>gi|77457134|ref|YP_346639.1| ATP-dependent transcriptional regulator, MalT related, LuxR family [Pseudomonas fluorescens Pf0-1]
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15236]
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family [Burkholderia sp. 383]
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family [Burkholderia sp. 383]
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>gi|46916437|emb|CAG23202.1| putative malT regulatory protein [Photobacterium profundum
SS9]
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SINKATNNACLKTQAMAERRQFACLTTLFSELFGELSDYGEQTYLVLDDYHVINNEEIHEGMRFFLKHMPDCVTLVVTSR
TQPPLGTANLRVRDLLIEVDNHLLAFDQEETERFFHKRVSSEIETTVLNSLREQVEGWPSALQLIALHAQQKPNNLAESA
LSMANFNRGHLWDYLAEEVFDQLDRETQQFLLQCSVLDIFNAELVSDLTGRSDALSMLESLNRFGLFLNTLEGADNWYRF
HNLFAEFLRHQRYSQIPQQRTELHNNAAKAWLKQNRPQQALMHAMKSKNEDLTIEILTDYGWNMYHHGELKLLEDSISAL
STEKLFSAPRLTLLRAWLAQSQHRYDDVGELIAESEEEMKQRNLVLDDGLQGEFNALRAQVAINQSKPVDALVLSEQALG
QLPSTTYRSRIVATSVVGEVHHCLGNLSRALPMMQQTEKMARQYHVYHQALWALLQQSEILVAQGYVQAAFELLDQAYRL
VKEQHLQQVPLHEFLLRLRAQILWCWNRLDEAEECAHKSLEVLAPFDDTKSLHAYSMLARIALSRGEIDKAARYLELCNS
LMERADYHIDWRANTDLSNLFYWQIKGEKDNIANWLHQAERPDSACNHFQQLQWRNIARACIILEDYHQAEEIFAMLEDN
CKAHNLITDSNRNLVIQSILCKKQGQRKIALEHLKQALTLTNSTGMIGNFLCDANEICDLLQELVDTKQLNELELHRVQQ
LLREMTSKERNRSVHFDENFVEKLLNLPDVPELIRTSPLTQREWQVLGLIYAGFSNEQIASELDVASTTIKTHIRNLYQK
LNIANRQQAINTAENLLKLMGF
>gi|73537667|ref|YP_298034.1| regulatory protein, LuxR [Ralstonia eutropha JMP134]
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RGAPPVRTDVARLVALARDGGPGALSTRQLAAELGVSPASVSRHWRASGLPPRRGVALADKQPASGGVTVRAAEIVGLYI
AEPEHAIVVALEADPGPAGMAPALDAAARNSATYRRTLAASFMTALKVIHSGTATAFQAGRASGWQGFLHALAEHQPAGR
PLLILADNPVSHNDPEVRDVIAGQPWTVSFAAGQAAWMRAVQSLLRDADGLPAGIPQVLAVIGEHARGPFQWIRSAGDAG
YAQGQGAVPRALTAQAAFAPSTFAGKSAGRSFEAFTGTEFDSVATLPSAEPGLPRQFSALPAQPFLSLVPALDTRPGPMR
PLQPVASAKLLPPRHARKLLPREGLMNRLLDARRQRCVVIQGQAGAGKTSTLMAWRKALISLGFDVSWLSLAAEDNEPTR
FFDCLLASLAEIDPAMARDAAMQVGGAEDDDAIEQWVIALVQALGPRERELVLMIDDLHHITDARIYRALQRLLDYAPPH
LHLAFSSRSALSLALEALRAQGLLTEIDMRDLRFTAEESARFLEEQLGTIAPRDAAALHALTDGWVAGLQLFAVDLRARR
SADYPLTKVRDPRTFAAFFEREVLGLLAPDDLELLTRMSTCHRFCADLCTAMPGETETPSRIGDRLARLEADNLFITQVD
