

Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastp suite-2sequences/](#) **Formatting Results - FE7RC5JT114**[Formatting options](#)[Download](#)[Blast report description](#)

Blast 2 sequences

emb|CCX10916| (2332 letters)

RID [FE7RC5JT114](#) (Expires on 02-10 13:23 pm)Query ID [gi|549049991|emb|CCX10916.1|](#)Description Similar to Acetyl-CoA carboxylase; acc. no.
P78820 [Pyronema omphalodes CBS 100304]

Molecule type amino acid

Query Length 2332

Subject ID [gi|171504|gb|AAA20073.1|](#)Description acetyl-CoA carboxylase [Saccharomyces
cerevisiae][See details](#)

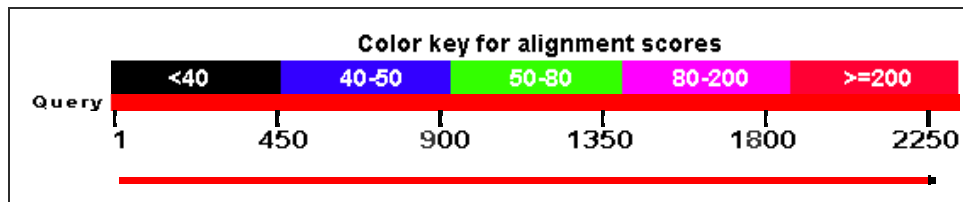
Molecule type amino acid

Subject Length 2237

Program BLASTP 2.2.29+

[Graphic Summary](#)

Distribution of 2 Blast Hits on the Query Sequence



Dot Matrix View



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
acetyl-CoA carboxylase [Saccharomyces cerevisiae]	2881	2902	96%	0.0	64%	AAA20073.1

Alignments

acetyl-CoA carboxylase [Saccharomyces cerevisiae]

