Type of file: table
Label: Table 1
Filename: mmc7.xls

Supplementary Table 1, Park et al.

Mouse PH-domains that translocated in response to PDGF stimulation in NIH3T3 cel

#	Name of construct	NM or XM #	Alternative names
1	Akap13-PH	XM_907140, XM_133543	
2	AKT1-PH	NM_009652	PKB; PKBalpha
3	AKT2-PH	NM_007434	PKBbeta
4	AKT3-PH	NM_011785	PKBgamma
5	BTK-PH	NM_013482	
6	CNKSR2-PH	NM_177751	Cnk2
7	DAPP1-PH	NM_011932	Bam32
8	FGD6-PH2	NM_053072	ETOHD4
9	FGD6-PHT	NM_053072	ETOHD4
10	Gab1-PH	NM_021356	
11	Gab2-PH	NM_010248	
12	ITK-PH	NM_010583	
13	Myo10-PH	NM_019472	
14	Myo10-PHT	NM_019472	
15	Osbpl3-PH	NM_027881	
16	Osbpl7-PH	XM_193637	
17	PDPK1-PH	NM_002613	PDK1
18	PHLDB1-PH	NM_153537	L15alpha, L15a
19	PHLPP-PH	XM_984950	

20	Plek2-PH	NM_013738	
21	Plek2-PH2	NM_013738	
22	PLEKHA1-PH	NM_133942	TAPP1
23	Plekha2-PH2	NM_031257	
24	PSCD1-PH	NM_011180	CTH1
25	PSCD2-PH	NM_011181	ARNO, CTH2
26	PSCD3-PH	NM_011182	GRP1, CTH3
27	Rasa2-PH	NM_053268	
28	SH3bp2-PH	NM_011893	
29	TEC-PH	AK139329 (BC037071)	

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	Current alias	**n**	**CNI**	**ORF**	**AFCSID**	**NM_number**
1	F024	E1	VAV2-PH1A	GGACAAGG	A002361	NM_009500
2	F024	E2	VAV2-PH1B	GGACAAGG	A002361	NM_009500
3	F026	E1	VAV3-PH1A	AGATAATG		NM_020505
4	F028	E1	VAV1-PH1A	GGAGAACC		NM_011691
5	F038	E1	GAB1-PH1A	CGGCGAAG		NM_021356
6	F041	E1	GAB2-PH1A	CGGCGGC		NM_010248
7	F058	E1	DOK1-PH1A	GGCTGTGA		NM_010070
8	F066	E1	CTH1-PH1A	ATTCATCG		NM_011180
9	F082	E1	BAM32-PH1A	GCCTTTGA		NM_011932
10	H001	E1	3BP2-PH1A	TGAGGAGA		NM_011893
11	H007	E1	CTH2-PH1A	GGAGGATG	A000330	NM_011181
12	H009	E1	CTH3-PH1A	AGAAGACG	A000332	NM_011182
13	H010	E1	DBS-PH1A	TCTCATCG	A000755	NM_178076
14	H011	E1	DNM1-PH1A	AGGGAACC	A000794	NM_010065
15	H012	E1	DNM2-PH1A	CCAGATTC	A000795	NM_007871
16	H013	E1	FGD1A-PH1A	GAAAATGG	A000912	NM_008001
17	H013	G1	FGD1B-PH2A	GAGCAGTC	A000912	NM_008001
18	H014	E1	RASGRF1-PH	AGCCATCC	A002032	NM_011245
19	H014	G1	RASGRF1-PH	TGAAACCG	A002032	NM_011245
20	H015	E1	GRB7-PH1A	CTTCGCCA	A000071	NM_010346
21	H016	E1	GRB10-PH1A	AGAAAGAA	A000064	NM_010345
22	H017	E1	IRS1-PH1A	CCCCCCGG	A001281	NM_010570
23	H019	E1	ITK-PH1A	CTTCATCC	A000832	NM_010583
24	H020	E1	KIF1A-PH1A	CCGGCCC		NM_008440
25	H021	E1	KIF1B-PH1A	CAACTCTC		NM_207682
26	H024	E1	LFC -PH1A	GAAGGAGT		NM_008487
27	H025	E1	SNTB1-PH1A	GACCCGTG	A002246	NM_016667
28	H026	E1	SH2B-PH1A	GGGTGGT	A002149	NM_011363
29	H027	E1	SWAP-70-PH	AATAAACTT	A002961	NM_009302
30	H029	E1	FGD2-PH1A	CCAGAGAG	A003323	NM_013710
31	H030	E1	FGD3-PH1A	TGCCCCAG	A003324	NM_015759
32	H034	E1	RASGRF2-PH	GAGCGTGC	A002441	NM_009027
33	H034	G1	RASGRF2-PH	TGACACCG	A002441	NM_009027
34	H037	E1	Cool1-PH1A	GAGGAAGG		NM_017402
35	H038	E1	PLD1-PH1A	AGAGCAGT	A001811	NM_008875
36	H040	E1	SNTA1-PH1A	TGCAGCGG	A002245	NM_009228
37	H041	E1	SNTB2-PH1A	TAGCAGGA	A000691	NM_009229
38	H042	E1	CADPS-PH1A	AGACAAGG		NM_012061
39	H043	E1	OPHN1-PH1A	GACTGTGG		NM_052976
40	H044	E1	ARHGEF3-PH	GGAATCGG		NM_027871
41	H045	E1	FGDB-PH1A	AATGCACA	A000912	NM_008001
42	H046	E1	DOK4-PH1A	CAATTTCA	A000053	NM_053246
43	H048	E1	H048-PH1A	CCACTTGG		NM_024413
44	H050	E1	PSGAP-PH1A	AGGCCACG		NM_030113
45	H051	E1	OST-PH1A	AACTACTA	A000754	NM_133197
46	H052	E1	OSBPL5-PH1	TGACCCCC		NM_024289
47	H053	E1	GEFT -PH1A	CCTGGGGA		NM_028027
48	H054	E1	Capri -PH1A	GATGGAAC		NM_133914
49	H055	E1	VEPHA-PH1A	GCAGCTTC		NM_145820
50	H056	E1	H056-PH1A	AGCATCCG		XM_885890

51	H056	G1	H056-PH1A	CCAGAACC		XM_885890		
52	H057	E1	GNRPX-PH1	CAACGAGA		NM_023900		
53	H060	E1	H060-PH1A	CATTGATG		NM_028707		
54	H061	E1	ETOHD4-PH1	GCAAGGG	A003325	NM_053072		
55	H061	G1	ETOHD4-PH2	CCAGCTGT	A003325	NM_053072		
56	H065	E1	OSBPL3-PH1	CGAGAAGA		NM_027881		
57	H067	E1	COL4BP-PH1	TAACCAGA		NM_023420		
58	H070	E1	PLEKHA3-PH	GGTTCTGT	A003308	NM_031256		
59	H071	E1	Plekha2-PH1	TGTGGATC	A003307	NM_031257		
60	H071	G1	Plekha2-PH2	CGGTGGG	A003307	NM_031257		
61	H074	E1	PLEK-PH1A	AAAGCGGA	A003310	NM_019549		
62	H074	G1	PLEK-PH2A	CTTCTGTG	A003310	NM_019549		
63	H075	E1	NGEF-PH1A	GAGAGTGG		NM_019867		
64	H076	E1	APS-PH1A	ATTCTGGC	A000306	NM_018825		
65	H077	E1	TNFIDP-PH1	GAGCGGCT		NM_023320		
66	H078	E1	Myosin X-PH1	CCTCAAGC	A001583	NM_019472		
67	H078	G1	Myosin X-PH2	AGAGGAGA	A001583	NM_019472		
68	H080	E1	CENTB4-PH1	AAAATCCT	A000344	NM_010026		
69	H086	E1	PLCL2-PH1A	CCCCAGGG		NM_013880		
70	H088	E1	EVT2-PH1A	CGTGAAGA		NM_145516		
71	H090	E1	RASGRF1B-	AGCCATCC	A002032	NM_001039655		
72	H091	E1	TEC-PH1A	CAACACTA		AK139329	BC037071	There are only
73	H094	E1	PLEK2-PH1A	CGGCGTGC	A003311	NM_013738		
74	H094	G1	PLEK2-PH2A	TCTGGATG	A003311	NM_013738		
75	H101	E1	TIAM2-PH1A	ACAGAACA		NM_011878		
76	H102	E1	ESE1-PH1A	AGAGAAGG	A000086	NM_010587		
77	H103	E1	ESE2 -PH1A	GGAGAAGG	A000881	NM_011365		
78	H106	E1	NET1-PH1A	GCTTCTAG	A001630	NM_019671		
79	H109	E1	SKAP2-PH1A	TGAATATG	A002165	NM_018773		
80	H110	E1	RHOIP2-PH1	CGAATACG	A002082	NM_012026		
81	H111	E1	RHOIP3-PH1	GGCCAAGG		NM_201245		
82	H111	G1	RHOIP3-PH2	TAGAAAGC		NM_201245		
83	H112	E1	RASA2-PH1A	GTCCAGAA		NM_053268		
84	H113	E1	RASA3-PH1A	CAAGTCTG	A001026	NM_009025		
85	H114	E1	Rasa1-PH1A	GCAGCTGG	A002029	NM_013832		
86	H115	E1	SOS1-PH1A	CAAAAGTC	A002030	NM_009231		
87	H116	E1	SPNB2-PH1A	CATGGAAA	A002854	NM_175836		
88	H118	E1	Tiam1-PH1A	GGGTGTAC		NM_009384		
89	H118	G1	Tiam1-PH2A	ACACTACC		NM_009384		
90	H124	E1	SOS2-PH1A	GCAGCACT		XM_987825		
91	H128	E1	FARP1-PH1A	GGAGATCA		NM_134082		
92	H128	G1	FARP1-PH2A	CCCGGATG		NM_134082		
93	H129	E1	AMYLB-PH1A	GTTTAAAA		NM_019456		
94	H130	E1	TARA1-PH1A	GAAAAAGC		NM_001039156		
95	H132	E1	DOK5-PH1A	GACATAGT		NM_029761		
96	H133	E1	AFAPL-PH1A	ATATGATG		NM_027373		
97	H134	E1	PLCD4-PH1A	TCAGATTC		NM_148937		
98	H147	E1	GRB14-PH1A	TGAATTTTT		NM_016719		
99	K054	E1	PKD1-PH1A	TGGAGGTG	A001930	NM_008858		
100	K058	E1	AKT2-PH1A	GGTATCTG	A000250	NM_007434		
101	K061	E1	AKT3-PH1A	TGTTACCA	A000251	NM_011785		

102	K093	E1	Grk2-PH1A	CTCTGAGC		NM_130863
103	K099	E1	AKT1-PH1A	CGTAGCCA	A000249	NM_009652
104	K113	E1	CRIK-PH1A	AGCTGAAT	A000662	NM_007708
105	S005	E1	PLCDL-PH1A	CGGTCGG		NM_019676
106	S008	E1	Pld-t2-PH1A	CTTTATCC		NM_008876
107	S033	E1	BTK-PH1A	AGTGATAC		NM_013482
108	H032	E1	ROCK1-PH1A	AAATGAAC		NM_005406

AK and BC, not NM

construct name	filename for PIP strip	PI(3,4)P2	PI(3,5)P2	PI(4,5)P2
pEX_EF1_YFP-AKT2-PH1A	PIP05062002	44.675	17.024	15.805
pEX_EF1_YFP-SH3bp2-PH1A	PIP05062001	29.901	13.352	14.374
pEX_EF1_YFP-LL5l-PH1A	PIP05071320	135.2068	41.294	68.972
pEX_EF1_YFP-ITK-PH1A		23.6613	17.7206	26.15123
pEX_EF1_YFP-Gab1-PH1A	ETG03101402	48.4715	17.132	21.694
pEX_EF1_YFP-Gab2-PH1A	ETG03101403	65.3202	29.152	38.199
pEX_EF1_YFP-AKT1-PH1A	PIP05062023	14.9955	14.4439	16.2155
pEX_EF1_YFP-Bam32-PH1A	PIP05070517	98.7099	12.678	13.434
pEX_EF1_YFP-AKT3-PH1A	PIP05062003	156.982	12.87	37.538
pEX_EF1_YFP-Akap13-PH1A	PIP05062725	0.141	2.826	1.58
pEX_EF1_YFP-TEC-PH1A		45.86615	14.985	30.7655
pEX_EF1_YFP-CTH3-PH1A		19.07994	15.78294	40.1808
pEX_EF1_YFP-ETOH4-PHTA	PIP05071324	18.393	20.025	23.842
pEX_EF1_YFP-BTK-PH1A	PIP05062004	4.8301	10.2341	18.2073
pEX_EF1_YFP-CTH2-PH1A	PIP05062007	15.8233	18.6102	21.0506
pEX_EF1_YFP-CTH1-PH1A	PIP05062008	5.2215	7.6645	11.9847
pEX_EF1_YFP-Ost-PH1A	ETG03110410	9.612	14.969	13.882
pEX_EF1_YFP-GEFT-PH1A	ETG03110412	21.187	32.71	26.72
pEX_EF1_YFP-H056-PH2A	PIP05061313	13.989	16.995	16.739
pEX_EF1_YFP-ETOHD4-PH1A	ETG03110415	34.81	39.68	45.016
pEX_EF1_YFP-ETOHD4-PH2A	PIP05070505	8.4463	12.6733	14.7693
pEX_EF1_YFP-Ngef-PH1A	PIP05070513	8.126	10.644	11.316
pEX_EF1_YFP-DBS-PH1A	PIP05062010	14.9879	15.4225	16.1981
pEX_EF1_YFP-IRS1-PH1A	PIP05062019	26.529	22.105	40.1173
pEX_EF1_YFP-Rasgrf2-PH2A	PIP05072014	3.057	4.158	4.577
pEX_EF1_YFP-CADPS-PH1A	PIP05072020	11.331	13.069	14.837
pEX_EF1_YFP-RhoGEF3-PH1A	PIP05062714	1.152	4.089	1.778
pEX_EF1_YFP-FGDB-PH1B	PIP05062715	3.957	3.538	0.921
pEX_EF1_YFP-DOK4-PH1A	PIP05072012	29.238	40.9769	41.9422
pEX_EF1_YFP-H048-PH1A	PIP05062717	11.6437	12.4098	16.1038
pEX_EF1_YFP-Grk2-PH1A	PIP05062718	78.7049	6.804	13.684
pEX_EF1_YFP-VephA-PH1A	ETG03102805	39.183	35.228	38.718
pEX_EF1_YFP-H056-PH1A	ETG03110401	17.881	22.012	30.369
pEX_EF1_YFP-Osbpl3-PH1A	PIP05070506	82.1786	87.2819	84.4582
pEX_EF1_YFP-Plekha2-PH2A	PIP05072024	53.005	22.501	26.145
pEX_EF1_YFP-Plek-PH1A	PIP05070511	29.801	21.759	41.213
pEX_EF1_YFP-APS-PH1A	PIP05061314	29.698	15.081	28.608
pEX_EF1_YFP-TNFidp-PH1A	PIP05070514	37.8347	39.7172	51.5705
pEX_EF1_YFP-Myo10-PH1A	PIP05061312	13.89	8.223	59.911
pEX_EF1_YFP-CentB4-PH1A	PIP05070516	12.1253	10.9806	12.7632
pEX_EF1_YFP-Plcl2-PH1A	PIP05070518	12.703	12.937	29.7647
pEX_EF1_YFP-Dok1-PH1A	ETG03101404	42.6731	27.575	33.726
pEX_EF1_YFP-Plek2-PH1A	ETG03111803	16.414	13.768	15.25
pEX_EF1_YFP-PLCd1-PH1A	PIP05071104	1.9552	1.9992	41.835
pEX_EF1_YFP-Skap2-PH1A	ETG03111809	18.409	15.298	23.061
pEX_EF1_YFP-Rhoip3-PH1A	PIP05071108	1.5083	1.7029	5.7885
pEX_EF1_YFP-Rasa2-PH1A		14.595	17.93	15.0705
pEX_EF1_YFP-Rasa1-PH1A	ETG03111815	22.974	28.169	29.055
pEX_EF1_YFP-Spnb2-PH1A	PIP05071114	15.263	19.316	55.935
pEX_EF1_YFP-FARP1-PH1A	PIP05071118	2.258	4.002	3.675

pEX_EF1_YFP-FARP1-PH2A	PIP05071119	4.69	6.652	5.774
pEX_EF1_YFP-Taral-PH1A	PIP05071121	4.671	4.086	1.156
pEX_EF1_YFP-Dok5-PH1A	PIP05071122	4.406	7.77	20.253
pEX_EF1_YFP-Afapl-PH1A	PIP05061306	36.57687	31.47523	41.58657
pEX_EF1_YFP-PLCd4-PH1A	PIP05071124	7.19	10.742	15.861
pEX_EF1_YFP-RlGPS2-PH1A	PIP05071304	69.514	22.101	109.234
pEX_EF1_YFP-Osbpl7-PH1A	PIP05071307	18.911	21.485	23.381
pEX_EF1_YFP-RhoGap1-PH1A	PIP05071310	19.023	15.349	21.582
pEX_EF1_YFP-BCRa-PH1A	PIP05061316	28.674	34.371	40.064
pEX_EF1_YFP-Rhogefl-PH1A	PIP05071311	16.026	15.33	19.365
pEX_EF1_YFP-Net1-PH1A	PIP05071313	10.819	11.267	12.157
pEX_EF1_YFP-Hapipl-PH1A		11.3805	12.125	15.9435
pEX_EF1_YFP-Cnk2-PH1A	PIP05071315	47.986	53.792	73.057
pEX_EF1_YFP-Arl6l-PH1A	PIP05071318	23.702	17.223	29.541
pEX_EF1_YFP-Parxl-PH4A	PIP05071322	6.909	7.206	7.933
pEX_EF1_YFP-Scopl-PH1A	PIP05071323	-4.268	-2.135	-6.237
pEX_EF1_YFP-Plekha2-PHTA	PIP05071325	14.025	16.852	17.824
pEX_EF1_YFP-VAV1-PH1A	PIP05062006	7.944	11.337	11.959
pEX_EF1_YFP-DNM2-PH1A	PIP05062012	6.257	10.728	10.898
pEX_EF1_YFP-FGD1A-PH1A	PIP05062013	13.011	17.118	21.45
pEX_EF1_YFP-VAV2-PH1A	PIP05071302	9.24	10.701	9.683
pEX_EF1_YFP-VAV3-PH1A		0	0	0
pEX_EF1_YFP-SNTA1-PH1A	PIP05072018	4.292	6.013	5.309
pEX_EF1_YFP-PsGAP-PH1A	PIP05062719	-5.915	-3.162	-4.667
pEX_EF1_YFP-Plekha3-PH1A	PIP05070508	3.1784	2.6845	4.0211
pEX_EF1_YFP-Net1-PH1A	PIP05071105	9.196	12.586	12.8
pEX_EF1_YFP-Phdp1-PH1A	PIP05071309	4.312	3.695	2.84
pEX_EF1_YFP-Parxl-PH3A	PIP05071321	17.441	7.404	11.994
pEX_EF1_YFP-CRIK-PH1A	PIP05062005	2.108	3.825	5.156
pEX_EF1_YFP-DNM1-PH1A	PIP05062011	5.728	10.94	9.395
pEX_EF1_YFP-FGD1A-PH2A	PIP05062014	6.3131	9.4924	10.9979
pEX_EF1_YFP-Rasgrf1A-PH1A	PIP05062015	1.301	4.371	5.992
pEX_EF1_YFP-Rasgrf1-PH2A	PIP05062016	6.833	12.291	13.077
pEX_EF1_YFP-Grb7-PH1A	PIP05062017	-1.671	4.3	4.681
pEX_EF1_YFP-Grb10-PH1A	PIP05062018	-0.251	2.047	1.411
pEX_EF1_YFP-KIF1A-PH1A	PIP05072008	12.721	13.96	14.947
pEX_EF1_YFP-KIF1B-PH1A	PIP05062021	5.371	11.054	10.537
pEX_EF1_YFP-PKD1-PH1A	PIP05062022	15.3975	21.6703	23.1561
pEX_EF1_YFP-LFC-PH1A	PIP05062024	7.144	13.814	10.504
pEX_EF1_YFP-SNTB1-PH1A	PIP05062025	4.115	4.82	6.518
pEX_EF1_YFP-SH2B-PH1A	PIP05062026	-0.437	4.183	5.342
pEX_EF1_YFP-SWAP70-PH1A	PIP05071301	9.554	12.201	11.462
pEX_EF1_YFP-VAV2-PH1B	ETG03100703	13.988	5.89	11.915
pEX_EF1_YFP-FGD2-PH1A	PIP05072011	11.891	10.239	13.111
pEX_EF1_YFP-FGD3-PH1A	PIP05072021	14.717	15.204	19.109
pEX_EF1_YFP-Rasgrf2-PH1A	PIP05072013	6.933	8.172	9.593
pEX_EF1_YFP-Cool1-PH1A	PIP05072015	2.94	1.997	2.392
pEX_EF1_YFP-PLD1-PH1A	PIP05072016	5.374	5.459	5.559
pEX_EF1_YFP-Pldt2-PH1A	PIP05072017	3.678	7.076	6.599
pEX_EF1_YFP-SNTB2-PH1A	PIP05072019	0.188	-0.416	0.071
pEX_EF1_YFP-Ophn1-PH1A	ETG03110406	22.672	13.83	18.059

pEX_EF1_YFP-Osbpl5-PH1A	PIP05062721	4.1727	7.2088	3.6281
pEX_EF1_YFP-Capri-PH1A	ETG03110413	26.04	30.851	27.641
pEX_EF1_YFP-GNRPx-PH1A	PIP05070502	5.1322	10.3678	12.341
pEX_EF1_YFP-H060-PH1A	PIP05070503	25.96	36.5519	28.461
pEX_EF1_YFP-COL4BP-PH1A	PIP05070507	0.5783	-3.6509	-3.6233
pEX_EF1_YFP-Plekha2-PH1A	PIP05070509	7.6618	8.2166	6.3022
pEX_EF1_YFP-Plek-PH2A	PIP05070512	1.661	1.874	1.604
pEX_EF1_YFP-Myo10-PH2A	PIP05070515	9.529	10.405	10.263
pEX_EF1_YFP-Evt2-PH1A	ETG03111114	-0.176	1.333	2.881
pEX_EF1_YFP-Plek2-PH2A	PIP05070525	118.1531	1.943	4.448
pEX_EF1_YFP-Tiam2-PH1A	PIP05071101	2.816	2.482	1.802
pEX_EF1_YFP-Ese1-PH1A	PIP05071102	4.721	3.408	10.446
pEX_EF1_YFP-Ese2-PH1A	PIP05071103	-1.0244	9.0483	5.4986
pEX_EF1_YFP-Rhoip2-PH1A	PIP05071107	1.585	1.365	4.23
pEX_EF1_YFP-Rhoip3-PH2A	PIP05071106	5.629	7.112	7.715
pEX_EF1_YFP-Rasa3-PH1A	ETG03111814	-2.318	3.532	6.97
pEX_EF1_YFP-SOS1-PH1A	PIP05071113	10.9196	14.4548	16.2554
pEX_EF1_YFP-Tiam1-PH1A	PIP05071115	11.295	17.219	18.328
pEX_EF1_YFP-Tiam1-PH2A	PIP05071116	7.299	6.251	4.49
pEX_EF1_YFP-SOS2-PH1A	PIP05071117	2.373	4.119	3.714
pEX_EF1_YFP-AmylB-PH1A	PIP05071120	0.726	4.052	2.994
pEX_EF1_YFP-Grb14-PH1A	PIP05071125	4.434	6.625	5.95
pEX_EF1_YFP-ROCK1-PH1A	PIP05071303	6.769	3.499	6.828
pEX_EF1_YFP-Myo10-PHTA	PIP05071305	9.509	9.038	10.895
pEX_EF1_YFP-PHR1-PH1A	PIP05071306	3.067	3.465	2.781
pEX_EF1_YFP-PP3bp2l-PH1A	PIP05071308	22.224	22.697	26.006
pEX_EF1_YFP-Dagk4l-PH1A	PIP05071312	11.796	15.47	16.307
pEX_EF1_YFP-CentB5-PH1A	PIP05071314	6.459	6.771	12.374
pEX_EF1_YFP-CentD2l-PH1A	PIP05071316	11.456	10.86	10.561
pEX_EF1_YFP-CentD2l-PH2A	PIP05071317	6.629	6.824	6.661
pEX_EF1_YFP-Plekhc1-PH1A	PIP05071319	2.224	4.341	4.989
YFP		4.008	0.901667	-0.00833
VAV3-PH1A	PIP05072001	5.215	4.489	4.156
pEX_EF1_YFP-Rasgrf1B-PH1A	ETG03111801	30.601	10.648	18.12

PI(3,4,5)P3	PM loc	%Trans	Ves loc				
58.2685	Y	100	Y	1			
40.424	Y	89	Y	1			
149.9232	Y	51	Y	1			
46.27393	Y	50	Y	1			
54.4387	Y	90	N		1		
68.0547	Y	81	N		1		
24.5162	Y	80	N		1		
91.1513	Y	77	N		1		
156.5038	Y	74	N		1		
4.343	Y	72	N		1		
125.4444	Y	57	N		1		
123.7781	Y	53	N		1		
29.091	Y	39	N		1		
68.3401	Y	32	N		1		
27.2169	Y	22	N		1		
15.0232	Y	13	N		1		
10.951	Y	0	Y			1	
37.798	Y	0	Y			1	
18.771	Y	0	Y			1	
60.782	Y	0	Y			1	
15.8553	Y	0	Y			1	
10.137	Y	0	Y			1	
14.0433	Y	0	N				1
31.8256	Y	0	N				1
4.72	Y	0	N				1
20.173	Y	0	N				1
2.173	Y	0	N				1
1.164	Y	0	N				1
48.2855	Y	0	N				1
16.6465	Y	0	N				1
77.3594	Y	0	N				1
40.954	Y	0	N				1
36.194	Y	0	N				1
81.5544	Y	0	N				1
40.136	Y	0	N				1
50.9341	Y	0	N				1
14.944	Y	0	N				1
39.4693	Y	0	N				1
103.3201	Y	0	N				1
11.3138	Y	0	N				1
18.9291	Y	0	N				1
42.1056	Y	0	N				1
25.623	Y	0	N				1
3.3147	Y	0	N				1
26.043	Y	0	N				1
4.3359	Y	0	N				1
22.6055	Y	0	N				1
33.371	Y	0	N				1
12.822	Y	0	N				1
3.871	Y	0	N				1

14.171	Y	0	N	1	
-0.691	Y	0	N	1	
12.007	Y	0	N	1	
39.9215	Y	0	N	1	
11.848	Y	0	N	1	
115.401	Y	0	N	1	
36.077	Y	0	N	1	
25.605	Y	0	N	1	
39.852	Y	0	N	1	
19.811	Y	0	N	1	
13.957	Y	0	N	1	
11.537	Y	0	N	1	
78.327	Y	0	N	1	
26.946	Y	0	N	1	
16.397	Y	0	N	1	
-6.488	Y	0	N	1	
21.501	Y	0	N	1	
11.955	N	0	Y		1
13.936	N	0	Y		1
19.326	N	0	Y		1
10.233	N	0	Y		1
0	N	0	Y		1
8.78	N	0	Y		1
-4.487	N	0	Y		1
3.6623	N	0	Y		1
11.367	N	0	Y		1
5.503	N	0	Y		1
23.016	N	0	Y		1
7.724	N	0	N		
16.399	N	0	N		
13.9593	N	0	N		
6.935	N	0	N		
18.175	N	0	N		
5.19	N	0	N		
4.431	N	0	N		
17.595	N	0	N		
12.136	N	0	N		
24.6181	N	0	N		
13.358	N	0	N		
9.171	N	0	N		
3.658	N	0	N		
17.085	N	0	N		
23.526	N	0	N		
13.625	N	0	N		
23.287	N	0	N		
12.542	N	0	N		
4.453	N	0	N		
8.596	N	0	N		
10.169	N	0	N		
2.035	N	0	N		
26.973	N	0	N		

7.6804	N	0	N
28.594	N	0	N
8.8291	N	0	N
27.869	N	0	N
0.8276	N	0	N
8.5441	N	0	N
3.669	N	0	N
9.571	N	0	N
3.562	N	0	N
10.504	N	0	N
3.116	N	0	N
14.124	N	0	N
4.2546	N	0	N
2.621	N	0	N
2.098	N	0	N
4.04	N	0	N
16.4621	N	0	N
15.421	N	0	N
1.623	N	0	N
3.827	N	0	N
4.951	N	0	N
4.596	N	0	N
7.94	N	0	N
19.167	N	0	N
4.491	N	0	N
27.847	N	0	N
19.95	N	0	N
16.54	N	0	N
10.647	N	0	N
10.882	N	0	N
6.459	N	0	N
-0.99467	N	0	N
6.903			
32.517			

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Label:	Table 2
Filename:	mmc8.xls

Supplementary Table 2, Park et al.
Mouse PH-domains - translocation and localization in response to PDGF, basal localization, lipid blot binding data, and cloning information

#	SWISS-PROT	Name of construct	NM or XM #	Alternative names	Translocating/PM-localized/ or Cytosolic	NIH3T3 cell PM translocation
1	Q8BGR1_MOUSE	2610034M16Rik-PH	NM_027001	AV114557	P	N
2	Q8BGR1_MOUSE	2610034M16Rik-PH2	NM_027001	AV114557	P	N
3	Q3U5G0_MOUSE	ABR-PH	NM_198894	RP23-48B14.2, 6330400K15Rik, AU042359	C	N
4	ARBK1_MOUSE	ADRPK1-PH	NM_130863	Adrbk-1, Bark-1, GRK2, betaARK1	P	N
5	Q3UGX1_MOUSE	AFAP1-PH	NM_027373	AFAP; mKIAA3018, 9630044L16Rik, AI848729; AFAP-110	P	N
6	Q3T998_MOUSE	AKAP13-PH	XM_907140, XM_133543	1700026G02Rik, 5730522G15Rik, AKAP-Lbc, BRX, Ht31, LBC, PROTO-	T	Y
7	AKT1_MOUSE	AKT1-PH	NM_009652	Akt, PKB, PKB/Akt, PKBalpha	T	Y
8	AKT2_MOUSE	AKT2-PH	NM_007434	2410016A19Rik, AW554154, MGC14031, PKB, PKBbeta	T	Y
9	AKT3_MOUSE	AKT3-PH	NM_011785	AI851531, D930002M15Rik	T	Y
10	AB1IP_MOUSE	APBB1IP-PH	NM_019456	9930118P07Rik, Prp48	C	N
11	Q6A055_MOUSE	ARHGEF18-PH	NM_133962	AI467246, D030053O22Rik	P	N
12	Q6Y5D6_MOUSE	ARHGAP10-PH	NM_030113	A930033B01Rik, PSGAP-m, PSGAP-s	C	N
13	ARHG2_MOUSE	ARHGEF2-PH	NM_008487	AA408978, GEF, GEF-H1, GEFH1, LFP40, Lbcl1, Lfc, P40, mKIAA0651	C	N
14	ARHG3_MOUSE	ARHGEF3-PH	NM_027871	1200004I24Rik, 9830169H03Rik, C76747	C	N
15	ARHG7_MOUSE	ARHGEF7-PH	NM_017402	PIX, Pak3bp, betaPix-b, betaPix-c, mKIAA0142, p85Cool1, p85SPR	C	N
16	BTK_MOUSE	BTK-PH	NM_013482	AI528679, xid	T	Y
17	CAPS1_MOUSE	CADPS-PH	NM_012061	AU067781, CAPS, CAPS1, MGC90712, mKIAA1121	C	N
18	Q3UH98_MOUSE	CENTB5-PH	NM_207223	Kiaa1716-hp, mKIAA1716	C	N
19	CEND1_MOUSE	CENTD1-PH	XM_132099	ARAP2, Gm148, mKIAA0580	C	N
20	CEND1_MOUSE	CENTD1-PH2	XM_132099	ARAP2, Gm148, mKIAA0580	C	N
21	Q3UDD2_MOUSE	CENTD2-PH	NM_027180	2410002L19Rik, mKIAA0782	C	N
22	Q3UDD2_MOUSE	CENTD2-PH2	NM_027180	2410002L19Rik, mKIAA0782	C	N
23	CTRO_MOUSE	CIT-PH	NM_007708	C030025P15Rik, CRIK, CRIK-SK, Cit-k	C	N
24	CNKR2_MOUSE	CNKSR2-PH	NM_177751	C030004A01, Cnk2, Ksr2, mKIAA0902	T	Y
25	C43BP_MOUSE	COL4ABP3-PH	NM_023420	2810404O15Rik, 9230101K08Rik, AU016711, CERT, GPBP	C	N
26	DAPP1_MOUSE	DAPP1-PH	NM_011932	Bam32	T	Y
27	DDEF1_MOUSE	DDEF1-PH	NM_010026	AV239055, Asap1, PAP, mKIAA1249, s19	P	N
28	Q6A0B7_MOUSE	DGKD-PH	XM_906228	AI841987, D330025K09, DGKdelta, KIAA0145, dgkd-2	P	N
29	DYN1_MOUSE	DNM1-PH	NM_010065	AI838169, Dnm, KIAA4093, mKIAA4093	C	N
30	DYN2_MOUSE	DNM2-PH	NM_007871		C	N
31	DOK1_MOUSE	DOK1-PH	NM_010070	AW557123, p62DOK	P	N
32	DOK4_MOUSE	DOK4-PH	NM_053246		P	N
33	DOK5_MOUSE	DOK5-PH	NM_029761	2700055C10Rik	P	N
34	Q3UY58_MOUSE	FARP1-PH	NM_134082	AW228844, BC030329, Cdep	C	N
35	Q3UY58_MOUSE	FARP1-PH2	NM_134082	AW228844, BC030329, Cdep	C	N
36	FGD1_MOUSE	FGD1-PH	NM_008001	ZFYVE3	C	N
37	FGD1_MOUSE	FGD1-PHB	NM_008001	ZFYVE3	C	N
38	FGD2_MOUSE	FGD1-PH2	NM_008001	ZFYVE3	C	N
39	FGD2_MOUSE	FGD2-PH	NM_013710	ZFYVE4	C	N
40	FGD3_MOUSE	FGD3-PH	NM_015759	5830461L01Rik, ZFYVE5	C	N
41	FGD6_MOUSE	FGD6-PH	NM_053072	AA123052, Etohd4, ZFYVE24	C	N
42	FGD6_MOUSE	FGD6-PH2	NM_053072	AA123052, Etohd4, ZFYVE24	T	Y
43	FGD6_MOUSE	FGD6-PHT	NM_053072	AA123052, Etohd4, ZFYVE24	T	Y
44	GAB1_MOUSE	GAB1-PH	NM_021356	AA408973, AW107238	T	Y
45	GAB2_MOUSE	GAB2-PH	NM_010248	AI463667, D130058I17Rik, p97	T	Y
46	Q3TYF3_MOUSE	GEFT-PH	NM_028027	2410008H17Rik, p63RhoGEF, D10Ertd610e	P	N
47	GRB10_MOUSE	GRB10-PH	NM_010345	RP23-119N24.1, 5730571D09Rik, AI325020, Meg1, mKIAA0207	C	N
48	GRB14_MOUSE	GRB14-PH	NM_016719	AI505286	C	N
49	GRB7_MOUSE	GRB7-PH	NM_010346	KIAA4028, MGC78181, mKIAA4028	C	N
50	IRS1_MOUSE	IRS1-PH	NM_010570	G972R, IRS-1	P	N
51	ITK_MOUSE	ITK-PH	NM_010583	RP23-273O7.1, Emt, Tcsk, Tsk	T	Y
52	ITSN1_MOUSE	ITSN1-PH	NM_010587	AA517634, AA545208, AI316805, EHSH1, Ese1, Intersectin, Itsn, Sh3p17	C	N

53	ITSN2_MOUSE	ITSN2-PH	NM_011365	AI327390, Ese2, Sh3d1B, Sh3p18, mKIAA1256	C	N
54	Q3TXY8_MOUSE	KALRN-PH	XM_993034	2210407G14Rik, AV235988, DUET, E530005C20Rik, Gm539, Hapip,	C	N
55	KIF1A_MOUSE	KIF1A-PH	NM_008440	ATSV, C630002N23Rik, Gm1626, Kns1	C	N
56	KIF1B_MOUSE	KIF1B-PH	NM_207682	A530096N05Rik, AI448212, AI506502, D4Mil1e, KIF1Bp130, KIF1Bp204,	C	N
57	MCF2L_MOUSE	MCF21-PH	NM_178076	C130040G20Rik, Dbs, Ost, Ost gamma, mKIAA0362	C	N
58	Q2L4X0_MUSMM	MCF2-PH	NM_133197	B230117G22Rik, Dbl, MGC159138, Mcf-2	P	N
59	MRIP_MOUSE	M-RIP-PH	NM_201245	M-RIP; RHOIP3; p116Rip; KIAA0864, AA536749	P	N
60	MRIP_MOUSE	M-RIP-PH2	NM_201245	M-RIP; RHOIP3; p116Rip; KIAA0864, AA536749	C	N
61	P70316_MOUSE	MYO10-PH	NM_019472	AW048724, D15Ertd600e, mKIAA0799	T	Y
62	P70316_MOUSE	MYO10-PH2	NM_019472	AW048724, D15Ertd600e, mKIAA0799	C	N
63	P70316_MOUSE	MYO10-PHT	NM_019472	AW048724, D15Ertd600e, mKIAA0799	T	Y
64	ARHG8_MOUSE	NET1-PH	NM_019671	0610025H04Rik, 9530071N24Rik, AI604373, AU015857, Net1a, mNET1	C	N
65	NGEF_MOUSE	NGEF-PH	NM_019867	Tims2, ephexin	C	N
66	OPHN1_MOUSE	OPHN1-PH	NM_052976	C130037N19Rik, MGC6513	C	N
67	Q80UX3_MOUSE	OSBPL3-PH	NM_027881	1200014M06Rik, 6720421I08Rik, A530055M08, MGC102333, ORP3,	T	Y
68	OSBL5_MOUSE	OSBPL5-PH	NM_024289	1110006M06Rik, AI462538, ORP5, Obph1, Osbp2	C	N
69	Q3TAX1_MOUSE	OSBPL7-PH	XM_193637	4933437E18Rik	T	Y
70	PDPK1_MOUSE	PDPK1-PH	NM_011062	PDK1	T	Y
71	PHLB1_MOUSE	PHLDB1-PH	NM_153537	AU041016, D330037A14Rik, Ll5a, MGC32394	T	Y
72	PHLPP_MOUSE	PHLPP-PH	XM_129968	SCOP, Plekhe1	T	Y
73	Q05DG3_MOUSE	PLCD1-PH	NM_019676	AW212592, C79986	P	N
74	Q3USN9_MOUSE	PLCD4-PH	NM_148937	4921507K24Rik	C	N
75	Q3U4E2_MOUSE	PLCL2-PH	NM_013880	PLC-L2, Plce2, mKIAA1092	P	N
76	PLD1_MOUSE	PLD1-PH	NM_008875	AA536939, C85393, Pld1a, Pld1b	C	N
77	PLD2_MOUSE	PLD2-PH	NM_008876	RP23-122P1.1	C	N
78	PLEK2_MOUSE	PLEK2-PH	NM_013738		T	Y
79	PLEK2_MOUSE	PLEK2-PH2	NM_013738		T	Y
80	PKHA1_MOUSE	PLEKHA1-PH	NM_133942	AA960558, C920009D07Rik, TAPP1	T	Y
81	PKHA2_MOUSE	PLEKHA2-PH	NM_031257	6430512N22Rik, AI851530, AU041791, TAPP2, W91773	C	N
82	PKHA2_MOUSE	PLEKHA2-PH2	NM_031257	6430512N22Rik, AI851530, AU041791, TAPP2, W91773	T	Y
83	PKHA2_MOUSE	PLEKHA2-PHT	NM_031257	6430512N22Rik, AI851530, AU041791, TAPP2, W91773	C	N
84	PKHA3_MOUSE	PLEKHA3-PH	NM_031256	FAPP1	C	N
85	Q6ZPK1_MOUSE	PLEKHA5-PH	NM_144920	2810431N21Rik, AI428202, AK129423, Ayu21-9, Gt(pU21)9Imeg,	C	N
86	PKHB1_MOUSE	PLEKHB1-PH	NM_013746	AI315628, PHR1, Phret1, evt-1	P	N
87	PKHB2_MOUSE	PLEKHB2-PH	NM_145516	2310009M15Rik, AU018239, Evt2, Phdc, evt-2	C	N
88	PKHC1_MOUSE	PLEKHC1-PH	NM_146054	AA960555, Kindlin-2, MGC36305, Mig2	C	N
89	PKHF1_MOUSE	PLEKHF1-PH	NM_024413	1810013P09Rik, APPD, LAPF, PHAFIN1, ZFYVE15	P	N
90	Q8BQ13_MOUSE	PLEKHJ1-PH	NM_023900	9530063M10Rik	C	N
91	Q3U3L2_MOUSE	PLEKHM1-PH	NM_183034	AP162, B2, BC038943, D330036J23Rik	C	N
92	Q3U0Q7_MOUSE	PLEKHM2-PH	XM_924800	2310034J19Rik, AI854247, mKIAA0842	C	N
93	Q9CXH2_MOUSE	PLEKHO1-PH	NM_023320	2810052M02Rik, Ckip1, JZA-20, Jza2, MGC151380	C	N
94	PLEK_MOUSE	PLEK-PH2	NM_019549	RP23-348N2.1, 2010300B13Rik	C	N
95	KPCD1_MOUSE	PRKCM-PH	NM_008858	PPKD, PKD1, Pkcm	C	N
96	CYH1_MOUSE	PSCD1-PH	NM_011180	CLM1, CTH-1, CYTIP, KIAA4240, mKIAA4240	T	N
97	CYH2_MOUSE	PSCD2-PH	NM_011181	ARNO, CTH2, CLM2	T	Y
98	CYH3_MOUSE	PSCD3-PH	NM_011182	CTH3, AI648983, Grp1, KIAA4241, mKIAA4241	T	Y
99	Q6NZP0_MOUSE	PSD2-PH	NM_028707	6330404E20Rik, AW125584, EFA6C	C	N
100	Q2PFD7_MOUSE	PSD3-PH	NM_177698	4931420C21Rik, AI661273, BC003498, D430018P08, EFA6D, MGC6957	P	N
101	Q7TPZ6_MOUSE	RALGPS2-PH	NM_023884	1810020P17Rik, 2210408F11Rik, 4921528G01Rik, 9130014M22Rik,	P	N
102	RASA2_MOUSE	RASA2-PH	NM_053268	5430433H21Rik, AA517451, AU023900, GAP1m	T	Y
103	Q2PMI6_MOUSE	RASA4-PH	NM_133914	AA793972, AW112107, BB079060, CAPRI, GAPL, KIAA0538, mKIAA053	C	N
104	RASL1_MOUSE	RASAL1-PH	NM_013832	MRASAL	C	N
105	GNRP_MOUSE	RASGRF1A-PH	NM_011245	CDC25, CDC25Mm, Grf1, Grfbeta, P190-A, Ras-GRF1, p190, p190RhoGl	C	N
106	GNRP_MOUSE	RASGRF1A-PH2	NM_011245	CDC25, CDC25Mm, Grf1, Grfbeta, P190-A, Ras-GRF1, p190, p190RhoGl	C	N
107	GNRP_MOUSE	RASGRF1B-PH	NM_001039655	CDC25, CDC25Mm, Grf1, Grfbeta, P190-A, Ras-GRF1, p190,	C	N
108	P70392_MOUSE	RASGRF2-PH	NM_009027	Grf2, Ras-GRF2	C	N
109	P70392_MOUSE	RASGRF2-PH2	NM_009027	Grf2, Ras-GRF2	C	N
110	RGNEF_MOUSE	RGNEF-PH	NM_012026	9230110L08Rik, AI323540, D13Bwg1089e, RIP2, RhoGEF, Rhoip2, p190	C	N

111	ROCK1_MOUSE	ROCK1-PH	NM_009071	Rock-I; 1110055K06Rik	C	N
112	O54867_MOUSE	SH2B1-PH	NM_011363	AI425885, Irip, SH2-B, SH2-Bb, Sh2bpsm1, mKIAA1299	C	N
113	APS_MOUSE	SH2B2-PH	NM_018825	APS	P	N
114	3BP2_MOUSE	SH3BP2-PH	NM_011893	3BP2	T	Y
115	Q3UND0_MOUSE	SKAP2-PH	NM_018773	2610021A10Rik, AA960083, BB137539, RA70, SKAP-HOM, Saps, Scap2	C	N
116	SNTA1_MOUSE	SNTA1-PH	NM_009228	AW228934, Snt1	C	N
117	SNTB1_MOUSE	SNTB1-PH	NM_016667	A1B; SNT2; BSYN2; 59-DAP; DAPA1B; SNT2B1; TIP-43; FLJ22442; MG	C	N
118	SNTB2_MOUSE	SNTB2-PH	NM_009229	SNT3; SNTL; SNT2B2; EST25263; D16S2531E	C	N
119	SOS1_MOUSE	SOS1-PH	NM_009231	9630010N06, AI449023	C	N
120	SOS2_MOUSE	SOS2-PH	XM_987825		C	N
121	SPTB2_MOUSE	SPNB2-PH	NM_175836	RP23-189P1.1, 9930031C03Rik, AL033301, KIAA4049, SPTB2, SPTBN1	P	N
122	SWP70_MOUSE	SWAP70-PH	NM_009302	70kDa, AV235546	C	N
123	TEC_MOUSE	TEC-PH	AK139329(BC037071)		T	Y
124	TIAM1_MOUSE	TIAM1-PH	NM_009384	AI847750, D16Ium10, D16Ium10e	C	N
125	TIAM1_MOUSE	TIAM1-PH2	NM_009384	AI847750, D16Ium10, D16Ium10e	C	N
126	Q3TSM6_MOUSE	TIAM2-PH	NM_011878	3000002F19Rik, STEF, mKIAA2016	C	N
127	TARA_MOUSE	TRIOBP-PH	NM_001039156	AI428493, EST478828, Tara, mKIAA1662	C	N
128	VAV_MOUSE	VAV1-PH	NM_011691	Vav, vav-T	C	N
129	VAV2_MOUSE	VAV2-PH	NM_009500	2810040F13Rik, AI847175	C	N
130	VAV2_MOUSE	VAV2-PHB	NM_009500	2810040F13Rik, AI847175	C	N
131	VAV3_MOUSE	VAV3-PH	NM_020505	A530094I06Rik, AA986410, MGC27838	C	N
132	Q8K4P5_MOUSE	VEPH-PH	NM_145820	2810471M23Rik, Veph	P	N

NIH3T3 cell Basal PM loc	Lysophosphatidic Acid	Lysophosphatidylcholine	PtdIns	PI(3)P	PI(4)P	PI(5)P	Phosphatidylethanolamine	hosphatidylcholi	Sphingosine-1-phosphate
Y(H)	6.38	0.97	17.01	39.88	34.91	35.19	2.56	2.69	1.94
N	4.51	1.51	43.10	51.91	52.84	54.73	0.99	0.97	3.02
N	6.23	0.81	9.86	44.44	74.15	63.52	1.36	2.28	4.22
Y(H)	6.82	-1.28	18.33	26.46	28.17	25.04	-1.02	0.07	0.71
N	6.85	3.90	11.31	23.68	32.41	28.14	3.41	5.53	6.57
Y(L)	1.11	1.84	19.83	22.42	28.28	27.01	4.58	4.02	3.57
Y(L)	6.10	2.92	16.33	28.87	22.88	29.97	1.60	2.37	4.93
Y(L)	1.05	1.01	10.57	22.87	20.53	24.72	0.79	2.06	1.83
Y(L)	1.27	0.94	4.45	12.91	12.33	15.97	1.58	3.50	0.12
N	2.72	3.74	21.47	30.11	33.71	26.99	-1.40	4.07	5.30
N	3.79	-0.10	12.39	20.70	24.02	19.09	-1.37	-0.88	3.95
N	3.61	2.74	18.31	17.44	20.71	23.57	2.96	3.26	3.62
N	2.97	1.16	17.64	27.33	24.80	29.61	0.04	1.83	2.80
N	1.52	0.24	1.96	2.58	3.40	1.38	1.96	0.98	3.20
N	1.05	0.22	0.34	4.81	6.13	6.78	-0.10	-0.51	2.47
N	4.69	0.49	36.52	43.49	47.10	51.39	3.12	0.99	2.29
N	1.29	0.74	12.23	30.72	29.07	33.71	-1.36	-0.32	2.89
N	4.15	-0.84	2.76	5.65	12.66	8.66	0.43	-3.58	4.14
N	6.50	0.69	26.56	23.16	27.31	25.09	-0.87	-2.39	5.18
N	0.98	-3.90	15.11	23.84	19.96	22.48	0.68	1.43	-0.20
N	3.76	0.55	27.61	26.40	27.69	23.70	-0.70	0.51	2.18
N	4.22	2.41	33.65	34.55	35.19	34.33	3.99	1.74	1.49
N	0.93	3.11	3.63	9.27	10.66	14.31	-1.09	0.96	4.20
Y(H)	-0.14	-1.81	24.24	54.41	69.18	55.39	-2.81	-1.40	0.73
N	9.68	-2.04	5.84	8.02	16.37	7.51	6.12	9.58	12.43
N	5.44	1.83	15.00	34.05	31.03	38.93	3.07	3.06	4.83
N	5.79	3.93	20.20	27.78	22.84	25.67	4.09	3.41	4.91
Y(L)	4.61	1.64	34.09	47.26	51.02	49.94	1.18	0.96	2.19
N	-0.53	1.43	5.05	17.74	9.60	12.54	0.28	-3.34	1.50
N	2.97	1.11	19.79	30.94	30.64	35.31	1.41	2.78	3.30
Y(H)	3.71	-0.11	14.22	29.03	26.54	28.50	1.98	2.40	7.07
Y(H)	2.61	-0.56	20.24	37.96	38.02	43.95	0.15	0.48	2.87
Y(H)	9.83	4.14	28.12	44.04	47.42	45.80	5.54	4.70	6.88
N	6.74	4.47	20.76	29.27	31.65	32.12	2.39	1.80	5.03
N	6.08	3.29	11.65	17.63	20.87	19.40	3.15	3.70	10.26
N	3.29	0.87	6.71	20.63	21.98	26.02	3.33	1.96	5.19
N	0.08	1.79	8.66	15.43	14.97	26.19	0.26	-0.07	2.51
N	2.23	1.84	18.50	33.09	35.22	31.76	3.83	1.88	1.87
N	2.81	1.62	4.76	15.98	9.93	15.28	0.62	0.36	5.65
N	-0.12	-1.74	5.94	16.32	12.54	17.65	-1.37	-3.20	2.43
N	4.47	1.97	16.69	33.90	31.17	41.23	2.39	1.51	2.58
N	1.98	1.64	3.39	11.30	11.67	14.63	2.20	2.81	5.84
N	3.30	2.55	34.18	63.46	58.50	57.42	-1.55	-0.11	3.98
Y(H)	6.43	2.55	10.95	29.69	25.20	33.46	4.44	5.31	4.96
Y(H)	10.61	0.41	16.98	31.86	33.47	37.77	2.36	2.95	4.80
N	1.49	2.01	19.94	33.47	24.84	37.51	2.85	1.86	4.36
N	2.17	3.24	18.40	27.06	23.61	26.94	3.29	3.15	0.87
N	5.82	0.15	22.14	32.93	32.89	30.74	1.11	1.75	2.95
N	-0.66	-0.14	19.59	29.34	26.97	32.38	3.00	2.69	-1.13
Y(L)	10.71	0.30	12.49	44.34	55.86	54.16	-1.18	-0.73	4.99
N	4.25	2.62	22.94	35.86	37.58	38.51	3.90	1.82	2.71
N	-0.06	2.36	3.75	6.67	6.77	8.23	2.88	-0.21	2.84

N	-2.21	1.78	24.16	39.63	30.50	37.97	4.04	4.15	-1.32
N	2.90	2.88	21.70	20.20	26.05	23.58	3.79	4.40	4.09
N	0.91	0.08	9.02	19.03	15.09	15.94	-0.76	-1.85	4.40
N	4.92	3.78	17.84	27.19	27.46	31.15	3.45	4.18	0.24
N	8.09	6.77	24.18	44.58	39.66	50.49	1.58	0.46	4.47
Y(H)	3.00	1.56	9.91	18.56	11.56	23.50	1.65	1.68	6.44
N	4.73	3.68	6.98	13.39	11.24	14.61	3.46	2.46	5.54
N	3.80	1.84	11.00	16.76	15.79	18.04	2.53	3.15	4.96
N	0.78	0.76	8.06	11.01	12.64	12.50	2.93	2.59	2.00
N	1.74	4.72	4.19	8.20	10.24	9.86	0.41	5.80	3.90
N	2.97	1.36	16.28	23.94	26.12	26.09	1.69	-0.43	1.50
N	4.92	1.70	13.76	25.28	21.47	25.47	0.94	1.90	7.47
N	3.20	-0.37	11.29	18.91	17.05	19.27	-0.27	0.17	5.41
N	5.34	1.79	14.40	20.05	15.71	23.98	-2.38	2.89	3.43
Y(H)	10.35	2.57	11.97	83.30	121.18	90.62	1.17	1.44	3.62
N	-0.93	1.90	27.99	42.08	34.01	43.92	2.82	2.99	-4.59
Y(H)	4.38	1.30	23.27	38.69	46.17	38.35	2.22	1.31	2.23
Y(L)									
Y(H)	3.21	0.15	16.49	25.51	29.68	28.36	1.31	1.85	2.30
Y(H)	4.83	1.77	5.25	4.01	3.40	5.34	2.05	1.65	1.89
Y(H)	-0.14	-1.49	3.90	10.02	8.90	13.02	-1.44	0.45	2.72
N	4.72	-2.63	27.09	30.16	39.21	37.18	1.16	-1.11	5.48
Y(M)	2.07	2.53	11.71	18.03	19.51	21.61	3.49	2.74	6.81
N	0.07	0.76	6.94	17.82	16.34	17.92	0.13	1.87	0.53
N	1.80	0.62	1.45	10.40	11.10	13.22	1.46	-0.24	2.44
N	2.60	1.67	11.08	29.33	22.25	29.61	-0.23	0.88	5.14
N	2.93	0.68	12.02	29.16	21.36	29.05	1.08	1.63	4.86
N									
N	2.80	3.06	3.28	14.55	18.35	14.42	1.82	2.84	7.49
N	5.46	-0.43	5.87	28.51	29.60	37.99	-0.54	-0.91	1.58
N	4.14	1.64	22.60	36.39	39.18	38.71	-1.99	0.46	4.24
N	8.76	9.11	9.68	15.31	15.54	14.32	10.63	15.29	7.95
N	4.51	0.67	23.92	34.79	41.14	41.26	1.37	1.62	4.49
N	-1.23	-0.43	3.75	4.03	4.18	3.63	0.00	-0.92	-1.28
N	1.58	0.66	1.59	7.11	5.90	0.32	3.83	4.03	3.84
N	2.52	0.45	4.10	7.92	8.38	3.72	1.11	-0.96	0.00
Y(M)	-1.35	0.93	17.17	35.97	32.70	37.09	2.56	0.73	1.67
N	2.87	1.45	15.15	31.87	25.90	33.67	2.17	2.66	2.72
N	2.31	-1.28	13.11	21.67	21.41	19.60	-3.93	-2.06	4.35
N	1.75	2.26	8.62	19.63	23.27	18.70	0.71	0.12	3.52
N	8.78	0.86	23.20	74.35	91.33	83.80	0.73	2.24	-0.02
N	2.16	0.71	5.11	11.44	8.21	9.81	0.53	-0.58	0.86
N	3.49	-0.38	21.84	38.98	45.52	39.78	4.30	3.96	0.17
N	5.05	2.30	16.74	26.12	23.75	28.38	-0.27	3.28	1.90
Y(L)	0.88	1.66	15.28	26.46	23.06	28.60	-0.86	1.11	0.99
Y(L)	1.77	1.57	9.40	17.13	16.33	18.63	2.43	2.93	3.82
N	1.90	1.48	17.44	28.74	29.58	32.42	1.33	2.83	5.42
Y(M)	3.79	-0.36	25.02	36.47	42.12	42.17	-1.93	-1.33	6.63
Y(H)	2.87	0.74	6.19	10.50	15.65	12.44	1.76	1.42	3.60
Y(L)	3.79	1.44	19.00	44.76	39.47	47.56	-2.93	-1.29	3.55
N	-1.30	-0.37	12.73	28.57	23.83	31.82	0.50	0.95	7.01
N	6.95	5.52	28.20	37.64	29.95	40.88	6.06	6.20	8.54
N	2.13	2.09	5.13	17.23	16.16	21.39	4.43	2.58	2.33
N	2.93	1.69	17.83	33.60	38.28	30.96	2.63	3.35	2.89
N	6.36	1.64	34.44	56.79	41.83	57.05	-3.56	-1.81	2.16
N	-0.92	0.09	4.74	15.65	16.24	16.74	-0.08	0.30	2.84
N	1.56	1.26	6.71	15.05	10.14	13.87	0.68	1.28	7.08
N	4.27	1.78	12.13	25.58	18.79	21.28	0.70	-0.25	1.88

N	-0.73	1.32	6.87	7.62	9.37	6.52	-1.32	-2.08	-3.41
N	-4.13	0.96	3.06	7.84	12.58	8.25	0.71	1.13	0.70
Y(M)	2.42	2.81	10.17	16.72	16.94	12.00	1.70	2.66	4.01
N	6.81	3.14	20.82	37.38	30.07	26.84	14.29	1.98	5.79
N	0.95	0.51	13.05	25.82	19.00	23.29	3.09	2.63	0.50
N	1.16	1.54	11.32	13.37	12.07	14.96	-1.50	1.32	7.61
N	0.26	3.69	6.78	7.64	19.42	11.43	0.49	-1.51	0.38
N	0.60	0.42	3.93	7.61	6.01	9.57	0.13	-2.47	-0.15
N	7.21	4.04	22.32	40.63	36.63	44.13	2.03	2.57	7.51
N	2.24	2.36	21.26	16.65	20.71	20.75	3.51	4.22	3.99
Y(H)	5.26	2.28	6.40	32.57	57.06	45.73	1.54	0.94	1.95
N	-0.85	0.90	13.45	27.41	25.70	32.22	0.16	1.95	0.36
N	3.11	1.92	12.76	22.80	26.52	26.28	2.72	3.80	3.29
N	4.31	3.07	25.04	44.26	37.28	45.52	2.90	2.21	5.55
N	6.41	4.02	25.68	37.86	39.93	38.37	5.21	6.21	8.93
N	3.86	-1.80	11.03	31.28	22.91	31.50	0.76	0.06	3.43
N	6.29	4.17	20.61	25.32	29.98	29.51	1.33	3.31	4.99
N	-0.69	0.83	8.45	18.25	15.57	18.01	0.09	0.08	2.63
N	1.23	1.43	18.49	26.33	23.58	28.64	0.42	0.80	0.88
N	0.24	1.60	14.92	15.35	11.64	15.39	2.38	1.26	0.67
N	2.41	2.40	9.49	13.98	11.47	15.97	1.37	-0.05	0.90
Y(M)	2.48	0.77	22.24	27.46	25.26	35.19	0.68	0.25	1.04

PI(3,4)P2	PI(3,5)P2	PI(4,5)P2	PI(3,4,5)P3	Phosphatidic Acid	Phosphatidylserine	Blank	CNI sequence
17.58	21.30	28.84	30.21	18.69	25.84	6.31	ATGGTGGTAGCATCCGACATCAG
43.98	42.98	39.77	38.39	30.92	64.39	3.08	CCTGTCCACCAGAACCATGTCTG
51.88	56.00	53.80	71.16	30.38	23.36	2.97	GACATTGATCCTCGCCGGACTGC
57.72	17.65	27.71	53.94	13.09	36.17	2.76	CTCACCATCTCTGAGCGGTGGCA
41.15	34.09	44.55	49.28	17.34	15.71	5.95	TATGAGTCATATGATGAAGAGGA
19.79	17.27	23.22	16.76	11.56	39.89	3.31	AAAGTGGCAAGTTACGAGAAGAA
23.45	15.72	19.18	31.91	14.92	33.18	3.04	ATGAACGACGTAGCCATTGTGAA
58.82	19.04	23.65	68.35	18.52	23.74	3.36	ATGAATGAGGTATCTGTCATCAAA
162.99	12.26	26.80	162.02	7.30	10.01	2.55	ATGAGCGATGTTACCATTGTGAAA
19.62	15.60	32.39	20.97	21.31	53.35	4.80	TATACTGTGTTTAAAAACCCTCAG
25.20	21.09	28.06	23.30	14.74	36.96	-1.38	AAAGTCAGTGAGTATGAGAAGGA
14.32	13.39	19.00	15.73	10.27	37.66	6.37	TATCATCAAGGCCACGAGCTTTC
20.47	19.02	22.25	23.95	17.18	26.39	3.71	GGACTAGTGAAGGAGTTGTTGTC
3.77	5.41	4.11	2.61	5.79	3.73	3.15	AAGACTGGGGAATCGGAATGCCG
7.11	6.17	6.57	8.63	12.06	7.46	4.18	GTTCGCAAGAGGAAGGAGCTGGA
41.50	39.57	48.85	69.57	25.90	51.78	8.75	ATGGCTGCAGTGATACTGGAGAG
20.83	19.68	22.68	28.93	18.49	32.56	2.03	GCCTTGGAAGACAAGGAACTCGG
21.08	15.40	29.19	24.10	13.35	19.68	1.33	GCTGAGTTGGACCAGCTTGTGAT
42.86	17.40	24.96	37.39	15.61	52.99	2.20	GACCCCGTGCACAGTACCCCCTA
17.53	15.70	19.27	19.11	9.03	31.43	0.06	GAACGTCCACTTCACTACACAGA
22.90	18.50	25.67	19.56	19.51	47.93	3.01	CCTGAGGCCCCCACGCCCCTGG
23.41	16.25	22.64	18.69	14.73	47.44	0.22	ATGGAGGCCATGCTGTTGTACTT
7.16	2.26	10.59	10.65	8.14	16.91	5.50	GGCCTGCCAGCTGAATATGCCAC
70.45	62.15	86.08	86.33	31.86	56.15	-0.05	CAAGACATCATGGGCACACCTGT
17.52	13.29	13.31	17.77	19.95	19.34	16.94	ATGTCGGATAACCAGAGCTGGAA
105.77	28.35	30.89	95.23	21.59	35.51	3.97	GCAAATCAGCCTTTGATTGGAAG
19.04	12.85	22.15	24.18	15.52	31.95	3.04	GATCTAATAAAATCCTCTCTGCAA
41.28	37.89	45.80	40.82	28.39	64.10	3.22	ACCATCCTCAAAGAAGGCATGCT
5.09	9.02	9.96	12.69	12.00	18.72	2.86	AAGACTTCAGGGAACCAGGTCGA
21.04	23.70	25.24	30.69	22.18	38.67	3.99	ACCAAGGACCAGATTCTTCTTCTG
25.67	19.82	22.52	27.22	19.07	34.26	3.39	ATGGACGGGGCTGTGATGGAGG
28.92	35.78	38.60	48.62	35.02	40.71	3.39	ATGGCGACCAATTTCAACGACAT
39.24	27.87	50.08	38.01	28.41	56.85	10.78	AATTTTAATGACATAGTGAAGCAG
25.97	24.29	28.13	26.06	20.20	43.10	4.92	GCGCTGGCGGAGATCACAGAGAT
16.89	14.22	16.88	21.55	18.66	30.33	7.40	AACAAGTCCCCGGATGAAGCCAC
19.28	21.55	23.79	30.39	19.79	24.01	5.87	GCCATCCGGAAAATGGAACGAAT
9.20	11.61	12.63	18.89	4.51	24.55	3.99	ATGGAACGAATGCACAAGCTGCT
20.37	17.21	20.20	18.02	11.38	37.68	6.05	GCACCTGGGAGCAGTCCAGCCT
14.39	12.67	16.03	20.10	14.32	19.67	0.52	GAAGATGCCCAGAGAGCACTGGA
14.38	14.34	16.13	23.89	16.44	23.89	0.30	CCCAGGGATGCCCCAGACCGGA
24.45	28.21	32.84	41.02	21.73	37.31	4.40	ACCATGAAGCAAGGGGACAACTT
11.81	11.10	16.51	16.25	17.40	14.06	6.36	TTAGATCACCAGCTGTCGCCTAG
44.53	39.88	48.47	45.26	36.52	73.24	5.15	ACCATGAAGCAAGGGGACAACTT
41.00	18.92	20.44	44.94	24.86	41.17	7.95	ATGAGCGGCGGCGAAGTGGTTTG
53.54	20.76	29.70	54.79	22.49	35.95	2.86	ATGAGCGGCGGCGGCGGCGACG
16.21	21.72	17.80	25.54	19.90	40.99	5.82	ATGATGTCCCTGGGGAGACTTCG
13.92	11.26	16.07	18.13	10.79	25.11	1.54	TTCTTATTCAGAAAGAATTATGCG
22.37	19.90	24.69	20.44	15.29	36.07	3.06	GCCAAATATGAATTTTTTAAGAAC
16.96	16.47	23.71	25.13	15.93	36.35	4.25	CGTAAAAACTTCGCCAAGTATGAA
65.78	42.18	74.17	68.12	18.67	22.18	1.94	ATGGCGAGCCCCCCGGATACCG
34.51	28.00	36.17	56.49	32.19	44.19	4.42	ATGAACAACTTCATCCTCCTGGAA
11.96	12.19	18.28	17.63	7.60	9.00	4.79	GGAGTTCGAGAGAAGGAGAACTC

16.61	19.96	21.16	25.77	21.25	51.55	8.34	GGAGTCCGGGAGAAGGAAAATTC
43.71	17.03	23.80	19.09	16.01	30.69	4.17	GCCATGCATGTCAGCATGCTGGA
14.55	12.57	15.31	15.97	14.65	22.77	2.42	CCCTGCTCCCGGCCCGCCAGCC
22.00	21.05	23.90	25.21	18.32	31.71	6.75	CCAGAAGCCAACTCTCGTGCCTC
27.34	28.44	29.95	29.58	24.87	49.70	1.86	TCCATGCATCTCATCGCCATCACT
4.56	8.34	7.96	7.61	8.19	26.11	1.56	GGTGAAGGAACTACTAAATTAAA
10.75	11.76	13.28	15.49	11.01	14.35	7.54	ATGTCGGCGGCCAAGGAAAACCC
13.63	16.24	15.35	14.13	11.15	16.92	5.00	GCCATCCCTAGAAAGCGGGACTT
15.97	9.91	38.36	105.90	5.45	8.62	2.35	CAGGAAGCCCTCAAGCAAGGCTG
9.96	10.84	10.70	10.00	9.57	3.80	0.43	TACACCCCAGAGGAGATGCACCA
34.44	16.88	35.25	61.03	10.48	38.57	-0.91	CAGGAAGCCCTCAAGCAAGGCTG
18.44	17.14	22.27	22.39	14.53	33.22	1.65	AAGAAAGGCGAATCTGAGTGTCA
10.62	10.70	11.51	20.28	14.18	22.27	-1.16	ATCCTGAAGAGAGTGGAGGAGAG
15.06	10.98	12.47	18.25	12.06	25.93	7.11	AACAGCTTGACTGTGGAGCTCAC
91.61	91.08	90.29	108.13	46.20	27.42	2.99	ATGAGTGACGAGAAGAATCTCGG
20.80	23.49	25.15	28.90	18.09	39.35	2.32	CAGAAGACTGACCCCCGGAAAGT
38.58	33.34	43.34	48.22	24.11	51.51	0.70	ATGGACTTCCAGGAAAGAGACAC
							CAGAGGTCGGGCAGCAACATAGA
134.11	38.39	57.56	138.93	22.51	24.42	0.13	GAAGTCAAGCTCCGGGAAAAGCA
1.07	3.21	3.09	2.13	5.09	12.81	3.94	AAGCCTCATAGCACTGGGAGCTC
13.97	9.24	72.80	32.25	4.92	14.64	-0.45	ATGGACTCCGGTCGGGACTTCCT
30.26	31.01	31.41	30.63	22.34	49.77	2.77	ATGACATCTCAGATTCAAGACCTA
14.46	12.36	29.60	22.80	14.42	24.33	2.24	GGTCCGGTCCCCAGGGACAGCA
7.10	4.85	8.73	10.51	9.16	16.40	1.40	ATCCAGGAAGAGCAGTTCTTTGG
6.49	9.88	9.41	12.98	16.73	8.19	2.81	CAACTTTCCTTTATCCCAGACCTT
15.89	14.64	14.92	20.37	14.04	34.00	3.44	ATGGAGGACGGCGTGCTCAAGG
100.79	12.22	11.25	22.36	14.03	37.06	3.61	GAGCAGTTTCTGGATGACTCCAC
							ATGACTGACATTGTTGGTGGTGT
17.34	17.90	15.98	18.22	24.55	16.63	9.68	ATGCCTTATGTGGATCGGCAGAA
35.45	11.98	22.07	29.73	29.39	35.67	0.70	AGCCAGAACGGTGGGGATGGGC
24.92	22.38	28.26	27.50	27.67	70.77	2.28	ATGCCTTATGTGGATCGGCAGAA
11.14	10.64	11.98	11.62	14.83	13.27	7.96	ATGGAGGGGGTTCTGTACAAGTG
32.88	26.62	36.89	28.97	28.18	50.90	-0.42	TCCAATTCAATTAAAAGGAACCCT
1.42	1.26	3.16	2.17	-0.31	5.64	-0.05	ATGAGCCCGGCAACCCCGGTTCC
-1.04	0.70	0.18	2.93	4.31	3.59	-1.88	ATGGCGTTCGTGAAGAGTGGATG
9.73	6.14	-0.36	11.86	4.77	5.36	0.42	ATCAATAAGCTGTCAATCATGACA
28.40	25.88	26.01	27.30	26.23	49.35	1.24	ATGGTGGACCACTTGGCAAACAC
16.18	23.50	24.78	28.74	16.45	38.43	3.49	ATGCGGTACAACGAGAAAGAGTT
34.03	23.96	33.57	32.64	16.34	30.11	0.26	CTGTCCAACCCATTCCGGGGCCT
20.14	14.74	20.10	18.05	13.14	38.58	3.59	CTGGCGTTGGCGAAATTTGTCGC
67.81	60.38	78.36	85.55	43.38	45.05	7.88	ATGAAGAAGAGCGGCTCCGGCAA
7.80	3.20	5.90	10.20	3.70	4.80	0.46	AGTGGATTCTTCTGTGAGGAGAA
27.39	28.41	32.74	30.15	26.96	49.49	3.02	GGCCAGAGTGGAGGTGCAGAGA
21.02	18.60	25.73	27.35	19.37	28.33	4.74	GTGGAGAGATTCATCGCCATGAA
28.37	23.32	31.54	38.88	22.00	31.76	4.17	AAAATCCCGGAGGATGATGGGAA
24.91	17.62	32.10	132.63	9.67	19.04	3.96	AAGATCCCAGAAGACGACGGAAA
28.25	30.42	30.48	38.46	17.07	42.20	0.69	GAATGGGCCATTGATGAGGATGA
54.34	30.75	42.17	56.97	32.79	58.12	1.41	GAATGGGCAGTAGATGATGAAGA
88.32	25.54	122.98	112.89	7.46	17.51	2.36	GAGACCTCATGGCCGGCTTTTGA
28.80	33.09	30.86	35.98	34.58	38.34	5.50	GGATGTCAGTCCAGAAAAAAGTC
15.15	19.01	15.96	18.55	16.18	32.15	2.41	GAGTCGTGGATGGAACCACTCCA
21.03	23.51	24.52	27.82	21.89	40.99	9.19	CTGGGCCAGCAGCTGGGCCAGG
17.73	13.52	17.52	22.85	13.01	22.08	3.48	ATGCAGAAAGCCATCCGGCTTAA
28.55	27.63	33.00	28.06	28.58	51.45	5.28	GAAGTCAGTGAAACCGAGAACAT
30.77	10.82	18.29	32.69	22.68	87.16	0.17	ATGCAGAAAGCCATCCGGCTTAA
10.15	9.85	9.68	16.18	13.95	17.64	1.90	ATGCAGAAGAGCGTGCGCTACAA
8.43	8.33	9.99	12.28	8.26	16.37	3.42	GAAGTCAGTGACACCGAGAACAT
16.94	12.08	14.50	26.57	12.99	30.19	3.72	AAAGTCAGCGAATACGAGAAGAA