THDRDVWYRIHPLLRETLLARLETDKDDAADAVDMSDPDTAETPNDMADASRANDEPCAHGTARELHAAAWRWFDRRGHL
DDAVYHAVRAGDADAAATMVEGCGHALLKRGELPQLLGLVRRLPREQLQNRFGLLALVSFLQLYMRDVDGLGRSLERLDP
LCDRSNAVHQYVVCLLRAGHAVQVDDPDTVLGMLPALWAIPPEADDLWWTARRNVLSWLFILRGEFDEARRLQDDTERRS
SVPRSSLFGRYITAMSLVMEGEIERAGRSAREVLRESERQGATFLGLTCMAAGLLADILYELNDHEGACQLLEPRIGMLE
RVSLPDVVLRALTLLSNAHWLAGRRTQASACLDRLEAYAARNNLDRLQTEALTLRLRRHLQQAETERANTVFRQVQQLAQ
RYAGETGTVARHIALAAARAEVEMSLYTQDYATAAARLEALLAREAGAKPLRIAALWLQLALARHATGNTRGARPAFLSA
LRMGHGAGLIRTLLDVTGGAPQVFLELAGEGIDEPVLAFYARRLQAAAVASGAAISRPADEAAPIAVLSEREREILGLLA
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>gi|68553916|ref|ZP_00593261.1| regulatory protein, LuxR [Ralstonia metallidurans CH34]
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ARIWQALQWLLDYAPPHLHLVLCSRGELSLSLARLHSQGLVTKFDLRDLRFSPEESEAYLRDQLGGISPRDARRLHDLTD
GWVAGLQLFALDIKAKQGAGFSPTALRDASAFAEYFEREVLQKLAEDDQKLLTCVAICSRFCAPLCAALVGEPHAVARMT
TRLVRLDSSNLFIIQVSGHEHESWYRLHPLLREVLLARVEAMPVAQQQALHAAASRWFEQRDQVEEAVRHAVLAGEANAA
ADAIEARASELLARGGLGQLTSLLRMLPPEQVESRFSLQLMQAHINLRARRLDAAAQAIGRLAQQAATLGLRERYAVTVL
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LLMEGKILQAEPVLRQVLNEAEQLGGEYVGAAHMAAVLLSETFYELNEIDSVCELLENRIEQLEAVSVPDAVLRALLMLA
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ATGGQGLMRRLLDEQGLDPVVAFYARRLLEASSRWRGRAVAPASAVRRSTPIRTLSEREAEVLKLIAQAMSNKMVARTLS
ISPETVKWHLKNIYIKLGVSGRDEAVALLRDLAADTPDLGAPRPR
>gi|77633453|ref|ZP_00795583.1| COG2909: ATP-dependent transcriptional regulator
[Yersinia pestis Angola]
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AIQLATGGHCSKSEALSQKHQYANLSALFSQLFIELSNWDGPLYLVIDDYHLITNDAIHEAMRFFLRHQPENLTLIILSR
TLPSLGIANLRVRDQLLELGMQQLAFNHHEAQQFFECRLSSPLEQGDSSRLCDEVEGWVTALQLIALSSRQPNSSAQKSA
KRLAGLNASHLSDYLVDEVLDQVDSKARAFLLRCSVLRSMNDALIVRLTGEDNGQQLLEELERQGLFIHRMDDSAEWFCF
HPLFATFLRQRCQWELALELPELHHAAAEGWMALGYPAEAIHHALAAGDVGMLRDILLQHAWSLFHHSELALLEQCLTAL
PYPLLVQNPELALLQAWLAQSQHRYSEVNTLLEQAELAMQERKIPVDEILRAEFGALRAQVAINAGKPDEAEKLATDALK
YLPMAHYYSRIVATSVTGEVHHCKGELARALPMMQQTEQMARRHEAYHYALWALLQQSEILIAQGFLQAAYETQEKAFEL
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CNMVASITLIG
>gi|67908526|ref|ZP_00506925.1| regulatory protein, LuxR [Polaromonas sp. JS666]
