

Ralstonia metallidurans gi|48771323|ZP_00275665 406aa (Betaproteobacteria)
>Ralmet Betaproteobacteria
-----MLSAASRPYIDASVPLVRE-----HGLAITTHFYREMFARPELRKI---FNMG-----NQANGSQQQSLASAVFYAANI---DRADVLPVVERIVHKKHVAVG---L---TPAHYPIVGKYLLEIAAIVLGDAA---TPPLLAAWDEAYWLLAGELIAAEARLYERHGV-----
Ralstonia solanacearum gi|17548115|NP_521517 401aa (Betaproteobacteria)
-----MLSEQSKPLIDASVPLVRE-----HGLITITQTFYRNFASHPELTNL---FNMG-----NQANGSQQQSLASAVFYAANH---GNNALAPVVGRIVHKKHAAGV---I---RPSHYPIVGRHLLGAIAEVLGDAA---TPPELLAAWDEAYWLLAEELIAAEARLYAHTQS-----
>Ralool Betaproteobacteria
-----MLSEQSKPLIDASVPLVRE-----HGLITITQTFYRNFASHPELTNL---FNMG-----NQANGSQQQSLASAVFYAANH---GNNALAPVVGRIVHKKHAAGV---I---RPSHYPIVGRHLLGAIAEVLGDAA---TPPELLAAWDEAYWLLAEELIAAEARLYAHTQS-----
Salmonella typhimurium gi|16765876|NP_461491 396aa (Gammaproteobacteria)
>Saltyg Gammaproteobacteria
-----MLDAGTATYKATIPLLVE-----TGPKLTAHFYDRMFTHNPELKEI---FNMS-----NQRNGDQREALFNAIAYASNI---ENLPALLPAVEKIAQKHTSFQ---I---KPEQYNIVGHLLATLDEMFPN---GQEVLDAGKAYGVLANVFIHREAIYHENAS-----
Sinorhizobium meliloti gi|16263102|NP_435895 403aa (Alphaproteobacteria)
-----MLTQRTKRDIVKATAPVLAQ-----HGYAIIQHFYKRMFQAHPELKNI---FNMA-----HQERGEQQQALARAVYAYAANI---ENPELSAVLKDIAHKHASLG---V---RPEQYPIVGEHLLASIKEVLGDAA---TDEIISAWAQYGNLADILAGMESELYERSEE-----
>Simmel Alphaproteobacteria
-----MLTQRTKRDIVKATAPVLAQ-----HGYAIIQHFYKRMFQAHPELKNI---FNMA-----HQERGEQQQALARAVYAYAANI---ENPELSAVLKDIAHKHASLG---V---RPEQYPIVGEHLLASIKEVLGDAA---TDEIISAWAQYGNLADILAGMESELYERSEE-----
Staphylococcus aureus gi|15923230|NP_370764 381aa (Firmicutes)
-----MLTEQEKDIIKQTVPLLKE-----GTEITSIFYPKMFKAHPPELLNM---FNQT-----NQKRGMSALLAQVMAAAVNI---DNLSVIKPIVIMVAYKHCAIQ---V---YAEHYPIVGENLKAIQDVTGLEE---HDPVIQAKAKAYGVIAADVFIQIEKIDYQGMW-----
>Staur Firmicutes
-----MLTEQEKDIIKQTVPLLKE-----GTEITSIFYPKMFKAHPPELLNM---FNQT-----NQKRGMSALLAQVMAAAVNI---DNLSVIKPIVIMVAYKHCAIQ---V---YAEHYPIVGENLKAIQDVTGLEE---HDPVIQAKAKAYGVIAADVFIQIEKIDYQGMW-----
>Staepl Firmicutes
-----MLTEQEKDIIKQTVPLLQD-----KQTEITSIFYPKMFKAHPPELLNM---FNQT-----NQKRGMSALLAQVLAAMNI---NNGLAIKPIVIMVAYKHCAIQ---V---YAEHYPIVGENLKAIQDVTGLEE---HDPVIQAKAKAYGVIAADVFIQIEKIDYQGMW-----
Streptomyces avermitilis gi|29832496|NP_827130 400aa (Actinobacteria)
>Stravel Actinobacteria
-----MLSEQAATVRATLPAVGA-----AVGEITARFYDRFLAARPELLRDL---FNRG-----NQAAGTQRQALAGSIAAFATYL---VEHPDERPDAMLDRIAHKHASLG---I---APGQYAVVHEHLFAAIAEVLGDAV---TPEVAAAWDEVYWMANALIAIERRLYAQHEN-----
Streptomyces avermitilis gi|29830819|NP_825453 565aa (Actinobacteria)
-----PEASPDAVILRRITMAEAVGP-----VAGKVTSSYFALLFVRHPELRSI---F---PAAMDQRDRLLKALLTAAEHI---DNTEVLVAYLQNGRGRHK---Y---GTRPEHPYAVGECILGALSRYASGIW---DEETEAAWVRAYTTISQVIMDAAAADDELRAFA-----
>Strave2 Actinobacteria
-----PEASPDAVILRRITMAEAVGP-----VAGKVTSSYFALLFVRHPELRSI---F---PAAMDQRDRLLKALLTAAEHI---DNTEVLVAYLQNGRGRHK---Y---GTRPEHPYAVGECILGALSRYASGIW---DEETEAAWVRAYTTISQVIMDAAAADDELRAFA-----
Streptomyces coelicolor gi|21218667|NP_624446 435aa (Actinobacteria)
>Strcoe1 Actinobacteria
-----SVTDEDVALVRASLTVVTP-----HVSELAHFYSILFSRYQVRDL---F---PAELDVQRERLVRALLRIVELV---DDPDNLVAFCSRIGRGRHK---F---GTQSGHYPAVGECLLQALSHFAGFAW---HPALATAWQRAYTAAADVMVRAAEEADARSFA-----
Streptomyces coelicolor gi|21225376|NP_631155 403aa (Actinobacteria)
>Strcoe2 Actinobacteria
-----MLSQSAQIVRDLTLPVGA-----SLGTTIDLFYRMRFEERPELLRDL---FNRA-----NQASGVQREALAGAVAAFATAL---VKHPDERPDVGLRIANHASLG---I---TSDQYTLVGRHLLAAVAEVLGDAV---TPAVAAAWDEVYWMANALIAEAMLYARSQV-----
Streptomyces coelicolor gi|21225698|NP_631477 398aa (Actinobacteria)
>Strcoe3 Actinobacteria
-----MLSEQSPVVRATLPAVGA-----ATGDI AALFYKRLFDAPPELLRDL---FNRG-----NQANGEQQRALAGSVAAPAGLL---LENPDERADVLSRISHKHASLG---I---TPDQYTVHRRHMAAVDVLGDAV---TPEVARAWDEVYWMANALIAEARLYTEKGV-----
Thermobifida fusca gi|4883571|ZP_0002715 394aa (Actinobacteria)
>Thefus Actinobacteria
-----MLSTQSDIVRATLPPVGA-----HLDEITSRFYTMFSERPELLDGL---FNRG-----NQANGEQQRALAGSIAAGFASAL---LANPDERPDALLARIAHKAHAVA---V---TDDQYVIVKHVLEGAIVLGDAA---TPEVIAAWDEVYWMGGALIAEARLYAEKNA-----
Vibrio cholerae gi|15600953|NP_232583 394aa (Gammaproteobacteria)
>Vibcho Gammaproteobacteria
-----MLTQEHINIIKSTIPLES-----AGPALTQHFYQRMFSHNPELKHII---FNMT-----HQKTRGRQSVLFEAIAAYAKHI---DNLAALTSVERIAHKHTSFN---I---QPEHYQIVGHLLLETRELAPDAF---TQPVEEAWTAAYFFLAQVFDREAGALYLERKQ-----
Vibrio parahaemolyticus gi|28899583|NP_799188 394aa (Gammaproteobacteria)
>Vibpar Gammaproteobacteria
-----MLSNQITIVKATAPLAEET-----GPKLTAHFYDRMFTHNPELKDI---FNMS-----NQRNGDQREALFNAI CAYANI---ENLPALLGAVEKIAHKHTSFLL---I---TKDQYQIVGKHLIATIDELFNP---GQEVLDAAWAEYGVLANVFIQREQIYQNAS-----
Vibrio vulnificus gi|27364701|NP_760229 394aa (Gammaproteobacteria)
>Vibvul Gammaproteobacteria
-----MLSENTINIVKSTAPLAEET-----GPKLTAHFYDRMFTHNPELKDI---FNMS-----NQRNGDQREALFNAI CAYASNI---DNLPALLGAVEKIAHKHTSFLL---I---TADQYQIVGSHLLATIDELFSP---GQAVLDAAWAEYGVLANVFIQREQIYQDNQS-----
Xylella fastidiosa gi|15836658|NP_297346 397aa (Gammaproteobacteria)
>Xylfas Gammaproteobacteria
-----SFSPHPIIKSTVPLLAE-----HGTTIIEAMYHRLFD-PQIEAL---FNQA-----NQRNGTQIHALGAILAYARNI---DNPGVLAERIAQKHVGYA---I---HPEHYPHVATALLGAIKVLGDVA---TSEVLEAWGEAYWFIANLLKDREAVIREGIMT-----
Yersinia pestis gi|16123099|NP_406412 396aa (Gammaproteobacteria)
>Yerpes Gammaproteobacteria
-----MLDQTIIVKSTIPLLAA-----TGPKLTAHFYDRMFTHNPELKNII---FNMS-----NQRNGDQREALFNAI CAYATNI---ENLALALLPVERIAQKHTSLN---I---QPEHYPIVGEHLIATIDELFSP---GQAVLDAAWAEYGVLANVFIQRESIQYQSET-----

Bacterial SDGs

*Acinetobacter sp. ADP1 gi|50086221|YP_047731 254aa (1-141) (Gammaproteobacteria)
>Acinet* Gammaproteobacteria
-----MTPQQLVKSTVPLVRE-----HGVTLSYFYRMLNHPPELKNV---FNLD-----HQSTGRQPRALAAVLAAYAEHI---EQPEKLAKAVERITTKHVSIN---I---QPEQYAVGENLLHSISEVLNVFF---ESELIEAWKQAYLQLADILIEVEKEYHQYLAQ-----
>Aquifex aeolicus gi|15605769|NP_213146 139aa (1-137) (Aquificales)
>Aqaeo* Aquificales
-----MLSEETIRIVKSTVPLLKE-----HGTEITARMYELLF SKYPKPKEL---F---AGASEEQPKLANAIIAYATI---DRLDNAISTARSHVRRN---V---KPEHYPLVKELLLQAEIVLNP---GEEVLKAWEEAYDFLAKTLITLLEKLYSQP-----
>Bradyrhizobium japonicum gi|27377918|NP_769447 142aa (Alphaproteobacteria)
>Bradjap1* Alphaproteobacteria
-----MTEPEITLQKQSFQKAVP-----ISETAAVLFYDRFLFEVAPSVRAM---F---PEDMTEQRKMLMGLAAVVGGL---SNLDSILPAASALAKRHVA---Y---GAKAEHYPVVGGATLWLEKLGEEA---WTPELATAWTDAYGLVSGYMISEAYQAQAAE-----
>Bradyrhizobium japonicum gi|27379994|NP_771523 139aa (Alphaproteobacteria)
>Bradjap2* Alphaproteobacteria
-----TMTATISFNPIEQSFERAAS-----RCADLTPLVYRRLFDHEPETRAM---F---RSQSELVKGSMLALT---I---EALIDFAGTRSGHFLRIA---CEV---VSHDAYGTPRELFIAFFAVIRDTRLRDLGDA---WSAIEAQWDTLLTDIEAYVTVPA-----
>Campylobacter jejuni gi|15792891|NP_282714 140aa (Epsilonproteobacteria)
>Camjej* Epsilonproteobacteria
-----MTKQEQIILKDCVPLQK-----NGEDLTNEFYKMFNDYPEVKPM---FNME-----KQISGEQPKALAMAILMAAKNI---ENLERNMRSFVKVVAITHVNLG---V---KEEHYPVIGACLLKAIKLNLPDE---ATLKAEVAYGKIAYFIDIEKLYDK-----
>Campylobacter coli gi|32527608|AAP86201.1 142aa
>Camcol* Epsilonproteobacteria
-----mtqeqgiikdcvplqk-----ngedltkefykimfndyvevcpm---fnme-----kqasgeqpkalamailmaakni---enlernmrsfvkvaithvnlk---v---keehypviggacilkaikevlyade---ttlkaweeankiaqfyidiekiyakak-----
>Chromobacterium violaceum gi|34498391| 148aa (Betaproteobacteria)
>Chrvio2* Betaproteobacteria
-----PLTQQQIRLVQESFAKVEP-----IADDEAAKLFYDKLFYAPDLRPL---F---KKDMAAQQRMLMSTLKLAVKGL---DDEQLTTPVLRKLAQRHVDYG---V---KPGDYTPVGNALLWTKQGLGEAS---WTQELRAAWVDAFRIMATVMKQAAYPEIQFIQD-----
>Clostridium perfringens gi|18310935|NP_562869 144aa (Firmicutes)
>Cloper* Firmicutes
-----MLDQKTDIIKSTVPLVKS-----NGLEITKTFYKMFQNPVVKPL---FNMI---KQESEQPKALAMAILAQAONI---DNLEAIKPVVNRIGVHCNAC---V---QPEHYPIVGHKLLGAIKEVLGDGA---TEDIINAWAKTYGVAEVIINNEKEMYASR-----
>Desulfobacterium hafniense gi|23119439|ZP_00102525 267aa (Firmicutes)
>Deshaf* Firmicutes
-----ALNEAAAVVRAVTPALAA-----HGHAVTAMRYRRLFRDE-RIAL---FNHAN-----QGGDNAQAHLAGAILAYAQHI---DDLPAISGALERIAQKHVGYH---I---LPEHYPFVAGALLGAIEETLGEAA---TPQVLAWGEAYWFLADLQRREARLGEAQ-----
>Gloeobacter violaceus gi|37521141|NP_924518 142aa (Cyanobacteria)
>Glovio*
-----TAMALQVKLLEQSFGEKVP-----NAHAFASFDNLSDFPQTAL---FA---HSDMQAQKQLLASLVLVVENL---RQPQVLSLALQDLGNRHGAC---I---VPEHYPMVGTSLKTFETYLGDAN---TPEVQAWVDAYGAIITGLMLTGAES-----
>Hosnoc punctiforme gi|23129187|ref|ZP_00111020.1| 126aa (Cyanobacteria)
>Nosup* Cyanobacteria
-----MYEIMQNFHPEVKEQ---F---FMSA-----AQADGSPARLATAVYANQI---DNLPALKSMVEKIAHRHVQTH---V---TPEQYPIVGESELLQAMKQVLEGEA---TEEVMAWTEAYQALSEVFIHREDIYVGEDK-----
>Novosphingobium aromaticivorans gi|23110290|ZP_00096448 148aa (Alphaproteobacteria)
>Novaro* Alphaproteobacteria
-----IASEHAKTIVKATAPAEK-----HGVDITAMYKRLQND-EVKAM---FDQA-----AQDSGEQPRRLAGAILAYAKNI---DKLENLSAVQRMVQRHVDTG---V---KAEHYPVVAELLPALRDLVLEGEA---TDEVLAAWGEAYWMLADILIAEKQAYLEAVA-----
>Photobacterium profundum gi|46915547|CAG22319.1 133 aa (Gammaproteobacteria)
>Photpro Gammaproteobacteria

