

Supplementary Figure 3. Bacterial protein sequence similarities in the *Haplomitrium ensiformis* mitogenome.

Shown are the top similar alignments indicating length of the native protein entry, the numbers of identical and similar residues and total alignment length separated by slashes followed by percentages of identical and similar residues, respectively.

A. HscA-RmuC

Fe-S protein assembly chaperone HscA [*Caedimonas varicaedens*], Part 1

Sequence ID: [WP_062141505.1](#) Length: 595, 134/149/163, 83/91 %

Query	1	RSAQVPIDQIKGIVLVGGATRIPLVLKKVKQFFNQPTPLTDINPDEVVALGAALQAETLTQ	180
		R AQ+ +DQIKG+VLVGGATRIPLV +KV++FF Q PLT+INPDEVVALGAALQAE LT+	
Sbjct	305	RDAQISLDQIKGVVLVGGATRIPLVRQKVERFFEQVPLTNINPDEVVALGAALQAEALTE	364
Query	181	GSNRllldvpslsglETYGGIVEKIIPRNSPIPATYEQDFTTFQDNQGTGSLHVVQGER	360
		GS RLLLDV+PLSLGLETYGG+VEKII RNSPIPA++ QDFTTFQDNQGTG+SLH+VQGER	
Sbjct	365	GSQRLLLDVAPLSLGLETYGGVVEKIILRNSPIPASHWQDFTTFQDNQGTGMSLHIVQGER	424
Query	361	ELAHDCPSLAHFELRGIPPMKAGIARIRVTFTIDADGILTVS	486
		EL DC SLAHFELRGIP MKAG+ARIRVTFTIDADGILTVS	
Sbjct	425	ELVQDCRSLAHFELRGIPLMKAGMARIRVTFTIDADGILTVS	466

Fe-S protein assembly chaperone HscA [*Caedimonas varicaedens*], Part 2

Sequence ID: [WP_062141505.1](#) Length: 595, 70/96/119, 59/80 %

Query	802	STGIHQSIIEVKPSYGLSEEDLLKIIIESHVYGYLDMEERLLRETRVEAERLFHAVregle	981
		+TGIHQ I+VKPSYGL+EEDLL++IEESH + DM+ERLLRE RVEAERL HAV+E L+	
Sbjct	471	TTGIHQYIDVKPSYGLTEEDLLRMIEESHSHARSMDERLLREARVEAERLLHAVKEALK	530
Query	982	ddadlleenerrGIEQAINELATVLNSSHRGLIKEKIDEIKKMTHTSWAERRLNRSMSKA	1158
		+D+DLLEE+E+ ++Q L +VLNS R I+ K + +++T+SWAERR+N++M KA	
Sbjct	531	NSDDLLEESEKIEVKQEAELISVLNSVKRDDIERKTERLRQVTNSWAERRMNQAMRKA	589

DNA recombination protein RmuC [*Caedimonas varicaedens*], Part 1

Sequence ID: [WP_062141503.1](#) Length: 475, 111/128/142, 78/90 %

Query	1198	MNIQQYEFAQLLIGIALGGSVGFLWMLRIKKLAHRTFDNLNEEMRNLRERFILSEDKAQR	1377
		MNIQQYE AQ+L G LGGS+GF +++R+K+LA TFD LNEEM+N+RER ILSEDKAQR	
Sbjct	1	MNIQQYELAQVLTGAILGGSIGFFFIMRVKRLAQLTFDRNLNEEMQNVRERLILSEDKAQR	60
Query	1378	HDNLVEDKNQLFERLSEARTKHAEEVLLIQERKQLQEKFKVIEDARQELSNAFQALSAQ	1557
		++ + E+KNQLFERLS+AR K+AEV+VLL QERKQ QEKFKVIE+ARQELSNAFQALSAQ	
Sbjct	61	YETMTEKNQLFERLSARAKYAEVDVLLGQERKQFQEKFKVIEEARQELSNAFQALSAQ	120
Query	1558	ALERNNRSFLDLAKSTLEKFHE	1623
		ALERNNRSFLDLAKSTLEKFHE	
Sbjct	121	ALERNNRSFLDLAKSTLEKFHE	142

B. DNA recombination protein RmuC [*Caedimonas varicaedens*], Part 2

Sequence ID: [WP_062141503.1](#) Length: 475, 188/193/200, 94/96%

Query	1	AKSTLEKFHETAKGDLQLKEKAISELVSPIRESLHNVDQKIGEIEKIRLSAYEVLRHQVG	180
		AKSTLEKFHETAKGDLQLKEKAISELVSPIRESLHNVDQKIGEIEKIRLSAYEVLRHQVG	
Sbjct	133	AKSTLEKFHETAKGDLQLKEKAISELVSPIRESLHNVDQKIGEIEKIRLSAYEVLRHQVG	192
Query	181	DLILSQKELRLETANLVKALRTPHVRGRWGEIQLRRVVMESGMSIHCDFIEQKTLEGEV	360
		DLILSQKELR ETANLVKALRTPHVRGRWGE+QLRRVVMESGMS+HCDFIEQ TLEGE+	
Sbjct	193	DLILSQKELRSETANLVKALRTPHVRGRWGEMLRRVVMESGMSVHCDFIEQTTLEGEI	252
Query	361	KLRPDMIVRLPGGKRLIIDAKAPLSAYLDALEAKEEVLRQDLLKDHRQVRTHILSLSTH	540
		KLRPDMIVRLPGGKRLIIDAKAPL+AYLDALEAKEE LRQD LKDHRQVRTHILSLST	
Sbjct	253	KLRPDMIVRLPGGKRLIIDAKAPLAAYLDALEAKEETLRQDFLKDHRQVRTHILSLSTR	312
Query	541	AYWNQFYKSGETPEFVVMFL	600
		AYW+Q KSGETPEFVVMFL	
Sbjct	313	AYWDQLSKSGETPEFVVMFL	332

C. Hypothetical protein BGO77_01970 [*Caedibacter* sp. 37-49]

Transglycosylase SLT domain-containing protein

Sequence ID: [OJX11001.1](#) Length: 642, 136/201/308, 44/65 %

Query	1	ALSHFKKLEPVVKTPISCSRVGWLGRTYEAMGKAKEARTSYQKAAQYKGTIFYGQKAFSK	180
		A HF +L V +P S S+ YW GR +A +EA YQKAA Y T+YGQ A	
Sbjct	334	AFHHFNQLYQKVTSPYSRSKAAWAGRAAQAKKLPEAHLWYQKAAYYPATYYGQLALKA	393
Query	181	LGHTDKEIILETLRFTPAQQAKFESHKAVKLIRLLAKEEIDEHILSFAYVFAKQTASPLE	360
		L + + LE+L F ++ KFE+H+ V+ ++LL K + + +LSF Y++A QT+S E	
Sbjct	394	L-NKPQTFRLESLTFPISEVRKFENHEFVRAVKLLHKAGLTDELLSFGYMYA-QTSSSHE	451
Query	361	RKQILALVHELAPHYGVEIAQVIAPYQSTLYSEAFPRPKPIYLKHMEKVDAALAHAVIRK	540
		+L+L +AP + V +A ++ +T Y EA+P++ ++ A+ HA+IRK	
Sbjct	452	ALMMLSLASTIAPQFAVGMADEMSILHNTHYKEAYPQVCRDNNSAQACLEDAMIHALIRK	511
Query	541	ESKFNPKIVSWAGAQGLMQLMPETAQLMADQCGVTCSEKQLLTDPLLNVKLGTLYLKEQL	720
		ESKFNP+ S AGA G+MQ++P TA+++A + GV +E +L +D N+ +GT YLKE+L	
Sbjct	512	ESKFNPRAKSEAGACGMMQVVPSTAKMVAQKMGVHFNEARLKSDMNYNMLIGTAYLKERL	571
Query	721	EKYDHSFPLTLASYNAGPGTVSRWLD RFPDPRHPSINTIDWIEVLPYSETRDYIHRVLEN	900
		+ Y S LTLA+YNAGPG+V +W++R+ DPR P ++TIDW+E +PYSETR+YI RV+EN	
Sbjct	572	QDYQGSIVLTLAAYNAGPGSVKWKWIERYGDPDPKVDITDWVEKIPYSETRNYIQVMEN	631
Query	901	YTIYKAIL 924	
		Y IY+AI	
Sbjct	632	YIIYQAIF 639	

G. SerS, Serine tRNA ligase [*Caedimonas varicaedens*]

Sequence ID: [WP_062139602.1](#) Length: 429, 268/297/317, 85/93 %

Query	1	EGQTDADNMEVRRWGSPTFDFTPPLPHYEIGEKLQEMDFENAAKIAGARFLILKGNLARL	180
		EG+TD++N+E+R+WG+PRTFDFTPPLPHYEIGEKLQ MDF+ A KI+GARF++LKG LARL	
Sbjct	113	EGRDSENIEIRKWTGTPRTFDFTPPLPHYEIGEKLQGMDFDTATKISGARFVVLKGALARL	172
Query	181	ERALGQFMLDLHTQ*FGYQEVSPPLLVRDETVYGVGQLPKFKENLFQTTDGRWLISTAEV	360
		ERALGQFMLDLHTQ FGYQEVSPPLLVRD+ VYGVGQLPKF+E+LFQT+DGRWLISTAEV	
Sbjct	173	ERALGQFMLDLHTQEFGYQEVSPPLLVRDDAVYGVGQLPKFREDLFQTS DGRWLISTAEV	232
Query	361	SLTNLVREKIVDEGVLP LRF TALTPCFRSEAGSAGRDRTRGMIRQH QFHKVELVSIVHPDA	540
		SLTNLVRE+I+DEG LPLRFTA TPCFRSEAG+AGRDRTRGMIRQH QFHKVELVSIVHPDA	
Sbjct	233	SLTNLVREIRILDEGSLPLRFTAFTPCFRSEAGAAGRDRTRGMIRQH QFHKVELVSIVHPDA	292
Query	541	AEEEHQRMVNAAETVLQ LKIPYRIMLLSSGDTGTQSRRTYDL DVWLPG*NLYREISSCS	720
		AE EHQRMVNAAETVLQ L+IPYR+MLLS GDT SRRTYDL+VWLPG N+YREISSCS	
Sbjct	293	AETEHQRMVNAAETVLQRLEIPYRVMLLSCGDTSGASRRTYDLEVWLPGENMYREISSCS	352
Query	721	NCGDYQARRMQARFRPKNGAGNKNSEPFVFTINGSGVAVGRALIAVIENSQNSDGSITIP	900
		NCGDYQARRMQARFRPKN G+KN+ EFVFT+NGSGVAVGRALIAVIEN QNSDGS+TIP	
Sbjct	353	NCGDYQARRMQARFRPKNDTGSKNTTEFVFTLNGSGVAVGRALIAVIENYQNSDGSMTIP	412
Query	901	DILRPYMKGMERISLHD	951
		+ LRPYMKGM+RIS+HD	
Sbjct	413	EALRPYMKGMKRISIH D	429