MSTLSKAPIIELLRKSSMSWIVVYAYCDRTHKCNGRFAEAAQSLREAQVKFEDASSPYGLMWVRVISAASLLKAGRHRDA
LADSASALAEAPAFTPGAAGLAAMLRAIRALLLYERNQCTDAMVEVEAALPLLPHQGIIDAMIAGYVAASRLQAARGDLS
AALDVAAEGERVGLARGFARLQLTMVAERALLLLRAGDVKAAQRMASDHGLLPQGPQTNLHRDKAERLCARLDLAQGRPD
LALQWADSGIARARRSHQQHKLAELLMLRSLALARTGDTEGGHDALMESLRIAASNGYVRLYLDEGVELEGLLRRVVDKP
QSPTPAFSYARTLLLAAGAASARQDAAPAEQERPTERELQILGLLADGLSNGEVAGRLVLTEGTVKWHLHNIYAKLGVKN
RTGALREARARAWL
>gi|71066001|ref|YP_264728.1| probable transcriptional regulator, luxR family
[Psychrobacter arcticus 273-4]
MHKKEADNIRLPLILTKLNAPTDSVHLVLRPRLMSKLIENINHRVMLIHGPAGFGKTSLAMQLREFLITQEHRVAWLSLD
AQDNDPARYINYIVAAIHSVEDSIVVNTTALSESQSNYAINFILSELVNQLELLNEQMYLVLDDWHFITNQATNDALNFL
IECAPDHFHLIICSRTQPPLPIYTLHVKHQLCVIDSTELRFDETETSHFLHKSNKVNLRPEDIHTLWKKTEGWVASLQLI
LLMLRTQKSKDDFTNLFDDIGKIHSINEYFAENVLNNLPIDMLNFLLQTSILERLNDDLCNTVTQRTNSQSLLESLYKQG
MFIRPLDQERCWFQYHHLFAYFLQQRLKLQMPEKIKTLHLSAAQWFANNNQTNEAVDHAIAAKEMDRAISFIEKDSMWLV
EHSFMGTLLRLIDKIPEKDIEMSCELQLAIAWAHCLTHHPQKAQQALNFVEIALANKKYSNEANIRIEARVLQACINMYA
DRLDKIEQILPTHFDKEDNHNPWVVVVANNIQTYVLIHNYNFDDAIQLQQQVGRFHQHTRGPFSGVYGDCFAGIAYLKQC
KLDIAEQYFKKAQKKAWDKAGKHSHAAYLSGALLGQIYYERNQLDEAEALLMDSWLLGAEGGIANFYIATYCFSSRLAIV
KNNFSEAHAILDKGQLVAQALCIPRLEFLLKAELIKLYISQGNIQSAQHTMQQWNRLIIPKQASSIIEQLFEIRACAEAR
LLCRTGEDKKAIEILSTILQDNILKKRCYYEVCTRTLLAKSLNKAGRHTEAEDILLPALLKGFEQGMIRVFIDEDQNVIK
VIERLAKRCRQQHTTNATAEFNRWLLSLLALDKIQTENMDITRTYIENPSQARELAVKTLKKKEILILEMLEKGLSNKEI
ARNLNIGVNTVKWYLKAIYNTLGVSRRVQAVIEAKNLNILD
>gi|9947737|gb|AAG05148.1| probable transcriptional regulator [Pseudomonas aeruginosa
PAO1]
MDAVQDPAAGSLSRSRIVPPQVPAEYSLRPAIRNLLDRNPHSRVLMFSAPAGFGKTCALAALARERTVADQAVAWLSLAE
EDDDPARFCRQLIEALGEAVPQLGDDAQTYLQNTMRVPVVAVIESLLGDLDRYARPLLLVLDDLHLVSNPDIFTGLNRLV
QYAPPGLVLALGTRSQPALSLATWRAKGLLLEIGLEELRLGFEETREYLERSGLYLDEPCLKALYGQTEGWVVGVHLVSL
WLRQQPQVQEMALLDGDKQAVSAYLLAAVFERLPGDLQEALLALGVASQLSGDLANALTGRQDGQALLERLESMQLFLLP
LDRERQWYRFHLLFADFLRNRLRDSDPDRFKQLHFNASLWFTNHHMPTFAIEHACAAEDPEMIAALVDGCGLELINRGQL
SLIYRWRKHVPDEIAERYPILVLTDVWSRASDLSLGEANRIIDELLARWGESRGDGPMGDQYLSALAVKAVVALQKDDLE
LCIALARRVEVQLGQNAAFLEVAVLITAALAQVVRGQGDQARRLLGLAQQRNHFLEGRYLDMQLANVEVILALEQGQVKQ
AQLLIERLRQRARPLFEKSRSALALPTITEALTAYYRIELDGLEERLGWALGHVDVINPIDFYAQGQICLARTQRLLGRP
