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Electronic Supplementary Information for

Green-fluorescent protein from the bioluminescent jellyfish *Clytia gregaria*: cDNA cloning, expression, and characterization of novel recombinant protein

Svetlana V. Markova,[a,b] Ludmila P. Burakova,[a] Ludmila A. Frank,[a,b] Stefan Golz,[c] Kseniya A. Korostileva,[a,b] and Eugene S. Vysotski*[a]

[a] Photobiology Lab, Institute of Biophysics, Russian Academy of Sciences Siberian Branch, Akademgorodok 50, Bldg. 50, Krasnoyarsk 660036, Russia.

[b] Siberian Federal University, Krasnoyarsk 660041, Russia

[c] Bayer Schering Pharma AG, BSP-GDD-GTR-TD-GT, 42096 Wuppertal, Germany

*Corresponding author:
Fax: 7 391 433400; Tel: 7 391 494430;
E-mail: <eugene_vysotski@ibp.ru> or<eugene.vysotski@gmail.com>

```
                                                                                             1
            stop                              stop                                stop       M  T  A
G45     1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATCTCATTTCACCAAAACAGAGTAAAAACAAAATGACTGC
G10     1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATTTCATTTCACCAAAACAGAGTAAAAACAAAATGACTGC
G2      1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATTTCATTTCACCAAAACAGAGTAAAAACAAAATGACTGC
G25     1 GGTTAAAGTCATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATTTCATTTCACCAAAACAGAGTAAAAACAAAATGACTGC
G12     1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAG------------------------AGTAAAAACAAAATGACTGC
G4      1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAG------------------------AGTAAAAACAAAATGACTGC
G44     1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATTTCATTTCACCAAAACAGAGTAAAAACAAAATGACTGC
G20     1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAG------------------------AGTAAAAACAAAATGACTGC
G1      1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATTTCATTTCACCAAAACAGAGTAAAAACAAAATGACTGC
G3      1 ---------GATCTTCAATCAGAAAGTCAGACGACATAGTTAAAAGGTATATTTCATTTCACCAAAACAGAGTAAAAACAAAATGACTAC
                                                                                                 A3T

                             10                            20                            30
            L  T  E  G  A  K  L  F  E  K  E  I  P  Y  I  T  E  L  E  G  D  V  E  G  M  K  F  I  I  K
G45    82 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G10    82 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G2     82 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G25    91 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G12    68 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G4     68 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G44    82 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G20    68 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G1     82 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA
G3     82 ACTTACCGAAGGAGCAAAACTGTTCGAGAAAGAAATTCCCTACATTACAGAGTTGGAAGGAGACGTTGAAGGAATGAAATTCATCATCAA

                             40                            50                            60
            G  E  G  T  G  D  A  T  T  G  T  I  K  A  K  Y  I  C  T  T  G  D  L  P  V  P  W  A  T  I
G45   172 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G10   172 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G2    172 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G25   181 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G12   148 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G4    148 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G44   172 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G20   148 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G1    172 AGGTGAAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGTGACCTTCCTGTACCATGGGCTACCAT
G3    172 AGGTGTAGGTACTGGCGACGCTACTACTGGCACCATCAAAGCGAAATATATTTGCACAACTGGAGACCTTCCTGTACCATGGGCTACCAT
            E35V

                             70                            80                            90
            L  S  S  L  S  Y  G  V  F  C  F  A  K  Y  P  R  H  I  A  D  F  F  K  S  T  Q  P  D  G  Y
G45   262 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G10   262 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G2    262 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G25   271 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G12   238 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G4    238 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G44   262 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G20   238 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G1    262 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA
G3    262 CTTGAGTAGTTTGTCGTATGGTGTTTTCTGTTTCGCTAAGTATCCACGCCACATTGCCGACTTTTTCAAGAGCACACAACCAGATGGTTA

                             100                           110                           120
            S  Q  D  R  I  I  S  F  D  N  D  G  Q  Y  D  V  K  A  K  V  T  Y  E  N  G  T  L  Y  N  R
G45   352 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G10   352 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G2    352 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G25   361 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G12   328 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G4    328 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G44   352 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
