

Cytochrome *bcc-aa₃* Oxidase Supercomplexes in the Aerobic Respiratory Chain of
Streptomyces coelicolor A3(2)

Dörte Falke¹, Marco Fischer¹, Bianca Biefel¹, Christian Ihling², Claudia Hammerschmidt¹,
Kevin Reinefeld¹, Alexander Haase¹, Andrea Sinz², and R. Gary Sawers^{1*}

¹ Institute of Microbiology, Martin-Luther University Halle-Wittenberg, Kurt-Mothes-Str. 3,
06120 Halle (Saale), Germany

² Institute of Pharmacy, Charles Tanford Protein Center, Martin-Luther University Halle-Wittenberg,
Kurt-Mothes-Str. 3a, 06120 Halle (Saale), Germany

* For correspondence: R.G. Sawers, Institute of Microbiology, Martin-Luther University Halle-
Wittenberg, Kurt-Mothes-Str. 3, 06120 Halle (Saale) Germany

Tel., +49 345 5526350; Fax., +49 345 5527010; Email, gary.sawers@mikrobiologie.uni-
halle.de

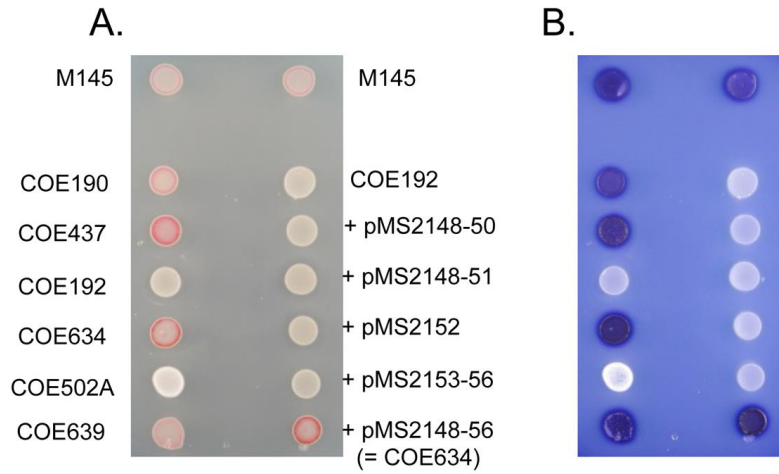


Figure S1. Cytochrome *c*-dependent electron transfer from TMPD by whole cells. The indicated strains were grown on DNB agar plates for 48 h and the colonies were photographed prior (A), and subsequent (B), to determining TMPD-oxidizing activity. Strains on the left side of each panel: M145 (wild type); COE190 (Δ SCO3945-3946); COE190 comp., COE190 transformed with pMS3945-46; COE192 (Δ SCO2148-56); COE192 comp., COE192 transformed with pMS2148-56; COE502A (transposon insertion in SCO2155); COE502A comp., COE502A transformed with pMS2148-56. Strain COE192 on the right side of each panel was transformed with the plasmids indicated beside the respective colony.

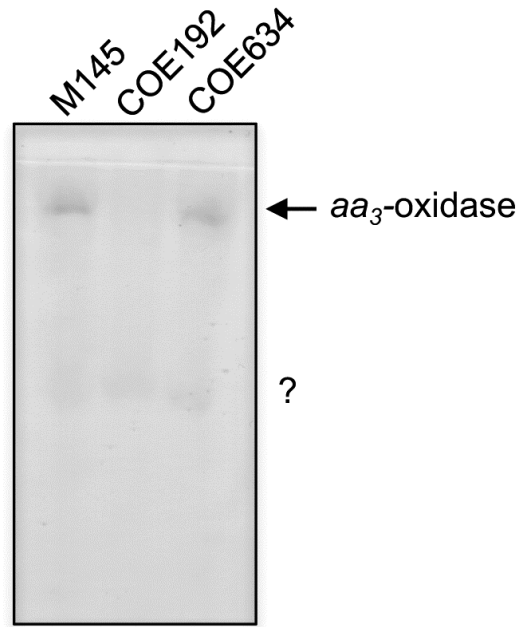


Figure S2. In-gel cytochrome *c* oxidase activity analysis of crude extracts derived from exponentially grown mycelium. Crude extracts (70 μ g of protein) from the strains indicated above the lanes were separated in non-denaturing 10% (w/v) native PAGE and stained for cytochrome *c* oxidase activity (see Experimental Procedures for details). The weak DAB-oxidizing activity indicated by a question mark represents an unidentified peroxidase or catalase activity, and was used as a loading control for the experiment.

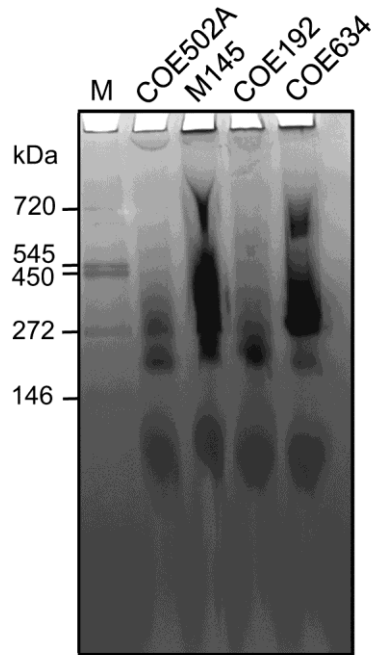


Figure S3. Coomassie-stained BN-PAGE gel of solubilized membrane fractions from mycelium. The same gel as shown in part G of Fig. 4 was stained with Coomassie Brilliant Blue to reveal the protein standards, after it had been stained for cytochrome oxidase activity. BN-marker proteins (Serva Electrophoresis GmbH) included ferritin (720 kDa), urease (hexamer 545 kDa), ferritin (450 kDa), urease (trimer 272 kDa), and lactate dehydrogenase (146 kDa).

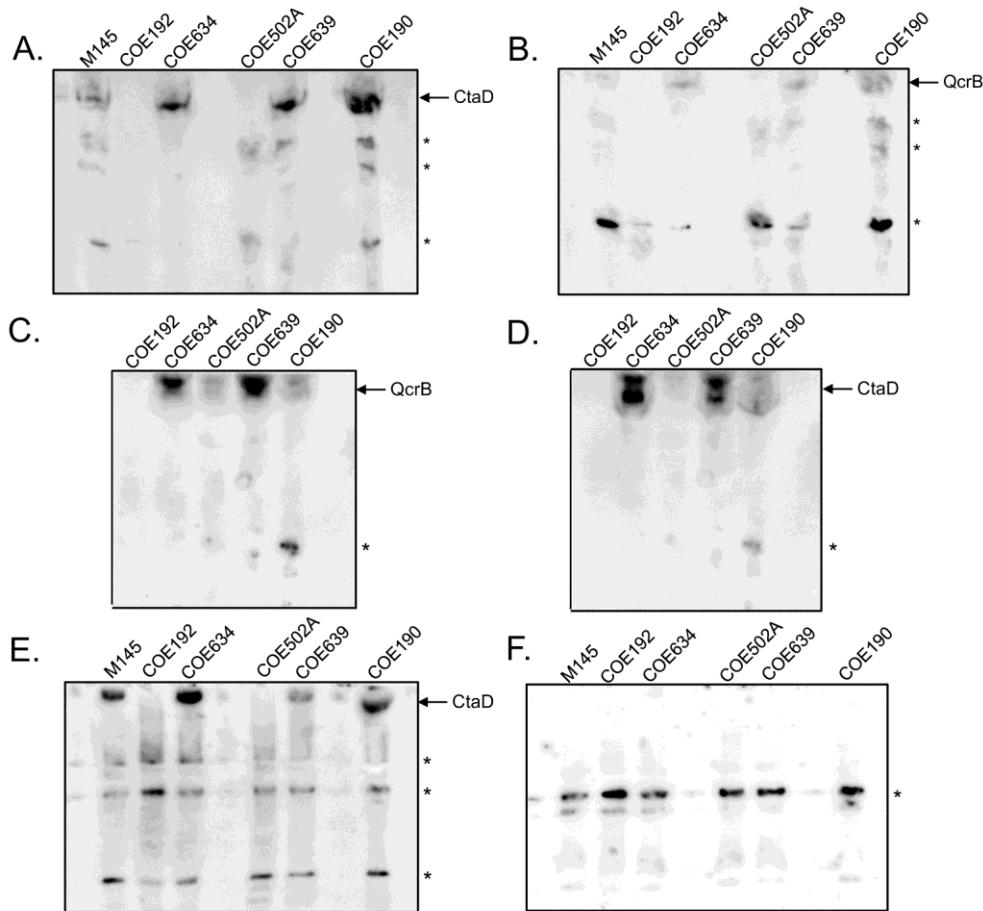


Figure S4. Evidence for co-migration of the *bcc* complex and *aa₃* oxidase subunits as supercomplexes in extracts of mycelium and spores. Western blots of protein complexes in crude extracts (60 μ g of protein) derived from mycelium (A, B, C, D) or spores (E, F) were separated in clear-native PAGE (10% w/v polyacrylamide). In parts A and B, the blot was challenged first with peptide-antibodies against CtaD (A), and subsequently with peptide-antibodies against QcrB (B). In the blot shown in C, anti-QcrB was used first and then after mild stripping to remove the primary and secondary antibodies, the membrane was challenged with anti-CtaD antibodies (D). In the blot shown in E, anti-CtaD was used first and then after stripping of the blot, the membrane was challenged with anti-QcrB (E). The location of the complex including CtaD and QcrB is shown at the right of each gel. The asterisks denote uncharacterized, fast-migrating complexes that react with the corresponding antibodies, but which are either absent or significantly reduced in signal intensity in extracts of COE192 (Δ *qcr*-

cta). Strains used include: M145, wild type; COE192 ($\Delta qcr-cta$); COE634 indicates COE192 complemented with pMS2148-56; COE502A, is mutated in the *ctaD* gene; COE639, COE502A complemented with pMS2148-56; and COE190 ($\Delta cydAB$). The gels shown in parts A through D were repeated on two separate occasions.

Table S1 Oligonucleotides used in this study.