KEALASLAAMQALASRNQSWRFFAQAMAEEINLILQDSGPDRLKRAEQRLKSVDWNKMAAHYRNMAFNPVNWSLGVSRVR
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EKLKVRNRTQAIRRARELSLL
>gi|76259013|ref|ZP_00766665.1| transcriptional activator domain [Chloroflexus
aurantiacus J-10-fl]
MVSQAVTGEYNEYLLRPRLLPPPAPLHRIRRSRVEQRLAVSLEAPLTIVVAPPGSGKTVALAMLATHGGWPAAWCRADAS
DDPASLLRHLVAALSRVVAFDTDNPPATIDALINVLTSELDDETLLVIDDAHLIDERPDLRALIERLIGAQPPRLHLVLA
GRSEPVSPLIATARLRGEVLLIEPADLAFQAEEAMALWHQAGRSAPTDLDELISLSGGWALALRIALDATDWRRALGLRD
QPSPMLDEYLEREVFAPLPPLLRRCLQRSAGLRWIDADACSALDPSLNASQLIAELQRRRLFVTPFGERGVQFQPIIAAW
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LMQAENWANRGRVDIGQRLERAAYRMAEAYRLTDVYQARVESLQPRLLLRSGRLREARQLLEERLWMERPLVRASAHREP
LLLLALIHALLGIGPQALAFAHRMLSEAQQSHNPVTEAIAELRLGHAYQVIARSDEQIARQHYSRGLRLLQQVSVPRTRA
EGYLGLTLLHGHAGDLARAEADAREGLLLAASAGDEWVAALILLALGSVTLMADDPRGYEWLDQAEKRFQTGRDTFGLFL
VHLWRALAALRAGRTTEVDQLVDQVIREAVEYGYESVLIGPSLFGPRDIAALVPLLLRARSMPVHRDTAMYLLRQGFPSI
AADDTVDDYHPGFTLRVQMLGAFRVWRGNQEIQAREWQREKAKQLFQLLLTMRGNWVQREQICAWLWPDADLEAAERQFK
VTLNTLNAALEPHRPPRVPPFFIRRQGLAYSFAPSFGAWIDVDEFELRASGALTSTDPDFARRSAQAALQLYRGDYLAEA
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ALREELGIEPLPETEALYHRIRQNEPI
>gi|48781484|ref|ZP_00278092.1| COG2909: ATP-dependent transcriptional regulator
[Burkholderia fungorum LB400]
MIPPRDTARVVARERLLTQLLEARRNRCVVLQGPAGCGKTSLLIAWREALLSLGFDIAWLTLAPEDNELAHFLDYLVASL
AQVDPAMCHEAALLGGRGMDDEAVERTIIALVRGIAAHSNDVVLVLDDLHHVANARNHEALQWLLDYAPANLHLVLVSRG

AVPLSLGRPRDQGLVLELDMRDLRFTAAESEAFLKAQLGEIGQREARHMHELTDGWVAGLQLFAIRLKRKKQGITDLAPS
DPLANAQLLDARGFAAYFEREVLSRLAPSEVEMLVRMASCTRVCAPLCIALIGHGQSPAEVRALLTRLENDNLFIAPIES
SGSETWYRLNPLFRETLLERFRARSELHQREVHLAAWLWFRDHRQHDDAVRHALLAGEPAAAADLVLRVARTMQIEGDLR
KLVGLIRLLPLAEVQTRIGLRLWMLHLQLYAREFDACAAAIARLHADIPESDTHSRYRLILLRAALAVQRDDTDEALSVL
PHLRQIPAHADSLTVGGRNNLLSWIHMRRGEYDEARRVQSEAPQPLVDGVPLMGTSAGILNGRCIAGFSYALEGKFIQVE
RISRDVLFEADQRGSAAAEAACFAAALLGEVLYEFNDLEAARKLLEDRVDVLERVSIPDSVLRVLTVLSAVHWAEGHHLD
AFAYLERLEEYATQYGLPRLVAHSVAEQIHRHLLSGQFDAAEAGLARLDMIAARAAGTVTDAATGTAAEIHAMTESSHIN
WCIAHEDFEGAACRLQALIPFCEARGWQRHVAHFQMQAAVVDAGRGRAEAAREAVLAALRRGHRLGLVRSLLDADPSALD
LIAAVVQGEPHDPVLSFYVSRLNAAKAASSSGAEPPAKPASRSAPPTAAETLSEREVRVVGLLAQALPNKKIARTLGISP
