

Query= EEY58132 Phytophthora infestans hydroxymethylglutaryl-CoA lyase, mitochondrial precursor

> AAX80809 hydroxymethylglutaryl-CoA lyase, putative;
3-hydroxy-3-methylglutarate-CoA lyase, putative
Length = 431

Score = 115 bits (289), Expect = 2e-026, Method: Compositional matrix adjust.
Identities = 82/284 (28%), Positives = 127/284 (44%), Gaps = 25/284 (8%)

Query: 15 SFVKIVEVGPRDGLQNEKTNVSTDDKVKFINLLSETGLSAIEATSFVSPKWVPQMADNAY 74
S +++VE PRD +Q + T+ K++++ L + G A++ SFVSP+ VPQM D+
Sbjct: 9 SSIRMVEC-PRDAMQGLPHFIPTQKIRYLKALLKCGFYALDCGSFVSPRAVPQMRDSTE 67
Query: 75 VLKGISR-----KQGVSYFVLTPNIKGFDSAV-AAGAE EVAIFGAASEAFSQKNINCSIE 128
V+ + K V+ ++ GF A+ G + E F Q+N SI
Sbjct: 68 VIANCWKTMQEEKAAPKLSVVVASLAGFKQALETGPVSVIGYPIGCCERFQQRNAKKSIA 127
Query: 129 ESLERFR-----PVCEKANSLGIRVRGYVSCVLGCPYQGPVDPASAVATV 172
SL+ R PV + G + Y+S G PY V +
Sbjct: 128 MSLDEIRNIKEATDAFNAQRSSNPVAPNEDVNGRELLIYISMAFGNPYGESHSIDLVEKL 187
Query: 173 ALKMLEMGCYEVS LGDTIGVGNPASTLAMLQATKQVIPAERLAVHFHDTYGQALSNILIA 232
+++ G ++SL DT GV P ++ P A HFH +A I+ A
Sbjct: 188 VGELVASGARDISLADTTGVAQPPLIFDTFTQLRKKFPDVTFAGHFHSNAVEARGKIVAA 247
Query: 233 LQEGIAVVDSSAAGLGGCPYA--SGASGNVATEDVLYMVHGLGI 274
L G ++DS+ G+GGCP+A G GNVATE V+ + G+
Sbjct: 248 LDAGCTMIDSALCGMGGC PFAKDDGLVGNVATEV VVKALEERGV 291

> AAX70704 hypothetical protein, conserved
Length = 215

Score = 59.7 bits (143), Expect = 2e-009, Method: Compositional matrix adjust.
Identities = 50/154 (32%), Positives = 79/154 (51%)

Query: 355 AQITSKDKAILDLKNARDRLKKYQSRLDIEANQLHDSAKRLLQAGKRDRAKLALKLKYYK 414
A ITS D+ L+LK RD++ + + A H A LL+ GKR+ A LK +K +
Sbjct: 21 AVITSLDRVQLELKLQRDKIMAAIRKYERAAEGEHVRAAE LLRNGKRELALYCLKRRKAQ 80
Query: 415 EQQM HQADEHLIQVLGMLDTVEWETQQLQVFEG LKAGNSILNAIHKEMSVEAVEELMLET 474
Q+ L V ++ TVE+ + +V E LK G L+ ++ ++++ V ELM T
Sbjct: 81 MSQITLVTSMLNVERLICTVEFAQIEREVVEALKCGKDELSKLNAILNMDDVLELMDST 140
Query: 475 EEAQVTANEISRIIGGNLTVEDEDAVLSELAIE 508
+ + +I+ I+ L V DE +LSEL E
Sbjct: 141 ADVVEESKQINEILAQQLVVYDESELLSELCSAE 174

Query= EDQ88211 Monosiga brevicollis MX1 predicted protein

> AAX70833 glutamine hydrolysing (not ammonia-dependent) carbomoyl phosphate synthase, putative

Length = 1833

Score = 1150 bits (2975), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 611/1235 (49%), Positives = 796/1235 (64%), Gaps = 62/1235 (5%)