Oligonucleotide name	Oligonucleotide sequence
BCF	5'- CCAACCGCGCGGGCGAGACTCTCGGGAAGGCGCTACGTGATTC CGGGGATCCGTCGACC-3'
BCR	5'- GGGGCCCTTCGACCGTGGTGTGGCGACGCTGGAGGGTCATGTA GGCTGGAGCTGCTTC-3'
BDF	5'- ACCACGGCGGTGTGGCGATGTGAGGAGAGTGAAGACGTGATT CCGGGGATCCGTCGACC-3'
BDR	5'- GTTTCGCTTCGTTTCACGTGAAACGCCTCCCGGGACTCATGTAG GCTGGAGCTGCTTC-3'
Sco2156_Hind III_fw	5'- GGCGGCAAGCTTAGAAGGCAGGCCGCAGCC-3'
Sco2153_NsiI_rv	5'- GGCGGCATGCATGTCGCGCAGTCCCCGC-3'
Sco2150_Hind III_fw	5'- GGCGGCAAGCTTCACCAGAAGCATCGACAG-3'
Sco2148_KpnI_rv	5'- GGCGGCGGTACCAACGGGGCCCTTCGACCG-3'
Sco2151_Hind III_fw	5'- GGCGGCAAGCTTTACTCCCTCGAACGTCCC-3'
Sco2152_Hind III_fw	5'- GGCGGCAAGCTTAACCAGTGCTGACGGGAC-3'
Sco2152_KpnI_rv	5'- GGCGGCGGTACCTACAAGGACCCGCACTCC-3'

RT- SCO7233_228 fw	5'-ACGGGTGGAGTTCCACACCGC-3'
RT- SCO7233_805 rv	5'-CCTGGCCGTTGATGCCGTTGG-3'
RT- SCO7234_254 fw	5'-TGCAGTTGTTTCAGCAACGAGC-3'
RT- SCO7234_961 rv	5'-AGAGAAAGGTGATGGCGATGG-3'
RT- SCO7236_211 fw	5'-TTCTTCAAGCCCTCCATGACG-3'
RT- SCO7236_806 rv	5'-GTGGAGTTCGTCATGAACTGC-3'
RT- SCO2150_150 fw	5'-CGAGGGCAAGAAGCTCTACG-3'
RT- SCO2150_630 rv	5'-CCAGGTAGGCGATGATGTCC-3'

Table S2 Mass spectrometry analysis of oxidase activity bands isolated after BN-PAGE.

A complete list of the polypeptides identified by mass spectrometric analysis of the *aa₃* oxidase activity band isolated from membrane fractions of strain M145 and COE634 is shown in the Excel spreadsheet (Dataset) labelled Table S2. Polypeptides of the Qcr and Cta subunits are highlighted in gray.

Band A BN-PAGE		Wt M145										
SCO number	Accession	Description	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pI	Score	Sequest HT	Sequest HT
SCO2149	Q9X807	Cytochrome bc1 complex Rieske iron-sulfur subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=qcrA PE=3 SV=1	11	3	5	3	353	38,6	5,44	8,32		
SCO2155	Q9X813	Probable cytochrome c oxidase subunit 1-alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaD1 PE=3 SV=1	13	8	16	8	578	64,1	7,17	23,32		
SCO2156	Q9X814	Probable cytochrome c oxidase subunit 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaC PE=3 SV=1	32	9	25	9	319	35,4	8,07	68,57		
SCO3945	Q9ZB7	Putative cytochrome oxidase subunit I OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3945 PE=4 SV=1	6	3	9	3	501	55,9	8,63	20,4		
SCO3946	Q9ZB6	Putative cytochrome oxidase subunit II OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3946 PE=4 SV=1	4	2	7	2	334	37,0	6,70	15,24		
	Q9RI32	Nitrate reductase alpha chain NarG2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0216 PE=3 SV=1	2	2	3	2	1233	137,0	6,48	4,98		
	Q9RI31	Nitrate reductase beta chain NarH2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0217 PE=4 SV=1	4	2	3	2	522	57,2	5,62	7,98		
	Q93IU2	BldKB, putative ABC transport system lipoprotein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5113 PE=4 SV=1	29	16	35	16	600	65,5	5,52	105,79		
	O86572	Putative oligopeptide-binding lipoprotein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5477 PE=4 SV=1	33	18	29	18	600	65,3	6,51	80,57		
	O50494	Glutamate binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5776 PE=3 SV=1	45	10	23	10	278	29,5	5,90	61,21		
	Q9L292	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1517 PE=4 SV=1	39	6	16	6	169	17,8	4,54	51,48		
	O50503	Solute-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6009 PE=4 SV=1	22	6	11	6	371	39,2	5,48	23,74		
	Q9FCI4	UPF0182 protein SCO5204 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5204 PE=3 SV=2	6	6	11	6	1000	109,5	5,97	27,17		
	P54919	Delta-aminolevulinic acid dehydratase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=hemB PE=3 SV=2	21	5	6	5	330	35,4	5,05	16,64		
	Q9K4D7	ATP synthase subunit b OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpF PE=3 SV=1	27	4	4	4	184	20,2	5,03	7,67		
	Q9RD72	Putative prolyl aminopeptidase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0805 PE=4 SV=1	3	2	4	2	433	47,6	5,81	7,48		
	Q9XAU5	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3607 PE=4 SV=1	4	2	4	2	489	51,6	5,25	10,95		
	Q9S2U4	Putative membrane protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2041 PE=4 SV=1	24	2	3	2	83	8,6	8,98	7,06		
	Q9S2I5	Putative branched chain amino acid binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2008 PE=4 SV=1	7	2	3	2	418	43,5	5,47	9,24		
	Q9X832	Putative secreted substrate-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6065 PE=4 SV=1	7	2	3	2	320	33,7	5,78	7,91		
	Q9F2R8	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4471 PE=4 SV=1	7	2	2	2	432	47,0	7,94	5,48		
	Q9K4D4	ATP synthase gamma chain OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpG PE=3 SV=1	8	2	2	2	305	33,0	6,29	4,44		
	O54095	Putative oxidase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5897 PE=4 SV=1	6	2	2	2	395	44,9	7,12	4,29		
Band B BN-PAGE		COE634 (COE192 comp.)										
SCO number	Accession	Description	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pI	Score	Sequest HT	Sequest HT
SCO2148	Q9X806	Cytochrome bc1 complex cytochrome b subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=qcrB PE=3 SV=1	3	2	4	2	545	60,8	7,85	6,36		
SCO2149	Q9X807	Cytochrome bc1 complex Rieske iron-sulfur subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=qcrA PE=3 SV=1	18	5	8	5	353	38,6	5,44	10,1		
SCO2155	Q9X813	Probable cytochrome c oxidase subunit 1-alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaD1 PE=3 SV=1	15	9	28	9	578	64,1	7,17	49,43		
SCO2156	Q9X814	Probable cytochrome c oxidase subunit 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaC PE=3 SV=1	37	10	44	10	319	35,4	8,07	118,58		
SCO3945	Q9ZB7	Putative cytochrome oxidase subunit I OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3945 PE=4 SV=1	6	3	9	3	501	55,9	8,63	13,52		
	Q9RI32	Nitrate reductase alpha chain NarG2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0216 PE=3 SV=1	14	13	38	13	1233	137,0	6,48	95,85		
	Q9RI31	Nitrate reductase beta chain NarH2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0217 PE=4 SV=1	11	6	10	6	522	57,2	5,62	26,65		
	O86572	Putative oligopeptide-binding lipoprotein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5477 PE=4 SV=1	40	19	47	19	600	65,3	6,51	161,69		
	Q9S227	Alanine dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1773 PE=3 SV=1	33	10	36	10	371	39,5	6,11	89,22		
	Q9L292	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1517 PE=4 SV=1	71	9	34	9	169	17,8	4,54	97,72		
	Q9RNU9	Phosphoenolpyruvate carboxylase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ppc PE=1 SV=1	12	9	18	9	911	101,2	5,74	54,67		
	P54919	Delta-aminolevulinic acid dehydratase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=hemB PE=3 SV=2	33	8	14	8	330	35,4	5,05	34,97		
	O86655	30S ribosomal protein S15 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rpsO PE=3 SV=1	44	5	14	5	95	10,8	11,14	37,4		
	Q9L0I6	Putative inosine-5'-monophosphate dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4771 PE=4 SV=1	25	7	14	7	374	40,1	5,87	39,95		
	Q93IU2	BldKB, putative ABC transport system lipoprotein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5113 PE=4 SV=1	17	9	14	9	600	65,5	5,52	36,93		
	Q9X929	Na(+)/H(+) antiporter NhaA 3 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=nhaA3 PE=3 SV=1	15	6	13	6	474	49,7	5,36	34,56		
	Q9K4D5	ATP synthase subunit alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpA PE=3 SV=1	22	8	12	8	529	57,2	5,07	45,64		
	P40174	Elongation factor Tu-1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tuf1 PE=3 SV=1	19	6	11	6	397	43,8	5,12	32,02		
	Q9L0I7	Inosine-5'-monophosphate dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=guaB PE=3 SV=1	15	5	11	5	501	52,4	6,64	38		
	Q9F2R8	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4471 PE=4 SV=1	11	4	9	4	432	47,0	7,94	18,8		
	P0A3H5	DNA-binding protein HU 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=hup1 PE=3 SV=1	41	3	9	3	93	9,8	9,47	23,21		
	P40171	60 kDa chaperonin 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=groL1 PE=3 SV=3	11	4	9	4	541	57,1	4,98	19,57		
	Q9ZB75	Putative ABC transporter OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3947 PE=4 SV=1	4	4	8	4	1172	122,7	9,25	18,79		
	Q9FCI4	UPF0182 protein SCO5204 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5204 PE=3 SV=2	5	5	7	5	1000	109,5	5,97	17,46		
	O50494	Glutamate binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5776 PE=3 SV=1	13	3	6	3	278	29,5	5,90	4,2		
	O50503	Solute-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6009 PE=4 SV=1	13	4	5	4	371	39,2	5,48	11,8		
	Q9K4D4	ATP synthase gamma chain OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpG PE=3 SV=1	7	2	3	2	305	33,0	6,29	2,42		
	Q9RI42	Putative luxR family two-component response regulator OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0204 PE=4 SV=1	12	2	2	2	233	25,4	5,10	3,5		
	Q9L0C8	50S ribosomal protein L5 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rplE PE=3 SV=1	14	2	2	2	185	20,8	9,69	3,03		
	Q9XXU5	60 kDa chaperonin 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=groL2 PE=3 SV=1	5	2	2	2	541	56,8	4,87	4,92		
	Q9X930	Putative integral membrane transport protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3565 PE=4 SV=1	22	2	2	2	162	16,8	9,92	6,22		
	Q9S2Q6	Dihydropyridol dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2180 PE=3 SV=1	5	2	2	2	486	51,4	6,34	6,08		
	Q9S2I5	Putative branched chain amino acid binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2008 PE=4 SV=1	8	2	2	2	418	43,5	5,47	5,45		
	P0A300	ATP synthase subunit beta OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpD PE=3 SV=2	4	2	2	2	478	52,1	4,89	4,91		

Table S3 Mass spectrometry analysis of oxidase activity bands isolated after clear-native PAGE analysis of membrane fractions from spores and mycelium.

