Find-A-Gene Project Assignment

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# Q1:

Name: CCCTC-binding factor (CTCF)

Accession: isoform 1 isoform 2 isoform 3

NP\_006556.1 NP\_001177951.1 NP\_001350845.1

Species: *Homo Sapiens*

# Q2:

Isoform 1 will be used for downstream analysis, as it is the longest isoform.

Query: NP\_006556.1

Method: TBLASTN (2.13.0+) search against with default parameters

Database: Expressed Sequence Tags (est)

Organism: Papilionoidea (taxid:37572)

TBLASTN Setting:

Graphical user interface, application

Description automatically generated

**Chosen Match:** Accession GE695232.1, a 750 base pair clone from *Bicyclus anynana*. Alignment details see below.

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Alignment Details:

**CBUN9529.b1 B.anynana\_wing.0-3d\_2-10kb Bicyclus anynana cDNA clone CBUN9529, mRNA sequence**

**Sequence ID:**[**GE695232.1**](https://www.ncbi.nlm.nih.gov/nucleotide/GE695232.1?report=genbank&log$=nuclalign&blast_rank=1&RID=NCCEP04Y013) **Length: 750 Number of Matches: 3**

Range 1: 3 to 734

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Alignment statistics for match #1** | | | | | | |
| Score | Expect | Method | Identities | Positives | Gaps | Frame |
| 154 bits (389) | 1e-41 | Compositional matrix adjust. | 95/284(33%) | 144/284(50%) | 47/284(16%) | +3 |

Query 267 QCELCSYTCPRRSNLDRHMKSHTDERPHKCHL----CGRAFRTVTLLRNHLNTHTGTRPH 322

C++C Y C +R NL H+++HT E+P+ C + C R R LR+H+ THTG +P

Sbjct 3 SCDICHYKCAQRGNLVCHIRTHTCEKPYSCEMYNYKCARKSR----LRHHMTTHTGEKPF 170

Query 323 KCPDCDMAFVTSGELVRHRRYKHTHEKPFKCSMCDYASVEVSKLKRHIRSHTGERPFQCS 382

C C+ LV H R HT EKPF C +C+Y L H+++HTGE+PF C

Sbjct 171 SCGICNYKTGVKNSLVCHLR-THTGEKPFCCEICNYKFALKRNLLNHMKTHTGEKPFSCG 347

Query 383 LCSYASRDTYKLKRHMRTHSGEKPYECYICHARFTQSGTMKMHILQKHTENVAKFHCPHC 442

+C+Y + L H+RTH+GEKP+ C IC+ +F

Sbjct 348 ICNYKTGVKNSLVCHLRTHTGEKPFCCEICNYKF-------------------------- 449

Query 443 DTVIARKSDLGVHLRKQHSYIEQGKK---CRYCDAVFHERYALIQHQKSHKNEKRFKCDQ 499

A K +L H++ I G+K C C+ + +L+ H ++H EK F C+

Sbjct 450 ----ALKHNLVNHMK-----IHTGEKPFSCEICNYKTRVKNSLVSHLRTHTGEKPFSCEI 602

Query 500 CDYACRQERHMIMHKRTHTGEKPYACSHCDKTFRQKQLLDMHFK 543

C+Y ++R+++ H +THTGEKP++C C+ K L H +

Sbjct 603 CNYKSARKRYLLNHMKTHTGEKPFSCDICNYKTGIKNSLVRHMR 734

Range 2: 84 to 749

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Alignment statistics for match #2** | | | | | | |
| Score | Expect | Method | Identities | Positives | Gaps | Frame |
| 142 bits (358) | 1e-37 | Compositional matrix adjust. | 89/255(35%) | 125/255(49%) | 33/255(12%) | +3 |

