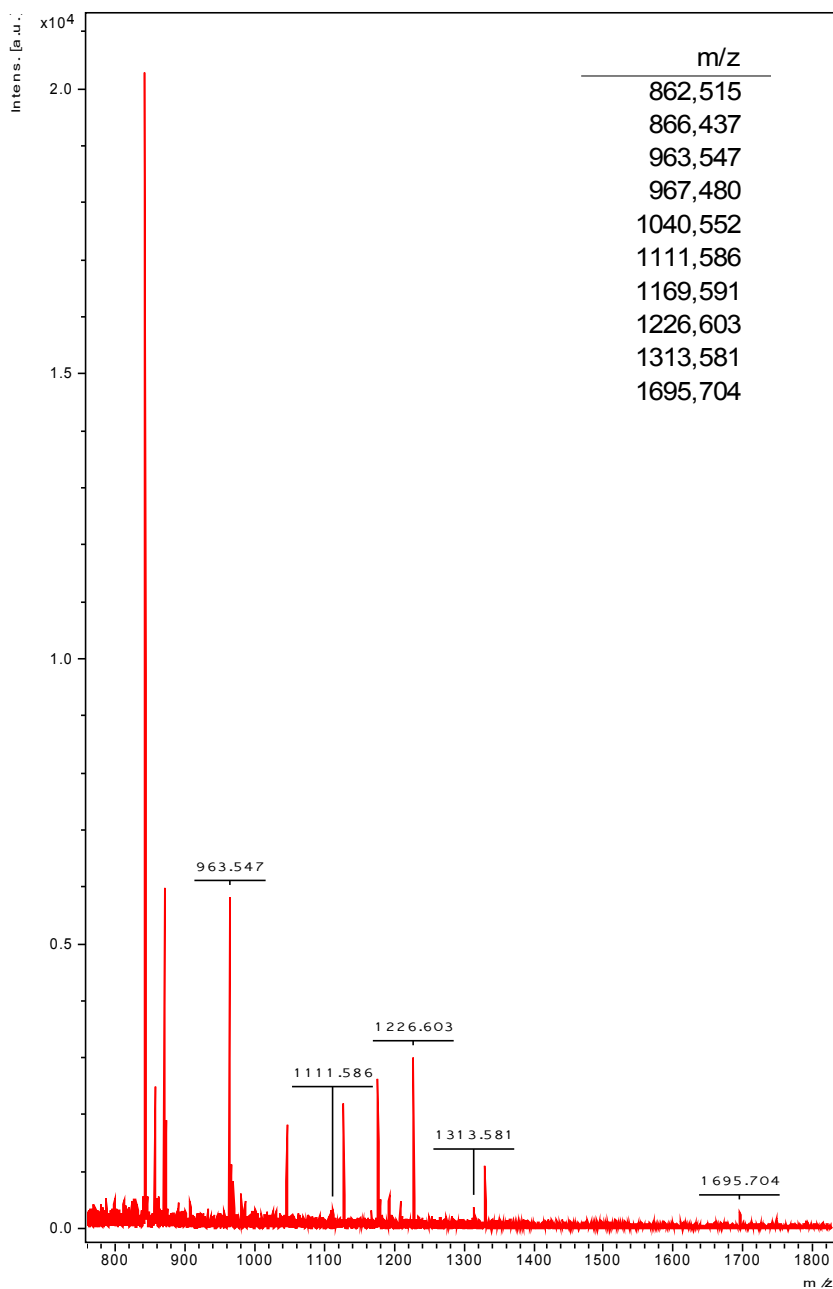


# Peptide Mass Fingerprint for spot 6149: SCO0379

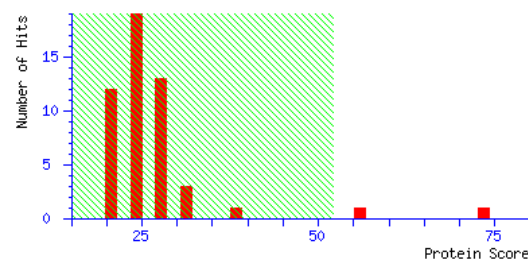


## Mascot Search Results

**(MATRIX) SCIENCE**  
 User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6149  
 Database : NCBI nr 20100529 (11111565 sequences; 3786451707 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 4 Jun 2010 at 08:16:29 GMT  
 Top Score : 73 for [gi|21218922](#), catalase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21218922</a>	55139	73	catalase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 2052219</a>	55463	56	catalase [Streptomyces coelicolor]
3. <a href="#">gi 21234037</a>	35740	39	putative transposase [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21225946</a>	45243	30	cytochrome P450 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21220009</a>	46650	30	histidyl-tRNA synthetase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21220698</a>	194331	30	bi-functional protein (secreted alpha-amylase/dextrinase) [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21218820</a>	114800	29	hypothetical protein SCO0269 [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21226044</a>	10980	28	hypothetical protein SCO7792 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21225001</a>	39963	28	ATP-dependent DNA ligase [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21220329</a>	57941	27	ABC transporter ATP binding protein [Streptomyces coelicolor A3(2)]

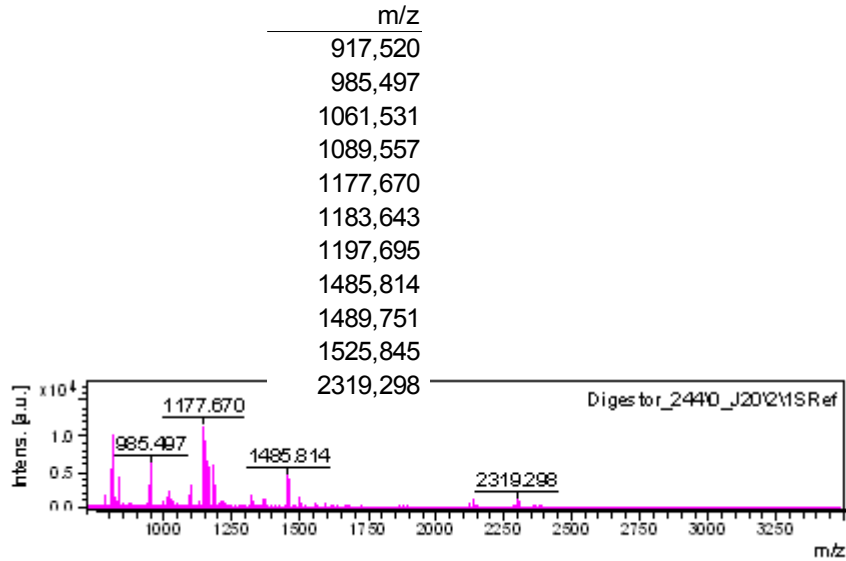
Sequence Coverage: 13%

Matched peptides shown in **Bold Red**

```

1 MPENNQKPLT TVAGAPVPDM QNSLTSGPRG PMLLDQVWFL EKLAHFDREV
51 IPERRMHAKG SGAFGTFTVT HDITRYTSAK IFSEIGKKTP LTRFSTVAG
101 ERGAADAERD IRGFAVKFYT DEGNWDLVGN NTPVFFFRDP LKFPDLNHAV
151 KRDPRTNLRN AENNWDFWTN LPEALHQVTI VMSDRGIPAS YRHHGFGSH
201 TYSLINAEGE RFVVKFHRT QQGIKNLTD AEAALVGKDR ESHQRDLFDA
251 IEDGDFPKWK LFIQVMPEAD AENYRFHFPD LTKVWSKKDY PLIEVGWEL
301 NRNPDNYFAD VEQAAFSPAN VVPGISFSPD RMLQGRLFSY GDAQRYRLGV
351 NHHQIPVNAP KNPVNSYHRD GAMRVDSGNG ATPGVEPNYSY GRWQEQPAYR
401 DPAQAVGAVA DRFNYREDD NYFEQPGNLF RQMSPEQQQV LFENTARAID
451 GASAQTIERH IGNTCTQADPA YGAGVRKAIE ALAAGNL
  
```

# Peptide Mass Fingerprint for spot 6577: SCO1570

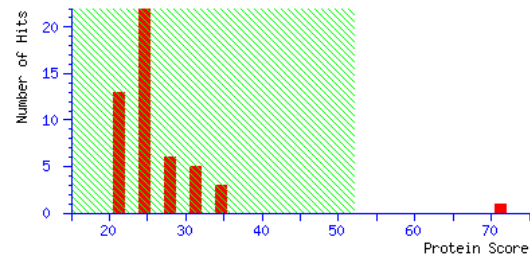


## *MATRIX* SCIENCE Mascot Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6577  
**Database** : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 8 Jun 2010 at 17:42:51 GMT  
**Top Score** : 71 for **gi|21220068**, argininosuccinate lyase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
 Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220068</a>	50967	71	argininosuccinate lyase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21225548</a>	34681	34	ion channel subunit [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21218772</a>	28703	34	nitrate reductase delta chain NarJ2 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21219843</a>	32751	33	oxidoreductase [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21224934</a>	38541	33	hypothetical protein SCO6637 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21234058</a>	32616	32	putative DNA-binding protein [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21223145</a>	32307	32	transcriptional regulator [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21234061</a>	65898	31	putative atp/GTP-binding protein [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21219988</a>	35753	30	aspartate carbamoyltransferase catalytic subunit [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21218824</a>	55178	28	alpha-galactosidase SCF8502 [Streptomyces coelicolor A3(2)]

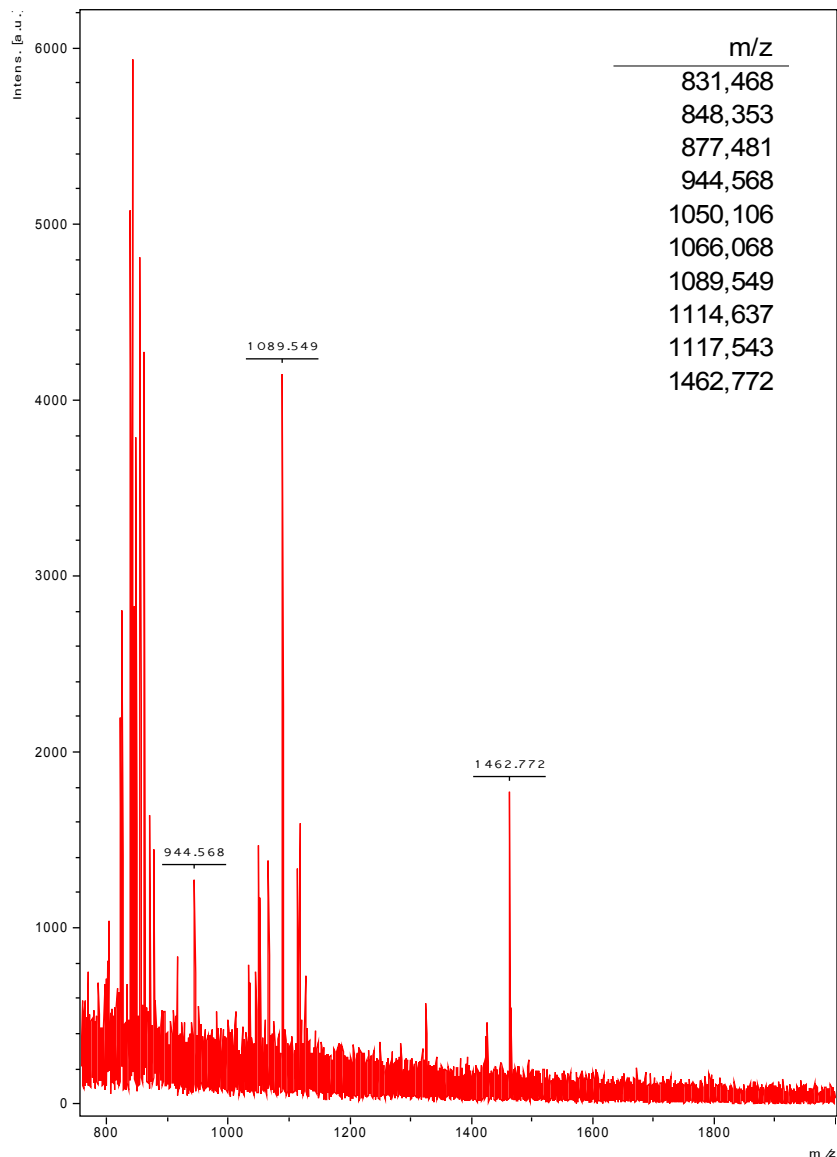
Sequence Coverage: 11%

Matched peptides shown in **Bold Red**

```

1  MSSNSGDVRL  WGRFADGPA EALAKLSASV  HFDWRLAPYD  IAGSRAHARV
51 LHAAGLLTED  ELTRMIAGLD  RLEADVADGS  FTGTIAD EDV  HTALERGLLE
101 RLGPDLGGKL  RAGRSRNDQV  ATLFRMYLRD HARTV  GSLIA  DLQDALVGLA
151 EAHPDVAMPG  RTHLQHAQPV  LFAHHVLAHA  QALGRDAERL  RQWDARTAVS
201 PYGSGALAGS  SLGLDPEAVA  RDLGFEHGSV  GNSIDGTASR  DFVAEFAFIT
251 AMIGVNVSRI  AEEIIIWNTK  EFSFVTLHDA  FSTGSSIMPQ  KKNPDIAELA
301 RGKSGRLIGN  LTGLMATLKA  LPLAYNRDLQ  EDKEPVFDSI  DQLEVLLPAF
351 TGMMATLTVH  RERMEELAPA  GFSLATDIAE  WLVKQGVFPR  VAHEVAGECV
401 KVAEADGKEL  DELTDEQFAK  ISEHLTPEVR  TVLNVPGALA  SRDGRGGTAP
451 SAVAVQLAEV  KADVAAQHAW  ADAKK
    
```

# Peptide Mass Fingerprint for spot 6655: SCO1580

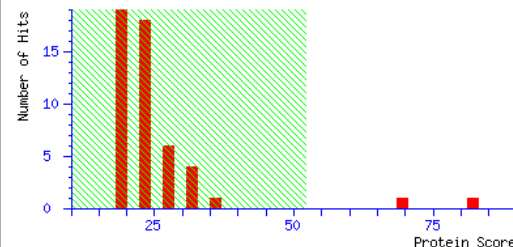


## Mascot Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6655  
**Database** : NCBI nr 20100529 (11111565 sequences; 3786451707 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 4 Jun 2010 at 09:03:29 GMT  
**Top Score** : 82 for [gi|21220077](#), N-acetyl-gamma-glutamyl-phosphate reductase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \times \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220077</a>	34708	82	N-acetyl-gamma-glutamyl-phosphate reductase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 146824</a>	25360	71	N-acetyl-gamma-glutamyl-phosphate reductase [Streptomyces coelicolor]
3. <a href="#">gi 32141213</a>	66287	38	molecular chaperone DnaK [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21220801</a>	5705	33	hypothetical protein SCO2333 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21224333</a>	98902	31	hypothetical protein SCO5996 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21223060</a>	40967	31	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21224045</a>	41169	31	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21219150</a>	48301	29	hypothetical protein SCO0618 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21218860</a>	42898	28	acyl-CoA dehydrogenase [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21220744</a>	41758	27	lipoprotein [Streptomyces coelicolor A3(2)]