19.88	9.39	13.63	13.46	6.99	19.50	2.05	ACACATAGAAATGAACTTCAAATG
6.50	9.65	8.29	9.69	4.96	6.79	5.16	AACTCCTCGGGTGGTGCTGGGAC
25.87	19.02	26.57	22.46	6.94	14.66	4.21	CGAAAGGGATTCTGGCTGCGTAA
29.29	21.92	23.64	30.84	14.87	28.94	4.56	ATGGCGGCTGAGGAGATGCAGT
13.67	13.91	17.79	19.39	13.04	29.89	6.01	GACGGCGATGAATATGACGATCC
13.56	15.43	14.42	15.10	15.17	21.05	5.78	GAGATCTGTGCAGCGGACGGCC
7.38	6.77	7.60	10.47	7.22	15.74	0.80	GACTTGCTGACCCGTGTGGTTGC
8.82	5.32	3.54	7.50	5.03	8.67	2.01	TCTCCTGATAGCAGGAACACCTT
32.94	34.23	36.22	41.08	23.69	42.37	4.87	ATTTGCTCCAAAAGTCTTGCAAAA
16.17	15.75	20.19	20.45	9.88	31.96	6.19	ATTTACAAGCAGCACTCCCCCAG
13.84	24.62	54.79	24.95	8.62	8.29	-0.91	GCAGGAACCATGGAAACGAGTGA
19.45	18.90	17.37	22.02	16.14	30.37	1.80	CATTACAAAATAAACTTTGATGAC
45.50	24.37	36.63	131.17	7.80	18.71	6.16	ATGAATTTCAACACTATCCTAGAA
34.20	33.40	33.33	37.43	18.87	36.25	2.22	CGCCAGGGGGTGTACGAGAACTT
26.09	30.13	35.03	25.94	18.49	43.99	7.79	AGCGAGGAACACTACCACCTGGA
14.45	14.04	16.55	26.79	13.57	34.09	5.50	CCCCTCCGACAGAACATCTATGA
24.18	20.88	24.33	19.09	15.74	38.98	7.43	GGAGAGTGGAAAAAGCATTGGTT
12.56	11.59	13.84	16.50	12.24	16.66	1.23	ACAGAGAAGGAGAACCTGCGGTT
29.57	19.21	28.72	30.49	13.86	27.85	0.52	GTGAAGCGGGACAAGGAGACCTT
7.77	3.64	6.69	13.18	5.26	19.88	1.29	GTGAAGCGGGACAAGGAGACCTT
8.28	5.42	7.57	11.54	9.58	19.68	2.10	GTAAAAAGAGATAATGAGACCCTT
21.85	20.95	23.49	24.80	19.45	41.49	2.56	GATCTGGAGCAGCTTCAGCTCCA

Type of file: table
Label: Table 3
Filename: mmc9.xls

Supplementary Table 3, Park et al:
Mouse PH-domains -number of criteria met from Isakoff et al. (1998)

	Translocating?	8-criteria	3-criteria	Criteria 1	Criteria 2	Criteria 3	Criteria 4	Criteria 5	Criteria 6	Criteria 7	Criteria 8
2610034M16Rik-PH	N	7	3	1	1	1	0	1	1	1	1
2610034M16Rik-PH2	N	3	0	1	1	0	0	1	0	0	1
ABR-PH	N	4	2	0	0	0	1	1	0	1	1
ADRPK1-PH	N	6	2	1	0	1	1	1	1	0	1
AFAP-PH	N	2	0	0	1	0	0	1	0	0	1
AKAP13-PH	N	3	1	0	0	0	1	1	0	1	1
APBB1IP-PH	N	6	2	1	1	0	0	1	1	1	1
ARFGEF18-PH	N	2	1	0	0	0	0	1	0	1	0
ARHGAP10-PH	N	3	0	1	1	0	0	1	0	0	1
ARHGEF2-PH	N	3	1	0	0	0	0	1	1	1	0
ARHGEF3-PH	N	3	0	1	1	0	0	1	0	0	1
ARHGEF7-PH	N	4	1	1	0	0	0	1	1	0	1
CADPS-PH	N	7	2	1	1	0	1	1	1	1	0
CENTB5-PH	N	7	2	1	1	1	1	1	1	0	0
CENTD1-PH	N	4	0	1	1	0	1	1	0	0	1
CENTD1-PH2	N	4	1	1	1	0	0	1	0	0	0
CENTD2-PH	N	6	2	1	1	1	1	1	0	0	1
CENTD2-PH2	N	5	1	1	1	0	0	1	1	0	0
CIT-PH	N	3	0	1	1	0	0	1	0	0	1
COL4ABP3-PH	N	4	2	1	0	1	0	1	0	0	1
DDEF1-PH	N	6	2	1	1	1	1	1	0	0	0
DGKD-PH	N	6	3	1	0	1	0	1	1	1	0
DNM1-PH	N	5	1	1	1	0	0	1	1	1	0
DNM2-PH	N	5	1	1	1	0	0	1	1	1	1
DOK1-PH	N	5	1	1	1	0	1	1	0	1	1
DOK4-PH	N	6	1	1	1	0	1	1	1	1	1
DOK5-PH	N	5	0	1	1	0	1	1	1	0	0
FARP1-PH	N	6	2	0	1	1	1	1	1	0	0
FARP1-PH2	N	3	0	1	1	0	0	1	0	0	0
FGD1-PH	N	7	2	1	1	1	1	1	1	0	0
FGD1-PHB	N	7	2	1	1	1	1	1	1	0	1
FGD1-PH2	N	4	0	1	1	0	0	1	1	0	1
FGD2-PH	N	7	2	1	1	1	1	1	1	0	0
FGD3-PH	N	7	2	1	1	1	1	1	1	0	0
FGD6-PH	N	6	2	0	1	1	1	1	1	0	0
GEFT-PH	N	6	2	1	1	0	1	1	0	1	1
GRB10-PH	N	4	1	1	1	0	0	1	0	1	1
GRB14-PH	N	5	1	1	1	0	0	1	1	1	0
GRB7-PH	N	5	1	1	1	0	1	1	0	1	1

IRS1-PH	N	4	2	0	0	1	0	1	1	0	1
ITSN1-PH	N	3	2	0	0	1	0	1	0	1	1
ITSN2-PH	N	3	2	0	0	1	0	1	0	1	1
KALRN-PH	N	6	2	1	1	0	0	1	1	1	0
KIF1A-PH	N	3	1	1	0	0	0	1	0	0	1
KIF1B-PH	N	2	0	1	0	0	0	1	0	0	0
MCF21-PH	N	5	1	1	1	0	0	1	1	0	1
MCF2-PH	N	4	1	1	1	0	0	0	1	0	0
M-RIP-PH	N	6	1	1	1	0	1	1	1	0	0
M-RIP-PH2	N	4	2	0	0	1	0	1	1	1	0
MYO10-PH2	N	7	3	1	1	1	0	1	1	1	1
NET1-PH	N	2	0	0	0	0	1	1	0	0	1
NGEF-PH	N	6	1	1	1	0	1	1	1	1	0
OPHN1-PH	N	3	0	1	1	0	0	1	0	0	0
OSBPL5-PH	N	3	0	0	1	0	1	1	0	0	1
PLCD1-PH	N	4	3	0	0	1	0	1	0	1	0
PLCD4-PH	N	6	2	1	1	0	0	1	1	1	1
PLCL2-PH	N	5	2	1	1	1	0	0	1	0	1
PLD1-PH	N	7	2	1	1	1	1	1	1	0	0
PLD2-PH	N	7	2	1	1	1	1	1	1	0	1
PLEKHA2-PH	N	4	1	1	0	0	0	1	1	0	0
PLEKHA3-PH	N	5	2	1	0	1	0	1	1	0	0
PLEKHA5-PH	N	7	3	1	1	1	0	1	1	1	1
PLEKHB1-PH	N	6	1	1	1	0	1	1	1	1	0
PLEKHB2-PH	N	6	1	1	1	0	1	1	1	1	1
PLEKHC1-PH	N	4	1	1	1	0	0	1	0	1	1
PLEKHF1-PH	N	6	3	0	1	1	0	1	1	1	0
PLEKHJ1-PH	N	6	2	1	1	0	1	1	0	1	0
PLEKHM1-PH	N	3	1	0	0	0	1	1	0	1	0
PLEKHM2-PH	N	5	1	1	1	0	1	1	0	1	0
PLEKHO1-PH	N	6	3	1	1	1	0	1	0	1	0
PLEK-PH	N	5	2	1	0	1	1	1	0	1	0
PLEK-PH2	N	8	3	1	1	1	1	1	1	1	1
PRKCM-PH	N	4	1	1	1	0	0	1	0	1	1
PSD2-PH	N	4	1	1	1	0	0	1	0	1	1
PSD3-PH	N	4	1	1	1	0	0	1	0	1	0
RALGPS2-PH	N	3	0	1	1	0	0	1	0	0	0
RASA4-PH	N	5	1	1	1	0	0	1	1	1	1
RASAL1-PH	N	7	3	1	1	1	0	1	1	1	1
RASGRF1A-PH	N	5	1	1	0	1	1	1	1	0	1
RASGRF1A-PH2	N	5	1	1	1	0	1	1	0	0	1
RASGRF1B-PH	N	5	1	1	0	1	1	1	1	0	1
RASGRF2-PH	N	5	1	1	0	1	1	1	1	0	0
RASGRF2-PH2	N	5	1	1	1	0	1	1	0	0	1

RGNEF-PH	N	2	1	0	0	0	0	1	0	1	0
ROCK1-PH	N	4	1	1	1	0	0	1	0	1	0
SH2B1-PH	N	5	0	1	1	0	1	1	1	0	0
SH2B2-PH	N	3	0	1	0	0	0	1	1	0	0
SKAP2-PH	N	5	2	1	1	1	0	1	0	0	0
SNTA1-PH	N	1	0	0	0	0	0	1	0	0	0
SNTB1-PH	N	4	1	1	1	0	0	1	0	1	0
SNTB2-PH	N	5	1	1	1	0	1	1	0	1	0
SOS1-PH	N	3	1	0	0	0	1	1	0	0	0
SOS2-PH	N	3	1	0	0	0	1	1	0	0	0
SPNB2-PH	N	3	0	1	1	0	0	1	0	0	0
SWAP70-PH	N	7	2	1	1	1	1	1	1	0	0
TIAM1-PH	N	4	1	1	1	0	0	1	0	1	1
TIAM1-PH2	N	4	0	1	1	0	0	1	1	0	1
TIAM2-PH	N	5	1	1	1	0	1	1	0	1	1
TRIOBP-PH	N	2	1	0	0	0	0	0	1	1	0
VAV1-PH	N	5	1	1	1	0	1	1	0	0	1
VAV2-PH	N	5	1	1	0	0	1	1	1	0	1
VAV2-PHB	N	5	1	1	0	0	1	1	1	0	1
VAV3-PH	N	5	2	1	1	0	0	1	0	1	0
VEPH-PH	N	6	2	1	1	0	0	1	1	1	0
AKT1-PH	Y	8	3	1	1	1	1	1	1	1	1
AKT2-PH	Y	8	3	1	1	1	1	1	1	1	1
AKT3-PH	Y	8	3	1	1	1	1	1	1	1	1
BTK-PH	Y	8	3	1	1	1	1	1	1	1	1
CNKSR2-PH	Y	6	2	1	1	1	0	1	1	1	0
DAPP1-PH	Y	8	3	1	1	1	1	1	1	1	1
FGD6-PH2	Y	5	1	1	1	0	0	1	1	1	1
GAB1-PH	Y	8	3	1	1	1	1	1	1	1	1
GAB2-PH	Y	8	3	1	1	1	1	1	1	1	1
ITK-PH	Y	8	3	1	1	1	1	1	1	1	1
MYO10-PH	Y	8	3	1	1	1	1	1	1	1	1
OSBPL3-PH	Y	6	2	1	1	1	0	1	1	0	1
OSBPL7-PH	Y	6	2	1	1	1	0	1	1	0	0
PDK1-PH	Y	5	3	0	0	1	0	1	1	1	1
PHLDB1-PH	Y	8	3	1	1	1	1	1	1	1	1
PHLPP-PH	Y	4	1	1	1	0	0	1	0	0	1
PLEK2-PH	Y	7	3	1	0	1	1	1	1	1	1
PLEK2-PH2	Y	8	3	1	1	1	1	1	1	1	1
PLEKHA1-PH	Y	7	3	1	1	1	1	0	1	1	1
PLEKHA2-PH2	Y	7	3	1	1	1	1	0	1	1	1
PSCD1-PH	Y	8	3	1	1	1	1	1	1	1	1
PSCD2-PH	Y	8	3	1	1	1	1	1	1	1	1
PSCD3-PH	Y	8	3	1	1	1	1	1	1	1	1

RASA2-PH	Y	8	3	1	1	1	1	1	1	1	1
SH3BP2-PH	Y	5	2	1	0	1	1	1	0	0	1
TEC-PH	Y	8	3	1	1	1	1	1	1	1	1

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Label: Table 4
Filename: mmc11.xls

Supplementary Table 5, Park et al:
Translocation data from mouse, human, C.elegans, Drosophila, and Dictostyelium PH-domains used as Input to RFC algorithm for Fig. 6D to F

Species	SWISS-PROT name	Gene Name	Cloned and Tested Translocating?	Sequence
Mouse	Q3U5G0_MOUSE	ABR-PH1	C	DIDPRRTAVTTPKGETRQLVKDGFLVEVSESSRKLRHVFLFTDVLLCAKLKKTSAGKHQQYDCKWYIPLADLVFPSPEESEASPQVHPFPDH
Mouse	Q3T998_MOUSE	AKAP13-PH1	C	KVASYEKKVRLGEIYTKTDSKSIMRMKSGQMFAKEDLRRKKLVRDGSVFLKSTTGRLKEVQAVLLTDILVFLQEKDQKYVFASLDHKSTVISLK
Mouse	AB1IP_MOUSE	APBB1IP-PH1	C	YTVFKNPQNFYLDNKGKKENKETNEKMNAKNKEYLLEESFCGTSIIVPELEGALYLKEDGKKSWKRRYFLLRASGIYYVPKGKTKTSRDLACF
Mouse	Q6Y5D6_MOUSE	ARHGAP10-PH1	C	YHQGHELSKDFNHYKMELQINIQNTRNRFEGTRSEVEELMNKIRQNPKDQKRASQFTAEGYLYVQEKRPAPFGSSWVKHYCMYRKTAKKF
Mouse	ARHG2_MOUSE	ARHGEF2-PH1	C	GLVKELLSNVDQDVHELEKEARLQEIYNRMDPRAQTPVPGKGPFGRDELLRRKLIHEGCLLWKTATGRFKDVLLLLMTDVLVFLQEKDQKYI
Mouse	ARHG3_MOUSE	ARHGEF3-PH1	C	KTGESECRYYKERLLYLEEGQKDSLIDSSRVLCCHGELKNNRGVKLHVFLFQEVLVITRAVTHNEQLCYQLYRQPIPVKDLTLEDLQDGEVRL
Mouse	ARHG7_MOUSE	ARHGEF7-PH1	C	VRKRKELELQILTEPIRSWEGDDIKTLGSVTYMSQVTIQCAGSEEKNERYLLLFPNLLLMLSASPRMSGFIYQGKLPTTGMTITKLEDSENHRN
Mouse	CAPS1_MOUSE	CADPS-PH1	C	ALEDKELGRVILHPTPNSPKQSEWHKMTVSKNCPDQDLKIKLAVRMDKPQNMKHSGYLWTIGKNVWKRWKKRFFVLVQVSQYTFAMCSYR
Mouse	Q3UH98_MOUSE	CENTB5-PH1	C	AELDQLVIDSAVEKREMERKHAAIQQRDFSYDEPKVEFDVDAPSGVVMEGYLFKRASNAFKTWNRRWFSIQNSQLVYQKKLKDALTVVVDD
Mouse	CEND1_MOUSE	CENTD1-PH1	C	DPVHSTPYLLAKKAGQSLQMEFLYHNKFSDFPQHDIHSEGVLSQESSQSTFLCDFLYQAPSAASKLSSEKKLLEETNKKWCVLEGGFLSYYE
Mouse	CEND1_MOUSE	CENTD1-PH2	C	ERPLHYTENVLEQVLQWSSLAEPGSAYLVVKRFLTIDSIKQCREKSIKEGILKLKEEPSKILSGNKFQDRCVVLRDGHLFIYKDPKSSKHDKMF
Mouse	Q3UDD2_MOUSE	CENTD2-PH1	C	PEAPTPLALAEQAGQTLQMEFLRNNRTTEVPRLDSMKPLEKHYSVVLPTVSHSGFLYKTASAGKLLQDRRAREEFSRRWCVLGDGVLSYFE
Mouse	Q3UDD2_MOUSE	CENTD2-PH2	C	MEAMLLYLASRVGDTKHGMMKFREDRSLLGLGLPSGGFHDRYFILNSSCLRLYKEVRSHRPEKEWPVKSLKVYLGVKKKLRPPTCWGFTV
Mouse	CTRO_MOUSE	CIT-PH1	C	GLPAEYATHFTEAFCRDKMNSPGLQSKEPGSSLHLEGWMKVPRNNKRGQQGWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGD
Mouse	C43BP_MOUSE	COL4ABP3-PH1	C	MSDNQSWNSSGSEEDPETESGPPVERCGVLSKWTNYIHGWQDRWVVLKNNTLSYYKSEDETEYGCRGSICLSKAVITPHDFDECRFDISV
Mouse	DYN1_MOUSE	DNM1-PH1	C	KTSGNQVEILVIRKGWLTINNIGIMKGGSKEYWFVLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGFMSSKHIFALFNTEQRNVYKDYR
Mouse	DYN2_MOUSE	DNM2-PH1	C	TKDQILLLIDIEQSYINTNHEDFIGFANAQQRSTQLNKKRAIPNQVIRRGWLTINNISLMKGGSKEYWFVLTAESLSWYKDEEEKEKKYMLPLD
Mouse	Q3UY58_MOUSE	FARP1-PH1	C	ALAEITEMVAQLHGTMIKMENFQKLHELKKDLVGIDNLVIPGREFIRLGSLSKLSGKGLQQRMFFLFNDVLLYTSRGLTASNQFKVHGQLPLY
Mouse	Q3UY58_MOUSE	FARP1-PH2	C	NKSPDEATAADQESEDDLSASRTSLERQAPHRGNTMVHVCWHRSTSVSMVDFSIAVENQLSGNLLRKFKNSNGWQKLWVVFTNFCLFFYK
Mouse	FGD1_MOUSE	FGD1-PH1	C	AIRKMERMHKLLKVYELLGGEEDIVSPTKELIKEGHILKLSAKNGTTQDRYLILFNDRLLYCVPRLRLLGQKFSVRARIDVDGMELKESSNLNM
Mouse	FGD1_MOUSE	FGD1-PH1B	C	MERMHKLLKVYELLGGEEDIVSPTKELIKEGHILKLSAKNGTTQDRYLILFNDRLLYCVPRLRLLGQKFSVRARIDVDGMELKESSNLNMPRTF
Mouse	FGD2_MOUSE	FGD1-PH2	C	APGSSPACSQHTPQRRRSILEKQASVAAENSVICSFLHYMEKGGKGWHKAWFVVPENEPLVLYIYGAPQDVKAQRSLPLIGFEVGPPEAGE
Mouse	FGD2_MOUSE	FGD2-PH1	C	EDAQRALDMIFSAAQHSNAAIAEMERLQGLWDVYQRLGLEDDIVDPSNTLLREGPVLKISFRRSDPMERYLVLFNNMLLYCVPRVLQVGAQF
Mouse	FGD3_MOUSE	FGD3-PH1	C	PRDAPDRKDAERSLELISTAADHSNAAIRKMEKMHKLLEVYEQLGGEEDIVNPANELIKEGSIQKLSAKNGTTQDRHLFLFNNVMLYCVPKLR
Mouse	FGD6_MOUSE	FGD6-PH1	C	TMKQGDNFQKLMQIQYSLSGHHEIVQPGRVFLKEGTLMKLSRKVMQPRMFFLFNDALLYTTPMQSGMYKLNNMLSLAGMKVRKPTQEAYQ
Mouse	GRB10_MOUSE	GRB10-PH1	C	FLFRKNYAKYEFFKNPVNFFPDQMVNWCQQSNGGQAQLLQNFLNTSSCPEIQGFLQVKEVGRKSWKKLYVCLRRSGLYYSTKGTSKEPRH
Mouse	GRB14_MOUSE	GRB14-PH1	C	AKYEFFKNPMYFFPEHMVSFAAEMNGDRSPTQILQVFLSSSTYPEIHGFLHAKEQGKKSWKKAYFFLRRSGLYFSTKGTSKEPRHLQLFSEF
Mouse	GRB7_MOUSE	GRB7-PH1	C	RKNFAKYELFKSPPHTLFPEKMVSSCLDAQTGISHEDLIQNFLNAGSFPEIQGFLQLRGSGRGSGRKLWKRFFCFLRRSGLYYSTKGTSKDP
Mouse	ITSN1_MOUSE	ITSN1-PH1	C	GVREKENSDRLEWIQAHVQCEGLSEQLVFNSVTNCLGPRKFLHSGKLYKAKSNKELYGFLFNDFLLLTQITKPLGSSGTDKVFSPKSNLQYK
Mouse	ITSN2_MOUSE	ITSN2-PH1	C	GVREKENSDRLEWIQAHVQCEGLAEQLIFNSLTNCLGPRKLLHSGKLYKTKSNKELHAFLFNDFLLLTYLVRQFAAASGHEKLFNSKSSAQF
Mouse	Q3TXY8_MOUSE	KALRN-PH1	C	AMHVSMLEGFDENLDVQGELILQDAFQVWDPKSLIRKGRERHLFLFEISLVFSKEIKDSSGHTKYVYKNKLLTSELGVTEHVEGDPCKFALWS
Mouse	KIF1A_MOUSE	KIF1A-PH1	C	PCSRPASPEPELLPELDSKKTPSPVRATETEKEPQRLLVPDIQEIRVSPIVSKKGYLHFLEPHTAGWAKRFVVVRRPYAYMYNSDKDTVERFV
Mouse	KIF1B_MOUSE	KIF1B-PH1	C	PEANSRASSPCQEFEQFQIVPTVETPYLARAGKNEFLNLVPDIEEVRAGSVVSKKGYLHFKEPLSSNWAKHFVVVRRPYVFIYNSDKDPVER
Mouse	MCF2L_MOUSE	MCF21-PH1	C	SMHLIAITGYDGNLGDLGKLLMQGSFSVWTDHKKGHTKVKELARFKPMQRHLFLHEKAVLFCKKREENGEGYEKAPSYSYKQSLNMTAVGI
Mouse	MRIP_MOUSE	M-RIP-PH2	C	AIPRKRDFASEAPTAPLSDACPLSPHRRAKSLDRRSTESSMTPDLLNFKKGWLTKQYEDGQWKKHWFVLADQSLRYYRDSVAEEAADLDG
Mouse	P70316_MOUSE	MYO10-PH2	C	YTPEEMHHWITLLQRSKGDTRVEGQEFIVRGWLHKEVKNSPKMSSLKLKKRWFVLTHNSLDYYKSSEKNALKLGTLVLNSLCSVVPPDEKIF
Mouse	ARHG8_MOUSE	NET1-PH1	C	KKGESECQYYINKLEYLDEKQKDPRIEASKVLLCHGELKNKSGHKLYIFLFQDILVLTRPVTRNERHLYQVYRQPIPVQELVLEDLQDGDVRM
Mouse	NGEF_MOUSE	NGEF-PH1	C	ILKRVEERSEREGTALDAHKELEMVVKACNEGVRKMSRTEQMISIQKKMEFKIKSVPIISHSRWLLKQGELQQMSGPKTSRTLRTKKLFREIYL
Mouse	OPHN1_MOUSE	OPHN1-PH1	C	NSLTVELTQDFLPYKQQLQLSLQNTRNHFSSTREEMEELKKRMKEAPQTCKLPGQPTIEGYLYTQEKWALGISWAKYYCRYEKETRMLTMI
Mouse	OSBL5_MOUSE	OSBPL5-PH1	C	QKTDPRKVPRNLLLGCENELGPITPGRDMESNGPSQPRDEEPQTPGSATKVPLAEYRLCNGSDKECTSPTTRVSKKDALKAQKENYRQEK
Mouse	Q3USN9_MOUSE	PLCD4-PH1	C	MTSQIQDLLATDQDLLLMQEGTMMRKVRTKSWKKLRYFRLQNDGMTVWHGSQPESMPKPTFSISDVERIRKGQDSELLRYLVEEFPLEQG
Mouse	PLD1_MOUSE	PLD1-PH1	C	IQEEQFFGRRKQLEDYLTKILKMPMYRNYHATTEFLDVSQLSFIHDLGPKGLEGMIMKRSGGHRIPGVNCCGHGRACYRWSKRWLIVKDSFL
Mouse	PLD2_MOUSE	PLD2-PH1	C	QLSFIPDLGSKGLEGVIRKRSGGHRVPGFTFCGRDQVCYRWSKRWLVVKDSFLLYMRPETGAISFVQLFDPGFEVQVGKRSTETRYGVRID
Mouse	PKHA2_MOUSE	PLEKHA2-PH1	C	MPYVDRQNRICGFLDIEDNENSGKFLRRYFILDTQANCLLWYMDNPQNLAVGAGAVGSLQLTYISKVSIATPKQKPKTPFCFVINALSQRYFL
Mouse	PKHA3_MOUSE	PLEKHA3-PH1	C	MEGVLYKWTNYLTGWQPRWFVLDNGILSYYDSQDDVCKGSKGSIKMAVCEIKVHPADNTRMELIIPGEQHFYMKAVNAAERQRWLVALGS
Mouse	Q6ZPK1_MOUSE	PLEKHA5-PH1	C	SNSIKRNPNAPVVRRGWLYKQDSTGMKLWKKRWFVLSDLCLFYYRDEKEEGILGSILLPSFQIAMLTAEDHINRKYAFKAAHPNMRTYYFCT
Mouse	PKHB2_MOUSE	PLEKHB2-PH1	C	MAFVKSGWLLRQSTILKRWKKNWFDLWSDGHLIYYDDQTRQSIEDKVHMPVDCINIRTGHECRDIQPPDGKPRDCLLQIVCRDGKTISLCAE
Mouse	PKHC1_MOUSE	PLEKHC1-PH1	C	INKLSIMTSENHLNNSDKEVDEVDAALSDLEITLEGGKTSTILGDITSIPELADYIKVFKPKKLTLKGYKQYWCTFKDTSISCYKSKEESSGTPAH
Mouse	Q8BQ13_MOUSE	PLEKHJ1-PH1	C	MRYNEKELQALSRQPAEMAAELGMRGPKKGSVAKRRLVKLVVNFLFYFRPDEAEPLGALLLERCRVAQEEPGGFSISFVEDLSRKYHFECC
Mouse	Q3U3L2_MOUSE	PLEKHM1-PH1	C	MSNPFRGLMKLGTVARRGAMGIWKEFFCELSPLEFRLYLSDEERTCVESCSLLRCEAVGPAHSDGRFELVFSGKKLALRASSQDEAEDWLD
Mouse	Q3U0Q7_MOUSE	PLEKHM2-PH1	C	MALAKFVAQESKCEASAVTVHFYGLVHWEDPMEEALGPVPCQCSPAEGTITKEGMLHYKASTSYLGKEHWKACFVVLSNGILYQYPDRTD
Mouse	Q9CXH2_MOUSE	PLEKHO1-PH1	C	MKKSGSGKRGPPDGNHQSAAPEKVGWVRKFCGKGIFREIWKNRYVVLKGDQLYVSEKEVKDEKNSQEVFDLSDYEKCEELRKSKSRSKK
Mouse	PLEK_MOUSE	PLEK-PH2	C	SGFFCEENSSDDDVILKEEFRGVIIKQGCLLKQGHRRKNWKVRKFILREDPAYLHYYDPAGGEDPLGAVHLRGCVVTSVESSHDGKKSDEE

Mouse	KPCD1_MOUSE	PRKCM-PH1	C	GQSGGAEMQDPDADQEDSNRTISPSTSNNIPLMRVVQSVKHTKRRSSTVMKEGWMVHYTSKDTLRKRHYWRLDSKCITLFQNDTGSRYYK
Mouse	Q6NZP0_MOUSE	PSD2-PH1	C	EWAIDEDELRKSLSELVDDKFGTGTKKVTRILDGGNPFLDVPQALNATTYKHGVLTRKTHADMDGKRTPRGRRGWKKFYAVLKGTILYLQKD
Mouse	Q2PMI6_MOUSE	RASA4-PH1	C	ESWMEPLQPTVRQGVAQLKDFIMKLVDIEEKEELDLQRALNSQAPPVKEGPLFIHRTKGKGPLASSSFKKLYFSLTTEALSFAKTSSSKKSTF
Mouse	RASL1_MOUSE	RASAL1-PH1	C	MGQQLGQGKEQWLAPLHPFLLQSISRVRDFLDQLVDVDEDEEAGGPACALVQPSTIVREGFLLKRKEEPGGLATRFAFKKRYFRLSGRDLS
Mouse	GNRP_MOUSE	RASGRF1A-PH1	C	MQKAIRLNDGHVVTLGLLAQKDGTRKGYLSKRSADNPKWQTKWFALLQNLLFYFESDSSPRPSGLYLLEGSICKRAPSPKRGTSSKESGEK
Mouse	GNRP_MOUSE	RASGRF1A-PH2	C	EVSETENIRKNLAIERMITEGCEILLDTSQTFVRQGSLMQMSLSEKSKSSRGRLGSLSTKKEGERQCFLFSKHLIICTRGSGGKLHLTKNGVIS
Mouse	GNRP_MOUSE	RASGRF1B-PH1	C	MQKAIRLNDGHVVTLGLLAQKDGTRKGYLSKRSADNPKWQTKWFALLQNLLFYFESDSSPRPSGLYLLEGSICKRAPSPKRGTSSKESGEK
Mouse	P70392_MOUSE	RASGRF2-PH1	C	MQKSVRYNEGHALYLAMLARKEGTKRGFLSKKAAEASRWHEKWFALYQNVLFYFEGEQSGRPAGMYLLEGCSCERTPAPPRTNAGPAGA
Mouse	P70392_MOUSE	RASGRF2-PH2	C	EVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQGSLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRSSGGKLHLLKTGGVLS
Mouse	RGNEF_MOUSE	RGNEF-PH1	C	KVSEYEKNQKWLEILNKIENKTYTKLKNGHVFRKQALLSQERALLHDGLVYWKTATGRFKDILALLLTDVLLFLQEKDQKYIFAAVDQKPSVISL
Mouse	ROCK1_MOUSE	ROCK1-PH1	C	THRNELQMQLASKESDIEQLRAKLLDLSDSTSVASFPSADETDGNLPESRIEGWLSVPNRGNIKRYGWKKQYVVVSSKKILFYNDEQDKEQS
Mouse	O54867_MOUSE	SH2B1-PH1	C	NSSGGAGTVGRALANDGTSPGERWTHRFERLRLSRGGGTLKDGAGMIQREELLSFMGAEEAAPDPAGVGRGGGAAGLTSGGGGQPQW
Mouse	Q3UND0_MOUSE	SKAP2-PH1	C	DGDEYDDPFAGPADTISLASERYDKDDDGPSDGNQFPPIAAQDLPFVIKAGYLEKRRKDHSFLGFEWQKRWCALSKTVFYYYGSDKDKQQK
Mouse	SNTA1_MOUSE	SNTA1-PH1	C	EICAADGQDAVFLRAKDEASARSWAGAIQAQIGTFIPWVKDELQALLTATGTAGSQDIKQIGWLTEQLPSGGTAPTLALLTEKELLFYCSLPQS
Mouse	SNTB1_MOUSE	SNTB1-PH1	C	DLLTRVVADIREQLGKTGIAGSREIRHLGWLAEKVPGESEKQWKPALVVLTEKDLLIYDSMPRRKEAWFSPVHSYPLLATRLVHSGPGKGSP
Mouse	SNTB2_MOUSE	SNTB2-PH1	C	SPDSRNTLILRCKDTATAHSWFVAIHTNIMALLPQVLAELNAMLGATSTAGGSKEVKHIAWLAEQAKLDGGRQQWRPVLMAVTEKDLLLYDC
Mouse	SOS1_MOUSE	SOS1-PH1	C	ICSKSLAKRRLSESACRFYSQQMKGKQLAIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQPRLPC
Mouse	SOS2_MOUSE	SOS2-PH1	C	IYKQHSPRRRPGDPVCLFYNRQLRSKHLAIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGPLTRIGAKHERHIFLFDGLMISCKPNHGQTRLPG
Mouse	SWP70_MOUSE	SWAP70-PH1	C	HYKINFDDNKDGLSAWELIELIGNGQFSKGMDRQTVSMAINEVFNELILDVLKQGYMMKKGHKRKNWTERWFVLKPNIISYYVSEDLKDKKG
Mouse	TIAM1_MOUSE	TIAM1-PH1	C	RQGVYENFRRELEMSTTNSESLEEAGSAHSDEQSSGTLSSPGQSDILLTAAQGTVRKAGALAVKNFLVHKKNKKVESATRRKWKHYWVSLK
Mouse	TIAM1_MOUSE	TIAM1-PH2	C	SEEHYHLDVAIKTMNKVASHINEMQKIHEEFGAVFDQLIAEQTGEKKEVADLSMGDLLLHTSVIWLNPPASLGKWKKEPELAAFVFKTAVVLV
Mouse	Q3TSM6_MOUSE	TIAM2-PH1	C	PLRQNIYENFMRELEMSRSNTEHVETSTETMESSSESVSSLEQLDLLFEKEQGVVRKAGWLFFKPLVTLQKERKLELVARRKWKQYWVTLK
Mouse	TARA_MOUSE	TRIOBP-PH1	C	GEWKKHWFVLTDSSLKYYRDSTAEEADELDGEIDLRSCTDVTEYAVQRNYGFQIHTKDAVYTLSAMTSGIRRNWIEALRKTVRPTSAPDVTK
Mouse	VAV_MOUSE	VAV1-PH1	C	TEKENLRLALDAMRDLAQCVNEVKRDNETLRQITNFQLSIENLDQSLANYGRPKIDGELKITSVERRSKTDRYAFLLDKALLICKRRGDSYDLK
Mouse	VAV2_MOUSE	VAV2-PH1	C	VKRDKETLKKISEFQCSIGNLQVKLEEFGRPKIDGELKVRSIVNHTKQDRYLFLFDKVVIVCKRKGYSYELKEVIELLFHKMTDDPMHNKDIKKV
Mouse	VAV2_MOUSE	VAV2-PH1B	C	VKRDKETLKKISEFQCSIENLQVKLEEFGRPKIDGELKVRSIVNHTKQDRYLFLFDKVVIVCKRKGYSYELKEVIELLFHKMTDDPMHNKDIKKS
Mouse	VAV3_MOUSE	VAV3-PH1	C	VKRDNETLREIKQFQLSIENLNQPVLLFGRPQGDGEIRITTLDKHTKRERHIFLFDLAVIVCKRKGDNYEMKEIIDLQQYKIANNPTTDKENKKW
Mouse	Q8BGR1_MOUSE	2610034M16Rik-PH1	P	MVVASDISRCPNTPWPTCRGYLHKRTHSGFVKGWRKRWFVLKHDGFLLYYKHRKDEGKWPPLDMIKLEGAEVDIDNSLGKPFVFNCMPQS
Mouse	Q8BGR1_MOUSE	2610034M16Rik-PH2	P	PVHQNHVWEDVTVHNSSLPPLAIKHPECLGLLHQLERSTDVWIQHYCILKDGCLYFYASIRSTQASGGLYLQGYSVSEQTHGFEQPVIELKPS
Mouse	ARBK1_MOUSE	ADRPK1-PH1	P	LTISERWQQEVAETVFDTINAETDRLEARKKAKNKQLGHEEDYALGKDCIVHGYMSKMGNPFLTQWQRRYFYLFPNRLEWRGEGEAPQSLL
Mouse	Q3UGX1_MOUSE	AFAP-PH1	P	YESYDEEEEDGKGKKTRHQWPSEEASMDLVKDAKICAFLLRKKRFGQWTKLLCVIKDTKLLCYKSSKDQQPQMELPLQGCSITYIPRDSKKK
Mouse	Q6A055_MOUSE	ARFGEF18-PH1	P	KVSEYEKDQRLREIAGKMDLKSSSKLKNGLTFRKEDMLQRQLHLEGMLCWKTTSGRLKDILAILLTDVLLLLQEKDQKYVFASVDSKPPVISL
Mouse	DDEF1_MOUSE	DDEF1-PH1	P	DLIKSSLQLDPKEVGGLYVASRANSSRRDSQSRQGGYSMHQLQGNKEYGSEKKGFLLKKSDGIRKVWQRRKCAVKNGILTISHATSNRQPA
Mouse	Q6A0B7_MOUSE	DGKD-PH1	P	TILKEGMLTKQNNSFQRSKRRYFKLRGRTLYYAKTAKSIIFDEVDLTDASVAESSTKNVNNSFTVITPCRKLILCADNRKEMEDWIAALKTVQN
Mouse	DOK1_MOUSE	DOK1-PH1	P	MDGAVMEGPLFLQSQRFGTKRWRKTWAVLYPASPHGVARLEFFDHKGSSSRGGRGGSRRLDCKMIRLAECVSVVPVTVESPPEPGAAAF
Mouse	DOK4_MOUSE	DOK4-PH1	P	MATNFNDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLEKYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDDSARTFT
Mouse	DOK5_MOUSE	DOK5-PH1	P	NFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASSKGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAIGIYFNDDTSKTFACES
Mouse	Q3TYF3_MOUSE	GEFT-PH1	P	MMSLGRLRGFEGKLTAQGKLLGQDTFLVTEPEAGGLLSSRGRERRVFLFEQIIIFSEALGGGGRGGAQPGYVYKNSIKVSCLGLEGNLQGNF
Mouse	IRS1_MOUSE	IRS1-PH1	P	MASPPDTDGFSDVRKVGYLRKPKSMHKRFFVLRAASEAGGPARLEYYENEKKWRHKSSAPKRSIPLESCFNINKRADSKNKHLVALYTRDE
Mouse	Q2L4X0_MUSMM	MCF2-PH1	P	GEGTTKLKEALDSMLELLRSVNDSMHQTAINGYVGNINELGKMVLQGSFNVWLGHRKGATKMKDFARFKPMQRHLFLYEKAVMFCKRRFES
Mouse	MRIP_MOUSE	M-RIP-PH1	P	MSAAKENPCRKFQANIFNKSKCQNCFKPRESHLLNDEDLTQAKPIYGGWLLLAPDGTDFDNPVHRSRKWQRRFFILYEHGLLRYALDEMPTT
Mouse	Q05DG3_MOUSE	PLCD1-PH1	P	MDSGRDFLTLHGLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIEDIQEVRMGHRTEGLEKFARDII
Mouse	Q3U4E2_MOUSE	PLCL2-PH1	P	GPVPRDSKPGGLPRRSSIIKDGTKQKRERKKTVSFSSMPTEKKISSASDCINSMVEGSELKKVRSNSRIYHRYFLLDADMQSLRWEPSKKDS
Mouse	PKHB1_MOUSE	PLEKHB1-PH1	P	MSPATPVPPDSILESPFEEMALVRGGWLWRQSSILRRWKRNWFALWLDGTLGYYHDETAQDEEDRVVIHFNVRDIKVGQECQDVQPPEGR
Mouse	PKHF1_MOUSE	PLEKHF1-PH1	P	MVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVLTKECRKKAKPRIFFLFNDILVYGSIVLSKRKYRSQHIIPLEEVTLEPLPETLQ
Mouse	Q2PFD7_MOUSE	PSD3-PH1	P	EWAVDDEEKKKSPSESTEEKANGTHPKTISRIGSTTNPFLDIPHDPNAAVYKSGFLARKIHADMDGKKTPRGKRGWKTFYAVLKGTVLYLQK
Mouse	Q7TPZ6_MOUSE	RALGPS2-PH1	P	ETSWPAFESSAESEDLAVHLYPGAVTIQGVLRRKTLLKEGKKPTVASRTKYWAALCGTQLFYYAAKSLKATERKHFKSTSNKNVSVVGWMV
Mouse	APS_MOUSE	SH2B2-PH1	P	RKGFWLRNMSLCVVDGVRDLWHRRSSPEPDGGATPKAAEPASEPRDKWTRRLRLARTLAAKVELVDIQREGALRFMVADDAASGPGGTA
Mouse	SPTB2_MOUSE	SPNB2-PH1	P	AGTMETSEMVNGAAEQRTSSKESSPVPSPTLDRKAKSALPAQSAATLPARTLETPAAQMEGFLNRKHEWEAHNKKASSRSWHNVYCVINN
Mouse	Q8K4P5_MOUSE	VEPH1-PH1	P	DLEQLQLHLEEVRFFDVFGFSETAGAWQCFMCNNPEKATVVNQDGQPLIEGKLKEKQVRWKFIKRWKTRYFTLAGNQLLFQKGKSKDDPD
Mouse	AKT1_MOUSE	AKT1-PH1	T	MNDVAIVKEGWLHKRGEYIKTWRPRYFLLKNDGTFIGYKERPQDVDQRESPLNNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVET
Mouse	AKT2_MOUSE	AKT2-PH1	T	MNEVSVIKEGWLHKRGEYIKTWRPRYFLLKSDGSFIGHKERPEAPDQTLPPLNNFSVAECQLMKTERPRPNTFVIRCLQWTTVIERTFHVDS
Mouse	AKT3_MOUSE	AKT3-PH1	T	MSDVTIVKEGWVQKRGEYIKNWRPRYFLLKTDGSFIGYKEKPQDVDLPYPLNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPE
Mouse	BTK_MOUSE	BTK-PH1	T	MAAVILESIFLKRSQQKKKTSPLNFKKRLFLLTVHKLSYYEYDFERGRRGSKKGSIDVEKITCVETVIPEKNPPPERQIPRRGEESSEMEQISIIE
Mouse	CNKR2_MOUSE	CNKSR2-PH1	T	QDIMGTPVPETTLYHTFQQSSLQHKSKKKNKGPIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKDASLYWYINEED
Mouse	DAPP1_MOUSE	DAPP1-PH1	T	ANQPLIGSETGTLMVLKHPYPREVEEPCIYESVRVHTAMQTGRTENDLVPTAPSLGTKEGYLTKQGGLVKTWKTRWFTLQRNELKYFKDQM
Mouse	FGD6_MOUSE	FGD6-PH2	T	LDHQLSPRVGSPGNHKSPSSALSSVLHSIPSGRKQKKIPAALKEVSANTEDSTMSGYLYRSKGSKKPWKHLWFVIKNKVLYTYAASEDVAAL
Mouse	GAB1_MOUSE	GAB1-PH1	T	MSGGEVVCSGWLRKSPPEKKLKRYAWKRRWFVLRSGRLTGDPDVLEYYKNDHAKKPIRIIDLNLCQQVDAGLTFNKKEFENSYIFDINTIDRI

Mouse	GAB2_MOUSE	GAB2-PH1	T	MSGGGGDDVVCTGWLRKSPPEKKLRRYAWKKRWFILRSGRMSGDPDVLEYYKNEHSKKPLRIINLNLCEQVDAGLTFNKKELQDSFVFDIK
Mouse	ITK_MOUSE	ITK-PH1	T	MNNFILLEEQLIKKSQQKRRTSPSNFKVRFFVLTKASLAYFEDRHGKKRTLKGSIELSRIKCVEIVKSDISIPCHYKYPFQVVHDNYLLYVFAPD
Mouse	P70316_MOUSE	MYO10-PH1	T	QEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMYFENDSEEKLKGTVEVRTAKEIIDNTSKENGIDIILADRTFHLIAESPEDASQWF
Mouse	Q80UX3_MOUSE	OSBPL3-PH1	T	MSDEKNLGVSQKLVSPSRSTSSCSSKQGSRQDSWEVVEGLRGEMTYTQEPPVQKGFLLKKRKWPLKGWHKRFFCLEKGILKYAKSQADIE
Mouse	Q3TAX1_MOUSE	OSBPL7-PH1	T	MDFQERDTPSLAESTQSSKPSSTQQASELWEVMEEPRGRLGADDIMPERQEGHLLKKRKWPLKGWHKRYFVLEDGILHYATTRQDITKGK
Mouse	PDPK1_MOUSE	PDPK1-PH1	T	QRSGSNIEQYIHDLDTNSFELDLQFSEDEKRLLLEKQAGGNPWHQFVENNLILKMGPVDKRKGLFARRRQLLLTEGPHLYYVDPVNKVLKGE
Mouse	PHLB1_MOUSE	PHLDB1-PH1	T	EVKLREKQFSQARPLTRYLPNRKEDFDLKTHIESSGHGVDTCLHVVLSSKVCRGYLIKMGGKIKSWKKRWFVFDRLKRTLSYYVDKHETKLK
Mouse	PLEK2_MOUSE	PLEK2-PH1	T	MEDGVLKEGFLVKRGHIVHNWKARWFILRQNTLLYYKLEGGRRVTPPKGRIVLDGCTITCPCLEYENRPLLIKLKTRTSTEYFLEACSREERD
Mouse	PLEK2_MOUSE	PLEK2-PH2	T	EQFLDDSTALYTFAESYKKKVSSKEEISLSTMELSGTVVKQGYLSKQGHKRKNWKVRRFVLRKDPAFLHYYDPSKEENRPVGGFSLRGSLV
Mouse	PKHA1_MOUSE	PLEKHA1-PH1	T	MTDIVGGVPIITPTQKEEVNECGESLDRNNLKRSQSHLPYFAPKPPSDSAVIKAGYCVKQGAVMKNWKRRYFQLDENTIGYFKSELEKEPLR
Mouse	PKHA2_MOUSE	PLEKHA2-PH2	T	SQNGGDGQEGCEPGTHAFLRRSQSYIPTSGCRPSTGPPLIKSGYCVKQGNVRKSWKRRFFALDDFTICYFKCEQDREPLRTIPLKDVLKTHE
Mouse	PLEK_MOUSE	PLEK-PH1	T	MEPKRIREGYLVKKGSVFNTWKPMWVVLLEDGIEFYKKKSDNSPKGMIPLKGSTLTSPCQDFGKRMFVLKITTTKQQDHFFQAAFLEERDAV
Mouse	CYH1_MOUSE	PSCD1-PH1	T	VERFIAMNRGINDGGDLPEELLRNLYESIKNEPFKIPEDDGNDLTHTFFNPDREGWLLKLGGGRVKTWKRRWFILTDNCLYYFEYTTDKEPR
Mouse	CYH2_MOUSE	PSCD2-PH1	T	KIPEDDGNDLTHTFFNPDREGWLLKLGGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVDDPRKPNCFELYIPNNKGQLIKA
Mouse	CYH3_MOUSE	PSCD3-PH1	T	KIPEDDGNDLTHTFFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVEDPRKPNCFELYNPSHKGQVIKA
Mouse	RASA2_MOUSE	RASA2-PH1	T	GCQSRKKSRFKKSVMCEFLKMFQEERYFTDVKKFLDEISSTETKESSGTSEPVHLKEGEMYKRAQGRTRIGKKNFKKRWFCLTSRELTYHR
Mouse	RASA3_MOUSE	RASA3-PH1	T	SKSKSASFKESYMATFYEFFNEQKYADAVKNFLDLISSSGRRDPKSIEQPILLKEGFMIKRAQGRKRFGMKNFKKRWFRLTNHEFTYQKSKG
Mouse	3BP2_MOUSE	SH3BP2-PH1	T	MAAEEMQWPVPMKAIGAQNLLTMPGGVAKAGYLHKKGGTQLQLLKWPLRFVIIHKRCIYYFKSSTSASPQGAFSLSGYNRVMRAAEETTSN
Mouse	TEC_MOUSE	TEC-PH1	T	MNFNTILEEILIKRSQQKKKTSPLNYKERLFVLTKSVLSYYEGRAEKKYRKGVIDISKIKCVEIVKNDDGVIPCQNKFPFQVVHDANTLYIFAPSP
Mouse	PHLPP_MOUSE	PHLPP-PH1	T	KPHSTGSSERIQLSGMYNVRKGKMQLPVNRWTRRQVILCGTCLIVSSVKDSVSGKMHVLPLIGGKVEEVKKHQHCLAFSSSGPQSQTYYIC
Human	ARHGAP25-PH1H	ARHGAP25-PH1H	C	mslklprnwdfnlkveaakiarsrsvmtgeqmaafhpsstpnplerpikmgwlkkqrsivknwqqryfvlraqqlyyykd□eedtkpqgcmylpgctikeiatnpeeagkfvfeiipaswdqnrmg
Human	NM_001040118.1	CENTD2-PH1H	C	TCFEVNEREEAERPLHFAEKVLPILHGLGTDSHLVVKKHQAMEAMLLYLASRVGDTKHGMMKFREDRSLLGLGLPSGGFH□DRYFILNSSC
Human	NM_080612.2	GAB3-PH1H	T	MSAGDAVCTGWLVKSPPERKLQRYAWRKRWFVLRRGRMSGNPDVLEYYRNKHSSKPIRVIDLSECAVWKHVGPSFVRKEF□QNNFVFIV
Human	XM_928224.2	LOC653583-PH1H	T	SSGPAVPAITAPPTPPHPPGPRILDLRQHLEGWGHNPENCPHVQVSGCCCRGPLVKMGGRIKTWRKRWFCFDRQARRLAY□YADKEETKL
Human	NM_145739.1	OSBPL6-PH1H	T	MSSDEKGISPAHKTSTPTHRSASSSTSSQRDSRQSIHILERTASSSTEPSVSRQLLEPEPVPLSKEADSWEIIEGLKIGQ□TNVQKPDKHEGF
Human	NM_145753.1	PHLDB2-PH1H	T	EKEVKIRERQRAQARPLTRYLPVRKEDFDLRSHVETAGHNIDTCYHVSITEKTCRGFLIKMGGKIKTWKKRWFVFDRNKR□TFSYYADKHET
Human	NM_013385.2	PSCD4-PH1H	T	PFERFVSMNRGINNGSDLPEDQLRNLFDSIKSEPFSIPEDDGNDLTHTFFNPDREGWLLKLGGRVKTWKRRWFILTDNCL□YYFEFTTDKEP
Human	NM_022047.2	DEF6-PH1H	C	QVAQTTGGLSVWQFLELFNSGRCLRGVGRDTLSMAIHEVYQELIQDVLKQGYLWKRGHLRRNWAERWFQLQPSCLCYFGS□EECKEKRG
Human	NM_002972	SBF1-PH1H	T	MRQAARRSTSTLYSQFQTAESENRSYEGTLYKKGAFMKPWKARWFALDKTKHQLRYYDHRVDTECKGVIDLAEVEAVAPGTPTMGAPKTV
Human	NM_030962	SBF2-PH1H	C	MNLPSYQKRSLLHLPDSSMGEEQNSSISPSNGVERRAATLYSQYTSKNDENRSFEGTLYKRGALLKGWKPRWFVLDVTKHQLRYYDSGED
Human	NM_020715	PLEKHH1-PH1	C	MRGVSMSSLSSEGDYAIPPDACSLDSDYSEPEHKLQRTSSYSTDGLGLGGESLEKSGYLLKMGSQVKTWKRRWFVLRQGQIMYYKSPSDV
Dros	dCG12467-PH1	dCG12467-PH1	C	MLSFESGLSDDYALPPDAVSESTCMDASMPSLLMRQSYVDSPSKKIESLEKMGHLAKLGGKLKTWRKRWFVLKNGSLNYW□KSQHDVQR
Dros	CG5004-PH1-DR	CG5004-PH1-DR	C	SDRKRVLPKHQRPLTRYLPIFSPDLNLRHHIETAGHQIDPCPHVFVDAHSCRGYLHKLGATFHAWSRRWFVLDRQRSALI□YYSDKSERKPR
Dros	vap-PH1-DR	vap-PH1-DR	C	NHPVVNGIQPEFNQQYVVEKAAEKIYATLRECRDQIGLKKIKGIKHHGHLNKKSDKTTKWKQLYFALINDGSETQLCFYD□NPKKTKPKGLIDL
Dros	Akt1-PH1-DR	Akt1-PH1-DR	T	SAEKFSWQQSWPSRTSAAPTHDSGTMSINTTFDLSSPSVTSGHALTEQTQVVKEGWLMKRGEHIKNWRQRYFVLHSDGRL□MGYRSKPA
Dros	CG14366-PH1-DR	CG14366-PH1-DR	T	PKATPSSEESSSNSTKSPSHAPLDRKKSAGSIQALKSPITKRPPSTPVTLSGWLHKQGSDGLKVWRKRWFVLAEYCLYYY□KGPEEEKLLG
Dros	Grp1-PH1-DR	Grp1-PH1-DR	T	KIPQDDGNDLMHTFFNPDKEGWLWKQGGRYKSWKRRWFILNDNCLYYFEYTTDKEPRGIIPLENISVREIHDRSKPHCFE□LFATGGADIIKA
Dros	dBTK29A-PH1B(1-223)	dBTK29A-PH1-DR	T	**MMGTKHRNSHVNGSIKSSSSLRSSSKSFQAKMDLMSERLYDVVKSGSMVKRAQNKKRFTPVNYKHRWFELTKRTFSYFDVENVERRRER**
Dicty	CRAC-PH-DICTY	CRAC-PH-DICTY	T	mgkterkkellelfeyekikgdvsyssimkkaggngkgfldryfalhrnyilyyklgksslkpddkqepqgyinlmdcnp□ddtkeiaplmfqishkhrtyivkakdessmkqfltlliarirslekididkl
Dicty	AKT-PH-DICTY	AKT-PH-DICTY	T	mstapikhegfltkegggfkswkkrwfilkggdlsyyktkgelvplgvihlntsghiknsdrkkrvngfevqtpsrtyfl□cseteeerakwieilinerellnggkqpkksekvgvadfellnlvgkgsfgk
Dicty	PHDA-PH-DICTY	PHDA-PH-DICTY	T	mrlerdelllqalnyksikdkviystvmkkaggnkkgflsrlfvlykgfviyyktktlltspekpqggyidlrecdpskvk□tilddtdmtfqivhragrtflikgeepkpfrrffeickcvalkltqitftlpvekqtlln
Celegans	F59A6.5-PH1-CE	F59A6.5-PH1-CE	C	shcdvhvhascaprvnntcgmplqcatyyrenhttvsssgvsegrmngwlrvyrddmtgstwiaswammdltrisfytnd□gadlekpffsidlnkeqwvlrtgqempvdcddsmrannvlmi
Celegans	let-502-PH1-CE	let-502-PH1-CE	C	DMQTTQDALRDELKECKEELANRNVNTRYEDKRSLDSREGIPSSLSNQHIQMEGWLSLRDNTKKSRKPKWTNCFVALNEY□SFTIYVDEKA
Celegans	obr-1-PH1-CE	obr-1-PH1-CE	C	MPSLSEFLRKRRARQRRLQAVPSNNKKKSNNNNIMSSTSSGKSRRAASLSSINNFEHLASVEKAGWLNKWTNYLKGYRQR□WFVLDSNAT
Celegans	sec7-PH1-CE	sec7-PH1-CE	C	KIPDEVSTSGKGTVNDILLHAEREGWLFKQSSNPLFSGALSWKKRWFVLSENCLYYFDQMTDKEPKGIITLANVGIRKVE□APSRPFMFEIFS
Celegans	akt-1-PH1-CE	akt-1-PH1-CE	T	MSMTSLSTKSRRQEDVVIEGWLHKKGEHIRNWRPRYFMIFNDGALLGFRAKPKEGQPFPEPLNDFMIKDAATMLFEKPRP□NMFMVRCLQ
Celegans	akt-2-PH1-CE	akt-2-PH1-CE	T	MSTENAHLQKEDIVIESWLHKKGEHIRNWRPRYFILFRDGTLLGFRSKPKEDQPLPEPLNNFMIRDAATVCLDKPRPNMF□IVRCLQWTTVIE

ELEDMKMKISALKSEIQKEKANKGQSRAIERLKKKMFENEFLLLLNSPTIPFRIHNRNGKSYLFLLSSDYERSEWREAIQKLQKKDLQAFVLSSVELQVLTGSCFKLRTVHNIPVTSNKDDDESPGLYGF*

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FTSLDKPSVVSLQNLIVRDIANQAKGMFLISSGPPEMYEVHAASRDDRTTWIRVIQQSVRL**

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AFEISGSMIERILVSCTSQQDLHEWVEHLQKQTKVTSVSNPTIKPHSVPSHTLPSHPLTPSSKHADSKPVALTPAYHTLPHPSH*

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DLRLCSVKPCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWVQAVQASIASAYRESPDSCYSERLDRTASPSTSSIDSTTDSRERGVKG*

ENDKSTTPNGTININEVICLAIHKEDFYLNTGPIFIFEIYLPSERVFLFGAETSQAQRKWTEAIAKHFVPLFAENLTEADYDLIGQLFYKDCHALDQWRKGWFAMDKSSLHFCLQTQE*

PLRAMKFYLGVKKKMKPPTR*

ENERAVTPNREIRASEIVCLAVPPPDTHGFEHTFEVYTEGERLYLFGLESAEQAHEWVKCIAKAFVPPLAEDLLARDFERLGRLPYKAGLSLQRAREGWFSLRGSELRAVFPEGP*

VHETEKHEKQQWYLCCDTQMELREWFATFLSVQHDGLVWPSEPSRVSRAVPEVRMGSVSLIPLRGSENEMRRSVAAFTADPLS*

DVSIHGAVGASELANTAKADVPYILKMESHPHTTCWPGRTLYLLAPSFPDKQRWVTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDR*

NDSVWYLRAQDPEHRQQWVDAIEQHKTESGYGSESSLRRHGSMVSLVSGASGYSATSTSSFKKGHSLREKLAEMETFRDI*

QLELACETQEEVDSWKASFLRAGVYPERVGDKEKASETEENGSDSFMHSMDP*

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ENELKIESVERSFILSASSAAERDDWLEAISSSIEEYAKKRITFCPSRSLDEDSERKEEVSPLGAKA*

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GIINLSTAQVEYSEDQQAMVKTPNTFAVCTKHRGVLLQALNDKDMNDWLYAFNPLLAGTIRSKLPRRCPSQPKY*

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FTVVFHGRRPNLDLVANSVEEAQIWMRGLQLLVDLVASMDHQEQMDQ*

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QANDQKDLKDWVEALNQASKITVPKAGTVPLATEVLKNLTAPPTLEKKPQVAYKTEIIGGVVVQTPI*

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CYH1_MOUSE	PSCD1-PH1	T	VERFIAMNRGINDGGDLPEELLRNLYES
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NM_002972.1	SBF1-PH1	C	STAPHHRRSLGVYLQEGPVGSTLSLSL
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NM_001040118.1	CENTD2-PH1	C	TCFEVNEREEAERPLHFAEKVLPILHGL
NM_133268.1	OSBPL1A-PH1	C	HKQCALKLLRSGADPNLKNKNDQKPLD
NM_020715.2	PLEKHH1-PH1	C	YAIPPDACSLDSDYSEPEHKLQRTSSYS

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NV

Cerevisiae	SLM2-PH1	NP_01435	C		448..553	20.63529	8.396013	9	EVKSGFL
Cerevisiae	BOI1-PH1	NP_00946	C		779..893	16.96294	8.511027	9	ADCSGW
Cerevisiae	BUD4-PH1	NP_01262	C		1306..1412	0.692037	-2.74539	7	IYKEGYLL
Cerevisiae	ATG26-PH	NP_01329	C		241..333	0.510442	-5.36333	4	VKMSGNL
Pombe	reserved_r	NP_59415	C		722..835	6.859368	5.492493	4	AQKEGVL
Pombe	SPAC26A	CAA93232	C		722..835	6.859368	5.492493	4	AQKEGVL
Pombe	csx2-PH1	NP_59589	C		513..612	5.550006	0.909318	5	SAKQGLL
Pombe	SPAPYUG	NP_59470	C		584..684	5.464721	5.732295	6	LLCDGYL
Pombe	ksg1-PH1	NP_58844	C		<495..570	3.883014	1.060725	10	ISKIGTLN
Pombe	SPAC11E	NP_59493	C		683..806	-0.83699	-9.89105	8	YIKQGILK
Pombe	SPCPB16	NP_58802	C		225..317	-7.08751	-2.91975	6	VLMQGTI

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QDG....gdLKGKIENRFFKLHG.......SQLSGYHEI-......-SRKAKIDINLL..KVTKVLRN.........ediqadnggqrn
NIRT......KLIRSTRYWCVLKN.......HLFSMYTSST....eIYFPVLTIDLREV.qKIETQKHT........................lng
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LKYI......ENSGLVSRYFYLKD.......NILYFAENRN......SPVLGTIHLKDA..QVNRYNAN..........lpifsiidpphef
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SATKTFKLYTdES....................-TFKFNADSEFSAKSWVNALKKEQF
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.NNEHGWVVETpTK....................-SWSFEDPNG-PASAWVELLDKASS
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Celegans	sec7-PH1	NP_498764	C	263..391	49.55871	12.60603
Celegans	let-502-PH1	NP_491440	C	952..>1034	13.01202	2.55186
Celegans	obr-1-PH1	NP_499448	C	64..152	11.7475	10.13831
Celegans	F59A6.5-PH1	NP_494921	C	834..940	11.48228	0.762221
Cerevisiae	SLM2-PH1	NP_014351	C	448..553	20.63529	8.396013
Cerevisiae	BOI1-PH1	NP_009468	C	779..893	16.96294	8.511027
Cerevisiae	BUD4-PH1	NP_012625	C	1306..1412	0.692037	-2.74539
Cerevisiae	ATG26-PH1	NP_013290	C	241..333	0.510442	-5.36333
Drosophila	CG5004-PH1	NP_573195	C	1143..1237	30.65888	7.631296
Drosophila	vap-PH1	NP_996482	C	394..483	11.86322	3.56381
Pombe	reserved_name_rga2-PH1	NP_594152	C	722..835	6.859368	5.492493
Pombe	SPAC26A3.09c-PH1	CAA93232	C	722..835	6.859368	5.492493
Pombe	csx2-PH1	NP_595897	C	513..612	5.550006	0.909318
Pombe	SPAPYUG7.03c-PH1	NP_594704	C	584..684	5.464721	5.732295
Pombe	ksg1-PH1	NP_588442	C	<495..570	3.883014	1.060725
Pombe	SPAC11E3.11c-PH1	NP_594936	C	683..806	-0.83699	-9.89105
Pombe	SPCPB16A4.02c-PH2	NP_588026	C	225..317	-7.08751	-2.91975
Celegans	akt-2-PH1	NP_001024612	T	13..114	20.79403	11.46032
Celegans	akt-1-PH1	NP_001023647	T	16..117	9.549298	12.17148
Drosophila	Grp1-PH1	NP_001036375	T	356..480	65.83189	24.28059
Drosophila	Akt1-PH1	NP_732113	T	107..210	34.2812	16.92682
Drosophila	CG14366-PH1	NP_650310	T	375..468	11.99604	5.974204
Celegans	mtm-5-PH1	NP_508888		1646..1742	16.80814	12.46176
Cerevisiae	OSH3-PH1	NP_011940		224..313	17.18968	8.150776
Cerevisiae	BOI2-PH1	NP_011039		771..882	15.47084	6.390439
Cerevisiae	OPY1-PH1	NP_009687		218..315	7.47558	-0.75313
Cerevisiae	SLM1-PH1	NP_012161		471..577	7.089197	0.307673
Cerevisiae	SWH1-PH1	NP_009421		284..377	2.664051	1.000236
Cerevisiae	SPO14-PH1	NP_012956		498..660	1.270814	1.375714
Cerevisiae	CLA4-PH1	NP_014101		64..174	-1.96565	-6.26106
Cerevisiae	OSH2-PH1	NP_010265		292..384	-2.48795	2.301501
Drosophila	Btk29A-PH1	NP_723369		43..182	21.29646	8.839298
Drosophila	Sbf-PH1	NP_731633		1872..1972	18.98951	11.60579
Drosophila	CG12467-PH1	NP_477389		654..742	15.5075	16.54281
Pombe	SPCPB16A4.02c-PH1	NP_588026		28..106	11.78241	3.929772
Pombe	SPAC26A3.10-PH1	NP_594153		529..630	10.73578	2.185209
Pombe	pob1-PH1	NP_596828		701..806	6.27789	1.345219
Pombe	SPBC1289.04c-PH1	CAB38684		701..806	6.27789	1.345219
Pombe	SPBC17G9.08c-PH1	CAB52806		513..612	5.550006	0.909318
Pombe	SPAC6G9.04-PH1	NP_594113		1053..1154	4.629944	-3.21248
Pombe	SPCC576.15c-PH1	CAA21194		<495..570	3.883014	1.060725
Pombe	SPAC19A8.02-PH1	NP_593790		292..388	1.384858	0.630635
Pombe	plc1-PH1	NP_594734		161..271	1.197574	5.504969
Pombe	SPAC22F8.11-PH1	CAB52721		161..271	1.197574	5.504969
Pombe	SPAC637.13c-PH1	NP_594631		303..403	0.276965	2.858547
Pombe	SPBC2F12.05c-PH1	NP_595710		257..340	-0.45491	4.188521
Pombe	SPAC23H3.01-PH1	NP_001018249		<707..768	-1.7977	-2.02607
Pombe	SPAC19A8.01c-PH1	CAB16232		<285..346	-1.7977	-2.02607
Pombe	SPAC1F5.09c-PH1	NP_592864		26..122	-4.7572	-11.8294
Pombe	SPAC2F7.16c-PH1	NP_592986		394..510	-7.01332	-8.7836
Pombe	SPBC428.07-PH1	NP_595185		<194..256	-9.84818	-9.0019

Pombe	SPAC23H4.01c-PH1	NP_593405	152..241	-14.2623	1.69321
Pombe	SPCp054-PH1	NP_588075	805..898	-23.5296	-10.8256
Pombe	SPCC4B3.15-PH1	CAB60689	805..898	-23.5296	-10.8256

