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      10          20          30          40          50
TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

      60          70          80          90         100
TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     110         120         130         140         150
CCCAACGACC CCCGCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     160         170         180         190         200
AACGCCAATA GGGACTTTC ATTGACGTCA ATGGGTGGAG TATTTACGGT
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     210         220         230         240         250
AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCC
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     260         270         280         290         300
CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     310         320         330         340         350
CATGACCTTA TGGGACTTTC CTA CTTGGCA GTACATCTAC GTATTAGTCA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     360         370         380         390         400
TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     410         420         430         440         450
TAGCGGTTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     460         470         480         490         500
TGGGAGTTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     510         520         530         540         550
ACAACCTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     560         570         580         590         600
GTCTATATAA GCAGAGCTGG TTTAGTGAAC CGTCAGATCC GCTAGCGCTA
_____/NOTE=1 TO 612 OF CLONTECH PEGFP-C1_____>

     610         620         630         640         650
CCGGTGCCCA CCATGGTGTC TAAGGGCGAA GAGCTGATTA AGGAGAACAT
_____a____>
_____1 TO 732 OF TSIEN PCDNATAGRFPT_____>

     660         670         680         690         700
GCACATGAAG CTGTACATGG AGGGCACCGT GAACAACCAC CACTTCAAGT
_____1 TO 732 OF TSIEN PCDNATAGRFPT_____b_____>

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710          720          730          740          750
GCACATCCGA GGGCGAAGGC AAGCCCTACG AGGGCACCCA GACCATGAGA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

760          770          780          790          800
ATCAAGGTGG TCGAGGGCGG CCCTCTCCCC TTCGCCTTCG ACATCCTGGC
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

810          820          830          840          850
TACCAGCTTC ATGTACGGCA GCAGAACCTT CATCAACCAC ACCCAGGGCA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

860          870          880          890          900
TCCCCGATTT CTTTAAGCAG TCCTTCCCTG AGGGCTTCAC ATGGGAGAGA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

910          920          930          940          950
GTCACCACAT ACGAAGACGG GGGCGTGCTG ACCGCTACCC AGGACACCAG
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

960          970          980          990          1000
CCTCCAGGAC GGCTGCCTCA TCTACAACGT CAAGATCAGA GGGGTGAACT
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1010         1020         1030         1040         1050
TCCCATCCAA CGGCCCTGTG ATGCAGAAGA AAACACTCGG CTGGGAGGCC
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1060         1070         1080         1090         1100
AACACCGAGA TGCTGTACCC CGCTGACGGC GGCCTGGAAG GCAGAACCGA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1110         1120         1130         1140         1150
CATGGCCCTG AAGCTCGTGG GCGGGGGCCA CCTGATCTGC AACTTCAAGA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1160         1170         1180         1190         1200
CCACATACAG ATCCAAGAAA CCCGCTAAGA ACCTCAAGAT GCCCGGCGTC
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1210         1220         1230         1240         1250
TACTATGTGG ACCACAGACT GGAAAGAATC AAGGAGGCCG ACAAAGAGAC
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1260         1270         1280         1290         1300
CTACGTCGAG CAGCACGAGG TGGCTGTGGC CAGATACTGC GACCTCCCTA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1310         1320         1330         1340         1350
GCAAACCTGG GCACAAACTT AATGGCATGG ACGAGCTGTA CAAGACTCGA
_____ 1 TO 732 OF TSIEN PCDNATAGRFPT__b_____ >

1360         1370         1380         1390         1400
GAAATGTTAA GGAGGATTTT ACAGAGGACT CCTGGGAGAG TTGGCTCTCA
_____ c_____/NOTE=EEA1 CLONE NM_003566__c_____ >