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Query: 1      MCDSTIKSLQKVLQNEGDAIKPVFGICLGHQLLSIAIGAKTYKLTFGNRGHNQPCSNNQS 60
              +C TI++++ L E      KP+FG+C+G+ +L++A G TYK+ FG+RG NQP ++NQ
Sbjct: 231    LCTKTIENVRWALTQE----KPIFGVCMGNHMLALAAGGTTYKMKFGHRGQNQPSTSNQD 286
Query: 61      GRCYITSQNHGFATDASALPAG-WVPIFTNENDSTNEGIAHESLPFFSVQFHPEATAGPE 119
              GR IT+QNHGFA D +LP G W      F N ND NEG+ H + PF SVQFHPE GP+
Sbjct: 287    GRVVITTQNHGFAVDFKSLPQGDWEEYFFNPNDQCNEGLRHRTKPFSSVQFHPEGCCGPQ 346
Query: 120     DLELLFDVFLMQCRDKAARAQPLPQTIADFLIEKSYGKPSPPPATLPTKVVLGSGGLTI 179
              D E LF F+      D+ R++ + A F                      P KV+VLG+GG+ I
Sbjct: 347    DTEYLFGEFI----DQVKRSKT--KLAAQFK-----PRKVLVLGAGGIVI 385
Query: 180     GQAGEFDYSGSQAIKALKEEGVQTVLINPNIAITVQTMKGLADKVYFLPVTPEYVEQVIAY 239
              QAGEFDYSGSQ +KAL+EEGV+++L+NPNIATVQT +AD+VYF+PVTPE VE+VI
Sbjct: 386    AQAGEFDYSGSQCLKALREEGVKSILVNPNIATVQTDDEMADQVYFVPVTPEAVERVIEK 445
Query: 240     ERPDGLLLAFFGGQTALNCGVELYEKGFIEKYSVRVLGTPVQAIVDTEDREIFSQKLSQID 299
              ERPDG++L +GGQTALNCG++L + G+ +KY+V+VLGT + I TEDRE+F L QI+
Sbjct: 446     ERPDGIMLGWGGQTALNCGQLQDLKGLVKKYNVQVLGTAISTITVTEDRELFRNALLQIN 505
Query: 300     EKCCPNIACTTVDEVVAAAEKIGYPVMMRSSFALGGLGSGVVDNVDDLREKARVALNNTT 359
              E      ++A T+V E + AA IG+P+M+R++F LGG GSG+V++ ++L K VAL
Sbjct: 506     EPVAKSVAVTSVAEALKAAADIGFPMVRAAFCLGGQGSGIVNSEEELS NKVEVALTVAP 565
Query: 360     QVMLERSLHGWEIEIEYEVVRDCEDNTITVCNMENFDPLGIHTGESIVIAPSQTLSNDEYN 419
              QV+LE S+ GWKEIEYE+VRD DN ITVCNMENFDP+G+HTGESIV+APSQTL+N+EY+
Sbjct: 566     QVLLEESVAGWEIEIEYEVIRDIHDNCITVCNMENFDPMGVHTGESIVVAPSQTLTNEEYH 625
Query: 420     MLRTTAVKVVRHIGIVGECNIQYALNPFSSREYYIVEVNARLSRSSALASKATGYPLAYVA 479
              MLRT A+K++RH+G+VGECENIQY L P SR Y ++EVNARLSRSSALASKATGYPLA+VA
Sbjct: 626     MLRTAAIKIIRHLGVVGECENIQYGFLEPHSRRYVIEVNARLSRSSALASKATGYPLAHVA 685
Query: 480     AKLALGHTLPKLNRNSTRKTACFEPKSLDYCVVKIPRWDLSKFPTVDKRLGTSMKSVGEV 539
              K+ALG L +++N VT+ T ACFEPSLDY VK PRWD++KF V + +G+ MKSVGEV
Sbjct: 686     TKIALGKGLFEIKNGVTKTTMACFEPSLDYVTVKAPRWDVAKFNMVSQEIGSMMKSVGEV 745
Query: 540     MAIGRIFEEAFQKALRMVDLGFMGF-----EAGKVEINQEELVHGSEQRPFMLATALK 592
              MAIGR FEEA QKALRMVD GF      E G      L + R F + ALK
Sbjct: 746     MAIGRTFEEAVQKALRMVDPSNNGFDTPKRLAEMGDKWDYMRALRVPTPDRIFAICRAK 805
Query: 593     RGYTVDQLYDLTKIDKWFLYRLQRIV-MHGDLLKQY--DMHSVPAPILREAKQLGFSDAH 649
