

Unigene20083_All (DNA-binding protein DF1)

	10	20	30	40	50	60	70
Peu_1	AACCCTACAA	ATCCTCCTCA	TACTAATATT	TCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Peu_2	AACCCTACAA	ATCCTCCTCA	TACTAATATT	TCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Peu_3	AACCCTACAA	ATCCTCCTCA	TACTAATATT	TCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Peu_4	AACCCTACAA	ATCCTCCTCA	TACTAATATT	TCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Peu_5	AACCCTACAA	ATCCTCCTCA	TACTAATATT	TCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Ppr_1	AACCCTACAA	ATCCTCCTCA	TACTAATATT	CCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Ppr_2	AACCCTACAA	ATCCTCCTCA	TACTAATATT	CCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Ppr_3	AACCCTACAA	ATCCTCCTCA	TACTAATATT	CCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Ppr_4	AACCCTACAA	ATCCTCCTCA	TACTAATATT	CCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA
Ppr_5	AACCCTACAA	ATCCTCCTCA	TACTAATATT	CCACCCTCTT	TTCCAAACTT	CTCCTCAGAT	CTCATCTCCA

	80	90	100	110	120	130	140
Peu_1	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Peu_2	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Peu_3	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Peu_4	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Peu_5	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Ppr_1	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Ppr_2	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Ppr_3	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Ppr_4	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA
Ppr_5	ATTCCACTTC	TTCATCGACA	TCCTCGGACG	TGGAACTGCA	AGAGCGTTGC	AAGAGGAAAA	GGAAATGGAA

	150	160	170	180	190	200	210
Peu_1	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Peu_2	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Peu_3	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Peu_4	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Peu_5	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Ppr_1	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Ppr_2	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Ppr_3	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Ppr_4	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA
Ppr_5	GGACTTCTTT	GAAAGGCTCA	TGAAGGAGGT	GATCCAGAAG	CAAGAGGAGA	TGCAGAAGAA	GTTCTTGGAA

	220	230	240	250	260	270	280
Peu_1	GCAATTGAGA	GACTCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AATGCAGGAA	ATGACAAGAA
Peu_2	GCAATTGAGA	GACTCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AATGCAGGAA	ATGACAAGAA
Peu_3	GCAATTGAGA	GACTCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AATGCAGGAA	ATGACAAGAA
Peu_4	GCAATTGAGA	GACTCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AATGCAGGAA	ATGACAAGAA
Peu_5	GCAATTGAGA	GACTCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AATGCAGGAA	ATGACAAGAA
Ppr_1	GCAATTGAGA	GACGCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AACGCAGGAA	ATGACAAGAA
Ppr_2	GCAATTGAGA	GACGCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AACGCAGGAA	ATGACAAGAA
Ppr_3	GCAATTGAGA	GACGCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AACGCAGGAA	ATGACAAGAA
Ppr_4	GCAATTGAGA	GACGCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AACGCAGGAA	ATGACAAGAA
Ppr_5	GCAATTGAGA	GACGCGAACA	TGAAAGAATG	GTTAGAGAAG	AATCTTGGAG	AACGCAGGAA	ATGACAAGAA

	290	300	310	320	330	340	350
Peu_1	TCAATAGAGA	GAGCGAGATC	TTAGCCCAAG	AAAGATCCGT	TGCGGCAAGT	AAAAATGCTG	AGGTAATGGC
Peu_2	TCAATAGAGA	GAGCGAGATC	TTAGCCCAAG	AAAGATCCGT	TGCGGCAAGT	AAAAATGCTG	AGGTAATGGC
Peu_3	TCAATAGAGA	GAGCGAGATC	TTAGCCCAAG	AAAGATCCGT	TGCGGCAAGT	AAAAATGCTG	AGGTAATGGC
Peu_4	TCAATAGAGA	GAGCGAGATC	TTAGCCCAAG	AAAGATCCGT	TGCGGCAAGT	AAAAATGCTG	AGGTAATGGC
Peu_5	TCAATAGAGA	GAGCGAGATC	TTAGCCCAAG	AAAGATCCGT	TGCGGCAAGT	AAAAATGCTG	AGGTAATGGC
Ppr_1	TCAATAGAGA	GCGCGAGATC	TTAGCCCAAG	AAAGATCCGC	TGCGACAAGT	ATAGATGCTG	CGGTAATGGC
Ppr_2	TCAATAGAGA	GCGCGAGATC	TTAGCCCAAG	AAAGATCCGC	TGCGACAAGT	ATAGATGCTG	CGGTAATGGC
Ppr_3	TCAATAGAGA	GCGCGAGATC	TTAGCCCAAG	AAAGATCCGC	TGCGACAAGT	ATAGATGCTG	CGGTAATGGC
Ppr_4	TCAATAGAGA	GCGCGAGATC	TTAGCCCAAG	AAAGATCCGC	TGCGACAAGT	ATAGATGCTG	CGGTAATGGC
Ppr_5	TCAATAGAGA	GCGCGAGATC	TTAGCCCAAG	AAAGATCCGC	TGCGACAAGT	ATAGATGCTG	CGGTAATGGC

	360	370	380	390	400	...

Peu_1	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGGTCAA	ATACAAAATA	ATC
Peu_2	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGGTCAA	ATACAAAATA	ATC
Peu_3	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGGTCAA	ATACAAAATA	ATC
Peu_4	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGGTCAA	ATACAAAATA	ATC
Peu_5	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGGTCAA	ATACAAAATA	ATC
Ppr_1	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGTTCAA	ATACAAAATA	ATC
Ppr_2	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGTTCAA	ATACAAAATA	ATC
Ppr_3	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGTTCAA	ATACAAAATA	ATC
Ppr_4	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGTTCAA	ATACAAAATA	ATC
Ppr_5	ATTTTTGCAA	AAATTATCCG	AAGAGCAACA	TCCGGTTCAA	ATACAAAATA	ATC

Unigene26469_All (pentatricopeptide (PPR) repeat-containing protein)