MDIHEVFNDSYTRCNR--NPHEMPLFYERFLEKDETFRSM--F-----THVDMENQMKMIKASLLIIMLAA-----TSEQARATVKFKGRHRGPDG--L-----GIKPLDIDLWFECFLDITIKCEDPA-----YNSQVEQAWRQCFNEGITIMKAECKS-----
>Pirellula sp.1 gi|32471656|ref|NP_864649.166aa (Planctomycetes)
>Pirell* Planctomycetes
*Pseudomonas aeruginosa gi|15599162|ref|NP_252656.130aa (Gammaproteobacteria)
>Pseae* Gammaproteobacteria
*Rhodospseudomonas palustris gi|3993677|NP_949047.141aa (Alphaproteobacteria)
>Rhopal* Alphaproteobacteria
*Rhodospseudomonas palustris gi|22960924|ZP_00008530.146aa (Alphaproteobacteria)
>Rhopal2* Alphaproteobacteria
*Silicibacter gi|52009457|ZP_00336820.143aa (Alphaproteobacteria)
>Silici Alphaproteobacteria
*Thermobifida fusca gi|48835900|ZP_00292898.177aa (Actinobacteria)
>Thefus* Actinobacteria
*Vibrio parahaemolyticus gi|28900962|NP_800617.142aa (Gammaproteobacteria)
>Vibar* Gammaaproteobacteria
*Vitreoscilla stercoraria gi|70622|pir||GGZLB|70622.146aa (Betaproteobacteria)
>Vitste* Betaproteobacteria
-----MLDQQTINIKAIVPVLKE-----HGVITITTFYKNFLAKHPEVRPL--FDMG-----RQESLEQPKALAMTVLAAQNI-----ENLPAILPAVKKIAVKHCQAG--V-----AAAHYPIVGQELLGAIKEVLGDA--TDDILDAWGKAYGVIAVDFIQVEADLYAQAVE-----

Eukaryote FHbs

Aspergillus nidulans gi|40739893|gb|EAA59083|AN3522.2.410aa (Ascomycota; Pezizomycotina)
>Aspnid1 Ascomycota; Pezizomycotina
Aspergillus nidulans gi|40742233|gb|EAA61421|AN7169.2.426aa (Ascomycota; Pezizomycotina)
>Aspnid2 Ascomycota; Pezizomycotina
Candida albicans >gi|46432319|EAK91807.1.398aa also EAK91821.1 GI:46432334 (Ascomycota; Saccharomycotina)
>Canalb1 Ascomycota; Saccharomycotina
Candida albicans gi|46432322|EAK91810.1.400aa (Ascomycota; Saccharomycotina)
>Canalb2 Ascomycota; Saccharomycotina
Candida albicans gi|46441212|EAL00511.1.400aa (Ascomycota; Saccharomycotina)
>Canalb3 Ascomycota; Saccharomycotina
Candida albicans gi|46433276|EAK92722.1.563aa (region 300-430) (Ascomycota; Saccharomycotina)
>Canalb4 Ascomycota; Saccharomycotina
Candida glabrata gi|50291201|XP_448033.1.432aa (124-264) (Ascomycota; Saccharomycotina)
>Cangla1 Ascomycota; Saccharomycotina
Candida glabrata gi|50293309|XP_449066.398aa (Ascomycota; Saccharomycotina)
>Cangla2 Ascomycota; Saccharomycotina
Cryptococcus neoformans gi|50259618|EAL22289.1.504aa (Basidiomycota; Hymenomycetes)
>Cryneo Basidiomycota
Debaromyces hansenii gi|50428015|XP_462620.1.403aa (Ascomycota; Saccharomycotina)
>Debhan1 Ascomycota; Saccharomycotina
Debaromyces hansenii gi|50304451|XP_452175.1.395aa (Ascomycota; Saccharomycotina)
>Debhan2 Ascomycota; Saccharomycotina
Debaromyces hansenii gi|50428041|XP_462633.1.401aa (Ascomycota; Saccharomycotina)
>Debhan3 Ascomycota; Saccharomycotina
Dictyostelium discoideum gi|5821408|BAA83810 (Mycetozoa)
>Dicdis1 Mycetozoa
Dictyostelium discoideum gi|5821410|BAA83811 (Mycetozoa)
>Dicdis2 Mycetozoa
Eremothecium gossypii gi|45185029|NP_982746.1.436aa (181-330) (Ascomycota; Saccharomycotina)
>Eregos Ascomycota; Saccharomycotina
Fusarium oxysporum gi|3551511|BAA33011.415aa (Ascomycota; Pezizomycotina)
>Fusoxy Ascomycota; Saccharomycotina
Giardia lamblia (intestinalis) gi|27981493|458aa (Diplomonadida)
>Gialam Diplomonadida
Giberella zeae gi|3551511|EAA73242.415aa (Ascomycota; Pezizomycotina)
>Gibzeal Ascomycota; Pezizomycotina
Giberella zeae gi|42547868|EAA70711.457aa (Ascomycota; Pezizomycotina)
>Gibzeal2 Ascomycota; Pezizomycotina
Kluyveromyces lactis gi|50304451|XP_452175.1.395aa (Ascomycota; Saccharomycotina)
>Klulac1 Ascomycota; Saccharomycotina
Kluyveromyces lactis gi|50307891|XP_453939.430aa (181-319) (Ascomycota; Saccharomycotina)
>Klulac2 Ascomycota; Saccharomycotina
Magnaporthe grisea gi|38101598|EAA48540.447aa (Ascomycota; Pezizomycotina)

