FTM1 >Fugu thrombomodulin on Scaffold_195
(sequence length=542)
HTM1 >gi|1070535|thrombomodulin precursor [validated] - human
(sequence length=575)

Number of matches = 202
Fraction of identities per length = 0.372694

```
 M N D V T R L I A I   V C A L L W G R T G G V K P N N I Y C
 M_L G V_L V L_G A_L A L A G L_G F P A P A E P Q P_G G S Q C_

 I G N Q C F T V S K I L G D F S A A Q S E C Q D R G G N L M
 V E H D C_F_A L Y P G P A T F_L N A_S Q I C_D G L R G_H L_M_

 T V R S S V A H D V L L M L L         G D A S S R F W I G L
 T_V_R_S_S_V_A_A D_V_I S L L_L_N G D G G_V G R R R_L W_I_G_L_

 H L P T G C     P D R S A E L K G F L W V A G D N E S D F S
 Q L_P_P G_C_G D P_K R_L G P L_R G_F_Q W_V_T G_D_N_N T S Y S_

 N W P T   T F N S S     C S S H R C V S V S P A D G F
 R W_A R L D L N_G A P L C_G P L   C_V_A V_S_A A_E A T V P S

    K W T R E P C D T R T D G F L C E Y S F N E T C N S L E
 E P I W_E E Q Q C_E V K A D_G_F_L_C_E_F H F_P A T_C_R P L_A

 A G A G E          T L T Y S T P I G F E G E D L L S L P P
 V E P G_A A A A A A V S I T_Y_G T_P_F A A R G_A D_F Q A L_P_V

 G S T A V R M P T E T K Y I C             F S G Q W T Q
 G_S_S A_A V A P_L G L Q L M C_T A P P G A V Q G_H W_A R E A

   A P W N C D V L G G G C E Y K C T Q D P E K M P L C Y C P
 P G A W_D C_S V_E N G_G_C_E_H A C_N A I P_G   A P_R C_Q C_P_

 R G K T I N P E N E V T C E E T Q E D P C A S L R C A H I C
 A G_A A L Q A D G R   S C_T A S A T Q S C_N D L_  C_E H_F C_

 Y       E N G G S F A C T C R E G F K L A A D G R S C V D F
 V P N P D Q P G_S_Y S C_M C_E T G_Y R L_A_A_D_Q H R C_E D_V

 N D C T   D P R Q C P G E N S R C V N T A G G F Q C V C K D
 D D_C_I L E P_S P C_P_      Q R_C_V_N_T_Q G_G_F_E C_H C_Y P

 G Y R Y K G G V C V D   V N E C T S A P C E H M C D N L   P
 N Y_D L V D G_E C_V_E P V_D P C_F R A_N C_E_Y Q C_Q P L_N Q

 G S Y V C S C Y P G Y K E D P E E P H R C K L Y C G E E E C
 T S_Y_L C_V C_A E G_F A P I P_H E_P_H_R_C_Q M F C_N Q T A C_

 L A E C D P N D R Y Q C F C P E G Y I L E E R Q Q D A V C L
 P A_D C_D_P_N_T Q A S C_E C_P_E_G_Y_I_L_D D       G F I C_T

 D I D E C   S S F Y C D Q D C E N T Y G S Y V C I C S P G Y
 D_I_D_E_C_E N G G F C_S G V C_H N_L P G_T F E C_I_C_G P_D S

 K L V D N Y     K C V K N E V G P D E G S G A S S T P P S L
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 A L_V_R H I G T D C_D S G K V_D G G D   S_G_S G E P P_P_S_P

 T T E P P D A T I Q P S I L T R G G I V G I V L C T L   F I
 T_P G S T L T P P A V G L V H S G_L L I G_I_S I A S L_C L V

 T A L L M F L A Y       R V L C G K G K M E S A D G V K A S
 V A_L_L_A L L_C H L R K K Q G A A R A K_M_E_Y K C A A P S K

 E N E A H T L Q P V T S D A
 E_V V L Q H V R T E R T P Q R L


FTFI >fugu TFPI on scaf611, from tbn
   (sequence length=288)
TFPI >gi|125932|sp|human Tissue factor pathway inhibitor (TFPI)
   (sequence length=304)

Number of matches = 102
Fraction of identities per length = 0.354167

 M I F N S P D P Q G N Q T         L L N Y   P G E I S S V Y
 M_I_Y T M K K V H A L W A S V C L L_L_N_L A P_A P L N A D S

 L K T H K L H L L          Q I \/ P E H L I F N E L C A L K D E K
 E E D E E H T I I T /\ D T E L    P_P L K L M H S F C_A_F K_A D D

 G P C K A I K D R F F F N V D N G H C E L F E Y G G C G G N
 G_P_C_K_A_I_M K R_F_F_F_N_I F T R Q C_E_E F_I Y_G_G_C_E G_N_

 A N N F E T L E E C E E T C V            V S G K S H D K \/ Y
 Q N_R F_E_S L_E_E_C_K K M C_T R D N A N R I I K T T L Q Q /\ E

 N K T P C H L S E A P G P C R G L L S R Y Y Y D S R S Q Q C
 K P D F C_F L_E E_D P_G_I C_R_G_Y I T R_Y_F Y_N N Q T K Q_C_

 T H F F Y G G C F G N A N N F R S M A E C Q A K C Q S
 E R F_K Y_G_G_C_L G_N_M N_N_F_E T L E E_C_K N I C_E D G P /\ N

       P \/ D N V N K N M I S N N T S L S A Q T E A I N Q D M I
 G F Q V    D_N_Y G T Q L N A V N_N S_L_T P Q_S T K V   P S L F

 P \/ Y V K P T D L C S F P T D P G T C D G K E R R F T Y N S I
 E F H G P_S   W C_L T P_A D_R G_L C_R A N E_N R_F_Y Y_N_S_V

 T K R C Q A F I Y S G C G G N E N N F V F R K N C I A K C K
 I G K C_R P F_K Y_S_G_C_G_G_N_E_N_N_F_T S K Q E C_L R A C_K_

 A    A R K \/ Q K K K R E K N E K S A E S Q K S D   V A F N R R N
 K /\ G F I    Q_R I S K G G L I K_T K R K R K_K Q R V_K I A Y E E

 E L L H L L D P A
 I F V K N M


FTM2 >fugu thrombomodulin candidata2 on Scaffold195
   (sequence length=472)
HTM1 >gi|1070535|thrombomodulin precursor [validated] - human
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(sequence length=575)

Number of matches = 138
Fraction of identities per length = 0.292373

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 M S P S A N P C L L V L V F L C G L E E A L L S H S G    R
 M_L G V L V L G A L_A L_A G L_  G_F P A P A E P Q P G_G S Q

 C T D N R C V A V F V D S T D F P G A Q K S C K S F N G Q L
 C_V E H D C_F A_L Y P G P A T F_L N A_S Q I C_D G L R G_H L_

 F K Y N M T T L A D I F K L L P S G            K L W
 M T V R S S V A A_D_V I S L_L_L N G_D G G V G R R R L_W_I G

 L E Q Q E A V A T P Q N
 L_Q L P P G C G D P_K R L G P L R G F Q W V T G D N N T S Y

                                C S S I A V S T D S F A
 S R W A R L D L N G A P L C G P L C_V A V S A A E A T V P S

   Q S W E    P C H K N L S G Y L C Q Y P L T N P C G P V K
 E P I W_E_E Q Q C_E V K A D G_F L_C_E F H F P A T C_R P_L A

 V         A G A P Q V V Y T A P M D F E V R D S Q T F P E
 V_E P G A A A_A A_V S I T Y_G T P_F A A R G A D_F Q_A L P_V

 G T T A M V I T A G D K H L  E S K H V C F G D Q W L K
 G_S S A_A V_A P L G_L Q L M C T A P P G A V Q G H W_A R E A

   A P W N C E V M L G G C E R G C N K T T N T    C T C P G
 P G A W_D C_S V_E N G_G_C_E_H A C_N_A I P G A P R C_Q C_P_A

 E Q S L N S N G V T C
 G A A L_Q A D G_R S C_T A S A T Q S C N D L C E H F C V P N

                                  E D V N K C E D S A L C
 P D Q P G S Y S C M C E T G Y R L A A D_Q H R C_E_D_V D D C_

        T R A G E V C V K K E G G F E C V C R N G F I E E E
 I L E P S P C P Q R C_V_N T Q G_G_F_E_C_H C_Y P N Y D L V D

 G V C V N N  S I C F    E C E H P L C V K R Q G V Y K C A
 G_E C_V_E P V D P C_F_R A N C_E_Y Q C Q P L N Q_T S Y_L C_V

 C Y E G Y Q V R V G D L T K C D R L C T E R Q C L A S C D R
 C_A E_G_F A P I P H E P H R C_Q M F C_N Q T A C_P A_D C_D_P

 N A E S N V Q C F C P T G F I L D T S N G S N I C T D I D E
 N_T Q A S    C_E C_P_E G_Y I_L_D_     D G F I_C_T_D_I_D_E_

 C D M G K Q C E H T C V N L F G G F R C G C F E G F R L
 C_E N G_G F C_S G V C_H N_L_P G_T F_E C_I C_G P D S A L_V R

 H G E H Q C L P V D  D G Q E D G S S S T A S Y L I P V T P
 H_I G T D C_D S G K V D_G_G D S G_S_G E P P P S P T P_G S T

 Q P A L V P S Y I K A G S V L G I T V F L L L C A T L I F F
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 L T P P A V G L V H S G_L L I G_I_S I   A S L_C_L V V A L L

   L I Y N A V K R     C R R F D L T S L K H T N I D I F H L
 A L_L C H L R K_K Q G A A R_A K M E Y K C A A P S K E V V L_

 Q Q V T T D T Y K R L S L
 Q_H V_R T_E R   T P Q R L_


FTFI >fugu tissue factor inhibitor on scaf1267
   (sequence length=241)
TFI2 >gi|5730091| tissue factor pathway inhibitor 2 [Homo sapiens]
   (sequence length=235)

Number of matches = 103
Fraction of identities per length = 0.438298

 M D S I G N E F I S G I L V L L E V T K E V G T V R Q E A Q
 M_D_P   A R P L G L S I_L_L L_F L T E A A L G_D A A Q_E_P T

    R K S S E E I Y G \/ S V C L L Q V D E G P C R G D I E R Y Y Y
 /\ G N N A E_            I C_L_L_P L D_Y G_P_C_R_A L L L R_Y_Y_Y_

 N T I T Q K C E L F S Y G G C Q G N A N N F K S Y Q E C Q K
 D R Y T_Q_S C_R Q F_L Y_G_G_C_E G_N_A_N_N_F_Y T W E A C_D D

 T C F R I P \/ K V P Q I C R F P S E V   G P C R A L L R K Y F
 A C_W R_I_E /\ K_V_P_K V C_R_L Q V S V_D D Q C_E G S T E K_Y_F_

 F N M T S M Q C E L F Y Y G G C L G N     S N R F G D R A S
 F_N_L S S_M_T C_E_K F_F S G_G_C_H R N_R I E N_R_F_P D_E A_T

 C E E Y C S P K K \/ S L P V L C L D P L D K G K C S A S I P R
 C_M G F C_A P_K_K_/\   I P_S F C_Y S P_K D_E G_L C_S_A_N V T R_

 Y Y Y N A A T K R C E E F A Y S G C G G S S N N F V S R Q S
 Y_Y_F N_P R Y R T C_D A F_T Y_T G_C_G_G_N D N_N_F_V_S_R_E D

 C K D V C V R \/ G R K I R T R E G K T V P L R R N R N N R I T
 C_K_R A C_A K /\ A L K_K K K K M P K_L R F A S R_I R_K I R_K K

 F M Q A
 Q F


FALF >part of the genscan of alpha on Scaffold_3291
   (sequence length=697)
FALC >gi|971185|gb|AAB60686.1| fibrinogen alpha-E subunit [Gallus gallus
   (sequence length=741)

Number of matches = 258
Fraction of identities per length = 0.370158

 M E R V T      L L V Y L T L Y          C A A F V V \/ V G S
 M_I P V_T_I L C V L_L C L_N L_A W A Q D G K T T F_E K    E G_G

 L D P R G A R P V E P S T R S E K C A S Q K E W P F C S D D
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  G G R_G_P R_I L E_  N M H E S S C_K Y E K_N W_P_I C_V D_D_

D W G \/ P K C P S G C R I Q G L M D K H D I D L L K K I E K I
D_W_G_   T K_C_P_S_C C_R_M Q_G_I I D_D T D_Q N Y S Q R I_D N I_

R N L L D Q N K A K F R S A D Q V S E Q T Y N Y L K E K L T