ETVKWHLKNIYGKLSVTSRDEAVARVRDLELGSTPVAGEETD
>gi|78062243|ref|YP_372151.1| ATP-dependent transcriptional regulator, MalT-like, LuxR family [Burkholderia sp. 383]
MLVADVTPARRPPSLVATKVLPPRLPAGLVDRPRLVELAETAESKRLTVIQAPAGFGKTSLARLWLDCLRTRGALAGWLS
LDVGDDEPARFFHYFAQALQQACGDIGIAAGLSADASLLPPDAIVSTLINELVDVDDELYLFIDDYHLIGSPAIHAGVAY
FIDHAPSQVHVVICTRTEPPLPLARLRAHNELMEIDAAELRFSFDETQSFVRRECPGTLADATVKSLFVSTEGWAAALRI
AASVLKRGGAPGHDGAARIPSGASRPFAAYLEGMLERLPADLVDFMLRTSVLDRLSAPLCEAVTGVATSRPMLDTIVARQ
LLLQPLDQDGEWFRYHPLMAEYLRQRLATQCPDAIPDLHRRASRWYASQALWTDAVTHALAAGARDEAVALMAHCAMTLV
MRGDLLTLLGWQRQFPADLMQGQVRVSLAIAWGMALAMRFDDALAMLDAIERTPGAGVDPADIRHECQAVRSVIAALQDD
PRRAFALAQPCLDRPSTDTWTTNVVSNVVRFGHWKAGNLEALYATPWIPQSGDDRRLVFASVYRLSLLGHAEMQQMHFEL
AERYFSEAMQLGTRHCGPQSISVAICAPMLGQIRYEQGRLDEARALVIDLMPVIDVAVLLDSLLTAYKLLIRIAIARAEF
PHAYALLDRAQALAHARGWPRLTAAVLVERTRLHIAEGRLTEAAACVMQFDRLAGGDRGAQVDTSLEIDTYRALVTACVA
TARNDLQGAVAALDDGLRCASLRHSDYLALRLKTVLALVQLRGGERAAALDTFAEVLEVAEPAGIYRSIVDQGPEIGELL
QAMRDQARASSQTRDRLAYIERLLDGCRAQYQQDAQPARAAQRDMLSVRERDIVELIAHGQSNKEIARTLGIAPETVKSH
IKSLFMKLEVDKRARAVAVAQSLGLLGTRRLDS
>gi|15610217|ref|NP_217596.1| PROBABLE SERINE/THREONINE-PROTEIN KINASE TRANSCRIPTIONAL REGULATORY PROTEIN PKNK (PROTEIN KINASE K) (STPK K) [Mycobacterium tuberculosis H37Rv]
MTDVDPHATRRDLVPNIPAELLEAGFDNVEEIGRGGFGVVYRCVQPSLDRAVAVKVLSTDLDRDNLERFLREQRAMGRLS
GHPHIVTVLQVGVLAGGRPFIVMPYHAKNSLETLIRRHGPLDWRETLSIGVKLAGALEAAHRVGTLHRDVKPGNILLTDY
GEPQLTDFGIARIAGGFETATGVIAGSPAFTAPEVLEGASPTPASDVYSLGATLFCALTGHAAYERRSGERVIAQFLRIT
SQPIPDLRKQGLPADVAAAIERAMARHPADRPATAADVGEELRDVQRRNGVSVDEMPLPVELGVERRRSPEAHAAHRHTG
GGTPTVPTPPTPATKYRPSVPTGSLVTRSRLTDILRAGGRRRLILIHAPSGFGKSTLAAQWREELSRDGAAVAWLTIDND
DNNEVWFLSHLLESIRRVRPTLAESLGHVLEEHGDDAGRYVLTSLIDEIHENDDRIAVVIDDWHRVSDSRTQAALGFLLD
NGCHHLQLIVTSWSRAGLPVGRLRIGDELAEIDSAALRFDTDEAAALLNDAGGLRLPRADVQALTTSTDGWAAALRLAAL
SLRGGGDATQLLRGLSGASDVIHEFLSENVLDTLEPELREFLLVASVTERTCGGLASALAGITNGRAMLEEAEHRGLFLQ
RTEDDPNWFRFHQMFADFLHRRLERGGSHRVAELHRRASAWFAENGYLHEAVDHALAAGDPARAVDLVEQDETNLPEQSK
MTTLLAIVQKLPTSMVVSRARLQLAIAWANILLQRPAPATGALNRFETALGRAELPEATQADLRAEADVLRAVAEVFADR
VERVDDLLAEAMSRPDTLPPRVPGTAGNTAALAAICRFEFAEVYPLLDWAAPYQEMMGPFGTVYAQCLRGMAARNRLDIV
