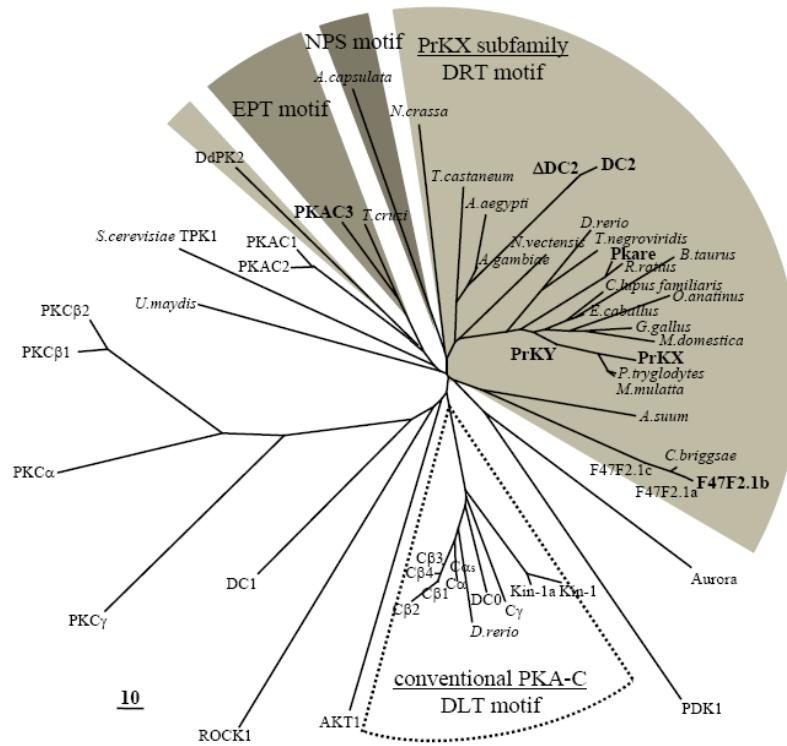
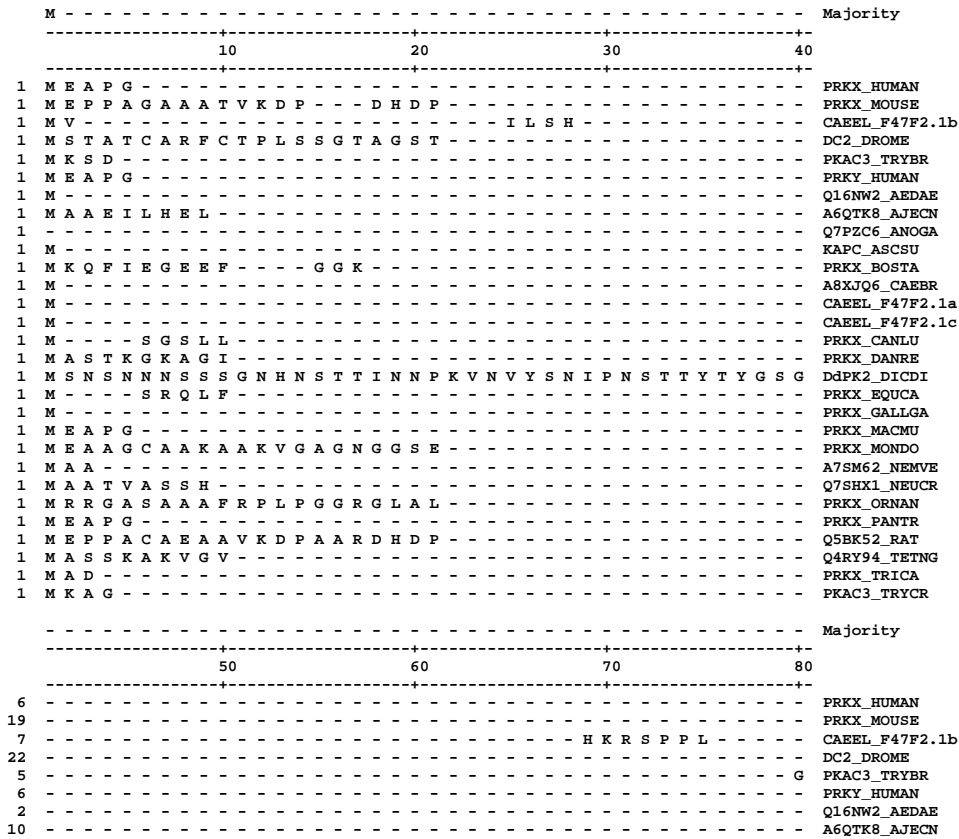


A



B



1	-----	Q7PZC6_ANOGA
2	-----	KAPC_ASCSU
14	-----	PRKX_BOSTA
2	-----	A8XJQ6_CAEBR
2	-----	CAEEL_F47F2.1a
2	-----	CAEEL_F47F2.1c
7	-----	PRKX_CANLU
11	-----	PRKX_DANRE
41	G G G T L S G N N T N N N N T N N N N N N N N N S S G D N K N H S P V T S A T D	DgPK2_DICDI
7	-----	PRKX_EQUCA
2	-----	PRKX_GALLGA
6	-----	PRKX_MACMU
22	-----	PRKX_MONDO
4	-----	A7SM62_NEMVE
10	-----	Q7SHX1_NEUCR
22	-----	PRKX_ORNAN
6	-----	PRKX_PANTR
22	-----	Q5BK52_RAT
11	-----	Q4RY94_TETNG
4	-----	PRKX_TRICA
5	-----	PKAC3_TRYCR

Majority

-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----
	90	100	110	120	
-----	-----	-----	-----	-----	-----
6	-----	-----	-----	-----	PRKX_HUMAN
19	-----	-----	-----	-----	PRKX_MOUSE
14	L M R	-----	L F R I	-----	CAEEL_F47F2.1b
22	-----	-----	-----	S K L	DC2_DROME
6	C L T R K D V S S - W	-----	-----	-----	PKAC3_TRYBR
6	-----	-----	-----	-----	PRKY_HUMAN
2	-----	-----	-----	-----	Q16NW2_AEDAE
10	-----	-----	-----	-----	A6QTK8_AJECN
1	-----	-----	-----	-----	Q7PZC6_ANOGA
2	-----	-----	-----	-----	KAPC_ASCSU
14	-----	-----	-----	-----	PRKX_BOSTA
2	-----	-----	-----	-----	A8XJQ6_CAEBR
2	-----	-----	-----	-----	CAEEL_F47F2.1a
2	-----	-----	-----	-----	CAEEL_F47F2.1c
7	-----	-----	-----	-----	PRKX_CANLU
11	-----	-----	-----	-----	PRKX_DANRE
81	R L T K M D I E E K W D N K N Y E K D E R E K S P L F H I L A S N L N S F G N F	-----	-----	-----	DgPK2_DICDI
7	-----	-----	-----	-----	PRKX_EQUCA
2	-----	-----	-----	-----	PRKX_GALLGA
6	-----	-----	-----	-----	PRKX_MACMU
22	-----	-----	-----	G N P	PRKX_MONDO
4	-----	-----	-----	-----	A7SM62_NEMVE
10	-----	-----	-----	-----	Q7SHX1_NEUCR
22	-----	-----	-----	A P P	PRKX_ORNAN
6	-----	-----	-----	-----	PRKX_PANTR
22	-----	-----	-----	V D A	Q5BK52_RAT
11	-----	-----	-----	-----	Q4RY94_TETNG
4	-----	-----	-----	-----	PRKX_TRICA
6	T V T K E E V A E - W	-----	-----	-----	PKAC3_TRYCR

Majority

-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----
	130	140	150	160	
-----	-----	-----	-----	-----	-----
6	L A Q A A A	-----	A E S D S R K V A E E T P	-----	PRKX_HUMAN
22	K V S A P	-----	A	-----	PRKX_MOUSE
21	-----	-----	A D P K P R T S S Q K A	-----	CAEEL_F47F2.1b
25	T T G N G S G N T M T S A Y K K K I P S N N S T T A N D S S N T E T T F T F K	-----	-----	-----	DC2_DROME
16	-----	-----	-----	-----	PKAC3_TRYBR
6	P A Q A A A	-----	A E S N S R E V T E D A A	-----	PRKY_HUMAN
2	-----	-----	R H G L S I M L E T F T D R	-----	Q16NW2_AEDAE
10	-----	-----	Q L Q H T T P Q N A L Q N Q D I D I D V T T T E	-----	A6QTK8_AJECN
1	-----	-----	-----	-----	Q7PZC6_ANOGA
2	-----	-----	-----	-----	KAPC_ASCSU
14	P P W G S C E K A D	-----	D D L N G W L H P A G S	-----	PRKX_BOSTA
2	-----	-----	S S S T S S V E S V E D E S C S	-----	A8XJQ6_CAEBR
2	-----	-----	S S S T S S V E S V E D E S C S	-----	CAEEL_F47F2.1a
2	-----	-----	-----	-----	CAEEL_F47F2.1c
7	C	-----	-----	-----	PRKX_CANLU
11	-----	-----	-----	-----	PRKX_DANRE
121	K V P S T F S L T P P E P N K Q Q Q P Q Q Q P Q Q Q Q P Q Q Q P Q Q	-----	-----	-----	DgPK2_DICDI
7	-----	-----	-----	-----	PRKX_EQUCA
2	-----	-----	-----	D A F S A A K	PRKX_GALLGA
6	-----	-----	-----	-----	PRKX_MACMU
25	P P P P P P P P P P P A P	-----	P G S S G S G D S E P A H	-----	PRKX_MONDO
4	-----	-----	-----	-----	A7SM62_NEMVE
10	-----	-----	P F - G G G L H P L Q A K G L	-----	Q7SHX1_NEUCR
25	P V P A P F A L H E A V A	-----	R A E G A H V Y G E I R P C C F F A L	-----	PRKX_ORNAN
6	-----	-----	-----	-----	PRKX_PANTR
25	K I S A P	-----	A	-----	Q5BK52_RAT
11	-----	-----	-----	-----	Q4RY94_TETNG
4	-----	-----	-----	-----	PRKX_TRICA
16	-----	-----	-----	-----	PKAC3_TRYCR