Query 266 FQCELCSYTCPRRSNLDRHMKSHTDERPHKCHLCGRAFRTVTLLRNHLNTHTGTRPHKCP 325

+ CE+ +Y C R+S L HM +HT E+P C +C L HL THTG +P C

Sbjct 84 YSCEMYNYKCARKSRLRHHMTTHTGEKPFSCGICNYKTGVKNSLVCHLRTHTGEKPFCCE 263

Query 326 DCDMAFVTSGELVRHRRYKHTHEKPFKCSMCDYASVEVSKLKRHIRSHTGERPFQCSLCS 385

C+ F L+ H + HT EKPF C +C+Y + + L H+R+HTGE+PF C +C+

Sbjct 264 ICNYKFALKRNLLNHMK-THTGEKPFSCGICNYKTGVKNSLVCHLRTHTGEKPFCCEICN 440

Query 386 YASRDTYKLKRHMRTHSGEKPYECYICHARFTQSGTMKMHILQKHTENVAKFHCPHCDTV 445

Y + L HM+ H+GEKP+ C IC+ + ++ H L+ HT F C C+

Sbjct 441 YKFALKHNLVNHMKIHTGEKPFSCEICNYKTRVKNSLVSH-LRTHTGE-KPFSCEICNYK 614

Query 446 IARKSDLGVHLRKQHSYIEQGKKCRYCDAVFHERYALIQHQKSHKNEKRFKCDQCDYACR 505

ARK RY L+ H K+H EK F CD C+Y

Sbjct 615 SARK--------------------RY----------LLNHMKTHTGEKPFSCDICNYKTG 704

Query 506 QERHMIMHKRTHTGE 520

+ ++ H R HTGE

Sbjct 705 IKNSLVRHMRIHTGE 749

Range 3: 6 to 728

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Alignment statistics for match #3** | | | | | | |
| Score | Expect | Method | Identities | Positives | Gaps | Frame |
| 136 bits (343) | 2e-35 | Compositional matrix adjust. | 87/250(35%) | 126/250(50%) | 9/250(3%) | +3 |

