

alpha_Thermobifida : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLESDFLNAGQGRPAINVGISVSRVGGAAQTKRAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Nocardioopsis : DVFYLHSRLLERC AKLSDEMGAGSMTALPIIETKAGDVSAIYIPTNVISITDGGVFLNSDLFNAGQGRPAIDVGVSVSRVGGAAQTKRATKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Kitasatospora : DVFYLHSRLLERC AKLINDALGGGSMGTGLPIIETKANDVSAYIPTNVISITDGGVFLESDFLNAGIRPAVNVGISVSRVGGSAQIKAMRSVAGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

subf1_Streptomyces : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIVETKANDVSAYIPTNVISITDGGVFLESDFLNAGQGRPALNVGISVSRVGGSAQHKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Bifidobacterium : DVFYLHSRLLERC AKLSDMGAGSMTGLPIVETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVNVGISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Gardnerella : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQKALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Scardovia : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Parascardovia : DVFYLHSRLLERC AKLSDMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Brevibacterium : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Actinomyces : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Cellvibrio : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIVETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Cellularmonas : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIVETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Isopteribacter : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIVETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Sanguibacter : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIVETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Jonesia : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Clavibacter : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Leifsonia : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Aeromicrobium : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Janibacter : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNAGQGRPAVDVGVISVSRVGGAAQTKRALKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Kytococcus : DVFYLHSRLLERC AKLSDMGAGSMTGLPIIETKAGDISAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Frankia : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 450

alpha_Pseudonocardia : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 449

alpha_Saccharopolyspora : DVFYLHSRLLERC AKLSEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 449

alpha_Mycobacterium : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 449

alpha_Rhodococcus : DVFYLHSRLLERC AKLSDEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 449

alpha_Nocardia : DVFYLHSRLLERC AKLSEMGAGSMTGLPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 449

alpha_Corynebacterium : DVFYLHSRLLERC AKLSDMGAGSMTALPIIETKANDVSAYIPTNVISITDGGVFLNSDLFNSGVRPAINVGISVSRVGGAAQIKAMKRVSGRLRLDLACFRLEAFAAFASDLDLAAASKACITRGCARLMELLKQCQYCFPMEEVSVW : 449

alpha_Thermobifida : AGTTGHLDDVFEVDIRRESEFLAYLRREHSGKLDVIRETDFGDDTAEALTDAIKEFKFTQTS DGTILGTEAPEALDESEVGGQETIKVAKTSGK----- : 547

alpha_Nocardioopsis : AGTTGKVDVFEVDIRREEDFLAYLRREHSGKLDVIRETDFGSEETQTLTAEIKFKQSFQTSAGTLLGTEAPEALDESEVGGQETIKVAKGKK----- : 546

alpha_Kitasatospora : AGTTGQLDVEVADIRREEREFLDNVRLEHKGILLAGIVETGFLLEQGTIDALTAITSFQGFTTADGKLLSEQA----- : 524

subf1_Streptomyces : AGTTGKMDVFEVADIRREKELLEYLHRQEQGLMSTIREGGKMSDDTLQAVAEIAAFKQFETS DKGKLLGEDAPSAAK----- : 529

alpha_Bifidobacterium : AGTHGKMDVFEVADIRREKAMLDYLDH-NTDILKTIREDTDFADTEALDKAVEAFRETFVTSAGKPLVEKK--PNVKNATPVEQEKIVAGEK----- : 542

alpha_Gardnerella : AGTHGKLDVFEVADIRRESELLDYLDK-GTDILQVIRDTDFTKETEAKLDAIDDFRRTFKTSAGKPLIVKDSLPAPENPAVEQEQLVAKPKADSREPEGK----- : 553

alpha_Scardovia : TGTHGWLDDVFEVADIRRESEGLLDYVDH-NTDILSLVIRETDFADTEAKLEAVKAFRRVYVVKDGTPLVNAKEGKEAPTKEVQETIATRRRSERNQSGSAQDGGQTNQADQAGRKAE : 567

alpha_Parascardovia : TGTHGKLDVFEVADIRRESEGLLDYVDH-NTDILLDVIRHTGDFATAETERKLEQAVDAFRVYVVKDGTPLVNVKAEAAKLTKEVQEQEVI SARPSGDRSGNSGPEKAE----- : 556

alpha_Brevibacterium : AGTHGYLDVFEVADIRRESEGLLDYVDH-NTDILSLVIRETDFADTEAKLEAVKAFRRVYVVKDGTPLVNVKAEAAKLTKEVQEQEVI SARPSGDRSGNSGPEKAE----- : 544

alpha_Actinomyces : AGTKGYLDVFEVADIRRESEAFLDHLRR-NTDILDSIESTGQLTDETEALVEAVEAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 543

alpha_Cellvibrio : AGTKGHLDDVFEVADIRRESEAFLDHLRR-NTDVLTTIAETGKLDDATEQSLAGAVSDFRNGFLKFDGTPLVGG-GDEDAEVEVEQEQIVRQKKA----- : 542

alpha_Cellularmonas : AGTKGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIAETGKLDDEQTEKALGDAIDDFRNGFLKFDGSPVGT-ADDEDVDEVEQEQIVRQKKA----- : 542

alpha_Isopteribacter : AGTKGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIAETGKLEDDTEALAAAVDDFRKGFVKSGGAPLVG--GAVEGEADVQEQLVVRQKKA----- : 541

alpha_Sanguibacter : AGTKGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIKSSGKLEDDTEALAAAVDDFRKGFVKSGGAPLVG--GAVEGEADVQEQLVVRQKKA----- : 543

alpha_Jonesia : AGTHGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIAQTNDFNKDTESALGDAIDAFRNQFIKGDGEALVDAEAEAEAEAEVEQEIVRSKKA----- : 543

alpha_Clavibacter : AGTKGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIKKKNVLTDDIVDAMKAVDQFKLEFQTGEGKPLASVSGSEKFEPAKAEDVNVQEIVKQKR----- : 545

alpha_Leifsonia : AGINGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 545

alpha_Aeromicrobium : AASAGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 546

alpha_Janibacter : AGTTGQLDVEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 545

alpha_Kytococcus : AGTNHGLDDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 549

alpha_Frankia : AGTTGHLDDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 550

alpha_Pseudonocardia : LGTSGKLDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 545

alpha_Saccharopolyspora : IATKGHLDDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 548

alpha_Mycobacterium : LGTGHLDDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 549

alpha_Rhodococcus : LAGEGVLDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 547

alpha_Nocardia : LVDAGYLDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 546

alpha_Corynebacterium : LASNGHLDDVFEVADIRRESEAFLDHLRR-NTDVLSTIREDTNVLDDETEAKLEAVKAFRRTFASGEQMLGAQVAEPPEEPTAERTTEQLVVKRG----- : 549

Fig. S5. Comparison of amino acid sequences of α -subunits of F_1 -part of F_0F_1 ATPase operon in various actinobacteria genera. Conserved residues are shown in black.