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10 AEREGWLFKQSsnplfsGALSWKKRWFVLSE.......NCLYYFDQMT.....dKEPKGIITLANV..GI
 8 IQMEGWLSLRD.ntkksRKPKWTNCFVALNE.......YSFTIYVDE-......-KAVSVILLIEA..GAMA
 6 VEKAGWLNKWT.....nYLKGYRQRWFVLDS......nATLSYYRNPS...evgHTCRGSINLQEA..
 3 GRMNGWLRVYR...ddmTGSTWIASWAMMDL.......TRISFYTNDG...adIEKPFFSIDLNKE..
 9 EVKSGFLEKRS.....kFLKSYSRGFYVLTP.......SFLHEFKTPD..khkfSTPLMSIPLVEC..TVTE
 9 ADCSGWMSKKG....tgAMGTWKQRFFTLHG.......TRLSYFTNTN.....dEKERGLIDITAH..RV
 7 IYKEGYLLQDG....gdLKGKIENRFFKLHG.......SQLSGYHEI-......-SRKAKIDINLL..KVTKVL
 4 VKMSGNLNIRT......KLIRSTRYWCVLKN.......HLFSMYTSST....eIYFPVLTIDLREV.qKIETQ
 8 HSCRGYLHKLG.....aTFHAWSRRWFVLDR.....qrSALIYYSDKS.....eRKPRGGAYFATI.dEV
 9 IKHHGHLNKKS.....dKTTKWKQLYFALIN...dgseTQLCFYDNPK.....kTKPKGLIDLSCA..YLY
 4 AQKEGVLLKYI......ENSGLVSRYFYLKD.......NILYFAENRN......SPVLGTIHLKDA..QVNRY
 4 AQKEGVLLKYI......ENSGLVSRYFYLKD.......NILYFAENRN......SPVLGTIHLKDA..QVNRY
 5 SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK...qslELHTEPIDLLMA..T
 6 LLCDGYLCQQG.....gDCPYWRRRYFQLIG.......SKLVAFQQFS......KVRRATIDLSEA.tHIV
10 ISKIGTLNVYSfrffssLFRKRKPRTFILTN.....fgRYLCVASDGE....grKTVKEEIPIKSV..GMRC
 8 YIKQGILKFQSeshkfrKKEVWSTVLAVLQR.......DVFTLYNLNTdpkdldISKVGKPVIKTT..IIA
 6 VLMQGTIHWLH.....gNLHRWSKCWAVVRG.......YGMTIYNTNR.....eYKPVKVIPIADI.qDV
 9 IVIESWLHKKG.....eHIRNWRPRYFILFR......dGTLLGFRSKP.....kEDQPLPEPLNNF..MIRD
 9 VVIEGWLHKKG.....eHIRNWRPRYFMIFN......dGALLGFRAKP.....kEGQPFPEPLNDF..MI
12 PDKEGWLWKQG.....gRYKSWKRRWFILND.......NCLYYFEYTT.....dKEPRGIIPLENI..SVR
 8 VVKEGWLMKRG.....eHIKNWRQRYFVLHS......dGRLMGYRSKPsastpsDFLLNNFTVRGC
 8 VTLSGWLHKQG....sdGLKVWRKRWFVLAE.......YCLYYYKGPE.....eEKLLGSVLLPSY..R
 8 PLCTGYLSKRG.....aKLKLWVPRFFVLYP.....dsPKVYYYEDFE.nwktaEKPSGCIDLVDF..K
10 RYLQGYLLKKR....rkRLQGFKKRFFTLDF.....ryGTLSYYLNDH.....nQTCRGEIVISLS..SVS
 9 ADFSGWMSKKG....sgAMSTWKTRFFTLHG.......TRLSYFSSTT.....dTRERGLIDITAH..RV
14 QVCSGILYTKVkkkklfNRAKWQKFNVELTN.....tsFNLYSFKTG-......-KLKKSIKLDKI.iDCIEL
11 EIKSGFLERRS.....kFLKSYSKGYYVLTP.......NFLHEFKTAD..rkkdLVPVMSLALSEC..TVTE
 6 PTYKGYLKKWT.....nFAQGYKLRWFILSS......dGKLSYYIDQA...dtkNACRGSLNMSSC..SL
 7 QGKQGYLVIRSkhafkdMIDRHTTKWFLVRN.......SYLTYVSDLS.....sTTPLDVFLIDWK.fKV
 9 KKKSGWVSYKD...dgiLSFIWQKRYLMLHD.......SYVALYKNDK....qnDDAILKIPLTSI.iSVS
 8 PTYKGFLKKWT.....nFAHGYKLRWFILSG......dGNLSYYKDQS....hvDRPRGTLKVSTC..RL
13 VVKSGSMVKRAqnkkrfTPVNYKHRWFELTK.......RTFSYFDVEN...verRRERGRIHLKGV.rL
 7 RTHEGHLYKRG.....aLLKGWKQRWFVLDS.....ikHQLRYYDTSE.....dTAPKGIIELAEV.qSV
10 LEKMGHLAKLG.....gKLKTWRKRWFVLKN.......GSLNYWKSQH...dvqRKPQGQIQLDEV.c
 6 VLKSGWLIKKG.....hATSTKKQLWAVLRR.......DQLSFYKDE-......---------KDI.sAVAYYKEK.
 6 IFKEGLLLVFGtdlamvSKAAWHKHWIVVEN.......GSLWEYANWK...dsvKSNVSSISLKHA..
 8 ADCHGWMRKRS.....dRYGVWKSRYFVLKG.......TRLSYYHSLN.....dASEKGLIDMTSH..R
 8 ADCHGWMRKRS.....dRYGVWKSRYFVLKG.......TRLSYYHSLN.....dASEKGLIDMTSH..R
 5 SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK...qslELHTEPIDLLMA..T
 9 WHRRGMISYKKsknnrwVAGYWKKKYCIVDS.......GKLIFYKSDHnacsnvSPIHREFGLQSC.
10 ISKIGTLNVYSfrffssLFRKRKPRTFILTN.....fgRYLCVASDGE....grKTVKEEIPIKSV..GMRC
 6 TKRQGWLLRNIssskadNKAIWRKYWFFVDN.......GYVGYLINDA...nggVFESEKIGVLLC..K
12 SIQNGCSLLRI......TKKKVRQRKVSLDP.....isGYLMLDKNTG....kaYKKLCVDDIKEI.rQGRD
12 SIQNGCSLLRI......TKKKVRQRKVSLDP.....isGYLMLDKNTG....kaYKKLCVDDIKEI.rQGRD
10 PIMAGYLIRKT......SFLKKKQRGFYAFT.....hsGYLYEFKSSD..slqdPEPEFALYIPDC..LIGR
 7 QHMSGYLKKWT.....nYKSGYKLRWFTLNN.......GVLSYYKNQD...dasSACRGSINLKLA..R
 3 AQKKAYERRYK......NFTTTSSSFDTLQG.....idTEAMEYEFPKtppleeFSPDTSYSLVNA.fAY
 3 AQKKAYERRYK......NFTTTSSSFDTLQG.....idTEAMEYEFPKtppleeFSPDTSYSLVNA.fAY
 8 IIRSGWVMLKE...dkmKYLPWTKKWLVLSS.......NSLSIYKGSK.....sESAQVTLLLKDI.qKVE
 5 HGKEGFATLKRccnttmMKTRSQPFWIIVSE.......SCIILCDNML......SMQPADVFIWDV..DF
 2 PSLASEQMHDS.....dADSLFQSANDHLNRakatqdcRGLLFYSKSQ....stSVPSGIINLTDA.vS
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10 QIISGTLLKKR....rkKGQGYARRYFTLNM.....veGTISYYANEN.....sSVMRGKIPLSIA..VISV
 7 LYNEGYLYRLE......-DSSIRRRFVVLRS.......KQLNFYAEKG......GQYLDTFQLSKT..VVSIP
 7 LYNEGYLYRLE......-DSSIRRRFVVLRS.......KQLNFYAEKG......GQYLDTFQLSKT..VVSIP
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IRKVEAP...........................SRPFMFEIFSlSD..gqikackteqdgrlvegrhSIYKICAVNDEDMRSWINAISRMM
HVR-...........................-HVTAADLRNvDD................sqlpKIFHIMYDD--------ASCNSSRH
RVHTDKT-...........................--TSCIVISGqSQ.....................-TFHVKPQNEMDRQQWTNSLEYMRH
QWVLRTGQ.................empvdcddsmRANNVLMIKMpRR.....................-CLYILAPSQPSARRWAECLQT
EHSKK.....................tksnseQGKNKFILRTnSN...............glihrgHNWVFKVDSYDDMIEWFGNIKALSS
LPASDD...............drlislyaaslgKGKYCFKLVPpQP..........gskkgltftepRVHYFAVENKSEMKAWLSAIIKAT
RN..........ediqadnggqrnftdwvLFNECFQLVFdDG.....................ERITFNAECSEEKSDWYNKLQEVVE
QKHT........................lngSATKTFKLYTdES.....................-TFKFNADSEFSAKSWVNALKKEQF
YLDHLN......................asksgRPHCTFIVKTkKR.....................-SYNLQAASDSAARIWIDAIITGAQ
QCHDS.........................lwERPYCFQIVErAL.................pclaTVTYLCAPSQESYVEWINSLKAQCD
NAN..........lpifsiidpphefltgeNYQSAFVIQEkQT..............etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
NAN..........lpifsiidpphefltgeNYQSAFVIQEkQT..............etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
TVRPAQSV...........................SRKFCFEVITpQT.....................-KRTYQATSKAEMHSWIEAIQYSIS
DNHY.................sdeeelegylYFESGFRIIFsNG.....................DYIDFYAETVGEKDEWMSTLRQHLG
RMVK...........................NNEHGWVVETpTK.....................-SWSFEDPNG-PASAWVELLDKASS
SLAKP...............fpssedavvlksTNSLYFDLETsSQ.....................LKLRFAGPSPKDAQGWIDALNYWAA
AEINVP.........................esSHKYFFTVITqNK.....................-PIEFRVDNEDSLILWVAALKTSID
AATV.......................cldkPRPNMFIVRClQW..................ttvIERTFYADSADFRQMWIEAIQAVSS
KDAATM.......................lfekPRPNMFMVRClQW..................ttvIERTFYAESAEVRQRWIHAIESISK
EIHDR...........................SKPHCFELFAtGG.adiikacktdsegkvvegkhTVYRMSAATEEDQQEWIKRLTQS
..QIMTVDRP...........................-KPFTFIIRGlQW..................ttvIERTFAVESELERQQWTEAIRNVSS
VSACLPE........................dkiYRKFAFKCEHqNM.....................RTYWLAADNSEAMMQWVRALAAASL
SFNLEQT...........................GRRGLIELHMkNK.....................-THRLLSENINEAIRWKECIEQVIR
ANKK-...........................--DKIIIIDSgME.....................-VWVLKATTKENWQSWVDALQTCFD
VPAKED...............dklvslyaastgKGRYCFKLLPpQP..........gskkgltftqpRTHYFAVDNKEEMRGWMAALIKT
DNN.......................skmkNDDTNFALITfDE.....................-RLSFKAANDQDMVDWIINFKSGIL
EHSRK..................nstsspnstGSDAKFVLHAkQN...............giirrgHNWVFKADSYESMMSWFDNLKILTS
LHLDSS-...........................-EKLKFEIIGgNN...................gvIRWHLKGNHPIETNRWVWAIQGAIR
RFSGNKleefgiendannildkngkskthqkksNISSKLLLLTlEN...................seRKLKIICKSESSLKQWMSSIIKM
RTQL-...........................-KQYCFELVRcSDrnsvssgsssslnvssdsnskKSIYIATKTESDLHSWLDAIFAKCP
LHIDSS-...........................-EKLNFELLGgIT...................gtTRWRLKGNHPIETTRWVNAIQSAIR
LVEEATVS...................geggdpfaPDGYPFQVGYcEIgngggsgvgiegqqsgravpqYTLYVIANSEKERSEWIR
TAAQPA....................qigakgvDEKGFFDLKTsKR.....................-IYNFYAINANLAQEWIEKLQACLQ
RINRAEG-...........................--ASTFEIDTgKK.....................-VYYLTADSHATMDDWIRVLQNVQR
...........................-SPKTFFLYLnEK.....................-IIRLIATSNEDAEEWVHVLRSTTG
SADKVRKQ...........................GRRFCFEVVTpKL.....................-KRLYQATSAEEMDSWIEAICEAAK
VTKTDDI........................vlsGGKTAIKLIPpAP.........gaakaavmftppKVHYFTCENNEELHRWSSAFLKAT
VTKTDDI........................vlsGGKTAIKLIPpAP.........gaakaavmftppKVHYFTCENNEELHRWSSAFLKAT
TVRPAQSV...........................SRKFCFEVITpQT.....................-KRTYQATSKAEMHSWIEAIQYSIS
LLASPNLPP.......................sinsNRNNVFYLNIpGN.....................ECYLFEAPSVLAMNEWIHSLNFNAA
RMVK...........................NNEHGWVVETpTK.....................-SWSFEDPNG-PASAWVELLDKASS
KFSVLPSN...........................HRKFCFQIKTkSV.....................-SYILQAETHMEMLEWGSVINNARE
DARNY..................reqykisseNEKRWFTIIYcAD..................nklKAMHMISPTLDAHNQWIMALEGLKT
DARNY..................reqykisseNEKRWFTIIYcAD..................nklKAMHMISPTLDAHNQWIMALEGLKT
PSE-...........................-KKPKFKITGkDA.............tkkifgarNDYAFRASNNTELMRWWEALNTHIA
LVHDPK-...........................-QPTVFQVIGkGS.....................VRYSVKANSPVEAKKWIAAISSAIE
YCDRDKK..........................nVRNCSFTVIFrDG.....................SEETLCAPTEESMIEWVAKINYIST
YCDRDKK..........................nVRNCSFTVIFrDG.....................SEETLCAPTEESMIEWVAKINYIST
ERSKS-...........................-RTFCFKLRFkSS...............tknfeiQACELSVADNMECYEWMDLISSRAL
EITRKN.............frkahskdtnekirLSHHSFKIKNrQK.....................-VMKLSVRSG----RWLQQFINSVQ
SIEPGTG-...........................---NKFTINFnNG.....................KSETLEALDPESKNTWITDLKNAIA
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AAE-...........................--THEINVDSgVE.....................-LWNLRAHTHQDWLRWCNALEKAKN
MVN...................fseavsnlGLVAGILATSvDR.....................RHVQLFADSKKVCQKWLQVMNSRSF
MVN...................fseavsnlGLVAGILATSvDR.....................RHVQLFADSKKVCQKWLQVMNSRSF
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A

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vap-PH1-D	NP_99648	C	IKHHGHL	T_Dros
CG5004-P	NP_57319	C	HSCRGYL	T_Dros
CG14366-	NP_65031		VTLSGWL	T_Dros
CG12467-	NP_47738	T	LEKMGHL	T_Dros
Btk29A-PH	NP_72336	T	VVKSGSM	T_Dros
Akt1-PH1-	NP_73211	T	VVKEGWL	T_Dros
Grp1-PH1-	NP_00103	T	PDKEGWL	T_Dros

F59A6.5-P	NP_49492	C	GRMNGW	T_Celegans
obr-1-PH1-	NP_49944	C	VEKAGWL	T_Celegans
let-502-PH	NP_49144	C	IQMEGWL	T_Celegans
akt-1-PH1-	NP_00102	T	VVIEGWL	T_Celegans
akt-2-PH1-	NP_00102	T	IVIESWLH	T_Celegans
sec7-PH1-	NP_49876	C	AEREGWL	T_Celegans

Type of file: table
Label: Table 5
Filename: mmc10.xls

Supplementary Table 4, Park et al:
Scoring of tested mouse PH-domains (used to make Fig. 5C)

Species	Name	Score	NP_number	Cloned and Tested Translocating?
Mouse	PSCD3-PH	100.6	NP_035312	T
Mouse	PSCD2-PH	99.9	NP_035311	T
Mouse	PSCD1-PH	98.1	NP_035310	T
Mouse	AKT3-PH	66.5	NP_035915	T
Mouse	AKT2-PH	64.9	NP_031460	T
Mouse	AKT1-PH	64.6	NP_033782	T
Mouse	RASA2-PH	60.2	NP_444498	T
Mouse	TEC-PH	58.5	BAE23957	T
Mouse	BTK-PH	57.5	NP_038510	T
Mouse	ITK-PH	54.6	NP_034713	T
Mouse	GAB1-PH	50.1	NP_067331	T
Mouse	GAB2-PH	44.4	NP_034378	T
Mouse	PLEKHA1-PH	40.8	NP_598703	T
Mouse	PLEKHA2-PH2	38.4	NP_112547	T
Mouse	DAPP1-PH	37.0	NP_036062	T
Mouse	PHLDB1-PH	36.4	NP_705765	T
Mouse	SH3BP2-PH	34.5	NP_036023	T
Mouse	PLEK2-PH	33.8	NP_038766	T
Mouse	PLEK2-PH2	31.7	NP_038766	T
Mouse	PDPK1-PH	28.1	NP_001074242	T
Mouse	MYO10-PH	25.5	NP_062345	T
Mouse	OSBPL3-PH	24.6	NP_082157	T
Mouse	CNKSR2-PH	23.5	NP_808419	T
Mouse	OSBPL7-PH	23.4	NP_001074903	T
Mouse	PHLPP-PH	20.2	XP_990044	T
Mouse	FGD6-PH2	19.1	NP_444302	T
Mouse	PLEK-PH2	17.0	NP_062422	N
Mouse	PLEKHO1-PH	5.6	NP_075809	N
Mouse	MYO10-PH2	4.7	NP_062345	N
Mouse	IRS1-PH	4.5	NP_034700	N
Mouse	PLEKHB2-PH	4.5	NP_663491	N
Mouse	SKAP2-PH	4.3	NP_061243	N
Mouse	PLEKHA5-PH	3.5	NP_659169	N
Mouse	DGKD-PH	3.4	XP_911321	N
Mouse	TRIOBP-PH	3.3	NP_613045	N
Mouse	RASAL1-PH	2.8	NP_038860	N
Mouse	2610034M16Rik-PH	1.7	NP_081686	N
Mouse	M-RIP-PH2	0.6	NP_957697	N
Mouse	PLEKHM2-PH	0.2	XP_985312	N
Mouse	PSD3-PH	-2.2	NP_808366	N
Mouse	PSD2-PH	-2.2	NP_082983	N
Mouse	CENTD2-PH	-2.3	NP_001035201	N
Mouse	M-RIP-PH	-3.5	NP_957697	N
Mouse	CENTB5-PH	-4.3	NP_997106	N
Mouse	DNM2-PH	-4.7	NP_001034609	N
Mouse	SWAP70-PH	-5.0	NP_033328	N
Mouse	ARHGAP10-PH	-5.1	NP_598723	N

Mouse	DNM1-PH	-5.4	NP_034195	N
Mouse	OPHN1-PH	-6.6	NP_443208	N
Mouse	PLEKHB1-PH	-7.1	NP_038774	N
Mouse	PLEKHJ1-PH	-7.9	NP_076389	N
Mouse	RALGPS2-PH	-8.0	NP_076373	N
Mouse	FARP1-PH2	-8.2	NP_598843	N
Mouse	DOK4-PH	-8.2	NP_444476	N
Mouse	CENTD1-PH	-8.7	XP_001001345	N
Mouse	PLEKHF1-PH	-8.8	NP_077724	N
Mouse	AFAP-PH	-8.8	NP_081649	N
Mouse	PLEKHA3-PH	-9.1	NP_112546	N
Mouse	PLCD1-PH	-9.3	NP_062650	N
Mouse	2610034M16Rik-PH2	-9.6	NP_081277	N
Mouse	VEPH-PH	-10.6	NP_082633	N
Mouse	CADPS-PH	-11.4	NP_001036082	N
Mouse	PLCL2-PH	-11.9	NP_038908	N
Mouse	RASA4-PH	-11.9	NP_598675	N
Mouse	ABR-PH	-12.4	NP_942598	N
Mouse	PRKCM-PH	-12.8	NP_032884	N
Mouse	RASGRF1B-PH	-13.0	NP_001034744	N
Mouse	FGD6-PH	-14.0	NP_444302	N
Mouse	PLCD4-PH	-14.4	NP_683739	N
Mouse	COL4ABP3-PH	-14.4	NP_075909	N
Mouse	PLEKHM1-PH	-14.8	NP_898855	N
Mouse	SH2B2-PH	-15.0	NP_061295	N
Mouse	DOK1-PH	-15.3	NP_034200	N
Mouse	NGEF-PH	-15.7	NP_063920	N
Mouse	KIF1A-PH	-16.0	NP_032466	N
Mouse	CIT-PH	-16.2	NP_031734	N
Mouse	PLEKHA2-PH	-16.5	NP_112547	N
Mouse	DDEF1-PH	-17.3	NP_034156	N
Mouse	TIAM1-PH2	-17.4	NP_033410	N
Mouse	FGD1-PH2	-17.7	NP_032027	N
Mouse	SNTA1-PH	-17.9	NP_033254	N
Mouse	PLD2-PH	-18.1	NP_032902	N
Mouse	CENTD1-PH2	-18.3	XP_001001345	N
Mouse	FGD2-PH	-18.7	NP_038738	N
Mouse	GEFT-PH	-18.7	NP_082303	N
Mouse	NET1-PH	-18.8	NP_062645	N
Mouse	SNTB2-PH	-19.0	NP_033255	N
Mouse	KIF1B-PH	-19.2	NP_997565	N
Mouse	DOK5-PH	-19.3	NP_084037	N
Mouse	TIAM1-PH	-19.5	NP_033410	N
Mouse	SH2B1-PH	-19.9	NP_035493	N
Mouse	PLEKHC1-PH	-20.7	NP_666166	N
Mouse	APBB1IP-PH	-21.3	NP_062329	N
Mouse	ADRPK1-PH	-21.3	NP_570933	N
Mouse	SPNB2-PH	-22.6	NP_787030	N
Mouse	ITSN1-PH	-22.9	NP_034717	N
Mouse	CENTD2-PH2	-24.0	NP_001035201	N
Mouse	FARP1-PH	-24.3	NP_598843	N
Mouse	TIAM2-PH	-24.5	NP_036008	N
Mouse	PLD1-PH	-25.5	NP_032901	N

Mouse	SNTB1-PH	-25.6	NP_057876	N
Mouse	RASGRF2-PH	-25.9	NP_033053	N
Mouse	RASGRF2-PH2	-27.2	NP_033053	N
Mouse	ARHGEF7-PH	-28.9	NP_059098	N
Mouse	OSBPL5-PH	-29.1	NP_077251	N
Mouse	KALRN-PH	-29.5	XP_998128	N
Mouse	RASGRF1A-PH	-30.3	NP_035375	N
Mouse	ARHGEF3-PH	-30.7	NP_082147	N
Mouse	ROCK1-PH	-30.8	NP_033097	N
Mouse	FGD1-PH	-31.6	NP_032027	N
Mouse	FGD1-PHB	-31.6	NP_032027	N
Mouse	GRB14-PH	-32.5	NP_057928	N
Mouse	FGD3-PH	-32.9	NP_056574	N
Mouse	MCF2-PH	-33.0	NP_573460	N
Mouse	ITSN2-PH	-33.0	NP_035495	N
Mouse	AKAP13-PH	-34.6	XP_984499	N
Mouse	ARHGEF2-PH	-35.0	NP_032513	N
Mouse	ARFGEF18-PH	-35.0	NP_084389	N
Mouse	MCF21-PH	-35.4	NP_835177	N
Mouse	GRB7-PH	-36.7	NP_034476	N
Mouse	RASGRF1A-PH2	-38.5	NP_035375	N
Mouse	RGNEF-PH	-39.3	NP_036156	N
Mouse	VAV3-PH	-40.8	NP_065251	N
Mouse	GRB10-PH	-42.0	NP_034475	N
Mouse	VAV2-PH	-42.1	NP_033526	N
Mouse	VAV1-PH	-43.5	NP_035821	N
Mouse	VAV2-PHB	-43.9	NP_033526	N
Mouse	SOS1-PH	-46.6	NP_033257	N
Mouse	SOS2-PH	-48.4	XP_992919	N

Sequence
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PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.....dKEPRGIIPLENL..SIREVDDP..........................RKPNCFELYIpNNkgqlikackteadgrvvegnhMVYRISAPTQEEKDEWIKSIQAAVS
PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.....dKEPRGTIPLENL..SIREVEDS..........................KKPNCFELYIpDDkdqvikackteadgrvvegnhTVYRISAPTPEEKEDWIKCIKAAIS
IVKEGWVQKRG.....eYIKNWRPRYFLLKT......dGSFIGYKEKP.qdvdlPYPLNNFSVAKC..QLMKTERP..........................-KPNTFIIRCIQW.................ttvIERTFHVDTPEEREEWTEAIQAVAD
VIKEGWLHKRG.....eYIKTWRPRYFLLKS......dGSFIGHKERPeapdqtLPPLNNFSVAEC..QLMKTERP..........................-RPNTFVIRCIQW.................ttvIERTFHVDSPDEREEWMRAIQMVAN
IVKEGWLHKRG.....eYIKTWRPRYFLLKN......dGTFIGYKERPqdvdqrESPLNNFSVAQC..QLMKTERP..........................-RPNTFIIRCIQW.................ttvIERTFHVETPEEREEWATAIQTVAD
HLKEGEMYKRAqgrtriGKKNFKKRWFCLTS.......RELTYHRQQG......KDAIYTIPVKNI.IAVEKLEEG........................sfNKKNMFQVIHtEK....................-TLYIQANNCVEANEWIDVLCRVSR
TILEEILIKRSqqkkktSPLNYKERLFVLTK.......SVLSYYEGRA....ekKYRKGVIDISKI..KCVEIVKN...................ddgvipcQNKFPFQVVHdAN....................-TLYIFAPSPQSRDRWVKKLKEEIK
VILESIFLKRSqqkkktSPLNFKKRLFLLTV.......HKLSYYEYDF.ergrrGSKKGSIDVEKI..TCVETVIPeknppperqiprrgeessemeqisiieRFPYPFQVVYdEG....................-PLYVFSPTEELRKRWIHQLKNVIR
ILLEEQLIKKSqqkrrtSPSNFKVRFFVLTK.......ASLAYFEDRH...gkkRTLKGSIELSRI..KCVEIVKS....................disipcHYKYPFQVVHdNY....................-LLYVFAPDCESRQRWVLTLKEETR
VVCSGWLRKSP.pekklKRYAWKRRWFVLRSgrltgdpDVLEYYKNDH.....aKKPIRIIDLNLC.qQVDAGLTF.....................nkkefENSYIFDINTiDR....................-IFYLVADSEEDMNKWVRCICDICG
VVCTGWLRKSP.pekklRRYAWKKRWFILRSgrmsgdpDVLEYYKNEH.....sKKPLRIINLNLC.eQVDAGLTF.....................nkkelQDSFVFDIKTsER....................-TFYLVAETEADMNKWVQSICQICG
VIKAGYCVKQG.....aVMKNWKRRYFQLDE.......NTIGYFKSEL.....eKEPLRVIPLKEV.hKVQECKQS.......................dimMRDNLFEIVTtSR....................-TFYVQADSPEEMHSWIKAVSGAIV
LIKSGYCVKQG.....nVRKSWKRRFFALDD.......FTICYFKCEQ.....dREPLRTIPLKDVlkTHECLVKS......................gdllMRDNLFEIITtSR....................-TFYVQADSPEDMHSWIEGIGAAVQ
GTKEGYLTKQG.....gLVKTWKTRWFTLQR.......NELKYFKDQ-......-MSPEPIRILDL.tECSAVQFD.......................ysqERVNCFCLVFpFR....................-TFYLCAKTGVEADEWIKILRWKLS
KVCRGYLIKMG.....gKIKSWKKRWFVFDR.....lkRTLSYYVDKH.....eTKLKGVIYFQAI.eEVYYDHLR....................saakspNPALTFCVKThDR....................-LYYMVAPSAEAMRIWMDVIVTGAE
VAKAGYLHKKG..gtqlQLLKWPLRFVIIHK.......RCIYYFKSST.....sASPQGAFSLSGY.nRVMRAAEE.......................ttsNNVFPFKIIHiSK..................khRTWFFSASSEDERKSWMALLRREIG
VLKEGFLVKRG.....hIVHNWKARWFILRQ.......NTLLYYKLEG..grrvTPPKGRIVLDGC..TITCPCLE........................yeNRPLLIKLKTrTS....................TEYFLEACSREERDSWAFEITGAIH
VVKQGYLSKQG.....hKRKNWKVRRFVLRK.....dpAFLHYYDPSK....eeNRPVGGFSLRGS..LVSALEDN.................gvptgvkgnVQGNLFKVITkDD....................THYYIQASSKAERAEWIEAIKKL-T
ILKMGPVDKRK......-GLFARRRQLLLTE......gPHLYYVDPVN......KVLKGEIPWSQE.IRPEAKNF-..........................---KTFFVHTpNR....................-TYYLMDPSG-NAHKWCRKIQEVWR
ALKQGWLHKKGggsstlSRRNWKKRWFVLRQ.......SKLMYFENDS.....eEKLKGTVEVRTA.kEIIDNTS-..........................-KENGIDIILaDR....................-TFHLIAESPEDASQWFSVLSQVHS
PVQKGFLLKKR....kwPLKGWHKRFFCLEK.......GILKYAKSQ-......-ADIEREKLHGC.iDVGLSVMS........................vkKSSKCIDLDTeEH....................-IYHLKVKSEELFDEWVSKLRHHRM
GDCEGWLWKKK.daksyFSQKWKKYWFVLKD.......ASLYWYINEE.....dEKAEGFISLPEF..KIDRASEC..........................RKKYAFKACHpKI....................KSFYFAAEHLDDMNRWLNRINMLTA
ERQEGHLLKKR....kwPLKGWHKRYFVLED.......GILHYATTRQ..ditkGKVHGSIDVRLS..VMSINKK-..........................--AQRIDLDTeDN....................-IYHLKIKSQDLFHSWVAQLRAHRL
IQLSGMYNVRK.gkmqlPVNRWTRRQVILCG.......TCLIVSSVKD....svSGKMHVLPLIGG..KVEEVKK-..........................-HQHCLAFSSsGP..................qsQTYYICFDTFTEYLRWLRQVSKVAS
STMSGYLYRSK.....gSKKPWKHLWFVIKN.......KVLYTYAASE.....dVAALESQPLLGF..TVTLVKDE.........................nSESKVFQLLHkGM....................VFYVFKADDAHSTQRWIDAFQEGTV
IIKQGCLLKQG.....hRRKNWKVRKFILRE.....dpAYLHYYDPAG.....gEDPLGAVHLRGC..VVTSVESS....................hdgkksDEENLFEIITaDE....................VHYYLQAATSKERTEWIKAIQVASR
PEKVGWVRKFC..gkgiFREIWKNRYVVLKG.......DQLYVSEKEV...kdeKNSQEVFDLSDY.eKCEELRKS.....................ksrskKNHSKFTLARcRQ...............pgttaPNLIFLAVSPEEKESWINALSSAIT
FIVRGWLHKEVknspkmSSLKLKKRWFVLTH.......NSLDYYKSSE....knALKLGTLVLNSL.cSVVPPDEK........................ifKETGYWNVTVyGR...................kHCYRLYTKLLNEATRWSSAIQNVTD
VRKVGYLRKPK......---SMHKRFFVLRAaseaggpARLEYYENEKkwrhksSAPKRSIPLESC.fNINKRADS..........................KNKHLVALYTrDE....................-HFAIAADSEAEQDSWYQALLQLHN
FVKSGWLLRQS.....tILKRWKKNWFDLWS......dGHLIYYDDQT...rqsIEDKVHMPVDCI..NIRTGHEC.................rdiqppdgkPRDCLLQIVCrDG....................KTISLCAESTDDCLAWKFTLQDSRT
VIKAGYLEKRR.kdhsfLGFEWQKRWCALSK.......TVFYYYGSDK.....dKQQKGEFAIDGY..DVRMNNTL......................rkdgKKDCCFEICApDK....................RIYQFTAASPKDAEEWVQQLKFILQ
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ILKEGMLTKQN.....nSFQRSKRRYFKLRG.......RTLYYAKTAK......SIIFDEVDLTDA..SVAESSTK..........................NVNNSFTVITpCR....................-KLILCADNRKEMEDWIAALKTVQN
-----------......--GEWKKHWFVLTD.......SSLKYYRDST..aeeaDELDGEIDLRSC.tDVTEYAVQ..........................-RNYGFQIHTkDA....................-VYTLSAMTSGIRRNWIEALRKTVR
IVREGFLLKRKepgglaTRFAFKKRYFRLSG.......RDLSYSKTPE......WQVHTSIPLSCI..RAVEHVDE.......................gafQLPHVMQVVTqDG................agtsHTTYLQCKNVNDLNQWLSALRKASA
PTCRGYLHKRT...hsgFVKGWRKRWFVLKH......dGFLLYYKHRK..degkWPPLDMIKLEGA..EVDIDNSL..........................GKPFVFNCMPqSG...................sRILCLCATSNQEMKRWLEAMQRAAR
NFKKGWLTKQY......EDGQWKKHWFVLAD.......QSLRYYRDSV..aeeaADLDGEINLSTC.yDVTEYPVQ..........................-RNYGFQIHTkEG....................-EFTLSAMTSGIRRNWIQTIMKHVL
ITKEGMLHYKA.stsylGKEHWKACFVVLSN.......GILYQYPDRT.....dVIPLLSVNMGGE..QCGGCRRS.......................nttDRPHAFQVILaDR....................PCLELSADSEAEMADWMQHLCQAVS
VYKSGFLARKIgkktprGKRGWKTFYAVLKG.......TVLYLQKDEYekalseEDLKNAVSVHHA..LASKATDY..........................eKKPNVFKLKTaDW....................RVLLFQTQSPEEMQGWINKINCVAA
TYKHGVLTRKTgkrtprGRRGWKKFYAVLKG.......TILYLQKDEYdkalseGDLKNAIRVHHA..LATRASDY..........................sKKSNVLKLKTaDW....................RVFLFQAPSKEEMLSWILRINLVAA
VSHSGFLYKTAllqdrrAREEFSRRWCVLGD.......GVLSYFENER.....aVTPNREIRASEI..VCLAVPPP.......................dthGFEHTFEVYTeGE....................RLYLFGLESAEQAHEWVKCIAKAFV
PIYGGWLLLAPfdnpvhRSRKWQRRFFILYE.......HGLLRYALDE...mptTLPQGTINMNQC.tDVVDGEAR..........................tGQKFSLCILTpDK....................-EHFIRAETKEIISGWLEMLMVYPR
VVMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKKLK.....dALTVVVDDLRLC..SVKPCEDI..........................ERRFCFEVVSpTK....................-SCMLQADSEKLRQAWVQAVQASIA
VIRRGWLTINN...islMKGGSKEYWFVLTA.......ESLSWYKDEE.....eKEKKYMLPLDNL..KIRDVEKG........................fmSNKHVFAIFNtEQ.............rnvykdlRQIELACDSQEDVDSWKASFLRAGV
VLKQGYMMKKG.....hKRKNWTERWFVLKP.......NIISYYVSED.....lKDKKGDILLDEN.cCVESLPDK.........................dGKKCLFLIKCfDK....................-TFEISASDKKKKQEWIQAIYSTIH
FTAEGYLYVQE.krpapFGSSWVKHYCMYRK...takkFNMIPFEHRS...ggkLGDGEAFFLKEC..TKRHMDST..........................DRRFCFDIEAaDR..................pgVPLTVQAFSEEERKQWLEALGGKEA

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VIRKGWLTINN...igiMKGGSKEYWFVLTA.......ENLSWYKDDE.....eKEKKYMLSVDNL..KLRDVEKG.........................fmSSKHIFALFNtEQ.............rnvykdyRQLELACETQEEVDSWKASFLRAGV
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AEMAAELGMRG....pkKGSVAKRRLVKLVV.......NFLFYFRPDE......AEPLGALLLERC..RVAQEE--..........................--PGGFSISFvED..................lsRKYHFECCSQEQCQDWMEALQRASY
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NQLSGNLLRKF.....kNSNGWQKLWVVFTN.......FCLFFYKSHQ.....dSHPLASLPLLGY..SLTIPSES.......................eniHKDYVFKLHFkSH....................-VYYFRAESEYTFERWMEVIRSATS
IVKQGYVKMKS.....rKLGIYRRCWLVFRK.ssskgpQRLEKYPDEK..svclRGCPKVTEISNV.kCVTRLPKE..........................tKRQAVAIIFTdDS....................-ARTFTCDSELEAEEWYKTLSVECL
TFLCDFLYQAPlssekkLLEETNKKWCVLEG.......GFLSYYENDK.....sTTPNGTININEV..ICLAIHKE....................dfylntGPIFIFEIYLpSE....................RVFLFGAETSQAQRKWTEAIAKHFV
LLGEGVLTKEC......-RKKAKPRIFFLFN.......DILVYGSIVL..skrkYRSQHIIPLEEV..TLEPLPET.........................lQAKNRWMIKTaKK....................-SFVVSAASTTERQEWISHIEECVR
AKICAFLLRKK......RFGQWTKLLCVIKD.......TKLLCYKSSK.....dQQPQMELPLQGC..SITYIPRD........................skKKKHELKITQqGT....................DPLVLAVQSKEQAEQWLKVIKEAYS
--MEGVLYKWT.....nYLTGWQPRWFVLDN.......GILSYYDSQD...dvcKGSKGSIKMAVC..EIKVHPA-..........................-DNTRMELIIpGE....................QHFYMKAVNAAERQRWLVALGSSKA
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PECLGLLHQLE.....rSTDVWIQHYCILKD.......GCLYFYASIR.....sTQASGGLYLQGY..SVSEQTHG..........................FEQPVIELKPsSE..................efKTFYFCAENKTENQRWIAALKTSIK
PLIEGKLKEKQ..vrwkFIKRWKTRYFTLAG.......NQLLFQKGKS....kdDPDDPPIELSKV..QSVKAVAK.....................krrdrSLPRAFEIFTdSK....................-TYVFKAKDEKNAEEWLQCINVALA
MKHSGYLWTIG....knVWKRWKKRFFVLVQ..vsqytFAMCSYREKK......AEPQELLQLDGY..TVDYTDPQ.....................pglegGRAFFNAVKEgD-....................-TVIFASDDEQDRILWVQAMYRATG
SMVEGSELKKV.....rSNSRIYHRYFLLDA.....dmQSLRWEPSKK......DSEKAKIDIKSI.kEVRTGKNT..............difrsngiseqiSEDCAFSVIYgEN...................yESLDLVANSADVANIWVTGLRYLIS
PVKEGPLFIHRkgkgplASSSFKKLYFSLTT.......EALSFAKTSS...skkSTFIKLASIRAA.eKVEEKSFG..........................-SSHIMQVIYaDD................vgraQTVYLQCKCVNELNQWLSALRKAST
LVKDGFLVEVS......-ESSRKLRHVFLFT.......DVLLCAKLKKfpdhelEDMKMKISALKS..EIQKEKAN...kgqsraierlkkkmfenefllllnSPTIPFRIHNrNG....................KSYLFLLSSDYERSEWREAIQKLQK
VMKEGWMVHYT.....sKDTLRKRHYWRLDS.......KCITLFQNDT.....gSRYYKEIPLSEI.ICLEPAKPS....................altpvgATPHCFEITTaNV....vyyvgenvvnpssppnNSVLPSGIGPDVARMWEVAIQHALM
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.....sPRPSGLYLLEGS..ICKRAPSP........krgtsskesgekqrhsrsrRRRNVLRRQPtRI...................sKTFRLVAIELTGMT---ATLEVSFS
FLKEGTLMKLS......-RKVMQPRMFFLFN.......DALLYTTPMQ...sgmYKLNNMLSLAGM..KVRKPTQE..........................AYQNELKIESvER....................-SFILSASSAAERDDWLEAISSSIE
LMQEGTMMRKV.....rTKSWKKLRYFRLQN.......DGMTVWHGSQ....peSMPKPTFSISDV.eRIRKGQDS................ellrylveefPLEQGFTVVFhGR...................rPNLDLVANSVEEAQIWMRGLQLLVD
VERCGVLSKWT.....nYIHGWQDRWVVLKN.......NTLSYYKSED...eteYGCRGSICLSKA..VITPHDF-..........................-DECRFDISVnDS....................-VWYLRAQDPEHRQQWVDAIEQHKT
LMKLGTVARRG......AMGIWKEFFCELSP.....leFRLYLSDEE-......RTCVESCSLLRC..EAVGPAH-..........................-SDGRFELVFsGK....................-KLALRASSQDEAEDWLDRVREALQ
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AVMEGPLFLQS...qrfGTKRWRKTWAVLYP.asphgvARLEFFDHKGgrggsrRLDCKMIRLAEC.vSVVPVTVE......................sppePGAAAFRLDTaQR....................-SHLLAADAVSSTA-WVQTLCRTAF
LLKQGELQQMStsrtlrTKKLFREIYLFLFN.......DLLVICRQIP...gdkYQVFDSAPRGLL..RVEELEDQ........................gqTLANVFILRLIEN...............addreATYMLKASSQSEMKRWMTSLAPNRR
VSKKGYLHFLE.....pHTAGWAKRFVVVRR.......PYAYMYNSDK.....dTVERFVLNLSTA..QVEYSEDQ......................qamlKTPNTFAVCTeHR....................-GILLQANSDKDMHDWLYAFNPLLA
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SEKKGFLLKKS....dgIRKVWQRRKCAVKN.......GILTISHATS......NRQPAKLNLLTC..QVKPNAE-..........................-DKKSFDLIShNR....................-TYHFQAEDEQDYIAWISVLTNSKE
DLSMGDLLLHTpaslgkWKKEPELAAFVFKT.......AVVLVYKDGSyeewdpFRFRHMIPTEAL..QVRALPSA........................daEANAVCEIVHvKS.............esegrpeRVFHLCCSSPESRKDFLKSVHSILR
SVICSFLHYME.....kGGKGWHKAWFVVPE....nepLVLYIYGAPQ.....dVKAQRSLPLIGF..EVGPPEAG.......................erpDRRHVFKITQsHL....................-SWYFSPETEELQRRWMAVLGRAGR
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KGLEGVIRKRSfcgrdqVCYRWSKRWLVVKD.......SFLLYMRPET....gaISFVQLFD-PGF..EVQVGKRS.........................tETRYGVRIDTsHR....................-SLILKCSSYRQARWWGQEITELAQ
SIKEGILKLKEepskilSGNKFQDRCVVLRD.......GHLFIYKDPK.....sSKHDKMFPLRAM..KFYLGVKK..........................------KMKPpTR....................------------------------
LLREGPVLKIS.....fRRSDPMERYLVLFN.......NMLLYCVPRVlqvgaqFQVRTRIDVAGM..KVRELTDA..........................EFPHSFLVSGkQR....................-TLELQARSRDEMVSWMQACQAAID
RGFEGKLTAQGpeagglLSSRGRERRVFLFE.......QIIIFSEALGggaqpgYVYKNSIKVSCL..GLEGNLQG..........................-NPCRFALTSrGP................eggiQRYVLQASDPAVSQAWIKQVAQILE
LLCHGELKNKS......----GHKLYIFLFQ.......DILVLTRPVTnerhlyQVYRQPIPVQEL..VLEDLQDG..........dvrmggsfrgafgnsdKAKNIFRVRFqDP.................spgHSHTLQANDVFHKQQWFNCIRAAIA
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VSKKGYLHFKE.....pLSSNWAKHFVVVRR.......PYVFIYNSDK.....dPVERGIINLSTA..QVEYSEDQ......................qamvKTPNTFAVCTkHR....................-GVLLQALNDKDMNDWLYAFNPLLA
IVKQGYVRIRS.....rRLGIYQRCWLVFKK.asskgpKRLEKFSDER...aayFRCYHKVELNNV.kNVARLPKS..........................TKKHAIGIYFnDD....................TSKTFACESDLEADEWCKVLQMECV
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IQREELLSFMGltsgggGQPQWQKCRLLLRSegeggggSRLEFFVPPK.....aSRPRLSIPCSTI.tDVRTATAL.......................empDRENTFVVKVeGP....................SEYILETSDALHVKAWVSDIQECLS
PELADYIKVFK..pkklTLKGYKQYWCTFKD.......TSISCYKSKE...essGTPAHQMNLRGC..EVTPDVNI.........................sGQKFNIKLLIpVA.................egmNEIWLRCDNEKQYAHWMAACRLASK
PELEGALYLKE.....dGKKSWKRRYFLLRA.......SGIYYVPKGK..tktsRDLACFIQFENV..NIYYGIQC....................kmkykaPTDHCFVLKHpQI................qkesqYIKYLCCDDARTLSQWVMGIRIAKY
CIVHGYMSKMG....npFLTQWQRRYFYLFP.......NRLEWRGEG-......EAPQSLLTMEEI..QSVEETQI..........................KERKCLLLKIrGG....................KQFVLQCDSDPELVQWKKELRDAYR
AQMEGFLNRKHahnkkaSSRSWHNVYCVINN.......QEMGFYKDAKaasgipYHSEVPVSLKEA..ICEVALDY.........................kKKKHVFKLRLsDG....................NEYLFQAKDDEEMNTWIQAISSAIS
FLHSGKLYKAK......---SNKELYGFLFN.......DFLLLTQITKksnlqyKMYKTPIFLNEV..LVKLPTDP.........................sGDEPIFHISHiDR....................-VYTLRAESINERTAWVQKIKAASE
DTKHGMMKFREllglglPSGGFHDRYFILNS.......SCLRLYKEVR.....sHRPEKEWPVKSL..KVYLGVKK......................klrpPTCWGFTVVHeTE................khekQQWYLCCDTQMELREWFATFLSVQH
FIRLGSLSKLS......-GKGLQQRMFFLFN.......DVLLYTSRGL.tasnqFKVHGQLPLYGM..TIEESEEE..........................wGVPHCLTLRGqRQ....................-SIIVAASSRSEMEKWMEDIQMAID
VRKAGWLFFKPrklelvARRKWKQYWVTLKG.......CTLLFYETYGnsteqnSAPRCALFAEDS..IVQSVPEH.........................pKKEHVFCLSNsCG....................DVYLFQATSQTDLENWVTAIHSACA
KGLEGMIMKRSccghgrACYRWSKRWLIVKD.......SFLLYMKPDS......GAIAFVLLVDKE.fRVKVGRKE..........................tETKYGLRIDNISR....................-TLILKCNSYRHARWWGGAIEEFIR
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IRHLGWLAEKV...pgeSEKQWKPALVVLTE.......KDLLIYDSMPrrkeawFSPVHSYPLLAT..RLVHSGPG....................kgspqaGMDLSFATRTgTK.................qgiETHLFRAEISRDLSHWTRSIVQGCH
GTKRGFLSKKA.....aEASRWHEKWFALYQ.......NVLFYFEGEQ.....sGRPAGMYLLEGC..SCERTPAP............prtnagpagardalDKQYYFTVLFgHD..................gqKPLELRCEEEQAGKEWMEAIHQASY
FIRQGSLIQVPvrlgslSLKKEGERQCFLFT.......KHFLICTRSSggklhlLKTGGVLSLIQC..TLIEEPDG.............sdddpkgsghmfgHLDFKIVVEPpDA..................asFTVVLLAPSRQEKAAWMSDISQCVD
VTYMSQVTIQC.....aGSEEKNERYLLLFP.......NLLLMLSASP..rmsgFIYQGKLPTTGM..TITKLEDS.........................eNHRNAFEISGsMI....................ERILVSCTSQQDLHEWVEHLQKQTK
VIMADSLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTPK.....vGQWVGTVLLHCC..ELIERPSK..........................KDGFCFKLFHpLDvwavkgpkgesvgsitqplpsSYLIFRAASESDGRCWLDALELALR
LILQDAFQVWD...pksLIRKGRERHLFLFE.......ISLVFSKEIKssghtkYVYKNKLLTSEL..GVTEHVEG..........................-DPCKFALWSgRT................pssdNKTVLKASNIETKQEWIKNIREVIQ
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.....sPRPSGLYLLEGS..ICKRAPSP................krgtsskesgeKQQHYFTVNFsND..................sqKTLELRTEDAKDCDEWVAAIARASY
YYKERLLYLEEcchgelKNNRGVKLHVFLFQ.......EVLVITRAVTneqlcyQLYRQPIPVKDL..TLEDLQDG...........evrlggslrgafsnneRVKNFFRVSFkNG.................sqsQTHSLQANDTFNKQQWLNCIRQAKE
SRIEGWLSVPN..rgniKRYGWKKQYVVVSS.......KKILFYNDEQ..dkeqSNPSMVLDIDKL.fHVRPVTQG..................dvyraeteEIPKIFQILYaNE................gecrKDVEMEPVQQAEKT----NFQNHKG
LIKEGHILKLS.....aKNGTTQDRYLILFN.......DRLLYCVPRLrllgqkFSVRARIDVDGM..ELKESSNL..........................NMPRTFLVSGkQR....................-SLELQARTEEEKKDWVQAINSTLL
LIKEGHILKLS.....aKNGTTQDRYLILFN.......DRLLYCVPRLrllgqkFSVRARIDVDGM..ELKESSNL..........................NMPRTFLVSGkQR....................-SLELQARTEEEKKDWVQAINSTLL
PEIHGFLHAKE.....qGKKSWKKAYFFLRR.......SGLYFSTKGT.....sKEPRHLQLFSEF.sTSHVYMSL..................agkkkhgaPTPYGFCLKPnKA................ggprDLKMLCAEEEQSRTCWVTAIRLLKD
LIKEGSIQKLS.....aKNGTTQDRHLFLFN.......NVMLYCVPKLrlmgqkLSVREKMDISDL..QVQDIVKP..........................NAACTFIITGrKR....................-SLELQTRTEEEKKEWIQVIQATVE
GHRKGATKMKD.....fARFKPMQRHLFLYE.......KAVMFCKRRFadrypsYSFKHCLKMEDV..GITEHVKG..........................-DNRKFEIRYsEK...................eEIYIVQAPNVDVKMLWLKEIRKILV
LLHSGKLYKTK......---SNKELHAFLFN.......DFLLLTYLVRkssaqfRMYKTPIFLNEV..LVKLPTDP.........................sSDEPVFHISHiDR....................-VYTLRTDNINERTAWVQKIKGASE
LVRDGSVFLKS......TTGRLKEVQAVLLT.......DILVFLQEKDyvfaslDHKSTVISLKKL..IVREVAHE..........................-EKGLFLISMgVK..................dpEMVEVHASSREERNSWIQIIQDTIN
LIHEGCLLWKT......ATGRFKDVLLLLMT.......DVLVFLQEKDkyiftsLDKPSVVSLQNL..IVRDIANQ..........................-AKGMFLISSgPP....................EMYEVHAASRDDRTTWIRVIQQSVR
LHLEGMLCWKT......TSGRLKDILAILLT.......DVLLLLQEKDyvfasvDSKPPVISLQKL..IVREVANE..........................-EKAMFLISAsLQ..................gpEMYEIYTSSKEDRNAWMAHIQRAVE
LLMQGSFSVWTtkvkelARFKPMQRHLFLHE.......KAVLFCKKREyekapsYSYKQSLNMTAV..GITENVKG..........................-DTKKFEIWYnAR...................eEVYIIQAPTPEIKAAWVNEIRKVLT
PEIQGFLQLRG.sgrgsGRKLWKRFFCFLRR.......SGLYYSTKGT..skdpRHLQYVADVNES..NVYVVTQG....................rklygmPTDFGFCVKPnKL...............rnghkGLHIFCSEDEQSRTCWLAAFRLFKY
FVRQGSLMQMSgrlgslSTKKEGERQCFLFS.......KHLIICTRGS.ggklhLTKNGVISLIDC..TLLDEPEN...............lddeakgagpeIEHLEFKIGVePK................dslpFTVILVASTRQEKAAWTSDIIQCVD
LLHDGLVYWKT......ATGRFKDILALLLT.......DVLLFLQEKDyifaavDQKPSVISLQKL..IAREVANE..........................-ERGMFLISAsSA..................gpEMYEIHTNSKEERNNWMRRIQQAVE
PQGDGEIRITT.....lDKHTKRERHIFLFD.......LAVIVCKRKG....dnYEMKEIIDLQQY..KIANNPTT.....................dkenkKWSYGFYLIHtQG...................qNGLEFYCKTKDLKKKWLEQFEMALS
PEIQGFLQVKE.....vGRKSWKKLYVCLRR.......SGLYYSTKGT..skepRHLQLLADLEES..SIFYLIAG....................kkqynaPNEHGMCIKPnKA...............ktemkELRLLCAEDEQIRTCWMTAFRLLKY
PKIDGELKVRS.....iVNHTKQDRYLFLFD.......KVVIVCKRKG....ysYELKEVIELLFH..KMTDDPMH.....................nkdikKWSYGFYLIHlQG...................kQGFQFFCKTEDMKRKWMEQFEMAMS
PKIDGELKITS.....vERRSKTDRYAFLLD.......KALLICKRRG....dsYDLKASVNLHSF..QVRDDSSG.....................erdnkKWSHMFLLIEdQG...................aQGYELFFKTRELKKKWMEQFEMAIS
PKIDGELKVRS.....iVNHTKQDRYLFLFD.......KVVIVCKRKG....ysYELKEVIELLFH..KMTDDPMH................nkdikkshgkMWSYGFYLIHlQG...................kQGFQFFCKTEDMKRKWMEQFEMAMS
FIMEGTLTRVG......---AKHERHIFLFD.......GLMICCKSNHgassaeYRLKEKFFMRKV..QINDKDDT.........................sEYKHAFEIILkDG....................NSVIFSAKSAEEKNNWMAALISLQY
FIMEGPLTRIG......---AKHERHIFLFD.......GLMISCKPNHgyssaeYRLKEKFVMRKI..QICDKEDA.........................cEYRHAFELVSkDE....................NSVIFAAKSAEEKNNWMAALISLHY

111	T_Mouse	PSCD3-PH	MouseDom	T	100.6262	31.89749	12	13.98169
112	T_Mouse	PSCD2-PH	MouseDom	T	99.94955	29.71226	12	13.98169
113	T_Mouse	PSCD1-PH	MouseDom	T	98.12305	29.71226	12	13.98169
127	T_Mouse	AKT3-PH1	MouseDom	T	66.54652	31.89749	8	14.12436
128	T_Mouse	AKT2-PH1	MouseDom	T	64.85858	21.37874	8	12.92688
129	T_Mouse	AKT1-PH1	MouseDom	T	64.60328	21.37874	9	12.92688
20	T_Mouse	RASA2-PH	MouseDom	T	60.19405	11.85552	12	7.197588
7	T_Mouse	TEC-PH1	MouseDom	T	58.45845	27.78836	12	13.94467
120	T_Mouse	BTK-PH1	MouseDom	T	57.54618	27.78836	13	13.54181
19	T_Mouse	RASA3-PH	MouseDom	T	55.79247	18.5865	12	9.697588
87	T_Mouse	ITK-PH1	MouseDom	T	54.58805	20.97401	12	12.25406
96	T_Mouse	GAB1-PH1	MouseDom	T	50.05182	11.87752	13	7.376668
95	T_Mouse	GAB2-PH1	MouseDom	T	44.3796	12.80969	13	7.782133
67	T_Mouse	PLEKHA1-	MouseDom	T	40.79698	19.45923	9	10.69288
65	T_Mouse	PLEKHA2-	MouseDom	T	38.37364	16.14802	10	8.74665
110	T_Mouse	DAPP1-PH	MouseDom	T	36.9857	20.497	7	11.77316
69	T_Mouse	PHLDB1-P	MouseDom	T	36.41728	20.54062	10	12.15971
131	T_Mouse	SH3BP2-P	MouseDom	T	34.53185	10.93954	8	6.1609
54	T_Mouse	PLEK2-PH	MouseDom	T	33.76889	22.15875	9	13.45775
55	T_Mouse	PLEK2-PH	MouseDom	T	31.67357	15.10798	8	8.577063
70	T_Mouse	PDPK1-PH	MouseDom	T	28.13585	6.732081	9	4.815186
73	T_Mouse	MYO10-PH	MouseDom	T	25.53585	16.46003	10	8.837797
26	T_Mouse	OSBPL3-P	MouseDom	T	24.61724	8.015123	10	5.302999
115	T_Mouse	CNKSR2-P	MouseDom	T	23.52208	3.053269	9	3.093661
48	T_Mouse	OSBPL7-P	MouseDom	T	23.39965	6.649137	10	4.749225
56	T_Mouse	PLEK-PH1	MouseDom	T	22.62968	14.41739	7	8.408871
68	T_Mouse	PHLPP-PH	MouseDom	T	20.18313	9.461556	8	5.959526
97	T_Mouse	FGD6-PH2	MouseDom	T	19.13196	12.27738	5	7.560051
88	T_Mouse	IRS1-PH1	MouseDom	P	4.52796	3.491613	10	3.321827
31	T_Mouse	DGKD-PH	MouseDom	P	3.390404	1.764742	9	2.473069
24	T_Mouse	2610034M	MouseDom	P	1.654989	9.397778	12	5.865881
51	T_Mouse	PSD3-PH1	MouseDom	P	-2.20621	-14.6482	12	-7.10921
79	T_Mouse	M-RIP-PH	MouseDom	P	-3.45277	-5.74347	6	-2.05755
63	T_Mouse	PLEKHB1-	MouseDom	P	-7.11446	-2.56218	7	-0.20638
27	T_Mouse	RALGPS2-	MouseDom	P	-8.02542	-11.9821	13	-5.77365
107	T_Mouse	DOK4-PH1	MouseDom	P	-8.24788	-17.0933	9	-8.68325
60	T_Mouse	PLEKHF1-	MouseDom	P	-8.77847	6.761305	11	4.96691
38	T_Mouse	AFAP-PH1	MouseDom	P	-8.81854	-8.27346	7	-3.42332
53	T_Mouse	PLCD1-PH	MouseDom	P	-9.26913	-0.86444	9	0.556861
25	T_Mouse	2610034M	MouseDom	P	-9.55625	-18.6114	3	-9.46285
22	T_Mouse	VEPH1-PH	MouseDom	P	-10.589	-0.91382	11	0.55365
42	T_Mouse	PLCL2-PH	MouseDom	P	-11.9024	-8.1226	9	-3.38032
126	T_Mouse	SH2B2-PH	MouseDom	P	-14.9566	-11.1846	4	-5.33384
108	T_Mouse	DOK1-PH1	MouseDom	P	-15.3327	-17.0358	12	-8.61398
109	T_Mouse	DDEF1-PH	MouseDom	P	-17.3438	-2.47524	9	-0.17146
45	T_Mouse	GEFT-PH1	MouseDom	P	-18.6789	-6.08618	6	-2.25916
106	T_Mouse	DOK5-PH1	MouseDom	P	-19.2796	-18.3878	8	-9.27135
125	T_Mouse	ADRPK1-P	MouseDom	P	-21.2903	1.49895	4	2.206273
10	T_Mouse	SPNB2-PH	MouseDom	P	-22.6344	-9.85365	7	-4.40766
52	T_Mouse	MCF2-PH1	MouseDom	P	-32.9825	-16.3673	11	-8.49827
32	T_Mouse	ARFGEF18	MouseDom	P	-35.0323	-25.5585	5	-14.5978

57	T_Mouse	PLEK-PH2	MouseDom	C	16.98692	19.24822	6	10.11167
21	T_Mouse	PLEKHO1-	MouseDom	C	5.64373	1.620825	8	2.216154
74	T_Mouse	MYO10-PH	MouseDom	C	4.739982	9.167004	12	5.56816
62	T_Mouse	PLEKHB2-	MouseDom	C	4.527408	1.331255	8	2.139154
36	T_Mouse	SKAP2-PH	MouseDom	C	4.342004	-4.3906	11	-1.52465
28	T_Mouse	PLEKHA5-	MouseDom	C	3.518519	10.20971	8	6.0546
8	T_Mouse	TRIOBP-P	MouseDom	C	3.319646	-1.76073	3	0.049064
18	T_Mouse	RASAL1-P	MouseDom	C	2.8033	1.427833	8	2.190496
80	T_Mouse	M-RIP-PH2	MouseDom	C	0.569569	0.00855	4	1.113177
44	T_Mouse	PLEKHM2-	MouseDom	C	0.157531	-1.18346	5	0.40386
30	T_Mouse	PSD2-PH1	MouseDom	C	-2.22542	-19.2232	14	-9.60921
39	T_Mouse	CENTD2-P	MouseDom	C	-2.29737	-10.0165	10	-4.6648
37	T_Mouse	CENTB5-P	MouseDom	C	-4.26434	6.459244	9	4.733255
104	T_Mouse	DNM2-PH1	MouseDom	C	-4.66261	-11.2473	9	-5.35131
9	T_Mouse	SWAP70-P	MouseDom	C	-4.98782	11.39746	10	6.808048
29	T_Mouse	ARHGAP1	MouseDom	C	-5.10301	-10.5789	6	-5.07223
105	T_Mouse	DNM1-PH1	MouseDom	C	-5.44484	-11.2473	9	-5.35131
76	T_Mouse	OPHN1-PH	MouseDom	C	-6.63977	-10.5806	5	-5.07223
23	T_Mouse	PLEKHJ1-	MouseDom	C	-7.88884	5.047737	9	4.256374
34	T_Mouse	FARP1-PH	MouseDom	C	-8.19076	-9.49061	5	-4.27736
116	T_Mouse	CENTD1-P	MouseDom	C	-8.69454	-5.52161	6	-1.99241
64	T_Mouse	PLEKHA3-	MouseDom	C	-9.11254	-1.18346	5	0.396189
118	T_Mouse	CADPS-PH	MouseDom	C	-11.3893	3.959244	9	3.542885
50	T_Mouse	RASA4-PH	MouseDom	C	-11.9261	-10.9678	10	-5.25627
41	T_Mouse	ABR-PH1	MouseDom	C	-12.4433	-2.26368	9	-0.05698
82	T_Mouse	PRKCM-PI	MouseDom	C	-12.7959	-1.27641	6	0.250509
93	T_Mouse	RASGRF1	MouseDom	C	-13.0423	-5.41003	6	-1.96591
98	T_Mouse	FGD6-PH1	MouseDom	C	-14.0154	-0.27131	6	1.055298
35	T_Mouse	PLCD4-PH	MouseDom	C	-14.3543	-14.5273	10	-7.08666
119	T_Mouse	COL4ABP3	MouseDom	C	-14.3874	-6.3498	4	-2.33589
43	T_Mouse	PLEKHM1-	MouseDom	C	-14.8386	-13.9517	6	-6.84987
78	T_Mouse	NGEF-PH1	MouseDom	C	-15.6602	-17.585	8	-8.70421
84	T_Mouse	KIF1A-PH1	MouseDom	C	-16.0109	-10.1593	5	-4.7058
114	T_Mouse	CIT-PH1	MouseDom	C	-16.2152	-12.4441	8	-5.88761
66	T_Mouse	PLEKHA2-	MouseDom	C	-16.5443	-7.60173	4	-2.91949
6	T_Mouse	TIAM1-PH2	MouseDom	C	-17.3668	-7.37381	8	-2.76331
100	T_Mouse	FGD1-PH2	MouseDom	C	-17.7219	-3.82106	5	-1.21869
15	T_Mouse	SNTA1-PH	MouseDom	C	-17.911	-9.89788	4	-4.43429
58	T_Mouse	PLD2-PH1	MouseDom	C	-18.1026	-2.71999	8	-0.35948
117	T_Mouse	CENTD1-P	MouseDom	C	-18.2504	-22.2886	9	-11.301
101	T_Mouse	FGD2-PH1	MouseDom	C	-18.6759	-4.16068	8	-1.37216
121	T_Mouse	NET1-PH1	MouseDom	C	-18.8253	-8.83715	5	-3.83069
13	T_Mouse	SNTB2-PH	MouseDom	C	-18.991	1.375319	5	2.151071
83	T_Mouse	KIF1B-PH1	MouseDom	C	-19.2249	-3.14081	5	-0.78088
5	T_Mouse	TIAM1-PH	MouseDom	C	-19.4766	-3.34446	8	-0.87617
77	T_Mouse	SH2B1-PH	MouseDom	C	-19.906	-3.93396	4	-1.30817
61	T_Mouse	PLEKHC1-	MouseDom	C	-20.6828	-11.5125	7	-5.53548
130	T_Mouse	APBB1IP-P	MouseDom	C	-21.2817	-5.83346	12	-2.10495
86	T_Mouse	ITSN1-PH1	MouseDom	C	-22.8564	-1.32801	8	0.246029
40	T_Mouse	CENTD2-P	MouseDom	C	-23.9611	-16.9155	8	-8.5378
33	T_Mouse	FARP1-PH	MouseDom	C	-24.3282	-2.90864	5	-0.61868

47	T_Mouse	TIAM2-PH	MouseDom	C	-24.539	-3.34446	8	-0.87617
59	T_Mouse	PLD1-PH1	MouseDom	C	-25.4941	-11.3197	8	-5.35948
14	T_Mouse	SNTB1-PH	MouseDom	C	-25.603	7.502175	7	5.186903
71	T_Mouse	RASGRF2	MouseDom	C	-25.9121	-2.41792	6	-0.1335
72	T_Mouse	RASGRF2	MouseDom	C	-27.2194	-1.0896	7	0.413275
122	T_Mouse	ARHGEF7	MouseDom	C	-28.864	-19.7666	5	-10.1688
75	T_Mouse	OSBPL5-P	MouseDom	C	-29.0949	-12.0358	7	-5.79644
46	T_Mouse	KALRN-P	MouseDom	C	-29.4503	-8.56954	11	-3.54998
94	T_Mouse	RASGRF1.	MouseDom	C	-30.2578	-5.41906	6	-1.96591
123	T_Mouse	ARHGEF3	MouseDom	C	-30.662	-22.7438	5	-11.4701
16	T_Mouse	ROCK1-P	MouseDom	C	-30.837	-2.58497	8	-0.21445
102	T_Mouse	FGD1-PH1	MouseDom	C	-31.5606	-18.7438	9	-9.5071
103	T_Mouse	FGD1-PH1	MouseDom	C	-31.5606	-18.8818	9	-9.5071
90	T_Mouse	GRB14-P	MouseDom	C	-32.4657	-3.31577	10	-0.86845
99	T_Mouse	FGD3-PH1	MouseDom	C	-32.8666	-22.7438	9	-11.9086
85	T_Mouse	ITSN2-PH	MouseDom	C	-33.023	-9.37175	8	-4.2002
49	T_Mouse	AKAP13-P	MouseDom	C	-34.5638	-26.5001	6	-15.7542
124	T_Mouse	ARHGEF2	MouseDom	C	-34.9632	-25.5585	6	-14.468
81	T_Mouse	MCF21-P	MouseDom	C	-35.4329	-16.3673	11	-8.49827
89	T_Mouse	GRB7-PH1	MouseDom	C	-36.6746	-3.03616	11	-0.7078
92	T_Mouse	RASGRF1.	MouseDom	C	-38.5344	-11.3442	8	-5.36364
17	T_Mouse	RGNEF-P	MouseDom	C	-39.3173	-26.8893	5	-15.8354
1	T_Mouse	VAV3-PH1	MouseDom	C	-40.8317	-19.4713	8	-9.74982
91	T_Mouse	GRB10-P	MouseDom	C	-42.0324	-4.94031	11	-1.79368
2	T_Mouse	VAV2-PH1	MouseDom	C	-42.0733	-23.6387	8	-12.6939
4	T_Mouse	VAV1-PH1	MouseDom	C	-43.5485	-24.7061	8	-13.2411
3	T_Mouse	VAV2-PH1	MouseDom	C	-43.9299	-23.6646	8	-12.6939
12	T_Mouse	SOS1-PH1	MouseDom	C	-46.556	-11.8582	7	-5.70905
11	T_Mouse	SOS2-PH1	MouseDom	C	-48.4066	-11.7303	7	-5.70905
640	Pombe	SPCp054-	NP_58807	805..898	-17.5762	-6.51671	7	-2.41889
643	Pombe	SPCC4B3.	CAB60689	805..898	-17.5762	-6.53239	7	-2.41889
630	Pombe	reserved_r	NP_59415	722..835	7.893253	-3.22634	4	-0.79655
649	Pombe	SPAC26A	CAA93232	722..835	7.893253	-3.22718	4	-0.79655
635	Pombe	pob1-PH1	NP_59682	701..806	7.048854	1.018837	8	1.776369
646	Pombe	SPBC128	CAB38684	701..806	7.048854	1.018837	8	1.776369
625	Pombe	SPAC11E	NP_59493	683..806	-2.46639	-15.5111	8	-7.79537
627	Pombe	SPAPYUG	NP_59470	584..684	7.412722	7.1358	6	5.127005
629	Pombe	SPAC26A	NP_59415	529..630	12.57498	4.027303	6	3.57941
636	Pombe	csx2-PH1	NP_59589	513..612	7.65289	-3.22718	5	-0.82185
644	Pombe	SPBC17G	CAB52806	513..612	7.65289	-3.27945	5	-0.82185
633	Pombe	SPAC2F7.	NP_59298	394..510	-10.1586	-10.5237	5	-5.06541
628	Pombe	SPAC637.	NP_59463	303..403	-6.77305	0.802741	10	1.576495
632	Pombe	SPAC19A	NP_59379	292..388	-2.9067	0.074765	6	1.187213
641	Pombe	SPCPB16	NP_58802	28..106	2.663912	-6.83352	6	-2.4654
634	Pombe	SPAC1F5.	NP_59286	26..122	-1.17018	-7.78566	8	-3.09871
637	Pombe	SPBC2F12	NP_59571	257..340	6.474466	-2.71999	7	-0.34772
642	Pombe	SPCPB16	NP_58802	225..317	-10.373	-4.38599	6	-1.49608
626	Pombe	plc1-PH1	NP_59473	161..271	-4.45531	-6.19282	12	-2.26644
645	Pombe	SPAC22F	CAB52721	161..271	-4.45531	-6.19282	12	-2.26644
624	Pombe	SPAC23H	NP_59340	152..241	-9.85844	1.698744	10	2.37737
631	Pombe	SPAC6G9.	NP_59411	1053..1154	5.617807	-8.73754	9	-3.69463

623	Pombe	SPAC23H	NP_00101	<707..768	-0.09846	-0.53616	3	0.863051
639	Pombe	ksg1-PH1	NP_58844	<495..570	3.00558	1.622565	10	2.269642
647	Pombe	SPCC576.	CAA21194	<495..570	3.00558	1.622565	10	2.269642
648	Pombe	SPAC19A	CAB16232	<285..346	-0.09846	-0.53754	3	0.863051
638	Pombe	SPBC428.	NP_59518	<194..256	-11.1684	-12.0319	2	-5.77692
476	Cerevisiae	SPO71-PH	NP_01038	980..1279	-6.14986	-2.89494	9	-0.55377
458	Cerevisiae	CAF120-P	NP_01412	92..204	-16.1067	-13.4099	10	-6.48231
469	Cerevisiae	BOI1-PH1	NP_00946	779..893	10.4628	2.78708	9	3.008196
466	Cerevisiae	BOI2-PH1	NP_01103	771..882	8.834833	8.614634	9	5.508196
475	Cerevisiae	TUS1-PH1	NP_01352	665..927	5.529107	4.327729	6	3.907399
459	Cerevisiae	CLA4-PH1	NP_01410	64..174	0.312161	-10.2053	9	-4.83293
453	Cerevisiae	BEM3-PH1	NP_01521	637..738	-9.25796	-3.53138	9	-0.89677
462	Cerevisiae	SPO14-PH	NP_01295	498..660	-2.15045	-0.08083	7	1.104243
470	Cerevisiae	CDC24-PH	NP_00935	479..668	0.076673	-5.05214	6	-1.83974
463	Cerevisiae	SLM1-PH1	NP_01216	471..577	9.280117	-3.27945	11	-0.82431
474	Cerevisiae	ASK10-PH	NP_01161	465..725	8.286208	4.855292	5	4.124394
456	Cerevisiae	SLM2-PH1	NP_01435	448..553	19.74367	2.080356	9	2.64987
471	Cerevisiae	YEL1-PH1	NP_00949	412..551	-5.46683	0.039599	6	1.15546
455	Cerevisiae	SKM1-PH1	NP_01452	4..113	-2.42455	-10.1684	8	-4.83293
457	Cerevisiae	SIP3-PH1	NP_01414	312..421	-21.3193	-10.9527	9	-5.24737
464	Cerevisiae	YSP1-PH1	NP_01202	311..421	-8.54804	-7.30928	8	-2.74737
467	Cerevisiae	OSH2-PH1	NP_01026	292..384	-1.25668	-5.72842	8	-2.05571
451	Cerevisiae	SWH1-PH	NP_00942	284..377	4.743527	-5.72634	6	-2.05571
477	Cerevisiae	NUM1-PH	NP_01043	2523..373	-10.2825	-1.45702	7	0.224625
460	Cerevisiae	ATG26-PH	NP_01329	241..333	4.977611	-14.3826	4	-6.95603
465	Cerevisiae	OSH3-PH1	NP_01194	224..313	16.08234	4.518779	10	3.971304
468	Cerevisiae	OPY1-PH1	NP_00968	218..315	8.069497	-5.67588	14	-2.01846
472	Cerevisiae	YHR131C-	NP_01199	194..306	0.482412	0.741968	6	1.569998
473	Cerevisiae	BEM2-PH1	NP_01108	1846..194	-20.8417	-10.2164	2	-4.94481
452	Cerevisiae	BUD4-PH1	NP_01262	1306..1412	9.501388	-0.39628	7	0.9957
461	Cerevisiae	SKG3-PH1	NP_01328	103..217	-22.5339	-13.0126	8	-6.25892
454	Cerevisiae	PLC1-PH1	NP_01505	<128..213	-1.36843	-12.4441	9	-5.83276

