APPENDIX A

Media formulation

Basal medium

KH_2PO_4	2.38g
$K_2HPO_4.3H_2O$	5.65g
$MgSO_4.7H_2O$	1.0g
Salt solution	6.2ml
Distilled water	1.0L

Glycerol-Asparagine agar medium (ISP5)

L-asparagine monohydrate	1.0g
Potassium phosphate, Dibasic	1.0g
Iron (II) Sulphate Heptahydrate	0.001g
Manganese (II) Chloride Tetrahydrate	0.001g
Zinc Sulphate Heptahydrate	0.001g
Agar	15.0g
Glyserol	10.0g

pH 7.0-7.4

Glycerol solution (30% v/v)

Glycerol	300ml
Yeast extract	1.0g
Glucose	3.75g
Casein	1.25g
Distilled water	0.7L

Inorganic salt- starch agar medium (ISP 4)

Soluble starch	10.0g
Potassium phosphate Dibasic	1.0g
Magnesium Sulphate Heptahydrate	1.0g
Sodium chloride	1.0g
Ammonium sulphate	2.0g
Calcium carbonate	2.0g
Iron (II) Sulphate Heptahydrate	0.001g
Manganese (II) Chloride Tetrahydrate	0.001g
Zinc Sulphate Heptahydrate	0.001g
Agar	15.0g
Distilled water	1.0L

pH 7.0 ~ 7.4

Nitrate Reduction test:

Solution I:

$CaCl_2$	0.5g
Distilled water	100ml

Solution II:

K_2HPO_4 (anhydrous)	0.5g
$MgSO_4.7H_2O$	0.2g
KNO_3	1.0g
Glucose	10.0g
Distilled water	900ml

Non-sporulating media

Casamino acid	20.0g
Soluble starch	20.0g
Yeast extract	4.0g
Agar	18.0g

Oatmeal agar (ISP 3)

Oatmeal	60.0g
Agar	12.5g
Distilled water	1.0L

pH 6.0 ± 0.2

Peptone Iron agar medium

Peptone	15.0 g
Proteose Peptone	5.0 g
Ferric Ammonium Citrate	0.5 g
Sodium Glycerophosphate	1.0 g
Sodium Thiosulfate	0.08 g
Agar	15.0 g

Peptone-Yeast Extract-Iron agar medium (ISP 6)

Peptone	15.0g
Proteose peptone	5.0g
Ammonium iron (III) citrate	0.5g
Potassium phosphate, Dibasic	1.0g
Sodium Thiosulphate	0.08g
Yeast extract	1.0g
Agar	15.0g

pH 7.0 – 7.2

Peptone-Yeast Medium (ISP 1)

Polypepton	5.0g
Yeast extract	3.0g
Distilled water	1.0L

pH 7.0 - 7.2

Sabouraud Dextrose Agar (SDA)

Enzymatic digest of casein	10.0g
Dextrose	20.0g
Agar	15.0g
Distilled water	1.0L

pH 5.4 – 5.8

Salt solution

$CuSO_4.5H_2O$	102mg
$FeSO_4.7H_2O$	176mg
$MnCl_2.4H_2O$	126mg
$ZnSO_4.7H_2O$	24mg
Distilled water	100ml

Starch-Glucose-Yeast Extract Yeast (SGY)

Soluble starch	10.0g
D(+)-glucose	10.0g
Glycerol	10.0g
Corn steep solids	2.5g
Bacteriological peptone	5.0g
Yeast extract	2.0g
CaCO3	3.0g
Instant ocean	16.7g
Distilled water	1.0L

pH 7.3

Tyrosine agar medium (ISP 7)

L-Tyrosine	0.5g
L-Asparagine Monohydrate	1.0g
Potassium phosphate	0.5g
Magnesium sulfate Heptahydrate	0.5g
Sodium chloride	0.5g
Iron (II) sulfate Heptahydrate	0.011g
Manganese (II) chloride Tetrahydrate	0.001g
Zinc sulfate Heptahydrate	0.001g
Agar	15.0g
Glycerol	15.0g

pH 7.0 – 7.4

Yeast extract-malt extract agar medium (ISP 2)

Yeast extract	4.0g
Malt extract	10.0g
Glucose	4.0g
Agar	15.0g
Distilled water	1.0L

pH 7.2 - 7.4

Yeast extract-peptone-Glucose agar (YPG)

Yeast extract	10.0g
Peptone	20.0g
Glucose	20.0
Agar	18.0g
Distilled water	1.0L
pH 6.8	

APPENDIX B

Scanning electron microscopy (SEM) procedure

Agar block culture

↓

Fixation in 2% w/v osmium tetroxide (Agar Scientific) at 4°C

↓

Wash twice with distilled water (15 minute each)

↓

Gradual dehydration in ethanol (10-95%, v/v) (15 minute each % ethanol)

↓

Dehydrate twice with absolute ethanol (15 minute each)

↓

Dehydration with ethanol:acetone (3:1 → 1:1 → 1:3) (15 minute each wash)

↓

Dehydrate three times with 100% acetone (20 minute each)

↓

Critical point drying in liquid carbon dioxide

↓

Mount on 0.5” aluminium stubs (Agar Scientific)

↓

Leave overnight in vacuum dessicator

↓

Gold sputter-coating

↓

SEM viewing

(Leica Stereoscan 440)

APPENDIX C

Forward and reverse sequences of strains X34, X42 and X77 obtained from 1st Base using ABI system.

>1st_BASE_214384_strain X34_27f_

GNNNNNANTGGCTTACATATGTCGAGTCGAACGATGAACCACTTCGGTGGG
GATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACTCTG
GGACAAGCCCTGGAAACGGGGTCTAATACCGGATACTGATCCTCGCAGGCA
TCTGCGAGGTTCGAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCA
GCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGACGGGTAGCCGGCCTG
AGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGG
GAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGA
CGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGA
AGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGC
CAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGGGC
GTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTT
AACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGAGAT
CGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGG
TGGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTG
GGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGC
ACTAGGTGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAA
GTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC
GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCGAA
GAACCTTACCAAGGCTTGACATACACCGGAAAACCCTGGAAACAGGGTCCC
CCTTGGGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGGGA
AGATGTTGGGTTAAGTCCCGCAAACGAGCGCAACCCTTTGGTCCCGTGTTTG
CCAGCAGGCCCTTTGTGGTGCTGGGGACTCACGGGGAGGACCCGCCCGGGG
TCCAACTCGGGAGAAGGTGGGGACANCAANGTCAAAGTTNNTTCATGGC

>1st_BASE_214385_strain X34_1525r

GGGGGNAGCCGTTAATTCGTCTTCGTCCCAATCGCCAGTCCCACCTTCGACA
GCTCCCTCGCACAAGGGGTTGGGCCACCGGCTTCGGGTGTTACCGACTTTCG
TGACGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCAGCAA
TGCTGATCTGCGATTACTAGCGACTCCGACTTCATGGGGTCGAGTTGCAGAC
CCCAATCCGAACTGAGACCGGCTTTTTGAGATTCGCTCCACCTCGCGGTATC
GCAGCTCATTGTACCGGCCATTGTAGCACGTGTGCAGCCCAAGACATAAGG
GGCATGATGACTTGACGTCGTCCCCACCTTCCTCCGAGTTGACCCCGGCGGT
CTCCCGTGAGTCCCCAGCACCACAAGGGCCTGCTGGCAACACGGGACAAGG
GTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGA
CAGCCATGCACCACCTGTACACCGACCACAAGGGGGACCCTGTCTCCAGGG
TTTTCCGGTGTATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGCGTCGAATTA
AGCCACATGCTCCGCCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTTA
GCCTTGCGGCCGTACTCCCCAGGCGGGGCACTTAATGCGTTAGCTGCGGCA
CGGACAACGTGGAATGTTGCCCACACCTAGTGCCCACCGTTTACGGCGTGG
ACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTCCTCAGCGT
CAGTATCGGCCCAGAGATCCGCCTTCGCCACCGGTGTTCCTCCTGATATCTG
CGCATTTCACCGCTACACCAGGAATTCCGATCTCCCCTACCGAACTCTAGCC

TGCCCGTATCGACTGCAGACCCGGGGTTAAGCCCCGGGCTTTCACAACCGA
CGTGACAAGCCGCCTACAAGCTCTTTACGCCCAATAATTCCGGACAACGCTT
GCGCCCTACGAATTACCGCGGCTGCTGGCACGTAGTTAGCCGGCGCTTCTTC
TGCAGGTACGGGCACTATCGCTTCTTCCCTGGTGAAAAAGGTTTACAACCCG
AAAGGGCGTCATCCCCTCAACAGCGGCCGTGGCTGCATCAAGGGGTTACGC
CGATTGTGGCAATTATTTCCCCAACCTGGCCTGCCCTCCGTAAGGA

>1st_BASE_244193_strain X42_27f
NNGATNCGTTAACGTGATGCTCCTTACTTACGATGAACCGCTTTCGGGCGGG
GATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACTCTG
GGACAAGCCCTGGAAACGGGGTCTAATACCGGATATGACTGTCCGCCGCAT
GGTGGATGGTGTAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAG
CTTGTTGGTGAGGTAGTGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGA
GAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGG
AGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGAC
GCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA
GAAGCGAGAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCC
AGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGGGCG
TAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGAAAGCCCGGGGCTTA
ACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGAGATC
GGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGT
GGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTG
GGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGC
ACTAGGTGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAA
GTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGAC
GGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCGAA
GAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACAGGCCCCC
CCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGTGA
GATGTTGGGTTAAGTCTCGCAACGAGGCGCAATCCTTTGTCTCCGTGTTGCT
CAGCAGGCTTCTTGTGGTTGCTGGGGACTCACGGGNGNACCNNNCGGGGGN
NCAATNNCGGGAGGGANGNNGNGNNCNNCNNNCAAGNCAATCATGCCCCC
NTTANGTGNNNTTGGGNCNNN

>1st_BASE_244194_strain X42_1525r
NNNNNTNNACGCACGTGAACTGTATCTTGGCGCGAGGCCCACCTTACGGAC
AGCTCCCTCCCACAAGGGGTTGGGCCACCGGCTTCGGGTGTTACCGACTTTC
GTGACGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCAGCA
ATGCTGATCTGCGATTACTAGCGACTCCGACTTCATGGGGTCGAGTTGCAGA
CCCCAATCCGAACTGAGACCGGCTTTTTGAGATTCGCTCCACCTCACGGTAT
CGCAGCTCATTGTACCGGCCATTGTAGCACGTGTGCAGCCCAAGACATAAG
GGGCATGATGACTTGACGTCGTCCCCACCTTCCTCCGAGTTGACCCCGGCGG
TCTCCCGTGAGTCCCCAGCACCACAAGGGCCTGCTGGCAACACGGGACAAG
GGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACG
ACAGCCATGCACCACCTGTACACCGACCACAAGGGGGCGCCTGTCTCCAGA
CGTTTCCGGTGTATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGCGTCGAATT
AAGCCACATGCTCCGCCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTT
AGCCTTGCGGCCGTACTCCCCAGGCGGGGCACTTAATGCGTTAGCTGCGGC
ACGGACAACGTGGAATGTTGCCCACACCTAGTGCCCACCGTTTACGGCGTG

GACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTCCTCAGCG
TCAGTATCGGCCCAGAGATCCGCCTTCGCCACCGGTGTTCCTCCTGATATCT
GCGCATTTCACCGCTACACCAGGAATTCCGATCTCCCCTACCGAACTCTAGC
CTGCCCGTATCGACTGCAGACCCGGGGTTAAGCCCCGGGCTTTTACAACCG
ACGTGACAAGCCGCCTACGAGCTCTTTACGCCCAATAATTCCGGACAACGC
TTGCGCCCTACGTATTACCGCGGCTTCTGGCACGTAATTAGCCGGGGCTTTC
TTTCTTGCAGGTACCGTCACCTTTCGCTTCTTCCCTGCTGAAAGAGGTTTATC
AATCCCGAAGGCCGTTCATCTCCTTCACGCGGNGGTTTCGCTNNCATTCAGG
NNTNNCCGCCNCCTNNTTGTNNNAANANNCCTCCACCNGNNNNNCCCTCTC
TCCCNNTAGGNNN

>1st_BASE_244195_strain X77_27f
NNNNTTNGCGTGGGGCCTCTTTCTATGCCGTCGACGATGAAACCGCTTCGGT
GGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTTCAC
TCTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGATAATACTCCGGCCC
GCATGGGAGGGGGTTGAAAGCTCCGGCGGTGAAGGATGAGCCCGCGGCCT
ATCAGCTTGTTGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGG
CCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTA
CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAG
CGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAG
GGAAGAAGCGCAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACG
TGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTATTG
GGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGG
CTTAACCCCGGGTCTGCATTCGATACGGGCTAGCTAGAGTGTGGTAGGGGA
GATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACAC
CGGTGGCGAAGGCGGATCTCTGGGCCATTACTGACGCTGAGGAGCGAAAGC
GTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTG
GGAACTAGGTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCAT
TAAGTTCCCCGCCTGGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAAT
TGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTTCGACGCAAC
GCGAAGAATCTTTACCCAAGGCTTGACATATACCGGGAAAGCATCAGAGAT
GGTGCCCTCCCCTTGTGGTCGGGTATTACCAGGTGGGTGCATNNTGNCGTCA
GCTCGTGTCGTGAGATGTTTGGGGNTAAGTCCCGCANGAGCGCNNNNTGNN
NTTGTNNGCCAGCATGCCTTTTCGGGTGAT

>1st_BASE_244196_strain X77_1525r
NNNNNNTCCTNTCCGTACGTAGGTGGGCTGGCGCTAGTGGCGAGGCCCACC
TTCGACAGCTGCCTCGCACAGAGGGGTTGGGCCACCGGCTTCGGGTGTTAC
CGACTTTCGTGACGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCA
CCGCAGCAATGCTGATCTGCGATTACTAGCAACTCCGACTTCATGGGGTCGA
GTTGCAGACCCCAATCCGAACTGAGACCGGCTTTTTGAGATTCGCTCCGCCT
CACGGCATCGCAGCTCATTGTACCGGCCATTGTAGCACGTGTGCAGCCCAA
GACATAAGGGGCATGATGACTTGACGTCGTCCCCACCTTCCTCCGAGTTGAC
CCCGGCAGTCTCCTGTGAGTCCCCATCACCCCGAAAGGCATGCTGGCAACA
CAGAACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACAC
GAGCTGACGACAGCCATGCACCACCTGTATACCGACCACAAGGGGGGCACC
ATCTCTGATGCTTTCCGGTATATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGC
GTCGAATTAAGCCACATGCTCCGCTGCTTGTGCGGGCCCCCGTCAATTCCTT

TGAGTTTTAGCCTTGCGGCCGTACTCCCCAGGCGGGGAACTTAATGCGTTAG
CTGCGGCACCGACGACGTGGAATGTCGCCAACACCTAGTTCCCAACGTTTA
CGGCGTGGACTACCAGGGTATCTAATCCTGTTCGCTCCCCACGCTTTCGCTC
CTCAGCGTCAGTAATGGCCCAGAGATCCGCCTTCGCCACCGGTGTTCCTCCT
GATATCTGCGCATTTCACCGCTACACCAGGAATTCCGATCTCCCCTACCACA
CTCTAGCTAGCCCGTATCGAATGCAGACCCGGGGTTAAGTCCCCGGGCTTTC
ACATCCGACGTGACAAGCCGCCTACGAGCTCTTACGCCCAATAATTCCCGG
ACAACGCTTTGCGTCCCTACGTATTATCCGCGGGCTGCTGGCACGTAGNAGC
CGGCGCTTCTTTCTGCAAGTACNNCACTGCGCTNTNCTTGCTGAAAGAGGTT
TACANNCGAGGGCCGT

APPENDIX D

Combined forward and reverse sequences of strains X34, X42 and X77

>consensus_strain X34 (1109 nucleotides)

GTCGAACGATGAACCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAAC
ACGTGGGCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAACGGGGTCTA
ATACCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAAAGCTCCGGCG
GTGCAGGATGAGCCCGCGGCCTATCAGCTAGTTGGTGAGGTAACGGCTCAC
CAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGA
CTGAGACACGGCCCAGActCcTACGGgaGGCAGCAGTGGGGAAtATTGCACAA
TgGGCGaAAgCCTGATGCAGCgACGCcGcgtgaGGGATGACGgCCTTCGGGTTGT
AAACCTcTTTCAgCAGGGAAGAAGCGAaAGTGaCgGTACCTGCAGAAGAAGC
GCCGGCTAACTACGTGCCAGCAGCCGCGGTAATaCGTAGGGCGCAAGCGTT
GTCCGGAATTATTGGGCGTAAAGAGCTcGTAGGCGGCTTGTCACGTCGGTTG
TGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGA
GTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATA
TCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCCGATACTGACGCT
GAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCA
CGCCGTAAACGGTGGGCACTAGGTGTGGGCAACATTCCACGTTGTCCGTGC
CGCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAA
AACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTA
ATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATACACCGGAAAAC
CCTGGAGACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTC
GTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC
TTGTCCCGTGTTGCCAGCAGGCCCTTGTGGTGCTGGGGACTCACGGGAGACC
GCCGGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCC
TTATGTCTTGGGCTGCACACGTGCTACAATGGCCGGTACAATGAGCTGCGAT
ACCGCGAGGTGGAGCGAATCTCAAAAAGCCGGTCTCAGTTCGGATTGGGGT
CTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCAT
TGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACG
AAAGTCGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGCGAGGGAGCT
GTCGAAGGTGGGACTGGCGA

>consensus_ strain X42 (1342 nucleotides)

TGAGTAACACGTGGGCAATCTGCCCTGCACTCTGGGACAAGCCCTGGAAAC
GGGGTCTAATACCGGATATGACTGTCCGCCGCATGGTGGATGGTGTAAAGC
TCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAGT
GGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCggcCacAct
GGGActGAGacacggcCcGGactccTacgGGaggcagcagtggggaAtattGCacaatgggCgaAAgcc
tgatGcAgCgaCgcCGcGtgaGgGATGACGGCCTTCGGGtTgTAAACCTCTTTCAGCA
GGGAAGAAGCGAgAGTGACGGTACCTGCAgaAgAAGCgCCGGCTAAcTACGT
GCCAGcAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGG
GCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTgAAAGCCCGGGGC
TTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGAG
ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACC
GGTGGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGC
GTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTG
GGCACTAGGTGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATT

AAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTG
ACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGACGCAACGCG
AAGAACCTTACCAAGGCTTGACATACACCGGAAACGTCTGGAGACAGGCGC
CCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGT
GAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCCGTGTTGCCA
GCAGGCCCTTGTGGTGCTGGGGACTCACGGGAGACCGCCGGGGTCAACTCG
GAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTG
CACACGTGCTACAATGGCCGGTACAATGAGCTGCGATACCGTGAGGTGGAG
CGAATCTCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCC
CATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATA
CGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACA

>consensus_ strain X77 (1278 nucleotides)

GGGGTTGAAAGCTCCGGCGGTGAAGGATGAGCCCGCGGCCTATCAGCTTGT
TGGTGGGGTAATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGG
GCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC
AGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC
GTGAGGGATGACGGCCtTCGggTtGTAAACCTCTTTCAGCAgGgAagaAGCGCAa
GTGacGgTACcTGCAGAAGAAGCGCCGGCTaaCTACGTGCCAGCAGCCGCGGT
AATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGGGCGTAAGAGCTCGTA
GGCGGCTTGTCACGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGC
ATTCGATACGGGCTAGCTAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTG
TAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGA
TCTCTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGG
ATTAGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAGGTGTTGGC
GACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCCCGCCTGGG
GAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACA
AGCAGCGGAGCATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAG
GCTTGACATATACCGGAAAGCATCAGAGATGGTGCCCCCCTTGTGGTCGGT
ATACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA
GTCCCGCAACGAGCGCAACCCTTGTTCTGTGTTGCCAGCATGCCTTTCGGGG
TGATGGGGACTCACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGGGG
ACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAA
TGGCCGGTACAATGAGCTGCGATGCCGTGAGGCGGAGCGAATCTCAAAAAG
CCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTT
GCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTTCCCGGGCCTTGT
ACACACCGCCCGTCACGTCACGAAA

APPENDIX E

BLAST results (top 20) of strains X34, X42 and X77

BLAST Strain X34

(Formatting Results - 60HVH2YZ01S)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
GU263851.1	Streptomyces sp. 35034 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
GQ392058.1	Streptomyces rochei strain A-1 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
AB184529.2	Streptomyces fungicidicus gene for 16S rRNA, partial sequence, strain: NBRC 13848	2593	2593	100%	0	99%
GQ289142.1	Bacterium Kwm1 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ792577.1	Streptomyces rochei strain cfcc3165 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ792558.1	Streptomyces rochei strain cfcc3131 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ792552.1	Streptomyces rochei strain cfcc3115 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ481066.1	Streptomyces avidinii strain xsd08150 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ481055.1	Streptomyces rochei strain xsd08098 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ481635.1	Streptomyces enissocaesilis strain HBUM174552 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
FJ224362.1	Streptomyces sp. P-13 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU841560.1	Streptomyces rochei strain HBUM174096 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU621883.1	Streptomyces sp. YDG17 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU593731.1	Streptomyces rochei strain 173672 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU593730.1	Streptomyces rochei strain 173260 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU593640.1	Streptomyces avidinii strain 173969 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU570711.1	Streptomyces rochei strain 173609 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU570623.1	Streptomyces rochei strain 173342 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU570372.1	Streptomyces rochei strain 173315 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%
EU257263.1	Streptomyces sp. A53Ydz-XM 16S ribosomal RNA gene, partial sequence	2593	2593	100%	0	99%