Acidothermus : ----MTATIDNTQSQADRTGGVGRVARVIGPVDEVEBAADLPEIYNALTVDFATASEQVEGETKRTLTEVAQHIGDNMVRATLSMQPTDGLVVRGALVDTGAPISVPPGCDVTKGFVFNVIQGLTLDVPR---IEVTRW-IHRPAPA : 141
Frankia : ----MTVTTSSSTAPADGRVPGIGRVARVIGPVDEVEBAPDLEIY-----YALHVERTLGDETAFLTTEVAQHIGDNVVRATLSMQPTDGLVVRGALVDTGAPISVPPGCDATKGFVFNVIQGLRPLDVE---VDAETT-WIHRSAFP : 134
Thermomonospora : ----MTAQVETATATGRVARIIGPVDEVEBPADAMEIYN-----ALHVDVTLGEEETKLTLEVAQHIGDNMVRATLSMQPTDGLVVRGATVDTGAPISVPPGCDVTKGFVFNVIQGLTLDVPTS-SLEINER-WSIHRKAPD : 129
Streptosporangium : ----MTAQVTETGVRVARVIGPVDEVEBPVEAMPDIYN-----ALTVDVTLGEEETKLTLEVAQHIGDNVVRATLSMQPTDGLVVRGAAVDTSGAASVPPGCDVTKGFVFNVIQGLSDVPTA-SLKIEER-WIHRPSPA : 128
Thermobifida : ----MTATAEGTAAPTVTGRIARVIGPVDEVEBPVGLSPLPIYN-----ALKTEVLGGETRTITTEVAQHIGDNVVRATLSMQPTDGLVVRGAEVDTGAPISVPPGCDVTKGFVFNVIQGLCEPDIPKS-ELQVKEY-WIHRPAPA : 133
Saccharopolyspora : ----MTAEERDQKQVDFLYN-----ALTVEITPAEGMAKLTLEVAQHIGDSVVRATLSMQPTDGLVVRGAVDTSGAGISVPPGCDVTKGFVFNVIQGLCHLDEP---GYGSDAERW-IHRKAFS : 107
Mycobacterium : ----MTAAEQKEKTKTDNVGRVVRVIGPVDEVEBPGRGSVPELFN-----ALHAEISYKDLAKLTLEVAQHIGDSVVRATLSMQPTDGLVVRGAVDTGASISVPPGCEGVKGFVFNVIQGLCLDDP---GYKDFEKW-IHRKAPA : 133
Nocardia : ----MTAAVTQNTSRTGANTGRVVRVIGPVDEVEBPGRSIPDLFN-----ALHAEITLTSVAKLTLEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLCDLDP---GLTRDGEQW-IHRKAPA : 134
Rhodococcus : ----MTAAVTQINANGADTTSRVRVIGPVDEVEBPGRHVPDLFN-----ALHSEVTLSPVAKLTLEVAQHIGDNVVRATLSMQPTDGLVVRGAAVDTGKPIISVPPGCDVTKGFVFNVIQGLCDLDP---GLTRDGEQW-IHRKAPA : 134
Corynebacterium : ----MTTALQEQNTQSSATAGRVVRVIGPVDEVEBPGRGLPALYN-----ALTVEVTLAVAKTLEVAQHIGDNVVRATLSMQPTDGLVVRGAAVDTGKPIISVPPGCDVTKGFVFNVIQGLCDLDP---GLTRDGEQW-IHRKAPA : 133
Pseudonocardia : ----MTATADTATTTGRVVRVIGPVDEVEBPGRNVPDLFN-----ALTVEVFDLAKLTLEVAQHIGDNVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLCDLDP---DLITGELW-IHRKAPA : 128
Salinispora : ----MTVSATADGPAKTKTATGRVVRVIGPVDEVEBPGRDAMPDLFN-----ALHVDVTLGAGEKLTLEVAQHIGDNVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLCECLNLEPG-ETLSPDDHW-IHRKAPA : 136
Geodermatophilus : ----MTVTEDRPTTQTGRVVRVIGPVDEVEBPGRDAMPDLFN-----ALEVEVTLADLGLKLTLEVAQHIGDNVVRATLSMQPTDGLVVRGAEVDTGASISVPPGCDVTKGFVFNVIQGLCLDTP---GHGNDALRW-IHRHAPR : 130
Kitasatospora : ----MTTVEPTGAGLATGRVARVIGPVDEVEBPVDAIPDMFN-ALHVEVDNPDGS-----GKTLTTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGSAISVPPGCDVTKGFVFNVIQGLVNDKAEFQVQVW-IHRKAPN : 136
Streptomyces : ----MTTVEPATATGRVARVIGPVDEVEBPVDAMEIYN-ALTVQVADPAQDG-----AVKLTLEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLLNVDQYTT---ERW-IHRQAPA : 130
Catenulispora : ----MTVTTEATRAKAVGRVARIIGPVDEVEBPVDMGMDLLN-ALKIDYP-----FLG-----ETRTTLEVAQHIGDGVVRATLSMQPTDGLVVRGAEVDTGKPIISVPPGCDITLGRVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 131
Kytococcus : ----MNATIAAERSDDTQGGVGRGLARIIGPVDEVEBPDAVPSIYN-LLKVDVLDAGETKTLN-----TEVAQHIGDNVVRATLSMQPTDGLVVRGAEVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRNAPD : 138
Intrasporangium : ----MTATVSDNVGAAQSGAGVGRISRIIGPVDEVEBPDSAMPQYIN-LLTTEVLSGETKTLN-----TEVAQHIGDNVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 140
Nocardioideaceae : ----MTAQVDEKTTGRIARVIGPVDEVEBPVDMAMEIYN-KLEVEVTVNGETSFLP-----TEVAQHIGDGVVRATLSMQPTDGLVVRGAEVDTGKPIISVPPGCDITLGRVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 129
Nocardioides : ----MTATIEETQETGSAGVRIARVIGPVDEVEBPVDSMPEIYN-KLECELTLEGEAKILS-----TEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDATLGRVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 135
Isopterocola : ----MTATVSDNVAAGAPTEPGRVVRVIGPVDEVEBPEDAIPIYIN-ALTVDIDLSAQGEGEK-----VFTLTTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDITLGRVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 143
Xylanimonas : ----MTATTVDTPEVTRNGPVGRVVRVIGPVDEVEBPEDAIPIYIN-ALTVIQLSAQGEK-----VFTLTTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDITLGRVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 142
Cellvibrio : ----MTATVDETAAGTAPGVGRVVRVIGPVDEVEBPADQIPIYIN-ALTVDIDLSAQGEGEK-----VFTLTTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 144
Leifsonia : ----MTATAEAQASTAPAGVGRVVRVIGPVDEVEBPEDAIPIYIN-ALTKTTIPIGR-----STETITTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 137
Clavibacter : ----MTDTATREAVSDSVAGVGRVVRVIGPVDEVEBPVDSIPPIYIN-ALTKTTIPIGR-----STETITTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDITLGRVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 136
Actinomyces : ----MTDTHAIEGRVVRVIGPVDEVEBPDRIPPIYIN-ALTVENLAGQEGES--TFTMTTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 133
Bifidobacterium : ----MAENQTAEBATEPIAGRVTRIQGSSVDEVEBPVGLPIYIN-ALTVELSDMGTKEEGEGSHTIPIVEQHLQDSTIRAVALKPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 140
Gardnerella : --MAENQTTAPAEQEVDPAGRVTRVQGSVDEVEBPVGLPIYIN-ALTKVDIATVNGTEG--DTVHEITTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 144
Scardovia : --MENASATLKNEQLDESQAVKRVTRVQGSVDEVEBPVGLPIYIN-ALTVIPIAVGTVEG--ESSATITTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 144
Parascardovia : MAQEYASTSLQAEQLDEAEAVKRVTRVQGSVDEVEBPVGLPIYIN-ALTVDIPIAVGSVEG--ESSATITTEVAQHIGDGVVRATLSMQPTDGLVVRGAVDTGKPIISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 146
Brevibacterium : ----MSTATDTPQVQGTGVRISRVIGPVDEVEBPDAVPAIYN-ALLTTVELSEG-----TRKITREVELQENGLVIRAVSMQPTDGLVVRGAEVDTGAPISVPPGCDVTKGFVFNVIQGLNLDKKEGFI-AEERW-IHRKAPA : 134