A complete list of the polypeptides identified by mass spectrometric analysis of active bands after in-gel staining specifically for cytochrome *aa₃* oxidase enzyme activity. Bands were isolated and analyzed from membrane fractions of strain M145 and are shown in the Excel spreadsheet (Dataset) labelled Table S3. Polypeptides of the Qcr and Cta subunits are highlighted in gray.

Band a Spores

SCO number	Accession	Description	Coverage [%]	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pI	Score	Sequest HT	Sequest HT
SCO2148	Q9X806	Cytochrome bc1 complex cytochrome b subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=qcrB PE=3 SV=1	12	8	12	8	545	60.8	7.85	24.88		
SCO2149	Q9X807	Cytochrome bc1 complex Rieske iron-sulfur subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=qcrA PE=3 SV=1	21	6	10	6	353	38.6	5.44	17.55		
SCO2150	Q9X808	Cytochrome bc1 complex cytochrome c subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2150 PE=4 SV=1	9	2	2	2	269	27.5	7.39	4.85		
SCO2155	Q9X813	Probable cytochrome c oxidase subunit 1-alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaD1 PE=3 SV=1	17	11	27	11	578	64.1	7.17	74.02		
SCO2156	Q9X814	Probable cytochrome c oxidase subunit 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ctaC PE=3 SV=1	41	14	40	14	319	35.4	8.07	84.95		
SCO2371	Q9KY19	Pyruvate dehydrogenase E1 component OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2371 PE=4 SV=1	2	2	2	2	918	102.3	6.28	5.94		
SCO3945	Q9ZB77	Putative cytochrome oxidase subunit 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3945 PE=4 SV=1	8	3	6	3	501	55.9	8.63	18.96		
SCO4332	Q9XKM5	Putative integral membrane ATPase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4332 PE=4 SV=1	7	5	6	5	802	85.1	5.29	16.79		
SCO4569	Q9XAR1	NADH-quinone oxidoreductase subunit H OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=nuoH PE=3 SV=1	15	5	7	5	467	51.1	5.99	20.94		
SCO4573	Q9XAR5	NADH-quinone oxidoreductase subunit L OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=nuoL PE=3 SV=1	11	7	14	7	654	69.2	8.12	40.99		
SCO4574	Q9XAR6	NuoM, NADH dehydrogenase subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4574 PE=4 SV=1	4	4	7	4	523	55.9	6.74	15.23		
SCO4607	Q9F2V4	NADH dehydrogenase subunit NuoM2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4607 PE=4 SV=1	9	3	3	3	534	56.2	8.76	10.05		
SCO4855	Q9K291	Succinate dehydrogenase iron-sulfur subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4855 PE=3 SV=1	14	3	5	3	257	29.3	5.81	4.51		
SCO4856	Q9K290	Succinate dehydrogenase flavoprotein subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4856 PE=3 SV=1	10	5	7	5	584	64.7	5.71	19.3		
SCO4857	Q9K289	Putative succinate dehydrogenase membrane subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4857 PE=4 SV=1	14	2	4	2	160	17.6	9.77	9.32		
SCO4858	Q9K288	Putative succinate dehydrogenase membrane subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4858 PE=4 SV=1	18	2	2	2	126	14.1	9.47	5.21		
SCO4947	Q9EWF3	Nitrate reductase alpha chain NarG3 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4947 PE=3 SV=1	5	5	5	5	1227	135.0	6.67	14.72		
SCO4948	Q9EWF4	Nitrate reductase beta chain NarH3 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4948 PE=4 SV=1	3	2	2	2	548	59.8	5.68	0		
SCO5367	Q9K4D8	ATP synthase subunit a OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpB PE=3 SV=1	11	4	6	4	273	30.6	7.53	14.26		
SCO5369	Q9K4D7	ATP synthase subunit b OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpF PE=3 SV=1	18	2	3	2	184	20.2	5.03	11.64		
SCO5371	Q9K4D5	ATP synthase subunit alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpA PE=3 SV=1	53	24	38	24	529	57.2	5.07	117.55		
SCO5372	Q9K4D4	ATP synthase gamma chain OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpG PE=3 SV=1	21	6	6	6	305	33.0	6.29	13.16		
SCO5373	P0A300	ATP synthase subunit beta OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=atpD PE=3 SV=2	49	19	33	19	478	52.1	4.89	107.63		
Q952K5	30S ribosomal protein S1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1998 PE=4 SV=1	6	3	3	3	502	55.0	4.64	4.5			
O86655	30S ribosomal protein S15 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rrpD PE=3 SV=1	26	2	2	2	95	10.8	11.14	5.62			
O31212	30S ribosomal protein S2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rrpB PE=3 SV=3	11	4	5	4	310	33.5	5.25	14.75			
Q910D4	30S ribosomal protein S3 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rrpC PE=3 SV=1	8	2	3	2	277	30.3	10.45	6.92			
Q9XK95	30S ribosomal protein S4 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rrpD PE=3 SV=1	12	3	4	3	204	23.6	10.15	6.56			
PA6790	30S ribosomal protein S5 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rrpE PE=3 SV=3	21	2	3	2	201	20.5	10.20	8.03			
O86841	4-hydroxy tetrahydropyridicolinate synthase 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=dapA2 PE=3 SV=1	12	3	4	3	299	31.2	5.92	11.81			
Q910D3	50S ribosomal protein L16 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rlp1 PE=3 SV=1	27	3	3	3	139	15.8	11.02	6.87			
P0A477	50S ribosomal protein L19 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rlp5 PE=3 SV=1	20	2	3	2	116	13.1	10.89	0			
Q910D7	50S ribosomal protein L2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rlpB PE=3 SV=1	25	6	6	6	278	30.5	11.39	10.08			
Q910E0	50S ribosomal protein L3 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rlpC PE=3 SV=1	16	3	6	3	214	22.8	10.20	8.21			
Q910D9	50S ribosomal protein L4 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rlpD PE=3 SV=1	30	5	5	5	219	23.6	10.04	13.65			
Q910C8	50S ribosomal protein L5 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rlpE PE=3 SV=1	24	4	5	4	185	20.8	9.69	10.32			
P40171	60 kDa chaperonin 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=grp1 PE=3 SV=3	25	9	11	9	541	57.1	4.98	38.28			
Q9XKU5	60 kDa chaperonin 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=grp2 PE=3 SV=1	13	5	10	5	541	56.8	4.87	29.24			
Q9ZBK4	ABC transporter ATP-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3958 PE=4 SV=1	11	4	5	4	303	33.3	6.46	10.03			
Q910L5	Aminotransferase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4645 PE=3 SV=1	7	2	3	2	408	43.5	5.10	10.23			
Q9WVX8	Anti-sigma-B factor antagonist OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rsbv PE=1 SV=1	21	2	2	2	113	12.3	5.24	4.63			
Q9X814	ATP-dependent zinc metalloprotease FtsH OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ftsH PE=3 SV=1	10	4	7	4	668	72.0	5.76	24.45			
Q952N0	Bacterioferritin OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=bfr PE=3 SV=1	55	12	209	12	167	19.2	4.86	515.96			
Q93IU3	BldKA, putative ABC transport system integral membrane protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5112 PE=3 SV=1	6	2	2	2	343	37.4	5.15	4.33			
Q93IU2	BldKB, putative ABC transport system lipoprotein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5113 PE=4 SV=1	43	27	60	27	600	65.5	5.52	160.6			
Q93IU1	BldKC, putative ABC transport system integral membrane protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5114 PE=3 SV=1	7	2	4	2	325	35.6	8.16	9.81			
Q7AK50	Catalase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO666 PE=3 SV=1	9	5	6	5	759	81.2	5.53	17.26			
Q95558	Chaperone protein DnaK OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=dnaK PE=3 SV=1	4	2	2	2	618	66.2	4.87	5.76			
Q952Q5	Dihydrolipamide acetyltransferase complex of pyruvate dehydrogenase complex OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2181 PE=3 SV=1	10	4	10	4	590	59.0	4.67	34.22			
Q952Q6	Dihydrolypoyl dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2180 PE=3 SV=1	6	3	3	3	486	51.4	6.34	6.96			
P0A3H7	DNA-binding protein HU 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=hup2 PE=3 SV=1	17	3	5	3	218	22.3	11.21	13.84			
P60312	DNA-directed RNA polymerase subunit alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rpoA PE=3 SV=1	12	4	5	4	340	36.7	4.79	11.08			
Q910L0	DNA-directed RNA polymerase subunit beta OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rpoB PE=1 SV=1	11	10	13	10	1161	128.4	4.98	35.16			
Q8CJT1	DNA-directed RNA polymerase subunit beta' OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rpoC PE=3 SV=1	4	4	6	4	1299	144.5	6.86	17.51			
P40173	Elongation factor G 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=efusA PE=3 SV=2	7	5	6	5	708	77.6	5.07	14.54			
O31213	Elongation factor Ts OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tsf PE=3 SV=3	9	2	3	2	278	29.8	5.63	4.49			
P40174	Elongation factor Tu-1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=etu1 PE=3 SV=1	26	8	8	8	397	43.8	5.12	22.29			
Q9F2Q3	Enolase 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=enp1 PE=3 SV=1	27	8	13	8	426	45.5	4.60	51.07			
Q9KIM1	F43a OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=f43a PE=4 SV=1	32	8	12	8	312	33.3	5.19	32.43			
Q9X489	Glucose-6-phosphate 1 dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=gwf PE=3 SV=1	25	11	12	11	507	56.6	5.40	34.47			
OS0494	Glutamate binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5776 PE=3 SV=1	62	23	43	23	278	29.5	5.90	134.02			
OS0492	Glutamate permease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5774 PE=3 SV=1	8	2	2	2	299	32.0	9.42	5.68			
OS0493	Glutamate permease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5775 PE=3 SV=1	24	5	5	5	222	23.2	9.25	12.86			
OS0495	Glutamate uptake system ATP-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5777 PE=4 SV=1	10	2	2	2	258	28.1	6.55	7.76			
P15106	Glutamine synthetase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glnA PE=3 SV=1	14	5	7	5	469	52.5	5.29	18.32			
Q9Z518	Glyceroldehyde-3-phosphate dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=gap PE=3 SV=1	15	4	8	4	336	36.2	5.48	22.73			
Q93J08	Glyceroldehyde-3-phosphate dehydrogenase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO57511 PE=3 SV=1	7	2	2	2	332	34.9	5.69	5.54			
Q9RIJ2	Glycerol kinase 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glpK1 PE=3 SV=1	4	2	2	2	507	55.5	5.38	5.18			
Q9AD47	Glycerol kinase 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glpK2 PE=3 SV=1	15	7	8	7	512	56.0	4.92	20.84			
Q9ZB55	Histidine kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6163 PE=4 SV=1	9	2	2	2	303	32.8	5.85	4.36			
Q9KY11	Histidine kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7327 PE=4 SV=1	2	2	3	2	1331	142.1	4.87	8.08			
Q9RIJ9	Integral membrane protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5113 PE=4 SV=1	6	2	3	2	363	38.0	7.44	8.37			
Q9X913	K(+)-insensitive pyrophosphate-energized proton pump OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=hppA PE=1 SV=1	20	13	17	13	794	80.6	5.39	45.53			
Q9KYV5	Large-conductance mechanosensitive channel OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=mclL PE=3 SV=1	27	5	5	5	156	16.7	7.14	13.97			