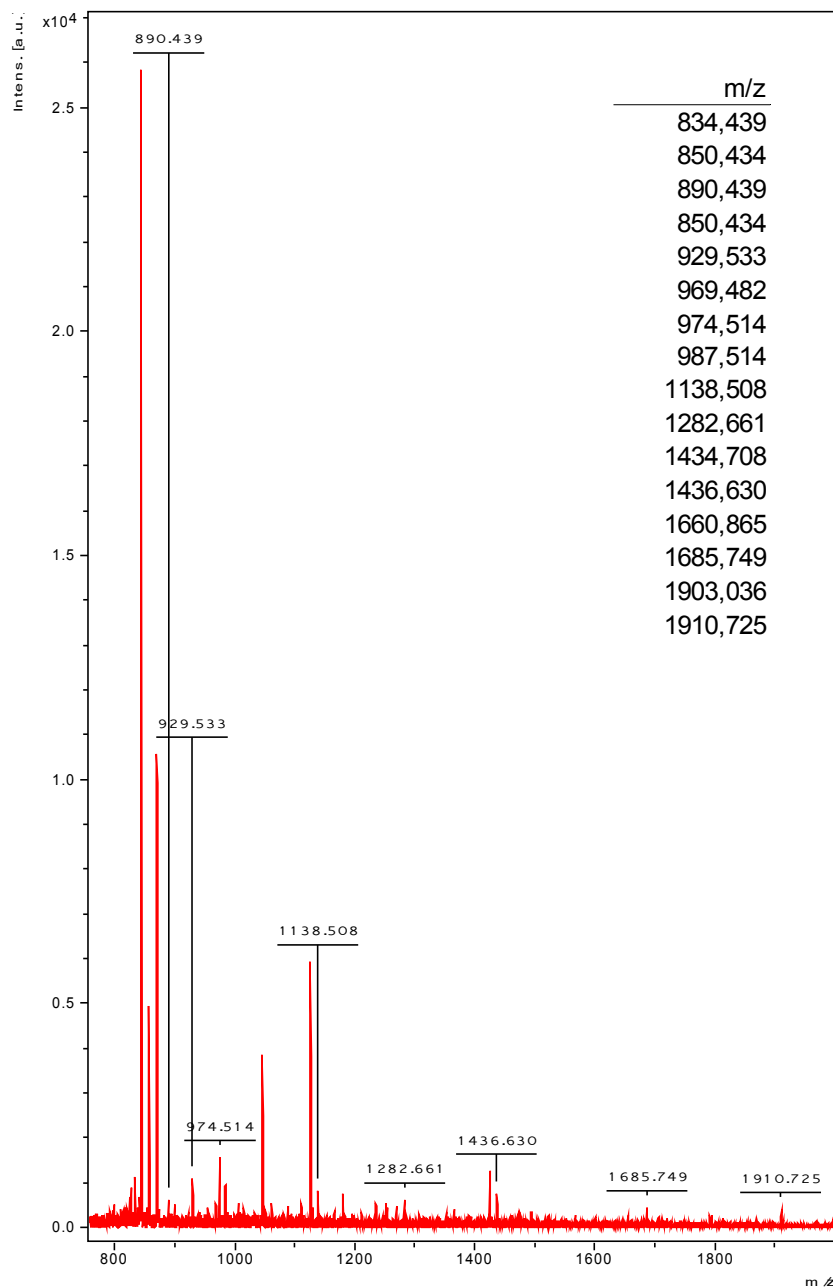
Sequence Coverage: 15%

Matched peptides shown in **Red**

```

1 MAVRAAVAGA SGYAGGELLR LLLTHPEVEI GALTGNSNAG QRLGALQPHL
51 LPLADRVLEA TTPEVLGGHD VVFLALPHGQ SAAVAEQLGP DVLVVDMGAD
101 FRLKADAGDWE RFYGSPHAGT WPYGLPELPG ARAALEGSKR IAVPGCYPTA
151 VSLALFPAYA ASLAEPEAVI VAASGTSGAG KAAKPHLLGS EVMGSMSPYG
201 VGGGHRHTPE MIQNLGAVAG EPVTVSFTPT LAPMPRGILA TCTAKAKPGV
251 TAESVRAAYE KALADEFFVH LLPEGQWPAT ASVYGSNAVQ VQVAHDAAG
301 RIIAISIDN LAKGTAGGAV QSMNLALGLD ETTGLTTIGV AP
    
```

# Peptide Mass Fingerprint for spot 6550: SCO1814

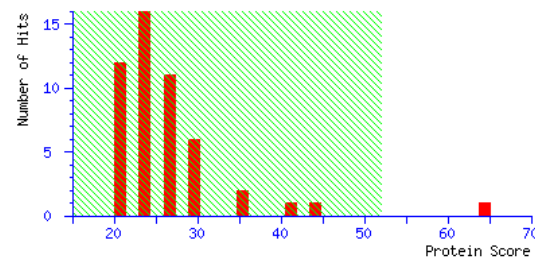


## MASCOT Search Results

**Matrix Science**  
 User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6550  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 8 Jun 2010 at 07:26:39 GMT  
 Top Score : 64 for **gi|21220304**, enoyl-(acyl carrier protein) reductase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <b>gi 21220304</b>	27250	64	enoyl-(acyl carrier protein) reductase [Streptomyces coelicolor A3(2)]
2. <b>gi 21223982</b>	20774	44	ribosome recycling factor [Streptomyces coelicolor A3(2)]
3. <b>gi 21223255</b>	34716	41	polysaccharide biosynthesis related protein [Streptomyces coelicolor A3(2)]
4. <b>gi 21223930</b>	15952	35	hypothetical protein SCO5574 [Streptomyces coelicolor A3(2)]
5. <b>gi 21223426</b>	56410	34	secreted protein [Streptomyces coelicolor A3(2)]
6. <b>gi 21220635</b>	36900	30	kinase [Streptomyces coelicolor A3(2)]
7. <b>gi 21219464</b>	31179	30	formamidopyrimidine-DNA glycosylase [Streptomyces coelicolor A3(2)]
8. <b>gi 21219445</b>	31682	30	hypothetical protein SCO0926 [Streptomyces coelicolor A3(2)]
9. <b>gi 21224699</b>	20339	29	hypothetical protein SCO6387 [Streptomyces coelicolor A3(2)]
10. <b>gi 21224661</b>	145012	29	hypothetical protein SCO6348 [Streptomyces coelicolor A3(2)]

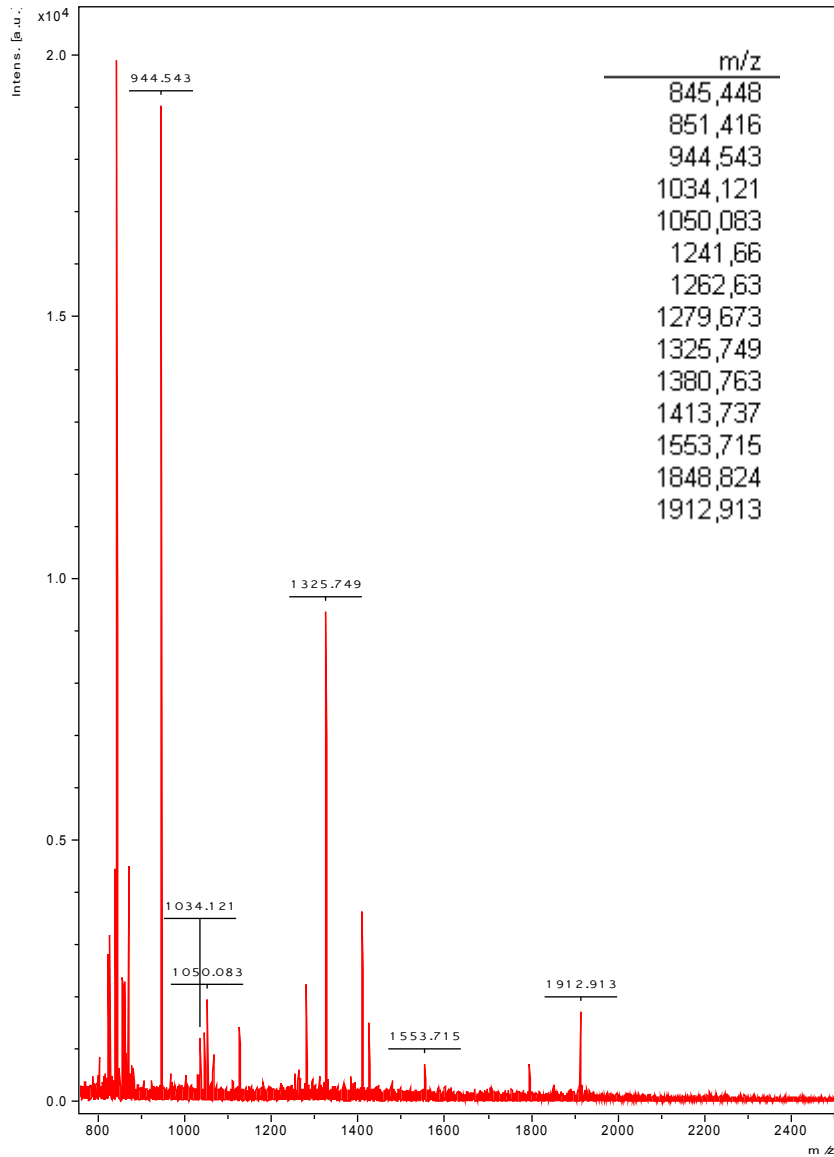
Sequence Coverage: 23%

Matched peptides shown in **Bold Red**

```

1  MSGILEGKRV LITGVLMSS IAFHAAKLAQ EQGAEIILTA FPRPTLTERI
51  AKKLPKPTRV IELDVTNDEH LARLADVVEG ELGGLDGVVH SIGFAPQDAL
101 GGNFLNTPFE SVATAMHVS A YSLKSLTMAC MPLMQNGGSV VGLTFDAQYA
151 WPQYDWMGPA KAAL EATSRY MARDLGKQNI RCNLVSA GPI GSMAAKSIPG
201 FSDLAAVWDS RSPLEWDLKD PEPAGRGIVA LLSDWFPKTT GEIIHVDGGL
251 HAIGA
  
```

# Peptide Mass Fingerprint for spot 6445: SCO1935

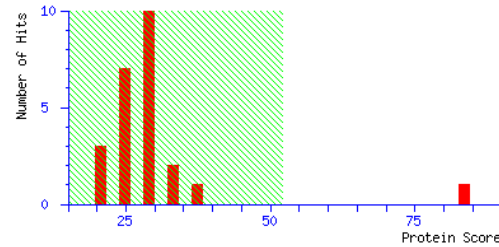


## MASCOT Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6445  
**Database** : NCBIInr 20100529 (11111565 sequences; 3786451707 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 3 Jun 2010 at 14:24:41 GMT  
**Top Score** : 84 for [gi|21220421](#), transketolase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220421</a>	75085	84	transketolase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 7481146</a>	21183	35	probable pantoate-amino acid ligase - Streptomyces coelicolor (fragment)
3. <a href="#">gi 21219522</a>	43650	35	insertion element [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21221636</a>	25020	34	TetR family transcriptional regulator [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21221716</a>	26860	32	cobalt-porphyrin-6x reductase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21222864</a>	25430	31	MerR family transcriptional regulator [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21220839</a>	102585	31	pyruvate dehydrogenase subunit E1 [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21222670</a>	34131	30	binding-protein-dependent transport lipoprotein [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 32141201</a>	35492	29	pantoate--beta-alanine ligase [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21218793</a>	33045	28	oxidoreductase [Streptomyces coelicolor A3(2)]

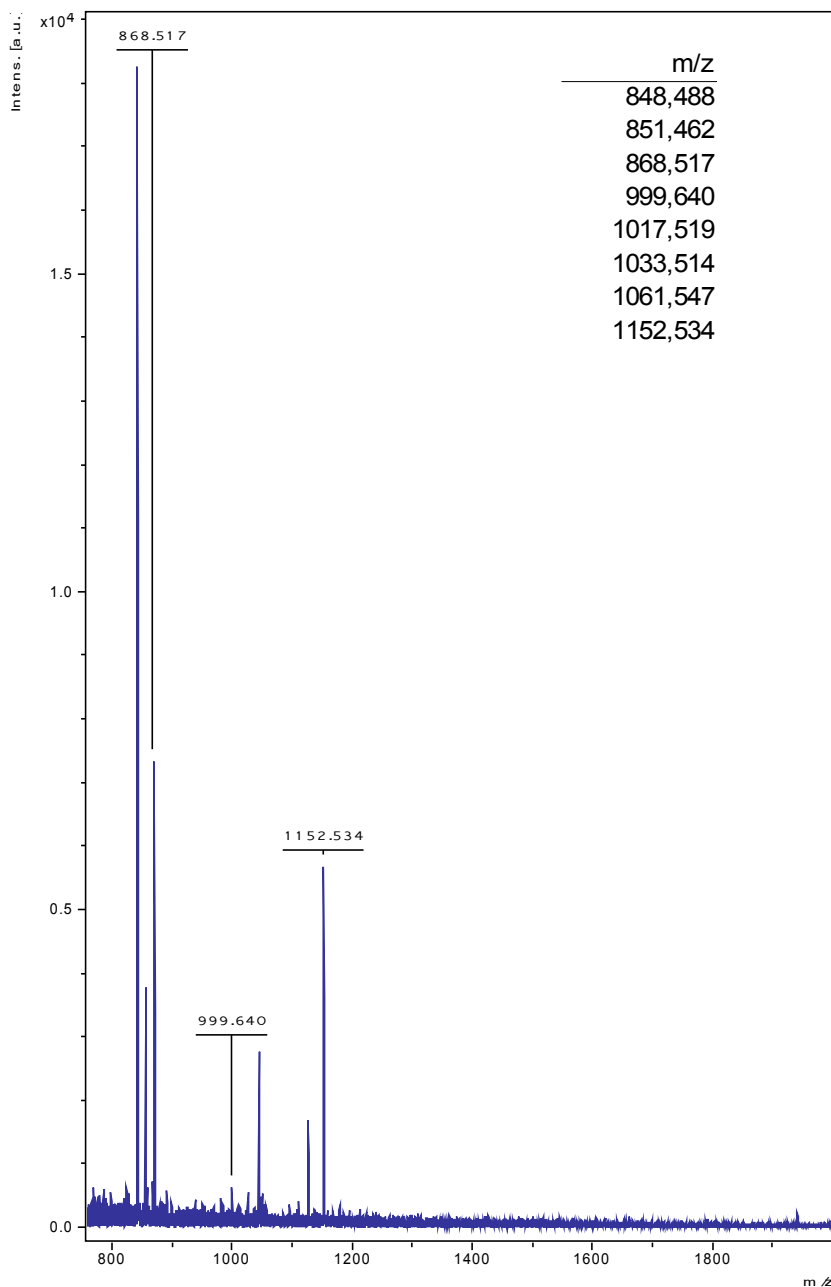
Sequence Coverage: 12%

Matched peptides shown in **Bold Red**

```

1  MSTKPTTDDL EWTELDQRAV DTARVLAADA VQKVGNGHPG TAMSLAPAA
51  TLFQKVMRHD PADANWVGRD RFVLSAGHSS LTLYTQLYLA GFGLELADLE
101 SFRTWGSKTP GHPEYGHHTG VETTTGPLGQ GVANAVGHAM AARYERGLFD
151 PEAAEGESPF DHFVYCIAGD GCLQEGISSE ASSTAGHQKL GNLVLLWDDN
201 HISIEGDDET AVSEDTCKRY EAYGWHVQRV APKPDGDLDP NAIYDAIEAA
251 KKVTRPSFI AMRSIIAWPA PNAQNTAAAH GSALGDDEVA ATRKVLGFDP
301 EKSFVSDDEV IEHTRKALEK QQAARAVWEK SFQQWRDNMP ERAAEYDRVA
351 KGELPAGWEE KIPVFEAGK LARAASGKV LQALGAVIPE LWGGSADLAG
401 SNNTTIDKTS SFLPAGNPLP EADPYGRTIH FGIREHAMAA EMNGIALHGN
451 TRIYGGTFLV FSDYMRNAVR LSALMHLPTV YVWTHDSIGL GEDGPTHQPV
501 EHLASLRAIP GLNVVRPADA NETAIAWREI LRRWTKEFGK GQPHGLALTR
551 QGVPTYEPNE DAAKGGYVLF EAEGGDAEVV LIATGSEVHV AVGARERLQA
601 DGVPTRVVSM PSVEWFEQQD QGYRDSVLPP SVKARVAVEA GIGLTHWKYV
651 GDAGRIVSLE HFGASADAKV LFKFEGFTA E NVASAARESL AAAQR
    
```