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6 PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.....dKEPRGIIPLENL..SIRE
6 PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.....dKEPRGIIPLENL..SIRE
6 PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.....dKEPRGTIPLENL..SIR
5 IVKEGWVQKRG.....eYIKNWRPRYFLLKT......dGSFIGYKEKP.qdvdlPYPLNNFSVAKC..Q
5 VIKEGWLHKRG.....eYIKTWRPRYFLLKS......dGSFIGHKERPeapdqtLPPLNNFSVAEC..Q
5 IVKEGWLHKRG.....eYIKTWRPRYFLLKN......dGTFIGYKERPqdvdqrESPLNNFSVAQC..Q
9 HLKEGEMYKRAqgrtriGKKNFKKRWFCLTS.......RELTYHRQQG......KDAIYTIPVKNI.lAVE
7 TILEEILIKRSqqkkktSPLNYKERLFVLTK.......SVLSYYEGRA....ekKYRKGVIDISKI..KCVEI
8 VILESIFLKRSqqkkktSPLNFKKRLFLLTV.......HKLSYYEYDF.ergrrGSKKGSIDVEKI..TCVE
9 LLKEGFMIKRAqgrkrfGMKNFKKRWFRLTN.......HEFTYQKSKG......DQPLCNIPIENI.lAVE
7 ILLEEQLIKKSqqkrrtSPSNFKVRFFVLTK.......ASLAYFEDRH...gkkRTLKGSIELSRI..KCVEI
8 VVCSGWLRKSP.pekklKRYAWKRRWFVLRSgrltgdpDVLEYYKNDH.....aKKPIRIIDLNLC.q
8 VVCTGWLRKSP.pekklRRYAWKKRWFILRSgrmsgdpDVLEYYKNEH.....sKKPLRIINLNLC.
5 VIKAGYCVKQG.....aVMKNWKRRYFQLDE.......NTIGYFKSEL.....eKEPLRVIPLKEV.hKVQ
6 LIKSGYCVKQG.....nVRKSWKRRFFALDD.......FTICYFKCEQ.....dREPLRTIPLKDVlkTHE
4 GTKEGYLTKQG.....gLVKTWKTRWFTLQR.......NELKYFKDQ-......-MSPEPIRILDL.tECSA
6 KVCRGYLIKMG.....gKIKSWKKRWFVFDR.....lkRTLSYYVDKH.....eTKLKGVIYFQAI.eEV
4 VAKAGYLHKKG..gtqlQLLKWPLRFVIIHK.......RCIYYFKSST.....sASPQGAFSLSGY.nRVM
4 VLKEGFLVKRG.....hIVHNWKARWFILRQ.......NTLLYYKLEG..grrvTPPKGRIVLDGC..TIT
6 VVKQGYLSKQG.....hKRKNWKVRRFVLRK.....dpAFLHYYDPSK....eeNRPVGGFSLRGS..
6 ILKMGPVDKRK......-GLFARRRQLLLTE......gPHLYYVDPVN......KVLKGEIPWSQE.lRPEA
7 ALKQGWLHKKGggsstlSRRNWKKRWFVLRQ.......SKLMYFENDS.....eEKLKGTVEVRTA.
7 PVQKGFLLKKR....kwPLKGWHKRFFCLEK.......GILKYAKSQ-......-ADIEREKLHGC.iDVGL
7 GDCEGWLWKKK.daksyFSQKWKKYWFVLKD.......ASLYWYINEE.....dEKAEGFISLPEF..
7 ERQEGHLLKKR....kwPLKGWHKRYFVLED.......GILHYATTRQ..ditkGKVHGSIDVRLS..VM
3 RIREGYLVKKG.....sVFNTWKPMWVVLLE.......DGIEFYKKKS.....dNSPKGMIPLKGS..TLT
6 IQLSGMYNVRK.gkmqlPVNRWTRRQVILCG.......TCLIVSSVKD....svSGKMHVLPLIGG..K
5 STMSGYLYRSK.....gSKKPWKHLWFVIKN.......KVLYTYAASE.....dVAALESQPLLGF..TVT
4 VRKVGYLRKPK......---SMHKRFFVLRAaseaggpARLEYYENEKkwrhksSAPKRSIPLESC.f
5 ILKEGMLTKQN.....nSFQRSKRRYFKLRG.......RTLYYAKTAK......SIIFDEVDLTDA..SVAES
6 PTCRGYLHKRT...hsgFVKGWRKRWFVLKH......dGFLLYYKHRK..degkWPPLDMIKLEGA.
8 VYKSGFLARKIgkktprGKRGWKTFYAVLKG.......TVLYLQKDEYekalseEDLKNAVSVHHA..
5 PIYGGWLLLAPfdnpvhRSRKWQRRFFILYE.......HGLLRYALDE...mptTLPQGTINMNQC.t
5 LVRGGWLWRQS.....sILRRWKRNWFALWL......dGTLGYYHDET...aqdEEDRVVIHFNVR..
7 VTIQGVLRRKTkegkkpTVASRTKYWAALCG.......TQLFYYAAKSerkhfkSTSNKNVSVVGW.
5 IVKQGYVKMKS.....rKLGIYRRCWLVFRK.ssskgpQRLEKYPDEK..svclRGCPKVTEISNV.k
6 LLGEGVLTKEC......-RKKAKPRIFFLFN.......DILVYGSIVL..skrkYRSQHIIPLEEV..TLEPLP
5 AKICAFLLRKK......RFGQWTKLLCVIKD.......TKLLCYKSSK.....dQQPQMELPLQGC..SITY
5 LLKGSQLLKVK......SSSWRRERFYKLQE.......DCKTIWQESR..kvmrSPESQLFSIEDI.qEV
1 PECLGLLHQLE.....rSTDVWIQHYCILKD.......GCLYFYASIR.....sTQASGGLYLQGY..SVSE
7 PLIEGKLKEKQ..vrwkFIKRWKTRYFTLAG.......NQLLFQKGKS....kdDPDDPPIELSKV..QS
5 SMVEGSELKKV.....rSNSRIYHRYFLLDA.....dmQSLRWEPSKK......DSEKAKIDIKSI.kEVR
1 IQREGALRFMVaasgpgGTAQWQKCRLLLRR.avagerFRLEFFVPPK.....aSRPKVSIPLSAI.i
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6 SEKKGFLLKKS....dgIRKVWQRRKCAVKN.......GILTISHATS......NRQPAKLNLLTC..QVKP
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4 IVKQGYVRIRS.....rRLGIYQRCWLVFKK.asskgpKRLEKFSDER...aayFRCYHKVELNNV.k
3 CIVHGYMSKMG....npFLTQWQRRYFYLFP.......NRLEWRGEG-......EAPQSLLTMEEI..QS
5 AQMEGFLNRKHahnkkaSSRSWHNVYCVINN.......QEMGFYKDAKaasgipYHSEVPVSLKE
4 GHRKGATKMKD.....fARFKPMQRHLFLYE.......KAVMFCKRRFadrypsYSFKHCLKMEDV..
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6 IIKQGCLLKQG.....hRRKNWKVRKFILRE.....dpAYLHYYDPAG.....gEDPLGAVHLRGC..VV
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7 FIVRGWLHKEVknspkmSSLKLKKRWFVLTH.......NSLDYYKSSE....knALKLGTLVLNSL.cS
5 FVKSGWLLRQS.....tILKRWKKNWFDLWS......dGHLIYYDDQT...rqsIEDKVHMPVDCI..NIR
6 VIKAGYLEKRR.kdhsfLGFEWQKRWCALSK.......TVFYYYGSDK.....dKQQKGEFAIDGY..D
5 VVRRGWLYKQD....stGMKLWKKRWFVLSD.......LCLFYYRDEK.....eEGILGSILLPSF..QIA
2 -----------......--GEWKKHWFVLTD.......SSLKYYRDST..aeeaDELDGEIDLRSC.tDVTEYAVQ
7 IVREGFLLKRKepgglaTRFAFKKRYFRLSG.......RDLSYSKTPE......WQVHTSIPLSCI..RAV
3 NFKKGWLTKQY......EDGQWKKHWFVLAD.......QSLRYYRDSV..aeeaADLDGEINLSTC.y
3 ITKEGMLHYKA.stsylGKEHWKACFVVLSN.......GILYQYPDRT.....dVIPLLSVNMGGE..QC
9 TYKHGVLTRKTgkrtprGRRGWKKFYAVLKG.......TILYLQKDEYdkalseGDLKNAIRVHHA..L
6 VSHSGFLYKTAllqdrrAREEFSRRWCVLGD.......GVLSYFENER.....aVTPNREIRASEI..VCL
5 VVMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKKLK.....dALTVVVDDLRLC..SV
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6 VLKQGYMMKKG.....hKRKNWTERWFVLKP.......NIISYYVSED.....lKDKKGDILLDEN.cCVE
3 FTAEGYLYVQE.krpapFGSSWVKHYCMYRK...takkFNMIPFEHRS...ggkLGDGEAFFLKEC
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2 PTIEGYLYTQE...kwaLGISWAKYYCRYEK...etrmLTMIPMEQKP......GAKQGPVDLTLK.yC
6 AEMAAELGMRG....pkKGSVAKRRLVKLVV.......NFLFYFRPDE......AEPLGALLLERC..RV
4 NQLSGNLLRKF.....kNSNGWQKLWVVFTN.......FCLFFYKSHQ.....dSHPLASLPLLGY..SLT
4 TFLCDFLYQAPlssekkLLEETNKKWCVLEG.......GFLSYYENDK.....sTTPNGTININEV..ICL
2 --MEGVLYKWT.....nYLTGWQPRWFVLDN.......GILSYYDSQD...dvcKGSKGSIKMAVC..EI
6 MKHSGYLWTIG....knVWKRWKKRFFVLVQ..vsqytFAMCSYREKK......AEPQELLQLDGY..
5 PVKEGPLFIHRkgkgplASSSFKKLYFSLTT.......EALSFAKTSS...skkSTFIKLASIRAA.eKVE
3 LVKDGFLVEVS......-ESSRKLRHVFLFT.......DVLLCAKLKKfpdhelEDMKMKISALKS..EIQK
4 VMKEGWMVHYT.....sKDTLRKRHYWRLDS.......KCITLFQNDT.....gSRYYKEIPLSEI.ICLE
4 GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.....sPRPSGLYLLEGS..ICK
4 FLKEGTLMKLS......-RKVMQPRMFFLFN.......DALLYTTPMQ...sgmYKLNNMLSLAGM..KV
7 LMQEGTMMRKV.....rTKSWKKLRYFRLQN.......DGMTVWHGSQ....peSMPKPTFSISDV.e
2 VERCGVLSKWT.....nYIHGWQDRWVVLKN.......NTLSYYKSED...eteYGCRGSICLSKA..VI
3 LMKLGTVARRG......AMGIWKEFFCELSP.....leFRLYLSDEE-......RTCVESCSLLRC..EAV
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2 VSKKGYLHFLE.....pHTAGWAKRFVVVRR.......PYAYMYNSDK.....dTVERFVLNLSTA..QV
5 LHLEGWMKVPR..nnkrGQQGWDRKYIVLEG.......SKVLIYDNE-......AREAGQRPVEEF..EL
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3 SVICSFLHYME.....kGGKGWHKAWFVVPE....nepLVLYIYGAPQ.....dVKAQRSLPLIGF..EV
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6 KGLEGVIRKRSfcgrdqVCYRWSKRWLVVKD.......SFLLYMRPET....gaISFVQLFD-PGF..E
4 SIKEGILKLKEepskilSGNKFQDRCVVLRD.......GHLFIYKDPK.....sSKHDKMFPLRAM..KFY
4 LLREGPVLKIS.....fRRSDPMERYLVLFN.......NMLLYCVPRVlqvgaqFQVRTRIDVAGM..KV
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5 PELADYIKVFK..pkklTLKGYKQYWCTFKD.......TSISCYKSKE...essGTPAHQMNLRGC..E
6 PELEGALYLKE.....dGKKSWKRRYFLLRA.......SGIYYVPKGK..tktsRDLACFIQFENV..NIYY
3 FLHSGKLYKAK......---SNKELYGFLFN.......DFLLLTQITKksnlqyKMYKTPIFLNEV..LVKLPT
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4 GTKRGFLSKKA.....aEASRWHEKWFALYQ.......NVLFYFEGEQ.....sGRPAGMYLLEGC..S
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5 PEIHGFLHAKE.....qGKKSWKKAYFFLRR.......SGLYFSTKGT.....sKEPRHLQLFSEF.sTSH
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5 LLMQGSFSVWTtkvkelARFKPMQRHLFLHE.......KAVLFCKKREyekapsYSYKQSLNMTAV
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4 FVRQGSLMQMSgrlgslSTKKEGERQCFLFS.......KHLIICTRGS.ggklhLTKNGVISLIDC..TLL
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4 PQGDGEIRITT.....lDKHTKRERHIFLFD.......LAVIVCKRKG....dnYEMKEIIDLQQY..KIANN
5 PEIQGFLQVKE.....vGRKSWKKLYVCLRR.......SGLYYSTKGT..skepRHLQLLADLEES..SI
3 PKIDGELKVRS.....iVNHTKQDRYLFLFD.......KVVIVCKRKG....ysYELKEVIELLFH..KMTD
4 PKIDGELKITS.....vERRSKTDRYAFLLD.......KALLICKRRG....dsYDLKASVNLHSF..QVRD
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3 FIMEGTLTRVG......---AKHERHIFLFD.......GLMICCKSNHgassaeYRLKEKFFMRKV..QIND
3 FIMEGPLTRIG......---AKHERHIFLFD.......GLMISCKPNHgyssaeYRLKEKFVMRKI..QICDK
4 LYNEGYLYRLE......-DSSIRRRFVVLRS.......KQLNFYAEKG......GQYLDTFQLSKT..VVSIP
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2 AQKEGVLLKYI......ENSGLVSRYFYLKD.......NILYFAENRN......SPVLGTIHLKDA..QVNRY
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3 LLCDGYLCQQG.....gDCPYWRRRYFQLIG.......SKLVAFQQFS......KVRRATIDLSEA.tHIV
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2 SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK...qslELHTEPIDLLMA..T
2 SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK...qslELHTEPIDLLMA..T
4 HGKEGFATLKRccnttmMKTRSQPFWIIVSE.......SCIILCDNML......SMQPADVFIWDV..DF
6 PIMAGYLIRKT......SFLKKKQRGFYAFT.....hsGYLYEFKSSD..slqdPEPEFALYIPDC..LIGR
5 TKRQGWLLRNIssskadNKAIWRKYWFFVDN.......GYVGYLINDA...nggVFESEKIGVLLC..K
4 VLKSGWLIKKG.....hATSTKKQLWAVLRR.......DQLSFYKDE-......---------KDI.sAVAYYKEK.
5 IIRSGWVMLKE...dkmKYLPWTKKWLVLSS.......NSLSIYKGSK.....sESAQVTLLLKDI.qKVE
4 QHMSGYLKKWT.....nYKSGYKLRWFTLNN.......GVLSYYKNQD...dasSACRGSINLKLA..R
2 VLMQGTIHWLH.....gNLHRWSKCWAVVRG.......YGMTIYNTNR.....eYKPVKVIPIADI.qDV
6 SIQNGCSLLRI......TKKKVRQRKVSLDP.....isGYLMLDKNTG....kaYKKLCVDDIKEI.rQGR
6 SIQNGCSLLRI......TKKKVRQRKVSLDP.....isGYLMLDKNTG....kaYKKLCVDDIKEI.rQGR
8 QIISGTLLKKR....rkKGQGYARRYFTLNM.....veGTISYYANEN.....sSVMRGKIPLSIA..VISV
7 WHRRGMISYKKsknnrwVAGYWKKKYCIVDS.......GKLIFYKSDHnacsnvSPIHREFGLQSC.
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2 AQKKAYERRYK......NFTTTSSSFDTLQG.....idTEAMEYEFPKtppleeFSPDTSYSLVNA.fAY
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0 PSLASEQMHDS.....dADSLFQSANDHLNRakatqdcRGLLFYSKSQ....stSVPSGIINLTDA.vS
3 LIQKGPLYQKP.....hKHSVFSKYYVVLIS.......GFIVLFHCFHakevleYAHYVTIPIDDC..YLYS
3 RYHEGVFLILQnnngthAARKWKDVYGVLLG.......TQLALWDAKEkklkevASKPTYINLTDA..
4 ADCSGWMSKKG....tgAMGTWKQRFFTLHG.......TRLSYFTNTN.....dEKERGLIDITAH..RV
4 ADFSGWMSKKG....sgAMSTWKTRFFTLHG.......TRLSYFSSTT.....dTRERGLIDITAH..RV
3 LVLSGTVYKKR.....dLWLDPTPVYIALLD.......NCLLITEEISgetqkyKLIERPIPIDYL..SLEKRK
3 KKKSGWVSYKD...dgiLSFIWQKRYLMLHD.......SYVALYKNDK....qnDDAILKIPLTSI.iSVSR
5 NVKDGSLLLRR.pktltGNSTWRVRYGILRD.......DVLQLFDKN-......-QLTETIKLRQS..SIELI
5 QGKQGYLVIRSkhafkdMIDRHTTKWFLVRN.......SYLTYVSDLS.....sTTPLDVFLIDWK.fKV
1 ISKFGELLYFDisttnsSSEPEREFEVYLFE.......KIIILFSEVVsslilkKKSSTSASISAS..NITDNN
5 EIKSGFLERRS.....kFLKSYSKGYYVLTP.......NFLHEFKTAD..rkkdLVPVMSLALSEC..TVTE
2 CIKAGYFLKKS.....eLLPTYHQGYFVLTS.......NYIHEFQSSDirkksyLAPIMSIPLNDC..TLKD
5 EVKSGFLEKRS.....kFLKSYSRGFYVLTP.......SFLHEFKTPD..khkfSTPLMSIPLVEC..TVTE
2 TSRRTSLSYLN......KDSEWERVKIQVKE.......GRIFIFKIKPdyfkdiSSSYFAYSLLEA..EAHV
3 VKKEGWISYKV...dglFSFLWQKRYLVLND.......SYLAFYKSDK....cnEEPVLSVPLTSI.tNVS
5 PEKSGWLYMKT.qvgkpTREIWVRRWCFLKN.....avFGMFLLSPSK..tyveETDKFGVFLTNV
5 KGLSGWLYMKTtvghdpKRVVWVRRWCFLQN.......NVFGVFSLSP..sktyVEETDKFGILWI..
3 PTYKGFLKKWT.....nFAHGYKLRWFILSG......dGNLSYYKDQS....hvDRPRGTLKVSTC..RL
3 PTYKGYLKKWT.....nFAQGYKLRWFILSS......dGKLSYYIDQA...dtkNACRGSLNMSSC..SL
4 TVIGEYLFKYYprlgpfGFESRHERFFWVHP.......YTLTLYWSASilenpaNTKTKGVAILGV.eS
4 VKMSGNLNIRT......KLIRSTRYWCVLKN.......HLFSMYTSST....elYFPVLTIDLREV.qKIETQ
9 RYLQGYLLKKR....rkRLQGFKKRFFTLDF.....ryGTLSYYLNDH.....nQTCRGEIVISLS..SVS
8 QVCSGILYTKVkkkklfNRAKWQKFNVELTN.....tsFNLYSFKTG-......-KLKKSIKLDKI.iDCIEL
2 RIHSDLVHRSD......QSQHLHHRLFTLPT.......RSASEFKKADsryltdEALYKSFTLQNA..RFG
1 KKIGGFFRRPFsiggfnTSSSNYSLNSILSQ....evsSNKSILPSILvdsmqlHDLKPSYSLKTF..EI
3 IYKEGYLLQDG....gdLKGKIENRFFKLHG.......SQLSGYHEI-......-SRKAKIDINLL..KVTKVL
2 RYHYGIFLILHktdgtpAARQWEECYGVLLG.......TQLALWDAKEstmkkaASRPSFINFTDA..S
6 VLQRGIMIRMT.....rRRRKFYEFKLINNN.......GQIIWKDGS-......-KYLELDSVKDI..RIGDTAS
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VEDP.........................RKPNCFELYNpSHkgqvikackteadgrvvegnhVVYRISAPSPEEKEEWMKSIKASI
VDDP.........................RKPNCFELYIpNNkgqlikackteadgrvvegnhMVYRISAPTQEEKDEWIKSIQAAV
EVEDS.........................KKPNCFELYIpDDkdqvikackteadgrvvegnhTVYRISAPTPEEKEDWIKCIKAAIS
MKTERP..........................-KPNTFIIRCIQW.................ttvIERTFHVDTPEEREEWTEAIQAVAD
LMKTERP..........................-RPNTFVIRCIQW.................ttvIERTFHVDSPDEREEWMRAIQMVAN
LMKTERP..........................-RPNTFIIRCIQW.................ttvIERTFHVETPEEREEWATAIQTVAD
KLEEG........................sfNKKNMFQVIHtEK....................-TLYIQANNCVEANEWIDVLCRVSR
KN...................ddgvipcQNKFPFQVVHdAN....................-TLYIFAPSPQSRDRWVKKLKEEIK
TVIPeknppperqiprrgeessemeqisiieRFPYPFQVVYdEG....................-PLYVFSPTEELRKRWIHQLKNVI
RLEEE........................sfRMKNMFQVIQpER....................-ALYIQANNCVEAKDWIDILTKVSQ
VKS....................disipcHYKYPFQVVHdNY....................-LLYVFAPDCESRQRWVLTLKEETR
QVDAGLTF.....................nkkefENSYIFDINTiDR....................-IFYLVADSEEDMNKWVRCICDICG
eQVDAGLTF.....................nkkelQDSFVFDIKTsER....................-TFYLVAETEADMNKWVQSICQICG
ECKQS........................dimMRDNLFEIVTtSR....................-TFYVQADSPEEMHSWIKAVSGAIV
LVKS.......................gdlIMRDNLFEIITtSR....................-TFYVQADSPEDMHSWIEGIGAAVQ
QFD........................ysqERVNCFCLVFpFR....................-TFYLCAKTGVEADEWIKILRWKLS
YDHLR.....................saakspNPALTFCVKThDR....................-LYYMVAPSAEAMRIWMDVIVTGAE
RAAEE........................ttsNNVFPFKIIHiSK..................khRTWFFSASSEDERKSWMALLRREIG
PCLE........................yeNRPLLIKLKTrTS....................TEYFLEACSREERDSWAFEITGAIH
LVSALEDN.................gvptgvkgnVQGNLFKVITkDD....................THYYIQASSKAERAEWIEAIKKL-T
KNF-..........................---KTFFVHTpNR....................-TYYLMDPSG-NAHKWCRKIQEVWR
EIIDNTS-.........................-KENGIDIILaDR....................-TFHLIAESPEDASQWFSVLSQVHS
SVMS......................vkKSSKCIDLDTeEH....................-IYHLKVKSEELFDEWVSKLRHHRM
KIDRASEC.........................RKKYAFKACHpKI....................KSFYFAAEHLDDMNRWLNRINMLTA
ISINKK-..........................--AQRIDLDTeDN....................-IYHLKIKSQDLFHSWVAQLRAHRL
SPCQD........................fgKRMFVLKITTtKQ....................QDHFFQAAFLEERDAWVRDIKKAIK
EEVKK-..........................-HQHCLAFSSsGP..................qsQTYYICFDTFTEYLRWLRQVSKVAS
LVKDE..........................nSESKVFQLLHkGM....................VFYVFKADDAHSTQRWIDAFQEGTV
INKRADS..........................KNKHLVALYTrDE....................-HFAIAADSEAEQDSWYQALLQLHN
STK...........................NVNNSFTVITpCR....................-KLILCADNRKEMEDWIAALKTVQN
EVDIDNSL.........................GKPFVFNCMPqSG...................sRILCLCATSNQEMKRWLEAMQRAA
LASKATDY.........................eKKPNVFKLKTaDW....................RVLLFQTQSPEEMQGWINKINCVAA
VVDGEAR.........................tGQKFSLCILTpDK....................-EHFIRAETKEIISGWLEMLMVYPR
DIKVGQEC..................qdvqppegrSRDGLLTVNLrEG....................SRLHLCAETRDDAIAWKTALMEA
MVMMADDP..........................EHPDLFLLTDsEK...................gNSYKFQAGSRMNAMLWLKHLSAA
VTRLPKE..........................tKRQAVAIIFTdDS....................-ARTFTCDSELEAEEWYKTLSVECL
T.........................lQAKNRWMIKTaKK....................-SFVVSAASTTERQEWISHIEECVR
PRD........................skKKKHELKITQqGT....................DPLVLAVQSKEQAEQWLKVIKEAYS
MGHRT.................eglekfardiPEDRCFSIVFkDQ....................rNTLDLIAPSPADVQHWVQGLRKIID
QTHG..........................FEQPVIELKPsSE...................efKTFYFCAENKTENQRWIAALKTSIK
KAVAK....................krrdrSLPRAFEIFTdSK....................-TYVFKAKDEKNAEEWLQCINVALA
GKNT...............difrsngiseqiSEDCAFSVIYgEN....................yESLDLVANSADVANIWVTGLRYLIS
EVRTTMPL........................empEKDNTFVLKVeNG....................AEYILETIDSLQKHSWVADIQGCVD
.vSVVPVTVE.......................sppePGAAAFRLDTaQR....................-SHLLAADAVSSTA-WVQTLCRT
NAE-..........................-DKKSFDLIShNR....................-TYHFQAEDEQDYIAWISVLTNSKE
LEGNLQG..........................-NPCRFALTSrGP.................eggiQRYVLQASDPAVSQAWIKQVAQILE
VARLPKS..........................TKKHAIGIYFnDD....................TSKTFACESDLEADEWCKVLQMECV
VEETQI...........................KERKCLLLKIrGG....................KQFVLQCDSDPELVQWKKELRDAYR
A..ICEVALDY.........................kKKKHVFKLRLsDG....................NEYLFQAKDDEEMNTWIQAISSAIS
ITEHVKG..........................-DNRKFEIRYsEK...................eEIYIVQAPNVDVKMLWLKEIRKILV
ANE..........................-EKAMFLISAsLQ..................gpEMYEIYTSSKEDRNAWMAHIQRAVE
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TSVESS....................hdgkksDEENLFEIITaDE....................VHYYLQAATSKERTEWIKAIQVASR
KCEELRKS.....................ksrskKNHSKFTLARcRQ...............pgttaPNLIFLAVSPEEKESWINALSSAIT
SVVPPDEK........................ifKETGYWNVTVyGR...................kHCYRLYTKLLNEATRWSSAIQNVTD
RTGHEC.................rdiqppdgkPRDCLLQIVCrDG....................KTISLCAESTDDCLAWKFTLQDSRT
VRMNNTL......................rkdgKKDCCFEICApDK....................RIYQFTAASPKDAEEWVQQLKFILQ
MLTAE.......................dhiNRKYAFKAAHpNM....................RTYYFCTDTGKEMELWMKAMLDAAL
..........................-RNYGFQIHTkDA....................-VYTLSAMTSGIRRNWIEALRKTVR
EHVDE.......................gafQLPHVMQVVTqDG................agtsHTTYLQCKNVNDLNQWLSALRKASA
DVTEYPVQ..........................-RNYGFQIHTkEG....................-EFTLSAMTSGIRRNWIQTIMKHVL
GGCRRS.......................nttDRPHAFQVILaDR....................PCLELSADSEAEMADWMQHLCQAVS
ATRASDY.........................sKKSNVLKLKTaDW....................RVFLFQAPSKEEMLSWILRINLVAA
AVPPP.......................dthGFEHTFEVYTeGE....................RLYLFGLESAEQAHEWVKCIAKAFV
KPCEDI..........................ERRFCFEVVSpTK....................-SCMLQADSEKLRQAWVQAVQASIA
DVEKG........................fmSNKHVFAIFNtEQ.............rnvykdlRQIELACDSQEDVDSWKASFLRAGV
ESLPDK.........................dGKKCLFLIKCfDK....................-TFEISASDKKKKQEWIQAIYSTIH
..TKRHMDST..........................DRRFCFDIEAaDR..................pgVPLTVQAFSEEERKQWLEALGGKE
RDVEKG........................fmSSKHIFALFNtEQ.............rnvykdyRQLELACETQEEVDSWKASFLRAGV
VRRKTES.........................iDKRFCFDIETnER...................pGTITLQAPSEANRRLWMEAMDGKEP
AQEE--..........................--PGGFSISFvED..................lsRKYHFECCSQEQCQDWMEALQRASY
TIPSES.......................eniHKDYVFKLHFkSH....................-VYYFRAESEYTFERWMEVIRSATS
AIHKE....................dfylntGPIFIFEIYLpSE....................RVFLFGAETSQAQRKWTEAIAKHFV
KVHPA-..........................-DNTRMELIIpGE....................QHFYMKAVNAAERQRWLVALGSSKA
TVDYTDPQ.....................pglegGRAFFNAVKEgD-....................-TVIFASDDEQDRILWVQAMYRATG
EKSFG..........................-SSHIMQVIYaDD................vgraQTVYLQCKCVNELNQWLSALRKAST
EKAN...kgqsraierlkkkmfeneflllnSPTIPFRIHNrNG....................KSYLFLLSSDYERSEWREAIQKLQK
PAKPS....................altpvgATPHCFEITTaNV....vyyvgenvvnpssspp nNSVLPSGIGPDVARMWEVAIQH
RAPSP........krgtsskesgekqrhsrsrRRRNVLRRQPtRI...................sKTFRLVAIELTGMT---ATLEVSFS
RKPTQE.........................AYQNELKIESvER....................-SFILSASSAAERDDWLEAISSSIE
RIRKGQDS................ellrylveefPLEQGFTVVFhGR...................rPNLDLVANSVEEAQIWMRGLQLLV
TPHDF-..........................-DECRFDISVnDS....................-VWYLRAQDPEHRQQWVDAIEQHKT
GPAH-..........................-SDGRFELVFsGK....................-KLALRASSQDEAEDWLDRVREALQ
LEDQ........................gqTLANVFILRLIEN...............addreATYMLKASSQSEMKRWMTSLAPNRR
EYSEDQ......................qamlKTPNTFAVCTeHR....................-GILLQANSDKDMHDWLYAFNPLLA
CLPDGD.........vsihgavgaselantakaDVPYILKMEShPH..............ttcwpgRTLYLLAPSFPDKQRWVTALE
VSIATPK.......................qkpKTPFCFVINAISQ....................-RYFLQANDQKDLKDWVEALNQASK
QVRALPSA........................daEANAVCEIVHvKS.............esegrpeRVFHLCCSSPESRKDFLKSVHSIL
GPPEAG.......................erpDRRHVFKITQsHL....................-SWYFSPETEELQRRWMAVLGRAGR
SGPS....................kgsvpyDAELSFALRTgTR.................hgvDTHLFSVESPQELAAWTRQLVDGCH
QVGKRS.........................tETRYGVRIDTsHR....................-SLILKCSSYRQARWWGQEITELAQ
LGVKK..........................------KMKPpTR....................-------------------------
RELTDA.........................EFPHSFLVSGkQR....................-TLELQARSRDEMVSWMQACQAAID
DG...........dvrmggsfrgafgnsdKAKNIFRVRFqDP.................spgHSHTLQANDVFHKQQWFNCIRAAIA
.RLVHSGSG....................crspslGSDLTFATRTgSR.................qgiEMHLFRVETHRDLSTWTRILVQG
SEDQ......................qamvKTPNTFAVCTkHR....................-GVLLQALNDKDMNDWLYAFNPLLA
IS..IVQAVPEH.........................pKKDFVFCLSNsLG....................DAFLFQTTSQTELENWITAIHSACA
DVRTATAL.......................empDRENTFVVKVeGP....................SEYILETSDALHVKAWVSDIQECLS
TPDVNI..........................sGQKFNIKLLIpVA.................egmNEIWLRCDNEKQYAHWMAACRLASK
GIQC....................kmkykaPTDHCFVLKHpQI................qkesqYIKYLCCDDARTLSQWVMGIRIAKY
DP.........................sGDEPIFHISHiDR....................-VYTLRAESINERTAWVQKIKAASE
YLGVKK......................klrpPTCWGFTVVHeTE................khekQQWYLCCDTQMELREWFATFLSVQ
ESEEE.........................wGVPHCLTLRGqRQ....................-SIIVAASSRSEMEKWMEDIQMAID
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IVQSVPEH........................pKKEHVFCLSNsCG....................DVYLFQATSQTDLENWVTAIHSACA
KVGRKE........................tETKYGLRIDNISR...................-TLILKCNSYRHARWWGGAIEEFIR
VHSGPG...................kgspqaGMDLSFATRTgTK.................qgiETHLFRAEISRDLSHWTRSIVQGC
ERTPAP............prtnagpagardalDKQYYFTVLFgHD.................gqKPLELRCEEEQAGKEWMEAIHQ
PDG.............sdddpkgsghmfgHLDFKIVVEPpDA.................asFTVVLLAPSRQEKAAWMSDISQCVD
LEDS........................eNHRNAFEISGsMI...................ERILVSCTSQQDLHEWVEHLQKQTK
PSK.........................KDGFCFKLFHpLDvwavkgpkgesvgsitqplpsSYLIFRAASESDGRCWLDALELAL
HVEG.........................-DPCKFALWSgRT................pssdNKTVLKASNIETKQEWIKNIREVIQ
RAPSP...............krgtsskesgeKQQHYFTVNFsND..................sqKTLELRTEDAKDCDEWVAAIARASY
EDLQDG..........evrlggslrgafsnneRVKNFFRVSFkNG................sqsQTHSLQANDTFNKQQWLNCIRQ
RPVTQG..................dvyraeteEIPKIFQILYaNE................gecrKDVEMEPVQQAEKT----NFQNHKG
SNL.........................NMPRTFLVSGkQR...................-SLELQARTEEEKKDWVQAINSTLL
SNL.........................NMPRTFLVSGkQR...................-SLELQARTEEEKKDWVQAINSTLL
VYMSL.................agkkkhgaPTPYGFCLKPnKA................ggprDLKMLCAEEEQSRTCWVTAIRLLKD
DIVKP.........................NAACTFIITGrKR...................-SLELQTRTEEEKKEWIQVIQATVE
DP........................sSDEPVFHISHiDR...................-VYTLRTDNINERTAWVQKIKGASE
AHE.........................-EKGLFLISMgVK..................dpEMVEVHASSREERNSWIQIIQDTIN
ANQ.........................-AKGMFLISSgPP....................EMYEVHAASRDDRTTWIRVIQQSVR
..GITENVKG.........................-DTKKFEIWYnAR...................eEVYIIQAPTPEIKAAWVNEIRKVLT
NVYVVTQG....................rklygmPTDFGFCVKPnKL...............rnghkGLHIFCSEDEQSRTCWLAAFRLF
DEPEN...............lddeakgagpeIEHLEFKIGVePK................dslpFTVILVASTRQEKAAWTSDIIQCVD
ANE.........................-ERGMFLISAsSA..................gpEMYEIHTNSKEERNNWMRRIQQAVE
TT....................dkenkKWSYGFYLIHtQG...................qNGLEFYCKTKDLKKKWLEQFEMALS
YLIAG....................kkqynaPNEHGMCIKPnKA...............ktemkELRLLCAEDEQIRTCWMTAFRLLKY
PMH.....................nkdikKWSYGFYLIHlQG...................kQGFQFFCKTEDMKRKWMEQFEMAMS
DSSG.....................erdnkKWSHMFLLIEdQG...................aQGYELFFKTRELKKKWMEQFEMAIS
PMH................nkdikkshgkMWSYGFYLIHlQG...................kQGFQFFCKTEDMKRKWMEQFEMAMS
KDDT........................sEYKHAFEIILkDG....................NSVIFSAKSAEEKNNWMAALISLQY
EDA........................cEYRHAFELVSkDE....................NSVIFAAKSAEEKNNWMAALISLHY
MVN..................fseavsnlGLVAGILATSvDR...................RHVQLFADSKKVCQKWLQVMNSRSF
MVN..................fseavsnlGLVAGILATSvDR...................RHVQLFADSKKVCQKWLQVMNSRSF
NAN.........lpifsiidpphefltgeNYQSAFVIQEkQT.............etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
NAN.........lpifsiidpphefltgeNYQSAFVIQEkQT.............etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
VTKTDDI......................vlsGGKTAIKLIPpAP........gaakaavmftppKVHYFTCENNEELHRWSSAFLKAT
VTKTDDI......................vlsGGKTAIKLIPpAP........gaakaavmftppKVHYFTCENNEELHRWSSAFLKAT
LAKP..............fpssedavvlksTNSLYFDLETsSQ...................LKLRFAGPSPKDAQGWIDALNYWAA
DNHY................sdeeelegylYFESGFRIIFsNG...................DYIDFYAETVGEKDEWMSTLRQHLG
ADKVRKQ.........................GRRFCFEVVTpKL...................-KRLYQATSAEEMDSWIEAICEAAK
VRPAQSV.........................SRKFCFEVITpQT...................-KRTYQATSKAEMHSWIEAIQYSIS
VRPAQSV.........................SRKFCFEVITpQT...................-KRTYQATSKAEMHSWIEAIQYSIS
ITRKN............frkahskdtnekirLSHHSFKIKNrQK...................-VMKLSVRSG----RWLQQFINSVQ
PSE-.........................-KKPKFKITGkDA............tkkifgarNDYAFRASNNTELMRWWEALNTHIA
FSVLPSN.........................HRKFCFQIKTkSV...................-SYILQAETHMEMLEWGSVINNARE
.........................-SPKTFFLYLnEK...................-IIRLIATSNEDAEEWVHVLRSTTG
RSKS-.........................-RTFCFKLRFkSS..............tknfeiQACELSVADNMECYEWMDLISSRAL
LVHDPK-.........................-QPTVFQVIGkGS....................VRYSVKANSPVEAKKWIAAISSAIE
EINVP.......................esSHKYFFTVITqNK...................-PIEFRVDNEDSLILWVAALKTSID
ARNY.................reqykisseNEKRWFTIIYcAD.................nklKAMHMISPTLDAHNQWIMALEGLKT
ARNY.................reqykisseNEKRWFTIIYcAD.................nklKAMHMISPTLDAHNQWIMALEGLKT
AE-.........................--THEINVDSgVE...................-LWNLRAHTHQDWLRWCNALEKAKN
..LASPNLPP.....................sinsNRNNVFYLNIpGN...................ECYLFEAPSVLAMNEWIHSLNFNAA
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CDRDKK..........................nVRNCSFTVIFrDG....................SEETLCAPTEESMIEWVAKINYIST
MVK...........................NNEHGWVVETpTK....................-SWSFEDPNG-PASAWVELLDKASS
MVK...........................NNEHGWVVETpTK....................-SWSFEDPNG-PASAWVELLDKASS
CDRDKK..........................nVRNCSFTVIFrDG....................SEETLCAPTEESMIEWVAKINYIST
IEPGTG-..........................---NKFTINFnNG....................KSETLEALDPESKNTWITDLKNAIA
TTTdrtfdeinygshalprvygdgwrsvedESSRCFTLWFgTRnsnvpsntdkihftkklgvsgKSMVFMARSRQERDLW
TLRTLDNS.................dnivmecgkNLTNALVVSTtLK....................NRYFLQFGNKESFNAWNSAIRLCL
LPASDD..............drlislyaaslgKGKYCFKLVPpQP..........gskkgltftepRVHYFAVENKSEMKAWLSAIIKAT
PAKED..............dklvslyaastgKGRYCFKLLPpQP..........gskkgltftqpRTHYFAVDNKEEMRGWMAALIK
IPkssgnhmstaygdrktsnteisnanpnTDEFSFKIRNtAT...................gESFKFFTESAEVLNQWIDAIMESFK
TQL-..........................-KQYCFELVRcSDrnsvssgssssInvssdsnskKSIYIATKTESDLHSWLDAIFAKCP
NL.....................pedrfGTRNGFLITEhKK..............sglstsTKYYICTETSKERELWLSAFSDYID
FSGNKleefgiendannildkngkskthqkksNISSKLLLLTIEN..................seRKLKIICKSESSLKQWMSSIIKM
SnnsnnsssssIfklsanepkldlrgriMIMNLNQIIPqNN........rslnitwesikeqGNFLLKFKNEETRDNWSSCLQQLI
HSRK.................nstsspnstGSDAKFVLHAkQN..............giirrgHNWVFKADSYESMMSWFDNLKILTS
SSThkflkgskpknkntksseldqfyaaaqKESNNYVTWTfKI....................VSPEPSEEELKHFKRWVQDLKNL
HSKK....................tksnseQGKNKFILRTnSN..............glihrgHNWVFKVDSYDDMIEWFGNIKALSS
QDN.........iiigsgamksnvcnkntkRKSGNFTVSFpEN...............ingpkLVLEFQTRSVEEAHKFMDCINFW
RIQL-..........................-KQNCFEILRaTD...qkenispinsyfyesnskRSIFISTRTERDLHGWLDAIFAKCP
..RYDPEED-..........................-RKFCFEVKIfGN.........kvteahdnmskdITLVFQTSNYLDLKSWLIAFEATK
TVEYLPKE..........................PRNFCFKLRIqNP...........nckteeentyIDIILQAESIDELKSWINTLTSHKR
HIDSS-..........................-EKLNFELLGgIT..................gtTRWRLKGNHPIETTRWVNAIQSAIR
HLDSS-..........................-EKLKFEIIGgNN..................gvIRWHLKGNHPIETNRWVWAIQGAIR
VTDPNPY.......................ptgLYHKSIVVTTeTR....................-TIKFTCPTRQRHNIWYNSLRYLLQ
KHT.......................lngSATKTFKLYTdES....................-TFKFNADSEFSAKSWVNALKKEQF
NKK-..........................--DKIIIIDSgME....................-VWVLKATTKENWQSWVDALQTCFD
DNN......................skmkNDDTNFALITfDE....................-RLSFKAANDQDMVDWIINFKSGIL
IPTDY.........................tKKSFVLRMSCeSE....................-QFLLRFSHIDDMIDWSMYLSIGIS
KSIMEI...................inhrnipAYYYAFKIVMqNG....................HEYLIQTASSSDLTEWIKMIKASKR
N..........ediqadnggqrnftdwvLFNECFQLVFdDG....................ERITFNAECSEEKSDWYNKLQEVVE
VRSLDAN............dqviiasenektkkDLDNVLVVSTtLK....................NRYFLKFKNSKSFKTWNAAIRLSL
T..............yqeevdpkrlrsDSKLWIAIIYkVS.................nkIKALHVVALNELDFNTFLSCICGLVK
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Park et al, Supplementary Table 6:
RFC scores calculated for mouse, human, Dictyostelium, C.elegans, Drosophila, zebrafish, S.Ce

Species	Name	Score	NP_number	Cloned and Tested Translocating?
Celegans	akt-2-PH1	57.5	NP_001024612	T
Celegans	akt-1-PH1	47.7	NP_001023647	T
Celegans	sec7-PH1	36.0	NP_498764	N
Celegans	mtm-5-PH1	5.9	NP_508888	
Celegans	W09C5.5-PH1	3.0	NP_493390	
Celegans	obr-1-PH1	0.7	NP_499448	N
Celegans	let-502-PH2	-0.1	NP_491440	N
Celegans	obr-4-PH1	-0.1	NP_491691	
Celegans	F31D4.5-PH1	-0.6	NP_508029	
Celegans	gap-1-PH1	-1.6	NP_508404	
Celegans	beta1-syntrophin-PH1	-3.0	NP_492521	
Celegans	max-1-PH1	-3.0	NP_001041092	
Celegans	pdk-1-PH1	-4.1	NP_001024743	
Celegans	egl-8-PH1	-4.3	NP_001021348	
Celegans	unc-31-PH1	-5.6	NP_502437	
Celegans	gap-2-PH1	-5.7	NP_509594	
Celegans	cnt-2-PH2	-5.9	NP_001022838	
Celegans	F59A6.5-PH1	-6.4	NP_494921	N
Celegans	plc-2-PH1	-6.7	NP_506752	
Celegans	soc-1-PH1	-6.8	NP_504250	
Celegans	T25E12.4-PH1	-7.5	NP_507240	
Celegans	F25H2.6-PH1	-7.5	NP_492762	
Celegans	F10G8.8-PH2	-7.8	NP_492655	
Celegans	sma-1-PH1	-8.2	NP_741632	
Celegans	pld-1-PH1	-8.2	NP_494939	
Celegans	K10B4.3-PH1	-9.0	NP_493664	
Celegans	C04D8.1-PH1	-9.1	NP_498877	
Celegans	let-502-PH1	-9.2	NP_491440	
Celegans	ani-1-PH1	-9.5	NP_499624	
Celegans	stn-2-PH1	-9.7	NP_001024610	
Celegans	exc-5-PH2	-10.0	NP_001023039	
Celegans	W02B8.2-PH1	-10.7	NP_496914	
Celegans	unc-70-PH1	-11.2	NP_001024053	
Celegans	ZK632.12-PH1	-12.0	NP_499183	
Celegans	ani-3-PH1	-12.7	NP_507814	
Celegans	cnt-2-PH1	-13.4	NP_001022838	
Celegans	F10G8.8-PH1	-13.7	NP_492655	
Celegans	cnt-1-PH1	-13.8	NP_001022413	
Celegans	F52D10.6-PH2	-14.7	NP_509935	
Celegans	tag-59-PH1	-15.9	NP_504599	
Celegans	mig-10-PH1	-16.0	NP_001021248	
Celegans	Y37D8A.25-PH1	-16.2	NP_001022833	
Celegans	dyn-1-PH1	-16.3	NP_001024332	
Celegans	phospholipase-PH1	-16.7	NP_501213	
Celegans	cnk-1-PH1	-17.2	NP_499274	
Celegans	exoc-8-PH1	-18.1	NP_001021703	

Celegans	unc-73-PH2	-18.2	NP_001021501	
Celegans	F22G12.5-PH1	-18.2	NP_493307	
Celegans	pll-1-PH1	-18.2	NP_741067	
Celegans	rga-2-PH1	-18.8	NP_493035	
Celegans	F52D10.6-PH1	-20.3	NP_509935	
Celegans	Y55D9A.1-PH1	-20.3	NP_502417	
Celegans	tag-218-PH1	-20.5	NP_494707	
Celegans	chimaerin-PH1	-20.5	NP_497989	
Celegans	obr-3-PH1	-20.6	NP_741924	
Celegans	ZK1248.10-PH1	-21.9	NP_495156	
Celegans	T04C9.1-PH1	-24.7	NP_741164	
Celegans	uig-1-PH1	-25.7	NP_506293	
Celegans	tag-77-PH1	-25.8	NP_501455	
Celegans	grk-2-PH1	-26.2	NP_497235	
Celegans	tag-150-PH1	-27.7	NP_741736	
Celegans	ani-2-PH1	-29.5	NP_495282	
Celegans	tag-52-PH1	-30.3	NP_508633	
Celegans	F38B7.3-PH1	-30.4	NP_505929	
Celegans	Y95B8A.12-PH1	-30.7	NP_001032993	
Celegans	vav-1-PH1	-30.8	NP_001041223	
Celegans	sos-1-PH1	-33.3	NP_504235	
Celegans	unc-73-PH1	-39.6	NP_001021501	
Celegans	exc-5-PH1	-45.4	NP_001023039	
Danio	zgc:152822-PH1	88.4	NP_999847	264..388
Danio	LOC569358-PH1	87.2	XP_697830	262..388
Danio	LOC100002753-PH1	86.8	XP_001342459	148..258
Danio	zgc:73134-PH1	82.9	NP_956016	264..385
Danio	LOC566849-PH1	65.2	XP_695228	265..375
Danio	akt2-PH1	65.0	NP_937789	6..107
Danio	akt2l-PH1	63.4	NP_997980	6..107
Danio	LOC100002849-PH1	63.3	XP_001342534	59..166
Danio	LOC100003513-PH1	51.8	XP_001343052	117..212
Danio	LOC560668-PH1	49.2	XP_689158	1211..1317
Danio	LOC556983-PH1	44.7	XP_685028	579..674
Danio	LOC566287-PH1	44.0	XP_694648	1105..1204
Danio	zgc:56412-PH1	39.0	NP_998522	8..115
Danio	LOC559185-PH1	38.2	XP_687595	19..118
Danio	LOC567921-PH1	36.5	XP_696327	45..135
Danio	LOC100004342-PH1	36.1	XP_001339977	73..163
Danio	LOC798084-PH1	30.6	XP_001338541	30..127
Danio	plekha1-PH2	27.1	NP_998601	193..284
Danio	zgc:111998-PH1	26.3	NP_001017691	152..240
Danio	LOC556974-PH2	25.2	XP_685018	194..285
Danio	LOC570275-PH1	24.5	XP_698830	1278..>1329
Danio	LOC100003662-PH2	24.3	XP_001343165	363..455
Danio	itk-PH1	23.9	NP_571179	6..108
Danio	LOC555290-PH1	22.6	XP_682853	1250..1343
Danio	plek-PH2	22.4	NP_957135	247..347
Danio	LOC567753-PH2	22.1	XP_696146	258..360
Danio	zgc:101089-PH1	20.1	NP_001004646	1..79
Danio	LOC100004188-PH1	19.6	XP_001343551	24..140

Danio	LOC567753-PH1	19.2	XP_696146	12..107
Danio	osbpl6-PH1	18.4	NP_001005927	72..161
Danio	zgc:63721-PH1	16.6	NP_957334	214..305
Danio	LOC100002149-PH2	16.3	XP_001342004	257..362
Danio	zgc:153787-PH1	14.5	NP_001070812	445..531
Danio	LOC569779-PH1	14.1	XP_698280	1191..1284
Danio	LOC565754-PH1	14.1	XP_694119	61..160
Danio	zgc:153920-PH1	14.0	NP_001070792	16..122
Danio	zgc:154018-PH1	13.9	NP_001070226	15..110
Danio	LOC558834-PH1	13.2	XP_687193	562..657
Danio	zgc:92634-PH1	12.6	NP_001038623	1746..1846
Danio	max1-PH1	12.5	NP_001070987	648..735
Danio	plek-PH1	12.2	NP_957135	7..99
Danio	LOC797259-PH1	12.0	XP_001337715	2..101
Danio	LOC568768-PH1	11.4	XP_697212	325..420
Danio	LOC570940-PH1	10.0	XP_699568	216..298
Danio	LOC568764-PH1	9.4	XP_697207	112..206
Danio	LOC571486-PH1	9.3	XP_700175	137..251
Danio	zgc:153733-PH1	9.2	NP_001038864	20..108
Danio	LOC567300-PH1	7.6	XP_695683	173..261
Danio	LOC564212-PH1	7.0	XP_692653	794..902
Danio	si:dkey-183c16.1-PH2	5.9	XP_684366	525..616
Danio	zgc:158404-PH1	5.5	NP_001074034	22..143
Danio	si:dkeyp-15g12.1-PH1	5.0	XP_692142	215..306
Danio	LOC562517-PH1	4.7	NP_001038452	952..1073
Danio	osbpl1a-PH1	4.4	NP_001038547	242..336
Danio	LOC100002282-PH1	4.4	XP_001342108	<37..82
Danio	LOC561507-PH1	4.3	XP_690002	61..108
Danio	LOC563491-PH2	3.8	XP_691944	<1331..1357
Danio	cnksr1-PH1	3.7	NP_991222	441..537
Danio	LOC792661-PH1	3.2	XP_001332225	38..132
Danio	LOC559281-PH1	1.9	XP_687702	13..113
Danio	si:ch211-193c2.2-PH1	1.7	XP_693644	19..112
Danio	LOC571767-PH2	1.3	XP_700481	167..258
Danio	LOC569779-PH2	1.2	XP_698280	1369..1473
Danio	LOC571341-PH1	0.9	XP_700015	16..112
Danio	LOC562490-PH1	0.7	NP_001038451	212..303
Danio	zgc:56306-PH1	0.3	NP_956609	24..121
Danio	LOC568653-PH1	0.3	XP_697087	5..96
Danio	LOC564823-PH1	0.0	XP_693245	749..846
Danio	LOC570918-PH1	-0.1	XP_699541	1337..1446
Danio	LOC562940-PH1	-0.2	XP_691398	71..177
Danio	LOC793364-PH2	-0.8	XP_001332264	658..753
Danio	LOC572001-PH1	-1.1	XP_700746	23..121
Danio	LOC100004413-PH1	-1.6	XP_001343730	71..177
Danio	LOC560305-PH2	-1.9	XP_688794	813..908
Danio	plekhf1-PH1	-2.1	NP_956634	33..128
Danio	LOC559690-PH1	-2.1	XP_688145	175..259
Danio	LOC559168-PH1	-2.1	XP_687576	6..118
Danio	LOC794462-PH1	-2.1	XP_001334425	110..222
Danio	LOC559353-PH1	-2.2	XP_687779	807..921

Danio	zgc:158267-PH1	-2.3	NP_001073541	9..99
Danio	LOC569229-PH1	-2.8	XP_697692	22..117
Danio	LOC562683-PH1	-3.2	XP_691150	133..234
Danio	LOC562468-PH1	-3.8	XP_690939	50..146
Danio	LOC561110-PH1	-3.9	XP_689604	58..149
Danio	LOC562124-PH1	-3.9	XP_690615	269..359
Danio	LOC559690-PH3	-4.1	XP_688145	522..601
Danio	LOC558831-PH1	-4.3	XP_687190	46..149
Danio	zgc:76914-PH1	-4.4	NP_998253	5..116
Danio	LOC798450-PH1	-4.4	XP_001338895	<4..25
Danio	LOC560919-PH1	-4.5	XP_689411	1..105
Danio	LOC100002931-PH1	-4.5	XP_001342598	5..81
Danio	LOC563283-PH1	-4.6	XP_691739	23..129
Danio	LOC564545-PH1	-4.6	XP_692968	316..415
Danio	LOC558931-PH1	-4.7	XP_687312	439..524
Danio	LOC558931-PH3	-4.8	XP_687312	825..940
Danio	skap2-PH1	-4.9	NP_956922	108..203
Danio	zgc:158223-PH1	-4.9	NP_001073480	114..210
Danio	LOC565122-PH1	-4.9	XP_693512	13..101
Danio	LOC562503-PH1	-5.0	XP_690970	145..248
Danio	LOC559690-PH2	-5.3	XP_688145	280..365
Danio	stap2-PH1	-5.4	NP_942103	22..108
Danio	LOC555479-PH1	-5.6	XP_683095	582..675
Danio	LOC558241-PH2	-5.6	XP_686524	530..619
Danio	LOC100001577-PH1	-5.6	XP_001341548	<6..66
Danio	LOC100003191-PH1	-6.1	XP_001342811	13..113
Danio	LOC100003662-PH1	-6.2	XP_001343165	11..111
Danio	zgc:63749-PH1	-6.4	NP_957501	1..88
Danio	LOC100003547-PH1	-6.4	XP_001343082	82..174
Danio	LOC100006857-PH1	-6.7	XP_001340547	<603..669
Danio	LOC566919-PH1	-6.7	XP_695297	14..114
Danio	zgc:154069-PH1	-6.8	NP_001071273	5..95
Danio	als2-PH1	-6.8	XP_685064	<916..988
Danio	zgc:77177-PH1	-6.8	NP_998453	22..106
Danio	LOC566523-PH1	-6.9	XP_694888	389..473
Danio	zgc:114084-PH1	-7.1	NP_001025384	217..308
Danio	si:dkey-19f21.3-PH1	-7.3	XP_686251	516..625
Danio	LOC555290-PH2	-7.4	XP_682853	1428..1533
Danio	LOC557337-PH1	-7.6	XP_685483	414..529
Danio	LOC561644-PH1	-7.7	XP_690149	96..184
Danio	LOC569681-PH1	-7.7	XP_698171	<5..61
Danio	si:dkey-121a11.4-PH1	-7.9	NP_001073306	5..107
Danio	LOC560525-PH1	-7.9	XP_689027	235..>284
Danio	LOC562244-PH1	-7.9	XP_690730	463..575
Danio	zgc:153779-PH2	-8.0	NP_001073487	<522..552
Danio	LOC560226-PH1	-8.0	XP_001337042	690..>750
Danio	LOC571713-PH1	-8.2	XP_700421	81..190
Danio	LOC100002149-PH1	-8.2	XP_001342004	134..230
Danio	zgc:136983-PH1	-8.3	NP_001038715	269..370
Danio	LOC569534-PH1	-8.5	XP_698022	145..250
Danio	zgc:153917-PH1	-8.6	NP_001074048	269..359

Danio	zgc:92360-PH2	-8.6	NP_001002715	257..361
Danio	LOC557123-PH1	-8.9	XP_685219	388..505
Danio	LOC100003431-PH1	-8.9	XP_001339198	5..107
Danio	LOC791497-PH1	-9.2	XP_001331742	22..106
Danio	LOC563267-PH1	-9.4	XP_691722	455..551
Danio	LOC555573-PH1	-9.5	XP_683216	43..144
Danio	LOC793629-PH1	-9.7	XP_001333425	<19..76
Danio	LOC558931-PH2	-9.8	XP_687312	<581..627
Danio	LOC571767-PH3	-9.8	XP_700481	465..567
Danio	LOC568912-PH1	-10.1	XP_697365	10..108
Danio	LOC558831-PH2	-10.1	XP_687190	390..479
Danio	LOC564814-PH1	-10.2	XP_693236	219..309
Danio	LOC100004997-PH1	-10.6	XP_001344159	61..147
Danio	LOC559329-PH1	-10.8	XP_683727	118..227
Danio	zgc:92360-PH1	-10.9	NP_001002715	134..230
Danio	LOC100004931-PH1	-11.0	XP_001344109	266..355
Danio	LOC564211-PH1	-11.1	XP_692652	684..780
Danio	LOC558237-PH1	-11.1	XP_686519	86..199
Danio	arhgap12-PH1	-11.2	NP_957168	448..541
Danio	LOC100005196-PH1	-11.4	XP_001344312	<4..30
Danio	LOC562404-PH1	-11.9	XP_690883	144..263
Danio	LOC556641-PH1	-12.0	XP_684582	218..321
Danio	plekhf2-PH1	-12.0	NP_956538	33..136
Danio	LOC560514-PH1	-12.0	XP_689013	33..125
Danio	LOC560078-PH1	-12.1	XP_688562	271..385
Danio	zgc:158388-PH1	-12.1	NP_001076484	271..361
Danio	LOC560186-PH1	-12.2	XP_688668	254..344
Danio	LOC796268-PH1	-12.3	XP_001336583	89..186
Danio	LOC565669-PH1	-12.4	XP_694028	14..123
Danio	zgc:77233-PH1	-12.4	NP_998407	516..624
Danio	LOC100000241-PH1	-12.6	XP_001335880	7..110
Danio	LOC558931-PH4	-12.8	XP_687312	954..1046
Danio	LOC100002454-PH1	-12.9	XP_001342238	<78..135
Danio	LOC569403-PH1	-12.9	XP_697878	249..359
Danio	LOC556146-PH1	-13.0	XP_683972	313..395
Danio	LOC567382-PH1	-13.0	XP_695768	92..201
Danio	LOC561879-PH1	-13.2	XP_690372	307..394
Danio	LOC792802-PH1	-13.3	XP_001332401	1037..1131
Danio	si:dkey-183c16.1-PH1	-13.3	XP_684366	279..373
Danio	quo-PH1	-13.3	NP_001004109	1617..1723
Danio	LOC557435-PH1	-13.5	XP_685598	483..599
Danio	LOC565859-PH1	-13.6	XP_694214	307..394
Danio	LOC100006233-PH1	-13.6	XP_001345053	155..263
Danio	LOC566207-PH1	-13.7	XP_694569	307..394
Danio	zgc:77021-PH1	-13.8	NP_998474	19..105
Danio	zgc:55868-PH1	-14.1	NP_956362	16..124
Danio	LOC556974-PH1	-14.1	XP_685018	10..110
Danio	LOC565988-PH1	-14.3	XP_694345	418..513
Danio	pld2-PH1	-14.4	XP_694649	208..308
Danio	LOC561366-PH1	-14.6	XP_689868	376..485
Danio	LOC560226-PH2	-14.6	XP_001337042	<809..849

Danio	LOC100007833-PH1	-15.0	XP_001346187	70..132
Danio	LOC561507-PH2	-15.0	XP_690002	393..507
Danio	elmo1-PH1	-15.0	NP_998256	<604..671
Danio	LOC555489-PH1	-15.0	XP_683105	652..763
Danio	plcg1-PH1	-15.1	NP_919388	29..140
Danio	LOC557560-PH1	-15.1	XP_685738	210..>240
Danio	LOC571767-PH1	-15.3	XP_700481	58..147
Danio	zgc:103749-PH1	-15.4	NP_001006011	8..95
Danio	veph-PH1	-15.4	NP_997996	698..798
Danio	LOC563722-PH1	-15.5	XP_692171	1..>45
Danio	LOC572192-PH1	-15.6	XP_700972	339..494
Danio	LOC561475-PH1	-16.0	XP_689964	15..122
Danio	zgc:101886-PH1	-16.3	NP_001007375	1..91
Danio	LOC566479-PH1	-16.3	XP_694841	1..108
Danio	LOC792246-PH1	-16.3	XP_001331566	294..406
Danio	apbb1ip-PH1	-16.3	NP_956928	294..406
Danio	LOC797756-PH1	-16.5	XP_001338219	3..104
Danio	LOC100002649-PH1	-16.5	XP_001342391	80..159
Danio	LOC100006357-PH1	-16.5	XP_001345128	80..159
Danio	LOC562244-PH2	-16.6	XP_690730	<789..851
Danio	LOC557435-PH2	-16.6	XP_685598	<680..>717
Danio	plekhk1-PH1	-16.6	NP_001005937	309..415
Danio	LOC798492-PH1	-16.6	XP_001338932	36..135
Danio	zgc:158353-PH1	-16.7	NP_001038398	308..395
Danio	LOC794414-PH1	-16.9	XP_001334384	23..110
Danio	LOC100003123-PH1	-17.1	XP_001342754	1179..1281
Danio	plekha1-PH1	-17.3	NP_998601	10..110
Danio	LOC566659-PH1	-17.4	XP_695030	67..173
Danio	zgc:114072-PH1	-17.8	NP_001025299	515..623
Danio	DDEFL1-PH1	-17.9	XP_695781	302..389
Danio	LOC568502-PH1	-18.1	XP_696927	159..250
Danio	LOC557199-PH1	-18.4	XP_685305	579..688
Danio	LOC100007743-PH1	-18.8	XP_001346123	17..104
Danio	LOC556000-PH1	-19.3	XP_683782	64..159
Danio	LOC100001680-PH1	-19.3	XP_001341631	18..139
Danio	LOC572024-PH1	-19.3	XP_700770	18..139
Danio	LOC561797-PH1	-19.4	XP_685953	73..160
Danio	zgc:153779-PH1	-19.4	NP_001073487	336..>399
Danio	LOC558044-PH1	-19.4	XP_706955	2222..2322
Danio	LOC100001532-PH1	-19.5	XP_001341509	18..112
Danio	LOC558241-PH1	-19.6	XP_686524	280..392
Danio	LOC560813-PH1	-19.6	XP_689306	754..840
Danio	LOC568676-PH1	-19.7	XP_697113	307..>360
Danio	LOC565810-PH1	-20.2	XP_694170	357..459
Danio	LOC100006718-PH1	-20.5	XP_001345392	73..179
Danio	LOC793730-PH1	-20.6	XP_001332688	216..327
Danio	LOC100005669-PH2	-20.7	XP_001340801	418..492
Danio	zgc:114084-PH2	-20.7	NP_001025384	418..492
Danio	LOC555443-PH1	-20.7	XP_683036	16..124
Danio	LOC561893-PH1	-21.5	XP_690387	84..170
Danio	LOC558152-PH1	-21.6	XP_686431	515..607

Danio	zgc:110459-PH1	-21.7	NP_001018432	11..98
Danio	LOC796543-PH1	-21.7	XP_001336898	545..647
Danio	LOC562821-PH1	-21.8	XP_691286	27..112
Danio	LOC567369-PH1	-22.0	XP_695754	184..271
Danio	LOC561700-PH1	-22.4	XP_690204	801..908
Danio	LOC567180-PH1	-22.4	XP_695565	467..558
Danio	LOC564372-PH1	-22.5	XP_685777	15..103
Danio	si:dkey-27p7.2-PH1	-22.5	NP_001038672	308..395
Danio	LOC557428-PH1	-22.7	XP_685591	169..277
Danio	LOC572850-PH1	-23.0	XP_686610	269..367
Danio	LOC555298-PH1	-23.2	XP_682861	<20..86
Danio	LOC560186-PH2	-23.2	XP_688668	411..489
Danio	zgc:92147-PH1	-23.5	NP_001017914	27..112
Danio	rock2a-PH1	-23.5	NP_777288	1142..1247
Danio	LOC100006718-PH2	-23.7	XP_001345392	221..328
Danio	LOC569090-PH1	-24.0	XP_697546	496..611
Danio	LOC566614-PH1	-24.3	XP_694984	128..241
Danio	LOC568356-PH2	-24.3	XP_696774	351..436
Danio	ect2-PH1	-24.3	NP_001003883	631..759
Danio	LOC569202-PH1	-24.4	XP_697662	746..862
Danio	LOC100003104-PH1	-24.8	XP_001342736	31..115
Danio	LOC570984-PH1	-25.0	XP_001342717	248..368
Danio	LOC569320-PH1	-25.1	XP_697793	298..423
Danio	LOC571004-PH1	-25.5	XP_699647	491..603
Danio	quo-PH2	-25.8	NP_001004109	1699..1802
Danio	zgc:92432-PH1	-26.1	NP_001002175	303..408
Danio	phlda3-PH1	-26.3	NP_001002455	10..97
Danio	LOC572445-PH1	-26.8	XP_701253	47..157
Danio	itsn1-PH1	-26.9	NP_997065	1463..1569
Danio	si:dkey-83d9.7-PH1	-27.0	XP_001336063	752..911
Danio	LOC562865-PH1	-27.0	XP_691324	118..229
Danio	LOC798042-PH1	-27.0	XP_001338493	269..380
Danio	LOC556216-PH1	-27.0	XP_684060	485..584
Danio	LOC558551-PH1	-27.7	XP_686873	422..529
Danio	LOC567621-PH2	-28.1	XP_696014	1260..1419
Danio	si:ch211-89p3.3-PH1	-28.2	NP_001038559	1067..1189
Danio	rasgrf2-PH1	-29.2	XP_001335795	25..127
Danio	LOC556834-PH1	-29.2	XP_684848	1366..1476
Danio	LOC560923-PH1	-29.3	XP_689415	333..441
Danio	LOC563649-PH1	-29.4	XP_692097	260..371
Danio	zgc:136817-PH1	-29.7	NP_001035483	237..344
Danio	LOC795760-PH1	-29.7	XP_001336024	518..631
Danio	LOC793364-PH1	-29.7	XP_001332264	421..520
Danio	cdc42bpb-PH1	-29.9	NP_001038590	1091..1212
Danio	LOC558288-PH1	-30.7	XP_686581	439..549
Danio	LOC794265-PH1	-30.7	XP_001334201	93..203
Danio	LOC556727-PH1	-31.0	XP_684692	339..435
Danio	LOC562264-PH1	-31.8	XP_690750	<1020..1071
Danio	sptb-PH1	-32.1	NP_571600	2204..2302
Danio	zgc:152893-PH1	-32.2	NP_001038433	18..129
Danio	LOC797187-PH1	-32.4	XP_001337643	714..819

Danio	LOC567369-PH2	-32.9	XP_695754	352..437
Danio	LOC568885-PH2	-32.9	XP_697339	478..584
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Danio	LOC565291-PH1	-33.4	XP_693663	1313..1419
Danio	LOC560461-PH1	-33.4	XP_688954	734..839
Danio	LOC795770-PH1	-33.5	XP_001336029	402..515
Danio	LOC799605-PH1	-33.5	XP_001339941	1024..1130
Danio	LOC560319-PH1	-33.6	XP_688811	469..581
Danio	LOC559907-PH1	-33.6	XP_688395	926..1061
Danio	LOC559145-PH1	-34.0	XP_687553	398..505
Danio	LOC559017-PH1	-34.0	XP_687404	428..535
Danio	rasgrf2-PH2	-34.4	XP_001335795	477..585
Danio	LOC565016-PH2	-34.4	XP_693419	477..585
Danio	fgd-PH1	-34.5	NP_571631	375..475
Danio	LOC560305-PH1	-34.7	XP_688794	578..676
Danio	si:dkey-158b13.2-PH2	-35.5	XP_685856	2170..2282
Danio	LOC562861-PH1	-35.6	XP_691320	388..489
Danio	LOC567912-PH1	-36.5	XP_696317	281..403
Danio	arhgef7b-PH1	-36.7	NP_001008624	447..556
Danio	LOC567621-PH1	-36.8	XP_696014	454..546
Danio	LOC561670-PH1	-36.9	XP_690171	436..542
Danio	LOC568885-PH1	-37.7	XP_697339	25..127
Danio	obscn-PH1	-37.8	XP_001341205	3334..3445
Danio	LOC561825-PH1	-38.4	XP_690316	8..133
Danio	LOC798516-PH1	-38.9	XP_001335484	624..729
Danio	LOC557201-PH1	-39.0	XP_685307	791..917
Danio	grb10-PH1	-39.6	NP_001004287	301..413
Danio	LOC561276-PH1	-40.6	XP_689770	504..606
Danio	LOC555340-PH1	-40.9	XP_682922	750..854
Danio	LOC553493-PH1	-41.4	XP_707992	447..556
Danio	LOC562032-PH1	-43.2	XP_690519	285..397
Danio	LOC793086-PH1	-44.8	XP_001332757	398..506
Danio	LOC569231-PH1	-45.3	XP_697695	801..935
Danio	arhgef1-PH1	-46.0	NP_001075100	481..577
Danio	LOC557441-PH1	-49.7	XP_685605	608..705
Dicty	secG-PH1	34.8	XP_637214	
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Dicty	pkbA-PH1	27.9	XP_646888	T
Dicty	dagA-PH1	24.7	XP_638365	T
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Dicty	DDBDRAFT_0217064-PH1	18.7	XP_644892	
Dicty	DDB_0233285-PH1	18.2	XP_643886	
Dicty	DDBDRAFT_0205671-PH1	17.7	XP_641747	
Dicty	DDBDRAFT_0218225-PH1	17.3	XP_641291	
Dicty	DDBDRAFT_0217777-PH1	15.3	XP_643210	
Dicty	DDBDRAFT_0202904-PH1	14.8	XP_645812	
Dicty	DDBDRAFT_0202066-PH1	14.4	XP_647081	
Dicty	DDB_0232013-PH1	14.0	XP_647308	
Dicty	DDBDRAFT_0184481-PH1	14.0	XP_629529	
Dicty	DDB_0231560-PH3	13.6	XP_638248	