Acidothermus : FDQLEKATMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 291
Frankia : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 284
Thermomonospora : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 279
Streptosporangium : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 278
Thermobifida : FDQLEKATMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 283
Saccharopolyspora : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 257
Mycobacterium : FDQLEKATMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 283
Nocardia : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 284
Rhodococcus : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 284
Corynebacterium : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 283
Pseudonocardia : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 278
Salinispora : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 286
Geodermatophilus : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 280
Kitasatospora : FSELESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 286
Streptomyces : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 280
Catenulispora : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 281
Kytococcus : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 288
Intrasporangium : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 290
Nocardioideaceae : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 279
Nocardioides : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 285
Isopterocola : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 293
Xylanimonas : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 292
Cellvibrio : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 294
Leifsonia : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 287
Clavibacter : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 286
Actinomyces : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 283
Bifidobacterium : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 290
Gardnerella : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 294
Scardovia : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 294
Parascardovia : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 296
Brevibacterium : FDQLESKTMELFPGIKVIDLLTPYVGGKIGLFGGAGVGKTVLIQEMIRVAKNFGGVSFVAGVGERREGNDLIFEMTESGVINDTVLVFGQMDEPGRRLRVLSALTMAEYFRDVQKQVLLFIDNIFRHTQAGSEVSTLLGRMPSA : 284

Acidothermus : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFGEHHRVFNQVKLLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFYAEFTGQP : 441
Frankia : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVSPLDSTSRILDARVGGHHYDTPAREVQRLLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQPFVFAEFTGIP : 434
Thermomonospora : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISHPMFAEFTGQP : 429
Streptosporangium : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPLILGEEHHRVAVQETKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISHPMFAEFTGQP : 428
Thermobifida : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFYAEFTGTP : 433
Saccharopolyspora : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFYAEFTGQE : 407
Mycobacterium : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGQP : 433
Nocardia : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILEASTVGERHFAVANEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGQV : 434
Rhodococcus : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILEPAGHHRVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGEP : 434
Corynebacterium : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILEPAGHHRVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGLP : 433
Pseudonocardia : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGQP : 428
Salinispora : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILEPAGHHRVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGQM : 436
Geodermatophilus : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNMFAEFTGQP : 430
Kitasatospora : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVD : 436
Streptomyces : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGLD : 430
Catenulispora : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGID : 431
Kytococcus : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGIE : 438
Intrasporangium : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGIE : 440
Nocardioidaceae : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGIE : 429
Nocardioides : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGIE : 435
Isoperitcola : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 443
Xylanimonas : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 442
Cellvibrio : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVS : 444
Leifsonia : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVE : 437
Clavibacter : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVE : 436
Actinomyces : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 433
Bifidobacterium : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 440
Gardnerella : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 444
Scardovia : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 444
Parascardovia : VGYQPHLADENGLQERITSTRGHSITSLQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVP : 446
Brevibacterium : VGYQPHLADENGLQERITSTRGHSITSMQAIYVPADDTDPAPATTHAHLDAATVLSREISEKGIYPAVDPLDSTSRILDPQFVGGHHYVAVQEVKRLQRYKLLCDIIAALGIDEI SEBDRVIVGRARRIERFISQNTYFAKFTGVE : 434

