Appendix A

The Tetraspanins

The Tetraspanins are expressed in a broad range of organisms. The following lists a range of tetraspanins which have been found through GenBank and PubMed.

TM4SF Member	**Organism**	**GenBank Accession**	**Characterisation**
29Fa	*Drosophila melanogaster*	AF274011	Todres *et al.*, 2000
29Fb	*Drosophila melanogaster*	AF274012	Todres *et al.*, 2000
3A	*Drosophila melanogaster*	AF274013	Todres *et al.*, 2000
42Ea	*Drosophila melanogaster*	AF274014	Todres *et al.*, 2000
42Eb	*Drosophila melanogaster*	AF274015	Todres *et al.*, 2000
42Ec	*Drosophila melanogaster*	AF274016	Todres *et al.*, 2000
42Eg	*Drosophila melanogaster*	AF274017	Todres *et al.*, 2000
42Ei	*Drosophila melanogaster*	AF274018	Todres *et al.*, 2000
42El	*Drosophila melanogaster*	AF274019	Todres *et al.*, 2000
97E	*Drosophila melanogaster*	AF274020	Todres *et al.*, 2000
CG8666	*Drosophila melanogaster*	AE003670	Adams *et al.*, 2000
CG9033	*Drosophila melanogaster*	AE003826	Adams *et al.*, 2000
A15 (TALLA-1)	*Mus musculus* (Mouse)	AF052492	Hosokawa *et al.*, 1999
B0563.2	*Caenorhabditis elegans*	U28740	Waterston, 1998
C14A11.1	*Caenorhabditis elegans*	U97592	Waterston, 1998
CD9	*Bos taurus* (Cattle)	M81720	Martin-Alonso *et al.*, 1992
CD9	*Felis catus* (Cat)	L35275	Willett & Neil, 1995
CD9	*Gallus gallus* (Chicken)	AB032767	Kobayashi & Mekada, 1999
CD9 (MRP-1/ DRAP27)	*Homo sapien* (Human)	L34068	Miyake *et al.*, 1991
CD9	*Mus musculus* (Mouse)	L08115	Rubinstein *et al.*, 1993
CD9	*Rattus norvegicus* (Rat)	X76489	Kaprielian *et al.*, 1995
CD37	*Homo sapien* (Human)	NM_001774	Tomlinson & Wright, 1996
CD37	*Mus musculus* (Mouse)	U18372	Tomlinson & Wright, 1996
CD37 (MRC OX-44)	*Rattus norvegicus* (Rat)	X53517	Bellacosa *et al.*, 1991
CD53	*Homo sapien* (Human)	M60871	Amiot, 1990
CD53	*Mus musculus* (Mouse)	X97227	Wright *et al.*, 1993

TM4SF Member	**Organism**	**GenBank Accession**	**Characterisation**
CD53	*Rattus norvegicus* (Rat)	NM_012523	Bellacosa *et al.*, 1991; Gulko *et al.*, 1998; Griffiths *et al.*, 1999; Wilder *et al.*, 1999
CD63	*Bos taurus* (Cattle)	AJ012589	Brooke *et al.*, 1999
CD63 (ME491/ Pltgp40)	*Homo sapien* (Human)	NM_001780	Hotta *et al.*, 1992; Hotta *et al.*, 1988; Hotta *et al.*, 1989; Rapp *et al.*, 1990; Ross *et al.*, 1985; Metzelaar *et al.*, 1991; Horejsi & Vlcek, 1991; Wang *et al.*, 1992; Nishibori *et al.*, 1993; Sincock *et al.*, 1997; Tachibana *et al.*, 1997; Serru *et al.*, 1999; Berditchevski, 2001
CD63	*Mus musculus* (Mouse)	NM_007653	Miyamoto *et al.*, 1994
CD63	*Oryctolagus cuniculus* (Rabbit)	D21264	Sohma *et al.*, 1994
CD63	*Rattus norvegicus* (Rat)	NM_017125	Nishikata *et al.*, 1992
CD81	*Chlorocebus aethiops* (African green monkey)	AF116599	Levy & Kuo, 1998
CD81	*Pan troglodytes* (Chimp)	AF116600	Levy & Kuo, 1998
CD81	*Saguinus oedipus* (Tamarind)	AJ250197	Meola *et al.*, 2000
CD81 (TAPA-1/ M38/ S5.7)	*Homo sapien* (Human)	NM_004356	Takahashi *et al.*, 1990
CD81	*Rattus norvegicus* (Rat)	NM_013087	Geisert *et al.*, 1991; Geisert *et al.*, 1996; Irwin & Geisert, 1993
CD82 (KAI-1/R2/C33/ IA4/ 4F9)	*Homo sapien* (Human)	S48196	Imai *et al.*, 1992
CD82	*Mus musculus* (Mouse)	D14883	Nagira *et al.*, 1994
CD151 (Peta-3)	*Cercopithecus aethiops* (African green monkey)	AF275666	Shanmukhappa & Kapil, 2000
CD151	*Homo sapien* (Human)	D29963	Fitter *et al.*, 1995
CD151	*Mus musculus* (Mouse)	U89772	Fitter *et al.*, 1998
CD151	*Macaca mulatta* (Rhesus Monkey)	AF275665	Shanmukhappa & Kapil, 2000

TM4SF Member	**Organism**	**GenBank Accession**	**Discovery / Gene Characterisation**
CO-029 (TM4SF3)	*Homo sapien* (Human)	M35252	Szala *et al.*, 1990
D6.1A	*Rattus norvegicus* (Rat)	Y13275	Claas *et al.*, 1998
D76	*Manduca sexta* (Tobacco hornworm)	AF274022	Todres *et al.*, 2000
D107	*Manduca sexta* (Tobacco hornworm)	AF274021	Todres *et al.*, 2000
E118	*Manduca sexta* (Tobacco hornworm)	AF274023	Todres *et al.*, 2000
F139	*Apis mellifera* (Honeybee)	AF274024	Todres *et al.*, 2000
F53B6	*Caenorhabditis elegans*	Z81086	Consortium, 1998
GH07	*Drosophila melanogaster*	AF220042	Page-McCaw *et al.*, 1999
il-TMP (TM4SF4)	*Homo sapien* (Human)	U31449	Wice & Gordon, 1995
L6	*Mus musculus* (Mouse)	L15443	Marken *et al.*, 1994
LBL	*Drosophila melanogaster*	U49081	Kopczynski *et al.*, 1996
LD16	*Drosophila melanogaster*	AF220043	Page-McCaw *et al.*, 1999
LD29	*Drosophila melanogaster*	AF220044	Page-McCaw *et al.*, 1999
M6	*Drosophila melanogaster*	AF253528	Werner *et al.*, 2001
M6B	*Mus musculus* (Mouse)	AF254869	Werner *et al.*, 2001
NET-1 (TSPAN-1)	*Homo sapien* (Human)	AF065388	Serru *et al.*, 2000
NET-2	*Homo sapien* (Human)	NM_012338	Serru *et al.*, 2000; Berditchevski, 2001
NET-4 (TM4SF9/TSPAN-5)	*Homo sapien* (Human)	AF065389	Serru *et al.*, 2000
NET-5	*Homo sapien* (Human)	NM_006675	Serru *et al.*, 2000; Berditchevski, 2001
NET-6	*Homo sapien* (Human)	NM_014399	Serru *et al.*, 2000; Berditchevski, 2001
NET-7	*Homo sapien* (Human)	AF120266	Serru *et al.*, 2000
PRPH (RDS)	*Felis catus* (Cat)	M94047	Gorin *et al.*, 1993
PRPH1	*Gallus gallus* (Chicken)	AF031238	Weng *et al.*, 1998
PRPH2	*Gallus gallus* (Chicken)	AF031239	Weng *et al.*, 1998
PRPH	*Canis familiaris* (Dog)	U36577	Moghrabi *et al.*, 1995

TM4SF Member	**Organism**	**GenBank Accession**	**Discovery / Gene Characterisation**
PRPH2	*Mus musculus* (Mouse)	NM_008938	Travis *et al.*, 1989; Ma *et al.*, 1995
PRPH	*Rattus norvegicus* (Rat)	NM_013021	Begy & Bridges, 1990
PRPH35	*Xenopus laevis*	L79913	Kedzierski *et al.*, 1996
PRPH36	*Xenopus laevis*	L79914	Kedzierski *et al.*, 1996
PRPH38	*Xenopus laevis*	L79915	Kedzierski *et al.*, 1996
ROM-1	*Bos taurus* (Cattle)	D83385	Wada *et al.*, 1996
ROM-1	*Homo sapien* (Human)	NM_000327	Bascom *et al.*, 1992; Bascom *et al.*, 1993; Courseaux *et al.*, 1996; Wang *et al.*, 2001
ROM-1	*Mus musculus* (Mouse)	NM_009073	Bascom *et al.*, 1993
SAS	*Canis familiaris* (Dog)	AJ388529	Pichon *et al.*, 2000
SAS	*Homo sapien* (Human)	U81031	Elkahloun *et al.*, 1997; Meltzer *et al.*, 1991; Jankowski *et al.*, 1995
Sh23	*Schistosoma haematobium*	U23771	Inal & Bickle, 1995
Sj25	*Schistosoma japonicum*	U77941	Fan *et al.*, 1997
Sj23	*Schistosoma japonicum*	M63706	Davern *et al.*, 1991
SM23	*Schistosoma mansoni*	L34755	Reynolds *et al.*, 1992; Lee *et al.*, 1995
TE736	*Schistosoma japonicum*	AF036955	Fan *et al.*, 1997; Fan & Brindley, 1998
TM4SF	*Gallus gallus* (Chicken)	AF206661	Perron & Bixby, 1999
TM4-A (TSPAN-3)	*Homo sapien* (Human)	AF133423	Puls *et al.*, 1999
Tm4-A	*Mus musculus* (Mouse)	NM_019793	Puls *et al.*, 1999
TM4-B	*Homo sapien* (Human)	AF133424	Puls *et al.*, 1999
TM4-D (TSPAN-6/TM4SF6/T245)	*Homo sapien* (Human)	AF133426	Puls *et al.*, 1999
TM4SF2	*Homo sapien* (Human)	NM_004615	Li *et al.*, 1993b; Emi *et al.*, 1993; Virtaneva *et al.*, 1994; Takagi *et al.*, 1995; Serru *et al.*, 1999; Zemni *et al.*, 2000; Castellvi-Bel & Mila, 2001; Berditchevski, 2001
TM4SF5 (L6H)	*Homo sapien* (Human)	AF027204	Muller-Pillasch *et al.*, 1998
Tm4sf6	*Mus musculus* (Mouse)	NM_019656	Todd *et al.*, 1998
TM4SF7 (NAG-2)	*Homo sapien* (Human)	NM_003271	Tachibana *et al.*, 1997; Todd *et al.*, 1998; Serru *et al.*, 1999; Berditchevski, 2001

TM4SF Member	**Organism**	**GenBank Accession**	**Discovery / Gene Characterisation**
TSPAN2	*Homo sapien* (Human)	AF054839	Todd *et al.*, 1998
Tspan2	*Rattus norvegicus* (Rat)	AJ271442	Birling *et al.*, 1999
Tspan5	*Mus musculus* (Mouse)	AF121344	Todd *et al.*, 1998
UPK1A	*Bos taurus* (Cattle)	Z29378	Yu *et al.*, 1994
UPK1A	*Homo sapien* (Human)	NM_007000	Lobban *et al.*, 1998
UPK1A	*Sus scrofa* (Pig)	AF178940	Kwon *et al.*, 1999
UPK1B	*Bos taurus* (Cattle)	Z29378	Yu *et al.*, 1994
UPK1B	*Homo sapien* (Human)	AF042331	Finch *et al.*, 1999; Lobban *et al.*, 1998; Yu *et al.*, 1994
UPK1B	*Mustela vison* (Mink)	M64428	Kallin *et al.*, 1991
UPK1B	*Mus musculus* (Mouse)	AF073956	Webb *et al.*, 1999
UPK1B	*Oryctolagus cuniculus* (Rabbit)	AF178936	Cho *et al.*, 1999
UPK1B (5' end)	*Xenopus laevis*	BF024799	Clifton *et al.*, 1999
UPK1B (3' end)	*Xenopus laevis*	BE507089	Clifton *et al.*, 1999

Appendix B

BAMBE Tree Data of UPKIB Homologues

Probability Scores

```
***** Posterior probabilities of clades in most probable tree topology *****
              Parent   Parent
              Branch   Branch
   Count  Prob.  Mean      SD        Tree topology
   49999  1.000  0.000000 0.000000 {1,2,3,4,5,6,7}
   49999  1.000  0.027853 0.009104 {1,2,3,4,5,6}
   49999  1.000  0.293813 0.033462 {1,2,3,4,5}
   35963  0.719  0.021890 0.010045 {1,4,5}
   23642  0.473  0.008178 0.004235 {1,5}
   18656  0.373  0.015419 0.010278 {2,3}
   49999  1.000  0.042858 0.008763 {1}
   49999  1.000  0.048302 0.020992 {2}
   49999  1.000  0.022272 0.010764 {3}
   49999  1.000  0.046947 0.009752 {4}
   49999  1.000  0.029427 0.007474 {5}
   49999  1.000  0.053668 0.017857 {6}
   49999  1.000  0.027853 0.009104 {7}
```

Newick Tree Format

```
************* Most probable tree in newick format *************

(((((1:0.042858,5:0.029427):0.008178,4:0.046947):0.021890,(2:0.048302,3:0.022272
):0.015419):0.293813,6:0.053668):0.027853,7:0.027853);
```

Appendix C

BAMBE Tree Data of Human Tetraspanins

Probability Scores

```
***** Posterior probabilities of clades in most probable tree topology *****
              Parent   Parent
              Branch   Branch
    Count  Prob.  Mean     SD       Tree topology
    10000  1.000  0.000000 0.000000
{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26}
    10000  1.000  0.127276 0.020134
{2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26}
     9425  0.943  0.108186 0.041017
{2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,25,26}
    10000  1.000  0.251383 0.050842
{2,3,4,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,25,26}
     8935  0.893  0.119338 0.040881
{2,3,4,6,7,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,25,26}
      856  0.086  0.052336 0.035035 {2,3,6,7,9,11,13,14,16,18,23}
     1438  0.144  0.080427 0.042920 {2,3,6,7,9,13,16,23}
     9446  0.945  0.128957 0.047716 {2,3,6,9,13}
    10000  1.000  0.299133 0.059157 {2,6}
    10000  1.000  0.192634 0.046118 {3,9,13}
     9988  0.999  0.115096 0.038530 {9,13}
     1930  0.193  0.131242 0.082756 {7,16,23}
    10000  1.000  1.621952 0.203930 {16,23}
     5595  0.559  0.207737 0.083128 {11,14,18}
    10000  1.000  0.850673 0.146416 {14,18}
     1431  0.143  0.083594 0.035219 {4,10,12,15,17,19,20,21,22,25,26}
     4155  0.415  0.099209 0.045836 {4,12,15,17}
     5525  0.552  0.200573 0.090175 {12,15,17}
     8180  0.818  0.228858 0.102570 {12,15}
     3243  0.324  0.100959 0.039937 {10,19,20,21,22,25,26}
     6542  0.654  0.114155 0.058893 {10,20,25,26}
    10000  1.000  0.276397 0.087437 {10,20}
    10000  1.000  0.587312 0.108017 {25,26}
     7514  0.751  0.116396 0.052789 {19,21,22}
    10000  1.000  0.337432 0.055137 {21,22}
    10000  1.000  0.127276 0.020134 {1}
    10000  1.000  0.609012 0.064920 {2}
    10000  1.000  0.501747 0.054221 {3}
    10000  1.000  0.528252 0.059715 {4}
    10000  1.000  0.413900 0.049596 {5}
    10000  1.000  0.353092 0.049351 {6}
    10000  1.000  0.555599 0.095959 {7}
    10000  1.000  0.581584 0.069301 {8}
    10000  1.000  0.314362 0.031714 {9}
    10000  1.000  0.359483 0.069059 {10}
    10000  1.000  0.778541 0.129152 {11}
    10000  1.000  0.517239 0.072850 {12}
    10000  1.000  0.230502 0.037739 {13}
    10000  1.000  0.326195 0.094237 {14}
```

```
10000  1.000  0.734877 0.084533 {15}
10000  1.000  0.141255 0.096207 {16}
10000  1.000  1.571227 0.164654 {17}
10000  1.000  0.352410 0.090382 {18}
10000  1.000  0.637405 0.089315 {19}
10000  1.000  0.898564 0.098494 {20}
10000  1.000  0.253762 0.041038 {21}
10000  1.000  0.306964 0.038898 {22}
10000  1.000  0.765808 0.108245 {23}
10000  1.000  0.594299 0.063803 {24}
10000  1.000  0.637274 0.083918 {25}
10000  1.000  0.624761 0.088118 {26}
```

Newick Tree Format

```
************* Most probable tree in newick format *************

(1:0.127276,((((((((2:0.609012,6:0.353092):0.299133,(3:0.501747,(9:0.314362,13
:0.230502):0.115096):0.192634):0.128957,(7:0.555599,(16:0.141255,23:0.76580
8):1.621952):0.131242):0.080427,(11:0.778541,(14:0.326195,18:0.352410):0.850
673):0.207737):0.052336,((4:0.528252,((12:0.517239,15:0.734877):0.228858,17:
1.571227):0.200573):0.099209,(((10:0.359483,20:0.898564):0.276397,(25:0.6372
74,26:0.624761):0.587312):0.114155,(19:0.637405,(21:0.253762,22:0.306964):0.
337432):0.116396):0.100959):0.083594):0.119338,8:0.581584):0.251383,5:0.413
900):0.108186,24:0.594299):0.127276);
```

Appendix D

BAMBE Tree Data of A Range of Tetraspanins

Probability Scores

```
***** Posterior probabilities of clades in most probable tree topology *****
                    Parent      Parent
                    Branch     Branch
Count      Prob.    Mean            SD           Tree topology
15000  1.000   0.000000 0.000000
{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,3
2,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,6
0,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,8
8,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105}
15000  1.000   0.513874 0.055398
{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,3
2,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,58,59,60,6
1,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,8
9,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105}
2340    0.156   0.099819 0.070128
{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,3
2,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,58,59,60,6
1,62,63,64,65,66,67,68,69,70,71,72,73,74,76,77,78,79,80,81,82,83,84,85,86,87,88,89,9
0,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105}
6395    0.426   0.102913 0.068608
{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,3
2,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,58,60,61,6
2,63,64,65,66,67,68,69,70,71,72,73,74,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,9
1,92,93,94,95,96,97,98,99,100,101,102,103,104,105}
12456  0.830   0.116116 0.053041
{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,3
2,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,51,52,53,54,55,56,58,60,61,62,63,6
4,65,66,67,68,69,71,72,73,74,76,77,78,79,80,82,83,84,85,86,87,88,89,90,91,92,93,94,9
5,96,97,98,99,100,101,102,103,104,105}
7420    0.495   0.057771 0.033227
{1,14,15,16,17,18,32,33,34,35,36,51,53,54,56,58,61,62,64,65,66,67,68,69,71,72,73,74,
83,85,86,87,88,89,90,91,92}
12946  0.863   0.101453 0.036378
{1,32,33,34,35,36,51,53,54,56,58,64,65,66,67,68,69,73,74,83,85,86,87,90,91,92}
11699 0.780 0.090626 0.037975 {1,32,33,51,53,54,58,83,85,86,87,91,92}
11096  0.740   0.126601 0.058260 {1,32,33,83,85,86,87,91,92}
15000 1.000 0.315974 0.068211 {1,85,86,92}
15000  1.000   0.301039 0.040915 {1,86}
15000  1.000   0.178923 0.033684 {85,92}
6851    0.457   0.184088 0.117565 {32,33,83,87,91}
15000  1.000   1.782185 0.349440 {32,33,87}
5357    0.357   0.098361 0.076433 {32,87}
15000  1.000   0.554283 0.123887 {83,91}
```

12910	0.861	0.212337	0.082485	{51,53,54,58}
15000	1.000	0.361971	0.093005	{51,53,54}
15000	1.000	0.113876	0.025388	{51,54}
9585	0.639	0.137191	0.047881	{34,35,36,56,64,65,66,67,68,69,73,74,90}
7677	0.512	0.126314	0.052537	{34,35,36,64,65,66,67,68,69,73,74}
14837	0.989	0.138850	0.050325	{34,67,68,69}
4918	0.328	0.079446	0.044313	{34,68,69}
606	0.040	0.091540	0.037113	{34,68}
6148	0.410	0.181870	0.054530	{35,36,64,65,66,73,74}
3363	0.224	0.111246	0.051034	{35,36,65,66,73}
15000	1.000	1.370471	0.243455	{35,36}
12925	0.862	0.116120	0.046520	{65,66,73}
14446	0.963	0.135356	0.047023	{65,66}
7070	0.471	0.066330	0.035193	{64,74}
11558	0.771	0.103007	0.043314	{56,90}
12216	0.814	0.059494	0.031665	{14,15,16,17,18,61,62,71,72,88,89}
15000	1.000	0.475146	0.059704	{14,15,16,17,18}
14751	0.983	0.044087	0.015471	{14,15,17}
15000	1.000	0.018813	0.006944	{15,17}
15000	1.000	0.070274	0.019231	{16,18}
14678	0.979	0.109707	0.042264	{61,62,71,72,88,89}
13503	0.900	0.119504	0.045261	{61,62,71,88,89}
5919	0.395	0.076532	0.039525	{61,62,88}
15000	1.000	0.298817	0.062474	{62,88}
15000	1.000	0.180167	0.063541	{71,89}
14189	0.946	0.134095	0.051657	{2,3,4,5,6,7,8,9,10,11,12,13,19,20,21,22,23,24,25,26,27,28,29,30,31,37,38,39,40,41,42,43,44,45,46,47,48,52,55,60,63,76,77,78,79,80,82,84,93,94,95,96,97,98,99,100,101,102,103,104,105}
8003	0.534	0.140631	0.050551	{2,3,4,5,6,7,19,20,21,22,23,30,31,78,93,95}
11928	0.795	0.123928	0.054225	{2,3,4,5,6,7,19,20,21,22,23,30,31,93,95}
15000	1.000	0.268388	0.053640	{2,3,4,5,6,7,19,20,21,22,23,93,95}
14605	0.974	0.102526	0.037793	{2,3,4,5,6,7,93,95}
15000	1.000	0.157685	0.035124	{2,3,4,5,6,7}
15000	1.000	0.116443	0.028669	{2,3,5,6,7}
14938	0.996	0.031106	0.010262	{3,5,6,7}
2026	0.135	0.015314	0.006819	{5,6,7}
15000	1.000	0.082498	0.012083	{6,7}
15000	1.000	0.533018	0.053615	{93,95}
15000	1.000	0.345737	0.045289	{19,20,21,22,23}
14609	0.974	0.053354	0.017763	{19,20,21,23}
14568	0.971	0.012854	0.005353	{19,20,21}
15000	1.000	0.013831	0.004514	{20,21}
15000	1.000	0.466275	0.057202	{30,31}

```
537    0.036  0.039321 0.021424
{8,9,10,11,12,13,24,25,26,27,28,29,37,38,39,40,41,42,43,44,45,46,47,48,52,55,60,6
3,76,77,79,80,82,84,94,96,97,98,99,100,101,102,103,104,105}
1488   0.099 0.062709 0.029810
{8,9,10,11,12,13,24,25,26,27,28,29,37,38,39,40,41,42,43,44,45,46,47,48,52,55,63,7
6,79,80,82,94}
15000  1.000  0.129484 0.040998 {8,9,10,11,12,13,24,25,76,80}
15000  1.000  0.256575 0.047244 {8,9,10,24,25}
15000  1.000  0.576871 0.057862 {8,9,10}
15000  1.000  0.129976 0.026514 {9,10}
15000  1.000  0.209422 0.044854 {24,25}
15000  1.000  0.218609 0.052088 {11,12,13,76,80}
15000  1.000  0.333246 0.042972 {11,12,13}
15000  1.000  0.062673 0.016749 {12,13}
15000  1.000  0.223661 0.044098 {76,80}
2505   0.167  0.061361 0.035223
{26,27,28,29,37,38,39,40,41,42,43,44,45,46,47,48,52,55,63,79,82,94}
15000  1.000  0.604965 0.058302 {26,27,28,29}
14862  0.991  0.048440 0.019933 {26,27,29}
15000  1.000  0.028437 0.006168 {26,29}
8588   0.573  0.119269 0.058089
{37,38,39,40,41,42,43,44,45,46,47,48,52,55,63,79,82,94}
14921  0.995  0.321138 0.110191 {37,38,39,40,41,42,43,44,45,46,47,48,52,55}
15000  1.000  0.780852 0.103868 {37,38,39,40,41,42,43,44,45,46,47,48}
14602  0.973  0.135435 0.049592 {37,38,40,41,42,43,44,45,46,47,48}
15000  1.000  0.124108 0.026160 {37,38,40,41,42,45}
15000  1.000  0.069957 0.016833 {37,38,40,41,42}
15000  1.000  0.138748 0.016993 {37,40,41,42}
14567  0.971  0.019118 0.007115 {37,40}
15000  1.000  0.064537 0.010039 {41,42}
15000  1.000  0.199380 0.036719 {43,44,46,47,48}
15000  1.000  0.174931 0.029751 {43,44}
15000  1.000  0.763093 0.052466 {46,47,48}
8135   0.542  0.019524 0.010557 {46,47}
15000  1.000  0.372881 0.092093 {52,55}
15000  1.000  0.255072 0.074850 {63,79,82,94}
14215  0.948  0.144195 0.055940 {63,82}
15000  1.000  0.544552 0.056468 {79,94}
14952  0.997  0.188885 0.062526 {60,77,84,96,97,98,99,100,101,102,103,104,105}
7219   0.481  0.112852 0.053376 {60,77,84}
15000  1.000  0.216308 0.061556 {77,84}
15000  1.000  0.765699 0.093987 {96,97,98,99,100,101,102,103,104,105}
15000  1.000  0.277420 0.064312 {96,99,100,101,102,103,104,105}
15000  1.000  0.087775 0.029462 {96,99,100,101,102,103}
```

6420	0.428	0.013542	0.009189	{96,99,102}
14934	0.996	0.022119	0.009903	{96,99}
11310	0.754	0.017561	0.008287	{100,101,103}
9684	0.646	0.007392	0.003422	{100,103}
15000	1.000	0.182628	0.031823	{104,105}
15000	1.000	0.536864	0.072159	{97,98}
15000	1.000	0.944334	0.134918	{49,50,70,81}
14596	0.973	0.189827	0.078686	{49,50,81}
15000	1.000	0.358142	0.052483	{49,50}
15000	1.000	0.025579	0.013950	{1}
15000	1.000	0.058923	0.013852	{2}
15000	1.000	0.041926	0.009689	{3}
15000	1.000	0.203160	0.028333	{4}
15000	1.000	0.035778	0.009260	{5}
15000	1.000	0.034481	0.007289	{6}
15000	1.000	0.025891	0.006181	{7}
15000	1.000	0.056320	0.022649	{8}
15000	1.000	0.006051	0.003849	{9}
15000	1.000	0.030404	0.005467	{10}
15000	1.000	0.083446	0.016250	{11}
15000	1.000	0.028526	0.008377	{12}
15000	1.000	0.028534	0.006919	{13}
15000	1.000	0.081615	0.012933	{14}
15000	1.000	0.062512	0.008179	{15}
15000	1.000	0.019397	0.006991	{16}
15000	1.000	0.075799	0.013559	{17}
15000	1.000	0.037284	0.008345	{18}
15000	1.000	0.020955	0.005905	{19}
15000	1.000	0.004607	0.002520	{20}
15000	1.000	0.003440	0.002493	{21}
15000	1.000	0.061132	0.020881	{22}
15000	1.000	0.023186	0.006479	{23}
15000	1.000	0.137052	0.018285	{24}
15000	1.000	0.102082	0.017747	{25}
15000	1.000	0.001017	0.000979	{26}
15000	1.000	0.022246	0.005975	{27}
15000	1.000	0.058379	0.019774	{28}
15000	1.000	0.001134	0.001320	{29}
15000	1.000	0.118687	0.026883	{30}
15000	1.000	0.162009	0.032985	{31}
15000	1.000	0.335592	0.122612	{32}
15000	1.000	0.381237	0.074253	{33}
15000	1.000	0.742848	0.090163	{34}
15000	1.000	1.422144	0.266865	{35}