1410         1420         1430         1440         1450

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AGGTTCTGAT TTAGATTCAT CAGCAACTCC TATAAACACA GTGGACGTCA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1460      1470      1480      1490      1500
ATAATGAAAG CTCTTCAGAA GGTTCATAT GTCCCCAGTG TATGAAATCT
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1510      1520      1530      1540      1550
CTTGATCTG CTGATGAACT TTTCAAACAT TATGAAGCTG TTCATGATGC
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1560      1570      1580      1590      1600
TGGTAATGAC TCAGGTCATG GAGGAGAGTC TAATCTTGCT TTGAAGCGAG
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1610      1620      1630      1640      1650
ATGATGTAAC ACTGCTCAGA CAAGAGGTCC AAGACCTACA GGCTTCACTT
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1660      1670      1680      1690      1700
AAGGAAGAAA AATGGTACTC GGAAGAATTA AAGAAGGAAT TAGAAAAATA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1710      1720      1730      1740      1750
TCAAGGGCTG CAGCAGCAAG AGGCCAAACC TGATGGGTTG GTGACTGATT
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1760      1770      1780      1790      1800
CATCAGCAGA ACTACAGTCT TTGGAACAGC AATTAGAAGA AGCCCAAACA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1810      1820      1830      1840      1850
GAAAATTTTA ATATTAAGCA AATGAAAGAC TTATTTGAAC AGAAAGCAGC
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1860      1870      1880      1890      1900
CCAACTTGCT ACTGAAATTG CAGATATAAA GTCAAAGTAT GATGAAGAAA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1910      1920      1930      1940      1950
GGAGTCTTCG AGAAGCTGCT GAACAAAAG TGACACGTCT GACAGAAGAA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      1960      1970      1980      1990      2000
TTAAACAAAG AGGCAACTGT AATTCAAGAT CTGAAGACGG AACTGCTTCA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      2010      2020      2030      2040      2050
GAGACCTGGT ATAGAAGATG TTGCCGTGCT AAAGAAAGAA CTGGTCCAAG
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      2060      2070      2080      2090      2100
TTCAAACACT AATGGATAAC ATGACCTTGG AACGTGAGCG AGAATCTGAA
_____c_/NOTE=EEA1 CLONE NM_003566_____c_____>

      2110      2120      2130      2140      2150
AAACTCAAAG ATGAATGCAA AAAATTGCAG TCACAATATG CTAGCTCAGA

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_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2160      2170      2180      2190      2200
GGCCACAATA AGCCAGCTAA GGAGTGA ACT TGCCAAAGGC CCCCAGGAAG
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2210      2220      2230      2240      2250
TTGCTGTATA TGTACAGGAA CTACAAAAAC TGAAAAGTTC AGTTAATGAA
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2260      2270      2280      2290      2300
TTAACACAAA AAAATCAGAC CTTGACAGAA AACTTGCTGA AAAAAGAACA
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2310      2320      2330      2340      2350
AGACTATACT AAGTTAGAGG AGAAACATAA TGAAGAATCT GTGAGTAAAA
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2360      2370      2380      2390      2400
AGAATATTCA GGCAACCCTT CATCAAAAAG ACCTAGATTG TCAACAGCTT
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2410      2420      2430      2440      2450
CAGTCAAGAT TGTCTGCATC TGAAACCTCA CTGCATAGAA TACATGTAGA
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2460      2470      2480      2490      2500
ACTAAGTGAA AAAGGAGAAG CTA CTCAAAA GCTCAAAGAA GAATTATCTG
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2510      2520      2530      2540      2550
AGGTAGAGAC CAAGTACCAG CATCTAAAGG CGGAGTTTAA GCAGCTACAA
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2560      2570      2580      2590      2600
CAACAGAGAG AAGAAAAGGA GCAGCATGGG TTACA ACTCC AAAGTGAAAT
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2610      2620      2630      2640      2650
TAATCAATTA CATAGCAAAC TTCTAGAGAC AGAGCGCCAA CTAGGGGAAG
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2660      2670      2680      2690      2700
CTCATGGTAG GCTGAAGGAA CAGAGACAGC TTTCAAGTGA AAAGTTGATG
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2710      2720      2730      2740      2750
GATAAAGAAC AACAAGTGGC TGATTTACAA CTCAA ACTTT CTCGGTTAGA
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2760      2770      2780      2790      2800
AGAGCAGTTG AAGGAAAAAG TTACAAATTC TACAGAATTG CAGCATCAAT
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>
      2810      2820      2830      2840      2850
TAGATAAAAC AAAGCAACAG CATCAAGAAC AACAGGCTCT TCAGCAAAGC
_____ c ___/NOTE=EEA1 CLONE NM_003566_____ c _____>