Acidothermus : GSFVPLDDEITDAARRICEGEIDHLPEQAFMCGGDDVQAKAKRIALERS : 490
Frankia : GKFPVVAETIDSEKRTTQCEFDHLPEQAFMCGGEDAQKNAENI : 479
Thermomonospora : GVFVLDDEITISSFKAVVEGKYDHPVEQAFMCGGEDVERRAKELAS : 476
Streptosporangium : GEFVPLDDEITIASFKICACAGEYDHLPEQAFMVGCEQAIAKAKGIAR : 475
Thermobifida : GVFVPLEDEITIASFKACIDGEYDHLPEQAFMVGCEQEMAVEKAKKIQS : 480
Saccharopolyspora : GSFVPLKBTIEAFDKICKGDFDHPVEQAFMSTIGGLDLEKQAYKRLTEK : 455
Mycobacterium : GSTVPLKBTIEAFDKICKGDFDHLPEQAFMVGCEFLIGGEDLQRKAESIGAKMEDTSGDGAPAQSDSKSDSGDDADKDA : 509
Nocardia : GSVVPLECTIDDFDRVCKGEFDFHPVEQAFMVGCEGDDVEAAAKKIAGK : 482
Rhodococcus : GSVVPLRDTIEAFDRVCKGEFDFHLPEQAFMVGCEGDDVEAAAKKIAGK : 482
Corynebacterium : GSVVPLADTIDAFERICNGEFDFHYPEQAFMVGCEGDDVEAAAKKIAGK : 482
Pseudonocardia : GSTVPLKBTIEAFDKICKGDFDHPVEQAFMVGCEGDDLEKAKELMAEG : 475
Salinispora : GSTVPIKBTIEAFKKISEGEYDHPVEQAFMVGCEGDDLEKAKELMAEG : 485
Geodermatophilus : GSFVPSSETIQAFKATDCEYDHPVEQAFMVGCEGDDLEKAKELMAEG : 478
Kitasatospora : GSTVPLSETIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 484
Streptomyces : GSTVPLDDEITIAAFNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 478
Catenulispora : GSFVPLDDEITIAAFNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 479
Kytococcus : GSTVPLSETIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 486
Intrasporangium : GSTVPLVDTIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 489
Nocardioidaceae : GSTVPSKBTIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 478
Nocardioides : GSTVPSSETIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 484
Isoperitcola : GSTVPLSETIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 494
Xylanimonas : GSTVPLTBTIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 493
Cellvibrio : GSTVPSSETIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 495
Leifsonia : GSTVPLKBTIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 487
Clavibacter : GSTVPLKBTIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 486
Actinomyces : GSTVPLSETIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 482
Bifidobacterium : GSVVPADEITIEAFTRICDGEYDHPVEQAFMVGCEGDDLEKAKELMAEG : 491
Gardnerella : GSVVPADEITIEAFTRICDGEYDHPVEQAFMVGCEGDDLEKAKELMAEG : 495
Scardovia : GSVVPADEITIEAFTRICDGEYDHPVEQAFMVGCEGDDLEKAKELMAEG : 495
Parascardovia : GSVVPADEITIEAFTRICDGEYDHPVEQAFMVGCEGDDLEKAKELMAEG : 497
Brevibacterium : GSTVSIKBTIEAFKNAADCKYDHPVEQAFMVGCEGDDLEKAKELMAEG : 483

Fig. S6. Comparison of amino acid sequences of b-subunits of F₁-part of F₀F₁ ATPase operon in various actinobacteria genera. Conserved residues are shown in black.

delta_Clavibacter : ----- : -
delta_Leifsonia : ----- : -
delta_Brevibacterium : ----- : -
delta_Geodermatophil : ----- : -
delta_Modestobacter : ----- : -
delta_Nocardia : ----- : -
delta_Rhodococcus : ----- : -
delta_Corynebacteriu : ----- : -
delta_Saccharopolysp : ----- : -
delta_Pseudonocardia : ----- : -
delta_Mycobacterium : MSTFIGQLVGFAAIVLVVRYVPPVRRILMAARQATVRRQQLKDAASDRLTESTTAHSKAVEDAKAESKRIVVEEAESDSKRITQLSAQAGVEAERIKSQGGQRVDLLRQLSRQLRLELGHEAVRQAGELVRNFVADSQRSATVDRFLDDLDAMAPA : 160
delta_Kitasatospora : ----- : -
subi' Streptomyces : ----- : -
delta_Catenulispora : ----- : -
delta_Acidothermus : ----- : -
delta_Frankia : ----- : -
delta_Thermobispora : ----- : -
delta_Streptosporang : ----- : -
delta_Thermomonospor : ----- : -
delta_Thermobifida : ----- : -
delta_Actinomyces : ----- : -
delta_Bifidobacteriu : ----- : -
delta_Parascardovia : ----- : -

