S2 Fig. Sequence Alignments of CCT subunits

CCT1

```
HUMAN       --------MEGPLSVFGDRSTGETIRSQNVMAAASIANIVKSSLGPVGLDKMLVDDIGDV
CtCCT1      MAAIFEQPRNGTLFLGGQKISGADIRDQNVLATQAIANVVKSSFGPSGLDKMMVDDIGDV
YEAST       MSQLFNNSRSDTLFLGGEKISGDDIRNQNVLATMAVANVVKSSLGPVGLDKMLVDDIGDF
                     .. * : *:: :*  **.***:*: ::**:****:** *****:******.

HUMAN       TITNDGATILKLLEVEHPAAKVLCELADLQDKEVGDGTTSVVIIAAELLKNADELVKQKI
CtCCT1      TVTNDGATILSLLDVEHPAGKILVDLAQQQDKEVGDGTTSVVLIAAELLKRANDLMKNRI
YEAST       TVTNDGATILSLLDVQHPAGKILVELAQQQDREIGDGTTSVVIIASELLKRANELVKNKI
            *:********.**:*:***.*:* :**: **:*:********:**:****.*::*:*::*

HUMAN       HPTSVISGYRLACKEAVRYINENLIVNTDELGRDCLINAAKTSMSSKIIGINGDFFANMV
CtCCT1      HPTTIITGYRLALREAVKYMNEHVSIKVENLGRESLLNIAKTSMSSKIIGADADFFANMV
YEAST       HPTTIITGFRVALREAIRFINEVLSTSVDTLGKETLINIAKTSMSSKIIGADSDFFSNMV
            ***::*:*:*:* :**:::** :  ..: **:: *:* *********** :.***:***

HUMAN       VDAVLAIKYTDIRGQPRYPVNSVNILKAHGRSQMESMLISGYALNCVVGSQGMPKRIVN-
CtCCT1      VDAIQAVKTTNNKNEVKYPVKAVNILKAHGKSATESMLIKGYALNCTVASQAMKTRITD-
YEAST       VDALLAVKTQNSKGEIKYPVKAVNVLKAHGKSATESLLVPGYALNCTVASQAMPKRIAGG
            ***: *:*  : :.: :***::**:*****:*  **:*: ******.*.**.* .**..

HUMAN       -AKIACLDFSLQKTKMKLGVQVVITDPEKLDQIRQRESDITKERIQKILATGANVILTTG
CtCCT1      -AKIACLDMNLQKERMKLGVQITIDDPEQLEAIRAREATMVLERIDMILKAGANVILTTK
YEAST       NVKIACLDLNLQKARMAMGVQINIDDPEQLEQIRKREAGIVLERVKKIIDAGAQVVLTTK
             .******:.*** :* :***: * ***:*: ** **: :. **:. *: :**:*:***

HUMAN       GIDDMCLKYFVEAGAMAVRRVLKRDLKRIAKASGATILSTLANLEGEETFEAAMLGQAEE
CtCCT1      GIDDLCLKAFVEKGAMAVRRCKKEDLRRIAKATGATLLVTFSDLNGDEKFEPSYLGHAEE
YEAST       GIDDLCLKEFVEAKIMGVRRCKKEDLRRIARATGATLVSSMSNLEGEETFESSYLGLCDE
            ****:*** ***   *.***  *.**:***:*:***:: ::::*:*:*.** : ** .:*

HUMAN       VVQERICDDELILIKNTKARTSASIILRGANDFMCDEMERSLHDALCVVKRVLESKSVVP
CtCCT1      VVQERIADDECILIKGTKAHSSASIILRGPNEFTLDEMERSVHDSLCAVKRTLESGSIVP
YEAST       VVQAKFSDDECILIKGTSKHSSSSIILRGANDYSLDEMERSLHDSLSVVKRTLESGNVVP
            *** ::.*** ****.*. ::*:****** *::  ******:**:*..***.*** .:**

HUMAN       GGGAVEAALSIYLENYATSMGSREQLAIAEFARSLLVIPNTLAVNAAQDSTDLVAKLRAF
CtCCT1      GGGAVETALHIFLEEFAGTVGSREQLAIGEFAQSLLVIPKTLAVNAAKDASELVAQLRSR
YEAST       GGGCVEAALNIYLDNFATTVGSREQLAIAEFAAALLIIPKTLAVNAAKDSSELVAKLRSY
            ***.**:** *:*:::* ::********.*** :**:**:*******:*:::***:**:

HUMAN       HNEAQVN------------PERKNLKWIGLDLSNGKPRDNKQAGVFEPTIVKVKSLKFAT
CtCCT1      HALSQRIQEGEGSEDEKTIAKKKAYKNYGLDLVRGKVVDEIKAGVVEPSISKIRQLKSAT
YEAST       HAASQMAKP--------EDVKRRSYRNYGLDLIRGKIVDEIHAGVLEPTISKVKSLKSAL
            *  :*                :::  :  **** .**  *: :***.**:* *::.** *

HUMAN       EAAITILRIDDLIKLHPESKDDKHGSYEDAVHSGALND
CtCCT1      EACIAIMRIDTLIKLDPEPQPEDDGHDH----------
YEAST       EACVAILRIDTMITVDPEPPKED-PHDH----------
            **.::*:*** :*.:.**   :.    .
```