	10	20	30	40	50	60	70
Peu_1	TTGTCC-ACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Peu_2	TTGTCC-ACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Peu_3	TTGTCC-ACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Peu_4	TTGTCC-ACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Peu_5	TTGTCC-ACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Ppr_1	TTGTCCGACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Ppr_2	TTGTCCGACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Ppr_3	TTGTCCGACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Ppr_4	TTGTCCGACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC
Ppr_5	TTGTCCGACC	CACTACACCT	TTGGGAACCT	GCTGAATGCC	TCTGCAAATC	TTGCTGATCT	GAAGCTTGGC

	80	90	100	110	120	130	140
Peu_1	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Peu_2	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Peu_3	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Peu_4	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Peu_5	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Ppr_1	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Ppr_2	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Ppr_3	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Ppr_4	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG
Ppr_5	AGGCAGGCAC	ATAGTCATGT	TGTTAAGCAT	GGATTTAGGT	TCCAGTCTGG	TGAAGAGCCT	GATATTTTTG

	150	160	170	180	190	200	210
Peu_1	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Peu_2	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Peu_3	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Peu_4	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Peu_5	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Ppr_1	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Ppr_2	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Ppr_3	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Ppr_4	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA
Ppr_5	TGGGAAATTC	TCTCATAGAC	ATGTATATGA	AATGTGGATC	TGTTGAAGAG	GGACTTCGGG	TTTTTGAAAA

	220	230	240	250	260	270	280
Peu_1	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CMCAAAATGG	CTACGGAATG
Peu_2	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CMCAAAATGG	CTACGGAATG
Peu_3	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CMCAAAATGG	CTACGGAATG
Peu_4	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CMCAAAATGG	CTACGGAATG
Peu_5	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CMCAAAATGG	CTACGGAATG
Ppr_1	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CACAAAATGG	CTTCGGAATG
Ppr_2	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CACAAAATGG	CTTCGGAATG
Ppr_3	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CACAAAATGG	CTTCGGAATG
Ppr_4	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CACAAAATGG	CTTCGGAATG
Ppr_5	CATGGTGGAA	AAGGATCATG	TATCATGGAA	CACCATGATA	ATAGGTTATG	CACAAAATGG	CTTCGGAATG

	290	300	310	320	330	340	350
Peu_1	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Peu_2	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Peu_3	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Peu_4	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Peu_5	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Ppr_1	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Ppr_2	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Ppr_3	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Ppr_4	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA
Ppr_5	GAGGCCCTTG	AACTATTTCA	GAAAATGCTG	GAATCTGGAG	AGAAACCAGA	CCATGTTACA	ATGATTGGTA

	360	370	380	390	400	410	420

Peu_1	CTCTATGTGC	TTGTAGCCAC	GCAGGGCTTG	TTGAAGAGGG	ACGRCATTAC	TTTCTCTCAA	TGACTAAGGA
Peu_2	CTCTATGTGC	TTGTAGCCAC	GCAGGGCTTG	TTGAAGAGGG	ACGRCATTAC	TTTCTCTCAA	TGACTAAGGA
Peu_3	CTCTATGTGC	TTGTAGCCAC	GCAGGGCTTG	TTGAAGAGGG	ACGRCATTAC	TTTCTCTCAA	TGACTAAGGA
Peu_4	CTCTATGTGC	TTGTAGCCAC	GCAGGGCTTG	TTGAAGAGGG	ACGRCATTAC	TTTCTCTCAA	TGACTAAGGA
Peu_5	CTCTATGTGC	TTGTAGCCAC	GCAGGGCTTG	TTGAAGAGGG	ACGRCATTAC	TTTCTCTCAA	TGACTAAGGA
Ppr_1	CTCTATGTGC	TTGTAGCCAT	GCAGGGCTTG	TTGAAGAGGG	ACGGCATTAC	TTTTTCTCAA	TGACTAAGGA
Ppr_2	CTCTATGTGC	TTGTAGCCAT	GCAGGGCTTG	TTGAAGAGGG	ACGGCATTAC	TTTTTCTCAA	TGACTAAGGA
Ppr_3	CTCTATGTGC	TTGTAGCCAT	GCAGGGCTTG	TTGAAGAGGG	ACGGCATTAC	TTTTTCTCAA	TGACTAAGGA
Ppr_4	CTCTATGTGC	TTGTAGCCAT	GCAGGGCTTG	TTGAAGAGGG	ACGGCATTAC	TTTTTCTCAA	TGACTAAGGA
Ppr_5	CTCTATGTGC	TTGTAGCCAT	GCAGGGCTTG	TTGAAGAGGG	ACGGCATTAC	TTTTTCTCAA	TGACTAAGGA

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 430 440 450 460 470 480 490

Peu_1	ACATGGTTTG	CTACCAAGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Peu_2	ACATGGTTTG	CTACCAAGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Peu_3	ACATGGTTTG	CTACCAAGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Peu_4	ACATGGTTTG	CTACCAAGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Peu_5	ACATGGTTTG	CTACCAAGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Ppr_1	ACATGGTTTG	CTACCGGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Ppr_2	ACATGGTTTG	CTACCGGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Ppr_3	ACATGGTTTG	CTACCGGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Ppr_4	ACATGGTTTG	CTACCGGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT
Ppr_5	ACATGGTTTG	CTACCGGTGA	AGGACCATTA	TACATGTATG	GTTGATTTAC	TAGGCCGAGC	TGGTTGCCTT

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 500 510

Peu_1	GAGGAAGCAA	RGGATTTGAT
Peu_2	GAGGAAGCAA	RGGATTTGAT
Peu_3	GAGGAAGCAA	RGGATTTGAT
Peu_4	GAGGAAGCAA	RGGATTTGAT
Peu_5	GAGGAAGCAA	RGGATTTGAT
Ppr_1	GAGGAAGCAA	AGGATTTGAT
Ppr_2	GAGGAAGCAA	AGGATTTGAT
Ppr_3	GAGGAAGCAA	AGGATTTGAT
Ppr_4	GAGGAAGCAA	AGGATTTGAT
Ppr_5	GAGGAAGCAA	AGGATTTGAT