15000	1.000	1.012013	0.257094	{36}
15000	1.000	0.029831	0.006484	{37}
15000	1.000	0.072817	0.012715	{38}
15000	1.000	0.226437	0.051887	{39}
15000	1.000	0.025264	0.005443	{40}
15000	1.000	0.020017	0.005442	{41}
15000	1.000	0.029042	0.005031	{42}
15000	1.000	0.019450	0.007456	{43}
15000	1.000	0.050416	0.008312	{44}
15000	1.000	0.176275	0.019672	{45}
15000	1.000	0.075882	0.009392	{46}
15000	1.000	0.055528	0.011968	{47}
15000	1.000	0.071634	0.013844	{48}
15000	1.000	0.012916	0.010750	{49}
15000	1.000	0.055560	0.017975	{50}
15000	1.000	0.059147	0.009307	{51}
15000	1.000	0.518629	0.062503	{52}
15000	1.000	0.047707	0.022872	{53}
15000	1.000	0.051468	0.008637	{54}
15000	1.000	0.503456	0.071018	{55}
15000	1.000	0.522224	0.053113	{56}
15000	1.000	0.513874	0.055398	{57}
15000	1.000	1.123723	0.122881	{58}
15000	1.000	1.230378	0.140262	{59}
15000	1.000	0.477910	0.077983	{60}
15000	1.000	0.599741	0.062845	{61}
15000	1.000	0.653405	0.061809	{62}
15000	1.000	0.619907	0.070634	{63}
15000	1.000	0.354467	0.044036	{64}
15000	1.000	0.324985	0.048688	{65}
15000	1.000	0.450739	0.063098	{66}
15000	1.000	0.730437	0.094362	{67}
15000	1.000	0.810403	0.101741	{68}
15000	1.000	0.496793	0.072488	{69}
15000	1.000	0.482235	0.082907	{70}
15000	1.000	0.734604	0.048321	{71}
15000	1.000	0.582444	0.064821	{72}
15000	1.000	0.504268	0.065392	{73}
15000	1.000	0.493856	0.063971	{74}
15000	1.000	0.648753	0.092913	{75}
15000	1.000	0.327027	0.031054	{76}
15000	1.000	0.369007	0.071312	{77}
15000	1.000	0.894659	0.100229	{78}
15000	1.000	0.028816	0.006776	{79}

```
15000  1.000   0.211960 0.029770 {80}
15000  1.000   0.264354 0.045910 {81}
15000  1.000   0.677199 0.067476 {82}
15000  1.000   0.051264 0.014839 {83}
15000  1.000   0.929346 0.074076 {84}
15000  1.000   0.053571 0.013867 {85}
15000  1.000   0.034311 0.014027 {86}
15000  1.000   0.508950 0.069242 {87}
15000  1.000   0.484802 0.060396 {88}
15000  1.000   0.397716 0.066438 {89}
15000  1.000   0.529151 0.067819 {90}
15000  1.000   0.029625 0.021185 {91}
15000  1.000   0.056556 0.010498 {92}
15000  1.000   0.063320 0.017747 {93}
15000  1.000   0.026035 0.007520 {94}
15000  1.000   0.070652 0.023852 {95}
15000  1.000   0.001330 0.001169 {96}
15000  1.000   0.011901 0.010436 {97}
15000  1.000   0.092660 0.018941 {98}
15000  1.000   0.001156 0.001136 {99}
15000  1.000   0.023932 0.005789 {100}
15000  1.000   0.039188 0.007781 {101}
15000  1.000   0.035611 0.015606 {102}
15000  1.000   0.037878 0.007983 {103}
15000  1.000   0.046201 0.015117 {104}
15000  1.000   0.054314 0.015940 {105}
```

Newick Tree Format

```
************* Most probable tree in newick format *************
(((((((((((1:0.025579,86:0.034311):0.301039,(85:0.053571,92:0.056556):0.178923):
0.315974,(((32:0.335592,87:0.508950):0.098361,33:0.381237):1.782185,(83:0.0512
64,91:0.029625):0.554283):0.184088):0.126601,(((51:0.059147,54:0.051468):0.113
876,53:0.047707):0.361971,58:1.123723):0.212337):0.090626,(((((34:0.742848,68:
0.810403):0.091540,69:0.496793):0.079446,67:0.730437):0.138850,(((35:1.422144,
36:1.012013):1.370471,((65:0.324985,66:0.450739):0.135356,73:0.504268):0.1161
20):0.111246,(64:0.354467,74:0.493856):0.066330):0.181870):0.126314,(56:0.522
224,90:0.529151):0.103007):0.137191):0.101453,(((14:0.081615,(15:0.062512,17:0
.075799):0.018813):0.044087,(16:0.019397,18:0.037284):0.070274):0.475146,(((61
:0.599741,(62:0.653405,88:0.484802):0.298817):0.076532,(71:0.734604,89:0.3977
16):0.180167):0.119504,72:0.582444):0.109707):0.059494):0.057771,(((((((2:0.058
923,(3:0.041926,(5:0.035778,(6:0.034481,7:0.025891):0.082498):0.015314):0.0311
06):0.116443,4:0.203160):0.157685,(93:0.063320,95:0.070652):0.533018):0.10252
```

```
6,(((19:0.020955,(20:0.004607,21:0.003440):0.013831):0.012854,23:0.023186):0.0
53354,22:0.061132):0.345737):0.268388,(30:0.118687,31:0.162009):0.466275):0.1
23928,78:0.894659):0.140631,(((((8:0.056320,(9:0.006051,10:0.030404):0.129976)
:0.576871,(24:0.137052,25:0.102082):0.209422):0.256575,((11:0.083446,(12:0.028
526,13:0.028534):0.062673):0.333246,(76:0.327027,80:0.211960):0.223661):0.218
609):0.129484,((((26:0.001017,29:0.001134):0.028437,27:0.022246):0.048440,28:0
.058379):0.604965,((((((((37:0.029831,40:0.025264):0.019118,(41:0.020017,42:0.0
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:0.763093):0.199380):0.135435,39:0.226437):0.780852,(52:0.518629,55:0.503456):
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1):0.087775,(104:0.046201,105:0.054314):0.182628):0.277420,(97:0.011901,98:0.0
92660):0.536864):0.765699):0.188885):0.039321):0.134095):0.116116,(((49:0.012
916,50:0.055560):0.358142,81:0.264354):0.189827,70:0.482235):0.944334):0.1029
13,59:1.230378):0.099819,75:0.648753):0.513874,57:0.513874);
```
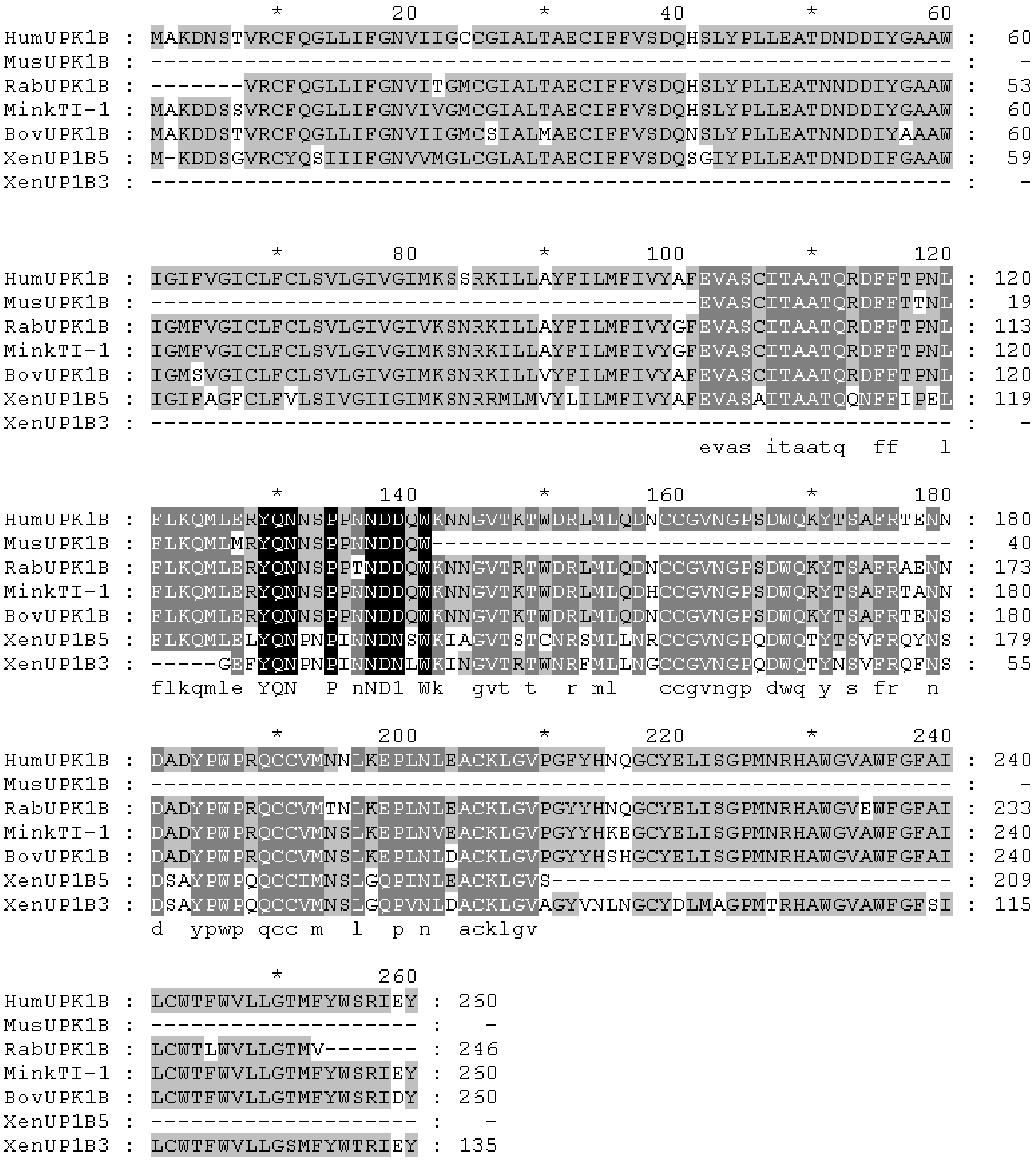

Appendix E

Amino Acid ClustalW Alignment of UPKIB Homologues



```
                    *        20         *        40         *        60
HumUPK1B : MAKDNSTVRCFQGLLIFGNVIIGCCGIALTAECIFFVSDQHSLYPLLEATDNDDIYGAAW :  60
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : -------VRCFQGLLIFGNVITGMCGIALTAECIFFVSDQHSLYPLLEATNNDDIYGAAW :  53
MinkTI-1 : MAKDDSSVRCFQGLLIFGNVIVGMCGIALTAECIFFVSDQHSLYPLLEATDNDDIYGAAW :  60
BovUPK1B : MAKDDSTVRCFQGLLIFGNVIIGMCSIALMAECIFFVSDQNSLYPLLEATNNDDIYAAAW :  60
XenUP1B5 : M-KDDSGVRCYQSIIIFGNVVMGLCGLALTAECIFFVSDQSGIYPLLEATDNDDIFGAAW :  59
XenUP1B3 : ------------------------------------------------------------ :   -

                    *        80         *       100         *       120
HumUPK1B : IGIFVGICLFCLSVLGIVGIMKSSRKILLAYFILMFIVYAFEVASCITAATQRDFFTPNL : 120
MusUPK1B : -----------------------------------------EVASCITAATQRDFFTTNL :  19
RabUPK1B : IGMFVGICLFCLSVLGIVGIVKSNRKILLAYFILMFIVYGFEVASCITAATQRDFFTPNL : 113
MinkTI-1 : IGMFVGICLFCLSVLGIVGIMKSNRKILLAYFILMFIVYGFEVASCITAATQRDFFTPNL : 120
BovUPK1B : IGMSVGICLFCLSVLGIVGIMKSNRKILLVYFILMFIVYAFEVASCITAATQRDFFTPNL : 120
XenUP1B5 : IGIFAGFCLFVLSIVGIIGIMKSNRRMLMVYLILMFIVYAFEVASAITAATQQNFFIPEL : 119
XenUP1B3 : ------------------------------------------------------------ :   -
                                                    evas itaatq  ff   l

                    *       140         *       160         *       180
HumUPK1B : FLKQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDNCCGVNGPSDWQKYTSAFRTENN : 180
MusUPK1B : FLKQMLMRYQNNSPPNNDDQW--------------------------------------- :  40
RabUPK1B : FLKQMLERYQNNSPPTNDDQWKNNGVTRTWDRLMLQDNCCGVNGPSDWQKYTSAFRAENN : 173
MinkTI-1 : FLKQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDHCCGVNGPSDWQRYTSAFRTANN : 180
BovUPK1B : FLKQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDNCCGVNGPSDWQKYTSAFRTENS : 180
XenUP1B5 : FLKQMLELYQNPNPINNDNSWKIAGVTSTCNRSMLLNRCCGVNGPQDWQTYTSVFRQYNS : 179
XenUP1B3 : -----GEFYQNPNPINNDNLWKINGVTRTWNRFMLLNGCCGVNGPQDWQTYNSVFRQFNS :  55
           flkqmle YQN  P nND1 Wk  gvt t  r ml   ccgvngp dwq y s fr  n

                    *       200         *       220         *       240
HumUPK1B : DADYPWPRQCCVMNNLKEPLNLEACKLGVPGFYHNQGCYELISGPMNRHAWGVAWFGFAI : 240
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : DADYPWPRQCCVMTNLKEPLNLEACKLGVPGYYHNQGCYELISGPMNRHAWGVEWFGFAI : 233
MinkTI-1 : DADYPWPRQCCVMNSLKEPLNVEACKLGVPGYYHKEGCYELISGPMNRHAWGVAWFGFAI : 240
BovUPK1B : DADYPWPRQCCVMNSLKEPLNLDACKLGVPGYYHSHGCYELISGPMNRHAWGVAWFGFAI : 240
XenUP1B5 : DSAYPWPQQCCIMNSLGQPINLEACKLGVS------------------------------ : 209
XenUP1B3 : DSAYPWPQQCCVMNSLGQPVNLDACKLGVAGYVNLNGCYDLMAGPMTRHAWGVAWFGFSI : 115
           d  ypwp qcc m  l  p n  acklgv

                    *       260
HumUPK1B : LCWTFWVLLGTMFYWSRIEY : 260
MusUPK1B : -------------------- :   -
RabUPK1B : LCWTLWVLLGTMV------- : 246
MinkTI-1 : LCWTFWVLLGTMFYWSRIEY : 260
BovUPK1B : LCWTFWVLLGTMFYWSRIDY : 260
XenUP1B5 : -------------------- :   -
XenUP1B3 : LCWTFWVLLGSMFYWTRIEY : 135
```

Appendix F

Nucleotide ClustalW Alignment of UPKIB Homologues

```
                    *        20         *        40         *        60
HumUPK1B : atggcgaaagacaactcaactgttcgttgcttccagggcctgctgatttttggaaatgtg :  60
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : ---------------------gttcgttgcttccagggcttgctgatttttggaaatgtg :  39
MinkTI-1 : atggcgaaagatgactcctctgttcgttgcttccagggcctgctgatttttggaaatgtg :  60
BovUPK1B : atggccaaagacgactccactgttcgttgcttccagggcctgctgatttttggaaatgtg :  60
XenUP1B5 : atg---aaggacgattctggagttcggtgttaccagtccatcattatcttcggcaatgtg :  57
XenUP1B3 : ------------------------------------------------------------ :   -

                    *        80         *       100         *       120
HumUPK1B : attattggttgttgcggcattgccctgactgcggagtgcatcttctttgtatctgaccaa : 120
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : attactggtatgtgtggcatcgccctgactgcagagtgcatcttctttgtatccgaccaa :  99
MinkTI-1 : attgttggtatgtgcggcatcgccctgaccgcagagtgcatcttcttcgtatctgaccag : 120
BovUPK1B : attatcggtatgtgcagcatcgccctgatggcagagtgcatcttctttgtatcagaccaa : 120
XenUP1B5 : gtcatggggctctgtggtttggccctgacggccgagtgcatcttctttgtgtcagaccag : 117
XenUP1B3 : ------------------------------------------------------------ :   -

                    *       140         *       160         *       180
HumUPK1B : cacagcctctacccactgcttgaagccaccgacaacgatgacatctatggggctgcctgg : 180
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : cacagcctctacccactgcttgaagccaccaacaatgacgacatctatggggctgcctgg : 159
MinkTI-1 : cacagcctctacccattgcttgaagccaccgacaacgatgacatctacggggcagcctgg : 180
BovUPK1B : aacagcctctacccactgcttgaagccaccaacaatgacgacatctatgcggcagcctgg : 180
XenUP1B5 : agtggcatctacccgctgctggaggctactgacaacgatgacatatttggcgccgcatgg : 177
XenUP1B3 : ------------------------------------------------------------ :   -

                    *       200         *       220         *       240
HumUPK1B : atcggcatatttgtgggcatctgcctcttctgcctgtctgttctaggcattgtaggcatc : 240
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : attggcatgtttgttggcatctgcctcttctgcctgtctgttctaggcattgtgggcatc : 219
MinkTI-1 : attggcatgtttgtcggcatctgcctcttctgtctgtccgttctaggcattgtaggcatc : 240
BovUPK1B : attggcatgtctgttggcatctgcctcttctgcctctctgtcctgggcatcgtaggcatc : 240
XenUP1B5 : attggcatctttgccggattctgtctcttcgtcttgtctatcgtcgggatcattggcatc : 237
XenUP1B3 : ------------------------------------------------------------ :   -

                    *       260         *       280         *       300
HumUPK1B : atgaagtccagcaggaaaattcttctggcgtatttcattctgatgtttatagtatatgcc : 300
MusUPK1B : ------------------------------------------------------------ :   -
RabUPK1B : gtgaagtccaacaggaaaatccttctggcgtatttcattctgatgtttatagtgtacggc : 279
MinkTI-1 : atgaagtccaacaggaaaattcttctggcgtatttcattctgatgtttatagtatatggc : 300
BovUPK1B : atgaagtccaacaggaaaattcttctggtgtatttcatcctgatgtttattgtatatgct : 300
XenUP1B5 : atgaagtcgaacaggagaatgctgatggtgtatctcatcctgatgttcattgtgtatgcc : 297
XenUP1B3 : ------------------------------------------------------------ :   -

                    *       320         *       340         *       360
HumUPK1B : tttgaagtggcatcttgtatcacagcagcaacacaacgagactttttcacacccaacctc : 360
MusUPK1B : ---gaagtggcatcttgtatcacagcagcaacacaacgcgactttttcacaaccaacctc :  57
RabUPK1B : tttgaagtggcatcttgtatcacagctgcaacacaacgagactttttcacacccaacctc : 339
MinkTI-1 : tttgaagtggcatcttgtatcacagcagcaacacaacgagacttcttcacgcccaacctc : 360
BovUPK1B : tttgaagtggcatcttgtatcacagcagcaacacaacgagactttttcacacccaacctc : 360
XenUP1B5 : ttcgaagtggcctctgccatcactgctgcaactcaacaaaattttttcattccagagctc : 357
XenUP1B3 : ------------------------------------------------------------ :   -
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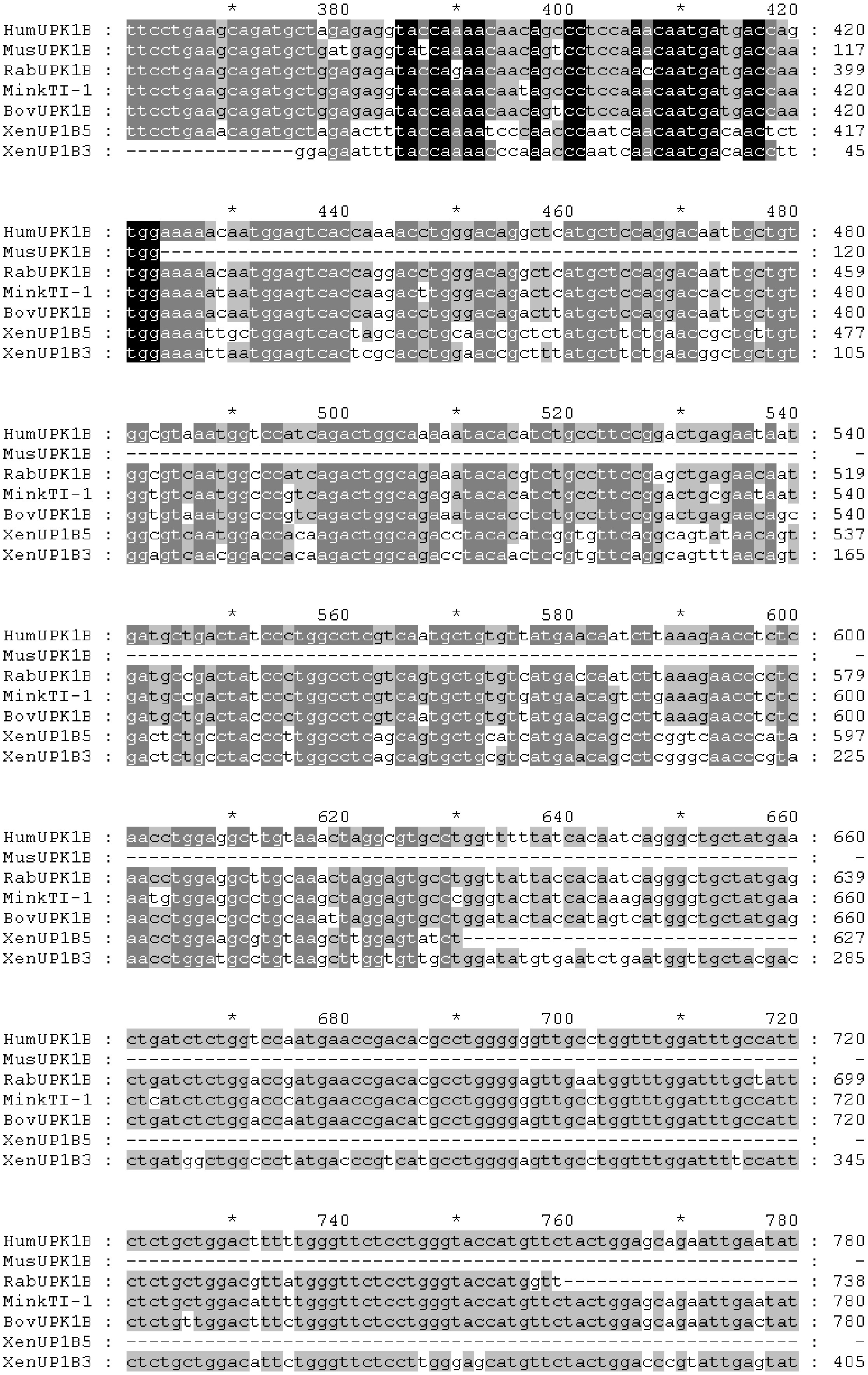

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                    *       380         *       400         *       420
HumUPK1B : ttcctgaagcagatgctagagaggtaccaaaacaacagccctccaaacaatgatgaccag :  420
MusUPK1B : ttcctgaagcagatgctgatgaggtatcaaaacaacagtcctccaaacaatgatgaccaa :  117
RabUPK1B : ttcctgaagcagatgctggagagataccagaacaacagccctccaaccaatgatgaccaa :  399
MinkTI-1 : ttcctgaagcagatgctggagaggtaccaaaacaatagccctccaaacaatgatgaccaa :  420
BovUPK1B : ttcctgaagcagatgctggagagataccaaaacaacagtcctccaaacaatgatgaccaa :  420
XenUP1B5 : ttcctgaaacagatgctagaactttaccaaaatcccaacccaatcaacaatgacaactct :  417
XenUP1B3 : ---------------ggagaatttaccaaaacccaaacccaatcaacaatgacaacctt :   45

                    *       440         *       460         *       480
HumUPK1B : tggaaaaacaatggagtcaccaaaacctgggacaggctcatgctccaggacaattgctgt :  480
MusUPK1B : tgg--------------------------------------------------------- :  120
RabUPK1B : tggaaaaacaatggagtcaccaggacctgggacaggctcatgctccaggacaattgctgt :  459
MinkTI-1 : tggaaaaataatggagtcaccaagacttgggacagactcatgctccaggaccactgctgt :  480
BovUPK1B : tggaaaaacaatggagtcaccaagacctgggacagacttatgctccaggacaattgctgt :  480
XenUP1B5 : tggaaaattgctggagtcactagcacctgcaaccgctctatgcttctgaaccgctgttgt :  477
XenUP1B3 : tggaaaattaatggagtcactcgcacctggaaccgctttatgcttctgaacggctgctgt :  105

                    *       500         *       520         *       540
HumUPK1B : ggcgtaaatggtccatcagactggcaaaaatacacatctgccttccggactgagaataat :  540
MusUPK1B : ------------------------------------------------------------ :    -
RabUPK1B : ggcgtcaatggcccatcagactggcagaaatacacgtctgccttccgagctgagaacaat :  519
MinkTI-1 : ggtgtcaatggcccgtcagactggcagagatacacatctgccttccggactgcgaataat :  540
BovUPK1B : ggtgtaaatggcccgtcagactggcagaaatacacctctgccttccggactgagaacagc :  540
XenUP1B5 : ggcgtcaatggaccacaagactggcagacctacacatcggtgttcaggcagtataacagt :  537
XenUP1B3 : ggagtcaacggaccacaagactggcagacctacaactccgtgttcaggcagtttaacagt :  165

                    *       560         *       580         *       600
HumUPK1B : gatgctgactatccctggcctcgtcaatgctgtgttatgaacaatcttaaagaacctctc :  600
MusUPK1B : ------------------------------------------------------------ :    -
RabUPK1B : gatgccgactatccctggcctcgtcagtgctgtgtcatgaccaatcttaaagaacccctc :  579
MinkTI-1 : gatgccgactatccctggcctcgtcagtgctgtgtgatgaacagtctgaaagaacctctc :  600
BovUPK1B : gatgctgactacccctggcctcgtcaatgctgtgttatgaacagccttaaagaacctctc :  600
XenUP1B5 : gactctgcctacccttggcctcagcagtgctgcatcatgaacagcctcggtcaacccata :  597
XenUP1B3 : gactctgcctacccttggcctcagcagtgctgcgtcatgaacagcctcgggcaacccgta :  225

                    *       620         *       640         *       660
HumUPK1B : aacctggaggcttgtaaactaggcgtgcctggtttttatcacaatcagggctgctatgaa :  660
MusUPK1B : ------------------------------------------------------------ :    -
RabUPK1B : aacctggaggcttgcaaactaggagtgcctggttattaccacaatcagggctgctatgag :  639
MinkTI-1 : aatgtggaggcctgcaagctaggagtgcccgggtactatcacaaagaggggtgctatgaa :  660
BovUPK1B : aacctggacgcctgcaaattaggagtgcctggatactaccatagtcatggctgctatgag :  660
XenUP1B5 : aacctggaagcgtgtaagcttggagtatct------------------------------ :  627
XenUP1B3 : aacctggatgcctgtaagcttggtgttgctggatatgtgaatctgaatggttgctacgac :  285

                    *       680         *       700         *       720
HumUPK1B : ctgatctctggtccaatgaaccgacacgcctggggggttgcctggtttggatttgccatt :  720
MusUPK1B : ------------------------------------------------------------ :    -
RabUPK1B : ctgatctctggaccgatgaaccgacacgcctggggagttgaatggtttggatttgctatt :  699
MinkTI-1 : ctcatctctggacccatgaaccgacacgcctggggggttgcctggtttggatttgccatt :  720
BovUPK1B : ctgatctctggaccaatgaaccgacatgcctggggagttgcatggtttggatttgccatt :  720
XenUP1B5 : ------------------------------------------------------------ :    -
XenUP1B3 : ctgatggctggccctatgacccgtcatgcctggggagttgcctggtttggattttccatt :  345

                    *       740         *       760         *       780
HumUPK1B : ctctgctggactttttgggttctcctgggtaccatgttctactggagcagaattgaatat :  780
MusUPK1B : ------------------------------------------------------------ :    -
RabUPK1B : ctctgctggacgttatgggttctcctgggtaccatggtt--------------------- :  738
MinkTI-1 : ctctgctggacattttgggttctcctgggtaccatgttctactggagcagaattgaatat :  780
BovUPK1B : ctctgttggactttctgggttctcctgggtaccatgttctactggagcagaattgactat :  780
XenUP1B5 : ------------------------------------------------------------ :    -
XenUP1B3 : ctctgctggacattctgggttctccttgggagcatgttctactggacccgtattgagtat :  405
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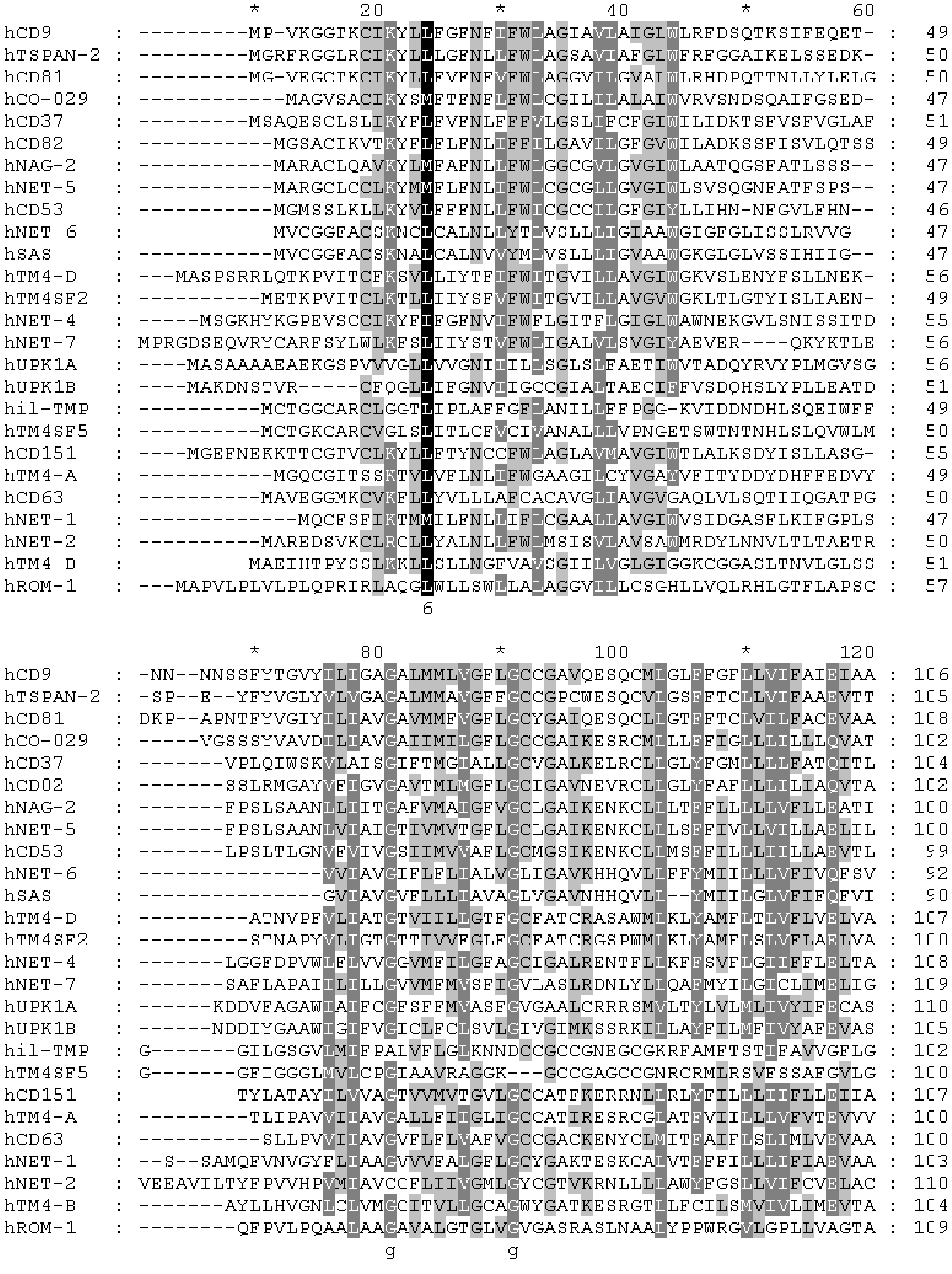
]]>

Appendix G

Amino Acid ClustalW Alignment of Human Tetraspanins