054569	Membrane protein insertase YidC OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=yidC PE=3 SV=1	5	2	2	2	431	47.3	10.08	5.04
Q952C8	Na(+)/H(+) antiporter NhaA 2 OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=nhaA2 PE=3 SV=1	6	6	8	6	629	67.7	6.32	20.36
Q9X929	Na(+)/H(+) antiporter NhaA 3 OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=nhaA3 PE=3 SV=1	10	4	4	4	474	49.7	5.36	7.22
Q9FC90	Oritriline aminotransferase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1223 PE=3 SV=1	6	2	2	2	407	42.9	6.04	3.36
Q9R162	Peptidylprolyl isomerase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1639 PE=4 SV=1	56	23	46	23	335	34.9	5.35	118.3
Q9F3K6	Permease OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5259 PE=3 SV=1	10	2	3	2	316	34.4	9.07	5.95
Q88054	Phenylalanine-tRNA ligase beta subunit OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=phcT PE=3 SV=1	3	2	2	2	840	89.9	5.14	4.84
Q9K2W0	Phosphate transport system permease protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4414 PE=3 SV=1	17	5	8	5	336	35.6	6.81	14.46
Q9K2V9	Phosphate-binding protein PstS OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4142 PE=3 SV=1	20	6	6	6	370	38.0	5.05	15.09
Q9RN9U	Phosphoenolpyruvate carboxylase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=ppc PE=1 SV=1	14	10	12	10	911	101.2	5.74	29.36
P56833	Phospho-N-acetylmuramyl-pentapeptide-transferase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=mraY PE=3 SV=1	4	2	3	2	363	38.9	9.06	4.16
Q8JCQ6	Polyribonucleotide nucleotidyltransferase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=ppn PE=3 SV=1	27	17	21	17	739	79.3	5.15	38.68
Q9K471	Possible integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO7214 PE=4 SV=1	6	2	2	2	355	36.3	9.85	4.97
Q9X811	Possible membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3411 PE=4 SV=1	9	3	3	3	303	33.7	7.47	4.25
O50505	Probable ABC-type transmembrane transport protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6011 PE=3 SV=1	2	2	2	2	430	44.7	9.28	2.91
P46105	Probable actinorhodin transporter OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=actI-2 PE=3 SV=1	8	6	9	6	578	59.7	6.95	25.85
Q952Q7	Probable cytosol aminopeptidase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=pepE PE=3 SV=1	2	3	2	2	517	52.0	5.60	9.39
Q9RD56	Probable glutamine synthetase [EC 6.3.1.2] OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2241 PE=3 SV=1	5	2	4	2	453	50.5	5.11	10.98
P19255	Probable glycerol uptake facilitator protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=glpF PE=2 SV=2	2	13	2	2	264	26.8	5.77	37.36
Q9RL34	Probable secreted solute-binding lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0453 PE=1 SV=1	10	3	3	3	429	45.8	6.46	5.72
Q9XA16	Probable serine/threonine-protein kinase SCO3848 OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3848 PE=3 SV=1	16	8	9	8	673	71.4	4.93	15.96
Q9K2H3	Probable secreted solute-binding lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6979 PE=4 SV=1	33	8	12	8	340	35.5	6.28	35.54
Q952U8	Protoprotein diacylglycerol transferase 1 OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=igt1 PE=3 SV=1	19	4	4	4	343	36.8	5.72	9.25
Q7AKI7	Propionyl-CoA carboxylase complex B subunit OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4926 PE=4 SV=1	9	4	5	4	530	57.1	5.26	8.92
Q9RKN3	Protease HtpX homolog 1 OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=htpX1 PE=3 SV=1	16	3	4	3	304	33.0	9.64	12.94
Q93956	Protein translocase subunit SecY OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=secF PE=3 SV=1	8	2	2	2	373	39.7	7.06	2.72
P46785	Protein translocase subunit SecY OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=secY PE=3 SV=2	12	5	6	5	437	47.3	9.42	14.75
Q9FBR4	Putative 2-oxoglutarate dehydrogenase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5281 PE=4 SV=1	8	9	11	9	1272	139.1	6.33	22.69
Q9RKT5	Putative ABC transporter system sugar binding lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6257 PE=4 SV=1	13	3	4	3	334	35.2	5.19	4.8
Q9ZBK6	Putative ABC transporter ATP-binding protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3956 PE=4 SV=1	11	3	4	3	320	34.3	5.80	11.58
Q9AD75	Putative ABC transporter ATP-binding protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4963 PE=4 SV=2	10	3	3	3	335	35.9	5.49	7.63
Q9K486	Putative ABC transporter ATP-binding subunit OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5395 PE=4 SV=1	22	6	10	6	346	37.5	7.08	32.01
Q9K487	Putative ABC transporter integral membrane subunit OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5394 PE=4 SV=1	14	4	5	4	258	27.3	9.74	8.89
Q9L2F2	Putative ABC transporter OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2464 PE=4 SV=1	4	3	4	3	642	69.4	5.72	6.99
Q9K5Y2	Putative acyl CoA dehydrogenase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5693 PE=3 SV=1	43	23	32	23	658	71.5	7.31	86.97
Q9AD84	Putative aldehyde dehydrogenase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO9113 PE=4 SV=1	7	2	2	2	480	51.3	5.69	3.08
Q9R1V8	Putative alpha-mannosidase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0948 PE=4 SV=1	4	3	3	3	1007	110.8	5.67	8.52
Q9FBM2	Putative amino acid permease OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5057 PE=4 SV=1	10	4	6	4	460	47.7	7.06	18.57
Q9X7P5	Putative BCCT family transporter OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6739 PE=3 SV=1	14	9	21	9	578	61.7	5.68	47.7
Q952J5	Putative branched chain amino acid binding protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2008 PE=4 SV=1	65	24	59	24	418	43.5	5.47	206.37
Q952J3	Putative branched chain amino acid transport permease OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2010 PE=3 SV=1	6	3	5	3	608	63.4	5.68	18.28
O69844	Putative cationic amino acid transporter OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6014 PE=4 SV=1	18	9	18	9	503	53.5	7.87	39.17
Q9KZP3	Putative CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyl-transferase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1389 PE=3 SV=1	2	2	2	2	215	23.8	9.76	9.58
Q956T8	Putative Ctp-family ATP-binding protease OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3373 PE=4 SV=1	3	2	4	2	841	93.0	6.01	6.28
Q9R1J0	Putative conserved secreted protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0378 PE=4 SV=1	22	4	5	4	244	25.4	5.00	14.85
Q9K2Y7	Putative D-alanyl-D-alanine carboxypeptidase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4439 PE=3 SV=1	12	7	12	7	832	84.2	4.63	41.94
Q9Z501	Putative export associated protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1965 PE=4 SV=1	10	2	2	2	192	20.6	6.18	5.14
Q9KZK5	Putative export protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4451 PE=4 SV=1	6	2	2	2	541	56.8	8.47	7.56
Q9L1L4	Putative extracellular solute-binding lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5430 PE=4 SV=1	11	4	6	4	458	49.7	4.96	19.18
Q9KYU9	Putative fructose-specific permease OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3196 PE=4 SV=1	15	7	14	7	699	70.1	5.26	29.29
Q9XA18	Putative FtsW/RodA/SpoVE family cell cycle protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3846 PE=3 SV=1	3	2	2	2	479	51.2	8.81	3.33
Q9XAM4	Putative glutathione-dependent aldehyde dehydrogenase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6706 PE=3 SV=1	18	5	6	5	396	42.7	5.12	16.93
Q9LDI3	Putative glycerol phosphate dehydrogenase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4774 PE=4 SV=1	42	21	32	21	568	62.0	6.84	76.45
Q9ADA6	Putative glycerol-3-phosphate dehydrogenase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1661 PE=4 SV=1	19	7	8	7	538	57.5	7.55	24.27
Q8CJ18	Putative glycerophosphoryl diester phosphodiesterase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1565 PE=4 SV=1	9	3	3	3	392	42.6	6.77	9.38
Q8CK05	Putative integral membrane efflux protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2164 PE=3 SV=1	4	3	3	3	1041	108.0	4.91	4.4
O69916	Putative integral membrane lysyl-tRNA synthetase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6384 PE=4 SV=1	7	4	5	4	589	66.4	9.29	12.81
Q9RCX8	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0932 PE=4 SV=1	26	4	5	4	254	27.7	4.68	13.52
Q9K3K9	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1051 PE=4 SV=1	9	3	3	3	357	38.3	7.25	5.57
Q9FCB6	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1251 PE=4 SV=1	12	4	4	4	468	48.9	4.94	14.87
Q9FCB5	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1252 PE=4 SV=1	15	4	4	4	337	36.5	8.24	10.14
Q9KXK3	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1363 PE=4 SV=1	10	2	2	2	240	26.3	8.24	7.8
Q9KXK6	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3214 PE=4 SV=1	9	3	5	3	289	29.1	6.87	9.67
Q9KY24	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2366 PE=4 SV=1	7	2	2	2	380	41.0	5.07	6.32
Q9KYW6	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3015 PE=4 SV=1	2	2	4	2	462	46.2	5.52	8.91
Q9RKD3	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3154 PE=4 SV=1	9	5	5	5	591	66.2	8.54	10.21
Q9X880	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3288 PE=4 SV=1	11	2	4	2	243	24.7	3.74	11.19
Q9X8V8	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3676 PE=4 SV=1	8	2	3	2	350	36.1	8.87	5.94
Q9LOG8	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4789 PE=4 SV=1	3	3	3	3	171	18.3	9.35	8.17
Q9FBK5	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5153 PE=4 SV=1	16	3	5	3	198	22.9	8.68	9.31
Q9ADF6	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6107 PE=4 SV=1	6	2	2	2	344	37.6	6.02	5.04
O86495	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6327 PE=4 SV=1	41	9	18	9	154	17.1	8.16	48.91
Q9K459	Putative integral membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO7226 PE=4 SV=1	13	2	3	2	146	15.6	5.10	1.7
Q9X9X2	Putative integral membrane sugar transport protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1900 PE=3 SV=1	6	2	2	2	292	30.9	9.33	3.56
Q95237	Putative iron-sulphur protein (putative secreted protein) OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1763 PE=4 SV=1	21	3	3	3	131	13.2	7.64	4.86
Q9X8V5	Putative iron-sulphur-binding reductase OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3673 PE=4 SV=1	18	12	20	12	760	83.3	5.74	54.04
Q9X881	Putative large membrane protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3289 PE=4 SV=1	30	15	16	15	536	58.9	7.24	39.61
Q9X9W4	Putative large secreted protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1908 PE=4 SV=1	7	3	6	3	613	64.7	5.39	20.65
Q9RJ53	Putative lipoprotein oligopeptide binding protein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1655 PE=4 SV=1	33	13	19	13	534	57.7	4.81	49.07
Q9FPZ8	Putative lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3101 PE=4 SV=1	26	6	8	6	215	23.5	6.57	19.82
Q9LOR0	Putative lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4231 PE=4 SV=1	12	3	4	3	241	23.5	4.41	8.09
Q9AK42	Putative lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4884 PE=4 SV=1	14	3	3	1	347	35.7	5.11	7.57
Q9AK41	Putative lipoprotein OS=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4885 PE=4 SV=1	24	5	5	3	348	36.0	5.06	11.18