BLAST Strain X42

(Formatting Results - DNYC2HWM01S)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
GU002076.1	Streptomyces sp. FXJ6.047 16S ribosomal RNA gene, partial sequence	2405	2405	100%	0	99%
AB362247.1	Streptomyces sampsonii gene for 16S rRNA, partial sequence	2405	2405	100%	0	99%
EU384262.1	Streptomyces sp. A556 Ydz-TA 16S ribosomal RNA gene, partial sequence	2405	2405	100%	0	99%
EU368806.1	Streptomyces sp. A52 Ydz-XM 16S ribosomal RNA gene, partial sequence	2405	2405	100%	0	99%
EU257255.1	Streptomyces sp. A93Ydz-QZ 16S ribosomal RNA gene, partial sequence	2405	2405	100%	0	99%
EF063487.1	Streptomyces sp. JXHM-A-12 16S ribosomal RNA gene, partial sequence	2405	2405	100%	0	99%
EF063445.1	Streptomyces sp. C19-17 16S ribosomal RNA gene, partial sequence	2405	2405	100%	0	99%
EU257240.1	Streptomyces sp. A46Ydz-XG 16S ribosomal RNA gene, partial sequence	2399	2399	100%	0	99%
AM412550.1	Streptomyces sp. 45zhy partial 16S rRNA gene, strain 45zhy	2399	2399	100%	0	99%
AB045867.1	Streptomyces griseus subsp. griseus gene for 16S rRNA	2399	2399	100%	0	99%
EF588223.2	Streptomyces griseus strain NRRL B-2165 16S ribosomal RNA gene, partial sequence	2394	2394	100%	0	99%
EU181249.1	Streptomyces sp. 94P32-5 16S ribosomal RNA gene, partial sequence	2394	2394	100%	0	99%
AM412551.1	Streptomyces sp. 41zhy partial 16S rRNA gene, strain 41zhy	2394	2394	100%	0	99%
HQ132794.1	Streptomyces albus strain N64 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%
HM797397.1	Streptomyces sp. L131D 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%
HM481475.1	Streptomyces albus strain XJ-17 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%
GU722183.1	Streptomyces sp. JV186 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%
HM222696.1	Streptomyces sp. 401K3-1 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%
GU213490.1	Streptomyces sp. HB094 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%
HM007152.1	Actinomycetales bacterium B3(2010) strain B3 16S ribosomal RNA gene, partial sequence	2388	2388	100%	0	99%

BLAST Strain X77

(Formatting Results - DNWTHD5701N)

Accession	Description	Total score	Query coverage	E value	Max ident
HM018120.1	Streptomyces sp. VAN21 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018109.1	Streptomyces sp. WALP25 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018108.1	Streptomyces sp. WALP24 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018107.1	Streptomyces sp. WALP23 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018106.1	Streptomyces sp. WALP22 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018082.1	Streptomyces sp. MEC01 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018079.1	Streptomyces sp. LEN01 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
HM018076.1	Streptomyces sp. HS7003 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
AB184777.2	Streptomyces roseochromogenus gene for 16S rRNA, partial sequence, strain: NBRC 3442	2220	100%	0	99%
EU647478.1	Streptomyces anulatus strain Malaysia 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EU741221.1	Streptomyces globisporus subsp. globisporus strain 13669A 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EU741191.1	Streptomyces sp. 13661T 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EU741124.1	Streptomyces globisporus subsp. globisporus strain 13638A 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
FJ792550.1	Streptomyces bacillaris strain cfcc3101 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
FJ572022.1	Actinomycetales bacterium JH105 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
FJ238114.1	Streptomyces sp. DS3024 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EU368787.1	Streptomyces sp. A306 Ydz-ZZ 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EU273549.1	Streptomyces globisporus subsp. globisporus isolate XSD-114 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EU257275.1	Streptomyces sp. A10Ydz-XM 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%
EF192235.1	Streptomyces griseus 16S ribosomal RNA gene, partial sequence	2220	100%	0	99%

APPENDIX F

Ribosomal Database Project (RDP) results (top 20 lists) of strains X34, X42 and X77

SeqMatch :: Detail Hierarchy –Strain X34

Query Sequence: unknown, 1309 unique oligos
short ID, orientation, similarity score, S_ab score, unique common oligomers and sequence full name.

Lineage:

no rank Root (0/20/609523) (selected/match/total RDP sequences)
domain Bacteria (0/20/600316)
phylum "Actinobacteria" (0/20/115554)
class Actinobacteria (0/20/115554)
subclass Actinobacteridae (0/20/110191)
order Actinomycetales (0/20/109342)
suborder Streptomycineae (0/20/6703)
family Streptomycetaceae (0/20/6703)
genus Streptomyces (0/20/6449)

S000015282 not_calculated 0.995 1382 Streptomyces maritimus; BD26; AF233338

S000607425 not_calculated 0.995 1368 Streptomyces sp.; NT90(K15); AJ002089

S000651961 not_calculated 0.995 1354 Streptomyces rochei (T); NBRC 12908; AB184237

S000652015 not_calculated 0.995 1371 Streptomyces plicatus; NBRC 13071; AB184291

S000652035 not_calculated 0.995 1364 Streptomyces vinaceusdrappus; NBRC 13099; AB184311

S000652337 not_calculated 0.995 1341 Streptomyces rubrocyanodiastaticus subsp. piger; NBRC 14692; AB184613

S000652454 not_calculated 0.995 1371 Streptomyces olivaceus; NBRC 3119; AB184730

S000711645 not_calculated 0.995 1378 Streptomyces enissocaesilis; NRRL B-16365; DQ026641

S000712498 not_calculated 0.995 1384 Streptomyces sp. 3194; DQ663150

S000892542 not_calculated 0.995 1378 Streptomyces rochei; NRRL B-1559; EF626598

S000967652 not_calculated 0.995 1338 Streptomyces sp. A53Ydz-XM; EU257263

S001096907 not_calculated 0.995 1342 Streptomyces rochei; 173315; EU570372

S001097158 not_calculated 0.995 1335 Streptomyces rochei; 173342; EU570623

S001097246 not_calculated 0.995 1341 Streptomyces rochei; 173609; EU570711

S001097744	not_calculated	0.995	1337	Streptomyces avidinii; 173969; EU593640
S001097834	not_calculated	0.995	1340	Streptomyces rochei; 173260; EU593730
S001097835	not_calculated	0.995	1344	Streptomyces rochei; 173672; EU593731
S001098348	not_calculated	0.995	1359	Streptomyces sp. YDG17; EU621883
S001154764	not_calculated	0.995	1344	Streptomyces rochei; HBUM174096; EU841560
S001189021	not_calculated	0.995	1328	Streptomyces sp. P-13; FJ224362

Query Sequence: unknown, 1233 unique oligos
short ID, orientation, similarity score, S_ab score, unique common oligomers and sequence full name.

Lineage:

no rank Root (0/20/615916) (selected/match/total RDP sequences)
domain Bacteria (0/20/606188)
phylum "Actinobacteria" (0/20/115729)
class Actinobacteria (0/20/115729)
subclass Actinobacteridae (0/20/110300)
order Actinomycetales (0/20/109449)
suborder Streptomycineae (0/20/6711)
family Streptomycetaceae (0/20/6711)
genus Streptomyces (0/20/6457)

☑	S000004207	not_calculated	0.989	1382	Streptomyces griseus; IFO 13550; AB045867
☐	S000006304	not_calculated	0.982	1377	Streptomyces sp.; ATCC10246; Y15503
☐	S000393985	not_calculated	0.982	1413	Streptomyces sp. VTT E-99-1329 (A52); AF429393
☐	S000439349	not_calculated	0.982	1425	Streptomyces sampsonii (T); ATCC25495; D63871
☐	S000651942	not_calculated	0.982	1353	Streptomyces sp.; NBRC 12883; AB184218
☐	S000652367	not_calculated	0.982	1353	Streptomyces albidoflavus; NBRC 15392; AB184643
☐	S000711646	not_calculated	0.982	1426	Streptomyces champavatii (T); NRRL B-5682; DQ026642
☐	S000770062	not_calculated	0.989	1388	Streptomyces sp. 45zhy; AM412550
☐	S000770063	not_calculated	0.983	1388	Streptomyces sp. 41zhy; AM412551
☐	S000770111	not_calculated	0.994	1392	Streptomyces sp. C19-17; EF063445
☐	S000770153	not_calculated	0.994	1392	Streptomyces sp. JXHM-A-12; EF063487
☐	S000966532	not_calculated	0.986	1392	Streptomyces sp. 94P32-5; EU181249
☐	S000967629	not_calculated	0.989	1344	Streptomyces sp. A46Ydz-XG; EU257240
☐	S000967644	not_calculated	0.994	1348	Streptomyces sp. A93Ydz-QZ; EU257255
☐	S000981689	not_calculated	0.994	1347	Streptomyces sp. A52 Ydz-XM; EU368806
☐	S001015127	not_calculated	0.994	1347	Streptomyces sp. A556 Ydz-TA; EU384262
☐	S001093294	not_calculated	0.994	1306	Streptomyces albidoflavus; JAM-AC0101; AB362247

GU002076	S001613869	not_calculated	0.994	1301	Streptomyces sp. FXJ6.047;
B-2165; EF588223	S001793115	not_calculated	0.984	1305	Streptomyces griseus; NRRL
GU263861	S001873751	not_calculated	0.983	1362	Streptomyces sp. 163003;

SeqMatch :: Detail Hierarchy –X77

Query Sequence: unknown, 1147 unique oligos
short ID, orientation, similarity score, S_ab score, unique common oligomers and sequence full name.

Lineage:

no rank Root (0/20/615916) (selected/match/total RDP sequences)
domain Bacteria (0/20/606188)
phylum "Actinobacteria" (0/20/115729)
class Actinobacteria (0/20/115729)
subclass Actinobacteridae (0/20/110300)
order Actinomycetales (0/20/109449)
suborder Streptomycineae (0/20/6711)
family Streptomycetaceae (0/20/6711)
genus Streptomyces (0/20/6457)

S000406301 not_calculated 0.997 1391 Streptomyces sp. YIM 80038; AY299622

S000587694 not_calculated 0.997 1383 Actinomycetales bacterium HPA66; DQ144230

S000651790 not_calculated 0.997 1376 Streptomyces globisporus subsp. globisporus; NBRC 12208; AB184066

S000651988 not_calculated 0.997 1383 Streptomyces cavourensis subsp. cavourensis; NBRC 13026; AB184264

S000652149 not_calculated 0.997 1373 Streptomyces albolongus (T); NBRC 13465; AB184425

S000652163 not_calculated 0.997 1373 Streptomyces bacillaris (T); NBRC 13487; AB184439

S000652202 not_calculated 0.997 1338 Streptomyces tsusimaensis; NBRC 13782; AB184478

S000711020 not_calculated 0.997 1361 Streptomyces griseobrunneus (T); NBRC 12775; AB249912

S000770104 not_calculated 0.997 1388 Streptomyces sp. M10; EF034030

S000805317 not_calculated 0.997 1332 Streptomyces griseus; EF192235

S000967664 not_calculated 0.997 1350 Streptomyces sp. A10Ydz-XM; EU257275

S000968181 not_calculated 0.997 1371 Streptomyces globisporus subsp. globisporus; XSD-114; EU273549

S000981670 not_calculated 0.997 1347 Streptomyces sp. A306 Ydz-ZZ; EU368787

S001198885 not_calculated 0.997 1408 Streptomyces sp. DS3024; FJ238114

S001292987 not_calculated 0.997 1320 Actinomycetales bacterium JH105; FJ572022

S001351242 not_calculated 0.997 1359 Streptomyces bacillaris; cfcc3101; FJ792550

S001416303 not_calculated 0.997 1373 Streptomyces anulatus;

Malaysia; EU647478

S001416786 not_calculated 0.997 1395 Streptomyces globisporus subsp. globisporus; 13638A; EU741124

S001416853 not_calculated 0.997 1395 Streptomyces sp. 13661T; EU741191

S001416883 not_calculated 0.997 1392 Streptomyces globisporus subsp. globisporus; 13669A; EU741221

APPENDIX G

Details information of closely related *Streptomyces* spp. to *S. rochei* (strain X34), *S. albidoflavus* (strain X42) and *S. cavourensis* (strain X77) – from NCBI GenBank

***Streptomyces rochei* gene for 16S rRNA, partial sequence, strain: NBRC 12908**

GenBank: AB184237.1
LOCUS AB184237, 1472 bp DNA linear BCT 01-APR-2006
DEFINITION Streptomyces rochei gene for 16S rRNA, partial sequence, strain: NBRC 12908.
ACCESSION AB184237
VERSION AB184237.1 GI:90960053
ORGANISM Streptomyces rochei
REFERENCE 1
AUTHORS Tamura,T., Oguchi,A., Kikuchi,T., Kikuchi,H., Nishii,T., Tsuji,K.,Yamaguchi,Y., Tase,A., Takahashi,M., Sakane,T., Suzuki,K. and Hatano,K.
TITLE Phylogenic analysis of the genus Streptomyces
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1472)
AUTHORS Tamura,T., Oguchi,A., Kikuchi,T., Kikuchi,H., Nishii,T., Tsuji,K., Yamaguchi,Y., Tase,A., Takahashi,M., Sakane,T., Suzuki,K. and Hatano,K.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2004) Tomohiko Tamura, National Institute of Technology and Evaluation, Department of Biotechnology; 2-5-8, Kazusakamatari, Kisarazu, Chiba 292-0818, Japan

ORIGIN
1 acgaacgctg gcgncgtgct taacncatgc aagtcgaacg atgaaccact tcggtgggga
61 ttagtggcga acgggtgagt aacacgtggg caatctgccc tgcactctgg gacaagccct
121 ggaaacgggg tctaataccg gatactgatc ctcgcaggca tctgcgaggt tcgaaagctc
181 cggcggtgca ggatgagccc gcggcctatc agctagttgg tgaggtaacg gctcaccaag
241 gcgacgacgg gtagccggcc tgagagggcg accggccaca ctgggactga gacacggccc
301 agactcctac gggaggcagc agtggggaat attgcacaat gggcgaaagc ctgatgcagc
361 gacgccgcgt gagggatgac ggccttcggg ttgtaaacct ctttcagcag ggaagaagcg
421 aaagtgacgg tacctgcaga agaagcgccg gctaactacg tgccagcagc cgcggtaata
481 cgtagggcgc aagcgttgtc cggaattatt gggcgtaaag agctcgtagg cggcttgtca
541 cgtcggttgt gaaagcccgg ggcttaaccc cgggtctgca gtcgatacgg gcaggctaga
601 gttcggtagg ggagatcgga attcctggtg tagcggtgaa atgcgcagat atcaggagga
661 acaccggtgg cgaaggcgga tctctgggcc gatactgacg ctgaggagcg aaagcgtggg
721 gagcgaacag gattagatac cctggtagtc cacgccgtaa acggtgggca ctaggtgtgg
781 gcaacattcc acgttgtccg tgccgcagct aacgcattaa gtgccccgcc tggggagtac
841 ggccgcaagg ctaaaactca aaggaattga cgggggcccg cacaagcggc ggagcatgtg
901 gcttaattcg acgcaacgcg aagaacctta ccaaggcttg acatacaccg gaaaaccctg
961 gagacagggt ccccttgtg gtcggtgtac aggtggtgca tggctgtcgt cagctcgtgt
1021 cgtgagatgt tgggttaagt cccgcaacga gcgcaaccct tgtcccgtgt tgccagcagg
1081 cccttgtggt gctggggact cacgggagac cgccggggtc aactcggagg aaggtgggga
1141 cgacgtcaag tcatcatgcc ccttatgtct tgggctgcac acgtgctaca atggccggta
1201 caatgagctg cgataccgcg aggtggagcg aatctcaaaa agccggtctc agttcggatt
1261 ggggtctgca actcgacccc atgaagtcgg agtcgctagt aatcgcagat cagcattgct
1321 gcggtgaata cgttcccggg ccttgtacac accgcccgtc acgtcacgaa agtcggtaac
1381 acccgaagcc ggtggcccaa ccccttgtgg gagggagctg tcgaaggtgg gactggcgat
1441 tgggacgaag tcgtaacaag gtagccgtac cg

***Streptomyces albidoflavus* (DSM 40455T) 16S rRNA gene**

GenBank: Z76676.1

LOCUS Z76676, 1476 bp DNA linear BCT 25-APR-1997
DEFINITION S.albidoflavus (DSM 40455T) 16S rRNA gene.
ACCESSION Z76676
VERSION Z76676.1 GI:2052194
ORGANISM Streptomyces albidoflavus
REFERENCE 1
AUTHORS Hain,T., Ward-Rainey,N., Kroppenstedt,R.M., Stackebrandt,E. and Rainey,F.A.
TITLE Discrimination of Streptomyces albidoflavus strains based on the size and number of 16S-23S ribosomal DNA intergenic spacers
JOURNAL Int. J. Syst. Bacteriol. 47 (1), 202-206 (1997)
REFERENCE 2 (bases 1 to 1476)
AUTHORS Rainey,F.A.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1996) F.A. Rainey, DSM - Dt.Sammlung von Mikroorganismen, und Zellkulturen, Mascheroder Weg 1b, D-38124 Braunschweig, FRG

ORIGIN

1 aacgctggcg gcgtgcttaa cacatgcaag tcgaacgatg aaccgctttc gggcggggat
61 tagtggcgaa cgggtgagta acacgtgggc aatctgccct gcactctggg acaagccctg
121 gaaacggggt ctaataccgg atatgactgt ccatcgcatg gtggatggtg taaagctccg
181 gcggtgcagg atgagcccgc ggcctatcag cttgttggtg aggtagtggc tcaccaaggc
241 gacgacgggt agccggcctg agagggcgac cggccacact gggactgaga cacggcccag
301 actcctacgg gaggcagcag tggggaatat tgcacaatgg gcgaaagcct gatgcagcga
361 cgccgcgtga gggatgacgg ccttcgggtt gtaaacctct ttcagcaggg aagaagcgaa
421 agtgacggta cctgcagaag aagcgccggc taactacgtg ccagcagccg cggtaatacg
481 tagggcgcaa gcgttgtccg gaattattgg gcgtaaagag ctcgtaggcg gcttgtcacg
541 tcggttgtga aagcccgggg cttaaccccg ggtctgcagt cgatacgggc aggctagagt
601 tcggtagggg agatcggaat tcctggtgta gcggtgaaat gcgcagatat caggaggaac
661 accggtggcg aaggcggatc tctgggccga tactgacgct gaggagcgaa agcgtgggga
721 gcgaacagga ttagataccc tggtagtcca cgccgtaaac ggtgggcact aggtgtgggc
781 aacattccac gttgtccgtg ccgcagctaa cgcattaagt gccccgcctg gggagtacgg
841 ccgcaaggct aaaactcaaa ggaattgacg ggggcccgca caagcggcgg agcatgtggc
901 ttaattcgac gcaacgcgaa gaaccttacc aaggcttgac atacaccgga aacgtctgga
961 gacaggcgcc cccttgtggt cggtgtacag gtggtgcatg gctgtcgtca gctcgtgtcg
1021 tgagatgttg ggttaagtcc cgcaacgagc gcaacccttg tcccgtgttg ccagcaggcc
1081 cttgtggtgc tggggactca cgggagaccg ccggggtcaa ctcggaggaa ggtggggacg
1141 acgtcaagtc atcatgcccc ttatgtcttg ggctgcacac gtgctacaat ggccggtaca
1201 atgagctgcg ataccgngag gtggagcgaa tctcaaaaag ccggtctcag ttcggattgg
1261 ggtctgcaac tcgaccccat gaagtcggag tcgctagtaa tcgcagatca gcattgctgc
1321 ggtgaatacg ttcccgggcc ttgtacacac cgcccgtcac gtcacgaaag tcggtaacac
1381 ccgaagccgg tggcccaacc ccttgtggga gggagctgtc gaaggtggga ctggcgattg
1441 ggacgaagtc gtaacaaggt agccgtaccg gaaggt

***Streptomyces cavourensis* subsp. *cavourensis* gene for 16S rRNA, partial sequence, strain: NBRC 13026**

GenBank: AB184264.1 1479 bp DNA linear BCT 01-APR-2006

LOCUS AB184264

DEFINITION *Streptomyces cavourensis* subsp. cavourensis gene for 16S rRNA, partial sequence, strain: NBRC 13026.

