

Collection of published 5S, 5.8S and 4.5S ribosomal RNA sequences

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The 1985 collection of published 5S, 5.8S and 4.5S ribosomal RNA sequences (1) is updated. We would like to thank those colleagues who have sent us their pre- or reprints on small ribosomal RNAs in 1985, and who have pointed out mistakes in our previous collection.

The 5S, 5.8S and 4.5S rRNA databases are part of the Berlin RNA Databank which uses the formats of the EMBL Nucleotide Sequence Data Library. The Berlin RNA Databank, including pure data as well as complete alignments, is online accessible worldwide via the I.P.Sharp Timesharing Network. Magnetic tapes or diskettes are also available from our laborator

THE ALIGNMENT

This year, the alignment is divided into 4 groups: eubacteria including plastids, mitochondria, archaebacteria, and eukaryotes. Since plastidial 5S rRNA exhibits no exclusive features distinct from cyanobacterial 5S rRNA, it is included in the eubacterial alignment. The alignment has been obtained by running the programs ALIGNSTAT or ALIGNSEC (2) and adjusted manually to account for potential secondary structure interactions. The programs were purchased as part of the genetic engineering program package, SAGE, for the IBM PC/XT from Technoma GmbH, Heidelberg, F.R.Germany. It was run on the IBM 3081 computer of I.P.Sharp Associates in Toronto, Canada. We do not want to give the impression that there are no alignment problems, so that changes must be considered when more sequence data come up.

One improvement of the alignment output is the presentation of the sequence references. They occur opposite the sequence

page and are numbered according to the sequence numbers. In addition, all available publications are listed, even if a sequence is determined several times.

The taxonomic position for each species is indicated in parentheses following the species name. We tried to adhere to the concept of phylogenetic systematics sensu Hennig (3), therefore only recognized monophyla are given without any rank. These are taken mainly from the following references: Hennig (metazoa)(4), Strasburger et al. (plants and algae)(5), Ainsworth et al.(eu-mycota)(6), International Society of Protozoologists (protozoa) (7), Schnabel et al.(archaeabacteria)(8),and Woese(eubacteria)(9).

THE NOMENCLATURE

An achievement of this year's compilation is the introduction of a generalized numeration. We adopted the idea of Sprinzl and Gauss for tRNA who took the best understood molecule as a basis, namely tRNA^{Phe} of the yeast Saccharomyces cerevisiae. Similary Delihas and Andersen (10) have proposed to use the E.coli 5S rRNA as a basis, and we would like to elaborate this proposal in which positions not present in the E.coli sequence are designated by a decimal fraction. The advantage of this is the universal comparability of 5S rRNA sequences,for example G44 in eubacteria will also be G44 in eukaryotes as well as in archaeabacteria. The disadvantage lies in the fact that the generalized numeration might be changed in the future in those regions of alignment uncertainties.

A new loop nomenclature has been developed, assigning small letters to the loops following the helices. One may refer to Helix B and Loop b, but also to segment B, segment B', segment b, segment b', corresponding to the 5' and 3' portions of the respective structures (see alignment).

THE MINIMAL MODEL

Another feature of this year's compilation is the formulation of a minimal model most researchers agree to. This was first proposed in 1974 by Nishikawa and Takemura for eukaryotes (11) and by Fox and Woese in 1975 for eubacteria (12). First attempts to use 5S rRNA as a phylogenetic marker were made in

1975 by Hori (13) and subsequently further developed to gain common secondary structure models (14,15,16). The present minimal model is based on investigation published in the early eighties by Studnicka et.al.(17), MacKay et al. (18), Delihas and Andersen (10), DeWachter et al. (19), and Küntzel et al.(20).

The minimal model could be constructed for eubacteria (covering to date 3 of the 9-10 recognized phylogenetic divisions), eukaryotes, and halophilic-methanogenic archaebacteria (Figures 1-3) and also includes deviations (insertions/deletions) for special monophyla that are represented by at least two species. Other archaebacterial divisions are only covered by single species and are shown separately (Figures 4-6).

Due to the lack of compensating base changes as a proof, the following base-pairs have been expelled from helices: 23/60 at the end of Helix B, G69/U107 at the beginning of Helix D in eukaryotes and archaebacteria, and U74/A102 at the end of Helix D in some eukaryotes.

To avoid problems concerning the variability of positions (discussed in detail by Fox (21), page 277) the bases indicated in the minimal models are the ones supposedly ancestral to the respective groups. Where a different base is present in the majority of the species, this is indicated with an arrow.

This new nomenclature and the minimal model resolved from discussions with George E. Fox and N. Delihas, we would like to extend this discussion to all researchers in the field during 1986.

ACKNOWLEDGEMENT

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Figures 1-6: Minimal models of 5S rRNA secondary structure. Squares indicate conserved base-pairing, circles unpaired nucleotides. Dotted lines indicate possible helix extensions. Filled squares and circles indicate positions that are unique to one group. Bases indicated in the minimal models are supposedly ancestral for the respective group. Different bases in the majority of species are marked with an arrow. Hypervariable positions remain blank. The occurrence of AC and UU odd base-pairs is also marked.