Unigene2702_All (UDP-glucuronosyl/UDP-glucosyl transferase family protein)

	10	20	30	40	50	60	70		
Peu_1	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Peu_2	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Peu_3	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Peu_4	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Peu_5	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Ppr_1	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Ppr_2	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Ppr_3	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		
Ppr_4	TATTCCACAT	CAAATGTTGA	TATTCTTCCT	CTTAGTCAGG	GCGAACATCC	TCAAAAGAAA	TCTTCCAGTG		

	80	90	100	110	120	130	140		
Peu_1	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Peu_2	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Peu_3	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Peu_4	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Peu_5	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Ppr_1	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Ppr_2	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Ppr_3	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		
Ppr_4	GACAGAGCAG	TGCAGATGAA	TTGTATCCAT	CTGATCATGC	TGCAGCCTTC	CTTTCCTTAA	TGAAAAGCAG		

	150	160	170	180	190	200	210		
Peu_1	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Peu_2	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Peu_3	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Peu_4	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Peu_5	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Ppr_1	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Ppr_2	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Ppr_3	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		
Ppr_4	CGGAACACTG	GATGTATTAT	TATCACAGGG	AAAGGAGTAC	GTACATGTGG	TGAGCTCCGA	TAATGTAGCT		

	220	230	240	250	260	270	280		
Peu_1	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Peu_2	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Peu_3	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Peu_4	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Peu_5	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Ppr_1	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Ppr_2	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Ppr_3	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		
Ppr_4	GCAGCTGTTG	ATCCAAGAAT	CATGAGTCAT	TTGAGCCAAA	ACAATATTGA	ATACTGTATG	GAGGTGACAC		

	290	300	310	320	330	340	350		
Peu_1	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAGTCA	GCAGCAAGGA	AAGTTTGAGC	TTGCAGAAAT		
Peu_2	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAGTCA	GCAGCAAGGA	AAGTTTGAGC	TTGCAGAAAT		
Peu_3	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAGTCA	GCAGCAAGGA	AAGTTTGAGC	TTGCAGAAAT		
Peu_4	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAGTCA	GCAGCAAGGA	AAGTTTGAGC	TTGCAGAAAT		
Peu_5	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAGTCA	GCAGCAAGGA	AAGTTTGAGC	TTGCAGAAAT		
Ppr_1	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAAATCA	GCAGCAAGGA	ATGTTTGAGC	TTGCAGAAAT		
Ppr_2	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAAATCA	GCAGCAAGGA	ATGTTTGAGC	TTGCAGAAAT		
Ppr_3	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAAATCA	GCAGCAAGGA	ATGTTTGAGC	TTGCAGAAAT		
Ppr_4	CAACCACTTC	ATATCTTTCA	AAAAGTAAAA	TGGCCAAATCA	GCAGCAAGGA	ATGTTTGAGC	TTGCAGAAAT		

	360	370	380	390	400	410	420		
Peu_1	AGCGCGAGCA	CTTCTTAAAG	ATTCAACGGA	GAAGTTTCAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT		
Peu_2	AGCGCGAGCA	CTTCTTAAAG	ATTCAACGGA	GAAGTTTCAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT		
Peu_3	AGCGCGAGCA	CTTCTTAAAG	ATTCAACGGA	GAAGTTTCAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT		
Peu_4	AGCGCGAGCA	CTTCTTAAAG	ATTCAACGGA	GAAGTTTCAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT		
Peu_5	AGCGCGAGCA	CTTCTTAAAG	ATTCAACGGA	GAAGTTTCAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT		

Ppr_1	AGCGCGAACA	CTTCCTAAAG	ATTCAACGGA	GAAGTTCAAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT	
Ppr_2	AGCGCGAACA	CTTCCTAAAG	ATTCAACGGA	GAAGTTCAAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT	
Ppr_3	AGCGCGAACA	CTTCCTAAAG	ATTCAACGGA	GAAGTTCAAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT	
Ppr_4	AGCGCGAACA	CTTCCTAAAG	ATTCAACGGA	GAAGTTCAAA	TTTATCGACA	CAAGAAGTTT	GTGGGTGAAT	
	
		430	440	450	460	470	480	490
Peu_1	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Peu_2	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Peu_3	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Peu_4	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Peu_5	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Ppr_1	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Ppr_2	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Ppr_3	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
Ppr_4	TTGAAAGCAA	TCAGAAGGCT	TGTTGATACC	AATGCCCTGA	AGATAGAGAA	CCTGTCTATT	TCAAAGGAAG	
	
		500	510	520	530	540	550	560
Peu_1	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Peu_2	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Peu_3	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Peu_4	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Peu_5	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Ppr_1	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Ppr_2	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Ppr_3	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
Ppr_4	TGGAAGGTGA	TCAAATGGTT	TTGCAAGAGA	CAGCAGCCGG	TTGACAATA	CAGTTATTTG	ATAAAGCCAT	
	
		570	580	590	600	610	620	630
Peu_1	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Peu_2	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Peu_3	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Peu_4	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Peu_5	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Ppr_1	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Ppr_2	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Ppr_3	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
Ppr_4	CGGCGTTAAT	GTCCCTCAAT	TTCGGGTTGT	GCAACTAAAT	GCAACATCAG	ACTTGCTTCT	TCTTCAGTCA	
	
		640	650	660	670	680	690	700
Peu_1	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Peu_2	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Peu_3	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Peu_4	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Peu_5	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Ppr_1	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Ppr_2	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Ppr_3	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
Ppr_4	GATCTGTACT	CCACCTCTGA	AGGTGTTTTA	GTTTCGGAACA	CAGCTCAAGC	TAACCCTGCA	AATCCATGTA	
	...							
Peu_1	TTG							
Peu_2	TTG							
Peu_3	TTG							
Peu_4	TTG							
Peu_5	TTG							
Ppr_1	TTG							
Ppr_2	TTG							
Ppr_3	TTG							
Ppr_4	TTG							

Unigene37561_All (heat stress transcription factor A3)