>Magri Ascomycota; Pezizomycotina
SITPEQVAVVKSTAPVLKE-----HGVTITTFYKNMIDAHPELHNV---FSTT-----SQATGAQPRALASAVLAYATHI-----DDLRLSHAVSRIAHKVSLH---I---TPDQYDIVGKYLIEAQVGLGDA-----TPEIVAIAAYAGVLADVFIVGEGKMYQEHSD
Neurospora crassa gi|28919225|EAA28703 418aa (Ascomycota; Pezizomycotina)
>Neural Ascomycota; Pezizomycotina
PLDQAQISIVKSTAPVLKQ-----HGEALITTFYFNLDITENPSLKI---FSLT-----SQATGAQPRALAHAVLAYATYI-----DNLSALSEAVARIAHKVSLQ---V---EPAQYAIYVQYLIQAIQVGLGDA-----TPEIVDAWTAAYGVLANVFIGVEGGMYEENEK
Neurospora crassa gi|28925744|EAA34752 537aa (Ascomycota; Pezizomycotina)
>Neura2 Ascomycota; Pezizomycotina
ALTYQSKLVRDTIPALKE-----HGERITSIFYKTMLDHPELNNY---FNSV-----NQKNGRQPRALTAIVLGFASNI-----NHLSELVFKFERMCKHCSLQ---I---QPEHYEVGKYLIQAFGEVLGPAM-----TPEVQTAWTAKYWMKLMIGREAGLYRDFES
Fichia norvegensis gi|417109|Q0331 388aa (Ascomycota; Saccharomycotina)
>Picnor Ascomycota; Saccharomycotina
VPLTPEINFLQSLAPVVKKE-----HGVTITTFYKMYFQTYPEVRSY---FNMT-----NQKTGRQPKVAFSLYQYILHL-----NDLTFISGFVQIVLKHGCLG---I---KPDQYFVVGESLQVAFKRMVLGEEA-----DEHFVEVFKYAGNLAQTLIDAEASVYKTLAW
Saccharomyces cerevisiae gi|1362285|S57699|FHP_YEAST 399aa (Ascomycota; Saccharomycotina)
>Saccr1 Ascomycota; Saccharomycotina
MLAEKTRSIKATVPVLEQ-----GQVTITRTFYKMLTEHTELLNI---FNRT-----NQKVGQAQNALATTVLAAAKNI-----DDLVLMDHVVKQIGHKRALQ---I---KPEHYPIVGEYLLKAIKEVLGDA-----TPEIINANGAYQAIADIFITVEKMYEEALW
Saccharomyces cerevisiae gi|6324095|NP_014165.1 426aa (Ascomycota; Saccharomycotina)
>Saccr2 Ascomycota; Saccharomycotina
APDGMISKTIDPTARPKTKQRDNDNKVDLFCFSQFYDNLIAMDPLEEY---F-----PSLKHQVAVSFCKVLDASIDNL-----ENVHVLDDYIVKLGKRHSRLG---I---KTVGFVEMKGFAMTTLQDRFGSFL-----TLELKNLWGLQVLYLANCMITAGDKPMEKIQP
Schizosaccharomyces pombe gi|19115929|NC003424 427aa (Ascomycota; Schizosaccharomycetes)
>Schpom1 Ascomycota; Schizosaccharomycetes
ELNESQKQYIRSSIPILEY-----SGVNLTKAFYQKMLGNYPEVLVY---FNKA-----HQISLSQPRILAFALLNYAKNI-----DDLTSLSAFMDQIVVHVGLQ---I---KAEHYPIVGHCLSTMQELLPSDVA-----TPAFLEAWTAYGNLAKILIDSEKKVYQSQPW
Yarrowia lipolytica gi|50548235|XP_502088 374aa (Ascomycota; Saccharomycotina)
>Yarlip1 Ascomycota; Saccharomycotina
MLTDAQIKIINDSAPFLAE-----NGTDFAKMYKYMFATVPEVIRF---FNQS-----DQKNLQPKILAHALVAYASNI-----DNLGVLSDVVEQIVVHVGLQ---I---QPEQYPIVAASIIHTLKEMLGEEA-----TPEFIEAWTAVYQLANILDAEKLKYEKQAS
Yarrowia lipolytica gi|50550817|XP_502881 463aa (186-321) (Ascomycota; Saccharomycotina)
>Yarlip2 Ascomycota; Saccharomycotina
LMSDPESELQSTAYGFT-----ALFCEQFYTNLMASHAELASI---F-----PSIKRQSVAVAGVGLAISL-----ERIEEMDFLRSVGRKRNRM-----I---GVEPIHYRWLGEAMVKTADFRRGDF-----TLEVETAWIKIYSYLAHLKLSADEEPNVLMA
Yarrowia lipolytica gi|50543406|XP_499869 471aa (193-329) (Ascomycota; Saccharomycotina)
>Yarlip3 Ascomycota; Saccharomycotina
LMDPELLESAAAYGFT-----ALFCEQFYTNLMASHAELTSI---F-----PSIKRQSVAVAGVGLAISL-----DHIEKLEDFLRSVGRKRNRM-----I---GVEPIHYRWLGEAMIKTADFRRGDSF-----TLEMETAWIKIYSYLANLKADEEPNVLMA
Cyanidioschyzon merolae CMR319C (Rhodophyte)
>Cyanmer
EPQESIAIVQSTWSQAVQ-----CERLRLQVYDRFLALYPELQPM---F-----RSDPALQRILRDMVDAQVRLK-----NSRRDLQALRDLGKRHVK-----Y---GTQEEQYPIVGENLLHALESILGSKHF-----SEDMRKAWLDVYAYWSSVMLEGAREAQ
Thalassiosira pseudonana 120695 (Stramenopiles; Bacillariophytes)
>Thapsel
GLSPEDLSLVQKSWAKVVF-----IASVAADLFYTKLFELDPRLPL---F-----PSDLADQKMLMAMI SVAVDGL-----TDLEALVPAVQDLGRRHAKY-----Y---KVTAPMFDVGAALDITLQKLGEGW-----DEEHKEAWTLVYGVL
Bacterial 2/2Hbs
Gemmata obscuriglobus (Planctomycete) 2/2Hb1
>Gemobs
LMDRLGG-----ESVVKAVVHDFALAALED-PRKN---FTRG-----GRYKPSAAALEKSIIVDMI SDVSGGP-----FKYSGSKMKEAKGMA-----I---TDAEFDALAVHLVSLKRF-----KVADPEIAELVKVVA
Haloarcula marismortui (Euryarcheota) gi|55379358|YP_137208 120aa 2/2Hb1
>Halmar
MASQSFPERIGG-----RDAVAVVSDFYDRVRDD-PLLEPY---FEET-----DMDQLRSHQQFISTVAGGP-----VDYDGDMDTAHEGMG-----I---TEDAFASVATHLEAALRANGVP-----DDDVEAILTEVAAMKDDIVEA
Hypomonas neptunium (Alphaproteobacteria) 2/2Hb1
>Hypnep
LYEVFGG-----EAGVSRIVDDLVERSIND-PRIDAI---FAAS-----DLVRLRRLTKQFCFILAGE-----CDYTGMDMASSHHDHG-----I---TNREFNALVENLQHAMNAESVFF-----RAQNKLLAALPMQRDVVT
Legionella pneumophila (Gammaproteobacteria) gi|53752322|CAH13754 124aa 2/2Hb1
>Legpne
MTESLERLGG-----QNAVNTAVDIFYRKMMD-RVNYF---FDDV-----DMEQQILKQKGLTFMVFGGP-----NQYTKGSMREHGHL-----L---ARGLNDSHVDIVIEHGLTKELGANEE-----DIQKVAALANSYRGDVLGRSS
Microbulbifer degradans (Gammaproteobacteria) gi|4886128|ZP_00315184 2/2Hb1
>Micdegl
CSSLQGNQTLKQLGG-----QDGVSAITRQLINMADN-RIAPR---FRGV-----NIGKFGTLDTYLSITDGG-----CVYGSDSITIHSGYN-----Y---TATEFNALVENLQAMETLQIPT-----ATQNKLLAKLAPSYQDVVYQ
Mycobacterium avium (Actinobacteria) (HbN) 131aa 2/2Hb1
>Mycavil
ILARFRKAEPASIIDRIGG-----HEALEVVVDFYVRVLAD-QLSGF---FTGT-----NMNRLKKGQVEFFAALGGP-----HPYTGAPMKQVHQGRG-----I---TMHFGVLVAGHLADALTAAGVPS-----ETVSEILGAIAPLAPEIATGEA
Mycobacterium bovis (Actinobacteria) gi|31618318|NP_855221 136aa (HbN) 2/2Hb1
>Mychov1
LSRLRKRREPISYDKIGG-----HEALEVVVDFYVRVLAD-QLSAF---FSGT-----NMSRLKKGQVEFFAALGGP-----EPYTGAPMKQVHQGRG-----I---TMHFGVLVAGHLADALTAAGVPS-----ETITEILGVIAPLAVDVTSGESTTAPV
Mycobacterium marinum (Actinobacteria) 136aa (HbN) 2/2Hb1
>Mycmar1
LSRFRKRAPVSIYDKIGG-----YEAIEAVVDFYVRVLAD-QLGGF---FTGT-----NMNRLKKGQVEFFAALGGP-----EPYTGAPMKQVHQGRG-----I---TMAHFLVAGHLGDSLTAAGVPS-----ETVTDILKVLAPLATDIASGETTATG
Mycobacterium paratuberculosis (Actinobacteria) 120aa 2/2Hb1
>Mycpar1
ILARFRKAEPASIIDRIGG-----HEALEVVVDFYVRVLAD-QLSGF---FTGT-----NMNRLKKGQVEFFAALGGP-----HPYTGAPMKQVHQGRG-----I---TMHFGVLVAGHLADALTAAGVPS-----ETVSEILGAIAPLAPEIATGEA
Mycobacterium smegmatis (Actinobacteria) (HbN) 125aa 2/2Hb1
>Mycsm1
MYSIEYIGG-----AEALEVVVDFYVRVLAD-ELAGF---FTGT-----NMSRLKGRQVEFFATALGGP-----DEYTGAPMRQVHQGRG-----I---TMHFGVLVAGHLGDSALAMPG-----ATTSQIIAIAIAPLAPEIATARTA
Mycobacterium tuberculosis (Actinobacteria) gi|15608680|NP_216058 HbN 136aa 2/2Hb1
>Myc tub1
LSRLRKRREPISYDKIGG-----HEALEVVVDFYVRVLAD-QLSAF---FSGT-----NMSRLKKGQVEFFAALGGP-----EPYTGAPMKQVHQGRG-----I---TMHFGVLVAGHLADALTAAGVPS-----ETITEILGVIAPLAVDVTSGESTTAPV
Nostoc punctiforme (Cyanobacteria) gi|23126739|ZP_00108627 159aa 2/2Hb1
>Nospun1
MSTLYDNIGG-----QPAIEQVVDLHKRIAD-SLLSPT---FAGT-----DMAQRNHLVAFLGQIFEGP-----KQYGGPRMDKTHAG-----I---NLQQPHFDAIAKHLGEAMVARGVSAE-----NTKAALDRVTNMKGAILNK
Nostoc punctiforme (Cyanobacteria) gi|23126739|ZP_00108627 159aa 2/2Hb1
>Nospun2
AHSAGSSLYKRLGG-----YNAIAAVIDSAKNIFAD-PLIGKY---FIGL-----STNSKQRLRELLIAQFCQAAGP-----CIYGTGRMKLSHSG-----I---GRGLNGEYAFVFNIALALDKNVQKPE-----KNQVGLFANSLRDQIVEKP
Pseudomonas syringae (Gammaproteobacteria) gi|28871348|NP_793967 140aa 2/2Hb1
>Psesyr1
AGCAQQPPRDDSLYQLGQ-----RAGIQRIVEGMLLNIAKDE-RIVEH---FKKV-----NIVRLRDLKVEQLCVAEGP-----CRYTGDSMAESHKQGN-----I---TPSDFNALVENLIAAMD TENVPVF-----VQNRILIARLAPMRGEVLGK
Pseudomonas syringae gi|23471254|ZP_00126585 142aa 2/2Hb1
>Psesyr2
CAQQQPPKDDSLYQLGQ-----RAGIQRIVEGMLINVARDO-RIVEH---FRKV-----DIVRLRDLKVEQLCVESGGP-----CRYTGDSMAEAHKQGN-----I---TPSDFNALVEDLIASMDTEKVPVF-----AQNRILIARLAPMRGEVIGK
Rhodospirillum baltica gi|32475444|NP_868438 127aa 2/2Hb1
>Rhoab1
MSQSESLDQLGG-----MDGVRVVDMEVMYRVLAD-PELTFH---FDGV-----PIEKLRMQTEFIASITSGD-----IQYTGADLTKVHAGRG-----I---TGVFHFKFCHGLTDALANNVSSH-----AIDQVGLKIAMSKDVTGSSNVDG
Xanthomonas axonopodis (Gammaproteobacteria) gi|21243436|NP_643018 131aa 2/2Hb1
>Xanaxo
TSACASTQSRQTLYDELGG-----QAGIEALVETMLSIADD-PRIVDK---FARV-----NIVMLNERLVQKFCHVADGP-----CPDTAKSMQQAHAHLA-----I---REGDFNALVEDLNWMDQRKIP-----RRTQNRLLARLAAMHGEIVNH
Xanthomonas campestris (Gammaproteobacteria) gi|21231965|NP_637882 142aa 2/2Hb1
>Xancam

