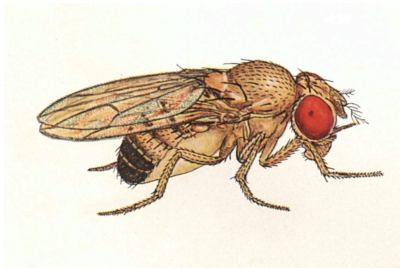




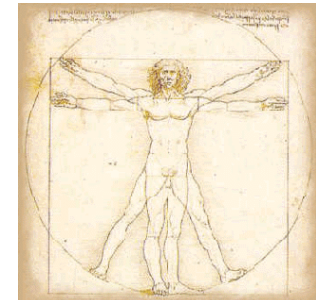
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Exploring Similarities between Man and Beast Using Publicly Available Genomic Resources



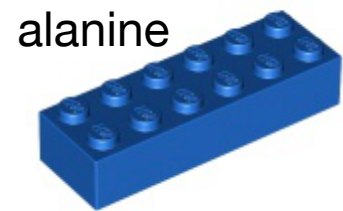
Frederick J Tan
Bioinformatics Research Faculty
23 November 2013



<http://emb.carnegiescience.edu/cty>

*Special thanks to Valeriya Gaysinskaya, Pavol Genzor, Safia Malki,
Zehra Nizami, and Gaëlle Talhouarne for devising these examples*





alanine

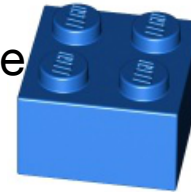
tryptophan



lysine



arginine



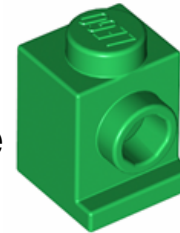
glycine



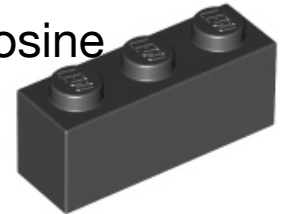
glutamate



aspartate



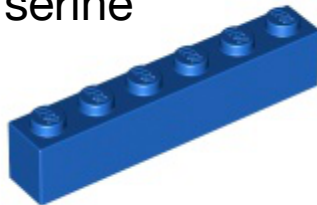
tyrosine



threonine



serine



proline



phenylalanine



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The mission of **UniProt** is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

What we provide

UniProtKB	Protein knowledgebase, consists of two sections: ★ Swiss-Prot, which is manually annotated and reviewed. ★ TrEMBL, which is automatically annotated and is not reviewed. Includes complete and reference proteome sets .
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UniParc	Sequence archive, used to keep track of sequences and their identifiers.
Supporting data	Literature citations , taxonomy , keywords , subcellular locations , cross-referenced databases and more .

NEWS



UniProt release 2013_11 - Nov 13, 2013

Forever young and cancer-free, in a black hole

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Sequences

Sequence		Length	Mass (Da)	Tools
☐ P02417 [UniParc].	FASTA	149	16,311	Blast go

Last modified May 1, 1991. Version 2.
Checksum: 8252B98C1677C130

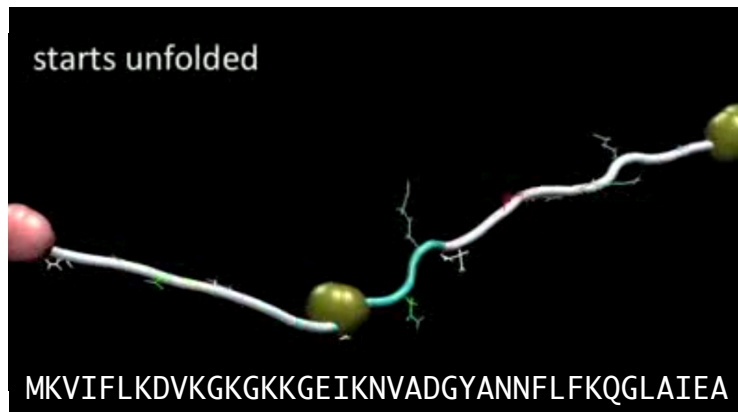
<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>
MKVIFLKDVK	GKGKKGEIKN	VADGYANNFL	FKQGLAIEAT	PANLKALEAQ	KQKEQRQAAE
<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>
ELANAKKLKE	QLEKLTVTIP	AKAGEGGRLF	GSITSKQIAE	SLQAQHGLKL	DKRKIELADA
<u>130</u>	<u>140</u>				
IRALGYTNVP	VKLHPEVTAT	LKVHVTEQK			

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Simulation of a millisecond folder: NTL9

youtube.com/watch?v=gFcp2Xpd29I



CTY Family Day 2013

Carnegie Institution for Science
Department of Embryology

Recent technological [advancements](#) have led to an explosion in the amount of information available about the genes and proteins present in organisms ranging from viruses to bacteria to plants to humans. In this workshop, you will be introduced to some of the publicly accessible [tools](#) and genomic [databases](#) that allow anyone with an internet connection to explore how genes in fundamental biological processes are conserved between model organisms and man.