Alignment Scores

1: HUMAN	100.00	63.92	62.39
2: CtCCT1	63.92	100.00	72.89
3: YEAST	62.39	72.89	100.00

CCT2

```
HUMAN       MASLSLAPVNIFKAGADEERAETARLTSFIGAIAIGDLVKSTLGPKGMDKILLSSGRDAS
CtCCT2      --MSSFSPTQIFEEGTTEEKGENARLSAFVGAIAVGDLVKSTLGPKGMDKILQSA-STGE
YEAST       ------MSVQIFGDQVTEERAENARLSAFVGAIAVGDLVKSTLGPKGMDKLLQSA-SSNT
                     .:**   . **:.*.***::*:****:***************:* *:

HUMAN       LMVTNDGATILKNIGVDNPAAKVLVDMSRVQDDEVGDGTTSVTVLAAELLREAESLIAK-
CtCCT2      IMVTNDGATILKSIALDNAAAKVLVNISKVQDDEVGDGTTSVAVLAAELLREAEKLVNQ-
YEAST       CMVTNDGATILKSIPLDNPAAKVLVNISKVQDDEVGDGTTSVTVLSAELLREAEKLIDQS
             ***********.* :** ******::*:*************:**:********.*: :

HUMAN       KIHPQTIIAGWREATKAAREALLSSAVDHGSDEVKFRQDLMNIAGTTLSSKLLTHHKDHF
CtCCT2      KIHPQTIIEGYRIASQAALKALEASAVDHSNNPEQFKKDLQAIARTTLSSKVLAQDRDHF
YEAST       KIHPQTIIEGYRLASAAALDALTKAAVDNSHDKTMFREDLIHIAKTTLSSKILSQDKDHF
            ******** *:* *: ** .**  :***:. :   *::**  ** ******:*::.:***

HUMAN       TKLAVEAVLRLKGSGNLEAIHIIKKLGGSLADSYLDEGFLLDKKIGVNQPKRIENAKILI
CtCCT2      AKLAVEAVLRLKGSSDLSHIQIIKKAGGKLCESYLDEGFILDKKIGVNQPKRLEKAKILI
YEAST       AELATNAILRLKGSTNLEHIQIIKILGGKLSDSFLDEGFILAKKFGNNQPKRIENAKILI
            ::**.:*:****** :*. *:***  **.*.:*:*****:* **:* *****:*:*****

HUMAN       ANTGMDTDKIKIFGSRVRVDSTAKVAEIEHAEKEKMKEKVERILKHGINCFINRQLIYNY
CtCCT2      ANTPMDTDKVKIFGARLKVSSTSKLAELERAEREKMKAKVEKIKAHGINCFINRQLIYNW
YEAST       ANTTLDTDKVKIFGTKFKVDSTAKLAQLEKAEREKMKNKIAKISKFGINTFINRQLIYDY
            *** :****:****::.:*.**:*:*::*:**:**** *: :*  .*** ********::

HUMAN       PEQLFGAAGVMAIEHADFAGVERLALVTGGEIASTFDHPELVKLGSCKLIEEVMIGEDKL
CtCCT2      PEQLFTDAGIMSIEHADFDGIERLALVTGGEIASTFDHPEQVKLGYCDLIEEIMIGEDTL
YEAST       PEQLFTDLGINSIEHADFEGVERLALVTGGEVVSTFDEPSKCKLGECDVIEEIMLGEQPF
            *****   *: :****** *:**********:.****.*.  *** *.:***:*:**: :

HUMAN       IHFSGVALGEACTIVLRGATQQILDEAERSLHDALCVLAQTVKDSRTVYGGGCSEMLMAH
CtCCT2      IKFSGVAAGEACTIVLRGATDQLLDEAERSLHDALAVLSQMVKEPRTILGGGCAEMIMAK
YEAST       LKFSGCKAGEACTIVLRGATDQTLDEAERSLHDALSVLSQTTKETRTVLGGGCAEMVMSK
            ::***   ************:* ************.**:* .*: **: ****:**:*::

HUMAN       AVTQLANRTPGKEAVAMESYAKALRMLPTIIADNAGYDSADLVAQLRAAHSEGNTTAGLD
CtCCT2      AVEAAATRVEGKKQTAVGAFAVALRQLPTILADNAGLDSGDLVARLRKAIYDGLTTYGLD
YEAST       AVDTEAQNIDGKKSLAVEAFARALRQLPTILADNAGFDSSELVSKLRSSIYNGISTSGLD
            **   * .  **:  *: ::* *** ****:***** **.:**::** :  :* :* ***

HUMAN       MR--EGTIGDMAILGITESFQVKRQVLLSAAEAAEVILRVDNIIKAAPRKRVPDHHPC
CtCCT2      LMTPGGGIADMRELGVIESYKLKRAVVSSASEAAELLLRVDDIIRAAPRKREKH----
YEAST       LN--NGTIADMRQLGIVESYKLKRAVVSSASEAAEVLLRVDNIIRARPRTANRQHM--
            :    * *.**  **: **::** *: **:****::****:**:* **.   .
```