              G TVD+++ LT+IDK+FL +LQ ++ M +L Y + ++ L K GFSD
Sbjct: 806     EGITVDEIHRLTRIDKFFLNKLQLLIEMQRELTTLYRGKLDTITYDHLLAMKAHGFSDVQ 865
Query: 650     IGAIVNGNEVGVRTRRQTLNLPVVKQIDTVSAEYP-AYTNYLYLTNGTANDVEFEGDY 708
              I +      VR RR LNI P VKQIDTV+ EYP A YLY TYN +DVEF
Sbjct: 866     IAEYLQCTTDDVRKRRYKLNITPKVKQIDTVAGEYPAAQCCYLYTTYNAQHDDVEFNDRM 925
Query: 709     VMVLGSGVYRIGSSVEFDYCAVGCVRELRLRGFKTIMVNYPETVSTDYDECRLYFDQL 768
              VLG GVYRIGSSVEFDY V RELRLG K I++NYPETVSTDYDECRLYF+++
Sbjct: 926     YAVLGCGVYRIGSSVEFDYGGVLVARELRLGNKVILINYPETVSTDYDECRLYFEEV 985
Query: 769     TFETVMDIYELETARGIVLSMGGQIPNNIANALQRANAKVLGTTTPDMIDNAENRYKFSRM 828
              + ETV+DI E G+++S+GGQI N+A L+ +LGT P +D AE+R KFS+M
Sbjct: 986     SEETVLDILLKEKISGVIIISLGGQIVQNMAIRLKEHGLPILGTPVNVDKAEDRNKFSKM 1045
Query: 829     CDSIGVDQPEWKELTSVESAKFAEKVSYPCLMRPSYILSGTAMRVAHSAHDLENDFRTA 888
              CD +GV QPEW TSV+ AF ++V +P L+RPSY+LSG+AM V S D++ A
Sbjct: 1046    CDQLGVPQPEWILSTSVQDVHAFQCQRVGFTLVLPSPYVLSGSAMAVISSPEDIDRYLTKA 1105
Query: 889     VVVS RDYPVVL SKFILD AKEIEVDAVASNGELVASCISEHVENAGVHSGDATIVHPPVDL 948
              +VS +PVV+SK+ A E +VD VA +G ++ I EH+ENAGVHSGDAT+ PP
Sbjct: 1106    SLVSGTHPVVVS KYEYEGAMEYDVDIVAHGRVLCYAICEHLENAGVHSGDATMFLPPQHT 1165
Query: 949     TQKTMNGCLAIAAGKIAKALHITGPFNIQF-IAKDDNLKVIETNVRASRSFPFVSKTANVD 1007
              ++ M      A +IA L + GP N+QF + KD+ L+VIE N+R+SRS PFVSKT +
Sbjct: 1166    KKEVMKRIYEAATQIAGELDVVGPMNVQFLLTKDEQLRVIEANIRSSRSVPFVSKTLGIS 1225
Query: 1008    MIAIATRVMLGL-DPEVPP--QVKPDRVGKVQPQFSFNRLAGADPTLGVDMISTGEVACF 1064
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      A+   +L   D E+ P   + K   +G K P FSNRLAGADP LGV+M STGE+   F
Sbjct: 1226 FPAVMVSALLSRPDSELVPIRRAKMTTHIGCKAPMFSFNRLAGADPILGVEMASTGEIGVF 1285
Query: 1065 GKTREEAYLKAMISTSFRLPRPQGNVLLSIGGYDGKLEFLDSTRRLQQLGFKLFGSMGTA 1124
      G   + E   + KAM+   +FR   P   V +S           E L   ++ +   LF S   T
Sbjct: 1286 GCDKREVFVRKAMLCQNFY--PTKGVFISSDVAVTEELLPHLEKISK-T-LPLFASTHTG 1342
Query: 1125 DFYLSHGVEIKPVDWLADTEDIESIKDNLDDGHYDMVINLPMRNKYR-----RP 1173
      HG+   +   +   D   + +   L   +D+VI L   RNK   +           P
Sbjct: 1343 AVLTKHGIPHTVLTQRHEDGDNPTYEVELAARRFDLVIQL--RNKRKDFILRSCTRENAP 1400
Query: 1174 ASYMTSGSLARRMAVESKVPLITNIKCAKLFIAAL 1208
      Y           RR+AV+   V L+T           K+F   L
Sbjct: 1401 PDYW-----VRLAVDYNVALLTEPNVVKMFCETL 1430