SurE, 5'/3'-nucleotidase [*Caedimonas varicaedens*]

Sequence ID: [WP_062139600.1](#) Length: 258, 246/252/258, 95/97 %

Query	947	MIKIMDQKPRILISNDDGIHAPGLKVLEDIASTITDDIWIVAPEWEQSGAAHFLSIGRPL	1126
		MIKIM QKPRILISNDDGIHA GLKVLEDIAS++TDDIWIVAPEWEQSGAAH LSIGRPL	
Sbjct	1	MIKIMHQKPRILISNDDGIHAAGLKVLEDIASSMTDDIWIVAPEWEQSGAAHLSIGRPL	60
Query	1127	RFRELGP KRYTVNGTPTDCVMIAVNKLMTACRPDLMLSGVNHGANLGEDVTYSGTVAAAM	1306
		RFRELGP KRYTVNGTPTDCVMIAVNKLMT CRPDLMLSGVNHGANLGEDVTYSGTVAAAM	
Sbjct	61	RFRELGP KRYTVNGTPTDCVMIAVNKLMT ECRPDLMLSGVNHGANLGEDVTYSGTVAAAM	120
Query	1307	EATLLGIPAIALSQSLITDHENGYDPARHYGPILIKKLISQTWPRHVLININFPDISVDK	1486
		EATLLGIPAIALSQSL+TDHEN YDPARHYGP+L+KKLISQTWPRHVLININFPDISVDK	
Sbjct	121	EATLLGIPAIALSQSLITDHENAYDPARHYGPLLVKKLISQTWPRHVLININFPDISVDK	180
Query	1487	IQGARVVHQGLRNINDNLVKWKDPHGKPPFFWIGGNRDDSPTEETDLEAIHQGSISITPL	1666
		IQGARVV QGLRNINDNLVKWKDPHGKPPFFWIGGNRDDSPTEETDLEAIHQG+ISITPL	
Sbjct	181	IQGARVVRQGLRNINDNLVKWKDPHGKPPFFWIGGNRDDSPTEETDLEAIHQGAISITPL	240
Query	1667	HLDLTHHSTLET LKLA FI	1720
		HLDLTHHSTLET LKLA FI	
Sbjct	241	HLDLTHHSTLET LKLA FI	258

J. MurA, UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rickettsiaceae bacterium]

Sequence ID: [RYE05808.1](#) Length: 422, 287/341/420, 68/81 %

Query	1278	MDSiiikggkpligKVNISGAKNaalpiitaallAEGNLNLINIPKLTDIYTMKTLQNH	1099
Sbjct	1	MDSI+IKGG PL G V I+GAKNAALPI+ AALL + L NIPKLT+ TM +LL++H	60
Query	1098	GILIDIKDLGDYYALSINSNKVDNFVAPYDIVRKMRASIWVLGPLLARFGKAQVSLPGGC	919
Sbjct	61	G ++ D + L I+ +K+ +F+APY+IVRKMRASIWVLGPLLARFG+A++SLPGGC	120
Query	918	AIGARQVDLHIDVLRAMGADIEITHGYIKAKSKGRKGVHFNFNKISVGATINAIMAATL	739
Sbjct	121	AIGARQVD+HI VL AM A IEI GYIKA SKG+LKG HFN++ISVGATI AI+AA+L	180
Query	738	AKGETVLLNCAREPEIIDLCKCLTAMGANIDGDSTGEIKITGVESLKGANYKVMPDRIEA	559
Sbjct	181	A+GET L NCA+EPEI+DLCK L MGA I G T EIKI GV SLKG Y VMPDRIEA	240
Query	558	GTYMIAAAITKGKLDILGIDYHIIENLGLKLIDAGVEVSPLENGVLKYSNGNIKSVDIQT	379
Sbjct	241	GTYMIAAAITKG+LDI+GIDY I+ENL LKL+++G V+ +G+ +++SG IK DI T	300
Query	378	EAYPGFSTDLQAQFMSLMTLAEGAAVITENIF*NRFMHIPELCRMGANITISGHSAMIRG	199
Sbjct	301	E YPGF+TDLQAQFMSL+T+A+GA+VITENIF NR+MH+PEL RMGANI I H+A+I+G	360
Query	198	VEHLSGAEVMASDLrasvslvlaglaAKGETIIRRVYHLDRGYQQLEQKLSHCGADIKRI	19
Sbjct	361	V++L GAEVMASDLRAS L+LA LAA GET I RVYHLDRGYQ E KLS CGADI RI	420

Acyl-CoA carboxylase subunit beta [Rickettsiaceae bacterium]

Sequence ID: [RYE05809.1](#) Length: 514, 453/485/514, 88/94 %

Query	1503	MNQITLPDQDLLEEKRSIARAGGGHDIRALQHKKGKLTARQRVEAFLDPDSEETGMFVE	1682
Sbjct	1	MNQ +L QDLLEEKRSIARAGGG +RIALQHKKG+LTAR+R+E LDPDSFEETGMFVE	60
Query	1683	HRCDNFGMKDKKFAGDGVVTGHGTINGRLVFIYSQDFTVLGGSLEGEYHAKKICNVIDSAL	1862
Sbjct	61	HRCDNFGMKDKK AGDGVVTGHGTINGRLVFIYSQDFTVLGGSLEGEYHAKKIC+V+DSAL	120
Query	1863	QVGAPVIGINDSGGARIQEGVDALGGYGELFQRNVIASGVIPQITLIMGPCAGGAVYSPA	2042
Sbjct	121	Q GAPVIGINDSGGARIQEGVDALGGYGELFQRNVI+ASGVIPQI+LIMGPCAGGAVYSPA	180
Query	2043	LTDFIFMVRDSSYMFVTGPDVVKTVTGEEVSQEKLGARMHTTKSGVADLAFKNDIEALL	2222
Sbjct	181	LTDFIFMVRDSSYMFVTGP+VVK VTGEEVSQEKLGAR+HTTKSG+ADL+FKNDIEALL	240
Query	2223	ETRRFFNFLPLSNRAPLPTRYTKDPADRVMSLNTLVPLAANKSYDMKELIQRIVDEG*F	2402
Sbjct	241	ETRR FNFLPLSNRAPLP+R TKDPADRVMSLNTLVP NKSYSYDMKELI+RIVDEG F	300
Query	2403	FELQPDFAKNILIGFGYMEGRSIGFVANQPLYLAGCLDINASRKAARFIRFCDAFNIPIV	2582
Sbjct	301	FEL +FAKNI+IGFGYMEGR +GFVANQPLYLAGCLDIN+SRKAARFIRFCDAFNIPI+	360
Query	2583	SLVDVPGFLPGTAQEHDGIIKHGAKLLYAYAEATVPKITVITRKAYGGAYIVMNSKHLRG	2762
Sbjct	361	SLVDVPGFLPGT QE++G+IKHGAKLLYAYAEATVPKITVITRKAYGGAYIVMNSKHLRG	420
Query	2763	DVNYAWVNPEIAVMGAEGAAEIIIFKEDCKDSLKKKKIQEYKDTVTSLFVAASRGYDDI	2942
Sbjct	421	DVNYAW+N EIAVMGAEGAAEIIIFK +CKD + KK IQEYKDT+TS F+AASRGY+DDI	480
Query	2943	IKPQNTRWRICKALNFLQGKNTQMPWKKHDNLPL	3044
Sbjct	481	IKPQNTRWR+CKALNFL+ K Q+PWKKHDNLPL	514

Acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha [Rickettsiaceae bacterium]Sequence ID: [RYE05810.1](#) Length: 665, 571/626/665, 86/94 %

Query	3077	MNKPLFDKVLIANRGEISLRIMRSLKMGIKSVAVYSEADTGSKHVQEADEAYYVGNSPA	3256
Sbjct	1	M+KPLFDKVLIANRGEI+LRIMRSLKMGIKSVA+YSEADT S HVQ ADEAYYVGNSPA	60
Query	3257	TESYLSIKNIVNAARASGAQAVHPGYGFLAENFNFANILKREGITLIGPSAQAIKQMGDK	3436
Sbjct	61	TESYLSIKNI+NA RASGAQAVHPGYGFLAEN NFA+ LKREGITLIGPSA AIKQMGDK	120
Query	3437	IEAKKIATEAGVTTVPGYMGIIGNVNQAISIAEEIGFPVIVKaaaggggrgMRVVKNSSE	3616
Sbjct	121	IEAKKIATEAGVTTVPGYMGII N+ QAISIAEEIGFPVIVKAAAGGGGRMRVVKNS+E	180
Query	3617	MAAAFESAKLEAENSFNDGRVFIEKLIENPRHIEIQLIADQFGNAVCLGEREC SIQRHHQ	3796
Sbjct	181	MA AFESAK+EAENSF+DGRVFIE+LIE+PRHIEIQL+ADQFGNAVCLGEREC SIQRHHQ	240
Query	3797	KIIEEAPSSFITEEIRQKMYAEVIALTHKVGYYSGAGTVEFIMDPDKHYFME MNTRLQVE	3976
Sbjct	241	KIIEEAPS FITEEIR++MYAEVIAL++KVGYYSGAGTVEFIMD K Y YFME MNTRLQVE	300
Query	3977	HPVTELVGTGIDIVEEMIKIAAGEKLSFTQDDIKLKWAIESRICSEDPTRGFLPSSGRIT	4156
Sbjct	301	HPVTELVGTGIDI+EEMIKIAAGEKLSFTQ+DIK+KGWAIE+RICSEDPTRGFLPSSGRIT	360
Query	4157	GYAEPLKSPHIRIDSGVSGIGGEVSMFYDPMIAKLCTYHDTREQAIEIMQTALSSYVIQGI	4336
Sbjct	361	YAEPLKSP+IR+DSGV GGEVSMFYDPMIAKLCTYHD R QAIE M++ALSSYVIQGI	420
Query	4337	SHNISFLEAVMSHPRFISGNINTGFIAEEYPAGFSGASLTSEITDVFLATAIYTYITEQK	4516
Sbjct	421	SHNISFLEAV+SH RFI GNINTGFIAEEYPAGFSGA+LTSEITDVFL+TAI+ YITEQK	480
Query	4517	RAASIEGQMVDQASKIGTRWVVSIDDLFPVLIKVPDPGYNIRQGYTRIYIRSNWNLGSH	4696
Sbjct	481	RA+SI GQ++DQ S IGTRWVVSIDD+LFPVLIKPV +GYNIRQGYTRIYIRSNW++GSH	540
Query	4697	LFSAVVNGRKVNVKIENISTGYRLTHSGITVKTFVRSPLMSELESIMPVKLQLDDLTALT	4876
Sbjct	541	LFSA +NGRKVNVKIE+I TGY+LTHSGITVK +VRSP MSELES+M K+ ++D ELT	600
Query	4877	APLAGQIIAVKVQEGDEVIVSQEIMILTAMKMENIILAECAGKIAKIFVKDKQVSAGQV	5056
Sbjct	601	APLAGQIIAVK++E +EV+V QE+++LTAMKMENIILAE +GKIAKIF+++KDQVSAGQV	660
Query	5057	LLEFE 5071	
		L+EFE	
Sbjct	661	LMEFE 665	