G20   328 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGGACACTTTATAATAG
G1    352 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTGTGAAAACGGAACACTTTATAATAG
G3    352 TTCACAAGACAGAATCATTAGTTTTGACAATGATGGACAATACGATGTCAAAGCCAAGGTTACTTATGAAAACGGAACACTTTATAATAG
                                                                       Y115C
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                  130                                     140                                     150
         V  T  V  K  G  T  G  F  K  S  N  G  N  I  L  G  M  R  V  L  Y  H  S  P  P  H  A  V  Y  I
G45  442 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G10  442 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G2   442 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G25  451 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G12  418 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G4   418 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G44  442 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G20  418 AGTCGCAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G1   442 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
G3   442 AGTCACAGTCAAAGGTACTGGCTTCAAATCAAACGGCAACATCCTTGGTATGAGAGTTCTCTACCATTCACCACCACACGCTGTCTACAT
          T125A


                     160                                     170                                     180
         L  P  D  R  K  N  G  G  M  K  I  E  Y  N  K  A  F  D  V  M  G  G  G  H  Q  M  A  R  H  A
G45  532 CCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G10  532 CCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G2   532 CCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G25  541 CCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G12  508 CCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G4   508 CCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G44  532 TCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G20  508 TCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G1   532 TCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC
G3   532 TCTTCCTGACCGTAAAAATGGTGGCATGAAAATTGAATACAATAAGGCTTTCGACGTTATGGGCGGTGGTCACCAAATGGCGCGTCACGC


               190                                     200                                     210
         Q  F  N  K  P  L  G  A  W  E  E  D  Y  P  L  Y  H  H  L  T  V  W  T  S  F  G  K  D  P  D
G45  622 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCGTTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G10  622 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCGTTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G2   622 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCGTTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G25  631 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCGTTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G12  598 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCGTTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G4   598 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCGTTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G44  592 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCATTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G20  598 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCATTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G1   622 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCATTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAAGATCCGGA
G3   622 CCAATTCAATAAACCACTAGGAGCCTGGGAAGAAGATTATCCATTGTATCATCATCTTACCGTATGGACTTCTTTCGGAAAGGATCCGGA


                     220                                     230
         D  D  E  T  D  H  L  T  I  V  E  V  I  K  A  V  D  L  E  T  Y  R  stop
G45  712 TGATGATGAAACTGACCATTTGACCATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G10  712 TGATGATGAAACTGACCATTTGACCATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G2   712 TGATGATGAAACTGACCATTTGACCATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAAC---------
G25  721 TGATGATGAAACTGACCATTTGACCATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G12  688 TGATGATGAAACTGACCATTTGACCATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G4   688 TGATGATGAAACTGACCATTTGACCATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G44  712 TGATGATGAAACTGACCATTTGAACATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G20  688 TGATGATGAAACTGACCATTTGAACATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G1   712 TGATGATGAAACTGACCATTTGAACATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
G3   712 TGATGATGAAACTGACCATTTGAACATCGTCGAAGTCATCAAAGCTGTTGATTTGGAAACATACCGTTGATAGCGTTAAACAAAGAAAAA
                                T221N


G45  802 TTACTC--------------GAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G10  802 TTACTC--------------GAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G2   793 ------------------------------------------------------------------------------------------