-----LSACATTQPRQTLVEELGG-----QPGIEALVEITMSRIADD-PRIVEH-----FARV-----NIVMLNERLVKQFCHVADGP-----CPDTAKSMAQAHQHMA-----I-----REDDFNALVEDLNWAMDQRNIP-----RRTQNRLLARLAAMHGEIVNH-----
Methylococcus capsulatus (Gammaproteobacteria) 134aa 2/2Hb1
>Metcap1
-----KLADWNESHGSLVEKLG-----EAAVNAADVIFRYKVLAD-PRINRF-----FEGV-----DMEKQAAKQKAFITMAFGGP-----HNYTGMDMRGHAHL-----V-KQGLNDAHFDAVMEHLGATMKELN-----VPDELTQAQAAIAESTRNDVLGR-----
Mycococcus xantus (Deltaproteobacteria) 116aa 2/2Hb1
>Myxxan1
-----SVYEQLG-----EPAMAAAVEVFYRKLADD-HISHF-----FEDV-----DMERQAAKQKAFITMVTGGP-----VHYSKGMFRAGHAPL-----V-KRGLNDSHFDAVGHKATLEEL-----GVAAPLVARVMITAESARADV-----
Synecococcus sp.PCC7002 (Cyanobacteria) gi|18766961|AAL79195.1 124aa 2/2Hb1
>Syncc
-----MASLYEKLGG-----AAAVDLAVEKFKVLAD-RVNR-----FVNT-----DMAKQKQKQKDFMTYAFGGT-----DRFPGRSMRAHQDLVNA-G-I-----TDVHFDAIENLVLTQLQNV-----SQDLIDEVVTIVGVSQHRNDVLNR-----
Synecocystis sp.PCC6803 (Cyanobacteria) gi|16330583|ref|NF_441311 124aa 2/2Hb1
>Synycs
-----MSTLYEKLGG-----TTAVDLAVKFKYERVLQD-RIKHF-----FADV-----DMAKQRAHQKAFITYAFGGT-----DKYDGRYMRHAHELVENH-G-I-----NGEHFDAVAEDLLATLKEMGV-----PEDLIAEVAAVAGAPAKRVDLWQ-----
Acidithiobacillus ferrooxidans (Gammaproteobacteria) TIGR_243159|contig:10428:a 129aa 2/2Hb2
>Acifer1
-----MLEPESTPYVRLGG-----EAAVRNLVNFYDLMDS-ACWOTPLRDIHAK-----DLSESEKELFLFLSGWLGPP-----YVQFGRHPLRARHASP-----V-----DDQARDQWMACLMQAMHEV-----GIEPELYGHLQAGFQRTADFMNRN-----
Agrobacterium tumefaciens (Alphaproteobacteria) gi|15889651|NF_355332 2/2Hb2
>Agrtum1
-----SKEATMSSETVLYEAI GG-----DATVRALTRRFYELMDTL-PEAARCRA-IHPA-----DLSGSEAKFYDYLTGYLGGP-----PVYVEKHGHPMLRRRHVAP-----I-----GPAERDEWLLCFRRAMDETIE-----NAKLREI IWAPVERLAFHMNQAEADNF-----
Azotobacter vinelandii (Gammaproteobacteria) gi|23105627|ZP_00092083 2/2Hb2
>Azovin
-----MIVNLVTFYQLGG-----EGVRRLLCNAFYRMEGL-PEAEGIRR-M-----HGADTTAVREKLFYELSGWLGPP-----YLEKYGVSMGLHRPFA-----I-----GPKERDQWMLCLNKALDDIGAS-----ETAKGLIKAPHFADHVRNRETSD-----
Bacillus anthracis (Firmicutes) gi|30261307|NP_843684 2/2Hb2
>Bacant
-----MSKQMPFFFAI GG-----EQCIELVDTFYYSVSKH-PDLSPI-----FP-----DDLTTETARKQKQFLTYQLGGP-----YTEEHGHPMLRARHLFFP-----I-----TPKRAEAWLSCMEQAMDDTGVHG-----HIREFVFERLALTAQHMVNTFNETGE-----
Bacillus cereus (Firmicutes) gi|30019349|NP_830980 132aa 2/2Hb2
>Baccer
-----MSKQMPFFFAI GG-----EQCIALVDTFYYSVSKH-PDLSPI-----FP-----EDLTETARKQKQFLTYQLGGP-----YTEEHGHPMLRARHLFFP-----I-----TPKRAEAWLSCMEQAMDDTGVHG-----IREFVFERLALTAQHMVNTFNETGEV-----
Bacillus halodurans (Firmicutes) gi|15615417|NP_243720 2/2Hb2
>Bachal
-----MVELNRTVYERIGG-----DKTVSALVDAFYTVAGD-PILAPI-----FP-----NDLTETARKQKQFLTYQLGGP-----YTEEHGHPMLRARHLFFP-----I-----TPRRAKAWLTCMERAMDEINLSP-----EREEMARLMTAHHMVNQPEHR-----
Bacillus licheniformis (Firmicutes) gi|52079659|YP_078450 132aa 2/2Hb2
>Baclic
-----MGQSFNAPYEAIG-----EELLSQLVDTFYYSVSKH-PDLSPI-----FP-----DDLTTETARKQKQFLTYQLGGP-----PLYTEEHGHPMLRARHLFFP-----I-----TPERADAWLSCMEAMDHVGLKGE-----IREFLFERLALTARHMVNQPKMEDGSH-----
Bacillus subtilis (Firmicutes) gi|16078221|NP_389038 2/2Hb2
>Bacsu2
-----MGQSFNAPYEAIG-----EELLSQLVDTFYYSVSKH-PDLSPI-----FP-----SDLTETARKQKQFLTYQLGGP-----YTEEHGHPMLRARHLFFP-----I-----TNERADAWLSCMEAMDHVGLGE-----IREFLGRLELTARHMVNQTEADRS-----
Bacillus thuringiensis (Firmicutes) gi|49477128|YP_035435.1 132aa 2/2Hb2
>Bachtu
-----MSKQMPFFFAI GG-----EQCIALVDTFYYSVSKH-PDLSPI-----FP-----DDLTTETARKQKQFLTYQLGGP-----NLYTEEHGHPMLRARHLFFP-----I-----TPKRAEAWLSCMEQAMDDTGVHG-----IREFVFERLALTAQHMVNTFNETGEI-----
Bdellovibrio bacteriovorus (Deltaproteobacteria) gi|39576266|NP_969438 137aa 2/2Hb2
>Bdebacl
-----MSEKKPYELGG-----EVLRLQCKRFYEMDTI-PEAKGIRD-MH-----PGNLRGSEKFLMFLSGWLGPP-----GLFVEKYGHPLRMHRHFFK-----I-----GKSERDQWMMCMQVAFDELNIAEP-----LRSELHSLRLLDHMRNVEEPESSE-----
Bordetella pertussis (Betaproteobacteria) gi|33593344|NP_880988 2/2Hb2
>Borper1
-----QPISEPLDTSKTFVDMGG-----EPGVRELVDRFYDLMDS-SD-----FKALR-----DAHPSLEQARDKLFWFLCGYGGP-----H-YIERFGHPRLRARHLFFS-----I-----GEIERDQWVACGRAMDQQL-----PAALVDRLLQAFYGTADWMRNRAG-----
Bradyrhizobium japonicum (Alphaproteobacteria) gi|27376186|NP_767715 131aa 2/2Hb2
>Braajpl
-----MMDSDVAISMFERIGG-----SATDILLVDRFYRMDT-PEAKV-----TRAM-----HAADLGLRDLVKRYLTEWTGGP-----RLYSVEKHGHPRLRQHIGFA-----I-----GDAERDAWLTCMRGALETVAD-----AAARQDLKALSGLDWMRNR-----
Burkholderia cepacia (Betaproteobacteria) gi|46323938|ZP_00224300 142aa 2/2Hb2
>Burcep1
-----AHSLHAHAPSPFDRLGG-----AALARLVDAFYRQMDTR-PDAQRIRA-MHGA-----DLGPVKTLVTYLCEWLGPP-----RHYSARQGHPLRMHRHFA-----I-----GMAERDAWLCMRALDECGVEP-----ALRDELQALFKLADWLENTGR-----
Burkholderia cepacia (Betaproteobacteria) gi|46311329|ZP_00211937 136aa 2/2Hb2
>Burcep2
-----TDVNDAPSPPTAFELVGG-----EARVREMDRFDYDLMDS-PE-----FAQIR-----ALHPDSDLGSRDKFFWFLCGWLGPP-----DHYISRFGHPRLRARHLFFP-----I-----ASVERDQWLRCAWAMDDIGLPE-----FLRERLMSFYDTADWMRNRPG-----
Burkholderia fungorum (Betaproteobacteria) gi|48786054|ZP_00282263 139aa 2/2Hb2
>Burfun1
-----AIPSSQQLPRATHFDRLGG-----PAVIRLVDAFYRMDTR-PDAQRIRA-MHHP-----DLSSTKAVLVLYLCEWLGDD-----KYSAQRGHPLRMHRHFA-----I-----GLAERDAWLTCMRGALETVGDP-----ALRDELQALFKLADWLENTGR-----
Burkholderia fungorum (Betaproteobacteria) gi|48784261|ZP_00280627 137aa 2/2Hb2
>Burfun2
-----DLNDEVSAQPTAFELVGG-----ARVRELVDRFYDLMDS-AD-----FAGIR-----ALHPDSDLGSRDKFFWFLCGWLGPP-----HYISRFGHPRLRARHLFFP-----I-----ASSERDQWLRCAWAMDDIGLPE-----LRELLGSFFETADWMRNRNG-----
Burkholderia mallei (Betaproteobacteria) gi|52428830|AAU49423 135aa 2/2Hb2
>Burmal
-----TDVNDAPSPPTAFELVGG-----ARVRELVDRFYDLMDS-PE-----FAGIR-----ALHPPTLEGSRDKLFWFLCGWLGPP-----HYIERFGHPRLRARHLFFP-----I-----ASSERDQWLRCAWAMDDIGLPE-----LRELLMSFHDADWMRNRPG-----
Burkholderia pseudomallei (Betaproteobacteria) gi|13774099|gb|AAK38159 170aa (36-170) 2/2Hb2
>Burpsel
-----TDVNDAPSPPTAFELVGG-----ARVRELVDRFYDLMDS-PE-----FAGIR-----ALHPPTLEGSRDKLFWFLCGWLGPP-----HYIERFGHPRLRARHLFFP-----I-----ASSERDQWLRCAWAMDDIGLPE-----LRELLMSFHDADWMRNRPG-----
Chloroflexus aurantiacus (Chloroflexi; Green non-sulfur bacteria) gi|22973316|ZP_00020053 140aa 2/2Hb2
>Chlaur
-----HYGEVYIMSEPTIYIGG-----EATFRIRVIDFYARVAD-PRLRHL-----FP-----ADLEPGKEHQRLFLMQLYFGGP-----TYSERRGHPLRMHRHAFP-----I-----GPRERDAWLEHMLAALNEAGVPE-----PARSVMENYFRHAAQAMNRLGED-----
Chromobacterium violaceum (Betaproteobacteria) gi|34499146|NP_903361 129aa 2/2Hb2
>Chrvioc
-----MSEVQEMTPYQLGG-----EGVVRWLTDRFYDMDSE-PSVKPLRD-M-HP-----ADLAGSRQKLFMFLSGWLGPP-----LYMEAFGHPLRMHRMFA-----V-----DEDARDQWMCRRRAVSEL-----VVEDWLKDKLEAFENTADFMNRN-----
Corynebacterium diphtheriae (Actinobacteria) gi|38234371|NP_940138.1 2/2Hb2
>Cordip
-----MNTPASFYESVGG-----EETFLIIVHRFYERMRND-LIGPM-----YP-----DDWEGAEEDLRWFLAQYGGP-----TFSENHRGHPRLMRHAFP-----I-----GMNEAQRLWIDMSDITDISEATLPP-----AHRAMWDMHQVAMQLINQAP-----
Corynebacterium efficiens (Actinobacteria) gi|25028901|NP_738955 2/2Hb2
>Coreff
-----MTSTENFYDSVGG-----EETFLIIVHRFYEQVTRDD-ILGPM-----YP-----DDWEGAEARLWFLVQYGGP-----DYEQRGHPLRMHRHAFP-----I-----GVTAERWELMTRALDSLEECTL-----TDDQRAAIWDMHVRADMLINSNPPDHR-----
Corynebacterium glutamicum (Actinobacteria) gi|19553644|NP_601646 2/2Hb2
>Corglu
-----MTSTENFYDSVGG-----EETFLIIVHRFYEQVTRDD-ILGPM-----YP-----DDFEGAEQRLWFLSQQYGGP-----DYEQRGHPLRMHRHAFP-----I-----GVTAERWELMTRALDSLEECTL-----TDDQRAAIWDMHVRADMLINSNPPDHR-----
Cytophaga hutchinsonii (Bacteroidetes/Chlorobi; green sulfur bacteria) gi|23136839|ZP_00118553 2/2Hb2 2/2Hb2
>Cythut
-----MEKALYVRLGK-----ENLDDLVDYFDLVVND-QIAHL-----FKN-----DKKEIKGKQRLFLQPLGGP-----LYSEKFGHPQMRMRHHP-----I-----TETDAIWLHMSQAIGSLVSEA-----LKDELFAFPPTAMFVNKKEEQ-----
Deinococcus radiodurans (Thermus/Deinococcus) gi|15806025|NP_294726 2/2Hb2
>Deirad
-----MTPLDLARGSLYDRIG-----DTALLVHRFYARVARN-PDLAPI-----FPA-----DLSETARKQKQFLTYQLGGP-----LYHELYGHPLRARHLFFP-----I-----TPGRARAWLCMNAALRETPGLAEA-----DAHELYAALARAVHVMNTEAPDSD-----
Exiguobacterium (Firmicutes) gi|45532753|ZP_00183753 126aa 2/2Hb2
>Exiguo
-----MLYEDLGG-----KQAEQVLFYRERYVADH-LLRPL-----FP-----SDRRQVEQATRFILQTLGGP-----KQYESYDERMMLAMHRLPL-----I-----TEVHAIWIELMTMTIETISDSEA-----ATRLIERIRIGALVLRICDAHQRN-----
Chloroflexus aurantiacus (Chloroflexi; Green non-sulfur bacteria) gi|53799877|ZP_00359558 127aa 2/2Hb1