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>AAX70835 aspartate carbamoyltransferase, putative [1191671 - 1192654] MW:35910.64 Length = 327

Score = 289 bits (740), Expect = 4e-078, Method: Compositional matrix adjust.
Identities = 157/325 (48%), Positives = 216/325 (66%), Gaps = 19/325 (5%)

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Query: 1613 LAPPSILKGRNLSVEQFGKRELHALFNRAHEFHSTKGAS---KLLDGKVMANIFYEPST 1669
      L P + LKG++I++   QF + ++ AL   A           A   + L+G++M   +F+E S+
Sbjct: 4     LQPVTSLKGKSIITAAQFTRPDIDALIRLATALKEKICAGEVLRFLGRIMTPLFFEDSS 63
Query: 1670 RTMCSFASAMQRLGGTVITLSDMKSTSVSKGESLSDTVRTMECYTDVIVLRHPAKGAMRE 1729
      RT+ SF +AM RLGG V+           +++SV+KGE+L DTVRT++ Y+DV+VLRHP + A+ E
Sbjct: 64    RTLNSFCAAMARLGGRVVYFK-AETSSVNKGETLGDVVRTLDSYSDVLVLRHPKQEAITE 122
Query: 1730 ASELLRRPLINAGDGVGEHPTQALLDVFTIREELGTVNGLHIAMVGDLKNGRTVHSLARL 1789
      A           P++NAG+G GEHPTQALLDV TI   ELG V+G   IAM+GDLK GRTVHSL +L
Sbjct: 123   AVAKATHPVNLNAGNGAGEHPTQALLDVLTIHSELGRVDGSTIAMIGDLKMGRTVHSLKL 182
Query: 1790 LSR--YNVTLHYISPPSLAMPDDVVEFVK---ASGITQHTHASI-EEIVADIDVLYVTR 1842
      L R           T+ +++P +L MP DVV+ +K           ASG+T +   S+ EEI+   DVLY TR
Sbjct: 183   LVRNFKMKTIFFVAPDALQMPQDVVDSLKQEIAASGV TIRSSNSL TEEILGQCDVLYATR 242
Query: 1843 VQKERFEDEAE-----YERVKNELVVTPETLINAKKRMIVMHPLPRVNEISPDVDTD 1894
      +QKERF   A           +E K ++V+   E +   AK +MIVMHPLPR +E+   VD D
Sbjct: 243   LQKERFAAAALDEAKALQAFEAAKADIVINAERMKKAKAKMIVMHPLPRNDELCTSVDED 302
Query: 1895 PRAAYFRQM EYGVSVRMALLASVLG 1919
      PRAAYFRQM+YG+ +RMA+L SVL
Sbjct: 303   PRAAYFRQM QYGYMRMAILYSVLA 327

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Query= EAL47672 Rab GTPase activating protein, putative

> EAN78273 GTPase activating protein, putative
Length = 418

Score = 107 bits (268), Expect = 6e-024, Method:Compositional matrix adjust.
Identities = 96/335 (28%), Positives = 156/335 (46%), Gaps = 38/335 (11%)

Query: 303 TDEFGYVKDQTQ---TEDEIKKITSQE---REKKWEIMLDEWNKSGKVPRA-LFHRVYKF 355
DEFG++ D+ + + I+ I + RE KW+ M W K R+ + R K
Sbjct: 92 VDEFGFIIDEEHDRVQRYIRGIDGKRVARREVWQKMQANWESMSKKRRSKVKSRCRKG 151

Query: 356 VPLNKRKKYWEIELKINQSIQEYN---GYF--ARITELPERGKDDEQIHKDVMAHQNN 409
+P + R W+ L I ++ N G + R+ ++ + G I +D+ R +
Sbjct: 152 IPSSFRGAAWQ--LLIGSYLEMLNPGNEGTYDCLRLKDISDEGLKG-TISRDLPTTFPKH 208

Query: 410 IHFMAKFNDGQRTLFRVLRAWMSQD-DLGYVQGMSDLGFLILILQEEEEVYWGFSALMN 468
+ F + GQ L VL A++ D ++GYVQGM+ + G L + EEE +W LMN
Sbjct: 209 VLFREEGGIGQTFLRNVLHAYANIDPEVGIVQGMFVVGALYTQMTEEE-TFWALHTLMN 267