# Peptide Mass Fingerprint for spot 6947: SCO1945

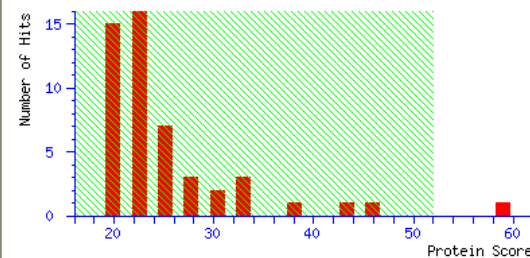


## Mascot Search Results

**Matrix Science**  
 User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6947  
 Database : NCBI nr 20100529 (11111565 sequences; 3786451707 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 4 Jun 2010 at 10:58:50 GMT  
 Top Score : 59 for [gi|21220430](#), triosephosphate isomerase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220430</a>	27947	59	triosephosphate isomerase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21219210</a>	49783	47	ferredoxin/ferredoxin-NADP reductase (putative secreted protein) [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21222497</a>	17654	43	lipoprotein [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21223671</a>	32237	37	hypothetical protein SC05308 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21220012</a>	5061	32	hypothetical protein SC01512 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21219314</a>	37039	32	hypothetical protein SC00792 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21219714</a>	50275	32	succinic semialdehyde dehydrogenase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21223435</a>	8955	31	hypothetical protein SC05063 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21222189</a>	48000	30	threonyl tRNA synthetase [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21219658</a>	64596	28	ABC transporter ATP-binding protein [Streptomyces coelicolor A3(2)]

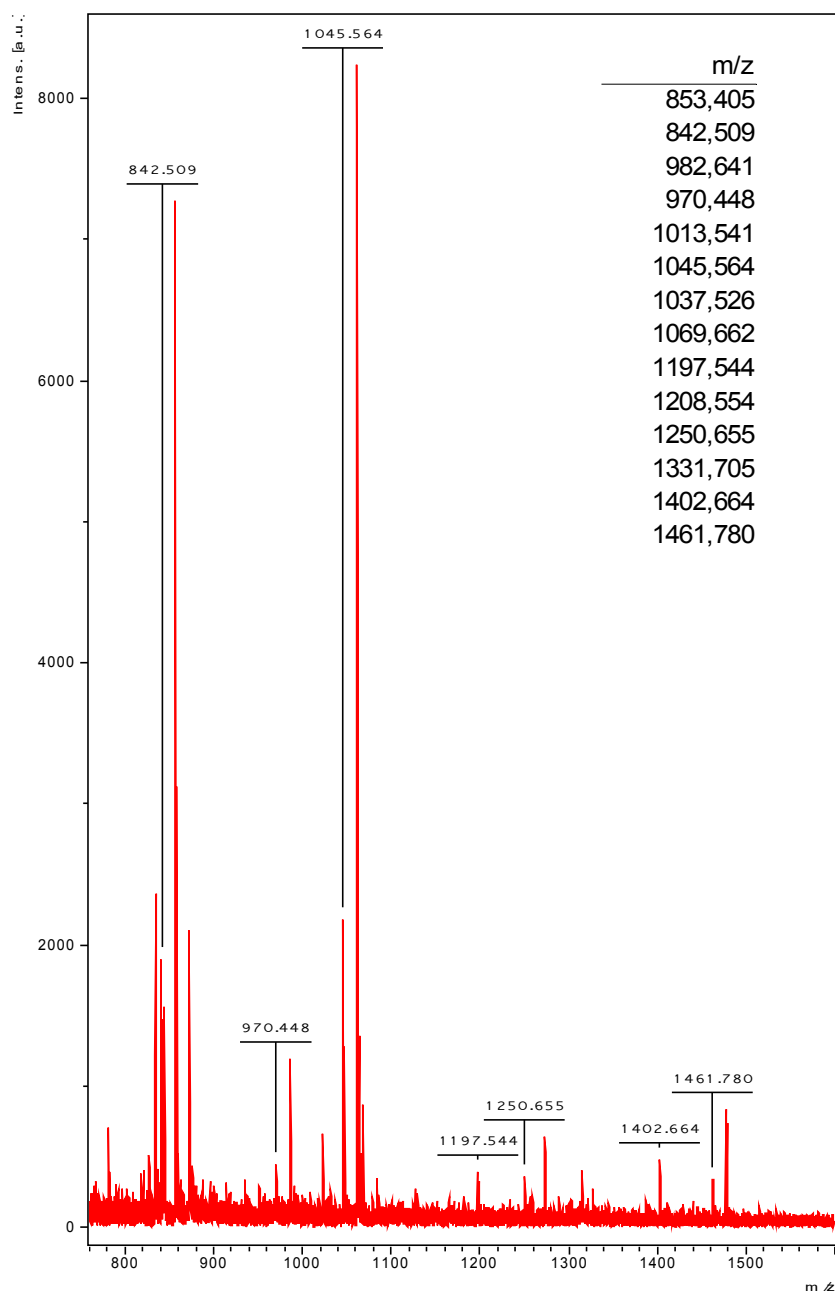
Sequence Coverage: 13%

Matched peptides shown in **Bold Red**

```

1  MTTRTPLMAG NWKMNLNHL E AIAHVQKLAF ALADKDYDAV EVAVLAPFTD
51  LRSVQTLVDG DKLKIKYGAQ DISAHDGGAY TGEISGPMLA KLKCTYVAVG
101 HSERRQYHAE TDEIVNAKVK AAYKHGLTPI LCVGEELDVR EAGNHVEHTL
151 AQVEGGLKDL AAEQAESVVI AYEPVWAIGT GKVCGADDAQ EVCAAIRGKL
201 AELYSQELAD KVRIQYGGSV KSGNVAEIMA KPDIDGALVG GASLDSDEFV
251 KIVRFRDQ
  
```

# Peptide Mass Fingerprint for spot 6233: SCO1946

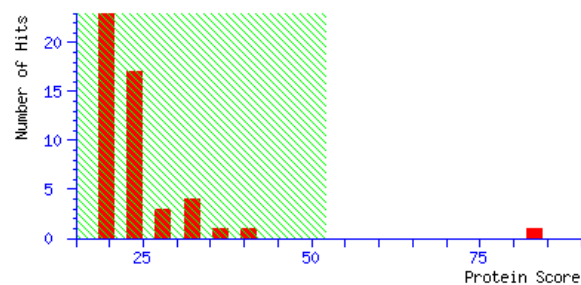


## MASCOT SCIENCE Mascot Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6233  
**Database** : NCBIInr 20100529 (11111565 sequences; 3786451707 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 4 Jun 2010 at 11:23:26 GMT  
**Top Score** : 83 for [gi|21220431](#), phosphoglycerate kinase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220431</a>	41740	83	phosphoglycerate kinase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21224012</a>	26447	41	hypothetical protein SC05661 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21225247</a>	19601	35	hypothetical protein SC06960 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21222919</a>	47816	34	integral membrane protein [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21223436</a>	86651	32	bifunctional protein [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21224983</a>	122963	31	hypothetical protein SC06688 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21225211</a>	26499	30	hypothetical protein SC06923 [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21223951</a>	27759	30	signal peptidase I [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21224180</a>	88928	27	DNA topoisomerase IV subunit A [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21222693</a>	9560	26	hypothetical protein SC04300 [Streptomyces coelicolor A3(2)]

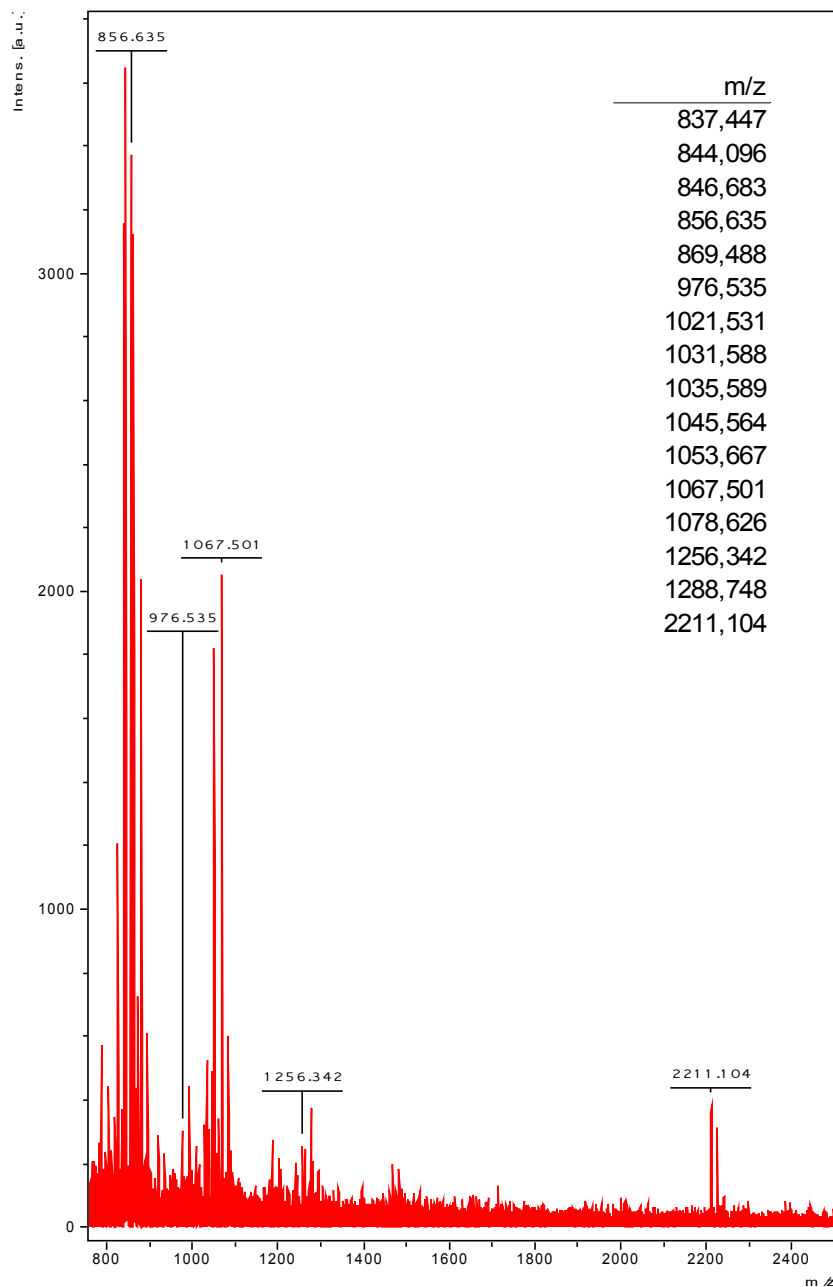
Sequence Coverage: 16%

Matched peptides shown in **Bold Red**

```

1  MKTIDELLSE GVAGKRVFVR ADLNWPLDGT TITDDGRIRRA VVPTVKALAD
51 AGARVIVASH LGRPKGAPDP AFSLAPAAAR LGELLGADVA FAEDTVGSSA
101 EAVVTGLADG GVAVIENLRF NAGETSKDDA ERAMFADKLA GLADVYVGDG
151 FGAVHRKHAS VFDLPKRLPH YAGYLIADEV GVLKKLTDEV KRPYVVALGG
201 AKVSDKLAVI DQLLGKADRL LIGGGMAYTF LKAGGYEVGI SLLQEDQIPA
251 VKEYIERAEK NGVELVLPVD VLVAFEPFDL KTKAPANPTT VAADAIPADQ
301 EGLDIGPETR KLYASKLADA GTVFWNGPMG VFEHPDYAEG TKAVAQALVD
351 APGFTVVGGG DSAAAVRTLG FDENAFGHIS TGGGASLEYL EGKTLPLGLAA
401 LED
    
```

# Peptide Mass Fingerprint for spot 6193: SCO1947

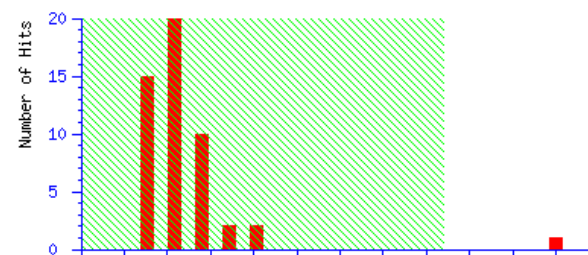


## MASCOT SCIENCE Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6193  
 Database : NCBI nr 20100529 (11111565 sequences; 3786451707 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 4 Jun 2010 at 11:38:51 GMT  
 Top Score : 65 for **gi|21220432**, glyceraldehyde-3-phosphate dehydrogenase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220432</a>	36417	65	glyceraldehyde-3-phosphate dehydrogenase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21218661</a>	25682	30	hypothetical protein SC00095 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21223676</a>	31813	29	membrane protein [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21225026</a>	77958	28	fatty acid oxidative multifunctional enzyme [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 32141232</a>	31838	26	aminoglycoside phosphotransferase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21220047</a>	9476	25	hypothetical protein SC01548 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21219602</a>	39255	25	aldolase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21222458</a>	40462	25	alcohol dehydrogenase [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21224018</a>	42554	24	polyamine ABC transporter ATP-binding protein [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21223774</a>	11954	24	hypothetical protein SC05414 [Streptomyces coelicolor A3(2)]

Sequence Coverage: **13%**

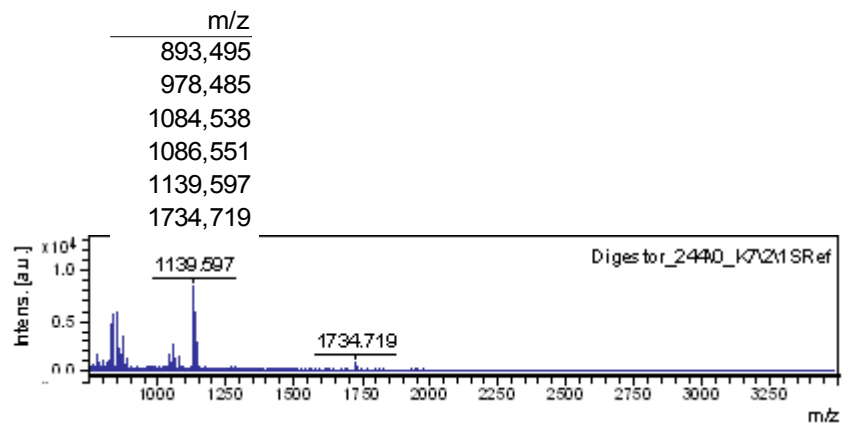
Matched peptides shown in **Red**

```

1  MTIRVGINGF GRIGRNYFRA LLEQGADIEI VAVNDLGDTA TTAHLKYDT
51 ILGRLKAEVS HTEDTITVDG KTIKVLSEFN PADIPWGLG WDIVIESTGI
101 FTKKADAEKH IAGGAKVLI SAPAKDEDIT IVMGVNQDKY DPANHHVISN
151 ASCTTNCVAP MAKVLDFNFG IVKGLMTIVH AYTNDQRILD FPHKDLRRAR
201 AAANIIPIT TGAAKATLV LPQLKGKLDG IRMRVPTG SATDLVVELQ
251 REVTKDEVNA AFKKAAADDGD LKGIIFYTED AIVSSDITGD PASCTFDSSL
301 TMVQEGKSVK ILGWYDNEWG YSNRLVDLTV FVGNQL
  
```



# Peptide Mass Fingerprint for spot 6666: SCO1965



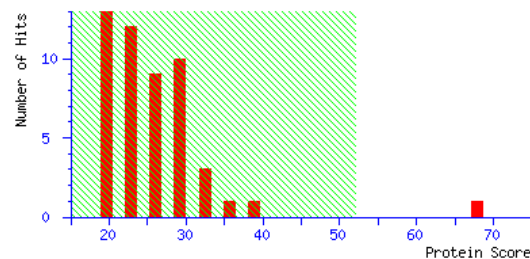
## *{MATRIX}* Mascot Search Results

*{SCIENCE}*

User : irene  
Email : isanh@unileon.es  
Search title : spot 6666  
Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
Taxonomy : Streptomyces coelicolor (8575 sequences)  
Timestamp : 8 Jun 2010 at 10:54:38 GMT  
Top Score : 68 for **gi|21220450**, export associated protein [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