ACCESSION AB184264

VERSION AB184264.1 GI:90960080

ORGANISM *Streptomyces cavourensis* subsp. cavourensis

REFERENCE 1
AUTHORS Tamura,T., Oguchi,A., Kikuchi,T., Kikuchi,H., Nishii,T., Tsuji,K., Yamaguchi,Y., Tase,A., Takahashi,M., Sakane,T., Suzuki,K. and Hatano,K.
TITLE Phylogenic analysis of the genus Streptomyces
JOURNAL Unpublished

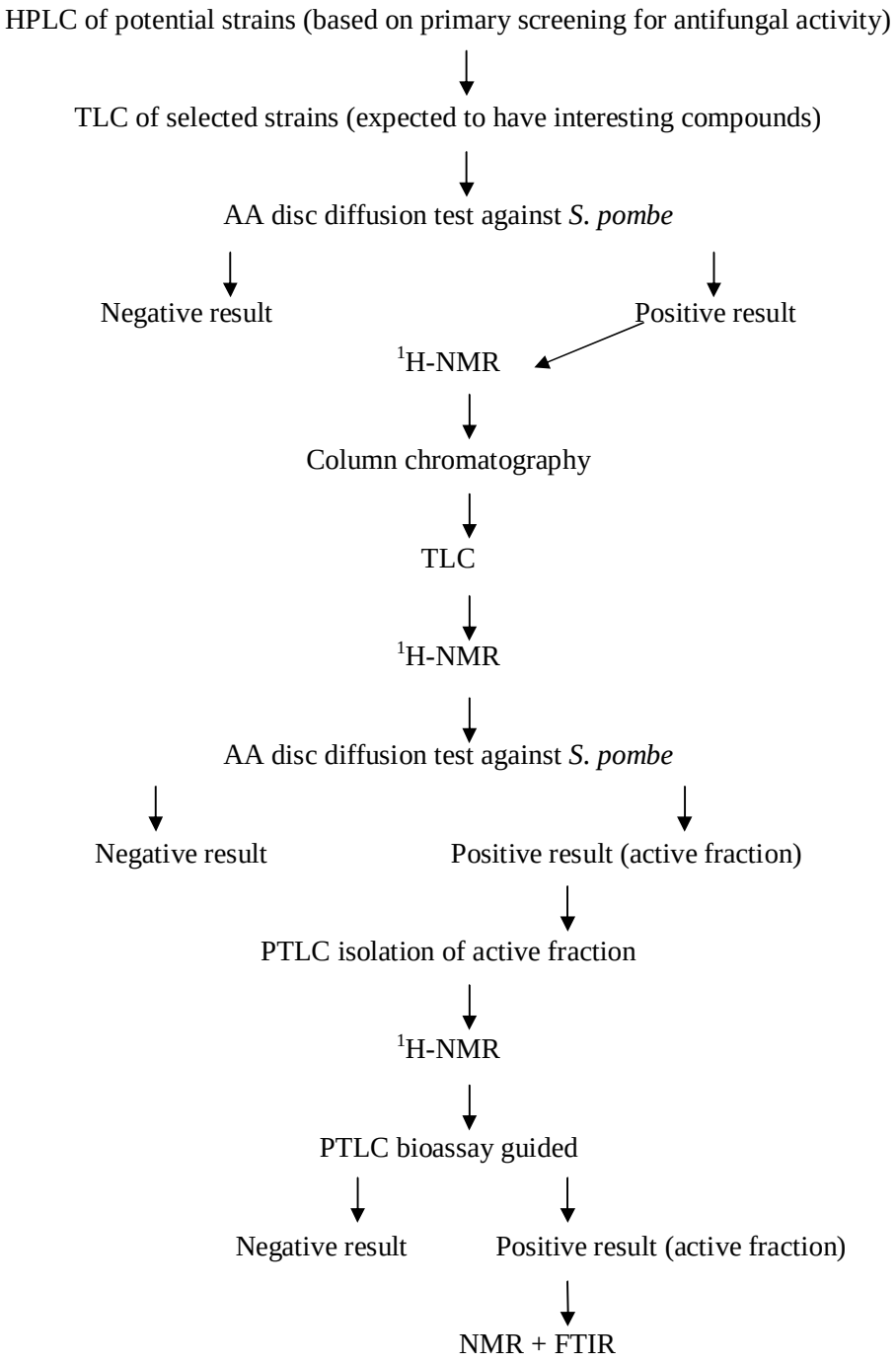
REFERENCE 2 (bases 1 to 1479)
AUTHORS Tamura,T., Oguchi,A., Kikuchi,T., Kikuchi,H., Nishii,T., Tsuji,K., Yamaguchi,Y., Tase,A., Takahashi,M., Sakane,T., Suzuki,K. and Hatano,K.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2004) Tomohiko Tamura, National Institute of Technology and Evaluation, Department of Biotechnology; 2-5-8, Kazusakamatari, Kisarazu, Chiba 292-0818, Japan

ORIGIN

1 acgaacgctg gcggcgtgct taacacatgc aagtcgaacg atgaaaccgc ttcggtggtg
61 gattagtggc gaacgggtga gtaacacgtg ggcaatctgc ccttcactct gggacaagcc
121 ctggaaacgg ggtctaatac cggataatac tcctgcctgc atgggtgggg gttgaaagct
181 ccggcggtga aggatgagcc cgcggcctat cagcttgttg gtggggtaat ggcctaccaa
241 ggcgacgacg ggtagccggc ctgagagggc gaccggccac actgggactg agacacggcc
301 cagactccta cgggaggcag cagtggggaa tattgcacaa tgggcgaaag cctgatgcag
361 cgacgccgcg tgagggatga cggccttcgg gttgtaaacc tctttcagca gggaagaagc
421 gcaagtgacg gtacctgcag aagaagcgcc ggctaactac gtgccagcag ccgcggtaat
481 acgtagggcg caagcgttgt ccggaattat tgggcgtaaa gagctcgtag gcggcttgtc
541 acgtcggatg tgaaagcccg gggcttaacc ccgggtctgc attcgatacg ggctagctag
601 agtgtggtag gggagatcgg aattcctggt gtagcggtga aatgcgcaga tatcaggagg
661 aacaccggtg gcgaaggcgg atctctgggc cattactgac gctgaggagc gaaagcgtgg
721 ggagcgaaca ggattagata ccctggtagt ccacgccgta aacgttggga actaggtgtt
781 ggcgacattc cacgtcgtcg gtgccgcagc taacgcatta agttccccgc ctggggagta
841 cggccgcaag gctaaaactc aaaggaattg acgggggccc gcacaagcag cggagcatgt
901 ggcttaattc gacgcaacgc gaagaacctt accaaggctt gacatatacc ggaaagcatc
961 agagatggtg ccccccttgt ggtcggtata caggtggtgc atggctgtcg tcagctcgtg
1021 tcgtgagatg ttgggttaag tcccgcaacg agcgcaaccc ttgttctgtg ttgccagcat
1081 gcctttcggg gtgatgggga ctcacaggag actgccgggg tcaactcgga ggaaggtggg
1141 gacgacgtca agtcatcatg ccccttatgt cttgggctgc acacgtgcta caatggccgg
1201 tacaatgagc tgcgatgccg tgaggcggag cgaatctcaa aaagccggtc tcagttcgga
1261 ttggggtctg caactcgacc ccatgaagtc ggagttgcta gtaatcgcag atcagcattg
1321 ctgcggtgaa tacgttcccg ggccttgtac acaccgcccg tcacgtcacg aaagtcggta
1381 acacccgaag ccggtggccc aacccccttgt gggagggagc tgtcgaaggt gggactggcg
1441 attgggacga agtcgtaaca aggtagccgt accggaagg

APPENDIX H

Flow chart of chemical profiling and compound isolation procedure



APPENDIX I

^{1}H-NMR chromatograms of fractions F1 – F6 of *S. rochei* after column chromatography

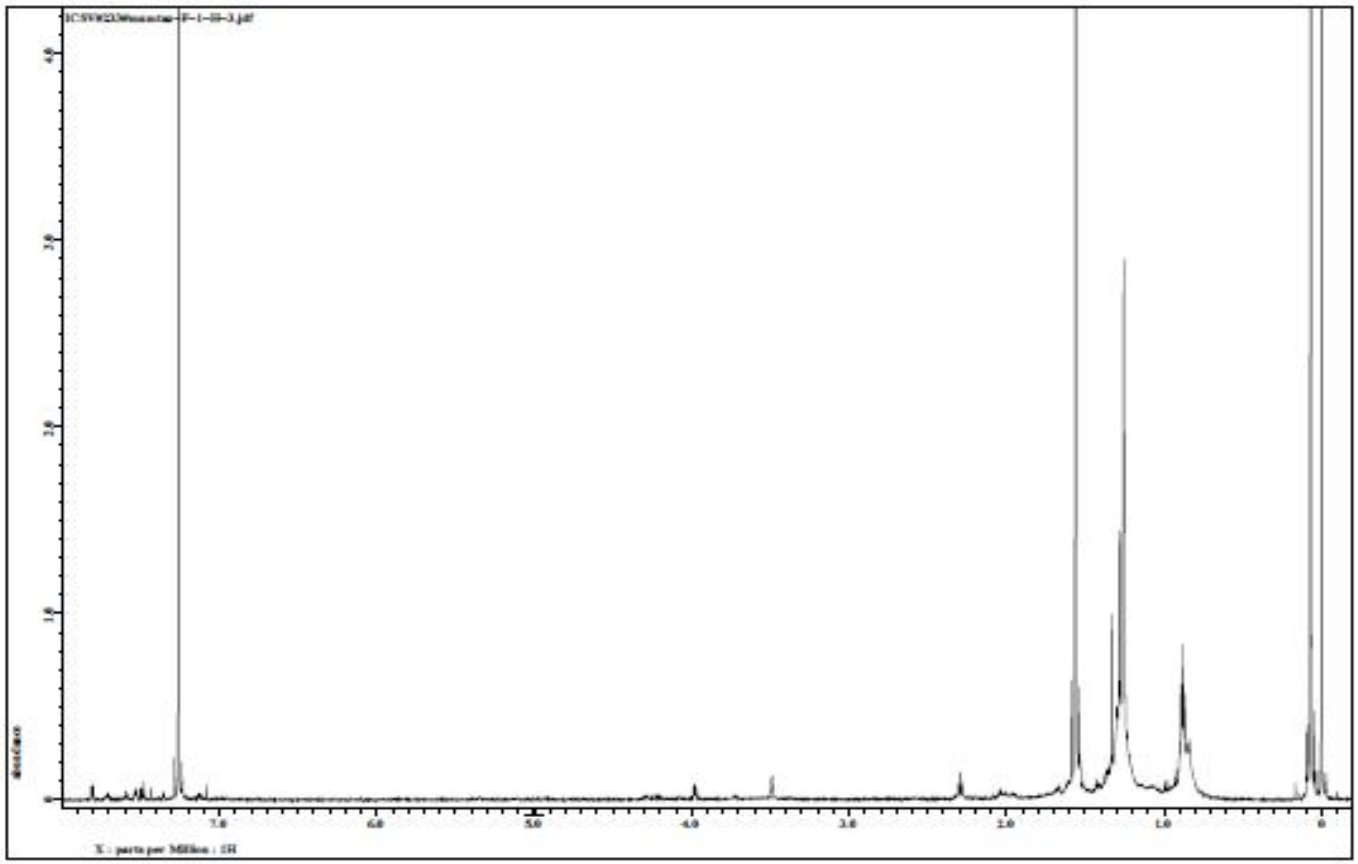


Figure I-1: ^{1}H-NMR chromatograms of fraction F1 of *S. rochei* (strain X34)

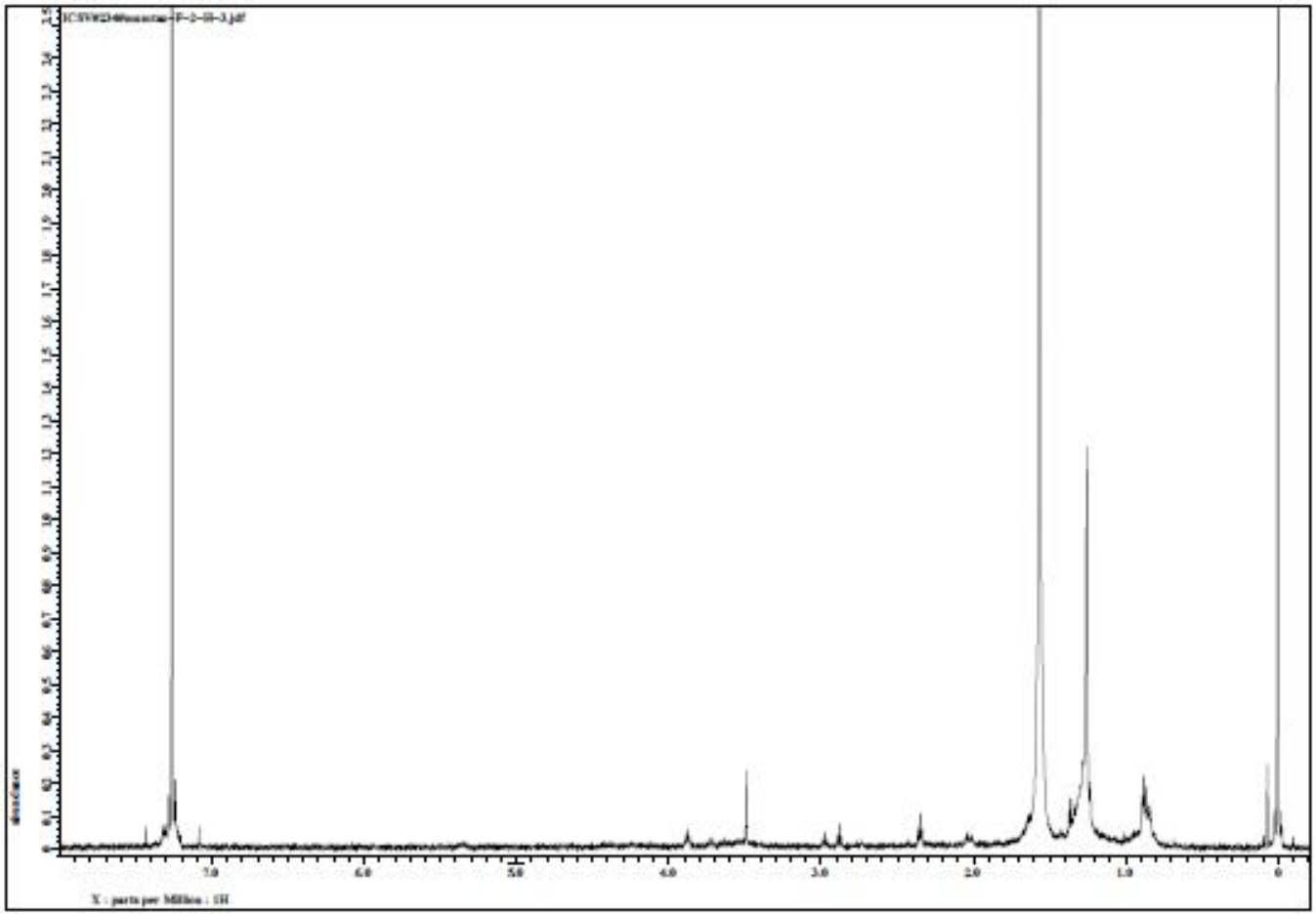


Figure I-2: ^{1}H-NMR chromatograms of fraction F2 of *S. rochei* (strain X34)

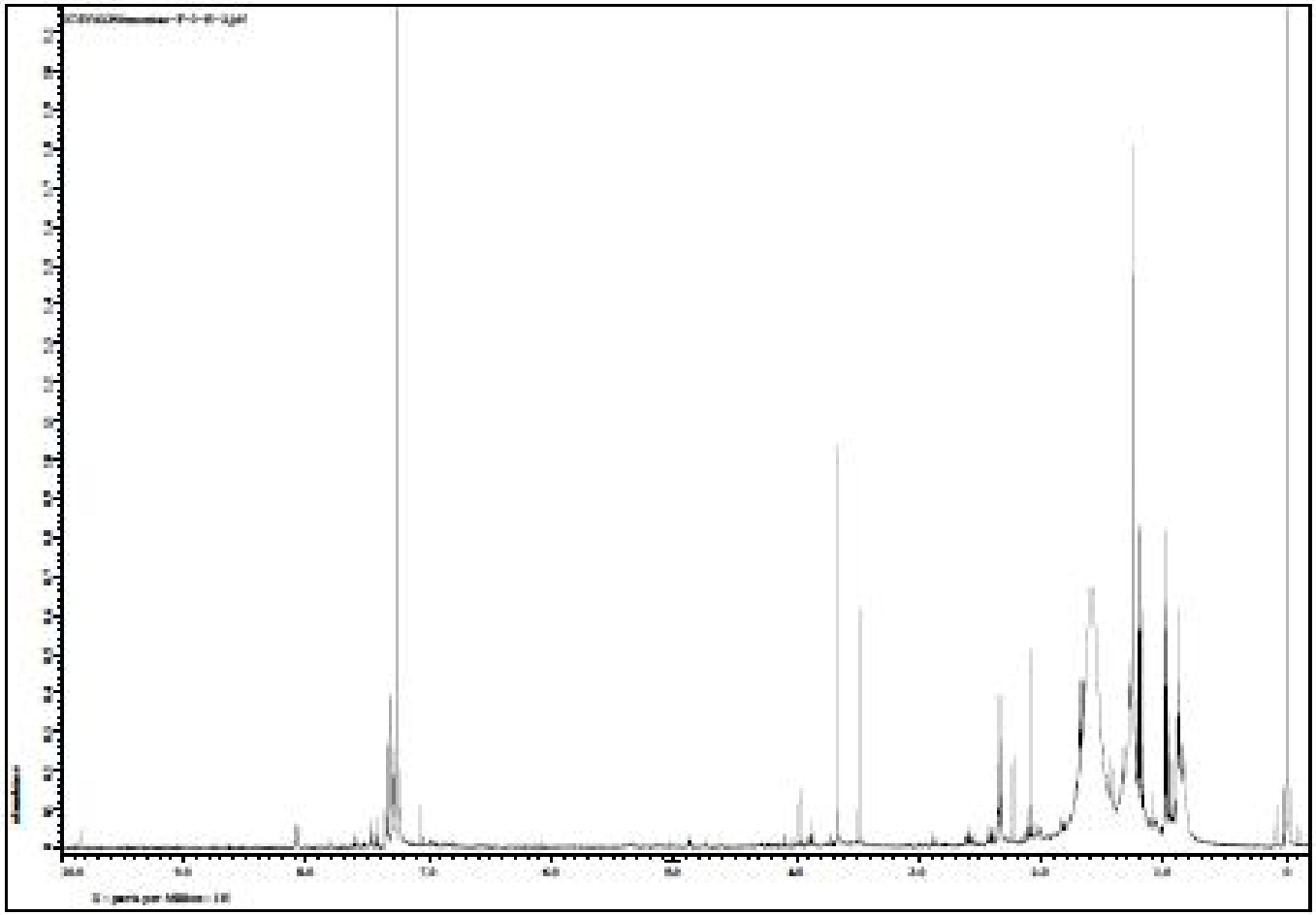


Figure I-3: ^{1}H-NMR chromatograms of fraction F3 of *S. rochei* (strain X34)

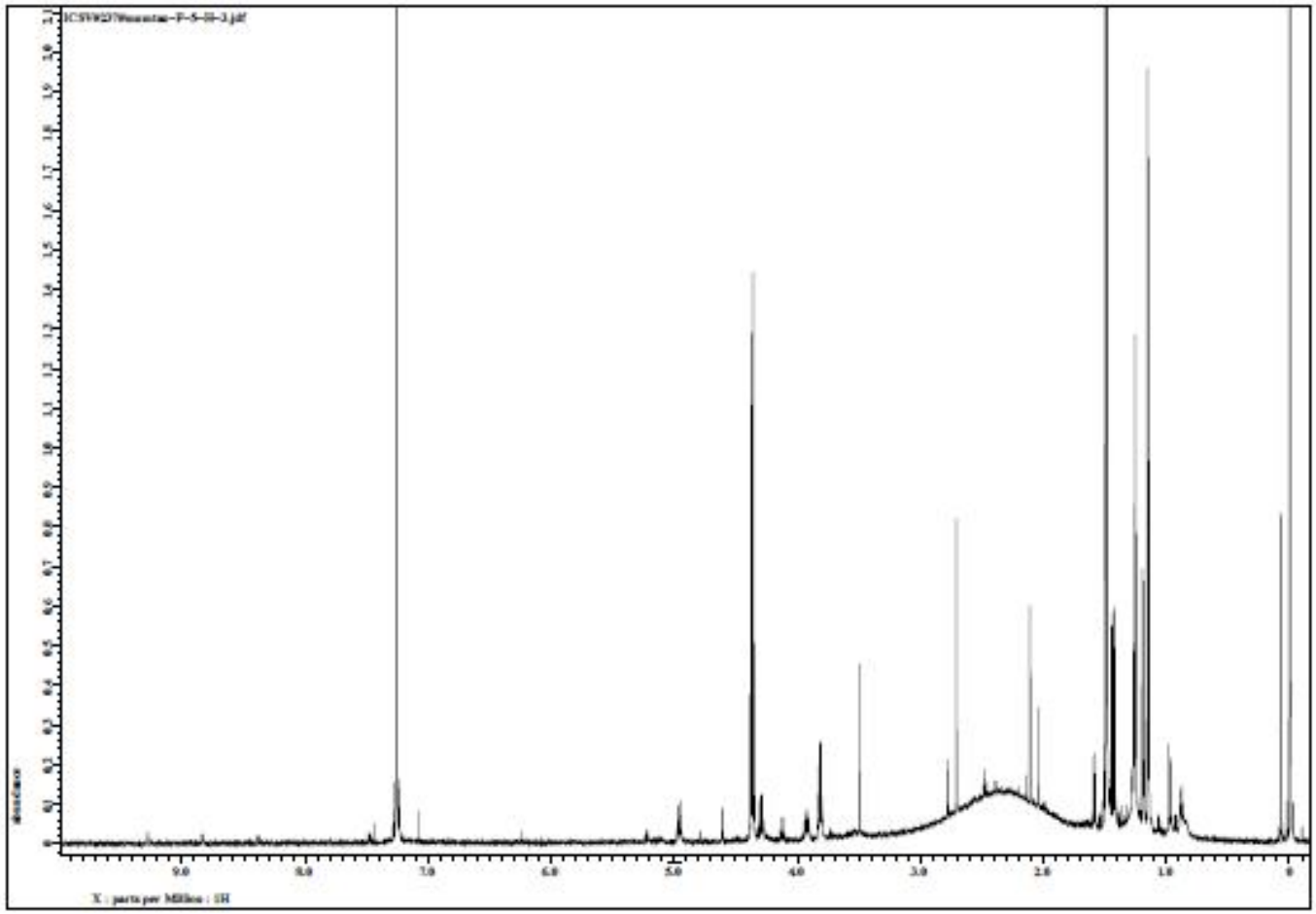


Figure I-4: ^{1}H-NMR chromatograms of fraction F4 of *S. rochei* (strain X34)