Query: 469 NPKYNLREMFLPGFPGINKCAFVAMKVMKKYHPKIFYHLKSKEYDFDNWKTMYMLEYFMLW 528
KY LREM+ PGFP ++K + ++M K P ++ H F+ + Y W
Sbjct: 268 GEKYRLREMYKPGFPMHLKLFYQLQRLMAKLLPNLYEH-----FEELGVHPTYYASRW 320

Query: 529 FCRCFHPEFE----VRILDLILMEGWEIVF--SIFSAILHYSKVEILKMDEYIFIDKAL- 581
F F +F +RI D+ L EGW+I+F +I L ++ + +E IF K L
Sbjct: 321 FMTLFVYDFNFRAVLRIWDIFLSEGWKIIFRIAIVLLKLEERRLLAMSFEETIIFATKTLE 380

Query: 582 --ADPMTLM----GSQFDQDKFINFVKKARITPKE 610
DP L+ G +F + F ++ + +E
Sbjct: 381 QGKDPDELIRRAHGVRFKTAELEAFAREYELNKRE 415

> EAN76787 huntingtin interacting protein (HIP), putative
Length = 820

Score = 48.9 bits (115), Expect = 4e-006, Method:Compositional matrix adjust.
Identities = 39/129 (30%), Positives = 57/129 (44%), Gaps = 16/129 (12%)

Query: 95 VKQLLAAGITKSAQDINGNNALIRGVIAGRTNACVYLARKMNKTGIDSQNNLGEC AIYIA 154
V L G +A+D +G AL V G A V + + LGEC
Sbjct: 58 VVTFLLGADVNARDKDGATALHVAVTQGNDIATV-----CTLGREPFLGEC----- 104

Query: 155 CRRNNLKLEKLIKYGGNVNIQNNKGITPLMVACFYMNLEMINLLIKAGANIDTVDSKDS 214
+N ++ LI G ++N +N G TPLMVA N+ + LL++ GA I D
Sbjct: 105 ---SNEMIIRFLIDNGADINARNASGETPLMVAAAKGNITAMRLLLLERGAVITQRDDAGC 161

Query: 215 NCLHYMAKS 223
LH+ ++S
Sbjct: 162 TVLHHASRS 170

Query= EDP05938 Chlamydomonas reinhardtii partial DNA topoisomerase I

>AAX79872 DNA topoisomerase IB, large subunit
Length = 661

Score = 432 bits (1112), Expect = e-122, Method:Compositional matrix adjust.
Identities = 232/467 (49%), Positives = 302/467 (64%), Gaps = 22/467 (4%)

Query: 23 SSKSGQVMWKTLLKHAGVLFPPPEYEPHGKPLYDGKPVDLTPDQEEVATMFAVMKETDYMN 82
++K G+ W TL H GVLFP Y PHG+ LY+ + ++TP++EEVATMFAV++E DY
Sbjct: 66 TTKKGKRWDTLLHNGVLFPPAYVPHGIPILYNQQKFEMTPEEEVATMFAVLRHEDYYR 125
Query: 83 KKVFLDNFWEGFKEVLGK-GHVIKDLKKCDFTPIIDWHMAQREAKKGISKEEKDRIKKEK 141
+VF NF++ ++E+L K H I+ L+ CDF+ IY+WH + E +K ++EEK +K+
Sbjct: 126 NEVFRNFFQSWREILDKRKHPIRCLELCDFSAIYEWHQREVEKRKSRTREEKKELKRIA 185
Query: 142 DEKEAKYKVAYVDGRPEPVGNFRVEPPGLFRGRGEHPKMGKIKKRVYPRDITINIGENEP 201
DE+ YK +G+ E V NFRVEPPGLFRGRGEHP GK+KKR+ P D+ +NIG+ P
Sbjct: 186 DEEAEPYKWCIIWNGKKEQVANFRVEPPGLFRGRGEHPMRGKLLKRILPEDVVLNIGKEAP 245
Query: 202 VPEHPYPGQTWKEVKHDHTVTWLAYWKDTISTKDYKYVFLGATSTFKADSDLAKEYEKARK 261
+P+ P G WK V HD VTWLA W + + KYV L +ST K SD AK+E AR+
Sbjct: 246 IPQAP-AGHKWKGVVDQNVTLAMWYEP-TIGQCKYVMLAPSSTLKGQSDYAKFETARE 303
Query: 262 LKEIIVDKRKNYERDWDSSDQRKRQMGVAMFYIDKLALRAGHEKDEDEADTVGCCCTLKVE 321
LK I D+R++Y +D+ S+D+ +RQ VA YFIDKLALR GHEK E+EADTVGCC+L+ E
Sbjct: 304 LKNHIDDIRESYTKDFSSTDEMERQRAVATYFIDKLALRVGHEKGEEADTVGCCSLRKE 363
Query: 322 NIEIMGDNKVKFDFLGKDSIRYENIVEVDPVRYKNLEKF-KRIDHTGKRKQQGDQLFETF 380
+IE+ DN V+FDLFGKDSIRY N V V P VYK L F KR D ++F
Sbjct: 364 HIELRPDNNVRFDFLGKDSIRYVNEVTLPPEVYKLLGSFIKRTD-----SEIFRKV 414
Query: 381 DAQDLNKLKNIMDGLSVKVFRTYNASIVLDRLSEWEATKKGHSTAQTVDQKKVDYDIA 440
LN LK+ + LS KVFRTYNASI LD EW K A D K V ++ A
Sbjct: 415 TPTTLNNYLSFLKDLKSAKVFRTYNASITLD----EWFREKPVDPKASLSD-KLVYFNKA 469
Query: 441 NKEVAILCNHQRSVPKTHTNQMEKIQEKLGMNKELELEDELRAAQ 487
N EVA LCNHQRS+PKT ++ I+ KL + + + D LR AQ
Sbjct: 470 NTEVAKLCNHQRSIPKTFHVSQSIKYKLEDIKRTI---DTLRAQ 512