>Chlaur
-----MSEPTIYEQIGG-----EATFRRIVDIFYARVEAD-FRLRHL--FP-----ADLEPGKEHQRLFLMQYFGGP-----RTYSERRGHPRLMRHAPFP-----I-----GPRERDAWLEHMLAALNEAGVPE-----PARSVMENYFRHAAQAMNRLGED-----
Kineococcus radiotolerans (Actinobacteria) gi|46365419|ZP_00227907.1 149aa 2/2Hb2
>Klnrad
-----RKPAGPDGGRSFFDEVGG-----HEFTVRLVDVDFYEGVADE-VLRHM--YP-----EADLGPARGMLMFLEQYWGVP-----ATYSEQRGHPRLMRHASFK-----V-----NPDARDRWLTHMRAAVVSLGLAP-----AQEGVLDVYDRAAHSMLNTFED-----
Leifsonia xylaii (Actinobacteria) gi|50954582|YP_061870 135aa 2/2Hb
>Leixyl
-----TGIPVGPAGPTFFFEQAGG-----HDTFRRLVDVDFYEGVAAD-VLRLRM--YP-----EEDLEPAERLTLFLFEQYWGVP-----AAAYSEQRGHPRLMRHLPFR-----V-----NPDARDRWLNMRAAVLELALP-----PLQEETLSYLERAAFAMVNTFEE-----
Leptospira interrogans (Spirochaetes) gi|24216675|NP_714156 145aa 2/2Hb2
>Lepint
-----GGFPQIPGLQLVFGVSGE-----NSLRKLVSDFYDQIPSS-SIS-FM--FP-----ENLEDSKIKSADFLIQVTGGP-----LYSQNYGPFKMRARHLFPF-----I-----DEKARRVWLSYCRVRLDDWADEV-----SAKEVLWIFFKDFSTWVMNLESKTEE-----
Mesorhizobium loti (Alphaproteobacteria) gi|13470534|NP_102102 160aa 2/2Hb2
>Meslot
-----MSRDVPTLYEWAGG-----SDALNRLTQTFYDKVAKD-PVVGVP--FKAM-----SPDHPSHVAAFIGEVEFGP-----YSEKFGHREMVMHHLGKH-----L-----TEEQRRRWLNLLADADEVGLPDD-----PEFRSAFMGYVEWGSRLAKMNSNLGET-----
Methylobacillus flagellatus (Betaproteobacteria) gi|46120937|ZP_00201861 137aa 2/2Hb2
>Metfla
-----DKIGEPGSKATFELLGG-----AEQVRAIVERFYDMDTD-PRAAGIRA-MHAP-----DLTSAREKLFMFLTGWGTGGP-----QLYMERYGHPRLMRHMSFF-----I-----DDSDARQWVMYCMVKAMHDTGVDE-----AIIEKMGAALYGVADFMNRREG-----
Methylococcus capsulatus (Gammaproteobacteria) 131aa 2/2Hb2
>Metcap2
-----MQEPTVQTPYQRLGG-----EAVLHELVERFYGMDEL-PEAAP IRA-MHA-----DDLSGAKSLKFKFLSGWLGGP-----LFVQEGHFLRARHFFFS-----I-----GVPERDQWLLCMRKALDDIPLDGPF-----EALYEALARTAHMINRED-----
Microbulfiber degradans (Gammaproteobacteria) gi|48862691|ZP_00316586 137aa 2/2Hb2
>Micdeg2
-----MNEYGYGQGDASYKAAAGE-----IGETRLVDVDFYHFMDTL-PEAAKILRS-MHAQ-----SLAESRKRLAYFLSGWLGGP-----RLYAQHGFSINIPGAHRH-----L-----AATPEDADANWLMCAKAVDLQPYEP-----SFKQYLLQLRVPADRIVEAGRKPL-----
Mycobacterium avium (Actinobacteria) gi|41408389|NP_961225 (HbO) 129aa 2/2Hb2
>Mycavi2
-----SFYDAVGG-----AETQAVISRFYAQVPEDE-ILREL--YPL-----DDLEGAERLRMFLEQYWGVP-----TYSDRRHGHPRLMRHVPFR-----I-----TPLARDAWLRCMHTAVASIDSKTLD-----DEHRELLDYLEMAAHSLVNSP-----
Mycobacterium bovis (Actinobacteria) gi|31793651|NP_856144 128aa (HbO) 2/2Hb2
>Mycbov2
-----MPKSFYDAVGG-----AKTFDAIVSRFYAQAQVADE-VLRRV--YPE-----DDLGAEEERLRMFLEQYWGVP-----TYSEQRGHPRLMRHAPFR-----I-----SLIERDAWLRMHTAVASIDSSETLD-----DEHRELLDYLEMAAHSLVNSP-----
Mycobacterium leprae (Actinobacteria) gi|15827640|NP_301903 128aa 2/2Hb2
>Myclep2
-----MQQSFYDAIGG-----AETFKAVISRFYAQVPEDE-ILREL--YPA-----DDLGAEEERLRMFLEQYWGVP-----TYSSQRGHPRLMRHAPFR-----I-----TAIERDAWLRMHTAVASIDSHTL-----DNEHRELLDYLEMAAHSLVNSAS-----
Mycobacterium smegmatis (Actinobacteria) 136aa (HbO) 2/2Hb2
>Mycsme2
-----MGDVTVQVRSFYDEVGG-----HDTTHAIVSRFYQLVREDE-ILHPL--YPE-----DDFEGAEERLRMFLEQYWGVP-----TYSQQRGHPRLMRHAPFR-----I-----GFLERDAWLRMHTAVASIDSQTLDDA-----HRRALLDYLMADSMVNSAF-----
Mycobacterium tuberculosis (Actinobacteria) gi|15609607|NP_216986 HbO 128aa 2/2Hb2
>Myc tub2
-----MPKSFYDAVGG-----AKTFDAIVSRFYAQAQVADE-VLRRV--YPE-----DDLGAEEERLRMFLEQYWGVP-----RTYSEQRGHPRLMRHAPFR-----I-----SLIERDAWLRMHTAVASIDSSETLDDE-----HRELLDYLEMAAHSLVNSP-----
Nocardia farcinica (Actinobacteria) gi|54014789|BAD56159 134aa
>Nocfar
-----MSSQGTATSFYEAAGG-----AETFRRLVAAFYREVADE-ILRPL--YPE-----DDLGAEEERLRMFLEQYWGVP-----RTYSERGHPRLMRHMFPK-----V-----GFLERDAWLRMHTAVASIEVEPLDDE-----HRKALLDYLEMAAHSLVNSPI-----
Novosphingobium aromaticivorans (Alphaproteobacteria) gi|48850360|ZP_00304602 131aa 2/2Hb2
>Novarol
-----MATEAPALSPYDRIGG-----REVLRITDRFYDMDTD-PA--YAE LR-----AMHAPDLSPMREALAGFLSGCGGP-----RGWFEANPKCKMCKMHPFP-----I-----TRQTATQWADCMRAIADAAPEDTE-----VADAMAQVLQMAKGMARD-----
Novosphingobium aromaticivorans (Alphaproteobacteria) gi|48847810|ZP_00320259 133aa 2/2Hb2
>Novaro2
-----MTVPGTPYEAFGG-----EAAIRALCGRFYSYLMDEL-PGAACRA-VHPP-----SLERAERLFEYLTGWLGGP-----PLYTDKYGHPRLMRHFIAF-----I-----GREEVEGWLLCFRQAWSETIPASPL-----ADAIMEKVEGLAHWMKNDPIAGS-----
Oceanobacillus ihyensii (Firmicutes) gi|23098673|NP_692139 128aa 2/2Hb2
>Oceihe2
-----MEQMEHRTIYEAIIGG-----YRTMNIIVHAFYTRVEVH-PDLKPI--F-----PDDLTEITIRQMMFLTQFFGGP-----LYEEERGHPLRRRHLFPF-----I-----TPTRDAWLTMAAAEEAEIKEP-----YRTAMERLTLTANHMNTPE-----
Parachlamydia sp. UWE25 (Chlamydiae) gi|46446613|YP_007978.1 146aa 2/2Hb2
>Parach
-----SGFPQITPDSRIYLSMG-----EDNIYKMLDFYLELEKS-SIRHL--FP-----ADMKAASKSAAFFVFCGGP-----PLYQQQFSPMRQRHLFPA-----I-----DEEARQVWLHSFKHILQGAQKYC-----FMEYMGSFYRFLDQFSTWMTNQSE-----
Photobacterium profundum (Gammaproteobacteria) gi|46913965|CAG20747 160aa
>Phopro
-----QKTPYVGMGDTALLAAGG-----EEGVKLVDAFYDYMOTL-PEAEVVR-AHMKP-----DLTDSREKLTFTLGTWGGP-----SRYAEKYSGMNIPGAHRHLS-----I-----GIAEKEAWLQCMQKALDDQGYDD-----VFKRYVMVQLSFFAEMCRNRS-----
Polaromonas sp. JS666 (Betaproteobacteria) gi|54032073|ZP_00364205 146aa 2/2Hb2
>Polaro
-----ENPFGNPFPTFFANIGG-----EERVKALVERFYDLMLE-PG--YALR-----AAHGSLTDNARQRLFWFLCGWLGGP-----QHYTERFGHPRLMRHMPQQTGG-GAI--GSIGILLERDQWLACMQAMRETGVDD-----ALRTRLNASFQQTADWMNRNGE-----
Ralstonia eutropha (Betaproteobacteria) gi|46132529|ZP_00202928 139aa 2/2Hb2
>Raleut
-----PESTQAGTEVTAFDLVGG-----EARVRELVDRFYDLMLE-PE--FAGLR-----ALHPASLDGSRDKLFWFLCGWLGGP-----NHFIERFGHPRLRARHMPFE-----I-----GISERDQWNRCMALAMQDVGLSED-----LQMRMQAFQQTADWMNRNVAR-----
Ralstonia metallidurans (Betaproteobacteria) gi|22977370|ZP_00023178 2/2Hb2
>Ralmet
-----SNQPEEQREITAYELIGG-----EARVRELVDRFYDLMLE-TE--FAGLR-----ALHPSPLESGRDKLFWFLCGWLGGP-----NYFIERFGHPRLRARHLFPE-----I-----GTSERDQWNRCMALAMQDVGLSED-----LQMRMQALFQQTADWMNRNVR-----
Ralstonia solanacearum (Betaproteobacteria) gi|17546809|NP_520211 2/2Hb2
>Ralsol
-----MTDAASGQETLAFDLGG-----EARVRELVDRFYDLMLE-PA--FA--R-----ALHPSSLDGSRDKLFWF--HYI-----ERFHPRLRARHLFPE-----I-----GTRERDQWNRCMALAMQDLGIDDA-----LQMRMQAFQQTADWMNRNVR-----
Rubrivivax gelatinosus (Betaproteobacteria) gi|47573541|ZP_00243579 136aa 2/2Hb2
>Rubgel
-----TPPESTAPATFYEYVGG-----EHAVRALVDRFYDLMLE-PG--FHDLR-----RLHPSLTDGSRDKLFWFLCGWLGGP-----DLYVERFGHPRLRARHLFYS-----I-----GVRERDQWMCMEQAMHECEDP-----LLVSRKASFANTADWMNRNRT-----
Shewanella oneidensis (Gammaproteobacteria) gi|24371639|NP_715681 145aa 2/2Hb2
>Sheone
-----KVQDRDPNQSNAYDLIGG-----DKVIRAIANSFYQKASSE-ETRAL--FA-----IHRAPAESEQKLYEFLTWLGGP-----QKYGHPALRARHMFPA-----V-----DEAMRDQWLFCKMFAIEKHKKP-----EHRAAIYEAISTLADHMRNQ-----
Sinorhizobium meliloti (Alphaproteobacteria) gi|15966172|NP_386525 130aa 2/2Hb2
>Sime11
-----MTEPQTTLIYEALIGG-----DATVRLTQRFYELMDSL-PEAACRA-VHPP-----DLTGSSEKFYEYLTGWLGGP-----YVQKRGHPLMRHRRHFIAG-----I-----GPAERDEWLCFTRALEETVSHPK-----LREIILEPTLRAHMQNKE-----
Staphylococcus aureus (Firmicutes) gi|15923993|NP_371527 121aa 2/2Hb2
>Staur
-----MITTFYDIIG-----KEALYDMIDFYTLVEKDE-RLNHL--FP-----GDFAEISRKQKQFLTQFLGGP-----YTEEHGHPLMRHMDFT-----I-----TEFERDAWLNMQTAINRAAFPQG-----VGDYLFERLRLTANHMVNS-----
Staphylococcus epidermidis (Firmicutes) gi|27467610|NP_764247 121aa 2/2Hb2
>Stae1
-----MSKTPYELIG-----QKALYQMDHFYQLVEKDS-RINHL--FP-----GDFKTSRQKQKFLTQFLGGP-----DLYTQEHGHPLMRHMEFT-----I-----SEYERDAWLNMQTAINRAAFPQG-----VGDYLFERLRLTANHMVNS-----
Streptomyces avermitilis (Actinobacteria) gi|29831913|NP_826547 134aa 2/2Hb2
>Strave
-----NEIRRGTLQEQTFYEQVGG-----EETFRRLVHRFYEGVAGD-PLLKPM--YP-----EEDLGAERFRLFLLQYWGVP-----YSEQRGHPRLMRHAPFA-----V-----DRAAHDWLRKHMRAVAVDELGLS-----EEHEHTLWNYLYTAAASMVNTES-----
Streptomyces coelicolor (Actinobacteria) gi|21221127|NP_626906 137aa 2/2Hb2
>Strcoe
-----NEIRRGTLQEQTFYEQVGG-----EETFRRLVHRFYEGVAGD-PILRPM--YP-----EEDLGAERFRLFLLQYWGVP-----YSDNRGHPRLMRHPFA-----V-----DRAAHDWLRKHMRAVAVDELGL-----SEEHEQTLWKYLYTAAASMVNTFG-----
Thermobifida fusca (Actinobacteria) gi|48835434|ZP_00292434 163aa 2/2Hb2
>Thefusc
-----MTSQDDQMTFYEAVGG-----EETFRRLARFYEGVAAD-PVLRPM--YP-----EEDLGAERLRLFLLQYWGVP-----YSERRGHPRLMRHFPYR-----I-----GAEERDRWLTHMRAAVDDLALPA-----HLEQQWLEYLYTAAASMVNPEDAQFP-----