R_Q Q L_A D S Q N K_Y K T S N R V_I V E T_I N_I L_K_P G L_E

\/ Q N V H Q N I S Y Q Y T Q Y T L A K      L L D S \/ D P S L Q
   G A Q Q L D E N Y_G H V S T E L_R R R I V T L_K Q    R V A T Q_

R G S Q T H R A H T Y A G Q S P G L R K R \/ Q V D I D I K L R
V N R I K A L Q N S I Q E Q_V V E M K R L    E V_D_I_D_I_K_I R_

S C K G S C E R Y S A Y Q M E V G S Y V A L E K Q \/ L T Q L D
A C_K_G_S_C_A R_S F D Y_Q_V D K E G Y_D N I Q K_H    L_T_Q_A S

S Q S A Q R V E S V K T L Y V M K S R P L K D D P V D S L L
S_I D M H P D F Q T T T_L_S T L K_M R_P_L_K_D_S N V_P E H F

K S K P V D G Q Q R E D M F H E V R P S P Y F F N I P N L P
K_L K_P_S P E M Q_A M S A F_N N I K Q M Q V V L E R P_E T D

S F L F S Q I F K V F \/ I S T V K L I L E Q E G S S S S P A T
H V A E A R G D S S P    S H T_G K_L_I_T S S H   R R E S_P_S L

V S K L P G T S     Y S S T R S          S P S V A T S S K
V_D K_T S S A S_S V H R C T_R_T V T K K V I S G P D G P R E

S I T E     L S G Q G G G   G L F D G G              F D G
E I_V E_K M V S_S D G_S D C S H L Q G_G_R E G S T Y H F_S G_

M S S K T H I S T K M A E C T K R I K T T I I H T     K E G
T G D F H K L D R L L P D L E S F F T H D S V S T_S S R H S

P V E Q R E E V V E G G P E C Q T A T D F S K G E L S S L
I G S S T S S H V_T G_A G S S H L G T_G   G K_D K F T D L_G

            F P T L T Q T S S S S S S S S S S S S S S S S S
E E E E D D F_G G L_Q P S G F A A G S_A S_H S_K T V L T S_S_

S S S I H P G G A K G S L L G S S K A I L V D P F D F G A F
S_S_S_F N K G_G_    S T F E T K S_L K T R E T S E Q L G_G V

T T A N A D D D L P D L H A R S V K S T H V K R N A D Y V G
Q H D Q S A E D_T P_D_F K A_R_S_F R P A A M S T R R S Y_N G_

K \/ D C V E A H Q Y H L K G E T N G L F Q I R P G G T Q S D Q
K_   D_C_D D I R Q_K H_T S G_A K S G_I F_K I_K P_E G_    S_N K

V V E V Y C Q Q E G L M G G W L L V Q Q R E S G A V S F N Q
V_L S V_Y_C_D Q_E_T T L G_G_W_L_L_I Q_Q_R_M D G_S V_N F_N_R

S W D E Y R S G F G S V D A D G R G E F W L G N Q N L H W L
T W_Q D Y_R_R G_F_G_S_V_D_G K G_Q G_E_L W_L_G_N_E N_I H_L L_

T S Q S E T L L K V E M E D W E G G A A T A E Y T L R V G S
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 T_  Q_N D T_L_L_R V_E_L E_D_W_D G_N A_A_Y A_E_Y_I V Q V_G_T

 E E E G F P L H V S G Y S G E G G D A L V L S G S D M A P S
 E_A E_G_Y A L_T V_S_S Y_E G_T A G_D_A_L_V_A G W L E E G S E

 L   S H D G M K F S T F D K D N D K W D Q N C A E V Y G G G
 Y T S_H_A Q M_Q F_S_T_F_D_R D_Q D_H W_E E S C_A_E_V_Y_G_G_G_

 W W Y N R C Q S A N L N G V Y Y R G S   Y N P E K N P A
 W_W_Y_N_S C_Q_A A_N_L_N_G_I Y_Y_P G_G H Y_D P_R Y N_V P Y E

 V H N G V V W S T F N S S   Y S L K A
 I E N_G_V_V_W_I P F_R A S_D Y_S_L_K_V V R M K I R P L E T L


FAPL >fugu antiplasmin on scaf1092
   (sequence length=460)
HAPL >gi|178751|gb|AAA35543.1| alpha-2-antiplasmin precursor
   (sequence length=488)

Number of matches = 159
Fraction of identities per length = 0.345652

 M A L W F R R L S L L N R K \/ K P E N N S A T K V P A    A A N T
     L_W_    G L_L V L_S W S    C L Q G P C S V F S P_V /\ S A_M E

 S Q P D S    S E D G R N E D     Y C L I G R S L E S R    E A I A
 P L G R Q /\ L T S G_P N_Q E Q V S P L_T L L K L_G N Q /\ E_P G G

 A A I Q K L G V Q L L Q N L E A T P E Q P N I I I S P L S \/ A
 Q T A L K_  S P P G V C S R D P T_P_E_Q_T H R L A R A M M    A_

 F T A S P L S F V       S I F P K F   M A A W R C P H A L I
 F_T_A_D L F S_L V_A Q T S_T C P_N L I L S P L S V A L A_L_S

 A L F L   A G A V N E T R E L L M H H L H E R A L P C Y H E S
 H L_A L_/\  G_A_Q N_H T_L Q R L_Q Q V L_H_A G S G P_C_L P H L

 L H N I L A G L R K N D L Q I A T Q I F L R Q \/ G F Q P K Q D
 L_S R L C Q D L_G P G A F R L A_A R M Y L_Q K /\ G_F_P I K_E D_

 F V N K S R H L Y G S E P A E L K S          L Q Q I N D W
 F_L E Q S_E Q L_F G_A K P_V S L_T G K Q E D D L_A N I_N_Q W_

 V Y N A T N G K M P Q F L S A L P L N V L V M L I N A V H F
 V_K E A_T_E G_K_I Q E F_L_S_G L_P_E D T V L L L_L N_A_I H_F_

 K \/ G   W V A R F D P R F T S R G A F Y L D D N N M I D V E V
 Q /\ G_F W_R N K F_D_P_S L T_Q R_D S F_H L_D_E Q F T V P V_E_M

 M E D A K H P L S L F I D N E M D A Q \/ V M Q V    A R F R F R K
 M_Q A R T Y P_L_R W F_L       L E Q P    E I Q_V_/\ A_D F_P F_K N

 L M S L L V V M P T S S Q V S V A S L L P K L N V S K L Y S
 N M_S_F V V_L V P_T_H F E W N V_S Q V L_A N L_S W D T L_H P

 R L P K E R A V Q V K V P K F K L E Y S Q E L Q E V F T K I \/
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 P L_V W E_R_P T K V_R L P_K_L Y L_K H Q M D L_V A T L S Q L /\

 G G L G E I F S R P N L A E I A D G P L L V S S V M H K S T
   G_L_Q E_L F_Q A P_D L_R G I_S E Q S L_V V_S_G V_Q H_Q S_T_

 M E I N E E G A E A A A A T T V V I S R A S S P V F H M T Q
 L E_L S E_V G_V E_A_A_A_A_T_S I A M S_R_M S_L S S F_S V N R

 P F F F A V M D D T T E V P I F M G V V N N P N P G A P
 P_F_L F_F I F E D_T_T_G L P_L F_V G_S V_R N_P_N_P_S A_P_R E

 V M Q         T G D K             V G F P I D K S M
 L K E Q Q D S P G_N K_D F L Q S L K G_F_P_R G D K L F G P D

                T R F E     G P P K
 L K L V P P M E E D Y P Q F G_S P_K_


FUAT >fugu antithrombin-III scandidate on Scaffold_1063
   (sequence length=437)
HSAT >gi|113936|sp|P01008|ANT3_HUMAN Antithrombin-III precursor (ATIII)
   (sequence length=464)

Number of matches = 241
Fraction of identities per length = 0.551487

                M P A S D W L L L L A S L H V V S
 M Y S N V I G T V T S G K R K V Y L_L S_L_L L I G F W D C V

       A D V L D I C G A K P R D L A L E P R C I Y R S P D P
 T C H G S P V D_I_C_T A_K_P_R_D_I P M N P_M C_I_Y_R_S_P_E K

 E A P E P L   T T H P V P G S T N P R V W E L S K A N A R F
 K A_T E_D E G S E Q K I P_E A T_N_R R_V_W_E_L_S_K_A_N_S R_F_

 A M S L Y K Q V A S S R G P E S N I F M S P I S I S T A F A
 A_T T F Y_Q H L A_D S_K N D N D N_I_F_L S_P_L S_I_S_T_A_F_A_

 M T K L G A C N Q T L E Q L M R \/ V F E F D T I K E K T S D Q
 M_T_K_L_G_A_C_N_D T_L_Q Q_L_M_E /\ V_F_K F_D_T_I_S E_K_T_S_D_Q_

 V H F F F A K L N C R L Y R K K D K S N E L V S A N R L F G
 I H_F_F_F_A_K_L_N_C_R_L_Y_R_K_A N K_S_S K L_V_S_A_N_R_L_F_G_

 D K S L A F D Q T Y Q N I S E T V Y G A K L L P L D F K \/ D D
 D_K_S_L_T F_N E T_Y_Q_D I_S_E_L V_Y_G_A_K_L_Q P_L_D_F_K_/\ E N

 P E K A R V T I N N W I S N K T E N L I Q D T L P P G G  \/ G
 A E_Q S R_A A I_N_K W_V S_N_K_T_E_G R I_T D_V I P_S E A I   N

 H W K N K F D K D N V Y V          S E F H S S Q T R S W L
 E L T V L V L V N T I Y_F K /\ G L W K S_K F_S P E N T_R_K E L_

        G Q H D V P G G P A F R \/ R   P F R Y K H F P E D Q V
 F Y K A D G E S C S A S M M Y Q E G K F_R_Y_R R V A E_G   T

 Q L L E M P Y R G D D I T M V I I L P S Q G T A L S Q \/ V E E
```

```
 Q_V L_E_L P_F K G_D_D_I_T_M_V_L I_L_P_K P E K S L_A K V_E_K

 V L D L K K L S A W L D Q M K E T T V S V H V P R F R V E D
 E L_T P E V L_Q E W_L_D_E L E E_M M L V V_H_M P_R_F_R_I E_D_

 S F S L K E K L Q L L G L T D L F D P N K A S L P \/ G M L E D
 G F_S_L_K_E_Q L_Q_D M G_L_V D_L_F_S P_E K_S K L_P_/\ G_I V A E

 G V E G L H I S D A Y H K A F L E \/ V N E E G S E A A A A T A
 G_R D D L_Y V S_D_A_F H_K_A_F_L_E_/\ V_N_E_E_G_S_E_A_A_A_S T_A_

 A V A T G R S I N L N R E I F Q A N R P F L L L I R E A S I
 V V_I A G_R_S_L N_P N_R_V T F_K A_N_R_P_F_L_V F I_R_E_V P L

 N T L L F I A R V A E P C D R
 N_T_I I F_M G R_V_A_N P_C_V K


FUPC >fugu protein C on scaffold 8062
   (sequence length=448)
HSPC >gi|21707771|gb|AAH34377.1| human protein
   (sequence length=461)

Number of matches = 204
Fraction of identities per length = 0.455357

    M L R P V L C A S V A V W   W S A S V L G L     S \/ V F S N
 M W Q L_T S L L_  L F V_A_T W_G I S_G T P A P L_/\ D S_   V_F_S_S

 A P D A H M L L R S R   R A N S F L E E L K P P S M E R E C
 S E R A_H_Q V L_R_I R_K R_A_N_S_F_L_E_E_L_R H S S_L E_R_E_C_

 V E E N C D F E E A R E I F Q T R E A T V R V A V N A C \/ I L
 I E_E_I C_D_F_E_E_A_K E_I_F_Q_N V D D T_L A F W S K H V /\ D G

 G N H E L L P D G N Q C D N N M C V N G T C V D K Y Q A Y A
 D Q C L V L_P_L E H P C_A S L C C_G H G_T_C_I D_G I G S F S

 C S C N H G Y E G R Y C D Q \/ P L T A T N C S L D N G N C D H
 C_D C_R S G_W E_G_R_F C_Q R /\ E V S F L N_C_S_L_D_N_G_G C_T H_

 E C T D G A D G L T R R C G C V N G Y N L Q D D S R T C R P
 Y C_L E E V G    W R_R_C_S C_A P G_Y_K L_G D_D_L L Q C_H P_

 K \/ G P S S C G        Q L L I G R S S Y T K S I D G
 A /\ V K F P C_G_R P W K R M E K K R_S_H L K R D T E D Q E D Q

 L L P W M V G G E V G K K G E S P W Q \/ V L V L N A V G K F H
 V D P_R L I D G_K M T R R G_D S_P_W_Q_/\ V_V L L_D S K K K_L A

 C G G V L I D E S W V L T A A H C L E D S L T F R V R L   G D
 C_G_A V_L_I_H P S_W_V_L_T_A_A_H_C_M D E S_K K L L V_R_L_/\ G_E

 Y E R L R A E G T E V T L K V T K T F K H P K Y N R R S V D
 Y_D L R R_W E_K W E_L D L_D I K E V F_V H_P_N Y_S K S T T D_

 N D I S L L R L \/ E T P A P L S D Y I V P V C L P G R H L A Q
```

```
 N_D_I_A L_L_H L_   A Q P_A_T L_S_Q T I_V_P_I C_L_P_D S G L_A_E

 R V L N K N G T M T V V S G W G        K E N L E S S R F S