G25  811 TTACTC--------------GAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G12  778 TTACTC--------------GAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G4   778 TTACTC--------------GAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAA------
G44  802 TTACTCCTCGAGTTTAACTCGAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G20  778 TTACTCCTCGAGTTTAACTCGAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G1   802 TTACTCCTCGAGTTTAACTCGAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTTCGTAGAAAGCTGCC
G3   802 TTACTCCTCGAGTTTAACTCGAGTGGTGGGCATCAATCATCATTTTTTTAAATTTGAAAGAATATTTTCAATAGTCCGTAGAAAGCTGCC
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G45  878 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G10  878 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G2   793 ------------------------------------------------------------------------------------------
G25  887 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G12  854 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G4   848 ------------------------------------------------------------------------------------------
G44  892 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G20  868 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G1   892 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAGAAGCACTGCTTTTTTCATTAGGTATGTATG
G3   892 GTCTATTATAATATTTATATATTTTGTTTTATTTCAACCCACTTTTAAAGATCATTCTAAAAGCACTGCTTTTTTCA-------------

                                                                 PAS
G45  968 ATGTATTTATTTACAAATGAATAATTACTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTTC-------------
G10  968 ATGTATTTATTTACAAATGAATAATTACTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTTC-------------
G2   793 ------------------------------------------------------------------------------------------
G25  977 ATGTATTTATTTACAAATGAATAATTACTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTTCAAATATCCAAGC-
G12  944 ATGTATTTATTTACAAATGAATAATTACTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTCC-------------
G4   848 ------------------------------------------------------------------------------------------
G44  982 ATGTATTTATTTACAAATGAATAATTGCTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTTCAAATATCCATAAT
G20  958 ATGTATTTATTTACAAATGAATAATTGCTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTCCG------------
G1   982 ATGTATTTATTTACAAATGAATAATTGCTTTGAGTAAGTTTTCTAATCTTCTTCAAGAAATAAAATTACACTTGTTCAAATATCCCG---
G3   969 ------------------------------------------------------------------------------------------

G45 1045 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
G10 1045 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA--
G2   793 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA-
G25 1066 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA-
G12 1011 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
G4   848 AAAAAAAAAAAAAAAAAAAAAAAAAAAA---
G44 1072 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
G20 1036 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
G1  1069 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA-
G3   969 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA--
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Fig. S1. A nucleotide alignment of ten complete cDNA sequences of the cgreGFP genes isolated from one specimen of the jellyfish *Clytia gregaria*: G1, G2, G3, G4, G10, G12, G20, G25, G44 and G45. Start codons (ATG) are marked in bold; stop codons – in bold and underlined. There are four stop-codons in 5-untranslated region of the clone cgreGFP25 before the start codon; other clones have 3 stop-codons in 5-untranslated region. A consensus polyadenylation signal PAS (AAATAA) is indicated by blue box. The amino acid sequence encoded by the cDNAs of the first group (cgreGFP2, 4, 10, 12, 25 and 45) having the same coding part is shown over the alignment. The residues forming the chromophore of cgreGFP are highlighted in green. Nucleotide replacements, making cgreGFP clones (44, 1, 3 and 20) different from the first group of cDNA genes are indicated by grey boxes; the resulting amino acid replacements in cgreGFP44 (T221N), cgreGFP20 (T221N and T125A), cgreGFP1 (T221N and Y115C), and cgreGFP3 (T221N, A3T, and E35V) are shown in yellow boxes under the alignment.

The six isolated cgreGFP cDNAs (cgreGFP2, 4, 10, 12, 25, and 45) are evidently various transcripts of one gene. The heterogeneity of untranslated regions seems to result from an alternative splicing, an imprecise cleavage after polyadenylation signal, and/or from annealing of oligo(dT) primer on any poly(A)-stretch in the 3'-untranslated regions instead of the terminal poly(A) tail.

The cgreGFP clones 44, 1, 3, and 20 differing from each other in 1-2 amino acids have four common nucleotide differences resulting in one common amino acid T221N replacement in coding sequences. These clones initially isolated at library screening were not so bright in comparison with other six cgreGFP clones of the first group. However after multiple passages with selection of bright colonies, these clones became brighter that seems to be the result of additional mutations. Thus, these four cgreGFP cDNAs (44, 1, 3, and 20) might originate from various transcripts of the second GFP gene (allelic gene, for example).