Thiobacillus denitrificans (Betaproteobacteria) gi|52006448|ZP_00333828 126aa 2/2Hb
>Thiden
-----MQTHYDLGG-----ADTIRRLVDRFYDLMDED-PDY-----YG-IR-----KLPHTDLTESRNKLAFLSGWTGGP-----PEYTDRFGHPFLRRRHLPFV-----I-----GESERDQWGMCMIRAMQDVLDA-----ALQQELTAALFQTADFMRNQ
Verruimicrobium spinosum (Chlamydiae/Verruimicrobia) gml|TIGR_240016|contig:335 121aa 2/2Hb2
>Verspi
-----MVDFFYRLGE-----EALTRVLAFAFYRKKADD-LLGFM-----YFP-----EDWEGAERRLRDFLIFRFGGP-----DQYIQERGHPRMLRHAPFK-----I-----GVAERDRWLDLGMGAAMKEVGIPE-----DLAPTLOGGFAQVADFMRN
Acidithiobacillus ferrooxidans (Gammaproteobacteria) TIGR_243159|contig:10428:a 132aa 2/2Hb3
>Acifer3
-----MEQVSPKRRLEFLCEK-----ITPLVIRAVDDFYNRIQHH-PTLAEP-----FSIV-----QDWELHKLRVHYWVTVSGGL-----PYKDYRYALGDKHAPLG-----I-----THSLVDDWLALFHETMLDHDMDAD-----MARRWHGMAAGISESLRMFAPR
Agrobacterium tumefaciens (Alphaproteobacteria) gi|15887600|NP_353281 2/2Hb3
>Agrtum2
-----VHNAEQDRAEKAMAEIGV-----DAAFIDLLVETFYGRVLEHQTLGPV-----FD-----AGRWPEHMRMARMQFWTAIAFKN-----GSYGGKPVQAHLG-----V-----QGMSAELFPQWLALFSVTLDDIAPSRKAHD-----WFMETAERIAARSLTSLFLYFNPAMDDP
Agrobacterium tumefaciens (Alphaproteobacteria) gi|17934166|NP_530956 2/2Hb3
>Agrtum3
-----MARIGV-----DAAFIDLLVETFYGRVLEHQTLGPV-----FDARL-----AGRWPEHMRMARMQFWTAIAFKN-----GSYGGKPVQAHLG-----V-----QGMSAELFPQWLALFSVTLDDIAPSRKAHD-----WFMETAERIAARSLTSLFLYFNPAMDDP
Bdellovibrio bacteriovorus (Deltaproteobacteria) gi|42523942|NP_969322 128aa 2/2Hb3
>Bdebac2
-----MTPTSRKPLES-----REDVMVLVDSFYAKVRAD-GYIGPI-----FTDV-----AKVDWEHLPKLYNFWSDLLLGE-----DSYRGRFPFPHTKLN-----L-----ERGHFEQWLRLEFVETVDEHFVGLKANE-----AKERAYRIARNFMINLQLLSLE
Bordetella pertussis (Betaproteobacteria) gi|33593122|ref|NP_880766 2/2Hb3
>Borper2
-----NGAPDLCTE-----EDITQLVHQFYAEVRDD-AELGPI-----FN-----THVDDVHVLAKLVDFWSSILRGT-----RGTPMPRHVALPGLHAG-----L-----FERWLRFRATAAAQPNQAMAEQ-----ACLMAGRIAQSLWYGYQLHRSPDQA
Bradyrhizobium japonicum (Alphaproteobacteria) gi|27381333|NP_772862 154aa 2/2Hb3
>Braajap2
-----AAAARRNLLTQDAERTGI-----TEEMIAELVTRFYGRVRDD-ALLGPV-----FAV-----VQNWDEHLAKLGFDFWSSVVLMS-----S-----PMRAHPLGLVLQDGHDFRW-----L-----DLFEQTARDVCCPAAAAALFDKA-----RRIADSFEMASATVAGRIASPRHVLRS
Brucella melitensis (Alphaproteobacteria) gi|17988743|NP_541376 141aa 2/2Hb3
>Brumel3
-----MTILINQPH-----SIDRDSIDRLVEIFYGRAREDE-IIGPI-----FNRT-----VKDWDHHLARISEFWSVILKT-----R-----PMPPHLALNLENEHDFRW-----L-----ELFEQTAREIFPPEAAIIFVDRA-----RRIADSFEMAIATHSGRIAPRHSRRP
Burkholderia cepacia (Betaproteobacteria) gi|46315472|ZP_00216054 186aa (1-155) 2/2Hb3
>Burcep3
-----MTALPASPDAPARPD-----TEPTEENIRDLVYAFYDRVRAD-PLLGPV-----FDAK-----LEGRWDDHLPKMTVFWSSVLGT-----K-----GYRGNVQAAHQPLDG-----I-----EPAHFSRWLWLFKLVETRYAPPAA-----IRFMFEPALRIAQSLQSRFGWDYQIPP
Burkholderia cepacia (Betaproteobacteria) gi|46323547|ZP_00223911 190aa (1-155) 2/2Hb3
>Burcep4
-----MTSLPASDAPARPD-----AEPTEANIRDLVYAFYDRVRAD-PLLGPV-----FD-----AKLDGRWDHLPKMTVFWSSVLGT-----R-----GYRGNVQAAHQPLDG-----I-----EPAHFSRWLWLFKLVETRYAPPAA-----AVRFMEPALRIAQSLQSRFGWDYRIPA
Burkholderia fungorum (Betaproteobacteria) gi|48783812|ZP_00280193 181aa (1-154) 2/2Hb3
>Burfun3
-----MNPSPAAPAVERAAHP-----TEANIRDLVYAFYERVRAD-ALLGPV-----FDAT-----LADRDWDDHLPKMTVFWSSVLGA-----VQAAHQPLEGIEPQHSRW-----L-----YLFLDTVQSRYPAAAVR-----FMFEPALRIAQSLQSRFGWDYKIFE
Burkholderia mallei (Betaproteobacteria) 144aa 2/2Hb3
>Burmal4
-----TQAFSASSAAKPARDAEP-----TPENIRALVDAFYDRVRDD-ALLGPV-----FE-----SKLAGRWQDHLPKMGFEWSSVLGT-----KSYRGNVQAAHQPLDG-----L-----EPVHFSRWLWLFKLVETRYAPPAA-----AVRFMEPALRIAQSLQSRF
Burkholderia pseudomallei (Betaproteobacteria) gi|53719116|YP_108102 180aa (36-170) 2/2Hb
>Burpse2
-----TQAFSASSAAKPARDAEPT-----PENTRALVDAFYDRVRDD-ALLGPV-----FE-----SKLAGRWQDHLPKMGFEWSSVLGT-----KSYRGNVQAAHQPLDG-----L-----EPVHFSRWLWLFKLVETRYAPPAA-----AVRFMEPALRIAQSLQSRFGWDYR
Campylobacter jejuni (Epsilonproteobacteria) gi|15791829|NP_281652 2/2Hb3
>Camjej
-----MKFETINQ-----ESIAKIMEIFYEKVRKDK-DLGPV-----FNNAI-----GTSDEWEKHAKKIGNFWAGMLLGE-----GDYNGQPLKXHL-----L-----PPFPQEFFEIKLFEESINIVYNEE-----MKNVILQRAQMIASHQNMILYKYGGH
Caulobacter crescentus (Alphaproteobacteria) gi|16127286|NP_421850 2/2Hb3
>Cauce
-----MSLSPRSQARADA-----APFDEEIDRLVETFYARIRQHH-RLGPI-----FEAA-----IGPDGWEHLAKLDFWSSVLNLS-----GRYKQGVAAHQGVGEG-----V-----TEGLFTPWGLFHMTCALFDAP-----RAAIIQKAEARIAATKLGFRHPGAVA
Desulfitobacterium hafniense (Firmicutes) gi|23119438|ZP_00102524 2/2Hb3
>Deshaf
-----MFKRGMRSDD-----LDEAALALVRRFYAAVREDD-RLGPV-----FA-----AAIDWDWAHERLLIDFTSMLGS-----GRYRGNPAQMLHRHAGR-----I-----QPELFAHWLWLRRCSEHTLPPAAQ-----AAVQAARAGIAEHLQRLLAQA
Helicobacter hepaticus (Epsilonproteobacteria) gi|32261711|gb|AAP76761 2/2Hb3
>Helhep
-----MTFKEINVDISIR-----KLMDFYAKVRADKSLGDI-----FNTKI-----GTSDEVNKHAKIANFQGMMLNS-----GDYNGQPLKAHL-----L-----PPFPRELFVWNLNLFEEISLAVYAKEE-----HISLILQRAQMIARFQYIIESGLHH
Mesorhizobium sp. BNC1 (Alphaaproteobacteria) gi|45680999|ZP_00192444 154aa 2/2Hb3
>Mesorhi
-----MSKQSAGRTTIIVDGVFLPE--ILDERMIHDVHGFYBEIRNDD-LLGPI-----FNQA-----INSEAWPHHLAKMCDFWSATLLRRT-----KRYEGRPLPPHLA-----I-----PGLGEVHFRWMLFRATVDRLCPADVA-----VLFMDRALRIASFRLAVAFSRGDDTL
Methylococcus capsulatus (Gammaproteobacteria) gi|53804116|YP_114018 140aa 2/2Hb3
>Metcap3
-----MATHCTSSMSTHLP-----EQIAEMVRRFYRQVLADD-RLRPI-----FD-----AAITDWDTHRRVQDFWSSRTLLD-----DRYRGHYPVHAQPL-----L-----QPEHFDIWELEFRKAAREVLPADSAA-----RAIARAEMHMAESFKAGMFSFRVYEGP
Mycobacterium avium (Actinobacteria) 148aa 2/2Hb3
>Mycavi3
-----MPDLRD-----RADVEALLRRFYGRALDDE-VLAEP-----FARL-----RATGLDDHVP TCMDFVETVLFRA-----GRYRGSALQAHDRHRA-P-L-----SDRHFRRWLTWHITVDEMYRGAAD-----RAKIQAAIRIAWAMHRLTGADSPPELL
Nitrosomonas europaea (Betaproteobacteria) gi|30249138|NP_841208 141aa 2/2Hb3
>Niteur3
-----MIPRP IPEFSPDLYTE-----EEVSKLVHEFYAKARD-AALGPI-----FEEH-----VIDWDAHFVQMTNFWSAQLRGT-----SRFGAFMPKHIALPE-----L-----NETLFRKWLQFRQTTLELGNPLL-----KQHADTVAEFIAGRLWMGYQMSHFFHRE
Novosphingobium aromaticivorans (Alphaproteobacteria) gi|48849793|ZP_00303907 127aa 2/2Hb3
>Novaro
-----MNDLSITE-----GDIDRLVPEFYARVKDE-VLGPV-----FNQA-----IEDWPHDLERLKFVSSIMLTS-----GRYKQGLIAHVKEAH-----M-----TPENFARWLEWRQTTGDIIGPD-----KAELFRQKAARIESLTMGVQFYRERQRA
Rhodospseudomonas palustris (Alphaproteobacteria) gi|39935786|NP_948062 139aa 2/2Hb3
>Rhopal
-----MAYIVAMSLAHS-----ILNDDQIAQLVVRTFYGRAREDE-VIGPI-----FASA-----VHDWDHIIAQITDFWSSMLKT-----PMRPHMLNLNLAPEHDFRW-----L-----KLFEATATELFTPEVAT-----EFIIRARRIADSFEMGIATTQGVAT
Silicobacter pomeroyi (Alphaproteobacteria) 2/2Hb3
>Silpom3
-----IFPAQIDH-----VVRVFYARIRTH-ABELGPV-----FAAH-----VRDWAHEARIAAFWRNALIKE-----MRVHVSVPDIRPDHFP-----L-----WLALFHEVLTLQELAAETAA-----RWGALADRIGHGLKMGIL
Silicibacter sp. TM1040 (Alphaproteobacteria) gi|52009563|ZP_00336926 137aa 2/2Hb3
>Sillici
-----MQDQVQIARFQISA-----DTRRNVVSVFYGEVRRH-PVLAAPV-----FNA-----HVEDWPQHEEKIANFWRNALIRE-----R-----VYDGFPMREHLRSPD-----V-----RAEHFPVWGLFHAVLEREVTAEE-----QALQWGHADRIAGEFRTGIESIRQ
Sinorhizobium meliloti (Alphaproteobacteria) gi|15966331|NP_386684 155aa 2/2Hb3
>Simme12
-----VQSAAMREAEEMKALGI-----DEAFIGKLVDFYARVLAH-PELGPV-----FDA-----RLSGRWPEHMERKMSFWSAVAFRS-----GAYGGKPVQAHLG-----V-----ANMSPPELFPKWGLFAATLDDIAPNEE-----AKANFMATAERIAARSLTSLFLYFNP
Chlamydomonas reinhardtii 2/2Hbs
Chlamydomonas reinhardtii 160981
>Chlrei1
-----MAADTAPADSLSYRMGG-----EAAVEKAVDFYERIVAD-PQLAPF-----FANV-----DMKKQRKQVAFMITYVFGS-----GAYGRDLGASHRRL-----IREQGMNHFFDLVAHLDSTLQELGVAQ-----ELKAEAMAVASARPLIFGTGEAGAA
Chlamydomonas reinhardtii 160982
>Chlrei2
-----AAGVDAAPPSIFDRLGG-----EAAVEKAVDFYERIVAD-PQLAPF-----FEGV-----DMRTQRKQVAFMITYVFGA-----TGYTRDLAAHRRLL-----IRDKGLKEEHFDMVAGHLAGTLQLLIGGA-----DLVDEVIALVATKPIFIVER
Chlamydomonas reinhardtii 157690
>Chlrei3

-----GQSKSAATTRSTLHAKLGG-----AAVAATVDVYFKKLMND-PDLEFF-FRGMV-----DMVTLIAKQNRFLAYAFGAT-----THYHGKDIVMGAHL-----IINRGLNLTHFDKVGAGHFDVSLKEMGVGQ-----ELIDEAAGVLIGVRFLDFPERYKGVKD-----

Ciliate 2/2Hbs

Paramecium caudatum gi|121272|P15160 117aa
>Parcau -----SLFEQLGG-----QAAVQAVTAQFYANIQADATVATF-----FN-----GIDMPNQTKNTKTAFLCAALGGP-----NAWTGRNLKEVHANMG-----V-SNAQFTTVIGHLRSALTSAGVAAALV-----EQTVVAEETVRGDOVTV-----
Paramecium jenningsi gi|2147462|S60030 117aa
>Parjen -----MTLFEQLGG-----EAAVAVTTFQFYANIQADATVANF-----FN-----GINMDQTKNTKTAFLCAALGGP-----KAWGGRNLKEVHANMG-----V-TNAQFTTVIGHLRSALTSAGVAAALV-----EQTVVAEETVRGDOVTV-----
Paramecium multimicronucleatum gi|2147463|S60031 118aa
>Parmul -----MTLFEQLGG-----EAAVAVTTFQFYANIQADATVANF-----FN-----GINMPQTQTKTAFLCAALGGP-----NAWAGRNLKEVHANMG-----V-TNAQFTTVIGHLRSALTSAGVAAALV-----EQTVVAEETVRGDOVTV-----
Paramecium triaurelia gi|7428636|S60032 117aa
>Partri -----MTLFEQLGG-----EAAVAVTTFQFYANIQADATVANF-----FN-----GINMDQTKNTKTAFLCAALGGP-----KAWGGRNLKEVHANMG-----V-TNAQFTTVIGHLRSALTSAGVAAALV-----EQTVVAEETVRGDOVTV-----
Tetrahymena pyriformis gi|121274|P17724 121aa
>Tetpyr -----MNRKQPIYKELGG-----ENAMKAAVFLFYKVLADE-RVKHF-----FK-----NTMDHQTKQQTDFLTMLLGGP-----NHYKGNMTEAHKGMN-----L-QNLHFDIAIENLAATLKELGVT-----DAVINEAAKVIETHTRKDMLGK-----
Tetrahymena thermophila gi|417052|Q03459 121aa
>Tetthe -----MRKQPTVFEKGG-----QAAMHAAVFLFYKVLADD-RVKHY-----FK-----NTNMEHQAKQEDFLTMLLGGP-----NHYKGNMAEAHKGMN-----L-QNSHFDIAIENLAATLKELGVS-----DQIIEAAKVIETHTRKDCCLGK-----