Alignment Scores

1: HUMAN	100.00	69.13	65.59
2: CtCCT2	69.13	100.00	73.66
3: YEAST	65.59	73.66	100.00

CCT3

```
HUMAN       MMGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMKMLLDPMGGIVMT
CtCCT3      -MQAPVLVMNTQSGDRTTGRRAQISNIAAAKTVADIIRSCLGPKAMLKMLLDPMGGIVLT
YEAST       -MQAPVVFMNA-SQERTTGRQAQISNITAAKAVADVIRTCLGPKAMLKMLLDPMGGLVLT
             *    :.: : . .* :**:.* .** ***::**:**:*****:*:*********:*:*

HUMAN       NDGNAILREIQVQHPAAKSMIEISRTQDEEVGDGTTSVIILAGEMLSVAEH-FLEQQMHP
CtCCT3      NDGHAILREIEVSHPAAKSMIELSRTQDEEVGDGTTTVIILAGEILAQALPQ-LERNIHP
YEAST       NDGHAILREIDVAHPAAKSMLELSRTQDEEVGDGTTTVIILAGEILAQCAPYLIEKNIHP
            ***:******:* *******:*:*************:*******:*: .    :*:::**

HUMAN       TVVISAYRKALDDMISTLKKISIPVDISDSDMMLNIINSSITTKAISRWSSLACNIALDA
CtCCT3      VNIIAAFKRALKDALEIIEEISMPIDVNDDKAMYKLINASIGTKFVSRWSDLMCSLALKA
YEAST       VIIIQALKKALTDALEVIKQVSKPVDVENDAAMKKLIQASIGTKYVIHWSEKMCELALDA
            . :* * ::** * :. ::::* *:*:.:.  * ::*::** ** : :**.  *.:**.*

HUMAN       VKMVQF------EENGRKEIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTHPRMRRYI
CtCCT3      VRTVTW------EANGKREVDIKRYARVEKVPGGEIEDSRVLDGVMLNKDITHPKMRRRI
YEAST       VKTVRKDLGQTVEGEPNFEIDIKRYVRVEKIPGGDVLDSRVLKGVLLNKDVVHPKMSRHI
            *: *        * : . *:***:*.****:*** : ** ** **::***:.**:* * *

HUMAN       KNPRIVLLDSSLEYKKGESQTDIEITREEDFTRILQMEEEYIQQLCEDIIQLKPDVVITE
CtCCT3      ENPRIVLLDCPLEYKKGESQTNIEITKEDDWNRILQIEEEQVKAMCDAILAVKPDLVITE
YEAST       ENPRVVLLDCPLEYKKGESQTNIEIEKEEDWNRILQIEEEQVQLMCEQILAVRPTLVITE
            :***:****. **********:*** :*:*:.****:*** :: :*: *: ::* :****

HUMAN       KGISDLAQHYLMRANITAIRRVRKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIK
CtCCT3      KGVSDLAQHYLMKANVTALRRVRKTDNNRIARAVGATIVNRVEDLQESDVGTGCGLFEIE
YEAST       KGVSDLAQHYLLKGGCSVLRRVKKSDNNRIARVTGATIVNRVEDLKESDVGTNCGLFKVE
            **:*********::.. :.:***:*:*******. ** **.* *:*:*.****..**::::

HUMAN       KIGDEYFTFITDCKDPKACTILLRGASKEILSEVERNLQDAMQVCRNVLLDPQLVPGGGA
CtCCT3      KIGDEYFTFLTQCKNPKACTILLRGPSKDVLNEIERNLQDAMGVARNVMFHPRLSPGGGA
YEAST       MIGDEYFSFLDNCKEPKACTIMLRGGSKDILNEIDRNLQDAMAVARNVMLSPSLSPGGGA
             ******:*: :**:******:*** **::*.*::******* *.***:: * * *****

HUMAN       SEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRTLIQNCGASTIRLLTSLRAKHTQE
CtCCT3      TEMAVSVRLAQMARQIEGVQQWPYKAVAEALEVIPRTLVQNAGKSPVRVLTELRAKHAEG
YEAST       TEMAVSVKLAEKAKQLEGIQQWPYQAVADAMECIPRTLIQNAGGDPIRLLSQLRAKHAQG
            :****:  *:: :: : *::****:***:*:* *****:**.* . :*:*:.*****::

HUMAN       NCETWGVNGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGHKKKGDDQ
CtCCT3      K-HSFGVNGDTGAVVDMKEYGVWEPQAIKVQSMKTAIEAACLLLRVDDICSAKKAQPGVG
YEAST       N-FTTGIDGDKGKIVDMVSYGIWEPEVIKQQSVKTAIESACLLLRVDDIVSGVRKQE---
            :  : *::*:.* :*** . *:*** .:* *: ***:*:* ****:*** *. : :

HUMAN       SRQGGAPDAGQE
CtCCT3      T--GGAAQDD--
YEAST       -------
```