Dicty	DDBDRAFT_0185494-PH1	13.3	XP_639048	
Dicty	DDBDRAFT_0189208-PH1	12.1	XP_635449	
Dicty	DDBDRAFT_0191864-PH1	11.3	XP_629187	
Dicty	DDBDRAFT_0188916-PH1	11.0	XP_635612	
Dicty	DDBDRAFT_0187100-PH1	10.3	XP_637627	
Dicty	DDBDRAFT_0185955-PH1	9.6	XP_638566	
Dicty	pdkA-PH1	8.4	XP_640699	
Dicty	DDBDRAFT_0204119-PH1	8.3	XP_640920	
Dicty	DDB_0229957-PH1	6.7	XP_643307	
Dicty	DDB_0229869-PH2	6.4	XP_645484	
Dicty	gpaC-PH1	6.3	XP_637414	
Dicty	DDBDRAFT_0218370-PH1	5.6	XP_640297	
Dicty	DDB_0220701-PH1	5.1	XP_645246	
Dicty	DDBDRAFT_0205468-PH1	5.0	XP_642378	
Dicty	DDBDRAFT_0168417-PH1	4.7	XP_645597	
Dicty	roco6-PH1	3.8	XP_641642	
Dicty	DDBDRAFT_0189127-PH1	3.5	XP_635506	
Dicty	DDB_0233183-PH1	3.2	XP_001134564	
Dicty	DDBDRAFT_0167432-PH1	2.7	XP_643800	
Dicty	DDB_0231765-PH1	1.8	XP_001134600	
Dicty	DDBDRAFT_0218370-PH2	1.5	XP_640297	
Dicty	DDBDRAFT_0219504-PH1	1.0	XP_635981	
Dicty	DDBDRAFT_0191604-PH1	0.8	XP_629952	
Dicty	DDBDRAFT_0217683-PH1	0.5	XP_643465	
Dicty	ugt52-PH1	0.3	XP_636616	
Dicty	DDBDRAFT_0203449-PH1	0.2	XP_642501	
Dicty	fimB-PH1	-0.7	XP_643269	
Dicty	DDBDRAFT_0186714-PH1	-0.8	XP_637967	
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Dicty	pdkB-PH1	-1.7	XP_638523	
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Dicty	Unc104-PH1	-6.3	XP_635456	
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Dicty	DDBDRAFT_0219353-PH1	-7.5	XP_636680	
Dicty	vilA-PH2	-7.8	XP_636652	
Dicty	DDBDRAFT_0184166-PH1	-8.1	XP_629771	
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Dicty	DDB_0231560-PH2	-10.6	XP_638248	
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Dicty	DDBDRAFT_0205307-PH1	-14.7	XP_640320	
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Dicty	DDBDRAFT_0217791-PH1	-17.9	XP_643203	
Dicty	DDBDRAFT_0191859-PH1	-18.5	XP_629210	
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Dicty	gxcC-PH1	-19.3	XP_638371	
Dicty	DDB_0233316-PH1	-19.5	XP_642161	
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Dicty	DDB_0233355-PH1	-20.0	XP_641233	
Dicty	roco5-PH1	-21.1	XP_001134523	
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Dicty	DDB_0233358-PH1	-22.4	XP_642829	
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Drosophila	Sbf-PH1	8.6	NP_731633	
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Drosophila	rok-PH2	6.2	NP_536796	
Drosophila	CG31772-PH1	5.3	NP_608806	
Drosophila	Gap1-PH1	1.3	NP_729562	
Drosophila	PKD-PH1	0.1	NP_732327	
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Drosophila	chico-PH1	-2.5	NP_723540	
Drosophila	RhoGEF2-PH1	-4.2	NP_995869	
Drosophila	CG32560-PH1	-4.5	NP_573240	
Drosophila	Syn2-PH1	-5.0	NP_788381	
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Drosophila	Syn1-PH1	-9.7	NP_730686	
Drosophila	shi-PH1	-10.5	NP_001036279	
Drosophila	rok-PH1	-10.5	NP_536796	
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Drosophila	siz-PH1	-12.7	NP_001036618	
Drosophila	Caps-PH1	-13.2	NP_001027031	
Drosophila	CG17360-PH1	-13.6	NP_650115	
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Drosophila	blow-PH1	-15.2	NP_724580	
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Drosophila	RhoGEF3-PH1	-33.5	NP_728517	
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Human	PLEKHA1-PH2	33.5	NP_001001974	
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Human	CENTD1-PH1	8.9	NP_056045	
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Human	SBF1-PH1	7.7	NP_002963	T
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Human	FAM109A-PH1	6.3	NP_653272	
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Human	CENTA2-PH2	3.8	NP_060874	

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Human	PLEKHH1-PH2	1.7	NP_065766	
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Human	CENTD3-PH2	-5.3	NP_071926	
Human	CENTD2-PH3	-5.3	NP_001035207	
Human	CENTD2-PH1	-5.5	NP_001035207	
Human	CENTB2-PH1	-5.5	NP_036419	
Human	FARP2-PH2	-5.8	NP_055623	
Human	M-RIP-PH1	-6.2	NP_055949	
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Mouse	Osbpl1a-PH1	3.2	NP_997413	
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Mouse	CENTD1-PH1	-15.4	XM_132099	N
Mouse	Rasal2-PH1	-15.5	NP_808312	
Mouse	Arhgap22-PH1	-15.9	NP_722495	
Mouse	Afap1l1-PH1	-15.9	NP_849259	
Mouse	Centg1-PH2	-16.0	NP_001028435	
Mouse	VEPH1-PH1	-16.1	NM_145820	N
Mouse	Plekhf1-PH1	-16.1	NP_077724	N
Mouse	AA536749-PH2	-16.2	NP_957697	N
Mouse	Dnm2-PH1	-16.3	NP_001034609	N
Mouse	Fgd5-PH1	-16.4	NP_766319	
Mouse	RALGPS2-PH1	-16.5	NM_023884	N
Mouse	Centg1-PH1	-16.7	NP_001028435	
Mouse	Elmo1-PH1	-17.0	NP_932761	
Mouse	Plekhj1-PH1	-17.1	NP_076389	N
Mouse	Farp1-PH2	-17.3	NP_598843	N
Mouse	LOC669434-PH1	-17.3	XP_980149	
Mouse	Fgd1-PH2	-17.5	NP_032027	N
Mouse	Arhgap12-PH1	-17.6	NP_001034781	
Mouse	Dok6-PH1	-17.9	NP_001034262	
Mouse	Sntb2-PH1	-18.4	NP_033255	N
Mouse	Arhgap10-PH1	-18.6	NP_084389	N
Mouse	CENTD1-PH2	-18.7	XM_132099	N
Mouse	Fgd4-PH2	-18.7	NP_631978	
Mouse	Plekhn1-PH1	-19.0	NP_001008234	
Mouse	Skap1-PH1	-19.1	NP_001028358	
Mouse	Cdc42bpg-PH1	-19.2	XP_983816	
Mouse	Veph1-PH1	-19.2	NP_082633	
Mouse	Fgd6-PH1	-19.3	NP_444302	N
Mouse	Plcb4-PH1	-19.4	NP_038857	
Mouse	Adrbk2-PH1	-19.5	NP_796052	
Mouse	Col4a3bp-PH1	-19.5	NP_075909	N
Mouse	Ddefl1-PH1	-19.8	NP_001008233	
Mouse	Als2-PH1	-19.9	NP_082993	
Mouse	Prkd2-PH1	-19.9	NP_849231	
Mouse	Osbp-PH1	-20.0	NP_001028346	
Mouse	Ngef-PH1	-20.1	NP_063920	N
Mouse	Plcd4-PH1	-20.2	NP_683739	N
Mouse	BC067047-PH1	-20.2	NP_808450	
Mouse	Plekhg3-PH1	-20.3	NP_722499	

Mouse	Osbp2-PH1	-20.5	NP_690031	
Mouse	Spnb4-PH1	-20.5	NP_115999	
Mouse	Trio-PH2	-20.7	NP_001074771	
Mouse	4933428G20Rik-PH1	-20.7	NP_067468	
Mouse	Psd2-PH1	-21.5	NP_082983	N
Mouse	Arhgap9-PH1	-21.8	NP_666123	
Mouse	Ralgps1-PH1	-21.9	NP_780420	
Mouse	AI586015-PH1	-22.1	NP_064376	
Mouse	Ddef2-PH1	-22.1	NP_001091637	
Mouse	Rasgrf1-PH1	-22.3	NP_001034744	
Mouse	Centd2-PH1	-22.6	NP_001035201	
Mouse	Osbpl8-PH1	-22.7	NP_001003717	
Mouse	Apbb1ip-PH1	-22.8	NP_062329	N
Mouse	Ddef1-PH1	-22.8	NP_034156	N
Mouse	Prkcm-PH1	-22.8	NP_032884	N
Mouse	Psd4-PH1	-23.0	NP_808279	
Mouse	Arhgef19-PH1	-23.1	NP_766108	
Mouse	Pld2-PH1	-23.1	NP_032902	N
Mouse	Afap1l2-PH1	-23.2	NP_666214	
Mouse	RASGRF1B-PH1	-23.2	NM_001039655	N
Mouse	2610034M16Rik-PH2	-23.5	NP_081277	N
Mouse	Plcd1-PH1	-23.5	NP_062650	N
Mouse	Ect2-PH1	-23.5	NP_031926	
Mouse	Sh2b3-PH1	-23.8	NP_032533	
Mouse	Lnk-PH1	-23.8	XP_995739	
Mouse	Osbpl5-PH1	-24.0	NP_077251	N
Mouse	ABR-PH1	-24.3	NM_198894	N
Mouse	Raph1-PH1	-24.5	NP_001038978	
Mouse	Plcl2-PH1	-24.5	NP_038908	N
Mouse	Arhgef6-PH1	-24.5	NP_690014	
Mouse	Iqsec2-PH1	-24.7	NP_001005475	
Mouse	Arhgef16-PH1	-25.0	XP_994560	
Mouse	Rasgrf2-PH1	-25.0	NP_033053	N
Mouse	Tiam1-PH2	-25.3	NP_033410	N
Mouse	Itsn1-PH1	-25.5	NP_034717	N
Mouse	Adrbk1-PH1	-25.7	NP_570933	N
Mouse	DOK1-PH1	-26.0	NM_010070	N
Mouse	4631416L12Rik-PH1	-26.1	NP_001074764	
Mouse	Sh2b2-PH1	-26.1	NP_061295	N
Mouse	Bcr-PH1	-26.3	NP_001074881	
Mouse	E130112L23Rik-PH1	-27.0	NP_937892	
Mouse	Snta1-PH1	-27.1	NP_033254	N
Mouse	Exoc8-PH1	-27.2	NP_932771	
Mouse	Cdc42bpa-PH1	-27.3	XP_999345	
Mouse	Fgd2-PH1	-27.8	NP_038738	N
Mouse	Fgd4-PH1	-28.1	NP_631978	
Mouse	Spnb1-PH1	-28.1	NP_038703	
Mouse	LOC671775-PH1	-28.7	XP_994163	
Mouse	Plcg2-PH1	-28.8	NP_758489	
Mouse	Arhgef4-PH1	-29.2	NP_898840	
Mouse	Rasa4-PH1	-29.3	NP_598675	N

Mouse	Pld1-PH1	-29.5	NP_032901	N
Mouse	Spnb2-PH1	-30.2	NP_787030	N
Mouse	Net1-PH1	-30.2	NP_062645	N
Mouse	Centd1-PH4	-30.3	XP_001001345	
Mouse	KIF1A-PH1	-30.4	NM_008440	N
Mouse	SH2B1-PH1	-30.5	NM_011363	N
Mouse	Plekhm1-PH1	-31.6	NP_898855	N
Mouse	Sntb1-PH1	-31.7	NP_057876	N
Mouse	Iqsec3-PH1	-31.7	NP_001028526	
Mouse	DOK5-PH1	-31.9	NM_029761	N
Mouse	Farp1-PH1	-32.1	NP_598843	N
Mouse	Rock2-PH1	-32.1	NP_033098	
Mouse	Farp2-PH1	-32.2	NP_663494	
Mouse	E130306D19Rik-PH1	-32.2	NP_001013395	
Mouse	Arhgef9-PH1	-32.4	NP_001028501	
Mouse	Plekhg1-PH1	-32.4	NP_001028425	
Mouse	Spata13-PH1	-32.7	XP_998034	
Mouse	Dok5-PH1	-32.8	NP_084037	
Mouse	Sh2b1-PH1	-32.9	NP_035493	
Mouse	D10Ertd610e-PH1	-33.5	NP_082303	N
Mouse	Arhgef15-PH1	-34.2	NP_808234	
Mouse	Fgd3-PH1	-34.2	NP_056574	N
Mouse	PLEKHC1-PH1	-35.2	NM_146054	N
Mouse	Plekhg6-PH1	-35.3	NP_941006	
Mouse	KIF1B-PH1	-35.5	NM_207682	N
Mouse	Trio-PH1	-35.9	NP_001074771	
Mouse	Itsn2-PH1	-36.0	NP_035495	N
Mouse	Tiam1-PH1	-36.0	NP_033410	N
Mouse	Kalrn-PH1	-36.0	XP_998128	N
Mouse	Cdc42bpb-PH1	-36.8	NP_898837	
Mouse	LOC640526-PH1	-37.4	XP_622736	
Mouse	Kalrn-PH2	-37.4	XP_998128	
Mouse	Spnb3-PH1	-37.9	NP_067262	
Mouse	Centd2-PH4	-38.2	NP_001035201	N
Mouse	Grb7-PH1	-39.0	NP_034476	N
Mouse	Plekhg5-PH1	-39.8	NP_001004156	
Mouse	Arhgef7-PH1	-41.2	NP_059098	N
Mouse	Afap1l2-PH2	-41.3	NP_666214	
Mouse	ARHGEF3-PH1	-41.5	NM_027871	N
Mouse	Tiam2-PH1	-41.6	NP_036008	N
Mouse	Grb14-PH1	-41.8	NP_057928	N
Mouse	Mcf2-PH1	-42.6	NP_573460	N
Mouse	Plekhg4-PH1	-42.9	NP_001074802	
Mouse	Arhgef18-PH1	-42.9	NP_598723	N
Mouse	RASGRF1A-PH2	-43.2	NM_011245	N
Mouse	ARHGEF2-PH1	-44.3	NM_008487	N
Mouse	VAV2-PH1B	-45.3	NP_033526	N
Mouse	ROCK1-PH1	-45.7	NP_033097	N
Mouse	Arhgef2-PH1	-46.0	NP_032513	
Mouse	Fgd1-PH1	-46.9	NP_032027	N
Mouse	Mcf2l-PH1	-48.4	NP_835177	N

Mouse	Vav3-PH1	-49.1	NP_065251	N
Mouse	Vav1-PH1	-51.3	NP_035821	N
Mouse	Grb10-PH1	-51.6	NP_034475	N
Mouse	Sos2-PH1	-53.4	XP_992919	N
Mouse	Akap13-PH1	-55.4	XP_984499	N
Mouse	Sos1-PH1	-55.9	NP_033257	N
Mouse	RGNEF-PH1	-58.3	NM_012026	N
S.Cerevisiae	SLM2-PH1	14.2	NP_014351	N
S.Cerevisiae	OSH3-PH1	12.5	NP_011940	
S.Cerevisiae	BOI2-PH1	5.8	NP_011039	
S.Cerevisiae	BOI1-PH1	5.0	NP_009468	N
S.Cerevisiae	SLM1-PH1	0.2	NP_012161	
S.Cerevisiae	SWH1-PH1	-0.5	NP_009421	
S.Cerevisiae	BUD4-PH1	-2.7	NP_012625	N
S.Cerevisiae	CLA4-PH1	-3.9	NP_014101	
S.Cerevisiae	OPY1-PH1	-5.0	NP_009687	
S.Cerevisiae	SPO14-PH1	-6.0	NP_012956	
S.Cerevisiae	ASK10-PH1	-6.1	NP_011611	
S.Cerevisiae	YSP1-PH1	-7.3	NP_012025	
S.Cerevisiae	OSH2-PH1	-7.5	NP_010265	
S.Cerevisiae	SKM1-PH1	-8.8	NP_014528	
S.Cerevisiae	PLC1-PH1	-8.9	NP_015055	
S.Cerevisiae	TUS1-PH1	-9.3	NP_013529	
S.Cerevisiae	ATG26-PH1	-12.1	NP_013290	N
S.Cerevisiae	YHR131C-PH1	-12.2	NP_011999	
S.Cerevisiae	CDC24-PH1	-13.5	NP_009359	
S.Cerevisiae	BEM3-PH1	-15.5	NP_015210	
S.Cerevisiae	SPO71-PH1	-18.8	NP_010389	
S.Cerevisiae	BEM2-PH1	-21.1	NP_011082	
S.Cerevisiae	NUM1-PH1	-24.1	NP_010434	
S.Cerevisiae	YEL1-PH1	-26.0	NP_009493	
S.Cerevisiae	SIP3-PH1	-30.6	NP_014142	
S.Cerevisiae	CAF120-PH1	-32.0	NP_014121	
S.Cerevisiae	SKG3-PH1	-33.0	NP_013288	
S.Pombe	csx2-PH1	3.0	NP_595897	N
S.Pombe	SPBC17G9.08c-PH1	3.0	CAB52806	
S.Pombe	SPAC26A3.10-PH1	0.2	NP_594153	N
S.Pombe	ksg1-PH1	-3.1	NP_588442	N
S.Pombe	SPCC576.15c-PH1	-3.1	CAA21194	
S.Pombe	SPAC23H3.01-PH1	-3.8	NP_001018249	
S.Pombe	SPAC19A8.01c-PH1	-3.8	CAB16232	
S.Pombe	SPBC2F12.05c-PH1	-5.2	NP_595710	
S.Pombe	SPAC11E3.11c-PH1	-5.8	NP_594936	N
S.Pombe	reserved_name_rga2-PH1	-7.7	NP_594152	N
S.Pombe	SPAC26A3.09c-PH1	-7.7	CAA93232	
S.Pombe	SPAC19A8.02-PH1	-8.0	NP_593790	
S.Pombe	pob1-PH1	-8.4	NP_596828	
S.Pombe	SPBC1289.04c-PH1	-8.4	CAB38684	
S.Pombe	SPAC1F5.09c-PH1	-8.5	NP_592864	
S.Pombe	plc1-PH1	-10.9	NP_594734	
S.Pombe	SPAC22F8.11-PH1	-10.9	CAB52721	

S.Pombe	SPCPB16A4.02c-PH1	-11.2	NP_588026	N
S.Pombe	SPAC23H4.01c-PH1	-11.3	NP_593405	
S.Pombe	SPAC6G9.04-PH1	-12.8	NP_594113	
S.Pombe	SPAC637.13c-PH1	-17.7	NP_594631	
S.Pombe	SPAPYUG7.03c-PH1	-21.1	NP_594704	N
S.Pombe	SPAC2F7.16c-PH1	-23.0	NP_592986	
S.Pombe	SPCPB16A4.02c-PH2	-25.8	NP_588026	
S.Pombe	SPCp054-PH1	-27.5	NP_588075	
S.Pombe	SPCC4B3.15-PH1	-27.5	CAB60689	
S.Pombe	SPBC428.07-PH1	-28.5	NP_595185	

erevesaie, and S.Pombe PH-domains

Sequence
IVIESWLHKKG.....eHIRNWRPRYFILFR......dGTLLGFRSKP.......kEDQPLPEPLNNF..MIRDAATV.....................
VVIEGWLHKKG.....eHIRNWRPRYFMIFN......dGALLGFRAKP.......kEGQPFPEPLNDF..MIKDAATM...................
AEREGWLFKQSsnplfsGALSWKKRWFVLSE.......NCLYYFDQMT.......dKEPKGIITLANV..GIRKVEAP..................
PLCTGYLSKRG.....aKLKLWVPRFFVLYP.....dsPKVYYYEDFE...nwktaEKPSGCIDLVDF..KSFNLEQT.................
KKLEGWMMHFI....lsDPERRLKHYWMMQS.......NAIHLYNEYS.egigvnpNRVYRIIPLAEI.tSVVQNNGK................
VEKAGWLNKWT.....nYLKGYRQRWFVLDS......nATLSYYRNPS.....evgHTCRGSINLQEA..RVHTDKT-................
RTFCDVCNKKL......-------------.......------SDI-........IRPTPAFECKNC..HFKTHKDH.........................VAQGSLPMC
--MEGPLSKWT.....nMVHGWQYRWFKIEN.......DTLLYYTSRE....kmlkGQQRGQIRLTGA..VVGIDGE-.................
VQNYGILMKKY..krknRSARWAKRFFVLKE.......CFLIYYSTSYfektrridLHPKGIIPLIGC..SIVSGGDV......................
VFKFGNLQQVDsrlawkKVLHYKKRYVQLTN.......THLIWQKDVQ........CAPKGTVPLSDI..KFVNVDN-..................
VRHMGWIAEQV...senGISMWKPKFMTLTN.......SEILFYEAVP..qlkaewAEPRLVRPLVAT..RVVQTSSR...............
MEKSGYWTQLT....dsRIKSLKRRYVVFKN.......GQISFYRKHN.....nrdEEPASKISISDI.rSVTKLEQQ......................
ILKQGYLEKKR......--GLFARRRMFLLT.....egPHLLYIDVPN........LVLKGEVPWTPC..MQVELKN-.........................
IDENGFFLRWL......---IEGKDAVVLDM.......GQIWEARTGG......lpKDGRIMFELEQR..GASETIA-.........................-
LKYCGYCYCIG....rnAWKKWKKRFFCLVQ..vsqyaFAVCSFRQKK........ADPTEFIQLDGF..TIDYMPES.................
PFRSNPLKRTK......SVSKMEKSLAEANQ.......HSLHRVDASNqpparrhlSQPAREGSLRAC.rSHESLLSS...............
AIKE---NQRQ......-------------.......---HFSPPA-........-MPQTVAGKKKR..ESRKIGTN....................skhndEEDECFE
GRMNGWLRVYR...ddmTGSTWIASWAMMDL.......TRISFYTNDG.....adlEKPFFSIDLNKE..QWVLRTGQ............
ILRDGKLIFFK.....yEENWTSRNAVRLHV....dptPYILYWRYKDkvfntkelAYEKNYIYLERI.yDVRAGKPT................df
IILEGSLKRCK..kyklFKTKWVEHYFVLHCrdrernlFAIDEFKTSR.kndlkkrFKLEFVIRVESN.lSVSDPSIL..............cta
ADSEGAGSYSS......-FSSIASTASRMLG....raaDCLVLMTKR-........---------NGW..SGDAGSP-.........................----
LPTNGVMKKWT.....nYVNGWQDRYFEITE.......GNLVYYLSKA.....eksHGCRGSIFLKSA..IIAAHEF-....................
TLRKGWLMLRG.....kSDNDWCKHWVVLAG.......LQLKLYKDVW....aedsTEPLLTVDLSQC.eNVYPSASA.............
IDMKGFFDRKQsggkraTIRSWKNYYGILCG.......QLLCFFKDEQ...qflenVAAAPPVYIYGA..QCEQYPEY................
KHTEGFVKKRPkqccvrYLLPWSKRWLMVRD.......SFVAYMDHR-........TEQIRMVLLMDR..DFKVAAGG...............
KVLEGQLKEKK..grwrFLKRWNTKYFTLSS.......AALNYSTQHM....ptdsRALLPSIDLRSI.rSVRSLGRG..................
VARQTWVKHQEalgksgKRNNWEDRWAVLCR.......RSLYLCVESP.......aYTTEKTIELGSH.tRVDVCNAI.............v
IQMEGWLSLRD.ntkksRKPKWTNCFVALNE.......YSFTIYVDE-........-KAVSVILLIEA..GAMAHVR-........................
ITYHGFLSMYQ..rtgeGLGSWTRYWCALEN.......GEMKFWKQPE.......dEGTKGYTALMDL.sTCCRSEGA.............
ISYIGWVNEYLdddqeeLKIRWQPRFLILKG.......SDVCFFDVPP.....lnsEDLNKCVYLYKC.yDVAVKQVP................
VLHSSQIRFRG......SLGKLLDRFMVVRD......dFCMYTYSSEE.......dICALAMLPLPGC..EVKMCGE-....................
GRMNGWLRVYR...ddlPESTWTSLWAMMDS.......NHVKFYRDAG....adnlENPYFTIDLNKE..QWILRTGQ............
EAFEGTLIRKHsldrkaANRSWEKLYAVLRQ.......NELSFYKDPK...hrdesVHGEPPMALPGC..SVNVASDY..............
LVGEGVLVKMC......-RKKPKQRQFFLFN.......DILVYGNIVI....skkrYNKQRILRLEGV..QVEDLEDD.......................
MEYRGFLHILHplerakKVPIWHKYWSLLHR.......GAILFWSTPQ...eevheKVPIFQIDLTKC..TNNSIEES...................
PIKQGNLYKKS..sksaLNREWKKKYVCLYS......dGRLTYHTNLK...eymdkTAHGKEMDLKLA..TIRITGRL................
VTACGFLYVAPfsmqshSAKRWQRRWFTLFD......sGDLTYAIDNS......mdTLPQLSIDMSLC.yRVSEAHAI..............
VMMEGYLYKRS....snAFKTWNRRWFQIKD.......KQLLYSHRST.....dlePATIMEENLRIC..LVRPAPSN...................
NTMCGYLKRKL.....rNSSGWQDLWVVMCC.......HTLYFYRNHN.......eREPLAHLSLMDY..GVGLPTVA................
TAYEGLVKTPR...aggVRKGWQTAYVVVCD.......FKLYLYDCTVqnkmqdvkNEIRLVLDMRDP..DFTVCGVS...........
PEMEGFLYLKS.....dGRKSWKKHYFVLRP.......SGLYYAPKSK....kpttKDLTCLMNLHSN..QVYTGIGW.................
RRFSGPLQLQQ......-DFQWRAGWGVLKA.......NMLFVYNKTE....eetsAPPFLLLIIEDC..FIELCDEN.....................
VIRKGWLSLSN....vsFVRGSKDNWFVLMS.......DSLSWYKDDE.......eKEKKYMLPLDGV..KLKDIEGG.................
AEKGSLLCRIK......NQKVKEMALVTIKS......kQFLNYYSSYW....fnfvPNALKSVALSEL.lEVRSGYQT...........dnlqras
KLFEGWVRRRKelnaneLTNKWPKIWMCLRG.......HYLLLYTNQN.......tKRPEMVINLIKA..TISDSTDL..................
VILYGEMEQFD....veTKKPVQKCMLILLS.......HRLIIGNINA.....agkYVMESTLSLNSV..APVNVKDR....................e