Sequence ID: **gb|AAA20073.1|** Length: 2237 Number of Matches: 2

Range 1: 27 to 2214

Score	Expect	Method	Identities	Positives	Gaps	Frame
2881 bits(7469)	0.00	Compositional matrix adjust.	1419/2234(64%)	1725/2234(77%)	57/2234(2%)	
Features:						
Query 24		KLPEHFYGGNSLDAAAPSKVKDFVAANDGHTVITKVLIANNGIAAVKEIRSVRKWAYETF				83
Sbjct 27		+LP HF G N++D S ++DFV ++ GHTVI+K+LIANNGIAAVKEIRSVRKWAYETF				86
Query 84		ELPGHFIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSVRKWAYETF				
Sbjct 87		GNRAIQFTVMATPEDLQANADYIRMADQYVEVPGGTNNNNYANVELIVDVAERMGVHAV				143
Query 144		G++R +OF MATPEDL+ANA+YIRMADQY+EVPGGTNNNNYANV+LIVD+AER V AV				
Sbjct 147		GDDRTVQFVAMATPEDLEANAERYIRMADQYIEVPGGTNNNNYANVDLIVDIAERADVDAV				146
Query 204		WAGWGHASENPLLPELSAASKOKIVFIGPPGSAMRSLGDKISSTIVAQAHAEPVPCIPWSGT				203
Sbjct 147		WAGWGHASENPLLPEL+SK+K++FIGPPG+AMRSLGDKISSTIVAO A+VPCIPWSGT				206
Query 262		WAGWGHASENPLLPEKLSQSKRVIFIGPPGNAMRSLGDKISSTIVAQAHAEPVPCIPWSGT				
Sbjct 207		GVNQVEVGED-GLVTVADDIYQOGCTKTAEEALAKARSIGFPIMIKASEGGGGKGIKVE				262
Query 263		GV+ V V E GLV+V DDIYO+GC + E+ L KA+ IGFP+MIKASEGGGGKGIKVE				
Sbjct 267		GVDTVHVDEKTLGLVSVDDDIYQKGCCTSPEDGLQAKRIGFPMIKASEGGGGKGIKVE				266
Query 323		SEEGFSQLYNQVAGEVPGSPIFVMKLAGSARHLEVOLLADQYGNNTLSGRDCSVORRHQ				322
Sbjct 327		EE F LY+Q A E+PGSPIF+MKLAG ARHLEVOLLADQYGNNTLSGRDCSVORRHQ				326
Query 383		REEDFIALYHOAAANEIPGSPFIMKLAGRARHLEVQLLADQYGNNTLSGRDCSVORRHQ				
Sbjct 327		KIIEEAPVTIAKQDTFQAMERAAVRLGRLVGYVSAGTVEYLYSHDDKFYFLELNPRLQV				382
Query 383		KIIEEAPVTIAK+TF ME+AAVRLG+LVGYVSAGTVEYLYSH D KFYFLELNPRLQV				
Sbjct 387		KIIEEAPVTIAKAETFHEMEKAARVLGRLVGYVSAGTVEYLYSHDDKFYFLELNPRLQV				386
Query 443		EHPVTMTGVLNPAALQIAMGIPHLRIRDIRLLYGVNPTSSEIDFDFSKEGSETTOR				442
Sbjct 447		EHPVTMTGVLNPAALQIAMGIP+HRI DIR LYG+NP+++SEIDF+F + + OR				446
Query 503		EHPVTMTGVLNPAALQIAMGIPMHRISDIRTYGMNPHSASEIDFEFKTQDATKKQR				
Sbjct 507		RPTPKGHCTACRITSEDPGEGFKPSNGMMHFNFRSSSNVWGYFSVSTAGGIHSFSDSOF				502
Query 563		RP PKGHCTACRITSEDP +GFKPS G +HELNFRSSSNVWGYFSV G IHSFSDSOF				