		10	20	30	40	50	60	70		
Peu_1	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Peu_2	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Peu_3	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Peu_4	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Peu_5	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Ppr_1	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Ppr_2	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Ppr_3	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Ppr_4	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			
Ppr_5	GATGGCCATC	TCATATTGAT	TTTACTGGGG	AAATGTTGGG	GGCAAAGAAG	CTTAGGAAGA	CTATGTCACA			

		80	90	100	110	120	130	140		
Peu_1	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Peu_2	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Peu_3	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Peu_4	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Peu_5	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Ppr_1	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Ppr_2	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Ppr_3	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Ppr_4	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			
Ppr_5	TCCAGCTAAT	GGTAGCGCTG	ATGATCTAGT	TTTTGGAAAT	GAAGTTAGAC	CTCGTAAGGA	ATTTTTCCGA			

		150	160	170	180	190	200	210		
Peu_1	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Peu_2	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Peu_3	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Peu_4	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Peu_5	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Ppr_1	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Ppr_2	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Ppr_3	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Ppr_4	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			
Ppr_5	AATGACTCTC	TTCCTAATGA	GACGTTTGTA	ACTATTTCTC	ACGTCAGTCT	TAAAAC TCAC	CCCTCTCAGT			

		220	230	240	250	260	270	280		
Peu_1	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Peu_2	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Peu_3	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Peu_4	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Peu_5	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Ppr_1	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Ppr_2	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Ppr_3	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Ppr_4	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			
Ppr_5	TGCCACCACC	TTCTAGACCA	CCGCCTGCAT	TAGATGTCAA	CAAGAGGGAT	TCTTG TAAAT	CAACTCCAAA			

		290	300	310	320	330	340	350		
Peu_1	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Peu_2	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Peu_3	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Peu_4	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Peu_5	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Ppr_1	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Ppr_2	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Ppr_3	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Ppr_4	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			
Ppr_5	CTGTCACAGC	GCTGCTTCCT	CAGGAAGTGC	TGGTGATAGT	TCTCCACCTT	ACTTTGATGT	TGAGGTAGAT			

		360	370	380	390	400	410	420		

Peu_1	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Peu_2	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Peu_3	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Peu_4	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Peu_5	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Ppr_1	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Ppr_2	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Ppr_3	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Ppr_4	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA
Ppr_5	GCAAGTTCCT	CTGCTGCTGC	CTCTGCTGCT	GCTATAAAAAG	AAGCTATGGA	GAAAGCTCAA	GTCAAGCTGA

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 430 440 450 460 470 480 490

Peu_1	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Peu_2	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Peu_3	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Peu_4	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Peu_5	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Ppr_1	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Ppr_2	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Ppr_3	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Ppr_4	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA
Ppr_5	AAAGTGCAAA	AGAATTGATG	GACAGGAAGA	GGGGTGGTTT	TCAAAAACCAT	ACAAAATCGG	CTTCAAAAAA

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 500 510 520 530 540 550 560

Peu_1	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Peu_2	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Peu_3	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Peu_4	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Peu_5	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Ppr_1	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Ppr_2	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Ppr_3	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Ppr_4	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG
Ppr_5	TGACAAAAAG	GATAGAGAAG	GTAGGGTGGT	TAAGATTGTT	GATGTGTCTG	GTAGTACAAA	ATATGAAGGG

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 570 580 590 600 610 620 630

Peu_1	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Peu_2	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Peu_3	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Peu_4	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Peu_5	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Ppr_1	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Ppr_2	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Ppr_3	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Ppr_4	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT
Ppr_5	GTGCAAGGCA	CTTGTGAAAAG	TGAAGAGAAT	GGAATGGATG	ACAGGCWAAA	GGTTAAAATT	CCAGATTCTT

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 640 650 660 670 680 690 700

Peu_1	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Peu_2	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Peu_3	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Peu_4	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Peu_5	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Ppr_1	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Ppr_2	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Ppr_3	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Ppr_4	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC
Ppr_5	TAGAAGGGAA	AAGGCATCAA	AATGCAGCAA	AAAAGTCTTC	TGATGAGAAG	CATGGAAGGG	AATCCTTGTC

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 710 720 730 740 750 760 770

Peu_1	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGAAATGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Peu_2	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGAAATGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Peu_3	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGAAATGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Peu_4	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGAAATGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG

Peu_5	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGAAATGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Ppr_1	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGARTGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Ppr_2	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGARTGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Ppr_3	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGARTGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Ppr_4	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGARTGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG
Ppr_5	ATCTCAAGGA	TCTGATAAAA	TTGATGAAGC	TAGTGARTGG	AAAGAAGCTA	CTCAATTTTT	TGAACTGGTG

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 780 790 800 810 820 830 840

Peu_1	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Peu_2	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Peu_3	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Peu_4	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Peu_5	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Ppr_1	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Ppr_2	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Ppr_3	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Ppr_4	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA
Ppr_5	AGAACAAATG	TACCCAGGAA	AGTCGTTGAC	TTGTCAAATA	ATGAAAACAT	TTTTCTGCAG	AACACAAATA

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Peu_1	TCCATGAACA	A
Peu_2	TCCATGAACA	A
Peu_3	TCCATGAACA	A
Peu_4	TCCATGAACA	A
Peu_5	TCCATGAACA	A
Ppr_1	TCCATGAACA	A
Ppr_2	TCCATGAACA	A
Ppr_3	TCCATGAACA	A
Ppr_4	TCCATGAACA	A
Ppr_5	TCCATGAACA	A

Unigene38057_All (with no lysine kinase)

	10	20	30	40	50	60	70		
Peu_1	GTAACAAACC	CGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Peu_2	GTAACAAACC	CGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Peu_3	GTAACAAACC	CGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Peu_4	GTAACAAACC	CGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Peu_5	GTAACAAACC	CGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Ppr_1	GTAACAAACC	AGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Ppr_2	GTAACAAACC	AGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Ppr_3	GTAACAAACC	AGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Ppr_4	GTAACAAACC	AGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		
Ppr_5	GTAACAAACC	AGGAGCTCTC	CTCCGTAACA	ATGGACGAAA	GCGCCTCTTA	TGACCCGACT	ATAAACCCACA		