delta_Clavibacter : -----MGSASRASLDSARRVLAELG-----GVDLSTAGQLLGAGRAIGGSTHLSAADTGIAPVVKHSIVDRVFGATVQEPTLRVLRVAVDGRSSSHDELAGIEELGIRAVAI SAPEG---TPVSESEFTFGRA : 123
delta_Leifsonia : -----MGSATREARARSVSALAGLGS-----KADLATAEDLFAAGRVVADSVQFRAVSDPAADRSGRDVLVKRVFG-ALSAPAVELLVGIAGERSSGQDDVLDLAEELGIRSIASAAPRT---VDIPAEFLAFGGA : 123
delta_Brevibacterium : -----MLQSSRLSIQAVLEAANAELISR-----GDAREIGTGELAIIVAVLLENVTRKAPADSSESAEKKQHLLRTEFSTRTSETVLRLESELAVSHRARTQDVTSLVAVGVTIAAASQASQQLGQVEEVEFRFARL : 128
delta_Geodermatophil : -----MDASSREALAVRERLELTPASGLLERARDRLTGQERAATDEELVALAEELFAVAHLLDQVSRRAISDPGSGPADRAGVARRLLSGRVSGATLDLVETAARQRWSRPLDVEATETLATEAALDAADARGELADVEEELFRFGRI : 149
delta_Modestobacter : -----MHASSRAAMEQSRAALTAQTG-----GARSRTGEALLVLADELFAVAHLLDQQLSERRAISDSVSRPDRAGLAQRIFGGKVGGEATLDVVQTVARQRGSRPLDVEATETLATEAALDAADARGELADVEEELFRFGRI : 135
delta_Nocardia : -----MYAASREASRSREALRAALT-----GSDS----VAATTGSELFAVVAVLDSQRSRVAVADVSVPGSARAEELSERVFGGKVS PATLAVLT TAVAQDTSRTADVDTLELLGQEAALLESAADSGRLDAVEEELFRLGRI : 130
delta_Rhodococcus : -----MYAASREALTQTRALSSALG-----SVSAGAATAAAAQIGAEELFSVVEILDEQRTSRASISDTSTPGNVREGLAEQVFGGKVS AETLAVLKAAVGQDNRSVTSDLLNSLVLVGRESLLKAAADQQLDAVEEELFRLGRI : 135
delta_Corynebacteriu : -----MHAASRESLAALSQRLDAAIG-----GDNVA--VAQAAQTGSELF DIVEVLDSDRGRVAVADTSATAEQRSGLVRSLFAGKVSETTLNLVVDAAQVWSTPREVREGVLVGRALLRS AEGGQLETVESEELFQLGHI : 133
delta_Saccharopolysp : -----MNAASREALAATELQLLQATD-----GAQAA---EITGLADELFGVAALLGRESTERRADADASTDPRSREDLARGLLADKLGARALPVAVEAVRARRSSPTDLDGLERLARTALLVQAERAGRLDAVEEELFRLGRI : 131
delta_Pseudonocardia : -----MAASTETQLQSASRESLADAVRRLDAVVD-----SSAGADLAILGDLLFAVERLLESEPAERRHADPAVAPEARTELARRLLEGGKIGAAALDLVSTLVSARRSRSIDLLDALEALARRAVLVAEKDGSLEDEVEELFRFGRI : 139
delta_Mycobacterium : -----SADVQYPLMTKMRSSSRVALTNLSEWFSTITK-----DLLDNKGLSTLSEGLVSVVAQMLDREIVTRYITVPAEDAEBETRLIERLLAGQVGDATLDVLRSAVSESRASSDLLIDALEHVSRAQALLEVAERDKDVEEELFRFGRI : 302
delta_Kitasatospora : -----MIGASREALAAGRENLESITDNNTS-----VDSAKLAEELAAVTALLDREVSRRVITDPAQAGEAKAEELAGRLLAGQVGGETADLVGMVRSRGRSRSDVDAIEELASTAELIAAQRSGALDDVEEELFRFGRI : 130
subi' Streptomyces : -----MNGASREALAARERLDAITDNNTS-----VDAAKLAEELAAVTGLLDREVSRRVITDPAQAGEAKAEELAGRLLAGQVGGETADLVGMVRSRGRSRSDVDAIEELASTAELIAAQRSGALDDVEEELFRFGRI : 130
delta_Catenulispora : -----MQGASREALAAGADRLDALTSAPG-----ADIAAVADDLSAVAVAFKGDASRRRITDPAQAGEAKAEELAGRLLAGQVGGETADLVGMVRSRGRSRSDVDAIEELASTAELIAAQRSGALDDVEEELFRFGRI : 130
delta_Acidothermus : -----MQGASRESLAAAWREAEELLVRRPR-----GAQPPEEVG-----TQLFSVTAILDEHPARRASDPDPAVEPGRKVS LADRLFGERIGETARRIVATVVRARRSRVRDSDALETLGV LALLVAERSRAVDDEEELFRFGRI : 133
delta_Frankia : -----MDGSSRRSLAVARARLDELTA LPPP-----GTTTPRPAANLARLADDDGVDLLDRELVRRAITDPGVPGSARSELARLFGSKISPTALEIVQAVTGRMARPLDQQALAE LAVEVLLAQQRNNVLDDEEELFRFGRI : 139
delta_Thermobispora : -----MRGLSKAAMAQVEARFNVLAASAD-----LGSLAEELFAIAGLFDREHGRRRNSDPARPAETRAEILRSLLNGKVS DTAIEVAVAAVEAKRSRAGDTPDALERLGVIAAAAEEAESFGEIDDEEELFRFGRI : 128
delta_Streptosporang : -----MLRGLSRASLAEVEERFNAVAGSAD-----LGSLADELFAVADLFDREHGRRRNSDPARPAEQQAQAVRVLLEGKVS GALETVIAAVSAKARRSGDADVLERLGVIAAAAEEAASRLDDVEEELFRFGRI : 129
delta_Thermomonospor : -----MSAAVIGAVARASLAEARERLETVLATAD-----LAELGGELFAVLHLVDREHGRRAISDPARPAEQKADLVAGLLDGKVSAAAASSVVQDVVRLRTRPSEADALET LAVTTEAARAEDGVLDDEEELFRFGRI : 133
delta_Thermobifida : -----MQGVSRSTLTVIRRLDDILPSAN-----TATLGHELFEVVALLDQHSERRRWDAPAGSPDSRSELVNSLLETQKVS PATLLVSDVVVRAQMSRPRDLDAVEQAAVLATVAEHASARELEGEVEEELFRFGRI : 128
delta_Actinomyces : -----MRAASEKSLKAASAVLNRLSETD-----ADVMTVAENLFGSLSDLSQDNSSVRNATDTPGRSSDRRTLRNLLGDNVLPQTVSVVEELASGNSSPEDNEAFETLGTAEVFAAEKAGK LADVEEELFRVNTF : 130
delta_Bifidobacteriu : -----MRGEASRIADRESRDSLAPKLRDTH-----EDAWRIGNELFTITSALDNNIQERAITDPSRPTAKVVVFKEMVGDQVHPMTTEIMTDLVSRRRSRARDANAVEDFGVDAMMYADATDSTLHVSIETSR LHSS : 131
delta_Parascardovia : -----MHGETSLASEQSVRRYFGRSLKEDG-----LSAGRISQELFGFSAVLDSNRKLERAITDPSRPAEQKQALVSTLLEGKVPRTLELRLALVACQSRVTDLSNGVEDLAIDAVLYQADAEKGIRVAVELAKIHST : 131