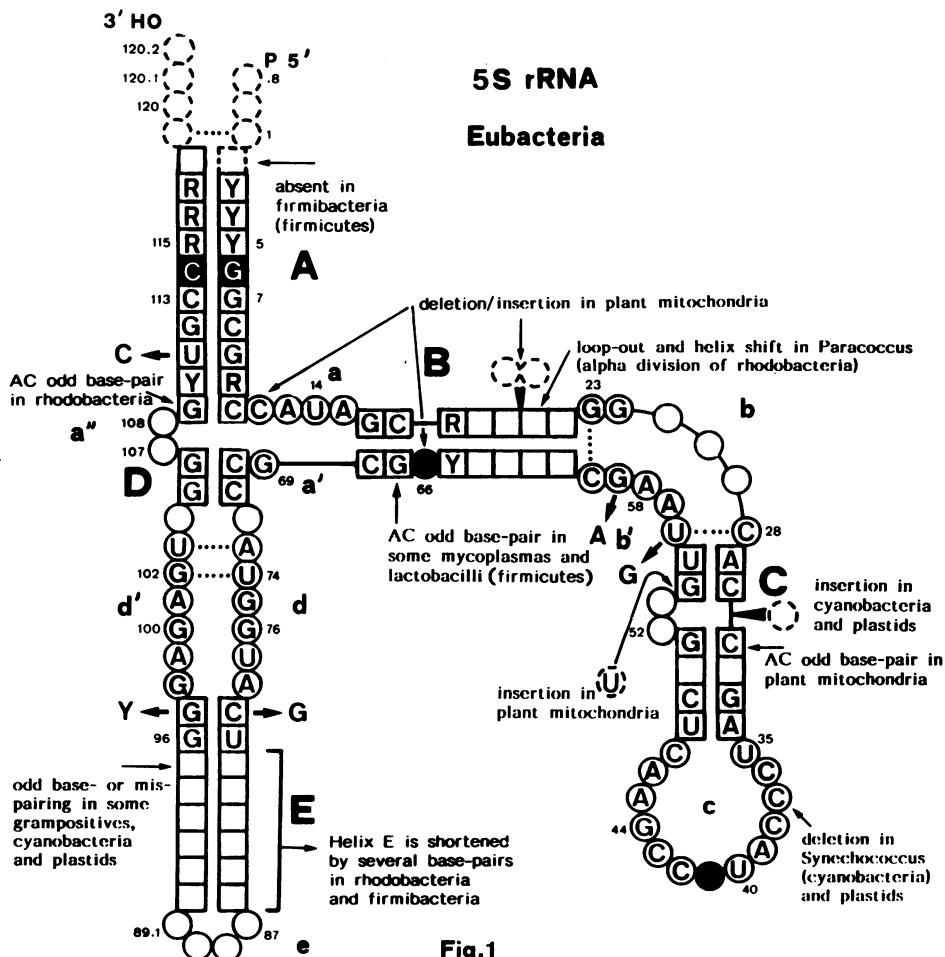


Fig.1

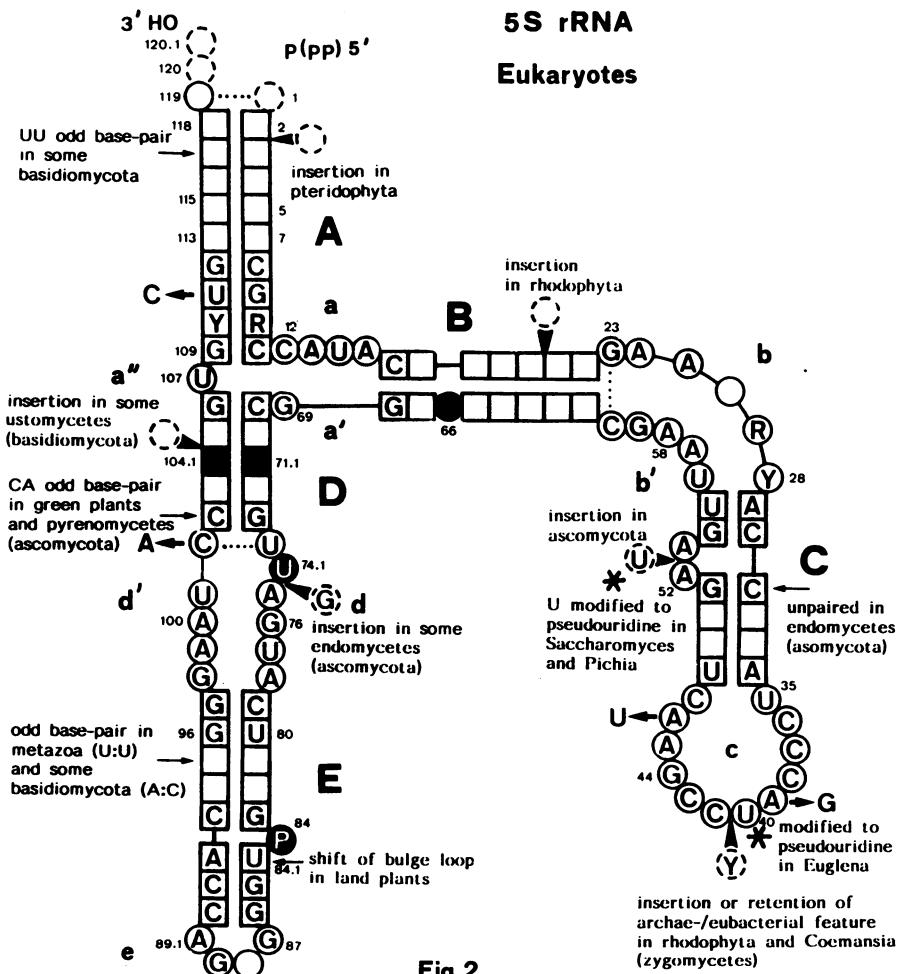


Fig.2

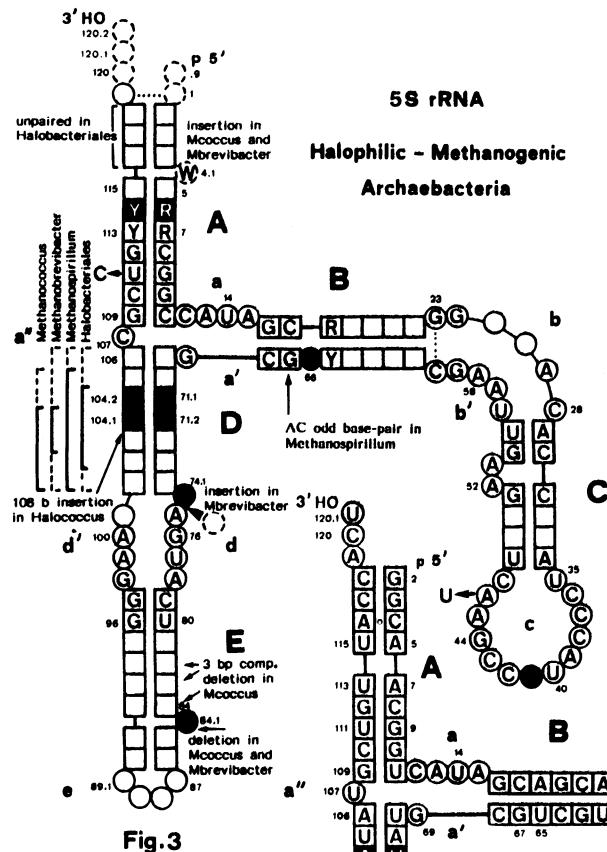


Fig.3

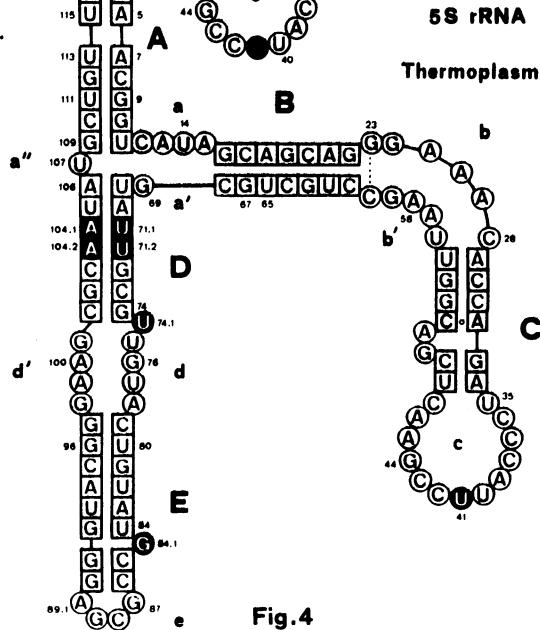
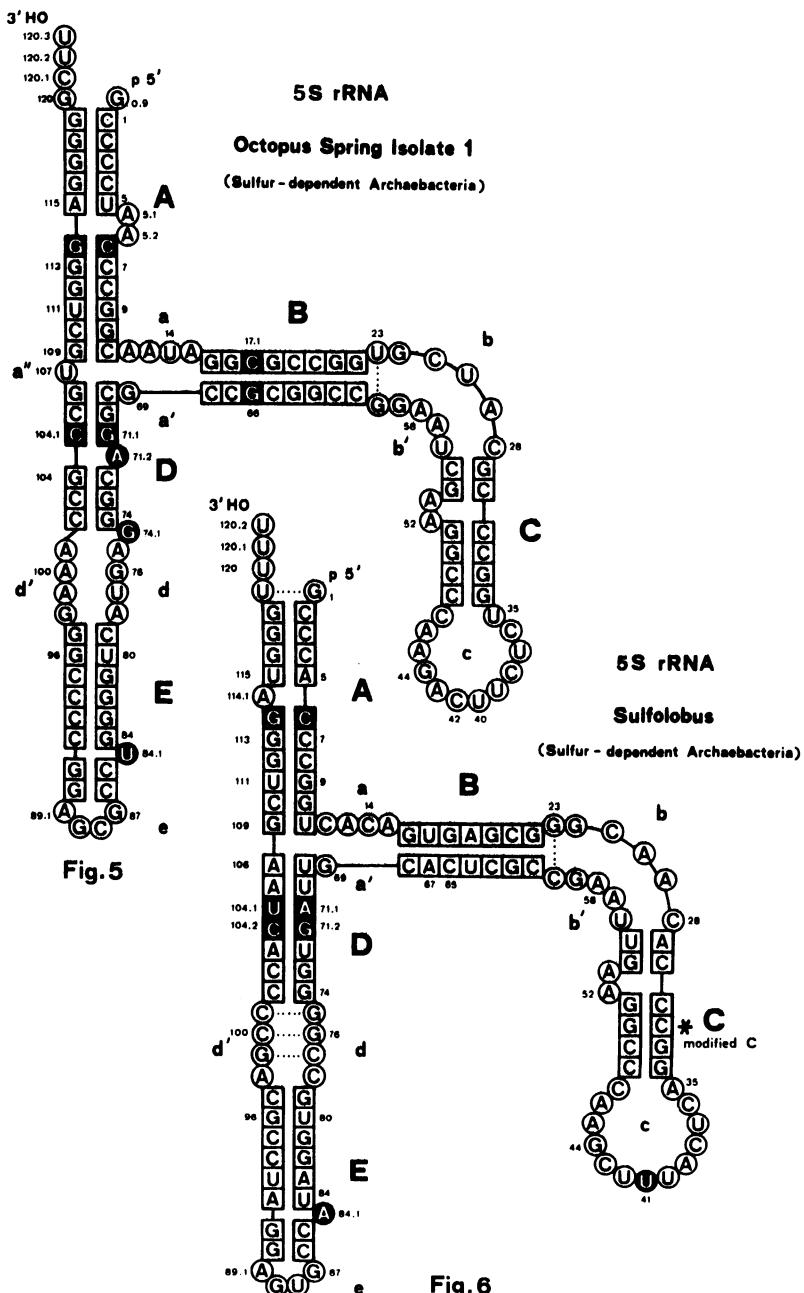