Sbjct 567		RPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGYFSVGNNGNIHSFSDSOF				506
Query 623		GHIFAYGETRSASRKHMVVALKELISIRGDFRTTVEYLIKLETPAFEDNTITGWLDEL I				562
Sbjct 627		GHIFA+GE R ASRKHMVVALKELISIRGDFRTTVEYLIKLETFEDNTITGWL+LI				
Query 683		GHIFAFGENRQASRKHMVVALKELISIRGDFRTTVEYLIKLETFEDNTITGWLDEL I				566
Sbjct 687		SKKLTSERPDPPIVAVVCGAVAKAHIAEACVSEYKTSLEKGOVPAKDTLKTVPVDFIYE				622
Query 743		+ K+T+E+PDP +AV+CGA KA +ASE +Y SL+KGOV +KD L+T+FPVDFI+E				
Sbjct 747		THKMTAEKPDPTLAVICGAATKAFLASEEARHKYIESLQKGQVLSKDLLQTMFPVDFIHE				626
Query 803		GTRYKFTATRSSHDSYNLFVNGSKATVGWVALSDGGLLVLLDGKSHNVYWKKEEVSATRLS				682
Sbjct 807		G RYKFT +S +D Y LF+NGSK + + LSDGGLL+ + GKSH +YWKEEV+ATRLS				686
Query 863		GKRYKFTVAKSGNDRYTLFINGSKCDIILRQLSDGGLLIAIGGKSHTIYWKEEVAATRLS				
Sbjct 867		VDSKTCLLEQENDPTQLRTPSPGKLVKFLVNGEHVKKGOAYAEVEMMKMYPLLTSEDG				742
Query 923		VDS T LLE ENDPTQLRTPSPGKLVKFLVNGEH+ KGO YAE+EVMMK MPL++ E+G				
Sbjct 927		VDSMTTLLEQENDPTQLRTPSPGKLVKFLVNGEHIKGOYAEIEVMMKMQPLVSQENG				746
Query 983		IVQFVKOPGATLEAGDIIGILALDDPSRVKHAAPFSGQLPAFGPPRIVGNKPSQRFATLQ				802
Sbjct 987		IVQ+KOPG+T+ AGDI+ I+ LDDPS+VKHA PF G LP FG P I G KP+ +F +L				
Query 1043		IVQLLKQPGSTIVAGDIMAIMTLDDPSKVKHALPFEGMLPDFGSPVIEGTPAYKFKSLV				806
Sbjct 1047		SILVNILDGYNQMVLSNTLKELEIIVLRNPPEYGEFSAQFSALHSRMPNKLQNLQSII				862
Query 1103		S L NIL GYDNO++++ +L+LIEVLRNP+LPY E+ SALHSR+P KLD+ + +++				
Sbjct 1107		STLENILKGYDNOQVIMNASLQQLIEVLRNP+LPYSEWKLHISALHSRLPAKLDEQMELV				866
Query 1163		EKAASRNAEFPAKQLHKALDKFLAESVAPSEVEMMKQSLAPLIKIMDDYADGLKAHEYKV				922
Sbjct 1167		++ R A FPA+OL K +D ++ + +++ + PL I Y++GL+AHE+ +				
Query 1223		ARSLRRGAVFPAQRLSKLID -MAVKNPEYNPDKLLGAVVEPLADIAHKYSNGLEAHEHSI				926
Sbjct 1227		FITFLENFVNVEKLFSGYNTREEDTILKLRDENKEDIAKAVNIVFHSRVRGAKNNLVLA I				982
Query 1283		F+ FLE + VEKLF+G N REE+ ILKLRDEN +D+ K V SHS+V AKNNL+LAI				
Sbjct 1287		FVHFLEEYVEKLFNGPNVREENIILKLRDENPKDLKVALTVLSHSHSVSAKNNLILAI				986
Query 1343		LEEYRPGKPNVQVAKYFRPVLQQLTELETRATAKVSLSKAREVLIQCSLPSLEERASQME				1042