>EAN76725 DNA topoisomerase type IB small subunit
Length = 273

Score = 71.6 bits (174), Expect = 5e-013, Method:Compositional matrix adjust.
Identities = 32/74 (43%), Positives = 49/74 (66%)

Query: 505 LPWALNSKIDKKKQAIKVELQARSKEDLKTVALGTSKINYMDPRITVAWCKRNEVPIEK 564
P + ++I K ++ + VE + K+D KTV+LGTSK+NY+DPRI +W N VPI +
Sbjct: 193 FPRDIEAEIGKHEKRLKDVENMLKMQDNKTVSLGTSKVNYIDPRIVCSWANENNVPISR 252
Query: 565 IFNKSLLAKFNWAM 578
+F+ +L KF WA+
Sbjct: 253 LFSATLQKKFPWAL 266

Query= EDP08267 Iron-sulfur subunit of mitochondrialsuccinate dehydrogenase

> AAX79657 electron transfer protein, putative
Length = 242

Score = 98.2 bits (243), Expect = 2e-021, Method: Compositional matrix adjust.
Identities = 48/116 (41%), Positives = 77/116 (66%), Gaps = 6/116 (5%)

Query: 60 FQIYRWNPDSDDEKPKYASYQVDINNCGPMMLDVLLKIKDEQDQTLSLRRSCREGICGSCA 119
++ R++P+++ K + SY+ D ++ M+LD++ +K QD TL+ R SC EG+CGSCA
Sbjct: 30 LRLIRFDPETN-KQRVESYEYDKHH-DYMVLDLITAVKAHQDPTLAFRASCCEGVCGSCA 87

Query: 120 MNIDGSNTLACLCKVNRDPGHVGKVAPLPHMFVVKDLVVDMANFYAQYKSIKPYLQ 175
MNI+G N+LAC+ V V PLP+ V+KD VVD+ +F+ QY I+P+++
Sbjct: 88 MNINGVNSLACITF----SQQVTTVGPLPNFPVIKDFVVDLRHFFRQYAYIRPFVR 139

> EAN76651 succinate dehydrogenase, putative
Length = 188

Score = 108 bits (269), Expect = 2e-024, Method: Compositional matrix adjust.
Identities = 46/93 (49%), Positives = 62/93 (66%)

Query: 191 SRAKLDGLYECILCACCSTSCPSYWWNSDKYLGPVLLAAYRWIIDSRDDMTSERMKEVD 250
+R +L+GLYEC+LCA C+ SCP YWWN + +LGPVLL +YRW+I+ D R+K +
Sbjct: 74 NNRLEGLYECVLCASCTGSCPQYWWNRELFLGPVLLQSYRWLIEPLDRDFDSRVKMFE 133
Query: 251 DAYKLYRCKTIMNCATVCPKGLNPGKAINKIKQ 283
+ C I NC+ CPK LNPG A +IK+
Sbjct: 134 HGPLVNFCHNIFNCSITCPKFLNPGMASKEIKR 166