 R_E L_N_Q A G_Q E T_L V_T G_W_G_Y H S S R E_K E A K R N R T

 S A L N V I K V P L V D T D T C R G Q M Y Y N I T S N M L C
 F V L_N_F I_K_I P_V V_P H N E C_S E V M_S N M V S E N_M_L_C_

 A G I V G Q K M D A C E G D S G G P M V T L Y R D T W F L V
 A_G_I_L G_D R Q D_A_C_E_G_D_S_G_G_P_M_V_A S F H G T_W_F_L_V_

 G L V S W G E G C G N V E K L G I Y T K V S N Y I D W I N K
 G_L_V_S_W_G_E_G_C_G_L L H N Y G_V Y_T_K_V_S_R Y_L D_W_I_H G

 V R E D W D T S P V E R Q R P
 H I R D_K E A P Q K S W A P


PSFU >fugu protein S on Scaffold_2356 646_aa
   (sequence length=646)
PSHU >gi|190442|gb|AAA60180.1| protein S alpha [Homo sapiens]
   (sequence length=650)

Number of matches = 331
Fraction of identities per length = 0.512384

 L S P S T A S Q F L R R H R R A N S L F E E S K P G N L E R
 L_S_K Q Q A_S_Q_V L_V R_K R_R_A_N_S_L_L E_E_T K_Q G_N_L_E_R_

 E C I E E L C N K E E A R E I F E N Q P E T \/ E Y F Y P K Y V
 E_C_I_E_E_L_C_N_K_E_E_A_R_E_V F_E_N_D P_E_T_/\ D Y_F_Y_P_K_Y_L

 \/ V C L G S H R V G I      G N Q H P G I P S D L R T C V T \/ E
    V_C_L_R S_F Q T G_L F T A A R Q_S T N A Y P D_L_R_S C_V_N /\ A

 I N N Q C S P Y P C Y K E G S L R C V D G Q A S F T C V C K
 I_P D Q_C_S_P_L P_C_N E D G_Y M S C_K D_G_K A_S_F_T_C_T C_K_

 P G W K G Q R C E D \/ D I D E C L D P   E F P A G C N Q K C N
 P_G_W_Q G_E K C_E_F /\ D_I_N E_C_K D_P_S N I N G G_C_S Q_I C_D

 N I P G S F Q C Q C E S G H Y F L   N Q I T C V \/ D V D E C Q
 N_T P_G_S_Y H C_S C_K N G_F V M L_S N_K K D C_K /\ D_V_D_E_C_S

 L Y P S I C K E P A R C V N S P G M Y E C R C P K G F R Y N
 L_K P_S_I_C_  G T A_V C_K N_I P_G_D F E_C_E C_P_E G_Y R_Y_N_

 F T S K T C S \/ D V D E C E M S V C D G I C I N T V G S Y E C
 L K S_K_S C_E /\ D_I D_E_C_S E N M C_A Q L C_V N_Y P G_G Y_T C_

 H C D G R L G L R L A E N S R Y C Q   R I P V C V D L Y D H K
 Y C_D_G_K K G_F K L_A_Q D Q K S C_E /\ V V S V_C_L P L_N L D T

 H S E M L Y L G E Q F S G L P A M F L R Y R L P E N T K \/ F A
 K Y E_L L_Y_L_A E_Q_F_A G_V  V L Y L_K F R_L_P_E_I S R /\ F_S

 A E F D F R T F D P E G V V L Y A E S  S Q G S W F M L G L
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 A_E_F_D_F_R_T_Y D_S E_G_V_I L_Y_A_E_S_I D H S A W_L L I A L_

 R G G H I E V Q F K N Q H T F K L T S G G K A I N D G
 R_G_G_K I_E_V_Q_L K_N_E H_T_S K_I T_T G_G_D V I_N_N G_L W N

 T \/ I S V D E L E S S I S V K I S K E A V M S I N S P Q S L F
 M /\ V S_V_E E_L_E_H S_I_S_I K_I_A K_E_A_V_M_D I_N_K P_G P L_F_

 T A V N G K V E T K V Y I A G L P E R A D T    I K P \/ I N P
 K P E N_G_L L E_T_K_V_Y_F A_G_F P_R K V E S E L I_K_P_/\ I_N_P_

 R L D G C I R G W N L M N Q G A S R V K E V I Q E L K S K Q
 R_L_D_G_C_I_R_S W_N_L_M_K Q_G_A_S_G I K_E_I I_Q_E_K Q N K_H

 C F I S V E K G S F F S G M G L A S F N V D Y \/ S D      S G
 C_L V T V_E_K_G_S_Y Y P G_S G_I A_Q F_H I D_Y_/\ N N V S S A E

 S W S V D I E M N I R P S S S T G V I F A L V S   N D T V P
 G W_H V_N V T L N_I_R_P_S_T G T_G_V_M L A_L_V_S_G N_N T_V_P_

 L S I A V V   T Q G E G E A \/ N L Q V F L G G V S V A T L D S
 F A V S L V_D S T S E_K S Q /\ D I L L S V E N T V I Y R I Q A

 L M L C Y P E R L T V S L K I T P A A V Q V S G N S S T V T
 L_S L_C_S D Q Q S H L E F R V N R N N L E L S_  T P L K I E

 Y V T S E S L Q E A L E H L N A T M Q N P L T T Y I G G I P
 T I S H E_D L_Q_R Q L_A V L_D K A M_K A K V A T_Y_L G_G_L P_

 \/ D D I P L P A T P V T A Y Y H G C M D I S V N G Q Q L D F D
 /\   D_V P_F S A_T_P_V_N A_F Y_N G_C_M_E V N I N_G_V Q_L_D_L D_

 E A L S K H N S I K S H S C P P V S A P D R Q G D V L Q P P
 E_A_I S_K_H_N_D I_R A H_S_C_P_S V_W K K T K N S

 A E


FUPT >fugu prothrombin on scaffold 403
   (sequence length=618)
HSPT >gi|339641|gb|AAC63054.1| prothrombin [Homo sapiens
   (sequence length=622)

Number of matches = 323
Fraction of identities per length = 0.522654

 M A G P T V K P L T V L L L F L L H S C L    A N H \/ V F L S
 M_A_H V R G L Q L_P G C L_A L A A L C S L_V H S Q H_/\ V_F_L_A

 S R S A S Q V L V R S R R A N Q M F E E I K A \/ G N L E R E C
 P Q Q A_R S L L_Q R_V R_R_A_N_T F L E_E_V R K   G_N_L_E_R_E_C_

 M E E K C N Q E E A R E V F E Q P D T T \/ E A F W K K Y L \/ D C
 V E_E_T C_S Y E_E_A_F E_A L E_S S T A T_/\ D V F_W_A K_Y_T   A C_

 N G   N Q L P R T E A N I I A F K E C L D \/ G F C I S G R G L N
 E T /\ A R T P_R_D K         L A A C_L_E /\ G_N C_A E G_L G_T N_
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Y A G N V N I S K S G I Q C Q H W K H S F P H P I M R \/ E Y N
Y_R G_H V_N_I_T R S_G_I_E C_Q_L W_R S R Y P_H_K P E I /\ N   S

A S E P D S I L Q E N F C R N P N N S P D G P W C F T T D P
T T H P_G A D L_Q_E_N_F_C_R_N_P_D S S_T T G_P_W_C_Y T_T_D_P_

T V Q K E T C R V P I C G \/ V F L I P G E A F V P P T P T P K
T_V_R R Q E C_S I P_V C_G_/\ Q D Q V T V A M T P R S E G S S V

H F K T I Q S S C I S N Y G V D Y V G D L D V S A K G H A C
N L S P P L E Q C_V P D R G_Q Q Y_Q G_R L_A V_T T H G_L P C_

L M W S S P E A V T L S Q N K E F D P D I N L L C N K C R N
L_A W_A S_A Q A_K A L_S_K H Q D F_N S A V Q L_V E N_F C_R_N_

P D K D P E G P W C Y V N A S G K V I V D Y C D L P V C \/ E D
P_D_G D_E E_G_V W_C_Y_V_A G K P G D F   G Y_C_D_L_N Y C_/\ E_E

L L S Q E     E T L D T G A Q Q R T       T L S S S K K R F
A V E E E_T G D G L_D_E D S D R A I E G R T_A T S_E Y Q T F_

F N P R T F G E G E D \/ E C G R R P L F E Q K N K K D A S E D
F_N_P_R_T_F_G_S G_E_A /\ D C_G_L R_P_L_F_E_K K_S L E D_K T E_R

E L L Q S Y R E K R I V G G D E A E V A S A P W \/ Q V M L Y K
E_L_L_E S_Y_I D G R_I_V_E G_S D A_E_I G M S P_W_/\ Q_V_M_L_F R

R S P Q E L L C G A S L I S N E W V L T A A H C I L Y P P W
K S_P_Q_E_L_L_C_G_A_S_L_I_S_D R W_V_L_T_A_A_H_C_L L_Y_P_P_W_

N K N F S A S D I L V R L G K H N R A K \/ F E Q G I E K I M V
D K_N_F_T E N D_L L_V_R_I G_K_H_S R_T R /\ Y E_R N I_E_K_I_S M

V D L I I V H P K Y N W K E N L N R D I A L L H L R R P I P
L E K I_Y I H_P_R Y_N_W_R E_N_L_D R_D_I_A_L_M K L_K K P_V A

F S N V I H P I C L P N K K V A R M \/ L M T T G F K G R V T G
F_S_D Y I_H_P_V C_L_P_D R E T A_A S /\ L_L Q A G_Y K_G_R_V_T_G_

W G N L K E S F D P   A A R N L P T K L Q Q I H L P I V E E
W_G_N_L_K_E_T W T A N V G K G Q P_S V L_Q_V V N L_P_I_V_E_R

D V C R S S T S I R I T D N M F C A \/ G Y K P E D N K R G D A
P V_C_K D S_T_R I_R_I_T_D_N_M_F_C_A_/\ G_Y_K_P_D E G K_R_G_D_A_

C E G D S G G P F V M K H P E E N R W Y Q M G I V S W G E G
C_E_G_D_S_G_G_P_F_V_M_K_S P_F N N_R_W_Y_Q_M_G_I_V_S_W_G_E_G_

C D R D G K Y G F Y T H V F R M T K W M R K V I E Q
C_D_R_D_G_K_Y_G_F_Y_T_H_V_F_R_L K K_W_I Q K_V_I_D Q_F G E
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TAFI >Fugu thrombin-activatable fibrinolysis inhibitor on scaf123
(sequence length=421)
TAFI >gi|4503005|thrombin-activatable fibrinolysis inhibitor(TAFI)
(sequence length=423)

Number of matches = 216
Fraction of identities per length = 0.513064

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               M S Y I F L F C           L I   S D Q V L S
 M K L C S L A V L V P I_V L_F_C_E Q H V F A F Q /\ S_G Q_V_L_A

 I T P K T Q E H V D I L K N V S T Q Y E \/ T S L W Q P D S P Q
 A L P_R T_S R Q V_Q V L_Q N_L T T_T Y_E_/\ I V L_W_Q_P_V T A D

 Y I Q E E M E V H L Y V P A R T L K T V K D L L N K H T I \/ V
 L I_V K K K Q V_H_F F V_N A_S D V D N V_K_A H L_N_V S G I_   P

 C   F R V L L A N A K E L I E M Q T K N E T T D P R S S A S Y
 C_/\  S V_L_L_A_D V E D L_I_Q Q Q_I S N_D T_V S P_R_A S_A_S_Y_

 Y E K Y H S L N D \/ I Y F W I N Q T Q Q D N P N I V K V I L I
 Y_E_Q Y_H_S_L_N_E /\ I_Y_S W_I_E F I T E R H P_D M L T K I_H I_

 G S S S E K R P L Y V L K \/ L S R N K G P E K K A M W I D C G
 G_S_S_F E_K_Y P_L_Y_V_L_K_/\ V S_G K E Q T A K_N A_I W_I_D_C_G_

 I H A R E W I S P A F C L W F V R H \/ S L S F Y G Q N Q D I T
 I_H_A_R_E_W_I_S_P_A_F_C_L_W_F_I G H_/\ I T Q F_Y_G_I I G Q Y T_

 H I L D N L D V Y I L P V M N P D G Y E Y T W T T \/ Q N R M W
 N L L_R L V D_F Y_V M P_V_V N_V D_G_Y_D Y_S W_  K /\ K N_R_M_W_

 R K N R S V S K S D N C I G A D L N R N F D A   N W C \/ T E G
 R_K_N_R_S_F Y A N N H C_I_G_T D_L_N_R_N_F_A S K H W_C_/\ E E_G_

 A S D D P C S E I Y C G A F P E S E P E S Q S V A H F L R S
 A_S_S S S C_S_E_T Y_C_G_L Y P_E_S_E_P_E_V K A V_A_S F_L_R_R

 H K D S V K L Y F S I H S Y S Q M L L F P Y S C T L D E A E
 N I N Q I K_A Y_I S_M H_S_Y_S_Q_H I V F_P_Y_S_Y T_R S K S K

 N H N E L V S \/ L D M A Q E A A Q K I R R Y Y R N T   Y K Y G
 D H_E E_L_  S_/\ L_  V A_S E_A_V R A I_E K T S K N_T_R Y_T H G_

 A G G K T I \/ Y L A P G G S D D W V Y N L G I K Y S F T F E L
 H G_S E T_L /\ Y_L_A_P_G_G_G D_D_W_I Y_D L_G_I_K_Y_S_F_T_I E_L_

 Q D R G R Y G F L L P P S H I T Q A C N E A L T A L K T I A
 R D_T G_T Y_G_F_L_L_P_E R Y I_K P T C_R E_A_F A A_V S K I_A_

 R K V I E K M E A S T S S P P T V
 W H V_I_R N V
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FBEF >fugu fibrinogen beta homolog no signal
   (sequence length=467)
BEHU   (31->491=461)>FIBB_HUMAN1 gi|39949
   (sequence length=461)

Number of matches = 262
Fraction of identities per length = 0.568330