AALQNFRTAFEVGTAVGAHSHAARLAGSLLAELLYETGDLAGAGRLMDESYLLGSEGGAVDYLAARYVIGARVKAAQGDH
EGAADRLSTGGDTAVQLGLPRLAARINNERIRLGIALPAAVAADLLAPRTIPRDNGIATMTAELDEDSAVRLLSAGDSAD
RDQACQRAGALAAAIDGTRRPLAALQAQILHIETLAATGRESDARNELAPVATKCAELGLSRLLVDAGLA
>gi|54022251|ref|YP_116493.1| putative serine/threonine protein kinase [Nocardia farcinica IFM 10152]
MEIGRGGFGVVYRCLQTALERVVAVKVLPPDMDAESRERFLREEQAMGRLSGHPNIVDILQVDVTASGLPFIVMPYCTHG
SLEQLIHEQGPLGWADTLRVGVKLAGAIESAHRAQILHRDVKPGNVLLSSYGEPQLTDFGIARIPGGFRTSSSMITGSPA
FTAPEVLKGEEPTVRSDVYGLGATLFALLTGHAAFERQAGEKVVAQFLRITTQPVPDLREQDIPAPVAEAIERAMSPDPQ
QRPESAFEFGEMLRAAQRALGQLPDEMALLDTAVLLDDLGEVRATEPHPSIRTQFSTRARPSVTARRSWPLTLRPNVSQH
PPGATSTTPPPTAATKFRPPTPARAPVPRPRLLEVLRAGGRRRLALIHAPAGFGKSTVAAQWRAELTDQGVPVAWIGLDH
DDDNEVWFLAHLLQAIHRVRPAIGAGLDQALEERPADAVAFVISTLIDEVHAGGETIVVVIEDWHRITDPGAHRAMAALL
DNGCHHLRFVVTSRDQSGLPVNSMRVHDELVEIGSAQLRLTRAETGQILVERNGFELTDKQVEQIHRVTDGWPAAVQLVS
LALRGNPDPQRLISALPEGGHGIREYLAENVLDTLEPRMLDFLTAISVTERVNASLAAALSEDSEAELLLAQAEQRELFL
RRIEHDPEWYRMQPLFAEHLRARLERTDAAKLRALHRKASRWYAEHQFLRKSVDHALAATDLKLALDLVEGGGMDLIDGS
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TDGVLDQVADCLDNPDDLPAWTVSTAANVVSYVRLCTFDFDGARQIQEWAQPYHEKSKDPLGTVFGLCAQGAAAYEQLDI
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GELHLSPENADETRLPTHFLDEVLG
>gi|46164562|ref|ZP_00137359.2| COG2909: ATP-dependent transcriptional regulator [Pseudomonas aeruginosa UCBPP-PA14]
MTDFSRTFSGTPSAVLPTANRFFRPPLPSAHVARPRLCRRLRDGLDGRLLLIAAPAGFGKSSLAIEFCESLDPRWQSLWL
GLSSRESDPGRFLERLLDGLRQYHPTLGEEALGLLKMRQRHQPFAFETWLDDLLDELAPCLDPQRPLLLVLDDYHLAQGA
VLDRCLQFLLNHLPEGLVLLVTSRQRPDWHLARLRLSRQLLELSEQDLRLTAEESGALMAASGLELDEDALDALLERSEG
WVAGLRLWLLARGDPEEQVSPGVHGADELIRDYLLEEVIERQPPEVQAFLAQTARFERFCAELCDTVREAGDSAAILDHL
QQHQVFLVPLDENGQWFRYHHLFSDLLLARPLPDFGPSAGSLHLRACGWFSRHGLLDQAVEQALRAGQPDVAASLVQNLS
EEQLLAEQNIATLLRWKMDLPDSLLASTPRLILLYGWALALACQLDAAEELAGQLARFLPAPDESAQRDLLAQWQALSGV
IARGRGDIDKAEAHCREALQDLAGERYGTRLQCLSTLSNLAVTRGDFWQARNYNRDALEFAQRYGNPLFEALVHYDRARV
LQARGEVARAEEEVRQGLERLQHLPAQRRYAVRGRLLLYRGYLRSLALQPDEARKWIKQGIEETRSCRDVSLVIGYCVLA
SLEGRLGNYAAAFARLGDVERLMHAWDIPPIYYLAAITLIKCELWLAQGQTELAGVWLQRLGGTYGGQAATPPECSPLLP
LHVELLQAGLERREGRPEEAARRLDRLARSTRENGALLPARLALGQLAALHLEQGRREREALATLQQAMEGAVGGALLPLH