Fig. 4



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Table 1: Alignment of 5S rRNAs. The sequences are numbered sequentially, the number is repeated on the opposite page in order to correlate the sequences with the corresponding publication. Identical sequences are only listed once with the name of the species first examined. Additional species are listed on the opposite page. Only the corrected sequence appears in the alignment, if the published sequence has been reexamined later. If different publications led to different sequences of the same species or strain, all sequences are aligned and given a capital letter suffix. If different variants within one species or strain have been isolated and sequenced, all sequences are aligned and numbered sequentially. DNA sequences are indicated by T occurring instead of U. Heterogeneity in specific positions is indicated as recommended by the IUB-IUPAC joint commission on biochemical nomenclature (22). If all 4 nucleotides are present, this is indicated by N, incomplete sequence analysis is indicated by X. Length heterogeneity is indicated by lower case letters. Modified bases are indicated as follows: F for Pseudouridine, 2'-O-Methyl-riboses by underscoring. Helix segments are boxed and named according to the secondary structure model in Figure 1. Plastidial and mitochondrial sequences are preceeded by pt and mt, respectively. The term Firmicutes for Grampositives, comprising the two subdivisions Firmibacteria (low GC-content, "clostridia") and Thallobacteria (high GC-content, "actinomycetes") has been proposed by Gibbons and Murray (23), the term Rhodobacteria for purple bacteria and their relatives by Wolters and Erdmann (24). Because of their phylogenetic ancestry mycoplasmas are classified as Firmicutes.

EUKARYOTA

1	HOMO SAPIENS	(CHORDATA, MAMMALIA)
2	GALLUS GALLUS 1	(CHORDATA, AVES)
3	GALLUS GALLUS 2	(CHORDATA, AVES)
4	IGUANA IGUANA	(CHORDATA, SQUAMATA)
5	TERRAPENE CAROLINA	(CHORDATA, CHELONIA)
6	NOTOPHTHALMUS VIRIDESCENS	(CHORDATA, AMPHIBIA)
7	XENOPUS LAEVIS [SOM]	(CHORDATA, AMPHIBIA)
8	XENOPUS BOREALIS [OCJC]	(CHORDATA, AMPHIBIA)
9	XENOPUS LAEVIS [OCJC] 1	(CHORDATA, AMPHIBIA)
10	XENOPUS LAEVIS [OCJC] 2	(CHORDATA, AMPHIBIA)
11	XENOPUS LAEVIS [OCJC] 3	(CHORDATA, AMPHIBIA)
12	XENOPUS LAEVIS [OCJC] 4	(CHORDATA, AMPHIBIA)
13	XENOPUS BOREALIS [OCJC] 1	(CHORDATA, AMPHIBIA)
14	XENOPUS BOREALIS [OCJC] 2	(CHORDATA, AMPHIBIA)
15	XENOPUS BOREALIS [OCJC] 3	(CHORDATA, AMPHIBIA)
16	SALMO GAIRDNERI	(CHORDATA, OSTEICHTHYES)
17	TINCA TINCA [SOM]	(CHORDATA, OSTEICHTHYES)

