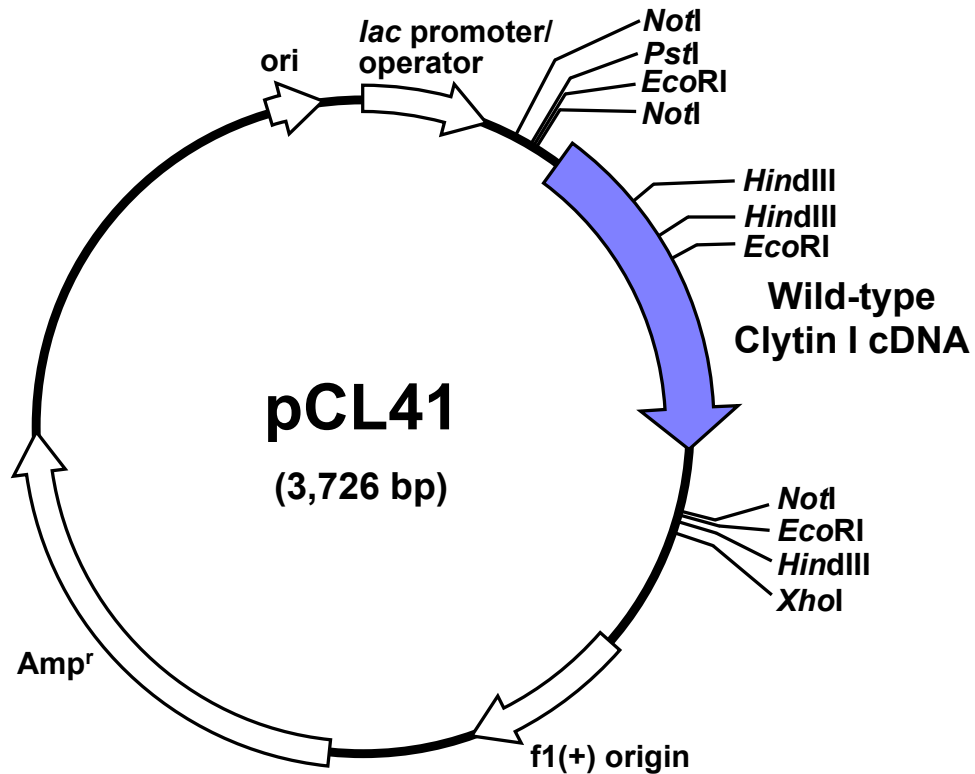


| pCL41                                    |   |
|--|---|
| <b>Cat. No.</b>                          | P-008   |
| <b>Gene/Insert name:</b>                 | Wild-type Clytin I ( <i>C. gregaria</i> )                     |
| <b>Vector backbone:</b>                  | pBluescript SK  |
| <b>Vector type:</b>                      | <i>E. coli</i>  |
| <b>Backbone size w/o insert (bp):</b>    | 2,958   |
| <b>Bacterial resistance:</b>             | Ampicillin  |
| <b>Growth strain:</b>                    | JM83  |
| <b>Growth temperature (°C):</b>          | 37  |
| <b>Growth instructions:</b>              | pCL41 is resistant to ampicillin (50 µg/mL)                   |
| <b>High or low copy:</b>                 | High copy   |
| <b>Vector map:</b>                       | <a href="#">pCL41</a>   |
| <b>Coding sequence:</b>                  | <a href="#">Nucleotide sequence &amp; Amino acid sequence</a> |
| <b>Plasmid sequence:</b>                 | <a href="#">pCL41 (3,726 bp)</a>                              |
| <b>Restriction enzyme list:</b>          | <a href="#">Restriction enzyme sites of pCL41</a>             |
| <b>GenBank Accession No.:</b>            | <a href="#">L13247</a>  |
| <b>Size:</b>                             | 10 µg   |
| <b>Terms and Licenses:</b>               | MTA   |
| Laboratory Reagent For Research Use Only |   |

# Ca<sup>2+</sup>-Binding Photoprotein, Clytin I

Cat. No. P-008

Name: pCL41  
Insert: Wild-type Clytin I cDNA  
Vector: pBluescript SK



• DNA fragment:

M A D T - - - F V P \*\*\*  
ATG-GCT-GAC-ACT-.....-TTT-GTT-CCT-TAA

• Feature for pCL41:

| Residue     | Source      | Comments                                      |
|-------------|-------------|---|
| 1-331       | 1-331       | pBluescript SK backbone                       |
| 1-230       | 1-230       | <i>lac</i> promoter/operator                  |
| 380-973     | 1-594       | Wild-type Clytin I ORF                        |
| 1,094-3,726 | 326-2,958   | pBluescript SK backbone                       |
| 1,356-1,662 | 588-894     | f1(+)-origin                                  |
| 3,553       | 2,785       | ori: Origin of replication                    |
| 1,925-2,785 | 1,157-2,017 | Amp <sup>r</sup> : Ampicillin resistance gene |

Ref.