Majority

-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	-----
	170	180	190	200	
-----	-----	-----	-----	-----	-----
25	-----	-----	D G A P A L	-----	PRKX_HUMAN
	-----	-----	C P S P	-----	

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40 - - - - - G H S L Q - - - - - PRKX_MOUSE
45 - - - - - N E C S A S F T F D T CAEEL_F47F2.1b
64 - - - - - L G R S N G R S S S N V A S S E S S D P L E S D Y DC2_DROME
16 - - - - - K L Q D L E I R E - - - - - PKAC3_TRYBR
25 - - - - - D W A P A L - - - - - C P S P - - - - - PRKY_HUMAN
16 - - - - - Q16NW2_AEDAE
34 K P L Q Q N N S L D H P K K R F A L E R - - - - - A6QTK8_AJECN
1 - - - - - Q7PZC6_ANOGA
13 - - - - - K A P C A S C S U - - - - - KAPC_ASCSU
39 - - - - - E P L R R T K E P A H L R L G V A S G S - - - - - PRKX_BOSTA
18 - - - - - N E C S A S F T F D T A8XJQ6_CAEBR
18 - - - - - N E C S A S F T F D T CAEEL_F47F2.1a
2 - - - - - CAEEL_F47F2.1c
8 - - - - - T - - - - - PRKX_CANLU
11 - - - - - PRKX_DANRE
161 Q Q Q Q Q P Q Q Q Q Q P Q Q Q L Q Q N N Q Q Q Q Q L Q Q Q Q L Q Q Q L Q Q Q Q DdPK2_DICDI
7 - - - - - PRKX_EQUCA
11 - - - - - M R A K S G D A A - - - - - PRKX_GALLGA
25 - - - - - D G A P A L - - - - - C P S P - - - - - PRKX_MACMU
51 - - - - - S S S P A V - - - - - G P G S - - - - - PRKX_MONDO
4 - - - - - A7SM62_NEMVE
29 Q R Q Q Q Q T Q S Q P Q - - - - - L H P - - - - - Q7SHX1_NEUCR
57 - - - - - L R L K S E G G S G H L Q A R D C P G G - - - - - PRKX_ORNAN
25 - - - - - D W A P A L - - - - - C P S P - - - - - PRKX_PANTR
43 - - - - - G H S L Q - - - - - Q5BK52_RAT
11 - - - - - Q4RY94_TETNG
24 - - - - - D Y - - - - - PRKX_TRICA
16 - - - - - Q L H D L E L G E - - - - - PKAC3_TRYCR

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Majority

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-----+-----+-----+-----+
                210                220                230                240
-----+-----+-----+-----+
35 - - - - - E A L - - - - - S P - - - - - E P P V Y S - - - - - PRKX_HUMAN
45 - - - - - D W - - - - - PRKX_MOUSE
56 N N N S R G N N Q - - - - - CAEEL_F47F2.1b
89 S E E D P E Q E Q Q R P - - - - - D P A T K S R S S S T A T T T T S S A DC2_DROME
25 - - - - - PKAC3_TRYBR
35 - - - - - E A R - - - - - S P - - - - - E A P A Y R - - - - - PRKY_HUMAN
16 - - - - - S - - - - - Q16NW2_AEDAE
54 - - - - - A6QTK8_AJECN
1 - - - - - Q7PZC6_ANOGA
13 - - - - - K A P C A S C S U - - - - - KAPC_ASCSU
59 - - - - - P A A - - - - - E K A G - L C S V - - - - - G T A S F K S - - - - - PRKX_BOSTA
29 N N N S R G D Q Q - - - - - A8XJQ6_CAEBR
29 N N N S R G N N Q - - - - - CAEEL_F47F2.1a
2 - - - - - CAEEL_F47F2.1c
9 - - - - - P P S - - - - - G N I N - V C M G - - - - - T - - - - - PRKX_CANLU
11 - - - - - PRKX_DANRE
201 Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q Q H L H Q D G I V N T P S T T Q T S DdPK2_DICDI
7 - - - - - PRKX_EQUCA
21 - - - - - PRKX_GALLGA
35 - - - - - E A R - - - - - S P - - - - - E P P A Y R - - - - - PRKX_MACMU
61 - - - - - P A P - - - - - S P - - - - - E L P A Y K - - - - - PRKX_MONDO
4 - - - - - A7SM62_NEMVE
45 - - - - - Q7SHX1_NEUCR
77 - - - - - Q W G - - - - - H P V D W A C L R F F K Q A A G T R Q C PRKX_ORNAN
35 - - - - - E A R - - - - - S P - - - - - E A P A Y R - - - - - PRKX_PANTR
48 - - - - - D W - - - - - Q5BK52_RAT
11 - - - - - S E D D K E G - - - - - Q4RY94_TETNG
26 - - - - - PRKX_TRICA
25 - - - - - PKAC3_TRYCR

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Majority

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-----+-----+-----+-----+
                250                260                270                280
-----+-----+-----+-----+
46 - - L Q D F D T L A - - - - - PRKX_HUMAN
47 - - - - - PRKX_MOUSE
65 - - - - - V N E L A E E T H M K L S I T P T R E S F - - - - - CAEEL_F47F2.1b
121 D H D N D V D E E D E D D E - - - - - D E G E G N - - - - - DC2_DROME
25 - - - - - PKAC3_TRYBR
46 - - L Q D C D A L V - - - - - PRKY_HUMAN
17 - - - - - Q16NW2_AEDAE
54 - - - - - C N P G P P A S - - - - - A6QTK8_AJECN
1 - - - - - Q7PZC6_ANOGA
13 - - - - - V S I T I D P N N N K L - - - - - KAPC_ASCSU
77 - - - - - K S K T A R - - - - - D D C F R R - - - - - PRKX_BOSTA
38 - - - - - V D E L A E E T H M K L S I T P T R E S F - - - - - A8XJQ6_CAEBR
38 - - - - - V N E L A E E T H M K L S I T P T R E S F - - - - - CAEEL_F47F2.1a
2 - - - - - K L S I T P T R E S F - - - - - CAEEL_F47F2.1c
21 - - - - - F K L V P - - - - - F T L F T S - - - - - PRKX_CANLU
11 - - - - - N N E S S G R D S G - - - - - R T E A G S - - - - - PRKX_DANRE
241 T T T T T T T T T N P H T S G L S L Q H A H S S Y T P S N V L H S P T H F Q S DdPK2_DICDI
9 - - - - - R R - - - - - S Y F S S - - - - - PRKX_EQUCA
21 - - - - - A A A G L A A P Q P A - - - - - A T A P S P - - - - - PRKX_GALLGA
46 - - L Q D F D T L A - - - - - PRKX_MACMU
72 - - L Q D F D T L A - - - - - PRKX_MONDO
4 - - - - - A7SM62_NEMVE
45 - - - - - C M L S Q H H S Y - - - - - Q7SHX1_NEUCR
100 A L L Q G E D G Q A G R E E G - - - - - R P T L G S - - - - - PRKX_ORNAN
46 - - L Q D F D A L V - - - - - PRKX_PANTR
50 - - - - - Q5BK52_RAT
11 - - - - - N M E T N A V K E N K - - - - - S S A G S S - - - - - Q4RY94_TETNG
33 - - - - - PRKX_TRICA

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25 - - - - - PKAC3_TRYCR
-----
Majority
-----
290 300 310 320
-----
54 - - - - - PRKX_HUMAN
47 - - - - - PRKX_MOUSE
86 - - - - - CAEEL_F47F2.1b
142 GRDADDDATHDSSSESI EEDDGN ETDD EDDDESEESS SVQT DC2_DROME
25 - - - - - PKAC3_TRYBR
54 - - - - - PRKY_HUMAN
17 - - - - - Q16NW2_AEDAE
62 - - - - - A6QTK8_AJECN
1 - - - - - Q7PZC6_ANOGA
25 - - - - - KAPC_ASCSU
89 PLGSPSGTWD AVH - - - - - PRKX_BOSTA
59 - - - - - A8XJQ6_CAEBR
59 - - - - - CAEEL_F47F2.1a
13 - - - - - CAEEL_F47F2.1c
32 CAVSPTP - - - - - PRKX_CANLU
28 PTL PAGAASLT TN - - - - - PRKX_DANRE
281 SLPTRLDNTNPI TTP I RQQQQSQQQLQQQI PPP TVNS DgPK2_DICDI
16 PAPETES - - - - - PRKX_EQUCA
38 AGPGSPSAPEPTA - - - - - PRKX_GALLGA
54 - - - - - PRKX_MACMU
80 - - - - - PRKX_MONDO
4 - - - - - VST A7SMG2_NEMVE
54 - - - - - QNDQRRNDPSQTQKNN D TSGGFEM Q7SHX1_NEUCR
121 SPPKSSGGSGDCG - - - - - PRKX_ORNAN
54 - - - - - PRKX_PANTR
50 - - - - - Q5BK52_RAT
28 AGETS P SANL - - - - - Q4RY94_TETNG
33 - - - - - PRKX_TRICA
25 - - - - - PKAC3_TRYCR