Q9EWW2	Putative lipoprotein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4934 PE=4 SV=1	57	15	21	15	414	43.5	6.44	49.08
OS0499	Putative lipoprotein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6005 PE=4 SV=1	35	15	21	15	469	50.6	5.41	48.07
Q9L126	Putative lipoprotein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO7434 PE=4 SV=1	11	2	3	2	253	26.6	4.97	3.74
Q7AKP1	Putative maltose-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2231 PE=4 SV=1	13	4	4	4	423	44.6	5.54	8.55
Q9K2P4	Putative mannose-1-phosphate guanylyltransferase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1388 PE=4 SV=1	5	3	4	3	831	89.6	5.15	9.33
OS3902	Putative membrane protein ActII-3 O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=actII-3 PE=3 SV=1	12	4	5	4	711	74.8	6.62	9.21
Q9RK30	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0686 PE=3 SV=1	6	2	2	2	407	43.5	6.44	5.86
Q9RCW1	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0850 PE=4 SV=1	21	3	3	3	141	14.7	10.14	7.12
Q9S290	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1740 PE=4 SV=1	22	6	10	6	354	36.0	8.94	30.61
Q9RJ36	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1832 PE=4 SV=1	28	3	4	3	195	21.0	10.24	9.98
Q9S2U7	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2035 PE=4 SV=1	24	6	9	6	275	29.4	8.28	24.23
Q9S2U4	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2041 PE=4 SV=1	24	2	3	2	83	8.6	9.98	3.9
Q9RKN9	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2289 PE=4 SV=1	19	3	4	3	180	17.7	8.83	11.14
Q8CJ22	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2534 PE=4 SV=1	9	2	2	2	434	46.6	4.96	7.85
Q9L0V8	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3746 PE=4 SV=1	9	3	3	3	428	46.5	9.45	7.35
Q9X9U1	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3927 PE=4 SV=1	8	3	4	3	513	52.5	8.88	14.15
Q9EWF8	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4957 PE=4 SV=1	27	6	10	6	372	40.7	5.87	28.08
OS0485	Putative membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5767 PE=4 SV=1	2	2	2	2	402	43.9	9.13	6.13
Q9L282	Putative membrane transferase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO15227 PE=3 SV=1	16	3	5	3	241	25.2	9.16	12.16
Q9KZB9	Putative membrane transport protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO06970 PE=3 SV=1	6	3	3	3	714	75.3	8.16	7.56
Q9XKW8	Putative metalloproteinase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4273 PE=4 SV=1	5	2	2	2	473	51.5	4.59	5.25
Q9F3L8	Putative Na+/H+ antiporter O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5246 PE=4 SV=1	16	7	9	7	530	56.9	5.95	23.49
OS6572	Putative oligopeptide-binding lipoprotein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5477 PE=4 SV=1	52	30	58	30	600	65.3	6.51	166.03
Q8CJQ0	Putative oxidase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5966 PE=4 SV=1	11	9	9	9	1047	113.8	5.64	18.12
Q9ZBW7	Putative oxidoreductase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6551 PE=4 SV=1	10	2	2	2	277	30.2	5.25	3.23
Q8CJJ7	Putative oxidoreductase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO7525 PE=3 SV=1	3	2	3	2	764	84.2	6.86	7.6
Q8CJX4	Putative penicillin acylase (EC 3.5.1.11) O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3184 PE=4 SV=1	17	16	19	16	936	102.4	5.55	43.75
Q9F3F0	Putative peptide transport system ATP-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5120 PE=3 SV=1	19	7	6	6	327	35.9	6.54	10.76
Q9F3F3	Putative peptide transport system secreted peptide-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5117 PE=4 SV=1	56	31	60	31	544	58.8	5.43	181.73
Q7AKN1	Putative permease binding-protein component O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2933 PE=4 SV=1	32	8	9	8	322	34.5	5.34	25.7
Q9AR32	Putative permease membrane component O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2933 PE=4 SV=1	13	3	4	3	290	30.3	10.29	10.29
Q9XKY7	Putative phosphate binding protein [Putative secreted protein] O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2428 PE=4 SV=1	5	6	5	5	522	55.4	6.81	13.51
Q9L0U6	Putative proton transport protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4498 PE=3 SV=1	9	3	4	3	440	46.4	6.10	7.68
Q9S2H5	Putative PTS transmembrane component O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2906 PE=4 SV=1	17	5	9	4	431	46.4	6.54	31.4
Q9S2H4	Putative PTS transmembrane component O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2907 PE=4 SV=1	9	3	3	2	416	44.1	7.62	10.12
Q9XA07	Putative regulatory protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3857 PE=4 SV=1	3	6	8	6	232	24.8	9.45	19.65
Q9KZU9	Putative secreted 5'-nucleotidase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4152 PE=3 SV=1	7	3	4	3	612	64.4	5.73	10.44
Q9J3J3	Putative secreted hydrolase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1968 PE=4 SV=1	12	3	3	3	289	31.4	5.50	5.03
Q9S1Z5	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0131 PE=4 SV=1	23	5	7	5	279	30.0	7.14	19.62
Q9X9Z6	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1796 PE=4 SV=1	23	6	10	6	319	34.7	5.35	23.07
Q9XKJ9	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2321 PE=4 SV=1	16	6	8	6	419	42.4	4.98	15.77
Q9L057	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2978 PE=4 SV=1	28	10	15	10	465	48.4	5.02	45.76
Q9J3J0	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3966 PE=1 SV=1	19	3	3	3	216	23.1	5.49	4.8
Q9F2R7	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4472 PE=4 SV=1	13	3	5	3	223	23.7	9.33	8.42
Q9FBL6	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5142 PE=4 SV=1	25	4	5	4	119	12.7	5.30	11.42
Q9J3D2	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5995 PE=4 SV=1	9	2	3	2	240	25.0	7.01	6.87
Q9K458	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO7227 PE=4 SV=1	10	3	3	3	343	37.2	5.82	4.24
Q9K4I8	Putative secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO7237 PE=4 SV=1	54	7	11	7	119	12.9	5.87	22.93
Q9X832	Putative secreted substrate-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6065 PE=4 SV=1	2	2	2	2	320	33.7	5.78	8.19
Q9RKF3	Putative secreted sugar-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3484 PE=4 SV=1	8	4	4	4	436	46.2	4.94	9.69
Q9L0R2	Putative sensor kinase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4229 PE=4 SV=1	5	2	2	2	426	45.3	6.13	5.89
Q9X885	Putative small integral membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3293 PE=4 SV=1	26	5	6	5	167	18.5	7.94	13.47
Q9X9I2	Putative small secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3546 PE=4 SV=1	19	3	5	3	196	20.4	4.94	17.04
OS6753	Putative solute binding lipoprotein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5646 PE=4 SV=1	46	14	16	14	373	40.0	5.55	40.43
Q9X9X4	Putative substrate binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1898 PE=4 SV=1	13	6	7	6	456	49.9	5.14	18.72
Q9X8V6	Putative substrate-binding transport protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3704 PE=4 SV=1	8	8	13	8	269	27.2	5.53	30.92
Q9AKA0	Putative sugar ABC transporter ATP-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4886 PE=4 SV=1	19	7	8	7	537	57.5	5.52	23.4
Q9AK39	Putative sugar ABC transporter integral membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4887 PE=3 SV=1	7	3	5	3	374	39.3	7.06	16.54
Q9KZR2	Putative sugar transport protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2889 PE=4 SV=1	8	4	6	4	504	53.6	7.14	6.88
Q9ZB01	Putative sugar transporter O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5578 PE=3 SV=1	8	5	2	5	472	50.4	6.55	18.32
Q9L1U8	Putative sugar transporter sugar-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2946 PE=4 SV=1	5	2	2	2	432	44.8	6.81	4.38
Q9RDN3	Putative sugar-binding receptor O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2094 PE=4 SV=1	62	25	69	25	332	39.6	5.44	194.65
Q9XKW4	Putative tellurium resistance protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4277 PE=4 SV=1	13	2	2	1	191	20.3	4.65	6.55
Q9F3F7	Putative tetR-family transcriptional regulatory protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4421 PE=4 SV=1	2	2	2	2	211	22.7	9.61	9.8
Q9XA42	Putative transcriptional regulator O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3571 PE=1 SV=1	11	2	2	2	224	24.7	6.16	5.57
Q9AK60	Putative transport integral membrane protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO4057 PE=3 SV=1	3	8	3	3	296	31.9	6.33	17.75
Q9KZM0	Putative transport protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO3024 PE=4 SV=1	15	3	4	3	326	34.2	5.91	14.57
OS4186	Putative transport protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5957 PE=4 SV=1	2	3	2	2	533	54.3	5.86	13.13
Q9KY50	Putative zinc metalloprotease SC05695 O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5695 PE=3 SV=1	14	5	6	5	430	46.2	6.29	13.77
Q9L286	Pyridoxal 5'-phosphate synthase subunit PdxS O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=pdxS PE=3 SV=1	10	2	2	2	303	32.2	5.25	6.69
Q9L299	Pyruvate kinase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5423 PE=3 SV=1	5	2	2	2	476	51.1	5.71	5.67
OS6842	Ribonuclease J O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=rnj PE=1 SV=1	6	3	3	3	561	61.0	6.54	4.66
Q9K3U0	Ribose-phosphate pyrophosphokinase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=rps PE=3 SV=1	18	4	5	4	324	35.2	6.46	12.93
Q9F3K5	Secreted protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO5260 PE=4 SV=1	33	7	12	7	320	33.4	5.31	42.79
OS6565	Serine hydroxymethyltransferase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=glyA PE=3 SV=1	5	2	2	2	420	44.7	6.30	6.16
Q9ZB99	Signal recognition particle receptor FtsY O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=ftsY PE=3 SV=1	24	10	15	10	412	43.6	4.89	47.4
Q04943	Signal transduction histidine-protein kinase AfsQ2 O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=afsQ2 PE=3 SV=1	9	4	7	4	535	57.4	5.35	21.15
OS0503	Solute-binding protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO6009 PE=4 SV=1	52	16	28	16	371	39.2	5.48	80.66
Q9KY56	Succinate-CoA ligase [ADP-forming] subunit beta 1 O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=sucC1 PE=3 SV=1	25	7	8	7	394	41.6	4.89	23.2
Q9X908	Thymidylate kinase O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=tnk PE=3 SV=1	3	3	3	3	1089	115.7	5.52	5.08
Q9RDB5	Uncharacterized protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO0792 PE=4 SV=1	8	2	3	2	343	36.9	8.09	9.77
Q9AK96	Uncharacterized protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO1366 PE=4 SV=1	52	10	18	10	217	22.8	7.15	54.44
Q9KY22	Uncharacterized protein O5=Streptomyces coelicolor [strain ATCC BAA-471 / A3(2) / M145] OX=100226 GN=SCO2368 PE=4 SV=1	13	2	2	1	191	20.4	4.70	5.27