A. C15:645..2066, virB8 and virB9

virB8 family protein [Rickettsia endosymbiont of Culicoides newsteadii]

Sequence ID: [WP_094649370.1](#) Length: 231 133/177/231 (58/76 %)

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Query   645   MEPILNSVQEYIKFGEYFKDAKKWYNFKYIYPLSQRSFLLIIRSILLTLFIGLALNISYL 824
        M+ + +SVQEYIK GEYF DA++WYNF+Y+YPL RSFLLI + L LF+G+ ++++ L
Sbjct   1    MDKVSSSVQEYIKSGEYFVDARRWYNFEYLYPLVHRSFLLIFTVVFLALFLGVVSVNSL 60

Query   825   FPMVNVQVRYLLQAQS*SSANIIRADLVKNDPLASIADIMVRNYLIHREKYDYDNLKGQFI 1004
        P V QVRY + A+S SA I A+ +K++ + SIADIM++NY+IHRE YDYD L+ QF+
Sbjct   61   LPTVRQVRYAISAESLKSATITNANHIKSNAINSIADIMIKNYVIHRESYDYDFLRPQFM 120

Query   1005  FIQNSTIIVFRKLFNYMNIIDNPSSPVMCYQQYTRRSINILSFTYKKADKAEIIFSSIAK 1184
        FIQN+ST I+FR+ N+MNIDN SPVM YQ+ RRS+NILS Y K +KAE+IF+S+AK
Sbjct   121  FIQNSSTRIIFRQFANFMNIIDNLSLSPVMRYQRSRLRSVNILSVVYHKNNKAEVIFTSVAK 180

Query   1185  TAGSKIFENMVWQATINFIDIDKINLGLPSDSRFNFAVTNYCLKILQDKMSK 1337
        + + I ENMVWQATINF+ID IN+ LP +S FNF VT Y LK++DK K
Sbjct   181  NSANDILENMVWQATINFDAINIHLPNSNFNFVVTGYKCLKLIEDKSKK 231
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P-type conjugative transfer protein VirB9 [Rickettsiaceae bacterium]

Sequence ID: [RVE05781.1](#) Length: 248

```
Query   1356  ILIFYANSSFAIRKSRPTSIDSRRIRIMVYNPDNVFKYTGYYGYQASIELLKDEEI*HFY- 1532
        I++ + N+S AIR+SRPT IDSRRIRIMVYNPD+VFKY GYY YQASIEL K EEI
Sbjct   10    IILLFVNTSQAIRESRPTPIDSRIRIMVYNPDVFKYGVYNYQASIELAKSEEIISISM 69

Query   1533  -----WRYRYLANCSLR**NFIKLMEQDATNMTLITNKLTFFELYVEETDMRDPDIL 1697
        W+ N FIK ME DATNMTLITNK TYFFELY EET+D+RDPD+
Sbjct   70    GDTTSWQIVPSGNRI-----FIKPMEHDATNMTLITNKRTYFFELYAEETS DIRDPDMA 124

Query   1698  FNVRFVYPD---EEEHLRSFSATSSSAPDLTHPEKSNFSYSISSHEEIIAPIKVFDGGEFTY 1871
        FNVRF+YPD EEEHLR+F A++ + PDL+HPEK NF+YSIS E++APIK+FDDGGEFTY
Sbjct   125  FNVRFIYPDEEEEEHLRTF-ASALAGPDLSHPEKYNFNYSISGSEQVAPIKIFDDGGEFTY 183

Query   1872  L*FRDKNAELSSNFC--H**RAARVNGQL*IIKRRK*HCYFRASISKIIHKAW*KIICVF 2045
        L FRDKNA+L + F R + VN + I K+ ++ KI+CVF
Sbjct   184  LQFRDKNAQLPAIFAVDEDRRESMVNYR--ISTENNTIVIVEQVFQKLAIRSGKKIVCVF 241

Query   2046  NEVFKSY 2066
        NE FK Y
Sbjct   242  NESFKPY 248
```

B. C15:3263..4537: murA

UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Rickettsia endosymbiont of Culicoides newsteadii] Sequence ID: [WP_094648791.1](#) Length: 424

```
Query   4537  MDSIIKGGKPLIGKVNISGAKNAALPIITAALLAEGNLNLINIPKLTDIYTMKTLNQNH 4358
        MDS+IIKGG PL G ++ISGAKN+ALPI+TAALL + L++ NIPKLTDI TMK LL+N
Sbjct   1    MDSLIIKGGIPLEGNISISGAKNSALPIMTAALLTD-KLSINNIPKLTDIITMKKLENL 59

Query   4357  GILIDIKDLGDYALSSINSNKVDNFVAPYDIVRKMRASIWVLGPLLARFGKAQVSLPGGC 4178
        G ++ + D DY ++ I+S+ ++NF APYDIVRKMRASIWVLGPLL+RF KA+VSLPGGC
Sbjct   60    GSVVTVTDHQDYLSDIDSSNINFTAPYDIVRKMRASIWVLGPLLRSRFSKAKVSLPGGC 119

Query   4177  AIGARQVDLHIDVLRAMGADIEITHGYIKAKSKGRCLKGVHFNFNKISVGATINAIMAATL 3998
        AIGARQVDLHI L+AMGADI++ HGVI AK GRLK VHF F +ISVGATIN+IMAATL
Sbjct   120  AIGARQVDLHIAALQAMGADIDVDHGYINAKITGRLKAVHFVFKQISVGATINSIMAATL 179

Query   3997  AKGETVLLNCAREPEIIDLCKCLTAMGANIDGDSTGEIKITGVESLKGANYKVMPDRIEA 3818
        AKGET+L NCAREPEI+DLC CL MGA I+G T EI I G LK NY +MPDRIEA
Sbjct   180  AKGETILSNCAAREPEIVDLCHCLNKMGAIEINGIGTSEITIIGKSYLKHTNYSIMPDRIEA 239

Query   3817  GTYMAAAAITKGKLDILGIDYHIIENLGLKLIDAGVEVSPLENGVRCLKYSGNIKSVDIQT 3638
        GTYM+AAAITKG L+I GI+ +I+EN+ LKLI+AG++V P++NG+R+ Y + VDI T
Sbjct   240  GTYMAAAAITKGSINIYGINGNIVENIVLKLIEAGIKVEPIDNGLRVS YVDKLN PVDIHT 299

Query   3637  EAYPGFSTDLQAQFMSLMTLAEGAAVITENIF*NRFMHIPELCRMGANITISGHSAMIRG 3458
        YPGF+TD QAQFMSLMTL G++ ITE IF NRFMH+PELCRMGANI I G+SA+I G
Sbjct   300  SPYPGFATDFQAQFMSLMTLCSSGSTITETIFENRFMHVPELCRMGANIIIGKNSAIIHG 359

Query   3457  VEHLSGAEVMASDLRASVSLVLAGLAAGKETIIRRVYHLDRGYQQLEQKLSHCGADIKRI 3278
        V L+GAEVMASDLRASVSLVLAGLAA T IRR+YHLDRGYQ LE+KLS+CGA+I R+
Sbjct   360  VPFLTGAEVMASDLRASVSLVLAGLAANDTTKIRRIYHLDRGYQTEKKLSNCGANIVRV 419
```

Query 3277 LGESI 3263
G+++
Sbjct 420 TGDNV 424

C. C15:4762-6303, Acyl-CoA carboxylase subunit beta

acyl-CoA carboxylase subunit beta [Rickettsiaceae bacterium]

Sequence ID: [RYE05809.1](#) Length: 514

Query 4762 MNQTILPDQDILLEEKRSIARAGGGHDRIALQHKKGKLTARQRVEAFDLPDSFEETGMFVE 4941
MNQ +L QDILLEEKRSIARAGGG +RIALQHKKG+LTAR+R+E LDPDSFEETGMFVE
Sbjct 1 MNQNVLQGGDILLEEKRSIARAGGGLERIALQHKKGRLTARERIEVLDPDSFEETGMFVE 60

Query 4942 HRCDNFGMKDKKFAGDGVVTHGHTINGRLVFIYSQDFTVLGGSUGEYHAKKICNVIDSAL 5121
HRCDNFGMKDKK AGDGVVTHGHTINGRLVFIYSQDFTVLGGSUGEYHAKKIC+V+DSAL
Sbjct 61 HRCDNFGMKDKKTAGDGVVTHGHTINGRLVFIYSQDFTVLGGSUGEYHAKKICSVDSAL 120

Query 5122 QVGAPVIGINDSGGARIQEGVDALGGYGELFQRNVIASGVIPQITLIMGPCAGGAVYSPA 5301
Q GAPVIGINDSGGARIQEGVDALGGYGELFQRNV+ASGVIPQI+LIMGPCAGGAVYSPA
Sbjct 121 QAGAPVIGINDSGGARIQEGVDALGGYGELFQRNVLASGVIPQISLIMGPCAGGAVYSPA 180

Query 5302 LTDFIFMVRDSSYMFVTGPDVVKTVTGEEVSQEKLGARMHTTKSGVADLAFKNDIEALL 5481
LTDFIFMVRDSSYMFVTGP+VVK VTGEEVSQEKLGAR+HTTKSG+ADL+FKNDIEALL
Sbjct 181 LTDFIFMVRDSSYMFVTGPEVVKAVTGEEVSQEKLGARIHTTKSGIADLSFKNDIEALL 240