```
G D D L E Y D D Y E V S \/ A T V D A R G H R P L Q R G R E P Y
  Q G V N D N E       E /\ G F F S A_R_G_H_R_P_L_D K K R_E_E A

S P T R Y A P P T V T S G N R \/ Y G G R P G T A R V T Q G Q V
P S L R_P A_P_P_P I S G G_G     Y_R A R_P_A K A_A A T_Q_K K V_

Q E K Q E Q P E A G G C T H A S E E L \/ G V L C P N G C E L K
E R K_    A P_D A_G_G_C_L H_A_D P D L_/\ G_V_L_C_P_T G_C_Q L_Q

T A L L K Q E R T V R T \/ S L G E L K P Q V D E L M R S S N Q
E A_L_L_Q Q_E_R_P I R_N    S_V D E_L_N N N V_E A V S Q T S_S S

I Y N Y V S S V S V S L R E R Q R V I D \/ A N N A V V S V Y T
S F Q Y_M Y L L K D L W Q K R_Q_K Q V K /\ D N_E N V_V_N E Y_S

E N V E E Q H A Y I K E T V D T I F P S N I R I L Q \/ G V L D
S E L E_K H Q L Y_I_D E_T_V_N S N I P_T N_L R_V L_R    S I L_E

R V R Q K I Q K L E K A I Q A Q R E D C K E P C K T K C P I
N L R_S K_I_Q_K_L_E_S D V S A_Q_M E_Y C_R T P_C_T V S C_N I_

P V V S \/ G K E C E D I F R R G G R D S Q M Y M V Q P D S S V
P_V_V_S_/\ G_K_E_C_E_E I_I R_K G_G_E T S_E M_Y_L I Q_P_D_S_S_V_

H P Y R V F C D Q T T Q K G \/ G W L L I Q N R L D G S V D F G
K P_Y_R_V_Y C_D_M N T_E N G_/\ G_W_T V I_Q_N_R_Q D_G_S_V_D_F_G_

R R W D D Y R R G F G N I A F D A   G K G H C E T P \/ G E Y W
R_K W_D_P Y_K Q G_F_G_N_V A_T N T D G_K_N Y C_G L P_/\ G_E_Y_W_

L G N D R I S Q L T K M G P T E V L I E M Q D W T G A K \/ V H
L_G_N_D_K I_S_Q_L_T_R M_G_P_T_E_L L_I_E_M_E D_W_K G_D K_   V_K

A Q Y R Q F T V Q S D T S N Y V L S V D G Y S G N A G N S F
A_H Y_G G F_T_V_Q_N E A N K Y_Q I S_V_N K Y_R G_T A_G_N_A L

M E G A L E L F G V N R T M T I H N A M R F S T Y D R D N D
M_D G_A_S Q L_M G_E N_R_T_M_T_I_H_N_G M_F F_S_T_Y_D_R_D_N_D_

N W \/ S P G D P S K Q C S R E D G G G W W Y N R C H S S N P N
G W_   L T S D_P_R K_Q_C_S_K E_D_G_G_G_W_W_Y_N_R_C_H_A A N_P_N_

G R Y Y M G G A Y T R Y M A K H G T D D G V V W M N W K G S
G_R_Y_Y_W G_G_Q Y_T_W D M_A_K_H_G_T_D_D_G_V_V_W_M_N_W_K_G_S_

W Y S L K T I S M K I R P F F A S K
W_Y_S_M R K M S_M_K_I_R_P_F_F_P Q Q
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FUFX >fugu f10 on scaf2859
   (sequence length=467)
HSFX >gi|20336663|gb|AAM19347.1|AF503510_1 coagulation factor X [Homo sapiens
   (sequence length=488)

Number of matches = 207
Fraction of identities per length = 0.443255

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M F R                         L F F I A       F L D K    T G
M_G R_P L H L V L L S A S L A G L_L L L G E S L F_I R R /\ E Q

A S Q L L S R Q R R A N S L F E E V K Q G N M E R E C N E E
A_N N I L_A R_V T R_A_N_S_F L E_E_M K_K G_H L E_R_E_C_M E_E_

H C S K E E A R E I F E D D D K T \/                D G D A C
T C_S_Y E_E_A_R_E_V F_E_D_S D_K_T_/\ N E F W N K Y K D_G_D_Q C_

K S T P C V N K G R C K D G I G S Y T C F C L S G Y Q G F N
E T S P_C_Q N_Q G_K C_K_D_G_L G_E Y_T_C_T C_L_E G_F E G_K N_

C E I \/ V I P Q L C E N E N G G C E H F C K V V R G N V R C S
C_E_L /\ F T R K L_C_S L D N_G_D C_D Q F_C_H E E Q N S V_V C_S_

C A D G Y E L G P D D K S C Q S N \/ E T F R C G G I I T E N V
C_A_R G_Y_T L_A D N G K_A C_I P T /\ G P Y P C_G_K Q T L E_R R

R T I L R Y R P N T N T N G T K S D N S S S T N S T E Q E D
K R S V A Q A T S S S G E A P D S_I T W K P Y D A A D L D P

E E F S S G T S Q R K A H A A S D H E M S T M T R I V N G E
T E_N P F D L L D F N   Q T Q P E R G D N N L T_R_I_V_G G_Q

D C P P G E C P W Q \/ A V L L N E E H H W F C G G T I L N P Y
E C_K D G_E_C_P_W_Q_/\ A_L L_I N_E_E_N E G F_C_G_G_T_I_L_S E F

I I L T A A H C M N E T R Y F Y I R L \/ G E S D M L E N E G T
Y I_L_T_A_A_H_C_L Y Q A K R F_K V R_V   G_D R N T E Q E E_G_G

E A M Y E V E T I L A H Y N Y K P N T Y H N D I A L I K L T
E_A_V H E_V_E_V V I K H_N R F T K E T_Y_D F D_I_A_V L R L_K

K P I K Y S R F I L P A C I P E Q E F A E S \/ V L M Q Q S D G
T P_I_T F R M N V A P_A_C_L P_E_R D W A_E_S_   T L_M_T Q_K T G_

M I S G F G R L G G N R Q T S P I L K R L T I P Y V E R R T
I V S_G_F_G_R_T H E K G R Q S_T R L_K_M L_E V P_Y_V_D R_N S

C M E S T S L R I S A R M F C A G Y D E I A K D A C Q G D S
C_K L S_S S_F I I_T Q N M_F_C_A_G_Y_D_T K Q E D_A_C_Q_G_D_S_

G G P H V T R Y R S T Y F I T G I V S W G E G C A Q K G K Y
G_G_P_H_V_T_R_F K D T_Y_F_V T_G_I_V_S_W_G_E_G_C_A_R K_G_K_Y_

G V Y T Q V S K Y I R W I R D G I N T L   I P K G Q S T R L
G_I Y_T_K V_T A F L K W_I_D R S M K T_R G L P_K_A K S_H A P

K R H Y G P I R R I V G
E V I T S S P L K
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13A1 >fugu f13 on Scaffold_3692
(sequence length=742)

H13A >gi|20379735| coagulation factor XIII [Homo sapien]
(sequence length=732)

Number of matches = 344
Fraction of identities per length = 0.469945

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 M S D P A P V V D P S P A P A A P S G P R P K V T N R G R T
 M_S_E T                                 S R T A F G G_R_R

 A V A V A S S N S E S T E V P E F E S F V A L S P R G F P P
 A_V_P P N N S_N_A A E D D L P_T V E_  L Q G V V P_R_G_  V N

 L T D Y \/ L D I V A V D M M S Q S D G V N K Q Q H R T M F Y N
 L_Q E F /\ L_N V T S V_H L F K E R W D T N_K_V D H_H T_D K Y_E

 S N Y L I V R R G Q E F H V K L T F N R P Y N P K E D K F A
 N N_K L_I_V_R_R_G_Q_S F_Y V_Q I D F_S R_P_Y_D P_R R D_L F_R

 L E F V I G \/ A N P D Y S K G T Y I P V   F P N K E R Q S R W
 V E_Y V_I_G_/\ R Y P_Q E N K_G_T_Y_I_P_V_P I V S E L Q S G K W_

 A G R I A D S S N N D V T V G I T P L A N C I V G K Y H M Y
 G A K I_V M R E D R S V_R L S I_Q S S P K C_I_V_G_K_F R M_Y_

 I A V M T P F G I R R T R K D P V R D L Y I L F N P W \/ S P    A
 V A_V_W T_P_Y G_V L R_T_S R N P_E T D_T Y_I_L_F_N_P_W_   C E /\ D

 D D V F L D D E P E R Q E C V M N E M G I I Y H G A Y D D I
 D_A V_Y L_D_N E_K E_R_E E_Y V_L N_D I G_V I_F Y G_E V N D_I_

 A E R Q W N Y G Q \/ F N Y G V L D A C L Y I M D R S E M P I T
 K T R_S W_S Y_G_Q_/\ F_E D G_I L_D_T C_L_Y_V M_D_R_A Q M_D L S

 N R G D P I K V T R K A S A M \/L    N S R D D D G V L V G N W S
 G R_G_N P_I_K_V_S R_V G S_A_M_  V /\ N_A K D_D_E G_V_L_V_G_S W_D

 G D Y T Y G V A P T S W T G S T E I L L T Y A S S R M P V S
 N I Y_A Y_G_V_P P_S A W_T_G_S_V D I_L_L_E Y_R S_S_E N P_V_R

 Y A Q C W V Y A A V F N T \/ F L R C L G I P S R V V T N Y Y S
 Y_G Q_C_W_V_F A_G V_F_N_T_/\ F_L_R_C_L_G_I_P_A R_I V_T_N_Y_F S_

 A H D N D G N L K T D I I L D E N G K I D R S R T R D S I W \/
 A_H_D_N_D_A N_L_Q M D_I_F L_E E_D G_N V N S K L T_K D_S_V W_/\

 N Y H C W N E C Y M T R P D L P F G F G G W Q V V D A T P Q
 N_Y_H_C_W_N_E_A W M_T_R_P_D_L_P_V G_F_G_G_W_Q_A V_D_S T_P_Q_

 E T S D \/ G M Y R C G P A S V Q A I K H G E M C Y P F D A A F
 E_N S_D_/\ G_M_Y_R_C_G_P_A_S_V_Q_A_I_K_H_G_H V C_F Q F_D_A_P F_

 V F A E \/ V N S D V V F Y S R G K D G A M Q P V R V N Q T H V
 V_F_A_E_/\ V_N_S_D_L I Y I T A K K_D_G_T H V V E N V_D A T_H_I

 G R M V L T K A P G A T T R R D I T S Q Y K F P E G \/ T S E E
 G_K L I V T_K_Q I G_G D G M M D_I_T_D T Y_K_F_Q E_G_/\ Q E E_E_

 R T V L E K A E G F G C H R       E K S R P P E A D V D L
 R_L A L_E_T A_L M Y G_A K K P L N T E_G V M K S R S N V_D_M
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 V L P T L E V P V G Q D F E L S L E F V N R S D Q R R V V E
 D F E V E N A V L G_K D_F_K L_S_I T F_R N_N S_H N R_Y T I T

 A Y I S G N V V F Y T G V T S A E F M L R D P T V T M K P N
 A_Y_L S_A N_I T F_Y_T_G_V_P K A_E_F_K K E T F D V_T_L E P_L

 E \/ T V K E T V V V E S K K Y M K H L V E Q A N L H F I I T G
 S /\ F K K_E_A V_L I Q A G E Y_M_G Q L_L E_Q_A_S L_H_F_F V T_A

 K V K E T G Q I V T A M K V V A L H N P K L S V K \/ V S G E N
 R I N E_T_R D V L A K Q K_S T V L_T I P_E I I I K_/\ V_R G_T Q

 R V S E E M M A T V E F T N P F S F A L A D V Y I R M E G P
 V V_G S D M_T V I V_E_F_T_N_P_L K E T L_R N V_W V H L D G_P_

 G V M M P T Y K Y Y S \/ L I P N G S S L T W T E M F V P Q R A
 G_V_T R P_M K K_M F R /\ E I_R P N S_T V Q W_E E_V C R P_W V S

 G A T R V F A T L D C P A L R Q V Q G E V S L T I     K P
 G_H R K L I A_S M S S D S L_R_H V_Y G_E_L D V Q I_Q R R P_S


 M


FUF8 >fugu f8 candidate on scaf2929
   (sequence length=1583)
HSF8 >gi|66384|pir||EZHU coagulation factor VIII precursor [validated] - huma
   (sequence length=2351)

Number of matches = 658
Fraction of identities per length = 0.415666

 M R T D      T L L L P L P                      L P L L L
 M_Q I E L S T C F F L_C L_L R F C F S A T R R Y Y L_G A V E

 L V A A F C G G D A Q Q              P P A A V R Q Y   Y I
 L_S W D Y M Q S D_L G E L P V D A R /\ F P_P_R V P K S F P F N