Q9L2F9	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2524 PE=4 SV=1	48	29	46	29	614	68,7	5,31	121,13
Q9RDK4	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2582 PE=3 SV=1	12	5	5	5	402	43,9	6,39	11,09
Q8CJV0	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2999 PE=4 SV=1	17	23	30	23	1653	183,6	5,43	70,74
Q9X8L7	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3353 PE=4 SV=1	29	3	3	3	126	13,3	7,08	4,69
Q9X8I7	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3407 PE=4 SV=1	12	4	6	4	375	41,2	6,55	14,31
Q9X8S6	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3659 PE=4 SV=1	26	4	4	4	178	20,4	4,51	5,33
Q9F2I1	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3790 PE=4 SV=1	4	2	2	2	692	74,8	6,67	7,33
Q9XA19	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3845 PE=4 SV=1	11	4	4	4	515	54,3	4,89	8,49
Q9AK47	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4879 PE=4 SV=1	4	2	2	2	443	47,9	7,80	3,65
O86549	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6615 PE=4 SV=1	5	2	2	2	400	42,1	5,72	2,62
O88016	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6660 PE=4 SV=1	13	3	3	3	311	33,9	5,94	5
Q9K4M1	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7293 PE=4 SV=1	14	2	2	2	225	23,8	6,90	7,92
Q9K407	Undecaprenyl-diphosphatase 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=supp2 PE=3 SV=1	5	3	3	3	291	31,4	9,26	1,99
Q9FCI4	UPF0182 protein SCO5204 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5204 PE=3 SV=2	53	46	88	46	1000	109,5	5,97	279,63
Q9RIJ56	Zinc metalloprotease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1652 PE=3 SV=1	22	7	10	7	374	39,8	5,97	27,91

Band b Mycelium

Table with columns: SCO number, Accession, Description, Coverage [%], # Peptides, # PSMs, # Unique Peptides, # AAs, MW [kDa], calc. pi, Score. Contains detailed protein data for Mycelium band b, including entries like SCO0213, SCO0216, SCO0217, etc.