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delta_Clavibacter : VSTDGELAFGDKLGDPEAKSTLVHRLLDG----RASEQTVVVEQLVQVQPRGRRIQELVRHAATLVADQAGLTIATVSVASETSPECSERTAQALSRRYSRRTEINQVVDRIIVGGLRVGIGDDVIDGSAVTRINDLRLQFA----- : 263
delta_Leifsonia : VTSDAEDELALRSKLADPSAKAALVERLLVGG----KAAGQTVATIRQLVLQVPRGRSVRQALREAAIRIVAAQDQGTIATVVTATLPAQAQERLRASLAAKYG-DLKNQVVDPSILGGMRVGIGGDDVIDGSAVTRINDLRLQFA----- : 263
delta_Brevibacterium : CESEHDEARALESDAS-ASAKRALIADLLAG----KAQADTITLIEQAVLFPRLGRVATALDQYSDILAAARQQRSVADVTVAKELSEACTQKRTAALSASYGRDLYLVNVQVDPVAVVGGVVRVQVGDDEMSSTVADRIAEVQRRLAS----- : 268
delta_Geodermatophil : VGGDAEFSRILSDRTAPVTGKAALLDGLLAG----RVSPITAMILRNHLTGRTIGHAENVVERLSEAASTRRGQSVARVTTAVELTDAQERRLAELLGRLYHRETCIQVVVDPGVLGGLVTRVWGDEVIDGSAHRIEAGRRLVG----- : 290
delta_Modestobacter : VAGDDTARILGNRSAPREGKSALLDRLLSG----KVSPVTERIVRNALTSSSHVSAENEIERLSTAAARRRGQSVAVVSAVELTGMQQRIVAVLERIYGRVTCIQVQVDPVVLGGLVTRVWGDEVIDGSAHRIEAGRRLVG----- : 276
delta_Nocardia : IADNPDIEQALSDRAKPARARRDLITRLLTG----KAEPITVTLAEQTVIRQQ-TGLGAAFDELSDLAASRRDQIVAVRAAIALTPQCKERLAASLQRIYQKPFVTVHVQVDSASLGSGLVVRVGGDDVIDGSAVGRTERLRRELA----- : 269
delta_Rhodococcus : VAGNPKIEQSLSDRSVPAKRKRELLSKLLYG----KVTAVAEALATQAVGRLNKNSAPADAFDELSNLAAAQREAVVAVRSSAFLSSECSDRITATLTRYGKPFVTVHVEVDPELLSGLVVRVGGDEVIDGSGAGRIAAALRKSLEK----- : 275
delta_Corynebacteriu : LAEQSQIEQLLADKAATPEAKRGLLASVLYG----KVTSTVETLALQAVGRPS-KRPADDIDSLSRLAAGLRNHHVAVTSATVVSDEQERALADKLGRVYQKAMSHHTVIDKSLGGLVTRVWGDEVIDGSLSTRLEKLRVGLG----- : 272
delta_Saccharopolysp : IGSQVDEERLLSDPTGDEAGKYAVVQQLIEG----KVEPVTLISVQRQLVARPRGRRVSEGLEELAELSAKRRERSVAHVRSIAELISDEQQRISRTLQRIYARFIYVHLEVDPPGVGGGLLIRVWGDEVIDGSAITGRIQSLRRDLAD----- : 272
delta_Pseudonocardia : LDREPCARILLADRSTPADKRVLGSELLR----GKASTVTTTLEQAVRSRGLALDIVAGQLAELAAARRDRYVAHVRSVAVALTDQEQRTTESLGRLYGRFISIQVEHDPPELLGGLVVRVGGELIDGSAVGRIDAAARRGLPT----- : 280
delta_Mycobacterium : LDAQPPHAILLGDYAVPVEGRVALLRKVLDAS-TKVHPIAAAILTQTVELLRQPAEEAIQFLAEVAVARRGEVVAQVSAADLSDACRTRITTEVLSRIYGHFVAVQLQIDSELLGGLLISVADEVIDGTLASRIATAEAQLPD----- : 446
delta_Kitasatospora : VAGSHEPRAALTEPKADAAKAALVRKLLGG----RANAGTVRIIVANLVTNPRGRSLEGGLESYSKLAASRRGRVVAKVTSAIELSDVQKQRLAAALAGLHGRQVHINIDVDPEVQGGVVRVHGDEIIDGTVASRIEGARQGLEG----- : 271
delta_Streptomyces subsp : VASSPEPRAALAEERGTEAAAKAELLRLLGG----RANPVTERIVTRLVTRPRGRSLDGGDLALSKLAARRDRLVAVVTSAVELISDEQKRRIGDGLARLYGRQVHINLVDVDPVVLGGLIQRVHGDEVINGTIADRIDEVSRRMAG----- : 271
delta_Catenulispora : LDSNGEALALADGRVPADKRVALVDGLLGG----KVDVTTYRIVGRLVAAPRGRSISAGLTEIGKEAAARRQRLIAYVTAAVEMTEQQRDRLAAVLKRLYGRQVHINVDLDPVVLGGLSVRVRGDEVIDGTVATRIQQQRQLAG----- : 271
delta_Acidothermus : VASRPETRDALANRTLVENKVRVLERLLAD----RAHPVTVAIVTQLVRHPRGRTPEEGFADFGIAARFRQLVAVVTTAVALTDDBSRRLRAALSELYGRDVEHVEVDPRIGGGVVRVHGDEVIDGSAITIAETRQLAS----- : 274
delta_Frankia : LNRTPETSLALSAPAAEVSQAKQALVARLLDG----KAHPVTVRIVQRVATERHYHGDLERRLEQLTTIAAARRNRLVAVLSAVELAGDCIYRRTAISRYFGRVQLQVVDVDPVVLGGVVRVHGDEVIDGSAVLRITDARRLLR----- : 280
delta_Thermobispora : LAAYPEPRAALSDFNIPGDRKRALLTELLEG----KVTRAALRLITQLVHPRGRSLESALDEYQWIVARLKERLVGVVRSVAVELTEEQKQRLAAWLRAIYGRVHINVEVDPKVLGGSVQVGDHFIDTTIAGRTEDEVRRRLAG----- : 269
delta_Streptosporang : VASDLEPYRTLAPGVPAQAKQELLGSLLAG----KVAPTTLRILISQLVHPRGRSLDRGLEEFYGLVAAQRQRLVAVVRSVAVELSEEQKRRLATWLRTSYGRDVEHINVEVDPRVVGGSVHGGDDLIDTTIAGRTEDEVRRRLAG----- : 270
delta_Thermomonospor : VEGEPQRTALTDPALPDDRKDGLLSALLDG----KVTPSARRIIGELVHPRGRSLESGLAHYGRVLAQRQRLVAVVRSVAVELTERQRTRLAAVLSAAYGHVEHINIEIDPSVLGGLSICVHGDEVIDGTIAGRTEDEVRRRLAG----- : 275
delta_Thermobifida : VAGQPEPRAALTTDGASIEHKRTLVENLLSG----KVSTATLTVTEAVTRPRGRTLEQGLEHFSQLVAERAKHYIAVVRAAVELSEACQSRQQAALTRIYGRDVEHINIEITPEIVGGLSIRVWGDEVIDGTIAGRTEDEVRRRLAG----- : 269
delta_Actinomyces : LADQREPRIGLSDLVGSGPHDRAHFAARLFG---EALNVYTTFRVRRVRLSVHGRLLSRLRYLSDLASQRRQVPAVVTVAQELTVEVQRQLLANLEKRTGKNVILHEVVEPEVLGGSFHILVGNQAINATVSSNIEQAKRALA----- : 271
delta_Bifidobacteriu : LLNLPVYRSKLYDDQAPSEVRVLFRELFGDKN---LNKVTMRIAEHATCNLRRRRYLETIQWLKFKFSRHMGMQSMITVTTAAPELKEEQKRLIDVYSAKVGRQVHINNSVVDPTVLGGMRIQVHGDEVIDGTIAGRTEDEVRRRLAG----- : 278
delta_Parascardovia : ILNLTARSYLSDFTPVDPDKRVACLRTLLGGKND--LDPIITMTAEHATRDRLNRRYLSLTSWLIKESIDSHSGEEVVTSAVELTDQCTQRITDLYTQKLNHFVHINNSVVDPTVLGGLRIQVGAQVTDITVVAQIHDLQVRL----- : 272