- - - - - L - - - - ERI - TIGTGT FGRVHLVKDKKTA K - Majority
-----
330 340 350 360
-----
54 - - - - - T - - - - - VGTGT FGRVHLVKEKTA K - PRKX_HUMAN
47 - - - - - - - - - - DTIATVGTGT FGRVNLVKEK TGR - PRKX_MOUSE
86 - - - - - - SLSQLERIITIGKGT FGRV ELARDKITG - CAEEL_F47F2.1b
182 - - - - - AKGVRKYHLDDYQI IKT VGTGT FGRVCLCRDRISE - DC2_DROME
25 - - - - - - - - - - TIGTGT FGRVRLCRHRASG - PKAC3_TRYBR
54 - - - - - - - - - - MGTGT FGRVHLVKEKTA K - PRKY_HUMAN
17 - - - - - - FVFLAFLIT - - - - - GTGT FGRVCLCRDKETD - Q16NW2_AEDAE
81 - - - - - - SSEL SIGDFEL LQT LGTGT FARV L VRL LKHTG - A6QTK8_AJECN
1 - - - - - - - - - - TI - - - - - GTGT FGRVCLCRDKITN - Q7PZC6_ANOGA
25 - - - - - - NVDDDFRICTIGTGSFGRVYLVQHRASE - KAPC_ASCSU
102 - - - - - GWV CGRVDLALDDL LGTGT FGRVQLVQEKTSK - PRKX_BOSTA
59 - - - - - - SLSQLERIVTIGKGT FGRV ELARDKISG - A8XJQ6_CAEBR
59 - - - - - - SLSQLERIITIGKGT FGRV ELARDKITG - CAEEL_F47F2.1a
13 - - - - - - SLSQLERIITIGKGT FGRV ELARDKITG - CAEEL_F47F2.1c
39 - - - - - - - - - - GTGT FGRVQLVKDKKAAK - PRKX_CANLU
41 - - - - - - RTYTLDDLDTIATVGTGT FGRVFLVKDKKTR - PRKX_DANRE
321 FFLPPP VNARERLKEFKQIRVIGTGT FGKVVLIQNTKDG - DgPK2_DICDI
23 - - - - - - - - - - LRTGT FGRVQLVKEKKA K - PRKX_EQUCA
51 - - - - - - Y - - - - - KLEDELETLATVGTGT FGRVHLVKEKMGK - PRKX_GALLGA
54 - - - - - - - - - - VGTGT FGRVHLVKEKTA K - PRKX_MACMU
80 - - - - - - - - - - TQLDQVERIKF IGTGT FGRVHLVKEKTA K - PRKX_MONDO
7 - - - - - - RKKDKRTTLQDFELSKTLGTGT FGRV L LARDR RG - A7SMG2_NEMVE
78 - - - - - - ATRKPRLSDFHR - - - - - T FARV L V R PANGTE - Q7SHX1_NEUCR
134 - - - - - - FWTRDEEVEERRRLLSTGT FGRVHLVKEKTA K - PRKX_ORNAN
54 - - - - - - - - - - VGTGT FGRVHLVKEKTA K - PRKX_PANTR
50 - - - - - - - - - - DTIATVGTGT FGRVNLVKEK TGR - Q5BK52_RAT
38 - - - - - - RMYSLDELD TIATV - - - - - VKDKKTR - Q4RY94_TETNG
33 - - - - - - YDIDDFNI IKTIGTGT FGRV L LCKNKSTN - PRKX_TRICA
25 - - - - - - - - - - TIGTGT FGRVRLCKHKTS G - PKAC3_TRYCR

- - - - - HYFALKVMSIPDVIRL KQE QHVHNEKSVLKEVS - HP Majority
-----
370 380 390 400
-----
73 - - - - - HFFALKVMSIPDVIRL KQE QHVHNEKSVLKEVS - HP PRKX_HUMAN
70 - - - - - KYCALKIMSIPDVIRL KQE QHVQNEKAVLKEIN - HP PRKX_MOUSE
114 - - - - - AHYALKV LNI RRVVDMRQTQH V HNEKRVLLQLK - HP CAEEL_F47F2.1b
217 - - - - - KYCAMKILAMTEVIRL KQIEHVKNERNILREIR - HP DC2_DROME
44 - - - - - QYVVLKILK KQEILRMKQV DHI LAESSILQELS - HP PKAC3_TRYBR
73 - - - - - HFFALKVMSIPDVIRR KQE QHVHNEKSVLKEVS - HP PRKY_HUMAN
43 - - - - - KYWAMKILAMADVIRL KQIEHVKN EKNILREID - HP Q16NW2_AEDAE
115 KFKNGAYALKV LHKADVIRL KQVEHV RNEIETLNAVAGHP - HP A6QTK8_AJECN
20 - - - - - KYWAMKILAMADVIRL KQIEHVKN EKNILQEI D - HP Q7PZC6_ANOGA
53 - - - - - QYFALKKMAIREV VSMRQT EHVHSEKRLLSRLS - HP KAPC_ASCSU
133 - - - - - HFFALKVMTIPD IIRL KQE QHVHNEKSVLKEVN - HP PRKX_BOSTA
87 - - - - - AHYALKV LNI RRVVDMRQTQH V HNEKRVLLQLK - HP A8XJQ6_CAEBR
87 - - - - - AHYALKV LNI RRVVDMRQTQH V HNEKRVLLQLK - HP CAEEL_F47F2.1a
41 - - - - - AHYALKV LNI RRVVDMRQTQH V HNEKRVLLQLK - HP CAEEL_F47F2.1c
56 - - - - - HFFALKVMSIPDVIRL KQE QHVHNEKSVLKEVS - HP PRKX_CANLU
72 - - - - - GFFALKAMKIPDVIRL KQIEHVHNEKVELTEVN - HP PRKX_DANRE
360 - - - - - CYFAMKCLNKAYV VRLKQVEHLNS EKSILSSI H - HP DgPK2_DICDI
41 - - - - - HFFALKVMSIPDVIRL KQE QHVHNEKSVLKEVS - HP PRKX_EQUCA
80 - - - - - HYFALKVMSIPDVIRL KQE QHVHNEKSVLKEVN - HP PRKX_GALLGA
73 - - - - - HFFALKVMSIPDVIRL KQE QHVHNEKSVLKEVS - HP PRKX_MACMU
109 - - - - - HYFALKVMSIPDVIRL KQE QHVHNEKSVLKEVS - HP PRKX_MONDO

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42 - - - - E F Y A L K I M N I S E V I R L K Q V E H V Q N E K N I L M S I E - H P A7SM62_NEMVE
105 I D R Q K V Y A L K I L R K T E V I R L K Q I D H V R H E R Q I L Q D V T G H P Q7SHX1_NEUCR
165 - - - - H Y F A L K V M S I P D V I R L K Q E Q H V H N E K S V L K E V N - H P PRKX_ORNAN
73 - - - - H F F A L K V M S I P D V I R L K Q E Q H V H N E K S V L K E V S - H P PRKX_PANTR
73 - - - - R Y C A L K I M S I P D V I R L K Q E Q H V Q N E K A V L K E I N - H P Q5BK52_RAT
59 - - - - T F Y A L K Q M K I P D V I R L K Q E Q H V H N E K E V L T E V T - H P Q4RY94_TETNG
62 - - - - Q Y S A M K I L C L S D V I R L K Q V E H V K N E K N I L Q E I R - H P PRKX_TRICA
44 - - - - K Y M A L K I L K K Q E V L R M K Q V E H I L A E S S I L Q E L N - H P PKAC3_TRYCR

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F L V K L F W T F H D E R F L Y M L M E Y V P G G E L F S Y L R N R G R F S S N S Majority
-----+-----+-----+-----+-----+
                410                420                430                440
-----+-----+-----+-----+-----+

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108 F L I R L F W T W H D E R F L Y M L M E Y V P G G E L F S Y L R N R G R F S S T PRKX_HUMAN
105 F L I K L L W T G H D N R F L Y M L M E F V P G G E L F T Y L R N R G R F S S V PRKX_MOUSE
149 F I V K M Y A S E K D S N H L Y M I M E F V P G G E M F S Y L R A S R S F S N S CAEEL_F47F2.1b
252 F V I S L E W S T K D D S N L Y M I F D Y V C G G E L F T Y L R N A G K F T S Q DC2_DROME
79 F I V T M Y K G F M D D R L Y L L L E Y V V G G E L F S H L R K A G K F P N D PKAC3_TRYBR
108 F L I R L F W T W H E E R F L Y M L M E Y V P G G E L F S Y L R N R G H F S S T PRKY_HUMAN
78 F V V N M R W H A K D D C C L Y M L F E Y V S G G E L F S Y L R N A G R F D N A Q16NW2_AEDAE
155 F I T T L V A T F T D D L S L Y M L L E Y C P G G E I F T F L R R A R R F D V S A6QTK8_AJECN
55 F I V N M R W N S K D D C C L Y M L F E F V S G G E L F S Y L R N A G R F D S A Q7PZC6_ANOGA
88 F I V K M Y C A S W D K Y N L Y M L F E Y L A G G E L F S Y L R A S R T F S N S KAPC_ASCSU
168 F L V K L F W T G H D D R F L Y M L M E F V P G G E L F S Y L R N R G R F S S N PRKX_BOSTA
122 F I V K M Y A S E K D S N N L Y M I M E F V P G G E M F S Y L R A S R S F S N S A8XJQ6_CAEBR
122 F I V K M Y A S E K D S N H L Y M I M E F V P G G E M F S Y L R A S R S F S N S CAEEL_F47F2.1a
76 F I V K M Y A S E K D S N H L Y M I M E F V P G G E M F S Y L R A S R S F S N S CAEEL_F47F2.1c
91 F L V K L F W T C H D E R F L Y M L M E F V P G G E L F S Y L R N R G R F S S S PRKX_CANLU
107 F L V R L F W T H H D D R F L Y M L M E Y V N G G E L F S Y L R S R G H F S S S PRKX_DANRE
395 F I V N L Y Q A F Q D E K K L Y L L F E Y V A G G E V F T H L R K S M K F S N S DgPK2_DICDI
76 F L V K L F W T Y H D E R F L Y M L M E F V P G G E L F S Y L R N R G R F A S N PRKX_EQUCA
115 F L I R L F W T Y H D E R F L Y M L M E Y V P G G E L F S Y L R N M G R F N N S PRKX_GALLGA
108 F L I R L F W T W H D E R F L Y M L M E Y V P G G E L F S Y L R N R G R F S S T PRKX_MACMU
144 F L I R L Y W T Y H D E R F L Y M L M E Y D P G E Y L F S Y V R D M G R F N N S PRKX_MONDO
77 F I V N L L W T Q H D Q T F L Y M L L E Y A C G G E L F T Y L R T A G R F N N G A7SM62_NEMVE
145 F I T S L Q A S F S D H D F L Y L L L D Y I P G G E L F T Y L R K Y R R F D E E Q7SHX1_NEUCR
200 F L I R L Y W T Y H D E R F L Y M L M E Y V P G G E L F S Y L R N M G R F N N S PRKX_ORNAN
108 F L I R L F W T W H D E H F L Y M L M E Y V P G G E L F S Y L R N Q G C F S S T PRKX_PANTR
108 F L I K L L W T D H D N R F L Y M L M E F V P G G E L F T Y L R N R G R F S S V Q5BK52_RAT
94 F I R L F W T H H D Q R F L Y M L M D F V P G G E L F S Y L R S R G R F S N T Q4RY94_TETNG
97 F I V N M L W C S K D N T C I Y M L F E Y V C G G E L F S Y L R N A G R F S T S PRKX_TRICA
79 F I V N M L K G F M D N D R L Y I L L E Y V V G G E L F T H L R K A G K F P N D PKAC3_TRYCR