Q95205	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2181 PE=3 SV=1	11	5	10	5	590	59.0	4.67	31.71
Q95206	Dihydrolipoate dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2180 PE=3 SV=1	11	5	7	5	486	51.4	6.34	14.29
P35886	DNA gyrase subunit B	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ngyB PE=3 SV=1	6	3	3	3	686	75.4	5.41	6.18
Q9Y816	DNA integrity scanning protein DisA	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=disA PE=1 SV=1	15	4	4	4	374	40.0	5.38	11.72
Q95240	DNA polymerase I	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=polA PE=3 SV=1	4	3	4	3	907	98.9	5.14	10.39
P60312	DNA-directed RNA polymerase subunit alpha	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rp0A PE=3 SV=1	39	11	17	11	340	36.7	4.79	50.53
Q91010	DNA-directed RNA polymerase subunit beta	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rp0B PE=1 SV=1	34	31	43	31	1161	128.4	4.98	120.12
Q8JC11	DNA-directed RNA polymerase subunit beta'	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=rp0C PE=3 SV=1	41	44	62	44	1299	144.5	6.86	153.89
Q93R9V	Ectoine dihydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ectD PE=1 SV=2	12	3	5	3	299	32.8	5.31	11.52
P40173	Elongation factor G	1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=efuS PE=3 SV=2	18	9	10	9	708	77.6	5.07	21.64
P40174	Elongation factor Tu	1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=efu1 PE=3 SV=1	34	10	15	10	397	43.8	5.12	44.64
Q9F2Q3	Enolase 1	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=eno1 PE=3 SV=1	41	12	18	12	426	45.5	4.60	68.97
Q9R1M1	F42a OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=f42a PE=4 SV=1		38	11	17	11	312	33.3	5.19	48.19
Q9L131	Flavohemoprotein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7428 PE=3 SV=1	8	2	2	2	398	43.1	5.57	5.83
Q9L1G4	Folypolylglutamate synthase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2614 PE=3 SV=1	6	2	3	2	444	46.9	4.77	11.73
088017	Glucose-6-phosphate 1-dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=gnd PE=3 SV=1	5	2	3	2	592	65.6	5.48	10.28
050494	Glutamate binding protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5776 PE=3 SV=1	61	20	30	20	278	29.5	5.90	102.73
050492	Glutamate permease	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5774 PE=3 SV=1	14	3	4	3	299	32.0	9.42	12.65
050493	Glutamate permease	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5775 PE=3 SV=1	31	6	7	6	222	23.2	9.25	16.86
050495	Glutamate uptake system ATP-binding protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5777 PE=4 SV=1	45	8	13	8	258	28.1	6.55	36.05
P15106	Glutamine synthetase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glnA PE=3 SV=1	9	3	3	3	469	52.5	5.29	7.66
Q9L065	Glutamine-fructose-6-phosphate aminotransferase [isomerizing]	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glnS PE=3 SV=1	14	7	9	7	605	66.1	6.33	22.12
Q92518	Glyceraldehyde 3-phosphate dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=gap PE=3 SV=1	15	4	5	4	336	36.2	5.48	15.48
Q93108	Glyceraldehyde 3-phosphate dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7511 PE=3 SV=1	11	4	11	7	332	34.9	5.69	32.89
Q9R180	Glycine betaine transport ATP-binding protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1621 PE=4 SV=1	11	4	6	4	364	39.9	5.31	17.49
Q9R181	Glycine betaine transport system permease protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1620 PE=3 SV=1	23	16	20	16	871	95.0	5.31	44.83
Q9L2H9	Glycine-tRNA ligase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glyQS PE=3 SV=1	6	2	3	2	460	52.4	5.62	5.05
086522	Histidine kinase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5540 PE=4 SV=1	5	4	6	4	1111	119.8	5.08	20.11
086808	Histidine kinase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5748 PE=4 SV=1	2	3	3	3	1829	195.6	5.07	9.45
Q9AD84	Homoserine dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3564 PE=3 SV=1	6	2	2	2	429	44.0	5.49	6.65
Q9L017	Inosine 5'-monophosphate dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glmB PE=3 SV=1	22	7	8	7	501	52.4	6.64	20.78
Q9R1U9	Integral membrane protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0513 PE=4 SV=1	5	2	4	2	363	38.0	7.44	3.72
Q9FBK6	Iron-sulfur cluster carrier protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5152 PE=3 SV=1	8	2	2	2	377	39.0	5.34	4.17
Q9ZF3	Iscortate dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7000 PE=4 SV=1	23	15	20	15	739	79.5	5.19	56.59
Q9RYV5	Large-conductance mechanosensitive channel	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=mscL PE=3 SV=1	12	2	2	2	156	16.7	7.14	6.94
Q9L1C5	Lipoprotein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1557 PE=3 SV=1	11	2	2	2	275	29.0	4.94	6.18
054569	Membrane protein insertase YidC	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=yidC PE=3 SV=1	7	3	3	3	431	47.3	10.08	7.83
Q9Y929	Na ⁺ /H ⁺ antiporter NhaA	3 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=nhaA3 PE=3 SV=1	15	8	8	8	474	49.7	5.36	19.28
Q9R162	Peptidylprolyl isomerase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1639 PE=4 SV=1	36	12	18	12	335	34.9	5.35	41.81
Q9F3K6	Permease	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5259 PE=3 SV=1	25	5	8	5	316	34.4	9.07	15.21
088055	Phenylalanine-tRNA ligase alpha subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=phe5 PE=3 SV=2	15	3	3	3	358	39.1	4.93	8.23
088054	Phenylalanine-tRNA ligase beta subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=phe7 PE=3 SV=1	17	11	13	11	840	89.9	5.14	32.32
Q9Z8K6	Phosphatidylserine decarboxylase proenzyme	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=psd PE=3 SV=1	31	5	7	5	218	23.6	9.23	18.35
Q9RNU9	Phosphoenolpyruvate carboxylase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ppc PE=1 SV=1	28	20	29	20	911	101.2	5.74	76.64
Q9KZP1	Phosphoenolpyruvate-protein phosphotransferase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ptsI PE=3 SV=1	5	2	2	2	556	57.2	4.79	5.96
P56833	Phospho-N-acetylmuramoyl-pentapeptide-transferase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=mrpE PE=3 SV=1	4	2	3	2	363	38.9	9.06	4.17
Q9RKL4	Phosphoribosylamine-glycine ligase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=purD PE=3 SV=1	19	5	6	5	416	42.6	4.94	19.28
Q9RKK5	Phosphoribosylformylglycinamide synthase subunit PurL	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=purL PE=3 SV=1	4	2	3	2	752	79.8	2.8	8.94
Q9RKK6	Phosphoribosylformylglycinamide synthase subunit PurQ	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=purQ PE=3 SV=1	23	5	6	5	226	24.5	6.00	13.32
Q8CJ06	Polyribonucleotide nucleotidyltransferase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=pnp PE=3 SV=1	23	11	13	11	739	79.3	5.15	34.52
Q9L178	Possible binding-protein-dependent transport lipoprotein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7399 PE=4 SV=1	23	6	11	6	327	34.1	4.81	28.13
Q9X811	Possible membrane protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3411 PE=4 SV=1	8	3	3	3	303	33.7	7.47	5.2
Q9R1Z7	Possible regulator protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0168 PE=4 SV=1	53	10	18	10	190	21.1	7.25	35.36
Q95274	Probable 3-oxacyl-(Acyl-carrier-protein) reductase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1815 PE=1 SV=1	16	3	3	3	234	24.8	6.20	8.37
050505	Probable ABC-type transmembrane transport protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6011 PE=3 SV=1	14	8	13	8	430	44.7	9.28	30.91
Q9RDC0	Probable amino acid ABC transporter protein, ATP-binding component	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2831 PE=4 SV=1	12	2	2	2	261	28.8	5.43	7.69
Q952Q7	Probable cytosolic aminopeptidase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=pepA PE=3 SV=1	32	12	13	12	517	52.0	5.60	38.03
Q9RD56	Probable glutamine synthetase [EC 6.3.1.2]	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=speB PE=3 SV=1	5	2	3	2	453	50.5	5.11	3.61
P19255	Probable glycerol uptake facilitator protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glpF PE=2 SV=2	10	2	2	2	264	26.8	5.77	6.35
Q9YK76	Probable M18 family aminopeptidase 2	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=apeB PE=3 SV=1	45	13	24	13	432	45.9	6.37	60.54
Q9YK16	Probable serine/threonine-protein kinase	SCO3848 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3848 PE=3 SV=1	20	11	14	10	673	71.4	4.93	29.61
Q9RF22	Protease HtrX homolog 2	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=htrX2 PE=3 SV=1	10	2	3	2	287	31.1	9.91	11.78
Q9R1J8	Proteasome-associated ATPase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=arc PE=3 SV=1	7	4	5	4	588	65.1	4.98	9.73
Q9L100	Protein serine/threonine kinase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4777 PE=4 SV=1	4	2	3	2	599	63.9	6.35	8.69
P04466	Protein translocase subunit SecA	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=secA PE=3 SV=1	5	3	3	3	947	106.4	5.11	9.19
053956	Protein translocase subunit SecY	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=secY PE=3 SV=1	14	4	4	4	373	39.7	7.06	8.54
P46785	Protein translocase subunit SecE	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=secY PE=3 SV=2	10	4	5	4	437	47.3	9.42	13.12
Q9FB84	Putative 2-oxoglutarate dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5281 PE=4 SV=1	22	23	27	23	1272	139.1	6.33	71.95
Q9RKT5	Putative ABC transport system sugar binding lipoprotein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6257 PE=4 SV=1	9	2	2	2	334	35.2	5.19	3.16
Q9Z8K6	Putative ABC transporter ATP-binding protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3956 PE=4 SV=1	8	2	3	2	320	34.3	5.80	8.91
Q9F2X6	Putative ABC transporter ATP-binding protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4585 PE=4 SV=1	25	6	9	6	327	34.2	6.19	27.81
05A187	Putative ABC transporter ATP-binding subunit	SCO5958 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5958 PE=3 SV=1	7	2	2	2	284	29.6	5.74	5.14
Q9YK4D	Putative ABC transporter ATP-binding subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1922 PE=4 SV=1	13	2	3	2	254	27.6	5.41	14.26
Q9K4B8	Putative ABC transporter ATP-binding subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5393 PE=4 SV=1	38	17	27	16	423	44.0	8.38	82.02
Q9K4B6	Putative ABC transporter ATP-binding subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5395 PE=4 SV=1	23	7	17	6	346	37.5	7.08	41.63
Q9K4B7	Putative ABC transporter integral membrane subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5394 PE=4 SV=1	14	4	4	4	258	27.3	9.74	8.05
Q9L2F3	Putative ABC transporter	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2463 PE=4 SV=1	17	6	7	6	577	62.8	6.33	19.47
Q9L2F2	Putative ABC transporter	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2464 PE=4 SV=1	12	7	9	7	642	69.4	5.72	17.81
Q9ZB5	Putative ABC transporter	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3947 PE=4 SV=1	52	49	129	49	1172	122.7	9.25	359.58
Q9R1K15	Putative ABC transporter transmembrane protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0491 PE=4 SV=1	9	2	3	2	540	57.3	7.68	0
Q9R1K13	Putative ABC transporter transmembrane protein	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0493 PE=4 SV=1	21	8	11	8	601	62.1	5.74	34.71
Q9EWW4	Putative acyl-CoA carboxylase complex A subunit	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4921 PE=4 SV=1	6	2	2	2	590	62.5	5.25	5.92
Q9R147	Putative alcohol dehydrogenase	OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0199 PE=3 SV=1	6	6	10	6	340	35.3	6.18	25.45