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Fig. S7. Comparison of amino acid sequences of d-subunits of F₁-part of F₀F₁ ATPase operon in various actinobacteria genera. Conserved residues are shown in black.

Kitasatospora : MGAQLRVYKRRIRSVTATKIKKAMEMISASRIIVKQRAVAASTPYADEITRATVAVATRSTAKHPLTTENPN---AKRAAVLLITADRLGAGGSSNAIKQSLAARFREE-GKDVVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Streptomyces : MGAQIRVYKRRIRSVTATKIKKAMEMIAASRIIVKQRAVAASTPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLLVTSRDLGAGGSSNAIKAAETLREKLVAAE-GKEVVVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Thermobifida : MGAQLRVYRRIRSVTATKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVLTVMVGRGKGVYGFNLANAVANSWTCGSDRE : 144
Acidothermus : MGAQLRIYRRIRSVTATKIKKAMEMIAASRIIVKQRAVAASTPYAEITRVAVAATGNTQHPLETTETER---PVRAAVLLVTSRDLGAGGSSNAIKAAETLREKLVAAE-GLDVVVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Catenulispora : MGGQLRVYRRIRSVTATKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVVYVGRGKGVYGFNLANAVANSWTCGSDRE : 149
Saccharopolyspora : -MAQLRELNRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PKRAGVIVVTSRDLGAGGSSNAIKAAETLREKLVAAE-GKTPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 144
Pseudonocardia : MAAQIRVLRIRSVTATKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PKRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Mycobacterium : MAATLRELNRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PRAAGVIVVTSRDLGAGGSSNAIKAAETLREKLVAAE-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Rhodococcus : -MASIRELRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PKRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Nocardia : -MASIRELRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PKRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Corynebacterium : -MANLRELNRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PKRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 144
Frankia : MAGQLREYRRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Dermacoccus : MGAQQRVYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---VRAAGVIVVTSRDLGAGGSSNAIKAAETLREKLVAAE-GKEVVVYVGRGKGVYGFNLANAVANSWTCGSDRE : 146
Kytococcus : MAAGTREYRQIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEPVLYVGRGKGVYGFNLANAVANSWTCGSDRE : 146
Kineococcus : MAGQLRAYRRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---VKRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEIAPVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Arthrobacter : MGAQIRVYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Brevibacterium : MGAQQRVYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Leifsonia : MGAQLRVYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Clavibacter : MGAQLRVYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PVRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Nocardioidaceae : ---MRELNRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 141
Nocardioidea : MAVSLREYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Aeromicrobium : MAASVRELNRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Kribbella : MPASLREYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Actinomyces : MAGNQRVYRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 145
Bifidobacterium : -MSSQLALKSRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 144
Gardnerella : -MSSQLALKSRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 146
Parascardovia : -MASQLAFKSRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 144
Scardovia : -MASQLAFKSRIRSVKSTRKIKKAMEMIAAATRIITKAQRAEAEEAPYAREITRVAVAATGNTQHPLETTETER---PTRAAVLVITSDRGLAGAGYANAKAEERLTAALNEQ-GKEVTVYVGRGKGVYGFNLANAVANSWTCGSDRE : 144