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RHINDKLGVERRTQAVARAKHMGLLR

>gi|68557156|ref|ZP_00596497.1| regulatory protein, LuxR [Ralstonia metallidurans CH34]
MSAATSRKPGDSDTQRRGLVASKLVPPRALPNHLVRSRLVDVMVDAASARLILVRAAAGFGKTTLMQQYLERCQAGQRAC
VWLRCDAADNDLQRFLLHLHTGLLRLPGLTRHQRDERSDTIAGETIAHEIIEIAASYAHPFAILLDDLEVIQNDAITEYL
QQLVRVLSPQGVLVIGTRATPDLGLGGLRARGQLLDINPAALRFSAEEAASFIRDKCGLPLPDGEIATLWRCTEGWAAAV
YLATLSLRGHPNHAAFVRSFSGTNIELAEYLAEDILMGQSESCRDFLLQTSLLGQLSAPLCDAVTGRHDSREMLSFLERN
NLFITPLDGEHQWYRYHSLFASFLQHRLQVTYPDKARALHVAASRWYLSEDRPVPAIEHLLQAGLDDEALPLIAIHTPAL
FQAGRVRLLARWLDRIDRKRLLADPHRMGLAYAWVLLLNRRYSEAMQTMAALLAADVPADQQAKIAFEVETLRCVLLAMT
DQIEACLAAGLAHLERIPPDAPFRYASVVNSQAFSLVASHRYEDARRVLSRLMPGANDVRTGFQRGIADSLEGVIDLVQG
RLSNALARFRAVAERGWSPSEVSSLRHAFLPAWATALYEANALEDCARVLAEAMPYCKGYAPPDAMIAGFILSARLALLG
GDRDRWLRMLAELEEIGRGIQLPRAICSAWLERVRVATIEGRLDAADQALRSAELHADWAASDSYGHANDIDFPDSIGWR
LAIAHGEHEQTASELADAIAVATQRQRHWRALKLRLLLAMALDGAGRQSEAFEPLTEAMRLASHEGLVRTFVDEGDRLAD
LLRRWADAREAEIVRAGIDLQFVRTVLAQIPTPLAVAGEEVNKARGAAIAEPLTTREQEVLQMLAAGHRNRVIAEKMFVS
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>gi|76261137|ref|ZP_00768757.1| Transcriptional regulatory protein, C-terminal:Tetratricopeptide TPR_4 [Chloroflexus aurantiacus J-10-fl]
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IEQAIAFGLPITVDSGSTNGERVFRFHPLWQRLLANRALTRFNRVFVRELHERFGEVLARHDQIEAALRHLAMAENPTAI
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LFSQELWMQSLLLIVLGEGGEPQRALELANELVTQMAQRNDGLFRALVHIYRAYLVAQQRPDDPAIATDLATACAICDRT
GVESLPFLPQTVMNWAITAALRIGLSSRAMIAALRQFDTTTLSVILMPLLEETFPLAVRLRSINLVGELGLVNAYGTLRG
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ARAVGLIAE
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IGQQLGVKPFLGNEATADRLLKCQSPKQLIVATHGYYSQRKDKYLTLLKELLSSSQGKEVEILEKNYGLLDEEFLAFIER
YRNSENRDNKIREKLRAIAPLVKQQLKTTPVKPPVNNMDFETFKPNRHQAKIENPMMGSAVAFTGANTWLSGGQLPPEFP
TMAFAQDIAGLDLWETELVILIACESGLGDVQTGEGVFGLRRAFAVAGNQTLIMSLWSVPTLATMLLMEQFLDDSRSGMS
AGAALRKAQKYIRNITVGELQKSKLGSDILGELNLGKNLKIESKPLAHPYFWGAWICQSVSELGIRF
>gi|15026710|gb|AAK81534.1| Regulatory protein related to malT, positive regulator of mal regulon (ATPase and HTH-type DNA-binding domain) [Clostridium acetobutylicum ATCC 824]