Plant 2/2Hbs

Arabidopsis thaliana GLE3 gi|18418064|NP_567901.1 175aa
>Arabid -----DQAEAFIDESNLFDKGL-----QTFINLSTNFYTRYVDEE-EWFQSI-FS-----NSNKEDAIQNQYEFFVQRMGGP-----FLYSQRKGFALIGRHRFPF-----V-----THQAAERWLHMQNALDSDVD-----QDSKIKMKFFRHTAFFLVAGNELKNQ-----
Datisca glomerata 2/2Hb gi|31559437|CAD33536.1 169aa
>Datisc -----KQEDAFADINLNFQKLG-----QTFVNLSTNFYTRYVDEE-EWFRSI-FA-----SKKEDAIQNQYEFFVQRMGGP-----FLYSRRKGFALIGRHRFPF-----V-----THQAAERWLHMLALDSTPD-----IDVDSKVMINFRHTAFFLVAGDELKNQ-----
Glycine max 2/2Hb gi|44888958|AAS48191.1 (172aa,15-156)
>Glycin -----SIADAFADIANLNFHKLGL-----QTLVNLSTNFYTRYVDEE-QEWFRI-FA-----NSDKQNAIQNIEFLVQRMGGP-----TLYSQRKGFALIGRHRFPF-----L-----THEAANRWLHMQALDSTSA-----IDDDSKIKLINFRTAYFLVAGVEHKDQ-----
Hordeum vulgare 2/2Hb gi|14165165|AAK55410.1 171aa
>Hordeu -----AAADAFADIVNVFEALGG-----TPQPFVLDSTNFYTRYVEDE-EWFRFI-FS-----GSKKEDAIQNQYEFFVQRMGGP-----PLFSQRKGFALIGRHRFPF-----V-----THRAAERWLHMQALETTS-----INPDKTKMNFRTAYFLVAGNEMTRQ-----
Oryza sativa 2/2Hb gi|50725383|BAD32857.1 (172aa,15-158)
>Oryza -----AAGDAFADIDGQVFEALGG-----TPQPFVLDSTNFYTRYVEDE-EWFRQI-FA-----GSKKEDAIQNQYEFFVQRMGGP-----QLFSQRKGFALIGRHRFPF-----V-----THQAAERWLHMQALETTS-----IDAATKTKMNFRTAYFLVAGNEMTRQ-----
Triticum aestivum 2/2Hb gi|27085257|AAN85433.1 171aa
>Tritic -----AAADAFADIVNVFEALGG-----TPQPFVLDSTNFYTRYVEDE-EWFRFI-FS-----GSKKEDAIQNQYEFFVQRMGGP-----PLFSQRKGFALIGRHRFPF-----V-----THQAAERWLHMQALETTS-----INPDKTKMNFRTAYFLVAGNEMTRQ-----
Zea mays 2/2Hb gi|27085257|AAN85433.1 171aa
>Zeamay -----AAADAFADIVNVFEALGG-----TPQPFVLDSTNFYTRYVEDE-EWFRFI-FG-----GSKKEDAIQNQYEFFVQRMGGP-----PLFSQRKGFALIGRHRFPF-----V-----THRAAERWLHMQALETTS-----IDVDSKTKMNFRTAYFLVAGNEMTRQ-----

Thalassiosira pseudonana scaffold_18:64010:64489 160aa
>Thapse2 -----QSLIATTSITPILLERIGG-----SSGFIPLSTLFLYRNFVNDKAMPW-----FLGI-----PATSTKDEAIDNQFRFLVQTFGGG-----ELYRQKKGKYLTRVGRHANYQ-----I-----QIAAAERWVHMEGAIDEHEALVDDE-----ARECKLYFRYTFYIVVASEFMRDDQ-----

GCSs

Bacillus subtilis Firmicutes gi:37927254|NP388919 433aa (40)
>BacsubGCS -----VRLGDALYVLEQLQPLIQE-----NIVNIVDAFYKNDLSE-SLMDI-----INDHSS-----VDRLKQTLKRHIQEMFAGVID-----DEFIEKRNRIASIHRLIGL-----L-----PKWYMGAFQELLSMIDIYEAS-----ITNQELKKAIKATTKIINLEQQVLVE-----
Acidithiobacillus ferrooxidans Gammaproteobacteria TIGR243159|contig:10428 880aa (13)
>AciferGCS -----LGLQSDSFGVIDRYDALDK-----EASALAHAFYDYLISH-PATAAV-----FRDPSSA-----RLDALIQKQTEHAKGLVSRLD-----RPRESMRKIGALHHHLGIGPSW-I-----AGAYILYWRHWQKILQVDVVA-----DRGEEAAAVERDLRDLALFRLVGDLMVQLEGY-----
Agrobacterium tumefaciens Alphaproteobacteria gi|15888368|NP_354049 499aa (18)
>AgrtumGCS -----LGLGHGERQNLSDMKGVITC-----SLDASDRFYTKVRAV-PETAKF-----FSSEAH-----HHAQSMQLKHSRIASQTFNEDYTN-----AVTAIGRTHARLGLPERWYI-----GGYALMLDGIKAVIESMWP-----RGLLAKGSDRVDKLSATIKAAILLMDYISIVYL-----
Azotobacter vinelandii Gammaproteobacteria gi|23104391|ZP_00090857 472aa (23)
>AzovinGCS -----LLLGQFPAPVVAQIRELATT-----HQSELPGYFYQMLQDE-QAML-----FLTHE-----QVKSRLHGTLRQWVSVFSMSDDAALQ-----ALIAQKQIGIEHARIKIP IHLVL-----RGARHLRERFLVLLRESDI-----PRQRKLFQRLISETVDLAMEIMSRAFSDAY-----
Bacillus anthracis Firmicutes gi|30265443|BA5673 434aa (42)
>BacantGCS -----LHISKEDLQIVKVLQPFYIE-----EIDWITEKFSYNIQK-PNLITI-----IERYSS-----IPKIKQTLKTHIKELFSGDMH-----EDFIEQRVIAKRRHVQIGLHRKW-Y-----TAAYQELFRS IMKILKQV-----ESDFSYSINVKLFTLEQLVIAAYESKY-----
Bacillus cereus Firmicutes gi:30023454|NP_835085 434aa (42)
>BaccerGCS -----LHISKEDLQIVKVLQPFYIE-----EIDWITEKFSYNIQK-PNLITI-----IERYSS-----IPKIKQTLKTHIKELFSGDMH-----ENFIEQRVIAKRRHVQIGLHRKW-Y-----TAAYQELFRS IMKILKTS-----YSAEFSYSINVKLFTLEQLVIAAYESEY-----
Bacillus halodurans Firmicutes gi|15613068|NP_241371 441aa (44)
>BachalGCS -----IHLTDLDDLRKMKALQPLVE-----NMEVLADAFYSNIQK-PNLNEI-----IETHSS-----VERLKETLKHQILEMFGNEID-----QAFIQKRLQIAQAHVIRGLQTKW-Y-----VSAFQQLTDSLITQLLEQSSD-----YSAEIVLARSLLKLNLEQQVLVEAYENKR-----
Bacillus thuringiensis Firmicutes gi|49481265|YP_039413 433aa (41)
>BacthuGCS -----LHISKEDLQIVKVLQPFYIE-----EIDWITEKFSYNIQK-PNLITI-----IERYSS-----IPKIKQTLKTHIKELFSGDMH-----EDFIEQRVIAKRRHVQIGLHRKW-Y-----TAAYQELFRS IMKILKQIT-----TIDDFSYSINVKLFTLEQLVIAAYESEY-----
Bordetella bronchiseptica Betaproteobacteria gi|33600945|NP_888505 475aa (13)
>BorbroGCS -----DTCAHSPHEWAAARNVVTA-----NKAALADYFYECMLAD-PNAAF-----FLS-----DQLVKTKLHASMQDWLESVYAAAPTEEY-----ERTVAFQKRVGEVHARIDIPVHL-V-----MRGACALIRRICELLDORAS-----LSAAQAAATCRYVADVTMTAVEMMCHAYSVSHD-----
Bordetella pertussis Betaproteobacteria gi|33594381|NP_882025 475aa (69)
>BorperGCS -----DTCAHSPHEWAAARNVVTA-----NKAALADYFYECMLAD-PNAAF-----FLS-----DQLVKTKLHASMQDWLESVYAAAPTEEY-----ERTVAFQKRVGEVHARIDIPVHL-V-----TRGACALIRRICELLDORAS-----KDPKRAAATCRYVADVTMTAVEMMCHAYSVSHD-----
Burkholderia fungorum Betaproteobacteria gi|22984913|ZP_00030046 724aa (22)
>BurfunGCS -----HLYSQARASALTSLETVLRH-----NAVEIVKRFYDGLIRL-PKSKHT-----LAA-----LSEHELQHLKQIQNLALASPDLT-----AMDHRTMALRVGRHIAVIGLEWEDLI-----RSRGLLSAAIHDTLDTTVHGIAL-----AVLGRRLTQDLAWQTEAYQRLQTSRQDVLMRV-----
Carboxydothermus hydrogenoformans Firmicutes TIGR246194|CONTIG:4013 251aa (17)
>CarhydGCS -----LNLTAEDLQMAEFKELFIQ-----KAQEVNFKYQHLTKF-PYLQEL-----IKK-----HSTVEKLSKQAEYFISLTSEKID-----ADYIKNRLVAGKHMEDIAIYPNWYI-----GAYRLYEVVGVGLVARKYS-----PGTELYFKAQVAFYKRNIFDIQIATENYI-----
Caulobacter crescentus Alphaproteobacteria GI|16124683|NP_419247 537aa (17)
>CaucrelGCS -----MGIDDKARSALRDLRPIR-----AEIGKALDNFYKVRAT-PETKRF-----FSD-----DRHMNAASSRQAHWGVIAEGQFS-----DDYQAVRAIGQTHARIGLEPRWYI-----GGYAVGDHLVRAVIDSELK-----GLFMEKAKKAGEAVALMKAIFLDMDFAIISYLETLE-----