- 1) Clytin I amino acid seq. & cDNA seq.: GenBank Accession No. L13247  
Inouye, S. and Tsuji, F.I. *FEBS Lett.* (1993) 315: 343-346.

**Gene coding region (ORF: Clytin I)**

**Nucleotide sequence**

GAATTCGCGGCCGCATCAACTTTTGGCAACTCAAAGCAAATTTCAAACTTCAAC**ATGGCTGACACTGCAT**  
**CAAAATACGCCGTCAAACCTCAGACCCAACTTCGACAACCCAAAATGGGTCAACAGACACAAATTTATGTT**  
**CAACTTTTTGGACATTAACGGCGACGGAAAAATCACTTTGGATGAAATCGTCTCCAAAGCTTCGGATGAC**  
**ATTTGCGCCAACTTGGAGCAACACCAGAACAGACCAAACGTCACCAGGATGCTGTCTGAAGCTTTCTTCA**  
**AAAAGATTGGTATGGATTATGGTAAAGAAAGTCGAATTTCCAGCTTTTGTGATGGATGGAAAGAAGCTGGC**  
**CAATTATGACTTGAACTTTGGTCTCAAAACAAGAAATCTTTGATCCGCGACTGGGGAGAAGCTGTTTTT**  
**GACATTTTTGACAAAGACGGAAGTGGCTCAATCAGTTTGGACGAATGGAAGGCTTATGGACGAATCTCTG**  
**GAATCTGCTCATCAGACGAAGACGCCGAAAAGACCTTCAAACATTGCGATTTGGACAACAGTGGCAAAC**  
**TGATGTTGATGAGATGACCAGACAACATTTGGGATTCTGGTACACCTTGGACCCCAACGCTGATGGTCTT**  
**TACGGCAATTTTGTTCCTTAA**ACATCGAAACAAAAGCCAAAAGAAGTTTTGGAAGAATTATTTGATACT  
ATCATTGTACTATTTTCGTAACATGCTATATTTTGTAAACATGCTATATTTTATAATTTTGCGCGGCCGCA  
ATTC

**Amino acid sequence**

EFAAASTFATQSKFQNFN**M**ADTASKYAVKLRPNFDNPKWVNRHKFMFNFLDINGDGKITLDEIVSKASDD  
ICAKLGATPEQTKRHQDAVEAFFKKIGMDYGKEVEFPFVVDGWKELANYDLKLWSQNKKSLIRDWGEAVF  
DIFDKDGSISLDEWKAYGRISGICSSDEDAEKTFKHCDLNSGKLDVDEMTRQHLGFWYTLDPNADGL  
YGNFVP\*