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2860      2870      2880      2890      2900
ACCACGGCAA AACTTCGAGA AGCTCAGAAT GATTTGGAAC AAGTTCTACG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

2910      2920      2930      2940      2950
TCAAATTGGC GATAAGGACC AAAAGATCCA GAACCTTGAA GCTTTATTAC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

2960      2970      2980      2990      3000
AGAAGAGTAA AGAAAATATT TCATTACTAG AAAAAGAAAG AGAAGATCTT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3010      3020      3030      3040      3050
TATGCAAAAA TTCAGGCTGG TGAAGGAGAG ACTGCTGTTC TTAACCAGTT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3060      3070      3080      3090      3100
ACAAGAAAAA AACCATACAC TACAGGAGCA AGTAACTCAA CTAACAGAGA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3110      3120      3130      3140      3150
AGCTGAAGAA TCAGTCAGAA AGTCATAAAC AAGCCCAGGA GAATTTGCAT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3160      3170      3180      3190      3200
GACCAGGTAC AAGAGCAGAA GGCACATCTT AGAGCTGCAC AAGACCGTGT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3210      3220      3230      3240      3250
CCTTTCCCTA GAAACTAGTG TCAATGAATT AAATAGTCAA TTAAATGAAA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3260      3270      3280      3290      3300
GCAAGGAGAA GGTCTCCAG CTTGACATAC AGATTAAAGC CAAAACCGAA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3310      3320      3330      3340      3350
CTATTACTAT CAGCAGAAGC AGCAAAAAC TCTCAAAGAG CTGATCTTCA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3360      3370      3380      3390      3400
GAATCATTTG GACACAGCTC AAAATGCATT ACAAGATAAA CAGCAGGAGT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3410      3420      3430      3440      3450
TAAATAAGAT TACTACTCAG TTGGATCAGG TCACTGCAAA GTTACAAGAC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3460      3470      3480      3490      3500
AAGCAAGAAC ATTGCAGTCA GCTGGAAAGT CATCTTAAAG AATATAAAGA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3510      3520      3530      3540      3550
GAAATACCTC TCTTTAGAAC AGAAAACCGA AGAGCTAGAA GGTCAAATTA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
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3560      3570      3580      3590      3600
AGAAACTAGA AGCTGATAGT CTTGAAGTTA AAGCAAGCAA GGAGCAGGCT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3610      3620      3630      3640      3650
TTGCAAGATC TACAACAGCA AAGACAGCTG AACACAGATT TAGAGCTCAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3660      3670      3680      3690      3700
AGCCACAGAA TTGAGTAAAC AACTTGAAAT GGAGAAGGAA ATAGTATCCA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3710      3720      3730      3740      3750
GTACAAGATT GGATCTACAG AAAAAATCTG AAGCCCTTGA AAGTATCAAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3760      3770      3780      3790      3800
CAAAAGCTTA CCAAGCAAGA GGAAGAAAAA CAAATCCTGA AACCAAGATTT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3810      3820      3830      3840      3850
TGAAACTTTA AGTCAAGAAA CAAAGATTCA GCATGAGGAA TTGAATAACA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3860      3870      3880      3890      3900
GAATTCAAAC AACAGTAACA GAACTACAAA AAGTGAAAAT GGAGAAAGAA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3910      3920      3930      3940      3950
GCTTTAATGA CAGAGCTTTC TACAGTAAAG GACAAACTAT CAAAAGTTTC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