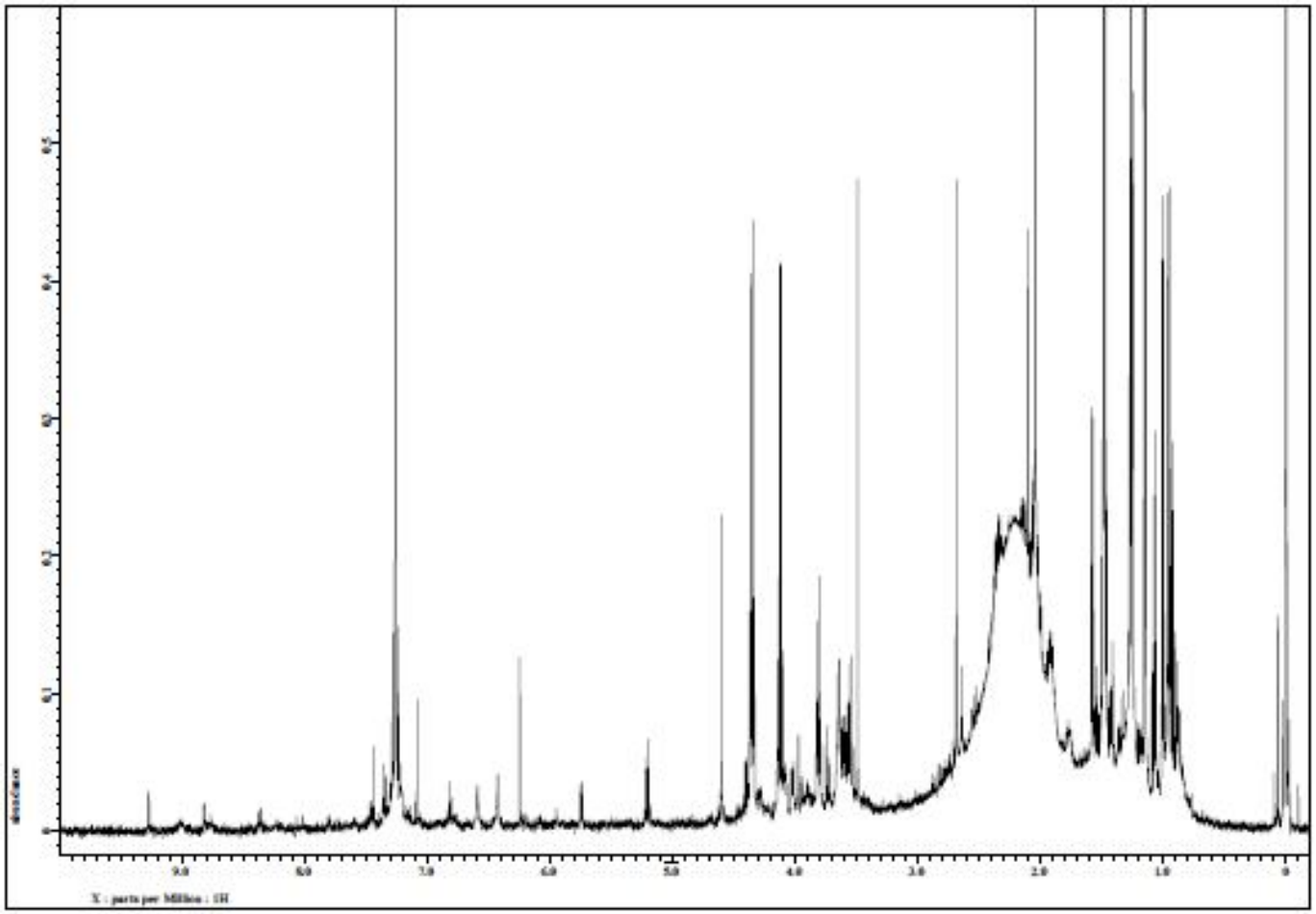


Figure I-5: ^{1}H-NMR chromatograms of fraction F5 of *S. rochei* (strain X34)

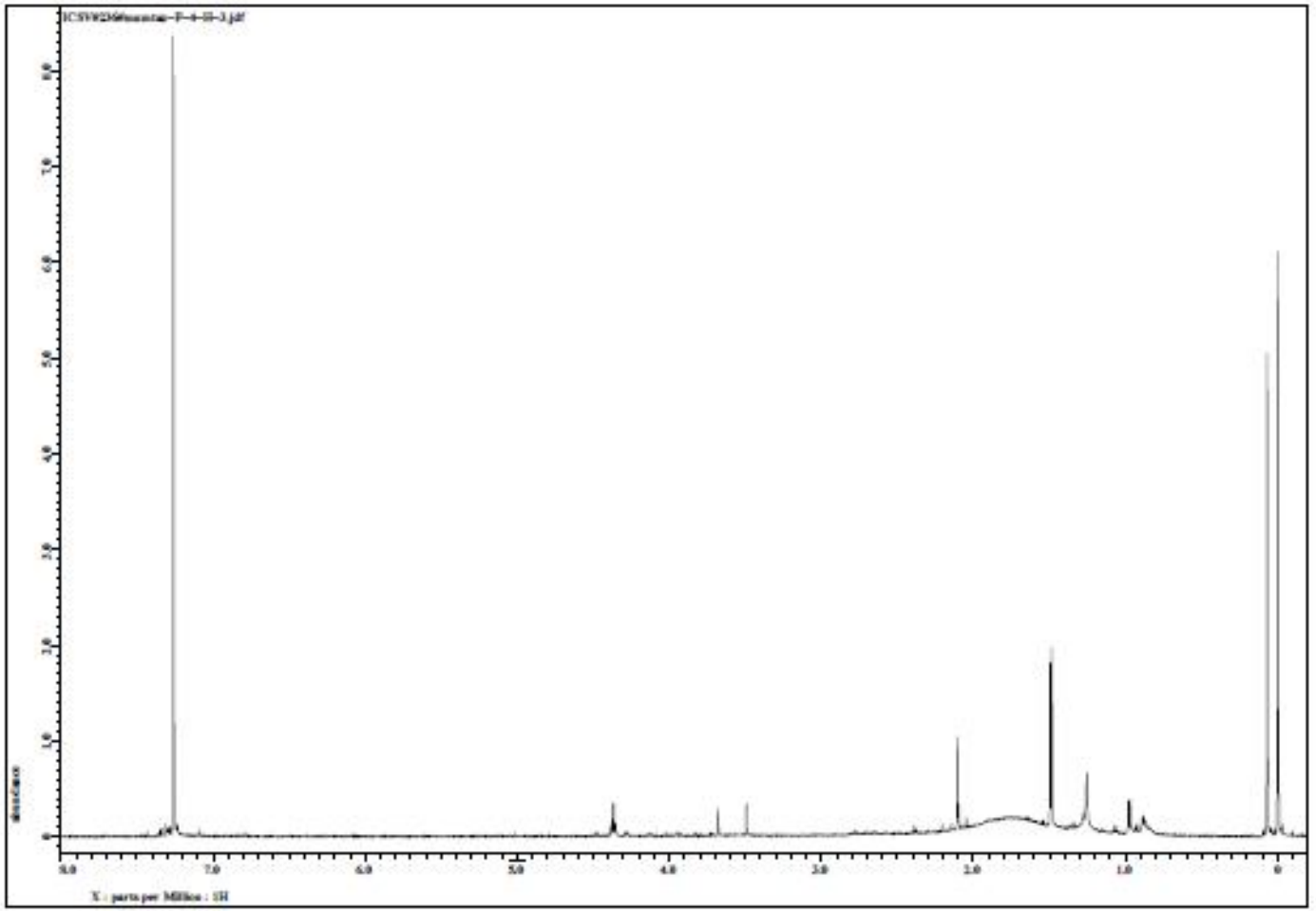
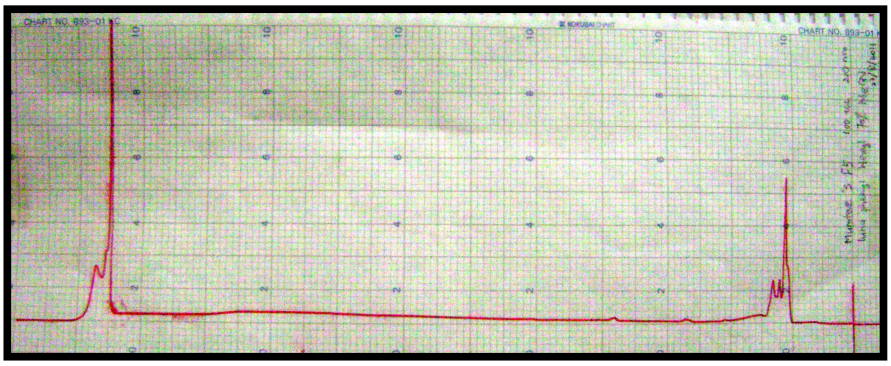


Figure I-6: ^{1}H-NMR chromatograms of fraction F6 of *S. rochei* (strain X34)

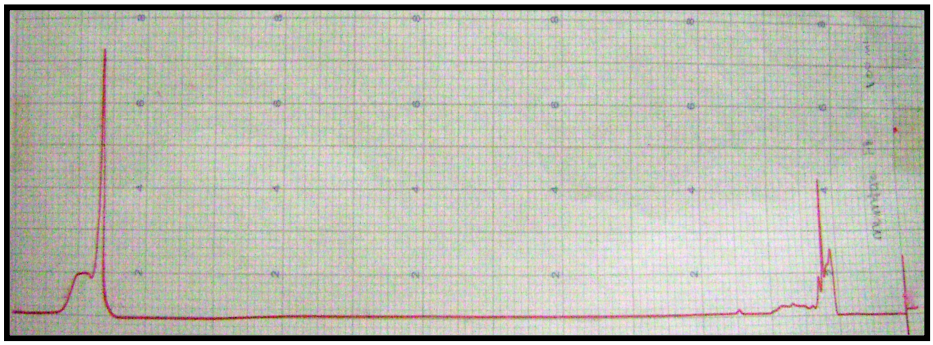
APPENDIX J

HPLC chromatograms of active fraction F5 of *Streptomyces rochei* (strain X34) using four parameters

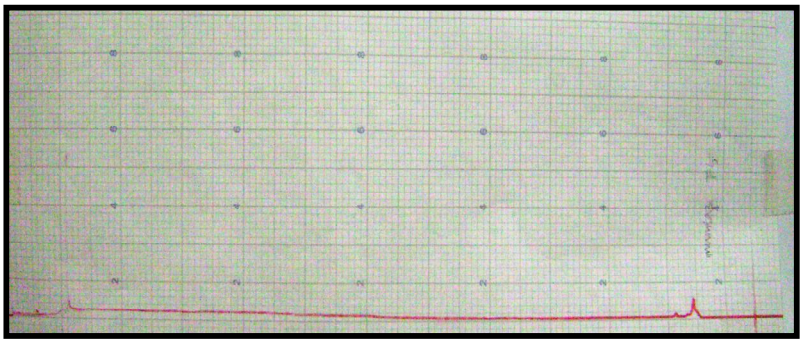
Column	:	Luna phenyl-Hexyl
Wavelength	:	210nm
Solvent	:	75% of 70% MeCN
Flow rate	:	2.0ml/min
Injection volume	:	100µl
Sample [ ]	:	5mg/ml MeCN
Sensitivity of plotter	:	0.050 AU



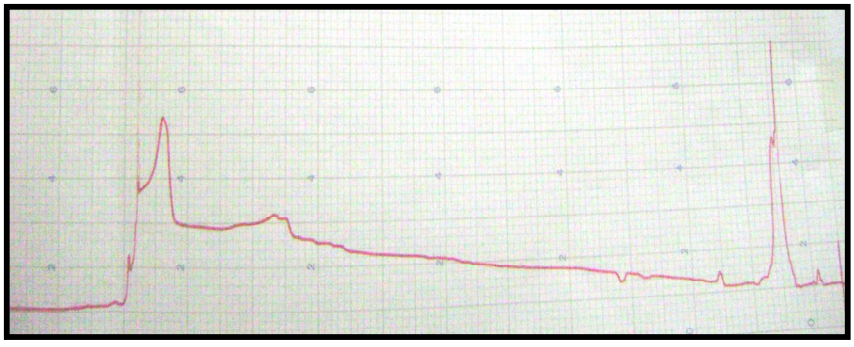
Column	:	Luna phenyl-Hexyl
Wavelength	:	210nm
Solvent	:	90% of 70% MeCN
Flow rate	:	2.0ml/min
Injection volume	:	100µl
Sample [ ]	:	5mg/ml MeCN
Sensitivity of plotter	:	0.050 AU



Column	:	C18 (2)
Wavelength	:	254 nm
Solvent	:	75% of 70% MeCN
Flow rate	:	2.0ml/min
Injection volume	:	100µl
Sample [ ]	:	5mg/ml MeCN
Sensitivity of plotter	:	0.050 AU



Column	:	C18 (2)
Wavelength	:	210 nm
Solvent	:	50% of 50% MeCN
Flow rate	:	2.0ml/min
Injection volume	:	100µl
Sample [ ]	:	5mg/ml MeCN
Sensitivity of plotter	:	0.050 AU



APPENDIX K

HPLC chromatograms of six potential strains of tested *Streptomyces* spp.

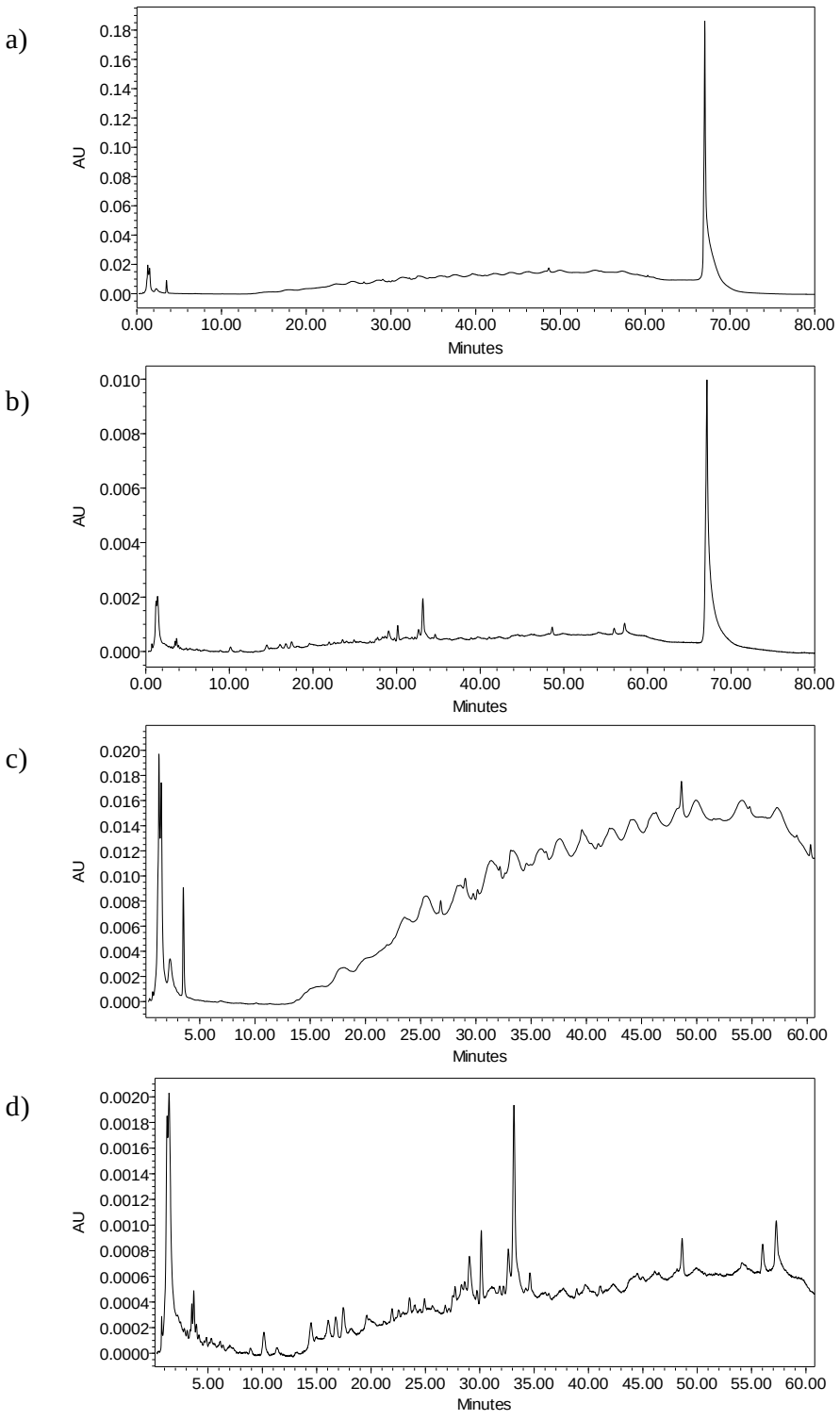


Figure K-1: HPLC chromatograms of strain X13 with different UV detector. a & c: 220nm, b & d: 254nm

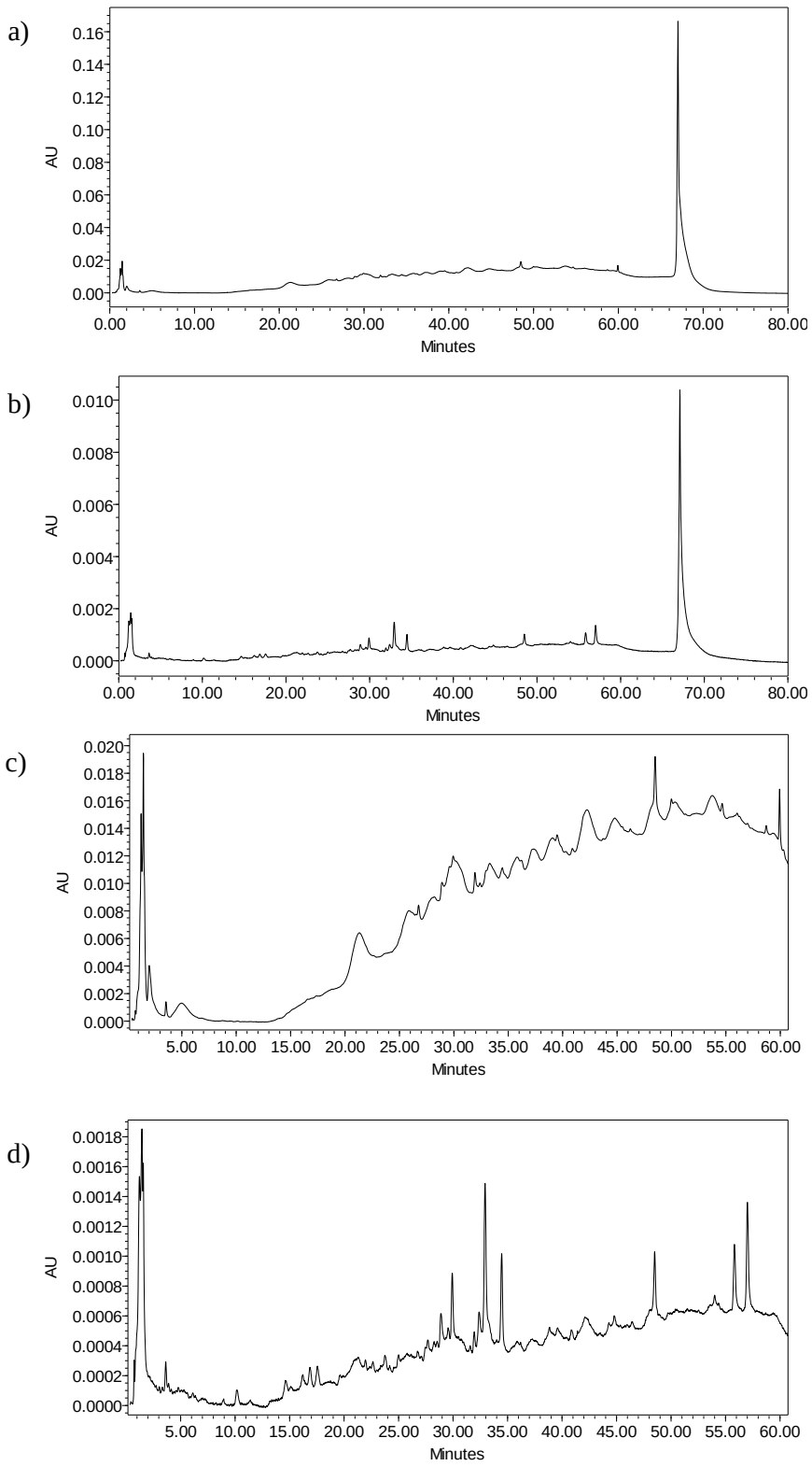


Figure K-2: HPLC chromatograms of strain X32 with different UV detector. a & c: 220nm, b & d: 254nm

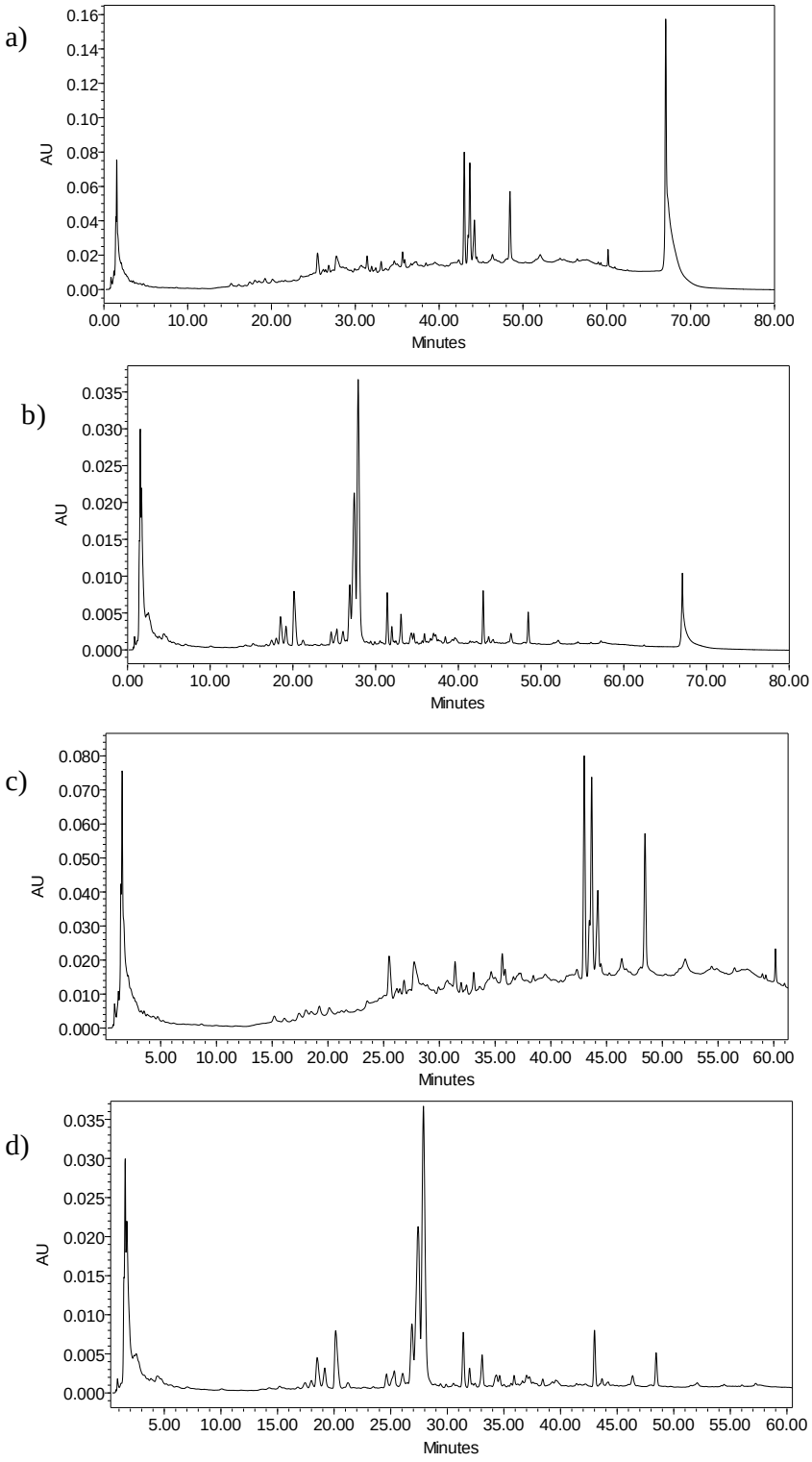


Figure K-3: HPLC chromatograms of strain X34 with different UV detector. a & c: 220nm, b & d: 254nm