Kitasatospora : TYGDAKTVSADIAAFTAETGG-----VDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----KNQIFPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 248
Streptomyces : SYADAKAVAAPLIEAAVQDTAE-----GGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----KAEILPLFDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 249
Thermobifida : SYMHAMELSSADMEKFIQTAE-----GGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----QGFPL-LYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 248
Acidothermus : SYLQAKDVYAAIAFAENTPADD-----GGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----VGGMFPQYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 246
Catenulispora : AYTDARTVADEVEIAFLAE-----GGMDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----AGGVFPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 248
Saccharopolyspora : DYSDAADIGETIVKAFVLAGADDYLDGGPD-----GTLGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----KTLRPVYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 254
Pseudonocardia : GYEHAAEAARTVDAFMAGEDD---GDGNAD---GVHGVDELHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----SQVESPGSKGLQSLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 277
Mycobacterium : EYEAHQEIGETIVKAFMAGVDDGDDAGAD---GILGLDELHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----EPHTLFSDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 255
Rhodococcus : GYADAAKASRIIVELFMAGSGAEVEAPNGE---GTIEGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----DGKSGPSAVYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 271
Nocardia : KYTDAASAACNIEVEAFMAGSDGTVPAPEGT---GDIAGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----SPTADVHAQYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 268
Corynebacterium : TWEKTHDVRRIIDGFVAGSNGQAKTREGINVEGETVIRGFDQVHVYVTEESMLTCTAVDHRILLPKLDELVELSDGAPA-----PNNQITPDYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 272
Frankia : SYSDAKAVADAITAFTPTPEE-----GGVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----GPLPNYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 246
Dermacoccus : KFENAEEIGERTADFHAGAEGG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----PDGFLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 252
Kytococcus : TVEDAREISDAIEAFLTPTEG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----GVDLSTPEYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 258
Kineococcus : SYDAKTIQDRIIVADFGKEFADG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----SDGELPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 247
Arthrobacter : VFATAQEIQAALIEAFATAYEEG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----LLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 246
Brevibacterium : TVEAAKEIGDIIIVSSFNNTDYEAG-----GIDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----AKDVVPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 256
Leifsonia : EFEQAQEVADITLESFLRDSADG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----QVLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 247
Clavibacter : EFETAQSGIDATIEFVTPASEG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----AVLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 247
Nocardioidaceae : DYDAAKEIGKIIIEVFVEGTEAE---KAAAP---GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----DVLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 248
Nocardioidea : SYDAALVGTIIVDAFLD-----EEGEH---AVDEHVHVVYTRERSMLTCEPTAVRILLPEVVEGTEAPEG-----EVLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 247
Aeromicrobium : EFSDARDITTVRAFNSGDDDDTVDPAR-----AADLHLVSTEQSMLTCEPTAVRILLPEVVEGTEAPEG-----ELLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 254
Kribbella : TFAAREVADAITAFLTPTEG-----GVDLHLVSTEQSMLTCTAVDHRILLPKLDELVELSDGAPA-----DVLPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 247
Actinomyces : GEEMEDIAQALLESFLPAEQ-----GVAEVLIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG-----TEYQKAAETGAAPLYDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 263
Bifidobacterium : GVEVAEISNATIDAYMKPDEEG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG-----AASPLYSDEEBSAEGVLDALLPRVVESRIYNALLQSAASE : 249
Gardnerella : DVTIAEKISDITMDAYMTPAEAG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG : 281
Parascardovia : SVENAAARISQITFDYMAPASKG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG : 278
Scardovia : TVGMAARISQITFDYMAPASEG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG-----GVSFLYIVFTREIVSMVSCVPEVRMLPLTVVDVDSGSELDREHDHVRG : 276

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Kitasatospora : HAARRR-AMKSATDNAGEI IKSLTIRLAN SARQAEITCEI SEIVGGANALADASAGSE : 304
Streptomyces : HAATRRRAMKSATDNAEETIKSLTIRLANAARQADITCEI SEIVGGACALADANAGSD : 306
Thermobifida : HASRRRA-AMKAATDNAEETVKTITRQANQARCAEITNEI SEIVGGADALAAASAGSE : 304
Acidothermus : IAARRR-ACKAATDNAEETIRTYTIRLANAARCAEITCEI SEIVGGADALVATGSE-- : 300
Catenulispora : HAARRR-AMKSATDNASTIDNITRQANAARCAEITCEI SEIVGGANALADANVGSD : 304
Saccharopolyspora : HAARRT-AMKSATDNADEIIRTISREANQARCAQITCEI SEIVGGVDEALSSAGSE-- : 308
Pseudonocardia : SANRQR-AMKAATDNAEETIRSTILEANQARCAQITCEI SEIVGGVDALASAGSES- : 332
Mycobacterium : SASRRR-AMKSASDNADDLIKDITLMANRERQSQITCEI SEIVGGANALADAANK-- : 309
Rhodococcus : SAARRT-AMKAATDNAEETVNTISRQANQARCAQITCEI SEIVGGANALASSAGSD- : 326
Nocardia : SAARRT-AMKAATDNAEETATDISRQANSVRCAQITCEI SEIVGGVNALAASSDRD- : 323
Corynebacterium : SAARRT-AMKSATDNAEETVVDISRVANQARCAQITCEI SEIVGGACALAESAESD- : 327
Frankia : SAARQR-AMKSATDNAEETIKTYTIRANRARCDAITCEI SEIVGGANALASGA---- : 298
Dermacoccus : LAARQR-AMKSATDNAEETIKTYTIRLANQARCAEITCEI SEIVGGASALADAS---- : 304
Kytococcus : LAARQR-AMKSATDNAEETIKDYTIRLANQARQADITCEI SEIVGGSAALADAK---- : 310
Kineococcus : LAARQR-AMKSATDNAEETIKKLTIRLANARQADITCEI SEIVGGADALASSGSR- : 302
Arthrobacter : LAARQR-AMKSAGDNATDIKKYTRLRNTARCAEITCEI SEIVAGADALNAS----- : 297
Brevibacterium : QAARQQ-AMKTATDNADEIIRTYYIRLAN SARQAEITCEI SEIVGGADALAGAGSND- : 311
Leifsonia : HAATQK-AMKAASDNADKITIDYTRLANARCAEITCQI SEIVGGADALSSAN---- : 299
Clavibacter : HAARQK-AMKSASDNADKITVTTYTRLRNARQTEITCQI SEIVGGADALASSK---- : 299
Nocardioidaceae : IAQRQK-AMKSATDNAEETIKKFTIRVANQARCAQITCEI SEIVGGVNALADAQAAND : 304
Nocardioides : LAARQK-AMKSATDNAEETIKKYTRIANQARCAQITCEI SEIVGGVNALADAQAGSE : 303
Aeromicrobium : LAARQK-AMKSATDNAEETIQKYTRTANQARCAQITCEI SEIVGGANALADATAGSE : 310
Kribbella : LANRQR-AMKSATDNAQDIERTITREANQARCAQITCEI SEIVGGACALADASAGSE : 303
Actinomyces : LASRQQ-AMHTATDNAEETINTYTRLANQARQGDITCEI SEIVSGADALAAE----- : 314
Bifidobacterium : TANRQN-AMHTATBNARSTIDDTIRKLNASRCASITCELTEI IGSADALNKKEE--- : 302
Gardnerella : TASRQN-AMHTATBNARNVDDTIRKLNASRCASITCELTEI IGSADALNNEED--- : 334
Parascardovia : TASRQN-AMHTATBNARKIVDEITRKLNASRCASITCELTEI VGSADALKTEIE--- : 331
Scardovia : TASRQN-AMHTATDNAGKIVDEITRKLNASRCASITCELTEI VGSADALKTEIE--- : 329

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Fig. S8. Comparison of amino acid sequences of g-subunits of F₁-part of F₀F₁ ATPase operon in various actinobacteria genera. Conserved residues are shown in black.