	80	90	100	110	120	130	140		
Peu_1	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Peu_2	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Peu_3	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Peu_4	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Peu_5	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Ppr_1	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Ppr_2	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Ppr_3	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Ppr_4	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		
Ppr_5	TCTCCATGGA	AGAGCTAAAA	GTCTCCACCA	AGAACTTCTC	CACCGATTTA	ATCATCGGCG	ATGGCAGTTT		

	150	160	170	180	190	200	210		
Peu_1	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCACG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Peu_2	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCACG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Peu_3	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCACG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Peu_4	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCACG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Peu_5	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCACG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Ppr_1	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCATG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Ppr_2	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCATG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Ppr_3	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCATG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Ppr_4	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCATG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		
Ppr_5	CGGCTTGGTT	TATAAAGCTG	CACTCTACAA	CGGCTCCATG	GTTGCTATTA	AAAAGCTTGA	CCCGGACGCT		

	220	230	240	250	260	270	280		
Peu_1	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Peu_2	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Peu_3	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Peu_4	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Peu_5	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Ppr_1	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Ppr_2	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Ppr_3	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Ppr_4	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		
Ppr_5	TTTCAAGGTT	TTCGTGAGTT	TCGTGCCGAG	ATGGAGACTC	TAGGTCAGTT	ACGCCATGGA	AATATTGTCA		

	290	300	310	320	330	340	350		
Peu_1	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Peu_2	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Peu_3	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Peu_4	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Peu_5	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Ppr_1	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Ppr_2	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Ppr_3	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		
Ppr_4	AGATTCTCGG	GTATTGTGTT	TCGGGTCGGG	ACCGGGTTTT	AATTCTGGAG	TTCGTTGAAA	GAGGGAGTCT		

Ppr_5 AGATTCTCGG GTATTGTGTT TCGGGTCGGG ACCGGGTTTT AATTCTGGAG TTCGTTGAAA GAGGGAGTCT

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360 370 380 390 400 410 420

Peu_1 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTGTGATA AGTITCCCATT ACCCTGGGAG

Peu_2 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTGTGATA AGTITCCCATT ACCCTGGGAG

Peu_3 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTGTGATA AGTITCCCATT ACCCTGGGAG

Peu_4 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTGTGATA AGTITCCCATT ACCCTGGGAG

Peu_5 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTGTGATA AGTITCCCATT ACCCTGGGAG

Ppr_1 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTATGATA AGCTCCCATT ACCCTGGGAC

Ppr_2 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTATGATA AGCTCCCATT ACCCTGGGAC

Ppr_3 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTATGATA AGCTCCCATT ACCCTGGGAC

Ppr_4 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTATGATA AGCTCCCATT ACCCTGGGAC

Ppr_5 TGACCAGTGG ATTCACGACA CATCATCAAT GGATAACGAT CACTATGATA AGCTCCCATT ACCCTGGGAC

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

430 440 450 460 470 480 490

Peu_1 ACGAGGATCA AGATTGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Peu_2 ACGAGGATCA AGATTGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Peu_3 ACGAGGATCA AGATTGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Peu_4 ACGAGGATCA AGATTGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Peu_5 ACGAGGATCA AGATTGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Ppr_1 ACGAGGATCA AGATAGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Ppr_2 ACGAGGATCA AGATAGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Ppr_3 ACGAGGATCA AGATAGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Ppr_4 ACGAGGATCA AGATAGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

Ppr_5 ACGAGGATCA AGATAGTTAT GGGCGTGGCC AATGGGCTTG CTTATTTGCA TGGGCTTGAT ACTCCCATTA

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500 510 520 530 540 550 560

Peu_1 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Peu_2 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Peu_3 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Peu_4 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Peu_5 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Ppr_1 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Ppr_2 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Ppr_3 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Ppr_4 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

Ppr_5 TTCATAGGGA TATTAAGGCT AGTAACGTTT TGTTGGACTC GAGCTTTCAG GCCCATATCT CTGATTTTGG

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570

Peu_1 GCTTGCCCGT

Peu_2 GCTTGCCCGT

Peu_3 GCTTGCCCGT

Peu_4 GCTTGCCCGT

Peu_5 GCTTGCCCGT

Ppr_1 GCTTGCCCGT

Ppr_2 GCTTGCCCGT

Ppr_3 GCTTGCCCGT

Ppr_4 GCTTGCCCGT

Ppr_5 GCTTGCCCGT

Unigene7669_All (ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase)

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      10          20          30          40          50          60          70
Peu_1 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA
Peu_2 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA
Peu_3 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA
Peu_4 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA
Peu_5 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA
Ppr_1 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA
Ppr_2 AAACAGGTGG GAATTGTAGG GTTATATGGA ATGGGGGGTG TCGGAAAAAC TACCCTCTTG ACTCAAATCA

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.....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
      80          90          100         110         120         130         140
Peu_1 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA
Peu_2 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA
Peu_3 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA
Peu_4 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA
Peu_5 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA
Ppr_1 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA
Ppr_2 ACAACGAGTC TCTCAAGACA CTCGATTATT TTGATATTGT GATATGGGTA GTGGTGTCAA AAGATTTGAA

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     150         160         170         180         190         200         210
Peu_1 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC
Peu_2 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC
Peu_3 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC
Peu_4 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC
Peu_5 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC
Ppr_1 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC
Ppr_2 ACTTAACACT ATTCAAGAAA GCATAGGGAG AAAAAATAGGC TGTTCCTGATG ATTTGTGGAA GAATAAAAAGC