Query 5482 ETRRFFNFLPLSNRAPLPTRYTKDPADRVMSLNTLVPLAANKSYDMKELIQRIVDEG*F 5661
ETRR FNFLPLSNRAPLP+R TKDPADRVMSLNTLVP NKS YDMKELI+RIVDEG F
Sbjct 241 ETRRLFNFLPLSNRAPLPSRCTKDPADRVMSLNTLVPNVPNKS YDMKELIKRIVDEGDF 300

Query 5662 FELQPDFAKNILIGFGYMEGRSIGFVANQPLYLAGCLDINASRKAARFIRFCDAFNIPIV 5841
FEL +FAKNI+IGFGYMEGR +GFVANQPLYLAGCLDIN+SRKAARFIRFCDAFNIPI+
Sbjct 301 FELHAEFAKNIIGFGYMEGRPVGFVANQPLYLAGCLDINSSRKAARFIRFCDAFNIPII 360

Query 5842 SLVDVPGFPLPGTAQEHDGIIKHGAKLLYAYAEATVPKITVITRKAYGGAYVMNSKHLRG 6021
SLVDVPGFPLPGT QE++G+IKHGAKLLYAYAEATVPKITVITRKAYGGAYVMNSKHLRG
Sbjct 361 SLVDVPGFPLPGTNQEYNGLIKHGAKLLYAYAEATVPKITVITRKAYGGAYVMNSKHLRG 420

Query 6022 DVNYAWVNPEIAVMGAEGAAEIIIFKEDCKDSLKKKKIQEYKDTVTSLFVAASRGYLDI 6201
DVNYAW+N EIAVMGAEGAAEIIIFK +CKD + KK IQEYKDT+TS F+AASRGY+DDI
Sbjct 421 DVNYAWINSEIAVMGAEGAAEIIIFKNECKDPEQKKILIQEYKDTITSPFIAASRGYIDDI 480

Query 6202 IKPQNTRWRICKALNFLQGKNTQMPWKKHDNLPL 6303
IKPQNTRWR+CKALNFL+ K Q+PWKKHDNLPL
Sbjct 481 IKPQNTRWRICKALNFLREKKVQVPWKKHDNLPL 514

D. C15: 6336-8333

acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha [Rickettsiaceae bacterium]

Sequence ID: [RYE05810.1](#) Length: 665

Query 6336 MNKPLFDKVLIANRGEISLRIMRSLKMGIKSVAVYSEADTGSKHVQEAEAYYVGNSPA 6515
M+KPLFDKVLIANRGEI+LRIMRSLKMGIKSVA+YSEADT S HVQ ADEAYYVGNSPA
Sbjct 1 MSKPLFDKVLIANRGEIALRIMRSLKMGIKSVAIYSEADTNSMHVQYADEAYYVGNSPA 60

Query 6516 TESYLSIKNIVNAARASGAQAVHPGYGFLAENFNANILKREGITLIGPSAQAIAKQMGDK 6695
TESYLSIKNI+NA RASGAQAVHPGYGFLAEN NFA+ LKREGITLIGPSA AIAKQMGDK
Sbjct 61 TESYLSIKNIINAIRASGAQAVHPGYGFLAENANFASALKREGITLIGPSAGAIAKQMGDK 120

Query 6696 IEAKKIATEAGVTTVPGYMGIIGNVQAISIAEEIGFPVIVKAAAGGGGRGMRVVKNSSE 6875
IEAKKIATEAGVTTVPGYMGII N+ QAISIAEEIGFPVIVKAAAGGGGRGMRVVKNS+E
Sbjct 121 IEAKKIATEAGVTTVPGYMGIIRNITQAISIAEEIGFPVIVKAAAGGGGRGMRVVKNSAE 180

Query 6876 MAAAFESAKLEAENSFNDGRVFIEKLIENPRHIEIQLIADQFGNAVCLGEREC SIQRHHQ 7055
MA AFESAK+EAENSF+DGRVFIE+LIE+PRHIEIQL+ADQFGNAVCLGEREC SIQRHHQ
Sbjct 181 MAQAFESAKIEAENSFDDGRVFIERLIESPRHIEIQLLADQFGNAVCLGEREC SIQRHHQ 240

Query 7056 KIIIEAPSSFITEEIRQKMYAEVIALTHKVGYYSGTVEFIMDPDKHYFFMEMNTRLQVE 7235
KIIIEAPS FITEEIR++MYAEVIAL++KVGYYSGTVEFIMD K YYFMEMNTRLQVE
Sbjct 241 KIIIEAPSVFITEEIRKQMYAEVIALSNKVGYYSGTVEFIMDSKKQYYFMEMNTRLQVE 300

Query 7236 HPVTELVTGIDIVEEMIKIAAGEKLSFTQDDIKLKGWAIESRICSEDPTRGFLPSSGRIT 7415
HPVTELVTGIDI+EEMIKIAAGEKLSFTQ+DIK+KGWAIE+RICSEDPTRGFLPSSGRIT
Sbjct 301 HPVTELVTGIDIIEEMIKIAAGEKLSFTQEDIKIKGWAIEARICSEDPTRGFLPSSGRIT 360

Query 7416 GYAEPLKSPHIRIDSGVSIGGEVSMFYDPMIAKLCTYHDTREQAIEIMQTALSSYVIQGI 7595

Sbjct	361	YAEPLKSP+IR+DSGV GGEVSMFYDPMIAKLCTYHD R QAIE M++ALSSYVIQGI EYAEPLKSPNIRVDSGVGAGGEVSMFYDPMIAKLCTYHDDRAQAIECMRSALSSYVIQGI	420
Query	7596	SHNISFLEAVMSHPRFISGNINTGFIAEEYPAGFSGASLTSEITDVFLATAIYTYITEQK SHNISFLEAV+SH RFI GNINTGFIAEEYPAGFSGA+LTSEITDVFL+TAI+ YITEQK	7775
Sbjct	421	SHNISFLEAVISHQRFIDGNINTGFIAEEYPAGFSGATLTSEITDVFLSTAIFAYITEQK	480
Query	7776	RAASIEGQMVDQASKIGTRWVVSIDDLRFPVLIKPVPDGYNIRQGYTRIYIRSNWNLGSH RA+SI GQ++DQ S IGTRWVVSIDD+LFPVLIKPV +GYNIRQGYTRIYIRSNW++GSH	7955
Sbjct	481	RASSISGQIIDQVSNIGTRWVVSIDDKLFPVLIKPVQEGYNIRQGYTRIYIRSNWHIGSH	540
Query	7956	LFSAVVNGRKVNVKIENISTGYRLTHSGITVKTFRSPLMSELESIMPVKLQLDDLTEL LFSA +NGRKVNVKIE+I TGY+LTHSGITVK +VRSP MSELES+M K+ ++D ELT	8135
Sbjct	541	LFSATINGRKVNVKIESILTGYKLTHSGITVKAYVRSPRMSELESVMLGKITVNDQAELT	600
Query	8136	APLAGQIIAVKVQEGDEVIVSQEIMILTAMKMENIILAECAGKIAKIFVKDKDQVSAGQV APLAGQIIAVK++E +EV+V QE++LTAMKMENIILAE +GKIAKIF++KDQVSAGQV	8315
Sbjct	601	APLAGQIIAVKIKEQEEVVVGQELIVLTAMKMENIILAERSGKIAKIFIQEKDQVSAGQV	660
Query	8316	LLEFE 8330 L+EFE	
Sbjct	661	LMEFE 665	

E. C12: R629..1594, IS481 family transposase [Rickettsia bellii]

Sequence ID: [WP_045799898.1](#) Length: 364

Query	1594	GYSRD--YRKFELYEAGGAEALY 1529 GYSRD YRKFELYE GG EALY	
Sbjct	32	GYSRDSYRKFELYETGGEALY 54	
Query	1547	GCRSFIHEVSRKKPIIANRV---VEKAVLDMAIKYPAYGQLQVSNKLKKEGILVSPGRVR G ++E+SR+KPIIANRV +EKAV+DMAI+YPAYGQL+VSN+LKK GILVSPG VR	1377
Sbjct	48	GGEALYEISRRKPIIANRVDPSIEKAVMDMAIEYPAYGQLRVSNELKKSGILVSPGGVR	107
Query	1376	SIWLRNDLNSLKKHLIALETK-EQDGIILTEAQLRVLENRKNAKEAQGKIETEHVILAV SIWLRNDLN++ K L ALE K QDGI+LTEAQL+VLE R+N KEA G+IET+HP L	1200
Sbjct	108	SIWLRNDLNNISKRLKALEAKMAQDGIIVLTEAQLQVLEKRRNEKEAHGEIETQHPGYLGC	167
Query	1199	KICIT*AVLKA*VKS LPKPLLIHIQG*QAQSFMLKRQLAITSADMLNDRVL----T*GIP + K + + + I A + + + AIT+ADMLNDRVL T GIP	1032
Sbjct	168	QDTYYVGNFKG-IGKVYSQVFIDSYTRVADAKLYTDKTAITAADMLNDRVLPWYETQGIP	226
Query	1031	YLEYLLIAVQNIRVT*RIMLLNC*VLKG*STLLK-HIPLKLTECVSDSIKL*NEFFDI L L + F ++G K + P C + + EFFD	855
Sbjct	227	ILRLITDRGSEYKGNIEHHAFELFLSIEGIEHTTTKAYSPQTNGMCERFNKTMKEFFDT	286
Query	854	VMRKKIYTSKELQQLDLDLTLHYNYE 774 MRKKIYT L +LQ DLD WL Y+N E	
Sbjct	287	AMRKKIYTELDDLQLDLDIWLEYFNNE 313	
Query	1212	YLSCQDMYYVGSFKGIGKVFTQTFIDTYSRVAGAKLYAEKTASYFC*YAK**GADLR-- YL CQD YYVG+FKGIGKV++Q FID+Y+RVA AKLY +KTA AD+	1039
Sbjct	164	YLGCDQDTYYVGNFKGIGKVYSQVFIDSYTRVADAKLYTDKTAIT-----AADMLND	214
Query	1038	-----YTLLRLITDRGTEYKGNLENHAFELFLSIEGIEHTTTKAYSP*TNGMCER +LRILTDRG+EYKGN+E+HAFELFLSIEGIEHTTTKAYSP TNGMCER	889
Sbjct	215	RVLWPWYETQGIPILRLITDRGSEYKGNIEHHAFELFLSIEGIEHTTTKAYSPQTNGMCER	274
Query	888	FHKTIK 871 F+KT+K	
Sbjct	275	FNKTMK 280	
Query	772	RPHYGKYYYGKTPMQTFQDSKKLALEKNNEILYPEYLSDSQNSADNQI 629 RPH GKY YGKTPMQTFQDSKKLA+EKNNEILY EY SDSQN DNQ+	
Sbjct	314	RPHSGKYCYGKTPMQTFQDSKKLAVEKNNEILYLEYSSDSQNLTDNQV 361	