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T G L F Y A A E I V C A I E Y L H S K E - - I V Y R D L K P E N I L L D R E G H Majority
-----+-----+-----+-----+
                450                460                470                480
-----+-----+-----+-----+

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148 T G L F Y S A E I I C A I E Y L H S K E - - I V Y R D L K P E N I L L D R D G H PRKX_HUMAN
145 A S V F Y A T E I V C A I E Y L H S K E - - I V Y R D L K P E N I L L D R E G H PRKX_MOUSE
189 M A R F Y A S E I V C A I E Y I H S L G - - I V Y R D L K P E N L M L S K E G H CAEEL_F47F2.1b
292 T S N F Y A A E I V S A L E Y L H S L Q - - I V Y R D L K P E N L L I N R D G H DC2_DROME
119 V A K F Y S A E I V L A F E Y I H E C G - - I V Y R D L K P E N V L L D K Q G N PKAC3_TRYBR
148 T G L F Y S A E I I C A I E Y L H S K E - - I V Y R D L K P E N I L L D R D G H PRKY_HUMAN
118 T A N F Y A C E I V L A L E F L H S H A L S - - I V Y R D L K P E N L L L D R D G H Q16NW2_AEDAE
195 T A Q F Y A A E I V L I L E F L H D V H G - I A Y R D L K P E N I L L D A D G H A6QTK8_AJECN
95 T A N F Y A C E I V L A L E Y L H S L S - - I V Y R D L K P E N L L L D R E G H Q7PZC6_ANOGA
128 M A R F Y A A E I V C A I Q Y L H S K N - - I A Y R D L K P E N L M L N K E G H KAPC_ASCSU
208 T G L F Y A A E I V C A I E Y L H S R D - - I V Y R D L K P E N I L L D R D G H PRKX_BOSTA
162 M A R F Y A S E I V C A I E Y I H S L G - - I V Y R D L K P E N L M L S K E G H A8XJQ6_CAEBR
162 M A R F Y A S E I V C A I E Y I H S L G - - I V Y R D L K P E N L M L S K E G H CAEEL_F47F2.1a
116 M A R F Y A S E I V C A I E Y I H S L G - - I V Y R D L K P E N L M L S K E G H CAEEL_F47F2.1c
131 T G L F Y S A E I I C A I E Y L H S K E - - I V Y R D L K P E N I L L D R E G H PRKX_CANLU
147 T G M F Y S A E I V C A I E Y L H S K E - - I V Y R D L K P E N I L L D S E G H PRKX_DANRE
145 T A K F Y A A E I V L A L E F L H K Q N - - I V Y R D L K P E N L L I D N Q G H DgPK2_DICDI
116 T G L F Y S A E I V C A I E Y L H S K E - - I V Y R D L K P E N I L L D R D G H PRKX_EQUCA
155 T G L F Y S T E I I C A I E Y L H S K E - - I V Y R D L K P E N I L L D K E G H PRKX_GALLGA
148 T G L F Y S A E I I C A I E Y L H S K E - - I V Y R D L K P E N I L L D R D G H PRKX_MACMU
184 T G L F Y S A E I I C A I E Y L H S K E - - I V Y R D L K P E N I L L D K E G H PRKX_MONDO
117 T G L F F G S E I V S A M D Y L H G H S - - I V Y R D L K P E N I L L D R D G H A7SM62_NEMVE
185 M A R F Y A A E I V L V L E Y L H E E Q G G I A Y R D M K P E N L L L D A D G H Q7SHX1_NEUCR
240 T G L F Y S T E I I C A I E Y I H S K E - - I V Y R D L K P E N I L L D K E G H PRKX_ORNAN
148 T G L F Y S A E I I C A M E Y L H S K E - - I V Y R D L E P E N I L L D R D G H PRKX_PANTR
148 A A I F Y A T E I V C A I E Y L H S K E - - I V Y R D L K P E N I L L D R E G H Q5BK52_RAT
134 T G L F Y T S E I V C A I E Y L H S K E - - I V Y R D L K P E N I L L D S E G H Q4RY94_TETNG
137 T G N F Y T S E I V S A L E Y L H S R S - - I V Y R D L K P E N L L L D K D G H PRKX_TRICA
119 V A K F Y S A E I V L A F E Y L H S N S - - I V Y R D L K P E N L L L D A Q G N PKAC3_TRYCR

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I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S Majority
-----+-----+-----+-----+
                490                500                510                520
-----+-----+-----+-----+

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186 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S PRKX_HUMAN
183 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S PRKX_MOUSE
227 I K M A D F G F A K K L - - - - R D R - - - T Y T I C G T P D Y L A P E S L A R CAEEL_F47F2.1b
330 L K I T D F G F A K K L - - - - R D R - - - T W T L C G T P E Y I A P E I I Q S DC2_DROME
157 I K I T D F G F A K R V - - - - R D R - - - T Y T L C G T P E Y L A P E I I Q S PKAC3_TRYBR
186 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S PRKY_HUMAN
156 L K I T D F G F A K K L - - - - K D R - - - T W T L C G T P E Y L A P E I I Q S Q16NW2_AEDAE
234 L K L V D F G F A K K L - - - - W S R E T Y T L C G T P E Y L A P E V I H N A6QTK8_AJECN
133 M K I T D F G F A K K L - - - - K D R - - - T W T L C G T P E Y L A P E I I Q S Q7PZC6_ANOGA
166 L K M T D F G F A K K E V - - - - I D R - - - T W T M C G T P E Y L A P E V I G N KAPC_ASCSU
246 V K L T D F G F A K K L - - - - V D K - - - T W T L C G T P E Y L A P E V I Q S PRKX_BOSTA
200 I K M A D F G F A K K L - - - - R D R - - - T Y T I C G T P D Y L A P E S L A R A8XJQ6_CAEBR
200 I K M A D F G F A K K E L - - - - R D R - - - T Y T I C G T P D Y L A P E S L A R CAEEL_F47F2.1a
154 I K M A D F G F A K K E L - - - - R D R - - - T Y T I C G T P D Y L A P E S L A R CAEEL_F47F2.1c

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169 I K L T D F G F A K K L - - - - V D K - - - T W T L C G T P E Y L A P E V I Q S PRKX_CANLU
185 I R L T D F G F A K K L - - - - S E R - - - T W T L C G T P E Y L A P E V I Q S PRKX_DANRE
473 I K I T D F G F A K R V - - - - E D R - - - T F T L C G T P E Y L A P E I I Q S DdPK2_DICDI
154 I K L T D F G F A K K L - - - - V D K - - - T W T L C G T P E Y L A P E V I Q S PRKX_EQUCA
193 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S PRKX_GALLGA
186 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S PRKX_MACMU
222 I K L T D F G F A K K L - - - - L D R - - - T W T L C G T P E Y L A P E V I Q S PRKX_MONDO
155 V K L T D F G F A K E V - - - - H D K - - - T W T L C G T P E Y L A P E I I Q S A7SM62_NEMVE
225 I K L V D F G F A K R L G Y N D V E R P V E T Y T L C G T P E Y L A P E V I Q N Q7SHX1_NEUCR
278 I K L T D F G F A K K L - - - - V D K - - - T W T L C G T P E Y L A P E V I Q S PRKX_ORNAN
186 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S PRKX_PANTR
186 I K L T D F G F A K K L - - - - V D R - - - T W T L C G T P E Y L A P E V I Q S Q5BK52_RAT
172 I R L T D F G F A K K L - - - - S D R - - - T W T L C G T P E Y L A P E V I Q S Q4RY94_TETNG
175 L K I T D F G F A K K L - - - - T D R - - - T W T L C G T P E Y L A P E I I Q S PRKX_TRICA
157 I K I T D F G F A K R V - - - - T E R - - - T F T L C G T P E Y L A P E V I Q S PKAC3_TRYCR

K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A Majority
-----+-----+-----+-----+
530 540 550 560