- MISBURNUS FOSSILIS (EUROPEAN LOACH, LOCHE D'ETANG, SCHLAMMPFETZGER)
1. SOMBAT (LIVER)
[1] SERENKOVA T.D., SERENKOVIA T.I., MIZO A.M., AVDONINA T.A.,
TINOFFEYVA M.YA., KISSELEV L.I., [1981]
NUCL. ACIDS RES. 11(2141-51)(1981).
- TINCA TINCA (TENCH, TANCHE, SCHLEI)
1. OOCYTES
MISBURNUS FOSSILIS (EUROPEAN LOACH, LOCHE D'ETANG, SCHLAMMPFETZGER)
1. OOCYTES
[1] SERENKOVA T.D., SERENKOVIA T.I., MIZO A.M., AVDONINA T.A.,
TINOFFEYVA M.YA., KISSELEV L.I., [1981]
NUCL. ACIDS RES. 11(2141-51)(1981).
- SCYLLOTHRINUS CANICULUS FROM PLUGABUSHOU, F (DOGxFISH, PETITE
ROUBSETTE, KATZENHAI) 1 LIVER AND OCYCTES
HALOXYNTHA RORETZI (SESSILE ASCIDIAN, SEESENKETIDE)
[1] BONADS, [22] BRANCHIAL POUCHES
[2] SERENKOVA T.D., SERENKOVIA T.I., MIZO A.M., AVDONINA T.A.,
TINOFFEYVA M.YA., KISSELEV L.I., [1981]
NUCL. ACIDS RES. 11(2141-51)(1981).
- SACCOGLOSSUS KOMALEVSKI FROM WOOD HOLE, USA (ACORN-WORM,
ETCHELINJANI)
LYTECHINUS VARIABILIS (SEA URCHIN, SEEIGEL)
1. CLOWN FLOPS
HETEROCENTROTUS POLCHRERATIS FROM SUGASHIMA, J (SEA URCHIN,
SEEIGEL)
1. OVARIES
ASTERIAS VOLGARTIS (PURPLE SEA STAR, PURPUR SEEESTERN)
1. OVARIES
ASTERINA PECTINIFERA FROM SUGASHIMA, J (SHORT-ARMED SEA STAR,
KURIL TIGER SEEESTER)
1. OVARIES
STICHOMYS DHITIME FROM SUGASHIMA, J (SEA CUCUMBER, SEEIGURE)
1. HOPPER INSECT
ACRYPTON ITHON MAGNOLIAE (ELDER APHID, HOLUNDERBLATTLAUS)
1. NOME OF IRBANI SHIM
DROSOPHILA MELANOGASTER (FRUIT FLY, FRUCHTFIEGE)
1. CLONE, CELL LINE, [C3] ADULTS, LARVAE AND EMERGOS, [4] CLONE P1201
1(-1) AND OTHERS
DROSOPHILA SIRULANS 204-1, SEYCHELLES 1, CLONE
DROSOPHILA TEISSIERI 201-5, COMBO 1, CLONE
- DROSOPHILA MELANOGASTER (FRUIT FLY, FRUCHTFIEGE)
1. CLONE PMS1
DROSOPHILA MELANOGASTER (FRUIT FLY, FRUCHTFIEGE)
1. CLONE PMS1
CALLIPHORA ERYTHROCEPHALA (-, TRAUFNUCKE)
- PHILOSAMIA CYNTHIA-RICINI (SILK MOTH, SEIDENSPIINNER)
1. POSTERIOR SILKGLANDS OF THE SILKWORM
- [18] [13] MASHKHOVA T.D., SERENKOVIA T.I., MIZO A.M., AVDONINA T.A.,
TINOFFEYVA M.YA., KISSELEV L.I., [1981]
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- DISEGIA JAPONICA FROM SANAGI, J (PLANARIAN, PLANARIE)
1 WHOLE ORGANISM
PHASCOLORIS DOLLDII
1 WHOLE ORGANISM
- RETTI PACHYLIA (VESTIMENTIFERAN TUBE WORM,)
1 TUBE WALL AND TROPHOSOME
L. LIMNAIA ANATINA FROM ARTAKAY, J (LAMP-SHELL,)
1 WHOLE ORGANISM
- BIGULIA NERITINA FROM SUGASHIMA, J (MUS-ANIMAL, MODSTIRCHEN)
CAENORHADITIS ELEGANS [1-3] BRISTOL, N2
CAENORHADITIS EBIGAE [1-3]
CAENORHADITIS EBIGAE [1-3]
1 WHOLE MERMAPHODITE ORGANISM
CONFLICT 113 INSTEAD OF G IN DNA [3]
- RHABDITIS TOKAI
1 WHOLE ORGANISM
BRACHIONUS PLICATILIS (PLANKTON ROTIFER, RAEDERTIER)
1 WHOLE ORGANISM
SPICRODON SALTMATRIX FROM SETO INLAND SEA NEAR USIMADO, J
1 OVARIES
NEOPSIS DOLLETTI FROM SETO INLAND SEA NEAR USIMADO, J (HYDROID,)
1 OVARIES
CHARYBDEA GLINDECIARIA FROM SETO INLAND SEA NEAR USIMADO, J
(OCCEANIC JELLYFISH, NOCHISEQUILL) 1 OVARIES
AURELLIA AURITA FROM SETO INLAND SEA NEAR USIMADO, J (WHITE SEA JELLY, QUALE) 1 OVARIES
AURELLIA AURITA FROM CANADA (WHITE SEA JELLY, QUALE)
1 OVARIES
ARTHROLEURA JAPONICA (SEA ANEMONE, SEEANEHOME)
1 WHOLE ORGANISM
1 WHOLE ORGANISM
PROTEIN ACTION, F (SLIMY PARTRILLED SPONGE,) AND HALICHONDRIA JAPONICA (CRUMB OF BREAD SPONGE,)
BROTHKERNEDCHAMPH 1 WHOLE ORGANISM
- HALICHONDRIA PANICEA FROM AUDRESELLES, F (CRUMB OF BREAD SPONGE,)
BROTHKERNEDCHAMPH
1 WHOLE ORGANISM
HALICLONA OVALATA FROM AUDRESELLES, F (DEADMAN'S FINGERS,)
1 WHOLE ORGANISM
- S2 [1] OHKA T., KUMAZAKI T., HORI H., OBAMA S., TAKAI M. 1
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NUCL. ACIDS RES. SYMP. SER. B115-22(1980).
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S6 [1] OHKA T., KUMAZAKI T., HORI H., OBAMA S. 1
NUCL. ACIDS RES. 12:5101-08 (1984).
S7 [1] BUTLER M.H., WALL S.M., LIEMHORN K.R., FOX G.E., HECHT R.M. 1
J. MOL. EVOL. 18:18-23 (1981).
[2] KUMAZAKI T., HORI H., OBAMA S., ISHII N., SUZUKI K. 1
NUCL. ACIDS RES. 10:7001-04 (1982).
[3] NELSON D.W., HONDA B.M. 1
GENE 38:245-251 (1985).
S8 [1] KUMAZAKI T., HORI H., OBAMA S., ISHII N., SUZUKI K. 1
NUCL. ACIDS RES. 10:17001-04 (1982).
S9 [1] KUMAZAKI T., HORI H., OBAMA S., ISHII N., SUZUKI K. 1
NUCL. ACIDS RES. 10:17001-04 (1982).
S0 [1] HORI H., OHMA T., KUMAZAKI T., OBAMA S. 1
NUCL. ACIDS RES. 10:17405-08 (1982).
S1 [1] HORI H., OHMA T., KUMAZAKI T., OBAMA S. 1
NUCL. ACIDS RES. 10:17405-08 (1982).
S2 [1] HORI H., OHMA T., KUMAZAKI T., OBAMA S. 1
NUCL. ACIDS RES. 10:17405-08 (1982).
S3 [1] HORI H., OHMA T., KUMAZAKI T., OBAMA S. 1
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S6 [1] KOTIYA H., OHMA T., KUMAZAKI T., OBAMA S. 1
NUCL. ACIDS RES. 10:17405-08 (1982).
S7 [1] DAVIS E., VANDENBERGE A., DE WACHTER R. 1
NUCL. ACIDS RES. 10:5297-5302 (1982).
[2] KOTIYA H., OHMA T., KUMAZAKI T., OBAMA S. 1
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S8 [1] DAVIS E., VANDENBERGE A., DE WACHTER R. 1
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- DICYCEA HISAKIENSE
BLASTOCLADIELLA SIMPLEX ATCC 24579
PHILICTOCYTRIUM IRREGULARE ATCC 32046
DIPLOCYDYES ACUIMINOSPORUS ATCC 14302
LINDERINA MACROSPORA
COPHEANIA MOJAVENSIS
CUNNINGHAMELLA ELEGANS ATCC 9245
BLAKESLEA TRISpora ATCC 14271
MORTIERELLA FORMOSENSIS ATCC 24542
PHYCOPHYCES BLAKESLEEAENSIS NRRL 15355 (ALBAL WATER MOLD, ALGENPILZ)
BASIDIOMOLUS MAGNUS ATCC 15379
SPHAGNUM CULSETAE ATCC 16244
GENISTELLOIDES HIBERNUS
CAPNIOCYDYES STELLATUS
SCHIZOBACCHARODYTES PORAE ((2) IF00045 (2) ADE6 SUP3-704
1 CLONES (2) PSPI. 11, 36 AND 41 (2) PYHS AND PYH116
PROTOPHYES INNADATUS ATCC 28130
YARROWIA LIPOLYTICA ATCC 8461
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- NEUROSPORA CRASSA [L11C5] EM2256 (ATCC 10815) AND PK052
; CONIDIA OR YOUNG MYCELIUM, CLONES PK051 AND PK052
- NEUROSPORA CRASSA OAK RIDGE 74-DRB-1A (F68C 98a) ; GENE 17
AND BEADLE AND TATUM 25A (F68C 333) ; GENE 17
- NEUROSPORA CRASSA OAK RIDGE 74-DRB-1A (F68C 98b)
- NEUROSPORA CRASSA OAK RIDGE 74-DRB-1A (F68C 98b)
- ACRENOMIUM PERSICINUM CBS 169-65 [=PACETILORYCES PERSICINUS]
ACRENOMIUM PERSICINUM CBS 169-65 [=PACETILORYCES PERSICINUS]
- ACRENOMIUM PERSICINUM CBS 169-65 [=PACETILORYCES PERSICINUS]
- ACRENOMIUM CHRYSEODERMIUM ATCC 14533 [=CEPHALOSPORIUM ACRENOMIUM]
- MONILIUM FRUCTICOLA ATCC 9684
- TRICHOPHAEA ARUNDINANS ATCC 26431
- AUREOBASIDIUM PULLULANS ATCC 269928
; YEAST PHASE
- USTILAGO VIOLOACEA (FLAG-SHOT, CHARBON, FLUGBRAND)
; YEAST PHASE
- RHODOSPORIDIUM TORULOIDES
; YEAST PHASE
- AESSOSPORON SALMONICOLOR
; YEAST PHASE
- USTILAGO SCABIOSAE GD 1425
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METZENBERG R.L.;
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- L16 MORZYCA-MROBLENSKA E., SELKER E.U., STEVENS J.N.,
METZENBERG R.L.;
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- L17 MORZYCA-MROBLENSKA E., SELKER E.U., STEVENS J.N.,
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- L18 MORZYCA-MROBLENSKA E., SELKER E.U., STEVENS J.N.,
METZENBERG R.L.;
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- L19 CHEN M.-H., ANNE J., VOLCKART G., HUYSHANS E.,
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- L20 CHEN M.-H., ANNE J., VOLCKART G., HUYSHANS E.,
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- L23 TEMPLETON A.R.I.,
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- L29 WALKER W.F., DOOLITTLE W.F.,
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- L30 BLANZ P.-A., GOTTSCHALK H.J.,
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- SPHAEROLETHRA SPEC GD 1127
- RHIZOTONIA CRICORUM ATCC 11070 ("HELICOBASILUM PURPUREUM")
[RHIZOTONIA, RHIZOTONIA, RHIZOTONIA]
RHIZOTONIA HEMIALS ATCC 14016 ("TRICHOPHAEA BULATATA")
- PACHNOCEBE FERRUGinea
1 MYCELLIA
RHODOSPORIDIUM MALVINELLUM CBS 6082
- AGARICOCLITUM PALMICOLUM
- 1 YEAST PHASE
TRICHOSPORONIDES DEDICEPHALIS ATCC 15988
- 1 MYCELLIA
MONILIELLA ACETABULANS ATCC 18455
- TILLETTARIA ANIMALIA ATCC 24038
- EXOBASIDIUM VACCINIUM ATCC 24312
- TRICHOSPORON ORYZAE ATCC 28323
USTILAGO LONGISTIHA GD 466 (SHUT, BRAND)
GIOVANNIELLA PRIMULICOLA GD 1394 (SHUT, BRAND)
TILLETTA CONTROVERSA
- USTILAGO HORDEI GD 935
HEITS
USTILAGO MAYDIS GD 115
USTILAGO MAYDIS GD 1042
20/100
- FARNSIA THURELENII GD 1309
- MICROSTROMA JUGLANDIS PB4142 (RUST, ROST)
- CHLONOSPHERE APOMASTIDIALES
1 YEAST PHASE
- 120 [1] BLANZ P. A., GOTTSCHALK M. I. SYSTEM, APPL. MICROBIOL. 5: 51B-526 (1984).
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Eukaryota		5S rRNA	
D.	A.		
F.			
0123456789012341345567901235678901			
CCCCCGAAUGGGAAGAUUCUA:::GGGCCGUUGGUU:::	137	STERIGMATOMYCES FENICILLATUS	(BASIDIOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	138	TREMELLA MESENTERICA	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	139	BULLERA ALBA	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	140	AGRICUS EDULIS	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	141	CRYPTOCOCCUS ALBIDUS	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	142	ITERSONIA PERPLEXANS	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	143	PHAFFIA RHODOZYMA	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	144	PHLOBASIDIUM FLORIFORME	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	145	FILOBASIDIUM CAPSULIGENUM	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	146	SCHIZOPHYLLUM COMMUNE	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	147	BJERKAANDERA ADUSTA	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	148	COPRINUS RADIATUS	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	149	RUSSULA CYANOXANTHA	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	150	PLEUROTUS OSTREATUS	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	151	AURICULARIA AURICULA-JUDAЕ	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	152	AURICULARIA DELIQUESCENS	(HYMENOMYCOTES)
CCCCCGCGGAAUUCUA:::GGGCCGUUGGUU:::	153	RHIZOCTONIA GLOBULARIS	(HYMENOMYCOTES)