Alignment Scores

1: HUMAN	100.00	63.94	59.96
2: CtCCT3	63.94	100.00	73.62
3: YEAST	59.96	73.62	100.00

CCT4

```
HUMAN       MPENVAPRSGATAGAAGGRGKGAYQDRDKPAQIRFSNISAAKAVADAIRTSLGPKGMDKM
CtCCT4      --------MATATQAGSGVTNQAFRDKEKPLAVRSANIVAARAVADAIRTSLGPRGMDKM
YEAST       -------------MSAKVPSNATFKNKEKPQEVRKANIIAARSVADAIRTSLGPKGMDKM
                          :.    : :::::::**  :* :** **::************:*****

HUMAN       IQDGKGDVTITNDGATILKQMQVLHPAARMLVELSKAQDIEAGDGTTSVVIIAGSLLDSC
CtCCT4      IRSGKGETIITNDGSTMLKSMSVMHPTAKMLVQLSKAQDVEAGDGTTSVVVICGSLLGAA
YEAST       IKTSRGEIIISNDGHTILKQMAILHPVARMLVEVSAAQDSEAGDGTTSVVILTGALLGAA
            *: .:*:  *:*** *:**.* ::**.*:***::* *** **********:: *:**.:.

HUMAN       TKLLQKGIHPTIISESFQKALEKGIEILTDMSRPVELSDRETLLNSATTSLNSKVVSQYS
CtCCT4      DRLLQKGIHPSVISESFQRAAAAAVQVLHDMSQPIALTDTAALLQAANTSLSSKIVSQYS
YEAST       ERLLNKGIHPTIIADSFQSAAKRSVDILLEMCHKVSLSDREQLVRAASTSLSSKIVSQYS
             :**:*****::*::*** *   .:::* :*.: : *:*   *:.:*.***.**:*****

HUMAN       SLLSPMSVNAVMKVIDPATATSVDLRDIKIVKKLGGTIDDCELVEGLVLTQKVS--NSGI
CtCCT4      NLLGPMAVNAVTKTIDIKTADNVDLKNIRVIKKVGGTIEDSELVDGLVLTQPVIKSAGGP
YEAST       SFLAPLAVDSVLKISD-ENSKNVDLNDIRLVKKVGGTIDDTEMIDGVVLTQTAIKSAGGP
            .:*.*::*::* *  *  .: .***.:*:::**:****:* *:::*:**** .    .*

HUMAN       TRVEKAKIGLIQFCLSAPKTDMDNQIVVSDYAQMDRVLREERAYILNLVKQIKKTGCNVL
CtCCT4      VRMEKARIGMIQFQLSPPKPDMENTIQVNDYRQMDKIVKEERQYLLNMVKKIKKAKCNVL
YEAST       TRKEKAKIGLIQFQISPPKPDTENNIIVNDYRQMDKILKEERAYLLNICKKIKKAKCNVL
            .* ***:**:*** :* ** * :* * *.** ***:::*** *:**: *:***: ****

HUMAN       LIQKSILRDALSDLALHFLNKMKIMVIKDIEREDIEFICKTIGTKPVAHIDQFTADMLGS
CtCCT4      FIQKSILRDAVNDLSLHFLQRLGILAVKDIERDEVEFICKSTGCKPIADIESFTEDKLGS
YEAST       LIQKSILRDAVNDLALHFLSKLNIMVVKDIEREEIEFLSKGLGCKPIADIELFTEDRLGS
            :*********:.**:****.:: *:.:*****:::**:.*  * **:*.*: ** * ***

HUMAN       AELAEEVNLNGSGKLLKITGCAS--PGKTVTIVVRGSNKLVIEEAERSIHDALCVIRCLV
CtCCT4      ADLVEEVHSAGSR-YVKVTGTKST--GKTVSVVVRGANSLILDEAERSLHDALCAVRCLV
YEAST       ADLVEEIDSDGSK-IVRVTGIRNNNARPTVSVVIRGANNMIIDETERSLHDALCVIRCLV
            *:*.**:.  **   ::**  .     **::*:**:*.::::*:***:*****.:****

HUMAN       KKRALIAGGGAPEIELALRLTEYSRTLSGMESYCVRAFADAMEVIPSTLAENAGLNPIST
CtCCT4      KKKALIAGGGAPEIEIAAQLNKQARALSGTEAICWKAFADAMEVIPTTLAENAGLNPIKV
YEAST       KERGLIAGGGAPEIEISRRLSKEARSMEGVQAFIWQEFASALEVIPTTLAENAGLNSIKV
            *::.************:: :*.: :*::.* ::   : **.*:****:********* *..

HUMAN       VTELRNRHAQGEKTAGINVRKGGISN-ILEELVVQPLLVSVSALTLATETVRSILKIDDV
CtCCT4      VTDLRHRHEMGEKNAGVSIKSGGVSSDITKENVLQPLLVSTSAIELAAETVKMILRIDDI
YEAST       VTELRSKHENGELNDGISVRRSGTTN-TYEEHILQPVLVSTSAITLASECVKSILRIDDI
            **:** :*  ** . *:.:: .* :.   :* ::**:***.**: **:* *: **:***:

HUMAN       VNTR
CtCCT4      ALSR
YEAST       AFSR
            . :*
```