3960      3970      3980      3990      4000
TGATTCTTTG AAAAACTCTA AAAGTGAATT TGAAAAGGAG AATCAGAAAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

4010      4020      4030      4040      4050
GAAAAGCCGC TATATTAGAC TTGGAAAAAA CTTGCAAAGA ATTAAAGCAT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

4060      4070      4080      4090      4100
CAACTTCAAG TGCAGATGGA AAACACACTT AAGGAACAGA AGGAACTGAA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

4110      4120      4130      4140      4150
AAAGTCACTT GAAAAAGAGA AGGAGGCTTC TCATCAGTTG AAATTGGAAC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

4160      4170      4180      4190      4200
TCAATTCAAT GCAGGAACAA CTTATACAGG CCCAGAATAC TTTAAAACAA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

4210      4220      4230      4240      4250
AATGAAAAAG AAGAGCAACA ACTTCAGGGG AACATAAATG AGCTAAAGCA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

4260      4270      4280      4290      4300

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ATCAAGTGAA CAGAAGAAAA AACAAATTGA AGCACTCCAA GGAGAGCTTA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4310      4320      4330      4340      4350
AAATTGCTGT TTTACAGAAG ACAGAGCTTG AGAATAAACT ACAGCAGCAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4360      4370      4380      4390      4400
TTAACACAGG CAGCCCAGGA ACTTGCAGCA GAGAAAGAGA AAATATCAGT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4410      4420      4430      4440      4450
ATTACAAAAC AACTATGAAA AAAGTCAGGA AACTTTCAAA CAGCTTCAAT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4460      4470      4480      4490      4500
CTGATTTCTA TGGGAGGGAA TCTGAACTTC TAGCCACCAG GCAAGATCTT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4510      4520      4530      4540      4550
AAGTCTGTAG AAGAGAAGCT TTCTCTAGCA CAGGAGGACT TGATTTCAAA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4560      4570      4580      4590      4600
CAGAAATCAA ATTGGAAATC AAAATAAATT GATTCAAGAA CTGAAGACTG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4610      4620      4630      4640      4650
CCAAGGCTAC ATTGGAGCAG GATTCAGCAA AGAAAGAACA GCAATTGCAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4660      4670      4680      4690      4700
GAGCGATGTA AAGCACTACA AGACATTCAG AAAGAAAAGT CACTGAAAGA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4710      4720      4730      4740      4750
AAAAGAAGTG GTAAATGAGA AGTCTAAATT GGCAGAGATA GAAGAAATTA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4760      4770      4780      4790      4800
AATGTAGACA AGAAAAAGAA ATCACTAAAC TAAACGAAGA ACTCAAGTCC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4810      4820      4830      4840      4850
CACAACTAG AAAGCATAAA GGAGATAACA AATCTTAAAG ATGCTAAACA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4860      4870      4880      4890      4900
GCTTCTAATT CAGCAGAAAT TAGAACTTCA AGGAAAAGCG GACTCCCTGA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4910      4920      4930      4940      4950
AGGCAGCTGT TGAACAGGAG AAGAGAAATC AGCAGATACT AAAAGACCAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>