```
                    *        20         *        40         *        60
hCD9     : ---------MP-VKGGTKCIKYLLFGFNFIFWLAGIAVLAIGLWLRFDSQTKSIFEQET- :  49
hTSPAN-2 : ---------MGRFRGGLRCIKYLLLGFNLLFWLAGSAVIAFGLWFRFGGAIKELSSEDK- :  50
hCD81    : ---------MG-VEGCTKCIKYLLFVFNFVFWLAGGVILGVALWLRHDPQTTNLLYLELG :  50
hCO-029  : ------------MAGVSACIKYSMFTFNFLFWLCGILILALAIWVRVSNDSQAIFGSED- :  47
hCD37    : ---------MSAQESCLSLIKYFLFVFNLFFFVLGSLIFCFGIWILIDKTSFVSFVGLAF :  51
hCD82    : -----------MGSACIKVTKYFLFLFNLIFFILGAVILGFGVWILADKSSFISVLQTSS :  49
hNAG-2   : -----------MARACLQAVKYLMFAFNLLFWLGGCGVLGVGIWLAATQGSFATLSSS-- :  47
hNET-5   : -----------MARGCLCCLKYMMFLFNLIFWLCGCGLLGVGIWLSVSQGNFATFSPS-- :  47
hCD53    : -----------MGMSSLKLLKYVLFFFNLLFWICGCCILGFGIYLLIHN-NFGVLFHN-- :  46
hNET-6   : -----------MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVG-- :  47
hSAS     : -----------MVCGGFACSKNALCALNVVYMLVSLLLIGVAAWGKGLGLVSSIHIIG-- :  47
hTM4-D   : ---MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEK- :  56
hTM4SF2  : ----------METKPVITCLKTLLIIYSFVFWITGVILLAVGVWGKLTLGTYISLIAEN- :  49
hNET-4   : -----MSGKHYKGPEVSCCIKYFIFGFNVIFWFLGITFLGIGLWAWNEKGVLSNISSITD :  55
hNET-7   : MPRGDSEQVRYCARFSYLWLKFSLIIYSTVFWLIGALVLSVGIYAEVER----QKYKTLE :  56
hUPK1A   : ----MASAAAAEAEKGSPVVVGLLVVGNIIILLSGLSLFAETIWVTADQYRVYPLMGVSG :  56
hUPK1B   : ----MAKDNSTVR-----CFQGLLIFGNVIIGCCGIALTAECIFFVSDQHSLYPLLEATD :  51
hil-TMP  : ----------MCTGGCARCLGGTLIPLAFFGFLANILLFFPGG-KVIDDNDHLSQEIWFF :  49
hTM4SF5  : ----------MCTGKCARCVGLSLITLCFVCIVANALLIVPNGETSWTNTNHLSLQVWLM :  50
hCD151   : ----MGEFNEKKTTCGTVCLKYLLFTYNCCFWLAGLAVMAVGIWTLALKSDYISLLASG- :  55
hTM4-A   : -----------MGQCGITSSKTVLVFLNLIFWGAAGILCYVGAYVFITYDDYDHFFEDVY :  49
hCD63    : ----------MAVEGGMKCVKFLLYVLLLAFCACAVGLIAVGVGAQLVLSQTIIQGATPG :  50
hNET-1   : -------------MQCFSFIKTMMILFNLLIFLCGAALLAVGIWVSIDGASFLKIFGPLS :  47
hNET-2   : ----------MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETR :  50
hTM4-B   : ---------MAEIHTPYSSLKKLLSLLNGFVAVSGIILVGLGIGGKCGGASLTNVLGLSS :  51
hROM-1   : ---MAPVLPLVLPLQPRIRLAQGLWLLSWLLALAGGVIILCSGHLLVQLRHLGTFLAPSC :  57
                                  6

                    *        80         *       100         *       120
hCD9     : -NN--NNSSFYTGVYILIGAGALMMLVGFLGCCGAVQESQCMLGLFFGFLLVIFAIEIAA : 106
hTSPAN-2 : -SP--E--YFYVGLYVLVGAGALMMAVGFFGCCGPCWESQCVLGSFFTCLLVIFAAEVTT : 105
hCD81    : DKP--APNTFYVGIYILIAVGAVMMFVGFLGCYGAIQESQCLLGTFFTCLVILFACEVAA : 108
hCO-029  : -----VGSSSYVAVDILIAVGAIIMILGFLGCCGAIKESRCMLLLFFIGLLLILLLQVAT : 102
hCD37    : -------VPLQIWSKVLAISGIFTMGIALLGCVGALKELRCLLGLYFGMLLLLFATQITL : 104
hCD82    : -------SSLRMGAYVFIGVGAVTMLMGFLGCIGAVNEVRCLLGLYFAFLLLILIAQVTA : 102
hNAG-2   : -------FPSLSAANLLIITGAFVMAIGFVGCLGAIKENKCLLLTFFLLLLLVFLLEATI : 100
hNET-5   : -------FPSLSAANLVIAIGTIVMVTGFLGCLGAIKENKCLLLSFFIVLLVILLAELIL : 100
hCD53    : -------LPSLTLGNVFVIVGSIIMVVAFLGCMGSIKENKCLLMSFFILLLIILLAEVTL :  99
hNET-6   : ---------------VVIAVGIFLFLIALVGLIGAVKHHQVLLFFYMIILLLVFIVQFSV :  92
hSAS     : ---------------GVIAVGVFLLLIAVAGLVGAVNHHQVLL--YMIILGLVFIFQFVI :  90
hTM4-D   : ---------ATNVPFVLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVA : 107
hTM4SF2  : ---------STNAPYVLIGTGTTIVVFGLFGCFATCRGSPWMLKLYAMFLSLVFLAELVA : 100
hNET-4   : -------LGGFDPVWLFLVVGGVMFILGFAGCIGALRENTFLLKFFSVFLGIIFFLELTA : 108
hNET-7   : -------SAFLAPAIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIG : 109
hUPK1A   : ------KDDVFAGAWIAIFCGFSFFMVASFGVGAALCRRRSMVLTYLVLMLIVYIFECAS : 110
hUPK1B   : ------NDDIYGAAWIGIFVGICLFCLSVLGIVGIMKSSRKILLAYFILMFIVYAFEVAS : 105
hil-TMP  : G-------GILGSGVLMIFPALVFLGLKNNDCCGCCGNEGCGKRFAMFTSTIFAVVGFLG : 102
hTM4SF5  : G-------GFIGGGLMVLCPGIAAVRAGGK---GCCGAGCCGNRCRMLRSVFSSAFGVLG : 100
hCD151   : --------TYLATAYILVVAGTVVMVTGVLGCCATFKERRNLLRLYFILLLIIFLLEIIA : 107
hTM4-A   : ---------TLIPAVVIIAVGALLFIIGLIGCCATIRESRCGLATFVIILLLVFVTEVVV : 100
hCD63    : ----------SLLPVVIIAVGVFLFLVAFVGCCGACKENYCLMITFAIFLSLIMLVEVAA : 100
hNET-1   : --S--SAMQFVNVGYFLIAAGVVVFALGFLGCYGAKTESKCALVTFFFILLLIFIAEVAA : 103
hNET-2   : VEEAVILTYFPVVHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELAC : 110
hTM4-B   : -------AYLLHVGNLCLVMGCITVLLGCAGWYGATKESRGTLLFCILSMVIVLIMEVTA : 104
hROM-1   : --------QFPVLPQAALAAGAVALGTGLVGVGASRASLNAALYPPWRGVLGPLLVAGTA : 109
                               g         g
```

```
                     *       140         *       160         *       180
hCD9      : A-----IWGYSHKDEVIKEV-QEFYKDTYN-KLKTKDEPQR---------ETLKAIHYAL : 150
hTSPAN-2  : G-----VFAFIGKGVAIRHV-QTMYEEAYNDYLKDRGKGNG---------TLITFPLQHF : 150
hCD81     : G-----IWGFVNKDQIAKDV-KQFYDQALQQAVVDDDANNAK--------AVVKTFHETL : 154
hCO-029   : G-----ILGAVFKSKSDRIVNETLYENTKLLSATGESEKQFQ--------EAIIVFQEEF : 149
hCD37     : G-----ILISTQRAQLERSL-RDVVEKTIQKYGTNPEETAAE--------ESWDYVQFQL : 150
hCD82     : G-----ALFYFNMGKLKQEM-GGIVTELIRDYNSSRED-SLQ--------DAWDYVQAQV : 147
hNAG-2    : A-----ILFFAYTDKIDRYA-QQDLKKGLHLYGT-QGNVGLT--------NAWSIIQTDF : 145
hNET-5    : L-----ILFFVYMDKVNENA-KKDLKEGLLLYHT-ENNVGLK--------NAWNIIQAEM : 145
hCD53     : A-----ILLFVYEQKLNEYV-AKGLTDSIHRYHS-DNST--K--------AAWDSIQSFL : 142
hNET-6    : S-----CACLALNQEQQGQL------------LEVGWNNTAS---------ARNDIQRNL : 126
hSAS      : S-----CSCLAINRSKQTDV------------INASWWVMSN--------KTRDELERSF : 125
hTM4-D    : A-----IVGFVFRHEIKNSF-KNNYEKALKQYNSTGDYRSH----------AVDKIQNTL : 151
hTM4SF2   : G-----ISGFVFRHEIKDTF-LRTYTDAMQTYNGN-DERSR----------AVDHVQRSL : 143
hNET-4    : G-----VLAFVFKDWIKDQL----YFFINNNIRAYRDDIDLQ--------NLIDFTQEYW : 151
hNET-7    : G-----VVALTFRNQTIDFL----NDNIRRGIENYYDDLDFK--------NIMDFVQKKF : 152
hUPK1A    : C-----ITSYTHRDYMVSNP-SLITKQMLTFYSADTDQGQE-------LTRLWDRVMIEQ : 157
hUPK1B    : C-----ITAATQRDFFTPN---LFLKQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQD : 157
hil-TMP   : A-----GYSFIISAISINKG-----PKCLMANSTWGYPFHD---------GDYLNDEALW : 143
hTM4SF5   : A-----IYCLSVSGAGLRNG-----PRCLMN-GEWGYHFEDT-------AGAYLLNRTLW : 142
hCD151    : G-----ILAYAYYQQLNTELKENLKDTMTRRYHQSGHEAVTS---------AVDQLQQEF : 153
hTM4-A    : V-----VLGYVYRAKVENEV-DRSIQKVYKTYNGTNPDAASR---------AIDYVQRQL : 145
hCD63     : A-----IAGYVFRDKVMSEF----NNNFRQQMENYPKNNHTAS--------ILDRMQADF : 143
hNET-1    : A-----VVALVYTTMAEHFLTLLVVPAIKKDYGSQEDFTQ-----------VWNTTMKGL : 147
hNET-2    : G-----VWTYEQELMVPVQWSDMVTLKARMTNYGLPRYRWLT--------HAWNFFQREF : 157
hTM4-B    : A-----TVVLLFFPIVGDVALEHTFVTLRKNYRGYNEPDDYS--------TQWNLVMEKL : 151
hROM-1    : GGGGLLVVALGLALALPGSLDEALEEGLVTALAHYKDTEVPG---HCQAKRLVDELQLRY : 166

                     *       200         *       220         *       240
hCD9      : NCCG-------------LAGGVEQFISDICPKK-DVL----------------------- : 173
hTSPAN-2  : QCCG-------------KES--SEQVQPTCPK---------------------------- : 167
hCD81     : DCCGSST---------LTALTTSVLKNNLCPSGSNII----------------------- : 182
hCO-029   : KCCGLVNGAADWGNNFQHYPELCACLDKQRPCQSYNG----------------------- : 186
hCD37     : RCCGWHYPQDWFQVLILRGNGSEAHRVPCSCYNLSATNDSTILDKVILPQL-------SR : 203
hCD82     : KCCGWVSFYNWTDNAELMNRPEVTY--PCSCEVKGEEDNSLSVRKGFCEAP--------- : 196
hNAG-2    : RCCGVSNYTDWFEVYNATRVP------DSCCLEFSES----------------------- : 176
hNET-5    : RCCGVTDYTDWYPVLGENTVP------DRCCMENSQG----------------------- : 176
hCD53     : QCCGINGTSDW------TSGP------PASCPSDRK------------------------ : 166
hNET-6    : NCCG-----------FRSVN-----PNDTCLASCVK------------------------ : 146
hSAS      : DCCG-----------LFNLTTLYQQDYDFCTAICKS------------------------ : 150
hTM4-D    : HCCGVTDYRDWTDTNYYSEKGFPKSCCKLE-DCTPQ------------------------ : 186
hTM4SF2   : SCCGVQNYTNWSTSPYFLEHGIPPSCCMNETDCNPQDLHNL------------------- : 184
hNET-4    : QCCGAFGADDWNLNIYFNCTDSNASRERCGVPFSCCTKDPAEDVINTQCG---------- : 201
hNET-7    : KCCGGEDYRDWSKNQYHDCSAPGP--LACGVPYTCCIRN-TTEVVNTMCG---------- : 199
hUPK1A    : ECCGTSGPMDWVNFTSAFRAATPEVVFPWPPLCCRRTGNFIPLNEEG------------- : 204
hUPK1B    : NCCGVNGPSDWQKYTSAFRTENNDADYPWPRQCCVMNNLKEPLNLEA------------- : 204
hil-TMP   : NKCR-------------------------------------------------------- : 147
hTM4SF5   : DRCE-------------------------------------------------------- : 146
hCD151    : HCCGSNNSQDWRDSEWIRSQEAGGRVVPDSCCKTVVALCGQ------------------- : 194
hTM4-A    : HCCGIHNYSDWENTDWFKETKNQSVPLSCCRETASNCNG--------------------- : 184
hCD63     : KCCGAANYTDWEKIPSMSKNRVPDSCCINVTVGCGINFN--------------------- : 182
hNET-1    : KCCGFTNYTDFEDSPYFKENSAFPPFCCNDNVTNTANET--------------------- : 186
hNET-2    : KCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQED-------------------- : 197
hTM4-B    : KCCGVNNYTDFSGSSFEMTTGHTYPRSCCKSIGSVSCDG--------------------- : 190
hROM-1    : HCCGRHGYKDWFGVQWVSSRYLDPGDRDVADRIQSNVEGLYLTDGVPFSCCNPHSPRPCL : 226
               cCg
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                    *       260         *       280         *       300
hCD9     : -------------------ETFTVKSCPDAIKEVFD---NKFHIIGAVGIGIAVVMIFGM : 211
hTSPAN-2 : -------------------ELLRHKNCIDEIETIIS---VKLQLIGIVGIGIAGLTIFGM : 205
hCD81    : -------------------SNLFKEDCHQKIDDLFS---GKLYLIGIAAIVVAVIMIFEM : 220
hCO-029  : -------------------KQVYKETCISFIKDFLA---KNLIIVIGISFGLAVIEILGL : 224
hCD37    : LGHLARSRHSADICAVPAESHIYREGCAQGLQKWLH---NNLISIVGICLGVGLLELGFM : 260
hCD82    : -GNRTQSGN------HPEDWPVYQEGCMEKVQAWLQ---ENLGIILGVGVGVAMVELLGM : 246
hNAG-2   : -------------CGLHAPGTWWKAPCYETVKVWLQ---ENLLAVGIFGLCTALVQILGL : 220
hNET-5   : -------------CGRNATTPLWRTGCYEKVKMWFD---DNKHVLGTVGMCILIMQILGM : 220
hCD53    : -----------------------VEGCYAKARLWFH---SNFLYIGIITICVCVIEVLGM : 200
hNET-6   : -------------------SDHSCSPCAPIIGEYAG---EVLRFVGGIGLFFSFTEILGV : 184
hSAS     : -------------------QSPTCQMCGEKFLKHSD---EALKILGGVGLFFSFTEILGV : 188
hTM4-D   : ----------------RDADKVNNEGCFIKVMTIIE---SEMGVVAGISFGVACFQLIGI : 227
hTM4SF2  : ---------------TVAATKVNQKGCYDLVTSFME---TNMGIIAGVAFGIAFSQLIGM : 226
hNET-4   : -------YDARQKPEVDQQIVIYTKGCVPQFEKWLQ---DNLTIVAGIFIGIALLQIFGI : 251
hNET-7   : -------YKTIDKERFSVQDVIYVRGCTNAVIIWFM---DNYTIMAGILLGILLPQFLGV : 249
hUPK1A   : -------------CRLGHMDYLFTKGCFEHIGHAID---SYTWGISWFGFAILMWTLPVM : 248
hUPK1B   : -------------CKLGVPGFYHNQGCYELISGPMN---RHAWGVAWFGFAILCWTFWVL : 248
hil-TMP  : -----------------------EPLNVVPWNLTLF---SILLVVGGIQMVLCAIQVVNG : 181
hTM4SF5  : -----------------------APPRVVPWNVTLF---SLLVAASCLEIVLCGIQLVNA : 180
hCD151   : -------------RDHASNIYKVEGGCITKLETFIQ---EHLRVIGAVGIGIACVQVFGM : 238
hTM4-A   : --------------SLAHPSDLYAEGCEALVVKKLQ---EIMMHVIWAALAFAAIQLLGM : 227
hCD63    : ------------------EKAIHKEGCVEKIGGWLR---KNVLVVAAAALGIAFVEVLGI : 221
hNET-1   : -------------CTKQKAHDQKVEGCFNQLLYDIR---TNAVTVGGVAAGIGGLELAAM : 230
hNET-2   : ------------------LSDLYQEGCGKKMYSFLRGT-KQLQVLRFLGISIGVTQILAM : 238
hTM4-B   : --------------RDVSPNVIHQKGCFHKLLKITK---TQSFTLSGSSLGAAVIQRWGS : 233
hROM-1   : QNRLSDSYAHPLFDPRQPNQNLWAQGCHEVLLEHLQDLAGTLGSMLAVTFLLQALVLLGL : 286
                                     c

                    *       320         *       340         *       360
hCD9     : IFSMILCCAIRRNREMV------------------------------------------- : 228
hTSPAN-2 : IFSMVLCCAIRNSRDVI------------------------------------------- : 222
hCD81    : ILSMVLCCGIRNSSVY-------------------------------------------- : 236
hCO-029  : VFSMVLYCQIGNK----------------------------------------------- : 237
hCD37    : TLSIFLCRNLD-HVYNRLARYR-------------------------------------- : 281
hCD82    : VLSICLCRHVHSEDYSKVPKY--------------------------------------- : 267
hNAG-2   : TFAMTMYCQVVKA-DTYCA----------------------------------------- : 238
hNET-5   : AFSMTLFQHIHRTGKKYDA----------------------------------------- : 239
hCD53    : SFALTLNCQIDKTSQTIGL----------------------------------------- : 219
hNET-6   : WLTYRYRNQKDPRANPS----------------AFL------------------------ : 204
hSAS     : WLAMRFRNQKDPRATPVPXYETLDPSDXLLLSLSFLFLP--------------------- : 227
hTM4-D   : FLAYCLSRAITNNQYEIV------------------------------------------ : 245
hTM4SF2  : LLACCLSRFITANQYEMV------------------------------------------ : 244
hNET-4   : CLAQNLVSDIEAVRASW------------------------------------------- : 268
hNET-7   : LLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN--------------- : 294
hUPK1A   : LIAMYFYTML-------------------------------------------------- : 258
hUPK1B   : LGTMFYWSRIEY------------------------------------------------ : 260
hil-TMP  : LLGTLCGDCQCCGCCGGDGPV--------------------------------------- : 202
hTM4SF5  : TIGVFCGDCRKK----QDTPH--------------------------------------- : 197
hCD151   : IFTCCLYRSLKLEHY--------------------------------------------- : 253
hTM4-A   : LCACIVLCRRSRDPAYELLITGGTYA---------------------------------- : 253
hCD63    : VFACCLVKSIRSGYEVM------------------------------------------- : 238
hNET-1   : IVSMYLYCNLQ------------------------------------------------- : 241
hNET-2   : ILTITLLWALYYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNT : 298
hTM4-B   : RYVAQAGLELLA------------------------------------------------ : 245
hROM-1   : RYLQTALEGLGGVIDAGGETQGYLFPSGLKDMLKTAWLQGGVACRPAPEEAPPGEAPPKE : 346
```

```
hCD9     : ------- :   -
hTSPAN-2 : ------- :   -
hCD81    : ------- :   -
hCO-029  : ------- :   -
hCD37    : ------- :   -
hCD82    : ------- :   -
hNAG-2   : ------- :   -
hNET-5   : ------- :   -
hCD53    : ------- :   -
hNET-6   : ------- :   -
hSAS     : ------- :   -
hTM4-D   : ------- :   -
hTM4SF2  : ------- :   -
hNET-4   : ------- :   -
hNET-7   : ------- :   -
hUPK1A   : ------- :   -
hUPK1B   : ------- :   -
hil-TMP  : ------- :   -
hTM4SF5  : ------- :   -
hCD151   : ------- :   -
hTM4-A   : ------- :   -
hCD63    : ------- :   -
hNET-1   : ------- :   -
hNET-2   : HFEMEEL : 305
hTM4-B   : ------- :   -
hROM-1   : DLSEA-- : 351
```

Appendix H

Nucleotide ClustalW Alignment of Human Tetraspanins

```
                      *        20         *        40         *        60
hCD9       : ------------------------------atgccggtcaaaggaggcaccaagtgcatc :   30
hCD37      : ---------------------------atgtcagcccaggagagctgcctcagcctcatc :   33
hCD53      : ---------------------------------atgggcatgagtagcttgaaactgctg :   27
hCD63      : ------------------------------atggcggtggaaggaggaatgaaatgtgtg :   30
hCD81      : ------------------------------atgggagtggagggctgcaccaagtgcatc :   30
hCD82      : ---------------------------------atgggctcagcctgtatcaaagtcacc :   27
hCD151     : ------------atgggtgagttcaacgagaagaagacaacatgtggcaccgtttgcctc :   48
hCO-029    : ------------------------------------atggcaggtgtgagtgcctgtata :   24
hNAG-2     : ---------------------------------atggcgcgcgcctgcctccaggccgtc :   27
hNET-1     : ---------------------------------------atgcagtgcttcagcttcatt :   21
hNET-2     : ------------------------------atggccagagaagattccgtgaagtgtctg :   30
hNET-4     : ---------------atgtccgggaagcactacaagggtcctgaagtcagttgttgcatc :   45
hNET-5     : ---------------------------------atggccaggggctgcctctgctgcttg :   27
hNET-6     : ---------------------------------atggtttgcgggggcttcgcgtgttcc :   27
hNET-7     : atgccgcgcggggactcggagcaggtgcgctactgcgcgcgcttctcctacctctggctc :   60
hil-TMP    : ------------------------------atgtgcactgggggctgtgccagatgcctg :   30
hROM-1     : ---------------------------atggcgccggtgttgcccctggtgctgcccctg :   33
hSAS       : ---------------------------------atggtttgtggcggctttgcctgctcc :   27
Hum        : ---------------------------------atgggccagtgcggcatcacctcctcc :   27
hTM4-B     : ---------------------------atggctgaaatccacactccgtattcttccttg :   33
hTM4-D     : ---------atggcgtccccgtctcggagactgcagactaaaccagtcattacttgtttc :   51
hTM4SF2    : ------------------------------atggagaccaaacctgtgataacctgtctc :   30
hTM4SF5    : ------------------------------atgtgtacgggaaaatgtgcccgctgtgtg :   30
hTSPAN-2   : ---------------------------atggggcgcttccgcgggggcctgcggtgcatc :   33
hUPK1A     : ------------atggcgtctgcggcagcagcggaggccgagaagggatctccagttgtg :   48
hUPK1B     : ---------------------------atggcgaaagacaactcaactgttcgttgcttc :   33
                                                                        t