F. C12:1890-5078, isoleucine tRNA ligase [Rickettsia endosymbiont of Bemisia tabaci]

Sequence ID: [WP_095568341.1](#) Length: 1091

Query	5078	MKKQNIYPEIESGADFP LIEKKILAYWKEHNIFQKSIDNRPATGGIDRAANNEFIFYDGP M YPE+ S ADF IEK+IL +W+++NIFQKSID R ++EFIFYDGP	4899
Sbjct	1	MTNTKYYPEVSSNADFATIEKEILKFWQDNNIFQKSIDR-----EGDDEFIFYDGP	52
Query	4898	PFANGLPHYGHLTGFIKDVYARYQATKGKKVERRFGWDCHGLPAEMGAKEKLGFSGRLA	4719

Sbjct	53	PFANGL HYGHLLTGFIKDVYARYQ +GKKVERRRFGWDCHGLPAEM +EKELG SGRLA PFANGLTHYGHLLTGFIKDVYARYQTVRGKKVERRRFGWDCHGLPAEMQSEKELGISGRLA	112
Query	4718	ITKFGIDKFNEHCRSSVMKYASEWEKYVNRQARWVDFNNSYKTMDSLFSMESVLWAFKELY IT FGI+KFN HCR SVMKYA EWE+YV RQARWVDF NSYKTM +FMESVLWAFKELY	4539
Sbjct	113	ITNFGIEKFNAHCRDSVMKYADEWEQYVTRQARWVDFKNSYKTM DKNFMESVLWAFKELY	172
Query	4538	KKGLIYESMRVMPYSWACETPLSNFETRLDNSYRERVDKAVTCSFTLTDK-----PAK KGL+YESMRVMPYSWACETPLSNFETRLDNSYRER DKA VT SF L PAK	4380
Sbjct	173	NKGLLYESMRVMPYSWACETPLSNFETRLDNSYRERADKAVTVSFELCHPENITDVI PAK	232
Query	4379	APAGFK-----EYKMLAWTTTPWTLPSNLALAVGPEVKYIFVPKEENCYIIAKFA A K EY++LAWTTTPWTLPSNLALAVG ++ Y VPK + CYIIA +	4230
Sbjct	233	AGIQEKVDPPLRGDDIEYRVLAWTTTPWTLPSNLALAVGSDIDYALVPKGDVCIYIIAASS	292
Query	4229	SYKYAKELGIEEGVKCQECRGNELDGITYKPVFDYFVDHPNSFRVLCAEFVAEGDGTGIV KYAKEL ++ + +G+EL G++YKP+FDYF DHPNSF++ +FV EGDGTG+V	4050
Sbjct	293	VSKYAKELELKGDEQFTIIKGSELQGLSYKPLFDYFKDHPNSFKIFAGDFVVEGDGTGVV	352
Query	4049	HLAPGFGEDDQVVVCVQAGIELVCPVDNAGKFTSEVYDFVGLNVFEANDNITIKLKEIGAW H+APGFGEDDQ++C GI+LVCPVDN+GKFT E+ D GL VF+AND I IKLKE G W	3870
Sbjct	353	HMAPGFGEDDQILCESKGIKLVCPVDNSGKFTKEIPDLEGLQVFDANDKII IKLKEQGNW	412
Query	3869	LKTEQVLHNYPHCWRTDTPLIYKAVSSWYVEVTKFKDRMVLELNQEIINWIPSNVKDNLF GK LKTEQ +HNYPHCWRTDTPLIYKAV SWYV+VT+FKDRMVLELNQ+INWIP +VKDNLF GK	3690
Sbjct	413	LKTEQYIHNYPHCWRTDTPLIYKAVPSWYVKVTEFKDRMVLELNQQINWIPFHVKNLFGK	472
Query	3689	WLENARDWSISRNRFWGTPIPIWRSDPKYPRIDVYASVEELEKDFGVKVTDLHRPYIDQ WLENARDWSISRNRFWGTP+P+W+S+DP+YPRIDVY S+EELE DFGVK+TDLHRP+ID+	3510
Sbjct	473	WLENARDWSISRNRFWGTPLPVWKSDDPQYPRIDVYGSIEELETDFGVKITDLHRPFIDE	532
Query	3509	LTRANPDDPTGKSIMQRVEDVDFDCWFESGSMYPYQGAHYPFENKEWFEKHFPADFIVEYSA LTR NP+DPTGKS M+R+EDVDFDCWFESGSMYPYQGAHYPF+NK+WFE HFPADFIVEYSA	3330
Sbjct	533	LTRTNPNDDPTGKSTMRRIEDVDFDCWFESGSMYPYQGAHYPFKNQWFE DHFPADFIVEYSA	592
Query	3329	QTRGWFYITLMVLSTALFDRPPFLNCICHGVILDSSSQKLSKKLRNYADPLELFDKYGSDA QTRGWFYITLMVLSTALFDRPPFLNCICHGVILD++ QKLSK+L NYADPLELFDKYGSDA	3150
Sbjct	593	QTRGWFYITLMVLSTALFDRPPFLNCICHGVILDATGQKLSKRLNNYADPLELFDKYGSDA	652
Query	3149	LRLTMLSSNVVKQGELLIDKEGKMVYETLRIFIKPIWSAYHFFFTLYANADGIRGENILAA LR+TMLSSNVVKQGELLIDK+GKMV++TLR+FIKPIW+AYHFFFT+YANAD I+GE	2970
Sbjct	653	LRVTMLSSNVVKQGELLIDKDGMVFDTLRLFIKPIWNAYHFFFTMYANADHIKGE-----	707
Query	2969	VSNLNRNVLDQYILAKLKTAVSGIAQGLDNFNTQIAYSNIANFFEV LNNWYIRRSRHRFW ++ + NVLD YIL+KLK AV I + LDNF+TQIAY ++ FFEVLNNWYIRRSR RFW	2790
Sbjct	708	LNFTSENVL DVYILSKLKIAVEKIKESLDNFDTQIAYHAVSEFFEVLNNWYIRRSRARFW	767
Query	2789	KSEKSDKRMAYNTLYTCLQMCMQAMSSSLAPLIMEDIYLG L-----	2667
Sbjct	768	KSEKD DK+ AYNTLYTCL+ M AMSSL PLI E IYLG L KSEKDLKQNA YNTLYTCL ETMAIAMSSLVPLISEAIYLG LHCHPRESGDPEKSVFLDSR	827
Query	2666	-----TGANNSSGGSVHLTNFPDLNEIEVDPNLIKNDLILDICNCALFIRSQENIRVRQ N SVHL N+P+L++ E++ L+ MD +LDIC+ +LFIRS EN RVRQ	2505
Sbjct	828	LRGNDIKDVQNDLSVHLCNYPNLKSF E INSELVDTMDTVLDICNSL FIRSSENARVRQ	887
Query	2504	PLAQITLIIKEVNNLRVFE DIIKDEINIKSIVYYNNLENFAIRKLSINFQLVGKRLSNKI PL+ IT+I K + L+ FED+IKDEIN+KS++Y ++LEN+A++KLSINF ++GKRL K+	2325
Sbjct	888	PLSSITII SKNNDKLKDFEDLIKDEINVKSVIYRDDLENYAVKKLSINFPMLGKRLPAKM	947
Query	2324	KNIITASKKGEWQLQGEQLEIAGEVLNSEEFSIVLEPKGDIKAKALSDNSGLVILDLEI K+II ASKK EW+ L I E LNS+E+ ++LEP IKGA + + NS L+ILDLE+	2145
Sbjct	948	KDIIAASKKNEWEATSGGLRICNETLNSDEYKLILEPHSHIKGASSFAHNSLLILDLEL	1007
Query	2144	TKELEEEGVARDLIRFIQQARKDAGFNVS DRIELEIKGTLRIIQISKVYEQ LITEQTL SK T EL +EG+ARD++R IQQARK+A F ++DRI ++I + +I +Y + I EQTL +	1965
Sbjct	1008	TSELIDEGIARDIVRSIQQARKNADF AITDRILIDID----LPKIIDIYGEFIKEQTLGE	1063
Query	1964	FGSINVAAYECSVELMNEKVKLALK 1890 F + +EL N K++L +K	
Sbjct	1064	FAKDFTPDHISEIELENHKLQLKIK 1088	

G. C12:9205-11498 penicillin-binding protein 1A [Caedimonas varicaedens]

Sequence ID: [WP_082168465.1](#) Length: 824

Query	9205	ILALFSHYSGSLPDYQHLADYKPPVVTRLYANDGHMFAEYAW EKRIYVP IQSIPKKVIQA +LALF HYGSGLPDYQHLADYKPPVVTRLYANDGHMFAEYAW EKRIYVP+QSIPK+VIQA	9384
Sbjct	1	MLALFYHYGSGLPDYQHLADYKPPVVTRLYANDGHMFAEYAW EKRIYVPVQSIPKRVIQA	60