Query 324 CPDCDMAFVTSGELVRHRRYKHTHEKPFKCSMCDYASVEVSKLKRHIRSHTGERPFQCSL 383

C C G LV H R HT EKP+ C M +Y S+L+ H+ +HTGE+PF C +

Sbjct 6 CDICHYKCAQRGNLVCHIR-THTCEKPYSCEMYNYKCARKSRLRHHMTTHTGEKPFSCGI 182

Query 384 CSYASRDTYKLKRHMRTHSGEKPYECYICHARFTQSGTMKMHILQKHTENVAKFHCPHCD 443

C+Y + L H+RTH+GEKP+ C IC+ +F + H ++ HT F C C+

Sbjct 183 CNYKTGVKNSLVCHLRTHTGEKPFCCEICNYKFALKRNLLNH-MKTHTGE-KPFSCGICN 356

Query 444 TVIARKSDLGVHLRKQHSYIEQGKKCRYCDAVFHERYALIQHQKSHKNEKRFKCDQCDYA 503

K+ L HLR E+ C C+ F ++ L+ H K H EK F C+ C+Y

Sbjct 357 YKTGVKNSLVCHLRTHTG--EKPFCCEICNYKFALKHNLVNHMKIHTGEKPFSCEICNYK 530

Query 504 CRQERHMIMHKRTHTGEKPYACSHCDKTFRQKQLLDMHFKRYHDPNFVPAAFVCSKCGKT 563

R + ++ H RTHTGEKP++C C+ +K+ L H K + F C C

Sbjct 531 TRVKNSLVSHLRTHTGEKPFSCEICNYKSARKRYLLNHMKTHTG----EKPFSCDICNYK 698

Query 564 FTRRNTMARH 573

+N++ RH

Sbjct 699 TGIKNSLVRH 728

# Q3:

**Chosen sequence:**

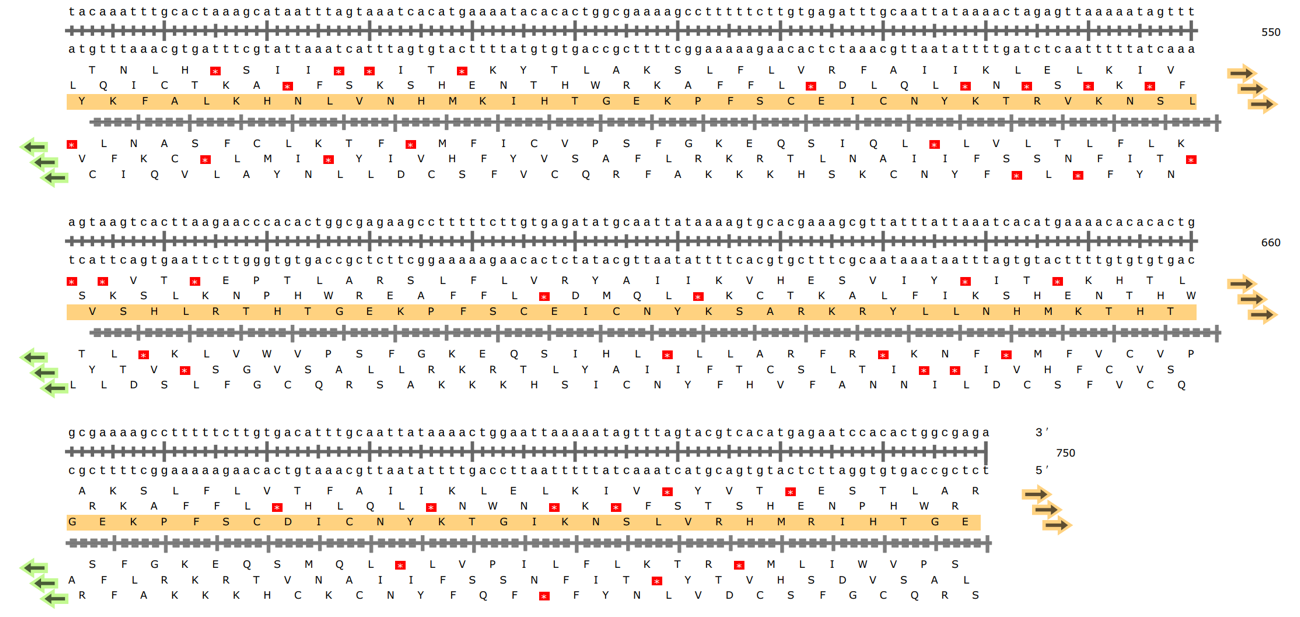
>B. anynana protein (from BLAST results)

SCDICHYKCAQRGNLVCHIRTHTCEKPYSCEMYNYKCARKSRLRHHMTTHTGEKPFSCGICNYKTGVKNSLVCHLRTHTGEKPFCCEICNYKFALKRNLLNHMKTHTGEKPFSCGICNYKTGVKNSLVCHLRTHTGEKPFCCEICNYKFALKHNLVNHMKIHTGEKPFSCEICNYKTRVKNSLVSHLRTHTGEKPFSCEICNYKSARKRYLLNHMKTHTGEKPFSCDICNYKTGIKNSLVRHMRIHTG

All six reading frame:

A picture containing diagram

Description automatically generated



Name: *Bicyclus* CTCF-like protein

Species: *Bicyclus anynana*

Taxonomy: Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

Ditrysia; Papilionoidea; Nymphalidae; Satyrinae; Satyrini;

Mycalesina; Bicyclus.

# Q4:

BLASTP search on non-redundant protein sequences (nr) hits top on zinc finger protein 84-like proteins on *Bicyclus anynana*, with identity percentage of 95.16%, suggesting a possible novel protein. See details below.

BLASTP setting: Graphical user interface, application

Description automatically generated

BLASTP results: Graphical user interface, application

Description automatically generated

Alignment details:

Graphical user interface, text, application

Description automatically generated

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