                      *        80         *       100         *       120
hCD9       : aaatacctgctgttcggatttaacttcatcttctggcttgccgggattgctgtccttgcc :   90
hCD37      : aagtacttcctcttcgttttcaacctcttcttcttcgtcctcggcagcctgatcttctgc :   93
hCD53      : aagtatgtcctgtttttcttcaacttgctcttttggatctgtggctgctgcattttgggc :   87
hCD63      : aagttcttgctctacgtcctcctgctggccttttgcgcctgtgcagtgggactgattgcc :   90
hCD81      : aagtacctgctcttcgtcttcaatttcgtcttctggctggctggaggcgtgatcctgggt :   90
hCD82      : aaatactttctcttcctcttcaacttgatcttctttatcctgggcgcagtgatcctgggc :   87
hCD151     : aagtacctgctgtttacctacaattgctgcttctggctggctggcctggctgtcatggca :  108
hCO-029    : aaatattctatgtttaccttcaacttcttgttctggctatgtggtatcttgatcctagca :   84
hNAG-2     : aagtacctcatgttcgccttcaacctgctcttctggctgggaggctgtggcgtgctgggt :   87
hNET-1     : aagaccatgatgatcctcttcaatttgctcatctttctgtgtggtgcagccctgttggca :   81
hNET-2     : cgctgcctgctctacgccctcaatctgctcttttggttaatgtccatcagtgtgttggca :   90
hNET-4     : aaatacttcatatttggcttcaatgtcatattttggtttttgggaataacatttcttgga :  105
hNET-5     : aagtacatgatgttcctcttcaatttgatattctggctctgtggctgtgggctgctggga :   87
hNET-6     : aagaactgcctgtgcgccctcaacctgctttacaccttggttagtctgctgctaattgga :   87
hNET-7     : aagttttcacttatcatctattccaccgtgttctggctgattggggccctggtcctgtct :  120
hil-TMP    : ggggggaccctcattccccttgcttttttttggcttcctggctaacatcctgttatttttt :   90
hROM-1     : cagccccgcatccgcctggcacaagggctctggctcctctcctggctgctggcgctggct :   93
hSAS       : aagaatgcgctttgcgctctcaacgtggtctacatgctggtgagcttgttgctcattgga :   87
Hum        : aagaccgtgctggtctttctcaacctcatcttctggggggcagctggcattttatgctat :   87
hTM4-B     : aagaaactgttatctttactcaatggcttcgtggctgtgtctggcatcatcctagttggc :   93
hTM4-D     : aagagcgttctgctaatctacactttttattttctggatcactggcgttatccttcttgca :  111
hTM4SF2    : aaaaccctcctcatcatctactccttcgtcttctggatcactggggtgatcctgctggct :   90
hTM4SF5    : gggctctccctcattaccctctgcttcgtctgcattgtggccaacgccctcctgctggta :   90
hTSPAN-2   : aagtacctgctgcttggcttcaacctgctcttctggctggctggatcggccgtcattgct :   93
hUPK1A     : gtgggcctgctagttgtgggcaatatcattatttctgctgtcaggcctgtccctgtttgct :  108
hUPK1B     : cagggcctgctgatttttggaaatgtgattattggttgttgcggcattgccctgactgcg :   93
              a        T         c    t  t tt     t     g        t  t g
```

```
                    *       140         *       160         *       180
hCD9     : attggactatggctccgattcgactctcagaccaagagcatcttc---gagcaagaaact :  147
hCD37    : ttcggcatctggatcctcatcgacaagaccagcttcgtgtcctttgtgggcttggccttc :  153
hCD53    : tttgggatctacctgctgatccacaac---aacttcggagtgctc---ttccataacctc :  141
hCD63    : gtgggtgtcggggcacagcttgtcctgagtcagaccataatccag------ggggctacc :  144
hCD81    : gtggccctgtggctccgccatgacccgcagaccaccaacctcctg---tatctggagctg :  147
hCD82    : ttcggggtgtggatcctggccgacaagagcagtttcatctctgtcctgcaaacctcctcc :  147
hCD151   : gtgggcatctggacgctggccctcaagagtgactacatcagc------ctgctggcctca :  162
hCO-029  : ttagcaatatgggtacgagtaagcaatgactctcaagcaatttttggttctgaagatgta :  144
hNAG-2   : gtcggcatctggctggccgccacacaggggagcttcgccacgctg---tcctcttccttc :  144
hNET-1   : gtgggcatctgggtgtcaatcgatggggcatcctttctgaagatcttcgggccactgtcg :  141
hNET-2   : gtttctgcttggatgagggactacctaaataatgttctcactttaactgcagaaacgagg :  150
hNET-4   : attggactgtgggcatggaatgaaaaaggagttctgtccaacatctcttccatcaccgat :  165
hNET-5   : gtgggcatctggctctccgtgtcccaaggcaactttgccaccttc---tcccccagcttc :  144
hNET-6   : attgctgcgtggggcattggcttcggg---------------------------ctgatt :  120
hNET-7   : gtgggcatctatgcagaggttgagcggcagaaa---------------tataaaaccctt :  165
hil-TMP  : cctggagga---aaagtgatagatgacaacgaccacctttcccaa---gagatctggttt :  144
hROM-1   : ggtggcgtcatcctcctctgtagtgggcacctcctggtccagctaaggcaccttggcacc :  153
hSAS     : gtggctgcttggggcaagggtctgggt---------------------------ctggtg :  120
Hum      : gtgggagcctatgtcttcatcacttatgatgactatgaccacttc---tttgaagatgtg :  144
hTM4-B   : ctgggcattggtggtaaatgtggaggggcctctctgacgaatgtcctcgggctgtcctcc :  153
hTM4-D   : gttggcatttggggcaaggtgagcctggagaattacttttctctt---ttaaatgagaag :  168
hTM4SF2  : gttggagtctggggcaaacttactctgggcacctatatctcccttt---attgccgagaac :  147
hTM4SF5  : cctaatggggagacctcctggaccaacaccaaccatctcagcttg---caagtctggctc :  147
hTSPAN-2 : tttggactatggtttcggttcggaggtgccataaaggagttatca---tcagaggacaag :  150
hUPK1A   : gagaccatatgggtgacagccgaccagtaccgtgtatacccactgatgggagtctcaggc :  168
hUPK1B   : gagtgcatcttctttgtatctgaccaacacagcctctacccactgcttgaagccaccgac :  153
            t g     t

                    *       200         *       220         *       240
hCD9     : aataataat------aattccagcttctacacaggagtctat---attctgatcggagcc :  198
hCD37    : gtgcct------------------ctgcagatctggtccaaa---gtcctggccatctca :  192
hCD53    : ccctcc---------------------ctcacgctgggcaat---gtgtttgtcatcgtg :  177
hCD63    : cctggc---------------------tctctgttgccagtg---gtcatcatcgcagtg :  180
hCD81    : ggagacaagcccgcgcccaacaccttctatgtaggcatctac---atcctcatcgctgtg :  204
hCD82    : agctcg------------------cttaggatgggggcctat---gtcttcatcggcgtg :  186
hCD151   : ggcacc------------------tacctggccacagcctac---atcctggtggtggcg :  201
hCO-029  : ggctctagc---------------tcctacgttgctgtggac---atattgattgctgta :  186
hNAG-2   : ccgtcc---------------------ctgtcggctgccaac---ctgctcatcatcacc :  180
hNET-1   : tccagt------------gccatgcagtttgtcaacgtgggctacttcctcatcgcagcc :  189
hNET-2   : gtagaggaagcagtcattttgacttactttcctgtggttcatccggtcatgattgctgtt :  210
hNET-4   : ctcggc---------------------ggctttgacccagtttggctcttccttgtggtg :  204
hNET-5   : ccttcg---------------------ttgtctgcagccaac---ctggtcattgccata :  180
hNET-6   : tccagt---------------------ctccgagtggtcggc---gtggtcattgcagtg :  156
hNET-7   : gaaagt------------------gccttcctggctccagccatcatcctcatcctcctg :  207
hil-TMP  : ttcggagga------------------atattaggaagcggt---gtcttgatgatcttc :  183
hROM-1   : ttcctggctccc------tcctgtcagttccctgtcctgccccaggctgccctggcagcg :  207
hSAS     : tccagc---------------------atccacatcatcggc---ggagtcattgctgtg :  156
Hum      : tacacg---------------------ctcatccctgctgta---gtgatcatagctgta :  180
hTM4-B   : gcatac---------------------ctccttcacgttggcaacctgtgcctggtgatg :  192
hTM4-D   : gccacc---------------------aatgtccccttc------gtgctcattgctact :  201
hTM4SF2  : tccaca---------------------aatgctccctat------gtgctcatcggaact :  180
hTM4SF5  : atgggcggc------------------ttcattggcgggggc---ctaatggtactgtgt :  186
hTSPAN-2 : tcccca------------gagtatttctatgtggggctgtat---gttctggttggagcc :  195
hUPK1A   : aaggatgac------------------gtcttcgctggtgcctggattgccatcttctgc :  210
hUPK1B   : aacgat------------------gacatctatggggctgcctggatcggcatatttgtg :  195
                                                          t  t  t
```

```
                    *       260         *       280         *       300
hCD9     : ggcgccctcatgatgctggtgggcttcctgggc---tgctgcggggctgtgcaggagtcc :  255
hCD37    : ggaatcttcaccatgggcatcgccctcctgggt---tgtgtgggggccctcaaggagctc :  249
hCD53    : ggctctattatcatggtagttgccttcctgggc---tgcatgggctctatcaaggaaaac :  234
hCD63    : ggtgtcttcctcttcctggtggcttttgtgggc---tgctgcggggcctgcaaggagaac :  237
hCD81    : ggcgctgtcatgatgttcgttggcttcctgggc---tgctacggggccatccaggaatcc :  261
hCD82    : ggggcagtcactatgctcatgggcttcctgggc---tgcatcggcgccgtcaacgaggtc :  243
hCD151   : ggcactgtcgtcatggtgactggggtcttgggc---tgctgcgccaccttcaaggagcgt :  258
hCO-029  : ggtgccatcatcatgattctgggcttcctggga---tgctgcggtgctataaaagaaagt :  243
hNAG-2   : ggcgcctttgtcatggccatcggcttcgtgggc---tgcctgggtgccatcaaggagaac :  237
hNET-1   : ggcgttgtggtctttgctcttggtttcctgggc---tgctatggtgctaagactgagagc :  246
hNET-2   : tgctgtttccttatcattgtggggatgttaggatattgt---ggaacggtgaaaagaaat :  267
hNET-4   : ggaggagtgatgttcattttgggatttgcaggg---tgcattggagcgctacgggaaaac :  261
hNET-5   : ggcaccattgtcatggtgacgggcttcctcggc---tgcctgggggccatcaaggaaaac :  237
hNET-6   : ggcatcttcttgttcctgattgctttagtgggt---ctgattggagctgtaaaacatcat :  213
hNET-7   : ggcgtcgtcatgttcatggtctccttcattggt---gtgctggcgtccctccgtgacaac :  264
hil-TMP  : cctgcgctggtgttcttgggcctgaagaacaatgactgctgtgggtgctgcggcaacgag :  243
hROM-1   : ggcgcggtggctctgggcacaggactagtgggt------gtaggagccagccgggcaagt :  261
hSAS     : ggagtcttccttctccttattgcagtggctgga---ctggtgggtgctgtcaaccaccac :  213
Hum      : ggagccctgcttttcatcattgggctaattggc---tgctgtgccacaatccgggaaagt :  237
hTM4-B   : ggatgcatcacggtactgcttggctgtgccggg---tggtatggagcgactaaagagagc :  249
hTM4-D   : ggtaccgtcattattcttttgggcacctttggt---tgttttgctacctgccgagcttct :  258
hTM4SF2  : ggcaccactattgttgtctttggcctgtttgga---tgctttgctacatgtcgtggtagc :  237
hTM4SF5  : ccagggattgcagccgttcgggcaggggcaag----------ggctgctgtggtgctggg :  237
hTSPAN-2 : ggggccctgatgatggccgtggggttcttcggg---tgctgcggaccatgctgggagtcg :  252
hUPK1A   : ggcttctccttcttcatggtagccagttttggt---gtgggtgccgcactctgccgccgc :  267
hUPK1B   : ggcatctgcctcttctgcctgtctgttctaggc---attgtaggcatcatgaagtccagc :  252
           gg     t  t  t     t g   t  t gg          G   c

                    *       320         *       340         *       360
hCD9     : cagtgcatgctgggactg------ttcttcggcttcctcttggtgatattcgccattgaa :  309
hCD37    : cgctgcctcctgggcctg------tattttgggatgctgctgctcctgtttgccacacag :  303
hCD53    : aagtgtctgcttatgtcg------ttcttcatcctgctgctgattatcctccttgctgag :  288
hCD63    : tattgtcttatgatcacg------tttgccatctttctgtctcttatcatgttggtggag :  291
hCD81    : cagtgcctgctggggacg------ttcttcacctgcctggtcatcctgtttgcctgtgag :  315
hCD82    : cgctgcctgctggggctg------tactttgctttcctgctcctgatcctcattgcccag :  297
hCD151   : cggaacctgctgcgcctg------tacttcatcctgctcctcatcatctttctgctggag :  312
hCO-029  : cgctgcatgcttctgttg------tttttcataggcttgcttctgatcctgctcctgcag :  297
hNAG-2   : aagtgcctcctgctcact------ttcttcctgctgctgctgctggtgttcctgctggag :  291
hNET-1   : aagtgtgccctcgtgacg------ttcttcttcatcctcctcctcatcttcattgctgag :  300
hNET-2   : ctgttgcttcttgcatgg------tactttggaagtttgcttgtcattttctgtgtagaa :  321
hNET-4   : actttccttctcaagttt------ttttctgtgttcctgggaattattttcttcctggag :  315
hNET-5   : aagtgcctcctcctcagc------tttttcatcgtcctgttggtcatcctcctagcagag :  291
hNET-6   : caggtgttgctatttttt------tatatgattattctgttacttgtatttattgttcag :  267
hNET-7   : ctgtaccttctccaagca------ttcatgtacatccttgggatctgcctcatcatggag :  318
hil-TMP  : ggctgtgggaagcgattt------gcgatgttcacctccacgatatttgctgtggttgga :  297
hROM-1   : ctgaatgcagctctataccctccctggcgaggggtcctgggcccgctgctggtggctggc :  321
hSAS     : caagtcctgctg------------tacatgatcatccttggtttggtcttcatcttccaa :  261
Hum      : cgctgtggacttgccacg------tttgtcatcatcctgctcttggtttttgtcacagaa :  291
hTM4-B   : agaggcacgctcttgttt------tgcatcctgtcaatggttattgtcctcatcatggaa :  303
hTM4-D   : gcatggatgctaaaactg------tatgcaatgtttctgactctcgtttttttggtcgaa :  312
hTM4SF2  : ccatggatgctgaaactg------tatgccatgtttctgtccctggtgttcctggctgag :  291
hTM4SF5  : tgctgtggaaaccgctgc------aggatgctgcgctcggtcttctcctcggcgttcggg :  291
hTSPAN-2 : caatgtgtgcttggatca------ttttttacctgcctcctggtgatatttgctgctgaa :  306
hUPK1A   : cggtccatggtcctcacg------tacctggtgctcatgctcatcgtctacatcttcgag :  321
hUPK1B   : aggaaaattcttctggcg------tatttcattctgatgtttatagtatatgcctttgaa :  306
                    ct             t   t        t     t  t  t       ga
```

```
                   *       380         *       400         *       420
hCD9      : atagctgcggccatctggggatattcccacaaggatgaggtgatt--------------- :  354
hCD37     : atcaccctgggaatcctcatctccactcagcgggcccagctggag--------------- :  348
hCD53     : gtgaccttggccatcctgctctttgtatatgaacagaagctgaat--------------- :  333
hCD63     : gtggccgcagccattgctggctatgtgtttagagataaggtgatg--------------- :  336
hCD81     : gtggccgccggcatctggggctttgtcaacaaggaccagatcgcc--------------- :  360
hCD82     : gtgacggccggggccctcttctacttcaacatgggcaagctgaag--------------- :  342
hCD151    : atcatcgctggtatcctcgcctacgcctactaccagcagctgaac--------------- :  357
hCO-029   : gtggcgacaggtatcctaggagctgttttcaaatctaagtctgat--------------- :  342
hNAG-2    : gccaccatcgccatcctcttcttcgcctacacggacaagattgac--------------- :  336
hNET-1    : gttgcagctgctgtggtcgccttggtgtacaccacaatggctgag--------------- :  345
hNET-2    : ctggcttgtggcgtttggacatatgaacaggaacttatggttcca--------------- :  366
hNET-4    : ctcactgccggagttctagcatttgttttcaaagactggatcaaa--------------- :  360
hNET-5    : ctgatcttactcatcctcttctttgtctacatggacaaggtgaac--------------- :  336
hNET-6    : ttttctgtatcttgcgcttgtttagccctgaac--------------------------- :  300
hNET-7    : ctcattggtggcgtggtggccttgaccttccggaaccagaccatt--------------- :  363
hil-TMP   : ttcttgggagctggatactcgtttatcatctca--------------------------- :  330
hROM-1    : acggctggtgggggggggctcctggtcgtcgccctcgggctagccctggctttgcctggg :  381
hSAS      : tttgtaatctcttgctcatgtctggctattaac--------------------------- :  294
Hum       : gttgttgtagtggttttgggatatgtttacagagcaaaggtggaa--------------- :  336
hTM4-B    : gttacagctgccacagtggtccttcttttctttccaattgttgga--------------- :  348
hTM4-D    : ctggtcgctgccatcgtaggatttgttttcagacatgagattaag--------------- :  357
hTM4SF2   : ctcgtagctggcatttcagggtttgtgtttcgtcatgagatcaag--------------- :  336
hTM4SF5   : gtgcttggtgccatctactgcctctcggtgtct--------------------------- :  324
hTSPAN-2  : gtaaccactggagtatttgcttttataggcaagggggtagctatc--------------- :  351
hUPK1A    : tgcgcctcctgcatcacgtcctacacccaccgtgactacatggtgtcc------------ :  369
hUPK1B    : gtggcatcttgtatcacagcagcaacacaacgagactttttcacacccaacctcttc--- :  363
             t       g

                   *       440         *       460         *       480
hCD9      : ---------aaggaagtccaggagttttacaaggacacctacaac---aagctgaaaacc :  402
hCD37     : ---------cgaagcttgcgggacgtcgtagagaaaaccatccaaaagtacggcaccaac :  399
hCD53     : ---------gagtatgtggctaagggtctgaccgacagcatccaccgttaccactcagac :  384
hCD63     : ---------tcagagtttaataacaacttccggcagcagatggagaattacccgaaaaac :  387
hCD81     : ---------aaggatgtgaagcagttctatgaccaggccctacagcaggccgtggtggat :  411
hCD82     : ---------caggagatgggtggcatcgtgactgagctcattcgagactacaacagcagt :  393
hCD151    : ---------acggagctcaaggagaacctgaaggacaccatgaccaggcgctaccaccag :  408
hCO-029   : ---------cgcattgtgaatgaaactctctatgaaaacacaaagcttttgagcgccaca :  393
hNAG-2    : ---------aggtatgcccagcaagacctgaagaaaggcttgcacctgtacggcacgcag :  387
hNET-1    : ---------cacttcctgacgttgctggtagtgcctgccatcaagaaagattatggttcc :  396
hNET-2    : ---------gtacaatggtcagatatggtcactttgaaagccaggatgacaaattatgga :  417
hNET-4    : ---------gaccagctgtatttctttataaacaacaacatcagagcatatcgggatgac :  411
hNET-5    : ---------gagaacgccaagaaggacctgaaggaaggcctgctgctgtaccacaccgag :  387
hNET-6    : ---------cag---gagcaacagggtcagcttctggaggttggttggaacaatacggca :  348
hNET-7    : ---------gacttcctgaacgacaacattcgaagaggaattgagaactactatgatgat :  414
hil-TMP   : ------------------gccatttcaatcaacaagggtcctaaatgcctcatggccaat :  372
hROM-1    : agtctggatgaggcgctggaggagggcctggtgactgccttggctcactacaaggacaca :  441
hSAS      : ---------cgaagcaaacagacagatgtcatcaatgcttcttggtgggtcatgagcaac :  345
Hum       : ---------aatgaggttgatcgcagcattcagaaagtgtataagacctacaatggaacc :  387
hTM4-B    : ---------gatgtggccttggaacacaccttcgtgaccctgaggaagaattacagaggt :  399
hTM4-D    : ---------aacagctttaagaataattatgagaaggctttgaagcagtataactctaca :  408
hTM4SF2   : ---------gacaccttcctgaggacttacacggacgctatgcagacttacaatggcaat :  387
hTM4SF5   : ------------------ggagctgggctccgaaatggacccagatgcttaatgaac--- :  363
hTSPAN-2  : ---------cgacatgttcagaccatgtatgaagaggcttacaatgattaccttaaagac :  402
hUPK1A    : ------------aacccatccctgatcaccaagcagatgctgaccttctacagcgcggac :  417
hUPK1B    : ------ctgaagcagatgctagagaggtaccaaaacaacagccctccaaacaatgatgac :  417
```

```
                    *       500         *       520         *       540
hCD9     : aaggatgag---ccc---cagcgg---gaaacgctgaaagccatccactatgcgttgaac :  453
hCD37    : cccgaggag------accgcggccgaggagagctgggactatgtgcagttccagctgcgc :  453
hCD53    : aat---------------agcaccaaggcagcgtgggactccatccagtcatttctgcag :  429
hCD63    : aac---------------cacactgcttcgatcctggacaggatgcaggcagattttaag :  432
hCD81    : gatgacgcc---aac---aacgccaaggctgtggtgaagaccttccacgagacgcttgac :  465
hCD82    : cgcgaggac---------agcctgcaggatgcctgggactacgtgcaggctcaggtgaag :  444
hCD151   : tcgggc------catgaggctgtgaccagcgctgtggaccagctgcagcaggagttccac :  462
hCO-029  : ggggaaagt---gaaaaacaattccaggaagccataattgtgtttcaagaagagtttaaa :  450
hNAG-2   : ggcaacgtg---------ggcctcaccaacgcctggagcatcatccagaccgacttccgc :  438
hNET-1   : caggaa------------gacttcactcaagtgtggaacaccaccatgaaagggctcaag :  444
hNET-2   : ttacctaga---tatcggtggcttactcatgcttggaatttttttcagagagagtttaag :  474
hNET-4   : attgat---------------ttgcaaaacctcatagacttcacccaggaatattggcag :  456
hNET-5   : aacaacgtg---------gggctgaagaacgcctggaacatcatccaggctgagatgcga :  438
hNET-6   : agt---------------------------gctcgaaatgacatccagagaaatctaaac :  381
hNET-7   : ctggac---------------ttcaaaaacatcatggactttgttcagaaaaagttcaag :  459
hil-TMP  : ----------------------------agtacatgggctaccccttccacgac------ :  399
hROM-1   : gaggtgcctgggcactgtcaggccaaaaggctggtggatgagctgcaactgaggtaccac :  501
hSAS     : aag---------------------------actcgggatgaactggaaagaagttttgat :  378
Hum      : aac---------cctgatgctgctagccgggctattgattatgtacagagacagctgcat :  438
hTM4-B   : tacaacgag---ccagacgactattctacacagtggaacttggtcatggagaagctaaag :  456
hTM4-D   : gga---------gat---tatagaagccatgcagtagacaagatccaaaatacgttgcat :  456
hTM4SF2  : ------------gat---gagaggagccgggcagtggaccatgtgcagcgcagcctgagc :  432
hTM4SF5  : ----------------------------ggcgagtgggctaccacttcgaagacaccgcg :  396
hTSPAN-2 : aggggaaaa---ggc---aatggg---acactcatcacctttccacttcaacatttccag :  453
hUPK1A   : accgaccag---ggccaggagctgacccgcctctgggaccgcgtcatgattgagcaagaa :  474
hUPK1B   : cagtggaaa---aacaatggagtcaccaaaacctgggacaggctcatgctccaggacaat :  474
                                                a     t

                    *       560         *       580         *       600
hCD9     : tgctgtggtttggctgggggc------------gtg------------------------ :  477
hCD37    : tgctgcggctggcactacccgcaggactggttccaagtcctcatcctgagaggtaacggg :  513
hCD53    : tgttgtggtataaatggcacgagtgattggaccagt------------ggc--------- :  468
hCD63    : tgctgtggggctgctaactacacagattgggagaaaatcccttccatgtcg--------- :  483
hCD81    : tgctgtggctccagcacactgactgctttgaccacc------------------------ :  501
hCD82    : tgctgcggctgggtcagcttctacaactggacagacaacgctgagctcatgaatcgc--- :  501
hCD151   : tgctgtggcagcaacaactcacaggactggcgagacagtgagtggatccgctcacaggag :  522
hCO-029  : tgctgcggtttggtcaatggagctgctgattggggaaat---------aat--------- :  492
hNAG-2   : tgctgtggcgtctccaactacactgactggttcgaggtg------tacaac--------- :  483
hNET-1   : tgctgtggcttcaccaactatacggattttgaggactcaccctacttcaaa--------- :  495
hNET-2   : tgctgtggagtagtatatttcactgactggttggaaatgaca------------------ :  516
hNET-4   : tgctgtggggcttttggagctgatgattggaacctaaatatttacttcaattgcacagat :  516
hNET-5   : tgctgtggtgtcactgactacacagactggtacccagtg------ctgggg--------- :  483
hNET-6   : tgctgtgggttccgaagtgttaac------------------------------------ :  405
hNET-7   : tgctgtggcggggaggactaccgagattggagcaagaatcagtaccacgactgcagtgcc :  519
hil-TMP  : ggggattatctcaatgatgaggccttatgg------------------------------ :  429
hROM-1   : tgctgcgggcgccacgggtacaaggattggtttggggtccagtgggtcagcagccgttac :  561
hSAS     : tgttgtggcttattcaacctcacaaccctg------------------------------ :  408
Hum      : tgttgtggaattcacaactactcagactggaaaatacagattggttcaaagaaaccaaa :  498
hTM4-B   : tgctgtggggtgaataactacacagattttctggctcttcc------------------ :  498
hTM4-D   : tgttgtggtgtcaccgattatagagattggacagatactaattattactca--------- :  507
hTM4SF2  : tgctgtggtgtgcagaactacaccaactggagcaccagcccctacttcctg--------- :  483
hTM4SF5  : ggagcttacttgctcaaccgcactctatgg------------------------------ :  426
hTSPAN-2 : tgctgtggaaaagaaagc------------------------------------------ :  471
hUPK1A   : tgctgtggcacatctggtcccatggactgggtgaacttcacgtcagccttccgggcggcc :  534
hUPK1B   : tgctgtggcgtaaatggtccatcagactggcaaaaatacacatctgccttccggactgag :  534
           tG tgtgg                   t
```

```
                   *       620         *       640         *       660
hCD9     : ---------------------------------------------------gaacagttt :  486
hCD37    : tcg---------------------------------------------gaggcgcaccgc :  528
hCD53    : ---------------------------------------------------cca------ :  471
hCD63    : ---------------------------------------------------aagaaccga :  492
hCD81    : ---------------------------------------------------tcagtgctc :  510
hCD82    : ------------------------------------------------cctgaggtcacc :  513
hCD151   : gcc---------------------------------------------ggtggccgtgtg :  537
hCO-029  : ---------------------------------------------------tttcaacac :  501
hNAG-2   : ---------------------------------------------------gccacgcgg :  492
hNET-1   : ---------------------------------------------------gagaacagt :  504
hNET-2   : ------------------------------------------------gagatggactgg :  528
hNET-4   : tcc---------------------------------------------aatgcaagtcga :  531
hNET-5   : ---------------------------------------------------gagaacacg :  492
hNET-6   : ------------------------------------------------------------ :    -
hNET-7   : cct---------------------------------------------ggacccctggcc :  534
hil-TMP  : ------------------------------------------------------------ :    -
hROM-1   : ctggatcccggtgaccgggatgtggctgaccggatccagagcaatgtagaaggcctatac :  621
hSAS     : ---------------------------------------------------tatcaacaa :  417
Hum      : ---------------------------------------------------aaccagagt :  507
hTM4-B   : ------------------------------------------------ttcgaaatgaca :  510
hTM4-D   : ---------------------------------------------------gaaaaagga :  516
hTM4SF2  : ---------------------------------------------------gagcatggc :  492
hTM4SF5  : ------------------------------------------------------------ :    -
hTSPAN-2 : ---------------------------------------------------tccgaacag :  480
hUPK1A   : act---------------------------------------------ccggaggtggtg :  549
hUPK1B   : ---------------------------------------------------aataatgat :  543

                   *       680         *       700         *       720
hCD9     : ------------atctcagacatctgccccaagaag---gac------------------ :  513
hCD37    : ------------gtgccctgctcctgctacaacttgtcggcgaccaacgactccacaatc :  576
hCD53    : ---------------ccagcatcttgcccctcagatcgaaaa------------------ :  498
hCD63    : ------------gtccccgactcctgctgcattaatgttactgtgggc------------ :  528
hCD81    : ------------aagaacaatttgtgtccctcgggcagcaac------------------ :  540
hCD82    : ------------tacccctgttcctgcgaagtcaagggggaagag--------------- :  546
hCD151   : ------------gtcccagacagctgctgcaagacggtggtggctctttgtgga------ :  579
hCO-029  : ------------tatcctgaattatgtgcctgtctagataagcag--------------- :  534
hNAG-2   : ------------gtacctgactcctgctgcttggagttcagtgag--------------- :  525
hNET-1   : ---------gcctttcccccattctgttgcaatgacaacgtcaccaac------------ :  543
hNET-2   : ------------cccccagattcctgctgtgttagagaattcccagga------------ :  564
hNET-4   : gagcgatgtggcgttccattctcctgctgcactaaagatcccgcagaagatgtcatcaac :  591
hNET-5   : ------------gttcccgaccgctgctgcatggagaactcccag--------------- :  525
hNET-6   : ------------ccaaatgacacctgttctggctagctgtgtt------------------ :  435
hNET-7   : tgtggg------gtgccctacacctgctgcatcaggaacacgacagaagttgtcaacacc :  588
hil-TMP  : ------------------aacaagtgccgagagcct------------------------ :  447
hROM-1   : ctgactgatggggtccctttctcctgttgcaacccccactcaccccggcct--------- :  672
hSAS     : ------------gattatgatttctgcactgcaatctgcaag------------------ :  447
Hum      : ------------gtccctcttagctgctgcagagagactgccagcaat------------ :  543
hTM4-B   : acgggccacacctaccccaggagttgctgtaaatccatcggaagtgtgtcctgtgac--- :  567
hTM4-D   : ------------tttcctaagagttgctgtaaa---cttgaagat--------------- :  546
hTM4SF2  : ------------atcccccccagctgctgcatgaacgaaactgat--------------- :  525
hTM4SF5  : ------------------gatcggtgcgaggcgccc------------------------ :  444
hTSPAN-2 : ------------gtccaacctacatgcccaaag--------------------------- :  501
hUPK1A   : ttcccc------tggcccccactgtgctgtcgccggacgggaaacttcatccccctcaac :  603
hUPK1B   : gctgactatccctggcctcgtcaatgctgtgttatgaacaat------------------ :  585
                                   TGc
```