Alignment Scores

1: HUMAN	100.00	62.00	58.78
2: CtCCT4	62.00	100.00	65.78
3: YEAST	58.78	65.78	100.00

CCT5

```
YEAST       MAARPQQPPMEMPDLSNAIVAQDEMGRPFIIVKDQGNKKRQHGLEAKKSHILAARSVASI
CtCCT5      -------MGSMNIDLSNATVMKDEQGRPFIVVRDQGKKKRQHGNEAVRAHILAARTVANI
HUMAN       -------------MASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVANT
                          * . :  ** ****:::::**..*.*  * ** ::**:**::**.

YEAST       IKTSLGPRGLDKILISPDGEITITNDGATILSQMELDNEIAKLLVQLSKSQDDEIGDGTT
CtCCT5      IKTSLGPRGLDKILISPDGDITVTNDGATILQQMEITNHVAKLLVELSKSQDDEIGDGTT
HUMAN       MRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAKLMVELSKSQDDEIGDGTT
            ::*****.****:::. **::*:********. *:: :.:****:*:**************

YEAST       GVVVLASALLDQALELIQKGIHPIKIANGFDEAAKLAISKLEETCDDISASNDELFRDFL
CtCCT5      GVVVLAGALLEQAAELIDKGIHPIRIADGYDQACDIACAELDRISDVIEFDR--ENTENL
HUMAN       GVVVLAGALLEEAEQLLDRGIHPIRIADGYEQAARVAIEHLDKISDSVLVDI--KDTEPL
            ******.***::* :*:::*****:**:*:::*. :*  .*:. .* :  .      : *

YEAST       LRAAKTSLGSKIVSKDHDRFAEMAVEAVINVMDKDRKDVDFDLIKMQGRVGGSISDSKLI
CtCCT5      IKVARTSLGSKIVSKAHDQFAKIAVDAVLSVADLERKDVDFDLIKVDGKVGGSLEDTMLV
HUMAN       IQTAKTTLGSKVVNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLEDTKLI
            ::.*:*:****:*.. * ::*::**:**:.* * :*:****:***::*:*** :.*: *:

YEAST       NGVILDKDFSHPQMPKCVLPKEGSDGVKLAILTCPFEPPKPKTKHKLDISSVEEYQKLQT
CtCCT5      KGVIIDKDFSHPQMPSEV------RDAKIAILTCAFEPPKPKTKHKLEISTVEEFKKLQN
HUMAN       KGVIVDKDFSHPQMPKKV------EDAKIAILTCPFEPPKPKTKHKLDVTSVEDYKALQK
            :****:**********. *       ..*:***** ************:::::**::: **.

YEAST       YEQDKFKEMIDDVKKAGADVVICQWGFDDEANHLLLQNDLPAVRWVGGQELEHIAISTNG
CtCCT5      YEREKFVEMIQQIKDAGANLAICQWGFDDEANHLLLQNNLPAVRWVGGPEIELIAIATNG
HUMAN       YEKEKFEEMIQQIKETGANLAICQWGFDDEANHLLLQNNLPAVRWVGGPEIELIAIATGG
            **::** ***:::*.:**::.*****************:********* *:* ***:*.*

YEAST       RIVPRFQDLSKDKLGTCSRIYEQEFGTTKDRMLIIEQSKETKTVTCFVRGSNKMIVDEAE
CtCCT5      RIVPRFEDLRPEKLGTAGLVREITFGTTREKMLVIEECANTRAVTVFVRGSNKMIIDEAK
HUMAN       RIVPRFSELTAEKLGFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEEAK
            ******.:*  :*** .. : *  ****::::**:**:. :::::** *:**.****::**:

YEAST       RALHDSLCVVRNLVKDSRVVYGGGAAEVTMSLAVSEEADKQRGIDQYAFRGFAQALDTIP
CtCCT5      RSLHDALCVVRNLVRDNRVVYGGGSAEVACSLAVEDAAVKTPGLEQYAMRAFAEALDTIP
HUMAN       RSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCPTLEQYAMRAFADALEVIP
            *:***:***:***::*.*******:**:: :***.: * *   ::***:*.**:**:.**

YEAST       MTLAENSGLDPIGTLSTLKSKQLKEK--ISNIGVDCLGYGSNDMKELFVVDPFIGKKQQI
CtCCT5      MTLAENSGLNPIATLAEIKSQQVKDPTARGRVGVDCMGTGKNNMKEAFVIDPLIGKKQQL
HUMAN       MALSENSGMNPIQTMTEVRARQVKEM--NPALGIDCLHKGTNDMKQQHVIETLIGKKQQI
            *:*:****::** *:: ::::*:*:      :*:**:  *.*:**: .*:: :******:

YEAST       LLATQLCRMILKIDNVIISGKDEY--
CtCCT5      MLATQLCRMVLKVNNVIVSGSGEEEF
HUMAN       SLATQMVRMILKIDDIRKPGESEE--
             ****: **:**::::   *..*
```