[Night and Day: Regulating circadian rhythm with cryptochromes](#)

[A Tight Squeeze: Packing 2 meters of DNA into each cell with histones](#)

[Muscle or Blood: Determining cell fate with transcription factors](#)

[Under Water: Transporting oxygen in blood with hemoglobin](#)

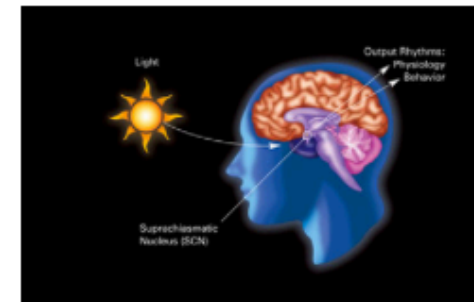
[The Sweet Life: Metabolising sugar with glucosidases](#)

[A Xerox Copier: Ensuring proper genome duplication with PCNA](#)

[\[BONUS\] Antifreeze Proteins: A Case of Convergent Evolution](#)

Night and Day: Regulating circadian rhythm with cryptochromes

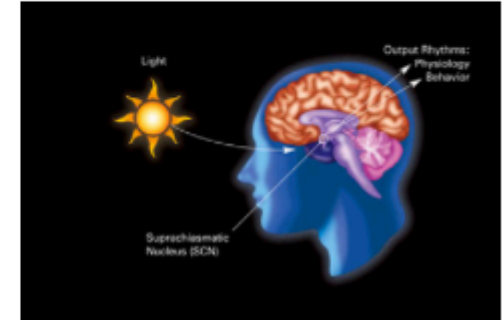
Many organisms vary their activities according to the time of day. These circadian (circa-"approximately" -dian "a day") rhythms help find prey and avoid predators. A protein called cryptochrome acts to coordinate circadian rhythms with changes in the daily sunrise and sunset.



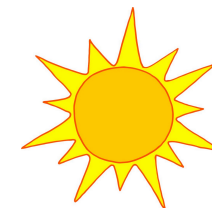
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- ★ Compare structure of fruitfly ([4GU5](#)) and mammalian ([4I6E](#)) proteins at [PDB](#)
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FB2013_06, released November 1st, 2013

A Database of *Drosophila* Genes & Genomes

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Species: ☐ include non-Dmel species

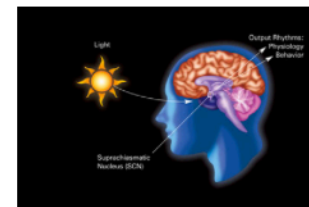
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- ★ BONUS: Determine where human cryptochrome ([cry2](#)) is expressed using [BioGPS](#)

General Information

Symbol	Dmellcry	Species	<i>D. melanogaster</i>
Name	cryptochrome	Annotation symbol	CG3772
Feature type	protein_coding_gene	FlyBase ID	FBgn0025680
Gene Model Status	Current	Stock availability	8 publicly available
Also Known As	dCRY, DmCRY		

Genomic Location

Cytogenetic map	91F11-91F11	Sequence location	3R:15,037,876..15,041,164 [+]
-----------------	-----------------------------	-------------------	-------------------------------

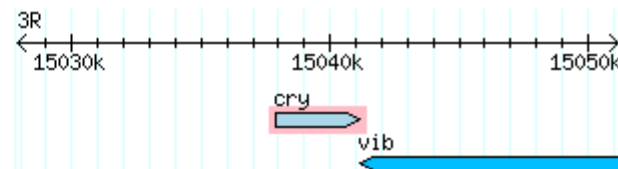
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[Decorated FastA](#) [↕](#)

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Families, Domains

[Protein Family \(UniProt\)](#)

[Sequence Similarity](#)