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LIHQGTLQISE..siagNVQKPKDRRIFLFE.......QSAIIADHIPkkefgnptYIFKSQFMVNKM..VFEPNVPD......................
VVKEGNLNVLKtlfdnlKSSSAKRRYCILRR..heggeCTFEIRKTAQ.......eAPKMLPLKVSAA..QIKSTKK-......................
QTGSDFVKLRG......-TNRQFRRFFSLDA.....dlSYIRWTPTNK........KPHKARIAIDEI.rEIRLGKNT.............ellrssdev
PLKEGSVQLTS.....ISTLLSHHRYFFLYH.......ETLIISKQKG.....acsYKLKEKLRLEKV..WIASSNT-..........................
QSLEEYIHVLQvgilthPNRKILRVGFVLRSarrapccRIMVLCSDRIgvnldgnfFTVHAEFKLKGM..MIDEGDTY...............
EYYSGFLMRKYggktpfGRRSWRMVYARLRG.......LVLYFDTDEH.pkatsryASLENAVSLHHA..LAEPAPDY.............
LVKKGVLTQLVssnilqSRQKARTLHVFLFS.......DMIMITKKKL...ngtfvCKDYAARRFVDM..QPIEPDNP...............kip
TIRCGDLERSEekvvkpKKREWITNYMYLTT.......AHLILYKDQKaekhgkhyDAPQGVWDLRGA..SVTWYQDN........
VVMADTLKIRG......ALKRWNRYYCVLKP.......GLLILYKHKK.....adrGDWVGTVLLNHC..ELIERPSK......................
SAICGYLHRIE..vrsiGLITRRRYWFALCD.....stPYLYWYKDSD.......dIKCIGRVSLSGA..AFTYDPR-.......................
SIKQGYVYMQEtigrdvLLGRWTKYYCVYSR...etriFTMVSANSAT.ktdmksaVAQTATFKFKSC..SRRPMDSI............
LSAYGDLLLEA...tfrQAGSKTTRLLFLFE.......EMLLIVKQRG......anYVCKDYIMCSNL..MLNEWICP......................
LIRQSEVMKQT......-RKELQPRYLVLFT.......DYLWICRVSS...sgqfdINRSYRIPLEYM..KFERMEED......................
VIVHGYIKKLG....gpFTSAWQTKYGKLYP.......SRLELYPESL........TAKPELVFMDQI..EDVCAEMQ.....................
LKSLGLLRLQTnrkkkaKLSRAQKRFIFFFD.......GAVMFCKKRVtlnsepeyFEHKFCIPIISL..GYDTSSRT...................
VEYRGFLYLFD.erspnGEAAWDRYWAMLHR.......GIIFFWKNPI........DEKNQKVPLSQI..DLTKCTNQ.................s
LLKEGMLYKRE....lnGSANYQETVVFLFN.......DILLYGIKRI.svmplckYEPSAILSLRHC..IVQLDDI-.........................
RLKDGEILKYT...sgiFSSKWKKMYAVLFS......dSRLVWFENRG.......dRKPKGSVLLKDV..IPYICVGL..........mtdrm
LIHEGPLELVE......-NGRTVDMYAFLFN.......DMFVLTKTKKpigksehyIVQRQPVPLDSC..VFCDADSN....................
VNLDGEVKMAE..stltQAGKPKQRYIFLFD.......KVIVVCKAANgasartntFTYKNAYVMSEL..TIDKNASL................dv
LEKDGDLGMIRsseitkNKKWKTERFVYIFD.......QMIVLCKRHR......ntLKFKDRLAVHSI..DVFDIPDS......................
FVTQDTLTFWE..prayFKGRGKERQVFLFD.......ISIVFAKRIEvspknikyVIKGKPLPLSEV..SIVEHVEG...................
LLKSGSVQKIS.....sTTEKTEERFIFLFN.......DLVILASERK..migvskYKLRAVFSASHM..QVCEGDNL.....................
====================================================================================================
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEDK.......................
PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEDP.......................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEEP.......................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEDS.......................
PDREGWLLKEG.....gRIKTWKRRWFILTD.......GCLYYFQYTT.......dKEPKGIIPLENL..CVKEVDDP......................
VVREGWLHKRG.....eYIKTWRPRYFILKS......dGSFIGYKEKP..etsdanQPPLNNFSVAEC..QLMKTERP................
VVKEGWLLKRG.....eYIKTWRPRYFILKS......dGSFIGYKEKP..eltdqsYAPLNNFSVEEC..QLMKTERP..................
PELMLWWSWRTlspaggRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..CVREVIFQ.....................
KMCKGFLVKMG.....gKIKSWKKRWFVFDR.....lkRTFSYYADKH.......eSKLKGVIYFQAI.eEVYYDHLR...................
KTCRGFLIKMG.....gKIKTWKKRWFVFDR.....nrRTLSYYADKH.......eAKLKGVIYFQAI.eEVYYDHLK..........sahkvif
MLKEGFMIKRAqgrnrfGLKNFKKRWFRLTN.......HEFTYHKTKG........EGALCSIPIENI.lAVERLEEE.......................
KMCKGHLVKMG.....gKIKSWKKRWFVFDR.....lkRTFSYYVDKH.......eTKLKGVIYFQAI.eEVYYDHLR................sa
VVYSGWLRKSP.pekklRRYAWKKRWFVLRSgrlsgdpDVLEYYKNDH.......aKKPIRVIDLNLC.eQVDAGLSF...........
VIGENSILPSPppdspgDSEAWKKRWFILRSgrmsgdpDVLEYYKSDH.......aKKPIRIIDLHCC.eQVDAGLTF.............
EKQAGFMLKKR....kwPMKGWHKRYFYLDK.......GILKYAKCAA....dvekGKLHGCIDV-GL..SVMAIKK-...................
EKHEGFMLKKR....kwPLKGWHKRFFVLDN.......GILKYSKSPV....diqkGKLHGSIDV-GL..SVMSIKK-......................
VNASGYLHKKG..gsqfSLMKWPLRFIIIHK.......GCVYYFKSST.......sAAPQGTFSLNGY.nRVLRAAEE...................
VIKAGYCVKQG.....aLMKNWKRRYFVLEQ.......NSMSYFKSDL.......eKEPLRIILLKEV.hKVQECKHS...................
GTKEGYLVKQG.....aFVKNWKQRWFTLNR.......YELKYFKDKM.......fVEPIRTLDLTEC..SAVQFDYS...................
VIKTGYCVKQG.....aVMKNWKRRYFMLDD.......NALSYFKTDM.......eREPLKVILLKEV.nKVQECKQS...................
KMCKGFLVKMG.....gKIKSWKKRWFVFDR.....lkRTFSYYADKH.......eSKLKGVIYFQAI.eEVYYDHLR................sa
ALRSGYCVKQG.....nVRKSWKRRFFILDD.......QTVSYYKSEM.......dKEPLRSIRLRDV.lKVNECLVK....................
VILKETLYKKSqqkrrtSPCNYKERTFILNT.......QDLAYFEQRP.....gkkPTQKGCIELSHI..KCVEIVRS....................dv
SLKSGWLYKKGggmstlSRRNWKMRWFVLRD.......SKLMYFENDS.......eEKLKGTIDIRAA.kEIVDNHE-................
IVKQGCLLKQG.....hRRKNWKVRKFILRD.....dpAYIHYYDPSK......geDDPLGSIHLRGS..VVTAVEFV...................
VVKRGYLLKQG.....hKVKNWKVRLFVLRA.....epGFLHYYDPSK......ddVTPAGSVSLRGC..LVSALDDN...............
--------MKG......----WHKRYFLLER.......GILTYAKTGS....dlkkGRLRGRIDV-GL..SVMAMKK-.........................-KSM
DLCSGFLYKSPpsgqirKMKSWKRRFFVLEK..knngsHELKYYKTTE.......kDKAIKSIEVSSI..TLLYVGPE..............sh
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ILKEGFMVKRG.....hVVQNWKVRWFALKS.......DRLLYYKYEG....gkrdSCHRGTILLRNC..KITCPYLE.........................
GICEGYLMKRR....kwPLKGWHKRYFVLDK.......GILRYTKNQH....dfsrGKMHGSLDVSLA..VMSVNKK-........................
VLKEGYLWKKG.....qLRRNWTERWFTLRP.......STLLYFTSED.......rKDHKGNIQLDGN.cCVEVLPDR........................
YLKEGYMEKTG....plQREPFKKRWFILDS.....mdRKLLYFKTQLielgvvfiGSENHGYSVREC..VPKGTRGN...................
IYKMGPVDKRK......-GLFARRRQLLLTE......gPHLYYVDPVN........KVLKGEIP--WS.pELRPEAK-...................................
ALKQGWLMKKGggsstlSRRNWRRRWFVLRQ.......SKLIYYENDT.......eERMKGMLDMHEA.kEIIDVTG-.......................
IVKKGYLLFNK.....gKGKRWKHLYFILEG.....ndAHLIYFESEK......raTKPKGLIDLSVC..SVYGVHDS..............................
EIRTGYLNKSP...pakGIKSWKRRFFVLSK..vdkdnYHLSYYRNNE......srDKPLGTIDLSKI..SLLSTAPE............ahsr
GDCQGWLYKRK.eskglLGWKWKKFWFVLKK.......CSLYWYTSDM.......aEKAEGYINLRDF..TIEQATEC..................
GDCEGWLWKKK.daksyFSQKWKKYWVVLKD.......ACLYWYTNEE.......dEKAEGFVSLPEF..NIDQASEC.................
RSFEGILYKKG.....aLLKPWKPRWFVLDK.....tkHQLRYYETRQ.......dKECKGMIELADV.eSVIPGTPA.......................
LEKTGYLLKMG.....sQVKAWKRRWFILRN.......GEILYYKSPS.....dviRKPQGQMELNSS.cHIARGEG-......................
TIREGYLVKKG.....tVLNSWKAVWVVLKD.......DAIEFFKKKT.......dRNAKGMIPLKGA..TLTSPCQD.........................
------MEKKQ.....sRAQSWRKRWFVLRRgrmsgnpDVLEYYRSKS.......sRKPIRTIDLQEC..EVTIEAEV.......................r
GDCEGWLWKKK.datgyFTQKWKKYWFVLKD.......SNLYWYTNQN.......dEKAEGFISLPEF..RIDRAIEC...................
VLKEGYLWKKG.....hLRRNWTERWFCLKP.......GSFSYYVSED.......aRDCRGVIEMDHN.cCVEVLPDR...................
VSRQGWLYKQA....ssGVKQWNKRWFVLTD.......RCLFYYKDEK.......eEGVLGSLPLLSF..KIGPVQTS......................
TISEASTTVTTgskdssGMRLWKRKWFVLAD.......FCLFYYKEWClyptdsreESVLGSIPLPSY..TIAPVGPE...................
VDKEGYLYKKR.....eRNTTYLRRWFVLKG.......NLLFYQERPG.......dRNLLGVIVLEGC..MVQACETD.......................
VIKNGWLHKQD....stGMKMWKKRWFVLSD.......MCLFYYRDEK..eegilgSILLPSFHISML..SVDDHIT-.........................
IWKCGYLRKQK......---HGHKRFFVLRG.psnlgpSRLEYYDSEKkaaasgvtCPAKRVIYLSQC.fTVNKRADA...................
SSMSGYLHRSK.....gHKKPWKRLWFVIKN.......KVLYTYAASE.......dVAALESQPLLGF..FLREEKTG..........................
EVYTGYLQKSPiaknllSQKSWKRRFFVLSK..tvdnnHQLTYYPSSE......rrDKPLGKIDLSKI.sLLFTSPDS..................hpt
IIKKGYLVKKG.....hVRRNWQERWFVLKP.......GSLIYYVAED.......qKEKKGEILLEES..SVVESVPD..............................
IEEKGFLTMFE...dvsGFGAWHRRWCVLSG.......YCISYWTYPD....dekrKNPMGRINLANC..TSRKVEPA...................
KMFEGPLWKSS......RFFGWRSYWVVLQD.......GVLSWYPKQT...dadsnTRRQGCKPLTQA..HCMIKAK-...........................
PLCQGFLKKRK......--------------.......--------DK.......mLDLRGQYYIYEV.qSVREVNKS...............................dNNRYMFE
LLYLGNVKRVD......----------SVKQ.......CCLIRFEDNS...efwvlRKDIHSFSSGGE..EVCCICDS............................pplKE
EACSKPLWHVF......--------------.......----------........-KPPPALECRRC..HVKCHKDH.............................ldKKEDMITPCK
PDCDGWLWKKRkeagvfMTQKWQRFWFVLKG.......PTLYWYNSQQ.......eEKAEGLIKIGSY..NIESAGEH................
SKLCGYLNKLT...gkgPLRGFKTRWFVYDP.....rkCFLYYFKTPQ.......dALPIGHIEIGDA..CFSYDVEA........................
VKKVGYLRKPK......---SMHKRFFVLRA.asasgpSRLEYYENEK..kwrhksGAPKRSIPLESC.fNINKRADS......................
PDKTGFLFKKG.....eRNTAYHRRWCILKG.......NMLFYFEERE.......sREPIGVIVLEGC..TVELCESE.............................
VSFEGYLEMLS......---PRTKVYTLINR.......DKLFLFKSH-........EEYFQGMGITDI.dMRMANVRD................................g
FIIRGWLYKEI.rgssqANLKLKKRWFVLTH.......NSVDYYKSSE......rnALKLGSLVLNSL.cSVLVPDER...........................
GLVRGWLLREV....qgGWLRQRRFWFVLTS.......DSLDYYSGPD......rdARRLGTLVLTSL.cSVLWPDKH...................
VLKQGYMMKKG.....hKRKNWTERWFLLKP.......SLISYYVSED.......lTEKKGDILLDGN.cCVESLPDK.........................
IRKHGYLKKQK......---HGHRRYFVLKD.tsdglpARLEYHENEK...kwknkSAPKRVIFLDSC.ISINKRADA.........................
FIKRSQQKKKT......SPLNFKERLFVLTH.......DKISYYDYDA...ekakrKSLKGYVDIEKI..RCVEVVLP...........................ed
STKEGPLLYRA.gssylGKEVWKSCYLVLSN.......GILYQYAERT.......dVTPLMSVTMGGG..HCGGCRRS....................
VYKNGFLVRKVgkktprGKRGWKTFYAILKG.......LILYLQKDEYrpdkqlsdEDLKNAVSIHHS..LAMRAADY...................
PDKTGWIRKFC..gkgiFREIWKNRFVILKG.......DQLLISEKEV.....kdeKKIQEVVDLTDY.eKSEELRKA...........................
SFLCGFLQYSD......RTKPSQRVWCVIPQ....hdaLVLYLYGAPQ.......dVKALCTIPLLGY..QVEDVQRS.........................
VKKCGYLRKQK......---HGHKRFFVLRE.psdgsrARLEYYESEK...kwknkSAAKRVIPLDSC.lNINKRADA.......................
PDKTGWIRKFC..gkgiFREIWKNRFVILKG.......DQLFISEKEV.....kdeKKIQEVVDLTDY.eKSEELRKA...........................
SVLCSFLHHME....kgSGRGWQKAWFVIPE....nepLVLYIYGAPQ.......dVKAQRSLPLIGF..EVSLPESG......................
LVGEGCLQKLC......-RRGPQPRVFYLFN.......DILVYGSIML....hgrwNNKQNIIPLEEV..QQEDLEDG............................
ATKAGWLDKLS....pqGNCVFQRRWVKLEG.......GNLTYYNSEK.......eMYSKGLIPLSAV.kQIRALGE-........................
HGKQGEVFLQH....qkHGEKWKRYWLALHP.asrhgiARLELSEAIQrstvvvrrHPERKVIRLADC.vSVVKLPPH..............
IRKCGYLRKQK......---HGHKRFFVLRA.sshvgpSRLEYYDSEKaaaapagaSPPKRVIYLYQC.fTVNKRADS...................
VQHEGFLTMFE...dvsGFGAWQRFYFLLEG.......GHLLYWNYPN....emgsKPADGSLSLYGF.cSVRPVERE..............
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NFKKGWMSKLD......ESGEWRKHWFVLTD.......AGLKYYRDSA....aeerDDVDGEIDLKAC.vKVSEFEVE............
AEKAGWLKKSS....gkFLSSYKDRYIQLDR.......TAIAVYENEE.......ITTCLEKLELDNY.eTCHELKSA...................
VSKHGWLYKANnsaisvTMKSFKRRYFHLTQ..lgdgsYNLNFYKDEK......isKEPKGTIFLDSC.mGVIQNSKV..........
PLKTGWLKKQR.....sIVKNWQLRFFVLRG.......NSLTYHKDDK.......eSTVQGTIPLFSC..QVNELPSN.................
TKLCGYLNKQG.....gPLKTWKSRWFAYEE.....ksCQLFYYRMAH.......dINSLGKVDLTRA..TFSYPLRG..............
IVMEGYLFKRA....snAFKTWNRRWFSIQN.......NQLVYQKKFK.......dNPTVVVEDLRLC..TVKHCEDI.................
SFMDGFLYCSAatldrkGKPDMVRRWCTLEG.......GFLSYYDNEK.......iATPIGRVDIGDV.vSLAINNNQ...............
PIYGGWLCLAPfdnpmqRSRKWQRRFFVLYE......hGCLRFALDES......psTLPQGTVNMNQC.tDVVDAEPR.........
HVKEGQLYVQH....qkFGKKWKKNWFVLYP.asqngiARLEFYDCSGasdkpstkKMDKKIIRLSEC.iSILPAVTE.........
MSTAKNLLLLA..ssqeDQQKWVSR------.......----LMKKIPpapdaphrSSPRVPVKVQSS.qSMRRPSRQ.................
MQAGSQMIKLR......GKSKALVRLFYLDE.....hkSCIRWRPSR-........KHERAKITIDSI.hEVCEGMRT.............evfrr
SIMEGPLSKWT.....nVMKGWQYRWFVLDY.....naGLLSYYTSKD....kmmrGSRRGCVRLRGA..VIGIDDE-...........
PDKVGWIRRFS..gkgiFREIWRNRFVMLKG.......DHLFIFEKEM.....knnGKTHEVFDLVHY.eRSEELRKA.............
QMMSGCLRVKL....ggEPQGWTNVYGVLKG.......TNLFCYHQKE...dmeanVEPVLTIGINKE.tRIRAAEKD............
PILSGWLDKLS....pqGNYVFQKRYVKFDG.......KNLMYFGSEK.......dAYPKGVIPLAAI..QMARLAK-..................
ILYSGFLYKSGtlsrrtRDADFQKYWCSV-E.......KSILFYESDR.......cHEPSMKIDVKDI..ICLGVSRP..............dssnn
VLKSGYLEKRR.kdhsfFGNEWQKRWCALNN.......SIFYYYGSEK.......dKQQKGEFNIVGY..TVKMNNTL.............
ILKQGYLEKKR.rdhsfFSMEWQKRWCVLNN.......TIFYYFGSDK.......dKQQKGSFYINGY..SAELVPSL...............
SVKEGLLLKQT.....sSFQRWKRRYFKLRG.......RTLYYAKDSK........SLIFDEVDLSDA..SVAETSTK...................
VVKAGWLKKQR.....sIMKNWQLRWFVLRT.......DHLYFYKDEE.......eTKPQGCIPLQGS..QVNELTAN...............
TNKSGYVELRG......---LKGRVYLSLMG.......TCFRLCKTDQ.......dFNAGLAIAVVDL..TAACVKQF.....................
CYYEGYLEKRG.....aKEKVARRLWTCLCG.......NTLYFYNNPK.......dTHYVEKLDLSGF.vSLIDDPSR................
NGKKGWMYLLD......EDEEWRKFWFVITD.......SGLRYYRDSE....aeerDEADGEVYLRHC.lRVEEFDAD............
GVMSGTLQRCR.....nSKRSWRSLWFLLKD.......KVLYTYPQPE.......eRVACETLPLLGF..SVRSEAEG...............
------MYKFI......-------------.......-------SS-........-KPKVSVPLSAI.vEVRTTMPL....................empDKDNTFVLKVeN
VRRSGYLRKQK......---SMHRRYFVLRA.asergpARLEYYESEK..kfrgkaPVPKKALALETC.fNINKRADS..............
NRTCGFLDIEE....neNSDRFSRRYFILDT.....dkNYLLWYMDNP..qnlpvgTEHVGSLRLSYI.sKVNEASLK.............
--MEGVLYKWT.....nYMTGWQPRWFVLDN.......GIISYYDSQD.....dvcKGSKGSIKMPVC..EIKVHPT-.................
VLKGEYLNKAKaeggkkLRKNWTLTWVVLSS.......NQLLFYKESKeavsnlkpGGKPDGVDLNGA..VIEWTTEK........
-LCEGSCFRKL.....gNRRRQEKFWFCRLS....lnhKLLHYGDLE-........ESPQGEVPLELL..TDKIAVSD...ikavltgkdcphr
VRKSGYLRKQK......---SMHRRFFVLRA.aseqgpARLEYYENEK..kfrsksPVPKKAVNLDSC.fNINKRADS.............
SIMEGPLSKWT.....nVMKGWQYRWFVLDY.....naGLLSYYTSKD....kmmrGSRRGCVRLRGA..VIGIDDE-...........
GKNLEALRKPSkgltlqNAGRFSASWFILFN.......DVLV---HAQ........FSSHYVYPLATL..WVEPISDE....................
TQRAAELGMRG....pkKGDVVKKRFVKLIV.......NFLFYFRTDE........DEPIGALLLEQC..RVEREDLQ..................
LEKAGILNKTKaengkrLRKNWAQSWTVLHD.......GVLTFHKDPKgmssktnqIVPEYTVELKGA..TLSWASKE.........
CHICAFLLRKK......RFGQWAKQLTVIRE.......NRLQCYKSSK.......dQSPYTDIPLSLC..SVIYVPKD....................
VIRKGWVIINN...islIKGGSKEYWFVLTA.......ESLSWFKDDE.......eKEKKYMLPLDNL..KVRDIEKS...................
FIVRGWLHKEMkssgksTSLKLKKRWFVLTN.......NSLDYYKSSE......rsASKLGTLVLNSL.cSVVQPDEK.............
VVKEGWMVHYT.....sKDNLRKRHYWRLDS.......KCLTLFQNDS.......gAKYYKEIPLSEI.lQVEVARDF.................
SVKEGLLLKQT.....sSFQRWKKRYFKLRG.......RTLYYAKDAK........SLIFDEVDLSDA..SVAESSTK...................
MAHMTQAEMAH......-------------.......----------........-TCRGTITLATV..HIEVGET-......................---CHFVLTSgGR
FVKSGWLHRQS.....tILRRWKKNWFDLWS......dGRLVFYDDQQrrdmedeiHMKVDCINIRNA.sACRELAPP.........
SMGSEHWSQKL..rlprGTQGHKTELLEIQR......eGALRYMVADD........TNCMGAAQWQKC..RLLLRKT-.............
IRKQGWLHYKQrkkvgsGMRQWKRVFSVLHS.......SLLFLYKDKRagshgigqEKDIQTISIQGC..LIDIAYSE............
SPPLGKEHMPS......-------------.......---SPMTDRK.......kKKRNRSINLKGD.aAAGQAEEE......................-ESVDF
PRRQSMTVKKGqfmvelVEGARKLRHVFLFT.......DILLCAKLKKqtggkgqqYDCKWYIPLADV..TFQTIDES...........
SMQTGTQMVKL.....rGGSKGLVRFFYLDE.....hkSCIRWRPSR-........KNEKAKISIDSI.rEVCEGKQS.............eifqr
DVYEGMLWKKG.....rDNGQFLERKFVLSV.....hdFTLKYYKEDE.......sKGPKATIYVKNL..NATFQPEK...............
ISSEGYLYVQE.krpppFGSSWVKRYSTFVK.......EQKILHMKTF.dqrsggkLGETESVTLKSC..VRKTTDAL............
WTMEGYLYVQE..krefGISVWSLHVLLINKlkrtsnsHCIYLLSQNG......vtSNPPEKFRLKSC..IRRKTDSI................
IAMEGYLYKRA....snAFKTWSRRWFSIQK.......NQLVYQKKHN.......eQITVVVEDLRLC..TVKPCSEQ................
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FLKEGYMEKTG....prQTEGFKKRWFTLDH.......RRLMYFKDPL.......dAFAKGEVFLGHR..DHGYRVTI................g
VMKEGWLVHFT.....sKDTLRKRHYWRLDS.......KCITLFQNDT.......gSKYYKEIPLSEV.ISLEPAKTF....................n
FVKSGWLHRQS.....tILRRWKKNWFDLWS......dGRLVFYDDQQrrdmedeiHMKVDCINIRNA.sACRELTPP............
TQRAAELGMRG....pkKGDVVKKRLVKLIV.......NFLFYFRTDE........DEPIGALLLEQC..RVEREDPQ......................
SEKCATLNMTKtehgkkVRKNWTSYWTVLQG.......SLLIFNKGQGgwfgrdqkSSVEYSVDLKGG..SVDWASKD........
VLKAGWLKKQR.....sIMKNWQLRWFVLRA.......DHLFFYKDEE.......eTKPQGCISLKGS..QVNELTAN.....................
RSHESLLSPSS......--------------.......----------.......AVEALDLSMEEE..VLIKPVHS.......................silGQDFCFEVTTs
CQKSGFLELKG......---TKSKIYTAIIM.......EQIWLYKSEQ......cfKNGIGITVIEAR..GATIRDG-..........................-KG
QSQCGYLFKTApitehkPKADFSQRWCCLGD.......GMFSYYRNEQ.......sHHKNGGMKISEI..ICLSVNSP.................
IVKQGYVRMRS.....rKLGIYRRCWLVFKK.ssskgpRRLEKYPDEK....sayiRACPKVTEISNV.kNVTRLPRD...............
NFKKGWMVKLD......EEGQWKKYWFVLTD.......HSLRYYKDSI....aeeaSDLDGEIDLSTC.yNVTEYQAQ...............
IAMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKRFR.......dNPTVVVEDLRLC..TVKHCEDV...................
NPRCGYLNVLV......-NQCWKERWCCVRN.......RTLYFHKDRG......dvHTHVRALALHGV..DVLPGLGP..................
VYKTGFLARKIgkktprGKRGWKTFYAVLKG.......MILYLQKDEYkpekalseDDLKNAISVHHA..LAIKAMDY................
ESRDGMLMKRG.....rDNGQFLNRRFVLSV.....reGILKYYTKLD.......aKEPKALMKVDTL.nACFQPDKI...................
GTIQGYLFKRS....rkKNKTWKRCWFSTEN.......NQLIYLKSH-........-KEQPVVLFDDL..RLCAVKSL.......................
LEKAGILNKTKsengkkVRKNWGHSWTVLHG.......GKLTFHKDPKgassktnqILPEFTVDLKGA..TINRAPKD.............
FRVTGFLSRRL.....kGSIKRTKSQPKLDR..nssfrHILPGFRPVDesrsheslLSPTSAVEALDL..SMEEEVLI..................
SEKCGVLNVTKtehgkkVRKNWASTWTVLQG.......SSLLFAKGQGtswfggnqSKPEFTVDLRGG..SVEWASKE........
VKRGSPVLLQA......--------------.......--ISEVNRKQ......wiEAMDGKEPIYHS.pIQKQAES-..........................----------.--
RRLKGSIKRAK..sqpkLDRTGSFRHMILPRsadqertRLMQSFKESH...sheslLSPSSAAEALDL..TLDEDAII.............kp
KGLEGIVYKRSccghneVCYRWSKRWLIVKD.......SFLLYMKPD-........TGAISFVLLVDN..EFSIKMDS....................
LIGEGVLTKLC......-RKRPKARQFFLFN.......DILVYGNIVI....qkkkYNKQHIIPLESV..TIDTVEDE.........................gE
EKVDGYLMKYT.....nLVTGWQYRYFVLNN.....eaGLLEYFVNEQ.....srnQKPRGSLPLGGA..VISPSDE-..................
FKVTGFLSRRL.....kGSIKRTKSQPKLDR..hssfrNILPGFKSAEesrsheslLSPSSAVEALDL..SMEEEVLI..................
VVMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKRLK.......dALTVVVEDLRLC..SVKPCEDI...................
SRICGYLWRKK......WLGHWSRQLFIIKQ.......NSLLCFKCAK.......dLHPLLDLNLMGC..NVVYKFKQ.....................
YIREGWLKTVP.....pKGTEAKPKMFYLFS.......DILLQAKPCSmhptngdkFTCQRVYPLKEC..TVDKVFGH...............
SMIVGTVMRKI.....kSRTWKKQRYFRLQE.......DCMTIWYQSK......kaGNAHSTFSVGDV.eAVREGHQS...............
VIRRGWLTINI....siMKGGSKDYWFVLTA.......ESLSWYKDEE.......eKEKKFMLPLDNL..KLRDVEKS.....................
VVHRGFLRKYG....gfMFKQWKEKYLVLTV......eGNLMVCRDA-........DAPADQVVALQS..HCESLVEG.............reil
FERVGVLRYKA....mIDPQQWKEGFFVLQK.......SNLFICPGND........GAAEDIINLKRL.qELSIASEM.......................
IAASDSATQPD......KCVSVSDACVPLSS......rSHLMPRLKES..rsheslLSPSSAVEALDL..SMEEEVLI..................kp
CIMHGYMLKLG....npFLTQWQRRYFYLFP.......NRVEWRGEG-........ESRQNLLTMEHI.vTVEETQIK...................
NDHEENVSTSQ......----WRKHWFVLTD.......QILRFYRDPV....aeeaADLDGEINLSTC.yDVTDYPVQ.....................
MKHCGYLWAIG....knLWKRWKRRFFVLVQ..vsqytFAMCSYREKK........AEPVELLQLDGY..TVDYTDPQ.............
TEKSGYLYKRS....dgLRKMWQKRKCTVQN.......CYLTIAHGTP........NKSPAKLNLLTC..QVKPSLE-.....................
FLKEGTLMKLS......-RKVMQPRMFFLFN.......DILLYTTPVQ.....sgqYKVNSMLSLAGM..KVSKPSQE.......................
FLKEGTLMKLS......-RKVMQPRMFFLFN.......DILLYTTPVQ.....sgqYKVNSMLSLAGM..KVSKPSQE.......................
LDLSSYLLKPV......---QRISKYSLLLQ.......DLLRECECVT..naelqrTEIHTALNIIQF..QLRHGNNL.......................lam
PEIEGVLWLKD.....dGKKSWKKRYFLLRA.......SGIYYVPKGKyflrplqtLRHYFGFYRDYI..NHIKNDR-.......................
CEKKGYLLKKS....dgLRKVWQRRKCSVKG.......GILTISHATS........NRQPVKLNLLTC..QVKPSAE-.......................
VKREGWLHFKQgkkvgsAIWPWRRVFSVLRT.......HSLFLYKDKRkgaqlgggAEDEQPISIRGC..LVDIAYSE............
SEKKGYLFKKS....dgIRKVWQRRKCSVKN.......GILTISHATS........NRQPVRLNLLTC..QVKPSGE-.......................
CYHEGFLEKKS.....iKDKMGRKLWTSLCG.......DSLFFFNSSK.......dSVYIEKLELSDL.nSVSDDGSR....................
LMNGGDLLKVR......SESWKKTRYFKLQE.......DCKTMWHESK......ktLKTKQTFSIEDI.eEVRTGRQT................ds
NRICGFLDIEE....meNSGKFLRRYFILDT.....mdSSLMWFMDNP..qnlpegTSNVGSIKLTYI.sKVSDATKL................
LVLEGSFRVQR......---VKKERAFFLFD.......KMLLIAKKRL........DHFIYSTHIFCC..NLLLVENM.........................KD
KGLEGYILKRScighhqFCFRWSRRWLVVKD.......SFLLYMSRDP....givsFVLLFDPELKVL..VGRVYTD-..................
MKACGYLWAVG....knVWKRWKKRFFVLVQ..vsqytFAMCSYREKK........SEPQELLQLDGY..TVDYTDPQ............
QIKNEIQREKR......-------------.......----VCKGGK.......vLDRLRKKLCEQE..SLLLLMS-..........................-PCMAFRV
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RDKDRKMTRRS......---TFQKGQYFVLD....pelGQLQYFINEH.....skvQKPRGSLPLIGS..SVAPSDE-......................
PSLESFLSRRLaksqpkLDRTSSFRHMILPRsadqertRLMQSFKESH...sheslLSPSSAAEALDL..TLDEDAII...............
RLCEGTCFRKI.....sSRRRQDKFWCRLSP.....nhKVLHYGDLEEspqgevphDSLQDKLPVADI.kAVVTGKDC............
LEKQGEVLEVNgtflgnLRPKFTPVYLFLFN.......DLLVIAIKK-........-SAERYVVLDHA..HRSLVQVQ..................syen
TVLTLYYSKKS......QRPERRTFQVKLET.......RQIIWTRGT-........DKIEGEIDIREI.kEIRTGQKS............rdferyvedv
DSKDSDIERLR......-------------.......SQLTSLSIH-........SLDTTSISSIGN..DLDSDEAY.........................pAAESGLE
IVKAGWLEKTP....pkGGRIYQRRWVQLDS.......EYLRYFQSIK........EVYSKRMVSLGS..VFKVVSV-.......................
VLKEGALEKRS....dgLLQLWKKKRCVLTE.......DGLVLHPHKHqqhdtgckVKELHFANMKTV..DCVERKG-..............
PLIEGKLKEKQ..vrwkFIKRWKTRYFTLAG.......NQLLFRRGKS......kdELDNNTIELSKV..QSVKVVAK....................
VMQSGTQMVKL.....kTGSKGLVRLFYLDE.....hrSCIRWRPSRK....sekaKRPKQDMIYDFW..RMVWQEN-.............
LMHSSVIWLNPfpslgrMKKDPELTVFVFKR.......AVILLYRENNsahgdqdsFKFRWLIPLSAL..QVRLGNTA................
AMKAGMFFRKV.....kSRMWRRQRHYKLQD.......DCKTIAYKSS......waINSYSTFSISDV.eAVREGHQS.................
--MEGVLYKWT.....nYISGWQPRWFVLEG.......GTLSYYDSQE.....dawKGCKGSIKISVC..EIQVHPSD...................
VMQSGTQMVKL.....kTGSKGLVRLFYLDE.....hrSCIRWRPSR-........KSEKAKITIDSL.yKVTEGRQS...............difh
PDLEGVLYLKE.....dGKKSWKQRYFLLRA.......SGLYYSPKGK....tkasRDLVCLVQFDNV..NVYYCKEY.................
PDLEGVLYLKE.....dGKKSWKQRYFLLRA.......SGLYYSPKGK....tkasRDLVCLVQFDNV..NVYYCKEY.................
MEKEGFLFLHRkdkcmpMTSPFKKYYVTLSK.......DTLSYSRTLH........SKKSSSISLPKI.rAVEKVEEK....................
KISQDAVLLMEahahltSSLQSKERLLLLFT.......DSLIIAKTKS......lyLKLKAQVSLSDI..WLASCIHC.....................vtd
KISQDAVLLMEahahltSSLQSKERLLLLFT.......DSLIIAKTKS......lyLKLKAQVSLSDI..WLASCIHC.....................vtd
ILHHTWFFSDDdtdktpEDQKQKEMQPVLNI.......DHLL------........SNIGRVVPLQDF..SVSVAEVE.........cvlegcksetl
TTSSGHVRSQS......-----------VVS.......SIFSEAWKRGqadepkasRDLVCFLQLDHV..NVYLGQDY....................rsky
DMMSGFLSQQQ...sieGLQRRCRLYCVLKA.......GKISCYYSPE...eiqakVEPILIIPINKE.tRIRVVEND.......................
IVCGGALELNPlkgqdgGVKGLIKRRLQGDD.......KRKSSTQLNTlsvaarygSKESLSIPVSAA.kSLNLSADQ..............
TERSGMLLKRS....egLRKVWQKRKCSVKN.......GLLTISHGTP........NAPPANLNLLTC..QVKRNPD-.......................
DTYKGWLFKWT.....nYLKGYQRRWFVLSN.......GLLSYYRTQA.....emaHTCRGTITLATV..HIEVGDT-...................
VHHEGFLYRKHgkerspNSKSWVNLFCVLKQ.......GEIGFYKDAR...htttpYNDEPLLNLAIC..EFDTTNGY................
NRICGFLDIED....veNSGKFLRRYFILDT.....qqGSLLWYMDNP..qnlpvgAKHVGFLSLTYI.sKVSDATKQ.................
LLKSGWLWRQS.....sVLKRWKLNWCDLID.......GSFVFYKSES.......rRDYETKVNLKSS..CVNVRSGL...............ec
VIRKGWLTLNI....siMKGGSKEYWFVLTA.......ESLSWYKDEE.......eKEKKYMLPLDNL..KLRDVEKG.....................
TEKSGFLLKKS....dgIRKVWQKRKCGVKY.......GCLTISHSTI........NRPPAKLNLLTC..QVRPNPE-........................
ARICAFLLRKK......RFGQWTKLLCVIKD.......NKLLCYKSSK.......dQTPQMELLLSGC..SITHIPKD........................
TYKHGVLTRKSgkrtprGRRGWKKFYAVLKG.......MILYLQKDEY......kpDKDLSEVDLKNA.vRVHHALAT.................
LLKLGQLERRS......AVGMWWDYYCELSP.......FELRLYVNA-........EERVCNENLSLL..RCEDIHLY........................
LVLEGSFRIHR......---AKNERTLFLFD.......RMLLITKRRG......ehYVYKTHISCSTL..MLIESAK-..........................-D
LKRGSKFIKWD.....eANSTPSLITLRVDP.......NGFFLYWTGG.......tSMEAEILDMSHI..RDTRTGKF......aktpkdqrire
LKRGSKFIKWD.....eANSTPSLITLRVDP.......NGFFLYWTGG.......tSMEAEILDMSHI..RDTRTGKF......aktpkdqrire
DTYKGWLFKWT.....nYIKGYQRRWFVLSN.......GLLSYYRTQA.....emaHTCRGTINLATA..HIDTEDA-...................
PIKQGTLWKRS...ersLNKEWKKKYVTLSN.......SGMLTYHSNIqnaqgkemDLLRVTVKVPGK..RLHRAAAP.............
EAMEGILCRKQshnkksANRSWQNVYCVLRK.......GSLGFYKDNK.sasngipYHGEVPISLGEA..VCEVAHDY...........
ALQLKPVSVNE......----------VLKR.......GSKFIKWDE-........--EAEILDMSHI..RDTRTGKF......aktpkdqriremlfsgkadg
FVKEGTLMKVS......-RKCKQPRHLFLNKeiteqrmNDIMLYTYPQ....qdgkYRLINRLPLAGM..KVSKPPME...............
CYCRLFEVPDP...nrlQKLGQHQREIFLFN.......DLLVVTKIFQ.kkknsvtYSFRQSFSLYGM..QVMLFENQ.................
LMRDGFVVDVC......-ESGHNLRHLFLYT.......DMLLCAKLTN..agrqaqYRFCWYLPLVGL..KLHWTAEH.................
VLKKGWLIHNT.....sTDTLKKRHYWVLDG.......KSITLYPNEN.......tSKYYKEISLSEV.lQVRGADQI........................
MIHSSKVRFRF.....lHCQDVHDCYLDLFQ.......THLHFVSNNT......tgLTYQGTLPLKEL..TICKVQNR.....................n
FKVPGFLSKRL.....kGSIKRTKSQTKLDR.ntsfrlPSLRPTENDRshesllspGSAVEALDLSME..EDVYIKPL..................
DPRCGYVGVLV......-NRCWREHWCRVRA.......GSLYLYQEKG......eqRVPHTTVGLKGC..EVVPGLG-.................
DPRCGYVGVLV......-NRCWREHWCRVRA.......GSLYLYQEKG......eqRVPHTTVGLKGC..EVVPGLG-.................
LLRGGDLIKVK......SNSWKKTRFLKLNE.......DCKTIYQSSS......kaFKRESSFELAEI.dSVRLGRQS................eglq
LLQEGDIQVCVkiltskFLRRWEPHHLTLTD.......SSLVSATPTG......ymEAPLSYSTIEDL..QLLSWDNA...................
LLHHGADSSVSggavggRGTRWHKCRLVLKEggdggleYFLEFYIPPK.......sSKPRLTVPCCSI.vDVRSTTAI.............
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ILKEGELEKRS....dnLLQFWKRKTCVLTT.......DSLNIYTDQQ.......kKNKSKELKLQSI.kKVDCVEHT......................
LVREGPVTELR.dfslkDREEERSVYMHLFN.......DYLLLSIRKEggrftvidHAPVSELRAENC..RFKLHSL-...................
DELGGKLSKWT.....nYIHGWQDRWIALKG.......NILSYYRSAD.....ekeYGCRGSICLSKA..VITPHEF-......................
ARICAFLWRKK......WLGQWAKQLCVVRE.......HRLLCYKSSK.......dQTPLLDISLLGC..SVVYKEKQ....................
LVRQGELCVCG....ggRRKKTGVRNVFLYQ.......NFMIFTKHKT.pnpgnsvYSFKHSIKTGEM..GLTQSVGE.............
LKKSGELAVYTdlsifrKAFSFKSYYLFLFN.......DVLIVTKKK-........-SEESYVVLDYA..TVEKVEVE...................eem
DTYKGWLFKWT.....nYIKGYQRRWFVLSN.......GLLSYYRTQA.....emgHTCRGTINLATA..NIAVEDS-..................
TERSGNLYKKS....dgLRKVWQKRKCTVKN.......GYLTISHGTA........NRPPAKLNLLTC..QVKHNPE-......................
LEKHGELQELSrgslfsMRNRCSPVYMFLFN.......DLLILTTRKS...gcpdrFTVIDYAHRSLV..QVQATVNS...................
ATMEGYLYVQE...kwaLGVTWVKNYCKYFK......dNKLFIMVPME...qkagiKQTTAQLTLKSC..IRRKTDST................
------MTKRC......--------------.......-TLFFYETDG.rsgidhnSVPKHAVWAENS..IVQAVPEH.........................pKKDFVF
KDRVAFLKVLM......-NCQWQSLWCWVKD.......GNLKMYRDEA......slEIPEYTVHLRGS..DVRPGPD-....................
DELGGKLSKWT.....nYIHGWQDRWIALKG.......NILSYYRSAD.....ekeYGCRGSICLSKA..VITPHEF-......................
IRLEGWLSLPV..rnntKRFGWERKYVVVSS.......KKILFYNSEQ....dkehSNPYMVLDIDKL.fHVRSVTQT..................
ITYVTKVKLQH.....mPCQEQYDRLLVLYP.......NYLIILSEES......dgLFYKGKLPLNMI..TVTTPCQD.........................
LLKKGEVQQMSstrtmrSRKLYHPIYLFLFN.......NLLLITKRNS......sgDKFQVLDSCSRS..MLRTEDLE.......................
IVMADWLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTNK.......nGQWVGTVLLNAC..ELIERPSK........................
VPTCGYLNVLS......-NNRWRERWCQLKD.......NQLFLHKDRA......dlKTHMASLPLRGC..EVIPGLDS.....................
SSHRSLVHRVEialgdkPCDRGEHVTLFLFN.......DCLEIARKRHgqtrppaqLKHITLMPLSQI.rRVLDIQDT..................
LVKHGELLEVDsisgskFKLTTRPVYLHLFN.......DCLLLSRRKE.....swkFMVFVHAKIEDL..KVKDLSQK...................
EECKGWLFKKT.....hYTRRWKMSWFHLKD.......GKLIYGLNE-........ESAEKVIDLAGA..RMEVHDGD...................
LLLQGNLLKIS......-AGNIQERVFFLFD.......NLLVYCKRKStksingpqYVFRGRINTEVM..EVENVEDG.................tac
IVHMGWVCEQTadadrdADAAHCCRFLALRG.......SALLIFRTPPwtqaeasfHLCEVLFKVHKL.wIAEDCWIQ...........t
VFHKGFLKRKAgkrtpwGKRSWKTFYAMLKG.......MVLYLQKDDY....vkdgQGSDEVLSVHHA..LAEQALQY............
LKEQGQLIRQD.efllTFRKKKCYRHIFLFQ.......DLILFSKTRK.tdigndtYIYKQSFKTSDI..GMTHNSGD......................
IRHLGWLAEKT....esERQSWKPVLVMLTE.......KDLLLFDSMP..rmrehwLTPTHTYPLLAT..RLVHSGPD................
VMNDGYLEKRS....ngLLQLWKKKRCVLSD.....egLRLYGCKGDS........GKEMRFEQMTTL..DCVEYKR-................
FMMEGCEMKKV.....rSNSRMYNRYFLLDP......dMRWLRWEPSK.......kDSEKAKLEIKSI.kEVRLGKKT..............pv
FLHSGKLYKAK......---SNKELYGFLFN.......DFLLLTQIIKsakshlqyRMYKTPIFLNEV..LVKLPTDP.........................s
LLKDGFMVELV......-EGARKLRHVFLFT.......DLLLCAKLKKliggksqqYDSKWYIPLSDL..TFQTAEESslrseiqrerrank
SMVDGSELRKV.....rSNSRVYHRYFLLDA.....dmQSLRWEPSKK........ESDKAKIDVKSI.kEVRTGKNT..............dtf
VCKEGQLRYLEddtisdTAPQWQRCRLQVRRehsasqrYLLELYDPPK......dyRMPKISVHCSDI.kEIRRCNRL...........
LIKEGHILKLA.....aRNTSAMDRYLFLFN.......NMLLYCVPKF..slvgqkFTVRTRIGIEGM..NVKETFNE......................
LVQEGTLKQLIggnhkaSIVSRKDLYIHLFN.......DLLLLSVRSG......qrFLVQDHALFPDH.vRAEEIKTT......................
DLSMGDLLLYDpsslmkGKRDPELAAFVFRT.......AVVFVCKDCSstlderdpFRFRHMISTDAL..QVRNLPSL...............
TAYEGHLRVPK...ptgVKKGWQRVWAVVCD.......FKLFLYELGE.gkgaqpgVVVNQVIDMRDE..EFSASSVL............
GTKRGYLSKKT.....tENSKWHEKFFALYQ.......NVLFYFDTDQ.......sARPSGIYLLEGC..TCERVPAL...............kvst
LNEQGQLIRQD.efwviFRKKRSLRRVFLFQ.......DVILFTKTKK...ndrgdDVYVYKLSIKTC..EIGMTQSC...................
LIYTGEMSWIY.....qPYGRSQQRVFFLFD.......HQLVLCKKDL...irrdiLYYKGRIDMDRY..AVRDAIDG...................r
PEIQGFLHVRE.....gGKKSWKKLYFVLRR.......SGLYCSSKGQ....skepRHLQFTGDLEDL..NVFTVFTG.................
LTAQGKLLQQDteqdsgVLSRSKERRVFLFE.......QIVIFSELLR.kgsstpgYQFKKSIKVSYL..SMEEQVES.................
ITAQGKLLQQDteqdssILSRAKERRVFLFE.......QLVIFSEPIDkkgfslpgYIFKNSIKISCL..GVEACVDG.......................
LIKEGQILKLA.....aRNTSSMERYLFLFN.......NMLLYCVPKF..slvgqrFTVRTRVRVEGM..KVLETSNE...................
TAYKGFVRIPK...ptgVKKGWQRAYAVVCD.......CKLFLYEVPE.gkstqpvVMASQVLDLRDE..EFSVSSVL...............
VIYMSQIHMQS.....sANEEKEERYFMLFP.......NVIIMLSASP....rmsgFIYQGRLPLTGT..SVTKQPED......................
VIYMSQIHMQS.....sANEEKEERYFMLFP.......NVIIMLSASP....rmsgFIYQGRLPLTGT..SVTKQPED......................
LVLEGTFRIQR......---AKNERTLFLFD.......KLLLITKKRE........ETYSYKAHILCC..NLMLVEVI.........................pKEF
LLFEGTVNWKA......ASGRLKDILALLLT.......DVLVLLQEKDqryvfstvDNKPSVISLQKL..IVREVAHE........................
VLMEGTLARKHgpnkkaPNRSWNNLYCVLKP.......GHLSIYKDAK.sfshsvtFHGEEPLTLTNS..SCEILTNY...............
TEYKKSLIKRDvmtvyrQRIERLTVQVIMET.......RQVAWSRTA-........NKTEGVLDIFEI.rEVRPGKNS............kefdrf
LVCCCQLHEVP.dpnrpQRSGVHQREVFLFN.......DLLVVTKIFQ.kkktsvtYSFRQSFPLVEM..QVHMFQNS.............
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VDTSGYLNVLV......-NTQWRSRWCSVKD.......RQLWIYSDKS......kgKVAQQPLSLEGC..MVLPDPSP..................
FVRQGSLIQVPgrlgslSLKKEGERQCFLFS.......KHLIICTRGS...ggklhLTKNGVVSLIDC..TLIEEPEG.............tddesk
IESQGELILQEvwdpktLIRKGRERHLFLFE.......MSLIFSKEVK.dsngrskYIYKSKLFTSEL..GVTEHVEG...................
SRLEGWLAIPN..raniKRYGWKKQYVVVSS.......KKILFYNDEQ....dkeqSNPSMVLDIDKL.fHVRPVTQG.................
LKEQGQLVRQD.eftisYGRKKCQRHVFLFE.......DLVLFSKPKR.ieggldvYIYKHSFKTADV..GMTETSGE...............
LVCCCQLYEVP.dpnrpQRSGVHQREVFLFN.......DLLVVTKIFQ.kkktsvtYSFRQSFPLVEM..QVHMFQNS............
LRAQGKLLQQDienensILSRPKERRVFLFE.......QLIILSEPMDkrgfslpgYVYKNSIKISCL..SIEDRCPE.....................
LIHSGELTRIV......RPGKTQQRSYFLFD.......HQLVFCKKDV...lrrdlLHYRGRMDTDLL..EPSDLPDG....................rh
PEIEGVLWLKE.....dGKKSWKKRYFLLRA.......SGIYFVPKGK....akasRDLVCFLQLDHV..NVYYGQDY..................
NHKKGPTRMKD.....mARFKPMQRHLFLHE.......RALLFCKKREeghdrtasYSFKHCLMMSAV..GITENVKG............
PKGDGEVRLVS.....nLDKRRQDRHIFLFD.......AAVIICKRRG......dnYEMKEVIDLSHF..KITNNLAD......................k
LIFSGDLTKIS.....qPQAKGQQRMFFLFD.......HQLVFCKKDL...lrrdiLYYKGRLDMDEM..EVVDVEDG...................k
FVRQGSLIQLPvrlgslSLKKEGERQCFLFT.......KHFLICTRSS..ggklhlLKQGGVLSLIEC.tLIEEPDAN..............deda
FVRQGSLIQLPvrlgslSLKKEGERQCFLFT.......KHFLICTRSS..ggklhlLKQGGVLSLIEC.tLIEEPDAN..............deda
LIKEGHIKKMS.....aKNGSAQDRYLYLFN.......NMVLYCVPKL..rlmgqkFSVRERIDIAGM..EVHENVKQ..................
LIKEGHILKLS.....aKNGTSQDRYLILFN.......DRLLYCVPKL..rligqkFGVRARIDVDGM..ELKETSSM.......................
IVAQGRLLLQDaepeggLLNRMKERRVFLFE.......QIVIFSEPLDkrgfsmpgYLYKYSIKVNCL..GLEDSVDG...............
LLLEGALKMKE......GKESRMDVYCFLFT.......DVLLITKPVK...rvekvKVIRQPLVIHNV..VCRELKD-........................
TAYEGHVKVPK...plgVKKGWQRAIAVVCD.......FKLFLYDLPE.gkaaqpgVVVNQVIDMRDE..EFSVSPVL...............
VLFMSQVIIQN.....hGAEEKNERYLLLFP.......HILLMLSASP....rmsgFIYQGKLPLTGM..SVSKTEDS......................
VRKAGMLAVKNkrvepaAKRKWKQYWVSLKG.......CTLFFYETDG.rsgidhnSIHKHAVWVENS..IVQAVPEH..........
FILEGALLRAG......---AKHERHNFLFD.......GLMISCKANQpgagsgaeFRLKEKFVLRKY..RIVDREDS.......................
GTRRGCLSKKS.....sDNTKWHTKWFALLQ.......NMLFYFESES.......sSRPSGLYLLEGC..VCDRSPSP................k
PIRQGHFTAWEeipevkSSQRGHHRHVFLFK.......DCIVFCKPKRevgthteaYIFKNKMKLSDI..DVKDTAEG.............
LQMGSEMTVYQ......KRTERITVQVIMET.......MQVALTRSG-........DRIVKVVDISEL.kEVRQWETFkdfqrfnenrgsafr
LVCCSRLFEVT.dinkaQKQAAHQREVFLFN.......DLLVILKLCP.kkkssaaYTFCKTMGLLGM..QFHLFENE...............
GHKKGPTRVKE.....mARFKPMQRHLFLHE.......HALLFCKRREenadktpsYSFKHCLKMSAV..GITENVKG.............
PEIQGFLYMKE.....tGRKSWKKLYMFLRR.......SGLYYSTKGM....skepRHLQLLSDLEES..NIFTVTTG...................
LIHEGALLWKT.....aQGSRLKDVHVLLMT.......DVLVFMQEKD.qkyvfptLDKPSVLCLQNL..IVRDIANQ..................
LVCCSRLYEVT.dvnkpQKQASHQREVFLFN.......DLIVILKLCP.kkktaatYTFCKAMGLLGM..QFHLFENE................
IKTLGSVLYMSamvqnhGCEEKNERYLLLFP.......HVLLILSASP....rmsgFIYQGKLPLSGM..TVTPLEDC................
PEIQGYLYVKE.....mGRKSWKKLYVFLRR.......SGLYFSTKGT....skepRHLQLLADLEDS..NVFTVITG...................
PKGDSEVRVAS.....vDKRAKQDRHIFLFD.......SAVIVCKRRG......dnYEMKEVIDLHSF..KITNNPTS.....................e
EHKRGHVKVME.....lARFKPMQRHLFLHE.......KALLFCKRREegyekapsYSFKQELSMAAI..GITEHAKG...............
LIHEGTLLWKT......PSSRLKDVQVLLMT.......DILVFLQEKD.qrfifasLDKSAVVSLQSL..LVRDIANQ........................
LLHDGPLQLKN......TAGRLKDVHALLLS.......DVLVFLQEKDqkyvfaslDQRATVISLQKL..IVREVAHE.....................
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VEKKGWLTKQG.....gRIKTWKKRWFILTA.......NCLLYYKTPQ.......dHEPCGIIPLENV..VVTIDPQ-........................
VIYSTVMKKAG.....gNKKGFLSRLFVLYK.......GFVIYYKTKT...lltspEKPQGYIDLREC..DPSKVKTI........................l
IKHEGFLTKEG.....gGFKSWKKRWFILKG.......GDLSYYKTKG.......eLVPLGVIHLNTS.gHIKNSDRK......................
VSYSSIMKKAG.....gNGKGFLDRYFALHR.......NYILYYKLGKsslkpddkQEPQGYINLMDC..NPDDTKEI.................
ALKYGYLKKLG...gkgISKNWKKRFFILTK......sGIFYYFKHRT.......sKEPVGIINLEEY.tKIYKDKS-.........................-
TIKEGSVIKQG.....gRIKNWKKRWCVLNE.......EGLHYFKSQH........SIEKGSILLAEI.iSVEGDDKP........................a
SDREGWLTKQG.....gSIRTWRRRWFVLKG.......KKLFYFKSKG.......dIEATGLIELEQN..SFVKEEKD....................
ALIKGWLNKMT.....sNEKTWQRRWFVLKN.......NCLYYFKNEK......deDHPKVIIPLEGL..KVTLLSD-.......................
IVREGYLNKQG.....hLRKNWLCRYFILTE.......TSLEYYKDKG........REFLNRIPLSEC..SITMAEIE.........................il
ALYSGWLQKKG...dkgVVLLWKKRYFSVDR.......NSINYYTDQT.......lQEQKGSISVSGI..EFTNASML...................
IAKEGFLIKKG.....hIRRNWNVRWFQLKR.......NILTYSKTPN.......dIKLSGTIILSPE.sEIDIATNM..........................K
PDKEGELKKQG.....hVVKNWKKRKFIIQN.......DMLFYFKDKE........ERPVGAVPLRMS..RCYENKSL....................
DVFSGYLVKLG.....aIRKNWLKRHFVVRY......dYSIDYFVDDK.......hTNKKGTINLCGY..SVNDDPNK..sgldrilkiaekm
VLVSGWMRKTK......ANKWWEKRFFQLTQ.......NSLIYYKEDP.......pQKTLGSIFLLVS..SCRIIKQK.......................
IVKQGYLTKKG.....aMRRNWTKRWFVLKQ.......GYLFYFKTSK.......dKKPKGIIQLTNV..VVSRSYY-......................
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KIIEGELIKRG.....hIFPSWRTRWFRIEN.......GFLLYFKSKN.......ePEPIDRVPLRGS..RVSKKPFH..........................
IVMQGYLTKIG.....eVVKNWKRRWFIFES.......NYLFYLKNEQ.......sSKVLGIIPLIGS..KIENIDQ-..........................--
-MYCGYIYKLG......QFLYKKRYFEIIYDnqphsssPKLCYYDNEN.......kKYKRGSIEIQDI.IYFNISKEY.......................s
ILLEGYLEKQG...ekgIYKSYKNRYFSLAK.....ngFDLHYFESPPssstqsstALSLGYLDIRQV.tSIKKVDG-....................
SKREGYVYKKG.....iIVKNWKRRFMKFIG......dDRLEYFKNEQ.......dKTPCGSISLHDC.gQIDSIQEL......................
DSIQGYLFKKGssllssSSTLWKKRWFSLEN.....gsTTLKYFKNSS.......dESPKGSINIQLI.eSIDILTTTtttttttttfgnkdntnn
VIYQGLVWKRK......-GFSIKKRQLILTD......tPRLIYIDPKK........MELKGEIPWSDS.iKPKLKSN-..........................---
PSKSGFLFKMN.....gLMKSWKTRWFSLER.......DVLFYYKYNN.......dPKPQGELIILEI.kSIEILPKD......................kl
VLHTGYLTKQG.....gRIQNWKIRWFVLKR.......GTLSYYLSPI....nweyTKPRGVIYLTKK.tELKEVDHR....................
VYLEGELGKKK......EGKGWKVRWMKLLE.......HSLVYYKSSK.......dKEPLGIVNLNEC.qDCEVNKE-....................
ETLRAYLSKKG.....hVVKNWKLRLFVLKP.....gsSYMEYFVDET....keqqHLPQGRVPLYGT..RVMEYVYN..............
ATMEGELLKKS.....rFAAGWKKYYFVLIG.......NHLHYFKTKK.......aRKPKGTITISFI..TPPIPLK-..........................-E
PDKSGYLIKEG.....hVIRSWKKRYFVLKD.......GLIYYFKHQS.......dQEPTGMIPVIGS..QIKRIGET.........................
IVKEGNLKKKG..ggegGRRNWTVRWFKLKN.......DSLSYYKKRK.......dTKPKGIIKLSHS..KVETHSG-...................
VLNEGFIQKKG.negffGSKMFQKRYFKIYE......eGRLAYFKNQN.......dVSPIGVIEMKGA.IACEDMEG-..................
GTKSDFITKKGrggstfGRKSWRLRWFVLSR.....fdKTLKYYSKQT.......dKEPSCSLILEGA..WLEEISPP....................
PVREGYLKKQD......KKKSWKTRYFKLTD.......KYLYWYKSPT.......aIKASGMIICKDY..HIKLAPST......................h
SEFSNVLEKKH......SEISWRSKKFYLKN.......THLYYHRYSS..tespkePTKIKCINLILC..SVKLAQVV.......................
SSKEGWLYKRG....ddLLRIWKKRYFVLRD.......SSLFYFKHQN.......dNFPCGVILLNHG.tKLKRASAS....................
PILSGYLKKQG...dkgLVRSFKKRWFLQRD.......TKLFYYEKEG.......dSEPYGFVNLPEM.iNVKTVDS-..................
KDKSGNLLIME...dsdDQITWKGYYFVLVE.......RCLYYYKSSK........MPPQGVITLKYT..DISVCDSP.....................
GVHSGYLFKKG.....hNFKSWRRRWFVLKD.......NILSYYKSPK.......dTAPAGIIPINEI.vNIEIECEI......................sqa
SDISGVLLKTK....nnNKRTKKERLCVIKY.......SRVLYYFSETinstevkkKRCKGLKFLDDC..KITEKGE-....................
PEKRGFLNILRyisptiGGDNWNQRWCVLKE.......GCLFIYESNK.......dEIEIEVLSLDKG..QVKEKEI-.......................
YVLENYLYKKG......-DFFWKKYWFVLTP.......DSISWYKSSI....lketHYPNGTILLSKI.vTVDKLDPE.......................
SDHKGWLKKYTssgtfrKTLQWKKRWFVLKD.......LVLYYYEGPE........SNLKGKISIPNW..SVEIEKTI.....................
PYFEGFIMRKRggglikGLKNWNKRWYSLRK.......NKLLYFKSKS.......dSTEMGCILMKTV.qTVRPCTEV................
IAANSKLKQDS......-----LKFHFILFQ.......TGLLKVEKSH......deLHVKQYYQIKDK.pIVLTVLQD......................vpsml
IIYSGELYKKN....rnLNIGWKKRFFILTA.......TSLIQSNSSS........EQPKSEIILSNY..ILNITSDS.........................SAK
ILACGITEKRS......-GLITKKRQLIITD......tPRIFYVDPVK........MTQKGEITVDGS.ISAQQKSS-.........................---K
YWKAGWLTMRT...dllAGSNWKPRWVVLRN.......ATIAIYTCPT.....dpaSKPLESFYLSTV.rGVTKISKE...................
CVKYGWIEKRC..gknqSFSSWKRMWFILKD.......SKLTYYIKEK......nlKKRSSTIGSTQE..FFKQQHGI....................
KIYEGWMEMYI......-QKKWKKKWCVLRG.......IHLEYYKGWWedqqgaqdSEECGKILLNYW.yTFSKPVLT............
IIYEGLLIKQT.....kILKRWDPKYFCLLN......sSLINFYDTTK........TRVHRVFYLDQI..SISYKKMA.........................tDT
IIKQGWMKKRG.....tKNKSWKKRYFILDM......kKTLRYYKDN-........SKIPHGNNSNNS..GGGSSSNN....................
PLKIGHLMKQQ.....kIIKLWKRIYVVLSS.......DCLFFYKPIAnnnlnnsiINPIGTVDLRDI.vSVTQVSLT...........kqtkisfssı
PTKQGILFKKS.....rYLKEWRNRFFVIEE.......DILYYFDIEKgnnsnkpiGTPLGIFNLLNC..SFTLITNE.....................
DETSGYLKKKS.....aFKEEWKPRWFVFKK.......PYLYYSHNQK.......dTHKLKKIDLTNS..SVAITQDE....................
ISKEGYLVRKA......-TTSWKKQYFIIQS.......NLLLRYKTKP....skkgKLPKETLDLIGT..DIQSSTI-..........................-A
KVVEGHLMKKS....kqVMGGWNKCWYVLKD.......GMLYCYKGKK.......eFHPENALNILLC..SVRVPQVI......stsspmt
LIREATFGELT....eeKDKISGRMHYYLFN.......DIIMRTQKDK.......kSIRLETLFIIAS..TNVDGEEN........................rgs
DYKKGLINRSN.....gKNKGWKKVWLVLNG.......QNLKSYQSEL......eiDTVLYEIQLKDI.eTITTEEQP.....................
IVIEGNLTELI...pglLWNSNTEKWYVVSE.......GMLYSYKNKS.....lkqLDPLETIHLEKA.iSAHKTKEI........................f
ITFSGYLGKKS.....kSKPEWNYKWFAIRD....tneHVLWYYDSPR.......dPSPINGIRLSNA..YIRECECG.....................
TIKSGNLYKKG.....kINKSWQKRWCMLSK......dSKLFYHKQAN........EKHSGFVDLRQC..IIKQSDCT......................
INQEGILDFVK....ksSLSKWKNRYVRLVD.......GGIYIYKTDK........DEDFKCIDLEFS..VLDSNPKE........................a
IKKKGYLFKEG.....kKLKSMSKYFFKASR.......GNLSYCKNES.......nKSKVKSIQLSEQ.iQLAIPHNV......................h
FITEGIVKQEI...egwLFNSYENRYLKIVK.......DKIYCFLNED....saqaIWDSPVLNIKYV..DIYDEDEN......................ts
KEHQGYLFKTS.sptsnNSSDWKKYLFVYKN.......DVLTYYKVSK.....knkRKEKGIIDLFHS.vKQESRPK-..................
GFKKGYLGVQG....gkLISKWKQRWVVLNQ.......ESISIYKSQE..qqetskKEPKKSIQIIFC..SAKVVKST.....................
LVKEGTLSMGGliqpgqTQQQQYQYYFILLT.......DILLYCKKQTsssssgnkYKFIGKFDLKNM..DIKNITDM................
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LVKEGTLSMGGliqpgqTQQQQYQYYFILLT.......DILLYCKKQTsssssgnkYKFIGKFDLKNM..DIKNITDM.................
ATMTGFLYKMG.....qLNKEWKKRFFFIQG.......TNLYYATLKEfekgtidsVTPTGSMPLERC..RIDQSPHS.................
FVTEGALTLKK......-----DKYYVFLFT.......DAMILTKPGK......ekKKFKNIINLSTA..SLNTTDE-..........................--QN
AVKKGWLNIRV...kgkVTDKWSRKWCVLSD.......GTLYFFRKP-........TDPSPVRYLRDT..VITSKKEI......................
FIYEGTLTKVC......-RKACKKRVVFLFS.......DILVYGSSIP......pkLLLHEKIELDHC..RIEDIPDG.............nlggsssisln
FVREGGLMKVC......-RKEDKFRWFFLFS.......DALMYCTSTNlpntsnhsFTFHRLMLLSDI.nKIRDVKDR..................
FIREGSLTKVC......-RKDHKKRWFILFS.......DALVYGNRID.tavgnpiYKFHRLLPLSNT..KIANLDDT.........................
LFKKGYLFKRS......EYNSYTRKFFELSN.......GKLSYYKTGN.......dTSPSHTHDLFLT..TVRIREDL.........................
LIKDGLMMESR......QKKVSKYRYFILFN.......DLLFITKQKK......nkYSIYKTIPLIDL..KVLEVPQS.....................annt
ILKECWVRIKE....gkNDNDNHNRYIFLFN.......DNIMFTKNSS....ftkkYQYQYSFSLPYH..STKLLPSV......................
FIREGAVHFGS...ssgSFKDKDPIVFLFND.......MVMMTIKHPN....kpneYKYRYSCQFSTT.tTIEELPS-.....................
FLKEGDLKKIS......-DRVVNTRHFFLFN.......DLLIYCKKER.....kntYRFKASFPLLTC..WVKDIPDT..........................c
YVREGMLTESG......KGSNSNQYYCFLFN.......DIFVLSTPIK....ksnqFSFKKKISLSEA..EVTMISDP.........................
YVYEGYILVGD......VSSKSKRVYVFLFN.......DILIFSKPTT.....nkiFNSKTKFKFLKC.eDLFPSPML...................tdip
FLKEGILIEQF......-NNQRISYYTFLFS.......DIILFTEKIEmmaydgsfYLLKKLERIVNI..QVDDPELG..........................f
FVRESQCNISA.....nKKSESGGFYLFFFN.......DMVLVTKKSS....lfsnYKYVYTIPLKNA..DIKDISS-..........................
FIKEGLVSKKL......---DKELLRCILLN.......DVLILAKNKK......snSTVKLIVYLENI..LIRDSIDS........................lpGYKE
DIYGGYLYVKF.....kAEGSYKKYYFNLLT.......NAKVLHQREEskkksnnnNVAIKILNLKRF..SLTRGNQF....................
LLMEGTVSAVK....eINSEDSLSRTLFLFN.......NLILICSFGTinqfktkkLKLKAKIPISDS..RLIFVSDT..........................d
FKIGLTILKIS....skGKPQKKKLIFDLAR.......NQIVCGKKK-........-----KVNFSEI.dEIRVGHKT..........nifnqfkssknlkedi
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PDKEGWLWKQG.....gRYKSWKRRWFILND.......NCLYYFEYTT.......dKEPRGIIPLENI..SVREIHDR.......................
VVKEGWLMKRG.....eHIKNWRQRYFVLHS......dGRLMGYRSKPadsastpsDFLLNNFTVRGC..QIMTVDRP...........
VVKSGSMVKRAqnkkrfTPVNYKHRWFELTK.......RTFSYFDVEN.....verRRERGRIHLKGV.rLVEEATVS.................
VTLSGWLHKQG....sdGLKVWRKRWFVLAE.......YCLYYYKGPE.......eEKLLGSVLLPSY..RVSACLPE.................
HSCRGYLHKLG.....aTFHAWSRRWFVLDR.....qrSALIYYSDKS.......eRKPRGGAYFATI.dEVYLDHLN..................
GDIQGHLYRRK..knhrGVTYWARIYFVMLD.......TILYGFRSKQ.......sTSASLVIFLPGF..TVSLAKEV.......................
RTHEGHLYKRG.....aLLKGWKQRWFVLDS.....ikHQLRYYDTSE.......dTAPKGIIELAEV.qSVTAAQPA..................
LEKMGHLAKLG.....gKLKTWRKRWFVLKN.......GSLNYWKSQH.....dvqRKPQGQIQLDEV.cRINRAEG-................
-----------......--------------.......----------........------------..--------..........................----MFDIKTpKR..............................-T
EVCPKPLWHMF......--------------.......------KPPA.......aYECKRCRNKIHK.eHVDKHDP-..........................--LAPCKL
PIFSGYLWRQSqakgapNSKKWVRRWFSLRP......dNCLYYYKTED.......dSQPVGAMIMAKH..TVDLCPVD............
LLKEGLMTKYP.tsrkrFGRQFKQRHFRLTT.......HSLSYAKSKG........KQPICDIPLQEI.aSVEQLKDK......................
ALKEGWLVHYT.....sLDKAVKRYYWRLDS.......KTITLFVSEQ.......gSKYHKELPLAEL.ISIESHLGD.......................
PIKQGYLYKRS...sksLNKEWKKKYVTLCD......dGRLTYHPSLH....dymdDVHGKEIPLQYV..TVKVPGQK...............
VEYKGFLTMFE...disGFGAWHRRWCYLNG.......SVINYWKYPD....dekrKTPMGSIDLNSC..TSQKVTTA................
FDMEGFLNKRG.....eVNKAFQRRYFVLKG.......NLLFYFESRL.......dKEPLGLIIVEGC..TIELSNEV.........................
TFIAGEVANAG......--------------.......NKLEAQTPN-........-VKKRHRRMKSS..SVKANEAD.........................dNDGYE
VSKCGYLFVAPfsnplyRTKRWQRRWFVLYD......dGELTYSVDDY......peTIPQACVDMTKV.IEVTSAVEV..............
MALSGYLKKLK......---TMKKKFFVLYE.etstsaARLEYYDTEK...kflqrAEPKRVIYLKNC.fNINRRLDT........................
LIHDGNLTIKKnpsvqlHGLLFENMIVLLTK......qDDKYYLKNLHplsitnkpVSPIMSIDADTL..IRQEAAD-.......................
SKKSNPLKRTK...svtKLERTKRGSGGLRG.......SRSHESLLSS........HAVMSTIDLSCT.gAVGVAPVH....................
IEYMGWVNEGV.innniSWQSYKPRFLLLKG.......TEVMLFETPP..lnvagiSKALVVYKVYQT..MFRIVKES................
LERGTIVTKLY.....gKQRRPDRRHLMLIR.....etRQLLWATVAT....qtprTDYEGAIQLREI.rEIRVGKHS.............kefrlf
GTLEGTLSKWT.....nVMKGWQYRFFVLDE.....naGLLSYYTSKD....kmikGVRRGCVRLKDA..LIGIDDQ-.................
IKHHGHLNKKS.....dKTTKWKQLYFALIN...dgseTQLCFYDNPK.......kTKPKGLIDLSCA..YLYQCHDS.....................
PDCFGYLLKLG.....sRWCGWSKRYCVLKD.......ACLYFYQDAN.......sKSAFGMACLHGY..KVASMSAN.................
TAYEGYVKVPK...sgvIKRGWIRQFVVVCD.......FKLFLYDISP.......dRCALPSVSVSQV.IDMRDPEFS...........vgsvr
PMIEGQLKEKK..gkwrLFRRWRTRYFTLSG.......AHLSCKGSS-........--GGESIDVNQI..RSVKVSRG......................
ITKQGYLLKGPrmfaniGNKSFKRRYCYLRQ..eidgtYILELHKDEK.......qGEAKATIVMDFC.tDVVQNPKR................
CRKEGTVNNLTsldqptGSQKWEKCRLVLVK...avggYMLEFYTPHK....atkpRSGVFCFLISEA.rETTALEMP............
FLNEGALIELD....snDYRPIQRVFFFLFN.......DVLIVCKVKH.....dkrLDFLTEYDPKKI..AVINIKDL.........................d
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SVVAGELVSPSssessdESDKWLPIFVAVTE.......REFRIYESAP..wsveawSRPLEIYALATT..RLAGAGNN...............
VIRKGHMVIQN...lgiMKGGSRPYWFVLTS.......ESISWYKDED.......eKEKKFMLPLDGL..KLRDIEQG...................
SVFEGWLSVPN.kqnrrRGHGWKRQYVIVSS.......RKIIFYNSDI...dkhntTDAVLILDLSKV.yHVRSVTQG..................
LVGEGVLTKMC......-RKRPKSRQFFLFN.......DILVYGNIVI....gkkkYNKQHIMPLEEV..SLESIADN.......................
VIKEGVLQKIT......HKGTEIKRYCVLMS.......DIFMYCKMIKpntvvensLECCCIFPLKKC..KVYEML--.......................
CYCRLYEIPDV...nkkERPGVHQREVFLFN.......DLLVITKIFS.kkktsvtYTFRNSFPLCGT..VVTLLDMP.....................
MKHCGYLYAIG....ksVWKKWKRRYFVLVQ..vsqytFAMCSYKEKK........SEPSEMMQLDGY..TVDYIEAA..............
PSMKGFLMHRRistsaaNRIFWQPGYFLLKA.......GVLYMFNDST.......qRLPSWAMALAEC.qGARRTVKS..............
LKLCGQLSKYT.....nVMKGWQYRWFTVDA.....ktGSLSYYLCDSapsphvlaSAPRGQVQLAGA..VVYPSDE-...........
PEMKGWLLKWT.....nYIKGYQRRWFVLSK.......GVLSYYRNQS.....einHTCRGTISLHGA..LIHTVDS-....................
FTKRGYLFLME...kkpFKATWTKYYCTFKK...qkreFTMLQFNQMN.hnftrpeARDDEKLTLFSC..QRRASEFE..........
STKYGQLQRIV..pkrlFFDQTRKCYCGILN.......DWMLCYADGP......taCRPSSTLYLKSS..SIEIEHFG......................
LNISDFLGKIK......KGLELHAMCFVFKS.......AVVFLCKERLnatneveiIRYQVLIPVTEV..QVRASSAK.......................
ILKKGFVNKRK......----------GLFA......rKRMLLLTTGP.......rLIYIDPVQMIKK.gEIPWSPDL........................rAEYKN
IVLADWLKVRG......TLKSWTKLWCVLKP.......GLLLIYKSQK.....tksSHWVGTVMLTSC..QVIERPSK.......................
KGKEGVILKRTyfcsdvVCGTWRNRWFFVKE.......TCFGYIRPTD........GSIRAVILFDQG..FDVSTGIY.....................
VTRQGHLLKKS...egkVRRVWQKRRCRVTS......dGFLDIFHADE........SKPPTRVNLLTC..QIKPVPD-.....................
VEIQGSLERKHsggkkaPVRSWKQFHTVLCG.......QLVCFFKDEN...dflqqKTATAPVNILGA..KCERADDY.............
IELRGYLSKWT.....nYIYGWQPRYIVLKD.......GTLSYYKSES.....esdFGCRGAISLTKA..TIKAHES-.......................
LQMDGPLYMKA.....dPKKGWKRYHFVLRS.......SGLYYFPKE-........-KTKNTRDLACL..NLFHGHNV............ytglgw
NKIEGYLFKKK....skGFKTWCRRWFYLSD.......NQLVYSDLDScrkrsnedSFSVMEEDLRIC..SVRPVNEG.............
TRFSGYLNVQD....pkSQHNWNRRWCSLDG.......VRLSVWQHED....nlesDIPIFTLELPGL.gQSLIAAAP................
NAKKGWLMKQD.....nRTCEWSKHWFTLSG.......AALFYYRDPL....ceerGVLDGVLDVNSL.tSVIPEPAA................
AAMHGCVRRKTkegrkpAVASWQRYWLQIWA.......NSLVYFPPKSgserndfkREPCKVCPLDGW..YAHVSDNT.......
HQLSGYLLRKF.....kNSSGWQKLWVVFTS.......FCLYFYKSYQ.......dEFALASLPLLGY..TVGPPGHQ...................
LIRQGCLLKHS......-KRGLQQRMFFLFS.......DLLLYGSKSP....ldqsFRILGHVPVRSL..-LTENAE-..........................
FDKEGLLIITDegflwrSSEVRVERWCKLRG.......NLLFYLKDKD......pkSAVAGLLVLENC..RARIQNEE...................
LLLDGELHIKA.....hEDQKTKLRYAFVFD.......KILIMVKALH.iktgdmqYTYRDSHNLADY..RVEQSHSR...................
PIKRGLLWQQR....drLFSRWKERYFVLTR.......DYLHCFKRASanerasdmGQFIFKVKLVDV.eKVEWLNRR............
VDKLGEVVLQDawdtkqIIRKGRERRVFLFE.......LYLLFAKEVK..esnvvkYQFKSKLMTTDM..GITEHIEG................
LQDGEKFIRWD.....dDSGTGTPVTMRVDA.......KGFFLYWVDQ........NNELDILDIATI..RDVRTGQY.......akrpkdnkl
EYKKGYVMRKCfkktpfGKRSWKMFYCTLRD.......LVLYLHKDEHgfrksqmsDNLHNAIRIHHA..LATKANDY.............
LSTLGDIIHMG...svaVGADHRDRYFVLFP.......QTLLFLSVSQ....rmsaFIYEGKLPLTGI..IVNRLEDT........................
LVKRGELTHLLakltfgKRLTKISIYAFLFS.......DLLLLCKRRG.escfsvfDYCPRSMLTLAA..GDSLPQLP...................t
EGHEGYVTRKHsttkkaSNRSWDKVYMAAKA.......GRISFYKDQKyksnpeltFRGEPSYDLQNA..AIEIASDY.............
CILHGYIKKLG....gsFASLWQTKYAKLYP.......NRLELHSESG.......NNKPELIFMDQV..EDISSDFI........................l
LRQEGLLMEQH......----NKQRLVLLFA.......TMLIITKQKE.......dGRLQFKTYISQN..NLMLSEHL..........................p
ITAQGSLLMQGmncvvdAAQKHRELQVFLFQ.......QIIIFADIEKknqyaspiFKYRSHIQLNHM..QMKELGD-...............
VRKAGFLSVKKhqielaRKRGWKGYWVCLKG.......TTLLFYPCDS.regrsveAAPKHLIIVDGA..IMQPIPEH................
DFERDALFKVD......------EYGFFLYWksegrdgDVIELCQVSD....iragGTPKDPKILDKV..TKKNGTNI........................
LRQNEFLVWQG......RGGKKTLRQVFLFE.......ELVLFSKARRpdhknldiYIYKNSIKTSDI..GLTAHTGD.................
SSNRSFILKCEnelsdsLSGRGDSLVLYLFS.......DSIELCKRRSkspstaktHKHLKLISLNTI..RLVIDISD.......................
HLHSARFFLQVdatrqkQNLWNSSYTLFLFD.......NQLVYCKRDI...ikrshFIYKGRIFLDRC..RVVNVRDG..................
LAKQGELLMQDskkdirLRMKPKRRHIFLYQ.......KSLLLCKQTSksgynkssYQFKSDVKMSQI..GLTESVSG.............
FIREDSLSKLG.....sGKRIWSERKVFLFD.......GLMVLCKANTsagataydYRLKEKYFMRRV..DINDRPDS.................
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PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEDP.......................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEDS.......................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPQENL..SIREVDDP......................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEFTT.......dKEPRGIIPLENL..SVQKVDDP.....................
IVKEGWLHKRG.....eYIKTWRPRYFLLKN......dGTFIGYKERP..qdvdqrEAPLNNFSVAQC..QLMKTERP................
IVKEGWVQKRG.....eYIKNWRPRYFLLKT......dGSFIGYKEKP...qdvdlPYPLNNFSVAKC..QLMKTERP................
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VIKEGWLHKRG.....eYIKTWRPRYFLLKS......dGSFIGYKERP..eapdqtLPPLNNFSVAEC..QLMKTERP................
CCCRGPLVKMG.....gRIKTWRKRWFCFDR.....qaRRLAYYADKE.......eTKLKGVIYFQAI.eEVYYDHLR.................
KTCRGFLIKMG.....gKIKTWKKRWFVFDR.....nkRTFSYYADKH.......eTKLKGVIYFQAI.eEVYYDHLK...................
HLKEGEMYKRAqgrtriGKKNFKKRWFCLTS.......RELTYHKQPG........KDAIYTIPVKNI.IAVEKLEES.......................
KVCRGYLVKMG.....gKIKSWKKRWFVFDR.....lkRTLSYYVDKH.......eTKLKGVIYFQAI.eEVYYDHLR..........saakk
TILEEILIKRSqqkkktSPLNYKERLFVLTK.......SMLTYYEGRA......ekKYRKGFIDVSKI..KCVEIVKN...................ddg
VLKEGFMIKRAqgrkrfGMKNFKKRWFRLTN.......HEFTYHKSKG........DQPLYSIPIENI.IAVEKLEEE......................
VVCSGWLRKSP.pekklKRYAWKRRWFVLRSgrltgdpDVLEYYKNDH.......aKKPIRIIDLNLC.qQVDAGLTF.............
VILESIFLKRSqqkkktSPLNFKKRLFLLTV.......HKLSYYEYDF...ergrrGSKKGSIDVEKI..TCVETVVPeknppperqiprrg
VVCTGWLRKSP.pekklRRYAWKKRWFILRSgrmsgdpDVLEYYKNDH.......sKKPLRIINLNFC.eQVDAGLTF............
AVCTGWLVKSP.perklQRYAWRKRWFVLRRgrmsgnpDVLEYYRNKH.......sSKPIRVIDLSEC..AVWKHVGP..........
PVQKGFLLKKR....kwPLKGWHKRFFYLDK.......GILKYAKSQT....dierEKLHGCIDV-GL..SVMSVKK-......................
ILLEEQLIKKSqqkrrtSPSNFKVRFFVLTK.......ASLAYFEDRH.....gkkRTLKGSIELSRI..KCVEIVKS....................disi
VLYSGWLRKSP.pekklRLFAWRKRWFILRRgqtssdpDVLEYYKNDG.......sKKPLRTINLNLC.eQLDVDVTL............
VIKAGYCVKQG.....aVMKNWKRRYFQLDE.......NTIGYFKSEL.......eKEPLRVIPLKEV.hKVQECKQS.....................
VAKAGYLHKKG..gtqlQLLKWPLRFVIIHK.......RCVYYFKSST.......sASPQGAFSLSGY.nRVMRAAEE....................
DKHEGFMLKKR....kwPLKGWHKRFFVLDN.......GMLKYSKAPL....diqkGKVHGSIDV-GL..SVMSIKK-....................
GTKEGYLTKQG.....gLVKTWKTRWFTLHR.......NELKYFKDQ-........-MSPEPIRILDL.tECSAVQFD.......................
GTKEGYLTKQG.....gLVKTWKTRWFTLHR.......NELKYFKDQ-........-MSPEPIRILDL.tECSAVQFD.......................
VLKEGFLVKRG.....hIVHNWKARWFILRQ.......NTLVYYKLEG....grrvTPPKGRILLDGC..TITCPCLE.......................
LIKSGYCVKQG.....nVRKSWKRRFFALDD.......FTICYFKCEQ.......dREPLRTIFLKDVlkTHECLVKS......................
ERQEGHLLKKR....kwPLKGWHKRYFVLED.......GILHYATTRQ....ditkGKLHGSIDVRLS..VMSINKK-.....................
VVKQGYLAKQG.....hKRKNWKVRRFVLRK.....dpAFLHYYDPSK......eeNRPVGGFSLRGS..LVSALEDN..............
SILEELLLKRSqqkkkmSPNNYKERLFVLTK.......TNLSYYEYDK.....mkrGSRKGSIEIKKI..RCVEKVNL...................
ILKMGPVDKRK......-GLFARRRQLLLTE......gPHLYYVDPVN........KVLKGEIPWSQE.lRPEAKNF-.........................
VLKQGYLWKRG.....hLRRNWAERWFQLQP.......SCLCYFGSEE.......cKEKRGIIPLDAH.cCVEVLPDR.................
IVKKGYLLKKG......KGKRWKNLYFILEG.....sdAQLIYFESEK......raTKPKGLIDLSVC..SVYVVHDS........................
ALKQGWLHKKGggsstlSRRNWKKRWFVLRQ.......SKLMYFENDS.......eEKLKGTVEVRTA.kEIIDNTT-..................
VCKQDYFIKSPpsqlfsSVTSWKKRFFILSK..ageksFSLSYYKDH-........-HHRGSIEIDQN.sSVEVGISS......................
CDLWDQLHLRS.rqgggRVKTWKRRWFILTD.......NCLYYFEYT-........------------..--------..........................----------.--
RIREGYLVKKG.....sVFNTWKPMWVVLLE.......DGIEFYKKKS.......dNSPKGMIPLKGS..TLTSPCQD...................
GDCEGWLWKKK.daksyFSQKWKKYWFVLKD.......ASLYWYINEE.......dEKAEGFISLPEF..KIDRASEC...............
IIKQGCLLKQG.....hRRKNWKVRKFILRE.....dpAYLHYYDPAG.......aEDPLGAIHLRGC..VVTSVESN...................
LEKSGYLLKMS.....gKVKSWKRRWFVLKG.......CELLYYKSPS.....dviRKPQGHIELSAS.cSILRGDN-...................
RSFEGTLYKRG.....aLLKGWKPRWFVLDV.....tkHQLRYYDSGE.......dTSCKGHIDLAEV..EMVIPAGP..................
VTKAGWLFKQA....ssGVKQWNKRWFVLVD.......RCLFYYKDEK.......eESILGSIPLLSF..RVAAVQPS...................
IQLSGMYNVRK.gkmqlPVNRWTRRQVILCG.......TCLIVSSVKD......slTGKMHVLPLIGG..KVEEVKK-....................
KVKSGWLDKLS....pqGKRMFQKRWVKFDG.......LSISYYNNEK.......eMYSKGIIPLSAI..STVRVQG-....................
VCKRGYLRKQK......---HGHRRYFVLKL.etadapARLEYYENARsgaaipplIPPRRVITLYQC.fSVSQRADA................
VVVRGWLHKQD....ssGMRLWKRRWFVLAD.......YCLFYYKDSR.......eEAVLGSIPLPSY..VISPVAPE...................
PYFHSFLYMKG.....gLMNSWKRRWCVLKD.......ETFLWFRSKQ........EALKQGWLHKKG.gGSSTLSRR.............
SSMSGYLYRSK.....gNKKPWKHFWFVIKN.......KVLYTYAASE.......dVAALESQPLLGF..TVIQVKDE.....................
RSYEGTLYKKG.....aFMKPWKARWFVLDK.....tkHQLRYYDHRV.......dTECKGVIDLAEV..EAVAPGTP.................
VRKCGYLRKQK......---HGHKRFFVLRGggsapqpPRLEYYESEK..kwrskaGAPKRVIALDCC.lNINKRADA..............
VEERGFLTIFE...dvsGFGAWHRRWCVLSG.......NCISYWTYPD....dekrKNPIGRINLANC..TSRQIEPA..................
AIKCGWLRKQG.....gFVKTWHTRWFVLKG.......DQLYYFKDED.......eTKPLGTIFLPGN..KVSEHPCN...................
VDNAGFLYKKG.....gRHAAYHRRWFVLRG.......NMLFYFEDAA.......sREPVGVIILEGC..TVELVEAA....................
LEKSGYLLKMG.....sQVKTWKRRWFVLRQ.......GQIMYYKSPS.....dviRKPQGQVDLNSR.cQIVRGEG-................
VIKQGWLHKANnstitvTMKVFKRRYFYLTQ..lpdgsYILNSYKDEK......nsKESKGCIYLDAC.iDVVQCPKM...............
PIKQGMLLKRS....gkWLKTWKKKYVTLCS......nGVLTYYSSLG....dymkYIHKKEIDLQTS..TIKVPGK-...................
YLKQGFMEKTG....pkQKEPFKKRWFALDC.....heRRLLYYKNPL.......dAFEQGQVFLGNK.eQGYEAYED.............
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VVRRGWLYKQD....stGMKLWKKRWFVLSD.......LCLFYYRDEK.......eEGILGSILLPSF..QIALLTSE......................
KRYEGPLWKSS......RFFGWRLFWVVLEH.......GVLSWYRKQP...davhnIYRQGCKHLTQA..VCTVKST-...............
PTVKGWLTKVK......-HGHSKVVWCALVG.......KIFYYYRSHE.......dKRPLGCLPVRDA..HIEEVDRS..........cdsded
KKLCGYLSKFG...gkgPIRGWKSRWFFYDE.....rkCQLYYSRTAQ.......dANPLDSIDLSSA..VFDCKADA..................
PDCDGWLLLRK.apggfMGPRWRRRWFVLKG.......HTLYWYRQPQ.......dEKAEGLINVSNY..SLESGHDQ...........
DACAKPLWHVF......-------------.......----------........-KPPPALECRRC..HVKCHRDH.....................ldkkeDLICPCKVS
PTMKGLLTKVK......-HGYSKRVWCTLIG.......KTLYYFRSQE.......dKFPLGQIKLWEV..KVEEVDRS...........cdsded
DACAKPLWHVF......-------------.......----------........-KPPPALECQRR..HVKCHRDH.....................ldkkeDLICPCKVS
VLKQGYMMKKG.....hRRKNWTERWFVLKP.......NIISYYVSED.......lKDKKGDILLDEN.cCVESLPDK.....................
YLKEGYMEKTG....pkQTEGFRKRWFTMDD.......RRLMYFKDPL.......dAFARGEVFIGSK..ESGYTVLH..................
ADCQGWLYKKK.ekgsfLSNKWKKFWVILKG.......SSLYWYSNQM.......aEKADGFVNLPDF..TVERASEC.............
SAISGYLSRCK.....rGKRHWKKLWFVIKG.......KVLYTYMASE.......dKVALESMPLLGF..TIAPEKEE........................
VQLYGVLWKRP...fgrPSAKWSRRFFIIKE.......SFLLYYSESEfetnkyfnIHPKGVIPLGGC..LVEPKEEP.....................
NGLSKDMDTGL......-------------G.......DSICFSPSIS..sttspkLNPPPSPHANKK..KHLKKKS-..........................--TNNF
FVKSGWLLRQS.....tILKRWKKNWFDLWS......dGHLIYYDDQT.....rqnIEDKVHMPMDCI..NIRTGQEC.................r
WTMEGYLYVQE...krpLGFTWIKHYCTYDK.gsktftMSVSEMKSSG.......kMGSPEMFKLKSC..IRRKTDSI................
LDKAGVLHRTKdkgkrlRKKHWSASWTVLEG.......GVLTFFKDSKglrqpskfSTPEYTVELRGA..TLSWAPKD............
VRKVGYLRKPK......---SMHKRFFVLRAaseaggpARLEYYENEK..kwrhksSAPKRSIPLESC.fNINKRADS.................
LKKGTKFVKWD......-DDSTIVTPIILRT....dpqGFFFYWTDQN......keTELLDLSLVKDA..RCGRHAKA..........pkdpklre
ANKKKHLKKKS......-------------T.......NNL---KDD-........----------GL..SSTAEEE-..........................--EEKFMIVSvTG..
FIVRGWLHKEVknspkmSSLKLKKRWFVLTH.......NSLDYYKSSE......knALKLGTLVLNSL.cSVVPPDEK................
VVHMGWVNEKL..qgadSSQTFRPKFLALKG.......PSFYVFSTPP..vstfdwVRAERTYHLCEV..LFKVHKFW.....ltedcv
AVKQGFLYLQQ...qqtFGKKWRRFGASLYG.gsdcalARLELQEGPE...kprrcEAARKVIRLSDC.lRVAEAGGE............
PIKQGMLLKRS....gkWLKTWKKKYVTLCS......nGVLTYYSSLG....dymkNIHKKEIDLQTS..TIKVPGKWpslatsactpis
AMLRGSRLRKI.....rSRTWHKERLYRLQE.......DGLSVWFQRR.....iprAPSQHIFFVQHI.eAVREGHQS................eg
IVYMGWCEARE..qdplQDRVYSPTFLALRG.......SCLYKFLAPP..vttwdwTRAEKTFSVYEI..MCKILKDS..................
PLLSGWLDKLS....pqGNYVFQRRFVQFNG.......RSLMYFGSDK.......dPFPKGVIPLTAI..EMTRSSK-.....................
IVVKGWLYREPrgggarPWLPPRRAWFVLTR.......DSLDQFSSSG......kgARRLGSLVLTSL.cSVTGPERR..............
PSISSTTSPKLpppsphANRKKHRR------.......----------........KKSTSNFKADGL..SGTAEEQE..........................-ENFE
DAFAGFLNQQQ...mveGLISWRRLYCVLRG.......GKLYCFYSPE...eieakVEPALVVPINKE.tRIRAMDKD...............
PIKMGWLKKQR.....sIVKNWQQRYFVLRA.......QQLYYYKDEE.......dTKPQGCMYLPGC..TIKEIATN.....................
NGLSKDMDIGL......-------------G.......DSICFSPSIS..sttspkLNPPPSPHANKK..KHLKKKS-..........................--TNNF
VLKEGVLEKRS....ggLLQLWKRKRCVLTE.......RGLQLFEAKG....tggrPKELSFARIKAV..ECVESTG-.....................
HNVRGLLKRLK......-----EKKKARLEP...rdgpPSALGSRES-........LATLSELDLGAE.rDVRIWPLH......................psll
ILKEGPMLKNC.....nSFKRWKLRYFLVQG.......QKLYFAHHPA........FAHFETIDLSQA..TVAESSCR......................
SLMCSFLQLIG....dkWGKSGPRGWCVIPR....ddpLVLYVYAAPQ.......dMRAHTSIPLLGY..QVTVGPQG................
IIKEGMLTKQN.....nSFQRSKRRYFKLRG.......RTLYYAKTAK........SIIFDEVDLTDA..SVAESSTK...........................
ITKHGWLYKGNnsaisvTMRSFKRRFFHLIQ..lgdgsYNLNFYKDEK......isKEPKGSIFLDSC.mGVVQNNKV.............
PIKQGMLLKRS...gksLNKEWKKKYVTLCD......nGVLTYHPSLH....dymqNVHGKEIDLLRT..TVKVPGKR.........pprat
PLRTGMLELRG......---HKAKVFAALSP.......GELALYKSEQ....afsIGIGICFIELQGC..SVRETKS-..........................--
VSHSGFLYKTAllqdrrAREEFSRRWCVLGD.......GVLSYFENER.......aVTPNGEIRASEI..VCLAVPPP...................
VIKAGWLDKNP....pqGSYIYQKRWVRLDT.......DHLRYFDSNK.......dAYSKRFISVACI..SHVAAIG-........................
IVMEGYLFKRA....snAFKTWNRRWFSIQN.......NQLVYQKKFK.......dNPTVVVEDLRLC..TVKHCEDI.....................
NQLSGYLLRKF.....kNSHGWQKLWVVFTN.......FCLFFYKTHQ.......dDYPLASLPLLGY..SVSIPREA......................
PIYGGWLLLAPfdnpvhRSRKWQRRFFILYE.......HGLLRYALDE.....mptTLPQGTINMNQC.tDVVDGEGR...............
ITKEGMLHYKA.gtsylGKEHWKTCFVVLSN.......GILYQYPDRT.......dVIPLLSVNMGGE..QCGGCRRA...................
VLKAGYLEKRR.kdhsfLGFEWQKRWCALSK.......TVFYYYGSDK.......dKQQKGEFAIDGY..SVRMNNTL................
--MEGVLYKWT.....nYLTGWQPRWFVLDN.......GILSYYDSQD.....dvcKGSKGSIKMAVC..EIKVHSA-......................
SIMEGPLSKWT.....nVMKGWQYRWFVLDY.....naGLLSYYTSKD....kmmrGSRRGCVRLRGA..VIGIDDE-.............
VIRKGWLTISN...igiMKGGSKGYWFVLTA.......ESLSWYKDDE.......eKEKKYMLPLDNL..KVRDVEKS...................
VDKAGWIKKSS....ggLLGFWKDRYLLLCQ.......AQLLVYENED.......dQKCVETVELGSY.eKCQDLRAL.................
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PALEGVLSKYT.....nLLQGWQNRYFVLDF.....eaGILQYFVNEQ.....skhQKPRGVLSLSGA..IVSLSDE-..................
GNREGFLWKRG.....rDNSQFLRRKFVLLA.....reGLLKYFTKEQ.......gKSPKAVISIKDL..NATFQTEK.......................
PTASGTLRVQQ....agEMQNWAQVHGVLKG.......TNLFCYRQPE...dadtgEEPLLTIAVNKE.tRVRAGELD...............
LRRGSKFIKWD.....eETSSRNLVTLRVDP.......NGFFLYWTGP........NMEVDTLDISSI..RDTRTGRY.....arlpkdpkirev
VHIRGWLHKQD....ssGLRLWKRRWFVLSG.......HCLFYYKDSR.......eESVLGSVLLPSY..NIRPDGPG.......................
SIKEGQLLKQT.....sSFQRWKKRYFKLRG.......RTLYYAKDSK........SLIFDEVDLSDA..SVAEASTK.........................
LVMEGHLFKRA....snAFKTWSRRWFTIQS.......NQLVYQKKY-........-KDPVTVVVDDL..RLCTVKLC.......................
TLREGWVVHYS.....nKDTLRKRHYWRLDC.......KCITLFQNNT.......tNRYYKEIPLSEI.ITVESAQNF....................sl
YTMEGYLYVQE...krhFGTSWVKHYCTYQR...dskqITMVPFDQKS.....ggkGGEDESVILKSC..TRRKTDSI...............
PIKQGILLKRS...gksLNKEWKKKYVTLCD.......NGLLTYHPSL...hdymqNIHGKEIDLLRT..TVKVPGKR.............lprat
VEKEGYLQKAKadggkkLRKNWSTSWIVLSS.......RRIEFYKESKqalsnmktGHKPESVDLCGA..HIEWAKEK..........
GYREGFLWKRG.....rDNGQFLSRKFVLTE.....reGALKYFNRND.......aKEPKAVMKIEHL..NATFQPAK....................
MVKEGWMVHYT.....sRDNLRKRHYWRLDS.......KCLTLFQNES.......gSKYYKEIPLSEI.IRISSPRDF....................t
TRKAGYLNARN..ktglVSSTWDRQFYFTQG.......GNLMSQARGD........VAGGLAMDIDNC..SVMAVDCE................
PEKVGWVRKFC..gkgiFREIWKNRYVVLKG.......DQLYISEKEV.....kdeKNIQEVFDLSDY.eKCEELRKS..................
ADHMGFLRTWGpgtpptPSGTGRRCWFVLKG.......NLLFSFESRE.......gRAPLSLVVLEGC..TVELAEAP................
SLLCGPLRLSE......SGETWSEVWAAIPM....sdpQVLHLQGGSQ.......dGRLPRTIPLPSC..KLSVPDPE....................
VVMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKKLK.......dALTVVVDDLRLC..SVKPCEDI....................
NRICGFLDIEE....heNSGKFLRRYFILDT.....qaNCLLWYMDNPnltlgagsSKVLQMLSVKKV..SIATPKQK......................
AMQEGMQMVKL.....rGGSKGLVRFYYLDE.....hrSCIRWRPSR-........KNEKAKISIDSI.qEVSEGRQS...............evf
LIGEGVLTKLC......-RKKPKARQFFLFN.......DILVYGNIVI....qkkkYNKQHIIPLENV..TIDSIKDE.........................gDI
PDRAGSLELRG......---FKNKLYVAVVG.......DKVQLYKNLE.......eYHLGIGITFIDM..SVGNVKEV..........................-
VPTCGYLNVLS......-NSRWRERWCRVKD.......NKLIFHKDRT......dIKTHIVSIPLRGC..EVIPGLDS....................
AAKEGWLHFRPgkrvggSIRPWKQMYVVLRG.......HSLYLYKDKR...eqttpSEEEQPISVNAC..LIDISYSE.................
WVKTGALQWWC....dwKPHKWVDVRLALEQghdgvrdSILFIYYVVH.......eEKKYIHIFLNEV..VALVPVLN................
ENVYGYLMKYT.....nLVTGWQYRFFVLNN.....eaGLLEYFVNEQ.....srnQKPRGTLQLAGA..VISPSDE-..................
VYKHGALVRKVcrktprGKRGWKSFHGILKG.......MILYLQKEEYkpgkalseTELKNAISIHHA..LATRASDY.................
ILKSGTLYRLT......VQNNWKAFTFVLSR.......AYLMAFQPGK......ldEDPLLSYNVDVC..LAVQMDNL.....................
IVREGYLLKRKepaglaTRFAFKKRYVWLSG.......ETLSFSKSPE........WQMCHSIPVSHI.rAVERVDEG....................
RLCEGSSFRKI......GNRRRQERFWYCRL...alnhKVLHYGDLDDnpqgevtfESLQEKIPVADI.kAIVTGKDC............ph
MKHSGYLWAIG....knVWKRWKKRFFVLVQ..vsqytFAMCSYREKK........AEPQELLQLDGY..TVDYTDPQ..............
YEEESFVFEPN......-------CLFKVDE.......FGFFLTWRSE........GKEGQVLECSLI.nSIRSGAIP..........kdpkilaaleavgk
VPCCGYLNVLV......-NQGWKERWCRLKC.......NTLYFHKDHM......dIRTHVNAIALQGC..EVAPGFGP..................
PIKQGMLLKRS....gkWLKTWKKKYVTLCS......nGVLTYYSSLG....dymkNIHKKEIDLRTS..TIKVPGKW..................
LHLEGWMKVPR..nnkrGQQGWDRKYIVLEG.......SKVLIYDNE-........AREAGQRPVEEF..ELCLPDGD.........vsihga
RPSQGFLSRRLsqpkldRTSSFRQILPRFRS.adhdraRLMQSFKESHesllspssAAEALELNLDED..SIIKPVHS...........
--MEGVLYKWT.....nYLSGWQPRWFLLCG.......GILSYYDSPE.....dawKGCKGSIQMAVC..EIQVHSV-...................
VYKSGFLARKIgkktprGKRGWKTFYAVLKG.......TVLYLQKDEYkpekalseEDLKNAVSVHHA..LASKATDY...............