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.....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
     220         230         240         250         260         270         280
Peu_1 CTTGACGAAA AATCTGTGGA CATATTTACT GCCTTTCGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA
Peu_2 CTTGACGAAA AATCTGTGGA CATATTTACT GCCTTTCGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA
Peu_3 CTTGACGAAA AATCTGTGGA CATATTTACT GCCTTTCGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA
Peu_4 CTTGACGAAA AATCTGTGGA CATATTTACT GCCTTTCGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA
Peu_5 CTTGACGAAA AATCTGTGGA CATATTTACT GCCTTTCGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA
Ppr_1 CTTGACGAAA AAGCTGTGGA CATATTTACT GCCTTACGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA
Ppr_2 CTTGACGAAA AAGCTGTGGA CATATTTACT GCCTTACGCC ATAAAAGGTT TGTGATGTTG TTGGATGATA

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.....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
     290         300         310         320         330         340         350
Peu_1 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT
Peu_2 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT
Peu_3 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT
Peu_4 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT
Peu_5 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT
Ppr_1 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT
Ppr_2 TCTGGGAGAG GTTTGATTTA AAAAAACTTG GAGTTCCTCT TCCTGATATG AAAAAACGGTT CCAAGGTAGT

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Peu_1 TTTCACAA
Peu_2 TTTCACAA
Peu_3 TTTCACAA
Peu_4 TTTCACAA
Peu_5 TTTCACAA
Ppr_1 TTTCACAA
Ppr_2 TTTCACAA

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Unigene25055_All (twin LOV protein 1)

	10	20	30	40	50	60	70
Peu_1	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGA	GTTGCCATTT	TAGGCCATCT
Peu_2	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGA	GTTGCCATTT	TAGGCCATCT
Peu_3	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGA	GTTGCCATTT	TAGGCCATCT
Peu_4	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGA	GTTGCCATTT	TAGGCCATCT
Peu_5	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGA	GTTGCCATTT	TAGGCCATCT
Ppr_1	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGG	GTTGCCATTT	TAGGCCATCT
Ppr_2	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGG	GTTGCCATTT	TAGGCCATCT
Ppr_3	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGG	GTTGCCATTT	TAGGCCATCT
Ppr_4	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGG	GTTGCCATTT	TAGGCCATCT
Ppr_5	TCTCTCCATC	TCCAGTTTTT	TATGCTAGAA	ATAAATTAAG	AGGAAATTGG	GTTGCCATTT	TAGGCCATCT

	80	90	100	110	120	130	140
Peu_1	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Peu_2	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Peu_3	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Peu_4	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Peu_5	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Ppr_1	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Ppr_2	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Ppr_3	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Ppr_4	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA
Ppr_5	GGATACGGAA	TCCAGACCCCT	TTTATTGTAT	TTTATTTCTT	ACAATATGTG	CGATAATTAT	ACTGTATTTA

	150	160	170	180	190	200	210
Peu_1	CATTATTAAT	GATATTTGCT	TTTGGGCATG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTA	CCTCCTGAAC
Peu_2	CATTATTAAT	GATATTTGCT	TTTGGGCATG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTA	CCTCCTGAAC
Peu_3	CATTATTAAT	GATATTTGCT	TTTGGGCATG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTA	CCTCCTGAAC
Peu_4	CATTATTAAT	GATATTTGCT	TTTGGGCATG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTA	CCTCCTGAAC
Peu_5	CATTATTAAT	GATATTTGCT	TTTGGGCATG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTA	CCTCCTGAAC
Ppr_1	CATTATTAAT	GATATTTGCT	TTTGGGCGTG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTG	CCTCCTGAAC
Ppr_2	CATTATTAAT	GATATTTGCT	TTTGGGCGTG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTG	CCTCCTGAAC
Ppr_3	CATTATTAAT	GATATTTGCT	TTTGGGCGTG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTG	CCTCCTGAAC
Ppr_4	CATTATTAAT	GATATTTGCT	TTTGGGCGTG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTG	CCTCCTGAAC
Ppr_5	CATTATTAAT	GATATTTGCT	TTTGGGCGTG	ACAGAATCGA	AGAAAGTACG	TGTAGATTTG	CCTCCTGAAC

	220	230	240	250	260	270	280
Peu_1	TTTGTGACGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Peu_2	TTTGTGACGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Peu_3	TTTGTGACGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Peu_4	TTTGTGACGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Peu_5	TTTGTGACGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Ppr_1	TTTGTGAYGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Ppr_2	TTTGTGAYGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Ppr_3	TTTGTGAYGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Ppr_4	TTTGTGAYGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT
Ppr_5	TTTGTGAYGT	AATTTTATCT	CCAGTATCAA	TCAGCACTCT	TTATTCTTAT	ACATTTATCC	CATCAATAAT

	290	300	310	320	330	340	350
Peu_1	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Peu_2	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Peu_3	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Peu_4	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Peu_5	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Ppr_1	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Ppr_2	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Ppr_3	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT
Ppr_4	GCATCGACTA	GAGTCCCTGC	TTATTGCTGT	CAACTTAAAG	AAGATGCATT	CGGATCATTG	CATGCAAAAT

Ppr_5 GCATCGACTA GAGTCCCTGC TTATTGCTGT CAACTTAAAG AAGATGCATT CGGATCATTG CATGCAAAAT
.....|.....||.....||.....||.....||.....||.....||.....|
 360 370 380 390 400 410 420
Peu_1 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Peu_2 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Peu_3 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Peu_4 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Peu_5 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Ppr_1 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Ppr_2 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Ppr_3 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Ppr_4 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT
Ppr_5 GTTGATATTC CAGCCATGAA GGTAATTTAT TCCGACTCTA ATTATGCCAA ATGTTTTGTT TTTTGGACTT

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 430 440 450 460 470 480 490
Peu_1 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Peu_2 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Peu_3 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Peu_4 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Peu_5 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Ppr_1 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Ppr_2 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Ppr_3 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Ppr_4 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT
Ppr_5 GTACTGACCA AACTTTATTA TATGGTAGGT ATTGGAAGCA ATTACCACAA AGAAGTGCCA GGAGAAATTT