 A A V E I G W D   Y I H V E D          G D P A S E Q R \/ G I
 T S V_V Y K K T L F V E F T D_H L F N I A K P_R P P W M /\ G_L

 Q G P V I V A Q A G E T V L V H F K N L A S Q P Y S I S P V
 L G_P_T I_Q A_E V Y D T_V_V I T L K_N_M A_S_H P_V S_L H A V_

 G I S Y W K H S E G \/ A G Y D D S T A G H E K E D D A V Y P G
 G_V S_Y_W_K_A S_E_G_/\ A_E Y_D_D_Q T_S Q R E_K_E_D_D_K V_F P_G_

 G Y Y E Y V W D I S P K D G P T G S D P E C L T Y S Y S S Q
 G_S H T Y_V_W_Q V L K E N G_P_M A S_D_P_L C_L_T_Y_S_Y_L S_H

 V D P V R D V N S G L I G A L L I C K \/ M S A F T D E G Q R R
 V_D_L V_K D_L N_S_G_L_I_G_A_L_L_V C_R /\ E G S L A K E_K T Q T

 N Q A F V L L F V V F D E   S K S W Y G E V G E R K S R D K
 L H K F_I L_L_F_A V_F_D_E_/\ G K_S_W_H S E_T K N S L M Q D_R D
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F K R S D S R K E F H T I N G Y I N A T L P \/ L K I C Q G R
A A S A R A W P K M H_T_V N_G_Y_V N_R S L_P_/\ G L_I G C_H R_

N P V I W H L I G M G T A P A I H L I Q F Q H H T L E \/ V L T
K S V_Y W_H_V I_G_M_G_T_T P_E V H_S I_F L E G H_T_F L V_R N

H R K V T V E V T P M T F V T A E M K P A T V G S F L I S C
H_R_Q A S L E_I S P_I T_F_L T_A_Q T L L M D L G_Q F_L_L F C_

Q I H A P R H \/ D G M S A M F L V E K C P D P V V L P G P D M
H I_S S H Q H_/\ D_G_M_E A_Y V K V_D S C_P_E E P_Q L

R N A K P S N D D D Y D Y N Y D G E E M F N I I N F K P K E
R_M K N N E E A E D_Y_D_D D L T D S E_M_ D V V R F_D D D N

L K P Q V R S S R G A N F Q V W E H Y I A I E E L T W D
S P S F I Q_I R_S_V A K K H P K T W_V H_Y_I_A_A E_E_E D W_D_

Y T P H L S S P T S S E L Q S R F F P T S A S R L S Y K Y K
Y_A P_L V L A P_D D R /\ S Y K S_Q Y L N N G P Q R_I G R K_Y_K_

K V A F V E Y T D K S F T R R K N T E K S L M G P L L K
K_V_R F_M A Y_T_D_E T F_K T R_E A I Q H E_S G I L G_P_L_L_Y

G K V G D Q I \/ H I M L K N T A S R P F N I Y P N G L S S I R
G_E V_G_D_T L /\ L I_I F K_N_Q A_S_R_P_Y N_I_Y_P_H G_I T D V R_

P M \/ K R S K N G K L E K D L R T M G V G P N E T F G Y I W E
P_L Y S R R L P K_G /\ V K_H L_K D F P I L P_G E_I F_K Y_K W_T

L T A N D R P L E E D P Q C L T Q L Y Q S T V D P E K D L A
V T_V E D_G P_T K S D_P_R C_L_T_R Y Y_S S_F V_N M E_R D_L_A_

S G L V G T L L I C K N E A I D Q R G R L \/ V G P D K D W S L
S_G_L_I G_P L_L_I_C_Y K E_S V D_Q_R_G_N Q /\ I M S D_K_R N V I

V F A V F D E N N S W Y M K E N I H N T T Q T P T G Y N D T
L F_S V_F_D_E_N_R S_W_Y_L T E_N_I_Q R F L P N P_A G_V Q L E

D P D V Y N S H V I Y S E F N G Y F I D \/ A V N G I M F R R
D_P_E F Q A S N I_M H S /\ I N_G_Y_V F D_ S L Q L S V C L H E

R Q F V I C K T D \/ R G H L T E F L S V Y F T G N L F Q H Q G
V A Y W Y I L S I G_A Q T_D F_L_S_V_F F_S G_Y T F_K H_K M

L Y Q S V L T L F P M S G L T V S M E P E V V \/ G E W E I G A
V Y_E D T L_T_L_F_P_F S_G_E T_V_F M_S M E_N P /\ G_L W_I L G_C

F D G S L K S R G M S I Q Y T V L T C E R E
H N S D F R N R_G_M_T A L L K V_S S C_D K N T G D Y Y E D S

Y E D I S A Y L L S K N N A I E P R S F S Q N S R H P S T R

Q K Q F N A T T I P E N D I E K T D P W F A H R T P M P K I

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          D L L V             D H         E L D E V D
Q N V S S S D_L_L_M L L R Q S P T P H_G L S L S D L_Q E_A K

F S D Y V D N M V L G             L R G M       R P R N H
Y E T F S D_D P S P G_A I D S N N S L_S E M_T H F R_P_Q L H_

                  T V L L K V C N K V P I N N S T H
H S G D M V F T P E S G L Q L_R L N E K_L G T T A A T_E L K

                          S V N T S T L N A T D G R R C
K L D F K V S S T S N N L I S T I P S D N L_A A_G T D N T S

Y L                                     K K V T L T P P
S L_G P P S M P V H Y D S Q L D T T L F G K K_S S P L_T_E S

G G
G_G_P L S L S E E N N D S K L L E S G L M N S Q E S S W G K

        E D A N I T S G E R I P E D I L       E E L
N V S S T E_S G R L F K G_K R_A H G P A L_L T K D N A L_F K

                                      Q L D G E     V
V S I S L L K T N K T S N N S A T N R K T H I D_G_P S L L I

T A A P S
E N S P_S_V W Q N I L E S D T E F K K V T P L I H D R M L M

       G I L R V G E                   Q A L R R R Q
D K N A T A L_R_L N H M S N K T T S S K N M E M V Q Q K K E

       A E D N S T D F D I Y
G P I P P D A Q N P D_M S F F K M L F L P E S A R W I Q R T

          S G D E G               G E E R S
H G K N S L N S G Q G_P S P K Q L V S L G_P E_K S_V E G Q N


F L S E K N K V V V G K G E F T K D V G L K E M V F P S S R

              E I Q E R P A E N R T T A N A T G I N R T K
N L F L T N L D N L H E_N N T H N_Q E K K I Q E E I_E K K E

E L E E G N E I L
T L_I Q E N_V V L_P Q I H T V T G T K N F M K N L F L L S T


R Q N V E G S Y D G A Y A P V L Q D F R S L N D S T N R T K

                        L T G
K H T A H F S K K G E E E N L_E G_L G N Q T K Q I V E K Y A

         N P G N S K R S F T V E                   P V
C T T R I S P_N T S_Q Q N F_V T Q R S K R A L K Q F R L P_L

T S E E M V Q N Y I M S E E             E K L K P
E E T E_L E K R I I_V D D T S T Q W S K N M K H L_T P_S T L
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         H H Q Q P G N I A V N E L S
T Q I D Y N E K E K G A I T Q S P L S D C L T R S H S I P Q

                                                V E Y D D
A N R S P L P I A K V S S F P S I R P I Y L T R V L F Q D N

               Y N Q E E
S S H L P A A S Y R K K D S G V Q E S S H F L Q G A K K N N

                                                  N S T S Y
L S L A I L T L E M T G D Q R E V G S L G T S A T N S V T Y

           V L
K K V E N T V L P K P D L P K T S G K V E L L P K V H I Y Q

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

             R S G E V R Y
I K W N E A N R P G K V P F L R V A T E S S A K T P S K L L


D P L A W D N H Y G T Q I P K E E W K S Q E K S P E K T A F


K K K D T I L S L N A C E S N H A I A A I N E G Q N K P E I


E V T W A K Q G R T E R L C S Q N P P V L K R H Q R E I T R


T T L Q S D Q E E I D Y D D T I S V E M K K E D F D I Y D E

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

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

S F R D P V S Q G E L E A H L G I L G P F I K A E V N D \/ L L
S F T Q P L Y R G E L N E H L G L L G P Y I R A E V E D   N I

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

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

C K T G T Y Y S T V D K \/ E E D L N S G L I G P L V I C K P
C K A W A Y F S D V D L /\ E K D V H S G L I G P L L V C H T N

T L S T R L H T \/ Q P D V Q E F A L L F H T F D E T K S W Y M
T L N P A H G R   Q V T V Q E F A L F F T I F D E T K S W Y F

E E N L R R Y C A P P C H A N T Q D P W Y H I S N K F A \/ A I
T E N M E R N C R A P C N I Q M E D P T F K E N Y R F H /\ A I
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N G Y V A E S L P G L L V A Q H Q R V R W H L L N V G S D G
N_G_Y_I M D T L_P_G_L_V M A_Q_D Q_R_I R_W_Y L_L_S M G_S_N E

E Y H A V H F H G L P F T V H A K K E H R M G V Y N L F P \/ G
N I H_S I H_F_S G_H V F_T_V_R K K_E E_Y K M_A L Y_N_L_Y P_/\ G_

V F G T V E M R P P T V G T W L V E C T V G E S Q L A G M R
V_F_E T_V_E_M_L P_S K A G_I W_R V_E_C_L I G_E_H L H A_G_M_S

A K L L V Y N P \/ Q C S R P L G M K S G R I G D S Q I K A S D
T L F L_V_Y_S N /\ K C_Q T P_L_G_M_A S_G_H I_R D_F Q_I_T A_S_G

Y I G   N           I L I F I S P V                   R S
Q Y G_/\ Q W A P K L A R L_H Y S G S I N A W S T K E P F S W I

K R N L         G Y R V Q T Q G V R S N L R N N Y I T A F
K_V D L_L A P M I I H G I K T_Q_G_A R_Q K F S S L Y_I_S Q F_

T V S Y S L D Q E T W S T Y R G S \/ G S S R S S S S S T A \/ K V
I I M Y_S_L_D_G K K W_Q T_Y_R_G_           N S_T G T_L M /\ V_

F N G N L D N S R V K N N P F V P P F V A R Y I R I H P L Y
F_F G_N_V D_S S_G I K_H N_I F_N P_P_I I A_R_Y_I_R_L H_P_T H

Y N Q R P A L R M E L L G C D L N \/ S C S L P L G L Q D R R I
Y_S I R_S T L_R_M_E_L_M G_C_D_L_N_/\ S_C_S_M P_L_G_M E S K A I_

P D E S F V A S S S Y W S L L R S W T P S L A R L H Q E G S
S D_A Q I T A_S_S_Y F T N M F A T W_S P_S_K A_R_L_H_L Q G_R

A N A W R P K \/ N N N P H E W L Q V D L G K V K R I T G V V T
S N_A_W_R_P_Q /\ V N_N_P_K E_W_L_Q_V_D_F Q K_T M K V T_G_V_T T_

Q G A R S L L T K M M V T E F S V T I S R D G Q A W S S \/ V L
Q_G_V K S_L_L_T_S M_Y V_K E_F_L I S S S_Q D_G_H Q W_T L   F F

E G S S Q R E K   I F Q G N N D S D E E A L T I F D A P L F G
Q N G    K V K_/\ V F_Q_G_N_Q D_S_F T P V V N S L D_P P_L_L T

R Y I R I H P L G W I N D I A L R L E V L G C D T Q Q A L
R_Y_L R_I_H_P_Q S W_V H Q I_A_L_R_M E_V_L_G_C_E A Q_D L Y


GAFU >fugu gamma on scaffold 39
   (sequence length=442)
GAHU >gi|4503715 fibrinogen, gamma chain
   (sequence length=437)

Number of matches = 223
Fraction of identities per length = 0.510297

      M L L A I R T V N K L C S W L H Q E E T L W T   P \/ V T E
M S W S L_H P R N L I L Y F Y A L L_F L S S T_C V A /\ Y   V_A T

R S F L S C C T F L G S P T S \/ G M Y C P T K C G V A D Y M L
R_D    N C_C_I L    D E R F   G_S Y_C_P_T_T C_G_I A_D_F L S
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 K Y F S    K T N D G L E Q M L I D L E N I A N M T Q D A E N R
 T Y_Q T /\ K_V D K             D_L_Q S L E D I L H Q V E_N_K

 V V Y M K D S M V A A Q K S I T P G \/ N T T N    I N P L E T S T
 T S E V K_Q L I K A_I Q_L T Y N P_D    E S S K /\ P N_M I D A A T_

    K S S M L D D V V R F Q K T I S V Q E Q Q I R \/ E V Q N M
 L K S R I M_L_E E I M K Y E A S I_L T H D S S I_R_/\ Y L Q_E I

 V S S N E R R M S E L K Q L S L Q L Q Q K C S E P C K D S V
 Y N S_N_N Q K I V N L_K_E K V A Q_L_E A Q C_Q E_P_C_K_D_T V_

 E I Q P I S G T \/ D C Q D I A N K G A T T S G L Y Y V K P Q K
 Q I_H D I_T G_K /\ D_C_Q_D_I_A_N_K_G_A_K Q S_G_L_Y_F I K_P_L K_

