Bioinformatics Analysis of Cryptochrome

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Background



Background



The absorption of light leads to an isomeric change in the retinal molecule.





By Uniprot

CRY1_HUMAN	MGVNAVHWFRKGIRLHDN PALKECIQGADTIRGVYILDPWFAGSSNVGINRWRFLLQCLE
CRY1_MACFA	MGVNAVHWFRKGIRLHDN PALKECIQGADTIRGVYILDPWFAGSSNVGINRWRFLLQCLE
CRY1_SPAJD	MGVNAVHWFRKGIRLHDN PALKECIQGADTIRGVYILDPWFAGSSNVGINRWRFLLQCLE
CRY1_MOUSE	MGVNAVHWFRKGIRLHDN PALKECIQGADTIRGVYILDPWFAGSSNVGINRWRFLLQCLE
CRY1_RAT	MGVNAVHWFRKGIRLHDN PALKECIQGADTIRGVYILDPWFAGSSNVGINRWRFLLQCLE
CRY1_HUMAN CRY1_MACFA CRY1_SPAJD CRY1_MOUSE CRY1_MOUSE CRY1_RAT	DLDANLERLINSELFVIRGOPADVFPELFEMNITELSIEVDSEPFCKEEDAAIKELATEA DLDANLERLINSELFVIRGOPADVFPELFEMNITELSIEVDSEPFCKEEDAAIKELATEA DLDANLERLINSELIVIRGOPADVFPELFEMNITELSIEVDSEFFCKEEDAAIKELATEA DLDANLERLINSELFVIRGOPADVFPELFEMNITELSIEVDSEFFCKEEDAAIKELATEA DLDANLERLINSELFVIRGOPADVFPELFEMNITELSIEVDSEFFCKEEDAAIKELATEA
CRY1_HUMAN	GVEVIVEISHTLYDLDEIIELNGGOPPLTYERFOTLISIMEPLEIPVETITSEVIEEGIT
CRY1_MACFA	GVEVIVEISHTLYDLDEIIELNGGOPPLTYERFOTLISIMEPLEIPVETITSEVIEEGIT
CRY1_SPAJD	GVEVIVEISHTLYDLDEIIELNGGOPPLTYERFOTLISIMEPLEIPVETITSEVIEEGIT
CRY1_MOUSE	GVEVIVEISHTLYDLDEIIELNGGOPPLTYERFOTLVSIMEPLENPADTITSDVIGEGIT
CRY1_RAT	GVEVIVEISHTLYDLDEIIELNGGOPPLTYERFOTLVSIMEPLENPADTITSDVIGEGIT
CRY1_HUMAN	PLSDDHDERYGVPSLEELGFDIDGLSSAVWPGGETEALTRLERHLERKAWVANFERPRM
CRY1_MACFA	PLSDDHDERYGVPSLEELGFDIDGLSSAVWPGGETEALTRLERHLERKAWVANFERPRM
CRY1_SPAJD	PLSDDHDERYGVPSLEELGFDIDGLSSAVWPGGETEALTRLERHLERKAWVANFERPRM
CRY1_MOUSE	PLSDDHDERYGVPSLEELGFDIDGLSSAVWPGGETEALTRLERHLERKAWVANFERPRM
CRY1_RAT	PLSDDHDERYGVPSLEELGFDIDGLSSAVWPGGETEALTRLERHLERKAWVANFERPRM
CRY1_HUMAN	ANSLLAS PTOLS PYLEFOCLSCELFYFRLTDLYKKVKNSS PPLSLYGOLLWEFFFYTAR
CRY1_MACFA	ANSLLAS PTOLS PYLEFOCLSCELFYFRLTDLYKKVKNSS PPLSLYGOLLWEFFYTAR
CRY1_SPAJD	ANSLLAS PTOLS PYLEFOCLSCELFYFRLTDLYKKVKNSS PPLSLYGOLLWEFFFYTAR
CRY1_MOUSE	ANSLLAS PTOLS PYLEFOCLSCELFYFRLTDLYKKVKNSS PPLSLYGOLLWEFFFYTAR
CRY1_RAT	ANSLLAS PTOLS PYLEFOCLSCELFYFRLTDLYKKVKNSS PPLSLYGOLLWEFFFYTAR