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 500 510
Peu_1 CATTTGGAAT CCTTAGAAAC TC
Peu_2 CATTTGGAAT CCTTAGAAAC TC
Peu_3 CATTTGGAAT CCTTAGAAAC TC
Peu_4 CATTTGGAAT CCTTAGAAAC TC
Peu_5 CATTTGGAAT CCTTAGAAAC TC
Ppr_1 CATTTGGAAT CCTTAGAAAC TC
Ppr_2 CATTTGGAAT CCTTAGAAAC TC
Ppr_3 CATTTGGAAT CCTTAGAAAC TC
Ppr_4 CATTTGGAAT CCTTAGAAAC TC
Ppr_5 CATTTGGAAT CCTTAGAAAC TC

	10	20	30	40	50	60	70		
Peu_1	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCG	TTATCTTCCT	CCAGCTCCCC	TCCTRCCTCC	AAAGAAGAAG		
Peu_2	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCG	TTATCTTCCT	CCAGCTCCCC	TCCTRCCTCC	AAAGAAGAAG		
Peu_3	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCG	TTATCTTCCT	CCAGCTCCCC	TCCTRCCTCC	AAAGAAGAAG		
Peu_4	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCG	TTATCTTCCT	CCAGCTCCCC	TCCTRCCTCC	AAAGAAGAAG		
Peu_5	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCG	TTATCTTCCT	CCAGCTCCCC	TCCTRCCTCC	AAAGAAGAAG		
Ppr_1	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCS	TTATCTTCCT	CCAGCTCCCC	TCCTACCTCC	AAAGAAGAAG		
Ppr_2	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCS	TTATCTTCCT	CCAGCTCCCC	TCCTACCTCC	AAAGAAGAAG		
Ppr_3	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCS	TTATCTTCCT	CCAGCTCCCC	TCCTACCTCC	AAAGAAGAAG		
Ppr_4	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCS	TTATCTTCCT	CCAGCTCCCC	TCCTACCTCC	AAAGAAGAAG		
Ppr_5	TCCAGAAGTC	CCGCTCTTTC	TATCCACTCS	TTATCTTCCT	CCAGCTCCCC	TCCTACCTCC	AAAGAAGAAG		

	80	90	100	110	120	130	140		
Peu_1	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Peu_2	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Peu_3	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Peu_4	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Peu_5	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Ppr_1	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Ppr_2	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Ppr_3	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Ppr_4	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		
Ppr_5	CCATTGTTCA	AGCCAAAACC	TGTCTCTCAA	CCACCCTAGA	GAAGCCCCCTA	AACAACCCAA	AACTAGCTGG		

	150	160	170	180	190	200	210		
Peu_1	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TAGATGACTC	GCCAACTTCT		
Peu_2	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TAGATGACTC	GCCAACTTCT		
Peu_3	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TAGATGACTC	GCCAACTTCT		
Peu_4	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TAGATGACTC	GCCAACTTCT		
Peu_5	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TAGATGACTC	GCCAACTTCT		
Ppr_1	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TRGATGACTC	GCCAACTTCT		
Ppr_2	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TRGATGACTC	GCCAACTTCT		
Ppr_3	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TRGATGACTC	GCCAACTTCT		
Ppr_4	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TRGATGACTC	GCCAACTTCT		
Ppr_5	CAAACCTAAG	AAACTGAAGC	AACCTAGATT	CCAGGTAGAA	ATCCCAGTCA	TRGATGACTC	GCCAACTTCT		

	220	230	240	250	260	270	280		
Peu_1	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Peu_2	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Peu_3	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Peu_4	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Peu_5	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Ppr_1	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Ppr_2	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Ppr_3	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Ppr_4	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		
Ppr_5	CTCTCTCAAC	TTGCCTCTGA	TGTTTTCAAA	GACCTGCCCA	TTAAGAGAAG	AGGGACACCG	GTCAAGATTT		

	290	300	310	320	330	340	350		
Peu_1	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Peu_2	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Peu_3	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Peu_4	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Peu_5	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Ppr_1	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Ppr_2	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Ppr_3	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Ppr_4	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		
Ppr_5	TAATCCTCTG	GCCGAGTCCC	ACATTGAAGA	ACAGAGGCAT	AGAAGCATTT	CAATCTTACA	ATTCATCAAA		

	360	370	380	390	400	410	420		

Peu_1	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Peu_2	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Peu_3	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Peu_4	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Peu_5	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Ppr_1	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Ppr_2	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Ppr_3	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Ppr_4	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG
Ppr_5	AAATGTTGAG	CACGTCGACG	TTTCTTCAGT	CAGAAATACA	GACAACAGAA	TTTTGAGTTC	TGCCGAAGTG

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430 440 450 460 470 480 490

Peu_1	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	CTGTACCCAA
Peu_2	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	CTGTACCCAA
Peu_3	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	CTGTACCCAA
Peu_4	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	CTGTACCCAA
Peu_5	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	CTGTACCCAA
Ppr_1	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	TTGTACCCAA
Ppr_2	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	TTGTACCCAA
Ppr_3	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	TTGTACCCAA
Ppr_4	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	TTGTACCCAA
Ppr_5	GCAGTGT TTC	TGGGGCCAGA	GACTTCACAG	TTGCCTGATA	TCAAAA CTGT	TACTGATATT	TTGTACCCAA

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500 510 520 530 540 550 560

Peu_1	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGC TTT
Peu_2	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGC TTT
Peu_3	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGC TTT
Peu_4	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGC TTT
Peu_5	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGC TTT
Ppr_1	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGY TTT
Ppr_2	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGY TTT
Ppr_3	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGY TTT
Ppr_4	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGY TTT
Ppr_5	AGCCAGTAGT	CATATTCAAC	CCCAAATGGG	GGTTTGGAGA	GGAGAACGAG	TTTGGTGATT	TGAGTGGY TTT

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570 580 590 600 610 620 630

Peu_1	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Peu_2	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Peu_3	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Peu_4	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Peu_5	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Ppr_1	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Ppr_2	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Ppr_3	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Ppr_4	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA
Ppr_5	TGTGGGATCC	TTTGAAGTGG	TATATTCATT	CATGGGGTTG	GAGGTTAGAG	GTATTTT GAG	CAAGCGAAAA