 A T E Q F L V Y C E I D A F G R G F T V I Q R \/ R R D G S V D
 A_N Q Q_F_L_V_Y_C_E_I_D_G S G_N G_W T_V_F Q_K /\ R_L D_G_S_V_D_

 F K K D W I Q Y R E G F G Y L S P D D T T E F W L G N E K I
 F_K_K_N W_I_Q_Y_K E_G_F_G_H L_S_P_T G T_T_E_F_W_L_G_N_E_K_I_

 H L L T A S T T M P T V L R I E L V D W E G N K K \/ Y A D Y N
 H_L_I S T Q S A I P_Y A L_R_V E_L_E D_W_N G_R T S /\ T A_D_Y_A

 M F R I G S E A D K Y R L T Y G F Y F G G D A E D A F D G Y
 M_F_K V G_P E_A_D_K_Y_R_L_T_Y_A Y F A G_G_D_A_G D_A_F_D_G_F

 D F G D D P S D K S Y T S H N G M Q F S T F D S D N D R Y D
 D_F_G_D_D_P_S_D_K_F F T_S_H_N_G_M_Q_F_S_T_W D_N D_N_D_K F E

 G N C A Q Q D G S G W W M N R C H A A H L N G K Y Y S \/ G G R
 G_N_C_A_E Q_D_G_S_G_W_W_M_N_K C_H_A_G H_L_N_G_V Y_Y_Q /\ G_G_T

 Y S E K D A G E F G F D N G I I W V T W H S R W Y S L K E T
 Y_S_  K_A S T P N G_Y D_N_G_I_I_W_A T_W_K T R_W_Y_S_M K_K T_

 T M K L I P L S R L A A G G        Q T T G V K E    F G G L G
 T_M_K_I I_P_F N R_L_T I G_E G Q Q H H L G G_A K_Q /\ A G_D V

 L
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FPAI >Fugu plasminogen activator inhibitor on scaf1754
(sequence length=406)
HPAI >gi|189545|gb|AAA36413.1| plasminogen activator inhibitor
(sequence length=415)

Number of matches = 181
Fraction of identities per length = 0.445813

```
 M A A I S G S N T A F A L E L L R T L S Q G N P S G N I F V
 M_E D L C V A N_T_L F_A_L_N L_F K H L_A K A S P_T Q N_L F_L

 S P L S I S S A L A M V Y L G A K G E T A A Q M A Q V M D S
 S_P_W S_I_S_S_T M A_M_V_Y_M G_S R G_S T_E D Q_M_A_K V_L Q F
```

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 N    G R I E S L Q W D K S D F   P C    L Q A L      S F
 N_E V G_A N A V T P M T P E N F_T S C_G F M Q_Q I Q K G S_Y

 S            S G K D V H A D F Q T L N G E I N S P S A S
 P D A I L Q A Q A A D K I H_S S F_R S L_S S A I_N_A S T G D

 Y T L K L A N R L Y G E S T A N F L S V G S G F T P I T N C
 Y_L L_E S V N_K L_F G_E_K S A_S F_     R E E Y I R L    C_

 Q K Y Y H A D L K A I D F I G A T E E C R A E I N S W V E E
 Q_K_Y_Y_S S E P Q A_V D_F_L E C A E_E_A R_K K I_N_S_W_V_K T

 Q T E N K I K D L L K P G T V S T M T R L A L V N A I Y F K
 Q_T_K G K_I_P N L_L_P E G_S V_D G D T_R_M V L_V_N_A_V Y_F_K_

 G N W M N R F D E A N T K E M P F K V N Q N E S K P V Q M M
 G_K W_K T P F_E K K L N G L Y P_F_R V_N_S A Q R T P_V_Q_M_M_

 Y Q M K K L P Y N Y I P E H G V Q I L E L P Y V E E E L S M
 Y_L R E K_L_N I G Y_I_E D L K A Q_I_L_E_L_P_Y_  A G D V S_M_

 F I L L P E E T T D G P S P L L K L E N E L T R E K L D E W
 F_L L_L_P_D E_I A D_V S T G L_E L L_E_S E_I T_Y D K_L_N K W_

 T N R E N M D V H S E V L V H L P K F K L E E D Y E M N E A
 T_S K D K M_  A E D E_V_E V_Y I P_Q F_K_L_E_E_H Y_E_L R S I

 L A K L G M T D V F C A A K A D L S G M N G D G G L F L S T
 L_R S M G_M_E D_A F_N K G R A_N F S_G_M_S E R N D L_F_L_S_E

 V A H K A F V E V N E E G T E A A A A T A G M V A F C M L R
 V_F H_Q A_M V_D V_N_E_E_G_T_E_A_A_A_G T_G G_V M T G R T G H

 E E   H F T A D H P F L F F I R H N K T K S I L F L G R Y S
 G G P Q F_V A_D_H_P_F_L_F_L I_M H_K I T_K_C I_L_F_F G_R_F C

 S P
 S_P_


FTPA >fugu tPA candidate
   (sequence length=524)
HTPA >gi|4505861| t-plasminogen activator [Homo sapiens]
   (sequence length=524)

Number of matches = 294
Fraction of identities per length = 0.561069

 \/ V Y C V D S K T S A M R S S G E T W L R     W R G Q R V E Y
 /\ V_I C_R D_E K_T_Q M I Y Q Q H Q S W_L_R_P V L R_S N R_V_E_Y_

 C R C A R G R E L C H I V P V I \/ S C Y T S Q C Y N G G T C K
 C_W C_N S G_R_A Q C_H_S V_P_V_K /\ S_C_S E P R C_F N_G_G_T_C_Q

 E A V Y T S D Y I C Q C P T G F S G T H C E I \/ D T N E K C A
 Q A_L Y_F S_D_F V C_Q_C_P_E G_F_A G_K C C_E_I_/\ D_T_R A T C_Y
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 V G R G E G Y R G T W S I S H S G A E C I N W N S T T L R G
 E D Q G_I S Y_R_G_T_W_S_T A E S_G_A_E_C_T N_W_N_S_S A L_A Q

 R R F T A R K T D A S S L G L G N H N F C R \/ N P D N D S T P
 K P Y S G R_R P D_A_I R L_G_L_G_N_H_N_Y C_R_/\ N_P_D_R D_S_K P_

 W C F V Y K G T Q I V W E F C S V P K C P E D \/ R Y H E C M L
 W_C_Y V_F K_A G K Y S S E_F_C_S_T P_A C_S E_G /\ N   S D C_Y F

 G S G L T Y R G T A S V T K S G S R C L P W D N P A I T H K
 G_N G_S A Y_R_G_T_H S_L T_E S_G_A S C_L_P_W_N S M I L I G K_

 L N N A W R S D A L K L G L G G H N F C R \/ N P D G D V G P W
 V Y T A_Q N P S A_Q A L_G_L_G_K H_N_Y C_R_/\ N_P_D_G_D_A K P_W_

 C H V Y K N M R L T W E L C D V P K C \/ S T   C G Q R L D N T L
 C_H_V_L K_N_R R_L_T_W_E_Y C_D_V_P_S C_   S_T_/\ C_G_L R_     Q Y

 N H P V F R M F G G R E S D I T E Q P W Q A V I N V F Q R R
 S Q P_Q F_R_I K G_G_L F A D_I_A S H P_W_Q_A_A I_F A K H R_R_

 Y K Q H L Y R C G G V L I D S C W I L T A A H C F E E \/ N E K
 S P G E R F L C_G_G_I L_I_S S_C_W_I_L_S A_A_H_C_F_Q E_/\ R F P

 V E N L E V I L G R T F R K M N S S S E Q I F G V E K Y L I
 P H H L_T V_I_L_G_R_T_Y R_V V P G E E E_Q_K F_E V_E_K_Y_I V

 H E K F E S E T F D N D I \/ A L L K L K T D I G I C A I N S P
 H_K E F_D D D T_Y D_N_D_I_/\ A_L_L_Q L_K_S D_S S R C_A_Q E S_S

 E V Y P V C L P E R G L V L P D W T E C E I S G Y G K T T E \/
 V V_R T V_C_L_P_P A D L_Q L_P_D_W_T_E_C_E_L S_G_Y_G_K_  H E_/\

 F V S A E Y S E R V K R G H V R L W P N E R C V P D V L S G
 A L S_P F Y_S_E_R_L K_E A H_V_R_L_Y P_S S R_C_T S Q H L_L N

 R T V T S N M L C A G D T R G           R D D A C K \/ G D S
 R_T_V_T_D N_M_L_C_A_G_D_T_R_S G G P Q A N L H D_A_C_Q /\ G_D_S_

 G G P L V C R N N D R M T L M G V I S W G D G C G Q K D K P
 G_G_P_L_V_C_L N_D G R_M_T_L_V G_I I_S_W_G_L G_C_G_Q_K_D_V P_

 G V Y T R V T R Y I D W I N G G M K A N P L
 G_V_Y_T_K V_T_N Y_L D_W_I_R D N M_R P
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FUTF >fugu tissue factor on scaf8956 238a
   (sequence length=264)
HSTF >gi|418689|pir||KFHU3 tissue factor precursor [validated] - huma
   (sequence length=295)

Number of matches = 88
Fraction of identities per length = 0.333333

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 M K C S A                         L F L M L L L H C V R
 M_E T P A_W P R V P R P E T A V A R T L_L L_G W V F A Q V_A
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 S V S \/ A S Y P R     A Y N V T W K S T N F K T V L T W D P K
 G A S_/\ G T T N T V A A_Y_N_L T_W_K_S_T_N_F_K_T_I L_E W_E P_K_

 P S H L Y S Y T V E F    F R \/ I G G D K M R N P H C I R S S F P
 P_V N Q   V Y_T_V_Q I /\ S T    K S G_D_    W K S K C_F Y T T D T

 Q C D L S N S   L T E L R S S Y M A E I L S E P P     L G E
 E C_D_L_T D E I V K D V K Q T Y_L A_R V F S_Y P_A G N V E S

 T S E L T E F P Y S R S P R F C P Y N D \/ T D I G K P D F K L
 T_G S A G E_P L Y_E N S_P_E F_T P_Y_L E /\ T_N L G_Q P_T I Q

 E V S A D K K K T S L F V T D P L T A L F K D G R Q L N I R
 S F E Q V G T K_V N V T V_E D_E R T_L V R R N N T F L_S L R_

 D I F S D Q L M Y K V T Y R K N K S T G K \/ K E H I S K T N V
 D_V F_G K D L_I Y_T L Y Y_W K_S S S_S G_K_/\ K_T A K T N T_N_E

 I E L T N L D Q G E S Y C F S I Q A Y I P S R T I T K Q
 F   L_I D V D_K G_E_N Y_C_F_S_V Q_A_V I_P_S_R_T_V N R K S T

           L G E E S \/ S       K H C F      A L A T F G    Q
 D S P V E C M G_Q E_K    G E F /\ R E I F_Y I I G A V V F_V V I I

 M S S Y M N V   L    C K R P A E W N L F T V I S K Y L P L
 L V I I L A I S L_H K C_R K A G V G Q S W K E N S_P   L_N V

 L
 S
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FPLG >suspect fugu plasminogen from scaf9368 and scaf145
   (sequence length=747)
HSPG    (16->810=795)>gi|4505881|ref|NP_000292.1| plasminogen [Homo sapiens
   (sequence length=795)

Number of matches = 420
Fraction of identities per length = 0.562249

 \/ S V S G S E V E G Y T K T A G A W I L S L S G R K Y S V M T
 /\ S_G Q G_E P L D D Y_V N T_Q G_A_S L F S_V T K K Q L G A G S

 A V E C A R K C D A E T T F T C R \/ S F I Y I E K D Q E C R T
 I E E_C_A_A K_C_E E D E E F_T_C_R_/\ A F_Q Y_H S K_E Q_Q C_V I

 V G Q N S K S E I V L R R S S T A L Y E K K \/ V Y L L E C V N
 M A E N_R K_S_S I_I I R_M R D V V L_F E_K_K_/\ V_Y_L_S E_C_K T

 G I G T D Y R G T K S R T K T G K L C Q R W G V N S P H R P
 G_N G_K N Y_R_G_T_M S_K T_K_N G_I T C_Q_K W_S S T S_P_H_R_P_

 N \/ Y K P Q T S P L A D L E S N F C R N P D A D S G G P W C Y
 R /\ F S P_A T_H P_S E G L_E_E N_Y C_R_N_P_D_N D_P Q G_P_W_C_Y_