      4960      4970      4980      4990      5000
GTGAAAAAGG AAGAAGAGGA GCTGAAGAAA GAATTTATTG AGAAAGAAGC

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_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5010      5020      5030      5040      5050
TAAGTTGCAT TCCGAAATAA AAGAAAAGGA AGTAGGAATG AAGAAGCATG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5060      5070      5080      5090      5100
AAGAAAATGA GGCTAAACTT ACCATGCAGA TTACAGCATT AAATGAAAAC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5110      5120      5130      5140      5150
TTAGGCACTG TGAAGAAGGA GTGGCAATCT AGTCAACGGA GAGTTAGTGA
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5160      5170      5180      5190      5200
GCTTGAGAAA CAAACGGATG ACTTACGGGG TGAAATTGCA GTATTAGAAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5210      5220      5230      5240      5250
CAACGGTTCA GAATAATCAA GATGAAAGGA GAGCACTACT GGAAAGATGT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5260      5270      5280      5290      5300
CTTAAAGGAG AAGGTGAAAT AGAAAAGCTT CAAACCAAAG TATTAGAATT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5310      5320      5330      5340      5350
GCAAAGAAAG CTGGATAATA CAACTGCAGC AGTGCAGGAG CTGGGCAGAG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5360      5370      5380      5390      5400
AAAACCAATC ACTTCAGATC AAACATACAC AAGCGTTGAA TAGAAAGTGG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5410      5420      5430      5440      5450
GCCGAAGACA ATGAAGTACA AAACGTATG GCCTGTGGGA AAGGCTTTTC
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5460      5470      5480      5490      5500
AGTAACAGTG AGACGGCATC ACTGCCGACA GTGTGGAAAT ATCTTCTGTG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5510      5520      5530      5540      5550
CTGAATGTTT AGCCAAAAAT GCCTTAACTC CTTCTCCAA GAAGCCTGTT
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5560      5570      5580      5590      5600
CGTGTCTGTG ATGCATGTTT CAATGACTTG CAAGGATAAC TCAAGCTTCG
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
_____c___/NOTE=EEA1 CLONE NM_003566_____c_____>
      5610      5620      5630      5640      5650
AATTCTGCAG TCGACGGTAC CGCGGGCCCG GGATCCACCG GATCTAGATA
_____d___/NOTE=PEGFP-C1_____d_____>
      5660      5670      5680      5690      5700
ACTGATCATA ATCAGCCATA CCACATTTGT AGAGGTTTTA CTTGCTTTAA

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_____d_____/NOTE=PEGFP-C1_____d_____>
5710      5720      5730      5740      5750
AAACCTCCC ACACCTCCC CTGAACCTGA AACATAAAAT GAATGCAATT
_____d_____/NOTE=PEGFP-C1_____d_____>
5760      5770      5780      5790      5800
GTTGTTGTTA ACTTGTTTAT TGCAGCTTAT AATGGTTACA AATAAAGCAA
_____d_____/NOTE=PEGFP-C1_____d_____>
5810      5820      5830      5840      5850
TAGCATCACA AATTTACAAA ATAAAGCATT TTTTTCCTG CATTCTAGTT
_____d_____/NOTE=PEGFP-C1_____d_____>
5860      5870      5880      5890      5900
GTGGTTTGTC CAAACTCATC AATGTATCTT AACGCGTAAA TTGTAAGCGT
_____d_____/NOTE=PEGFP-C1_____d_____>
5910      5920      5930      5940      5950
TAATATTTTG TTAAAATTCG CGTTAAATTT TTGTTAAATC AGCTCATTTT
_____d_____/NOTE=PEGFP-C1_____d_____>
5960      5970      5980      5990      6000
TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC AAAAGAATAG
_____d_____/NOTE=PEGFP-C1_____d_____>
6010      6020      6030      6040      6050
ACCGAGATAG GGTTGAGTGT TGTTCCAGTT TGGAACAAGA GTCCACTATT
_____d_____/NOTE=PEGFP-C1_____d_____>
6060      6070      6080      6090      6100
AAAGAACGTG GACTCCAACG TCAAAGGGCG AAAAACCGTC TATCAGGGCG
_____d_____/NOTE=PEGFP-C1_____d_____>
6110      6120      6130      6140      6150
ATGGCCCACT ACGTGAACCA TCACCCTAAT CAAGTTTTTTT GGGGTCGAGG
_____d_____/NOTE=PEGFP-C1_____d_____>
6160      6170      6180      6190      6200
TGCCGTAAAG CACTAAATCG GAACCCTAAA GGGAGCCCCC GATTTAGAGC
_____d_____/NOTE=PEGFP-C1_____d_____>
6210      6220      6230      6240      6250
TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG AAGAAAGCGA
_____d_____/NOTE=PEGFP-C1_____d_____>
6260      6270      6280      6290      6300
AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA
_____d_____/NOTE=PEGFP-C1_____d_____>
6310      6320      6330      6340      6350
ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG CGTCAGGTGG
_____d_____/NOTE=PEGFP-C1_____d_____>
6360      6370      6380      6390      6400
CACTTTTTCGG GGAAATGTGC GCGGAACCCC TATTTGTTTA TTTTCTAAA
_____d_____/NOTE=PEGFP-C1_____d_____>
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        6410          6420          6430          6440          6450
TACATTCAAA TATGTATCCG CTCATGAGAC AATAACCCTG ATAAATGCTT
_____d_____/NOTE=PEGFP-C1_____d_____>