Query	9385	QL 9390 L	
Sbjct	61	FL 62	
Query	9384	AAEDKNLYTHSGIDIPSIISAALTNIGRVAESKRVPVGASTITQQVAKNFLDLADIAHAVSY	9563
Sbjct	63	AAEDKN Y HSGIDIPSIISAALTNIGRVAESKRVPVGASTITQQVAKNFLDLADIAHAVSY AAEDKNFYQHSGIDIPSIISAALTNIGRVAESKRVPVGASTITQQVAKNFLDLADIAHAVSY	122
Query	9564	ERKIKEAILAFRL*SAYSKDYILEFFMNEISLGASSYGAAAAALNYFNKSLDELTISEVA	9743
Sbjct	123	ERKIKEAILAFRL SAYSKDYILE F+NEI LG+SSYGAAAAALNYFNKSLDELTISE+A ERKIKEAILAFRLSAYS KDYILELFLNEIYLGSSSYGAAAAALNYFNKSLDELTISEIA	182
Query	9744	YLAGLPKAPSRYPARYP--AKIRRNYYVIRRMLEDGYITMQEAKDAAAEPIILHERNPGD	9917
Sbjct	183	YLAGLPKAPSRYP RYP AKIRRNYYV+RRM EDGYIT QEAK+AAAEPI+LHERNPG+ YLAGLPKAPSRYPVRYPEAAKIRRNYYVRRMFEDGYITAEAKEAAAEPIVLHERNPGE	242
Query	9918	VVHGSYFAEEVRRELIEKFGEKALYQEGLVVRTSLDPRQLQELAQQLRQGLINYDRRHGW	10097
Sbjct	243	VVHGSYFAEEVRREL+EKFGKALYQEGLVVRTSLDP+LQE+A+QSLRQGLI+YDRRHGW VVHGSYFAEEVRRELMEKFGEKALYQEGLVVRTSLDPQLQEVARQSLRQGLIDYDRRHGW	302
Query	10098	RGAVLRRLPLSKEEKILPEKGKESTALWIPKLKTVVEPSGIGEWMAIVLSVDAQAVTIGF	10277
Sbjct	303	RGAT+L L LSKEEK LPEK KE+ A WIPKLK VVEPSGIG WHM++VL+V +Q VTIGF RGAILHLILSKEEKTLPKAKEALAPWIPKLKAVVEPSGIGAWHMSVVLAVGSQEVVTIGF	362
Query	10278	KDGTWGYITFKELQWARKYINEYALGGTITRPAVLAVGDVVLVEP-LNNQKQFSLCQIP	10454
Sbjct	363	KDGT G I+ KELQWARKYINEYALG + +P DVL+VGDV+LVEP LN++K+F LCQIP KDGTSGQISLQELQWARKYINEYALGSGVVKPGDVLVSGDVILVEPSLNDKKKFKLCQIP	422
Query	10455	VVSGAMVMDPHSGRVLALQGGFSFKISQFNRRATQAMRQIGSTFKPFAYLAALKEGLTPS	10634
Sbjct	423	VSGA++VMDPH+GRVLA+ GGFSFKISQFNRRATQAMRQIGSTFKPFAYLAALKEGLTPS AVSGAIIIVMDPHTGRVLAMHGGFSFKISQFNRRATQAMRQIGSTFKPFAYLAALKEGLTPS	482
Query	10635	TLLYDGPFFYLDLGYGLGIWKPRNYERDYLGSITLRRAFELSRNLAPVRMIHEYVGMQNVK	10814
Sbjct	483	TLLYDGPFF +DLG GLG+W PRNYERDYLGSITLRRAFELSRNLAPVRM HEYVGM+NVK TLLYDGPFFSIDLGPGLGVWSPRNYERDYLGSITLRRAFELSRNLAPVRMTHEYVGMKNVK	542
Query	10815	QVAEKLGLVEHLPLQLATVLDAAESTILKVTAYAMIANGGKKITPTLLDRVQDRHGKNL	10994
Sbjct	543	QVAEKLGL+V+HLPLQLATVL AEST+LKVTAYAMIANGG+KITPTLLDRVQDRHGKNL QVAEKLGVVDHLPLQLATVLGAAESTLLKVTAYAMIANGGRKITPTLLDRVQDRHGKNL	602
Query	10995	YVNKGRRLCEGCGNVYWMNSPPSLVDRRQQVIDPATAYQMISLLQGDVDRGTAKGIKDLNR	11174
Sbjct	603	YVN+GR CEGCGNVYWMNSPPSLVDRRQQVIDPATAYQMISLLQGDV+RGTAAG++DLNR YVNQGRFCEGCGNVYWMNSPPSLVDRRQQVIDPATAYQMISLLQGDVDRGTAKGVDRDLNR	662
Query	11175	PLAGKTGTSNDYRDTWFMGFTPDVLVVGVFVGFDAALRDMGQHENGARVALPIFKAFMAEAL	11354
Sbjct	663	PLAGKTGTSNDYRDTWF+GFTPDVLVVGVFVGFDRD+GQHENGARVALPIFK FMAEAL PLAGKTGTSNDYRDTWFGFTPDVLVVGVFVGFVPRDLGQHENGARVALPIFKTFMAEAL	722
Query	11355	KNVPAIPFRIPSGIKLIRVDAMTGLRASGSEPNVIFEAFKPGTDENS	11498
Sbjct	723	KN PAIPFRIPSGIK +RVDAMTGL A+GSEPNVIFEAFKPGTDENS+ KNTPAIPFRIPSGIKFVRVDAMTGLPAAGSEPNVIFEAFKPGTDENSF	770

H. C12:8104-8664, ribonuclease E/G [Caedimonas varicaedens]

Sequence ID: [WP_062138834.1](#) Length: 766

Query	8664	MAKMMIIDATHSEETRVALIEKNRLIDFDFESATKLTVKGNIYLAKVARVEPSLQAAFV	8485
Sbjct	1	M K MIIDATHSEETRVALI EKNRLIDFDFESATKLTVKGN+YLAK+ARVEPSLQAAFV MTKRMIIIDATHSEETRVALISEKNRLIDFDFESATKLTVKGNVYLAKIARVEPSLQAAFV	60
Query	8484	DYGGNRHGFLAFSEIHPDYFRIPVSDREALKEEMNKVSAAEKNPLKKQ*FKKKEAQQSFK	8305
Sbjct	61	DYGGNRHGFLAFSEIHPDYFRIPVSDREALKEEMNK S EE ++ +E Q+SFK DYGGNRHGFLAFSEIHPDYFRIPVSDREALKEEMNKASLEEH--AEEIILPAQEEQKSFK	118
Query	8304	SPQGV-----EESEESAFEMQIAILGGEAPPNDEDELRSKRPLLHQMYKIQEVIHK	8146
Sbjct	119	+ T EESEESAFEM IAILGGEAP ND+DEL KRPLLHQMYKIQEVIHK DEEKATEEGDEKQEESEESAFEMPIAILGGEAPLNDDDELTSKRPLLHQMYKIQEVIHK	178
Query	8145	NQILFVQVVKEERG	8104
Sbjct	179	NQIL VQVVKEERG NQILLVQVVKEERG	192

I. c12:7486-8016, aminopeptidase P family protein [Rickettsia hoogstraalii]

Sequence ID: [WP_040255827.1](#) Length: 579

Query	8016	TSTLAIGAPTLEEIRCYTNVLRGHINLSKIKFPRGI-TGANLDILARQYLWAESSDYPHS	7840
Sbjct	401	T T+ IG PT E+ + YT VL+GHI L+K KFP+ I TGANLDILARQYLW E DYPH	460
Query	7839	TGHGVGSYLSVHEGPQGINLRNNVSLKPGMILSNEPGYYVPGKFGIRIENLMYVKAADHP	7660
Sbjct	461	TGHGVGS+LSVHEGPQ INLRN LK GMILSNEPG+Y+ GK+GIRIENLMYVK ++	518
Query	7659	NFLQFETLSLVPYARKLIDFNMLDSSELEYLKQYYQKIHDNIYHLLSPLAKDWLKLQI	7486
Sbjct	519	+L+FETLSLVPYA KLID +L+ E+ Y+K+YY KI IY LLSP A+DWL +I	576

J. COQ9 family protein [Rickettsiaceae bacterium]

Sequence ID: [RYE06526.1](#) Length: 210

Query	5725	MILEIEQKYQAQRAELITALTELLPFYEWNEKIIHEAEEICGFLPEYTYIIFSSGLPEIR	5546
Sbjct	1	M EI +KYQ QR + + ELLP++ W+ ++I EAE +CGF Y +++F + I	60
Query	5545	DFHESQTDVLMVKYLQEEEEPLKI--RERISLALKIRIKKCVSKIICKKNRNYFLQPENL	5372
Sbjct	61	F+E+ D LM+ L +E KI R+ IS ALKIRIK C ++ KKN+ YFL+PEN	120
Query	5371	LEGARVAWRTCDLIWRYAGDDSTDFNHYSKRSLLTGVYLSSIMFYIKDESKDYIETDNYI	5192
Sbjct	121	G+++AW+TC+ IW YAGD S DFN+Y+KR LL VY+SSI +Y+ D+S + +TD +I	180
Query	5191	DRTLTKIINIASELKKFAKLPSIEDIPILRLF	5099
Sbjct	181	D+ L KIINIASLK K+P E+IPILRLF	209

K. 30S ribosomal protein S21 [Rickettsia endosymbiont of Culicoides newsteadii]

Sequence ID: [WP_094649364.1](#) Length: 66

Query	5867	VILNVHAGNGEQAIKNLKRKMQRRELVFRAMKMSRFYEPSPVKVRKAQETERRKRKVAR	6046
Sbjct	1	+ILNVHAGNGEQAIKNLKRKMQRRELVFR+MKMSRFYEPSPVKVRK QETERRKRKVAR	60
Query	6047	KQMME	6064
Sbjct	61	KQMMEG	66

L. amino acid ABC transporter ATP-binding protein [Caedimonas varicaedens]

Sequence ID: [WP_062138842.1](#) Length: 241

Query	11906	LVKEVLSVIQDLATQHTMTLAIVTH*MSFAKKFSDMIWFLDAGELVETAEPEHFFSKPQT	11727
Sbjct	171	+VKEVLSVI+DLA QHTMTLAIVTH M+FAK+ SDMIWFLDAGELVE EP+HFF+KPQT	230
Query	11726	IRAQEFLLDMVL	11694
Sbjct	231	+RAQ+FLDMVL	241

P. Type II secretion system protein D precursor XpsD and type IV leader (prepilin) peptidase [Caedimonas varicaedens]

Sequence ID: [GAO98863.1](#) Length: 550

Query	1845	MNFSVRGCLIVLILFMLSSTRTWDTENDLALdpstkmtkqqieenLLRPTSTHIRKARPF	1666
Sbjct	1	MNF GC+ VL+LF LSSC TWD +NDLALDP TKMTK+QI ENL R + +K RPF	60
Query	1665	AKNSSVPLILKPSKN	1621
Sbjct	61	K S VP+I KN	75
Query	1684	QKSAPFCKK**CSPYPEALKKPITLSTTEEVLKDVLFKIDARQGGVDLSLDPEVRGGVAL	1505
Sbjct	55	+K+ PF KK P LK P+TLSTTE VPLKDV F+IARQ VDL+DP V+GGVAL	114
Query	1504	HTTKRPLINIVKELCTLTCL*YKIENNILRIEPAKPY*INYNAQFLSLTRQNQSRI SVAT	1325
Sbjct	115	H T RPLI+IV+ELCTL L YKIENNILRIEPAKPY+NYNAQFLSLTRQNQSRI SVAT	174