 T T D A N T R W E H C N V S A C S \/ E D C I H C S G E D Y R G
 T_T_D_P E K R_Y D Y C_D I L E C_E /\ E_E C_M H_C_S_G_E_N Y_D G_
```

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K A S T T E K G Y T C Q R W D                     S K \/ Y
K_I S_K T_M S G_L E C_Q_A W_D_S Q S P H A H G Y I P S_K_/\ F P

     L E G N Y C R N P D G D P R P W C F T T N P A K R W D
N K N L_K K N_Y_C_R_N_P_D_R E L R_P_W_C_F_T_T_D P_N K_R_W_E

F C D I P R C   T S E \/ P P T I V P E T T C F T G E G G S Y R G
L C_D_I_P_R_C_/\ T_T P   P_P_S S G P_T Y Q C_L K G_T G_E N Y_R_G_

T I A V T E A G K T C Q S W S S Q T P H K H N R T P D N Y P
N V A_V_T_V S G_H T_C_Q_H W_S_A Q_T_P_H_T H_N_R_T_P_E N_F P_

C K \/                                                 E
C_K_/\ N L D E N Y C R N P D G K R A P W C H T T N S Q V R W E_

Y C Q V P T C G D S A G P D D A V I P               P E E E
Y_C_K I P_S C_D S S_P V S T E Q L A P_T A /\ P P E L T P_V V Q

D C Y E D N G S S Y R G I T S Q T V S G K R C Q A W S S M T
D_C_Y_H G D G_Q S_Y_R_G_T S S_T T_T T G_K_K C_Q_S W_S_S_M_T_

P H S H L K T P K N F P N A \/ T S G G I F C R N P D N D R A P
P_H_R H_Q K_T_P_E N_Y P_N_A_/\ G L T M N Y C_R_N_P_D_A D_K G P_

W C Y T T N P G V R W E Y C N L E K C S T N A P K P T P G T
W_C_F T_T_D P_S V_R_W_E_Y_C_N_L_K K_C_S_G T E      A S V V

A T Q P Q S P T T E D S G Q T E R \/ D C K I G N G E T Y R G K
A_P P P_V V L L P D V E T P S E_E /\ D_C_M F G_N_G_K G Y_R_G_K_

I S I T I L G V T C Q A W S A Q S P H T H N S F T E E T H G
R A T T_V T G_T P C_Q_D W_A A_Q_E P_H_R H_S I F_T_P E_T_N P

D K G L E S N \/ Y C R N P D G D V N G P W C Y T T D P N K K W
R A G_L_E_K N_/\ Y_C_R_N_P_D_G_D_V_G G_P_W_C_Y_T_T_N P_R K_L Y

D Y C L I P D C A \/    G L K C G S P A I K P K R C F G R I V
D_Y_C_D V P_Q C_A_/\ A P S F D C_G_K P_Q V E P_K_K C_P G_R_V V_

G G C V S K P H S W P W Q I S L R T S \/ R G I H F C G G T L I
G_G_C_V_A H P_H_S_W_P_W_Q_V S_L_R_T_R /\ F G_M H_F_C_G_G_T_L_I_

D R Q W V L T A A H C L E K \/ S T R P G Y Y K I V L G I H T E
S P E W_V_L_T_A_A_H_C_L_E_K_/\ S_P R_P_S S Y_K_V I L_G_A H_Q E_

R A I E A S K Q L R D L E K L V L G P N G A D I A L L K L Q
V N L E_P H V Q_E I E V S R L_F L_E P_T R K D_I_A_L_L_K_L_S

T \/ P A L L N E K V T P V C L P D K D Y I V P S H T E C Y V T
S /\ P_A_V I T D K_V_I P_A C_L_P_S P N Y_V V_A D R T_E_C_F I T_

G W G E T Q \/ G T G G N G V L K E A G F P V I E N K I C N R P
G_W_G_E_T_Q_/\ G_T_F G_A G_L L_K_E_A_Q L P_V_I_E_N_K_V C_N_R_Y

A Y L N G R V K D H E M C A G N I E G G T D S C Q \/ G D S G G
E F L_N_G_R_V_Q S T E_L C_A_G_H L A G_G_T_D_S_C_Q_/\ G_D_S_G_G_
```

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 P L V C N S N N R F I L Q G V T S W G L G C A N P M K P G V
 P_L_V_C_F E K D K Y I_L_Q_G_V_T_S_W_G_L_G_C_A_R P_N K_P_G_V_

 Y A R V S K F I D W I K N T M E L N
 Y_V R_V_S_R F_V T W_I_E G V M_R N N_


FUF7 >fugu factor7 candidate A
   (sequence length=398)
HSF7    (44->466=423)>gi|182801|gb|AAA88040.1| coagulation factor VI
   (sequence length=423)

Number of matches = 164
Fraction of identities per length = 0.412060

 \/ V F M E K P E A N V F L H R T R R A N F L F E E L K A G N L
 /\ V_F_V T Q E E_A_H G V L_H_R_R R_R_A_N_A F L E_E_L_R P G_S L_

 D R D F K G E K F S Y E G A K E I F A L P Q Q L E   S Q G K
 E R_E C K_E E_Q C S_F E_E A_R E_I_F_K D A E R T K L F W I S

 A E    Q F I T \/ C K L S P C K N G A T C T R R F E T Y A C K C A
 Y S /\ D G D Q    C_A S S_P_C_Q N_G_G S C_K D Q L Q S Y_I C_F C_L

 N G F H G H N C D Q \/ V R R T S N G C R Y R N G G C E H F C R
 P A F_E G_R N_C_E T /\ H K D D Q L I C_V N E N_G_G_C_E_Q Y C_S

 E F P D R S Y V C F C A P G Y R L D K D N S T C L P \/ Q V K V
 D H T G T K R S C_R C_H E G_Y_S L_L A D_G V S C_T P_/\ T V_E Y

 P C G R L Q I L          F S P    R V I N G L I C P K G H
 P_C_G_K I P I_L_E K R N A S K P_Q G R_I V G G_K V C_P_K_G_E

 C P W Q \/ A M L S E N N I Y T C G A I I L S E Q W V L T A A H
 C_P_W_Q_/\ V L L_L V N_G A Q L C_G_G T L I N T I W_V_V S A_A_H_

 C V W R   K P A H L F N V T V \/ G E H D R E I F E K T E Q H R
 C_F D K I K_N W R N L I A V L /\ G_E_H_D_L S E H D G D E_Q_S R_

 R V I K V L I H P G Y N K T S S D K D L A M L K L H R P V K
 R_V_A Q V_I I_P S T Y_V P G T T N H D_I A_L L_R L_H_Q P_V_V

 L G L Y V V P I C L P A Q N S T I S R T L A N I R Q S T V S
 L_T D H V_V_P_L C_L_P_  E R T F S E R_T_L_A_F V R_F S_L V_S_

 G W G R L S R F G P P A T I L Q R L T L P R V P L Q E C
 G_W_G_Q L_L D R G_A T A_L E L_M V L_N V P_R_L M T Q_D C_L Q

       R L H T K L N I T R N M L C A G L K T G G R D A C E G
 Q S R K V G D S P N_I_T_E Y M_F C_A_G_Y S D G_S K D_S C_K G_

 D S G G P L V T Y Y K K T W F L T G V V S W G K G C A N E N
 D_S_G_G_P_H A T_H Y_R G T_W_Y L_T_G_I V_S_W_G_Q G_C_A_T V G

 L Y G V Y V R V T N F L D W I G N I I A T N
 H F G_V_Y_T R_V_S Q Y I E W_L Q K L M R S E P R P G V L L R
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 A P F P


FUF9 >fugu factor 9 from scaf1343
   (sequence length=473)
HUF9 >gi|22385321|gb|AAM96188.1| coagulation factor IX
   (sequence length=461)

Number of matches = 215
Fraction of identities per length = 0.466377

 M A R D F L L A L I A A L L L E V S    G L P T E G S T G \/ V
 M_Q R_V N M I M A E S P G L_I T I C L L G_Y L L S A E C T /\ V_

 F V S P Q A A N M V L L R Q R R Y N S G H L E E L Q K D N L
 F_L D H E N A_N_K I L_N R_P K R_Y_N_S_G_K L_E_E_F V Q G N_L_

 E R E C K E E Q C T M E E A R E V F E D D E K T \/
 E_R_E_C_M E_E_K C_S F E_E_A_R_E_V_F_E_N T E_R T_/\ T E F W K Q

   V D G D Q C V P P P C Q N E G V C K D G I N S Y V C W C K
 Y V_D_G_D_Q_C_E S N P_C_L N_G G_S C_K_D_D I_N_S_Y_E C_W_C_P

 P D F S G R N C E I \/ E V S K Q C S V N N G G C S H F C V M Q
 F G F_E G_K N_C_E_L /\ D V_T     C_N I K N_G_R C_E Q F_C_K N S

 G D I S   V C H C A V G H R L G L D K K S C E P T D \/ Q F S C
 A D_N K V V_C_S C_T E G_Y R_L_A E N Q K_S_C_E_P_A V /\ P F_P C_

 G H I N M S F S S K S N V Q R R S L M Q K L E A N R T F S S
 G_R V S V S_Q T S_K_    L T R_               A_E T V F_P D

 I L L G D Y S D N S T E L \/ D P Y W A F P T L P T I P E K E N
 V       D_Y_V   N_S_T_E_A    E T I L D N I T_Q S T_Q S F N D F

 T D Q R I V G G D E A L P G E I P W Q    V Q L N P P \/ A E P F C
 T_    R_V V_G_G_E D A_K P_G_Q F P_W_Q_/\ V_V L_N_G K    V D A F_C_

 G G S L L S D L W V I T A A H C L I N E K I A K Q G Y F I R
 G_G_S_I V N E K W_I V T_A_A_H_C_V     E_T G V K_I T     V V

 V G \/ E H    D V S K D E G P E R D H T V A E Q H I H F M Y D Y K
 A G_   E_H_/\ N I E E T E_H T E_Q K R N V_I R I I P H_H N Y_N A A

 K S P Y N H D I A L L K L N K P V E L S N K R R P I C L G P
 I N K Y_N_H_D_I_A_L_L_E L_D E P_L V L_N S Y V T P_I_C_I A D

 K D F T E T L L R E S T S S L V S G W G R I K F F G L E A T
 K_E Y T_N I F L_K   F G S_G Y V_S_G_W_G_R_V F H K G_R S A_L

 K L Q K L E V P Y V D R T R C K Q S S R E Q V T R Y M F C A
 V L_Q_Y L_R V_P_L V_D_R_A T C_L R S_T K F T I Y N N M_F_C_A_

 G Y Q L Q A K D S C Q G D S G G P H A T K Y K D T W F L T G
 G_F H E G G R D_S_C_Q_G_D_S_G_G_P_H_V T_E V E G T_S F_L_T_G_
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 I V S W G E E C A K D G K Y G I Y T R V S R Y Y P W I S Q K
 I_I S_W_G_E_E_C_A_M K G_K_Y_G_I_Y_T_K V_S_R_Y_V N W_I_K E K_

 T G L
 T_K L_T


FUA2 >fugu uPA on scaf3932
   (sequence length=454)
HUPA >human urokianase
   (sequence length=431)

Number of matches = 175
Fraction of identities per length = 0.406032

   M T F W R V L A A A F A I L T T A E A V R T L L H \/
 M R A L L A R L_L L C V L V V S D S K G S N E L_H Q    V P S /\ N

 C G L C L H G G T S V P S L T S G E H M F C L C A D G F Q G
 C_D   C_L_N G_G_T_C V_S N K Y F S N I H W C_N C_P K K F_G G_

 K N C E T \/ V K N S Q C Y E G V G L F Y R G T A S Q S E S G R
 Q H C_E_I /\ D K_S K T C_Y_E_G_N G_H F_Y_R_G_K A_S_T D T M G_R_

 T C R V W D P Q T    R E S Y L A S          D I N S G R H
 P C_L P W_N S A T_V L Q Q T Y_H A_H R S D A L Q L G L G_K H_

 N Y C R \/ N L H F R R R P W C Y V T K N Q Q L L W E Y C A V P
 N_Y_C_R_/\ N_P D N R_R_R_P_W_C_Y_V_Q V G L K P L_V Q E C_M V_H

 R C S S D   L C R C I P V P Q K K N A L R V C D R G V L N L R
 D C_A D G /\                K_K_

 C P H F A A P S Q A P P T P A H P A T \/ S A C G Q R R R R K Q
                   P_S S P_P E E L K   F Q C_G_Q_K T L R_P R

 M K I V G G T V A T V E S H P W V A A I F W R A K S K E K V
 F K_I_I G_G_E F T T_I E_N Q P_W_F A_A_I_Y R R_H R G G S V T

 F R C G G S L I S S C W V L T A A H C F   P D G \/ S H L K T R R
 Y V C_G_G_S_L_M S_P C_W_V_I S A_T H_C_F_/\ I D_      Y P K_K E D

 F S V V L G K N A L N E S K S T T E Q K F G V E Q I I V H R
 Y I V_Y L_G_R S R L_N_  S_N T Q G E_M K_F_E V_E_N L I_L H_K

 D F D N T D G N F N N D I \/ A L L K L K S T R G T C A K K S R
 D_Y S A D T L A H H N_D_I_/\ A_L_L_K_I R S_K E G_R C_A_Q P S_R_

 T V G S V C L P Q H L L Q P    G L T C E I A G Y G K E Q H \/
 T_I Q T I C_L_P_S M Y N D P_Q F G_T S C_E_I_T G_F G_K_E_N S /\

 G S W F R T Q Y L R E T Q V N V I S D D V C R Q E D Y Y G N
 T D Y L Y P E Q L_K M T_V V_K L I_S_H R E C_Q Q_P H Y_Y_G_S

 L I T S N M F C A G Q P D W S R D A C K \/ G D S G G P L V C E
 E V T_T K M_L C_A_A D P_Q W_K T D_S C_Q /\ G_D_S_G_G_P_L_V_C_S
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 V N G R L F L F G V I S W G D G C A K E F R P G V Y T R V T
 L Q G_R_M T L_T G_I V S_W_G_R G_C_A_L K D K P_G_V_Y_T_R_V_S