219 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_HUMAN
216 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_MOUSE
260 T G H N K G V D W W A L G I L I Y E M M V G K P P F R G K T T S E I Y D A I I E CAEEL_F47F2.1b
363 K G H N K A V D W W A L G V L I Y E M L V G Y P P F Y D E Q P F G I Y E K I L S DC2_DROME
190 K G H D R A V D W W T L G I L L Y E M L V G Y P P F F D E S P F R T Y E K I L E PKAC3_TRYBR
219 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKY_HUMAN
189 K G H N K A V D W W A L G V L I Y E M M V G Y P P F Y D D N P F G I Y E K I L S Q16NW2_AEDAE
268 S G H G L A V D W W A L G V L I Y E F I V G Q P P F W D P N P M R I Y K Q I V D A6QTK8_AJECN
166 K G H N K A V D W W A L G V L I Y E M I V G Y P P F Y D D N P F G I Y E K I L S Q7PZC6_ANOGA
199 K G H D T A V D W W S L G V L I Y E M M I G I P P F R G K T L D E I Y E K I I L KAPC_ASCSU
279 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N A F G I Y Q K I L A PRKX_BOSTA
233 T G H N K G V D W W A L G I L I Y E M M V G K P P F R G K T T A E I Y D S I I E A8XJQ6_CAEBR
233 T G H N K G V D W W A L G I L I Y E M M V G K P P F R G K T T S E I Y D A I I E CAEEL_F47F2.1a
187 T G H N K G V D W W A L G I L I Y E M M V G K P P F R G K T T S E I Y D A I I E CAEEL_F47F2.1c
202 K G H G R A V D W W A L G I L I F E M H S G F P P F F D D N P F G I Y Q K I L A PRKX_CANLU
218 K G H G R A V D W W A L G V L I F E M L A G Y P P F F D D N P F G I Y Q K I L A PRKX_DANRE
506 K G H G K A V D W W A L G I L I F E M L A G Y P P F Y D D D T F A I Y N K I L A DdPK2_DICDI
187 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_EQUCA
226 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_GALLGA
219 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_MACMU
255 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_MONDO
188 K G H N K A V D W W A L G I L I Y E M L V G Y P P F F D D N P F G I Y E K I L S A7SM62_NEMVE
265 K G H T T A V D W W A L G I L I Y E F L T G Y P P F Y H N N P L E I Y R H - - - Q7SHX1_NEUCR
311 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A PRKX_ORNAN
219 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P L G I Y Q K I L A PRKX_PANTR
219 K G H G R A V D W W A L G I L I F E M L S G F P P F F D D N P F G I Y Q K I L A Q5BK52_RAT
205 K G H G R A V D W W A L G I L I F E M L A G Y P P F F D D N P F G I Y Q K I L A Q4RY94_TETNG
208 K G H N K A V D W W A L G V L I Y E M L A G Y P P F Y D D N P F G I Y E K I L S PRKX_TRICA
190 R G H N K A V D W W A L G I L L Y E M L V G Y P P F F D E S P F K I Y E K I L E PKAC3_TRYCR

G K I D F P R H L D - L A A K D L I K K L L V V D R T R R L G N M K N G A D D V Majority
-----+-----+-----+-----+
570 580 590 600

259 G K I D F P R H L D - F H V K D L I K K L L V V D R T R R L G N M K N G A N D V PRKX_HUMAN
256 C K I D F P R Q L D - F T S K D L I K K L L V V D R T R R L G N M K N G A E D I PRKX_MOUSE
300 H K L K F P R S F N - L A A K D L V K K L L E V D R T Q R I G C M K N G T Q D V CAEEL_F47F2.1b
403 G K I E W E R H M D P I - A K D L I K K L L V N D R T K R L G N M K N G A D D V DC2_DROME
230 G K L Q F P K W V E - M R A K D L I K S F L T I E E T K R L G S V K R G V Q D V PKAC3_TRYBR
259 G K L Y F P R H L D - F H V K T - - - - - - - - - - G R M M PRKY_HUMAN
229 G K I E W S R H I E P I - A K D L V K K L L V Q D R T K R L G N M K N G A E D I Q16NW2_AEDAE
308 G V L R F P A N M - P P A Q D I V S R L C Q T N E S E R L G H I K G G S A R V A6QTK8_AJECN
206 G K I E W S R H V D P I - A K D L V K K L L V L D R T K R L G N M K N G A E D V Q7PZC6_ANOGA
239 G K L R F T R S F D - L F A K D L V K K L L Q V D R T Q R L G N Q K D G A A D V KAPC_ASCSU
319 G K I D F P R H L E - F S V K D L I R K K L L V T D R T R R L G N M K N G A E D V PRKX_BOSTA
273 H K L K F P R S F N - L A A K D L V K K L L E V D R T Q R I G C M K N G T Q D V A8XJQ6_CAEBR
273 H K L K F P R S F N - L A A K D L V K K L L E V D R T Q R I G C M K N G T Q D V CAEEL_F47F2.1a
227 H K L K F P R S F N - L A A K D L V K K L L E V D R T Q R I G C M K N G T Q D V CAEEL_F47F2.1c
242 G K I D F P R H L D - F S V K D L I R K K L L V V D R T R R L G N M K N G A D D V PRKX_CANLU
258 G K L E F F P R H L D - L Y V K D L I K K F L V T D R E R R L G N M K N G A D D V PRKX_DANRE
546 G R I T F P L G F D - V D A K D L I K R L L T A D R T R R L G A L K D G A L D V DdPK2_DICDI
227 G K I D F P R H L D - F S V K D L V R K K L L V V D R T R R L G N M K N G A D D V PRKX_EQUCA
266 G K I D F P R H L D - L Y V K D L I K K L L V V D R T R R L G N M K N G A D D V PRKX_GALLGA
259 G K I D F P R H L D - F H V K D L I K K L L V V D R T R R L G N M K N G A N D V PRKX_MACMU
295 G K I D F P R H L D - L Y V K D L I K K L L V V D R T R R L G N M K N G A D D V PRKX_MONDO
228 G K V E W P K H M D N T S A K D L I K K L L V H D R T R R L G S M K N G S E D V A7SM62_NEMVE
302 - - - - - - - - - - E E A K D I R S F C T V D R T M R L G N M S G G A A R V Q7SHX1_NEUCR
351 G K I D F P R H L D - L Y V K D L I K K L L V V D R T R R L G N M K N G A D D V PRKX_ORNAN
259 G K L D F P R H L D - F R V K D L I K K L L V V D R T R R L G N M K N G A N D M PRKX_PANTR
259 C K I D F P R Q L D - F T S K D L I K K L L V V D R T R R L G N M K N G A E D I Q5BK52_RAT
245 G K L E F P R H L D - F Y V K D L I K K F L V I D R A R R L G N M K N G A D D V Q4RY94_TETNG
248 G K I E W P K H L D P V - A K D L I K K L L V Q D R T K R L G N M K S G A E D V PRKX_TRICA
230 G K L Q F P R W L E - A R A K D L I K K L L V L E E T K R L G S L N R G T Q D V PKAC3_TRYCR

K R H R W F R G V D W D A V P Q R K L K P P I V P K L - - - S H D G D T S N F D Majority
-----+-----+-----+-----+
610 620 630 640

298 K H H R W F R S V D W E A V P Q R K L K P P I V P K I - - - A G D G D T S N F E PRKX_HUMAN
295 K R H R W F R S V D W E S V P Q R K L K P P I V P K L - - - S G D G D I S N F E PRKX_MOUSE
339 K D H K W F E K V N W D D T L H L R V E P P I V P T L - Y - - H P G D T G N F D CAEEL_F47F2.1b
442 K R H R W F K H L N W D V S K K L K P P I L P D V - - - H H D G D T K N F D DC2_DROME
269 K R H K F Y S G V N W N V L L Q R G V A A P I H V R L - - - N N D G D T R Y F D PKAC3_TRYBR
277 PRKY_HUMAN
268 K R H R W F K H L D W D V I R K Q L K P P I V P K F V F - - - E G D T S N F D Q16NW2_AEDAE

347 K Q H S F F K G V N W D D I Y H R R M K G P I V P R V - - - D S P T D A G N F E A6QTK8_AJECN
 245 K R H R W F K H L D W N V V I R K Q L K P P I V P T Y V F S S K E D D T S N F D Q7PZC6_ANOGA
 278 M N H K W F T D I D W D D V Q N M K L T P P I I P T L - Y - - S N G D T G N F D KAPC_ASCSU
 358 K Q H R W F R V V D W G A V P E R K L K P P I I P K L - - - C S E D D T S N F E PRKX_BOSTA
 312 K D H K W F E K V N W D D T L H L R V E P P I V P T L - Y - - H P G D T G N F D A8XJQ6_CAEBR
 312 K D H K W F E K V N W D D T L H L R V E P P I V P T L - Y - - H P G D T G N F D Q20541_CAEBL
 266 K D H K W F E K V N W D D T L H L R V E P P I V P T L - Y - - H P G D T G N F D CAEBL_F47F2.1c
 281 K R H R W F R T V D W E A V P Q R K L K P P I V P K L - - - C G E G D T S N F E PRKX_CANLU
 297 K K H R W F K S V N W E S V P C R K L K P P I V P K V - - - S H E G D T S N F D PRKX_DANRE
 585 K N H R W F S D I N W E R L Y Q R R D N G P F I P K I - - - Q H Q G D S S N F E DdPK2_DICDI
 266 K R H R W F R T V D W E A V P Q R K L K P P I V P K V - - - C G E G D T S N F E PRKX_EQUCA
 305 K R H R W F R S I D W D A V P Q R R L K P P I V P K V - - - S N D G D T S N F E PRKX_GALLGA
 298 K R H R W F H S V D W E A V P Q R K L K P P I V P K I - - - A G D G D T S N F E PRKX_MACMU
 334 K K H R W F R S V D W D A V P Q R K L K P P I V P K V - - - S N D G D T S N F E PRKX_MONDO
 268 K N H K W F K V I D W N L V L Q R K L K P P I N P K I - - - S H P G D T R N F D A7SM62_NEMVE
 331 K A H P W F K G V D W E A V E Q R R H K G P I I P H L - - - S H P G D A S C F D Q7SHX1_NEUCR
 390 K R H R W F R S I D W E A V P Q R K L K P P I V P K V - - - S S D G D T S N F E PRKX_ORNAN
 298 K R H R W F R S V D W E A V P Q R K L K P P I V P T - - - A G D G D T S N F E PRKX_PANTR
 298 K R H R W F R G V E W E S V P Q R K L K P P I V P K L - - - S S D G D I S N F E Q5BK52_RAT
 284 K K H R W F K T V D W D A V P L R K L K P P I P K V - - - S H E G D T S N F D Q4RY94_TETNG
 287 K R H R W F K T V D W D H D V I M R K L N P P I V P K I M Y - - - D G D A S N F D PRKX_TRICA
 269 K R H K F Y S G V D W D I L L Q K K V T P P I P V R L - - - N K E G D T R Y F D PKAC3_TRYCR