CTPSGDLSPLS......-------------.......------REPPpspmvkkqRRKKLTTPSKTE.gSAGQAEE-..........................-ENFE
LSAFGELVLEGggggggPRLRGGERLLFLFS.......RMLLVAKRRG......leYTYKGHIFCCNL..SVSESPR-...................
TVMTLFYSKKS......QRPERKTFQVKLET.......RQITWSRGA-........DKIEGAIDIREI.kEIRPGKTS............rdfdryqed
IQKAGYLNLRN..ktglVTTTWERLYFFTQG.......GNLMCQPRG-........AVAGGLIDLDNC..SVMAVDCE.....................
CRICAFLLRKK......RFGQWAKQLTVIRE.......DQLLCYKSSK.......dRQPHLRLALDTC..SIIYVPKD...........................
LLGEGVLTKEC......-RKKAKPRIFFLFN.......DILVYGSIVL....nkrkYRSQHIIPLEEV..TLELLPET........................IQ
VLREGELEKRS....dsLFQLWKKKRGVLTS.......DRLSLFPASP........RARPKELRFHSI.IKVDCVERT........................
IVKQGYVKMKS.....rKLGIYRRCWLVFRK.ssskgpQRLEKYPDEK....svcIRGCPKVTEISNV.kCVTRLPKE.................
AEMAAELGMRG....pkKGSVLKRRLVKLVV.......NFLFYFRTDE........AEPVGALLLERC..RVVREE--....................
VIRKGWLTINN...igiMKGGSKEYWFVLTA.......ENLSWYKDDE.......eKEKKYMLSVDNL..KLRDVEKG...................
LVRGGWLWRQS.....sILRRWKRNWFALWL......dGTLGYYHDET.....aqdEEDRVLIHFNVR..DIKIGPEC.....................
LVKDGFLVEVS......-ESSRKLRHVFLFT.......DVLLCAKLKKtsagkhqqYDCKWYIPLADL..VFPSPEE-.......................
MKHSGYLYALG....qkVWKRWKKRYFVLVQ..vsqytFAMCSYREKK........SEPQELMQLEGY..TVDYTDPH.............
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RRLKGSIKRTK...sqpKLDRNHSFRHILPG......fRSAAAAAADNesrsheslLSPSSAVEALDL..SMEEEVVI....................
FTAEGYLYVQE.krpapFGSSWVKHYCMYRK...aakkFNMIPFEHRS.....ggkLGDGEVFFLKEC..TKRHTDSI.............
NQLSGNLLRKF.....kNSNGWQKLWVVFTN.......FCLFFYKSHQ.......dNHPLASLPLLGY..SLTIPSES.......................
VTIQGVLRRKTkegkkpTVASWTKYWAALCG.......TQLFYYAAKSaterkhfkSTSNKNVSVIGW..MVMMADDP..........
TFLCDFLYQAPlssekkLLEETNKKWCVLEG.......GFLSYYENDK.......sTTPNGTININEV..ICLAIHKE....................df
FLKEGILMKLS......-RKVMQPRMFFLFN.......DALLYTTPVQ.....sgmYKLNNMLSLAGM..KVRKPTQE.....................
PTIEGYLYTQE...kwaLGISWVKYYCQYEK.....etKTLTMTPMEQ......kpGAKQGPLDLTLK.yCVRRKTES.................
LVKSGELTALEaspglrRKLNTRPVHLHLFN.......DCLLLSRPRE.....gsrFLVFDHAPFSSI..RGEKCEMK.....................
MLMCGVLLKIS......-SGNIQERVFFLFD.......NLLVYCKRKHkastdghrYLFRGRINTEVM..EVENVDDG.................ta
PLIEGKLKEKQ..vrwkFIKRWKTRYFTLAG.......NQLLFQKGKS......kdDPDDCPIELSKV..QSVKAVAK.....................
NFKKGWMSILDpsltttSTSQWKKHWFVLTD.......SSLKYYRDST....aeeaDELDGEIDLRSC.tDVTEYAVQ................
SVVCSFLQYME......KSKPWQKAWCVIPK....qdpLVLYMYGAPQ.......dVRAQATIPLLGY..VVDEMPRS.................
LVLEGTFRVHR......---VRNERTFFLFD.......KTLLITKKRG......dhFVYKGNIPCSSL..MLIESTR-..........................-D
AKICAFLLRKK......RFGQWTKLLCVIKD.......TKLLCYKSSK.......dQQPQMELPLQGC..NITYIPKD.........................s
FLKEGTLMKVT......-GKNRRPRHLFLMN.......DVLLYTYPQK.....dgkYRLKNTLAVANM..KVSRPVME.....................
NFKKGWLTKQY......EDGQWKKHWFVLAD.......QSLRYYRDSV....aeeaADLDGEIDLSAC.yDVTEYPVQ..............
VIRRGWLTINN...islMKGGSKEYWFVLTA.......ESLSWYKDEE.......eKEKKYMLPLDNL..KIRDVEKG.....................
PIKQSFLLKRS...gnsLNKEWKKKYVTLSS.......NGFLLYHPSI...ndyihSTHGKEMDLLRT..TVKVPGKR...................
RLVEGTCFRKL.....nARRRQDKFWCRLSP.....nhKVLHYGDLEEspqgevphDSLQDKLPVADI.kAVVTGKDC..........
CIMHGYMLKLG....npFLTQWQRRYFYLFP.......NRLEWRGEG-........ESRQNLLTMEQI.ISVEETQIK.......................
SVICSFLHYME.....kGGKGWHKAWFVVPE....nepLVLYIYGAPQ.......dVKAQRSLPLIGF..EVGPPEAG..................
QEKYGLLNVTKaengkkVRKNWLSSWAVLQG.......SSLLFTKTQGtswfgsnqSKPEFTVDLKGA..TIEMASKD...........
VDPKGYYLYWT......-----------YQS.......KEMEFLDITS..irdtrfGKFAKMPKSQKL.rDVFNMDF-..........................-PDN
IVKQGYVKIRS.....rKLGIFRRCWLVFKK.asskgpRRLEKFPDEK....aayfRNFHKVTELHNI.kNITRLPRE...................
VEKSGLLNMTKaqggrkLRKNWGPSWVVLTG.......NSLVFYREPPssgwgpagSRPESSVDLRGA..ALAHGRHL........
LVRHGELVELAaappakLKLSSKAVYLHLFN.......DCLLLSRRKE.....lgkFAVFVHAKMAEL..QVRDLSLK...................
PEKCGYLELRG......---YKAKIFTVLSG.......NSVWLCKNEQ....dfksGLGITIIPMNVA..NVKQVDRT..........................
TAYEGFLSVPR...psgVRRGWQRVFAALSD.......SRLLLFDAPD.lrlsppsGALLQVLDLRDP..QFSATPVL................a
VMQSGTQMIKL.....kRGTKGLVRLFYLDE.....hrTRLRWRPSR-........KSEKAKILIDSI.yKVTEGRQS...............eifhrc
TEKVGFLYKKS....dgIRRVWQKRKCGVKY.......GCLTISHSTI........NRPPVKLTLLTC..QVRPNPE-..........................
NRICGFLDIEE....neNSGKFLRRYFILDT.....reDSFVWYMDNP..qnlpsgSSRVGAIKLTYI.sKVSDATKL...................
VKHIAWLAEQA..kldgGRQQWRPVLMAVTE.......KDLLLYDCMP..wtrdawASPCHSYPLVAT..RLVHSGSG............
ELSMGELLMHSflslgkARKDLELTVFVFKR.......AVILVYKENChnstdldpFKFRWLIPISAL..QVRLGNPA...................
ALVEGQVKLRD......-GKKWKSRWLVLRKpspvadcLLMLVYKDKS...erikgLRERSSLTLEDI.cGLEPGLPY..............
PTMEGSLEFKQpggrqpSSSSWDSCRGNLQG.......SSLSLFLDER......maAEKVASIALLDL..TGARCERL..............
QIKNDIQREKRaterlkKKLSEQESLLLLMS.......PSMAFRVHSR......ngKSYTFLISSDYE..RAEWRENI......................
VLKAGWLKKQR.....sIMKNWQQRWFVLRG.......DQLFYYKDKD.......eIKPQGFISLQGT..QVTELPPG...................
DSFEGWLLKWT.....nYLKGYQRRWFVLGN.......GLLSYYRNQG.....emaHTCRGTINLSTA..HIDTEDS-..................
GKMTDSLRKPEralslqHAGRFSVNWFILFN.......DALV---HAQ........FSTHHVFPLATL..WAEPLSEE........................
LLLQGTLLKIS......-AGNIQERAFFLFD.......NLLVYCKRKStksingslYIFRGRINTEVM..EVENVEDG.................tadyl
SAREGWLFKWT.....nYIKGYQRRWFVLSN.......GLLSYYRSKA.....emrHTCRGTINLATA..NITVEDS-.....................
FKVPGFFSKRL.....kGSIKRTKSQSKLDR.ntsfrlPSLRSTDDRSesrsheslLSPCSTVECLDL.gRGEPVSVK...............
LLKGSQLLKVK......SSSWRRERFYKLQE.......DCKTIWQESR....kvmrTPESQLFSIEDI.qEVRMGHRT.................e
VERCGVLSKWT.....nYIHGWQDRWVVLKN.......NALSYYKSED.....eteYGCRGSICLSKA..VITPHDF-...................
AVCASRVKLQH....lpAQEQW-DRLLVLYP.......TSLAIFSEEL......dgLCFKGELPLRAV..HINLEEKE........................
PTMEGPLRRKTkegrkpALSSWTRYWVILSG.......STLLYYGAKSgtdrkhykSTPGKKVSIVGW..MVQLPDDP............
LLKQGELQQMStsrtlrTKKLFHEIYLFLFN.......DLLVICRQIP.....gdkYQVFDSAPRGLL..RVEELEDQ........................
PVKEGPLFIHRkgkgplMSSSFKKLYFSLTT.......EALSFAKTPS........SKKSALIKLANI.rAAEKVEEK.........................s
PVTQGDVYRAE......-----------TE..eipkiFQILYANEG-........-ECRKDVEMEPV.qEAEKTNFQ.......................nhkGH
IVAQGKLLLQDtdqdagLLPRCRERRIFLFE.......QIVIFSEPLDkkgfsmpgFLFKNSIKVSCL..CLEENVEN..................
EALKEAVLRYSdeasmdSGARWQRGRLALRRpgpdgpdRVLELFDPPK.......sSRPKLQAACSSI.qEVRWCTRL.......
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TYKHGVLTRKTgkrtprGRRGWKKFYAVLKG.......TILYLQKDEYrpdkalseGDLKNAIRVHHA..LATRASDY...............
CYCRLFEVPDP...nkpQKLGLHQREIFLFN.......DLLVVTKIFQ.kkknsvtYSFRQSFSLYGM..QVLLFENQ.................
SMVEGSELKKV.....rSNSRIYHRYFLLDA.....dmQSLRWEPSKK........DSEKAKIDIKSI.kEVRTGKNT..............difrsı
TERNGSLYKKS....dgIRKVWQKRKCSVKN.......GFLTISHGTA........NRPPAKLNLLTC..QVKTNPE-......................
KGLEGMIRKRSccgrdqVCYRWSKRWLVVKD.......SFLLYMCLET......gaISFVQLFD-PGF..EVQVGKRS................
VMKEGWMVHYT.....sKDTLRKRHYWRLDS.......KCITLFQNDT.......gSRYYKEIPLSEI.ISLEPVKTS...................a
VQHEGFLLRKRdanrksSNRSWVSLYCVLSK.......GELGFYKDSK.gpasgstHGGEPLLSLHKA..TSEVASDY...........
IRREGWLYYKQgkkagsGLRQWKRVYAALRA.......RSLSLSKERRagaaaagaGEDEAAPVCIGS..CLVDISYS.........
PELEGALYLKE.....dGKKSWKRRYFLLRA.......SGIYYVPKGK....tktsRDLACFIQFENV..NIYYGTQH...................k
SEKKGYLLKKS....dgIRKVWQRRKCSVKN.......GILTISHATS........NRQPAKLNLLTC..QVKPNAE-.......................
IVMADWLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTQK.......nGQWVGTVLLNAC..EIIERPSK........................
LVKRGELTAYVdtvlfsRRTSKQQVYFFLFN.......DVLIITKKKSeesynvndYSLRDQLLVESC..DNEELNSS............pgl
LLKRGELFLVEetglfrKIASRPTCYLFLFN.......DVLVVTKKKS.....eesYMVQDYAQMNHI..QVEKIEPS..............elplp
DLSMGDLLLHTpaslgkWKKEPELAAFVFKT.......AVVLVYKDGSsiyedwdpFRFRHMIPTEAL..QVRALASA.............
TAYEGHVRIPK...pagVKKGWQRALAIVCD.......FKLFLYDIAE.......gKASQPSVVISQV.iDMRDEEFS...........vssvla
PVKEGPLFIHRkgkgplMSSSFKKLYFSLTT.......EALSFAKTPS........SKKSALIKLANI.rAAEKVEEK........................
VIMADSLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTPK.......vGQWVGTVLLHCC..ELIERPSK........................
ARICAFLWRKK......WLGQWAKQLCVIKD.......NRLLCYKSSK.......dHSPQLDVNLLGS..SVIHKEKQ.....................
VIKQGYLEKKS.kdhsfFGSEWQKRWCVVSR.......GLFYYYANEK.......sKQPKGTFLIKGY..GVRMAPHL................
PEIEGVLWLKD.....dGKKSWKKRYFLLRA.......SGIYYVPKGK....akvsRDLVCFLQLDHV..NVYYGQDY..................
LMQEGMPMRKV.....rSKSWKKLRYFRLQN.......DGMTVWHARQ......arGSAKPSFSISDV.eTIRNGHDS...............
VQMEGYLGRKHgpnkkaSNRSWNNLYCVLRN.......SELTFYKDAK.nlalgmpYHGEEPLALRHA..ICEIAANY...........
LVCCCQLYEVP.dpnrpQRLGLHQREVFLFN.......DLLVVTKIFQ.kkkilvtYSFRQSFPLVEM..HMQLFQNS................
LHCCDEEISFS....lrLYEHIHDLSLFLFN.......DALLVSSRGTfertskttYQFIASVALHRL..LIENIPDS........................kY
TYKQGILARKMgkktpwGKRGWKMFHTLLRG.......MVLYFLKQGElegeslvgQMVDEPVGVHHS..LATPATHY.........
IQREGALRFMVaaagsgGSAQWQKCRLLLRR.avaeerFRLEFFVPPK.......aSRPKVSIPLSAI.iEVRTTMPL............
FLHSGKLYKAK......---SNKELYGFLFN.......DFLLLTQITKspksnlqyKMYKTPIFLNEV..LVKLPTDP........................s
IKQIGWLTEQL......PSGGTAPTLALLTE.......KELLLYLSLP..etrealSRPARTAPLIAT..RLVHSGPS....................kgs
DMKMKISALKS......--------------.......---EIQKEKAnkgqsraiERLKKKMFENEF..LLLLNSP-.........................--TIPFRIH
TAYKGHVKVPK...ptgVKKGWQRAYAVVCD.......CKLFLYDLPE.......gKSTQPGVIASQV.lDLRDDEFS...........vssv
LKEQGQLLHRD.pftviCGRKKCLRHVFLFE.......HLLLFSKLKG.peggsemFVYKQAFKTADM..GLTENIGD.............
LMKLGTVERRG......AMGIWKELFCELSP.....leFRLYLSNEE-........HTCVENCSLLRC.eSVGPAHS-......................
FLRQGWLLVVP......PHGEPRPRMFFLFT.......DVLLMAKPRPlhllrsgtFACKALYPMAQC..HLSRVFGH.................
LLKDSFMVELV......-EGARKLRHVFLFT.......DLLLCTKLKKqsggktqqYDCKWYIPLTDL..SFQMVDEL...............eav
VGRGGGVAGPP..sgggGQPQWQKCRLLLRSegeggggSRLEFFVPPK.......aSRPRLSIPCSSI.tDVRTTTAL...........
LMKLGTVERQG......AMGIWKELFCELSP.....leFRLYLSNEE-........HTCVENCSLLRC.eSVGPAHS-......................
LVYNGDLVEYD....adHMAQLQRVHGFLMN.......DCLLVATWLP...qrrgmYRYNALYSLDGL..AVVNVKDN.............
VVHYAKVQLRF.....qHSQDVSDCYLELFP.......AHLYFQAHGS......egLTFQGLLPLTEL..SVCPLEGS....................
LLREGPVLKIS.....fRRNDPMERYLFLFN.......NMLLYCVPRV..iqvgaqFQVRTRIDVAGM..KVRELMDA..................
KGIEGMIMKRSccgqqrACYRWSKRWLIVKD.......SFLLYMKPDS........GAIAFVLLVDKE.fKIKVGKKE..................
FMQAGCELKKV.....rPNSRIYNRFFTLDT......dLQALRWEPSK.......kDLEKAKLDISAI.kEIRLGKNT..............etftnng
SSHRSLVQRVEislgehPCDRGEQVTLFLFN.......DCLEIARKRHgqtrppasLKHIHLMPLSQI.kKVLDIRET.................
CIMHGYMSKMG....npFLTQWQRRYFYLFP.......NRLEWRGEG-........EAPQSLLTMEEI..QSVEETQI...................
PIRQGHFIVWEgapgarMPWKGHNRHVFLFR.......NHLVICKPRRdsrtdtvsYVFRNMMKLSSI..DLNDQVEG............
AQMEGFLNRKHahnkkaSSRSWHNVYCVINN.......QEMGFYKDAK.taasgipYHSEVPVSLKEA..VCEVALDY..........
LLHSGKLYKTK......---SNKELHGFLFN.......DFLLLTYMVKssksnaqfKMYKTPIFLNEV..LVKLPTDP........................
LLLHGPFSVWTykmkdlIRFKPSQRQIYLFE.......RGIVFCKIRMgdqglsphYSFKKTMKLMTL..SIRQLGRG...............
IRHLGWLAEKV...pgeSKKQWKPALVVLTE.......KDLLIYDSMP..rrkeawFSPVHTYPLLAT..RLVHSGPG..................
VIFMSQVMVQY.....gACEEKEERYLMLFS.......NVLIMLSASP....rmsgFIYQGKIPIAGT..VVTRLDEI........................
LIKEGQILKLA.....aRNTSAQERYLFLFN.......NMLLYCVPKF..slvgskFTVRTRVGIDGM..KIVETQNE.....................
LLCHGELRSKS......----GHKLYIFLFQ.......DILVLTRPVT.rnerhsyQVYRQPIPVQEL..VLEDLQDG..........dvrmggsfr
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LRCRDEFIVCC......-GRKKYLRHVFLFE.......DLILFSKTQK.vegshdvYLYKQSFKTAEI..GMTENVGD.....................
RGFEGKLTAQGpeagglLSSRGRERRVFLFE.......QIIIFSEALGvrggtqpgYVYKNSIKVSCL..GLEGNLQG................
LELGTVMTVFS...frkSTPERRTVQVIMET.......RQVAWSKTA-........DKIEGFLDIMEI.kEIRPGKNS...............kdfera
LIYTGEMAWIY.....qPYGRNQQRVFFLFD.......HQMVLCKKDL...irrdiLYYKGRIDMDKY..EVVDIEDG...................r
LVCCSRLFEVT.dvnklQKQAAHQREVFLFN.......DLLVILKLCP.kkkssstYTFCKSVGLLGM..QFQLFENE.................
SIKEGILKIKEepskilSGNKFQDRYFVLRD.......GFLFLYKDVK.......sSKHDKMFSLSSM..KFYRGVKK.....................
IVKQGYVRIRS.....rRLGIYQRCWLVFKK.asskgpKRLEKFSDER.....aayFRCYHKVELNNV.kNVARLPKS................
FIRLGSLSKLS......-GKGLQQRMFFLFN.......DVLLYTSRGL...tasnqFKVHGQLPLYGM..TIEESEDE......................
SRLEGWLSLPV..rnntKKFGWVKKYVIVSS.......KKILFYDSEQ....dkeqSNPYMVLDIDKL.fHVRPVTQT..................
LIKEGQIQKLS.....aKNGTPQDRHLFLFN.......SMILYCVPKL..rlmgqkFSVREKMDISGL..QVQDIVKP.....................
LKEQGQLVRQD.efvvrTGRHKSVRRIFLFE.......ELLLFSKPRH.gptgvdtFAYKRSFKMADL..GLTECCGN................
GTKRGFLSKKT.....aEASRWHEKWFALYQ.......NVLFYFEGEQ.......sCRPAGMYLLEGC..SCERTPAP.............pra
FIREGCLHKLT......-KKGLQQRMFFLFS.......DMLLYTSKGV...agtshFRIRGLLPLQGM..LVEESDNE......................
LVLEGTFRIQR......---AKNERTLFLFD.......KLLLITKKRD......dtFTYKAHILCGNL.mLVEVIPK-..........................-EP
LTAQGKLLQQDieldagMQSRTKERRVFLFE.......QIVIFSELLR.kgsltpgYMFKRSIKMNYL..VLEENVDN..................
FIRQGSLIQVPvrlgslSLKKEGERQCFLFT.......KHFLICTRSS..ggklhlLKTGGVLSLIDC..TLIEEPDA.............sddds
LETSSYLNVLV......-NSQWKSRWCSVRD.......NHLHFYQDRN......rsKVAQQPLSLVGC..EVVPDPSP....................
IESQGELILQEvwdpktLIRKGRERHLFLFE.......MSLVFSKEVK.dssgrskYLYKSKLFTSEL..GVTEHVEG.................
VRKAGALAVKNkkvesaTRRKWKHYWVSLKG.......CTLFFYESDG.rsgidhnSIPKHAVWVENS..IVQAVPEH...........
LILQDAFQVWD...pksLIRKGRERHLFLFE.......ISLVFSKEIK.dssghtkYVYKNKLLTSEL..GVTEHVEG....................
LIYSGELTRVT.....qPQAKSQQRMFFLFD.......HQLIYCKKDL...lrrdvLYYKGRLDMDGL..EVVDLEDG...................
EQMEGMLCRKQafgkkaANRSWQNVYCVLRR.......GSLGFYKDAK...aasagVPYHGEVPVSLA..RAQGSVAF.......
PEIQGFLQLRG.....sGRKLWKRFFCFLRR.......SGLYYSTKGT....skdpRHLQYVADVNES..NVYVVTQG................
VRKAGWLFFKPrklelvARRKWKQYWVTLKG.......CTLLFYETYG.knsmdqsSAPRCALFAEDS..IVQSVPEH...........
LEFQGELTELGggvlfaSRPRFTPLCLLLFS.......DLLLITQPKS...gqrlqVLDYAHRSLVQA..QQVPDPSG...................
GTRKGYLSKRS.....sDNTKWQTKWFALLQ.......NLLFYFESDS.......sSRPSGLYLLEGC..VCDRAPSP................k
VTYMSQVLIQC.....aGSEEKNERYLLLFP.......NVLLMLSASP....rmsgFIYQGKLPTTGM..TITKLEDS.....................
PKIDGELKVRS.....iVNHTKQDRYLFLFD.......KVVIVCKRKG......ysYELKEIIELLFH..KMTDDPMN.....................nk
LLLEGPVRVKE......GREGKLDVYLFLFS.......DVLLVTKPQR...kadkaKVIRPPLMLDKL..VCQPLRD-......................
LLLEGSLRMKE......GKDSKMDVYCFLFT.......DLLLVTKAVK...kaertRVIRPPLLVDKI..VCRELRD-.........................
PEIHGFLHAKE.....qGKKSWKKIYFFLRR.......SGLYFSTKGT.......sKEPRHLQFFSEF.gNSDIYVSL..................ag
LIHSGELTKIT......KQGKSQQRTFFLFD.......HQLVSCKKDL...lrrdmLYYKGRLDMDEM..ELVDLGDG...................
DTKHGMMKFREllglglPSGGFHDRYFILNS.......SCLRLYKEVRwsgapetsHRPEKEWPIKSL..KVYLGVKK.............
LIHDGCLLWKT......ATGRFKDVLVLLMT.......DVLVFLQEKD.qkyifptLDKPSVVSLQNL..IVRDIANQ.........................
LHLEGMLCWKT......TSGRLKDILAILLT.......DVLLLLQEKDqkyvfasvDSKPPVISLQKL..IVREVANE........................
SRIEGWLSVPN..rgniKRYGWKKQYVVVSS.......KKILFYNDEQ....dkeqSNPSMVLDIDKL.fHVRPVTQG................
PEIQGFLHVKE.....lGKKSWKKLYVCLRR.......SGLYCSTKGT....skepRHLQLLADLEDS..NIFSLIAG...................r
LIKEGHILKLS.....aKNGTTQDRYLILFN.......DRLLYCVPRL..rllgqkFSVRARIDVDGM..ELKESSNL.........................
GHKKGATKMKD.....lARFKPMQRHLFLYE.......KAIVFCKRRVegsdrypsYSFKHCWKMDEV..GITEYVKG...............
PKIDGELKITS.....vERRSKMDRYAFLLD.......KALLICKRRG......dsYDLKDFVNLHSF..QVRDDSSG.....................
LLMQGSFSVWTtkvkelARFKPMQRHLFLHE.......KAVLFCKKREegyekapsYSYKQSLNMAAV..GITENVKG...........
PQGDGEIRITT.....lDKHTKQERHIFLFD.......LAVIVCKRKG......dnYEMKEIIDLQQY..KIANNPTT.....................dke
LVRDGSVFLKN......AAGRLKEVQAVLLT.......DILVFLQEKDqkyifaslDQKSTVISLKKL..IVREVAHE.......................
FIMEGPLTRIG......---AKHERHIFLFD.......GLMISCKPNHlpgytsaeYRLKEKFVMRKI..QICDKEDT.........................
FIMEGTLTRVG......---AKHERHIFLFD.......GLMICCKSNHlpgasnaeYRLKEKFFMRKV..QINDKDDT......................
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PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIVPLENL..SIREVEDP.......................
PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVEDS.......................
PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVDDP.......................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEFTT.......dKEPRGIIPLENL..SVQKVEDP.......................
IVKEGWLHKRG.....eYIKTWRPRYFLLKN......dGTFIGYKERP..qdvdqrESPLNNFSVAQC..QLMKTERP.................
IVKEGWVQKRG.....eYIKNWRPRYFLLKT......dGSFIGYKEKP...qdvdlPYPLNNFSVAKC..QLMKTERP.................
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VIKEGWLHKRG.....eYIKTWRPRYFLLKS......dGSFIGYKERP..eapdqtLPPLNNFSVAEC..QLMKTERP................
KTCRGYLIKMG.....gKIKTWKKRWFVFDR.....nkRTFSYYADKH.......eAKLKGVIYFQAI.eEVYYDHLK....................
GCCRGPLVKMG.....gRIKTWRKRWFCFDR.....qaRRLAYYADKE.......eTKLKGVIYFQAI.eEVYYDHLR................
KVCRGYLIKMG.....gKIKSWKKRWFVFDR.....lkRTLSYYVDKH.......eTKLKGVIYFQAI.eEVYYDHLR...................
LLKEGFMIKRAqgrkrfGMKNFKKRWFRLTN.......HEFTYQKSKG........DQPLCNIPIENI.IAVERLEEE.......................
TILEEILIKRSqqkkktSPLNYKERLFVLTK.......SVLSYYEGRA......ekKYRKGVIDISKI..KCVEIVKN....................ddgv
HLKEGEMYKRAqgrtriGKKNFKKRWFCLTS.......RELTYHRQQG........KDAIYTIPVKNI.IAVEKLEEG....................
VVCSGWLRKSP.pekklKRYAWKRRWFVLRSgrltgdpDVLEYYKNDH.......aKKPIRIIDLNLC.qQVDAGLTF...............
VILESIFLKRSqqkkktSPLNFKKRLFLLTV.......HKLSYYEYDF...ergrrGSKKGSIDVEKI..TCVETVIPeknppperqiprrge
TVCMGWLIKSP.perklQRYAWRKRWFVLRRgrmsgnpDVLEYYRNKH.......sNKPIRVIDLSEC..TVWKHAGP................
VVCTGWLRKSP.pekklRRYAWKKRWFILRSgrmsgdpDVLEYYKNEH.......sKKPLRIINLNLC.eQVDAGLTF...............
ILLEEQLIKKSqqkrrtSPSNFKVRFFVLTK.......ASLAYFEDRH.....gkkRTLKGSIELSRI..KCVEIVKS...................disi
VIKAGYCVKQG.....aVMKNWKRRYFQLDE.......NTIGYFKSEL.......eKEPLRVIPLKEV.hKVQECKQS...................
VAKAGYLHKKG..gtqlQLLKWPLRFVIIHK.......RCIYYFKSST.......sASPQGAFSLSGY.nRVMRAAEE...................
DRHEGFMLKKR....kwPLKGWHKRFFVLDN.......GMLKYSKAPL....diqkGKVHGSIDV-GL..SVMSIKK-.................
PVQKGFLLKKR....kwPLKGWHKRFFCLEK.......GILKYAKSQ-........-ADIEREKLHGC.iDVGLSVMS......................
VLKEGFLVKRG.....hIVHNWKARWFILRQ.......NTLLYYKLEG....grrvTPPKGRIVLDGC..TITCPCLE.....................
GTKEGYLTKQG.....gLVKTWKTRWFTLQR.......NELKYFKDQ-........-MSPEPIRILDL.tECSAVQFD......................
LIKSGYCVKQG.....nVRKSWKRRFFALDD.......FTICYFKCEQ.......dREPLRTIPLKDVlkTHECLVKS.....................
VVKQGYLSKQG.....hKRKNWKVRRFVLRK.....dpAFLHYYDPSK......eeNRPVGGFSLRGS..LVSALEDN..............
ERQEGHLLKKR....kwPLKGWHKRYFVLED.......GILHYATTRQ....ditkGKVHGSIDVRLS..VMSINKK-.................
SILEELLLKKSqqkkkmSPNNYKERLFVLTK.......TSLSYYEYDK.....mkrGSRKGSIEIKKI..RCVEKVNL...................
ILKMGPVDKRK......-GLFARRRQLLLTE......gPHLYYVDPVN........KVLKGEIPWSQE.IRPEAKNF-.....................
IVKKGYLLKKG......KGKRWKNLYFILEG.....sdAQLIYFESEK......raTKPKGLIDLSVC..SVYVVHDS......................
ALKQGWLHKKGggsstlSRRNWKKRWFVLRQ.......SKLMYFENDS.......eEKLKGTVEVRTA.kEIIDNTS-.................
VLKQGYLWKRG.....hLRRNWAERWFQLQP.......SSLCYFGSEE.......cKEKRGTIPLDAH.cCVEVLPDR...............
RIREGYLVKKG.....sVFNTWKPMWVVLLE.......DGIEFYKKKS.......dNSPKGMIPLKGS..TLTSPCQD...................
GDCEGWLWKKK.daksyFSQKWKKYWFVLKD.......ASLYWYINEE.......dEKAEGFISLPEF..KIDRASEC...............
VHKRDYFIKSPppqlffSGTSWKKRLFILSQ..srgtgLSLSYYKDH-........-QHRGSIEIDGS.sTVEVGINC..................
VTKAGWLYKQA....ssGVKQWNKRWFVLVD.......RCLFYYKDEK.......qESILGSIPLLSF..RVAAVQPS.................
LEKSGYLLKMS.....vRVKTWKRRWFVLKG.......GELLYYKSPS.....dviRKPQGHIELSAS.cSILRGDN-.................
RSYEGILYKKG.....aFMKPWKARWFVLDK.....tkHQLRYYDHRM.......dTECKGVIDLAEV..EAVAPGTP...............
RSFEGTLYKRG.....aLLKGWKPRWFVLDV.....tkHQLRYYDSGE.......dTSCKGHIDLAEV..EMVIPAGP.................
STMSGYLYRSK.....gSKKPWKHLWFVIKN.......KVLYTYAASE.......dVAALESQPLLGF..TVTLVKDE....................
PYFHSFLYMKG.....gLMNSWKRRWCVLKD.......ETFLWFRSKQ........EALKQGWLHKKG.gGSSTLSRR................
IQLSGMYNVRK.gkmqlPVNRWTRRQVILCG.......TCLIVSSVKD......svSGKMHVLPLIGG..KVEEVKK-.................
IIKQGCLLKQG.....hRRKNWKVRKFILRE.....dpAYLHYYDPAG.......gEDPLGAVHLRGC..VVTSVESS..................
VRKCGYLRKQK......---HGHKRFFVLRGggsppqpPRLEYYESEK..kwrskaGAPKRVIALDCC.lNINKRADA..............
--------MRA......--------------.......--LIYSTTT-........---------AGS..QMEHSGM-..........................----------.-R.................
NTKCGWLRKQG.....gFVKTWHTRWFVLKG.......DQLYYFKDED.......eTKPLGTIFLHGN.kVIEHPCNE................
VCKRGYLRKQK......---HGHRRYFVLKL.etadapARLEYYRNARsgaavpalIPPRRVIILYQC.fSVSQRADA...............
VIKQGWLHKANnstitvTMKVFKRRYFYLTQ..lpdgsYILNSYKDEK......nsKESKGCIYLDAC.iDVVQCPKM..............
VDNAGFLYKRG.....gRGTGSHRRWFVLRG.......NILFYFEAEG.......sREPLGVILLEGC..TVELVDAR...................
KKLCGYLSKFG...gkgPIKGWKCRWFFYDE.....rkCHLYYSRTAQ.......dANPLDSIDLSSA..VFDCKADA...............
VEEKGFLTIFE...dvsGFGAWHRRWCVLSG.......NCISYWTYPD....derrKNPIGRINLANC.iSHQIEPAN..................
MGIGDFSATVG......----------TLTA.......GKICAVHTG-........-MRALIYSTTTA.gSQMEHSG-..........................----------
LEKSGYLLKMG.....sRVKTWKRRWFVLRQ.......GQILYYKSPS.....dviRKPQGQVDLNSH.cQIVREEE-.................
SRLCGYLQKLS...gkgPLRGYRSRWFVFDS.....rrCYLYYFKSPQ.......dALPLGHLDIADA..CFSYQGRD................
KRYEGPLWKSS......RFFGWKLFWVVLEH.......GVLSWYRKQP...davhnSYRQGCKHLTQA..VCTVKPT-..................
MATEGNAEKAD......--------------.......----------........----GFVNLSDF..TVERASEC.......................KKKNAFKINHpQ
VVRRGWLYKQD....stGMKLWKKRWFVLSD.......LCLFYYRDEK.......eEGILGSILLPSF..QIAMLTAE....................
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PTCRGYLHKRT...hsgFVKGWRKRWFVLKH......dGFLLYYKHRK....degkWPPLDMIKLEGA..EVDIDNSL...............
EACAKPLWHVF......-------------.......----------........-KPPPALECRRC..HVKCHRDH.....................ldkkeDLISPCKVSY
PTVKGWLTKVK......-HGHSKLVWCALVG.......KTFYYYRSHE.......dKRPLGCLPVQDA..HIEEVDRS..........cdsdec
VQLYGVLWKRP...fgrSSAKWSRRFFIIKE.......SFLLYYSESEfetnkyfnIHPKGVIPLGGC..LVEAREEP......................
KEKCGWLDKLS....pqGKRMFQKRWVKFDG.......LSISYYNNDR.......eMYSKGIIPLTAI..STVRAQG-.....................
FVKSGWLLRQS.....tILKRWKKNWFDLWS......dGHLIYYDDQT.....rqsIEDKVHMPVDCI..NIRTGHEC.................rc
VRLCGHLRKQK......---SQRRRFFVLRA.....dpPRLECYESEKflasgcrpPRPRRTVSLEGA.cTISKRADA.....................
LDKAGVLHRTKdkgkrlRKKHWSTSWTVLEG.......GVLTFFKDSKglrqpsklSTPEYTVELKGA..SLSWAPKD............
VLKQGYMMKKG.....hKRKNWTERWFVLKP.......NIISYYVSED.......lKDKKGDILLDEN.cCVESLPDK.....................
LKKGTKLVKWD......-DDSTIVTPTILRT....dpqGFFFYWTDQN......keTELLDLSLVKDA..RCGKHAEA.........pkdpklr
ILLSGIYNVRK...gktQLHKWAERLVVLCG.......TCLIVSSVKD......cqTGKMHILPLVGG..KIEEVKR-..........................
VFKSGWLYKGNtvnntvTVRSFKKRYFQLTQ..lpdnsYIMNFYKDEK......isKEPKGCIFLDSC.tGVVQNNRL..............
VFKSGWLYKGNtvnntvTVRSFKKRYFQLTQ..lpdnsYIMNFYKDEK......isKEPKGCIFLDSC.tGVVQNNRL..............
SLVCSFLQLIG....dkCSRSLPRSWCVIPR....ddpLVLYVYAAPQ.......dTKAHTSIPLLGY..QVISGPQG....................
PEKVGWVRKFC..gkgiFREIWKNRYVVLKG.......DQLYVSEKEV.....kdeKNSQEVFDLSDY.eKCEELRKS...............
VRKVGYLRKPK......---SMHKRFFVLRAaseaggpARLEYYENEK..kwrhksSAPKRSIPLESC.fNINKRADS.................
PSISSSTSPKLpppsphANRKKHRR------.......----------........KKSTSNFKADGL..SGTAEEQE..........................-ENLE
ADKAGWIKKSS....ggLLGLWKDRYLLLCQ.......AQLLVYENED.......eQKCVETVELGSY.eKCQDLRTL..................
LRRGSKFIKWD.....eEASSRNLVTLRVDP.......NGFFLYWTGP........NMEVDTLDISSI..RDTRTGRY.....arlpkdpkirev
PDCDGWLLLRK.vpggfMGPRWRRCWFVLKG.......HTLYWYRQPQ.......dEKAEGLINLSNY..SLESGHDQ............
PDCDGWLLLRK.vpggfMGPRWRRCWFVLKG.......HTLYWYRQPQ.......dEKAEGLINLSNY..SLESGHDQ............
PLRTGTLELRG......---HKAKVFAALIP.......GELALYKSEQ....afslGIGICFIELQGC..SVRETKS-..........................---l
FIVRGWLHKEVknspkmSSLKLKKRWFVLTH.......NSLDYYKSSE......knALKLGTLVLNSL.cSVVPPDEK................
NQLSGYLLRKF.....kNSNGWQKLWVVFTN.......FCLFFYKTHQ.......dDYPLASLPLLGY..SVSLPREA.....................
PLLSGWLDKLS....pqGNYVFQRRFVQFNG.......RSLMYFGSDK.......dPFPKGVIPLTAI..EMTRSSK-.....................
YLKQGFMEKTG....pkHREPFKKRWFALDP.....qeRRLLYYKNPL......daFELGQVFLGSNE.qGYEVWEDL.............
IIVKGWLYREPrgggarPWLLPRRAWFVLTR.......DSLDQFSSSG......kgARRLGSLVLTSL.cSVTGPERR................
VLKEGVLEKRS....ggLLQLWKRKRCVLTE.......RGLQLFEAKG....tggrPKELSFARIKAV..ECVESTG-.....................
IVREGFLLKRKepgglaTRFAFKKRYFRLSG.......RDLSYSKTPE........WQVHTSIPLSCI..RAVEHVDE......................
HNVRKLLKRLK......EKKRAKSELGAYTP...rdgpPSALGSRES-........LATLSELDLGAE.rDVRVWPLH.....................
VVHMGWVNERL..qgadNSQNFRPKFLALRG.......SSFYIFGAPP..vstldwGRAERAYNLCEV..LFKVHKFW.....lsdny
VSHSGFLYKTAllqdrrAREEFSRRWCVLGD.......GVLSYFENER.......aVTPNREIRASEI..VCLAVPPP.....................
ILKEGMLTKQN.....nSFQRSKRRYFKLRG.......RTLYYAKTAK........SIIFDEVDLTDA..SVAESSTK.........................
LVMEGHLFKRA....snAFKTWSRRWFTIQN.......NQLVYQKKY-........-KDPVTVVVDDL..RLCTVKLC......................
SAISGYLSRCK.....sGKRRWKKLWLVIKG.......KVLYTYLASE.......dKVAMESIPLLGF..TIAPEKEE.......................g
IVYMGWCEARE..qeslQDRVYTPVFLALRG.......SCLYRFLSPP..vttwdwTRAEKTFSVCEI..MCKVLKDS...............
AVKQGFLHLQQ...qqtFGKKWRRFAAVLYG.esgcalARLELQDVPE...ktrrgEATRKVVRLSDC.lRVAEVGSE............
WTMEGYLYVQE...krpLGFTWTKHYCTYDK.......GSKMFTMSIPfffqnglvTGSPEMFKLKSC..IRRKTDSI................
ADHTGFLRSWGpgspptPSGTGRRYWFVLKG.......NLLFSFETRE.......sRVPLSLVVLEGC..TVELAEAP...............
PIKVGWLKKQR.....sIVKNWQQRYFVLRA.......QQLYYYKDEE.......dSKPQGCMYLPGS..TVKEIATN...................
GYREGLLWKRG.....rDNGQFLSRKFVLTE.....reGALKYFNKND.......aKEPKAVMKIEHL..NATFQPAK....................
ILKSGTLYRLT......VQNNWKAFTFVLSK.......AYLMAFHPGK......ldEDPLLSYNVDVC..LAVQIDNL.......................
ITKHGWLYKGNnsaisvTMRSFKRRFFHLIQ..lgdgsYNLNFYKDEK......isKEPKGSIFLDSC.mGVIQNNRV..............
ITKHGWLYKGNnsaisvTMRSFKRRFFHLIQ..lgdgsYNLNFYKDEK......isKEPKGSIFLDSC.mGVIQNNRV..............
IVMEGYLFKRA....snAFKTWNRRWFSIQN.......NQLVYQKKFK.......dSPTVVVEDLRLC..TVKHCEDI...................
SIKEGQLLKQT.....sSFQRWKKRYFKLRG.......RTLYYAKDSK........SLIFDEVDLSDA..SVAEASTK.......................
AMLRGSRLLKI.....rSRTWHKERLYRLQE.......DGLSVWFQRR.....iprAASKHIFFVQHI.eAVREGHQS................eg
GNREGFLWKRG.....rDNAQFLRRRFVLLS.....reGLLKYYTKEE.......gKAPKAVISIKDL..NATFQTEK......................
WVKTGALQWWC....dwKPHKWVDVRVALEQghdgardSILFIYYVVH.......eEKKYLHVFLNEV..TVLVPVLN............
TSIASPVILRV......-DPKGYYLYWTYQN.......QEMEFLDVTS..irdtrfGKFAKIPKSQKL.rEVFNMDF-.........................
VIKAGYLEKRR.kdhsfLGFEWQKRWCALSK.......TVFYYYGSDK.......dKQQKGEFAIDGY..DVRMNNTL...............
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PIKQGILLKRS...gksLNKEWKKKYVTLCD.......NGLLTYHPSL...hdymqNIHGKEIDLLRT..TVKVPGKR.............lpra
VHIRGWLHKQD....ssGLRLWKRRWFVLSG.......HCLFYYKDSR.......eESVLGSVLLPSY..SVRPDGPG.................
ILKEGPLLKNC.....nSFRRWKLRYCLVQG.......QKLHFAHHPS........FAHFETIDLSQV..VLAESSCR.......................
VVKEGWMVHYT.....sRDNLRKRHYWRLDS.......KCLTLFQNES.......gSKYYKEIPLSEI.IRVSSPQDF......................
VIRKGWLTVSN...igiMKGGSKGYWFVLTA.......ESLSWYKDDE.......eKEKKYMLPLDNL..KVRDVEKG...................
--MEGVLYKWT.....nYLTGWQPRWFVLDN.......GILSYYDSQD.....dvcKGSKGSIKMAVC..EIKVHPA-.......................
YTMEGYLYVQE...krhFGTSWVKHYCTYQR...dskqITMVPFDQKS.....ggkGGEDESVTLKSC..TRRKTDSI.............
LVRGGWLWRQS.....sILRRWKRNWFALWL......dGTLGYYHDET.....aqdEEDRVVIHFNVR..DIKVGQEC..............
AIIQNVEKQDG...gwwRGDYGGKKQLWFPS.......NYVEEMINPAldensplgDLLRGVLDVPAC..QIAIRPEG.............
TRKAGYLNARN..ktglVSSTWDRQFYFTQG.......GNLMSQARGD........VAGGLAMDIDNC..SVMAVDCE...............
RLCEGSSFRKI..gnrrRQERFWHCRLALNH.......KVLHYGDLDDnpqgevtfESLQEKIPVADI.kAIVTGKDC............ph
PTIEGYLYTQE...kwaLGISWAKYYCRYEK...etrmLTMIPMEQKP........GAKQGPVDLTLK.yCVRRKTES................
LVRSDDVIETV.yndrgEIVKTKQRRIFMLN.......DVLMCATASS.......rNSHESHAVMSQR.yLLKWSVPL...................
YLKEGYMEKTG....pkQTEGFRKRWFTMDD.......RRLMYFKDPL.....dafARGEVFIGSKES..GYTVLEGL.................
VEKEGYLQKAKadggkkLRKNWSTSWIVLSG.......RKIEFYKDSKqalpnmktRHNVESVDLCGA..HIEWAKEK...........
PLCDSGLHLNYsswptsPGLRWEKRWC----.......----------........--DLRLIPLLHA..RFSQYVPG......................tdlSRQ
ITKEGMLHYKA.stsylGKEHWKACFVVLSN.......GILYQYPDRT.......dVIPLLSVNMGGE..QCGGCRRS..................
PALEGVLSKYT.....nLLQGWQNRYFVLDF.....eaGLLQYFVNEQ.....skhQKPRGVLSLSGA..IVSLSDE-..................
PIYGGWLLLAPfdnpvhRSRKWQRRFFILYE.......HGLLRYALDE.....mptTLPQGTINMNQC.tDVVDGEAR..............
PIYGGWLLLAPfdnpvhRSRKWQRRFFILYE.......HGLLRYALDE.....mpnTLPQGTINMNQC.tDVVDGEAR.............
PDRAGSLELRG......---FKNKLYVAVTG.......DKVQLYKNLE.......eFHLGIGITFIDM..NVGNVKEV..........................-
LIGEGVLTKLC......-RKKPKARQFFLFN.......DILVYGNIVI....qkkkYNKQHIIPLENV..TIDSIKDE.........................gE
VVMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKKLK.......dALTVVVDDLRLC..SVKPCEDI...................
VYKSGFLARKIgkktprGKRGWKTFYAVLKG.......TVLYLQKDEYkpekslsdEDLKNAVSVHHA..LASKATDY.............
DAFAGFLNEQQ...tgkGLVGWRRLYCALRG.......GKLRCFYGPE...eieakVEPALVVPIDKE.tRIQAVEKD................
DAFAGFLNEQQ...tgkGLVGWRRLYCALRG.......GKLRCFYGPE...eieakVEPALVVPIDKE.tRIQAVEKD................
VSHSGFLYKTAplqdrrAREEFSRRWCVLSD.......GVLSYYENER.......aVTPNGEIRASEI..VCLAVSPL....................
SLLCGTLNLSD......DGTTWNEVWAAIPE....sdpQVLDLLAGSQ.......aGRLLYSIPLSGC..NITMPDPE.....................
MQSGTQMIKLK......RGTKGLVRLFYLDE.....hrTRLRWRPSR-........KSEKAKILIDSI.yKVTEGRQS...............eifhrq
LSAFGELVLEGggggggPRLRGGERLLFLFS.......RMLLVAKRRG......peYTYKGHIFCCNL..SVSETPR-.................
ESVNGYLMKYT.....nLVTGWQYRFFVLNN.....eaGLLEYFVNEQ.....srnQKPRGTLQLAGA..VISPSDE-.................
VYKHGALVRKVcrktprGKRGWKSFHGILKG.......MILYLQKEEYqpgkalseAELKNAISIHHA..LATRASDY................
PEKCGYLELRG......---YKAKIFTVLRG.......NSVWLCKNEQ....dfksGLGITIIPMNVA..NVKQVDRA........................
AMQEGTQMVKL.....rGSSKGLVRFYYLDE.....hrSCLRWRPSR-........KNEKAKISIDSI.qEVSEGRQS...............eifq
VPCCGYLNVLV......-NQGWKERWCRLRC.......NTLYFHKDRT......dlHTHVNSIALRGC..EVAPGFGP...................
MKHSGYLWTIG....knVWKRWKKRFFVLVQ..vsqytFAMCSYREKK........AEPQELLQLDGY..TVDYTDPQ.............
AAREGWLQFRPgkrvggSIRPWKQMYVVLRG.......HSLYLYKDRR...eqttpSEEEQPISVNAC..LIDISYSE..............
PIKQGMLLKRS...gksLNKEWKKKYVTLCD......nGVLTYHPSLH....dymqNVHGKEIDLLRT..TVKVPGKR................
LHLEGWMKVPR..nnkrGQQGWDRKYIVLEG.......SKVLIYDNE-........AREAGQRPVEEF..ELCLPDGD.........vsihga
RPSQGFLSRRLsqpkldRTSSFRQILPRFRS.adhdraRLMQSFKESHesllspssAAEALELNLDED..SIIKPVHS............
MKHSGYLYALG....qkVWKRWKKRYFVLVQ..vsqytFAMCSYREKK........SEPQELMQLEGY..TVDYTDPH...........
VYKSGFLARKIgkktprGKRGWKTFYAVLKG.......TVLYLQKDEYkpekalseEDLKNAVSVHHA..LASKATDY.............
VPTCGYLNVLS......-NSRWRERWCRVKD.......SKLILHKDRA......dlKTHLVSIPLRGC..EVIPGLDS.......................
TVMTLFYSKKS......QRPERKTFQVKLET.......RQITWSRGA-........DKIEGSIDIREI.kEIRPGKTS............rdfdryqed
SALKSEIQKEK..ankgQSRAIERLKKKMFE.......NEFLLLLNS-........------------..--------..........................-PTIPFRIHN
NFKKGWMSILD......EPGEWKKHWFVLTD.......SSLKYYRDST....aeeaDELDGEIDLRSC.tDVTEYAVQ................
PTASGALRVQQ....agELQNGTLVHGVLKG.......TNLFCYWRSE...dadtgQEPLFTIVINKE.tGVRAGELE.................
-----------......--GEWKKHWFVLTD.......SSLKYYRDST....aeeaDELDGEIDLRSC.tDVTEYAVQ..........................-RN
LIIPGEQYFYL....kaRSVAERQRWLVALG.......SAKACLTDS-........RTQKEKEFAENT.eNLKTKMSE......................
IVKQGYVKMKS.....rKLGIYRRCWLVFRK.ssskgpQRLEKYPDEK....svclRGCPKVTEISNV.kCVTRLPKE...............
IQKTGYLNLRN..ktglVTTTWERLYFFTQG.......GNLMCQPRG-........AVAGGLIDLDNC..SVMAVDCE.....................
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IQKTGYLNLRN..ktglVTTTWERLYFFTQG.......GNLMCQPRG-........AVAGGLIDLDNC..SVMAVDCE......................
ELSMGELLMHSflslgkARKDIELTVFVFKR.......AVILVYKENChnsadldpFKFRWLIPISAL..QVRLGNTA.....................
LVKSGELTALEvspglrRKLTTRPVHLHLFN.......DCLLLSRPRE.....gsrFLVFDHAPFSSI..RGEKCEMK......................
VIRKGWLTINN...igiMKGGSKEYWFVLTA.......ENLSWYKDDE.......eKEKKYMLSVDNL..KLRDVEKG.....................
NRICGFLDIED....neNSGKFLRRYFILDT.....qaNCLLWYMDNP..qnlavgAGAVGSLQLTYI.sKVSIATPK....................
LVKDGFLVEMS......-ESSRKLRHVFLFT.......DVLLCAKLKKtsagkhqqYDCKWYIPLADL..VFPSPEE-....................
AKICAFLLRKK......RFGQWTKLLCVIKD.......TKLLCYKSSK.......dQQPQMELPLQGC..SITYIPRD........................
SFLCDFLYQTAvssekkLLEDTNKKWCVLEG.......GFLSYYENDR.......cTTPNGTINISEV..ICLAVHKE......................
ILCEGELEKRS....dsLFQVWKKKRCVLTA.......DRLRLFSGKT......spAKELFFHSILKV..DCVEHTS-.......................
LLCQGPVKLKC......FQKTKKKRHLSLFN.......DVLVVSRILN.....kreFKIKCIIPLHLL.wVVVDDVAQ....................rrkr
VTIQGVLRRKTkegkkpTVASWTKYWAALCG.......TQLFYYAAKSaterkhfkSTSNKNVSVVGW..MVMMADDP.........
QIKSDIQREKRvmerlrKKLSEQESLLLLMS.......PSMAFRVHSR......ngKSYTFLISSDYE..RAEWRESI......................
TFLCDFLYQAPlssekkLLEETNKKWCVLEG.......GFLSYYENDK.......sTTPNGTININEV..ICLAIHKE....................d
FKVPGFFSKRL.....kGSIKRTKSQSKLDR....ntsFRLPSLRNADesrshgslLSPCSAVECLDL.gRGEPVSVK...............
-----------......-MKNWQQRWFVLRG.......DQLFYYKDKD.......eSKPQGFISLQGT..QVTELLPD........................pedP
CRICAFLLRKK......RFGQWAKQLTVIKE.......EQLLCYKSSK.......dRQPHLRLALDVC..TVIYVPKD.........................
SPMVKKQRRKK......-----------LST.......PSKTEGSAVQ.......aEAKRKMWKLKSF.gSLRNIYKA..........................EE
PLIEGKLKEKQ..vrwkFIKRWKTRYFTLAG.......NQLLFQKGKS......kdDPDDPPIELSKV..QSVKAVAK......................
LLGEGVLTKEC......-RKKAKPRIFFLFN.......DILVYGSIVL....skrkYRSQHIIPLEEV..TLEPLPET.........................IQ
NFKKGWLTKQY......EDGQWKKHWFVLAD.......QSLRYYRDSV....aeeaADLDGEINLSTC.yDVTEYPVQ..............
VIRRGWLTINN...islMKGGSKEYWFVLTA.......ESLSWYKDEE.......eKEKKYMLPLDNL..KIRDVEKG.....................
FLKEGTLMRVR......-GKSRHPRHLFLMN.......DTLLYTHPQK.....dgkYRLKSSLPVANM..KVSRPVMD....................
VTIQGVLRRKTkegkkpTVASRTKYWAALCG.......TQLFYYAAKSaterkhfkSTSNKNVSVVGW..MVMMADDP..........
PIKQSFLLKRS...gnsLNKEWKKKYVTLSS.......NGFLLYHPSI...ndyihSTHGKEMDLLRT..TVKVPGKR...................
RLVEGTCFRKL.....nARRRQDKFWCRLSP.....nhKVLHYGDLEEspqgevphDSLQDKLPVADI.kAVVTGKDC...........
AEMAAELGMRG....pkKGSVAKRRLVKLVV.......NFLFYFRPDE........AEPLGALLLERC..RVAQEE--.......................
NQLSGNLLRKF.....kNSNGWQKLWVVFTN.......FCLFFYKSHQ.......dSHPLASLPLLGY..SLTIPSES.....................
SITPSITLSIT......------------PS.......ITLSIATNSA.....angCALQAALSLSDL..QARYPFHN........................nrLRKYAF
SVICSFLHYME.....kGGKGWHKAWFVVPE....nepLVLYIYGAPQ.......dVKAQRSLPLIGF..EVGPPEAG..................
QEKYGLLNVTKtengkkVRKNWLSSWAVLQG.......SSLLFTKTQGtswfgsnqSKPEFTVDLKGA..VIEMASKD...........
IVKQGYVKIRS.....rKLGIFRRCWLVFKK.asskgpRRLEKFPDEK....aayfRNFHKVTELHNI.kNITRLPRE..................
VKHIAWLAEQA..kldgGRQQWRPVLMAVTE.......KDLLLYDCMP..wtrdawASPCHSYPLVAT..RLVHSGSG............
FTAEGYLYVQE.krpapFGSSWVKHYCMYRK...takkFNMIPFEHRS.....ggkLGDGEAFFLKEC..TKRHMDST............
SIKEGILKLKEepskilSGNKFQDRCVVLRD.......GHLFIYKDPK.......sSKHDKMFPLRAM..KFYLGVKK......................
SEVCSFLQYME......KSKPWQKIWCVIPK....qdpLVLYMYGAPQ.......dVRAQATIPLLGY..VVDDMPKS..................
AICASRVKLQH....lpSQEQW-DRLLVLYP.......ASLAIFSEEP......egLSFKGELPLSAI..HINLEEKE..........................
VIKQGYLEKKS.kdhsfFGSEWQKRWCVISR.......GLFLYYANEK.......sKQPKGTFLIKGY..SVRMAPHL..................
TAYEGFLSVPR...psgVRRGWQRVYAALSD.......SRLLLFDAPD......prGSLASGVLLQAL..DLRDPQFS............atpv
PLIEGKLKEKQ..vrwkFIKRWKTHYFTLAG.......NQLLFQKGKS......kdDPDDSPIELSKV..QSVKAVAK......................
FLKEGTLMKLS......-RKVMQPRMFFLFN.......DALLYTTPMQ.....sgmYKLNNMLSLAGM..KVRKPTQE..................
YEEESFVFEPN......-------CLFKVDE.......FGFFLTWKSE........GKEGQVLECSLI.nSIRQAAIP.........kdpkilaaleavgk
CIMHGYMLKLG....npFLTQWQRRYFYLFP.......NRLEWRGEG-........ESRQSLLTMEQI..MSVEETQI.....................
VERCGVLSKWT.....nYIHGWQDRWVVLKN.......NTLSYYKSED.....eteYGCRGSICLSKA..VITPHDF-....................
TEKVGFLYKKS....dgIRRVWQKRKCGVKY.......GCLTISHSMI........NRPPVKLPLLTC..QVRPNPE-.......................
GKMTDSLRKPEralslqHAGRFSVNWFILFN.......DALV---HAQ........FSTHHVFPLATL..WAEPLSEE........................
TLREGWVVHYS.....nKDTLRKRHYWRLDC.......KCITLFQNNT.......tNRYYKEIPLSEI..LAVEPAQN...................fsl
SAREGWLFKWT.....nYIKGYQRRWFVLSN.......GLLSYYRSKA.....emrHTCRGTINLATA..NITVEDS-....................
LLKQGELQQMStsrtlrTKKLFREIYLFLFN.......DLLVICRQIP.....gdkYQVFDSAPRGLL..RVEELEDQ......................
LMQEGTMMRKV.....rTKSWKKLRYFRLQN.......DGMTVWHGSQ......peSMPKPTFSISDV.eRIRKGQDS..............
LLLQGNLLKIS......-AGNIQERAFFLFD.......NLLVYCKRKStksingslYIFRGRINTEVM..EVENVEDG.................tady
LTTYGELVLEA...tfrVHRVRNDRTFFLFD.......KILLITKKRG......dhFVYKGHIPCSSL..MLIESTR-...........................-
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DSYKGWLLKWT.....nYLKGYQRRWFVLGN.......GLLSYYRNQG.....emaHTCRATINLAST..HFETEDS-.................
VQHEGFLLRKRdanrksSNRSWVSLYCVLSK.......GELGFYKDSK.gpasggtHGGEPLLSLHKA..TSEVASDY............
IVAQGKLLLQDtdqdagLLPRCKERRVFLFE.......QIVIFSEPLDkkgfsmpgFLFKNSIKVSCL..CLEENVES.................
IRREGWLYYKQgkkaggGLRQWKRVYAVLRA.......RSLSLSKERRagaaaagaGEDEAAPVCIGS..CLVDISYS..........
TYKHGVLTRKTgkrtprGRRGWKKFYAVLKG.......TILYLQKDEYrldkalseGDLKNAIRVHHA..LATRASDY.................
EERSGLLNMTKaqggrkLRKNWGPAWVVLTG.......SSLVFYRERPlqgwaragSRPESSVDLRGA..ALASGRQL.........
PTMEGPLRRKTkegrkpALSSWTRYWVVLSG.......ATLLYYGAKSgtdrkhykSTPGKKVSIVGW..MVQLPDDP..........
LYFEGFLLVKR.....sDHQEYKHYWTELRG.......TTLFFYTDKK.......sTIYVGKLDIIDL..VCLTGQHS.......................
TERNGNLYKKS....dgIRKVWQKRKCSVKN.......GFLTISHGTA........NRPPAKLNLLTC..QVKTNPE-......................
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.......sPRPSGLYLLEGS..ICKRAPSP........krgtssk
VIKAGWLDKNP....pqGSYIYQKRWVRLDA.......DYLRYFDSNK........DAYSKRFVPVAC..ICRVAPI-.......................
IVMADWLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTQK.......nGQWVGTVLLNAC..EIIERPSK........................
PELEGALYLKE.....dGKKSWKRRYFLLRA.......SGIYYVPKGK....tktsRDLACFIQFENV..NIYYGIQC...................kr
SEKKGFLLKKS....dgIRKVWQRRKCAVKN.......GILTISHATS........NRQPAKLNLLTC..QVKPNAE-........................
VMKEGWMVHYT.....sKDTLRKRHYWRLDS.......KCITLFQNDT.......gSRYYKEIPLSEI.ICLEPAKPS...................a
TYKQGILARKMgkktpwGKRGWKMFHTLLRG.......MVLYFLKGEGldgeslvgHMVDEPVGVHHS..LASPATHY..........
LVRHGELVELAaappakLKLSSKAVYLHLFN.......DCLLLSRRKE.....lgkFAVFVHANMAEL..QVRDLSLK...................
KGLEGVIRKRSfcgrdqVCYRWSKRWLVVKD.......SFLLYMRPET......gaISFVQLFD-PGF..EVQVGKRS................
ARICAFLWRKK......WLGQWAKQLCVIRD.......TRLLCYKSSK.......dHSPQLDVNLRGS..SVVHKEKQ...................
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.......sPRPSGLYLLEGS..ICKRAPSP........krgtssk
PECLGLLHQLE.....rSTDVWIQHYCILKD.......GCLYFYASIR.......sTQASGGLYLQGY..SVSEQTHG......................
LLKGSQLLKVK......SSSWRRERFYKLQE.......DCKTIWQESR....kvmrSPESQLFSIEDI.qEVRMGHRT................e
SSHRSLVQRVEvslgehPCDRGEQVTLFLFN.......DCLEIARKRHdrtrppasLKHIHLMPLSQI.kKVLDIRET.................
EALKEVVLRYSdeaamdSGARWQRGRLVLRS.pgpghsHFLQLFDPPK.......sSKPKLQEACSSI.rEVRPCTRL..........
EALKEVVLRYSdeaamdSGARWQRGRLVLRS.pgpghsHFLQLFDPPK.......sSKPKLQEACSSI.rEVRPCTRL..........
VIMADSLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTPK.......vGQWVGTVLLHCC..ELIERPSK.........................
LVKDGFLVEVS......-ESSRKLRHVFLFT.......DVLLCAKLKKhpfpdhelEDMKMKISALKS..EIQKEKAN...kgqsraierlkk
PEIEGVLWLKD.....dGKKSWKKRYFLLRA.......SGIYYVPKGK....akvsRDLVCFLQLDHV..NVYYGQDY..................
SMVEGSELKKV.....rSNSRIYHRYFLLDA.....dmQSLRWEPSKK........DSEKAKIDIKSI.kEVRTGKNT..............difrs
VIFMSQVVMQH.....gACEEKEERYFLLFS.......SVLIMLSASP....rmsgFMYQGKIPIAGM..VVNRLDEI.......................
LVCCCQLYEVP.dpnrpQRLGLHQREVFLFN.......DLLVVTKIFQ.kkkilvtYSFRQSFPLVEM..HMQLFQNS................
LLKRGELFLLEessifrKIASRPTCYLFLFN.......DVLVVTKKKS.....eesYLVQDYAQLDHV..QVRKLEPS..............epllp
GTKRGFLSKKA.....aEASRWHEKWFALYQ.......NVLFYFEGEQ.......sGRPAGMYLLEGC..SCERTPAP............prt
DLSMGDLLLHTpaslgkWKKEPELAAFVFKT.......AVVLVYKDGSsiyeewdpFRFRHMIPTEAL..QVRALPSA.............
FLHSGKLYKAK......---SNKELYGFLFN.......DFLLLTQITKspksnlqyKMYKTPIFLNEV..LVKLPTDP.........................
CIVHGYMSKMG....npFLTQWQRRYFYLFP.......NRLEWRGEG-........EAPQSLLTMEEI..QSVEETQI.....................
AVMEGPLFLQS...qrfGTKRWRKTWAVLYP.asphgvARLEFFDHKGrggrggsrRLDCKMIRLAEC.vSVVPVTVE.........
LVKRGELTAYVdtvlfsKRMSKQQVYFFLFN.......DVLIITKKKSeesynvndYSLRDQLLVESC..DNEELNSS............pg
IQREGALRFMVaasgpgGTAQWQKCRLLLRR.avagerFRLEFFVPPK.......aSRPKVSIPLSAI.iEVRTTMPL.............
LLKDSFMVELV......-EGARKLRHIFLFT.......DLLLCTKLKKqsggktqqYDCKWYIPLTDL..SFQMVDEL...............ealp
LKEQGQLLHRD.pftviCGRKKCLRHVFLFE.......DLLLFSKLKG.seggsetFVYKQAFKTADM..GLTENIGD.................
IKQIGWLTEQL......PSGGTAPTLALLTE.......KELLFYCSLP..qsrealSRPTRTAPLIAT.sSAHRLVHS.................gps
LVYNGDLVEYD....adHMAQLQRVHGFLMN.......DCLLVATWLP...qrrgmYRYNALYPLDRL..AVVNVKDN...............
TAYEGHVRIPK...pagVKKGWQRALAVVCD.......FKLFLYDIAE.gkasqptSVISQVIDMRDE..EFSVSSVL................
LLREGPVLKIS.....fRRSDPMERYLVLFN.......NMLLYCVPRV..lqvgaqFQVRTRIDVAGM..KVRELTDA...................
LIKEGQILKLA.....aRNTSAQERYLFLFN.......NMLLYCVPRF..slvgskFTVRTRVGIDGM..KIVETHNE.......................
VQMEGYLGRKHgpnkkaSNRSWNNLYCVLRN.......SQLTFYKDAK.nlalgvpYHGEEPLALRHA..ICEIAVNY............
IRHLGWLAEKV...rekEGTRWKPRLSKLLL.......KTLVAKDSLKgkkqewlsGILGNEFILITF..KLVHSGPG...................
LELGTVMTVFN...arkSTPERRTVQMIMET.......RQVAWSKTA-........DKIEGFLDIMEI.kEIRPGKNS...............kdfer
LIHSGELTRVT.....qPQARSQQRMFFLFD.......RQLIYCKKDL...lrrdvLYYKGRLDMDDL..EVVDVEDG..................
PVKEGPLFIHRkgkgplASSSFKKLYFSLTT.......EALSFAKTSS.....skkSTFIKLASIRAA.eKVEEKSFG......................
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KGLEGMIMKRSccghgrACYRWSKRWLIVKD.......SFLLYMKPDS........GAIAFVLLVDKE.fRVKVGRKE..................
AQMEGFLNRKHahnkkaSSRSWHNVYCVINN.......QEMGFYKDAK.saasgipYHSEVPVSLKEA..ICEVALDY............
LLCHGELKNKS......----GHKLYIFLFQ.......DILVLTRPVT.rnerhlyQVYRQPIPVQEL..VLEDLQDG..........dvrmggsfrg
SIKEGILKLKEepskilSGNKFQDRCVVLRD.......GHLFIYKDPK.......sSKHDKMFPLRAM..KFYLGVKK.....................
VSKKGYLHFLE.....pHTAGWAKRFVVVRR.......PYAYMYNSDK.......dTVERFVLNLSTA..QVEYSEDQ......................
IQREELLSFMGltsgggGQPQWQKCRLLLRSegeggggSRLEFFVPPK.......aSRPRLSIPCSTI.tDVRTATAL...............
LMKLGTVARRG......AMGIWKEFFCELSP.....leFRLYLSDEE-........RTCVESCSLLRC..EAVGPAH-....................
IRHLGWLAEKV...pgeSEKQWKPALVVLTE.......KDLLIYDSMP..rrkeawFSPVHSYPLLAT..RLVHSGPG.....................
LVCCSRLFEVT.dvnklQKQAAHQREVFLFN.......DLLVILKLCP.kkkssftYTFCKAVGLLGM..RFHLFENE...................
IVKQGYVRIRS.....rRLGIYQRCWLVFKK.asskgpKRLEKFSDER.....aayFRCYHKVELNNV.kNVARLPKS...............
FIRLGSLSKLS......-GKGLQQRMFFLFN.......DVLLYTSRGL...tasnqFKVHGQLPLYGM..TIEESEEE......................
SRLEGWLSLPV..rnntKKFGWVKKYVIVSS.......KKILFYDSEQ....dkeqSNPYMVLDIDKL.fHVRPVTQT...................
FIREGCLHKLT......-KKGLQQRMFFLFS.......DMLLYTSKSV...tgashFRIRGFLPLRGM..LVEESENE.......................
FLRQGWLLVVP......PTGEPRPRMFFLFS.......DVLLMAKPRPlhllksgtFVCRALYPMSQC..HLSRVFGH...................
LIYTGEMAWIY.....qPYGRNQQRVFFLFD.......HQMVLCKKDL...irrdiLYYKGRIDMDKY..EVIDIEDG..................rd
LVLEGTFRIQK......---AKKERTLFLLD.......QLLLITKKRD......dtFTYKAHILCGNL.mLVEVIPK-............................-EP
LIHSGELTKIT......RQGKSQQRIFFLFD.......HQLVSCKKDL...lrrdmLYYKGRMDMDEV..ELVDVEDG...................r
IMKQGYVRIRS.....rRLGIYQRCWLVFKK.asskgpKRLEKFSDER.....aayFRCYHKVELNNV.kNVARLPKS..............
GRGGGAAGLTS...gggGQPQWQKCRLLLRSegeggggSRLEFFVPPK.......aSRPRLSIPCSTI.tDVRTATAL.............
RGFEGKLTAQGpeagglLSSRGRERRVFLFE.......QIIIFSEALGgrggaqpgYVYKNSIKVSCL..GLEGNLQG...............
LELQGELTELGggvlftSRPRFTPLCLLLFS.......DLLLITQPKS...gqrlqVLDYAHRSLVQA..QQVPDPSG.....................
LIKEGSIQKLS.....aKNGTTQDRHLFLFN.......NVMLYCVPKL..rlmgqkLSVREKMDISDL..QVQDIVKP.......................
PELADYIKVFK..pkklTLKGYKQYWCTFKD.......TSISCYKSKE.....essGTPAHQMNLRGC..EVTPDVNI.......................
LLLEGPVRVKE......GREGKMDVYLFLFS.......DVLLVTKPQR...kadraKVIRPPLMLEKL..VCRPLRD-..................
VSKKGYLHFKE.....pLSSNWAKHFVVVRR.......PYVFIYNSDK.......dPVERGIINLSTA..QVEYSEDQ......................
IESQGELILQEvwdpktLIRKGRERHLFLFE.......MSLVFSKEVK.dssgrskYLYKSKLFTSEL..GVTEHVEG...................
LLHSGKLYKTK......---SNKELHAFLFN.......DFLLLTYLVRnskssaqfRMYKTPIFLNEV..LVKLPTDP........................
VRKAGALAVKNkkvesaTRRKWKHYWVSLKG.......CTLFFYETDG.rsgidhnSVPKHAVWVENS..IVQAVPEH...........
LILQDAFQVWD...pksLIRKGRERHLFLFE.......ISLVFSKEIK.dssghtkYVYKNKLLTSEL..GVTEHVEG.....................
TAYKGYVKVPK...ptgVKKGWQRAYAVVCD.......CKLFLYDLPE.gkstqpgVVASQVLDLRDE..EFAVSSVL...............
LTAQGKLLQQDieldagMQSRTKERRVFLFE.......QIVIFSELLR.kgsltpgYMFKRSIKMNYL..VLEDNVDG..................
LTAQGKLLQQDieldagMQSRTKERRVFLFE.......QIVIFSELLR.kgsltpgYMFKRSIKMNYL..VLEDNVDG..................
EQMEGMLCRKQafnkkaANRSWQNVYCVLRR.......GSLGFYKDAR...aasagVPYHGEVPVSLA..RAQGSVAF........
DTKHGMMKFRElglglPSGGFHDRYFILNS.......SCLRLYKEVR.......sHRPEKEWPVKSL..KVYLGVKK...................
PEIQGFLQLRG.sgrgsGRKLWKRFFCFLRR.......SGLYYSTKGT....skdpRHLQYVADVNES..NVYVVTQG................
LLLEGSLRMKE......GKDSKMDVYCFLFT.......DLLLVTKAVK...kaertKVIRPPLLVDKI..VCRELRD-.....................
VTYMSQVTIQC.....aGSEEKNERYLLLFP.......NLLLMLSASP....rmsgFIYQGKLPTTGM..TITKLEDS.......................
LETSSYLNVLV......-NSQWKSRWCFVRD.......SHLHFYQDRN......rsKVAQQPLSLVGC..DVLPDPSP.....................
YYKERLLYLEEcchgelKNNRGVKLHVFLFQ.......EVLVITRAVT.hneqlcyQLYRQPIPVKDL..TLEDLQDG..........evrl
VRKAGWLFFKPrklelvARRKWKQYWVTLKG.......CTLLFYETYG.knsteqnSAPRCALFAEDS..IVQSVPEH............
PEIHGFLHAKE.....qGKKSWKKAYFFLRR.......SGLYFSTKGT.......sKEPRHLQLFSEF.sTSHVYMSL..................a
GHRKGATKMKD.....fARFKPMQRHLFLYE.......KAVMFCKRRFegadrypsYSFKHCLKMEDV..GITEHVKG..................
LKEQGQLVRQD.eftvrAGRHKACRRVFLFE.......ELLLFSKPRR.gpagvdiFTYKRSFKMADL..GLTECCGE...............
LHLEGALCWKS......TSGRLKDVLAVLLT.......DVLLLLQEKDqkyvfasvDSKPPVISLQKL..IVREVANE......................
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.......sPRPSGLYLLEGS..ICKRAPSP................krg
LIHEGCLLWKT......ATGRFKDVLLLLMT.......DVLVFLQEKD.qkyiftsLDKPSVVSLQNL..IVRDIANQ.........................
PKIDGELKVRS.....iVNHTKQDRYLFLFD.......KVVIVCKRKG......ysYELKEVIELLFH..KMTDDPMH................nkdi
SRIEGWLSVPN..rgniKRYGWKKQYVVVSS.......KKILFYNDEQ....dkeqSNPSMVLDIDKL.fHVRPVTQG.................
LIHEGCLLWKT......ATGRFKDVLLLLMT.......DVLVFLQEKD.qkyiftsLDKPSVVSLQNL..IVRDIANQ.........................
LIKEGHILKLS.....aKNGTTQDRYLILFN.......DRLLYCVPRL..rllgqkFSVRARIDVDGM..ELKESSNL.......................
LLMQGSFSVWTtkvkelARFKPMQRHLFLHE.......KAVLFCKKREegyekapsYSYKQSLNMTAV..GITENVKG...........
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PQGDGEIRITT.....IDKHTKQERHIFLFD.......LAVIVCKRKG......dnYEMKEIIDLQQY..KIANNPTT.....................dke
PKIDGELKITS.....vERRSKTDRYAFLLD.......KALLICKRRG......dsYDLKASVNLHSF..QVRDDSSG.....................e
PEIQGFLQVKE.....vGRKSWKKLYVCLRR.......SGLYYSTKGT....skepRHLQLLADLEES..SIFYLIAG...................
FIMEGPLTRIG......---AKHERHIFLFD.......GLMISCKPNHlpgyssaeYRLKEKFVMRKI..QICDKEDA..........................
LVRDGSVFLKS......TTGRLKEVQAVLLT.......DILVFLQEKDqkyvfaslDHKSTVISLKKL..IVREVAHE.......................
FIMEGTLTRVG......---AKHERHIFLFD.......GLMICCKSNHlpgassaeYRLKEKFFMRKV..QINDKDDT.......................
LLHDGLVYWKT......ATGRFKDILALLLT.......DVLLFLQEKDqkyifaavDQKPSVISLQKL..IAREVANE......................
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EVKSGFLEKRS.....kFLKSYSRGFYVLTP.......SFLHEFKTPD....khkfSTPLMSIPLVEC..TVTEHSKK....................t
RYLQGYLLKKR....rkRLQGFKKRFFTLDF.....ryGTLSYYLNDH.......nQTCRGEIVISLS..SVSANKK-.........................
ADFSGWMSKKG....sgAMSTWKTRFFTLHG.......TRLSYFSSTT.......dTRERGLIDITAH..RVVPAKED..............dkl
ADCSGWMSKKG....tgAMGTWKQRFFTLHG.......TRLSYFTNTN.......dEKERGLIDITAH..RVLPASDD..............drli
EIKSGFLERRS.....kFLKSYSKGYYVLTP.......NFLHEFKTAD....rkkdLVPVMSLALSEC..TVTEHSRK.................nst
PTYKGYLKKWT.....nFAQGYKLRWFILSS......dGKLSYYIDQA.....dtkNACRGSLNMSSC..SLHLDSS-....................
IYKEGYLLQDG....gdLKGKIENRFFKLHG.......SQLSGYHEI-........-SRKAKIDINLL..KVTKVLRN..........ediqadnggqr
KKKSGWVSYKD...dgiLSFIWQKRYLMLHD.......SYVALYKNDK......qnDDAILKIPLTSI.iSVSRTQL-........................
QVCSGILYTKVkkkklfNRAKWQKFNVELTN.....tsFNLYSFKTG-........-KLKKSIKLDKI.iDCIELDNN......................s
QGKQGYLVIRSkhafkdMIDRHTTKWFLVRN.......SYLTYVSDLS.......sTTPLDVFLIDWK.fKVRFSGNKleefgiendanr
CIKAGYFLKKS.....eLLPTYHQGYFVLTS.......NYIHEFQSSDrgirkksyLAPIMSIPLNDC..TLKDASSThkflkgskpknknt
KGLSGWLYMKTtvghdpKRVVWVRRWCFLQN.......NVFGVFSLSP....sktyVEETDKFGILWI..TVEYLPKE.............
PTYKGFLKKWT.....nFAHGYKLRWFILSG......dGNLSYYKDQS......hvDRPRGTLKVSTC..RLHIDSS-...................
VKKEGWISYKV...dglFSFLWQKRYLVLND.......SYLAFYKSDK......cnEEPVLSVPLTSI.tNVSRIQL-........................
VLQRGIMIRMT.....rRRRKFYEFKLINNN.......GQIIWKDGS-........-KYLELDSVKDI..RIGDTAST..............yqeevdpk
LVLSGTVYKKR.....dLWLDPTPVYIALLD.......NCLLITEEIS.kgetqkyKLIERPIPIDYL..SLEKRKIPkssgnhmstaygdrkt
VKMSGNLNIRT......KLIRSTRYWCVLKN.......HLFSMYTSST......elYFPVLTIDLREV.qKIETQKHT.......................l
RIHSDLVHRSD......QSQHLHHRLFTLPT.......RSASEFKKADdrsryltdEALYKSFTLQNA..RFGIPTDY.....................
ISKFGELLYFDisttnsSSEPEREFEVYLFE.......KIIILFSEVVsasslilkKKSSTSASISAS..NITDNNGSnnsnnssssslfklsa
NVKDGSLLLRR.pktltGNSTWRVRYGILRD.......DVLQLFDKN-........-QLTETIKLRQS..SIELIPNL.....................ped
LIQKGPLYQKP.....hKHSVFSKYYVVLIS.......GFIVLFHCFHgfakevleYAHYVTIPIDDC..YLYSGTTTdrtfdeinygshalp
KKIGGFFRRPFsiggfnTSSSNYSLNSILSQ....evsSNKSILPSILpevdsmqlHDLKPSYSLKTF..EIKSIMEI...................
TVIGEYLFKYYprlgpfGFESRHERFFWVHP.......YTLTLYWSASnpilenpaNTKTKGVAILGV.eSVTDPNPY..............
TSRRTSLSYLN......KDSEWERVKIQVKE.......GRIFIFKIKPtidyfkdiSSSYFAYSLLEA..EAHVVQDN.........iiigsgamk
PEKSGWLYMKT.qvgkpTREIWVRRWCFLKN.....avFGMFLLSPSK....tyveETDKFGVFLTNV..RYDPEED-............
RYHEGVFLILQnnngthAARKWKDVYGVLLG.......TQLALWDAKEsekklkevASKPTYINLTDA..TLRTLDNS.............
RYHYGIFLILHktdgtpAARQWEECYGVLLG.......TQLALWDAKEntstmkkaASRPSFINFTDA..SVRSLDAN............d
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SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK.....qslELHTEPIDLLMA..TVRPAQSV...............
SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK.....qslELHTEPIDLLMA..TVRPAQSV...............
IFKEGLLLVFGtdlamvSKAAWHKHWIVVEN.......GSLWEYANWK.....dsvKSNVSSISLKHA..SADKVRKQ..............
ISKIGTLNVYSfrffssLFRKRKPRTFILTN.....fgRYLCVASDGE......grKTVKEEIPIKSV..GMRCRMVK.......................
ISKIGTLNVYSfrffssLFRKRKPRTFILTN.....fgRYLCVASDGE......grKTVKEEIPIKSV..GMRCRMVK.......................
AQKKAYERRYK......NFTTTSSSFDTLQG.....idTEAMEYEFPKvftppleeFSPDTSYSLVNA.fAYCDRDKK................
AQKKAYERRYK......NFTTTSSSFDTLQG.....idTEAMEYEFPKvftppleeFSPDTSYSLVNA.fAYCDRDKK................
QHMSGYLKKWT.....nYKSGYKLRWFTLNN.......GVLSYYKNQD.....dasSACRGSINLKLA..RLVHDPK-..................
YIKQGILKFQSeshkfrKKEVWSTVLAVLQR.......DVFTLYNLNTsydpkdldISKVGKPVIKTT..IIASLAKP..............fpss
AQKEGVLLKYI......ENSGLVSRYFYLKD.......NILYFAENRN........SPVLGTIHLKDA..QVNRYNAN..........lpifsiidpph
AQKEGVLLKYI......ENSGLVSRYFYLKD.......NILYFAENRN........SPVLGTIHLKDA..QVNRYNAN..........lpifsiidpph
TKRQGWLLRNIssskadNKAIWRKYWFFVDN.......GYVGYLINDA.....nggVFESEKIGVLLC..KFSVLPSN................
ADCHGWMRKRS.....dRYGVWKSRYFVLKG.......TRLSYYHSLN.......dASEKGLIDMTSH..RVTKTDDI..................
ADCHGWMRKRS.....dRYGVWKSRYFVLKG.......TRLSYYHSLN.......dASEKGLIDMTSH..RVTKTDDI..................
IIRSGWVMLKE...dkmKYLPWTKKWLVLSS.......NSLSIYKGSK.......sESAQVTLLLKDI.qKVERSKS-.....................
SIQNGCSLLRI......TKKKVRQRKVSLDP.....isGYLMLDKNTG......kaYKKLCVDDIKEI.rQGRDARNY.................req
SIQNGCSLLRI......TKKKVRQRKVSLDP.....isGYLMLDKNTG......kaYKKLCVDDIKEI.rQGRDARNY.................req
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VLKSGWLIKKG.....hATSTKKQLWAVLRR.......DQLSFYKDE-........---------KDI.sAVAYYKEK..........................-SP
QIISGTLLKKR....rkKGQGYARRYFTLNM.....veGTISYYANEN.......sSVMRGKIPLSIA..VISVAAE-..........................
WHRRGMISYKKsknnrwVAGYWKKKYCIVDS.......GKLIFYKSDHdpnacsnvSPIHREFGLQSC..LASPNLPP...........
PIMAGYLIRKT......SFLKKKQRGFYAFT.....hsGYLYEFKSSD....slqdPEPEFALYIPDC..LIGRPSE-.........................
LLCDGYLCQQG.....gDCPYWRRRYFQLIG.......SKLVAFQQFS........KVRRATIDLSEA.tHIVDDNHY................sde
HGKEGFATLKRccnttmMKTRSQPFWIIVSE.......SCIILCDNML........SMQPADVFIWDV..DFEITRKN............frkah
VLMQGTIHWLH.....gNLHRWSKCWAVVRG.......YGMTIYNTNR.......eYKPVKVIPIADI.qDVAEINVP.......................
LYNEGYLYRLE......-DSSIRRRFVVLRS.......KQLNFYAEKG........GQYLDTFQLSKT..VVSIPMVN..................fsea
LYNEGYLYRLE......-DSSIRRRFVVLRS.......KQLNFYAEKG........GQYLDTFQLSKT..VVSIPMVN..................fsea
PSLASEQMHDS.....dADSLFQSANDHLNRakatqdcRGLLFYSKSQ......stSVPSGIINLTDA.vSIEPGTG-.................
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cldkPRPNMFIVRCIQW............................ttvIERTFYADSADFRQMWIEAIQAVSS
...lfekPRPNMFMVRCIQW............................ttvIERTFYAESAEVRQRWIHAIESISK
.........SRPFMFEIFSISD............gqikackteqdgrlvegrhSIYKICAVNDEDMRSWINAISRMMA
..........GRRGLIELHMkNK...............................-THRLLSENINEAIRWKECIEQVIR
.....svlakHPPHCFEIRTtTN............tvfcvgedyhafsggppkkIPRSMSVRPSSNTTMWFQFIKESLQ
...........--TSCIVISGqSQ...............................-TFHVKPQNEMDRQQWTNSLEYMRH
RyNT............................glsRELVLMAPQTDNCNKWVSQLRRFIE
.........-NNSLFTITVeGK................................-TFHMQGRDLRERNQWVRILENSIR
....DKKNCLLIAHpQL..............................pSAIIVAASDHQTQEMWLKALRSATK
.......--KNIITIVCeTM...............................-QLQFEAPGGVEATDWLNAIERQRN
....tapvikglTDVISFRMRTgTQ............................qgvRTHTIRVETHAELARWVRAVVIGGY
.....GAAYAFQLITsTD...............................-KMNFMTESERTTHDWVTILSAAIK
.--SGTFFIHTpN-...............................-RVYYLFDLEKKADEWCKAINDVRK
--ERTIWITHgQD..........................lvnvQSFFLVAESVELAKTCRAGINDILK
...dpelsaqGGKHFFTAIKeGD...............................-ELKFATDDENERHLWVQALYRATG
.........aHSTHMIELNEdNR..............lhpvhpsifevpncfrlASTYYSCRTPLERAKWMENLRKTMN
VINnCL...............................MRWEFCAGSLEERDEWIQAIGGEIE
...empvdcddsmRANNVLMIKMpRR...............................-CLYILAPSQPSARRWAECLQTAQR
felvpsersYEPNFLTIVSgTS.........................itnlkfTHFVCMEKNEKRLHEFAATLFTVVQ
ggghqeesMLNCIFGVGFrFE............................nivKDLYLVAKNDEEMTLWVNEICKLCK
-----SdEK...............................-------GSSLDAQSWTTAIQSALM
.....-DENEFSISMgEN...............................VVWYLKAENSQSKLLWMRSVVRETV
..............-RNYGIEIKCrRT...............................-RYVLSAMTPGIRDSWVSALQQNRH
..........aKRKNSFRLLLqDG...............................SEFIFSCPDERQMLEWVAKIKFHAH
.......keteGIPTGLIITNsQH...............................-ELHLKCRRLQDTATWKYIIEQAMG
...kkarkSLRKAFEIFTaDN...............................TSMILKAKDEKNAEEWLHCLQIAMA
diaydwlsssfsKQRHVVRIVTqNR...............................SEHLIELNTESEMLSWISVLQSSSE
..-HVTAADLRNvDD...........................sqlpKIFHIMYDD--------ASCNSSRH
....svvedicpfPNSFHIDVWApKM.....................dtsdprgierLRVMLAADTAQDLQTWLSLINSTSK
..nssprrdKRDNCFLIETpLQ............................vpnHYLSFEAVSAFELF------EQAYY
.....--KFTFSVRVgAR...............................RMYTMTAEDEQTQMKWLAILDLAAN
.......evaipgdVMRNVLTIKLqTR...............................-SVHIVAPTPKSAERWAACLQNAQT
............qKKKNVLSLRLpIG...............................AEYLFQCGSEEDMQRWLTELQVATG
..gIEKHGWIIKTpAK...............................-SFAVYAATETEKREWMLHIERCVT
.remsqgaEHEFHIELLIdQD..........................pdliekRRVILAAESSDHLNSWLSAINDTLD
.........hpLHSHRVASSVdPM................ngggggtptlksyepRRSDVGANS-----------GDGTS
............tGNAHSILLAFnKT...........................redqpSIIYIKADTTEEIRWWQNGLSKYAN
.......iDRIGCFELVTpTR...............................-IHLLQADSESLCQDWMRALQRTIL
......dkidNHENCFKLFYgSH...............................-TYFFRTDSYYFFERWVDSIFQAAI
......eadvihaqkgDIPKIFRVTTtQI...................lnssseysssskFYTLFMAETEEEKRKWVVALSELKT
.ekkyksptPWCISIKLTAIQM............................krsqFIKYICAEDEMTFKKWLVALRIAKN
...kiGKDFTFEIKFkST..............................aRSFIFAADSFKSLGRWVSLLTISPI
.......fmSRNHKFALFYpDG.........................kniykdyKQLELGCTNLDEIDAWKASFLRAGV
skkyefqelaPESRCFSVIFsHA...........................kflhKSVDFSADSKETRDKWVSVLTHLIS
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esgaaNAGKVLKLLIfPE................................-SRCYLCESARIRTLWFDELEQAKR
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.....-DPLRFVIKSsDP..............................tqpTSFIANAQSQEEKDEWNRKMSELLD
.......-GKTVLEIRGsDA.................................dkAAILLESEETQMLEEWLVALHTAIA
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--ADSFLIGWpFT..................................-NYLVHFRNTEEKDEWFELLSCCVQ
.........kvmdGENNVITLHNaDI..................................-SIVFAAPD---RASWIEDITEAIK
.............kKKSFVFRVRIaHG.................................GEILFQTSNQKELQEWCEKINFVAA
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............rdvqkkKQRKYIQLELcNT..................................KKYLLRGPNDTEAVEWYKSLEEVVA
....KDGFCFKLFHpMD.........msiwgnrgplgqsfgsftlnplnTSFLICAPSDQAGRCWMDALELSFK
...-EKGRFEIHSnNE..................................-VIALECSSDKQRNEWMKALQSTRK
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...EEPLSFQVLSfDN................................prAQYVFMASSMEQKRTWMQELKRMML
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..tiKGETAIIVKLrDG...............................fkePKICLTNSDEISLKEWHTSLRTAHK
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veetrngrDHEFHIELLIdQT............................psllekRRVVLAAESSDHLASWLNAINDTLF
..--GGSIFIRCgDV..................................-GVDFTAYSLGGVTEWYNEICDAID
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..dqatpmSLKFAFVIIHITR............................yyqvvGIYTLQAADKADKELWIEKFQESIE
ksggtitrRTQYVIIMTRdRN............................enneiTQLTFYFKNEATRNNWMTALLLSKS
....EVTNCFKIEShDK..............................sslpKIYHFVCKNPEEKRQWMAVLVKVTT
......dTCRFGLRVGTvSS................................ndNRIDLKANNHHTKVKWVQKIRDLTA
.....EREHSFYLRGsDG..............................tgpkRCVELFTPTQKEKNDWVDSIFSIID
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....RKPNCFELYIpNN...........rgqlikackteadgrvvegnhMVYRISAPTPEEKDEWIHSIKSAVS
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...KKPNCFELFIpDN...........kdqvikackteadgrvvegnhTFYRISAPTTEEKEDWIKSIKSAIS
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.........-RPNTFMIRClQW...............................ttvIERTFHVDSSDERDEWMRAIQMVAN
.........RKPYCLELYNpNS...........rgqkikacktetdgrvvegkhQSYTISASTAEERDQWIESISLN-E
..satkspTPTLTFCVKThDR.................................-LYYMVAPSAEAMRIWMDVIVTGAE
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........krkefQDSFVFDIKTaER..................................-TFYLVAETEEEMNRWVRSICQLCG
........-KAKCIDLDTeEN..................................-IYHLKIKSQELFDEWVSKLRHHRL
.....-RARRIDLDTeEH..................................-IYHLKVKSPDVFDLWVCKLRHHRL
....ttsSNVFPFKIVHfSK..................................rhRTWYFSAASEDERKEWMRHLRREIN
...eimMRDNLFEVVTtSR..................................-TFFVQADSPEEMHGWIKAISGAIV
......qERVNCFCLVFpER..................................-TFYLCAKSGAEADEWIKILRWKLS
.....dlmMRDNLFELVTtTR..................................-TFYIQSDSPEEMHGWIKAISGAIV
atkvpvpseREKALFKRNSfSP................................spPAVLLLCSS-----------CTICF
.sgdllSRDNLFEIITsAR..................................-TFYIQTDTPEDMKGWIMDIASKIQ
pipcDYKYPFQIIHdSY..................................-YLYVFAPDNDCRLKWVKALKEAIQ
..........-KENALNIVTeDR..................................-TYQIYAESPEDASGWFNVLSRVHS
dakrheVDGNLFEIITsDE..................................IHYYLQAATADERKDWIRAVQSVAK
..gtpagvkgkVQGNLFKIITqMD..................................THYYIQAPTHEERMDWIQAIRRV-T
CIDLDTeDS.................................-IYHLKAKTRSLFDLWVMQLRHHRI
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.....yeNRPLVIKLETnTS...............................EEHFLEACMREERDEWAAAIDAAVQ
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.......dGKRCMFCLKTITK...............................-TYELSASDTKQRQEWTTAIQTAIR
.............KWKCGVIVETpDR...............................-QFVFMCEQERDQREWVEALKTVIS
-NFKTFFVHTpNR...............................-TYYLMDPSG-NADKWCKKIQEVWG
............-KENGIDIVMpGR...............................-TYHLVAETAEDSSHWFSVLSQVHM
..lfGRPNCFQIVVqHF...........................seeqYIFYFAGETPEQAQDWMKCLQTFCN
wpwiqkhfkcPPSSVLFLTVeTR...............................-DYFLIGQNSDDVDSWLNAITTALQ
.............KKKFAMKASHIHV...............................LTLYFAAESMKDMNKWLAKLTQASN
..............RKKFAFKACHpKI...............................KSFYFAADNIEDMNRWLSLMNMAAA
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........--AQTFQLITeKK...............................-TFYLAADSPNILEDWIRVLQNVLK
..fsKRALVFKVSTaKN...............................QDHYFQATHLEEREHWVKDIRRAIT
tkrqhQNQHLFLCQTaTR...............................-IFYLLAKTAEEMNDWVQNIGQICT
...........RRKHAFKACHpKI...............................KSFFFATDHLEEMNRWMNRLGLAAI
..........dGKRCMFCVKTINK...............................-TFEISAPDSRQKQ------ELLAE
.......dsiTRKFAFKVEHaGT...............................RTYYFSADSQKEQEEWIQAMSEAAR
.........dhiSRKYAFKAEHtGM...............................RTYYFSADTQEDMNGWVRAMNQAAL
.......-GQFCFSLVFtGP.............................glRTYRLAADDHPSQESWIAALFCASH
........-RKYAFKATHpNM...............................RTYYFSTDTAKDMESWMKVMSDAAM
............KNKYLIALYTkDE...............................-YFAVVAESEQEQEEWYLSITELMT
.....pAQKLQFKLYHkNT...............................LYYIFRAEDIPTAQRWIEAFQEAMI
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sspnstGSDAKFVLHAkQN.........................giirrgHNWVFKADSYESMMSWFDNLKILTS
.......-EKLKFEIIGgNN.............................gvIRWHLKGNHPIETNRWVWAIQGAIR
nftdwvLFNECFQLVFdDG...............................ERITFNAECSEEKSDWYNKLQEVVE
..-KQYCFELVRcSD...........rnsvssgssslnvssdsnskKSIYIATKTESDLHSWLDAIFAKCP
kmkNDDTNFALITfDE...............................-RLSFKAANDQDMVDWIINFKSGIL
ildkngkskthqkksNISSKLLLLTIEN............................seRKLKIICKSESSLKQWMSSIIKMST
ksseldqfyaaaqKESNNYVTWTfKI...............................VSPEPSEEELKHFKRWVQDLKNLTS
.............PRNFCFKLRIqNP.....................nckteeentyIDIILQAESIDELKSWINTLTSHKR
.......-EKLNFELLGgIT.............................gtTRWRLKGNHPIETTRWVNAIQSAIR
...-KQNCFEILRaTD.............qkenispinsyfyesnskRSIFISTRTERDLHGWLDAIFAKCP
rlrsDSKLWIAIIYkVS............................nklKALHVVALNELDFNTFLSCICGLVK
snteisnanpnTDEFSFKIRNtAT..............................gESFKFFTESAEVLNQWIDAIMESFK
gSATKTFKLYTdES...............................-TFKFNADSEFSAKSWVNALKKEQF
....tKKSFVLRMSCeSE...............................-QFLLRFSHIDDMIDWSMYLSIGIS
epkldlrgriMIMNLNQIIPqNN..................rslnitwesikeqGNFLLKFKNEETRDNWSSCLQQLIH
rfGTRNGFLITEhKK.........................sglstsTKYYICTETSKERELWLSAFSDYID
rvygdgwrsvedESSRCFTLWFgTRdppsapeadlnnsnvpsntdkihftkklgvsgKSMVFMARSRQERDLWVMSIY
inhrnipAYYYAFKIVMqNG...............................HEYLIQTASSSDLTEWIKMIKASKR
.........ptgLYHKSIVVTTeTR...............................-TIKFTCPTRQRHNIWYNSLRYLLQ
snvcnkntkRKSGNFTVSFpEN..........................ingpkLVLEFQTRSVEEAHKFMDCINFWAG
.............-RKFCFEVKIfGN...................kvteahdnmskdITLVFQTSNYLDLKSWLIAFEATKK
....dnivmecgkNLTNALVVSTtLK...............................NRYFLQFGNKESFNAWNSAIRLCLY
qviiasenektkkDLDNVLVVSTtLK...............................NRYFLKFKNSKSFKTWNAAIRLSLF
...........SRKFCFEVITpQT...............................-KRTYQATSKAEMHSWIEAIQYSIS
...........SRKFCFEVITpQT...............................-KRTYQATSKAEMHSWIEAIQYSIS
...........GRRFCFEVVTpKL...............................-KRLYQATSAEEMDSWIEAICEAAK
...NNEHGWVVETpTK...............................-SWSFEDPNG-PASAWVELLDKASS
...NNEHGWVVETpTK...............................-SWSFEDPNG-PASAWVELLDKASS
.........nVRNCSFTVIFrDG...............................SEETLCAPTEESMIEWVAKINYIST
.........nVRNCSFTVIFrDG...............................SEETLCAPTEESMIEWVAKINYIST
.........-QPTVFQVIGkGS...............................VRYSVKANSPVEAKKWIAAISSAIE
edavvlksTNSLYFDLETsSQ...............................LKLRFAGPSPKDAQGWIDALNYWAA
efltgeNYQSAFVIQEkQT........................etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
efltgeNYQSAFVIQEkQT........................etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
..........HRKFCFQIKTkSV...............................-SYILQAETHMEMLEWGSVINNARE
.....vlsGGKTAIKLIPpAP...................gaakaavmftppKVHYFTCENNEELHRWSSAFLKATV
.....vlsGGKTAIKLIPpAP...................gaakaavmftppKVHYFTCENNEELHRWSSAFLKATV
.....-RTFCFKLRFkSS.........................tknfeiQACELSVADNMECYEWMDLISSRAL
ykisseNEKRWFTIIYcAD............................nklKAMHMISPTLDAHNQWIMALEGLKT
ykisseNEKRWFTIIYcAD............................nklKAMHMISPTLDAHNQWIMALEGLKT
```