Query	1324	DIFTANEGQAHADNGSNTLLTGETKNDFWAELESNLSTILQDSEPKGGKQEKSAAYSLHK	1145
		DIFT NEGQ TADNGSNTLLTGETKNDFWAELESNLSTILQ+S+ K Q+KS+YSLHK	
Sbjct	175	DIFTTNEGQGSTADNGSNTLLTGETKNDFWAELESNLSTILQNSDAKEVGGQDKSSYSLHK	234
Query	1144	QAGIIYIHVTQAQHQQVEHF 1085	
		QAGII ++ TQAQHQQVEHF	
Sbjct	235	QAGIISVYGTQAQHQQVEHF 254	
Query	1088	FLKLLRLSTSSQVlieakivevilkDEFQAGINWNLLKGDVLVQSPMGDTITPGSFNKKK	909
		FLKLLRLSTSSQVLI EAKIVEVILKDEF+AGINWNLLKGDVLVQSP+GDTITPGSFNK A	
Sbjct	254	FLKLLRLSTSSQVLI EAKIVEVILKDEFKAGINWNLLKGDVLVQSP LGDTITPGSFNKNA	313
Query	908	TIVRDVFTFGASGKQLTEIVSLINKFGTVITLSSPRLTAMNNELGVIKVATNYVYFRN*	729
		T VRDVFTFG SGKQLTEIV LINKFGTV TLSSPRLTAMNNE GVIKVATNYVYFR N	
Sbjct	314	TPVRDVFTFGGSGKQLTEIVGLINKFGTVRTLSSPRLTAMNNEPGVIKVATNYVYFRIN	373
Query	728	NRDYGYSVREY EYVSSEVHTV SIGLIMVVHPSINIADGSIVLSLRPTISRVDDEKPDPA	549
		NRDYGYSVRE+EYVSSE+HTV IGLIMVVHPSIN+ADGSIVLSLRPTISRVDDEK DPA	
Sbjct	374	NRDYGYSVREHEYVSSEIHTVPIGLIMVVHPSINLADGSIVLSLRPTISRVDDEKADPA	433
Query	548	VAIVSKETQQSYVPVVRKQEFESLVCMNSGEFIVMGGLME*ISKNNQSGVLYISEVPLFG	369
		VAIVSKE QQSYVPVVRKQEFESLVCMNSGEFIVMGGLME ++KNNQSGV Y+SEVPL G	
Sbjct	434	VAIVSKEAQQSYVPVVRKQEFESLVCMNSGEFIVMGGLME EVAKNNQSGVPYLSEVPLLG	493
Query	368	NLAKGKSDDRVSSELVIFLKATIVDNKADFPVPITESTFS 249	
		NLAK KS+DRVVSELVIFLKATIVDNKAD FVP+TEST +	
Sbjct	494	NLAKAKSEDRVSELVIFLKATIVDNKADTFVPVTESTVA 533	

Q. prepilin peptidase [Caedimonas varicaedens]

Sequence ID: [WP_062141155.1](#) Length: 142

Query	2058	MSYDSlllllllVMAWIGIIYYDMRYRIVPDFlvlsllilgilhyslTYGHFLCAVILGGG	2237
		M YDSL LLLL++ W GIIYYDMRYRI+PD LVLSLLILG LHYSITY HFLCA +LG G	
Sbjct	2	MLYDSLALLLLLLITWGGIIYYDMRYRIIPDGLVLSLLILGCLHYSITYEHFLCAGVLGLG	61
Query	2238	GALLKISMEKIMNHPALGWGDVKLAGVLGIGMEPEQISLFLIYIGLVGCAWGGP*KNFER	2417
		GALLKISMEK++N ALGWGDVKLA LGIGM PEQISLFLI G +GC WG K +	
Sbjct	62	GALLKISMEKLLNRLALGWGDVKLAALGIGMIPEQISLFLICAGFIGICIWGLFYKIILK	121
Query	2418	TSL--NSPTL 2441	
		SL +P+L	
Sbjct	122	ESLFFFPAPSL 131	

R. tRNA (guanosine(37)-N1)-methyltransferase TrmD [Caedimonas varicaedens]

Sequence ID: [WP_062139502.1](#) Length: 236 204/231 identities (88%)

Query	24322	MTFEMKIFTLYPEHFFPGPQQY*LVGKALQEKKWSLETVNIRDFAFDRHKTVDDTACGGGP	24501
		MTF +KIFTLYPE FPGP QY LVG+ALQEKKWSLETVNIRDFAFDRHKTVDDTACGGGP	
Sbjct	1	MTFAIKIFTLYPEIFPGPLQYSLVGRALQEKKWSLETVNIRDFAFDRHKTVDDTACGGGP	60
Query	24502	GMVMRPDVIDRALKFHYPTFSKSLIYLSPRGIPLTQEYVKKLARPSLGLLCGRFEGIDQ	24681
		GMVMR DVIDRALKFHY PFSKSLIYLSPRGIPLTQEYVKKLA+RPS+GLLCGRFEG+DQ	
Sbjct	61	GMVMRADVIDRALKFHYPVFSKSLIYLSPRGIPLTQEYVKKLAQRPSVGLLCGRFEGVDQ	120
Query	24682	RILDAWEFEVVSIGDFILTTGGELPAMALIDACVRILPGVIGSSSELEESFSQGLLEYPQ	24861
		R+LDAWEFEVVSIGDFILTTGGELPAMALIDACVR+LPGVIGS+ESLEESFSQGLLEYPQ	
Sbjct	121	RVLDAWEFEVVSIGDFILTTGGELPAMALIDACVRVLPGVIGSAESLEESFSQGLLEYPQ	180
Query	24862	YTRPCTWEGREVPVLLKGYHKHIRCwrkaqaEEITRTRRPDLWEKYCDAR 25014	
		YTRP WEGREVP++LL+G+H+ IR WR+AQAEEITR RRPDLW+KYCD R	
Sbjct	181	YTRPRVWEGREVPDILLQGHHEQIRRWQAQAEEITRVRRPDLWKKYCDTR 231	

S. 16S rRNA processing protein RimM [Caedimonas varicaedens]

Sequence ID: [WP_062139500.1](#) Length: 179, 135/156/175 (77/89 %)

Query	23784	mdssskilmgFIMGAFGIRGGMRFKSYTESIGNLKYKVLQDQTGHQRFKIIQLLPYKEN	23963
		M+SSSKILMGFIMGA GIRGGMRFKSY ES +LK+YKV QDQTG Q+ KIIQ+LPYKEN	
Sbjct	1	MNSSSKILMGFIMGACGIRGGMRFKSYGESPKDLKSYKVFQDQTGCQQLKIIQILPYKEN	60
Query	23964	IITLYLEGITTRSQA EALKGVSLYIDRVqlkksreefydydlegLVVQDEHNCKRGHVK	24143
		IITLYLEGITTRSQA EAL+G+SLYID QLKK S++EFYY+DLEGL+V++E NC G VK	

Sbjct	61	IITLYLEGITTRSQAEALRGSMLYIDHTQLKKLSKDEFYYHDLEGLIVRNEENCVIGQVK	120
Query	24144	AVVNYGADSILSICLLEDLSAEILVPFRKEFVKevnqkekyiildTDYMRALLDL	24308
		VV+YGADS+L +CLED S+EIL+PFRKEFVK VNQ+EKYIILDTDY++A LDL	
Sbjct	121	TVVSYGADSMGLGVCLLEDPSSEILIPFRKEFVKAVNQKEKYIILDTDYVQAFLDL	175

T. 50S ribosomal protein L19 [Caedimonas varicaedens]

Sequence ID: [WP_062139504.1](#) Length: 141, 105/109/115 (91/94%)

Query	25038	MNIIQQFEQEQLAKLAANSLVPQFSAGDTLRihvkvegerertqAYEGVCIAIKNAGIN	25217
		MNIIQQFEQE+ KLAAN+ VPQFSAGDTLRihvkvegerertQAYEG CIA KNAGIN	
Sbjct	1	MNIIQQFEQEQVTKLAANNPVPQFSAGDTLRihvkvegerertQAYEGFCIARKNAGIN	60
Query	25218	SSVTVRKLSFGEGVERvfplyspNIRIEVVRHGDvrraklyylreRTGKAARIAK	25382
		SSVTVRKLSFGEGVERVFLYSPNIRIEVVR+GDVRRAKLYYLR RTGKAARI +	
Sbjct	61	SSVTVRKLSFGEGVERVFLYSPNIRIEVRYGDVRRAKLYYLRARTGKAARITE	115

U. transcription-repair coupling factor [Caedimonas varicaedens]

Sequence ID: [WP_082168494.1](#) Length: 1159, 82/90/105 (78/85 %)

Query	23457	DRYKIPGALPDEVSNLLKILTFKQLCRKAGIEKLDAGKKGCVLSTFFNQSFNPLALVSYI	23636
		DR+ G LPDEV NLLKIL KQLCRKAGIEKLDAG+KGCVLST NQSF NPLALV+YI	
Sbjct	1056	DRF---GTLPDEVGNLLKILALKQLCRKAGIEKLDAGEKGCVLSTFSNQSFNPLALVAYI	1112
Query	23637	NEHQGIIRLRPDHKLVLKLVWKTPLLKMEGVKKILQELVALATQK	23771
		N+HQG IR RPD KLVFLKLVWKT LPK+EGVKKILQEL++LA +	
Sbjct	1113	NHQGTIRFRPDQKLVLKLVWKTPLSKVEGVKKILQELISLADSR	1157