- STERIGMATOMYCETES PENICILLATUS ATCC 32127
 1 YEAST PHASE
 TREMELLA MESENTERICA
 1 YEAST PHASE
- BULLERA ALBA ATCC 18546
 1 YEAST PHASE (PSALLIOTA) / MUSHROOM, PSALLIOTE,
 ABARTICUS EUDIS (PSALLIOTA)
 FRUITBODY
- CHEIRODODUS ALBIODUS ATCC 10466 (=FILOBASIDIUM SPEC?)
 1 YEAST PHASE
- CHERMONILLA PERPLEXANS ATCC 15495
 MYCELLIA
- PHAFIA RHODOZYMA ATCC 24202
 1 YEAST PHASE
- FILOBASIDIUM FUSIFORME
 ENDOPHYLLUM SEPPENWIL R. BAUER 778 (RUST, + ROT)
 1 YEAST PHASE
 NETS 119 40/100 ENDOPHYLLUM ONLY
- FILOBASIDIUM CAPSULIGENUM
 1 YEAST PHASE
- SCHIZOPHYLLUM COMMUNE AND COPRINUS CINEREUS (INKY CAP, ENCRIER,
 TINTENBLAETTERLZ/HISTOSCHAMM) + MYCELLIA
 BIJERKANDERA ADUSTA
 1 MYCELLIA
- COPRINUS RADICATUS ATCC 20528 (INKY CAP, ENCRIER,
 TINTENBLAETTERLZ/HIS SCHAMM)
 PLASSERAUX KANTHAA (BLUE AND YELLOW RUSSULA, RUSSULE CHARBONNIERE,
 PRETTE KEUBLING)
 FRUITBODY 119
- PELEOTUTUS OSTRAEATUS (OYSTER MUSHROOM, NOURET, AUSTERSCHWARM)
 FRUITBODY
- ARTICULARIA AURICULA-JUDAEE (JEM'S EAR, HIRNOKE OREILLE DE JUDAS,
 JUNENOCH)
- FRUITBODY
- DACRYMYCES DELIQUESCENS ATCC 12292 (TEAR MUSHROOM, + TRAENENPILZ)
 RHIZOCTONIA GLOBULARIS ATCC 14015 (SERACINA SPEC?)
 1 MYCELLIA
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- ACANTHAMOEBA CASTELLANI 1 ATCC 30010
DICTYOSTELIUM DISCOIDEUM NC-4 (CELLULAR SLIME MOLD, + ZELLULÄRER SCHLEIM) [L12]
PHYSARUM POLYCEPHALUM (PLASMODIAL SLIME MOLD, + PLASMODIAL SP. EINHILTZ)
AMERICAN PARASITICUM
EUGLENA GRACILIS 2 HETEROZYGOTHEM (+, AUGENTIERCHEN)
EUGLENA GRACILIS 2 PLASTID-LESS MUTANT CM500 (+, AUGENTIERCHEN)
CRITHIDIA FASCICULATA (TRYPANOSOMATIDIAN, TRYFANGOSOMA)
TRYFANGOSOMA BRUCEI BRUCEI IATAT 1.2 : CLONES PSS-2 AND PSS-11.5
THRAUSTOCYTRIUM VISURGENSE ATCC 29208
SCHIZOCYTRIUM AGGREGATUM ATCC 29209
SECALE CEREALE E1-21 LOVASZPATONAI [C1] SONHO (RYE, SEIGLE, ROGGEN)
+ EMBRYO TRITICUM AESTIVUM [43] THATCHER (WHEAT, BLE, WEIZEN)
ZEA MAYS (MAIZE, MAIS, MAIS)
ONLY REPORTED IN C33 FOR SECALÉ
HEITS 120
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- LINUM USITATISSIMUM (FLAX, LIN, FLAXES/LEIN)
+ CLONES PR6 AND PC11;
VICIA FABA (ROAD BEAN, FEVE DE MARAIS, SAUROHNE)