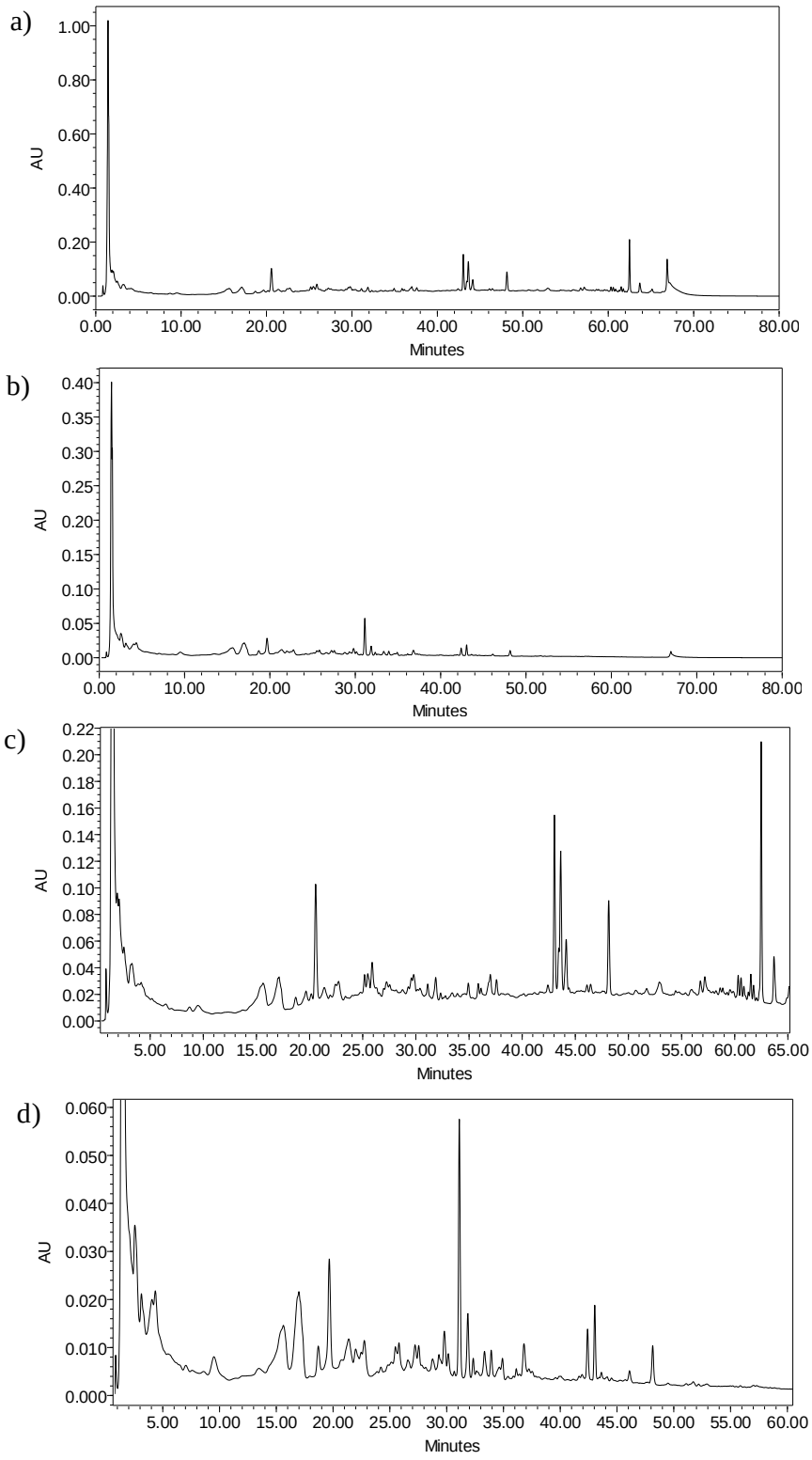


Figure K-4: HPLC chromatograms of strain X35 with different UV detector. a & c: 220nm, b & d: 254nm

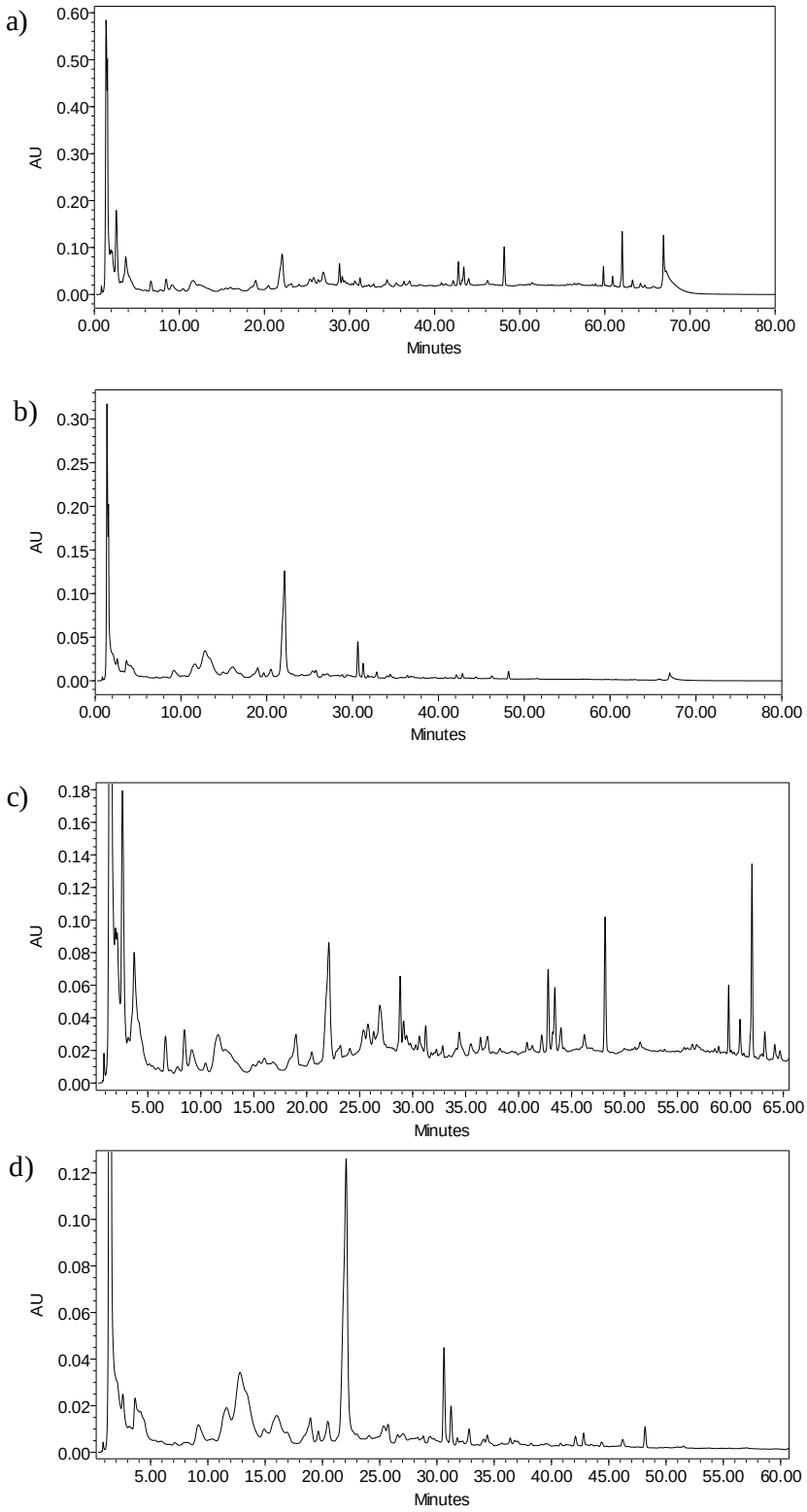


Figure K-5: HPLC chromatograms of strain X42 with different UV detector. a & c: 220nm, b & d: 254nm

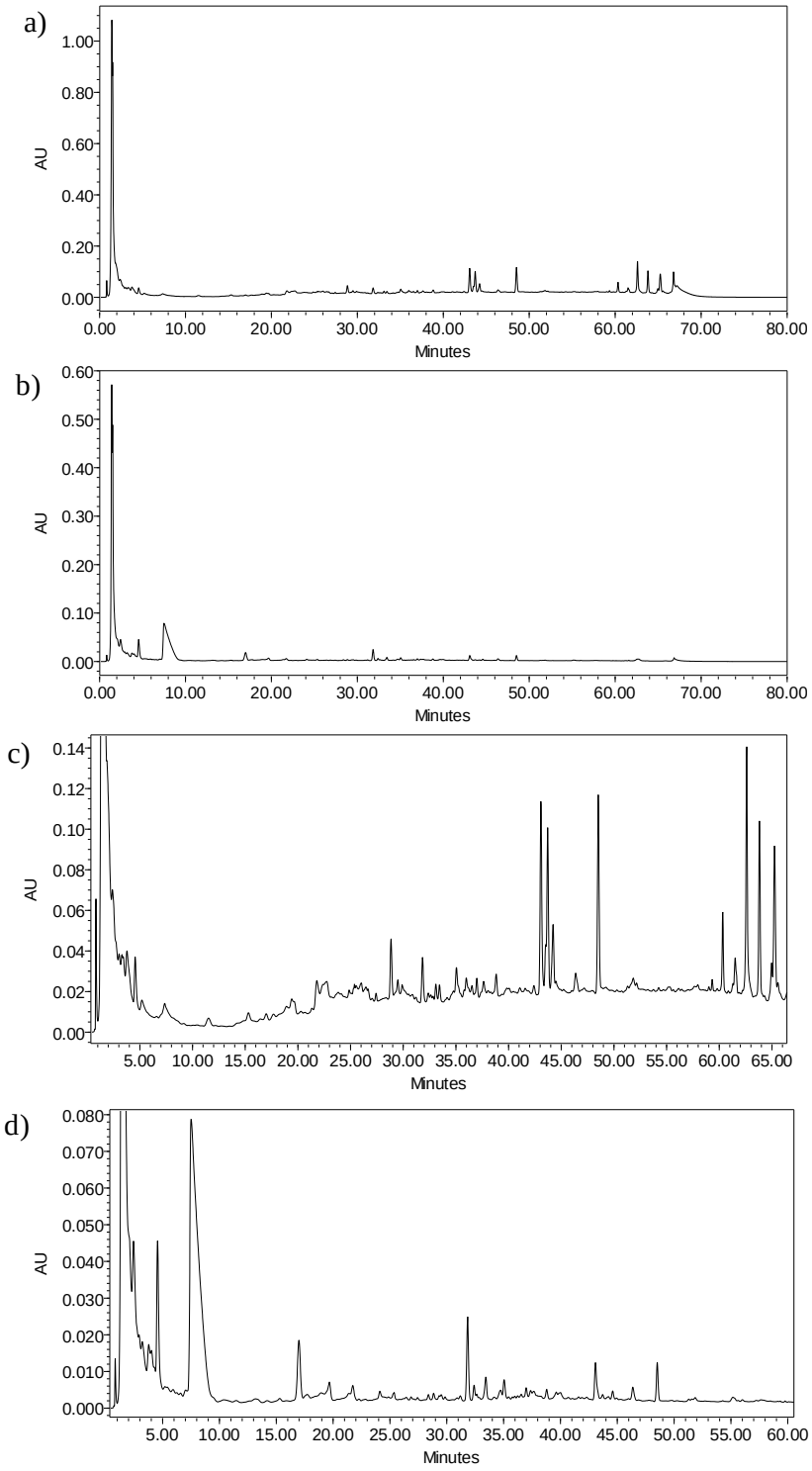


Figure K-6: HPLC chromatograms of strain X77 with different UV detector. a & c: 220nm, b & d: 254nm

APPENDIX L

^{1}H-NMR chromatograms of sub-fractions F5.1 – F5.6 of *S. rochei* (strain X34)

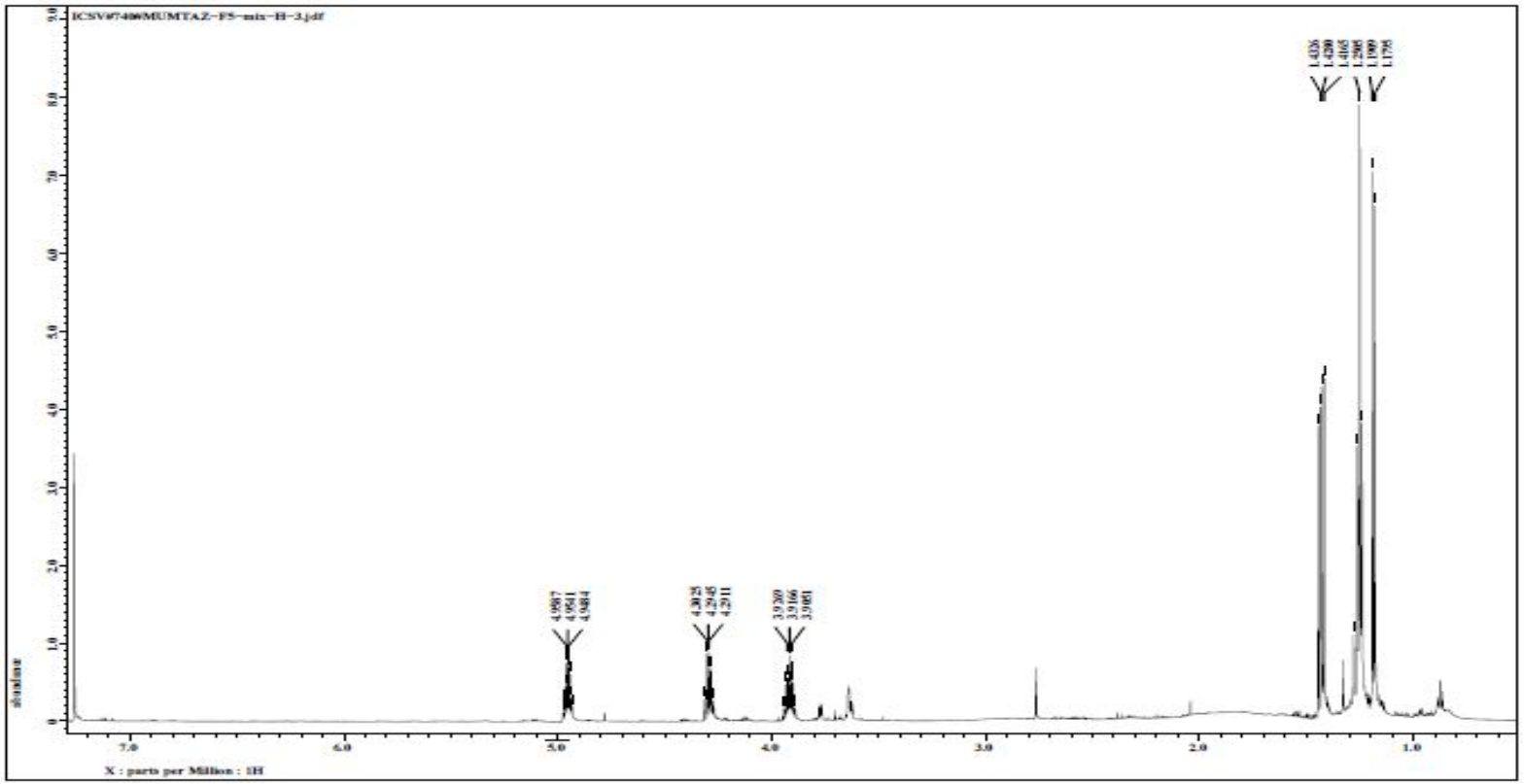


Figure L-1: ^{1}H-NMR chromatogram of sub-fraction F5.1 of *Streptomyces rochei* (strain X34)

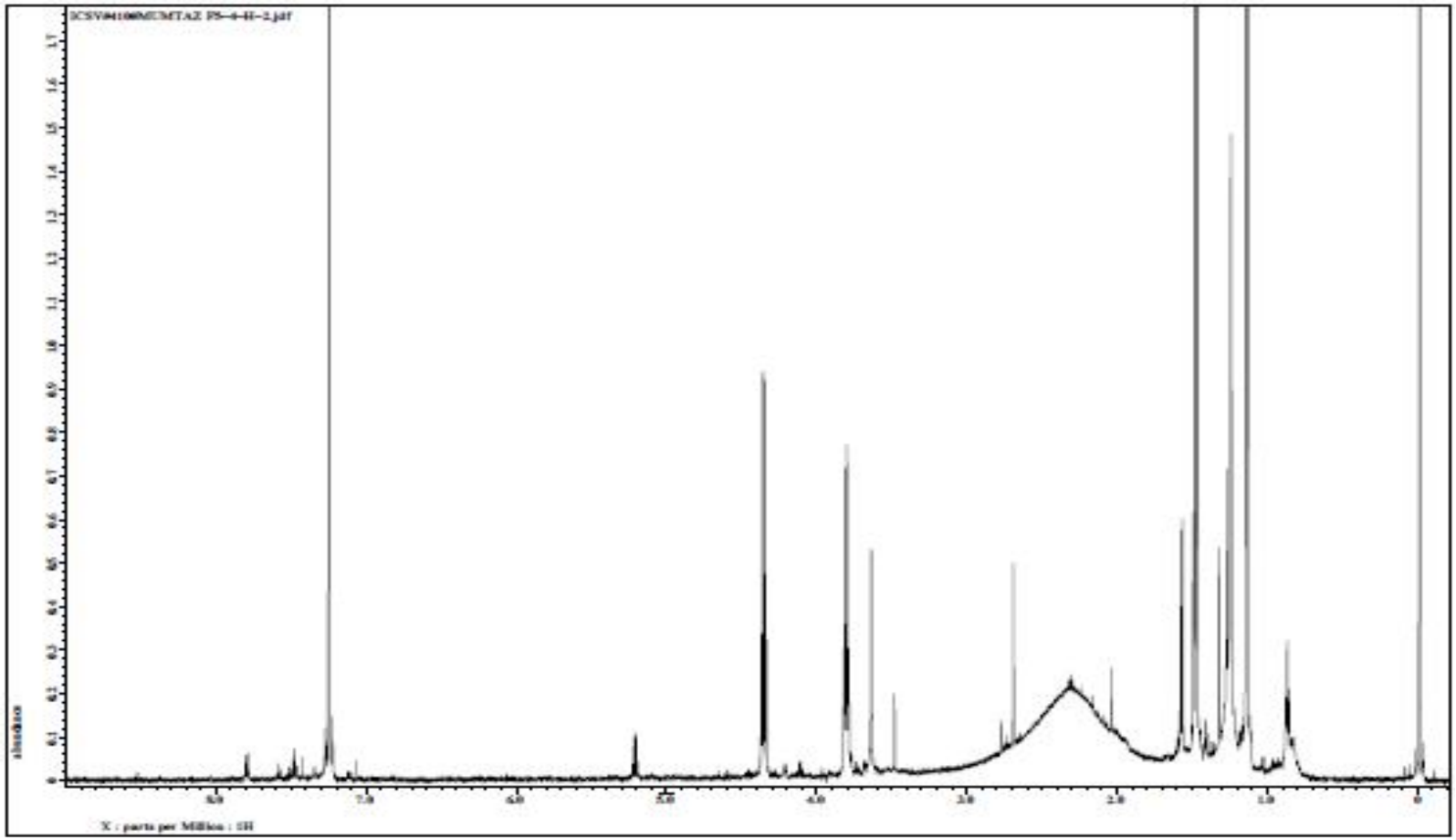


Figure L-2: ^{1}H-NMR chromatograms of sub-fraction F5.2 of *Streptomyces rochei* (strain X34)