Caulobacter crescentus Alphaproteobacteria GI|16126556|NP_421120 555aa (55)
>Caucres2GCS
-----MRFDESRRAHLRAIKPVID-----AEIGALGFQYSQVRLP-PDTRVK---FRD-----DGHMAGAERAQAHHWRIAEEAGY-----ESYVRDVERIGRSHADADIAPQWYI-----GGYAVVVEVMRALVAKRAK-GLFNSAKSDAELADGLSALIKAAFLMDLMSVSTYIDVLL
Chromobacterium violaceum Betaproteobacteria gi|34495694|NP_899909 375aa (25)
>Chrvi01GCS
-----FALAPREMLLRAAGNLVSES-----HLSEELVTRFVYELQTS-PEIALI---IGDA-----DTLQLRSLAQRYYVVDLFSGIY-----DLEYVNRILRIGLVHVKRIGVEPK-L-----YLAADVSLKFLAEKLE-LIPDAEVRHLTLQALDKLMMFDVALVFETVYIRSLVAIE
Chromobacterium violaceum Betaproteobacteria gi|34496333|NP_900548 295aa (15)
>Chrvi02GCS
-----FAIQEDDLKRVRAAGEAVLP-----RLDEAMDRFYEWLP-PEYEG-L-FARP-----SALRNAREAAQAYRVSFFSGVV-----DAAYLAERVCAGETHARIGLP-----L-----SSYFAGVNYAFTLFCYGLKS-----GSRETASQTLSTAKLHMDTALVETYSRL
Desulfitobacterium hafniense Firmicutes gi|23118817|ZP_00102172 157aa (15)
>DeshafGCS
-----LKLEQDQLLLKKEFKPVMEQ-----DVDQIVDQFYAHTIKI-SQLNGI---IKEF-----SSVERLRGLQRNYLLSIFPDVI-----DEGYIMSRIRIGDVHVKRINLPFFVYL-----SSYQTFDDLPRIFAHYR-----KKPEQALRSLAVLRIFSFDDQVVMASYI
Desulfotalea psychrophila Deltaproteobacteria gi|51244053|YP_063937 363aa (24)
>DesspyGCS
-----LFFTDDEQVQLVSLKEVVSE-----NIEEIVFAFYRIVPFD-EMDGV---IGDA-----ETLRRLKKNYQSYIKTLFAGQY-----DEEYVHSRLRVGVVHVKRIG-----V-----EPKFYISAIHTLLTILREIIT-----KNSSNDCCQACVRLRAVEKIIMFDLSLTFDITYINSL
Erwinia carotovora Deltaproteobacteria gi|50120615|YP_049782 442aa
>ErwcarGCS
-----MIATTSQGSFNLRRLTAVQ-----KASDFADEFYIMLKQ-Q-EASL---FLSS-----CQVHDLRLHSGMSKIADILTNTGDS-----LADLHNQKIKIGIHARIGIPVD-L-----VERGARRLKHWHYEHIAQVAD-----DKALCFDAMRFASISMDIAEIMSKTYSQSHDLAA
Escherichia coli Gammaproteobacteria gi|15801648|NP_287665 460aa (13)
>Escco1GCS
-----GLVEQADPPIRAKAAEIAVA-----HANYLSIEFYRIVRID-PHAE-----FLSN-----EQVERQLKSAMERWIINVLSAQVDD-----VERLIQIQHTVAEVHARIGIPVE-I-----VEMGFRVLKILYFVIFHAKC-----EKARKLQVYHFSINSIDIAMEVMTRAFT
Exiguobacterium Firmicutes gi|45532973|ZP_00183969 430aa (37)
>Exigu01GCS
-----IDLTVEDLQIVRLRHVDVAE-----WMPQMDAFYAEVLVR-PELKQL---IERH-----STLERLKGTLAKHLIQMDFQV-----TPDYINVRKRIADHRVIRIGLQNKWYI-----AAFQKVLNLSRQIEDSTLPES-----EQVRVRSAGKFLNLEQQIVLWTEYEMVAERQTV
Exiguobacterium Firmicutes gi|46113120|ZP_00182337 425aa (30)
>Exigu02GCS
-----MGYTEHLQTLKAMAPVNS-----ILDEVLEQVLDHLLH-PEMVQI---AQTS-----STRELRKLVFADFVGSLLTGNM-----DDKFLAMRTRMGTKHNRNFPVTFWI-----ASYAFAFNTLLIPKIVEHFQHEPA-----QLTNAIHALNHNLDQAIVTSQVVDAR
Geobacter metallireducens Deltaproteobacteria gi|48844286|ZP_00298606 300aa (11)
>GeometGCS
-----YLFGEDEAETLKSLLSIAQA-----NRELMIEDFYDLLGI-PETAA---FLQ-----DDTVLQRLKLSHGWFVNLFRGVY-----DNQYHDLQRGVHVHVKIGLNAHF-V-----NAAMQKVRVFAVGMIRENFPDRD-----ERRKTEAVEKILDINLIMTASYIEELKKV
Geobacter sulfurreducens Deltaproteobacteria gi|39998400|NP_954351 300aa (11)
>GeosulGCS
-----YRFDEDAEILGSLFPLAET-----NKRERLADQFYDYLGI-PETAE---FLK-----EDLVLQKQLQTHQDWFVSLFAGSY-----DNRYIHNLKQIGHAHVAVRGLNAHY-V-----NVMNVVRAQFTLSIQHQLQSPSD-----RRQREAVEKILDINLIMSASYIEEMRRF
Halocarula marismortui Euryarcheota gi|55229828|AAV45247 497aa (44)
>HalmarGCS
-----TGFDGSDVDNLTAMADETNA-----RAEAVDDFYDHLQSF-D-ETVEI---FGRS-----TKSVQDLKNTQYQLYLRDLVAGTY-----DKQVFNRAIRGKIHDMLDLPKIKYL-----GAYSIFYEHLRTIVEDLQSG-----DAARDEALEEMQSRALSIVFKLLNLDQ
Halobacterium salinarum Euryarcheota gi|15790497|NP_280321 489aa (39)
>HalsalGCS
-----TGIDDDTMAALAEQFLFEA-----TADALVTDFYDHLSEYE-RTQDL---FAN-----STKTVEQLKETAQAEYLLGLGRGEY-----DTEYAAQRARIGIHVDLGLGPDVYL-----GAYTRYTGLDALLADDVAD-----RGEAAAAVDELVARFLPMLKLLTFDQ
Magnetococcus sp. MC-1 Unclassified proteobacteria gi|48832082|ZP_00289126507 (20)
>Magnet1GCS
-----VGFTEKDAIILKLRPVAAK-----HATAVNTFYTRLSGFA-HLEKI---IGG-----AGSSVERLKRQTEEYLVQLDGEY-----GRDYFVRWRWIKQIHNKIGLEPDWYL-----GGYSYLQRQLLPIILLDKITTD-----DVQRAMAAIDKILDLSELAIGSYIDAV
Magnetococcus sp. MC-1 Unclassified proteobacteria gi|22998615|ZP_00042662 467aa (14)
>Magnet2GCS
-----DIYLVDAEKVNFVIGDLIKD-----RLNQTVRFYIELLESARFF---LDS-----ALVKERLHGSITELWQLMFSHKD-----DDTQMFQAKGNVHARINIPMLHV-----EGMRILRREIICFLSKYSPGTE-----LLVNDLVVLGEVLDHNLSLINESYVRNN
Magnetospirillum magnetotacticum Alphaproteobacteria gi|23014982|ZP_00054774 443aa (11)
>Magspi1GCS
-----LQIDEDTKRALREFREVLRSR-----HIDGVLDTFYRHVSNN-PATAKM---FAN-----PDRMAHARSQKHHMSEVFLGQ-----FDDRYFAQVTEIGKVHQRIQLDPKWYT-----AGYCFVLMNVIVAVEGSLYSYD-----ELTQVLAAVNKAFLMDLATSIVYIETNY
Magnetospirillum magnetotacticum Alphaproteobacteria gi|23014248|ZP_00054075 732aa (35)
>Magspi2GCS
-----LRLLDDAISTVKSVMQVSES-----SLPGIADGFYAHLMQW-PALKAL---LGG-----GAKIGHKQEQAHWASLFSGRF-----DDDYFTRAVAAIHAHERIGLEVNWYL-----GGYCFVLEKMAELAKLRSEA-----FPQAGAVLRAAFDMLDIASTYIEHGE
Moorella thermoacetica Firmicutes gi|49235973|ZP_00330036 245aa (13)
>MootheGCS
-----LTLSEAEGLMEAEKEIFIK-----EADAVKTFYDHLQY-PYLENM---IKQH-----STLERLTQTKAYISLTPAPI-----DGEYISGRLRIGKHKQKIGLYPKWYL-----GAYRIYSEIRRVINWHYHADDP-----DLCLRLLEAFTRKIFDMLAIENYI
Novosphingobium aromaticivorans Alphaproteobacteria gi|48849793|ZP_00304036 481aa (17)
>NovaroGCS
-----FNIDHKDFERFPHIAKVLN-----YAPPALDKLYDQIATP-PETASF---FGS-----RQAMRHARDKQIEHWAGMFSGRA-----DRSYFESAERIGNVHARIGLEPGWYI-----GGYAMVLEQVINAMFSGIGGIL-----GAKRTARSVGLVKMALLDMEVALSTYFAEE
Rhodobacter sphaeroides Alphaproteobacteria gi|46192658|ZP_00207372 341aa
>RhosphGCS
-----MN-----EAVGRALDRFHERMQT-SAAG---FFAD-----ATHMDSAKSRQARHWARLASGEI-----DAAYVEAVRGRTHARIGLEPFRWYL-----GGYALILEEIVQTMPLMRAGRGF-FGRRRAAALHALGYIVKALLDMDGVYSTYDVAQ
Rhodospirillum rubrum Alphaproteobacteria gi|22966565|ZP_00014161 442aa (11)
>RhorubGCS
-----LKADARLTEDLNEIHPMVS-----MIDDLGFEFYDTSRST-PELYAM---FGS-----AQSVRARLARQRHVVVFLKGD-----WKAHASQAQRKGAHVDRGITPS-I-----YFAAYSHVLCGLTGRMAQNFDP-----PEELARGLRAAIRAVDIMLAVLDVYFAEERDRAS
Shigella flexneri Gammaproteobacteria gi|24113095|NP_707605 381aa (13)
>ShifleGCS
-----GLVEQADPPIRAKAAEIALA-----HANYLSIEFYRIVRID-PHAE-----FLS-----NEQVERQLKSAMERWIINVLSAQV-----DDVERLIQIQHTVAEVHARIGIPVE-I-----VEMGFRVLKILYFVIFDASL-----SAAQKLQVYHFSINSIDIAMEVMTRAFT
Silicibacter sp. TM104 Alphaproteobacteria gi|52011617|ZP_00338974 308aa (25)
>Silici1GCS
-----FOITPADQERVRSIAPLADH-----VGEETIADFYAHILRFE-DAQQ---FAD-----DTQIERVKRQKQKYFQELINAEI-----DESYAERKRIGGHERAGITPTLYV-----GSYAYLQRLSQSILENGKE-----DPHKFLGLVLSMMKIAHYDMALAEITYV
Silicibacter sp. TM104 Alphaproteobacteria gi|52008958|ZP_00336325 485aa (11)
>Silici2GCS
-----YDLGNAQALLQKRAKMLG-----LILPELDHYDVRVGRE-PEMAAF---FKT-----EAMMERAKGEQLQHSRSLSGDF-----GEDYIQSARNIGRVHTRIGLPS-FF-----NAGYAHANAHIQALLKRRSG-GLMRRATETHALLGVLRSAMALDQLIFDAHAEMQ
Silicibacter sp. TM104 Alphaproteobacteria gi|52008710|ZP_00336080 487aa (12)
>Silici3GCS
-----FCLGEEDRSSIVGMAPLVER-----HIDAVLDDFYDLCLSR-PETKGY---FPT-----EQIVAHAAKAAQRAHWKLFSGRF-----DDSYMSSADKVGVRHFEVDLPFLFL-----GGYATVGDRLKVVLTQKNG-----WRGTAKRMQARALQRLILDFCERVIAGYIDAQL
Sinorhizobium meliloti Alphaproteobacteria gi|15964389|NP_384742 533aa (23) *REMOVED INSERT YAERVKVLADTES
>Sime1GCS
-----AGLDEDACALLDRHQALSP-----RIELALRALSRLQAS-PDAARH---FDS-----RQIDRLHLQSGSHWNVLDARFDGLRMLGDP-----RWQIASHAVLHELILGAIEDAWP-----KSLISLGRARRERLDLV-----AALVRAAFVDEIAVSLRNLQRHQHQRQ
Thermosynechococcus elongatus Cyanobacteria gi|22299532|ref NP_682779 194aa (24)
>TheoloGCS
-----RVQLTDEKSLAEAPWKG-----EIAQPMADTFYDYLGRDE-EMNAI---INAT-----EGRIHLRHQFVDFVDFYEMFTGMS-WG---KAYARRWKIGLVHVRIG-----I-----GFQVVPAMAVVNAVQK-----LREANKSEALSALGKICMIDLAFIEQAY
Thermus thermophilus Deinococcus/Thermus gi|46199407|YP_005074 203aa (32)
>TheheGCS
-----RTGFTAEHAALLRELEGVMV-----PIAHEVALAFYDYLGRD-PELGAI---LHAE-----PGRVERLYRTFARWYGEVLSGVY-----DRAYARRRRRIGLVHARLG-----I-----GPRAMIPAMGIVQELSLEH-----MRMALRGHEVYSAVEAFKLVAMEVALIEESYL
Vibrio vulnificus Gammaproteobacteria gi|27366532|NP_762059 306aa (20)
>VibvulGCS
-----HDLTEADLALIRKFGQIMVP-----KLDEYVKHFYDNLNRT-PEYQY---F-----GDAQKLRQVDSQVRYWKTFFDARI-----DSAYLERRDVGEIHARVGLP-----L-----PTYFAGNMISWIFTKRMYD-----TVHGIAYSSLVTAFTKLLHLDITVDDYSRLI

Pgbs

Aeropyrum pernix Crenarcheota gi|14600601|NP_147118 195aa (30)
>AerperPgb

-----VMLGEKDVMLKACDVLK-----DQVDEILDWYGVASNE-HLIYV--FSNP-----DTGEPKIEYLERVRARFGAWILDTC--RDYNREWLDYQYEVGLRHRHSKKGVTDGV-----RTVPHIPRLRYLIAFIYIPITATI-KPFLAKKGGSPEDIEGMYNAWFKSVVLQVAIWSHPYTK-----
Chloroflexus aurantiacus Chloroflexi gi|22974473|ZP00020712 227aa (63)
>ChlaurPgb
-----VLMFAEDEQLRMAGEVLC-----DQVDAILDWYGFVASH-AHLVYV--FTGS-----D-GQPIADYLSRVQRFGQWILDTCR--RPYDQDLWLNQMEIALRHRHTKKNQTDGV-----QSVFMIPLRMYIAFIYIPITATI-REFLARKGHSAAEVDRMHQAWFKSIVLQVTLWSYPYTR-----
Rubrobacter xylanophilus Actinobacteria gi|46106825|ZP_00200180 196aa (32)
>RubxylPgb
-----VLFTEDEEYIQRKAGEVLE-----GRLDELDDWYGFVASH-SHLVYV--FSSP-----E-GEPIQEYLERVRERFKRWILDACR--RPYDQEWLDYQYEQEIALRHTREKKNRTDGV-----EAPPEVSLRYMISFIYIPITATI-RPFLEEGGRPAEDVEKMHQAWFKAVVLHVTLWSQPYAR-----
Methanosarcina acetivorans Euryarcheota gi|20091705|NF_617780 195aa (31)
>MetacePgb
-----VMFTAEEDEYIQRKAGEVLE-----DQVEEILDWYGFVASH-PHLLYV--FTSP-----D-GTFPNEEYLAARVRFKRWILDTCN--RSYDQAWLDYQYEQEIALRHRHTKKNQTDNV-----ESVFNIGYRYLVAFIYIPITATI-KPFLARKGHTPEEVEKMYQAWFKATTLQVALWSYPYVK-----
Methanosarcina barkeri Euryarcheota gi|48837815|ZP_000294773195 197aa (31)
>MetbarPgb
-----VMFTEDEEYIQRKAGEVLE-----DQVEEILDWYGFVASH-PHLLYV--FTSP-----D-GTFPNEEYLAARVRFKRWILDTCN--RNYDQAWLDYQYEQEIALRHRHTKKNQTDNV-----ESVFNINRYLVAFIYIPITATI-KPFLARKGHTSEVEKMHQAWFKATVLQVALWSYPYVK-----
Thermobifida fusca Actinobacteria gi|48836482|ZP_00293478 197aa (33)
>ThfusPgb
-----VMFTSADEEALRMAGDVLE-----DQVEDVLDWYGFVADH-PHLLAY--FSTP-----D-GHPIQEYLDVRERFRFGQWILDTCR--RPYNQEWLDYQYEQEIALRHTPEKKNVTDNA-----NSVDNIPRLRYVIAFIYIPVTATI-RPFLAKKHSADQVEAMYQAWFKSVTMQIALWSQPYTR-----