- NITELLA FLEXILIS (STONEWORT, • ARTHROCHTERALGE)
SP TROGBYA SPEC (• SCHRAUBENALGE)
- CHLORELLA [1-4] PYRENODOSA SAB 211/88 [5] SPEC ATCC 11469
- SCENEDESMIUS QUADRICAUDA ATCC 11440
- SCENEDESMIUS OBLIQUUS
- ULVA PERTUSA FROM ISE-BAY NEAR SUGASHIMA, J (SEA LETTUCE, ULVE,
HEESEALAT)
- 1 WHOLE GAMETOPHYTE THALLUS
CHLAMYDOPHORAS REINHARDII CELL WALL DEFICIENT MUTANT CM15
- CHLAMYDOPHORAS REINHARDII CELL WALL DEFICIENT MUTANT CM15
- CHLAMYDOPHORAS SPEC
- PORPHYRA YEZDENSI FROM DENS IN HAMA BEACH, HOKKAIDO, J (LAVER,
PORPHYRE, PURPURITANG) 1 GAMETOPHYTE, PURPURITANG)
- PORPHYRA TENERA (LAVER, PURPHYRE, PURPURITANG)
- GRACILARIA COMPRESSA
- 205 [1] HORI H., LIH B.-L., OSAMA S.;
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J. MOL. EVOL. 1:9411-19(1983).
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216 [1] LIH B.-L., HORI H., OSAMA S.;
NUCL. ACIDS RES. 11:5185-88(1983).

- STREPTOMYCES GRISEUS 45-H
MICROCOCCUS LUTEUS ATCC 4898 [M. LYSODEIKTICIUS]
MICROCOCCUS LUTEUS ATCC 9341 (=SARCINA LUTEA)
CLOSTRIDIUM PASTERIANUM ATCC 6013
ASAG MAYBE AGAAAG [1] SELECTION
ACC. TO HOMOLOGY
UNBURE 97 101
- BACILLUS ACIDOCALDARATUS
BACILLUS BREVIS ATCC 8185
BACILLUS PASTERII ATCC 11889
- BACILLUS STEAROTHERMOPHILUS 1430R AND 1430FV
BACILLUS STEAROTHERMOPHILUS 799
- BACILLUS STEAROTHERMOPHILUS 14575
BACILLUS SUBTILIS BD170 AND 168
- BACILLUS MEGETHERIUM KH
- BACILLUS FIRMIUS ATCC 14575
- BACILLUS LICHENIFORMIS S244
BACILLUS SUBTILIS 168
- SIMONETSITS A.¹
NUCL. ACIDS RES. 8:4111-24 (1980).
217 [1] SIMONETSITS A.¹
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 SPYROPLASMA HONEYBEE BC3

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THERMUS THEROPHILUS HB8
RRNA 1 123 BAND 1
RRNA 1 122 BAND 2
RRNA 2 122 BAND 3
RRNA 3 122 BAND 4 (MEAK)
THERMUS AQUATICUS ATCC 25104

OCTOPUS SPRINGS ISOLATE 2, YELLOWSTONE NATIONAL PARK
OCTOPUS SPRINGS ISOLATE 3, YELLOWSTONE NATIONAL PARK

THIOBACILLUS NEAPOLITANUS X
THIOBACILLUS M1 (=THIOBACILLUS "FERROXIDANS")

THIOMICROSPORA PELOPHILA ATCC 27801

THIOMICROSPORA L12, GALAPAGOS SUBMARINE HYDROTHERMAL VENT

ACINETOBACTER CALCOACETICUS ITG 59

RIFTIA Symbiont
CALYPTOGENA Symbiont
SOLENIA Symbiont
ODONTELLA Symbiont
ALTOBACTER VINELANDII NCIB 8789
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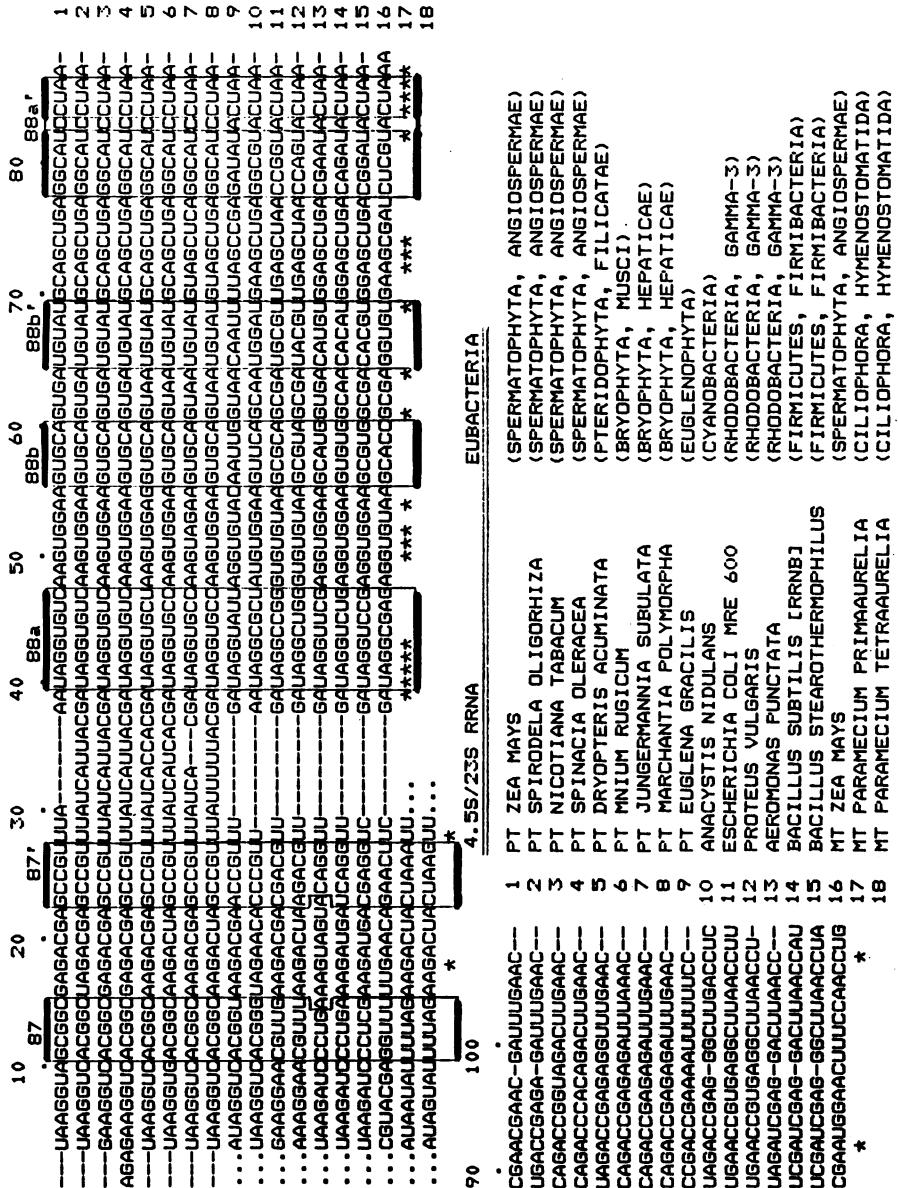
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- THIOBACILLUS FERRIDIDANS ATCC 19859
CHINO 1 (COPPER LEACHING POND ISOLATE AT CHINO MINE,
MARLEY, NEW MEXICO)
- THIOBACILLUS THIODIDANS ATCC 8055 AND
SULFUR SPRING ISOLATE, YELLOWSTONE NATIONAL PARK
- THIOBACILLUS THIOPARUS ATCC 8158
- CHINO 2 (COPPER LEACHING POND ISOLATE AT CHINO MINE,
MARLEY, NEW MEXICO)
- RHODOCYCLUS GEALATINOSUS (=RHODOPSEUDOMONAS GELATINOSA)
- THIOBACILLUS INTERMEDIA ATCC 15446
- THIOBACILLUS PERMETABOLIS ATCC 23370
NETS
- COPACIA ATCC 17616
ONLY PRESENT IN T. INTERMEDIA
- CONFLICT 8
- [1] G NOT PRESENT
[1] U [2] C
[1] C [2] U
- CONFLICT 9
- [1] C
[1] C
- CONFLICT 116
- [1] C
[1] C
- AQUASPIRILLUM SERPENS ATCC 11325
- ALCALIGENES FACIALIS NCIB 8156
- THIOBACILLUS AGRICOPILUS DSM 700 (ATCC 27807)
- ACIDIPHILUM CRYPTUM LHE12 (ATCC 33463)
- THIOBACILLUS NOVELLUS ATCC 8093
- AGROBACTERIUM TUNEFACIENS ICPB 112
- THIOBACILLUS VERSUTUS ATCC 23744 (=THIOBACILLUS A2)
- RHODOBACTER Sphaeroides (=RHODOPSEUDOMONAS S.)