```
                    *       740         *       760         *       780
hCD9     : ---------------------------------------------gtactcgaa------ :  522
hCD37    : ctagataaggtgatcttgccccagctcagcaggcttggacacctggcgcggtccagacac :  636
hCD53    : ------------------------------------------------------------ :    -
hCD63    : ------------------------------------------tgtgggattaat------ :  540
hCD81    : ---------------------------------------------atcatcagc------ :  549
hCD82    : ------------gacaacagcctttctgtgaggaagggcttctgcgaggcccccggcaac :  594
hCD151   : ---------------------------------------------cagcgagac------ :  588
hCO-029  : ------------agaccatgccaaagctataat---------------ggaaaa------ :  561
hNAG-2   : ------------agctgtgggctg------------------cacgcccccggc------ :  549
hNET-1   : ---------------------------------------------acagccaat------ :  552
hNET-2   : ---------------------tgttccaaacaggcccaccaggaagatctcagt------ :  597
hNET-4   : actcagtgtggctatgatgccagg------------------caaaaaccagaa------ :  627
hNET-5   : ------------ggctgcgggcgc------------------aacgccaccacg------ :  549
hNET-6   : ------------------------------------------------aaaagt------ :  441
hNET-7   : atgtgtggctacaaaactatcgac---------------------aaggagcgt------ :  621
hil-TMP  : ------------------------------------------------------------ :    -
hROM-1   : ------tgcctgcaaaaccgtctttcagactcctacgcccaccccctgttcgat------ :  720
hSAS     : ------------------------------------------------agccag------ :  453
Hum      : ------------------------------------------tgtaatggcagc------ :  555
hTM4-B   : ---------------------------------------------ggacgcgat------ :  576
hTM4-D   : ------------tgtactccacag------------------agagatgcagac------ :  570
hTM4SF2  : ------------tgtaatccccaggatctacacaatctgactgtggccgccacc------ :  567
hTM4SF5  : ------------------------------------------------------------ :    -
hTSPAN-2 : ---------------------------------------------------gag------ :  504
hUPK1A   : ---------------------------------------------gaggagggc------ :  612
hUPK1B   : ---------------------------------------------cttaaagaa------ :  594

                    *       800         *       820         *       840
hCD9     : ---------------------------------accttcaccgtgaagtcctgtcctgat :  549
hCD37    : agtgcagacatctgcgctgtccctgcagagagccacatctaccgcgagggctgcgcgcag :  696
hCD53    : ------------------------------------------gtggagggttgctatgcg :  516
hCD63    : ---------------------ttcaacgagaaggcgatccataaggagggctgtgtggag :  579
hCD81    : ---------------------------------aacctcttcaaggaggactgccaccag :  576
hCD82    : aggacccagagtggcaaccaccctgaggactggcctgtgtaccaggagggctgcatggag :  654
hCD151   : ------------------catgcctccaacatctacaaggtggagggcggctgcatcacc :  630
hCO-029  : ---------------------------------caagtttacaaagagacctgtatttct :  588
hNAG-2   : ---------------------------------acctggtggaaggcgccgtgctacgag :  576
hNET-1   : ------gaaacctgcaccaagcaaaaggctcacgaccaaaaagtagagggttgcttcaat :  606
hNET-2   : ---------------------------------gacctttatcaagagggttgtgggaag :  624
hNET-4   : ------------------gttgaccagcagattgtaatctacacgaaaggctgtgtgccc :  669
hNET-5   : ---------------------------------cctttgtggagaacgggctgctatgaa :  576
hNET-6   : ---------------------------------gaccactcgtgctcgccatgtgctcca :  468
hNET-7   : ------------------ttcagtgtgcaggatgtcatctacgtgcggggctgcaccaac :  663
hil-TMP  : ---------------------------------------------ctcaatgtggttccc :  462
hROM-1   : ---------------ccccgacaacccaaccaaaacctctgggcccaagggtgccatgag :  765
hSAS     : ---------------------------------agccccacatgccagatgtgtggagaa :  480
Hum      : ------------------ctggcccacccttccgacctctatgctgaggggtgtgaggct :  597
hTM4-B   : ---------------------gtgtctccaaacgtcatccaccagaagggctgtttccat :  615
hTM4-D   : ---------------------------------aaagtaaacaatgaaggttgttttata :  597
hTM4SF2  : ---------------------------------aaagttaaccagaagggttgttatgat :  594
hTM4SF5  : ---------------------------------------------cctcgcgtggtcccc :  459
hTSPAN-2 : ---------------------------------cttcttagacacaagaattgcatcgat :  531
hUPK1A   : ------------tgccgcctggggcacatggactacctgttcaccaagggctgcttcgaa :  660
hUPK1B   : ---------------------------------cctctcaacctggaggcttgtaaacta :  621
                                                              tg
```

```
                     *       860         *       880         *       900
hCD9      : gccatcaaagaggtcttcgacaat---------aaattccacatcatcggcgcagtgggc :   600
hCD37     : ggcctccagaagtggctgcacaac---------aaccttatttccatagtgggcatttgc :   747
hCD53     : aaagcaagactgtggtttcattcc---------aatttcctgtatatcggaatcatcacc :   567
hCD63     : aagattgggggctggctgaggaaa---------aatgtgctggtggtagctgcagcagcc :   630
hCD81     : aagatcgatgacctcttctccggg---------aagctgtacctcatcggcattgctgcc :   627
hCD82     : aaggtgcaggcgtggctgcaggag---------aacctgggcatcatcctcggcgtgggc :   705
hCD151    : aagttggagaccttcatccaggag---------cacctgagggtcattggggctgtgggg :   681
hCO-029   : ttcataaaagacttcttggcaaaa---------aatttgattatagttattggaatatca :   639
hNAG-2    : acggtgaaggtgtggcttcaggag---------aacctgctggctgtgggcatctttggg :   627
hNET-1    : cagcttttgtatgacatccgaact---------aatgcagtcaccgtgggtggtgtggca :   657
hNET-2    : aaaatgtattcctttttgagaggaaccaaa---caactgcaggtgctgaggtttctggga :   681
hNET-4    : cagtttgagaagtggttgcaggac---------aatttaaccatcgttgctggtattttc :   720
hNET-5    : aaggtgaagatgtggttcgatgac---------aataagcacgtgctgggcacggtgggg :   627
hNET-6    : atcataggagaatatgctggagag---------gttttgagatttgttggtggcattggc :   519
hNET-7    : gccgtgatcatctggttcatggac---------aactacaccatcatggcgggcatcctc :   714
hil-TMP   : tggaatctgaccctcttctcc------------atcctgctggtcgtaggaggaatccag :   510
hROM-1    : gtgctgctggagcacttgcaggacttggcaggcacactgggtagcatgctggctgtcacc :   825
hSAS      : aagtttcttaagcattcagacgaa---------gccctgaaaatcctagggggtgttgga :   531
Hum       : ctagttgtgaagaagctacaagaa---------atcatgatgcatgtgatctgggccgca :   648
hTM4-B    : aaactcctaaaaatcaccaagact---------cagagcttcaccctgagtgggagctct :   666
hTM4-D    : aaggtgatgaccattatagagtca---------gaaatgggagtcgttgcaggaatttcc :   648
hTM4SF2   : ctggtaactagtttcatggagact---------aacatgggaatcatcgctggagtggcg :   645
hTM4SF5   : tggaatgtgacgctcttctcg------------ctgctggtggccgcctcctgcctggag :   507
hTSPAN-2  : gaaattgagaccataatcagtgtt---------aagctccagctcattggaattgtcggt :   582
hUPK1A    : cacatcggccacgccatcgacagc---------tacacgtggggtatctcgtggtttggg :   711
hUPK1B    : ggcgtgcctggtttttatcacaatcagggc---tgctatgaactgatctctggtccaatg :   678
                t           t                             t        t

                     *       920         *       940         *       960
hCD9      : atcggcattgccgtggtcatgatattt---ggcatgatcttcagtatgatcttgtgctgt :   657
hCD37     : ctgggcgtcggcctactcgagctcggg---ttcatgacgctctcgatattcctgtgcaga :   804
hCD53     : atctgtgtatgtgtgattgaggtgttg---gggatgtcctttgcactgaccctgaactgc :   624
hCD63     : cttggaattgcttttgtcgaggttttg---ggaattgtctttgcctgctgcctcgtgaag :   687
hCD81     : atcgtggtcgctgtgatcatgatcttc---gagatgatcctgagcatggtgctgtgctgt :   684
hCD82     : gtgggtgtggccatggtcgagctcctg---gggatggtcctgtccatctgcttgtgccgg :   762
hCD151    : atcggcattgcctgtgtgcaggtcttt---ggcatgatcttcacgtgctgcctgtacagg :   738
hCO-029   : tttggactggcagttattgagatactg---ggtttggtgttttctatggtcctgtattgc :   696
hNAG-2    : ctgtgcacggcgctggtgcagatcctg---ggcctgaccttcgccatgaccatgtactgc :   684
hNET-1    : gctggaattgggggcctcgagctggct---gccatgattgtgtccatgtatctgtactgc :   714
hNET-2    : atctccattggggtgacacaaatcctg---gccatgattctcaccattactctgctctgg :   738
hNET-4    : ataggcattgcattgctgcagatattt---gggatatgcctggcccagaatttggttagc :   777
hNET-5    : atgtgcatcctcatcatgcagatcctg---ggcatggccttctccatgaccctcttccag :   684
hNET-6    : ctgttcttcagttttacagagatcctg---ggtgtttggctgacctacagatacaggaac :   576
hNET-7    : ctgggcatcctgcttccccagttcctg---ggggtgctgctgacgctgctgtacatcacc :   771
hil-TMP   : atggttctctgcgccatccaggtggtcaatggcctcctggggaccctctgtggggactgc :   570
hROM-1    : ttcctactgcaggctctggtgctcctt---ggcctgcggtacctgcaaacagcactggag :   882
hSAS      : ctcttctttagctttacagagatcctt---ggtgtttggctagcaatgagatttcggaat :   588
Hum       : ctggcatttgcagctattcagctgctg---ggcatgctgtgtgcttgcatcgtgttgtgc :   705
hTM4-B    : ctgggagctgcagtgatacagaggtgggggtctcgctatgttgcgcaggctggtcttgaa :   726
hTM4-D    : tttggagttgcttgcttccaactgatt---ggaatctttctcgcctactgcctctctcgt :   705
hTM4SF2   : tttggaatcgcattctcccagttaatt---ggcatgctgctggcctgctgtctgtcccgg :   702
hTM4SF5   : atagtactgtgtgggatccagctggtgaacgcgaccattggtgtcttctgcggcgattgc :   567
hTSPAN-2  : attggaattgcaggtctgacgatcttt---ggcatgatattcagcatggtcctctgctgt :   639
hUPK1A    : tttgccatcctgatgtggacgctcccg---gtcatgctgatagccatgtatttctacacc :   768
hUPK1B    : aaccgacacgcctggggggttgcctggtttggatttgccattctctgctggactttttgg :   738
             t     t            g t  t    g   t     t
```

```
                     *       980         *      1000         *      1020
hCD9      : gctatccgcagg------------------------------------------------ :  669
hCD37     : aacctggaccacgtctac---------------------------------------aac :  825
hCD53     : cagattgacaaa------------------------------------------------ :  636
hCD63     : agtatcaga--------------------------------------------------- :  696
hCD81     : ggcatccggaac------------------------------------------------ :  696
hCD82     : cacgtgcattccgaagac---------------------------------------tac :  783
hCD151    : agtctcaag--------------------------------------------------- :  747
hCO-029   : cagatcgggaac------------------------------------------------ :  708
hNAG-2    : caagtggtcaag------------------------------------------------ :  696
hNET-1    : aatctacaa--------------------------------------------------- :  723
hNET-2    : gctctgtattatgatagaagggagcctgggacagaccaaatgatgtccttgaagaatgac :  798
hNET-4    : gatatcgaagct------------------------------------------------ :  789
hNET-5    : cacatccaccgg------------------------------------------------ :  696
hNET-6    : cagaaagacccc------------------------------------------------ :  588
hNET-7    : cgggtggaggac------------------------------------------atcatc :  789
hil-TMP   : cagtgttgtggctgctgt---------------------------------------ggg :  591
hROM-1    : gggcttggaggggtcattgatgcgggaggagagacccagggctatctctttcccagtggg :  942
hSAS      : cagaaggatcct------------------------------------------------ :  600
Hum       : agaaggagtagagatcct---------------------------------------gct :  726
hTM4-B    : ctgctggcc--------------------------------------------------- :  735
hTM4-D    : gccataacaaat------------------------------------------------ :  717
hTM4SF2   : ttcatcacggcc------------------------------------------------ :  714
hTM4SF5   : aggaaaaaa--------------------------------------------------- :  576
hTSPAN-2  : gcgatacgaaac------------------------------------------------ :  651
hUPK1A    : atgctc------------------------------------------------------ :  774
hUPK1B    : gttctcctgggt------------------------------------------------ :  750
                t

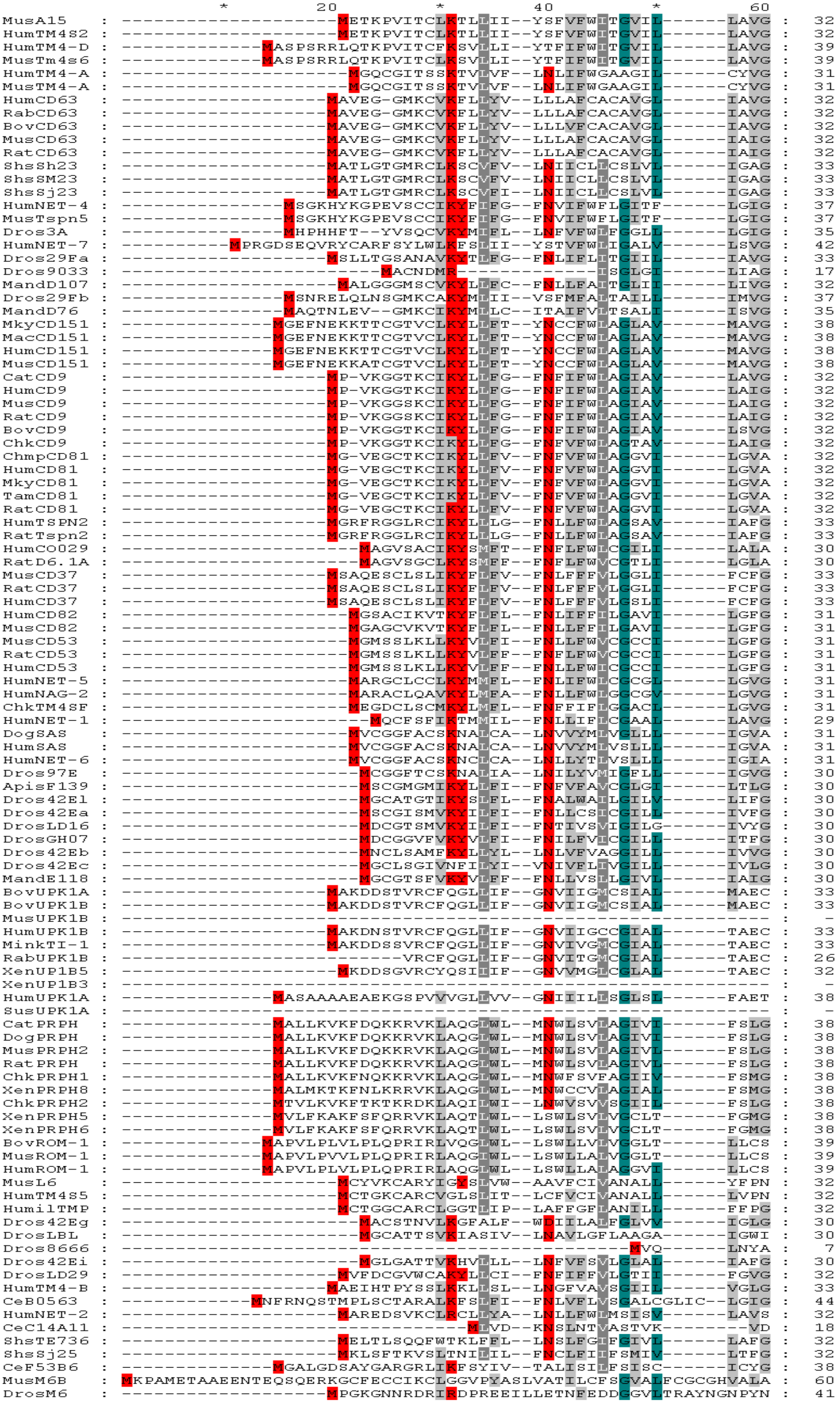
                     *      1040         *      1060         *      1080
hCD9      : aaccgcgagatggtc--------------------------------------------- :  684
hCD37     : cggctcgctcgataccgt------------------------------------------ :  843
hCD53     : accagccagaccatagggcta--------------------------------------- :  657
hCD63     : agtggctacgaggtgatg------------------------------------------ :  714
hCD81     : agc---tccgtg------------------------------------------------ :  705
hCD82     : agcaaggtccccaagtac------------------------------------------ :  801
hCD151    : ---ctggagcactac--------------------------------------------- :  759
hCO-029   : aaa--------------------------------------------------------- :  711
hNAG-2    : gcagacacctactgcgcg------------------------------------------ :  714
hNET-1    : ------------------------------------------------------------ :    -
hNET-2    : aactctcagcacctgtcatgtccctcagtagaactgttgaaaccaagcctgtcaagaatc :  858
hNET-4    : gtcagggcgagctgg--------------------------------------------- :  804
hNET-5    : actggtaagaagtacgacgca--------------------------------------- :  717
hNET-6    : cgcgcgaatcctagtgca------------------------------------------ :  606
hNET-7    : atggagcactctgtcactgatgggctcctggggcccggtgccaagcccagcgtggaggcg :  849
hil-TMP   : ggagatggacccgtt--------------------------------------------- :  606
hROM-1    : ctgaaagatatgctgaaaacagcatggctacagggaggggttgcctgcaggccagcacct : 1002
hSAS      : agagccaccccagtgcctttntatgagactttggatccttctgactngcttctgctctct :  660
Hum       : tacgagctcctcatcactggcggaacctatgca--------------------------- :  759
hTM4-B    : ------------------------------------------------------------ :    -
hTM4-D    : aaccagtatgagatagtg------------------------------------------ :  735
hTM4SF2   : aatcagtatgagatggtg------------------------------------------ :  732
hTM4SF5   : caggacacacctcac--------------------------------------------- :  591
hTSPAN-2  : tcacgagatgtgata--------------------------------------------- :  666
hUPK1A    : ------------------------------------------------------------ :    -
hUPK1B    : accatgttctactggagcagaattgaatat------------------------------ :  780
```

```
                    *      1100         *      1120         *
hCD9     : --------------------------------------------------------- :    -
hCD37    : --------------------------------------------------------- :    -
hCD53    : --------------------------------------------------------- :    -
hCD63    : --------------------------------------------------------- :    -
hCD81    : --------------------------------------------------------- :    -
hCD82    : --------------------------------------------------------- :    -
hCD151   : --------------------------------------------------------- :    -
hCO-029  : --------------------------------------------------------- :    -
hNAG-2   : --------------------------------------------------------- :    -
hNET-1   : --------------------------------------------------------- :    -
hNET-2   : tttgaacacacatccatggcaaacagctttaatacacactttgagatggaggagtta :  915
hNET-4   : --------------------------------------------------------- :    -
hNET-5   : --------------------------------------------------------- :    -
hNET-6   : ------ttcctt--------------------------------------------- :  612
hNET-7   : gcaggcacgggatgctgcttgtgctaccccaat------------------------ :  882
hil-TMP  : --------------------------------------------------------- :    -
hROM-1   : gaggaggccccaccaggagaagcacctcccaaggaggatctatctgaggcc------ : 1053
hSAS     : ctaagctttctcttcctccct------------------------------------ :  681
Hum      : --------------------------------------------------------- :    -
hTM4-B   : --------------------------------------------------------- :    -
hTM4-D   : --------------------------------------------------------- :    -
hTM4SF2  : --------------------------------------------------------- :    -
hTM4SF5  : --------------------------------------------------------- :    -
hTSPAN-2 : --------------------------------------------------------- :    -
hUPK1A   : --------------------------------------------------------- :    -
hUPK1B   : --------------------------------------------------------- :    -
```

Appendix I

Amino Acid ClustalW Alignment of Tetraspanin Family Members

Previously reported conserved amino acid residues (Section 1.5),
are highlighted in red in the alignment (Hemler *et al.*, 1996; Maecker *et al.*, 1997).
Other conserved motifs are highlighted in green.