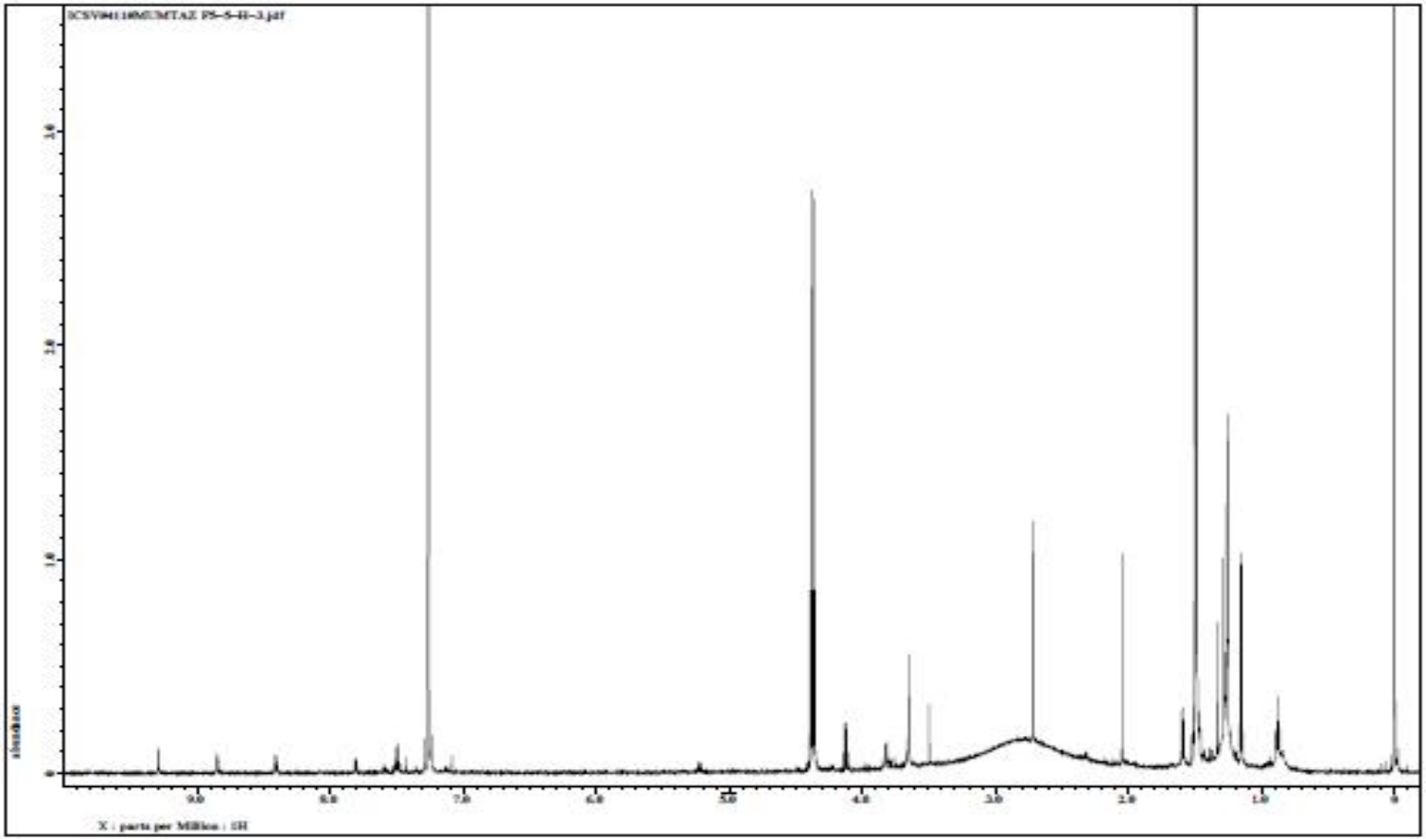


Figure L-3: ^{1}H-NMR chromatograms of sub-fraction F5.3 of *Streptomyces rochei* (strain X34)

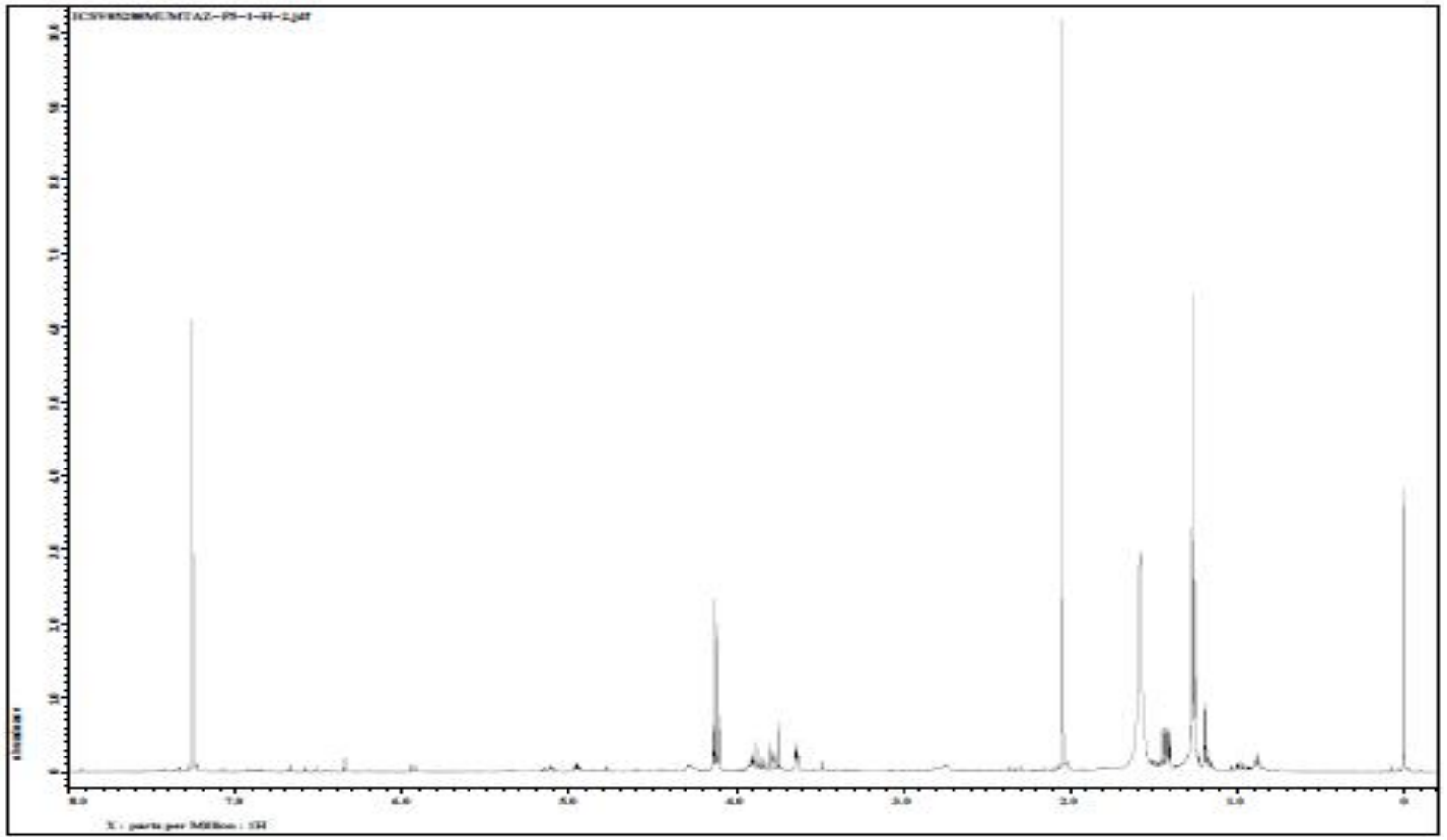


Figure L-4: ^{1}H-NMR chromatograms of sub-fraction F5.4 of *Streptomyces rochei* (strain X34)

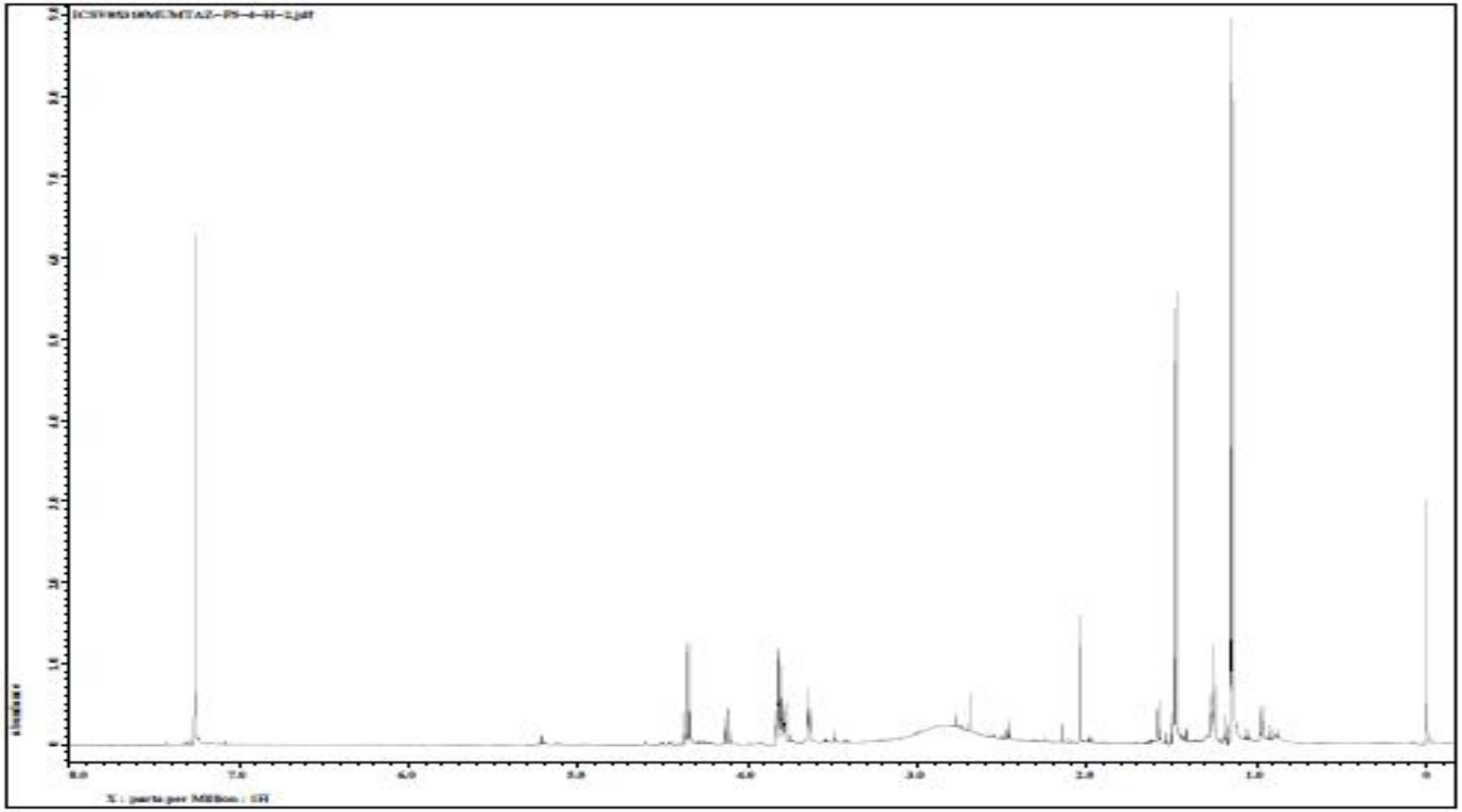


Figure L-5: ^{1}H-NMR chromatograms of sub-fraction F5.5 of *Streptomyces rochei* (strain X34)

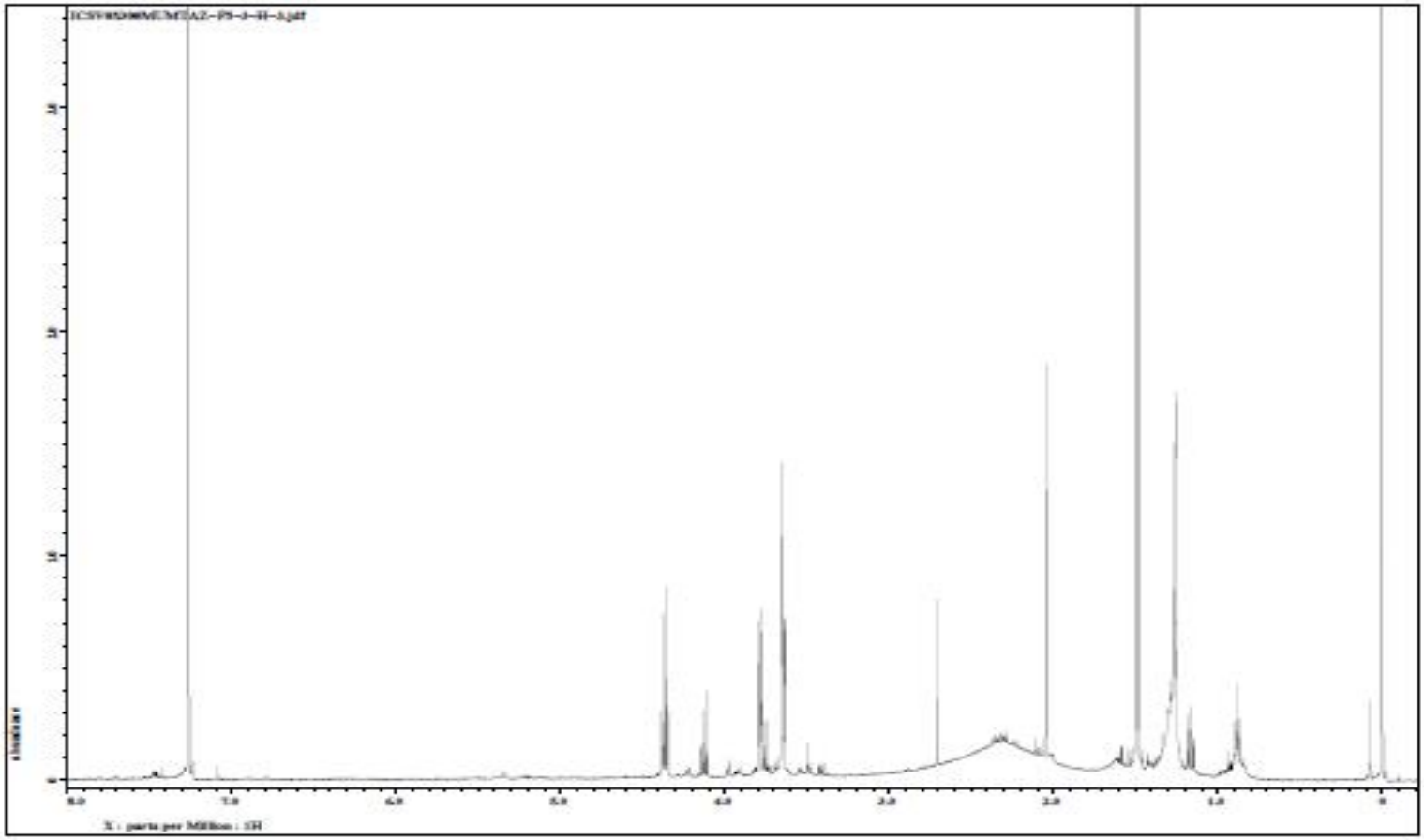


Figure L-6: ^{1}H-NMR chromatograms of sub-fraction F5.6 *Streptomyces rochei* (strain X34)

APPENDIX M

^{1}H-NMR and ^{13}C-NMR of active sub-fraction F5.4 of *S. rochei* (strain X34)

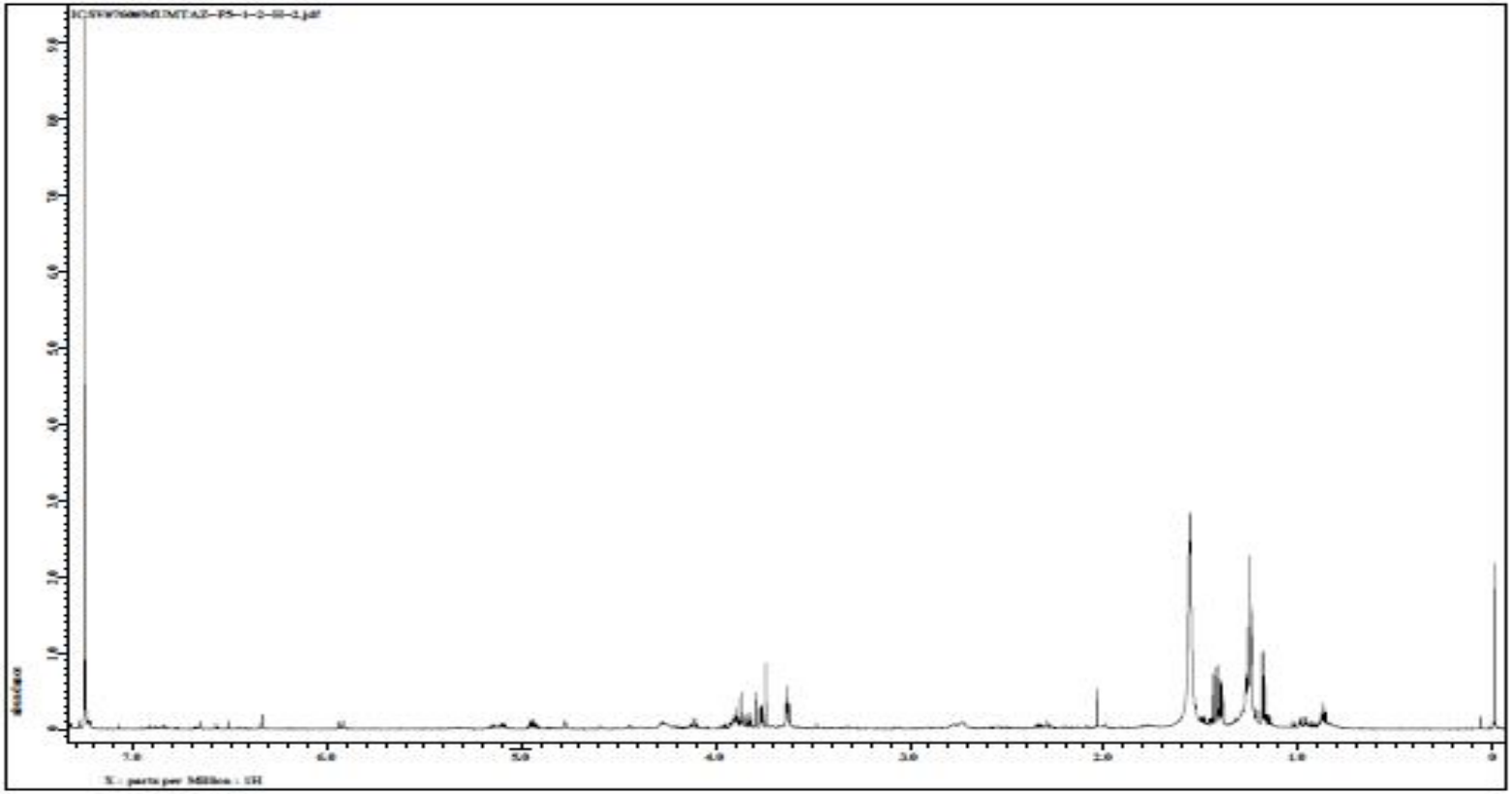


Figure M-1: ^{1}H-NMR chromatogram of active sub-fraction F5.4 of *S. rochei*.(strain X34)

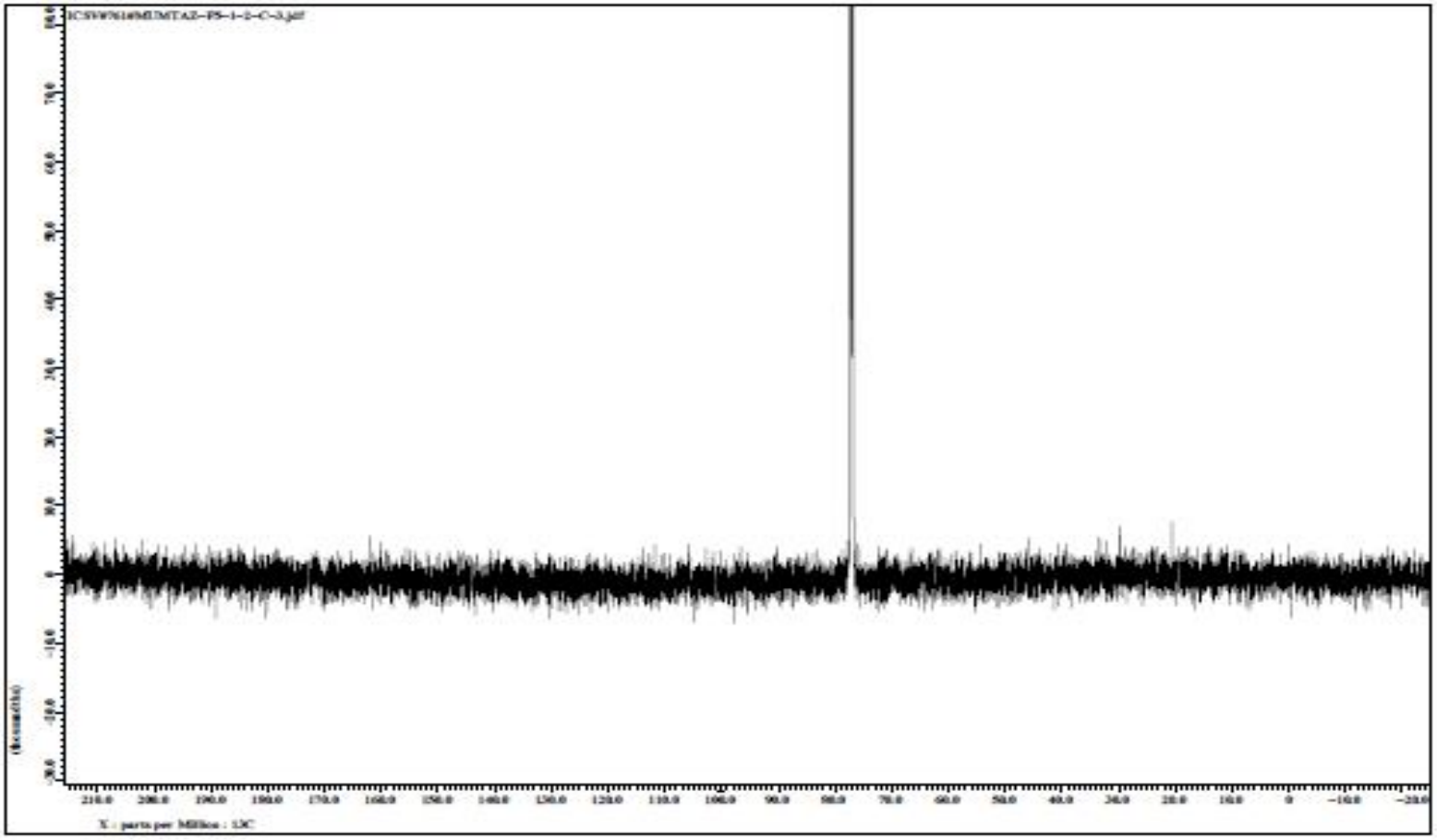


Figure M-2: ^{13}C-NMR chromatogram of active sub-fraction F5.4 of *S. rochei*.(strain X34)

APPENDIX N

Table N-1: Comparison of carbon sources utilization and NaCl tolerance between tested strains (X34, X42 and X77) and their most probably designated species.