Sbjct	986	L+ Y+P + +V+ F LO + ELE++ATAKV+L+ARE+LIO +LPS++ER O+E LKHYQPLCKLSSKVSIAIFSTPLQHIVELESKATAKVALQAREILIQGALPSVKERTEQIE	1045
Query	1043	HILRSSVVESRYGETGWEHRTPSIEALREVIDSKFTVFDVLPTEFFDHADPWVSLAALEVY HIL+SSVV+ YG + + P + L+++IDS + VFDVL F H DP V+ AA +VY	1102
Sbjct	1046	HILKSSVVKVAYGSSNPKRSEPDNLILKDLIDSNYVVFVLLQLFLTHQDPVVTAAAAQVY	1105
Query	1103	IRRAYRAYKIHGIHYQGTSDPPFVLTWDFQMRKVGAIEYGATQPSTPATPVSENGNPF5 IRRAYRAY I I + P ++ W FO+ ST T S+ G	1162
Sbjct	1106	IRRAYRAYTIGDIRVHEGVTVP - - IVEWKFQLPSAAF - - - - - STFPTVKSKMG - - - M	1152
Query	1163	KRVGSISDLSFLVAKSGEEPVRKGVIVPV5FLDEVEESLAKAIEFIPRRVEKSQ - PAPAL R S+SDLS+ VA S P+R+G+++ V LD+V+E L++++E IPR S PAP	1221
Sbjct	1153	NRAVSVDLSY - VANSQSSPLREGILMAVDHLDVDEILSQSLEVIPRHQSSSNGPAP - -	1209
Query	1222	MANLEGRRRPAAITTONDDDEDMSAVCNVAIRDVES - KDDKEVLDRIQPLVDDIKEDLIA ++ +S V NV + E + ++E+L R++ ++D K++LI	1280
Sbjct	1210	- - - - - DRSGSSASLSNVANVCVASTEGFESEEEILVRLREILDNLKQELIN	1255
Query	1281	RGIRRITFVCGHQDGSYPAYFTFRWPHFKEEESIRHIEPALAFQLELGRLSNFNKIPVFT IRRTIF+ G +DGSYP Y+TF P++ E E+IRHIEPALAFQLELGRLSNFNKIP+FT	1340
Sbjct	1256	ASIRRITFMFGFKDGSYPKYTYTNGPNYNENETIRHIEPALAFQLELGRLSNFNKIPIFT	1315
Query	1341	ENRNIHVYEAIGKESPADKRYFTRAVVRAGRLRDEIPTDYLISETDRLVNDILDAMEIV +NRNIHVYEA+ K SP DKR+FTR ++R G +RD+I +YL SE +RL++DILD +E+	1400
Sbjct	1316	DNRNIHVYEAIVSKTSPLDKRFFTRGIIRTHIRDDISIQEYLTSEANRLMSDILDNLEVT	1375
Query	1401	GNNNSDLNHIFINFSPVPLGPEETEPALGGFIERFGRRLWRLRVGAIRIVCTDPETG +NSDLNHIFINF VF + PE++E A GGF+ERFG+RL RLRV+ AEIRI+ DP+TG	1460
Sbjct	1376	DTSNSDLNHIFINFIIVFDISPEDEAAFGGFLERFGKRLRLRVSSAEIRI+IKDPQTG	1435
Query	1461	ASFPIRAIIQNVSGYVVQVEMYAERKSEQQWVHSHSIGSKPGSMHLRPTTTPYAAKEWLQ A P+RA+I NVSGYV++ EMY E K+ +G+WVF S+G KPGSMHLRP TPY KEWLQ	1520
Sbjct	1436	APVPLRALINNVSQYVVIKTEMYTEVKNAGGEWVFKSLG - KPGSMHLRPIATPYPVKEWLQ	1494
Query	1521	PKRYKAHLMGTQYVYDFPDLFRQAVFQSWRKLQATLPAVKEKMPDQSECLEYSELIVDEN PKRYKAHLMGT YVYDFP+LFRQA + + + K+ D + +ELI DEN	1580
Sbjct	1495	PKRYKAHLMGTTYVYDFPELFRQASSSQGKNFSADV - - - - - KLTD - - DFFISNELIEDEN	1547
Query	1581	GELAEVQREPNTNTHGMVGWILTAKTPEYPRGRFIVIANITFKIGSFGPOEDIFFNKC GEL EV+REP+ N GMV + +T KTEPYPRGR+F+V+ANDITFKIGSFGPOED FFNK	1640
Sbjct	1548	GELTEVEREPGANAIGMVAFKITVKTPEYPRGRQFVVVANDITFKIGSFGPOEDFFNKV	1607
Query	1641	TELARRLGIPRIYLSANSGARIGVAEELIPHFSVAWNADEKPELGFKYLYLT - - - DVYK TE AR+ GIPRIYL+ANSGARIG+AEE++P F VAWNDA P+ GF+YLYLT + K	1697