 N Y L R W I E E K V S G S M L V E K
 H F L_P W_I_R S H T K E E N G L A L


FUF7 >fugu f7 candidate B
   (sequence length=428)
HSF7    (44->466=423)>gi|182801|gb|AAA88040.1| coagulation factor VI
   (sequence length=423)

Number of matches = 187
Fraction of identities per length = 0.442080

 \/ V F L D A D K A H D V L V R T R R Y N S G W L E E L Q K G D
 /\ V_F_V T Q E E A_H_G V_L_H R_R R_R_  A N A F L_E_E_L_R P G_S

 L K R E C L E E I C S Y E E A R E V F E H T K T T \/ R Y L P E
 L_E R_E_C_K E_E_Q C_S_F E_E_A_R_E_I F_K D A E R T_   K L

 S D D Y Y V H H F F    G P N S C K S N P C L N G G S C S A E G
       F W I   S Y S /\ D G D Q C_A S_S P_C_Q N_G_G_S_C_K D Q L

 S S Y T C F C L P E F S G V D C E L \/ E Y Q T V P D T C L L E
 Q S_Y_I C_F_C_L_P_A F_E G_R N C_E_  /\ T H K D D Q L I C_V N E_

 N G G C E H F C H E N S A G R R G N C S C A D G Y D L D V D
 N_G_G_C_E_Q Y C_S D H T G T K R_  S C_R C_H E G_Y_S L_L A D_

 G L S C K A K \/ E S V A C G M V L S T Q F E H N Q L N P R A R
 G_V S_C_T P T /\ V E Y P C_G_K I P I L E   K R N_A S K P_Q G R_

 I V G G N E C P K G E C P W Q \/ V L L V Y K G K G F C G G V I
 I_V_G_G_K V C_P_K_G_E_C_P_W_Q_/\ V_L_L_L V N G_A Q L C_G_G_T L

 Y K P T W I L T A S H C M A D I D V   Q F L K V V A \/ G E H N
 I N T I W_V V S A_A H_C_F D K I_K N W R N L_I A V_L /\ G_E_H_D

 T E V D E G T E Q I I Q V S E I I M H E K Y V P R T A D N D
 L S E H D G_D E_Q_S R R V_A Q V I_I P S T Y_V_P_G T_T N H D_

 I A L L H L A V P I T Y T T Y A I P V C L P T R P L A E R E
 I_A_L_L_R L_H Q P_V V L T_D H V V P_L C_L_P_E R_T F S E_R_T

 L W A V S L H T V S G W G R R S E N G P T S H L L R Q L K V
 L_A F V_R F S L V_S_G_W_G_Q L L D R G_A T_A L E L_M V L_N V_

 P R I R T Q Q C I E E S G V V          L T Q N M F C A G Y
 P_R_L M T_Q_D C_L Q Q S_R K V_G D S P N I T_E Y M_F_C_A_G_Y_

 M E G R Q D S C K G D S G G P L V T K Y K K T V F L L G I V
 S D G_S K D_S_C_K_G_D_S_G_G_P_H A T_H Y_R G T_W Y L_T G_I_V_

 S W G K G C A R P G N Y G I Y T R V A N Y L E W I H N R T A
 S_W_G_Q G_C_A_T V G_H F G_V Y_T_R_V_S Q Y_I E_W_L Q K L M R
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 T V N Q P T N   N T E N F T T
 S E P R P_G V L L R A P F_P


FUF9 >fugu f9 candidate from scaf917
   (sequence length=476)
HUF9 >gi|22385321|gb|AAM96188.1| coagulation factor IX
   (sequence length=461)

Number of matches = 196
Fraction of identities per length = 0.425163

      M D L F R L P F S C L L      L V A L Q L D Y S \/ A P    L
 M Q R V N M I M A E S P G L_I T I C L_L G Y L L_S A E    C T /\ V

 F L P A E V A G S V L Q R P K R A N I G V F E E W L E G N L
 F_L_D H E_N A_N K I L_N R_P_K_R_Y N_S G_K L E_E_F V Q G_N_L_

 E R E C L E E T C D L E E V R E V F E D D E K T \/ S V M S R V
 E_R_E_C_M E_E_K C_S F E_E_A R_E_V_F_E_N T E_R T_/\ T E F W K Q

 L L V P S D G N Q C D S N P C L N Q G S C E D L L G S Y T C
 Y V      D_G_D Q_C_E S_N_P_C_L_N_G G_S_C_K D_D I N S_Y_E C_

 T C L P G F A G K D C E I \/ A K R C D V N N G D C A H F C E P
 W C_P F G_F_E G_K_N C_E_L /\ D V T C_N I K N_G_R C_E Q F_C_K N

 L G A F G A K C S C A T G Y R V T D D G L D C Q P \/ E T E F P
 S A D N K V V C_S_C_T E G_Y_R_L A E N Q K S C_E P_/\ A V P F_P_

 C G K T A L M Q V N S A F R R T L L G R L D S S L E N D T A
 C_G_R V S V S Q_  T S_K L T R_A E T V F P D_V D Y V N_S T_E

 P D   N \/ T N D T T L P G D E E P E P Y R R I V G G D L V I P G
 A E /\ T   I L D_N I T Q S T Q S F N D F T R_V V_G_G_E D A K P_G_

 E I P W Q \/ V A L M Q R S T G E V F C G G S I L S E R W V I T
 Q F P_W_Q_/\ V_V L_   N G K V D A F_C_G_G_S_I_V N E_K W_I V T_

 A A H C L L E E K V S F Y I R V \/ G E H   T L S I Q E G T E Q N
 A_A_H_C_  V E_T G V_K I T V V A   G_E_H_/\ N I E E T E_H T_E_Q_K

 Y D V L E Q H L H P L Y N A S I S L Y D H D I A L I Y L K S
 R N V_I R I I P H_H N Y_N_A_A I_N K Y_N H_D_I_A_L_L E L_D E

 P I A F S A N V R P I C I G P R A F T E F L I K S Y S P A R
 P_L V L N S Y V_T P_I_C_I_A D K E Y T_N I F L K_  F G S G Y

 V S G W G R T R Y L G L T A D S L Q K V D V P F T I R T E C
 V_S_G_W_G_R_V F H K G_R S A_L V L_Q_Y L R V_P_L V D R_A T C_

 K H S S S N R I T P Y M F C A G Y K D E A K D A C Q G D S G
 L R S_T K F T I_Y N N M_F_C_A_G_F H E G G R D_S C_Q_G_D_S_G_

 G P H T N S I R D T W F L T G I V S W G E E C A K E G K Y G
 G_P_H_V T E V E G T_S F_L_T_G_I_I S_W_G_E_E_C_A_M K G_K_Y_G_
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 V Y T R V S L Y Y H W I K Y V M G S T K K R L A F D V E N P
 I Y_T_K V_S_R Y_V N W_I_K_         E K_T K L_T

 D E


FUA1 >fugu uPA on scaf4367
   (sequence length=392)
HUPA >human urokianase
   (sequence length=431)

Number of matches = 164
Fraction of identities per length = 0.418367

 M K L L V    I L V I F V A F C S D V V S R N L E D I T S
 M_R A L_L A R L L_L C V L V V S D S K G S_N E L_H Q V P S_/\ N

    C L G \/                          C L C A
 C D C_L_N   G G T C V S N K Y F S N I H W C_N C_P K K F G G Q

          A T E T C W P G E R S S Y T G D V S K S L G G R R
 H C E I /\ D K S K T_C_Y E G_N G H F Y_R G_K A S_T D T M G_R_P

 C L N W          R N V F N P  W G D S    N G I G D H N
 C_L_P W_N S A T V L Q Q T Y H A H R S D_A L Q L G_L G_K H_N_

 Y C R \/ N P D Q S G R P W C Y V R R G R R I V W E F C V V P M
 Y_C_R_/\ N_P_D_N R R R_P_W_C_Y_V_Q V G_L K P L V Q E C_M V_H D

 C K P D \/ F S E L I L G V F A A L S C G E R Q E Q R T N K I V
 C_A D G /\ K K P S S P P E E L K F Q C_G_Q K T L R P R F K_I_I

 N G S F A D V E S H P W I A A I F G Q R S          L C G
 G G_E F_T T I E_N Q P_W_F A_A_I_Y R R H R G G S V T Y V C_G_

 G S L I S P C W V V T A A H C F   D D G \/ D A T D I R Q L S V H
 G_S_L_M S_P_C_W_V_I S A_T H_C_F_/\ I D_Y   P K K E    D Y I V_Y

 L G K K A I N E T N A K K E Q A F L V E K L I I H Q H F D S
 L_G_R S R L N_  S N_T Q G E_M K F_E V_E_N L_I_L H_K D Y S A

 S D L    N N D I \/ A L L K I K R R D G S C A A K S A S A R V
 D T L_A H H N_D_I_/\ A_L_L_K_I_R S K E G_R C_A_Q P S_R T I Q T

 V C L P P L R T Q L P A G F Q C T V A G Y G H E S Y \/ R T Y S
 I C_L_P_S M Y N D P Q F G_T S C_E I T G_F G_K E_N S /\ T D Y_L

 Y S Q Y L K K T E V K L I S H S L C Q S P S Y Y G K R I T D
 Y_P E Q L_K_M T_V V_K_L_I_S_H_R E C_Q_Q P_H Y_Y_G_S E V T_T

 N M L C A G S P D W T T D S C \/ Q G D S G G P L V C E A A G R
 K M_L_C_A_A D P_Q W_K T_D_S_C_/\ Q_G_D_S_G_G_P_L_V_C_S L Q G_R_

 M F L F G V V S W G D E C A K K N K P G V Y T Q V T N Y N K
 M_T L_T G_I V_S_W_G_R G C_A_L K_D K_P_G_V_Y_T_R V_S H F L P
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 W I A D E T G L S E Y T K G L M Y P E K
 W_I_R S H T_      K E E N G_L_A L


FF7C >fugu f7 candidate C
   (sequence length=426)
HSF7    (44->466=423)>gi|182801|gb|AAA88040.1| coagulation factor VI
   (sequence length=423)

Number of matches = 173
Fraction of identities per length = 0.408983

 \/ V F V E R D D A S T V L Q R R R R A N S G F L E E M Q Q G N
 /\ V_F_V_T Q E E A_H G V_L_H R_R_R_R_A_N_  A F_L_E_E_L R P G_S

 L K R E C I E E I C N Y E E A R E V F E D D A Q T \/
 L_E R_E_C_K E_E_Q C_S F E_E_A_R_E_I F_K D_A E R T_   K L F W I

       S G H D P C S V M P C Q N N G V C V S M G N T Y Q C H C
 S Y /\ S_D G D_Q C_A S S P_C_Q_N_G G_S C_K D Q L Q S Y_I C_F C_

 P E G F G G Q R C E T \/ K A E D F L K C L Y Q N G Q C Q H F C
 L P A F_E G_R N C_E_T_/\ H K D D_Q L_I C_V N E N_G_G C_E Q Y C_

  D G S G A S R K C F C A H G Y T L A S D G R Q C I A E \/ V E
 S D_H T G_T K R_S C_R C_H E G_Y_S L_L A D_G_V S C_T P T /\ V_E_

 F P C G Q L P P P E T G P D Q T V V G Q T R L V G T N H C P
 Y P_C_G_K I P_I L E_K    R N A S K P Q_G R_I V_G_G K V C_P_

 K G E C P W Q \/ V L V Q L H G Q S H C G G V L I R P D W V I T
 K_G_E_C_P_W_Q_/\ V_L_L L V N G_A Q L C_G_G_T L_I_N T I W_V_V S

 A A H C V T G K Q P Q H L S V V A G N R S L N \/ F I L    L P G E
 A_A_H_C_              F D K I K N W R_N L_I   A V L_ /\    G_E_

 H N L D N D D G T E Q K I P V A R V F A H E G Y V S E T G D
 H_D L_S E H D_G_D E_Q_S R R V_A_Q V_I I P S T Y_V_P G T_T N

 K D I A L L H L N A S V T L N R G V I P V C L P T K D L A E
 H D_I_A_L_L_R L_H Q P V_V L_T D H V_V P_L C_L_P_E R T F S E_

 R E L L M T R Y H T V S G W G K R T N G G N E D H G V V N T
 R_T L_A F V R_F S L V_S_G_W_G_Q L L D R G_A T A L E L M  V

 A P V S P F L R K F S V P I I P N P Q C S H R S Q F N F T D
 L N V_P R L M T Q D C L Q    Q S R K V G D S P    N_I T_E

 N M L C A G Y L E G N Q Q S C R G D D G S P L V T L Y G S T
 Y M_F C_A_G_Y_S D G_S K D S_C_K G_D_S G_G P_H A T_H Y_R G T_

 H F L I G V V G W G R G C P N P G Y Y G V Y T N M G N F V D
 W Y L_T G_I V_S W_G_Q G_C_A T V G_H F G_V_Y_T_R V S Q Y I E

 W A N G I M M A A N K A S T
 W_L Q K L M_R S E P R P G V L L R A P F P
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