Alignment Scores

1: YEAST	100.00	67.64	60.26
2: CtCCT5	67.64	100.00	67.84
3: HUMAN	60.26	67.84	100.00

CCT6

```
YEAST       -MSLQLLNPKAESLRRDAALKVNVTSAEGLQSVLETNLGPKGTLKMLVDGAGNIKLTKDG
CtCCT6      MSAAQLLNPKAESRRRQEALRVNISAGEGLQDVLKSNLGPMGTIKMLVDGAGQIKLTKDG
HUMAN       MAAVKTLNPKAEVARAQAALAVNISAARGLQDVLRTNLGPKGTMKMLVSGAGDIKLTKDG
              : : ******  * : ** **:::..***.**.:**** **:****.***:*******

YEAST       KVLLTEMQIQSPTAVLIARAAAAQDEITGDGTTTVVCLVGELLRQAHRFIQEGVHPRIIT
CtCCT6      NVLLREMQIQNPTAVMIARAATAQDDICGDGTTSVVLLVGELLKQADRYIQEGLHPRIIT
HUMAN       NVLLHEMQIQHPTASLIAKVATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPRIIT
            :*** ***** *** :**:.*:***:* *****: * ::****:**. :*.**:******

YEAST       DGFEIARKESMKFLDEFKISKTNLSNDREFLLQVARSSLLTKVDADLTEVLTPIVTDAVL
CtCCT6      DGFEIAKNEALKFLDKFKLPKD---IDRELLLNVARTSLSTKLSSSLAQHLTPSIVDAVL
HUMAN       EGFEAAKEKALQFLEEVKVSRE---MDRETLIDVARTSLRTKVHAELADVLTEAVVDSIL
            :*** *:::::::**::.*: :     *** *::***:** **: :.*:: **  :.*::*

YEAST       SVYDAQADNLDLHMVEIMQMQHLSPKDTTFIKGLVLDHGGRHPDMPTRVKNAYVLILNVS
CtCCT6      AIYQP-PAKPDLHMIEIMKMQHRTASDTQLIRGLALDHGARHPDMPKRVENAYILTLNVS
HUMAN       AIKKQ-DEPIDLFMIEIMEMKHKSETDTSLIRGLVLDHGARHPDMKKRVEDAYILTCNVS
            :: .      **.*:***:*:* : .** :*:**.****.***** .**::**:*  ***

YEAST       LEYEKTEVNSGFFYSSADQRDKLAASERKFVDAKLKKIIDLKNEVCGMDPDKGFVIINQK
CtCCT6      LEYEKSEINSGFFYSSAEQRDKLVESERKFVDLKLKKIVELKKQVCGNDPNKNFVVINQK
HUMAN       LEYEKTEVNSGFFYKSAEEREKLVKAERKFIEDRVKKIIELKRKVCGD-SDKGFVVINQK
            *****:*:******.**::*:**. :*****:: ::***::**.:***   :*.**:****

YEAST       GIDPMSLDVFAKHNILALRRAKRRNMERLQLVTGGEAQNSVEDLSPQILGFSGLVYQETI
CtCCT6      GIDPLSLDVLAKNGILALRRAKRRNMERLQLVCGGVAQNSVDDLTPDVLGWAGLVYEQQL
HUMAN       GIDPFSLDALSKEGIVALRRAKRRNMERLTLACGGVALNSFDDLSPDCLGHAGLVYEYTL
            ****:***.::*..*:************* *. ** * **.:**:*: ** :****:  :

YEAST       GEEKFTYVTENTDPKSCTILIKGSTHYALAQTKDAVRDGLRAVANVLKDKNIIPGAGAFY
CtCCT6      GEEKYTFVEDVKDPKSVTILIKGPNQHTITQVTDAVRDGLRSVYNCIVDKAVVPGAGAFH
HUMAN       GEEKFTFIEKCNNPRSVTLLIKGPNKHTLTQIKDAVRDGLRAVKNAIDDGCVVPGAGAVE
            ****:*:: . .:*:* *:**** .::::::* .********:* * : *  ::******.

YEAST       IALSRYLRSANMNKLGAKGKTKTGIEAFAEALLVIPKTLVKNSGFDPLDVLAMVEDELDD
CtCCT6      VACAAHLRSDEF-LKAVKGKAKFGVEAFADALLVIPKTLAANAGLDVQDAVALLQD----
HUMAN       VAMAEALIK--H-KPSVKGRAQLGVQAFADALLIIPKVLAQNSGFDLQETLVKIQAE---
            :* :  * .      ..**::: *::***:***:***.*. *:*:*  :.:. ::

YEAST       AQDSDETRYVGVDLNIGDSCDPTIEGIWDSYRVLRNAITGATGIASNLLLCDELLRAGRS
CtCCT6      --ELRAGNVAGIDLQTGQPMDPVLEGVFDSFRVLRNCIASSSSIASNLLLCDELLKARQM
HUMAN       --HSESGQLVGVDLNTGEPMVAAEVGVWDNYCVKKQLLHSCTVIATNILLVDEIMRAGMS
              .    . .*:**: *:    .  *::*.: * :: : ..: **:*:** **:::*

YEAST       TLKETPQ----------
CtCCT6      GRGGGPGGPGGMEGVEE
HUMAN       SLKG-------------
```