Sbjct	1608	TEYARKRGIPRIYLAANSGARIGMAEEIVPLFQVAWNAANPDKGFOYLYLTSEGMEITLK	1667
Query	1698	RFSASKKEVIAERIVEDGEERYKINTIIAEDGLGVECLRGSGLIAGATSRAYEDIFTI +F K+ V+ ER V +GEER+ I TIIG+EDGLGVECLRGSGLIAGATSRAY DIFTI	1757
Sbjct	1668	KF - - DKENSVLTERTVINGEERFVIKTIIGSEDGLGVECLRGSGLIAGATSRAYHDIFTI	1725
Query	1758	TLVTCRSVGIGAYLVRLGORAIQIEGQPII - - - - - LTGAPAINKLLGREVYTSNLQGGT TLVTCRSVGIGAYLVRLGORAIQ+EGQPII LTGAP GREVYTSNLQGGT	1812
Sbjct	1726	TLVTCRSVGIGAYLVRLGORAIQIEGQPIIYWYRCLLTGAPESTN - AGREVYTSNLQGGT	1784
Query	1813	QIMYKNGVSHLTATDDYEGVQKIIIEWMSFVPERKGAPVPISPAVDGWDRDVTVPNNKET QIMY NGVSHLTA DD GV+KI+EWMS+VP ++ PVPI D WDR V F P N ET	1872
Sbjct	1785	QIMYNNGVSHLTAVDDLAGEKIVEWMSYVPAKRNMVPVILETKDWDPRVDFTPTNDET	1844
Query	1873	YDCRWLIAGKETENGFEGLFDKGSFOETLSGWARTVVVGRARLAGIPIGVIAVETRSVE YD RW+I G+ETE+GFE GLFDKGSF ETLSGWA+ VVVGRARL GIP+GVI VETR+VE	1932
Sbjct	1845	YDVRWMIEGRETESGFEYGLFDKGSFFETLSGWAKGVVVGRARLGGIPLGVIGVETRIVE	1904
Query	1933	NVSPADPANPDSTETVSLEAGQVWYPNSAFKTAQAINDFNHGEQLPLMILANWRGFSGGQ N+ PADPANP+S ET+ E GOVW+PNSAFKTAQAINDFN+GEOLP+MILANWRGFSGGQ	1992
Sbjct	1905	NLIPADPANPNSAETLIQEPGQVWHPNSAFKTAQAINDFNNGEQLPMMILANWRGFSGGQ	1964
Query	1993	RDMYNEVLKYGSIYVDALVKYEQPIFYIYIPPFELRGGSWVVVDPTINENMMEMYADEES RDM+NEVLKYGSIYVDALV Y+OPT +YIPP GELRGGSWVVVDPTIN + MEMYAD +	2052
Sbjct	1965	RDMFNEVLKYGSIYVDALVDYKQPIIYIYIPTGELRGGSWVVVDPTINADQMEMYADVNA	2024
Query	2053	RAGVLEPEGIVGIKFRREKQOLDTMRDATYALRRRAAEKDLTPEEQNEIKAKMSEREQ RAGVLEP+G+VGIKFRREK LDTM RLD Y LR + + K L PE +I +++++RE+	2112
Sbjct	2025	RAGVLEPQGMVGIKFRREKLLDTMRLDDKYRELRSQLSNKS LAPVHQISKQLADRER	2084
Query	2113	LLLPVYAQVTLQFADLHDRAGMMAKGVIRMLPTWQHARRFFYWRLLRRRLNEELFLKKMV LLP+Y O++LOFADLHDR+ RM+AKGVI L W ARFFF+WRLRRRLNEE +K++	2172
Sbjct	2085	ELLPIYGQISLQFADLHDRSSRMVAKGVISKELEWTEARRFFFWRLLRRRLNEEYLIKRLS	2144
Query	2173	SADKSSTRAENLERLKS LVVDDDESSTVFEDNDRLVANWYEENMKDILQKIDGLKQDGIAA ++R E + R++S ++V ++DR VA W EEN K + K+ GLK + A	2232
Sbjct	2145	HQVGEASRLEKIARISWY - - - - PASVDHEDDRQVATWIEENYKTLDDKLKGLKLESFAQ	2200
Query	2233	QVASLIEENGKHAL 2246 +A I + +A+	
Sbjct	2201	DLAKKIRSDHDNAI 2214	

Range 2: 690 to 725

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.4 bits(41)	3.6()	Compositional matrix adjust.	12/36(33%)	19/36(52%)	1/36(2%)	
Features:						
Query	2234	VASLIE - ENGHKALRVAVEGGVRRMMEEEGRGIIEG + +L+E EN LR G + + + E G II+G		2268		
Sbjct	690	MTTLLEVENDPQLRTPSPGKLVLKFLVENGEHIIKG		725		