```
TFFLYLnEK................................-IIRLIATSNEDAEEWVHVLRSTTG
.--THEINVDSgVE................................-LWNLRAHTHQDWLRWCNALEKAKN
...........sinsNRNNVFYLNIpGN................................ECYLFEAPSVLAMNEWIHSLNFNAA
..-KKPKFKITGkDA........................tkkifgarNDYAFRASNNTELMRWWEALNTHIA
eelegylYFESGFRIIFsNG................................DYIDFYAETVGEKDEWMSTLRQHLG
kdtnekirLSHHSFKIKNrQK................................-VMKLSVRSG----RWLQQFINSVQ
...esSHKYFFTVITqNK................................-PIEFRVDNEDSLILWVAALKTSID
vsnlGLVAGILATSvDR................................RHVQLFADSKKVCQKWLQVMNSRSF
vsnlGLVAGILATSvDR................................RHVQLFADSKKVCQKWLQVMNSRSF
.........---NKFTINFnNG................................KSETLEALDPESKNTWITDLKNAIA
```

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Type of file:	table
Label:	Table 7
Filename:	mmc13.xls

Supplementary Table 7, Park et al.
Cloned and tested PH-domain constructs with total number of cells

Species	Name	Score	NP_number
Celegans	akt-2-PH1	57.5	NP_001024612
Celegans	akt-1-PH1	47.7	NP_001023647
Celegans	sec7-PH1	36.0	NP_498764
Celegans	obr-1-PH1	0.7	NP_499448
Celegans	let-502-PH2	-0.1	NP_491440
Celegans	F59A6.5-PH1	-6.4	NP_494921
Drosophila	Grp1-PH1	76.5	NP_001036375
Drosophila	Akt1-PH1	60.1	NP_732113
Drosophila	Btk29A-PH1	42.2	NP_723369
Drosophila	CG14366-PH1	26.9	NP_650310
Drosophila	CG5004-PH1	18.9	NP_573195
Drosophila	vap-PH1	-6.0	NP_996482
Human	PSCD4-PH1	79.4	NP_037517
Human	LOC653583-PH1	54.8	XP_933317
Human	PHLDB2-PH1	54.8	NP_665696
Human	GAB3-PH1	40.2	NP_542179
Human	OSBPL6-PH1	33.1	NP_665682
Human	DEF6-PH1	18.3	NP_071330
Human	RASA1-PH1	17.9	NP_002881
Human	SBF1-PH1	7.7	NP_002963
Human	PLEKHH1-PH1	6.2	NP_065766
Human	OSBPL1A-PH1	2.8	NP_579802
Human	ARHGAP25-PH1	-3.7	NP_001007232
Human	CENTD2-PH4	-41.8	NP_001035207
Mouse	Pscd3-PH1	89.6	NP_035312
Mouse	Pscd2-PH1	87.1	NP_035311
Mouse	Akt1-PH1	70.2	NP_033782
Mouse	Akt3-PH1	68.0	NP_035915
Mouse	Akt2-PH1	64.3	NP_031460
Mouse	Phldb1-PH1	53.7	NP_705765
Mouse	Rasa3-PH1	48.2	NP_033051
Mouse	TEC-PH1	47.9	BAE23957
Mouse	Rasa2-PH1	46.9	NP_444498
Mouse	Gab1-PH1	45.4	NP_067331
Mouse	Btk-PH1	44.8	NP_038510
Mouse	Gab2-PH1	41.2	NP_034378
Mouse	Itk-PH1	37.8	NP_034713
Mouse	Plekha1-PH1	33.5	NP_598703
Mouse	Sh3bp2-PH1	33.2	NP_036023
Mouse	Osbpl3-PH1	32.0	NP_082157
Mouse	Plek2-PH1	32.0	NP_038766
Mouse	Dapp1-PH1	30.2	NP_036062
Mouse	Plekha2-PH2	29.4	NP_112547
Mouse	Plek2-PH2	24.1	NP_038766

Mouse	Osbpl7-PH1	23.9	NP_001074903
Mouse	PDPK1-PH1	21.3	NM_011062
Mouse	Myo10-PH1	17.6	NP_062345
Mouse	Plek-PH1	16.0	NP_062422
Mouse	Cnksr2-PH1	13.0	NP_808419
Mouse	Fgd6-PH2	8.3	NP_444302
Mouse	Myo10-PH2	8.1	NP_062345
Mouse	Phlpp-PH1	8.0	XP_990044
Mouse	Plek-PH2	7.9	NP_062422
Mouse	Plekha5-PH1	2.3	NP_659169
Mouse	2610034M16Rik-PH1	2.2	NP_081277
Mouse	Plekhb2-PH1	0.1	NP_663491
Mouse	Swap70-PH1	-1.7	NP_033328
Mouse	Plekho1-PH1	-2.6	NP_075809
Mouse	Irs1-PH1	-2.6	NP_034700
Mouse	Myo10-PH3	-2.9	NP_062345
Mouse	Rasal1-PH1	-4.5	NP_038860
Mouse	CENTD2-PH1	-4.9	NM_027180
Mouse	DGKD-PH1	-5.0	XM_906228
Mouse	Skap2-PH1	-7.0	NP_061243
Mouse	Plekha3-PH1	-8.4	NP_112546
Mouse	Plekhb1-PH1	-8.6	NP_038774
Mouse	Ophn1-PH1	-9.2	NP_443208
Mouse	Plekhm2-PH1	-9.6	XP_985312
Mouse	AA536749-PH1	-9.7	NP_957697
Mouse	Centb5-PH1	-10.0	NP_997106
Mouse	Cadps-PH1	-11.2	NP_001036082
Mouse	Cit-PH1	-12.2	NP_031734
Mouse	PSD3-PH1	-12.7	NM_177698
Mouse	TRIOBP-PH1	-13.6	NP_001074771
Mouse	Dok4-PH1	-13.9	NP_444476
Mouse	Dnm1-PH1	-14.3	NP_034195
Mouse	Plekha2-PH1	-14.3	NP_112547
Mouse	Afap1-PH1	-14.6	NP_081649
Mouse	CENTD1-PH1	-15.4	XM_132099
Mouse	VEPH1-PH1	-16.1	NM_145820
Mouse	Plekhf1-PH1	-16.1	NP_077724
Mouse	AA536749-PH2	-16.2	NP_957697
Mouse	Dnm2-PH1	-16.3	NP_001034609
Mouse	RALGPS2-PH1	-16.5	NM_023884
Mouse	Plekhj1-PH1	-17.1	NP_076389
Mouse	Farp1-PH2	-17.3	NP_598843
Mouse	Fgd1-PH2	-17.5	NP_032027
Mouse	Sntb2-PH1	-18.4	NP_033255
Mouse	Arhgap10-PH1	-18.6	NP_084389
Mouse	CENTD1-PH2	-18.7	XM_132099
Mouse	Fgd6-PH1	-19.3	NP_444302
Mouse	Col4a3bp-PH1	-19.5	NP_075909
Mouse	Ngef-PH1	-20.1	NP_063920
Mouse	Plcd4-PH1	-20.2	NP_683739
Mouse	Psd2-PH1	-21.5	NP_082983

Mouse	Apbb1ip-PH1	-22.8	NP_062329
Mouse	Ddef1-PH1	-22.8	NP_034156
Mouse	Prkcm-PH1	-22.8	NP_032884
Mouse	Pld2-PH1	-23.1	NP_032902
Mouse	RASGRF1B-PH1	-23.2	NM_001039655
Mouse	2610034M16Rik-PH2	-23.5	NP_081277
Mouse	Plcd1-PH1	-23.5	NP_062650
Mouse	Osbpl5-PH1	-24.0	NP_077251
Mouse	ABR-PH1	-24.3	NM_198894
Mouse	Plcl2-PH1	-24.5	NP_038908
Mouse	Rasgrf2-PH1	-25.0	NP_033053
Mouse	Tiam1-PH2	-25.3	NP_033410
Mouse	Itsn1-PH1	-25.5	NP_034717
Mouse	Adrbk1-PH1	-25.7	NP_570933
Mouse	DOK1-PH1	-26.0	NM_010070
Mouse	Sh2b2-PH1	-26.1	NP_061295
Mouse	Snta1-PH1	-27.1	NP_033254
Mouse	Fgd2-PH1	-27.8	NP_038738
Mouse	Rasa4-PH1	-29.3	NP_598675
Mouse	Pld1-PH1	-29.5	NP_032901
Mouse	Spnb2-PH1	-30.2	NP_787030
Mouse	Net1-PH1	-30.2	NP_062645
Mouse	KIF1A-PH1	-30.4	NM_008440
Mouse	SH2B1-PH1	-30.5	NM_011363
Mouse	Plekhm1-PH1	-31.6	NP_898855
Mouse	Sntb1-PH1	-31.7	NP_057876
Mouse	DOK5-PH1	-31.9	NM_029761
Mouse	Farp1-PH1	-32.1	NP_598843
Mouse	D10Ertd610e-PH1	-33.5	NP_082303
Mouse	Fgd3-PH1	-34.2	NP_056574
Mouse	PLEKHC1-PH1	-35.2	NM_146054
Mouse	KIF1B-PH1	-35.5	NM_207682
Mouse	Itsn2-PH1	-36.0	NP_035495
Mouse	Tiam1-PH1	-36.0	NP_033410
Mouse	Kalrn-PH1	-36.0	XP_998128
Mouse	Centd2-PH4	-38.2	NP_001035201
Mouse	Grb7-PH1	-39.0	NP_034476
Mouse	Arhgef7-PH1	-41.2	NP_059098
Mouse	ARHGEF3-PH1	-41.5	NM_027871
Mouse	Tiam2-PH1	-41.6	NP_036008
Mouse	Grb14-PH1	-41.8	NP_057928
Mouse	Mcf2-PH1	-42.6	NP_573460
Mouse	Arhgef18-PH1	-42.9	NP_598723
Mouse	RASGRF1A-PH2	-43.2	NM_011245
Mouse	ARHGEF2-PH1	-44.3	NM_008487
Mouse	VAV2-PH1B	-45.3	NP_033526
Mouse	ROCK1-PH1	-45.7	NP_033097
Mouse	Fgd1-PH1	-46.9	NP_032027
Mouse	Mcf2l-PH1	-48.4	NP_835177
Mouse	Vav3-PH1	-49.1	NP_065251
Mouse	Vav1-PH1	-51.3	NP_035821

Mouse	Grb10-PH1	-51.6	NP_034475
Mouse	Sos2-PH1	-53.4	XP_992919
Mouse	Akap13-PH1	-55.4	XP_984499
Mouse	Sos1-PH1	-55.9	NP_033257
Mouse	RGNEF-PH1	-58.3	NM_012026
S.Cerevisiae	SLM2-PH1	14.2	NP_014351
S.Cerevisiae	BOI1-PH1	5.0	NP_009468
S.Cerevisiae	BUD4-PH1	-2.7	NP_012625
S.Cerevisiae	ATG26-PH1	-12.1	NP_013290
S.Pombe	csx2-PH1	3.0	NP_595897
S.Pombe	SPAC26A3.10-PH1	0.2	NP_594153
S.Pombe	ksg1-PH1	-3.1	NP_588442
S.Pombe	SPAC11E3.11c-PH1	-5.8	NP_594936
S.Pombe	reserved_name_rga2-PH1	-7.7	NP_594152
S.Pombe	SPCPB16A4.02c-PH1	-11.2	NP_588026
S.Pombe	SPAPYUG7.03c-PH1	-21.1	NP_594704

transfected and imaged and number of those cells expressing the phenotype (tran

Translocating (T), constitutively-PM localized (P), or cytosolic (C)	Total transfected	# of cells non-PM	# of cells PM prelocalized
T	17		
T	5		
C	41	41	
P	6		6
C	13	13	
C	11	11	
T	20		
T	7		
T	11		
T	5		
P	17		17
C	9	9	
T	14		
T	9		
T	15		
T	15		
T	21		
C	22	22	
C	21	21	
T	19		
C	22	22	
C	17	17	
C	10	10	
C	24	24	
T	8		
T	14		
T	23		
T	21		
T	42		
T	32		
T	9		
T	10		
T	9		
T	17		
T	13		
T	11		
T	8		
T	16		
T	35		
T	21		
T	17		
T	16		
T	16		
T	14		

T	25		
T	15		
T	26		
T	19		
T	38		
T	13		
T	13		
T	12		
C	17	17	
C	9	9	
P	7		7
C	9	9	
C	13	13	
C	12	12	
C	17	17	
C	6	6	
C	9	9	
C	25	25	
P	13		
C	15	15	
C	7	7	
C	4	4	
C	12	12	
C	5	5	
C	8	8	
C	5	5	
C	7	7	
C	13	13	
P	15		15
C	7	7	
P	15		15
C	6	6	
C	13	13	
C	10	10	
C	7	7	
P	5		5
P	17		17
C	8	8	
C	4	4	
P	13		13
C	5	5	
C	14	14	
C	11	11	
C	6	6	
C	5	5	
C	5	5	
C	13	13	
C	4	4	
C	6	6	
C	5	5	
C	4	4	

C	4	4	
C	7	7	
C	11	11	
C	9	9	
C	6	6	
C	13	13	
P	23		23
C	5	5	
C	7	7	
P	12		12
C	4	4	
C	8	8	
C	5	5	
C	8	7	
P	14		13
P	13		9
C	3	3	
C	7	7	
C	14	14	
C	10	10	
P	9		8
C	12	12	
C	4	4	
C	4	4	
C	7	7	
C	6	6	
P	17		15
C	9	9	
C	6	6	
C	21	21	
C	4	4	
C	8	8	
C	11	11	
C	6	6	
C	5	5	
C	5	5	
C	4	4	
C	16	16	
C	7	7	
C	9	9	
C	5	5	
C	9	9	
C	4	4	
C	6	6	
C	5	4	
C	23	19	
C	4	4	
C	7	7	
P	11		9
C	7	7	
C	9	9	

C	6	6	
C	5	5	
T	18		
C	16	16	
C	8	8	
C	25	25	
C	11	11	
C	12	12	
C	8	8	
C	8	8	
C	18	18	
P	12		12
C	13	13	
C	11	11	
C	13	13	
C	15	15	

slocating, PM-loc

# of cells PM translocated
17
5
20
7
11
5
13
9
11
12
13
6
6
10
23
21
40
30
9
6
8
12
8
11
8
7
32
13
7
16
5
9

14
15
15
11
27
7
7
7
5

17

alized or cytosolic)

Sequence
IVIESWLHKKG.....eHIRNWRPRYFILFR......dGTLLGFRSKP.......kEDQPLPEPLNNF..MIRDAATV......................
VVIEGWLHKKG.....eHIRNWRPRYFMIFN......dGALLGFRAKP.......kEGQPFPEPLNDF..MIKDAATM....................
AEREGWLFKQSsnplfsGALSWKKRWFVLSE.......NCLYYFDQMT.......dKEPKGIITLANV..GIRKVEAP..................
VEKAGWLNKWT.....nYLKGYRQRWFVLDS......nATLSYYRNPS.....evgHTCRGSINLQEA..RVHTDKT-.................
RTFCDVCNKKL......--------------.......------SDI-........IRPTPAFECKNC..HFKTHKDH.........................VAQGSLPMC
GRMNGWLRVYR...ddmTGSTWIASWAMMDL.......TRISFYTNDG.....adlEKPFFSIDLNKE..QWVLRTGQ.............
PDKEGWLWKQG.....gRYKSWKRRWFILND.......NCLYYFEYTT.......dKEPRGIIPLENI..SVREIHDR......................
VVKEGWLMKRG.....eHIKNWRQRYFVLHS......dGRLMGYRSKPadsastpsDFLLNNFTVRGC..QIMTVDRP...........
VVKSGSMVKRAqnkkrfTPVNYKHRWFELTK.......RTFSYFDVEN.....verRRERGRIHLKGV.rLVEEATVS................
VTLSGWLHKQG....sdGLKVWRKRWFVLAE.......YCLYYYKGPE.......eEKLLGSVLLPSY..RVSACLPE.................
HSCRGYLHKLG.....aTFHAWSRRWFVLDR.....qrSALIYYSDKS.......eRKPRGGAYFATI.dEVYLDHLN..................
IKHHGHLNKKS.....dKTTKWKQLYFALIN...dgseTQLCFYDNPK.......kTKPKGLIDLSCA..YLYQCHDS....................
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEFTT.......dKEPRGIIPLENL..SVQKVDDP......................
CCCRGPLVKMG.....gRIKTWRKRWFCFDR.....qaRRLAYYADKE.......eTKLKGVIYFQAI.eEVYYDHLR..................
KTCRGFLIKMG.....gKIKTWKKRWFVFDR.....nkRTFSYYADKH.......eTKLKGVIYFQAI.eEVYYDHLK....................
AVCTGWLVKSP.perklQRYAWRKRWFVLRRgrmsgnpDVLEYYRNKH.......sSKPIRVIDLSEC..AVWKHVGP.........
DKHEGFMLKKR....kwPLKGWHKRFFVLDN.......GMLKYSKAPL....diqkGKVHGSIDV-GL..SVMSIKK-..................
VLKQGYLWKRG.....hLRRNWAERWFQLQP.......SCLCYFGSEE.......cKEKRGIIPLDAH.cCVEVLPDR..................
IVKKGYLLKKG......KGKRWKNLYFILEG.....sdAQLIYFESEK......raTKPKGLIDLSVC..SVYVVHDS.......................
RSYEGTLYKKG.....aFMKPWKARWFVLDK.....tkHQLRYYDHRV.......dTECKGVIDLAEV..EAVAPGTP..................
LEKSGYLLKMG.....sQVKTWKRRWFVLRQ.......GQIMYYKSPS.....dviRKPQGQVDLNSR.cQIVRGEG-...............
KRYEGPLWKSS......RFFGWRLFWVVLEH.......GVLSWYRKQP...davhnIYRQGCKHLTQA..VCTVKST-..............
PIKMGWLKKQR.....sIVKNWQQRYFVLRA.......QQLYYYKDEE.......dTKPQGCMYLPGC..TIKEIATN...................
DTKHGMMKFREllglglPSGGFHDRYFILNS.......SCLRLYKEVRwsgapetsHRPEKEWPIKSL..KVYLGVKK.............
PDREGWLLKLG.....gRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIVPLENL..SIREVEDP......................
PDREGWLLKLG....ggRVKTWKRRWFILTD.......NCLYYFEYTT.......dKEPRGIIPLENL..SIREVDDP......................
IVKEGWLHKRG.....eYIKTWRPRYFLLKN......dGTFIGYKERP..qdvdqrESPLNNFSVAQC..QLMKTERP................
IVKEGWVQKRG.....eYIKNWRPRYFLLKT......dGSFIGYKEKP...qdvdlPYPLNNFSVAKC..QLMKTERP.................
VIKEGWLHKRG.....eYIKTWRPRYFLLKS......dGSFIGYKERP..eapdqtLPPLNNFSVAEC..QLMKTERP................
KVCRGYLIKMG.....gKIKSWKKRWFVFDR.....lkRTLSYYVDKH.......eTKLKGVIYFQAI.eEVYYDHLR....................
LLKEGFMIKRAqgrkrfGMKNFKKRWFRLTN.......HEFTYQKSKG........DQPLCNIPIENI.IAVERLEEE......................
TILEEILIKRSqqkkktSPLNYKERLFVLTK.......SVLSYYEGRA......ekKYRKGVIDISKI..KCVEIVKN...................ddg
HLKEGEMYKRAqgrtriGKKNFKKRWFCLTS.......RELTYHRQQG........KDAIYTIPVKNI.IAVEKLEEG......................
VVCSGWLRKSP.pekklKRYAWKRRWFVLRSgrltgdpDVLEYYKNDH.......aKKPIRIIDLNLC.qQVDAGLTF.............
VILESIFLKRSqqkkktSPLNFKKRLFLLTV.......HKLSYYEYDF...ergrrGSKKGSIDVEKI..TCVETVIPeknppperqiprrg
VVCTGWLRKSP.pekklRRYAWKKRWFILRSgrmsgdpDVLEYYKNEH.......sKKPLRIINLNLC.eQVDAGLTF............
ILLEEQLIKKSqqkrrtSPSNFKVRFFVLTK.......ASLAYFEDRH.....gkkRTLKGSIELSRI..KCVEIVKS....................dis
VIKAGYCVKQG.....aVMKNWKRRYFQLDE.......NTIGYFKSEL.......eKEPLRVIPLKEV.hKVQECKQS....................
VAKAGYLHKKG..gtqlQLLKWPLRFVIIHK.......RCIYYFKSST.......sASPQGAFSLSGY.nRVMRAAEE.....................
PVQKGFLLKKR....kwPLKGWHKRFFCLEK.......GILKYAKSQ-........-ADIEREKLHGC.iDVGLSVMS.......................
VLKEGFLVKRG.....hIVHNWKARWFILRQ.......NTLLYYKLEG....grrvTPPKGRIVLDGC..TITCPCLE.......................
GTKEGYLTKQG.....gLVKTWKTRWFTLQR.......NELKYFKDQ-........-MSPEPIRILDL.tECSAVQFD.........................
LIKSGYCVKQG.....nVRKSWKRRFFALDD.......FTICYFKCEQ.......dREPLRTIPLKDVlkTHECLVKS......................
VVKQGYLSKQG.....hKRKNWKVRRFVLRK.....dpAFLHYYDPSK......eeNRPVGGFSLRGS..LVSALEDN..............

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ERQEGHLLKKR....kwPLKGWHKRYFVLED.......GILHYATTRQ....ditkGKVHGSIDVRLS..VMSINKK-....................
ILKMGPVDKRK......-GLFARRRQLLLTE......gPHLYYVDPVN........KVLKGEIPWSQE.IRPEAKNF-....................
ALKQGWLHKKGggsstlSRRNWKKRWFVLRQ.......SKLMYFENDS.......eEKLKGTVEVRTA.kEIIDNTS-..................
RIREGYLVKKG.....sVFNTWKPMWVVLLE.......DGIEFYKKKS.......dNSPKGMIPLKGS..TLTSPCQD.....................
GDCEGWLWKKK.daksyFSQKWKKYWFVLKD.......ASLYWYINEE.......dEKAEGFISLPEF..KIDRASEC.................
STMSGYLYRSK.....gSKKPWKHLWFVIKN.......KVLYTYAASE.......dVAALESQPLLGF..TVTLVKDE....................
PYFHSFLYMKG.....gLMNSWKRRWCVLKD.......ETFLWFRSKQ........EALKQGWLHKKG.gGSSTLSRR...............
IQLSGMYNVRK.gkmqlPVNRWTRRQVILCG.......TCLIVSSVKD......svSGKMHVLPLIGG..KVEEVKK-...................
IIKQGCLLKQG.....hRRKNWKVRKFILRE.....dpAYLHYYDPAG.......gEDPLGAVHLRGC..VVTSVESS...................
VVRRGWLYKQD....stGMKLWKKRWFVLSD.......LCLFYYRDEK.......eEGILGSILLPSF..QIAMLTAE....................
PTCRGYLHKRT...hsgFVKGWRKRWFVLKH......dGFLLYYKHRK....degkWPPLDMIKLEGA..EVDIDNSL.............
FVKSGWLLRQS.....tILKRWKKNWFDLWS......dGHLIYYDDQT.....rqsIEDKVHMPVDCI..NIRTGHEC.................r
VLKQGYMMKKG.....hKRKNWTERWFVLKP.......NIISYYVSED.......lKDKKGDILLDEN.cCVESLPDK.....................
PEKVGWVRKFC..gkgiFREIWKNRYVVLKG.......DQLYVSEKEV.....kdeKNSQEVFDLSDY.eKCEELRKS.............
VRKVGYLRKPK......---SMHKRFFVLRAaseaggpARLEYYENEK..kwrhksSAPKRSIPLESC.fNINKRADS................
FIVRGWLHKEVknspkmSSLKLKKRWFVLTH.......NSLDYYKSSE......knALKLGTLVLNSL.cSVVPPDEK...............
IVREGFLLKRKepgglaTRFAFKKRYFRLSG.......RDLSYSKTPE........WQVHTSIPLSCI..RAVEHVDE.....................
VSHSGFLYKTAllqdrrAREEFSRRWCVLGD.......GVLSYFENER.......aVTPNREIRASEI..VCLAVPPP....................
ILKEGMLTKQN.....nSFQRSKRRYFKLRG.......RTLYYAKTAK........SIIFDEVDLTDA..SVAESSTK........................
VIKAGYLEKRR.kdhsfLGFEWQKRWCALSK.......TVFYYYGSDK.......dKQQKGEFAIDGY..DVRMNNTL................
--MEGVLYKWT.....nYLTGWQPRWFVLDN.......GILSYYDSQD.....dvcKGSKGSIKMAVC..EIKVHPA-.....................
LVRGGWLWRQS.....sILRRWKRNWFALWL......dGTLGYYHDET.....aqdEEDRVVIHFNVR..DIKVGQEC..............
PTIEGYLYTQE...kwaLGISWAKYYCRYEK...etrmLTMIPMEQKP........GAKQGPVDLTLK.yCVRRKTES................
ITKEGMLHYKA.stsylGKEHWKACFVVLSN.......GILYQYPDRT.......dVIPLLSVNMGGE..QCGGCRRS.................
PIYGGWLLLAPfdnpvhRSRKWQRRFFILYE.......HGLLRYALDE.....mptTLPQGTINMNQC.tDVVDGEAR..............
VVMEGYLFKRA....snAFKTWNRRWFSIQN.......SQLVYQKKLK.......dALTVVVDDLRLC..SVKPCEDI..................
MKHSGYLWTIG....knVWKRWKKRFFVLVQ..vsqytFAMCSYREKK........AEPQELLQLDGY..TVDYTDPQ.............
LHLEGWMKVPR..nnkrGQQGWDRKYIVLEG.......SKVLIYDNE-........AREAGQRPVEEF..ELCLPDGD.........vsihg
VYKSGFLARKIgkktprGKRGWKTFYAVLKG.......TVLYLQKDEYkpekalseEDLKNAVSVHHA..LASKATDY............
-----------......--GEWKKHWFVLTD.......SSLKYYRDST....aeeaDELDGEIDLRSC.tDVTEYAVQ..........................-RN
IVKQGYVKMKS.....rKLGIYRRCWLVFRK.ssskgpQRLEKYPDEK....svclRGCPKVTEISNV.kCVTRLPKE..............
VIRKGWLTINN...igiMKGGSKEYWFVLTA.......ENLSWYKDDE.......eKEKKYMLSVDNL..KLRDVEKG..................
NRICGFLDIED....neNSGKFLRRYFILDT.....qaNCLLWYMDNP..qnlavgAGAVGSLQLTYI.sKVSIATPK..................
AKICAFLLRKK......RFGQWTKLLCVIKD.......TKLLCYKSSK.......dQQPQMELPLQGC..SITYIPRD........................
TFLCDFLYQAPlssekkLLEETNKKWCVLEG.......GFLSYYENDK.......sTTPNGTININEV..ICLAIHKE....................d
PLIEGKLKEKQ..vrwkFIKRWKTRYFTLAG.......NQLLFQKGKS......kdDPDDPPIELSKV..QSVKAVAK...................
LLGEGVLTKEC......-RKKAKPRIFFLFN.......DILVYGSIVL....skrkYRSQHIIPLEEV..TLEPLPET.........................IQ
NFKKGWLTKQY......EDGQWKKHWFVLAD.......QSLRYYRDSV....aeeaADLDGEINLSTC.yDVTEYPVQ..............
VIRRGWLTINN...islMKGGSKEYWFVLTA.......ESLSWYKDEE.......eKEKKYMLPLDNL..KIRDVEKG....................
VTIQGVLRRKTkegkkpTVASRTKYWAALCG.......TQLFYYAAKSaterkhfkSTSNKNVSVVGW..MVMMADDP..........
AEMAAELGMRG....pkKGSVAKRRLVKLVV.......NFLFYFRPDE........AEPLGALLLERC..RVAQEE--......................
NQLSGNLLRKF.....kNSNGWQKLWVVFTN.......FCLFFYKSHQ.......dSHPLASLPLLGY..SLTIPSES.....................
SVICSFLHYME.....kGGKGWHKAWFVVPE....nepLVLYIYGAPQ.......dVKAQRSLPLIGF..EVGPPEAG................
VKHIAWLAEQA..kldgGRQQWRPVLMAVTE.......KDLLLYDCMP..wtrdawASPCHSYPLVAT..RLVHSGSG............
FTAEGYLYVQE.krpapFGSSWVKHYCMYRK...takkFNMIPFEHRS.....ggkLGDGEAFFLKEC..TKRHMDST..........
SIKEGILKLKEepskilSGNKFQDRCVVLRD.......GHLFIYKDPK.......sSKHDKMFPLRAM..KFYLGVKK....................
FLKEGTLMKLS......-RKVMQPRMFFLFN.......DALLYTTPMQ.....sgmYKLNNMLSLAGM..KVRKPTQE..................
VERCGVLSKWT.....nYIHGWQDRWVVLKN.......NTLSYYKSED.....eteYGCRGSICLSKA..VITPHDF-...................
LLKQGELQQMStsrtlrTKKLFREIYLFLFN.......DLLVICRQIP.....gdkYQVFDSAPRGLL..RVEELEDQ......................
LMQEGTMMRKV.....rTKSWKKLRYFRLQN.......DGMTVWHGSQ......peSMPKPTFSISDV.eRIRKGQDS..............
TYKHGVLTRKTgkrtprGRRGWKKFYAVLKG.......TILYLQKDEYrldkalseGDLKNAIRVHHA..LATRASDY................
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PELEGALYLKE.....dGKKSWKRRYFLLRA.......SGIYYVPKGK....tktsRDLACFIQFENV..NIYYGIQC....................k
SEKKGFLLKKS....dgIRKVWQRRKCAVKN.......GILTISHATS........NRQPAKLNLLTC..QVKPNAE-........................
VMKEGWMVHYT.....sKDTLRKRHYWRLDS.......KCITLFQNDT.......gSRYYKEIPLSEI.ICLEPAKPS....................a
KGLEGVIRKRSfcgrdqVCYRWSKRWLVVKD.......SFLLYMRPET......gaISFVQLFD-PGF..EVQVGKRS................
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.......sPRPSGLYLLEGS..ICKRAPSP........krgtsske
PECLGLLHQLE.....rSTDVWIQHYCILKD.......GCLYFYASIR.......sTQASGGLYLQGY..SVSEQTHG......................
LLKGSQLLKVK......SSSWRRERFYKLQE.......DCKTIWQESR....kvmrSPESQLFSIEDI.qEVRMGHRT................
VIMADSLKIRG......TLKSWTKLWCVLKP.......GVLLIYKTPK.......vGQWVGTVLLHCC..ELIERPSK........................
LVKDGFLVEVS......-ESSRKLRHVFLFT.......DVLLCAKLKKhpfpdhelEDMKMKISALKS..EIQKEKAN...kgqsraierlk
SMVEGSELKKV.....rSNSRIYHRYFLLDA.....dmQSLRWEPSKK........DSEKAKIDIKSI.kEVRTGKNT..............difrs
GTKRGFLSKKA.....aEASRWHEKWFALYQ.......NVLFYFEGEQ.......sGRPAGMYLLEGC..SCERTPAP............pr
DLSMGDLLLHTpaslgkWKKEPELAAFVFKT.......AVVLVYKDGSsiyeewdpFRFRHMIPTEAL..QVRALPSA............
FLHSGKLYKAK......---SNKELYGFLFN.......DFLLLTQITKspksnlqyKMYKTPIFLNEV..LVKLPTDP........................
CIVHGYMSKMG....npFLTQWQRRYFYLFP.......NRLEWRGEG-........EAPQSLLTMEEI..QSVEETQI...................
AVMEGPLFLQS...qrfGTKRWRKTWAVLYP.asphgvARLEFFDHKGrggrggsrRLDCKMIRLAEC.vSVVPVTVE........
IQREGALRFMVaasgpgGTAQWQKCRLLLRR.avagerFRLEFFVPPK.......aSRPKVSIPLSAI.iEVRTTMPL............
IKQIGWLTEQL......PSGGTAPTLALLTE.......KELLFYCSLP..qsrealSRPTRTAPLIAT.sSAHRLVHS.................gps
LLREGPVLKIS.....fRRSDPMERYLVLFN.......NMLLYCVPRV..lqvgaqFQVRTRIDVAGM..KVRELTDA..................
PVKEGPLFIHRkgkgplASSSFKKLYFSLTT.......EALSFAKTSS.....skkSTFIKLASIRAA.eKVEEKSFG.....................
KGLEGMIMKRSccghgrACYRWSKRWLIVKD.......SFLLYMKPDS........GAIAFVLLVDKE.fRVKVGRKE.................
AQMEGFLNRKHahnkkaSSRSWHNVYCVINN.......QEMGFYKDAK.saasgipYHSEVPVSLKEA..ICEVALDY.........
LLCHGELKNKS......----GHKLYIFLFQ.......DILVLTRPVT.rnerhlyQVYRQPIPVQEL..VLEDLQDG..........dvrmggsfr
VSKKGYLHFLE.....pHTAGWAKRFVVVRR.......PYAYMYNSDK.......dTVERFVLNLSTA..QVEYSEDQ..................
IQREELLSFMGltsgggGQPQWQKCRLLLRSegeggggSRLEFFVPPK.......aSRPRLSIPCSTI.tDVRTATAL............
LMKLGTVARRG......AMGIWKEFFCELSP.....leFRLYLSDEE-........RTCVESCSLLRC..EAVGPAH-......................
IRHLGWLAEKV...pgeSEKQWKPALVVLTE.......KDLLIYDSMP..rrkeawFSPVHSYPLLAT..RLVHSGPG................
IVKQGYVRIRS.....rRLGIYQRCWLVFKK.asskgpKRLEKFSDER.....aayFRCYHKVELNNV.kNVARLPKS.............
FIRLGSLSKLS......-GKGLQQRMFFLFN.......DVLLYTSRGL...tasnqFKVHGQLPLYGM..TIEESEEE.....................
RGFEGKLTAQGpeagglLSSRGRERRVFLFE.......QIIIFSEALGgrggaqpgYVVYKNSIKVSCL..GLEGNLQG............
LIKEGSIQKLS.....aKNGTTQDRHLFLFN.......NVMLYCVPKL..rlmgqkLSVREKMDISDL..QVQDIVKP....................
PELADYIKVFK..pkkITLKGYKQYWCTFKD.......TSISCYKSKE.....essGTPAHQMNLRGC..EVTPDVNI..................
VSKKGYLHFKE.....pLSSNWAKHFVVVRR.......PYVFIYNSDK.......dPVERGIINLSTA..QVEYSEDQ.......................
LLHSGKLYKTK......---SNKELHAFLFN.......DFLLLTYLVRnskssaqfRMYKTPIFLNEV..LVKLPTDP.........................
VRKAGALAVKNkkvesaTRRKWKHYWVSLKG.......CTLFFYETDG.rsgidhnSVPKHAVWVENS..IVQAVPEH.........
LILQDAFQVWD...pksLIRKGRERHLFLFE.......ISLVFSKEIK.dssghtkYVVYKNKLLTSEL..GVTEHVEG...................
DTKHGMMKFREllglglPSGGFHDRYFILNS.......SCLRLYKEVR.......sHRPEKEWPVKSL..KVYLGVKK.................
PEIQGFLQLRG.sgrgsGRKLWKRFFCFLRR.......SGLYYSTKGT....skdpRHLQYVADVNES..NVYVVTQG............
VTYMSQVTIQC.....aGSEEKNERYLLLFP.......NLLLMLSASP....rmsgFIYQGKLPTTGM..TITKLEDS.....................
YYKERLLYLEEcchgelKNNRGVKLHVFLFQ.......EVLVITRAVT.hneqlcyQLYRQPIPVKDL..TLEDLQDG..........evrl
VRKAGWLFFKPrklelvARRKWKQYWVTLKG.......CTLLFYETYG.knsteqnSAPRCALFAEDS..IVQSVPEH............
PEIHGFLHAKE.....qGKKSWKKAYFFLRR.......SGLYFSTKGT.......sKEPRHLQLFSEF.sTSHVYMSL..................a
GHRKGATKMKD.....fARFKPMQRHLFLYE.......KAVMFCKRRFegadrypsYSFKHCLKMEDV..GITEHVKG............
LHLEGALCWKS......TSGRLKDVLAVLLT.......DVLLLLQEKDqkyvfasvDSKPPVISLQKL..IVREVANE...................
GTRKGYLSKRS.....aDNPKWQTKWFALLQ.......NLLFYFESDS.......sPRPSGLYLLEGS..ICKRAPSP................krg
LIHEGCLLWKT......ATGRFKDVLLLLMT.......DVLVFLQEKD.qkyiftsLDKPSVVSLQNL..IVRDIANQ.......................
PKIDGELKVRS.....iVNHTKQDRYLFLFD.......KVVIVCKRKG......ysYELKEVIELLFH..KMTDDPMH................nkdi
SRIEGWLSVPN..rgniKRYGWKKQYVVVSS.......KKILFYNDEQ....dkeqSNPSMVLDIDKL.fHVRPVTQG................
LIKEGHILKLS.....aKNGTTQDRYLILFN.......DRLLYCVPRL..rllgqkFSVRARIDVDGM..ELKESSNL.......................
LLMQGSFSVWTtkvkelARFKPMQRHLFLHE.......KAVLFCKKREegyekapsYSYKQSLNMTAV..GITENVKG..........
PQGDGEIRITT.....lDKHTKQERHIFLFD.......LAVIVCKRKG......dnYEMKEIIDLQQY..KIANNPTT.....................dke
PKIDGELKITS.....vERRSKTDRYAFLLD.......KALLICKRRG......dsYDLKASVNLHSF..QVRDDSSG.....................
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PEIQGFLQVKE.....vGRKSWKKLYVCLRR.......SGLYYSTKGT....skepRHLQLLADLEES..SIFYLIAG....................
FIMEGPLTRIG......---AKHERHIFLFD.......GLMISCKPNHlpgyssaeYRLKEKFVMRKI..QICDKEDA.......................
LVRDGSVFLKS......TTGRLKEVQAVLLT.......DILVFLQEKDqkyvfaslDHKSTVISLKKL..IVREVAHE......................
FIMEGTLTRVG......---AKHERHIFLFD.......GLMICCKSNHlpgassaeYRLKEKFFMRKV..QINDKDDT......................
LLHDGLVYWKT......ATGRFKDILALLLT.......DVLLFLQEKDqkyifaavDQKPSVISLQKL..IAREVANE......................
EVKSGFLEKRS.....kFLKSYSRGFYVLTP.......SFLHEFKTPD....khkfSTPLMSIPLVEC..TVTEHSKK....................t
ADCSGWMSKKG....tgAMGTWKQRFFTLHG.......TRLSYFTNTN.......dEKERGLIDITAH..RVLPASDD..............drli
IYKEGYLLQDG....gdLKGKIENRFFKLHG.......SQLSGYHEI-........-SRKAKIDINLL..KVTKVLRN.........ediqadnggq
VKMSGNLNIRT......KLIRSTRYWCVLKN.......HLFSMYTSST......elYFPVLTIDLREV.qKIETQKHT......................l
SAKQGLLLAFSsdlqvvGKSGWHKYWVVLDH.......GKICEYANWK.....qslELHTEPIDLLMA..TVRPAQSV...............
IFKEGLLLVFGtdlamvSKAAWHKHWIVVEN.......GSLWEYANWK.....dsvKSNVSSISLKHA..SADKVRKQ.............
ISKIGTLNVYSfrffssLFRKRKPRTFILTN.....fgRYLCVASDGE......grKTVKEEIPIKSV..GMRCRMVK.......................
YIKQGILKFQSeshkfrKKEVWSTVLAVLQR.......DVFTLYNLNTsydpkdldISKVGKPVIKTT..IIASLAKP..............fpss
AQKEGVLLKYI......ENSGLVSRYFYLKD.......NILYFAENRN........SPVLGTIHLKDA..QVNRYNAN.........lpifsiidpph
VLKSGWLIKKG.....hATSTKKQLWAVLRR.......DQLSFYKDE-........---------KDI.sAVAYYKEK..........................-SP
LLCDGYLCQQG.....gDCPYWRRRYFQLIG.......SKLVAFQQFS........KVRRATIDLSEA.tHIVDDNHY................sde
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cldkPRPNMFIVRClQW............................ttvIERTFYADSADFRQMWIEAIQAVSS
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.........SRPFMFEIFSISD............gqikackteqdgrlvegrhSIYKICAVNDEDMRSWINAISRMMA
...........--TSCIVISGqSQ...............................-TFHVKPQNEMDRQQWTNSLEYMRH
RyNT............................glsRELVLMAPQTDNCNKWVSQLRRFIE
....empvdcddsmRANNVLMIKMpRR...............................-CLYILAPSQPSARRWAECLQTAQR
.....SKPHCFELFAtGG...........adiikacktdsegkvvegkhTVYRMSAATEEDQQEWIKRLTQSIS
................-KPFTFIIRGlQW............................ttvIERTFAVESELERQQWTEAIRNVSS
...geggdpfaPDGYPFQVGYcEIsasanshqlengngggsgvgiegqqsgravpqYTLYVIANSEKERSEWIRAIRQVCE
.......dkiYRKFAFKCEHqNM...............................RTYWLAADNSEAMMQWVRALAAASL
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.....lwERPYCFQIVErAL...........................pclaTVTYLCAPSQESYVEWINSLKAQCD
.....KKPFCLELYNpSC...........rgqkikacktdgdgrvvegkhESYRISATSAEERDQWIESIRASIT
...cafkspNPRLTFCVKTyER...............................-LFYMVAPSPEAMRIWMDVIVTAAD
nankspNPLLTFSVKThDR...............................-IYYMVAPSPEAMRIWMDVIVTGAE
...........sfvrkefQNNFVFIVKTtSR...............................-TFYLVAKTEQEMQVWVHSISQVCN
.........-KARRIDLDTeEH...............................-IYHLKVKSQDWFDAWVSKLRHHRL
.........dGKRCMFCVKTaNR...............................-TYEMSASDTRQRQEWTAAIQMAIR
.lfGRPNCFQIVVqHF...........................seehYIFYFAGETPEQAEDWMKGLQAFCN
..tmgapktvDEKAFFDVKTtRR...............................-VYNFCAQDVPSAQQWVDRIQSCLS
...........--SQTFQLISeKK...............................-TYYLTADSPSLLEEWIRVLQSLLK
............-DSCLFFIKCfDD.............................tiHGFRVPKNSLQSREDWLEAIEEHSA
....peeAGKFVFEIIPaSW.........................dqnrmgqDSYVLMASSQAEMEEWVKFLRRVAG
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.....RKPNCFELYNpSH...........kgqvikackteadgrvvegnhVVYRISAPSPEEKEEWMKSIKASIS
.....RKPNCFELYIpNN...........kgqlikackteadgrvvegnhMVYRISAPTQEEKDEWIKSIQAAVS
...........-RPNTFIIRClQW............................ttvIERTFHVETPEEREEWATAIQTVAD
..........-KPNTFIIRClQW............................ttvIERTFHVDTPEEREEWTEAIQAVAD
..........-RPNTFVIRClQW............................ttvIERTFHVDSPDEREEWMRAIQMVAN
saakspNPALTFCVKThDR...............................-LYYMVAPSAEAMRIWMDVIVTGAE
...sfRMKNMFQVIQpER...............................-ALYIQANNCVEAKDWIDILTKVSQ
vipcQNKFPFQVVHdAN...............................-TLYIFAPSPQSRDRWVKKLKEEIK
....sfNKKNMFQVIHtEK...............................-TLYIQANNCVEANEWIDVLCRVSR
.........nkkefENSYIFDINTiDR...............................-IFYLVADSEEDMNKWVRCICDICG
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...........nkkelQDSFVFDIKTsER...............................-TFYLVAETEADMNKWVQSICQICG
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....dimMRDNLFEIVTtSR...............................-TFYVQADSPEEMHSWIKAVSGAIV
....ttsNNVFPFKIIHiSK.............................khRTWFFSASSEDERKSWMALLRREIG
...vkKSSKCIDLDTeEH...............................-IYHLKVKSEELFDEWVSKLRHHRM
..yeNRPLLIKLKTrTS...............................TEYFLEACSREERDSWAFEITGAIH
ysqERVNCFCLVFpFR...............................-TFYLCAKTGVEADEWIKILRWKLS
.gdllMRDNLFEIITtSR...............................-TFYVQADSPEDMHSWIEGIGAAVQ
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.......--AQRIDLDTeDN...............................-IYHLKIKSQDLFHSWVAQLRAHRL
..---KTFFVHTpNR...............................-TYYLMDPSG-NAHKWCRKIQEVWR
...........-KENGIDIILaDR...............................-TFHLIAESPEDASQWFSVLSQVHS
....fgKRMFVLKITTtKQ...............................QDHFFQAAFLEERDAWVRDIKKAIK
............RKKYAFKACHpKI...............................KSFYFAAEHLDDMNRWLNRINMLTA
.....nSESKVFQLLHkGM...............................VFYVFKADDAHSTQRWIDAFQEGTV
...........NWKKRWFVLRqSK...............................-LMYFENDSE-------EKLKGTVE
........-HQHCLAFSSsGP.............................qsQTYYICFDTFTEYLRWLRQVSKVAS
..hdvkksDEENLFEIITaDE...............................VHYYLQAATSKERTEWIKAIQVASR
...dhiNRKYAFKAAHpNM...............................RTYYFCTDTGKEMELWMKAMLDAAL
.............GKPFVFNCMPqSG..............................sRILCLCATSNQEMKRWLEAMQRAAR
diqppdgkPRDCLLQIVCrDG...............................KTISLCAESTDDCLAWKFTLQDSRT
......dGKKCLFLIKCfDK...............................-TFEISASDKKKKQEWIQAIYSTIH
.........ksrskKNHSKFTLARcRQ..........................pgttaPNLIFLAVSPEEKESWINALSSAIT
...........KNKHLVALYTrDE...............................-HFAIAADSEAEQDSWYQALLQLHN
..........ifKETGYWNVTVyGR..............................kHCYRLYTKLLNEATRWSSAIQNVTD
...gafQLPHVMQVVTqDG...........................agtsHTTYLQCKNVNDLNQWLSALRKASA
....dthGFEHTFEVYTeGE...............................RLYLFGLESAEQAHEWVKCIAKAFV
..NVNNSFTVITpCR...............................-KLILCADNRKEMEDWIAALKTVQN
........rkdgKKDCCFEICApDK...............................RIYQFTAASPKDAEEWVQQLKFILQ
.......-DNTRMELIIpGE...............................QHFYMKAVNAAERQRWLVALGSSKA
....qdvqppegrSRDGLLTVNLrEG...............................SRLHLCAETRDDAIAWKTALMEANS
.........iDKRFCFDIETnER..............................pGTITLQAPSEANRRLWMEAMDGKEP
......nttDRPHAFQVILaDR...............................PCLELSADSEAEMADWMQHLCQAVS
............tGQKFSLCILTpDK...............................-EHFIRAETKEIISGWLEMLMVYPR
........ERRFCFEVVSpTK...............................-SCMLQADSEKLRQAWVQAVQASIA
........pglegGRAFFNAVKEgD-...............................-TVIFASDDEQDRILWVQAMYRATG
avgaselantakaDVPYILKMEShPH.........................ttcwpgRTLYLLAPSFPDKQRWVTALESVVA
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......------KMKPpTR...............................------------------------
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.......-DECRFDISVnDS...............................-VWYLRAQDPEHRQQWVDAIEQHKT
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..ellrylveefPLEQGFTVVFhGR...............................rPNLDLVANSVEEAQIWMRGLQLLVD
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.........tETRYGVRIDTsHR.............................-SLILKCSSYRQARWWGQEITELAQ
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..........empDRENTFVVKVeGP.............................SEYILETSDALHVKAWVSDIQECLS
....-SDGRFELVFsGK.............................-KLALRASSQDEAEDWLDRVREALQ
....kgspqaGMDLSFATRTgTK..........................qgiETHLFRAEISRDLSHWTRSIVQGCH
...........TKKHAIGIYFnDD.............................TSKTFACESDLEADEWCKVLQMECV
....wGVPHCLTLRGqRQ.............................-SIIVAASSRSEMEKWMEDIQMAID
...........-NPCRFALTSrGP.........................eggiQRYVLQASDPAVSQAWIKQVAQILE
......NAACTFIITGrKR.............................-SLELQTRTEEEKKEWIQVIQATVE
......sGQKFNIKLLIpVA..........................egmNEIWLRCDNEKQYAHWMAACRLASK
.qamvKTPNTFAVCTkHR.............................-GVLLQALNDKDMNDWLYAFNPLLA
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.......rklygmPTDFGFCVKPnKL........................rnghkGLHIFCSEDEQSRTCWLAAFRLFKY
....eNHRNAFEISGsMI.............................ERILVSCTSQQDLHEWVEHLQKQTK
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...dvyraeteEIPKIFQILYaNE.........................gecrKDVEMEPVQQAEKT----NFQNHKG
...NMPRTFLVSGkQR.............................-SLELQARTEEEKKDWVQAINSTLL
..............-DTKKFEIWYnAR............................eEVYIIQAPTPEIKAAWVNEIRKVLT
nkKWSYGFYLIHtQG............................qNGLEFYCKTKDLKKKWLEQFEMALS
rdnkKWSHMFLLIEdQG............................aQGYELFFKTRELKKKWMEQFEMAIS
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....-EKGLFLISMgVK..............................dpEMVEVHASSREERNSWIQIIQDTIN
....sEYKHAFEIILkDG................................NSVIFSAKSAEEKNNWMAALISLQY
.....-ERGMFLISAsSA..............................gpEMYEIHTNSKEERNNWMRRIQQAVE
snseQGKNKFILRTnSN..........................glihrgHNWVFKVDSYDDMIEWFGNIKALSS
islyaaslgKGKYCFKLVPpQP.....................gskkgltftepRVHYFAVENKSEMKAWLSAIIKATI
rnftdwvLFNECFQLVFdDG................................ERITFNAECSEEKSDWYNKLQEVVE
gSATKTFKLYTdES................................-TFKFNADSEFSAKSWVNALKKEQF
............SRKFCFEVITpQT................................-KRTYQATSKAEMHSWIEAIQYSIS
.............GRRFCFEVVTpKL................................-KRLYQATSAEEMDSWIEAICEAAK
...NNEHGWVVETpTK................................-SWSFEDPNG-PASAWVELLDKASS
edavvlksTNSLYFDLETsSQ................................LKLRFAGPSPKDAQGWIDALNYWAA
efltgeNYQSAFVIQEkQT.........................etrtgtaTVHVLLARDVEDQKSWLRAILRQVP
KTFFLYLnEK................................-IIRLIATSNEDAEEWVHVLRSTTG
elegylYFESGFRIIFsNG................................DYIDFYAETVGEKDEWMSTLRQHLG
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Supplementary Table 8, Park et al.
PH-domain constructs expressed in NIH3T3 cells and retested for PDGF-

	Species	Construct	RFC Score	NP_Number
1	Celegans	akt-2-PH	57.5	NP_001024612
2	Celegans	akt-1-PH	47.7	NP_001023647
3	Celegans	sec7-PH	36	NP_498764
4	Drosophila	Btk29A-PH	42.2	NP_723369
5	Drosophila	CG14366-PH	26.9	NP_650310
6	Drosophila	CG5004-PH	18.9	NP_573195
7	Human	OSBPL6-PH	33.1	NP_665682
8	Human	DEF6-PH	18.3	NP_071330
9	Human	RASA1-PH	17.9	NP_002881
10	Human	SBF1-PH	7.7	NP_002963
12	Mouse	Plek-PH	16	NP_062422
13	Mouse	Cnksr2-PH	13	NP_808419
14	Mouse	Fgd6-PH2	8.3	NP_444302
15	Mouse	Myo10-PH2	8.1	NP_062345
17	Mouse	Plekha5-PH	2.3	NP_659169
18	Mouse	2610034M16Rik-PH	2.2	NP_081277
19	S.Cerevisiae	SLM2-PH	14.2	NP_014351
20	S.Cerevisiae	BOI1-PH	5	NP_009468
21	S.Pombe	csx2-PH	3	NP_595897
22	S.Pombe	ksg1-PH	-3.1	NP_588442

induced translocation at 37deg

25 degC	37 degC
T	T
T	T
N	N
T	T
T	T
N	N
T	T
N	N
N	N
T	T
T	T
T	T
T	T
N	N
N	N
N	N
N	N
N	N
N	N
N	N