        6460          6470          6480          6490          6500
CAATAATATT GAAAAAGGAA GAGTCCTGAG GCGGAAAGAA CCAGCTGTGG
_____d_____/NOTE=PEGFP-C1_____d_____>

        6510          6520          6530          6540          6550
AATGTGTGTC AGTTAGGGTG TGGAAAGTCC CCAGGCTCCC CAGCAGGCAG
_____d_____/NOTE=PEGFP-C1_____d_____>

        6560          6570          6580          6590          6600
AAGTATGCAA AGCATGCATC TCAATTAGTC AGCAACCAGG TGTGGAAAGT
_____d_____/NOTE=PEGFP-C1_____d_____>

        6610          6620          6630          6640          6650
CCCCAGGCTC CCCAGCAGGC AGAAGTATGC AAAGCATGCA TCTCAATTAG
_____d_____/NOTE=PEGFP-C1_____d_____>

        6660          6670          6680          6690          6700
TCAGCAACCA TAGTCCC GCC TA ACTCCG CCCATCCC GC CCCTAACTCC
_____d_____/NOTE=PEGFP-C1_____d_____>

        6710          6720          6730          6740          6750
GCCCAGTTCC GCCCATTCTC CGCCCCATGG CTGACTAATT TTTTTTATTT
_____d_____/NOTE=PEGFP-C1_____d_____>

        6760          6770          6780          6790          6800
ATGCAGAGGC CGAGGCCGCC TCGGCCTCTG AGCTATTCCA GAAGTAGTGA
_____d_____/NOTE=PEGFP-C1_____d_____>

        6810          6820          6830          6840          6850
GGAGGCTTTT TTGGAGGCCT AGGCTTTTGC AAAGATCGAT CAAGAGACAG
_____d_____/NOTE=PEGFP-C1_____d_____>

        6860          6870          6880          6890          6900
GATGAGGATC GTTTCGCATG ATTGAACAAG ATGGATTGCA CGCAGGTTCT
_____d_____/NOTE=PEGFP-C1_____d_____>

        6910          6920          6930          6940          6950
CCGGCCGCTT GGGTGGAGAG GCTATTCGGC TATGACTGGG CACAACAGAC
_____d_____/NOTE=PEGFP-C1_____d_____>

        6960          6970          6980          6990          7000
AATCGGCTGC TCTGATGCCG CCGTGTTCCG GCTGTCAGCG CAGGGGCGCC
_____d_____/NOTE=PEGFP-C1_____d_____>

        7010          7020          7030          7040          7050
CGGTTCTTTT TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAAGTCAA
_____d_____/NOTE=PEGFP-C1_____d_____>

        7060          7070          7080          7090          7100
GACGAGGCAG CGCGGCTATC GTGGCTGGCC ACGACGGGCG TTCCTTGCGC
_____d_____/NOTE=PEGFP-C1_____d_____>