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KDLSIKVLNKYVVDYLTEEILKGLSNSEKDFLIKTSIMSYFNSELCNEILQIENSDEIINSLLNKNLFIITLDEEDGLFR
YHHLFKEFLNTNFNKLPDSTRKQFHLNAYTSLKNSGDISEAIIHLIKIKEYQKASSELEKNIEDTSCISLIRLIPLDALI
NSNELIIQKIFYHYSNMQIDECKSIISYLESFKKPELTALANIFKLYVYDFCNSMTLEDLNIVKTFKLTDITKAILYLNI

SPAFMIQGEYEKILYYSKESDKIATKYNIVFLSVFSKCLIASVLEEQGKLSDTLKVYNDLDTLIEKNKFISGFKFLVHLG
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campestris pv. vesicatoria str. 85-10]
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VALQLARLWLEGDTQRRQEVTVRFSGRSAQIAAYLAEQVVNDLDPDTRELLLRTSPLERFNAALADAVRQRQDSGRLLAR
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VELGLPAKAMLRSLRQHDPQTVGGTTRALTIQALLERLSGDDDPADDIFSERELEVLAQLARGYSNKQIARCLHLSENTV
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>gi|75428383|ref|ZP_00731653.1| ATP-dependent transcriptional regulator [Actinobacillus
succinogenes 130Z]
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>gi|70728347|ref|YP_258096.1| transcriptional regulator, LuxR family [Pseudomonas
fluorescens Pf-5]
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LuxR [Ralstonia metallidurans CH34]
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RSEAHTEFIDRFSGTSRSVADYLAEDVVARQPEPVRQFLLRTSILRYLNPQLCHVLLPDVDCEAILRQLESSSLIAPIES
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GSGSTQHYGYTGGNAWAGVMYAATVYEANDLAQAAHLLRVYVPLARDVLLGDHVTLGHVMLSRIAFARGDVDEAFETLTQ
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>gi|76260381|ref|ZP_00768018.1| TPR repeat:Bacterial transcriptional activator
domain:Tetratricopeptide TPR_4:Tetratricopeptide TPR_4 [Chloroflexus aurantiacus J-10-fl]
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[Actinobacillus pleuropneumoniae serovar 1 str. 4074]
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>gi|47572961|ref|ZP_00243002.1| COG2909: ATP-dependent transcriptional regulator
[Rubrivivax gelatinosus PM1]
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[Frankia sp. CcI3]
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DASRCRRWPVELPTVPSDYLSKLLATAHADAERAAIPIIDRPAERNPAPEEPLNAREIDILRLLDRGLSNKEIARNLGLT
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