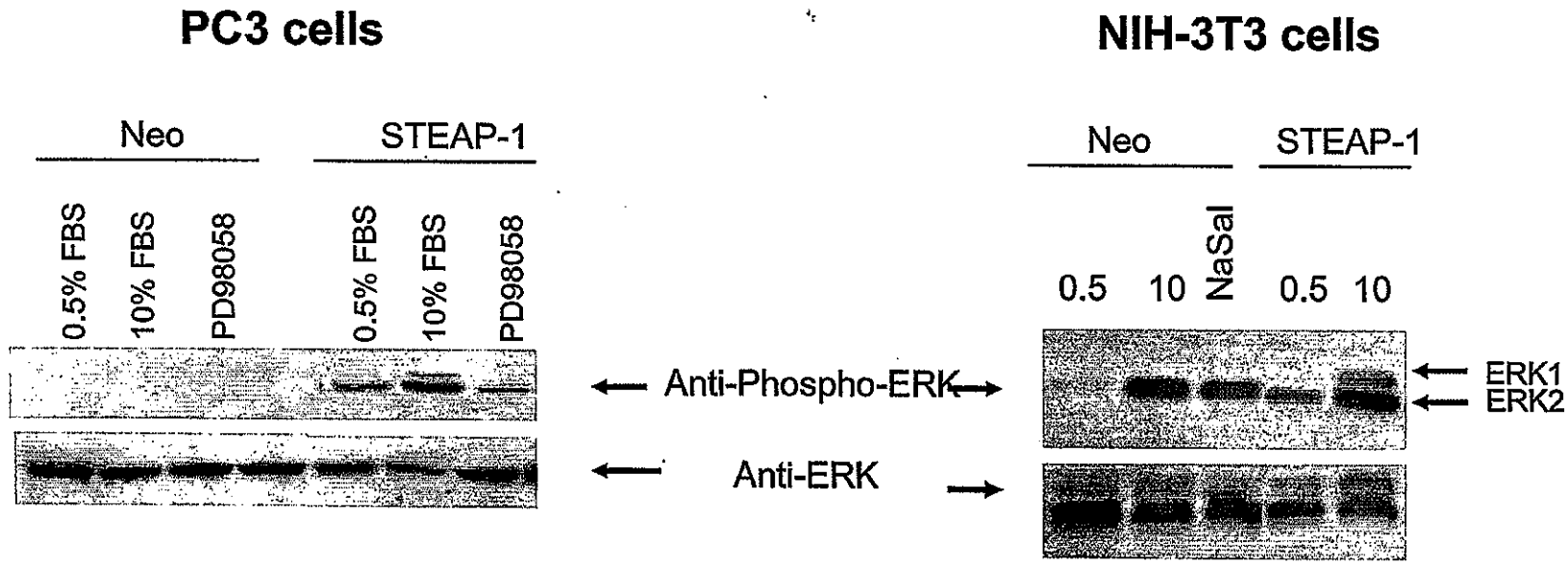
Figure 27: Effect of STEAP-1 MAbs on the Growth of LAPC9 Human Prostate Cancer Xenograft in Mice



- Treatment started on the same day of subcutaneous tumor cell injection (2 x 10^6/mouse; n=10/group)
- MAb ip injection – 100 or 500 µg/dose, 2/week, 12 injections (last day – d40)

* Significant difference compared to PBS and anti-KLH controls with $p<0.05$

Figure 28: STEAP-1 Induces ERK Phosphorylation



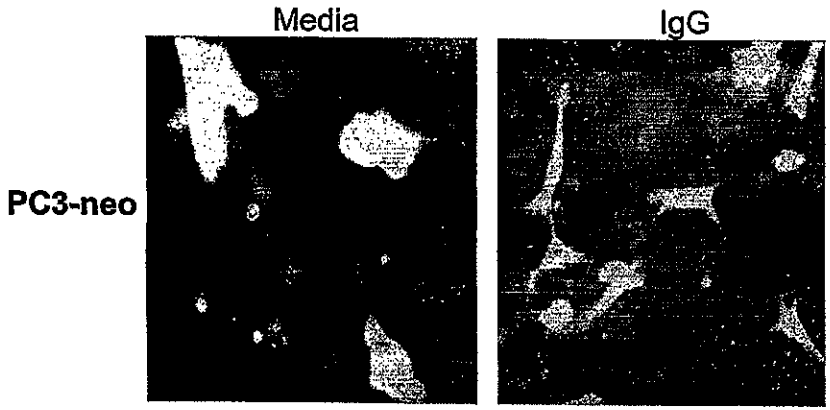
- **Expression of STEAP-1 induces ERK phosphorylation.**
- **FBS-mediated ERK1 phosphorylation is inhibited by the MEK inhibitor PD98038.**