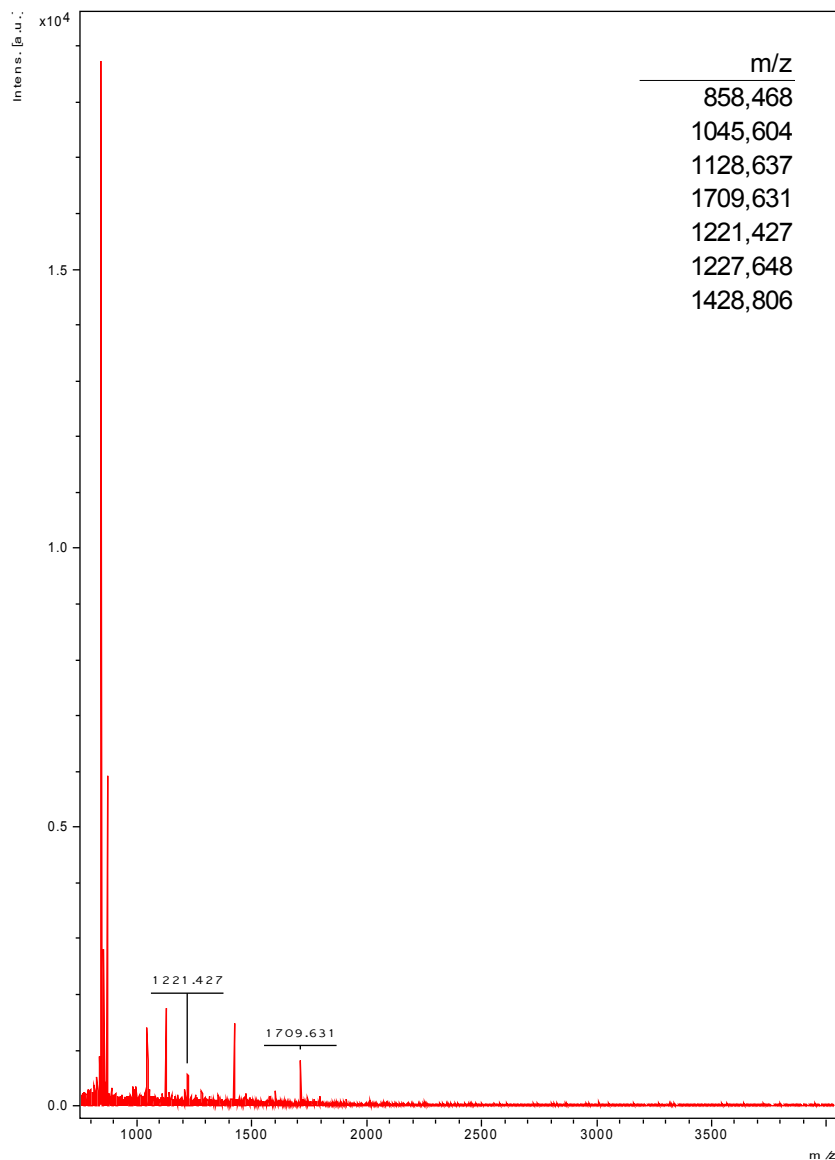
Accession	Mass	Score	Description
1. <a href="#">gi 21220450</a>	20619	68	export associated protein [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21225517</a>	81595	40	serine/threonine-protein kinase [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21220979</a>	47829	36	two-component sensor kinase [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 3451475</a>	60022	33	hypothetical protein [Streptomyces coelicolor]
5. <a href="#">gi 21223088</a>	30312	33	30S ribosomal protein S3 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21220759</a>	12371	32	hypothetical protein SCO2290 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21219250</a>	14151	30	hypothetical protein SCO0725 [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21219394</a>	10060	30	hypothetical protein SCO0873 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21222740</a>	62844	30	hypothetical protein SCO4349 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21222241</a>	14933	30	transcriptional regulator [Streptomyces coelicolor A3(2)]

Sequence Coverage: 19%

Matched peptides shown in **Bold Red**

1 MTVMNMTKGQA ISLQK**SDGGS LTVSRMGLGW QAAPRRGLFG SRTREIDLDA**  
51 SAVLFADKQP VDVVFFR**HLV SDDGSVRHTG** DNLVGGVGGG GDDEAILVDL  
101 QRVPVHIDQI VFTVNSFTGQ TFQEVQNAFC RLVDETNGQE LARYTLAGGG  
151 AFTAQIMAKV HRAGQGSMT AIGTPANGRT FQDLMPAILP VL

# Peptide Mass Fingerprint for spot 6494: SCO1998

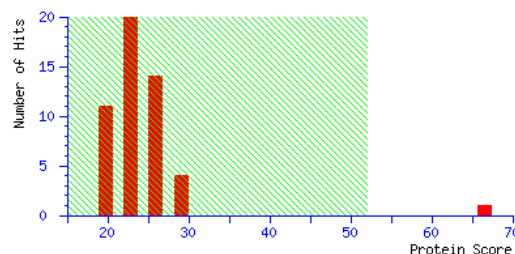


## *{MATRIX}* Mascot Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6494  
**Database** : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 8 Jun 2010 at 07:51:53 GMT  
**Top Score** : 66 for [gi|21220480](#), 30S ribosomal protein S1 [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21220480</a>	55001	66	30S ribosomal protein S1 [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21224283</a>	64042	30	transferase [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21225057</a>	75453	29	squalene-hopene cyclase [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21219928</a>	18002	28	transcription regulator $\Delta$ snC [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21222766</a>	16859	28	hypothetical protein SCO4376 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21222268</a>	19302	27	DNA-binding protein [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21223657</a>	21058	27	ATP/GTP-binding protein [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21221965</a>	20525	27	small secreted protein [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21219079</a>	55209	27	hypothetical protein SCO0544 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21224780</a>	21162	26	adenylosuccinate lyase [Streptomyces coelicolor A3(2)]

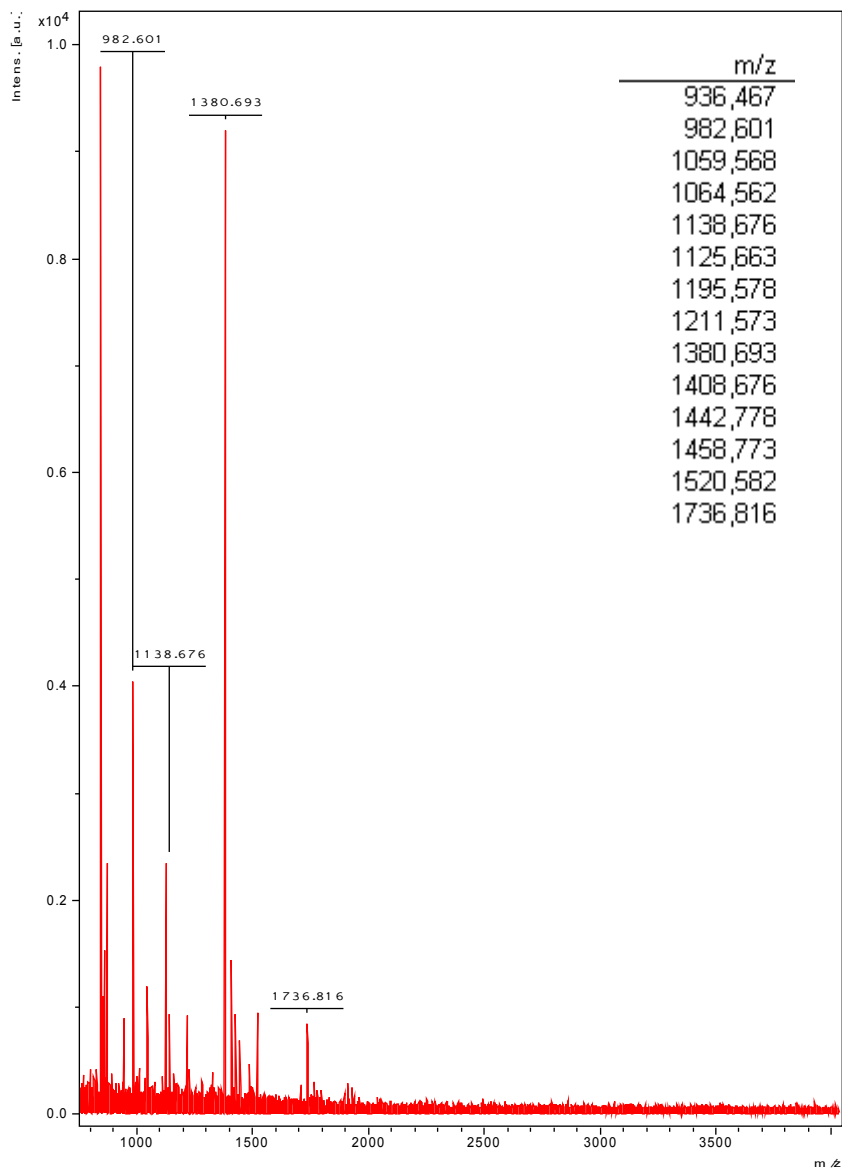
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```

1 MTSSTETTAT TPQVAVNDIG NEEAFLAAID ETIKYFNDGD IVDGVIVKVD
51 RDEVLLDIGY KTEGVIPSRE LSIKHDVDPN EVVAVGDEIE ALVLQKEDKE
101 GRLILSKKRA QYERAWGTIE KIKEEDGIIVT GTVIEWVKGK LILDIGLRGF
151 LPASLVEMRR VRDLQPYVGK ELEAKIIELD KNRNMVLSR RAWLEQTQSE
201 VRQTFLLTLQ KGQVRSGVVS SIVNFGAFVD LGGVDGLVHV SELSWKHIDH
251 PSEVVEVGQE VIVEVLVDVM DRERVSLSLK ATQEDPWQQF ARTHIGQVQV
301 PGKVTKLVPF GAFVRVDEGI EGLVHISELA ERHVEIPEQV VQVNDEIFVK
351 VIDIDLERRR ISLSLKQANE AFGADPSTVE FDPPLYGMAA SYDDQGNYYIY
401 PEGFDPETND ULEGYETQRE AWETQYAEAQ TRFEQHQAQV IKSREADEKA
451 AAEGVDTAGA APAASGGGGG GSYSSEGGDN SGALASDEAL AALREKLAGG
501 QS
    