[Protein Domains/Motifs](#)

```
>FBpp0083150 type=protein; loc=3R:join(15038063..15041164)
MATRGANVIWFRHGLRLHDPALLAALADKDGIALIPVFIIDGESAGTK
NVGYNMRMFLDLSLQDIDDQLQAATDGRGRLLVFEGEPAYIFRRLHEQVR
LHRICIEQDCEPIWNERDESIRSLCRELNIDFVEKVSHTLWDPQLVIETN
GGIPPLTYQMFLHTVQIIIGLPPRPTADARLEDATFVELDPEFCRSLKLF
QLPTPEHFNVYGDNMGFLAKINWRGGETQALLLLDERLKVEQHAFERGFY
LPNQALPNIHDSPKSMSAHLRFGLSVRRFYWSVHDLFKNVQLRACVRGV
QMTGGAHITGQLIWREYFYTMSVNNPNYDRMEGNDICLSIPWAKPNENLL
QSWRLGQTGFPLIDGAMRQLLAEGWLHHTLRNTVATFLTRGGLWQSWEHG
LQHFLKYLLDADWSVCAGNWMWVSSAFERLLDSSLVTCPVALAKRLDPD
GTYIKQYVPELMNVPKEFVHEPWRMSAEQQEQYECLIGVHYPERIIDLSM
AVKRNMLAMKSLRNSLITPPPHCRPSNEEEVRQFFWLADV VV
```

[NCBI/BLAST/blastp suite](#)

Standard Protein BLAST

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BLASTP programs search protein databases using a protein query. [more...](#)

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Enter accession number(s), gi(s), or FASTA sequence(s)
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Query subrange
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QMTGGAHITGQLIWREYFYTMSVNNPNYDRMEGNDICLSIPWAKPNENLL
 QSWRLGQTGFPLIDGAMRQLLAEGWLHHTLRNTVATFLTRGGLWQSWEHG
 LQHFLKYLLDADWSVCAGNWMWVSSSAFERLLDSSLVTCPVALAKRLDPD
 GTYIKQYVPELMNVPKFVHEPWRMSAEQQEQYECLIGVHYPERIIDLSM
 AVKRNMLAMKSLRNSLITPPPHCRPSNEEEVROFFWLADVVV

Or, upload file

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Enter a descriptive title for your BLAST search
 [?](#)

☐ Align two or more sequences
 [?](#)

Choose Search Set

Database

Non-redundant protein sequences (nr)

Organism

Optional

human

human (taxid:9606)

Human immunodeficiency virus 1 (taxid:11676)

Human immunodeficiency virus type 1 (taxid:...

human immunodeficiency virus 1 HIV-1 (taxi...

human immunodeficiency virus HIV-1 (taxid:...

human immunodeficiency virus type 1 HIV 1 ...

human immunodeficiency virus type 1 HIV-1 ...

human immunodeficiency virus type 1 HIV1 (...

human immunodeficiency virus type 1, HIV-1...

human immunodeficiency virus type I HIV-1 (...

human immunodeficiency virus type-1 HIV-1 ...

human immunodeficiency virus-1 HIV-1 (taxi...

Mycobacterium tuberculosis typus humanus ...

human hepatitis C virus (taxid:11103)

human hepatitis C virus HCV (taxid:11103)

human hepatitis virus C HCV (taxid:11103)

☐ Exclude

+

20 top taxa will be shown.
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Multiple sequences

Program Selection

Algorithm

BLAST

[+ Algorithm parameters](#)

(nr) using Blastp (protein-protein BLAST)

Graphic Summary

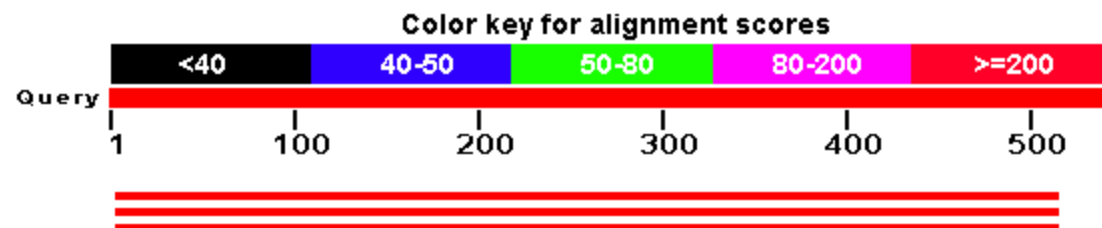
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 13 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Alignments

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Next Previous Descriptions

KIAA0658 protein [Homo sapiens]