***Streptomyces* spp. strain**	**Fru**	**Glu**	**Man**	**Xyl**	**Inos**	**Lact**	**Ara**	**Rha**	**Malt**	**Raff**	**Sorb**	**Suc**	**NaCl tolerance**	**References**
X34	+	+	+	±	±	+	+	+	+	-	-	±	8%	-
S. rochei	+	+	+	+	-	+	+	+	+	-	-	+	5%	Reddy *et al.* (2011) Berger *et al*. (1953)
S. plicatus	+	*	+	+	+	-	-	+	*	-	+	-	*	Aghighi *et al.* (2004)
S. enisssocaesilis	-	+	-	+	+	*	+	+	*	+	*	+	5%	Gause *et al.* (1983)
X42	+	+	+	±	±	-	+	±	±	-	+	±	10%	-
S. albidoflavus	+	+	+	-	-	-	+	-	-	-	*	-	5%	Atta *et al.* (2011) Waksman & Henrici (1948)
S. somaliensis	+	+	-	-	*	-	-	-	-	+	*	-	*	Lee *et al.* (2005)
S. hydrogenans	-	+	-	-	-	*	+	-	*	-	*	-	5%	Lindner *et al*. (1958)

+; good growth, ±; poor growth, -; no growth, *; not determined

Fruc; D-fructose, Glu; D-glucose, Man; D-mannitol, Xyl; D-xylose, Inos; Inositol, Lact; Lactose, Ara; L-arabinose, Rha; L-rhamnose, Malt; Maltose, Raff; Raffinose, Sorb; Sorbitol, Suc; Sucrose.

Continuation of Table N-1.

***Streptomyces* spp. strain**	**Fru**	**Glu**	**Man**	**Xyl**	**Inos**	**Ara**	**Rha**	**Raff**	**Suc**	**NaCl Tolerance**	**References**
X77	+	+	+	+	±	±	±	-	-	6%	-
S. cavourensis	+	+	+	+	-	-	-	-	-	7.5%	Skarbek & Brady (1978a)
S. celluloflavus	+	+	+	+	+	+	+	+	+	2.5%	Nishimura *et al.* (1953)
S. albolongus	-	+	-	-	-	+	-	-	-	*	Tsukiura *et al.* (1964)

+; good growth, ±; poor growth, -; no growth, *; not determined
Fruc; D-fructose, Glu; D-glucose, Man; D-mannitol, Xyl; D-xylose, Inos; Inositol, Lact; Lactose, Ara; L-arabinose, Rha; L-rhamnose, Malt; Maltose, Raff; Raffinose, Sorb; Sorbitol, Suc; Sucrose.

APPENDIX O

NMR chromatograms of active sub-fraction F5.1 (sampel in deuterated benzene, C_6D_6)