Alignment Scores

1: YEAST	100.00	63.93	57.55
2: CtCCT6	63.93	100.00	63.21
3: HUMAN	57.55	63.21	100.00

CCT7

```
HUMAN       ----MMPTPVILLKEGTDSSQGIPQLVSNISACQVIAEAVRTTLGPRGMDKLIVDGRGKA
CtCCT7      MAFAGQPPMIVVLKEGTDTSQGKGQILSNINACLAVQSTIKSTLGPYGGDLLLVDQNGKQ
YEAST       MNFGSQTPTIVVLKEGTDASQGKGQIISNINACVAVQEALKPTLGPLGSDILIVTSNQKT
                     :::******:***  *::***.** .: .::: **** * * *:*  . *

HUMAN       TISNDGATILKLLDVVHPAAKTLVDIAKSQDAEVGDGTTSVTLLAAEFLKQVKPYVEEGL
CtCCT7      TITNDGATVMKLLDIVHPAARILVDIARSQDAEVGDGTTSVVVLAGEILKEIKEHVEAGV
YEAST       TISNDGATILKLLDVVHPAAKTLVDISRAQDAEVGDGTTSVTILAGELMKEAKPFLEEGI
            **:*****::****:*****: ****:::************.:**.*::*: * .:* *:

HUMAN       HPQIIIRAFRTATQLAVNKIKEIAVTVKKADKVEQRKLLEKCAMTALSSKLISQQKAFFA
CtCCT7      STQIIIKGLRKAASMAVNKIREVAINA---EEGDRIDTLHKLAATAMTSKLIKRNSDFFT
YEAST       SSHLIMKGYRKAVSLAVEKINELAVDITS-EKSSGRELLERCARTAMSSKLIHNNADFFV
              ::*::. *.*..:**:**.*:*:     :: .  . *.: * **::**** .:  **.

HUMAN       KMVVDAVMMLD-DLLQLKMIGIKKVQGGALEDSQLVAGVAFKKTFSYAGFEMQPKKYHNP
CtCCT7      KMVVEAVLSLDQDDLNEKLIGMKKIPGGSLTDSIFVKGVAFKKTFSYAGFEQQPKKFVKP
YEAST       KMCVDAVLSLDRNDLDDKLIGIKKIPGGAMEESLFINGVAFKKTFSYAGFEQQPKKFNNP
            ** *:**: ** : *: *:**:**: **:: :* :: ************** ****: :*

HUMAN       KIALLNVELELKAEKDNAEIRVHTVEDYQAIVDAEWNILYDKLEKIHHSGAKVVLSKLPI
CtCCT7      KICCLNVELELKAEKDNAEVRVEQVSEYQAIVDAEWQIIYNKLEAIYKTGAKVVLSKLPI
YEAST       KILSLNVELELKAEKDNAEVRVEHVEDYQAIVDAEWQLIFEKLRQVEETGANIVLSKLPI
            **  ****************:**. *.:*********::::**. : .:**::*******

HUMAN       GDVATQYFADRDMFCAGRVPEEDLKRTMMACGGSIQTSVNALSADVLGRCQVFEETQIGG
CtCCT7      GDLATQYFADRDIFCAGRVTSEDMERVIQATGATIQSTCSDIRPEHLGTCGLFEERQIGG
YEAST       GDLATQFFADRNIFCAGRVSADDMNRVIQAVGGSIQSTTSDIKPEHLGTCALFEEMQIGS
            **:***:****::******  :*::*.: * *.:**:: . :  : ** * :*** ***.

HUMAN       ERYNFFTGCPKAKTCTFILRGGAEQFMEETERSLHDAIMIVRRAIKNDSVVAGGGAIEME
CtCCT7      ERFNFFEDCPEAKTCTLVLRGGAEQFIAEVERSLHDAIMIVKRAIKNKTTVAGGGATEME
YEAST       ERYNLFQGCPQAKTCTLLLRGGAEQVIAEVERSLHDAIMIVKRALQNKLIVAGGGATEME
            **:*:* .**:*****::*******.: *.***********:**::*.  ****** ***

HUMAN       LSKYLRDYSR-TIPGKQQLLIGAYAKALEIIPRQLCDNAGFDATNILNKLRARHAQGGTW
CtCCT7      VSAYLHRYADQTVRNKQQAIIKNFAKALEIIPRQLCDNAGFDATDILNRLRVEHRRGNIW
YEAST       VSKCLRDYSK-TIAGKQQMIINAFAKALEVIPRQLCENAGFDAIEILNKLRLAHSKGEKW
            :*  *: *:  *: .*** :*  :*****:******:****** :***:**  * :*  *

HUMAN       YGVDINNEDIADNFEAFVWEPAMVRINALTAASEAACLIVSVDETIKNPRSTVD-----A
CtCCT7      AGVDFQNEGVADMMEKFVWEPALVKINAINAATEAACLILSVDETIRNEESKTPPAPGSK
YEAST       YGVVFETENIGDNFAKFVWEPALVKINALNSATEATNLILSVDETITNKGSESANAGMMP
             ** ::.*.:.* :  ******:*:***:.:*:**: **:****** *  *

HUMAN       PTA--AGRGRGRGRPH-
CtCCT7      PARGGAGRGRGRGMPRR
YEAST       P----QGAGRGRGMPM-
            *     * ***** *
```