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7110      7120      7130      7140      7150
AGCTGTGCTC GACGTTGTCA CTGAAGCGGG AAGGGACTGG CTGCTATTGG
_____d_____/NOTE=PEGFP-C1_____d_____>

7160      7170      7180      7190      7200
GCGAAGTGCC GGGGCAGGAT CTCCTGTTCAT CTCACCTTGC TCCTGCCGAG
_____d_____/NOTE=PEGFP-C1_____d_____>

7210      7220      7230      7240      7250
AAAGTATCCA TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC
_____d_____/NOTE=PEGFP-C1_____d_____>

7260      7270      7280      7290      7300
GGCTACCTGC CCATTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC
_____d_____/NOTE=PEGFP-C1_____d_____>

7310      7320      7330      7340      7350
GTACTCGGAT GGAAGCCGGT CTTGTTCGATC AGGATGATCT GGACGAAGAG
_____d_____/NOTE=PEGFP-C1_____d_____>

7360      7370      7380      7390      7400
CATCAGGGGC TCGCGCCAGC CGAACTGTTC GCCAGGCTCA AGGCGAGCAT
_____d_____/NOTE=PEGFP-C1_____d_____>

7410      7420      7430      7440      7450
GCCCCGACGGC GAGGATCTCG TCGTGACCCA TGGCGATGCC TGCTTGCCGA
_____d_____/NOTE=PEGFP-C1_____d_____>

7460      7470      7480      7490      7500
ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTCATCGA CTGTGGCCGG
_____d_____/NOTE=PEGFP-C1_____d_____>

7510      7520      7530      7540      7550
CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT
_____d_____/NOTE=PEGFP-C1_____d_____>

7560      7570      7580      7590      7600
TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG
_____d_____/NOTE=PEGFP-C1_____d_____>

7610      7620      7630      7640      7650
GTATCGCCGC TCCCGATTTCG CAGCGCATCG CCTTCTATCG CCTTCTTGAC
_____d_____/NOTE=PEGFP-C1_____d_____>

7660      7670      7680      7690      7700
GAGTTCTTCT GAGCGGGACT CTGGGGTTCG AAATGACCGA CCAAGCGACG
_____d_____/NOTE=PEGFP-C1_____d_____>

7710      7720      7730      7740      7750
CCCAACCTGC CATCACGAGA TTTCGATTCC ACCGCCGCCT TCTATGAAAG
_____d_____/NOTE=PEGFP-C1_____d_____>

7760      7770      7780      7790      7800
GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG ATCCTCCAGC
_____d_____/NOTE=PEGFP-C1_____d_____>

7810      7820      7830      7840      7850

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GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCTAGGGG GAGGCTAACT
_____d_____/NOTE=PEGFP-C1_____d_____>

7860      7870      7880      7890      7900
GAAACACGGA AGGAGACAAT ACCGGAAGGA ACCCGCGCTA TGACGGCAAT
_____d_____/NOTE=PEGFP-C1_____d_____>

7910      7920      7930      7940      7950
AAAAAGACAG AATAAACGC  ACGGTGTTGG GTCGTTTGTG CATAAACGCG
_____d_____/NOTE=PEGFP-C1_____d_____>

7960      7970      7980      7990      8000
GGGTTCCGGT CCAGGGCTGG CACTCTGTCG ATACCCACC  GAGACCCCAT
_____d_____/NOTE=PEGFP-C1_____d_____>

8010      8020      8030      8040      8050
TGGGGCCAAT ACGCCCGCGT TTCTTCCTTT TCCCCACCCC ACCCCCCAAG
_____d_____/NOTE=PEGFP-C1_____d_____>

8060      8070      8080      8090      8100
TTCGGGTGAA GGCCAGGGC  TCGCAGCCAA CGTCGGGGCG GCAGGCCCTG
_____d_____/NOTE=PEGFP-C1_____d_____>