V. hypothetical protein BGO77_01970 [Caedibacter sp. 37-49]

Sequence ID: [OJX11001.1](#) Length: 642

Query	36642	ALSHFKKLEPVVKTPIISCSRVGYWLGRTYEAMGKAKEARTSYQKAAQYKGTIFYGQKAFSK	36821
		A HF +L V +P S S+ YW GR +A +EA YQKAA Y T+YGQ A	
Sbjct	334	AFHHFNQLYQKVTSFYRSKAAWAGRAAQAKKLQEAHLWYQKAAYPATYYGQLALKA	393
Query	36822	LGHTDKEIILETLRFTPAQQAKFESHKAVKLIRLLAKEEIDEHILSFAYVFAKQTASPLE	37001
		L + + LE+L F ++ KFE+H+ V+ ++LL K + + +LSF Y++A QT+S E	
Sbjct	394	L-NKPQTFRLESLTFPISEVRKFENHEFVRAVKLLHKAGLTDELLSFGYMYA-QTSSSHE	451
Query	37002	RKQILALVHELAPHYGVIEAQVIAPYQSTLYSEAFPRKPIYKHKMEKVDAALAHAVIRK	37181
		+L+L +AP + V +A ++ +T Y EA+P++ ++ A+ HA+IRK	
Sbjct	452	ALMMLSLASTIAPQFAVGMADSMILHNTHYKEAYPQVCRDNNSAQACLEDAMIHALIRK	511
Query	37182	ESKFNPKIVSWAGAQQGLMQLMPETAQLMADQCGVTCSEKQLLTDPLLNVKLGTLYLKEQL	37361
		ESKFN+ S AGA G+MQ++P TA+++A + GV +E +L +D N+ +GT YLKE+L	
Sbjct	512	ESKFNPRAKSEAGACGMMQVVPSTAKMVAQKMGVHFNEARLKSDMNYNMLIGTAYLKERL	571
Query	37362	EKYDHSFPLTLASYNAGPGTVSRWLDPRDPHPSINTIDWIEVLPSYSETRDYIHRVLEN	37541
		+ Y S LTLA+YNAGPG+V +W++R+ DPR P ++TIDW+E +PYSETR+YI RV+EN	
Sbjct	572	QDYQGSIVLTLAAYNAGPGSVKKWIERYGDPDPKVDITIDWVEKIPYSETRNYIQRVLEN	631
Query	37542	YTIYKAIL	37565
		Y IY+AI	
Sbjct	632	YIIYQAIF	639

W. DNA translocase FtsK [Rickettsia endosymbiont of Culicoides newsteadii]

Sequence ID: [WP_094649409.1](#) Length: 739 475/576/745 (64/77 %)

Query	3381	mtdyirKIFAYTITQILLYTSLGLICISISLITHSPDDPSFNLVLTQKDSNTLGHFSGSYLA	3560
		M YI +I + L +G ++ L+T++PDDPSFN VT K SN LG+FG YLA	
Sbjct	1	MLYYINRILTNRRVSALLMLVGCFTLLLVTYNPDPSFNSVTAKYPSNLLGYFGCYLA	60
Query	3561	DFLYQLFGLASYIFPLCFFSFAFILFKRGTSLSFLVKAIGMILASIALSVTLAKLSFKSL	3740
		D YQ FG+AS+I P+C F ++ ++ R ++ + M+L+ I+LS+ K+ L	
Sbjct	61	DIFYQFFGIASFILPICCFWWSLVSFVW-RLEKKWVTIRIMVLLSIISLSIVCTKIKIDYL	119
Query	3741	PAGGGGSFGLIYPLVSQFGPLANIACGIFALIMIFLITGVTYENYLNFLQKVRGLLNFK	3920
		PAG GG+ G IYPLV Q A+ A I I++FL+ + + + N+ K+ L+ +K	
Sbjct	120	PAGAGGTGVTIYPLVKQLDARADYALIIIVTFILLFLAEIKFSAFWNAIKLLKLIPIYK	179

Query	3921	--LPTPKLsqafinnpptivpqrttpvnseevfkipeiqsdlkvtsaaVTKSQAFKPVQ	4094
		+ P +S + P ++ + T VN EE ++ DL + + +	
Sbjct	180	KIISLPTISTNSNSTKPVLIKRA--FVNQEEASYADKM--DLGKNNDPQSHYLKKQSAS	235
Query	4095	NTSNNEVASLPPIDLLKMPNNQHIKAESVAELKTNAENLISVLTDFGVKGQIVDVSQGPV	4274
		N+++ LPPI+LLK ++Q+IK E+++EL+ NA+ L++VL DFGVKGQ++++QGPV	
Sbjct	236	RKENDQLPDLFPPIELLKQADSQNIKVETLSELQHNAQILLTVLNDFGVKGQVININQGPV	295
Query	4275	VTLYELEPAPGTKSSRVVGLSDDIARSLSAFSTRIAVVPGRNALGIELPNKQRAFFCLRE	4454
		VTLYE EPA GTKSSR++GLSDDIARSLSA STRIAV+PGRN LGIELPNKQRAFFCLRE	
Sbjct	296	VTLYEFEPAAGTKSSRIIGLSDDIARSLSAISTRIAVIPGRNVLGIELPNKQRAFFCLRE	355
Query	4455	LIETPEYQDPNILLPLILGKDLAGKPYVADLAKMPHLLVAGTTGSGKSVAINAMIMSLLY	4634
		LIETPEYQD +I+LPLILGKDLAGKP+VADLAKMPHLLVAGTTGSGKSVAINAMI+SLLY	
Sbjct	356	LIETPEYQDNSIMLPLILGKDLAGKPFVADLAKMPHLLVAGTTGSGKSVAINAMIIISLLY	415
Query	4635	RYTPAECRLIMIDPKMLELLVYDNiphlltpvVTGSGKAVVALKWAVREMENRYRLMSNV	4814
		RYTP ECRIMIDPKMLEL YD IPHLLTPVVT KAVVALKWAV+EMENRYR MSN+	
Sbjct	416	RYTPBEECRIMIDPKMLELSTYDGI PHLLTPVVT EPNKAVVALKWAVKEMENRYRAMSNI	475
Query	4815	GVRNIAGYNAKIAESLKEGKSLECVQTGFDPDTGKPIYKSIPIAMKKLPFIVVIVDEMA	4994
		GVRNIAGYNAKI E+ GK LE +QTGFD +TGKPIY+ I + M+KLPFIVVIVDEMA	
Sbjct	476	GVRNIAGYNAKILEAASSGKILERSIQTGFDSETGKPIYEKIEMNMEKLPFIVVIVDEMA	535
Query	4995	DLMIVAGKDIESSIQRQAQMARAAAGIHIIMATQRPSPVDVITGVIKANFPSRISFKvtski	5174
		DLM+VAGKDIE SIQRQAQMARAAAGIHIIMATQRPSPVDVITGVIKANFPSRISFKVTSKI	
Sbjct	536	DLMLVAGKDIELSIQRQAQMARAAAGIHIIMATQRPSPVDVITGVIKANFPSRISFKVTSKI	595
Query	5175	dsrtilgeqgseqllGMGMDMLYMGNSSRIIRVHGPFVDDKEVEKVTNYLSNTGTPDYVSA	5354
		DSRTILGEQGSEQLLGMGMDMLYMGNSS+I RVHGPFVDDKEVEKVT YL TGTP+Y+SA	
Sbjct	596	DSRTILGEQGSEQLLGMGMDMLYMGNSSKITRVHGPFVDDKEVEKVT EYLRATGTPEYLSA	655
Query	5355	VMESTDDDSINMEDFRDGD---DETIYKKAKQIVKIERKVSISYIQRCLRIGYNRAANV	5525
		V + DDD +N+E GDD DET+YK+A QIV++ERKVSISYIQRCLRIGYNRAA +	
Sbjct	656	VTQQLDDDEVNVES---SGDDSTSETLYKRAVQIVQLERKVSISYIQRCLRIGYNRAATL	713
Query	5526	IDRMERDGIISHPSHTGKREILIEE 5600	
		+++ME++G+IS P+HTGKREIL+ E	
Sbjct	714	VEKMEQNGVISPPNHTGKREILLPE 738	

X. NADH-quinone oxidoreductase subunit NuoF [Rickettsia rhipicephali]

Sequence ID: [WP_014408207.1](#) Length: 421 357/390/422 (85/92%)

Query	8232	MLQAQDKIFTNLYGEQGFIDLSSKARGDWDKTKDFIVKGRDWIIEEVKQSGLRGRGGAGF	8053
		ML+ +DKIFTNL+G+Q DL SSK RGDW+ TK + KGRD+I+EEVK+SGLRGRGGAGF	
Sbjct	1	MLKEEDKIFTNLHGQQSHDLKSSSKRGDWENTKALLDKGRDFIVEEVKKSGLRGRGGAGF	60
Query	8052	STGMKWSFMPKSSTKPSYLVVNADESEPGTCKDRDILRFEPHKLIEGCLLASHAVGAHVC	7873
		STGMKWSFMPK+S KP YLVVNADESEPGTCKDRDILRFEPHKLIEGCLLAS A+GA+ C	
Sbjct	61	STGMKWSFMPKNSKPCYLVVNADESEPGTCKDRDILRFEPHKLIEGCLLASFAIGANNC	120
Query	7872	YIYIRGEFYNEASNIQIAIDESYGAGLIGNACGSGYDLDIYLHRGAGAYICGEETALLE	7693
		YIYIRGEFYNEASNIQ A+DE+Y GLIGNACGSG+D +IYLHRGAGAYICGEETALLE	
Sbjct	121	YIYIRGEFYNEASNIQRALDEAYKEGLIGNACGSGFDCNIYLHRGAGAYICGEETALLE	180
Query	7692	SLEGKKGMPRLKPPFPAGTGLYGCPTTINNVESIAVVPTILRRGTSWFAGIGKPNNTGTK	7513
		SLEGKKGMPRLKPPFPAG GLYGCPTTINNVESIAVVPTILRRG SWFAGIGKPNNTGTK	
Sbjct	181	SLEGKKGMPRLKPPFPAGFGLYGCPTTINNVESIAVVPTILRRGASWFAGIGKPNNTGTK	240
Query	7512	LYCISGHVNPQPCNIEEAMGIPLKELIEKYAGGVRGGWNNLKAIIPGGSSVPMIPKEMCET	7333
		++CISGHVN+PCN+EEAMGI LKELIEKYAGGVRGGW+NLKAIIPGGSSVP++PK +CE	
Sbjct	241	IFCISGHVNKPCNVEEAMGISLKELIEKYAGGVRGGWNLKAIIPGGSSVPLPKLLCE-	299
Query	7332	VTMDFDTRLALGSLGTGGIIVMDKSTDVIYAIARLSKFMYESCQCTPCREGTGWMWR	7153
		V MDFD+LR GSGLTGGIIVMDKSTD+IYAIARLSKFYM+ESCQCTPCREGTGWMWR	
Sbjct	300	VEMDFDSLRTAGSGLGTGGIIVMDKSTDIIYAIARLSKFMYHESCQCTPCREGTGWMWR	359
Query	7152	VMMRLVKGQAKMEEIDQLLDVTKQVEGHTICALGDAAAWPIQGLIHHFRHEIEDRIKAYS	6973
		VMMRLVKG AK EID+LL+VTK++EGHTICALGDAAAWPIQGLI HFR EIE RIK+YS	
Sbjct	360	VMMRLVKGNAKKSEIDELLNVTKIEGHTICALGDAAAWPIQGLIRHFRSEIEARIKSYS	419
Query	6972	PI 6967	
		+	
Sbjct	420	VV 421	