```
                     *        20         *        40         *        60
MusA15    : --------------------METKPVITCLKTLLII--YSFVFWITGVIL------LAVG :  32
HumTM4S2  : --------------------METKPVITCLKTLLII--YSFVFWITGVIL------LAVG :  32
HumTM4-D  : -------------MASPSRRLQTKPVITCFKSVLLI--YTFIFWITGVIL------LAVG :  39
MusTm4s6  : -------------MASPSRRLQTKPVITCLKSVLLI--YTFIFWITGVIL------LAVG :  39
HumTM4-A  : ---------------------MGQCGITSSKTVLVF--LNLIFWGAAGIL------CYVG :  31
MusTM4-A  : ---------------------MGQCGITSSKTVLVF--LNLIFWGAAGIL------CYVG :  31
HumCD63   : -------------------MAVEG-GMKCVKFLLYV--LLLAFCACAVGL------IAVG :  32
RabCD63   : -------------------MAVEG-GMKCVKFLLYV--LLLAFCACAVGL------IAVG :  32
BovCD63   : -------------------MAVEG-GMKCVKFLLYV--LLLVFCACAVGL------IAVG :  32
MusCD63   : -------------------MAVEG-GMKCVKFLLYV--LLLAFCACAVGL------IAIG :  32
RatCD63   : -------------------MAVEG-GMKCVKFLLYV--LLLAFCACAVGL------IAIG :  32
ShsSh23   : -------------------MATLGTGMRCLKSCVFV--LNIICLLCSLVL------IGAG :  33
ShsSM23   : -------------------MATLGTGMRCLKSCVFV--LNIICLLCSLVL------IGAG :  33
ShsSj23   : -------------------MATLGTGMRCLKSCVFI--LNIICLLCSLVL------IGAG :  33
HumNET-4  : ---------------MSGKHYKGPEVSCCIKYFIFG--FNVIFWFLGITF------LGIG :  37
MusTspn5  : ---------------MSGKHYKGPEVSCCIKYFIFG--FNVIFWFLGITF------LGIG :  37
Dros3A    : ---------------MHPHHFT--YVSQCVKYMIFL--LNFVFWLFGGLL------LGIG :  35
HumNET-7  : ----------MPRGDSEQVRYCARFSYLWLKFSLII--YSTVFWLIGALV------LSVG :  42
Dros29Fa  : -------------------MSLLTGSANAVKYTLFG--FNLIFLITGIIL------IAVG :  33
Dros9033  : ------------------------MACNDMR-------------ISGLGI------LIAG :  17
MandD107  : --------------------MALGGGMSCVKYLLFC--FNLLFAITGLII------LIVG :  32
Dros29Fb  : ---------------MSNRELQLNSGMKCAKYMLII--VSFMFALTAILL------IMVG :  37
MandD76   : ---------------MAQTNLEV--GMKCIKYMLLC--ITAIFVLTSALI------ISVG :  35
MkyCD151  : --------------MGEFNEKKTTCGTVCLKYLLFT--YNCCFWLAGLAV------MAVG :  38
MacCD151  : --------------MGEFNEKKTTCGTVCLKYLLFT--YNCCFWLAGLAV------MAVG :  38
HumCD151  : --------------MGEFNEKKTTCGTVCLKYLLFT--YNCCFWLAGLAV------MAVG :  38
MusCD151  : --------------MGEFNEKKATCGTVCLKYLLFT--YNCCFWLAGLAV------MAVG :  38
CatCD9    : -------------------MP-VKGGTKCIKYLLFG--FNFIFWLAGIAV------LAVG :  32
HumCD9    : -------------------MP-VKGGTKCIKYLLFG--FNFIFWLAGIAV------LAIG :  32
MusCD9    : -------------------MP-VKGGSKCIKYLLFG--FNFIFWLAGIAV------LAIG :  32
RatCD9    : -------------------MP-VKGGSKCIKYLLFG--FNFIFWLAGIAV------LAIG :  32
BovCD9    : -------------------MP-VKGGTKCIKYLLFG--FNFIFWLAGIAV------LSVG :  32
ChkCD9    : -------------------MP-VKGGTKCIKYLLFG--FNFVFWLAGTAV------LAIG :  32
ChmpCD81  : -------------------MG-VEGCTKCIKYLLFV--FNFVFWLAGGVI------LGVA :  32
HumCD81   : -------------------MG-VEGCTKCIKYLLFV--FNFVFWLAGGVI------LGVA :  32
MkyCD81   : -------------------MG-VEGCTKCIKYLLFV--FNFVFWLAGGVI------LGVA :  32
TamCD81   : -------------------MG-VEGCTKCIKYLLFV--FNFVFWLAGGVI------LGVA :  32
RatCD81   : -------------------MG-VEGCTKCIKYLLFV--FNFVFWLAGGVI------LGVA :  32
HumTSPN2  : -------------------MGRFRGGLRCIKYLLLG--FNLLFWLAGSAV------IAFG :  33
RatTspn2  : -------------------MGRFRGGLRCIKYLLLG--FNLLFWLAGSAV------IAFG :  33
HumCO029  : ----------------------MAGVSACIKYSMFT--FNFLFWLCGILI------LALA :  30
RatD6.1A  : ----------------------MAGVSGCLKYSMFF--FNFLFWVCGTLI------LGLA :  30
MusCD37   : -------------------MSAQESCLSLIKYFLFV--FNLFFFVLGGLI------FCFG :  33
RatCD37   : -------------------MSAQESCLSLIKYFLFV--FNLFFFVLGGLI------FCFG :  33
HumCD37   : -------------------MSAQESCLSLIKYFLFV--FNLFFFVLGSLI------FCFG :  33
HumCD82   : ---------------------MGSACIKVTKYFLFL--FNLIFFILGAVI------LGFG :  31
MusCD82   : ---------------------MGAGCVKVTKYFLFL--FNLLFFILGAVI------LGFG :  31
MusCD53   : ---------------------MGMSSLKLLKYVLFI--FNLLFWVCGCCI------LGFG :  31
RatCD53   : ---------------------MGMSSLKLLKYVLFF--FNFLFWVCGCCI------LGFG :  31
HumCD53   : ---------------------MGMSSLKLLKYVLFF--FNLLFWICGCCI------LGFG :  31
HumNET-5  : ---------------------MARGCLCCLKYMMFL--FNLIFWLCGCGL------LGVG :  31
HumNAG-2  : ---------------------MARACLQAVKYLMFA--FNLLFWLGGCGV------LGVG :  31
ChkTM4SF  : ---------------------MEGDCLSCMKYLMFL--FNFFIFLGGACL------LGVG :  31
HumNET-1  : -----------------------MQCFSFIKTMMIL--FNLLIFLCGAAL------LAVG :  29
DogSAS    : ---------------------MVCGGFACSKNALCA--LNVVYMLVGLLL------IGVA :  31
HumSAS    : ---------------------MVCGGFACSKNALCA--LNVVYMLVSLLL------IGVA :  31
HumNET-6  : ---------------------MVCGGFACSKNCLCA--LNLLYTLVSLLL------IGIA :  31
Dros97E   : ----------------------MCGGFTCSKNALIA--LNILYVMIGFLL------IGVG :  30
ApisF139  : ----------------------MSCGMGMIKYLLFI--FNFVFAVCGLGI------LTLG :  30
Dros42El  : ----------------------MGCATGTIKYSLFL--FNALWAILGILV------LIFG :  30
Dros42Ea  : ----------------------MSCGISMVKYILFI--FNLLCSICGILL------IVFG :  30
DrosLD16  : ----------------------MDCGTSMVKYILFI--FNTIVSVIGILG------IVYG :  30
DrosGH07  : ----------------------MDCGGVFVKYVLFI--FNILFVICGILL------ITFG :  30
Dros42Eb  : ----------------------MNCLSAMFKYLLYL--LNLVFVAGGILL------IVVG :  30
Dros42Ec  : ----------------------MGCLSGIVNFILYI--VNIVFLIVGILL------IVLG :  30
MandE118  : ----------------------MGCGTSFVKYVLFF--FNLLVSLLGIVL------IAIG :  30
BovUPK1A  : -------------------MAKDDSTVRCFQGLLIF--GNVIIGMCSIAL------MAEC :  33
BovUPK1B  : -------------------MAKDDSTVRCFQGLLIF--GNVIIGMCSIAL------MAEC :  33
MusUPK1B  : ------------------------------------------------------------ :   -
HumUPK1B  : -------------------MAKDNSTVRCFQGLLIF--GNVIIGCCGIAL------TAEC :  33
MinkTI-1  : -------------------MAKDDSSVRCFQGLLIF--GNVIVGMCGIAL------TAEC :  33
RabUPK1B  : --------------------------VRCFQGLLIF--GNVITGMCGIAL------TAEC :  26
XenUP1B5  : --------------------MKDDSGVRCYQSIIIF--GNVVMGLCGLAL------TAEC :  32
XenUP1B3  : ------------------------------------------------------------ :   -
HumUPK1A  : --------------MASAAAAEAEKGSPVVVGLLVV--GNIIILLSGLSL------FAET :  38
SusUPK1A  : ------------------------------------------------------------ :   -
CatPRPH   : --------------MALLKVKFDQKKRVKLAQGLWL--MNWLSVLAGIVI------FSLG :  38
DogPRPH   : --------------MALLKVKFDQKKRVKLAQGLWL--MNWLSVLAGIVI------FSLG :  38
MusPRPH2  : --------------MALLKVKFDQKKRVKLAQGLWL--MNWLSVLAGIVL------FSLG :  38
RatPRPH   : --------------MALLKVKFDQKKRVKLAQGLWL--MNWLSVLAGIVL------FSLG :  38
ChkPRPH1  : --------------MALLKVKFNQKKRVKLAQGLWL--MNWFSVFAGIIV------FSMG :  38
XenPRPH8  : --------------MALMKTKFNLKRRVKLAQGLWL--MNWCCVLAGIAL------FSMG :  38
ChkPRPH2  : --------------MTVLKVKFTKTKRDKLAQILWI--LNWVSVVSGIIL------FSLG :  38
XenPRPH5  : --------------MVLFKAKFSFQRRVKLAQTLWL--LSWLSVLVGCLT------FGMG :  38
XenPRPH6  : --------------MVLFKAKFSFQRRVKLAQTLWL--LSWLSVLVGCLT------FGMG :  38
BovROM-1  : -------------MAPVLPLVLPLQPRIRLVQGLWL--LSWLLVLVGGLT------LLCS :  39
MusROM-1  : -------------MAPVLPVVLPLQPRIRLAQGIWL--LSWLLALVGGLT------LLCS :  39
HumROM-1  : -------------MAPVLPLVLPLQPRIRLAQGLWL--LSWLLALAGGVI------LLCS :  39
MusL6     : --------------------MCYVKCARYIGYSLVW--AAVFCIVANALL------YFPN :  32
HumTM4S5  : --------------------MCTGKCARCVGLSLIT--LCFVCIVANALL------LVPN :  32
HumilTMP  : --------------------MCTGGCARCLGGTLIP--LAFFGFLANILL------FFPG :  32
Dros42Eg  : ----------------------MACSTNVLKGFALF--WDIILALFGLVV------IGLG :  30
DrosLBL   : ----------------------MGCATTSVKIASIV--LNAVLGFLAAGA------IGWI :  30
Dros8666  : -----------------------------------------------MVQ------LNYA :   7
Dros42Ei  : ----------------------MGLGATTVKHVLLL--LNFVFSVLGLAL------IAFG :  30
DrosLD29  : --------------------MVFDCGVWCAKYLLCI--FNFIFFVLGTII------FGVG :  32
HumTM4-B  : -------------------MAEIHTPYSSLKKLLSL--LNGFVAVSGIIL------VGLG :  33
CeB0563   : ------------MNFRNQSTMPLSCTARALKFSLFI--FNLVFLVSGALCGLIC--LGIG :  44
HumNET-2  : --------------------MAREDSVKCLRCLLYA--LNLLFWLMSISV------LAVS :  32
CeC14A11  : --------------------------------MLVD--KNSLNTVASTVK--------VD :  18
ShsTE736  : --------------------MELTLSQQFWTKLFFL--LNSLFGIFGIVL------LAFG :  32
ShsSj25   : --------------------MKLSFTKVSLTNILIL--FNCLFIIFSMIV------LTFG :  32
CeF53B6   : --------------MGALGDSAYGARGRLIKFSYIV--TALISILFSISC------ICYG :  38
MusM6B    : MKPAMETAAEENTEQSQERKGCFECCIKCLGGVPYASLVATILCFSGVALFCGCGHVALA :  60
DrosM6    : -------------------MPGKGNNRDRIRDPREEILLETNFEDDGGVLTRAYNGNPYN :  41
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```
                     *        80         *       100         *       120
MusA15    : VWGKLTLGT--------------------YISLIAENSTNAP-YVLIGTGTTIVVFGLFG :  71
HumTM4S2  : VWGKLTLGT--------------------YISLIAENSTNAP-YVLIGTGTTIVVFGLFG :  71
HumTM4-D  : IWGKVSLEN--------------------YFSLLNEKATNVP-FVLIATGTVIILLGTFG :  78
MusTm4s6  : IWGKVSLEN--------------------YFSLLNEKATNVP-FVLIGTGTVIILLGTFG :  78
HumTM4-A  : AYVFITYDD--------------------YDHFFEDVYTLIPAVVIIAVGALLFIIGLIG :  71
MusTM4-A  : AYVFITYDD--------------------YDHFFEDVYTLFPAVVIIAVGALLFIIGLIG :  71
HumCD63   : VGAQLVLS---------------------QTIIQGATPGSLLPVVIIAVGVFLFLVAFVG :  71
RabCD63   : VGAQLVLS---------------------QTITHGATPGSLLPVVIIAVGAFLFLVAFVG :  71
BovCD63   : VGTHLVLN---------------------QTITHGATPSFLLPVVIIAVGAFLFLVAFVG :  71
MusCD63   : VAVQVVLK---------------------QAITHETTAGSLLPVVIIAVGAFLFLVAFVG :  71
RatCD63   : VAVQVVLK---------------------QAITHETTAGSLLPVVIIAVGAFLFLVAFVG :  71
ShsSh23   : AYVEVKFS---------------------QYGDNLHKVWQAAPIAIIVVGVIILIVSFLG :  72
ShsSM23   : AYVEVKFS---------------------QYGDNLHKVWQAAPIAIIVVGVIILIVSFLG :  72
ShsSj23   : AYVEVKFS---------------------QYEANLHKVWQAAPIAIIVVGVVILIVSFLG :  72
HumNET-4  : LWAWNEKGVLS-------------NISSITDLGGFDPVWL-----FLVVGGVMFILGFAG :  79
MusTspn5  : LWAWNEKGVLS-------------NISSITDLGGFDPVWL-----FLVVGGVMFILGFAG :  79
Dros3A    : VYAFRDKWEDA-------------NGS--VRLENFYDVFLNISLVMILAGTDIFLVSFSG :  80
HumNET-7  : IYAEVER----------------------QKYKTLESAFLAPAIILILLGVVMFMVSFIG :  80
Dros29Fa  : AGVGAVYTG--------------------YKLFLAGKFFSI-PTFLIVIGSFIIIISFFG :  72
Dros9033  : AVVLADVNE--------------------FNHFVEGRVLAP-PIVLIVTGLIIFLIASLG :  56
MandD107  : IKAQINSWP--------------------YIDLTDENFYTSGPVVLIIVGIIVFIVAFFG :  72
Dros29Fb  : TTIQTIFGD--------------------FSLFIDGHFSSP-PALLIAIGFILIAVAALG :  76
MandD76   : TTIYAIYHD--------------------VSFFLEDHFFSP-ATFVIVIGVIMLFVSLFG :  74
MkyCD151  : IWTLALKSD--------------------YISLLASGTYLATAYILVVAGAVVMVTGVLG :  78
MacCD151  : IWTLALKSD--------------------YISLLASGTYLATAYILVVAGAVVMVTGVLG :  78
HumCD151  : IWTLALKSD--------------------YISLLASGTYLATAYILVVAGTVVMVTGVLG :  78
MusCD151  : IWTLALKSD--------------------YISLLASSTYLATAYILVVAGVVVMVTGVLG :  78
CatCD9    : LWLRFDSQTKS-------------IFEQDSQP----SSFYTGVYILIGAGALMMLVGFLG :  75
HumCD9    : LWLRFDSQTKS-------------IFEQETNNN--NSSFYTGVYILIGAGALMMLVGFLG :  77
MusCD9    : LWLRFDSQTKS-------------IFEQENNH----SSFYTGVYILIGAGALMMLVGFLG :  75
RatCD9    : LWLRFDSQTKS-------------IFEQETNH----SSFYTGVYILIGAGALMMLVGFLG :  75
BovCD9    : LWLRFDSQTKS-------------IFEQENND----SSFYTGVYILIGAGALMMLVGFLG :  75
ChkCD9    : LWLRFDVQTKS-------------IFELESNN----MTFYTGVYILIGAGALMMLVGFLG :  75
ChmpCD81  : LWLRHDPQTTN-------------LLYLELGDKPAPNTFYVGIYILIAVGAVMMFVGFLG :  79
HumCD81   : LWLRHDPQTTN-------------LLYLELGDKPAPNTFYVGIYILIAVGAVMMFVGFLG :  79
MkyCD81   : LWLRHDPQTTN-------------LLYLELGDKPAPNTFYVGIYILIAVGAVMMFVGFLG :  79
TamCD81   : LWLRHDPQTTN-------------LLYLELGDKPAPNTFYVGIYILIAVGAVMMFVGFLG :  79
RatCD81   : LWLRHDPQTTT-------------LLYLELGDKPAPSTFYVGIYILIAVGAVMMFVGFLG :  79
HumTSPN2  : LWFRFGGAIKE-------------LSSEDKSP----EYFYVGLYVLVGAGALMMAVGFFG :  76
RatTspn2  : LWFRFGGTIKD-------------LSSEEKSP----EYFYVGLYVLVGAGALMMAVGFFG :  76
HumCO029  : IWVRVSNDSQA-------------IFGSEDVG----SSSYVAVDILIAVGAIIMILGFLG :  73
RatD6.1A  : IWLRVSKDGKE-------------IITSGDNG----TNPFIAVNILIAVGSIIMVLGFLG :  73
MusCD37   : TWILIDKT--S-------------FVSFVGLSF---VPLQTWSKVLAVSGVLTMALALLG :  75
RatCD37   : TWILIDKT--S-------------FVSFVGLSF---VPLQTWSKVLSVSGVLTMALALLG :  75
HumCD37   : IWILIDKT--S-------------FVSFVGLAF---VPLQIWSKVLAISGIFTMGIALLG :  75
HumCD82   : VWILADKS--S-------------FISVLQTSS---SSLRMGAYVFIGVGAVTMLMGFLG :  73
MusCD82   : VWILADKN--S-------------FISVLQTSS---SSLQVGAYVFIGVGAITIVMGFLG :  73
MusCD53   : IYFLVQN---T-------------YGVLFRN-----LPFLTLGNILVIVGSIIMVVAFLG :  70
RatCD53   : IHLLVQN---T-------------YGILFRN-----LPFLTLGNVLVIVGSIIMVVAFLG :  70
HumCD53   : IYLLIHN---N-------------FGVLFHN-----LPSLTLGNVFVIVGSIIMVVAFLG :  70
HumNET-5  : IWLSVSQG--N-------------FATFSPS-----FPSLSAANLVIAIGTIVMVTGFLG :  71
HumNAG-2  : IWLAATQG--S-------------FATLSSS-----FPSLSAANLLIITGAFVMAIGFVG :  71
ChkTM4SF  : IWVIVDPT--G-------------FREIVAANP----LLFTGAYIMLAMGAMLFLLGFLG :  72
HumNET-1  : IWVSIDGA--S-------------FLKIFGPLSSSAMQFVNVGYFLIAAGVVVFALGFLG :  74
DogSAS    : AWGKGLG----------------------------LVSSIHIIGGVIAVGVFLLLIAVAG :  63
HumSAS    : AWGKGLG----------------------------LVSSIHIIGGVIAVGVFLLLIAVAG :  63
HumNET-6  : AWGIGFG----------------------------LISSLRVVGVVIAVGIFLFLIALVG :  63
Dros97E   : VYARAAS----------------------------IVTNLPIVGGILACGVILICISMLG :  62
ApisF139  : VLIHL---------------------QILGVSKQIETGLAFPSITLIVLGSIIFVISFFG :  69
Dros42El  : GLGWG---------------------AMP----------DAYAIGILILGGTILVISLFG :  59
Dros42Ea  : ALLFS--------------------KVRNMDDFAEALRTQQVPVTMIILGTIILLISWFG :  70
DrosLD16  : VLILKSI------------------GVVEVNGQVGFPIQALMPIILISLGSIVVFISFLG :  72
DrosGH07  : SIMVS--------------------TIKDFSGVGETFTANSVAIIILVLGCVVFLVAFMG :  70
Dros42Eb  : SIMLS--------------------TMGNFTAFDGGVNTQTIPICIIVIGSVTFVVAFFG :  70
Dros42Ec  : SIMLS--------------------DLSRFDVAGSGTDPNTIPICVTVLGGLIFVVSFFG :  70
MandE118  : VVFVVN---------------------WKVVKDELQSHLTVAPWVFIIIGAVMFTIAFFG :  69
BovUPK1A  : IFFVSDQNS-----------------LYPLLEATNNDDIYAAAWIGMSVGICLFCLSVLG :  76
BovUPK1B  : IFFVSDQNS-----------------LYPLLEATNNDDIYAAAWIGMSVGICLFCLSVLG :  76
MusUPK1B  : ------------------------------------------------------------ :   -
HumUPK1B  : IFFVSDQHS-----------------LYPLLEATDNDDIYGAAWIGIFVGICLFCLSVLG :  76
MinkTI-1  : IFFVSDQHS-----------------LYPLLEATDNDDIYGAAWIGMFVGICLFCLSVLG :  76
RabUPK1B  : IFFVSDQHS-----------------LYPLLEATNNDDIYGAAWIGMFVGICLFCLSVLG :  69
XenUP1B5  : IFFVSDQSG-----------------IYPLLEATDNDDIFGAAWIGIFAGFCLFVLSIVG :  75
XenUP1B3  : ------------------------------------------------------------ :   -
HumUPK1A  : IWVTADQYR-----------------VYPLMGVSGKDDVFAGAWIAIFCGFSFFMVASFG :  81
SusUPK1A  : ----------------------------------------------IFCGFSFFVVASFG :  14
CatPRPH   : LFLKIELRK-------------------RSDVMN-NSESHFVPNSLIGMGVLSCVFNSLA :  78
DogPRPH   : LFLKIELRK-------------------RSDVMN-NSESHFVPNSLIVMGVLSCVFNSLA :  78
MusPRPH2  : LFLKIELRK-------------------RSEVMN-NSESHFVPNSLIGVGVLSCVFNSLA :  78
RatPRPH   : LFLKIELRK-------------------RSDVMD-NSESHFVPNSLIGVGVLSCVFNSLA :  78
ChkPRPH1  : LFLKIELRK-------------------RSEVMD-NSESHFVPNSLILMGILSCAFNGFA :  78
XenPRPH8  : VFLKIELRK-------------------RSEVMD-NDESHFVPNSLILMGSLACALNAFP :  78
ChkPRPH2  : LFLKIEIKK-------------------RNEVMA-KGDINSVPNMLISVGVIACVVNFLG :  78
XenPRPH5  : IFLKVQLWI-------------------HNEVME-NTSAHAVPNTVITAGLVGILLGIYA :  78
XenPRPH6  : IFLKVQLWI-------------------HNEVMD-NTTAHAVPNTVITAGLVGILLGYFA :  78
BovROM-1  : GHLLVQLWH-------------------LGTFLAPSCPFSALPQVALAASAVALGTGLVG :  80
MusROM-1  : GHLLVQLGH-------------------LGTFLAPSCSFPALPQTALAAGTVALGTGLGG :  80
HumROM-1  : GHLLVQLRH-------------------LGTFLAPSCQFPVLPQAALAAGAVALGTGLVG :  80
MusL6     : GETKYATED------------------HLSRFVWYFAGIVGGGLLMLLPAFVFIGMDEED :  74
HumTM4S5  : GETSWTNTN------------------HLSLQVWLMGGFIGGGLMVLCPGIAAVRAGGK- :  73
HumilTMP  : G-KVIDDND------------------HLSQEIWFFGGILGSGVLMIFPALVFLGLKNND :  73
Dros42Eg  : VHIIYKFEH-----------------------------FNTAAFVIIAVGVVVVLTALFG :  61
DrosLBL   : AYNADTET-------------------------------EEFVIAAYIACSLILVFALLG :  59
Dros8666  : HYSNFVSDH-----------------------------VWTAPIILMIVGAAVAVICFLG :  38
Dros42Ei  : IFFLISAAEN-----------------------AVSIGKNAAGGLIIALGVVILIIAIFG :  67
DrosLD29  : LWLAVDKHSLIALLKL--------VESERIEQFTQPQAIEQLAYVLLVIGAVMFFMSFLG :  84
HumTM4-B  : IGGKCGGAS------------------LTNVLGLSSAYLLHVGNLCLVMGCITVLLGCAG :  75
CeB0563   : LWLVLDKYAIDNLAFATAKVQGYDQDAGLRDLATKPTAVRQFGYLLFVGGFIVIVVAFLG : 104
HumNET-2  : AWMRDYLNN-----------VLTLTAETRVEEAVILTYFPVVHPVMIAVCCFLIIVGMLG :  81
CeC14A11  : LSQILSQVN--------------------------IQQLNSFLYVAIVIGGALLVLGFFG :  52
ShsTE736  : IKGYDILVKFN---------------------IILQGTIPVIFPITIFLGCFLLLSTLIG :  71
ShsSj25   : VIPQIYLLK---------------------FANILHGVRPSIFPIVCFTGSFVIIVACVG :  71
CeF53B6   : IWLLARRSQ--------------------YAELVSPSLYVDVGRILVIISILSILNYLIC :  78
MusM6B    : GTVAILEQHFS---------------TNTSDHALLSEVIQLMQYVIYGIASFFFLYGIIL : 105
DrosM6    : PTIQNRRRNSYR---------SDHSLDRYTERGGEGECCQSCMARIPYATLIATLMCLLG :  92
                                                             g         g
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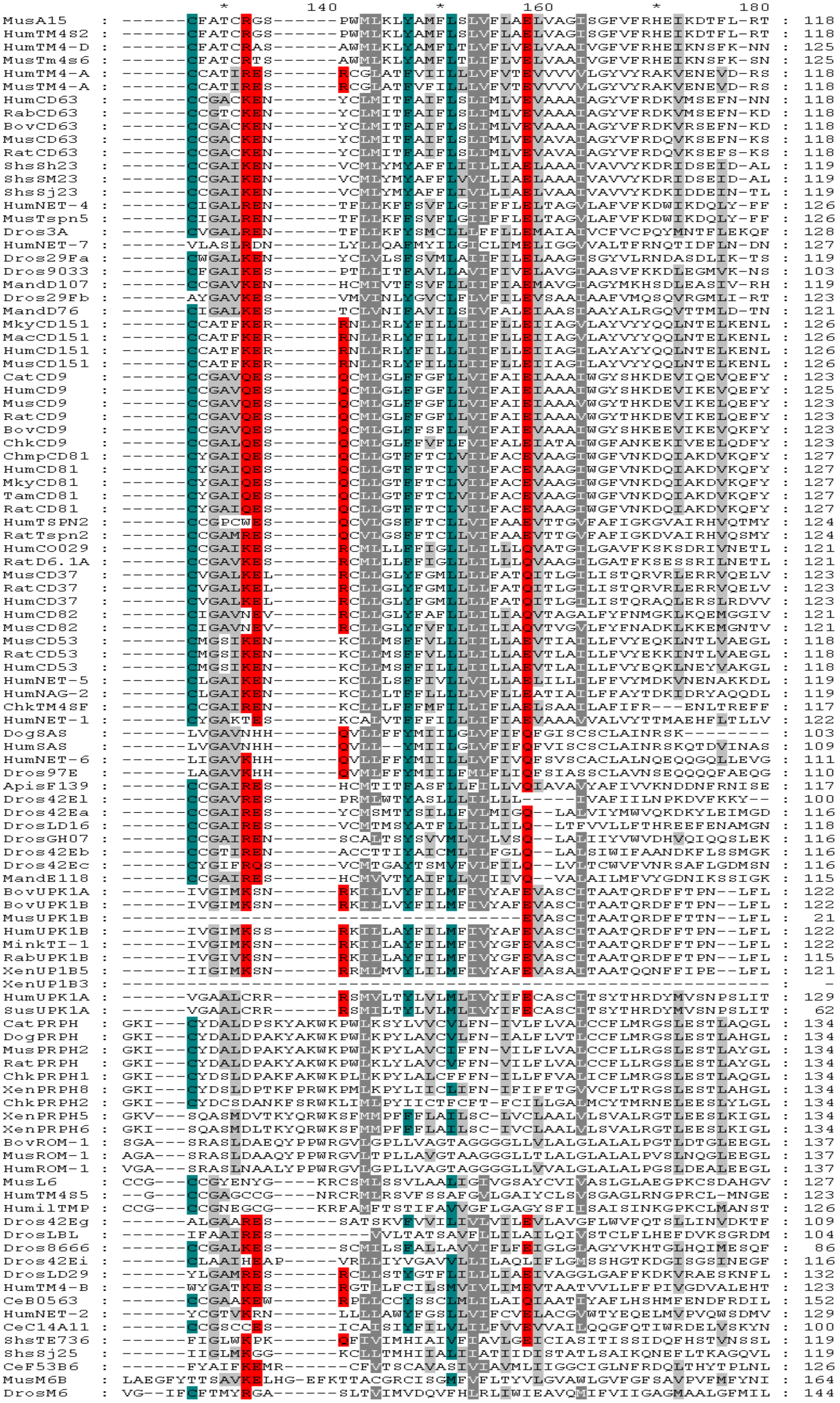