```

# Peptide Mass Fingerprint for spot 6143: SCO2198

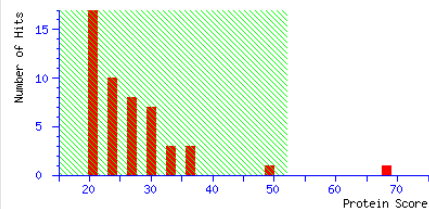


## (MATRIX) Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6143  
 Database : HCBInr 20100529 (11111565 sequences; 3786451707 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 3 Jun 2010 at 13:41:41 GMT  
 Top Score : 68 for **gi|21220671**, glutamine synthetase I [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

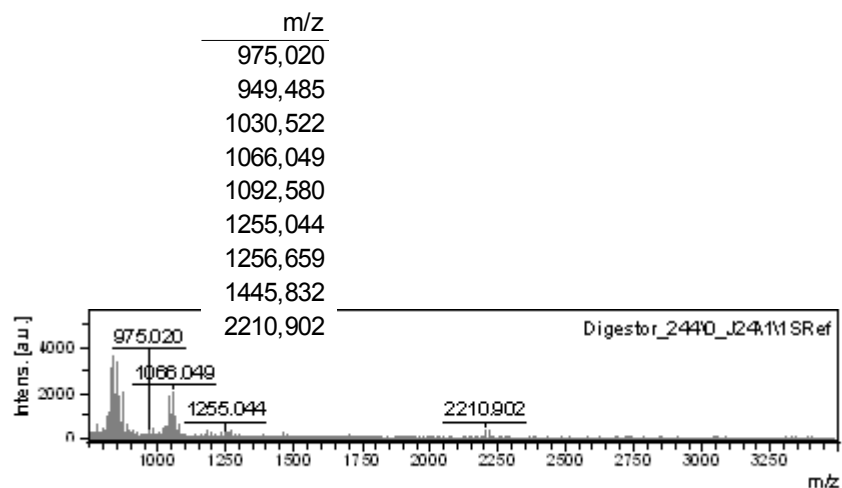
Accession	Mass	Score	Description
1. <a href="#">gi 21220671</a>	52592	68	glutamine synthetase I [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 212225936</a>	7597	48	ferredoxin [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 212221444</a>	17348	38	hypothetical protein SCO3001 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 212223700</a>	49278	37	plasmid transfer protein [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 212234112</a>	42059	35	ecf family sigma factor [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 212223661</a>	24234	33	TetR family transcriptional regulator [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 212225342</a>	24951	32	oxidoreductase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 212223654</a>	27622	32	hypothetical protein SCO5288 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 212220865</a>	16638	32	MarR family transcriptional regulator [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 212224042</a>	71920	31	acyl CoA dehydrogenase [Streptomyces coelicolor A3(2)]

Sequence Coverage: 18%

Matched peptides shown in **Bold Red**

**1 MFQNAADVKK FIADEDVKFV** DVRFCDLPGV MQHFTLPATA FDPDAEQAFD  
**51 GSSIRGFQAI** HESDMSLRPD LSTARVDPFR RDKTLNINFF IHDPIITGEQY  
**101 SRDPRNVAKK** AEAYLASTGI ADTAFPGPEA EYVFDVSRF ATRENESFYH  
**151 IDSEAGAWNT** GALEDNRYGK VRYKGGYFPV **PPVDHFADLR AEISLELERS**  
**201 GLQVERQHHE** VGTAGQAEIN YKFNTLLAAA DDLQLFKYIV **KNVAWKNGKT**  
**251 ATFMKPIFG** DNGSGMHVHQ SLWSGGEPLF YDEQGYAGLS DTARYYIGGI  
**301 LKHAPSLAF** TNPTVNSYHR LVPGFAPVN LVYSQRNRS **AMRIPITGSN**  
**351 PKAKRVEFRA** PDASGNPYLA FSALLLAGLD GIKNKIEPAE **PIDKDLIELA**  
**401 PEEHANVAQV** PTLGAVLDR LEADHEFLQ GDVFTPDIE TWIDFKRANE  
**451 IAPLQLRPH** HEFEMYFDV

# Peptide Mass Fingerprint for spot 6647: SCO2368

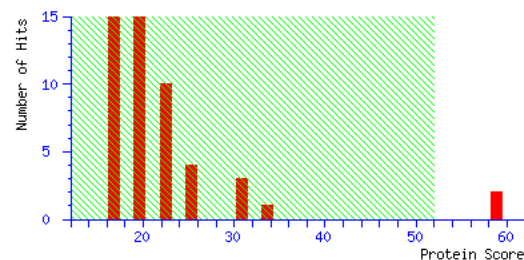


## *{MATRIX}* *{SCIENCE}* Mascot Search Results

User : irene  
Email : isanh@unileon.es  
Search title : spo7 6647  
Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
Taxonomy : Streptomyces coelicolor (8575 sequences)  
Timestamp : 8 Jun 2010 at 11:44:28 GMT  
Top Score : 59 for **gi|21220836**, hypothetical protein SCO2368 [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

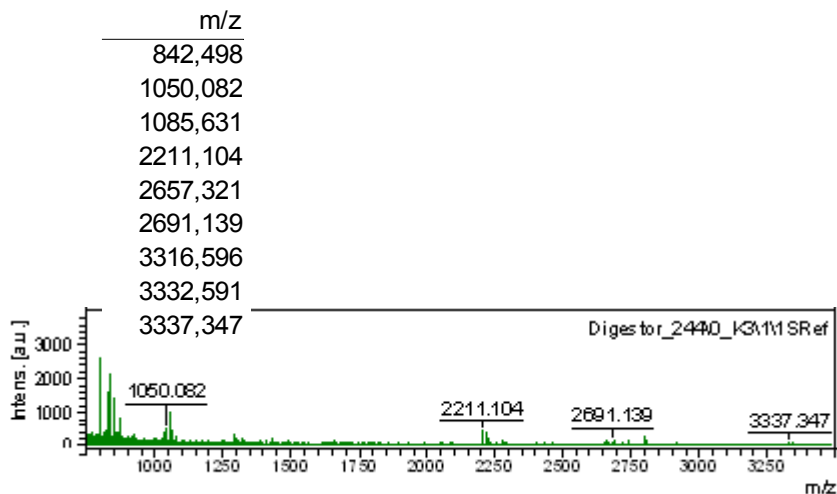
Accession	Mass	Score	Description
1. <a href="#">gi 21220836</a>	20375	59	hypothetical protein SCO2368 [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 256032870</a>	20335	59	Chain A, Crystal Structure Of Putative Tellurium Resistant Like Protein (Terd) From Strepton
3. <a href="#">gi 21219079</a>	55209	34	hypothetical protein SCO0544 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21222562</a>	9736	32	hypothetical protein SCO4165 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21225808</a>	44087	31	CRP family transcriptional regulator [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21225929</a>	36194	30	oxidoreductase [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 18077876</a>	16303	26	hypothetical protein 2_SCP2_p01 [Streptomyces coelicolor]
8. <a href="#">gi 21222099</a>	18803	25	hypothetical protein SCO3686 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21223227</a>	17639	25	hypothetical protein SCO4851 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21233998</a>	17404	25	putative regulatory protein [Streptomyces coelicolor A3(2)]

Sequence Coverage: 20%

Matched peptides shown in **Bold Red**

1 MGVSLSKGGN VSLTREAPGL TAVIVGLGWD IRTTGTDFD LDASALLLNS  
51 GQKVASDAHF IFFNMLKSPD GSVHTGDNI TGELEGDDEQ IKINLATVPA  
101 DIEKIVFPVS IYDAENR**QQS FGQVRNAFIR VVNQAGEAEI ARYDLSE**DAS  
151 TETAMVFGEL YR**HGAEWKFR AIGQGYASGL RGI**AQDFGVN V

# Peptide Mass Fingerprint for spot 6685: SCO2633

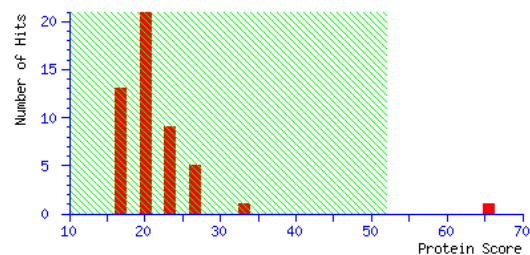


## *MATRIX* Mascot Search Results

User : irene  
Email : isanh@unileon.es  
Search title : spot 6685  
Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
Taxonomy : Streptomyces coelicolor (8575 sequences)  
Timestamp : 8 Jun 2010 at 10:18:46 GMT  
Top Score : 66 for **gi|21221090**, superoxide dismutase [Fe-Zn] [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

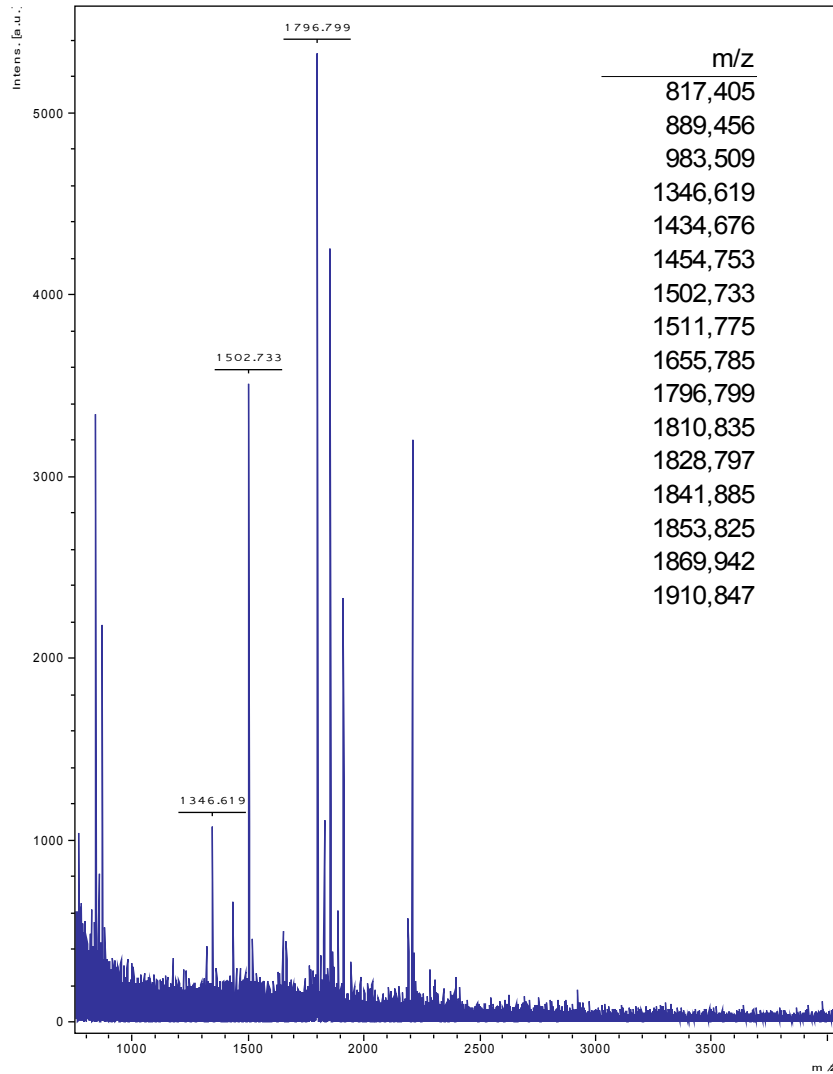
Accession	Mass	Score	Description
1. <a href="#">gi 21221090</a>	23513	66	superoxide dismutase [Fe-Zn] [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 286143258</a>	17854	33	Fe-containing superoxide dismutase [Streptomyces coelicolor]
3. <a href="#">gi 21221379</a>	30298	28	permease membrane component [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21223226</a>	28257	26	TetR family transcriptional regulator [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 167013500</a>	30656	26	Chain A, Crystal Structure Of A Tetr Family Transcriptional Regulator From Streptomyces Coeli
6. <a href="#">gi 21221880</a>	29237	25	ABC-transporter transport protein [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 32141144</a>	45263	25	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21223650</a>	24914	25	hypothetical protein SCO5284 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21222422</a>	25807	25	gntR family regulatory protein [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21220913</a>	37178	24	hypothetical protein SCO2449 [Streptomyces coelicolor A3(2)]

Sequence Coverage: 30%

Matched peptides shown in **Bold Red**

1 MSVYTLPELP YDYSALAPVI SPEIIEIHHDKHAAVYVKGANDTLEQLAEA  
51 RDKETWGSINGLEKNLAFHL**SGHILHSIYW****HMRTDGGGGE****PLDKDGVGEL**  
101 **ADAIAESFGS****FAGFRAQLTK**AAATTQSGWGVLAYEPLSGRLIVEQIYDH  
151 QGNVGGSTPILVFDWEHA FYLQYKQKVDFIDAMWAVVNWQDVARRYE  
201 **AAKSRTNTLL****LAP**

# Peptide Mass Fingerprint for spot 6366: SCO3649

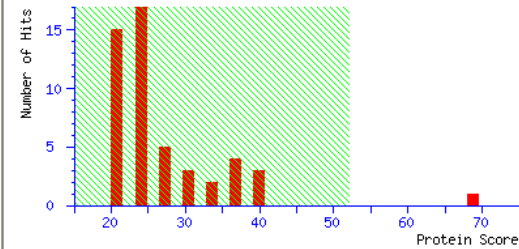


## Mascot Search Results

**MATRIX SCIENCE**  
 User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6366  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 7 Jun 2010 at 11:25:35 GMT  
 Top Score : 69 for **gi|21222064**, fructose-bisphosphate aldolase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

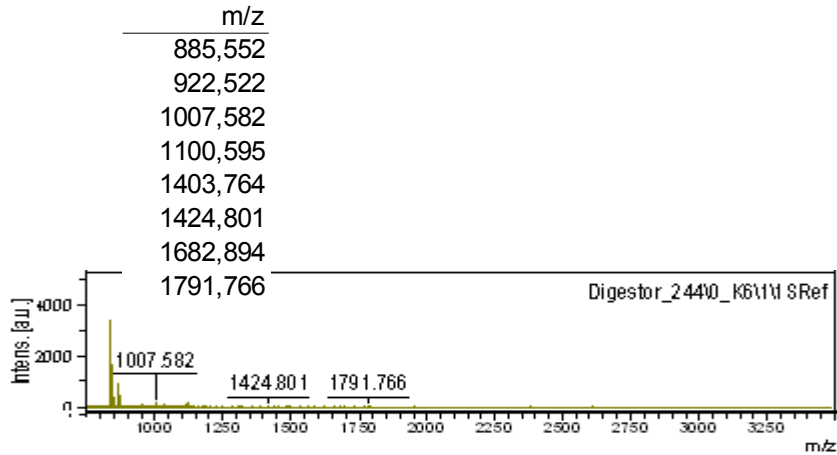
Accession	Mass	Score	Description
1. <a href="#">gi 21222064</a>	37018	69	fructose-bisphosphate aldolase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21219392</a>	34299	41	hypothetical protein SCO0831 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21221068</a>	35706	40	rod shape-determining protein MreC [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 2253080</a>	38571	39	mreC [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 4927470</a>	39068	38	transposase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21223078</a>	39170	38	IS1652 transposase [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21219973</a>	39144	38	transposase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21221089</a>	39158	38	transposase [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21223731</a>	57449	33	FOF1 ATP synthase subunit alpha [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21222741</a>	50035	33	integrase [Streptomyces coelicolor A3(2)]

Sequence Coverage: 17%

Matched peptides shown in **Bold Red**

**1 MPIATPEVYN EMLDR**AKAGK FAYPAINVTS SQTLLHAALRG FAEAESDGIV  
**51** QISTGGAEFL GGQHNKDMVT GAVALAEFAH IVAEK**YDVTV ALHTDHC**PKD  
**101** KLDGYVRPLI AVSEERVKAG RNPLFQSHMW DGS**AETLADN LSIAQELLAR**  
**151** ARAARIILEV EITPTGG**EED** GVSHEINDSL YTTVDDAVRT VEALGLG**EKG**  
**201** RYLLAASFGN VHGVYKPGNV VLRPELLKEL NEGIASKY**GQ** P**AGSKP**DFV  
**251** FHGGSGSTAE EIATALENGV VKMNIDTDQ YAFTRPVVDH MFRNYD**GV**LK  
**301** **VDGEVGN**KT YDPRTWG**KL**A **EAGMAARVVE** **ACGHLRSAGQ** **KIK**

# Peptide Mass Fingerprint for spot 6264: SCO4770



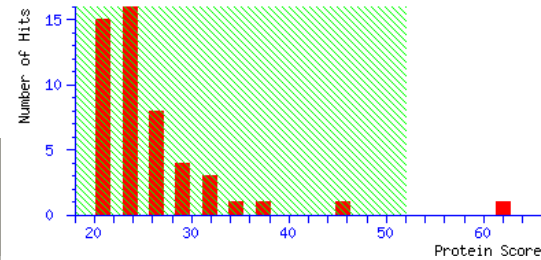
## *MATRIX* Mascot Search Results

*SCIENCE*

User : irene  
Email : isanh@unileon.es  
Search title : spot 6264  
Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
Taxonomy : Streptomyces coelicolor (8575 sequences)  
Timestamp : 9 Jun 2010 at 09:12:57 GMT  
Top Score : 62 for [gi|21223149](#), inosine 5' monophosphate dehydrogenase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \times \log(P)$ , where P is the probability that the observed match is a random event.  
Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

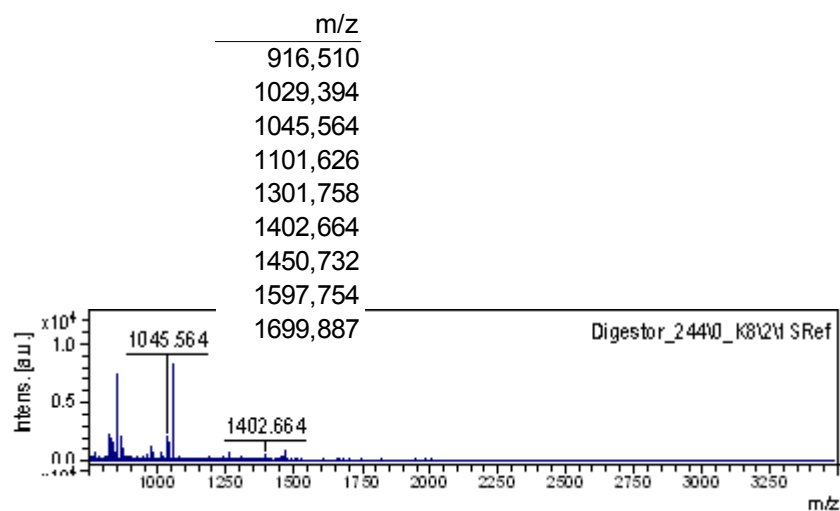
Accession	Mass	Score	Description
1. <a href="#">gi 21223149</a>	52614	62	inosine 5' monophosphate dehydrogenase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21224354</a>	59624	46	hypothetical protein SCO6022 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21223850</a>	80865	37	NAD-dependent DNA ligase LigA [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21220490</a>	43534	34	branched chain amino acid binding protein [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21226033</a>	34109	33	transcriptional regulator [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21223063</a>	49622	32	glutamate dehydrogenase [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21223616</a>	52389	31	nucleotide-binding protein [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21222098</a>	14747	29	hypothetical protein SCO3685 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21234249</a>	15421	28	hypothetical protein SCP1.250 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21223805</a>	71361	28	neutral zinc metalloprotease [Streptomyces coelicolor A3(2)]

Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

1 MTANVDGVPE KFATLGLTYD DVLLLPGASA VLPNAVDTSS RISRNVRVNI  
51 PLLSAAMDVK TEF**MAISMA RQGGVGLHR** NLSIEDQANQ VDLVKRSESG  
101 MVANPITIHP DATLGEADAL CA**KFRISGVP VTDGAGKLLG IVTNRDMAFE**  
151 TDRSRQVREV MTPMPLVTGQ VGISGVDAME LLRRHKIEKL PLVDGDGILK  
201 GLITVKDFVK AEQYPHAAKD AKGRLLVGAA VGASPEALDR AQLAEAGVD  
251 FLVVDTSHGH NSNALSWMSK IKSSVGIDVV GGNVATRDGA QALIDAGVDG  
301 IKVGVGPGSI CTTRVVAGIG VPQVTAIYEA SLAARAAGVP LIGDGGQLQYS  
351 GDIGKALAA**G** ADTVMLGSL**L** AGCEES**P**GEL QFINGKQ**F**K**S** YRGMGSLGAM  
401 QSRGQGRSYS KDRYFQAEVA SDDKL**V**PEGI EGQVPYR**G**PL ANVLHQLVGG  
451 LRQTMGYVGA ATIEEMESKG R**F**VRITSAGL KESH**P**HD**I**QM TVEAPNYR**S**  
501 K

# Peptide Mass Fingerprint for spot 6269: SCO4771

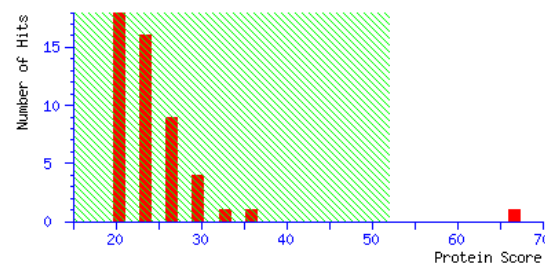


## *{MATRIX}* Mascot Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6269  
**Database** : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 9 Jun 2010 at 10:40:44 GMT  
**Top Score** : 67 for [gi|21223150](#), inosine 5-monophosphate dehydrogenase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21223150</a>	40205	67	inosine 5-monophosphate dehydrogenase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21223094</a>	20840	36	50S ribosomal protein L5 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21223258</a>	35743	33	lipoprotein [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21223436</a>	86651	31	bifunctional protein [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21223194</a>	49256	30	serine/threonine protein kinase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21224476</a>	51284	30	ADA-like regulatory protein [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21218689</a>	13519	29	hypothetical protein SCO0129 [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21225083</a>	66344	27	long chain fatty acid CoA ligase [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21222649</a>	101193	27	hypothetical protein SCO4254 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21221892</a>	56747	27	transposase [Streptomyces coelicolor A3(2)]

Sequence Coverage: 17%

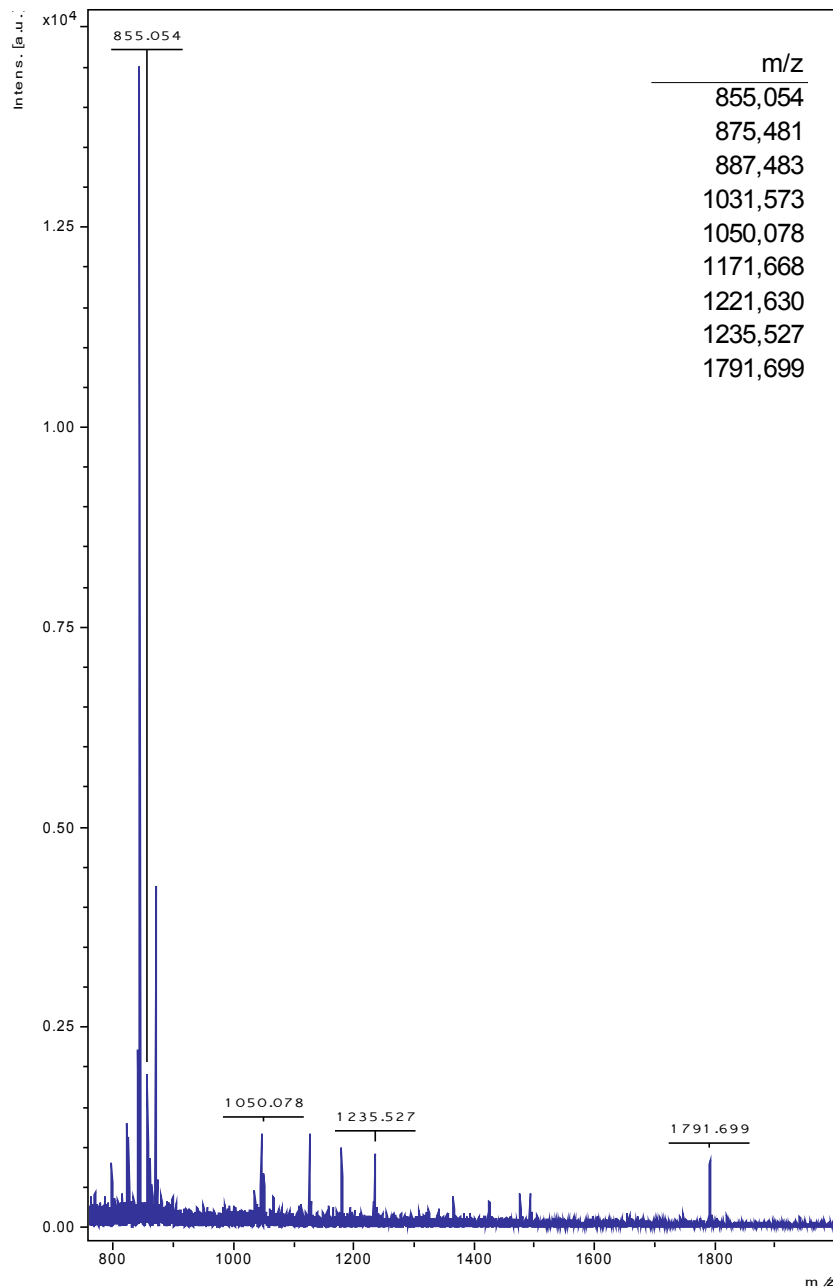
Matched peptides shown in **Bold Red**