CRY1_HUMAN CRY1_MACFA CRY1_SPAJD CRY1_MOUSE CRY1_RAT	INN PREDEMEGN PICUQI PHDEN PEALARMAEGRIGEPHIDAINTOL ROEGNIHHLARHA INN PREDEMEGN PICUQI PHDEN PEALARMAEGRIGEPHIDAINTOL ROEGNIHHLARHA
CRY1_HUMAN	VACFLISCOLWISWEECKEVFEELLLDADWSINACSWMWLSCSSFFQQFFHCYCPVCFCE
CRY1_MACFA	VACFLISCOLWISWEECKEVFEELLLDADWSINACSWMWLSCSSFFQQFFHCYCPVCFCE
CRY1_SPAJD	VACFLISSOLWISWEECKEVFEELLLDADWSINACSWMWLSCSSFFQQFFHCYCPVCFCE
CRY1_MOUSE	VACFLISCOLWISWEECKEVFEELLLDADWSINACSWMWLSCSSFFQQFFHCYCPVCFCE
CRY1_RAT	VACFLISCOLWISWEECKEVFEELLLDADWSINACSWMWLSCSSFFQQFFHCYCPVCFCE
CRY1_HUMAN	RIDPNGDYIRRYL PVLRGFPARYIYDPMNAPEGIQRVARCLIGVNYPRPMVNHAEASRLN
CRY1_MACFA	RIDPNGDYIRRYL PVLRGFPARYIYDPMNAPEGIQRVARCLIGINYPRPMVNHAEASRLN
CRY1_SPAJD	RIDPNGDYIRRYL PVLRGFPARYIYDPMNAPEGIQRVARCLIGVNYPRPMVNHAEASRLN
CRY1_MOUSE	RIDPNGDYIRRYL PVLRGFPARYIYDPMNAPEGIQRVARCLIGVNYPRPMVNHAEASRLN
CRY1_RAT	RIDPNGDYIRRYL PVLRGFPARYIYDPMNAPEGIQRVARCLIGVNYPRPMVNHAEASRLN
CRY1_HUMAN CRY1_MACFA CRY1_SPAJD CRY1_MOUSE CRY1_RAT	IEFMKQIYQQLSFYRGLGLLASVPSNPNCNCGENGYS-AENIPGCSSSG
CRY1_HUMAN	SCSQCSGILHYAHODS OTHLINOCRSSMCTGLSGCKRPSQEEDTQSICPKV
CRY1_MACFA	SCSQCSGILHYHCDS OTHLINOCRSSMCTGLSGCKRPSQEEDTQSICPKV
CRY1_SPAJD	SCSQCSGILHYAHODS OAHLINOCRSSACTGLSSGKRPSQEEDADSVCPKV
CRY1_MOUSE	NVPSCSGCXCSQCSGILHYAHODS OTHSINOCRSSACTGLSSGKRPSQEEDADSVCPKV
CRY1_RAT	CNCSQCSGILHYAHODS OTNPLKQCRSSMCTGLSSGKRPSQEEDADSVCPKV
CRY1_HUMAN	CROSTN
CRY1_MACFA	CROSTN
CRY1_SPAJD	CROSTN
CRY1_MOUSE	CROSSN

CRY1_HUMAN: Identity

CRY1_MACFA: 97.785% CRY1_SPAJD: 99.317% CRY1_MOUSE: 93.324% CRY1_RAT: 95.748%

emma(v6.0.1) - Multiple alignment program - interface to ClustalW program

OBOSSN

CRY1_RAT

Tandem Sequence Repeats Analysis

Hydrophilic and Hydrophobic Analysis

Average Flexibility

ProtScale output for user sequence

Alpha-helix

Coil

Transmembrane Tendency

Signal Protein

SignalP-4.1 prediction (euk networks): 4K0R_A_PDBID_CHAIN_SEQUENCE

Secondary Structure and Disorder Prediction

3D structure of Cryptochrome(4I6G)

Cry2 monomer with FAD ligand

Vacuum Electrostatics (416G)

Align Cry1_mouse with Cry1_Droso

FAD Binding Site Analysis

Another Druggable Pocket by CAVITY

Future work

Acknowledgement

Prof. Jingchu Luo Prof. Luhua Lai Xiuzhen Bai Zhe Yang Youjun Xu