**pCL41 (3,726 bp)**

GCGCCCAATACGCAAACC GCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAGCAGAGTTT  
CCCGACTGGAAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGG  
CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTTGTGAGCGGATAACAATTTACACAGGAAA  
CAGCTATGACCATGATTACGCCAAGCTCGAAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCCAC  
CGCGGTGGCGGCCGCTCTAGAAGTAGTGGATCCCCGGGCTGCAGGAATTCGCGGCCGCATCAACTTTTG  
CAACTCAAAGCAAATTTCAAACCTTCAAC**ATGGCTGACACTGCATCAAAATACGCCGTCAAACTCAGACC**  
**CAACTTCGACAACCCAAAATGGGTCAACAGACACAAATTTATGTTCAACTTTTTTGGACATTAACGGCGAC**  
**GGAAAAATCACTTTGGATGAAATCGTCTCCAAAGCTTCGGATGACATTTGCGCCAAACCTTGAGCAACAC**  
**CAGAACAGACCAAAACGTCACCAGGATGCTGTGCGAAGCTTTCTTCAAAAAGATTGGTATGGATTATGGTAA**  
**AGAAGTCGAATTTCCAGCTTTTTGTTGATGGATGGAAAGAACTGGCCAAATTAAGACTTGAAACTTTGGTCT**  
**CAAAACAAGAAATCTTTGATCCGCGACTGGGGAGAAGCTGTTTTTCGACATTTTTTGACAAAGACGGAAGTG**  
**GCTCAATCAGTTTGACGAATGGAAGGCTTATGGACGAATCTCTGGAATCTGCTCATCAGACGAAGACGC**  
**CGAAAAGACCTTCAAACATTTGCATTTGGACAACAGTGGCAAACCTTGATGTTGATGAGATGACCAGACAA**  
**CATTTGGGATTTCTGTACACCTTTGACCCCAACGCTGATGGTCTTTACGGCAATTTTTTCTTAAACAT**  
**CGAAACAAAAGCCAAAAGAAAGTTTGGAAAGAAATTTGATACACTATCATTGTTACTATTTTCGTAACAT**  
**GCTATATTTTGTAAACATGCTATATTTTATAATTTTTCGCGCCGCAATTCGATATCAAGCTTATCGATACC**  
**GTCGACCTCGAGGGGGGGCCCGGTACCCAAATTCGCCCTATAGTGAGTCTGATTACAATTCACTGGCCGTC**  
**GTTTTTACAACGTCGTGACTGGGAAAACCCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTT**  
**TCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGG**  
**CGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGGGTGGTGGTTACGCGCAGCGTGACCGCT**  
**ACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTCTCGCCACGTTGCGCCGGCT**  
**TTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCCTTACGGCACCTCGACCC**  
**CAAAAACCTTGATTAGGGTATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTG**  
**ACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACGGAACAACACTCAACCCCTATCTCGG**  
**TCTATTCTTTTGATTTATAAGGGATTTTGCAGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACA**  
**AAAAATTAACCGAATTTTAAACAAAATATTAACGCTTACAATTTAGGTGGCACTTTTTCGGGGAAATGTGC**  
**GCGGAACCCCTATTTGTTTATTTTCTAAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTG**  
**ATAAATGCTTCAATAATATTGAAAAAGGAAGAT**ATGAGTATTCAAACATTTCCGTGTCGCCCTTATTCCC****  
**TTTTTTGCGGCATTTTGCCTTCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAAGATGCTGAAG**  
**ATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTTCG**  
**CCCCGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATT**  
**GACCGGAGGCAAGAGCAACTCGGTGCGCCGATACACTATTTCTCAGAATGACTTGGTTGAGTACTCACAG**  
**TCACAGAAAAGCATTTACGGATGGCATGACAGTAAGAGAAATTAATGCAGTGTGCCATAACCATGAGTGA**  
**TAACTGCGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAAC**  
**ATGGGGGATCATGTAACCTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGC**  
**GTGACACCACGATGCTGTAGCAATGGCAACAACGTTGCGCAAACATTTAACTGGCGAACTACTTACTCT**  
**AGCTTCCCGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCCTTCTGCGCTCGGCC**  
**CTTCCGGCTGGCTGGTTTTATTGCTGATAAATCTGGAGCCGGTGGAGCGTGGGTCGCGGTATCATTCGAG**  
**CACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGA**  
**TGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTTGGTAACTGTCAGACCAAGTT**  
**TACTCATATATACTTTAGATTGATTTAAAACCTCATTTTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTT**  
**TTGATAATCTCATGACCAAAATCCCTTAACTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAA**  
**GATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCG**  
**CTACCAGCGGTGGTTTTGTTTGGCCGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAACCTGGCTTCAGCA**  
**GAGCGCAGATACAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCCTTCAAGAACTCTGTAGC**  
**ACCGCTACATACTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCTGTGCTT**  
**ACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGCGGCTGAACGGGGGGTTCTGTGCA**  
**CACAGCCAGCTTGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGC**  
**CACGCTTCCCGAAGGGAGAAAGGCGGACAGTTACCGGTAAAGCGGAGGGTCCGGAACGAGGAGCGCAGC**  
**AGGGAGCTTCCAGGGGAAACGCTGGTATCTTTATAGTCTGTCGGGTTTTCGCCACCTCTGACTTGAGC**  
**GTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGA AAAACGCCAG**C**AACGCGGCCTTTTTACG**  
**GTTCTTGGCCTTTTTGCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCTGATTCGTGGATAAC**  
**CGTATTACCGCTTTGAGTGAGCTGATACCGCTCGCCGACGCCGAACGACCGAGCGCAGCGAGTCAGTGA**  
**GCGAGGAAGCGGAAGA**

| Residue     | Source      | Comments                                      |
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| 3,553       | 2,785       | ori: Origin of replication                    |
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**Restriction enzyme sites of pCL41**

| Enzyme Name | Sequence  | Count | Cutting Positions |
|-------------|-----------|-------|-------------------|
| AccI        | GT!MKAC   | 1     | 1123              |
| ApaI        | GGGCC!C   | 1     | 1141              |
| Asp718I     | G!GTACC   | 1     | 1143              |
| BamHI       | G!GATCC   | 1     | 309               |
| BclI        | T!GATCA   | 0     | -                 |
| BglII       | A!GATCT   | 0     | -                 |
| EcoRI       | G!AATTC   | 3     | 327, 639, 1095    |
| EcoRV       | GAT!ATC   | 1     | 1103              |
| HincII      | GTY!RAC   | 2     | 446, 1124         |
| HindIII     | A!AGCTT   | 3     | 523, 595, 1107    |
| KpnI        | GGTAC!C   | 1     | 1147              |
| MluI        | A!CGCGT   | 0     | -                 |
| NcoI        | C!CATGG   | 0     | -                 |
| NdeI        | CA!TATG   | 0     | -                 |
| NheI        | G!CTAGC   | 0     | -                 |
| NotI        | GC!GGCCGC | 3     | 290, 334, 1088    |
| PstI        | CTGCA!G   | 1     | 325               |
| SacI        | GAGCT!C   | 1     | 277               |
| SalI        | G!TCGAC   | 1     | 1122              |
| ScaI        | AGT!ACT   | 1     | 2232              |
| SmaI        | CCC!GGG   | 1     | 317               |
| StuI        | AGG!CCT   | 0     | -                 |
| XbaI        | T!CTAGA   | 1     | 297               |
| XhoI        | C!TCGAG   | 1     | 1128              |

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