Sequence ID: [dbj|BAA31633.1](#) Length: 589 Number of Matches: 1

Range 1: 18 to 506 GenPept Graphics

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
375 bits(962)	4e-121	Compositional matrix adjust.	214/521(41%)	298/521(57%)	41/521(7%)

Query	5	GANVIWFRHGLRLHDPALLAALADKDQGIALLP-VFIFDGESAGTKNVGYNRMRFLLDS	63
		++V WFR GLRLHDPALLAA+ +G + V+I D A + +VG NR RFLL S	
Sbjct	18	ASSVHWFRKGLRLHDPALLAAV----RGARCVRCVYILDWPFAASSSVGINRWRFLQ	73
Query	64	LQDIDDQLQAATDGRGRLLVFEGEPAYIFRRLHEQVRLHRICIEQDCEPIWNERDESIRS	123
		L+D+D L+ RL V G+PA +F RL ++ + R+ E D EP ERD +I	
Sbjct	74	LEDLDTSLRKLNS---RLFVVRGQPADVFPRLFKEWGVTRLTTFEYDSEPFPGKERDAAIMK	130
Query	124	LCRELNIDFVEKVSHTLWDPQLVIETNGGIPPLTYQMFLHTVQIIGLPPRPTADARLEDA	183
		+ +E ++ V + SHTL+D +IE NG PPLTY+ F + + LP +P +	
Sbjct	131	MAKEAGVEVVTENSHTLYDLRIIELNGQKPPLTYKRFQAIISRMELPKKPVGLVTSQQM	190
Query	184	TFVELDPEFCRSLKLFELPTPEHFNVYG----DNMGF----LAKINWRGGETQALLLLD	235
		E CR+ ++ E H YG + +GF L W+GGET+AL LD	
Sbjct	191	-----ESCRA-EIQEN-----HDETYGVPSLEELGFPTEGLGPAVWQGGETEALRLD	237

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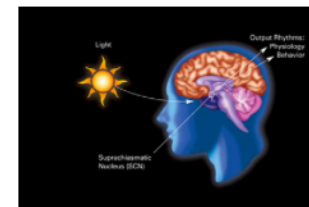
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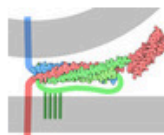
Full Description

Night and Day: Regulating circadian rhythm with cryptochromes

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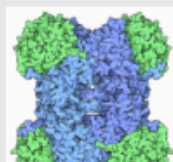
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are used inside cells to transport digestive enzymes from the Golgi to their final location in lysosomes. They are also used to deliver molecules out of the cell: for example, neurotransmitters are released from vesicles that fuse with the cell membrane at nerve synapses. The 2013 Nobel Prize was awarded to three researchers who have revealed the central molecular machinery for this process of vesicle fusion.

Full Article

Protein Structure Initiative Featured System Methylation of Arginine

The function of many proteins is tuned and regulated after they are synthesized by modification of key amino acids. These modifications change the chemistry of the amino acid, creating a distinctive mark that can be used as a signal or to customize interactions with other molecules. Phosphate groups, for



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DOI:10.2210/pdb4gu5/pdb

4GU5

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Updated structure of Drosophila cryptochrome.

Levy, C. , Zoltowski, B.D. , Jones, A.R. , Vaidya, A.T. , Top, D. , Widom, J. , Young, M.W. , Scrutton, N.S. , Crane, B.R. , Leys, D.

Journal: (2013) Nature **495**: E3-E4

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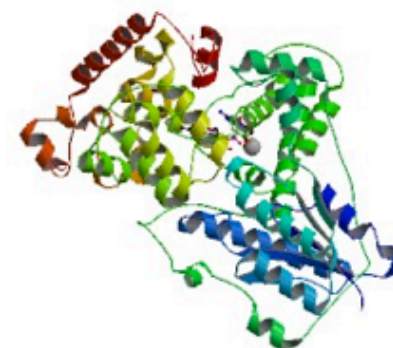
Structure of full-length Drosophila cryptochrome.
Zoltowski, B.D., Vaidya, A.T., Top, D., Widom, J., Young, M.W., Crane, B.R.
(2011) Nature **480**: 396 [PubMed](#)

↑ Molecular Description

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Classification: [Signaling Protein](#)

← **Biological Assembly 1** →



3D View

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No symmetry
Stoichiometry: **Monomer**
Biological assembly 1 assigned by authors
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4GU5

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Structure

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Symmetry C1

Stoichiometry A

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Subunit

Symmetry

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