A

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>Cre_CC-1690  Chlamydomonas reinhardti MEKHLA domain containing protein

MQMSHRVSRAATGLGCRRSVVAVPVVAAPRRICILAAKKGDKGGKGGKGAKKSALADLLKKKEEATGSAAATEGASNAVP
ADCVSPEGRMLVFTLADSYYRLTKKYLLEGVDFEKLPAALFRAPFALLAHNKFQEGVKDPVYIYGNRAALDLFEKSWDDL
LKMPSRLSAPVDESAQTDRDGLLEKAAKTGYVTGYEAWRVSSTGRRFKIKDVTLFNLIDRSGTKIGQAAVFSQYETEDGV
VHTIKGSEPDVEEEAAAAGPAIPTPEEIEAAEAAVAEQAAHVRSLKEVQGLQNNDIPVQIAVMELKKRKEKLAALQKALD
DALAASKAAFDDDDDE.
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B

Query sequence: Cre_CC-1690; selected matches from PSI-blast searches:

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gi|30138191|emb|CAD84197.1|  conserved hypothetical protein [Nitrosomonas
europaea ATCC 19718] + gi|30248305|ref|NP_840375.1|           Length=162

 Score =  101 bits (251),  Expect = 1e-20, Method: Composition-based stats.
 Identities = 61/150 (40%), Positives = 90/150 (60%), Gaps = 17/150 (11%)

Query  92   VFTLADSYYRLTKKYLLEGVDFEKLPAA-----LFRAPFALLAHNKFQEGVKDPVYIYGN  146
            V  L +SY   T +YL +     KL A+     L +APFAL++H        DP++ YGN
Sbjct  15   VAILQESYRHYTGRYLFD----PKLGASEAIVWLEQAPFALVSHGT----QPDPIFNYGN  66

Query  147  RAALDLFEKSWDDLLKMPSRLSA-PVDESAQTDRDGLLEKAAKTGYVTGYEAWRVSSTGR  205
            + AL LF  +WD+  +MPSRLSA PVD +   +R  LL+  ++ GY+  Y   R+++ GR
Sbjct  67   QTALQLFGMTWDEFTRMPSRLSAEPVDRA---ERTRLLDHVSRDGYIDDYTGVRIAADGR  123

Query  206  RFKIKDVTLFNLIDRSGTKIGQAAVFSQYE  235
            RF I+  T++NL+D SG   GQAA+  ++E
Sbjct  124  RFLIRHATVWNLLDESGRFYGQAAMIPEWE  153
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C

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gi|72121282|gb|AAZ63468.1|  PAS [Ralstonia eutropha JMP134] +
gi|46131006|ref|ZP_00169006.2|  COG0642: Signal transduction histidine kinase
[Ralstonia eutropha JMP134] + gi|73537945|ref|YP_298312.1|  PAS [Ralstonia
eutropha JMP134]          Length=639

 Score = 56.2 bits (135),  Expect = 4e-07, Method: Composition-based stats.
 Identities = 25/89 (28%), Positives = 37/89 (41%), Gaps = 4/89 (4%)

Query  146  NRAALDLFEKSWDDLLKMP-SRLSAPVDESAQTDRDGLLEKAAKTGYVTGYEAWRVSSTG  204
            NR A  +      +++    SR   P D  A+      LE A + G V   + WRV   G
Sbjct  45   NRGAQRIKGYEASEIIGSHFSRFY-PEDSIARGWPQKELELARRHGRVED-KGWRVRKDG  102

Query  205  RRFKIKDVTLFNLIDRSGTKIGQAAVFSQ  233
             RF   +V +  L + +G  IG A +
Sbjct  103  TRFW-ANVVITALHNEAGEIIGFAKITRD  130


 Score = 41.5 bits (97),  Expect = 0.011, Method: Composition-based stats.
 Identities = 21/89 (23%), Positives = 34/89 (38%), Gaps = 4/89 (4%)

Query  146  NRAALDLFEKSWDDLLKMP-SRLSAPVDESAQTDRDGLLEKAAKTGYVTGYEAWRVSSTG  204
            N  A  +      +++    S    P ++ A    + L+++A + G V   E WR+   G
Sbjct  173  NAGAAQIKGYRSSEIVGRHFSTFYLP-EDVAAGKPERLIQRAREHGSVQD-EGWRMRKDG  230

Query  205  RRFKIKDVTLFNLIDRSGTKIGQAAVFSQ  233
              F    VTL  + D      G A V
Sbjct  231  SLFW-ASVTLTAIYDEHRQLRGFAKVTRD  258
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D

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gi|27350430|dbj|BAC47441.1|  two-component hybrid sensor and regulator
[Bradyrhizobium japonicum USDA 110] + gi|27377287|ref|NP_768816.1|  two-
component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]
Length=634

  Score = 53.0 bits (126),  Expect = 2e-05, Method: Composition-based stats.
  Identities = 27/88 (30%), Positives = 38/88 (43%), Gaps = 2/88 (2%)

Query  146  NRAALDLFEKSWDDLLKMPSRLSAPVDESAQTDRDGLLEKAAKTGYVTGYEAWRVSSTGR  205
            N  A  L   S D+++     L  P ++ A+      L+ AA+TG  +  E WRV   G
Sbjct  18   NSGAERLKGYSADEIIGKSFSLFYPPEDRAKELPQTALKIAAETGRFSS-EGWRVRKDGT  76
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Query  206  RFKIKDVTLFNLIDRSGTKIGQAAVFSQ  233
            RF    V +  + D  G  IG A V
Sbjct  77   RFW-ALVVVDAIRDEQGQVIGFAKVTRD  103

  Score = 48.7 bits (115),  Expect = 3e-04, Method: Composition-based stats.
  Identities = 23/93 (24%), Positives = 34/93 (36%), Gaps = 4/93 (4%)

Query  146  NRAALDLFEKSWDDLLKMP-SRLSAPVDESAQTDRDGLLEKAAKTGYVTGYEAWRVSSTG  204
            N  A  +     D+++    SR   P ++          L +AAK G     E WRV
Sbjct  146  NPGAQRIKGYDPDEIIGQHFSRFYTP-EDIQTGVPKRALAEAAKLGRFEA-EGWRVRKDS  203

Query  205  RRFKIKDVTLFNLIDRSGTKIGQAAVFSQYETE  237
             RF    V +  + D +G  +G A V
Sbjct  204  SRFW-ASVVIDRITDEAGELVGFAKVTRDVTER  235
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