```

1 MTEIEIGRGK RRRAYAFDD IAVVPSRRTR DPKEVSIAWQ IDAYRFELPF
51 LAAPMDSVVS PATAIRIGEL GGLGVLNLEG LWTRHEDPQP LLEDEIAELDT
101 DNATRRLQEI YAAPIKEELI GQRIVEKVRDS GVVTAALASP QRTAQFSKAV
151 VDAGVDIFVI RGTTVSAEHV SGSHEPLNLK QFIYELDVPV IVGGCATYTA
201 ALHLMRTGAA GVLVFGGGA AHTRNVLGI QVPMATAVAD VAAARRDYMD
251 ESGGRYVHVI ADGGVGVSGD LPKAIACGAD SVMMGSPRAR ATDAPGRGNH
301 WGMEAVNEEL PRGKKVDLGT VGTIEEILTG PSRNPDGSMN FFGALRRAMA
351 TTGYSELKEF QRVEVTVADS QHRR
    
```



# Peptide Mass Fingerprint for spot 6400: SCO4809

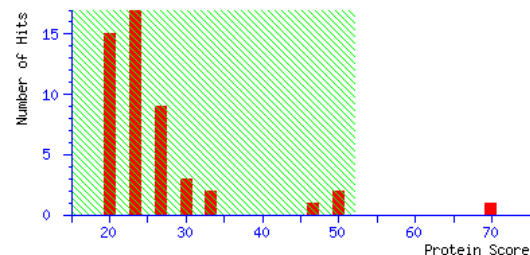


## Mascot Search Results

**Matrix Science**  
 User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6400  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 8 Jun 2010 at 09:03:25 GMT  
 Top Score : 70 for **gi|21223187**, succinyl-CoA synthetase subunit alpha [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 * \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

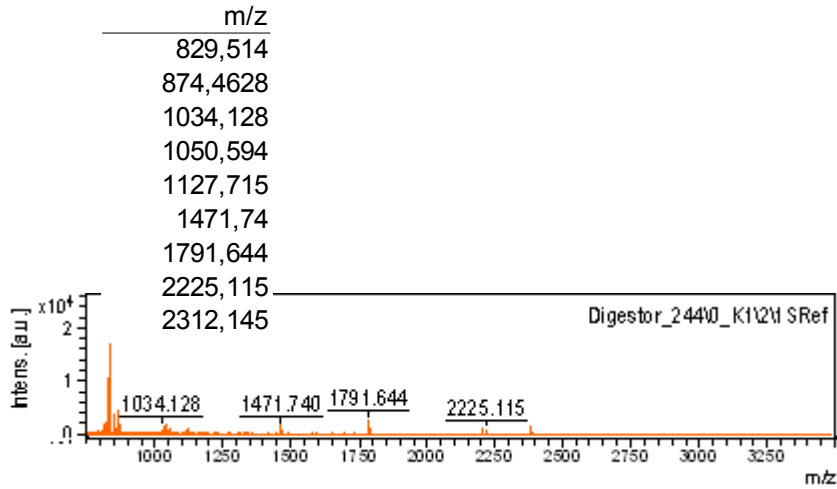
Accession	Mass	Score	Description
1. <a href="#">gi 21223187</a>	30277	70	succinyl-CoA synthetase subunit alpha [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21220340</a>	22223	51	cob(I)yrinic acid a,c-diamide adenosyltransferase [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 1532204</a>	38461	48	putative ABC transporter intracellular ATPase subunit BidK [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21223406</a>	38465	45	BidK, ABC transporter intracellular ATPase subunit [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21221650</a>	36991	33	hypothetical protein SCO3215 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21234217</a>	42020	32	putative plasmid partitioning protein, para2 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21223929</a>	32719	31	formamidopyrimidine-DNA glycosylase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21224337</a>	9513	30	hypothetical protein SCO6001 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21222312</a>	10483	30	hypothetical protein SCO3905 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21219532</a>	11954	28	hypothetical protein SCO1015 [Streptomyces coelicolor A3(2)]

Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

**1 MAIWLKDKS** VIVQMTGAT GMKHTKMLG DGTEVVGWV PRKAGTSVDF  
**51** DGNVVPVFGT VKEAIEKTGA NVSVIFVPEK FTKDAVVEAI DAEIPLAVVI  
**101** TEGIAVHDSA AFWSYAGKKG NKTRIIGPNC PGIITPGQSN VGIIPGDITK  
**151** PGRIGLVSKS GTLTYQMMYE LRDIGFSTAV GIGGDPIIGT THIDALAAFE  
**201** ADPETDLIVM IGEIGDAAE RAAEYISKNV TKPVVGYVAG FTAPEGKTMG  
**251** HAGAIVSGSS GTAQAKKEAL **EAAGVKVGKT** **PTETAKLARA** ILAG

# Peptide Mass Fingerprint for spot 6125: SCO4814

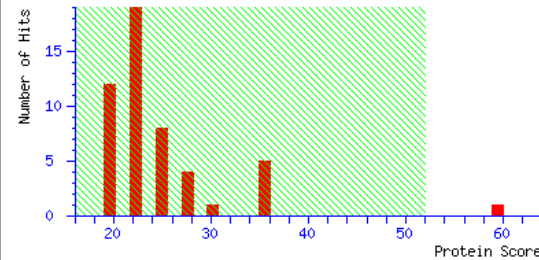


## *{MATRIX}* *{SCIENCE}* Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6125  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 9 Jun 2010 at 08:26:31 GMT  
 Top Score : 59 for [gi|21223192](#), bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase,

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21223192</a>	55351	59	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/
2. <a href="#">gi 21224356</a>	76616	37	transferase [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21220439</a>	34945	36	hypothetical protein SCO1950 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21220402</a>	27034	36	hypothetical protein SCO1915 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 256788439</a>	35147	35	hypothetical protein SlivT_28456 [Streptomyces lividans TK24]
6. <a href="#">gi 21219693</a>	185293	35	hypothetical protein SCO1182 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21220071</a>	49116	31	oxidoreductase membrane protein [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21223574</a>	15538	29	hydrogen peroxide sensitive repressor [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21221752</a>	12050	29	redoxin [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21902159</a>	61416	27	putative integral membrane ATPase [Streptomyces coelicolor A3(2)]

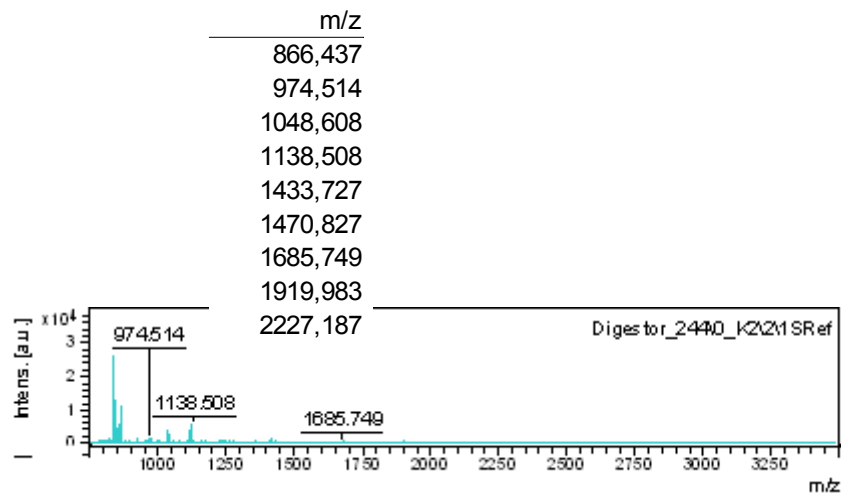
Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

```

1 MTATAGSNKR AIRRALVSVY DKTGLEDLAR GLHEAGVELV STGSTAGRIA
51 AAGVPVTKVE ELTGFPPECLD GRVKTLHPKV H&GILADLRL ESHRQQLDEL
101 GVAPFDLVVV NLYPFRETVA SGATPDECVE QIDIGGPMV RAA&KNHPSV
151 AVVTSPARYA DVLLAVEGGG FDLAARKRLA AEAFAQHTAAY DVAVASWF&AA
201 EYAPVDESGF PDLFGATYER ANTLRYGENP HQPAALYTSP EGGGLAQ&AEQ
251 LHGKEMSYNN YTDTAARRA AYDHA&EPCVA IIKHANPCGI AIGADVA&EAH
301 RKAHDCDPVS AYG&GVIAVNR PVSKEMA&ERV AGIFTEVIVA PDYEDG&ALEA
351 LTKKKNIRVL RAPAAPAAPV EVKPIDGGAL LQVTDRLQ&AE GDDPATWTLA
401 TGEALSE&AEL AELAF&AWRAC RAVKSNA&ILL AKD&GASVGVG MGVQVNRVDS&A
451 KLAVERAG&E RAQGAYA&ASD AFFFPPD&GLE ILTGAGVK&AV VQPGGSVRDE
501 LVVEA&AKKAG VTM&YFTGTRH FFH
  
```

# Peptide Mass Fingerprint for spot 6167: SCO4837



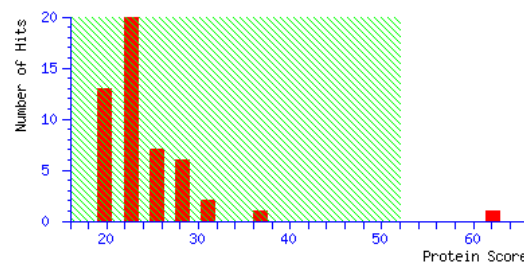
## Mascot Search Results

**{MATRIX}**  
**{SCIENCE}**

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6167  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 8 Jun 2010 at 20:08:55 GMT  
 Top Score : 62 for [gi|21223213](#), serine hydroxymethyltransferase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21223213</a>	51573	62	serine hydroxymethyltransferase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21224749</a>	33271	36	hypothetical protein SCO6443 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21223816</a>	42478	30	lipoprotein [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21219200</a>	54944	30	glycerol-3-phosphate dehydrogenase [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21221968</a>	12371	30	anti-sigma factor antagonist [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 32141268</a>	54491	30	gamma-aminobutyraldehyde dehydrogenase [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21225518</a>	57056	29	oxidoreductase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21221680</a>	64458	28	acyl CoA oxidase [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21219807</a>	108469	28	exonuclease [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21219211</a>	13484	28	hypothetical protein SCO0682 [Streptomyces coelicolor A3(2)]

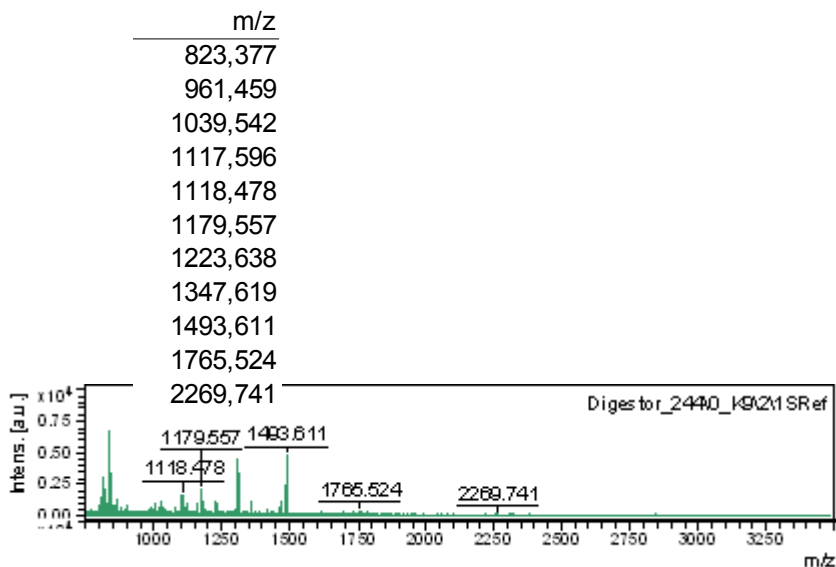
Sequence Coverage: 12%

Matched peptides shown in **Bold Red**