Alignment Scores

1: HUMAN	100.00	63.15	63.15
2: CtCCT7	63.15	100.00	68.25
3: YEAST	63.15	68.25	100.00

CCT8

```
HUMAN       MALHVPKAPGFAQMLKEGAKHFSGLEEAVYRNIQACKELAQTTRTAYGPNGMNKMVINHL
CtCCT8      MSLSIPGAPN-AGLFKQGYNSYDSEDGAVLRNIDACRAISSTVQTSLGPYGRNKVVINHL
YEAST       MSLRLPQNPN-AGLFKQGYNSYSNADGQIIKSIAAIRELHQMCLTSMGPCGRNKIIVNHL
            *:* :*  *. * ::*:* : :.. :  : :.* * : : .   *: ** * **:::***

HUMAN       EKLFVTNDAATILRELEVQHPAAKMIVMASHMQEQEVGDGTNFVLVFAGALLELAEELLR
CtCCT8      GKMILTSDAATILRELDVVHPAAKLLVMASQQQEAEMGDATNLVIVLAGELLRKAEDLLR
YEAST       GKIIITNDAATMLRELDIVHPAVKVLVMATEQQKIDMGDGTNLVMILAGELLNVSEKLIS
             *:::*.****:****:: ***.*::***:. *: ::**.**:*::** **. :*.*:

HUMAN       IGLSVSEVIEGYEIACRKAHEILPNLVCCSAKNLRDIDEVSSLLRTSIMSKQYGNEVFLA
CtCCT8      MGLKTSDIVNGYERAQKIALDALEELEVDKVEDLRNPEELKKALRTVIASKQNGSEDFLA
YEAST       MGLSAVEIIQGYNMARKFTLKELDEMVVGEITDKNDKNELLKMIKPVISSKKYGSEDILS
            :**.. :::**: * : : . * ::   .  : .: :*: . ::  * **: *.* :*:

HUMAN       KLIAQACVSIFPDS------GHFNVDNIRVCKILGSGISSSSVLHGMVFKKETEGDVTS-
CtCCT8      GLVAEAVLSVLPKN-----PVNFNVDNVRVVKIMGGSLDQSRVVRGMVFNKEPDGAVKK-
YEAST       ELVSEAVSHVLPVAQQAGEIPYFNVDSIRVVKIMGGSLSNSTVIKGMVFNREPEGHVKSL
             *:::*   ::*          ****.:** **:*..:..* *::*****:* :* *..

HUMAN       --VKDAKIAVYSCPFDGMITETKGTVLIKTAEELMNFSKGEENLMDAQVKAIADTGANVV
CtCCT8      --ARKAKVGVFTCPIDISQTETKGTVLLHNAKEMLNFSKGEEERLEAQIKELHDVGLRVV
YEAST       SEDKKHKVAVFTCPLDIANTETKGTVLLHNAQEMLDFSKGEEKQIDAMMKEIADMGVECI
               :. *:.*::***:*   ********::.*:*:::******: ::* :* : * * . :

HUMAN       VTGGKVADMALHYANKYNIMLVRLNSKWDLRRLCKTVGATALPRLTPPVLEEMGHCDSVY
CtCCT8      VAGSTVGELAMHYLNRYGILVIKIFSKFELRRLCRVVGATPLARLGAPMPDEMGTIDVVE
YEAST       VAGAGVGELALHYLNRYGILVLKVPSKFELRRLCRVCGATPLPRLGAPTPEELGLVETVK
            *:*. *.::*:** *:*.*:::: **::*****:. *** * **  *  :*:*  : *

HUMAN       LSEVGDTQVVVFKHEK-EDGAISTIVLRGSTDNLMDDIERAVDDGVNTFKVLTR--DKRL
CtCCT8      TQEIGGDRVTVFRQED-EATRTATIVLRGATQNHLDDLERAVDDGVNVIKAITK--DARL
YEAST       TMEIGGDRVTVFKQEQGEISRTSTIILRGATQNNLDDIERAIDDGVAAVKGLMKPSGGKL
              *:*. :*.**::*. *    :**:***:*:* :**:***:**** ..* : :  . :*

HUMAN       VPGGGATEIELAKQITSYGETCPGLEQYAIKKFAEAFEAIPRALAENSGVKANEVISKLY
CtCCT8      VPGAGATEIELVDRIQAAADKTPGLAQYSIKKYGEAFEVVPRTLAESAGLDATEVVSRLY
YEAST       LPGAGATEIELISRITKYGERTPGLLQLAIKQFAVAFEVVPRTLAETAGLDVNEVLPNLY
            :**.******* .:*   .:  *** * :**::. ***.:**:***.:*:...**: .**

HUMAN       AVHQEGN--------KNVGLDIEAE-VPAVKDMLEAGILDTYLGKYWAIKLATNAAVTVL
CtCCT8      AAHQK-------KDGWTTGVDIENQDNTGVLDAEDEGILDLLSSKQWAIKLATEAARTVL
YEAST       AAHNVTEPGAVKTDHLYKGVDIDGESDEGVKDIREENIYDMLATKKFAINVATEAATTVL
            *.*:               *:**: :   .* *  : .* *    * :**::**:** ***

HUMAN       RVDQIIMAKPAGGPKPPSGKK--DWDDDQND
CtCCT8      SVDQIIVARQAGGPKPP-GPN-PNWDED---
YEAST       SIDQIIMAKKAGGPRAPQGPRPGNWDQED--
             :****:*: ****: * * .  :**::
```

Alignment Scores

1: HUMAN	100.00	52.50	47.52
2: CtCCT8	52.50	100.00	60.15
3: YEAST	47.52	60.15	100.00