D Y P E E D W D K A P P V S Q K D L E L F K N F - - - - - Majority
 -----+-----+-----+-----
 -----+-----+-----+-----
 -----+-----+-----+-----
 335 T Y P E N D W D T A A P V P Q K D L E I F K N F PRKX_HUMAN
 332 T Y P E S E L D K T P S V S D K D L E T F K N F PRKX_MOUSE
 376 D Y - E E D T T G G P L C S Q R D R D L F A E W CAEBL_F47F2.1b
 479 D Y P E K D W K P A K A V D Q R D L Q E Y F N D F DC2_DROME
 306 R Y P E S P R H P L Q P L T E A Q Q E L F S G F C D G E Y T R I PKAC3_TRYER
 277 PRKY_HUMAN
 305 D Y P E T D W K S A R S L D K V E M Q L F E D F Q16NW2_AEDAE
 384 I Y P D P P H P S E L A P Y T K D M - - - R D A Y E H M F K T F A6QTK8_AJECN
 285 D Y P E T D W K S V R S L D K I E M Q L F E D F Q7PZC6_ANOGA
 315 S Y - D E C S D D E I A A P Q H E L E L F E D W KAPC_ASCSU
 395 A Y P E N D W T S A P P V S Q K E L D V F K N F PRKX_BOSTA
 349 D Y - E E D T T G G P L C S Q R E R D L F A E W A8XJQ6_CAEBR
 349 D Y - E E D T T G G P L C S Q R D R D L F A E W Q20541_CAEBL
 303 D Y - E E D T T G G P L C S Q R D R D L F A E W CAEBL_F47F2.1c
 318 A Y P E N D W N T A P P V S P K D L E V F K N F PRKX_CANLU
 334 S Y P D E E W K K D T P V P A K D L E I F K N F PRKX_DANRE
 622 M Y D E E E M V E E P P S N - - - - Y V D P P Y A H L F K D F DdPK2_DICDI
 303 A Y P E N D W N T A P P V S P K D L E V F K N F PRKX_EQUCA
 342 A Y P E D D W N K M P P V P P K D L E I F K N F PRKX_GALLGA
 335 T Y P E N D W D T A A P V P Q K D L E I F K N F PRKX_MACMU
 371 A Y P E D D W N K M P P V P P K D L E I F K N F PRKX_MONDO
 305 D Y P E E D W R G A P P L N A K H L E P F K D F A7SM62_NEMVE
 368 V Y P E Q D V H N E - - - A Y T E E M - - - F E K Y E K Y F G D F Q7SHX1_NEUCR
 427 A Y P E D D W N K T P P V P P K D M E I F K N F PRKX_ORNAN
 335 T Y P E N D W D T A A P V P Q K D L E I F K N F PRKX_PANTR
 335 T Y P E G E L D K T P S V S D E D L E T F K N F Q5BK52_RAT
 321 V Y P E D D W K K D P P V S P K D L E I F E N F Q4RY94_TETNG
 324 D Y P E G D W K S A R T L E D A E L K L F E D F PRKX_TRICA
 306 R Y P E S P R H P L P P L T A K Q Q E M F A G F C D G E Y T K A PKAC3_TRYCR

C

M - - - - - Majority
 -----+-----+-----+-----
 -----+-----+-----+-----
 -----+-----+-----+-----
 -----+-----+-----+-----
 1 M G N - - - - - A A A hCa_Homo_sapiens
 1 M A S - - - - - N S S hCas_Homo_sapiens
 1 M - - - - - G N A T hCb1_Homo_sapiens
 1 M A A Y R E P P C N Q Y T G T T T A L Q K L E G F A S R L F H R H S K G T A H D hCb2_Homo_sapiens
 1 M - - - - - G L - - - hCb3_Homo_sapiens
 1 M - - - - - hCb4_Homo_sapiens
 1 M G N - - - - - A P hCg_Homo_sapiens
 1 M - - - - - L K F L K P K S S D E G S CAEELP21137-2
 1 M A Q P K D P H F G H S S G T N S A L Q K L D T L A S R F F Y K C R K G - - - N Q7T374_DANRE
 1 M G - - - - - N N A T T S N K K V D A - - - - - K D C O D R O M E
 1 M P T - - - - - - - - - - - R L D I V G N L Q F - - - S S S T D N G D KAPC_CAEBL
 A K K - - E - E S - - - - - V - - - - - K E F L A K A K Majority
 -----+-----+-----+-----
 -----+-----+-----+-----
 -----+-----+-----+-----
 -----+-----+-----+-----
 7 A K K G S E Q E S - - - - - V - - - - - K E F L A K A K hCa_Homo_sapiens
 7 D - K E F L A K A K hCas_Homo_sapiens
 7 A K K G S E V E S - - - - - V - - - - - K E F L A K A K hCb1_Homo_sapiens
 41 Q K T A L E N D S - - - - - L H F S E H T A L W D - - - R S M K E F L A K A K hCb2_Homo_sapiens
 4 - K E F L A K A K hCb3_Homo_sapiens
 2 - - - - - S - - - - - V - - - - - - - - - - - K E F L A K A K hCb4_Homo_sapiens
 6 A K K D T E Q E - - - - - - - - - - - - - - - - E S V N E F L A K A R hCg_Homo_sapiens
 15 S K D N K N S A S - - - - - - - - - - - - - - - - L K E F L D K A R CAEELP21137-2
 38 H D K G L E N E G - - - - - P H V S E H T V L W D - - - T A M K E T L A K A K Q7T374_DANRE
 15 - A - E T V K E F L E Q A K K D C O D R O M E
 22 E D Q E A D V T A C F V L P S P S S F S K L S I L D D P V E D F K E F L D K A R KAPC_CAEBL

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EDFLKKWENPAQNTAGLDDFERIKKTLGTGSFGRVMLVKHK Majority
-----+-----+-----+-----+
          90          100          110          120
-----+-----+-----+-----+
25 EDFLKKWESPAQNTAHLDDQFERIKKTLGTGSFGRVMLVKHK hCa_Homo_sapiens
17 EDFLKKWESPAQNTAHLDDQFERIKKTLGTGSFGRVMLVKHK hCas_Homo_sapiens
25 EDFLKKWENPTQNNAGLEDDFERKKKTLGTGSFGRVMLVKHK hCb1_Homo_sapiens
72 EDFLKKWENPTQNNAGLEDDFERKKKTLGTGSFGRVMLVKHK hCb2_Homo_sapiens
13 EDFLKKWENPTQNNAGLEDDFERKKKTLGTGSFGRVMLVKHK hCb3_Homo_sapiens
12 EDFLKKWENPTQNNAGLEDDFERKKKTLGTGSFGRVMLVKHK hCb4_Homo_sapiens
25 GDFLLYRWGNPAQNTASSDQFERLRTLGMGSFGRVMLVRHQ hCg_Homo_sapiens
33 EDFKQRWENPAQNTACLD DFDRIKTLGTGSFGRVMLVKHK CAEELP21137-2
69 EDFLNKWECCQKSTACLD DFDKLTGTGSFGRVMLVKHK Q7T374_DANRE
27 EEFEDYKRRRNPNTNTAALDDFERIKKTLGTGSFGRVMIQHK KDCO_DROME
62 EDFKQRWENPAQNTACLD DFDRIKTLGTGSFGRVMLVKHK KAPC_CAEEL

ATGQYYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL Majority
-----+-----+-----+-----+
          130          140          150          160
-----+-----+-----+-----+
65 ETGNHYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL hCa_Homo_sapiens
57 ETGNHYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL hCas_Homo_sapiens
65 ATEQYYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL hCb1_Homo_sapiens
112 ATEQYYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL hCb2_Homo_sapiens
53 ATEQYYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL hCb3_Homo_sapiens
52 ATEQYYAMKILDKQKVVKLLKQIEHTLNEKRILQAVNFPFL hCb4_Homo_sapiens
65 ETGGHYAMKILNKKQKVVKMKQVEHILNEKRILQAIDFPFL hCg_Homo_sapiens
73 QSGNYAMKILDKQKVVKLLKQVEHTLNEKRILQAIDFPFL CAEELP21137-2
109 QSEQYFAMKILDKKQKVVKLLKQIEHTLNEKRILQAVSFPFL Q7T374_DANRE
67 PTKDYAMKILDKQKVVKLLKQVEHTLNEKRILQAIDFPFL KDCO_DROME
102 QSGNYAMKILDKQKVVKLLKQVEHTLNEKRILQAIDFPFL KAPC_CAEEL

VRLEFAFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA Majority
-----+-----+-----+-----+
          170          180          190          200
-----+-----+-----+-----+
105 VKLEFSFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA hCa_Homo_sapiens
97 VKLEFSFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA hCas_Homo_sapiens
105 VRLEYAFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA hCb1_Homo_sapiens
152 VRLEYAFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA hCb2_Homo_sapiens
93 VRLEYAFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA hCb3_Homo_sapiens
92 VRLEYAFKDNSNLYMVMEYVPGGEMFSHLRRIGRFS EPHA hCb4_Homo_sapiens
105 VKLQFSFKDNSYLYLVMEYVPGGEMFSRLQRVGRFS EPHA hCg_Homo_sapiens
113 VNMTFSFKDNSNLYMVLEFISGGEMFSHLRRIGRFS EPHS CAEELP21137-2
149 VKLECAFKDNSNLYMVVRYIQGEMFSHLRRIGRFS EQNA Q7T374_DANRE
107 VSLRYHFKDNSNLYMVLEFISGGEMFSHLRKVGRFS EPHS KDCO_DROME
142 VNMTFSFKDNSNLYMVLEFISGGEMFSHLRRIGRFS EPHS KAPC_CAEEL

RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT Majority
-----+-----+-----+-----+
          210          220          230          240
-----+-----+-----+-----+
145 RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT hCa_Homo_sapiens
137 RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT hCas_Homo_sapiens
145 RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT hCb1_Homo_sapiens
192 RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT hCb2_Homo_sapiens
133 RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT hCb3_Homo_sapiens
132 RFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDHQGYIQVT hCb4_Homo_sapiens
145 CFYAAQIVLAVQYLYHSLDLIHRDLKPENLLIDHQGYLQVT hCg_Homo_sapiens
153 RFYAAQIVLAFEYLHSLDLIYRDLKPENLLIDSTGYLKIT CAEELP21137-2
189 RFYAAQIVLTFEYLHMLDLIYRDLKPENLLIDHQGYIQVT Q7T374_DANRE
147 RFYAAQIVLAFEYLHSLDLIYRDLKPENLLIDSTGYLKVIT KDCO_DROME
182 RFYAAQIVLAFEYLHSLDLIYRDLKPENLLIDSTGYLKIT KAPC_CAEEL

DFGF AKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA Majority
-----+-----+-----+-----+
          250          260          270          280
-----+-----+-----+-----+
185 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCa_Homo_sapiens
177 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCas_Homo_sapiens
185 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCb1_Homo_sapiens
232 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCb2_Homo_sapiens
173 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCb3_Homo_sapiens
172 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCb4_Homo_sapiens
185 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA hCg_Homo_sapiens
193 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA CAEELP21137-2
229 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA Q7T374_DANRE
187 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA KDCO_DROME
222 DFGFAKRVKGR TWTLCGTPEYLAPEIILSKGYNKAVDWWA KAPC_CAEEL

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L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S Majority
-----+-----+-----+-----+
                290                300                310                320
-----+-----+-----+-----+
225 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S hCa_Homo_sapiens
217 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S hCas_Homo_sapiens
225 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S hCb1_Homo_sapiens
272 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S hCb2_Homo_sapiens
213 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S hCb3_Homo_sapiens
212 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F S S hCb4_Homo_sapiens
225 L G V L I Y E M A V G F P P F Y A D Q P I Q I Y E K I V S G R V R F P S K L S S hCg_Homo_sapiens
233 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V K F P S H F S N CAEELP21137-2
269 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R Y P S H F S S Q7T374_DANRE
227 L G V L V Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V R F P S H F G S KDCC_DROME
262 L G V L I Y E M A A G Y P P F F A D Q P I Q I Y E K I V S G K V K F P S H F S N KAPC_CAEEL

D L K D L L R N L L Q V D L T K R F G N L K N G V S D I K N H K W F A T T D W I Majority
-----+-----+-----+-----+
                330                340                350                360
-----+-----+-----+-----+
265 D L K D L L R N L L Q V D L T K R F G N L K N G V N D I K N H K W F A T T D W I hCa_Homo_sapiens
257 D L K D L L R N L L Q V D L T K R F G N L K N G V N D I K N H K W F A T T D W I hCas_Homo_sapiens
265 D L K D L L R N L L Q V D L T K R F G N L K N G V S D I K T H K W F A T T D W I hCb1_Homo_sapiens
312 D L K D L L R N L L Q V D L T K R F G N L K N G V S D I K T H K W F A T T D W I hCb2_Homo_sapiens
253 D L K D L L R N L L Q V D L T K R F G N L K N G V S D I K T H K W F A T T D W I hCb3_Homo_sapiens
252 D L K D L L R N L L Q V D L T K R F G N L K N G V S D I K T H K W F A T T D W I hCb4_Homo_sapiens
265 D L K H L L R S L L Q V D L T K R F G N L R N G V G D I K N H K W F A T T S W I hCg_Homo_sapiens
273 E L K D L L R N L L Q V D L T K R Y G N L K N G V A D I K N H K W F G S T D W I CAEELP21137-2
309 D L K D L L R N L L Q V D L T K R F G N L K N G V S D I K N H R W F A S T D W I Q7T374_DANRE
267 D L K D L L R N L L Q V D L T K R Y G N L K A G V N D I K N Q K W F A S T D W I KDCC_DROME
302 E L K D L L R N L L Q V D L T K R Y G N L K N G V A D I K N H K W F G S T D W I KAPC_CAEEL

A I Y Q R K V E A P - - - - - F I P K F R G P G D T S N F D D Majority
-----+-----+-----+-----+
                370                380                390                400
-----+-----+-----+-----+
305 A I Y Q R K V E A P - - - - - F I P K F K G P G D T S N F D D hCa_Homo_sapiens
297 A I Y Q R K V E A P - - - - - F I P K F K G P G D T S N F D D hCas_Homo_sapiens
305 A I Y Q R K V E A P - - - - - F I P K F R G S G D T S N F D D hCb1_Homo_sapiens
352 A I Y Q R K V E A P - - - - - F I P K F R G S G D T S N F D D hCb2_Homo_sapiens
293 A I Y Q R K V E A P - - - - - F I P K F R G S G D T S N F D D hCb3_Homo_sapiens
292 A I Y Q R K V E A P - - - - - F I P K F R G S G D T S N F D D hCb4_Homo_sapiens
305 A I Y E K K V E A P - - - - - F I P K Y T G P G D A S N F D D hCg_Homo_sapiens
313 A I Y Q K K I T P P S F S K G E S N G R L F E A L Y P R V D G P A D T R H F V E CAEELP21137-2
349 A I Y E K K V D A P - - - - - I I P K C R G P G D T S N F D E Q7T374_DANRE
307 A I F Q K K I E A P - - - - - F I P R C K G P G D T S N F D D KDCC_DROME
342 A I Y Q K K I T P P S F S K G E S N G R L F E A L Y P R V D G P A D T R H F V E KAPC_CAEEL

Y E E E - - E I R V S I T E K C A K E F G E F Majority
-----+-----+-----+-----+
                410                420
-----+-----+-----+-----+
331 Y E E E - - E I R V S I N E K C G K E F S E F hCa_Homo_sapiens
323 Y E E E - - E I R V S I N E K C G K E F S E F hCas_Homo_sapiens
331 Y E E E - - D I R V S I T E K C A K E F G E F hCb1_Homo_sapiens
378 Y E E E - - D I R V S I T E K C A K E F G E F hCb2_Homo_sapiens
319 Y E E E - - D I R V S I T E K C A K E F G E F hCb3_Homo_sapiens
318 Y E E E - - D I R V S I T E K C A K E F G E F hCb4_Homo_sapiens
331 Y E E E - - E L R I S I N E K C A K E F S E F hCg_Homo_sapiens
353 E V Q E P T E F V I A A T P Q L E E L F V E F CAEELP21137-2
375 Y D E E - - V I R V S V S E Q C S K E F L D F Q7T374_DANRE
333 Y E E E - - A L R I S S T E K C A K E F A E F KDCC_DROME
382 E V Q E P T E F V I A A T P Q L E E L F V E F KAPC_CAEEL

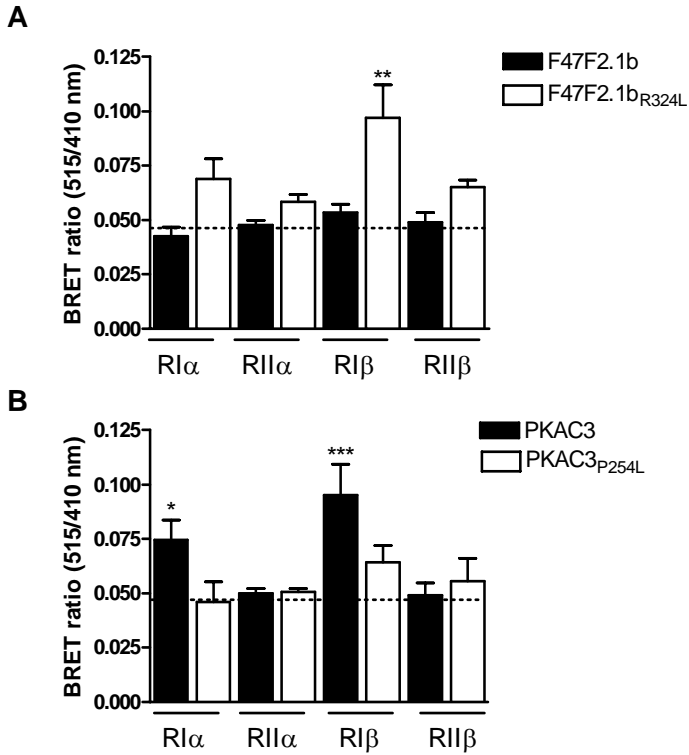
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Supplemental Fig. S1: Phylogenetic analysis of PKA, PrKX, PKC, ROCK1, AKT1, PDK1, and Aurora kinases. The sequences used in this study were identified by NCBI, Prosite, UniProt, and SwissProt database searches, aligned using Bioedit 7.0.5.3 (1), followed by ClustalW analysis (2). A table containing the accession numbers is provided below (Supplemental Tab. T1). (A) Depicted is an unrooted neighbor joining tree created with PAUP 4.0b10 (3). cAMP-dependent protein kinases: conventional PKA C subunits (dashed line), PrKX subfamily (shaded light grey) and putative members of the extended PrKX-like family (shaded dark grey) are highlighted. Written in bold are PrKX-like kinases experimentally addressed in this study. The bar represents 10 amino acid changes. (B) Alignment of PrKX subfamily of kinases and (C), alignment of conventional PKA C subunits performed with Megalign 7.0 (DNASar, Inc.). Marked in grey are the aminoacids corresponding to Arg283^{PrKX} and Leu277^{Cα} located in the αH-αI loop of the kinases.

