

```

1   MQV--QCQQSPVLAGS-ATLVALGALALYV-----AKPSGYGKHTES----- 39  P31213  S
1   MDLSAASHRIPLSDGNSIPIIIGLGTYSEPKSTPKGACATSVKVAIDTGYRHIDGAYIQQN 60  P51857  A
   *::  .:: *: * .  ::**::  :      *  :**  :  :

40  -----LK-----PAATRLPARAAWFLQELPSFAVPA----- 65  P31213  S
61  EHEVGEAIREKIAEGKVRREDIFYCGKLWATNHVPEMVRPTLERTLRVLQLDYVDLYIEE 120 P51857  A
   ::      :  .  *  ::*..  *:

66  -----GILARQPLS-----LF 76  P31213  S
121 VMAFKPGDEIYPRDENGKWLYHKSNLCATWEAMEACKDAGLVKSLGVSNFNRRQLELIL 180 P51857  A
   *::  :*  ::

77  GPPGT----VLLGLFCVHYFHRTFVYLLNRGRPYPAIILIRGTAFCTGNGVLQGYLIY 132 P31213  S
181 NKPGLKHKPVSNQVECHPYFTQPK-----LLKFCQQHDIVITAYSPL 222 P51857  A
   **  *  :  *  **  :      **  .  ::  *

133 CAEYPDGWYTDIRFSL--GVFLFILMGINIHSYILRQLRKPGEISYRIPQGGLFYVS 190 P31213  S
223 GTSRNPIWVNVSSPPLKDALNSLGKRYNKTAAQIV-----LRFNIQRGVV-VIPK 273 P51857  A
   :.  *  .  *  .:*  **  *  :  *:  :  :.*  :*  :  .  .

191 GAN--FLGEIIEWIGYALATWSLPALAFAPFSLCFLGLRAFHHHRFYLMKFEDYPKSRKA 248 P31213  S
274 SFNLERIKENFQIFDFSLTEEMKDIEALNKNVRFVLLMWRDHP-----EYPFHDEY 326 P51857  A
   .  *  :  *  ::  :  :*:  .:  :  .:  *  *  :*:  *  :**  :

249 LIPFIF 254 P31213 S5A2_HUMAN
327 ----- 326 P51857 AK1D1_HUMAN

```

Supporting Figure S4. 5AR type 2 and 5BR sequence alignment. Binding site residues are sharpened in light green; active site residues are sharpened in olive green.