8110      8120      8130      8140      8150
CCATAGCCTC AGGTTACTCA TATATACTTT AGATTGATTT AAAACTTCAT
_____d_____/NOTE=PEGFP-C1_____d_____>

8160      8170      8180      8190      8200
TTTTAATTTA AAAGGATCTA GGTGAAGATC CTTTTTGATA ATCTCATGAC
_____d_____/NOTE=PEGFP-C1_____d_____>

8210      8220      8230      8240      8250
CAAAATCCCT TAACGTGAGT TTTCGTTCCA CTGAGCGTCA GACCCCGTAG
_____d_____/NOTE=PEGFP-C1_____d_____>

8260      8270      8280      8290      8300
AAAAGATCAA AGGATCTTCT TGAGATCCTT TTTTTCTGCG CGTAATCTGC
_____d_____/NOTE=PEGFP-C1_____d_____>

8310      8320      8330      8340      8350
TGCTTGCAAA CAAAAAACC  ACCGCTACCA GCGGTGGTTT GTTTGCCGGA
_____d_____/NOTE=PEGFP-C1_____d_____>

8360      8370      8380      8390      8400
TCAAGAGCTA CCAACTCTTT TTCCGAAGGT AACTGGCTTC AGCAGAGCGC
_____d_____/NOTE=PEGFP-C1_____d_____>

8410      8420      8430      8440      8450
AGATACAAA  TACTGTCCTT CTAGTGTAGC CGTAGTTAGG CCACCACTTC
_____d_____/NOTE=PEGFP-C1_____d_____>

8460      8470      8480      8490      8500
AAGAACTCTG TAGCACCGCC TACATACCTC GCTCTGCTAA TCCTGTTACC
_____d_____/NOTE=PEGFP-C1_____d_____>

8510      8520      8530      8540      8550
AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG TCTTACCGGG TTGGACTCAA

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_____d_____/NOTE=PEGFP-C1_____d_____>
      8560      8570      8580      8590      8600
GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGGCTGAAC GGGGGGTTTCG
_____d_____/NOTE=PEGFP-C1_____d_____>
      8610      8620      8630      8640      8650
TGCACACAGC CCAGCTTGGA GCGAACGACC TACACCGAAC TGAGATACCT
_____d_____/NOTE=PEGFP-C1_____d_____>
      8660      8670      8680      8690      8700
ACAGCGTGAG CTATGAGAAA GCGCCACGCT TCCCGAAGGG AGAAAGGCGG
_____d_____/NOTE=PEGFP-C1_____d_____>
      8710      8720      8730      8740      8750
ACAGGTATCC GGTAAGCGGC AGGGTCGGAA CAGGAGAGCG CACGAGGGAG
_____d_____/NOTE=PEGFP-C1_____d_____>
      8760      8770      8780      8790      8800
CTTCCAGGGG GAAACGCCTG GTATCTTTAT AGTCCTGTCTG GGTTCGCCA
_____d_____/NOTE=PEGFP-C1_____d_____>
      8810      8820      8830      8840      8850
CCTCTGACTT GAGCGTCGAT TTTTGTGATG CTCGTCAGGG GGGCGGAGCC
_____d_____/NOTE=PEGFP-C1_____d_____>
      8860      8870      8880      8890      8900
TATGGAAAAA CGCCAGCAAC GCGGCCTTTT TACGGTTCCT GGCCTTTTGC
_____d_____/NOTE=PEGFP-C1_____d_____>
      8910      8920      8930      8940      8950
TGGCCTTTTG CTCACATGTT CTTTCCTGCG TTATCCCCTG ATTCTGTGGA
_____d_____/NOTE=PEGFP-C1_____d_____>
      8960      8970
TAACCGTATT ACCGCCATGC AT
_____/NOTE=PEGFP-C1___d___>

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