Supplemental Tab. T1: Listed are names and sequence identifiers used for the alignment and phylogenetic analysis of kinases.

Species	Name	UniProtKB/Swiss-Prot or NCBI accession number
<i>Homo sapiens</i>	PRKX_HUMAN	P51817
<i>Mus musculus</i>	PRKX_MOUSE (Pkare)	Q922R0
<i>Homo sapiens</i>	PRKY_HUMAN	O43930
<i>Rattus norvegicus</i>	Q5BK52_RAT	Q5BK52
<i>Pan troglodytes verus</i>	PRKX_PANTR	XP_001141503
<i>Bos taurus</i>	PRKX_BOSTA	XP_582115
<i>Macaca mulatta</i>	PRKX_MACMU	XP_001086667
<i>Canis lupus familiaris</i>	PRKX_CANLU	XP_852513
<i>Equus caballus</i>	PRKX_EQUCA	XP_001495714
<i>Ornithorhynchus anatinus</i>	PRKX_ORNAN	XP_001514495
<i>Monodelphis domestica</i>	PRKX_MONDO	XP_001362336
<i>Ajellomyces capsulata</i>	A6QTK8_AJECN	A6QTK8
<i>Neurospora crassa</i>	Q7SHX1_NEUCR	Q7SHX1
<i>Dictyostelium discoideum</i>	DdPK2_DICDI	XP_638835
<i>Ustilago maydis 521</i>	PRKX_USTMA	XP_757271
<i>Tetraodon nigroviridis</i>	Q4RY94_TETNG	Q4RY94
<i>Danio rerio</i>	PRKX_DANRE	XP_690430
<i>Nematostella vectensis</i>	A7SM62_NEMVE	A7SM62
<i>Drosophila melanogaster</i>	DC2_DROME	P16912
<i>Drosophila melanogaster</i>	ΔDC2_DROME	
<i>Anopheles gambiae</i>	Q7PZC6_ANOGA	Q7PZC6
<i>Aedes aegypti</i>	Q16NW2_AEDAE	Q16NW2
<i>Tribolium castaneum</i>	PRKX_TRICA	XP_973065
<i>Ascaris suum</i>	KAPC_ASCSU	P49673
<i>Caenorhabditis elegans</i>	CAEEL_F47F2.1a	Q20541
	CAEEL_F47F2.1b	NP_508671
	CAEEL_F47F2.1c	NP_741759
<i>Caenorhabditis briggsae</i>	A8XJQ6_CAEBR	XP_001676476
<i>Gallus gallus</i>	PRKX_GALLGA	XP_416852
<i>Trypanosoma brucei</i>	PKAC3_TRYBR	Q8WSK3
<i>Trypanosoma cruzi</i>	PKAC3_TRYCR	XP_809454
<i>Homo sapiens</i>	hCa	P17612
	hCas	P17612-2
	hCβ1	P22694-1
	hCβ2	P22694-2
	hCβ3	P22694-3
	hCβ4	P22694-4
	hCγ	P22612

<i>Drosophila melanogaster</i>	DC0	P12370
	DC1	P16911-2
<i>Caenorhabditis elegans</i>	Kin-1	P21137
	Kin-1a	P21137-2
<i>Danio rerio</i>	Q7T374_DANRE	Q7T374
<i>Homo sapiens</i>	PKC- α	P17252
	PKC- β 1	P05771-1
	PKC- β 2	P05771-2
	PKC- γ	P05129
<i>Homo sapiens</i>	Akt1/PKB	P31749
<i>Homo sapiens</i>	PDK1	O15530
<i>Homo sapiens</i>	Aurora-A	O14965
<i>Homo sapiens</i>	ROCK1	Q13464
<i>Saccharomyces cerevisiae</i>	KAPA_YEAST (TPK1)	P06244
<i>Trypanosoma brucei brucei</i>	PKAC1	Q3S1L1 (7)
	PKAC2	Q3S1K7 (7)



Supplemental Fig. S2: *C. elegans* F47F2.1b and *T. brucei* PKAC3 interaction with human R subunits. The BRET assay was performed as described in the Experimental Procedures section. (A) Holoenzyme formation of wildtype (black bars) and F47F2.1b_{R324L} (white bars) was assayed with four human R subunits. (B) Interaction analysis of PKAC3 (black bars) and PKAC3_{P254L} mutant protein (white bars) with R subunits. Depicted are original BRET values (\pm SEM) obtained from at least two independent experiments (n=6 wells). The dotted line represents the mean background value of the BRET assay. Significant values above the background are indicated in the plot (*; P<0.05; **, P<0.01, *** P<0.001).

Supplemental Tab. T2: Eukaryotic and prokaryotic protein expression vectors. *Renilla* luciferase (Rluc) as well as green fluorescent protein (GFP²) fusion protein expression vectors for the BRET assay (Rluc(h)-N1-3, GFP²-C1-3) were obtained from PerkinElmer Life and Analytical Sciences (Wellesley, U.S.A.). Oligonucleotides (MWG Biotech AG, Ebersberg, Germany) and vectors used for expression vector cloning and for mutagenesis are listed below.

construct	vector	(fusion) protein	restriction sites	primer_forward	primer_reverse
GFP-C3-PrKX	GFP2-C3	GFP-PrKX	HindIII/BamHI	GAT AAG CTT ATG GAG GCG CCC	GGT GGA TCC TCA GAA ATT CTT GAA
GFP-C3-PrKY	GFP2-C3	GFP-PrKY	HindIII/BamHI	ATA AAG CTT ATG GAG GCG CCC GG	TAT GGA TCC TCA CAT CAT TCG CCC CG
GFP-C3-Pkare	GFP2-C3	GFP-Pkare	HindIII/BamHI	CTC AAG CTT ATG GAG CCG CCC	CGC GGA GCC TCA GAA ATT TTT G
GFP-C2-DC2	GFP2-C2	GFP-DC2	EcoRI/HindIII	ATA GAA TTC ATG GAT TTG TGG CAT ATA TTT TTG GAA CG	ATT AAG CTT TTA GAA ATC ATT GAA GTA CTG CAA ATC TC
GFP-C2-A1-227 DC2	GFP2-C2	GFP-ADC2	EcoRI/HindIII	ATA GAA TTCATG GAT GCG GAT GAC GCC ACT C	ATT AAG CTT TTA GAA ATC ATT GAA GTA CTG CAA ATC TC
GFP-C3-PKAC3	GFP2-C3	GFP-PKAC3	HindIII/BamHI	ATC GAA GCTT ATG ACG ACA ACT CCC ACT GG	ACG CGG ATC CGA TCC TCG TGT ATT CAC CAT CG
GFP-C1-F47F2.1b	GFP2-C1	GFP-F47F2.1b	KpnI/BamHI	TAT GGT ACC ATG TCT TCG TCG ACA TCA TCA GTG G	ATA GGA TCC TCA CCA TTC GGC GAA AAG ATC GC
pRSET _B -hC α	pRSETb	hC α	NdeI/KpnI	CAT ATG GGC AAC GCC GCC GCC G	GGT ACC CTA AAA CTC AGA AAA CTC CTT GCC AC
pHis5BA-hC α	pHis5BA	His6-hC α	NruI/HindIII	-	-
pRSET _B -hRII β	pRSETb	hRII β	NdeI/EcoRI	CAT ATG AGC ATC GAG ATC CCG	GGA TTC TCA TGC AGT GGG TTC AAC AAT ATC C
Rluc-N1-hRII β	Rluc(h)-N1	hRII β -Rluc	XhoI/HindIII	ATA CTC GAG ATG GCC TCC CCG CCC GCC TGC	TAT AAG CTT CCG ACG GTG AGG GAG ATG AAG CTG TTG TAA CG
Rluc-N2-hRII β	Rluc(h)-N2	hRII β -Rluc	BglII/KpnI	AGA TCT ATG AGC ATC GAG ATC CCG GCG	GGT ACC TGC AGT GGG TTC AAC AAT ATC CAT G
				mutagenesis primer_forward	mutagenesis primer_reverse
GFP-C3-hC α K283A	GFP2-C3	GFP-hC α K283A	-	GGG AAC CTC GCC AAT GGG GTC	GAC CCC ATT GGC GAG GTT CCC
GFP-C3-hC α L277R	GFP2-C3	GFP-hC α L277R	-	G CAG GTA GAT CGC ACC AAG CGC	GCGCTTGGTGCATCT ACCTGC
pHis5BA-hC α	pHis5BA	His6-hC α L277R	-	G CAG GTA GAT CGC ACC AAG CGC	GCGCTTGGTGCATCT ACCTGC
GFP-C3-PrKXR283L	GFP2-C3	GFP-PrKXR283L	-	G CTC GTG GTT GAC CTA ACA AGG CG	CGCCTTGTTAGGTCAA CCACGAGC
pFastbac HTb-PRKXR283L	pFastbac HTb	His6-PrKXR283L	-	G CTC GTG GTT GAC CTA ACA AGG CG	CGCCTTGTTAGGTCAA CCACGAGC
GFP-C3-PKAC3P254L	GFP2-C3	GFP-PKAC3P254L	-	CTA ACA ATT GAA CTA ACG AAA CGC C	GGC GTT TCG TTA GTT CAA TTG TTA G
GFP-C1-F47F2.1bR324L	GFP2-C1	GFP-F47F2.1bR324L	-	G GAA GTA GAT CTA ACT CAA CGC	GCG TTG AGT TAG ATC TAC TTC C
Rluc-N2-hRII β S114A	Rluc(h)-N2	hRII β S114A-Rluc	-	CGG CGA GGA AGC GTG AGT GCC	GGC ACT CAC GCT TCC TCG CCG
Rluc-N1-hRII β G99S	Rluc(h)-N1	hRII β G99S-Rluc	-	GGC GTG CCG CAG TAT GTG CAG	CTG CAC ATA CTG CGG CAC GCC

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