

Rassf-GFP fusion proteins

Sequence: Translation of Rassf-GFP Range: 1 to 1050

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      10      20      30      40      50      60      70
MWKCHKCGKPVYFAERKQSIGYDWHPECLRCEECGKRLNPGQHAEHKSVPYCHVPCYGFALFGPQLFGHGT

      80      90     100     110     120     130     140
RVESHKSYGVKGAQKPTGAQANGPPLPRDHLESKLVYNQFYDNKSLEIRSREVNRLVLEGALRVYWGV

     150     160     170     180     190     200     210
QGVIIHLKEDDDQRILVRKRNSCRVSKAANESSDKENEASESLAPPTTTTAEVDQLSTDVSLSESMTFDS

     220     230     240     250     260     270     280
CSLNEISELPTTPEDASANTTANSKEQTNGNVCNDDDDTTTTDSSGTLVEAPTASTSCVSSTLPSKLDRL

     290     300     310     320     330     340     350
EKLDWDDIDDLLQVERRHNDKDRIYETMPVKLPSSQSSSSMSKGEELFTGVVPIVELDGDVNGHKFSV

     360     370     380     390     400     410     420
SGEGEGDATYGKLTLLKFICTTGKLPVPWPTLVTTLTLYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIF

     430     440     450     460     470     480     490
FKDDGNYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKANFKTRH

     500     510     520     530     540     550     560
NIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLLEFVTAAGITHGMDELYKA

     570     580     590     600     610     620     630
SSDSSPSKSTSTTTTTTESSTQSASTNTSSTDDFMTATGSLTANTNTQNTTTVSTTETSLDNFETCDDA

     640     650     660     670     680     690     700
TLKPIDFEDFKRSVHQDYVNGANSFTEPNEGTLKRNQPIDPSRIHDSLKLYGENSAMSFSFNCEHALRSI

     710     720     730     740     750     760     770
DPTLINDTMNLRSSVGSPhSAQRQYALQKSGSATVTSRDQKKPYQQGRQLFEKGINRSKSGPSCFVYSDS

     780     790     800     810     820     830     840
DDDDEATLRPQRMATIRRS DIPQRYIQIQMDCYPKENVAAASEGESSRADAPSITSGAAAGDELQTEDL

     850     860     870     880     890     900     910
YTASEGVDGPDGDSAGLHVTE DGVVLRPRPTGASAIKRRSGNRRSRTKLKRRCSINGHYNRETSFFT

     920     930     940     950     960     970     980
PPYGSQMSVWVSSMVTTEVINLVLEKYKVDSSPGNFSLFIVRDNGEQKRLKDDEYPLITRVTLGPHEDEV

     990    1000    1010    1020    1030    1040    1050
ARIFLVDSRKTDEISNEVAQFLNLSLPECRAILERYDQELAREVAKIKERYAELRRRIVSRMESLKVHL*
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Sequence: Translation of Rassf-C.GFP Range: 1 to 1055

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      10      20      30      40      50      60      70
MWKCHKCGKPVYFAERKQSIGYDWHPECLRCEECGKRLNPGQHAEHKSVPYCHVPCYGFALFGPQLFGHGT

      80      90     100     110     120     130     140
RVESHKSYGVKGAQKPTGAQANGPPLPRDHLESKLVYNQFYDNKSLEIRSREVNRLVLEGALRVYWGV

     150     160     170     180     190     200     210
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QGV IHLKEDDDQRILVRKRNSCRVSKAANESSDKENEASESLAPPTTTTAEVDQLSTDVSLSESMTFDS
220 230 240 250 260 270 280
CSLNEISELPTTPEASANTTANSKEQTNGNVCNDDDEDTTTTSSGTLVEAPTASTSCVSSTLPSKLDRL
290 300 310 320 330 340 350
EKLDWDDIDDLLQVERRHNDKDRIYETMPVKLPSSQSSSDSSPSKTSTETTTTTESSTQSASTNTSSTD
360 370 380 390 400 410 420
DFMTATGSLTANTNTQNTTTVSTTETSLDNFETCDDATLKPIDFEDFKRSVHQDYVNGANSFTEPNEGTL
430 440 450 460 470 480 490
KRNQPIDPSRIHDSLKLYGENSAMSFSNCEHALRSIDPTLINDTMNLRSSVGSPPHSAQRQYALQKSGSA
500 510 520 530 540 550 560
TVTSRDQKKPYQGRQLFEKGINRSKSGPSCFVYSDSDDDDEATLRPQRMATIRRS DIPQRYIQIQMDCY
570 580 590 600 610 620 630
PKENVAASEGESSRADAPSITSGAAAGDELDTQTEDLYTASEGVDGPDGDGSAGLHVTEGDVVLRRPPRT
640 650 660 670 680 690 700
GASAIKRRSGNRRSRTKLRRCSSINGHYNRETSFFTPPYGSQMSVWVSSMVTTEVINLVLEKYKVDSS
710 720 730 740 750 760 770
PGNFSLFIVRDNGEQRLKDDEYPLITRVTLGPHEVARIFLVDSRKTDEISNEVAQFLNLSLPECRAIL
780 790 800 810 820 830 840
ERYDQELAREVAKIKERYAELRRRIVSRMESLKVHFS SSSMSKGEELFTGVVPILEVELDGDVNGHKFSVS
850 860 870 880 890 900 910
GEGEGDATYGKLTLLKFICTTGKLPVPWPTLVTTLYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFF
920 930 940 950 960 970 980
KDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKANFKTRHN
990 1000 1010 1020 1030 1040 1050
IEDGGVQLADHYQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDHMLLEFVTAAGITHGMDELYKAL

KVHL*