Figure 29: STEAP-1 Mediates Cell-Cell Communication

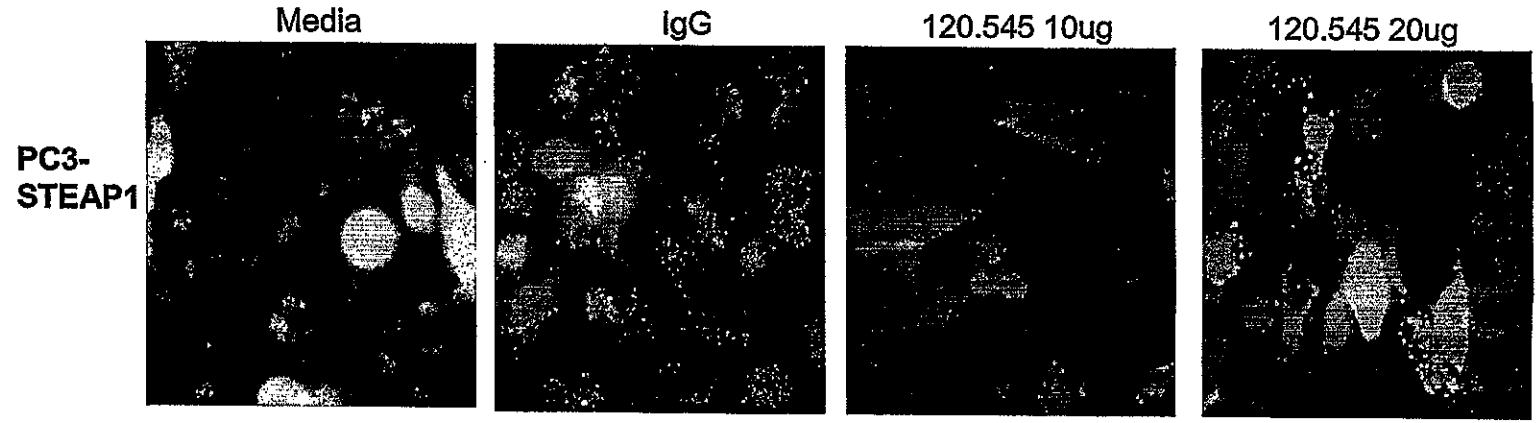


Figure 30: Cell Communication Requires STEAP-1 Expression on Donor and Recipient Cells