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                    *       140         *       160         *       180
MusA15   : ------CFATCRGS------PWMLKLYAMFLSLVFLAELVAGISGFVFRHEIKDTFL-RT : 118
HumTM4S2 : ------CFATCRGS------PWMLKLYAMFLSLVFLAELVAGISGFVFRHEIKDTFL-RT : 118
HumTM4-D : ------CFATCRAS------AWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFK-NN : 125
MusTm4s6 : ------CFATCRTS------AWMLKLYAMFLTLIFLVELVAAIVGFVFRHEIKNSFK-SN : 125
HumTM4-A : ------CCATIRES------RCGLATFVIILLLVFVTEVVVVVLGYVYRAKVENEVD-RS : 118
MusTM4-A : ------CCATIRES------RCGLATFVFILLLVFVTEVVVVVLGYVYRAKVENEVD-RS : 118
HumCD63  : ------CCGACKEN------YCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVMSEFN-NN : 118
RabCD63  : ------CCGTCKEN------YCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVMSEFN-KD : 118
BovCD63  : ------CCGACKEN------YCLMITFAIFLSLIMLVEVAAAIAGYVFRDKVRSEFN-KD : 118
MusCD63  : ------CCGACKEN------YCLMITFAIFLSLIMLVEVAVAIAGYVFRDQVKSEFN-KS : 118
RatCD63  : ------CCGACKEN------YCLMITFAIFLSLIMLVEVAVAIAGYVFRDQVKSEFS-KS : 118
ShsSh23  : ------CCGAIKEN------VCMLYMYAFFLIILLIAELAAAIVAVVYKDRIDSEID-AL : 119
ShsSM23  : ------CCGAIKEN------VCMLYMYAFFLVVLLIAELAAAIVAVVYKDRIDSEID-AL : 119
ShsSj23  : ------CCGAIKEN------VCMLYMYAFFLIVLLIAELVAAIVAVVYKDKIDDEIN-TL : 119
HumNET-4 : ------CIGALREN------TFLLKFFSVFLGIIFFLELTAGVLAFVFKDWIKDQLY-FF : 126
MusTspn5 : ------CIGALREN------TFLLKFFSVFLGIIFFLELTAGVLAFVFKDWIKDQLY-FF : 126
Dros3A   : ------CVGALREN------TFLLKFYSMCLLLFFLLEMAIAIVCFVCPQYMNTFLEKQF : 128
HumNET-7 : ------VLASLRDN------LYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFLN-DN : 127
Dros29Fa : ------CWGALKEN------YCLVLSFSVMLAIIFILELAAGISGYVLRNDASDLIK-TS : 119
Dros9033 : ------CFGAIKES------PTLLITFAVLLAVIFIVELAVGIAASVFKKDLEGMVK-NS : 103
MandD107 : ------CCGAVKEN------HCMIVTFSVFLLIIFIAEMAVGIAGYMKHSDLEASIV-RH : 119
Dros29Fb : ------AYGAVKES------VMVINLYGVCLFLVFILEVSAAIAAFVMQSQVRGMLI-RT : 123
MandD76  : ------CIGALKES------TCLVNIFAVILSIVFALEIAASIAAYALRGQVTTMLD-TN : 121
MkyCD151 : ------CCATFKER------RNLLRLYFILLLIIFLLEIIAGVLAYVYYQQLNTELKENL : 126
MacCD151 : ------CCATFKER------RNLLRLYFILLLIIFLLEIIAGVLAYVYYQQLNTELKENL : 126
HumCD151 : ------CCATFKER------RNLLRLYFILLLIIFLLEIIAGILAYAYYQQLNTELKENL : 126
MusCD151 : ------CCATFKER------RNLLRLYFILLLIIFLLEIIAGILAYVYYQQLNTELKENL : 126
CatCD9   : ------CCGAVQES------QCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIQEVQEFY : 123
HumCD9   : ------CCGAVQES------QCMLGLFFGFLLVIFAIEIAAAIWGYSHKDEVIKEVQEFY : 125
MusCD9   : ------CCGAVQES------QCMLGLFFGFLLVIFAIEIAAAVWGYTHKDEVIKELQEFY : 123
RatCD9   : ------CCGAVQES------QCMLGLFFGFLLVIFAIEIAAAVWGYTHKDEVIKELQEFY : 123
BovCD9   : ------CCGAVQES------QCMLGLFFSFLLVIFAIEVAAAIWGYSHKEEVIKEVQKFY : 123
ChkCD9   : ------CCGALQES------QCMLGLFFVFLFVIFALEIATAIWGFANKEKIVEELQDFY : 123
ChmpCD81 : ------CYGAIQES------QCLLGTFFTCLVILFACEVAAGIWGFVNKDQIAKDVKQFY : 127
HumCD81  : ------CYGAIQES------QCLLGTFFTCLVILFACEVAAGIWGFVNKDQIAKDVKQFY : 127
MkyCD81  : ------CYGAIQES------QCLLGTFFTCLVILFACEVAAGIWGFVNKDQIAKDVKQFY : 127
TamCD81  : ------CYGAIQES------QCLLGTFFTCLVILFACEVAAGIWGFVNKDQIAKDVKQFY : 127
RatCD81  : ------CYGAIQES------QCLLGTFFTCLVILFACEVAAGIWGFVNKDQIAKDVKQFY : 127
HumTSPN2 : ------CCGPCWES------QCVLGSFFTCLLVIFAAEVTTGVFAFIGKGVAIRHVQTMY : 124
RatTspn2 : ------CCGAMRES------QCVLGSFFTCLLVIFAAEVTTGVFAFIGKDVAIRHVQSMY : 124
HumCO029 : ------CCGAIKES------RCMLLLFFIGLLLILLLQVATGILGAVFKSKSDRIVNETL : 121
RatD6.1A : ------CCGAVKES------RCMLLLFFIGLLLILLLQVAAGILGATFKSESSRILNETL : 121
MusCD37  : ------CVGALKEL------RCLLGLYFGMLLLLFATQITLGILISTQRVRLERRVQELV : 123
RatCD37  : ------CVGALKEL------RCLLGLYFGMLLLLFATQITLGILISTQRVRLERRVQELV : 123
HumCD37  : ------CVGALKEL------RCLLGLYFGMLLLLFATQITLGILISTQRAQLERSLRDVV : 123
HumCD82  : ------CIGAVNEV------RCLLGLYFAFLLLILIAQVTAGALFYFNMGKLKQEMGGIV : 121
MusCD82  : ------CIGAVNEV------RCLLGLYFVFLLLILIAQVTVGVLFYFNADKLKKEMGNTV : 121
MusCD53  : ------CMGSIKEN------KCLLMSFFVLLLIILLAEVTIAILLFVYEQKLNTLVAEGL : 118
RatCD53  : ------CMGSIKEN------KCLLMSFFVLLLIILLAEVTLAILLFVYEKKINTLVAEGL : 118
HumCD53  : ------CMGSIKEN------KCLLMSFFILLLIILLAEVTLAILLFVYEQKLNEYVAKGL : 118
HumNET-5 : ------CLGAIKEN------KCLLLSFFIVLLVILLAELILLILFFVYMDKVNENAKKDL : 119
HumNAG-2 : ------CLGAIKEN------KCLLLTFFLLLLLVFLLEATIAILFFAYTDKIDRYAQQDL : 119
ChkTM4SF : ------CCGAIREN------KCLLLFFFMFILLIFLAELSAAILAFIFR---ENLTREFF : 117
HumNET-1 : ------CYGAKTES------KCALVTFFFILLLIFIAEVAAAVVALVYTTMAEHFLTLLV : 122
DogSAS   : ------LVGAVNHH------QVLLFFYMIILGLVFIFQFGISCSCLAINRSK-------- : 103
HumSAS   : ------LVGAVNHH------QVLL--YMIILGLVFIFQFVISCSCLAINRSKQTDVINAS : 109
HumNET-6 : ------LIGAVKHH------QVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVG : 111
Dros97E  : ------LAGAVKHH------QVMLFFYMIILFMLFLIQFSIASSCLAVNSEQQQQFAEQG : 110
ApisF139 : ------CCGAIRES------HCMTITFASFLLFILLVQIAVAVYAFIVVKNDDNFRNISE : 117
Dros42El : ------CCGAVRES------PRMLWTYASLLLILLLL-----IVAFIILNPKDVFKKY-- : 100
Dros42Ea : ------CCGAIRES------YCMSMTYSILLFVLMIGQ--LALVIYMWVQKDKYLEIMGD : 116
DrosLD16 : ------CCGAIRES------VCMTMSYATFLLILLILQ--LTFVVLLFTHREEFENAMGN : 118
DrosGH07 : ------CCGAIREN------SCALTSYSVVMLVLLVSQ--LALIIYVWVDHVQIQQSLEK : 116
Dros42Eb : ------CCGTIREN------ACCTTIYAICMLILFGLQ--LALSIWIFAANDKFLSSMGK : 116
Dros42Ec : ------CYGIFRQS------VCMTGAYTSMVFVLFILQ--LVLTCWVFVNRSAFLGDMSN : 116
MandE118 : ------CCGAIRES------HCMVVTYAIFLLVIIIVQ--VALAILMFVYGDNIKSSIGK : 115
BovUPK1A : ------IVGIMKSN------RKILLVYFILMFIVYAFEVASCITAATQRDFFTPN--LFL : 122
BovUPK1B : ------IVGIMKSN------RKILLVYFILMFIVYAFEVASCITAATQRDFFTPN--LFL : 122
MusUPK1B : -------------------------------------EVASCITAATQRDFFTTN--LFL :  21
HumUPK1B : ------IVGIMKSS------RKILLAYFILMFIVYAFEVASCITAATQRDFFTPN--LFL : 122
MinkTI-1 : ------IVGIMKSN------RKILLAYFILMFIVYGFEVASCITAATQRDFFTPN--LFL : 122
RabUPK1B : ------IVGIVKSN------RKILLAYFILMFIVYGFEVASCITAATQRDFFTPN--LFL : 115
XenUP1B5 : ------IIGIMKSN------RRMLMVYLILMFIVYAFEVASAITAATQQNFFIPE--LFL : 121
XenUP1B3 : ------------------------------------------------------------ :   -
HumUPK1A : ------VGAALCRR------RSMVLTYLVLMLIVYIFECASCITSYTHRDYMVSNPSLIT : 129
SusUPK1A : ------VGAALCRR------RSMILTYLVLMLIVYIFECASCITSYTHRDYMVSNPSLIT :  62
CatPRPH  : GKI---CYDALDPSKYAKWKPWLKSYLVVCVLFN-IVLFLVALCCFLMRGSLESTLAQGL : 134
DogPRPH  : GKI---CYDALDPAKYAKWKPWLKPYLAVCVLFN-IALFLVTLCCFLMRGSLESTLAHGL : 134
MusPRPH2 : GKI---CYDALDPAKYAKWKPWLKPYLAVCIFFN-VILFLVALCCFLLRGSLESTLAYGL : 134
RatPRPH  : GKI---CYDALDPAKYAKWKPWLKLYLAVCVFFN-VILFLVALCCFLLRGSLESTLAYGL : 134
ChkPRPH1 : GKI---CYDSLDPAKFAKWKPLLKPYLALCFFFN-ILLFFVALICFLMRGSLESTLAQGL : 134
XenPRPH8 : GKI---CYDSLDPTKFPRWKPMLKPYLIICLIFN-IFIFFTGVVCFLTRGSLESTLAHGL : 134
ChkPRPH2 : GKI---CYDCSDANKFSRWKLIMLPYIICTFCFT-FCILLGALMCYTMRNELEESLYLGL : 134
XenPRPH5 : GKV---SQASMDVTKYQRWKSFMMPFFFLAILSC-LVCLAALVLSVALRGTLEESLKIGL : 134
XenPRPH6 : GKI---SQASMDLTKYQRWKSFMMPFFFLAILSC-IVCLAALVLSVALRGTLEESLKIGL : 134
BovROM-1 : SGA---SRASLDAEQYPPWRGVLGPLLVAGTAGGGGLLVLALGLALALPGTLDTGLEEGL : 137
MusROM-1 : AGA---SRASLDAAQYPPWRGVLTPLLAVGTAAGGGLLTLALGLALALPVSLNQGLEEGL : 137
HumROM-1 : VGA---SRASLNAALYPPWRGVLGPLLVAGTAGGGGLLVVALGLALALPGSLDEALEEGL : 137
MusL6    : CCG---CCGYENYG----KRCSMLSSVLAALIGIVGSAYCVIVASLGLAEGPKCSDAHGV : 127
HumTM4S5 : --G---CCGAGCCG----NRCRMLRSVFSSAFGVLGAIYCLSVSGAGLRNGPRCL-MNGE : 123
HumilTMP : CCG---CCGNEGCG----KRFAMFTSTIFAVVGFLGAGYSFIISAISINKGPKCLMANST : 126
Dros42Eg : ------ALGAARES------SATSKVFVVILIVLVILEVLAVGFLWVFQTSLLINVDKTF : 109
DrosLBL  : ------IFAAIRES---------VVLTATSAVFLLILAILQIVSTCLFLHEFDVKSGRDM : 104
Dros8666 : ------CCGALKES------SCMILSFALLAVVIFLFEIGLGLAGYVKHTGLHQIMESQF :  86
Dros42Ei : ------CLAAIHEAP-----VRLLIYVGAVVLLILAQLIFLGMSSHGTKDGISGSINEGF : 116
DrosLD29 : ------YLGAMRES------RCLLSTYGTFLILLLIAEIVAGGLGAFFKDKVRAESKNFL : 132
HumTM4-B : ------WYGATKES------RGTLLFCILSMVIVLIMEVTAATVVLLFFPIVGDVALEHT : 123
CeB0563  : ------CCGAAKEW------RPLLCCYSSCLMLILAIQIAATIYAFLHSHMFENDFRDIL : 152
HumNET-2 : ------YCGTVKRN------LLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMV : 129
CeC14A11 : ------CCGSCCES------ICAISIYFILVLILFVVEVVAILQQGFQTIWRDELVSKYN : 100
ShsTE736 : ------FIGLWKPK------QFIVIMHIAIVFIAVLGEICIASITISSIDQFHSTVNSSL : 119
ShsSj25  : ------IIGLMKGG------KCLLTMHIIALIIATIIDISTATLSAIKQNEFLTKAGQVL : 119
CeF53B6  : ------FYAIFKEMR------CFVTSCAVASIVIAVMLIIGGCIGLNFRDQLTHYTPLNL : 126
MusM6B   : LAEGFYTTSAVKELHG-EFKTTACGRCISGMFVFLTYVLGVAWLGVFGFSAVPVFMFYNI : 164
DrosM6   : VG--IFCFTMYRGA------SLTVIMVDQVFHLRLIWIEAVQMIFVIIGAGMAALGFMIL : 144
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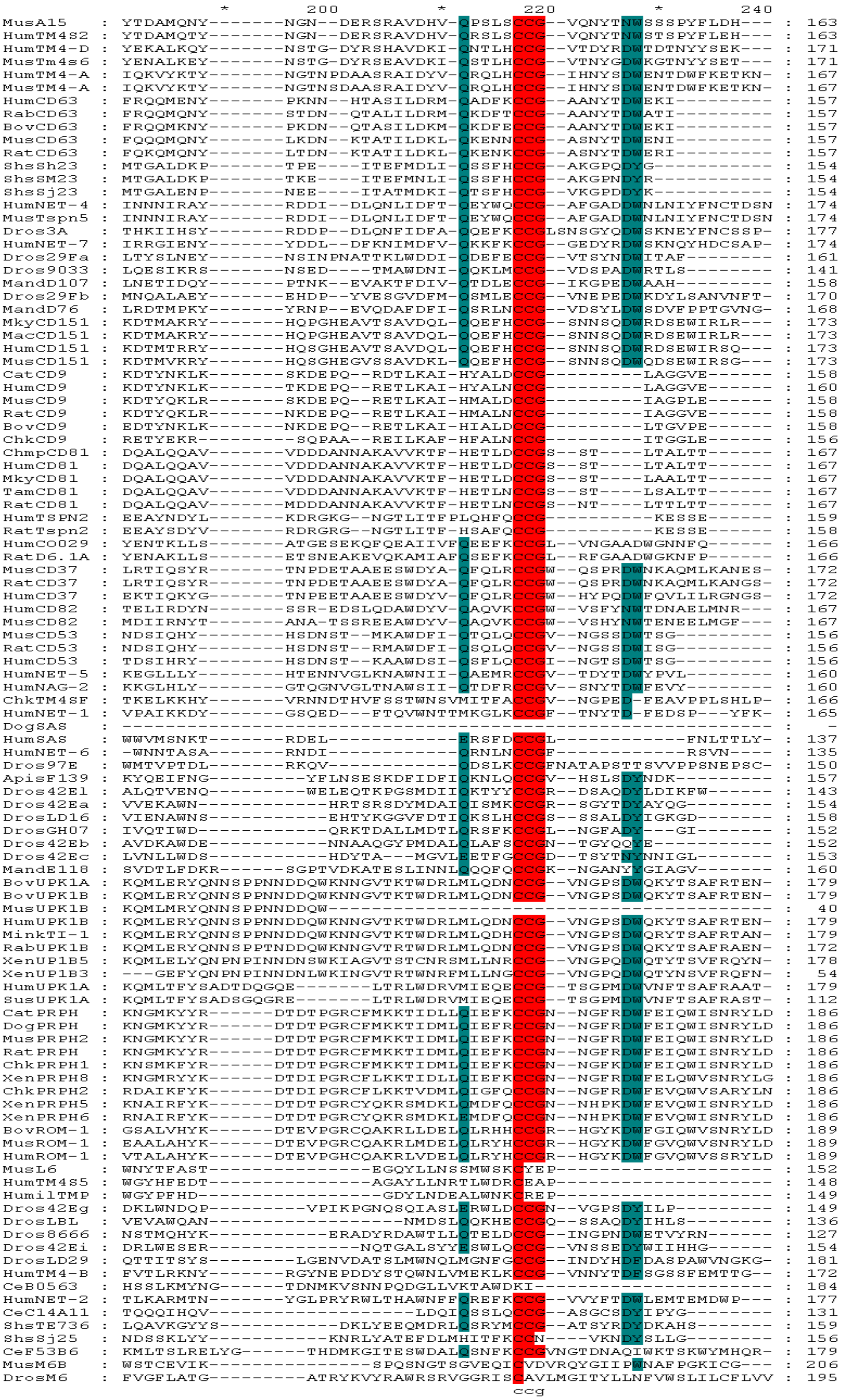