```
                          I
Cl-III   1 ------------------------------MTDTASKYAVKLKTNFEDPK
Cl-I     1 ------------------------------MADTASKYAVKLRPNFDNPK
Cl-II    1 MLWFTNRLLSMSALAARSRLQRTANFHTSILLATDSKYAVKLDPDFANPK

Cl-III  21 WVNRHKFMFNFLDINGNGKITLDEIVSKASDDICAKLGATPAQTQRHQEA
Cl-I    21 WVNRHKFMFNFLDINGDGKITLDEIVSKASDDICAKLGATPEQTKRHQDA
Cl-II   51 WINRHKFMFNFLDINGNGKITLDEIVSKASDDICAKLDATPEQTKRHQDA

Cl-III  71 VEAFFKKIGLDYGKEVEFPAFVNGWKELAKHDLKLWSQNKKSLIRNWGEA
Cl-I    71 VEAFFKKIGMDYGKEVEFPAFVDGWKELANYDLKLWSQNKKSLIRDWGEA
Cl-II  101 IEAFFKKMGMDYGKEVPFPEFIKGWEELAKHDLELWSQNKSTLIREWGDA

                II                                  III
Cl-III 121 VFDIFDKDGSGSISLDEWKTYGGISGICPSDEDAEKTFKHCDLDNSGKLD
Cl-I   121 VFDIFDKDGSGSISLDEWKAYGRISGICSSDEDAEKTFKHCDLDNSGKLD
Cl-II  151 VFDIFDKDASGSISLDEWKAYGRISGICPSDEDAEKTFKHCDLDNSGKLD

                                                   Identity
Cl-III  171 VDEMTRQHLGFWYTLDPNADGLYGNFVP
Cl-I    171 VDEMTRQHLGFWYTLDPNADGLYGNFVP                91.4%
Cl-II   201 VDEMTRQHLGFWYTLDPTSDGLYGNFVP                83.8%
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Fig. S2. A comparison of the cloned isotype of the Ca^{2+}-regulated photoprotein clytin from jellyfish *Clytia gregaria*, clytin-III (Cl-III), with clytin-I (Cl-I, AAA28293) [18] and clytin II (Cl-II, BAG49088) [19] isotypes. Colors mark amino acid similarity according to properties of the side chains. The letters colored by red show identical residues, blue letters represent similar residues, and black letters show nonidentical residues. The Ca^{2+}-binding sites I, II, and III are marked in yellow.

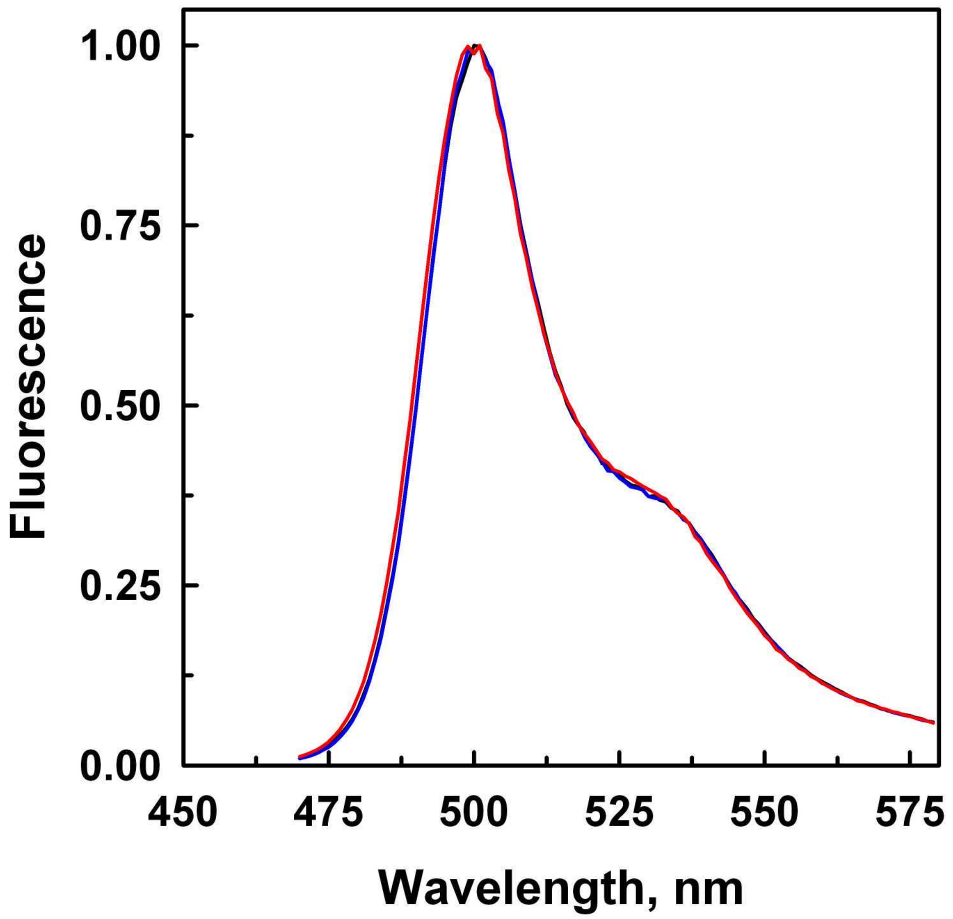

Fig. S3. Normalized fluorescence spectra (excitation at 470 nm) of pure recombinant cgreGFP at pH 5.5 (red), 7.0 (black), and 8.5 (blue).