Figure 31: STEAP1/120.545 MAb Effect on Gap Junction

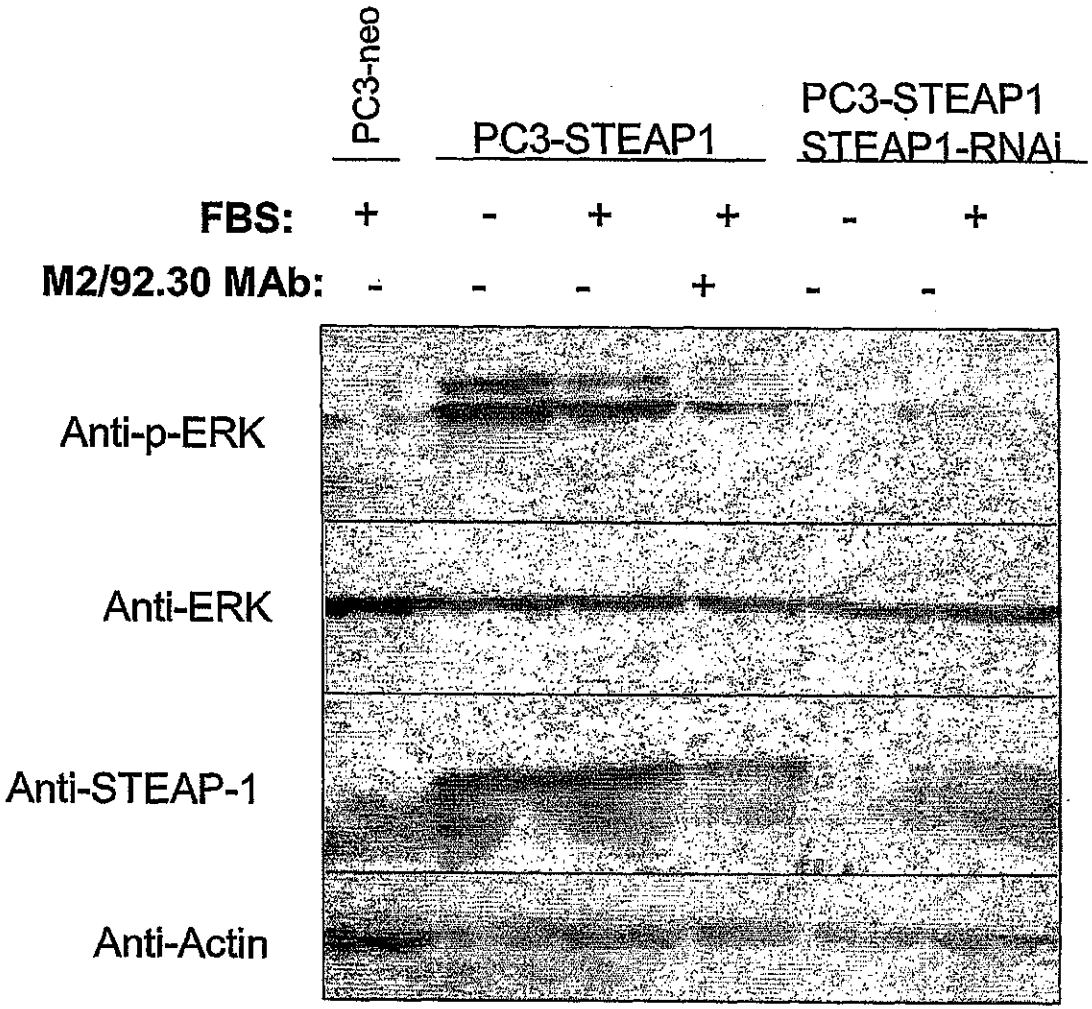


Cell Line	Treatment	% communication
PC3-neo	none	8%
	10ug/ml IgG2a	5%
PC3-STEAP1	none	70%
	10ug/ml IgG2a	85%
	1ug/ml X120.545	81%
	10ug/ml X120.545	37%
	20ug/ml X120.545	14%



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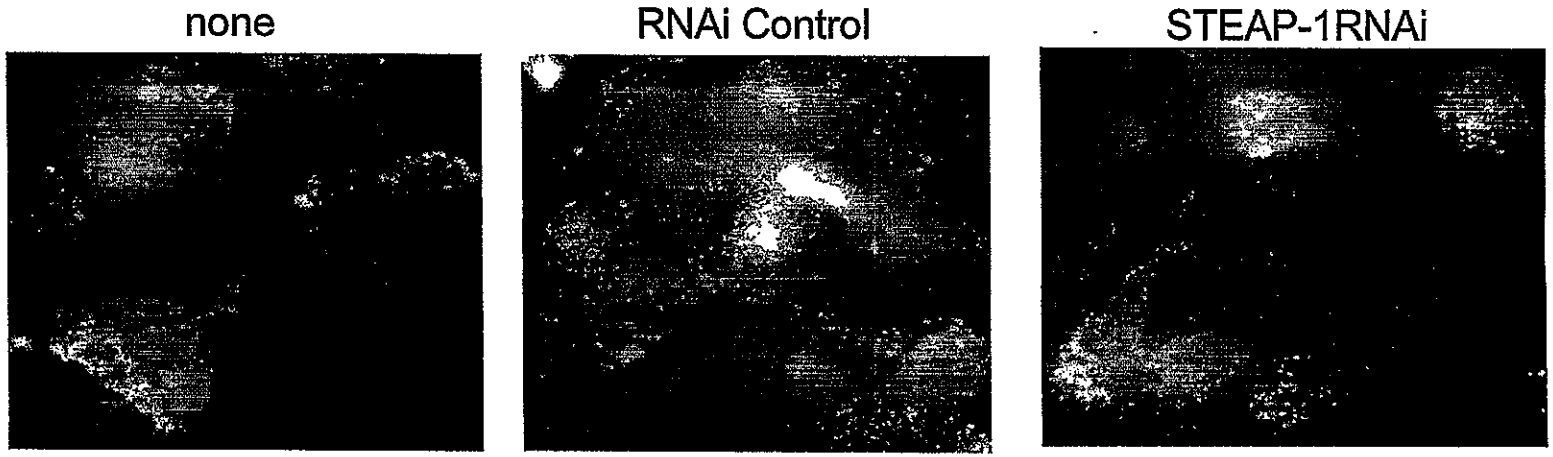
Figure 32: Inhibition of ERK Phosphorylation by STEAP-1 mAb and RNAi



- Blots on WCL
- Repeated 3 times

Figure 33: Effect of STEAP-1 RNAi on Cell-Cell Communication

PC3-STEAP1 Cells



Treatment		% Transfer
PC3-neo		5.2
PC3-STEAP1		76
	Control	47
	STEAP-1 RNAi	4.8