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640 650 660 670 680 690 700

Peu_1	GGAGTG AITTT	TCAAGTGTGT	CAGAGATGGG	GTTGTGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Peu_2	GGAGTG AITTT	TCAAGTGTGT	CAGAGATGGG	GTTGTGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Peu_3	GGAGTG AITTT	TCAAGTGTGT	CAGAGATGGG	GTTGTGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Peu_4	GGAGTG AITTT	TCAAGTGTGT	CAGAGATGGG	GTTGTGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Peu_5	GGAGTG AITTT	TCAAGTGTGT	CAGAGATGGG	GTTGTGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Ppr_1	GGAGTG GITTT	TCAAGTGTGT	CAGAGATGGG	GTTGYGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Ppr_2	GGAGTG GITTT	TCAAGTGTGT	CAGAGATGGG	GTTGYGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Ppr_3	GGAGTG GITTT	TCAAGTGTGT	CAGAGATGGG	GTTGYGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Ppr_4	GGAGTG GITTT	TCAAGTGTGT	CAGAGATGGG	GTTGYGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG
Ppr_5	GGAGTG GITTT	TCAAGTGTGT	CAGAGATGGG	GTTGYGAGTG	GAGAGAAATG	GACTGTTCTT	GTTGAAGAAG

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710 720 730 740 750 760 770

Peu_1	AAGGAGGAGA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Peu_2	AAGGAGGAGA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Peu_3	AAGGAGGAGA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Peu_4	AAGGAGGAGA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT

Peu_5	AAGGAGGAGA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Ppr_1	AAGGAGGACA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Ppr_2	AAGGAGGACA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Ppr_3	AAGGAGGACA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Ppr_4	AAGGAGGACA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT
Ppr_5	AAGGAGGACA	ATTGAAGGTT	GTTTCAAGGT	TCAAGGCACG	ACCATCCATT	GGTGAAGTAG	AGAATGTTTT

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 780 790 800 810 820 830 840

Peu_1	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Peu_2	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Peu_3	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Peu_4	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Peu_5	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Ppr_1	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Ppr_2	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Ppr_3	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Ppr_4	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT
Ppr_5	GTACAATCTG	ATGGCTATCA	ATTCGCCAAT	TACCAAGTCT	GCTAGGTTTT	TCAAGGATTT	GGTGTCAAAT

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Peu_1	GTA
Peu_2	GTA
Peu_3	GTA
Peu_4	GTA
Peu_5	GTA
Ppr_1	GTA
Ppr_2	GTA
Ppr_3	GTA
Ppr_4	GTA
Ppr_5	GTA

Unigene39162_All (proline-rich family protein)

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          10          20          30          40          50          60          70
Peu_1  AATTATSTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Peu_2  AATTATSTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Peu_3  AATTATSTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Peu_4  AATTATSTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Peu_5  AATTATSTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Ppr_1  AATTATCTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Ppr_2  AATTATCTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Ppr_3  AATTATCTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Ppr_4  AATTATCTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG
Ppr_5  AATTATCTAA TTTGTTTCAA ATTTTATAGGT GGATACGAGG AAAATGAAGA TGGATGTTAT TAGACCATGG

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          80          90          100          110          120          130          140
Peu_1  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Peu_2  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Peu_3  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Peu_4  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Peu_5  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Ppr_1  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Ppr_2  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Ppr_3  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Ppr_4  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC
Ppr_5  ATTGCTACTA GAGTGACGGA GCTTCTCGGA TTTGAAGATG AAGTTCCTTAT CAACTTCATT TATGGCCTGC

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          150          160          170          180          190          200          210
Peu_1  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Peu_2  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Peu_3  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Peu_4  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Peu_5  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Ppr_1  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Ppr_2  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Ppr_3  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Ppr_4  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT
Ppr_5  TTGATGGAAA GGTCTTATTG ATTTTCTGCA ATTAACCTAA CTTTTTTTATG TGTCTGAAAA TAGTTCATGT

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          220          230          240          250          260          270          280
Peu_1  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Peu_2  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Peu_3  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Peu_4  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Peu_5  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Ppr_1  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Ppr_2  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Ppr_3  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Ppr_4  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC
Ppr_5  TTTGCTTTTC AATTGAATAC TGCACGCGTG GATCCTCTGT CTTTGCTAAT ATAATTTTAC AATACTTGCC

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          290          300          310          320          330          340          350
Peu_1  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Peu_2  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Peu_3  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Peu_4  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Peu_5  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Ppr_1  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Ppr_2  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Ppr_3  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA
Ppr_4  TAAAGAATTG TTGAGAGTTC GTTTGGTGTT AGGCATTTTG TTTCTTAACA ATAGTCAAGT GGTTTGGTTA

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Ppr_5	TAAAGAATTG	TTGAGAGTTC	GTTTGGTGTT	AGGCATTTTG	TTTCTTAACA	ATAGTCAAGT	GGTTTGGTTA

	360	370	380	390	400	410	420
Peu_1	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Peu_2	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Peu_3	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Peu_4	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Peu_5	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Ppr_1	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Ppr_2	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Ppr_3	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Ppr_4	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC
Ppr_5	TCAATTTTTT	TTTGTGTAT	ACTGTATTGA	TGCAGGAAGT	GAACGGGAAG	GAGGTTCAAA	TATCGCTTAC

	430	440	450	460	470	480	490
Peu_1	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAG
Peu_2	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAG
Peu_3	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAG
Peu_4	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAG
Peu_5	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAG
Ppr_1	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAA
Ppr_2	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAA
Ppr_3	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAA
Ppr_4	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAA
Ppr_5	GGGATTCATG	GAGAAAAACA	CTGGGAAGTT	TATGAAAGAG	CTTTGGACAC	TTCTTCTTAG	TGCGCAGAAA

	500	510	520	
Peu_1	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Peu_2	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Peu_3	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Peu_4	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Peu_5	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Ppr_1	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Ppr_2	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Ppr_3	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Ppr_4	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC
Ppr_5	AATGAAAGTG	GTGTTCTCA	ACAGTTTTTG	GATGCC