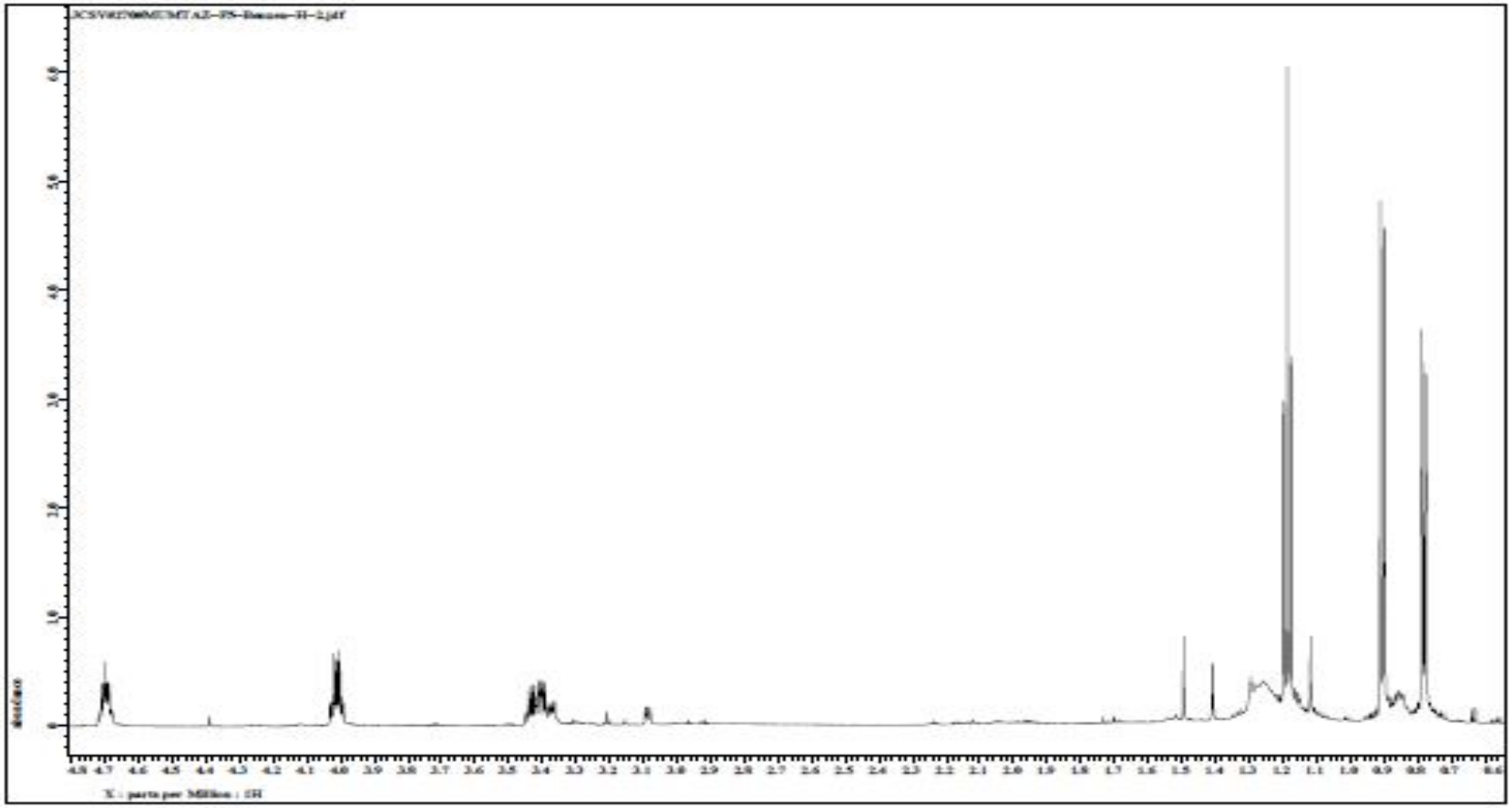


Figure O-1: ^{1}H-NMR chromatogram of active sub-fraction F5.1

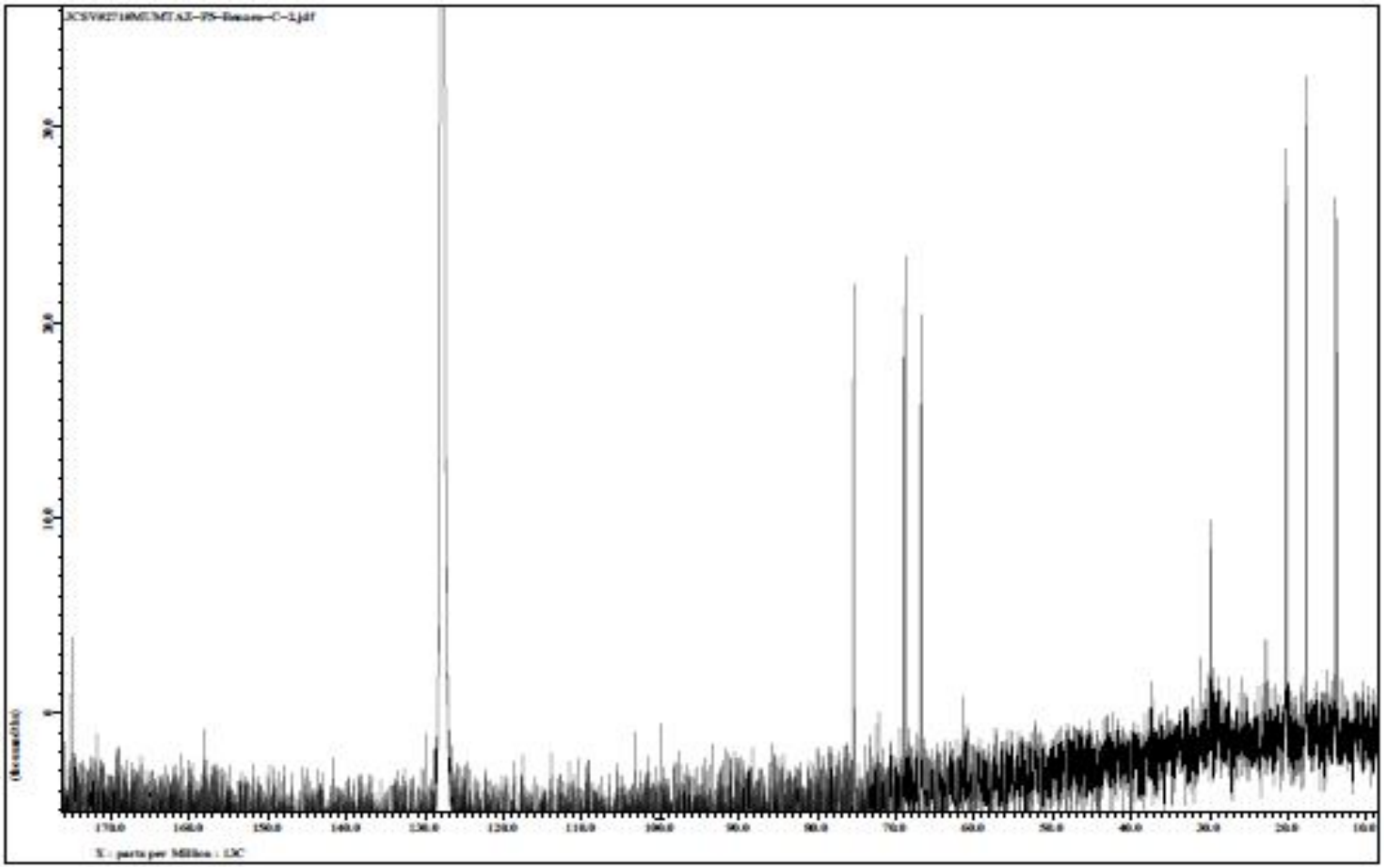


Figure O-2: ^{13}C-NMR chromatogram of active sub-fraction F5.1

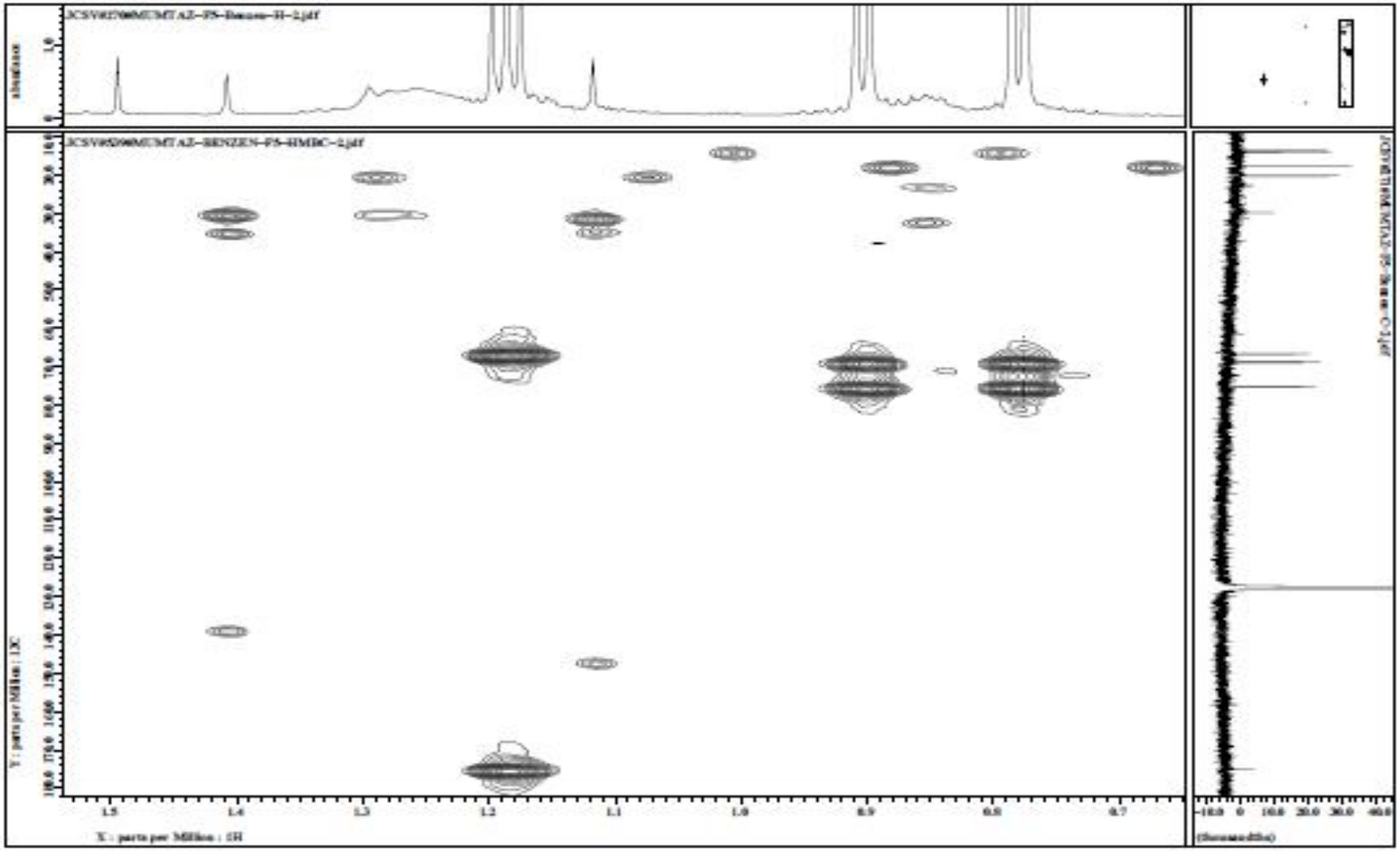


Figure O-3: HMBC chromatogram of active sub-fraction F5.1

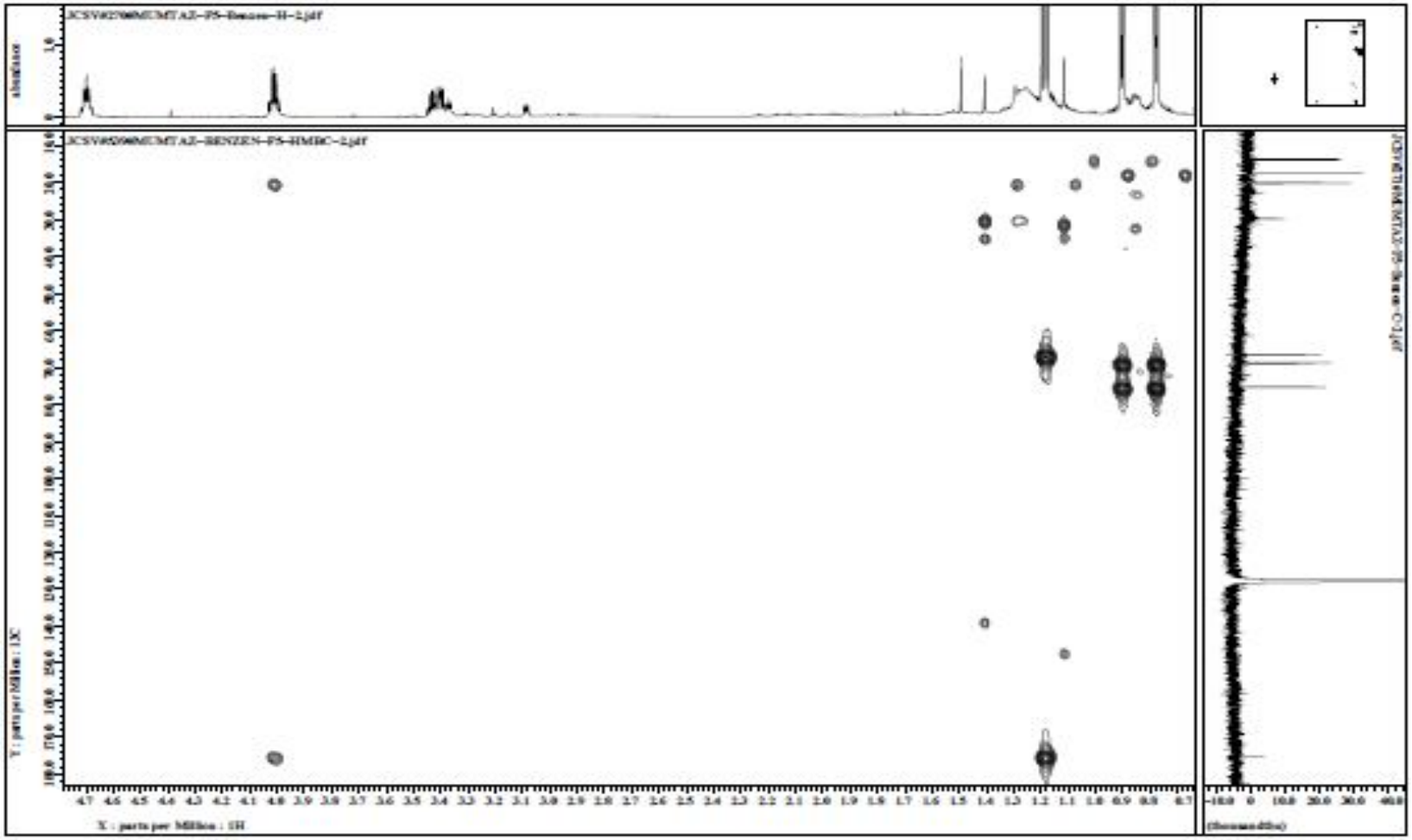


Figure O-4: HMBC chromatogram of active sub-fraction F5.1

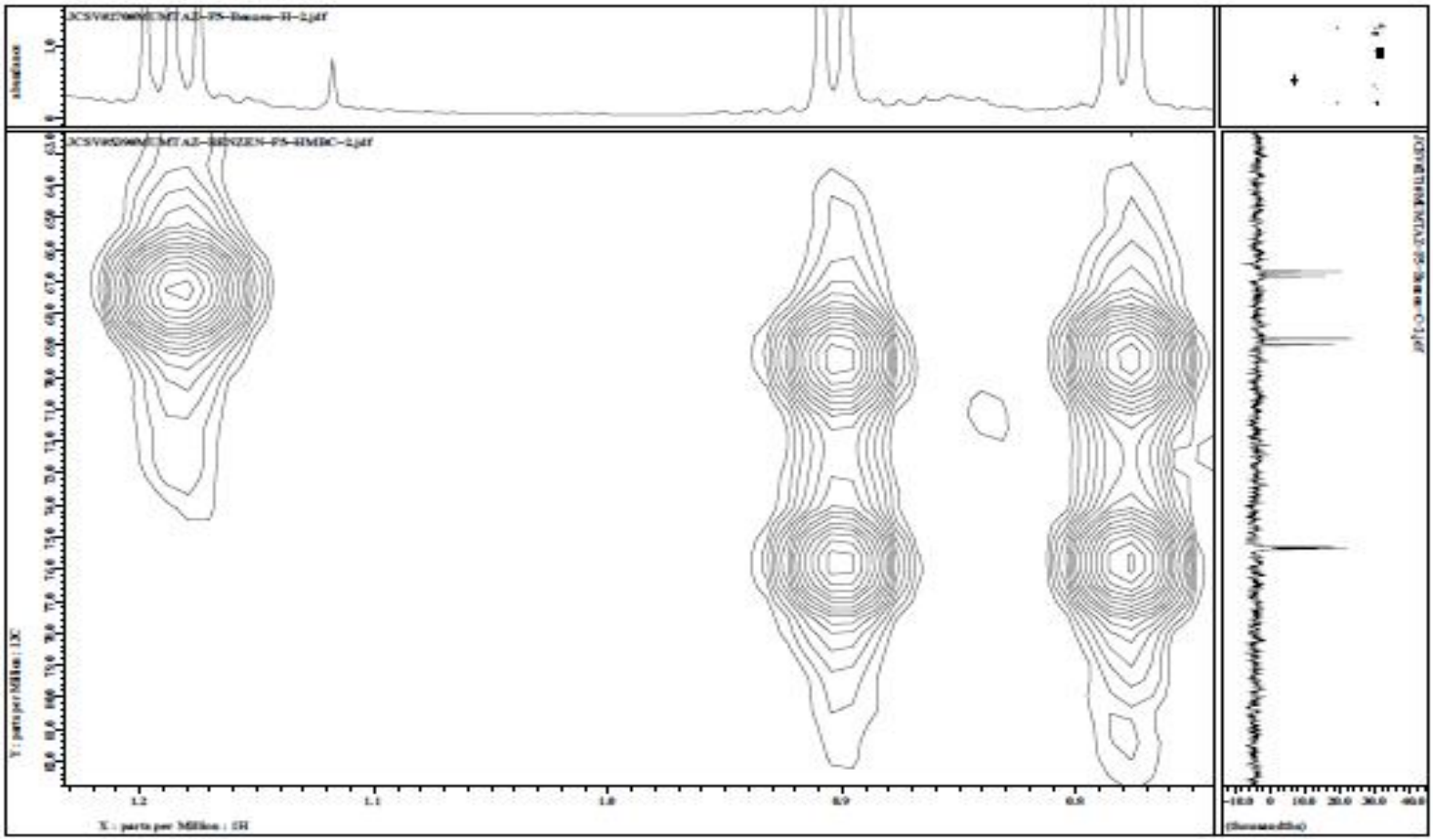


Figure O-5: HMBC chromatogram of active sub-fraction F5.1

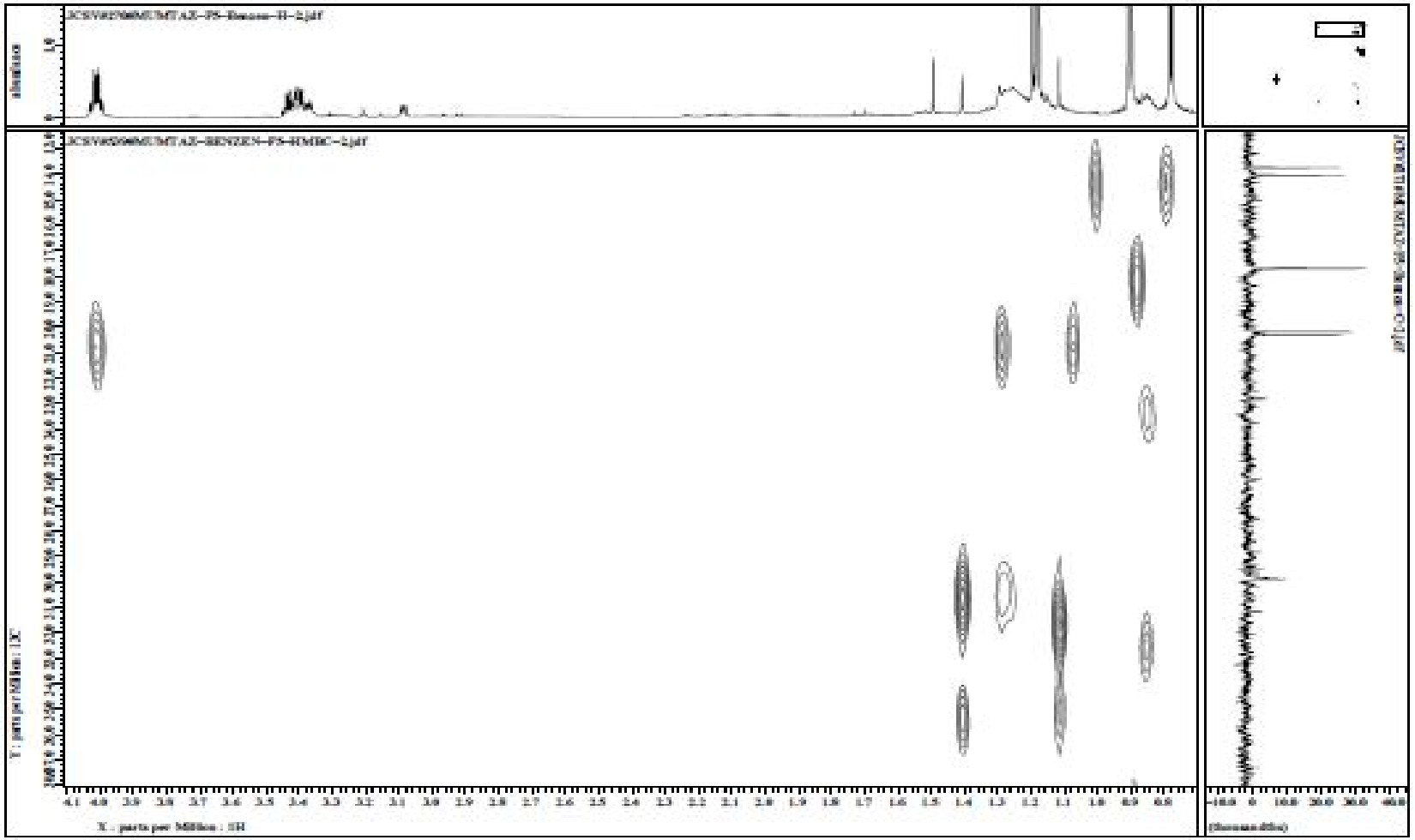


Figure O-6: HMBC chromatogram of active sub-fraction F5.1

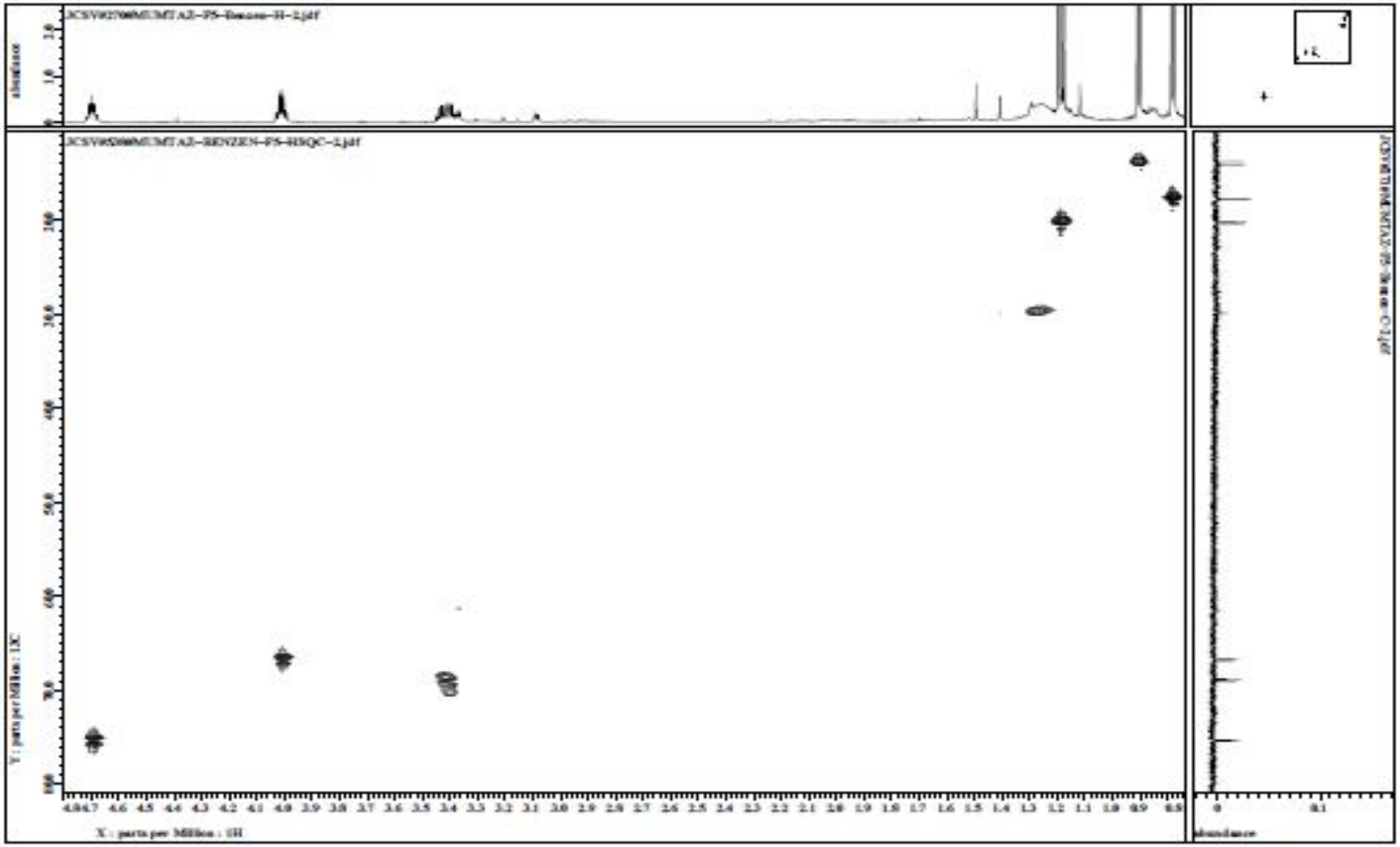


Figure O-7: HSQC chromatogram of active sub-fraction F5.1

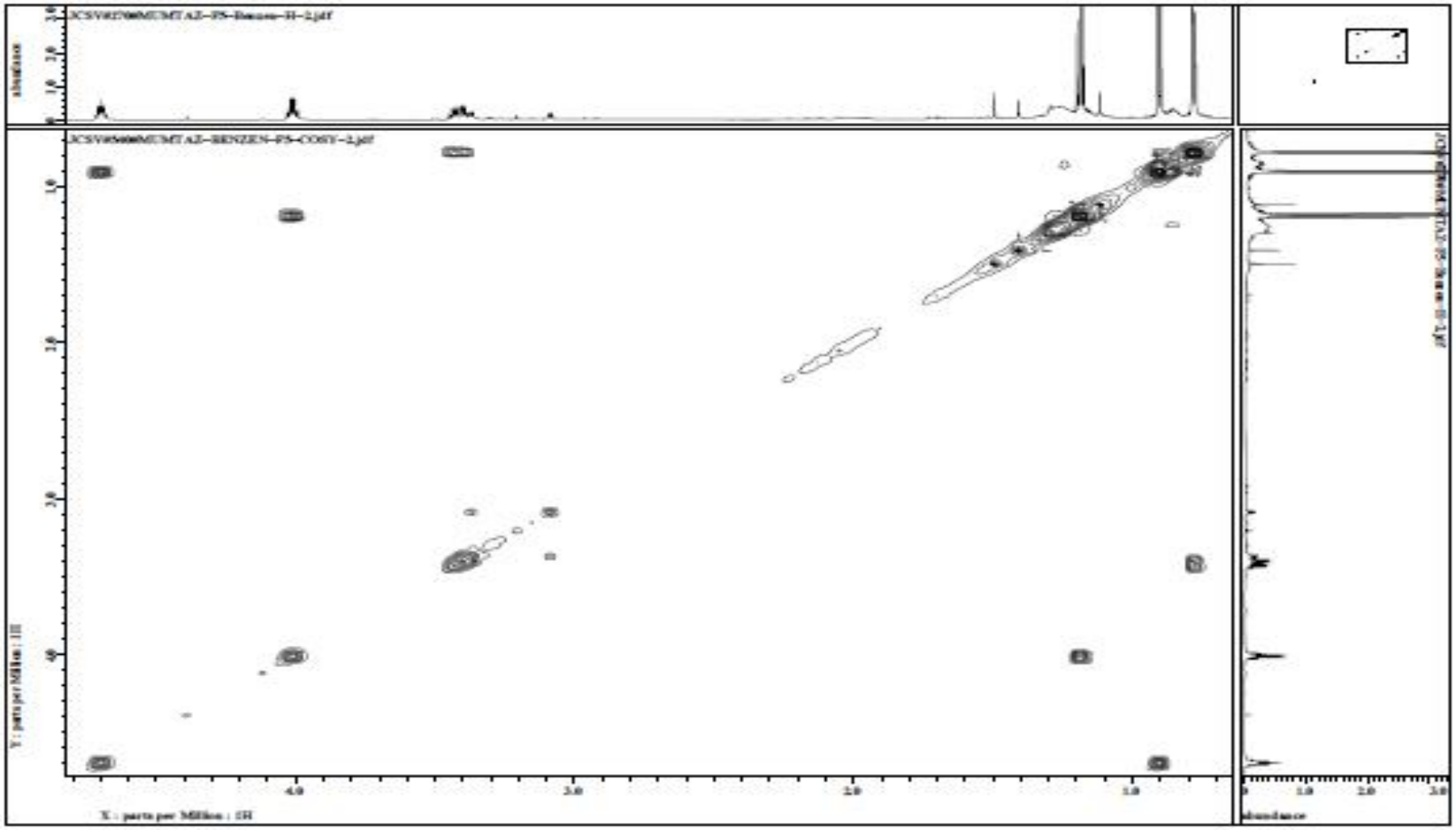


Figure O-8: COSY chromatogram of active sub-fraction F5.1

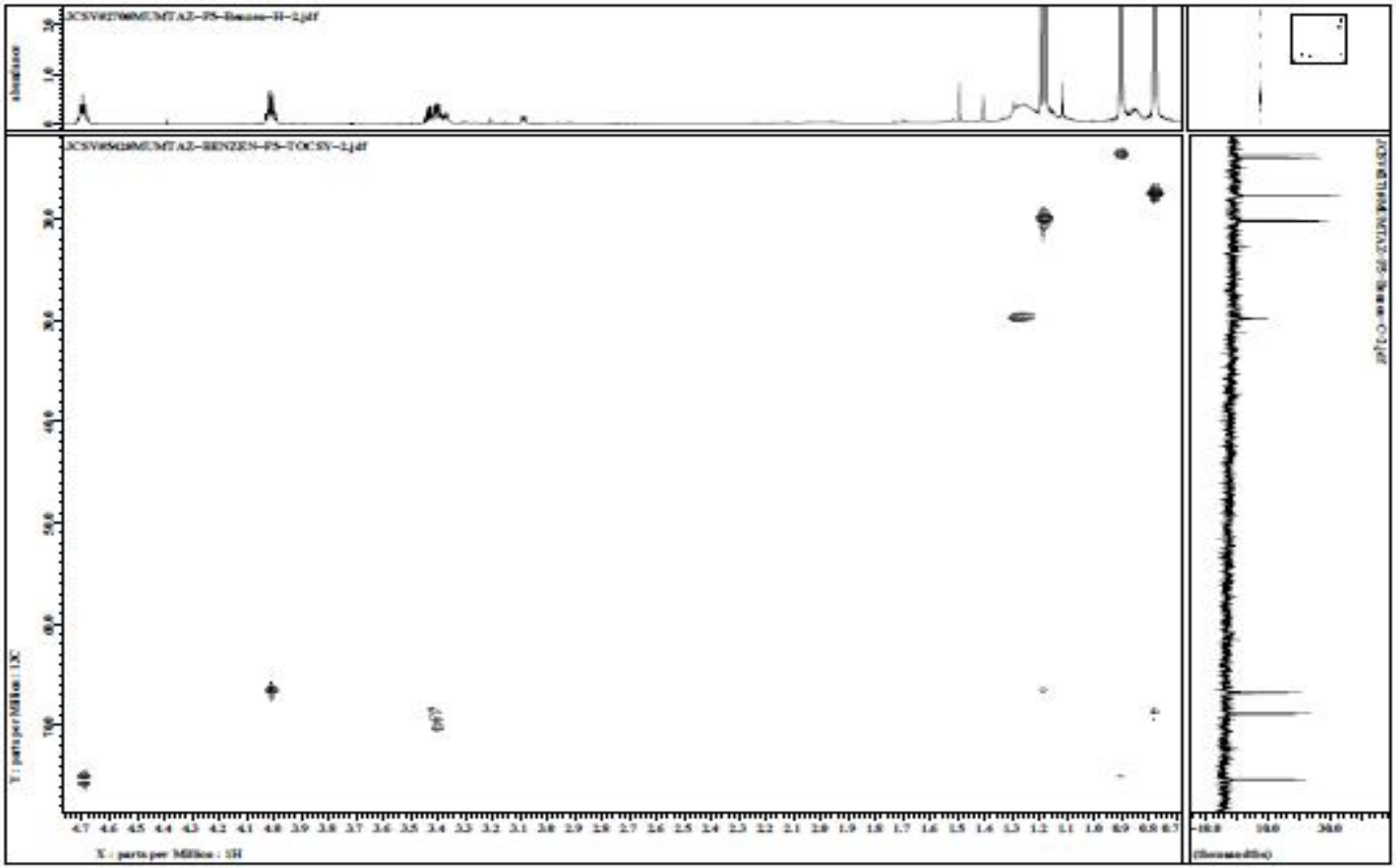


Figure O-9: TOCSY chromatogram of active sub-fraction F5.1

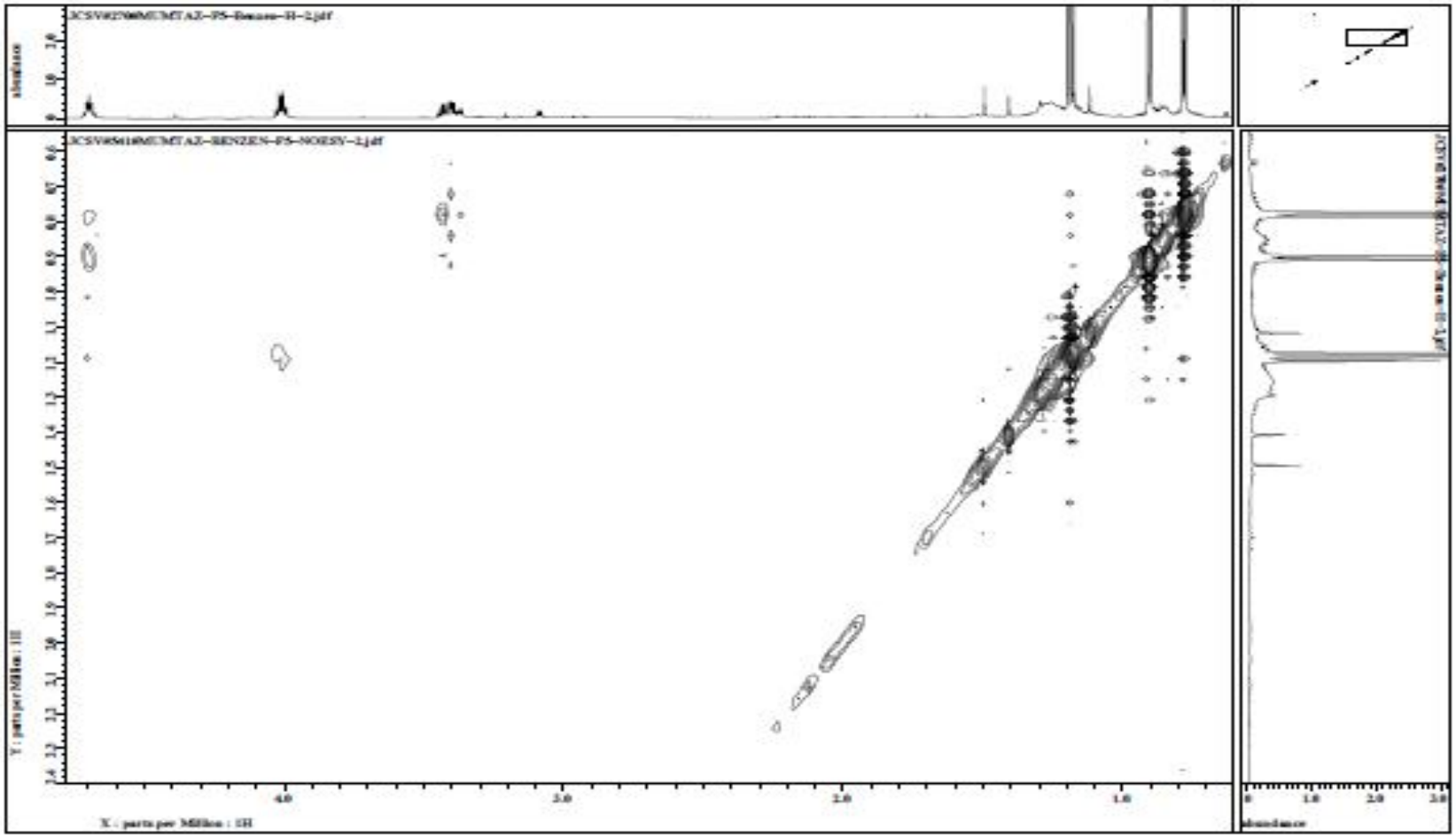
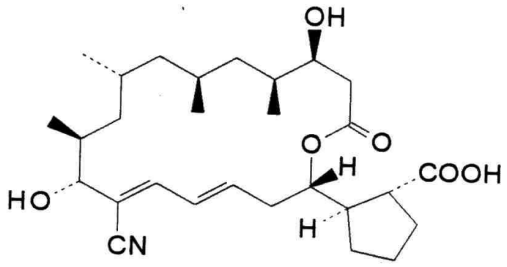


Figure O-10: NOESY chromatogram of active sub-fraction F5.1

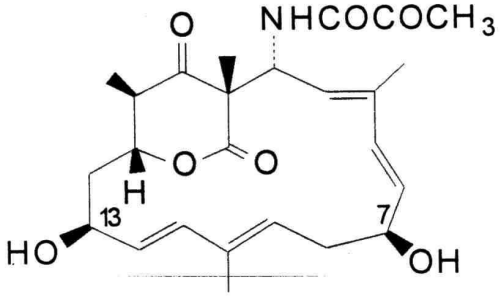
APPENDIX P

Secondary metabolites from *Streptomyces rochei* (Berger *et al.*, 1953; Kotake *et al.*, 1992)

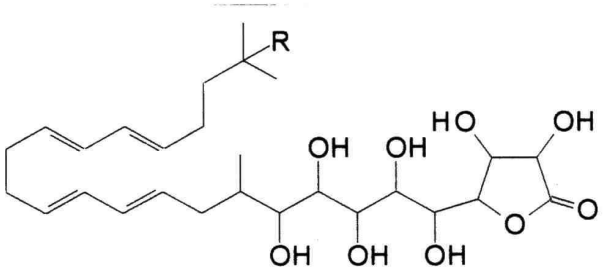
Borrelidin, macrolide antibiotic with antiviral activity



Bundlin, a macrocyclic compound active against gram-positive bacteria

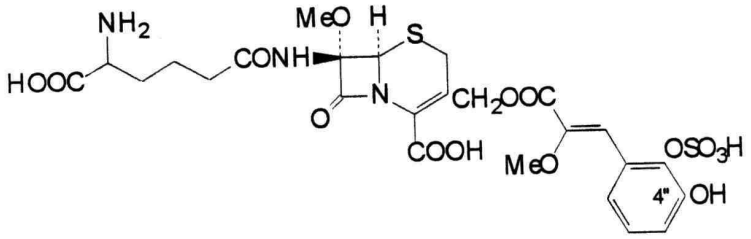


Butyrolactol A, active against fungi



R = CH_3

Cephalosporin antibiotic



Lankacyclinol, polyene-type antibiotic with antimicrobial activity