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 BACILLUS SUBTILIS CRRNB]
 1 CLONE PB6204
 BACILLUS STEAROTHERMOPHILUS 1054
 1 CLONES PW4223 AND PW4382
 ZEA MAYS A16B N (MAIZE, MAIS, MAIS) ; CLONES
 PARAMECIUM PRIMAURELIA (SLIPPER ANIMALCULE,
 PANTOFFELTIERCHEN) ; CLONES
 PARAMECIUM TETRAURELIA (SLIPPER ANIMALCULE,
 PANTOFFELTIERCHEN) ; CLONES

		5.8S rRNA		EUKARYOTA	
120	9	130	140	9,	150
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	1 RATTUS RATTUS	(CHORDATA, MAMMALIA)
GGCC	-CGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	2 TERRAPENE CAROLINA	(CHORDATA, CHELONIA)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	3 GALLUS GALLUS	(CHORDATA, AVES)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	4 XENOPUS LAEVIS	(CHORDATA, AMPHIBIA)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	5 XENOPUS BOREALIS	(CHORDATA, AMPHIBIA)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	6 SALMO GARDNERI	(CHORDATA, OSTEICHTHYES)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	7 LYTECHINUS VARIEGATUS	(ECHINODERMA, ECHINOIDEA)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	8 DROSOPHILA MELANOGASTER	(ARTHROPODA, INSECTA)
GGCC	-CGGGAUCCU	CCG-----GGGACGCC	-----UGUCUAGGCUCCGUU	9 SCIRIA COPROPHILA	(ARTHROPODA, INSECTA)
GGCC	-A TACTG	TGTAT-----GGGACGCC	-----UGUCUAGGCUCCGUU	10 BOMBYX MORI	(ARTHROPODA, INSECTA)
GGUC	-GUGGACUCA	GGACACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	11 PHYLLOSTITHIA CYNTHIA-RICINI	(ASCOMYCOTA, INSECTA)
GGUC	-GUGGACUCA	GGACACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	12 ACYRTHOSIPHON MAGNOLIAE	(ARTHROPODA, INSECTA)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	13 ARTEMIA SALINA	(ARTHROPODA, ANOSTRACA)
GGUC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	14 ARION RUFUS	(MOLLUSCA, GASTROPODA)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	15 HYMENIACEIDON SANGUINEA	(PORIFERA, SILICEA)
GGUC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	16 THERMOMYCES LANIGENOSUS	(ASCOMYCOTA, PLECTOMYCETES)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	17 NEUROSPORA CRASSA	(ASCOMYCOTA, ENDOMYCETIDAE)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	18 SACCHAROMYCES CEREVISIAE	(ASCOMYCOTA, PROTOMYCETIDAE?)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	19 SCHIZOSACHAROMYCES POMBE	(MYXOGLASTRIA)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	20 DICTYOSTELIUM DISCOIDEUM	(AMOEBAINA)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	21 PHYSARUM POLYCHYTRIUM	(KINETOPLASTIDA, TRYANOSOMAT.)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	22 ACANTHODEBA CASTELLANI	(DINOPHYTA)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	23 CRITHIDIA FASCICULATA	(CILIOPHORA, HYMENOSTOMATIDA)
GGCC	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	24 TRYANOSOMA BRUCEI	(CILIOPHORA, HYMENOSTOMATIDA)
JCCG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	25 CRYPTOCODIUM COMNII	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	26 TETRAHYMENA PYRIFORMIS A	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	27 TETRAHYMENA THERMOPHILA	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	28 TETRAHYMENA PARAVORAX	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	29 TETRAHYMENA PATULA	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	30 TETRAHYMENA CAMPYLLUM	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	31 COLPIDIUM COLFODA	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	32 GLAUCONIA CHATTONI	(CILIOPHORA, HYMENOSTOMATIDA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	33 CHAMYDOMONAS REINHARDII	(VOLVOPHYTA)
GGAGG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	34 SPERMATOphyta, ANGIOSPERMae	(SPERMATOphyta, ANGIOSPERMae)
GGCCG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	35 TRITICUM AESTIVUM	(SPERMATOphyta, ANGIOSPERMae)
GGCCG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	36 ORZA SATIVA	(SPERMATOphyta, ANGIOSPERMae)
GGCCG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	37 LUPINUS LUTEUS	(SPERMATOphyta, ANGIOSPERMae)
GGCCG	-GGGGUCCGCGC	GCGACU-----GGGACGCC	-----UGUCUAGGCUCCGUU	38 Vicia faba	(SPERMATOphyta, ANGIOSPERMae)