```

1  MPAEISPEST AYRAALDVIR AVEPRVADAI GOEVADQREM LKLIASENYA
51 SPATLLAMGN WFSDKYAEGT IGRRFYAGCR NVDTVESLAA EHARELFGAR
101 HAYVQPHSGI DANLVAFWAV LGARVEVPFL EKTGARQVND LTDADWAE LR
151 QAFGNQRLMG MSLDAGGHLT HGFRPNISGK MFDQRSYGTD PATGLIDYEA
201 LRASAREFKP LIIVAGYSAY PRLVNFRIMR EIADEVGATL MVDMAHFAGL
251 VAGKVLTGDF DPVPHAQIVT TTHKSLRGP RGGMVLCDSD LKDQVDRGCP
301 MVLGGPLPHV MAAKAVALAE ARRPAFQDYA QRIVDNARAL AEGLTKRGAT
351 LVTGGTDNHL NLIDVASSYG LTGRQAEAAAL LDSGIVTNRN AIPADPNGAW
401 YTSGIRIGTP ALTTRGLGTA EMDEVAGLID RVL TATEPGT TKSGAPSKAS
451 HVLDAKVADE ISHRATDLVA GFPLYPEIDL G
  
```

# Peptide Mass Fingerprint for spot 6678: SCO4856

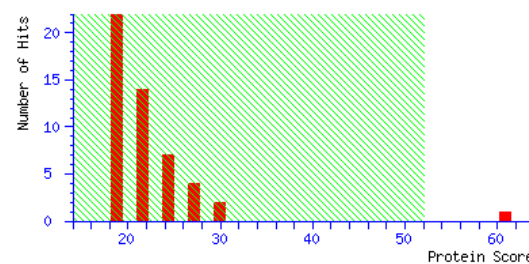


## *(MATRIX)* SCIENCE Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6678  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 9 Jun 2010 at 08:51:50 GMT  
 Top Score : 61 for **gi|21223232**, succinate dehydrogenase flavoprotein subunit [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
 Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21223232</a>	65033	61	succinate dehydrogenase flavoprotein subunit [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 31340548</a>	41926	29	two-component system sensor kinase [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21234243</a>	42698	29	putative oxidoreductase, mmfH [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21223100</a>	6884	28	SOS ribosomal protein L30 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21219011</a>	34461	27	AraC family transcription regulator [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21223969</a>	7047	27	transcriptional regulator [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21221938</a>	52401	26	ATP-binding protein [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21223988</a>	14373	25	mutT-like protein [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21223146</a>	12216	25	regulatory protein [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21223317</a>	32871	25	DNA-binding protein [Streptomyces coelicolor A3(2)]

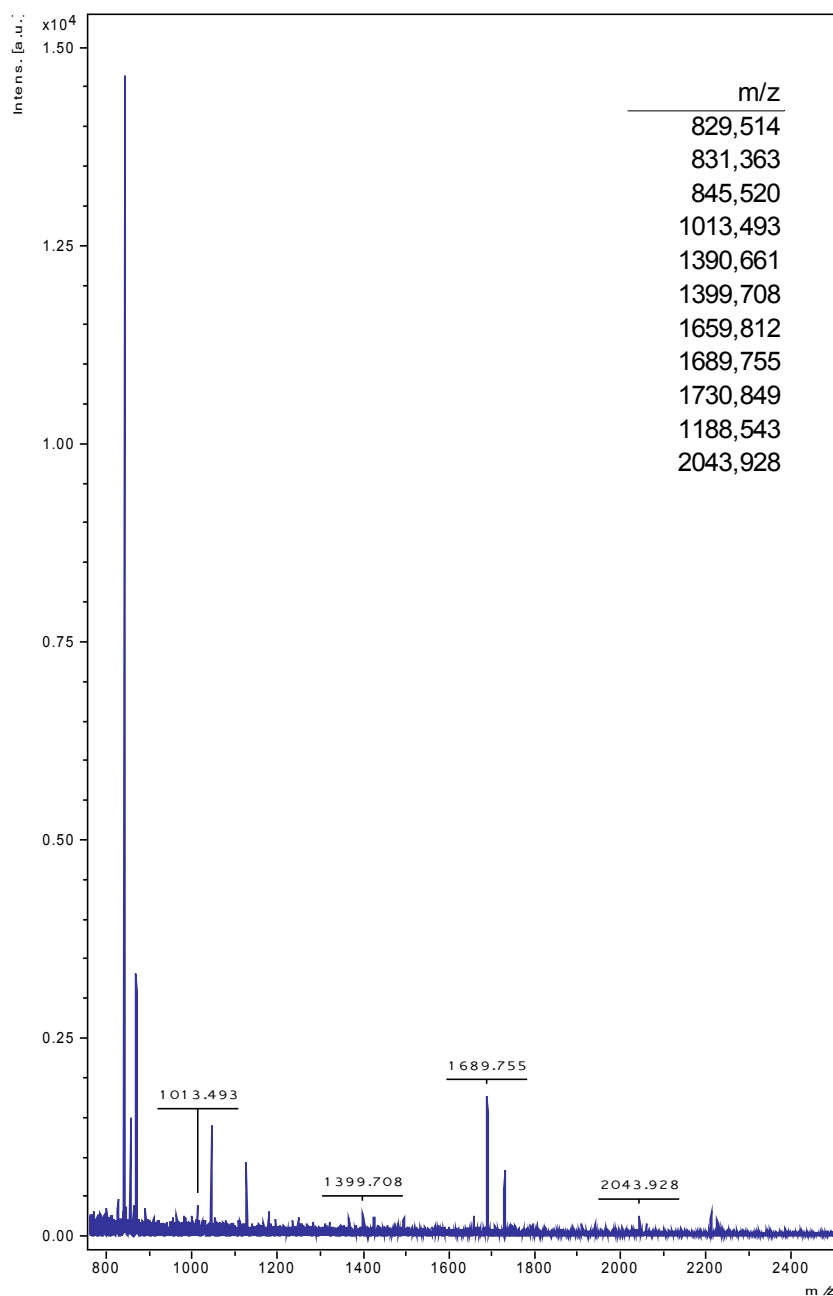
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```

1 MKVHKYDTVI VGAGGAGMRA AESTKRSRT AVLTkLYPTR SHTGAAQGGM
51 AAALANVEED NWEHTFDTV KGGDYLVQD AAEILAKEAI DSVLDLEKMG
101 LPFNRTPDGT IDQRRFGGHS RNHGEAPVRR SCYAADRTGH MILQTLYQNC
151 VKEGV EFFNE FYVLDQLITE VDGVKKSAGV VAYELATGEI HVFQAKSVIY
201 ASGGTGKFFK VTSNAHTLTG DGQAAVYRRG LPLEDMEFFQ FHPTGIWRMG
251 ILLTEGARGE GGILRNKDGE RFMEKYAPVM KDLASRDVVS RSIYTEIREG
301 RGGCGPEGDHV YLDLTHLPPE QLDAKLPDIT EFARTYLGIE PYTDPPIQIP
351 TAHYAMGGIP TNVEGEVLAD NTTVVPGLYA AGEVACSVH GANRLGTNSL
401 LDINVFGRRG GIAAAEYAQK ADFVELPEDP ETLVVEQIER LRSSTGTERV
451 ATIRRELQEC MDANVMVFRT EQTIKTAVEK IAE LRARYKN VSIQDKGRF
501 NTDLLEAVEL GNLLDLAEVM AVSALARKES RGGHYREDFP NRDDVNFMRH
551 TMAYREVGDD GAESIRLDYK PVVQTRYQPM ERKY
    
```

# Peptide Mass Fingerprint for spot 6257: SCO4958

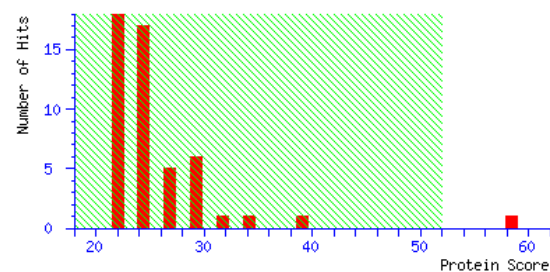


## *MATRIX* SCIENCE Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6257  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 8 Jun 2010 at 08:33:10 GMT  
 Top Score : 58 for [gi|21223331](#), cystathionine gamma-synthase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random even. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21223331</a>	40844	58	cystathionine gamma-synthase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21222182</a>	56949	40	secreted penicillin binding protein [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21218741</a>	68932	35	hypothetical protein SCO0184 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21224977</a>	100528	31	serine/threonine protein kinase [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21222513</a>	45928	30	hydroxyglutarate oxidase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 13122125</a>	49535	29	putative DNA damage inducible protein [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 161353682</a>	50783	29	DNA polymerase IV [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21220435</a>	34945	28	hypothetical protein SCO1950 [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21223401</a>	48275	28	ATP-binding protein [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21224785</a>	39246	28	hypothetical protein SCO6481 [Streptomyces coelicolor A3(2)]

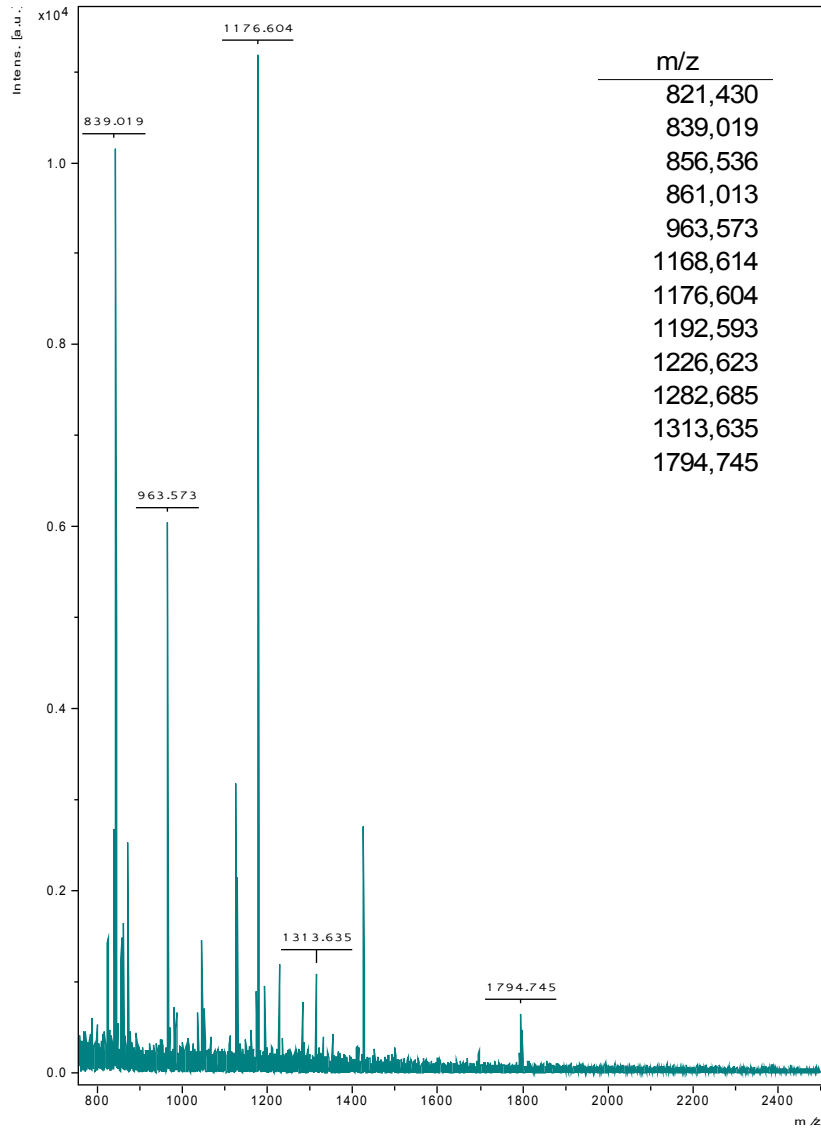
Sequence Coverage: 11%

Matched peptides shown in **Bold Red**

```

1  MPMSDRHISQ HFETLAIHAG NTADPLTGAV VPPIYQVSTY KQDGVGGLRG
51  GYEYSRSANP TRTAAEENLA ALEGGRRLA FASGLAAEDC LLRTLRLPGD
101 HVVIPNDAYG GTFRLFARKVA TRWGVENSVA DTSDAAAVRA ALTPKTKAVV
151 VETPSNPLLG ITDIAQVAQV ARDAGARLVV DNTFATPYLQ QPLALGADV
201 VHSLTKYMGG HSDVVGALI VGDQELGEEL AFHQNAMGAV AGPFDSWLVL
251 RGKTLAVRM DRHSENATKV ADMLSRHARV TSVLYPGLPE HPGHEVAAKQ
301 MKAFGGVSE RVEGGEQAAV EVCNRAKVFT LGESLGGVES LIEHPGRMTH
351 ASAAGSALEV PADLVRLSVG IENADLLAD LQQALG
  
```

# Peptide Mass Fingerprint for spot 6340: SCO6282

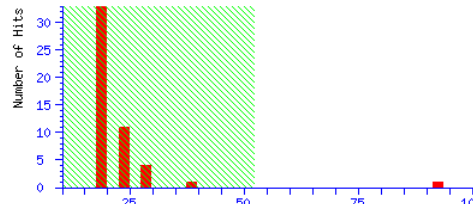


## MASCOT Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6340  
**Database** : NCBI nr 20100529 (11111565 sequences; 3786451707 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 3 Jun 2010 at 11:12:10 GMT  
**Top Score** : 92 for **gi|21224601**, 3-oxoacyl-[acyl-carrier protein] reductase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21224601</a>	27414	92	3-oxoacyl-[acyl-carrier protein] reductase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21225778</a>	34325	40	AraC family transcription regulator [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21234158</a>	6940	29	putative oxidoreductase subunit [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21220174</a>	25825	28	transcriptional regulator [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21223851</a>	80012	27	phosphodiesterase [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21219610</a>	36798	27	hypothetical protein SCO1095 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21220064</a>	24501	25	acyltransferase [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21219588</a>	44969	24	hydrogenase [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21225322</a>	13603	24	ABC transporter ATP-binding protein [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21219494</a>	12579	24	hypothetical protein SCO0977 [Streptomyces coelicolor A3(2)]