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                     *       200         *       220         *       240
MusA15    : YTDAMQNY-------NGN--DERSRAVDHV-QPSLSCCG--VQNYTNWSSSPYFLDH--- : 163
HumTM4S2  : YTDAMQTY-------NGN--DERSRAVDHV-QRSLSCCG--VQNYTNWSTSPYFLEH--- : 163
HumTM4-D  : YEKALKQY-------NSTG-DYRSHAVDKI-QNTLHCCG--VTDYRDWTDTNYYSEK--- : 171
MusTm4s6  : YENALKEY-------NSTG-DYRSEAVDKI-QSTLHCCG--VTNYGDWKGTNYYSET--- : 171
HumTM4-A  : IQKVYKTY-------NGTNPDAASRAIDYV-QRQLHCCG--IHNYSDWENTDWFKETKN- : 167
MusTM4-A  : IQKVYKTY-------NGTNSDAASRAIDYV-QRQLHCCG--IHNYSDWENTDWFKETKN- : 167
HumCD63   : FRQQMENY-------PKNN--HTASILDRM-QADFKCCG--AANYTDWEKI--------- : 157
RabCD63   : FRQQMQNY-------STDN--QTALILDRM-QKDFTCCG--AANYTDWATI--------- : 157
BovCD63   : FRQQMKNY-------PKDN--QTASILDKM-QKDFECCG--AANYTDWEKI--------- : 157
MusCD63   : FQQQMQNY-------LKDN--KTATILDKL-QKENNCCG--ASNYTDWENI--------- : 157
RatCD63   : FQKQMQNY-------LTDN--KTATILDKL-QKENKCCG--ASNYTDWERI--------- : 157
ShsSh23   : MTGALDKP-------TPE----ITEFMDLI-QSSFHCCG--AKGPQDYG----------- : 154
ShsSM23   : MTGALDKP-------TKE----ITEFMNLI-QSSFHCCG--AKGPNDYR----------- : 154
ShsSj23   : MTGALENP-------NEE----ITATMDKI-QTSFHCCG--VKGPDDYK----------- : 154
HumNET-4  : INNNIRAY-------RDDI--DLQNLIDFT-QEYWQCCG--AFGADDWNLNIYFNCTDSN : 174
MusTspn5  : INNNIRAY-------RDDI--DLQNLIDFT-QEYWQCCG--AFGADDWNLNIYFNCTDSN : 174
Dros3A    : THKIIHSY-------RDDP--DLQNFIDFA-QQEFKCCGLSNSGYQDWSKNEYFNCSSP- : 177
HumNET-7  : IRRGIENY-------YDDL--DFKNIMDFV-QKKFKCCG--GEDYRDWSKNQYHDCSAP- : 174
Dros29Fa  : LTYSLNEY-------NSINPNATTKLWDDI-QDEFECCG--VTSYNDWITAF-------- : 161
Dros9033  : LQESIKRS-------NSED----TMAWDNI-QQKLMCCG--VDSPADWRTLS-------- : 141
MandD107  : LNETIDQY-------PTNK--EVAKTFDIV-QTDLECCG--IKGPEDWAAH--------- : 158
Dros29Fb  : MNQALAEY-------EHDP--YVESGVDFM-QSMLECCG--VNEPEDWKDYLSANVNFT- : 170
MandD76   : LRDTMPKY-------YRNP--EVQDAFDFI-QSRLNCCG--VDSYLDWSDVFPPTGVNG- : 168
MkyCD151  : KDTMAKRY-------HQPGHEAVTSAVDQL-QQEFHCCG--SNNSQDWRDSEWIRLR--- : 173
MacCD151  : KDTMAKRY-------HQPGHEAVTSAVDQL-QQEFHCCG--SNNSQDWRDSEWIRLR--- : 173
HumCD151  : KDTMTRRY-------HQSGHEAVTSAVDQL-QQEFHCCG--SNNSQDWRDSEWIRSQ--- : 173
MusCD151  : KDTMVKRY-------HQSGHEGVSSAVDKL-QQEFHCCG--SNNSQDWQDSEWIRSG--- : 173
CatCD9    : KDTYNKLK-------SKDEPQ--RDTLKAI-HYALDCCG---------LAGGVE------ : 158
HumCD9    : KDTYNKLK-------TKDEPQ--RETLKAI-HYALNCCG---------LAGGVE------ : 160
MusCD9    : KDTYQKLR-------SKDEPQ--RETLKAI-HMALDCCG---------IAGPLE------ : 158
RatCD9    : KDTYQKLR-------NKDEPQ--RETLKAI-HMALNCCG---------IAGGVE------ : 158
BovCD9    : EDTYNKLK-------NKDEPQ--RETLKAI-HIALDCCG---------LTGVPE------ : 158
ChkCD9    : RETYEKR---------SQPAA--REILKAF-HFALNCCG---------ITGGLE------ : 156
ChmpCD81  : DQALQQAV-------VDDDANNAKAVVKTF-HETLDCCGS--ST----LTALTT------ : 167
HumCD81   : DQALQQAV-------VDDDANNAKAVVKTF-HETLDCCGS--ST----LTALTT------ : 167
MkyCD81   : DQALQQAV-------VDDDANNAKAVVKTF-HETLDCCGS--ST----LAALTT------ : 167
TamCD81   : DQALQQAV-------VDDDANNAKAVVKTF-HETLNCCGS--ST----LSALTT------ : 167
RatCD81   : DQALQQAV-------MDDDANNAKAVVKTF-HETLNCCGS--NT----LTTLTT------ : 167
HumTSPN2  : EEAYNDYL-------KDRGKG--NGTLITFPLQHFQCCG----------KESSE------ : 159
RatTspn2  : EEAYSDYV-------RDRGRG--NGTLITF-HSAFQCCG----------KESSE------ : 158
HumC0029  : YENTKLLS-------ATGESEKQFQEAIIVFQEEFKCCGL--VNGAADWGNNFQ------ : 166
RatD6.1A  : YENAKLLS-------ETSNEAKEVQKAMIAFQSEFKCCGL--RFGAADWGKNFP------ : 166
MusCD37   : LRTIQSYR-------TNPDETAAEESWDYA-QFQLRCCGW--QSPRDWNKAQMLKANES- : 172
RatCD37   : LRTIQSYR-------TNPDETAAEESWDYA-QFQLRCCGW--QSPRDWNKAQMLKANGS- : 172
HumCD37   : EKTIQKYG-------TNPEETAAEESWDYV-QFQLRCCGW--HYPQDWFQVLILRGNGS- : 172
HumCD82   : TELIRDYN-------SSR-EDSLQDAWDYV-QAQVKCCGW--VSFYNWTDNAELMNR--- : 167
MusCD82   : MDIIRNYT-------ANA-TSSREEAWDYV-QAQVKCCGW--VSHYNWTENEELMGF--- : 167
MusCD53   : NDSIQHY--------HSDNST--MKAWDFI-QTQLQCCGV--NGSSDWTSG--------- : 156
RatCD53   : NDSIQHY--------HSDNST--RMAWDFI-QSQLQCCGV--NGSSDWISG--------- : 156
HumCD53   : TDSIHRY--------HSDNST--KAAWDSI-QSFLQCCGI--NGTSDWTSG--------- : 156
HumNET-5  : KEGLLLY--------HTENNVGLKNAWNII-QAEMRCCGV--TDYTDWYPVL-------- : 160
HumNAG-2  : KKGLHLY--------GTQGNVGLTNAWSII-QTDFRCCGV--SNYTDWFEVY-------- : 160
ChkTM4SF  : TKELKKHY-------VRNNDTHVFSSTWNSVMITFACCGV--NGPED-FEAVPPLSHLP- : 166
HumNET-1  : VPAIKKDY-------GSQED---FTQVWNTTMKGLKCCGF--TNYTD-FEDSP---YFK- : 165
DogSAS    : ------------------------------------------------------------ :   -
HumSAS    : WWVMSNKT-------RDEL------------ERSFDCCGL------------FNLTTLY- : 137
HumNET-6  : -WNNTASA-------RNDI------------QRNLNCCGF------------RSVN---- : 135
Dros97E   : WMTVPTDL-------RKQV------------QDSLKCCGFNATAPSTTSVVPPSNEPSC- : 150
ApisF139  : KYQEIFNG---------YFLNSESKDFIDFIQKNLQCCGV--HSLSDYNDK--------- : 157
Dros42El  : ALQTVENQ---------WELEQTKPGSMDIIQKTYYCCGR--DSAQDYLDIKFW------ : 143
Dros42Ea  : VVEKAWN------------HRTSRSDYMDAIQISMKCCGR--SGYTDYAYQG-------- : 154
DrosLD16  : VIENAWNS-----------EHTYKGGVFDTIQKSLHCCGS--SSALDYIGKGD------- : 158
DrosGH07  : IVQTIWD------------QRKTDALLMDTLQRSFKCCGL--NGFADY---GI------- : 152
Dros42Eb  : AVDKAWDE-----------NNAAQGYPMDALQLAFSCCGN--TGYQQYE----------- : 152
Dros42Ec  : LVNLLWDS-----------HDYTA---MGVLEETFGCCGD--TSYTNYNNIGL------- : 153
MandE118  : SVDTLFDKR------SGPTVDKATESLINNLQQQFQCCGK--NGANYYGIAGV------- : 160
BovUPK1A  : KQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDNCCG--VNGPSDWQKYTSAFRTEN- : 179
BovUPK1B  : KQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDNCCG--VNGPSDWQKYTSAFRTEN- : 179
MusUPK1B  : KQMLMRYQNNSPPNNDDQW----------------------------------------- :  40
HumUPK1B  : KQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDNCCG--VNGPSDWQKYTSAFRTEN- : 179
MinkTI-1  : KQMLERYQNNSPPNNDDQWKNNGVTKTWDRLMLQDHCCG--VNGPSDWQRYTSAFRTAN- : 179
RabUPK1B  : KQMLERYQNNSPPTNDDQWKNNGVTRTWDRLMLQDNCCG--VNGPSDWQKYTSAFRAEN- : 172
XenUP1B5  : KQMLELYQNPNPINNDNSWKIAGVTSTCNRSMLLNRCCG--VNGPQDWQTYTSVFRQYN- : 178
XenUP1B3  : ---GEFYQNPNPINNDNLWKINGVTRTWNRFMLLNGCCG--VNGPQDWQTYNSVFRQFN- :  54
HumUPK1A  : KQMLTFYSADTDQGQE-------LTRLWDRVMIEQECCG--TSGPMDWVNFTSAFRAAT- : 179
SusUPK1A  : KQMLTFYSADSGQGRE-------LTRLWDRVMIEQECCG--TSGPMDWVNFTSAFRAST- : 112
CatPRPH   : KNGMKYYR------DTDTPGRCFMKKTIDLLQIEFKCCGN--NGFRDWFEIQWISNRYLD : 186
DogPRPH   : KNGMKYYR------DTDTPGRCFMKKTIDMLQIEFRCCGN--NGFRDWFEIQWISNRYLD : 186
MusPRPH2  : KNGMKYYR------DTDTPGRCFMKKTIDMLQIEFKCCGN--NGFRDWFEIQWISNRYLD : 186
RatPRPH   : KNGMKYYR------DTDTPGRCFMKKTIDMLQIEFKCCGN--NGFRDWFEIQWISNRYLD : 186
ChkPRPH1  : KNSMKFYR------DTDTPGRCFMKKTIDMLQIEFKCCGN--NGFKDWFEIQWISNRYLD : 186
XenPRPH8  : KNGMRYYK------DTDIPGRCFLKKTIDLLQIEFKCCGN--NGFRDWFELQWVSNRYLG : 186
ChkPRPH2  : RDAIKFYK------DTDIPGRCFLKKTVDMLQIGFQCCGN--NGFRDWFEVQWVSARYLN : 186
XenPRPH5  : KNAIRFYK------DTDTPGRCYQKRSMDKLQMDFQCCGN--NHPKDWFEVQWISNRYLD : 186
XenPRPH6  : RNAIRFYK------DTDTPGRCYQKRSMDKLEMDFQCCGN--NHPKDWFEVQWISNRYLD : 186
BovROM-1  : GSALVHYK------DTEVPGRCQAKRLLDELQLRHHCCGR--HGYKDWFGIQWVSNRYLD : 189
MusROM-1  : EAALAHYK------DTEVPGRCQAKRLMDELQLRYHCCGR--HGYKDWFGVQWVSNRYLD : 189
HumROM-1  : VTALAHYK------DTEVPGHCQAKRLVDELQLRYHCCGR--HGYKDWFGVQWVSSRYLD : 189
MusL6     : WNYTFAST---------------EGQYLLNSSMWSKCYEP-------------------- : 152
HumTM4S5  : WGYHFEDT---------------AGAYLLNRTLWDRCEAP-------------------- : 148
HumilTMP  : WGYPFHD----------------GDYLNDEALWNKCREP-------------------- : 149
Dros42Eg  : DKLWNDQP---------VPIKPGNQSQIASLERWLDCCGN--VGPSDYILP--------- : 149
DrosLBL   : VEVAWQAN------------------NMDSLQQKHECCGQ--SSAQDYIHLS-------- : 136
Dros8666  : NSTMQHYK-----------ERADYRDAWTLLQTELDCCG--INGPNDWETVYRN------ : 127
Dros42Ei  : DRLWESER--------------NQTGALSYYESWLQCCG--VNSSEDYWIIHHG------ : 154
DrosLD29  : QTTITSYS---------LGENVDATSLMWNQLMGNFGCCG--INDYHDFDASPAWVNGKG- : 181
HumTM4-B  : FVTLRKNY-------RGYNEPDDYSTQWNLVMEKLKCCG--VNNYTDFSGSSFEMTTG-- : 172
CeB0563   : HSSLKMYNG------TDNMKVSNNPQDGLLVKTAWDKI---------------------- : 184
HumNET-2  : TLKARMTN-------YGLPRYRWLTHAWNFFQREFKCCG--VVYFTDWLEMTEMDWP--- : 177
CeC14A11  : TQQQIHQV-------------------LDQIQSSLQCCG--ASGCSDYIPYG-------- : 131
ShsTE736  : LQAVKGYYS-----------DKLYEEQMDRLQSRYMCCG--ATSYRDYDKAHS------- : 159
ShsSj25   : NDSSKLYY-----------KNRLYATEFDLMHITFKCCN----VKNDYSLLG-------- : 156
CeF53B6   : KMLTSLRELYG------THDMKGITESWDALQSNFKCCGVNGTDNAQIWKTSKWYMHQR- : 179
MusM6B    : WSTCEVIK---------------SPQSNGTSGVEQICVDVRQYGIIPWNAFPGKICG--- : 206
DrosM6    : FVGFLATG---------ATRYKVYRAWRSRVGGRISCAVLMGITYLLNFVWSLILCFLVV : 195
                                                ccg
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                     *       260         *       280         *       300
MusA15    : ---------------------GIPPSCCMNETDCNPLDL--------------------- : 181
HumTM4S2  : ---------------------GIPPSCCMNETDCNPQDL--------------------- : 181
HumTM4-D  : ---------------------GFPKSCCKLE-DCTPQ----------------------- : 186
MusTm4s6  : ---------------------GFPKSCCKLE-GCYPQ----------------------- : 186
HumTM4-A  : --------------------QSVPLSCCRETASNCNG----------------------- : 184
MusTM4-A  : --------------------QSVPLSCCRETAKSCNG----------------------- : 184
HumCD63   : ---------------PSMSKNRVPDSCCIN---------------------------VTV : 175
RabCD63   : ---------------PGMTRDRVPDSCCVN---------------------------VTS : 175
BovCD63   : ---------------LAVT-NKVPDSCCVN---------------------------ITH : 174
MusCD63   : ---------------PGMAKDRVPDSCCIN---------------------------ITV : 175
RatCD63   : ---------------PGMAKDRVPDSCCIN---------------------------ITV : 175
ShsSh23   : --------------------PNIPASCRG------------------------------- : 163
ShsSM23   : --------------------GNVPASCKE------------------------------- : 163
ShsSj23   : --------------------GNVPASCKE------------------------------- : 163
HumNET-4  : ---------------ASRERCGVPFSCCT--KDPAEDVINT------------QCGYDAR : 205
MusTspn5  : ---------------ASRERCGVPFSCCT--KDPAEDVINT------------QCGYDAR : 205
Dros3A    : ----------------SVEKCGVPYSCCINATDISSGLVNI------------MCGYGVQ : 209
HumNET-7  : ----------------GPLACGVPYTCCIR---NTTEVVNT------------MCGYKTI : 203
Dros29Fa  : ------------------PNGDLPISCCN--------VHVG------------AVGTFTC : 183
Dros9033  : ------------------ANKTLPGSCCQ--------PQYI------------DSTVGHC : 163
MandD107  : -------------------NLTIPSTCCTG-------IEIN------------NSMAAQC : 180
Dros29Fb  : ---------------LGVDDVVVPNSCCG------------------------NQPTSLN : 191
MandD76   : ---------------ISVANISVPNSCCA------------------------ESRFEIV : 189
MkyCD151  : ----------------EARGRVVPDSCCKT-------------------------VVAGC : 192
MacCD151  : ----------------EARGRVVPDSCCKT-------------------------VVAGC : 192
HumCD151  : ----------------EAGGRVVPDSCCKT-------------------------VVALC : 192
MusCD151  : ----------------EADSRVVPDSCCKT-------------------------MVAGC : 192
CatCD9    : --------------------QFIS-DICPQ------------------------------ : 167
HumCD9    : --------------------QFIS-DICPK------------------------------ : 169
MusCD9    : --------------------QFIS-DTCPK------------------------------ : 167
RatCD9    : --------------------QFIS-DICPK------------------------------ : 167
BovCD9    : --------------------QFLT-DTCPP------------------------------ : 167
ChkCD9    : --------------------QQLM-ESCPK------------------------------ : 165
ChmpCD81  : --------------------SVLKNNLCPSG----------------------------- : 178
HumCD81   : --------------------SVLKNNLCPSG----------------------------- : 178
MkyCD81   : --------------------SVLKNNLCPSG----------------------------- : 178
TamCD81   : --------------------SMLKNNLCPSG----------------------------- : 178
RatCD81   : --------------------AVLRNSLCPSS----------------------------- : 178
HumTSPN2  : --------------------QVQP--TCPK------------------------------ : 167
RatTspn2  : --------------------QVQP--TCPK------------------------------ : 166
HumCO029  : --------------------HYPELCACLDKQRPCQ------------------------ : 182
RatD6.1A  : --------------------DAKESCQCTG--SDCE------------------------ : 180
MusCD37   : ------------------EEPFVPCSCYNSTATNDSTVFDKLFFSQLSRLGPRAKLRQTA : 214
RatCD37   : ------------------EELFVPCSCYNSTATNDSSGFDKLFLSQLSRLGPRAKLRQTA : 214
HumCD37   : ------------------EAHRVPCSCYNLSATNDSTILDKVILPQLSRLGHLARSRHSA : 214
HumCD82   : ------------------PEVTYPCSCEVKGEEDNS---------LSVRKGFCEAPGNRT : 200
MusCD82   : ------------------TKTTYPCSCEKIKEEDNQ---------LIVKKGFCEAD-NST : 199
MusCD53   : -----------------------PPSSCP----------------------------SGA : 165
RatCD53   : -----------------------PPSSCP----------------------------SGA : 165
HumCD53   : -----------------------PPASCP----------------------------SDR : 165
HumNET-5  : ------------------GENTVPDRCCM----------------------------ENS : 174
HumNAG-2  : ------------------NATRVPDSCCL----------------------------EFS : 174
ChkTM4SF  : ------------------LEETTPEACCQRNVQSRE------------------GMFVNR : 190
HumNET-1  : ------------------ENSAFPPFCCNDNVTN-----------------------TAN : 184
DogSAS    : ------------------------------------------------------------ :   -
HumSAS    : --------------------QQDYDFCTAIC----------------------------- : 148
HumNET-6  : ----------------------PNDTCLASC----------------------------- : 144
Dros97E   : --------------------ELINQQCCAHS----------------------------- : 161
ApisF139  : ----------------------PIPASCCNSP---------------------------E : 168
Dros42El  : --------------------NNTVPSSCCK-----------------------------D : 154
Dros42Ea  : ---------------------KFPPSCCSDTN---------------------------N : 166
DrosLD16  : ---------------------LVPPSCCSGS----------------------------- : 168
DrosGH07  : ---------------------TYPASCCDSPS---------------------------N : 164
Dros42Eb  : ---------------------TVPSSCCGYKD---------------------------R : 164
Dros42Ec  : ---------------------SVPGTCCGYLD---------------------------R : 165
MandE118  : ---------------------ANLPPSCCDPQ---------------------------F : 172
BovUPK1A  : ----------------SDADYPWPRQCCVMNSLKEP---------------------LNL : 202
BovUPK1B  : ----------------SDADYPWPRQCCVMNSLKEP---------------------LNL : 202
MusUPK1B  : ------------------------------------------------------------ :   -
HumUPK1B  : ----------------NDADYPWPRQCCVMNNLKEP---------------------LNL : 202
MinkTI-1  : ----------------NDADYPWPRQCCVMNSLKEP---------------------LNV : 202
RabUPK1B  : ----------------NDADYPWPRQCCVMTNLKEP---------------------LNL : 195
XenUP1B5  : ----------------SDSAYPWPQQCCIMNSLGQP---------------------INL : 201
XenUP1B3  : ----------------SDSAYPWPQQCCVMNSLGQP---------------------VNL :  77
HumUPK1A  : ----------------PEVVFPWPPLCCRRTGNFIP---------------------LNE : 202
SusUPK1A  : ----------------PEVVFPWPPLCCRRTGNFIP---------------------VNE : 135
CatPRPH   : FSSKEVKDRIKSNVDGRYLVDGVPFSCCNPNSPRPCIQYQLTNN------------SAHY : 234
DogPRPH   : FSSKEVKDRIKSNVDGRYLVDGVPFSCCNPSSPRPCIQYQLTNN------------SAHY : 234
MusPRPH2  : FSSKEVKDRIKSNVDGRYLVDGVPFSCCNPSSPRPCIQYQLTNN------------SAHY : 234
RatPRPH   : FSSKEVKDRIKSNVDGRYLVDGVPFSCCNPSSPRPCIQYQLTNN------------SAHY : 234
ChkPRPH1  : FSSKEVKDRIKSNVDGRYLVDGVPFSCCNPSSPRPCIQYQVTNN------------SAHY : 234
XenPRPH8  : GRSKEVKDRIQSNVDGKYLIDGVPFSCCNPSSPRPCIQLQVTNN------------SAHY : 234
ChkPRPH2  : MASKEVMDRFKSNVDGKFLVDGVPFSCCNPSSPRPCIQYHLTNN------------SAHY : 234
XenPRPH5  : FSSKEVKDRIKSNVDGRYLMDSVPFSCCNPSSPRPCIQMQITNN------------SAHY : 234
XenPRPH6  : FSSKEVKDRIKSSVDGRYLMDSVPFTCCNPSSPRPCIQIEITNN------------SAHY : 234
BovROM-1  : PNDPDVVDRIQSNVEGLYLIDGVPFSCCNPHSPRPCLQSQLSDP------------HAHP : 237
MusROM-1  : PSDQDVVDRIQSNVEGLYLIDGVPFSCCNPHSPRPCLQSQLSDP------------YAHP : 237
HumROM-1  : PGDRDVADRIQSNVEGLYLTDGVPFSCCNPHSPRPCLQNRLSDS------------YAHP : 237
MusL6     : ------------------------------------------------------------ :   -
HumTM4S5  : ------------------------------------------------------------ :   -
HumilTMP  : ------------------------------------------------------------ :   -
Dros42Eg  : -----------------------PNSCYNG------------------------------ : 156
DrosLBL   : --------------------LLIPPSCYAD------------------------------ : 146
Dros8666  : --------------------STLPAACCSVIN---------------------------L : 140
Dros42Ei  : ----------------------IPSSCCPES----------------------------- : 163
DrosLD29  : -------------------NRTIPDACCILKDVAKLVPR------------------DED : 204
HumTM4-B  : --------------------HTYPRSCCKSIG-------------------------SVS : 187
CeB0563   : ---------------------MIEKSCCG------------------------------- : 192
HumNET-2  : -----------------------PDSCCVREFPG------------------------CS : 190
CeC14A11  : ---------------------AFPTSCQCAT----------------------------- : 141
ShsTE736  : ----------------------IPPFSCLTG----------------------------- : 168
ShsSj25   : ------------------TLHLIPESCTHG------------------------------ : 168
CeF53B6   : -----------------APKLLIPESCCIPSEIERCR----------------------S : 200
MusM6B    : --------------------SALENICNTN------------------------------ : 216
DrosM6    : VTFIYTMFWN------MCTSVEHSQSCIDLTQFHFMFP---------------------- : 227
                                         c
```

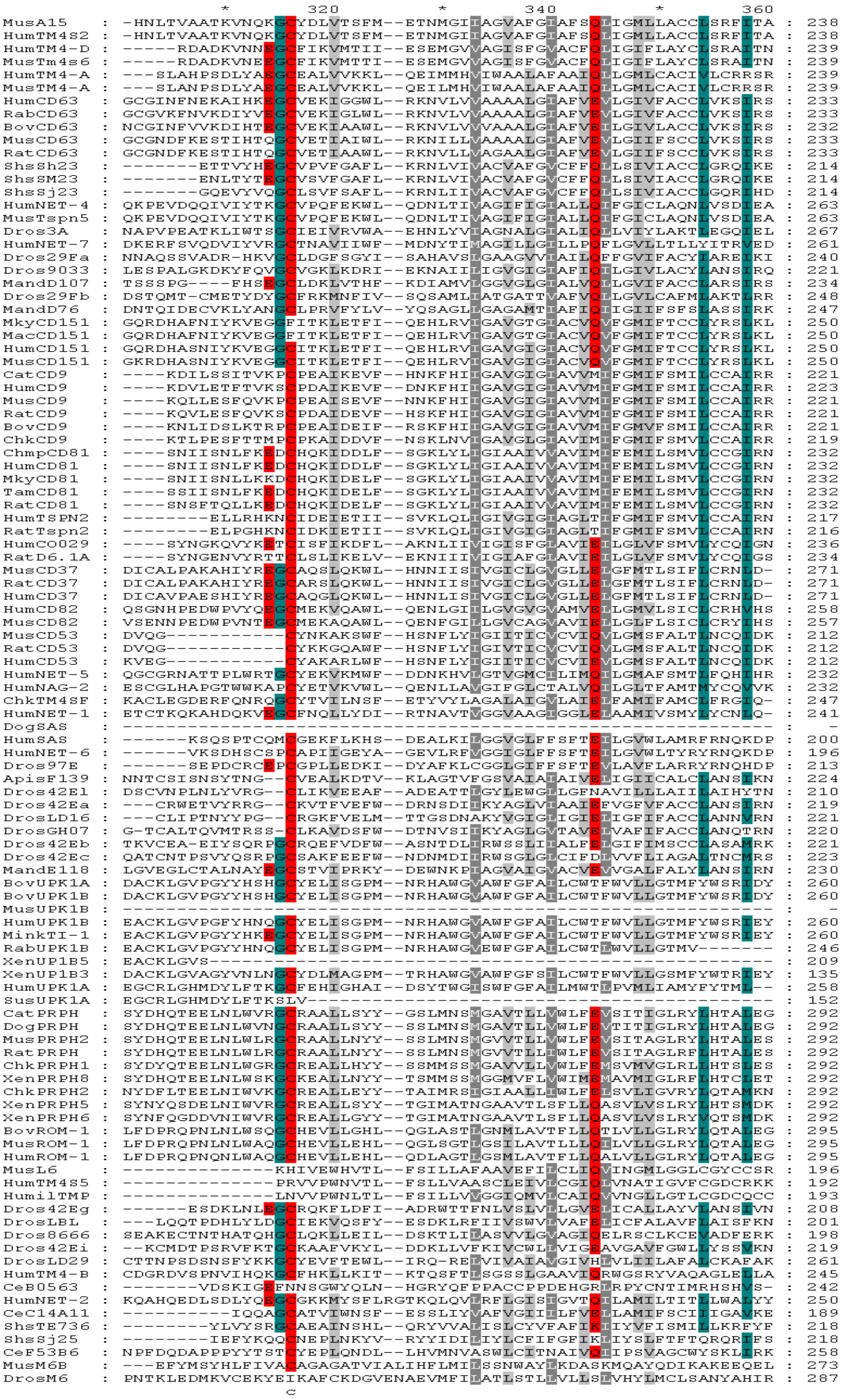

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                      *       320         *       340         *       360
MusA15     : -HNLTVAATKVNQKGCYDLVTSFM--ETNMGIIAGVAFGIAFSQLIGMLLACCLSRFITA : 238
HumTM4S2   : -HNLTVAATKVNQKGCYDLVTSFM--ETNMGIIAGVAFGIAFSQLIGMLLACCLSRFITA : 238
HumTM4-D   : -----RDADKVNNEGCFIKVMTII--ESEMGVVAGISFGVACFQLIGIFLAYCLSRAITN : 239
MusTm4s6   : -----RDADKVNEEGCFIKVMTTI--ESEMGVVAGISFGVACFQLIGIFLAYCLSRAITN : 239
HumTM4-A   : ---SLAHPSDLYAEGCEALVVKKL--QEIMMHVIWAALAFAAIQLLGMLCACIVLCRRSR : 239
MusTM4-A   : ---SLANPSDLYAEGCEALVVKKL--QEILMHVIWAALAFAAIQLLGMLCACIVLCRRSR : 239
HumCD63    : GCGINFNEKAIHKEGCVEKIGGWL--RKNVLVVAAAALGIAFVEVLGIVFACCLVKSIRS : 233
RabCD63    : GCGVKFNVKDIYVEGCVEKIGLWL--RKNVLVVAAAALGIAFVEVLGIVFACCLVKSIRS : 233
BovCD63    : NCGINFVVKDIHTEGCVEKIAAWL--RKNVLVVVAAALGIAFVEILGIVLACCLVKSIRS : 232
MusCD63    : GCGNDFKESTIHTQGCVETIAIWL--RKNILLVAAAALGIAFVEVLGIIFSCCLVKSIRS : 233
RatCD63    : GCGNDFKESTIHTQGCVETIAAWL--RKNVLLVAGAALGIAFVEVLGIIFSCCLVKSIRS : 233
ShsSh23    : -------ETTVYHEGCVPVFGAFL--KRNLVIVACVAFGVCFFQLLSIVIACCLGRQIKE : 214
ShsSM23    : -------ENLTYTEGCVSVFGAFL--KRNLVIVACVAFGVCFFQLLSIVIACCLGRQIKE : 214
ShsSj23    : -------GQEVYVQGCLSVFSAFL--KRNLIIVACVAFGVCFFQLLSIVIACCLGQRIHD : 214
HumNET-4   : QKPEVDQQIVIYTKGCVPQFEKWL--QDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEA : 263
MusTspn5   : QKPEVDQQIVIYTKGCVPQFEKWL--QDNLTIVAGIFIGIALLQIFGICLAQNLVSDIEA : 263
Dros3A     : NAPVPEATKLIWTSGCIEIVRVWA--EHNLYVIAGNALGIALIQLLVIYLAKTLEGQIEL : 267
HumNET-7   : DKERFSVQDVIYVRGCTNAVIIWF--MDNYTIMAGILLGILLPQFLGVLLTLLYITRVED : 261
Dros29Fa   : NNAQSSVADR-HKVGCLDGFSGYI--SAHAVSLGAAGVVIAILQFFGVIFACYIAREIKI : 240
Dros9033   : LESPALGKDKYFQVGCVGKLKDRI--EKNAIILIGVGIGIAFIQILGIVLACYLANSIRQ : 221
MandD107   : TSSSPG----FHSEGCLDKLVTHF--KDIAMVLGGVGLGIALVQLLGVIFACCLARSIRS : 234
Dros29Fb   : DSTQMT-CMETYDYGCFRKMNFIV--SQSAMLIATGATTVAFVQLLGVLCAFMLAKTLRR : 248
MandD76    : DNTQIDECVKLYANGCLPRVFYLV--YQSAGLLGAGAMTIAFIQIIGIIFSFSLASSIRK : 247
MkyCD151   : GQRDHAFNIYKVEGGFITKLETFI--QEHLRVIGAVGTGIACVQVFGMIFTCCLYRSLKL : 250
MacCD151   : GQRDHAFNIYKVEGGFITKLETFI--QEHLRVIGAVGTGIACVQVFGMIFTCCLYRSLKL : 250
HumCD151   : GQRDHASNIYKVEGGCITKLETFI--QEHLRVIGAVGIGIACVQVFGMIFTCCLYRSLKL : 250
MusCD151   : GKRDHASNIYKVEGGCITKLETFI--QEHLRVIGAVGIGIACVQVFGMIFTCCLYRSLKL : 250
CatCD9     : ----KDILSSITVKPCPEAIKEVF--HNKFHIIGAVGIGIAVVMIFGMIFSMILCCAIRR : 221
HumCD9     : ----KDVLETFTVKSCPDAIKEVF--DNKFHIIGAVGIGIAVVMIFGMIFSMILCCAIRR : 223
MusCD9     : ----KQLLESFQVKPCPEAISEVF--NNKFHIIGAVGIGIAVVMIFGMIFSMILCCAIRR : 221
RatCD9     : ----KQVLESFQVKSCPDAIDEVF--HSKFHIIGAVGIGIAVVMIFGMIFSMILCCAIRR : 221
BovCD9     : ----KNLIDSLKTRPCPEAIDEIF--RSKFHIIGAVGIGIAVVMIFGMVFSMILCCAIRR : 221
ChkCD9     : ----KTLPESFTTMPCPKAIDDVF--NSKLNVIGAVGLGIAVIMIFGMIFSMVLCCAIRR : 219
ChmpCD81   : ----SNIISNLFKEDCHQKIDDLF--SGKLYLIGIAAIVVAVIMIFEMILSMVLCCGIRN : 232
HumCD81    : ----SNIISNLFKEDCHQKIDDLF--SGKLYLIGIAAIVVAVIMIFEMILSMVLCCGIRN : 232
MkyCD81    : ----SNIISNLLKKDCHQKIDELF--SGKLYLIGIAAIVVAVIMIFEMILSMVLCCGIRN : 232
TamCD81    : ----SSIISNLFKEDCHQKIDELF--SGKLYLIGIAAIVVAVIMIFEMILSMVLCCGIRN : 232
RatCD81    : ----SNSFTQLLKEDCHQKIDELF--SGKLYLIGIAAIVVAVIMIFEMILSMVLCCGIRN : 232
HumTSPN2   : --------ELLRHKNCIDEIETII--SVKLQLIGIVGIGIAGLTIFGMIFSMVLCCAIRN : 217
RatTspn2   : --------ELPGHKNCIDKIETII--SVKLQLIGIVGIGIAGLTIFGMIFSMVLCCAIRN : 216
HumCO029   : ----SYNGKQVYKETCISFIKDFL--AKNLIIVIGISFGLAVIEILGLVFSMVLYCQIGN : 236
RatD6.1A   : ----SYNGENVYRTTCLSLIKELV--EKNIIIVIGIAFGLAVIEILGLVFSMVLYCQIGS : 234
MusCD37    : DICALPAKAHIYREGCAQSLQKWL--HNNIISIVGICLGVGLLELGFMTLSIFLCRNLD- : 271
RatCD37    : DICALPAKAHIYREGCARSLQKWL--HNNIISIVGICLGVGLLELGFMTLSIFLCRNLD- : 271
HumCD37    : DICAVPAESHIYREGCAQGLQKWL--HNNLISIVGICLGVGLLELGFMTLSIFLCRNLD- : 271
HumCD82    : QSGNHPEDWPVYQEGCMEKVQAWL--QENLGIILGVGVGVAMVELLGMVLSICLCRHVHS : 258
MusCD82    : VSENNPEDWPVNTEGCMEKAQAWL--QENFGILLGVCAGVAVIELLGLFLSICLCRYIHS : 257
MusCD53    : DVQG-----------CYNKAKSWF--HSNFLYIGIITICVCVIQVLGMSFALTLNCQIDK : 212
RatCD53    : DVQG-----------CYKKGQAWF--HSNFLYIGIVTICVCVIQVLGMSFALTLNCQIDK : 212
HumCD53    : KVEG-----------CYAKARLWF--HSNFLYIGIITICVCVIEVLGMSFALTLNCQIDK : 212
HumNET-5   : QGCGRNATTPLWRTGCYEKVKMWF--DDNKHVLGTVGMCILIMQILGMAFSMTLFQHIHR : 232
HumNAG-2   : ESCGLHAPGTWWKAPCYETVKVWL--QENLLAVGIFGLCTALVQILGLTFAMTMYCQVVK : 232
ChkTM4SF   : KACLEGDERFQNRQGCYTVILNSF--ETYVYLAGALAIGVLAIELFAMIFAMCLFRGIQ- : 247
HumNET-1   : ETCTKQKAHDQKVEGCFNQLLYDI--RTNAVTVGGVAAGIGGLELAAMIVSMYLYCNLQ- : 241
DogSAS     : ------------------------------------------------------------ :   -
HumSAS     : ------KSQSPTCQMCGEKFLKHS--DEALKILGGVGLFFSFTEILGVWLAMRFRNQKDP : 200
HumNET-6   : ------VKSDHSCSPCAPIIGEYA--GEVLRFVGGIGLFFSFTEILGVWLTYRYRNQKDP : 196
Dros97E    : ------SEPDCRCEPCGPLLEDKI--DYAFKLCGGLGIFFSFTEVLAVFLARRYRNQHDP : 213
ApisF139   : NNTCSISNSYTNG--CVEALKDTV--KLAGTVFGSVAIAIAIVELIGIICALCLANSIKN : 224
Dros42El   : DSCVNPLNLYVRG--CLIKVEEAF--ADEATTLGYLEWGLLGFNAVILLLAIILAIHYTN : 210
Dros42Ea   : ---CRWETVYRRG--CKVTFVEFW--DRNSDIIKYAGLVIAAIEFVGFVFACCLANSIRN : 219
DrosLD16   : ---CLIPTNYYPG--CRGKFVELM--TTGSDNAKYVGIGLIGIELIGFIFACCLANNVRN : 221
DrosGH07   : G-TCALTQVMTRSS-CLKAVDSFW--DTNVSIIKYAGLGVTAVELVAFIFACCLANQTRN : 220
Dros42Eb   : TKVCEA-EIYSQRPGCRQEFVDFW--ASNTDLIRWSSLIIALFELGIFIMSCCLASAMRK : 221
Dros42Ec   : QATCNTPSVYQSRPGCSAKFEEFW--NDNMDIIRWSGLGLCIFDLVVFLIAGALTNCMRS : 223
MandE118   : LGVEGLCTALNAYEGCSTVIPRKY--DEWNKPIAGVAIGVACVEVVGALFALYLANSIRN : 230
BovUPK1A   : DACKLGVPGYYHSHGCYELISGPM--NRHAWGVAWFGFAILCWTFWVLLGTMFYWSRIDY : 260
BovUPK1B   : DACKLGVPGYYHSHGCYELISGPM--NRHAWGVAWFGFAILCWTFWVLLGTMFYWSRIDY : 260
MusUPK1B   : ------------------------------------------------------------ :   -
HumUPK1B   : EACKLGVPGFYHNQGCYELISGPM--NRHAWGVAWFGFAILCWTFWVLLGTMFYWSRIEY : 260
MinkTI-1   : EACKLGVPGYYHKEGCYELISGPM--NRHAWGVAWFGFAILCWTFWVLLGTMFYWSRIEY : 260
RabUPK1B   : EACKLGVPGYYHNQGCYELISGPM--NRHAWGVEWFGFAILCWTLWVLLGTMV------- : 246
XenUP1B5   : EACKLGVS---------------------------------------------------- : 209
XenUP1B3   : DACKLGVAGYVNLNGCYDLMAGPM--TRHAWGVAWFGFSILCWTFWVLLGSMFYWTRIEY : 135
HumUPK1A   : EGCRLGHMDYLFTKGCFEHIGHAI--DSYTWGISWFGFAILMWTLPVMLIAMYFYTML-- : 258
SusUPK1A   : EGCRLGHMDYLFTKSLV------------------------------------------- : 152
CatPRPH    : SYDHQTEELNLWVRGCRAALLSYY--GSLMNSMGAVTLLVWLFEVSITIGLRYLHTALEG : 292
DogPRPH    : SYDHQTEELNLWVNGCRAALLSYY--SSLMNSMGAVTLLVWLFEVTITIGLRYLHTALEG : 292
MusPRPH2   : SYDHQTEELNLWLRGCRAALLNYY--SSLMNSMGVVTLLVWLFEVSITAGLRYLHTALES : 292
RatPRPH    : SYDHQTEELNLWLRGCRAALLNYY--SSLMNSMGVVTLLIWLFEVSITAGLRFLHTALES : 292
ChkPRPH1   : SYDYQTEELNLWGRGCREALLHYY--SSMMSSMGAVVLLVWLFEMSVMVGLRLLHTSLES : 292
XenPRPH8   : SYDHQTEELNLWSKGCKEALLNYY--TSMMSSMGGMVFLVWIMEMAVMIGLRFLHTCLET : 292
ChkPRPH2   : NYDFLTEELNIWVKGCREALLEYY--TAIMRSIGIAALLIWLFELSVLIGVRYLQTAMKN : 292
XenPRPH5   : SYNYQSDELNIWVRGCREALLSYY--TGIMATNGAAVTLSFLLQASVLVSLRYLHTSMDK : 292
XenPRPH6   : SYNFQGDDVNIWVRGCREALLGYY--TGIMATNGAAVTLSFLLQASVLVSLRYVQTSMDK : 292
BovROM-1   : LFDPRQPNLNLWSQGCHEVLLGHL--QGLASTLGNMLAVTFLLQTLVLLGLRYLQTALEG : 295
MusROM-1   : LFDPRQPNLNLWAQGCHEVLLEHL--QGLSGTLGSILAVTLLLQILVLLGLRYLQTALEG : 295
HumROM-1   : LFDPRQPNQNLWAQGCHEVLLEHL--QDLAGTLGSMLAVTFLLQALVLLGLRYLQTALEG : 295
MusL6      : --------------KHIVEWHVTL--FSILLAFAAVEFILCLIQVINGMLGGLCGYCCSR : 196
HumTM4S5   : --------------PRVVPWNVTL--FSLLVAASCLEIVLCGIQLVNATIGVFCGDCRKK : 192
HumilTMP   : --------------LNVVPWNLTL--FSILLVVGGIQMVLCAIQVVNGLLGTLCGDCQCC : 193
Dros42Eg   : ------ESDKLNLEGCRQKFLDFI--ADRWTTFNLVSLVLLGVELICALLAYVLANSIVN : 208
DrosLBL    : ---LQQTPDHLYLDGCIEKVQSFY--ESDKLRFIIVSWVLVAFELICFALAVFLAISFKN : 201
Dros8666   : SEAKECTNTHATQHGCLQKLLEIL--DSKTLILASVVLGVAGIQELRSCLKCEVADFERK : 198
Dros42Ei   : --KCMDTPSRVFKTGCKAAFVKYL--DDKLLVFKIVCWLLVIGEAVGAVFGWLLYSSVKN : 219
DrosLD29   : CTTNPSDSNSFYKKGCYEVFTEWL--IRQ-RELVIVAIAVGIVHLVLIILAFALCKAFAK : 261
HumTM4-B   : CDGRDVSPNVIHQKGCFHKLLKIT--KTQSFTLSGSSLGAAVIQRWGSRYVAQAGLELLA : 245
CeB0563    : -------VDSKIGEFNNSGWYQLN--HGRYQFPPACCPPDEHGRLRPYCNTIMRHSHVS- : 242
HumNET-2   : KQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYY : 250
CeC14A11   : ----------IQQAGCATVIWNSF--ESSLIYVAFVGIIILFVELLAMIFSCIIIGAVKE : 189
ShsTE736   : --------YLVYSRGCAEAINSHL--QRYVVALISLCYVFAFIKIIYVFISMILLKRFYF : 218
ShsSj25    : --------IEFYKQQCNEPLNKYV--RYYIDILIYLCFIFGFIKLIYSLFTFTQRQRIFS : 218
CeF53B6    : NPFDQDAPPPYYTSTCYEPLQNDL--LHVMNVASWLCITNAIVQIIPSVAGCWYSKLIRK : 258
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Dros42Ea  : ------------ :   -
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