- RATTUS RATTUS (RAT, RAT, WANDERFARTE)
HUS MUSCULUS (HOUSE MOUSE, SODIUS DOMESTIQUE, HAUSHAUSS)
HOMO SAPIENS (MAN, HOMME, MENSCH)
L. C. L. C. NOVIKOFF, HEPATICA ASCITES [C3] MPC-11 [C3] HELA
L6 [P-29] L77 CLONE F59 OF CHR-B4 IN PBR322 [B3] CLONE PHBES IN
PBR322 [B3] RAT LIVER.
HE75 1
HE75 2 US PARTIALLY (20/100 IN HELA)
MODBASE 14 F PARTIALLY
MODBASE 55 F
MODBASE 69 F
MODBASE 75 F
SITE 157 UNI NOT PRESENT IN RATTUS
- TERRAPENE CAROLINA (-) AMERIKANISCHE DOSENSENSCHILDKRÖTE)
1 HEART CELLS CCL50 US 50/100
MODBASE 14 F
MODBASE 69 F
MODBASE 75 F
MODBASE 75 G3
XENOPUS LAEVIS (CLAMED TOAD, XENOPE, KRALLENFROSCH)
1 HEART FIBROBLASTS US 70-90/100
HE75 2 F PARTIALLY
MODBASE 69 F
MODBASE 75 G3
XENOPUS BOREALIS (CLAMED TOAD, XENOPE, KRALLENFROSCH)
1 TRANSFORMED KIDNEY CELLS, [C3] CLONE PXL212 IN PRL1,
[C3] CLONE PLR101 IN PMLB9 40/100
HE75 1 20/100
HE75 3 40/100
MODBASE 15 US 30-40/100 (EXCLUDING MODBASE 19)
MODBASE 19 F 50/100 (EXCLUDING MODBASE 15)
MODBASE 70 F
MODBASE 76 G3
VARIANT 140 159 C MAYBE U LESS THAN 1/100
HE75 2 55/100
HE75 3 34/100
MODBASE 15 40/100
MODBASE 19 F
MODBASE 70 F
MODBASE 76 G3
VARIANT 140 159 C MAYBE U LESS THAN 1/100
HE75 2 20/100
HE75 3 40/100
MODBASE 15 30-40/100 (EXCLUDING MODBASE 19)
MODBASE 19 F 50/100 (EXCLUDING MODBASE 15)
MODBASE 70 F
MODBASE 76 G3
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- SOUND GARNIERI (RAINBOW TROUT, TRUITTE ARC-EN-CIEL,
SILVERBONED ORELLE) ; FIBROBLAST, CELL LINE RTG-2
HETS 1 40/100
MODBASE 8 LS
MODBASE 14 LS PARTIALLY
MODBASE 55 F
MODBASE 69 F PARTIALLY
MODBASE 75 LS
LYTECHINUS VARILEGATUS (SEA URCHIN) * SEE (GEL)
1 CLONE PLV134 IN PACYCB1, CLONE PBPH06
HETS 1 33/100
DENDROPHILA MELANOSTER OREGON R (FRUIT FLY, FRUCHTFLIEGE)
WHOLE TISSUE 1 64/100
RNA 123 HS, RNA
RNA 124- 153 2B, RNA
MODBASE 74 63
SCIRARA CORYPHILLA (SNAIL, TRÄUMERLECKE)
1 CLONE PBc22 123 HS, RNA
RNA 1 123 HS, RNA
RNA 124 153 2B, RNA
MODBASE 74 63
BOMBYX MORI (BILKMOH, SELDENSPINNER)
1 POSTERIOR BILKMOH OF SILKMOH
MODBASE 61 F
MODBASE 61 63
PHYLLOSTICIA CYNTHIA RICINI (BILKMOH, SELDENSPINNER)
1 POSTERIOR SILKMOH OF SILKMOH
MODBASE SEPIPHON MAGNOLIAE (ELDER APHID, HOLLUNDERBLATTLAUS)
WHOLE TISSUE 1 63
MODBASE 75 HS
AMERIA SEA 119 (BRINE SHRIMP, SALINEMERGEBE)
1,11 CYSTS 12 CLONE PBPS13 6 IS T [2] ARTIFICIAL DURING CLONING?
MODBASE 12 HS
CONFLICT 119 A IS AT [2]
MODBASE -2 -1 S/100 PROBABLY BU
HETS 1 25/100
HETS 2 25/100
HETS 3 45/100
MODBASE 45 C3
MODBASE 47 A3
MODBASE 105 F
MODBASE ? U SHOULD BE F
APION RUFUS (SNAIL, MEISCHNECKE)
1 WHOLE TISSUE
MODBASE 73 F
MODBASE 75 G3
HYMENOIDON SANGUINEA (SPONGE, EPONGE, SCHWAMM)
1 WHOLE TISSUE
HETS 1 LESS THAN 50/100
HETS 2 MORE THAN 50/100
MODBASE 43 A3
MODBASE 64 F
MODBASE 73 F
MODBASE 75 G3
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- THERMOPHYCES LAMINGINOSUS
HMDDBASE 19 F
HMDDBASE 45 A₂
HMDDBASE 51 F
HMDDBASE 73 F
HMDDBASE 75 F
HMDDBASE 93 G₂
- NEUROBESPA CRASSA
1 CLONE PYRC2 IN PBRZ22
SACCHAROMYCES CERESIAE (BAVERS YEAST, LEVURE, BAECERHEFE)
[C1] ATCC 22244 (ATCC4), [C2] 528BC HAPLOID
HETS 1 5/100
HETS 2 5/100
HETS 6 9/100
HMDDBASE 80 F
- SCHIZOSACCHAROMYCES FOBIUS (FISSION YEAST, LEVURE, SPALTHEFE)
1 CLONE PYRC2 AND PYM55 IN PBRZ22
HETS 1 POST ABUNDANT
HETS 2
HETS 3
HETS 4
HETS 5
HETS 6
HETS 7 POST ABUNDANT
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HETS 162 U MAYBE NOT PRESENT
- CRITHIDIA FASCICULATA (TRYPANOSOME, TRYFANSOM)
- HMDDBASE 7 UC 80/100
HMDDBASE 43 A₂
HMDDBASE 69 F
HMDDBASE 75 G₂
HMDDBASE 163 G₂
HETS 171 34/100
HETS 172 63/100
- TRYPANOSOMA BRUCEI BRUCEI
1 CLONE P162-5.85
- CRYPTOCODONIUM COMMUNIS (DINFLAGELLATE, DINFLAGELLAT) NOT DETERMINED
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- TETRAHYMENA PYRIFORMIS M
- NUDBASE 78 G³
TETRAHYMENA PYRIFORMIS M AND GL
TE TRAHYMENA VORAX VS
TE TRAHYMENA LEUCOPHRYNS TUR
- TE TRAHYMENA THERMOPHILA B-1648-VII
- TETRAHYMENA PARAVORAX RP
- TE TRAHYMENA PATULA L-FF AND NEI
- COPIDIUM CAMPYLUM
- COPIDIUM COLPODA
- GLAUCOMA CHATTONI
- CHLAMYDONAS REINHARDTII CN15 G³
- NUDBASE 42 G³
NUDBASE 74 G³
TRITICUM AESTIVUM (WHEAT, BLE, WEIZEN)
- 1 EMBRYO 1 79/100
HETS 1 79/100
HETS 2 16/100
NUDBASE 22 F
NUDBASE 47 A³
NUDBASE 78 F
NUDBASE 79 G³
NUDBASE 119 C MAYBE NOT PRESENT
UNSURE 123 A MAYBE NOT PRESENT
ORTIA SATIVA VAR. MANGE-SURUCHI (RICE, RIS, RETS)
1 CLONE PRZC17 GELBE LUPINE
- LUPINUS LUTEUS (YELLOW LUPINE, GELBE LUPINE)
- 1 CLONES PARIS AND PARTZ IN LAMBERT-67 CDS IN 15/100
VARIANT PARIS 1 CDS IN 15/100
Vicia faba (ROAD BEAN, SABORNE)
- 1 LEAVES, 22 F
NUDBASE 47 A³
NUDBASE 78 F
NUDBASE 79 G³
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