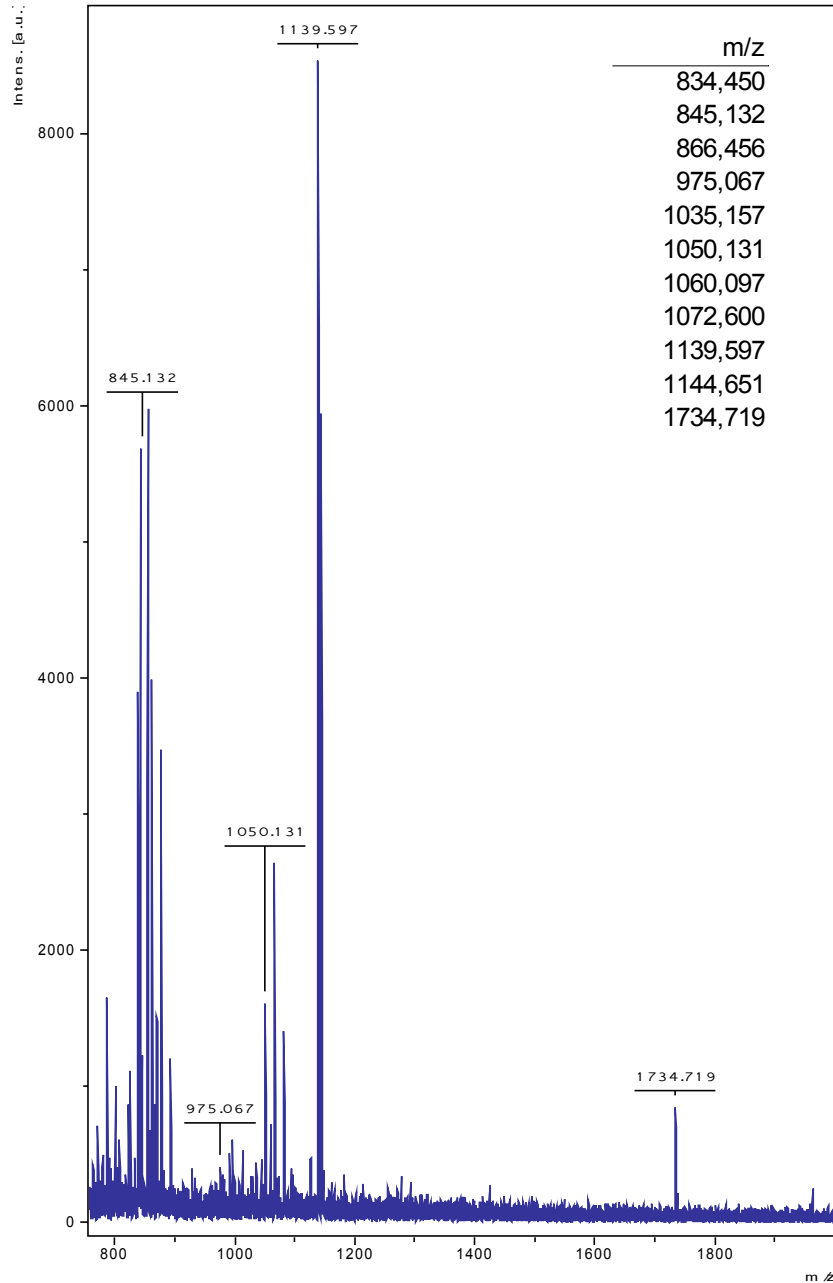
Sequence Coverage: 23%

Matched peptides shown in **Bold Red**

```

1 MTERLRSFRM TALTNKTALV TGGSRGIGRA IAQRLGKEGA LWALTYSSDE
51 AAAKETVHSI EAAGGRAFAF RSQLGVPGDA EALWQAFDAQ IGQYADGGSG
101 LDILVMNAGI AGPGLIHEVE EAEYDKVFAV NAKAPFFIIQ KGLERLRDGG
151 RIVNISSGVT KVAFPGMTSY AAAKGAVEVL TLTLAQTLGS RGITVNAVSP
201 GTIETDIHPW MADPAAKAHA AGFSVFNRVG QPDDVADVVA FLASDDARW
251 TGQNIDASGG SGLGL
  
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# Peptide Mass Fingerprint for spot 6513: SCO7036

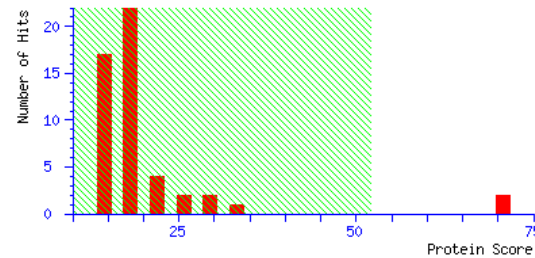


## Mascot Search Results

**User** : irene  
**Email** : isanh@unileon.es  
**Search title** : spot 6513  
**Database** : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
**Taxonomy** : Streptomyces coelicolor (8575 sequences)  
**Timestamp** : 8 Jun 2010 at 08:08:12 GMT  
**Top Score** : 71 for [gi|21225319](#), argininosuccinate synthase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 * \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

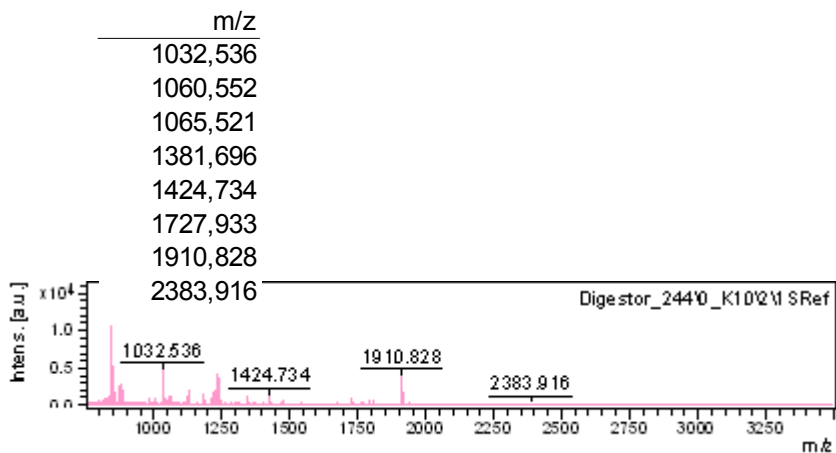
Accession	Mass	Score	Description
1. <a href="#">gi 21225319</a>	52408	71	argininosuccinate synthase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 216988</a>	53478	69	argininosuccinate synthetase [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 5459434</a>	2564	34	ADP glucose pyrophosphorylase [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21222200</a>	36058	30	integral membrane protein [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 32141263</a>	32546	28	hypothetical protein SCO5489 [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21223200</a>	6504	27	hypothetical protein SCO4823 [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21220231</a>	13242	26	hypothetical protein SCO1737 [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21224836</a>	60670	23	nitrate reductase beta chain NarH [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 21219805</a>	20177	23	hypothetical protein SCO1298 [Streptomyces coelicolor A3(2)]
10. <a href="#">gi 21219747</a>	22767	22	ATP-dependent Clp protease [Streptomyces coelicolor A3(2)]

Sequence Coverage: 12%

Matched peptides shown in **Bold Red**

**1** MSKVL**TL**SLPT **GER**VGIAFSG GLDTSVAVAW MRDKGAVPCT YTADIGQYDE  
**51** PDIASV**PD**RA **KTYGAE**VARL VDCRAALVEE GLAALTCGAF HIRSGGR**AYF**  
**101** **NTT**PLGRAVT GTLLVRAMLE DDVQIWGDGS TFRGNDIERF **YRYGLLAN**PQ  
**151** **LR**IYKPWLDA DFVTELGGRK EMSEWLVAHD LPYRD**ST**EKA **Y**STDANI**WGA**  
**201** **THE**AKTLEHL DTGVETVEPI MGVRFWDP**SV** EIAPEDVTIG FDQGRPV**TIN**  
**251** GKEFASAVDL VMEANAVGGR HGMGMSDQIE NRIIEAKSRG IYEAPGMALL  
**301** HAAYERLVNA IHNEDTLAQ HTEGRR**LG**RL MYEGRWLD**PQ** SLM**I**RESLQR  
**351** WVGSAVTGEV TLRRLRGEDY SILDTTGP**AF** SYHPDKLSME RTEDSA**FG**PV  
**401** DR**I**Q**L**TMRN LDIADSR**AK**L EQYAGLGLIG TANPAIGAAQ AAATGLIGAM  
**451** PEGGAQ**AI**AS RGEVSADDEL LDRA**AM**ESGT D

# Peptide Mass Fingerprint for spot 6771: SCO7510

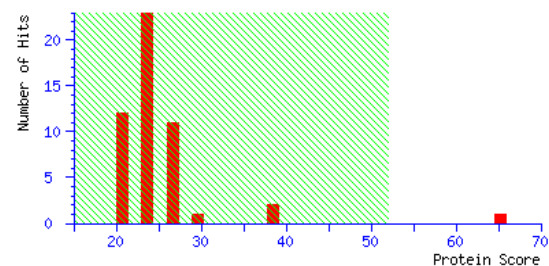


## *MATRIX* SCIENCE Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6771  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 9 Jun 2010 at 08:02:15 GMT  
 Top Score : 65 for **gi|21225776**, peptidyl-prolyl cis-trans isomerase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 \times \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

	Accession	Mass	Score	Description
1.	<a href="#">gi 21225776</a>	17878	65	peptidyl-prolyl cis-trans isomerase [Streptomyces coelicolor A3(2)]
2.	<a href="#">gi 32141251</a>	21837	39	TetR family transcriptional regulator [Streptomyces coelicolor A3(2)]
3.	<a href="#">gi 21225765</a>	24077	38	transcriptional regulator [Streptomyces coelicolor A3(2)]
4.	<a href="#">gi 21218759</a>	62886	28	two-component sensor [Streptomyces coelicolor A3(2)]
5.	<a href="#">gi 21224756</a>	17870	27	hypothetical protein SCO6450 [Streptomyces coelicolor A3(2)]
6.	<a href="#">gi 21221455</a>	72760	27	two-component system histidine kinase [Streptomyces coelicolor A3(2)]
7.	<a href="#">gi 21220835</a>	20515	26	hypothetical protein SCO2367 [Streptomyces coelicolor A3(2)]
8.	<a href="#">gi 21219601</a>	22107	26	hypothetical protein SCO1086 [Streptomyces coelicolor A3(2)]
9.	<a href="#">gi 21225981</a>	22061	26	hypothetical protein SCO7722 [Streptomyces coelicolor A3(2)]
10.	<a href="#">gi 21223596</a>	18258	26	acetyltransferase [Streptomyces coelicolor A3(2)]

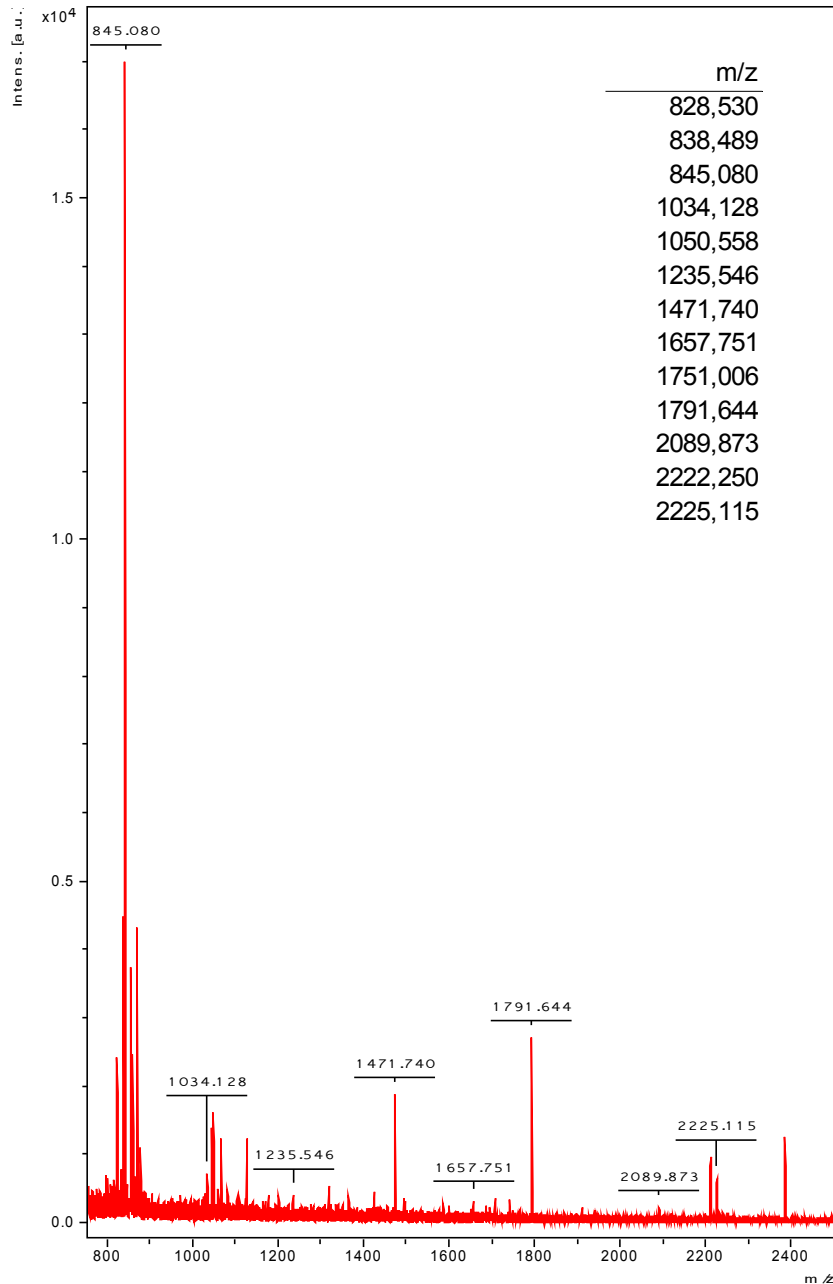
Sequence Coverage: 18%

Matched peptides shown in **Bold Red**

1 MSNSKVYFDI DIDGQDAGRI VFELFEDVTP KTARNFLELA TGEHGFYAG  
 51 SPFHRVIPQF MLQGGDFITNG NGTGGKSIYG EKFADEFNQL KHTEPYLLSM  
 101 ANAGPNTNGS QFFVTTVPTP WLDGK**HVVFG KVVEGTDVVD KIEGYGSSPA**  
 151 **GKTSKEIKVR** ASGKL



# Peptide Mass Fingerprint for spot 6317: SCO7511

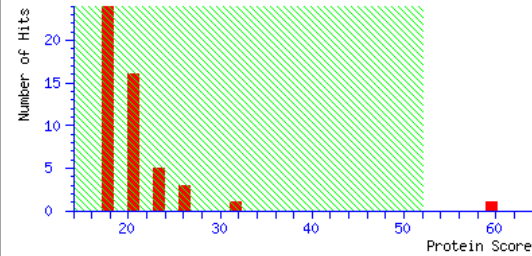


## Mascot Search Results

User : irene  
 Email : isanh@unileon.es  
 Search title : spot 6317  
 Database : NCBI nr 20100602 (11126451 sequences; 3793134231 residues)  
 Taxonomy : Streptomyces coelicolor (8575 sequences)  
 Timestamp : 7 Jun 2010 at 11:44:12 GMT  
 Top Score : 60 for **gi|21225777**, glyceraldehyde 3-phosphate dehydrogenase [Streptomyces coelicolor A3(2)]

### Mascot Score Histogram

Protein score is  $-10 * \log(P)$ , where P is the probability that the observed match is a random event. Protein scores greater than 52 are significant ( $p < 0.05$ ).



### Index

Accession	Mass	Score	Description
1. <a href="#">gi 21225777</a>	35003	60	glyceraldehyde 3-phosphate dehydrogenase [Streptomyces coelicolor A3(2)]
2. <a href="#">gi 21222306</a>	39433	31	hypothetical protein SCO3899 [Streptomyces coelicolor A3(2)]
3. <a href="#">gi 21234034</a>	10665	27	hypothetical protein SCP1.35 [Streptomyces coelicolor A3(2)]
4. <a href="#">gi 21223044</a>	12677	27	hypothetical protein SCO4663 [Streptomyces coelicolor A3(2)]
5. <a href="#">gi 21223028</a>	10468	26	preprotein translocase subunit SecE [Streptomyces coelicolor A3(2)]
6. <a href="#">gi 21223219</a>	17424	23	integral membrane protein [Streptomyces coelicolor A3(2)]
7. <a href="#">gi 21219711</a>	21020	23	regulatory protein [Streptomyces coelicolor A3(2)]
8. <a href="#">gi 21219378</a>	22366	23	TetR family transcriptional regulator [Streptomyces coelicolor A3(2)]
9. <a href="#">gi 119390540</a>	22225	23	Chain A, Crystal Structure Of Tetr-Family Regulator (Sco0857) From Streptomyces Coelicolor
10. <a href="#">gi 21221982</a>	71172	23	acetyl-CoA synthetase [Streptomyces coelicolor A3(2)]

Sequence Coverage: 13%

Matched peptides shown in **Bold Red**

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1 MTRIGINGFG RIGRNVLRAL LERDTKLEVV AVNDLTEPAT LARLLAFDST
51 AGRLGRPVTV DGDTLVVDGH RIKVLAREP ARLPWALGV DIVLEATGRF
101 TSADAARAHL TAGARKVLVS APSSGADVTL AYGVNTDAYD PAAHTIVSNA
151 SCTTNALAPL AAVLDELAGE EHGFMTTVHA YTQEQNLQDG PHRDARRARA
201 AGVNIPTTT GAAKAIGLVL PGLDGKLSGD SIRVVPVPGS IVELNTIVAR
251 DVTREDVLAA YRAAADGPLA GVLEYSDDPL VSSDITGNPA SSIFDSALTR
301 VEGRHIKVVVA WYDNEUGFSN RVIDTLALLA TR
  
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