Q9ADB4	Putative aldehyde dehydrogenase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4913 PE=4 SV=1	23	7	7	7	480	51.3	5.69	23.06
Q86519	Putative ATP/GTP binding protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5537 PE=4 SV=1	26	3	6	3	174	18.9	4.86	18.24
Q95215	Putative branched-chain amino acid binding protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2008 PE=4 SV=1	50	12	21	12	418	43.5	5.47	78.86
Q9XA60	Putative branched-chain alpha keto acid dehydrogenase E1 alpha subunit O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3817 PE=4 SV=1	6	2	3	2	417	45.4	5.39	9.04
Q9XA61	Putative branched-chain alpha keto acid dehydrogenase E1 beta subunit O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3816 PE=4 SV=1	7	2	4	2	326	35.7	5.58	10.87
Q9KZP3	Putative CDP-diacylglycerol-glycerol 3-phosphate 3-phosphatidyl-transferase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1389 PE=3 SV=1	10	3	5	3	215	23.8	9.76	12.82
Q95678	Putative Ctp-family ATP-binding protease O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3373 PE=4 SV=1	7	4	5	4	841	93.0	6.01	16.46
Q9F2R4	Putative cytochrome biogenesis related protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4475 PE=4 SV=1	8	2	2	2	380	40.5	9.28	5.76
Q9KZY7	Putative D-alanyl-D-alanine carboxypeptidase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4439 PE=3 SV=1	22	11	13	11	832	84.2	4.63	51.51
Q9XAQ1	Putative electron transfer oxidoreductase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4559 PE=4 SV=1	15	5	7	5	430	47.0	7.91	22.74
Q9L1E6	Putative enoyl-coA hydratase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5459 PE=3 SV=1	12	2	3	2	255	27.1	5.54	9.98
Q952N3	Putative eukaryotic-type serine/threonine protein kinase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2110 PE=4 SV=1	6	3	3	3	667	70.7	5.21	6.38
Q9Z501	Putative export associated protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1965 PE=4 SV=1	29	4	5	4	192	20.6	6.18	13.54
Q9RK35	Putative ferredoxin/ferredoxin-NADP reductase (Putative secreted protein) O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0681 PE=4 SV=1	21	7	7	7	454	49.8	5.05	20.66
Q9KYU9	Putative fructose-specific permease O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3196 PE=4 SV=1	33	18	39	18	699	70.1	5.26	108.26
Q9XA18	Putative FtsW/RodA/SpoVE family cell cycle protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3846 PE=3 SV=1	6	3	5	3	479	51.2	8.81	9.99
Q8CK22	Putative gluconate permease O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1680 PE=4 SV=1	6	2	3	2	465	47.9	7.66	9.21
Q9ADA6	Putative glycerol-3-phosphate dehydrogenase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1661 PE=4 SV=1	11	4	4	4	538	57.5	7.55	13.96
Q9K319	Putative glycine betaine ABC transport system integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4831 PE=3 SV=1	5	2	3	2	648	67.2	9.83	10
Q9RKY2	Putative glycosyl transferase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1423 PE=4 SV=1	11	3	3	3	302	32.5	5.94	9.31
Q9K426	Putative hydrogenase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1073 PE=4 SV=1	6	2	4	2	422	44.8	8.84	4.45
Q9L0N5	Putative hydrolytic protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4256 PE=4 SV=1	14	6	9	3	479	51.3	6.37	18.8
Q9L0N3	Putative hydrolytic protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4258 PE=4 SV=1	8	4	5	1	485	52.6	5.34	13.21
Q8KC05	Putative integral membrane efflux protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2164 PE=3 SV=1	9	7	11	7	1041	108.0	4.91	30.74
Q951P6	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0245 PE=4 SV=1	8	2	2	2	339	36.1	7.30	5.95
Q9RCU8	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0863 PE=4 SV=1	11	4	5	4	485	51.0	9.31	9.52
Q93J57	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0987 PE=4 SV=1	6	2	2	2	517	54.9	7.93	5.34
Q9FC98	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1215 PE=4 SV=1	10	2	5	2	316	34.6	9.09	18.3
Q9AK90	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1372 PE=4 SV=1	16	4	6	4	275	29.3	9.57	14.13
Q9KXP3	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1507 PE=4 SV=1	10	2	2	2	240	26.3	8.65	3.83
Q9RJ48	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1820 PE=4 SV=1	25	3	3	3	159	16.5	10.67	8.89
Q9S2P0	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2196 PE=4 SV=1	15	2	2	2	234	25.0	11.02	8.19
Q9KXK6	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2314 PE=4 SV=1	9	5	8	5	289	29.1	4.88	19.84
Q9KY24	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2366 PE=4 SV=1	7	2	3	2	380	41.0	5.07	8.34
Q9KYW6	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3015 PE=4 SV=1	5	2	5	2	462	46.2	5.52	10.97
Q9KYE1	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4129 PE=4 SV=1	8	2	2	2	420	42.6	7.02	7.35
Q9KYE0	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4130 PE=4 SV=1	30	8	11	8	266	27.5	6.81	28.77
Q9KZY8	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4438 PE=4 SV=1	5	2	2	2	625	67.9	7.87	4.59
Q9F2R5	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4474 PE=4 SV=1	16	6	7	6	574	61.9	5.38	21.63
Q9F2V1	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4610 PE=4 SV=1	17	2	2	2	138	14.9	9.52	5.79
Q9K3J5	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4825 PE=4 SV=1	8	2	2	2	178	18.9	8.82	4.36
Q9KZ97	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4849 PE=4 SV=1	8	3	5	3	436	45.9	9.26	7.78
Q9FBP3	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5034 PE=4 SV=1	6	4	4	4	778	82.8	7.50	11.15
Q86654	Putative integral membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5735 PE=4 SV=1	6	3	4	3	491	50.5	5.69	14.14
Q9RI45	Putative integral membrane protein SCJ12.13c O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0201 PE=4 SV=1	23	5	8	5	223	23.3	8.63	25.34
Q8CJL9	Putative integral membrane transferase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6752 PE=3 SV=1	19	10	16	10	605	63.1	8.32	51.02
Q9XAC6	Putative integral membrane transport protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1930 PE=4 SV=1	10	4	4	4	356	38.4	9.36	5.91
Q9X930	Putative integral membrane transport protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3565 PE=4 SV=1	19	2	3	2	162	16.8	9.92	3.25
Q9K467	Putative iron transport lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7218 PE=4 SV=1	23	5	8	5	345	37.2	5.74	22.75
Q9X8V5	Putative iron-sulphur-binding reductase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3673 PE=4 SV=1	5	4	6	4	760	83.3	6.04	18.89
Q9RJ53	Putative lipoprotein oligopeptide binding protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1655 PE=4 SV=1	31	14	18	14	534	57.7	4.81	47.3
Q9EX42	Putative lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0996 PE=4 SV=1	18	4	6	4	347	37.3	8.18	16.47
Q86780	Putative lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4739 PE=4 SV=1	8	2	2	2	268	26.6	4.39	6
Q9AK41	Putative lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4885 PE=4 SV=1	28	6	9	6	348	36.0	5.06	28.43
Q9EWW2	Putative lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4934 PE=4 SV=1	38	10	13	10	414	43.5	6.44	42.6
Q50499	Putative lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6005 PE=4 SV=1	6	2	3	2	469	50.6	5.41	8.76
Q9RI42	Putative luxR family two-component response regulator O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0204 PE=4 SV=1	16	3	4	3	233	25.4	5.10	5.15
Q7AKP1	Putative maltose-binding protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2231 PE=4 SV=1	13	4	6	4	423	44.6	5.54	14.33
Q9L269	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1540 PE=4 SV=1	15	2	5	2	150	16.4	10.64	16.2
Q952U4	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2041 PE=4 SV=1	24	2	3	2	83	8.6	8.98	4.61
Q95253	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2087 PE=4 SV=1	7	3	3	3	266	28.6	7.36	6.19
Q952X3	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2078 PE=4 SV=1	19	2	3	2	94	9.7	9.87	9.41
Q952V9	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2087 PE=4 SV=1	14	2	2	2	135	15.2	10.32	6.71
Q8CJ22	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2534 PE=4 SV=1	8	2	3	2	434	46.6	4.96	13.86
Q8CJ20	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2616 PE=4 SV=1	18	4	4	4	335	34.6	5.02	8.99
Q9KZK4	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2887 PE=4 SV=1	59	3	5	3	100	9.7	11.90	22.43
Q9KZQ3	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2900 PE=4 SV=1	22	2	2	2	110	12.0	9.86	6.57
Q93I54	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3048 PE=4 SV=1	8	2	3	2	397	42.4	6.83	10.72
Q9L0P9	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4242 PE=4 SV=1	16	3	4	3	468	48.5	7.93	10.95
Q9KYP4	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4489 PE=4 SV=1	14	2	2	2	100	11.1	7.18	5
Q9L050	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4524 PE=4 SV=1	33	5	6	5	239	24.4	5.80	10.1
Q9EWF8	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4957 PE=4 SV=1	41	12	23	12	372	40.7	5.87	69.91
Q9L2B1	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5409 PE=4 SV=1	12	3	5	3	114	12.7	9.99	17.68
Q7AKG6	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5414 PE=4 SV=1	19	2	2	2	109	11.9	9.35	4.8
Q54132	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5866 PE=4 SV=1	31	4	7	4	154	16.5	5.58	17.58
Q9K4J6	Putative membrane protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7318 PE=4 SV=1	4	3	5	3	752	79.6	7.17	14.9
Q9L282	Putative membrane transferase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1527 PE=3 SV=1	9	2	2	2	241	25.2	9.16	5.23
Q9RD59	Putative membrane transport protein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0623 PE=3 SV=1	6	2	2	2	539	55.6	9.14	5.86
Q9KYW0	Putative Na+/H+ antiporter O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3185 PE=4 SV=1	9	3	3	3	515	53.8	8.31	7.5
Q86572	Putative oligopeptide-binding lipoprotein O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5477 PE=4 SV=1	59	43	109	43	600	65.3	6.51	336.08
Q9XR74	Putative oxidoreductase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7286 PE=4 SV=1	12	3	3	3	327	35.8	4.87	10.18
Q9K3R0	Putative oxidoreductase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1088 PE=4 SV=1	20	3	4	3	272	28.6	5.82	12.66
Q9RJ37	Putative oxidoreductase O5-Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1831 PE=4 SV=1	15	2	3	2	251	25.7	5.35	7.02

Q92BW7	Putative oxidoreductase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6551 PE=4 SV=1	16	3	3	3	277	30.2	5.25	5.52
Q8CJX4	Putative penicillin acylase [EC 3.5.1.11] OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3184 PE=4 SV=1	30	32	46	32	936	102.4	5.55	98.1
Q9R008	Putative peptidase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0498 PE=4 SV=1	6	2	2	2	451	49.8	5.34	6.6
Q8CJS2	Putative peptide transport system ATP-binding subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5116 PE=3 SV=1	13	3	4	3	381	41.8	6.70	14.41
Q9F2R9	Putative phosphoglycerate mutase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4470 PE=4 SV=1	15	3	4	3	233	26.0	9.16	10.5
050512	Putative protease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5838 PE=4 SV=1	6	2	2	2	462	48.9	4.97	6.78
Q9I0U6	Putative proton transport protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4498 PE=3 SV=1	27	10	17	10	440	46.4	6.10	49.22
Q9S2H4	Putative P5 regulatory component OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2907 PE=4 SV=1	21	7	12	7	416	44.1	7.62	42.02
Q9KY14	Putative regulatory protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7324 PE=4 SV=1	25	5	8	5	299	31.8	5.50	30.74
Q9ADP3	Putative secreted penicillin-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4013 PE=4 SV=1	4	2	2	2	495	52.8	5.55	2.69
Q9I292	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1517 PE=4 SV=1	18	2	2	2	169	17.8	4.54	13.34
Q8CK18	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1793 PE=4 SV=1	20	3	5	3	260	28.4	4.86	15.73
Q9XZ6	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1796 PE=4 SV=1	38	11	19	11	319	34.7	5.35	48.13
Q9KXJ9	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2321 PE=4 SV=1	6	2	2	2	419	42.4	4.98	6.68
Q9RDL6	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2570 PE=4 SV=1	12	2	2	2	258	27.9	6.43	4.74
Q9I074	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2780 PE=1 SV=1	28	8	13	8	349	36.6	5.31	39.96
Q9XAJ5	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3607 PE=4 SV=1	39	19	26	19	489	51.6	5.25	69.63
Q9J340	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3966 PE=1 SV=1	49	8	11	8	216	23.1	5.49	30.76
Q9F2R8	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4471 PE=4 SV=1	34	14	26	14	432	47.0	7.94	57.94
Q9F2R7	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4472 PE=4 SV=1	45	8	9	8	223	23.7	9.33	13.29
Q9FBL6	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5142 PE=4 SV=1	34	5	6	5	119	12.7	5.30	21.75
Q8E589	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6224 PE=4 SV=1	21	5	8	5	271	27.8	4.84	24.43
Q8E590	Putative secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6225 PE=4 SV=1	29	9	15	9	421	44.1	4.89	46.82
Q9X832	Putative secreted substrate-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6065 PE=4 SV=1	20	4	5	4	320	33.7	5.78	14.68
Q9XAS7	Putative serine/threonine protein kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3820 PE=4 SV=1	7	3	3	2	522	53.5	4.67	8.13
Q9X912	Putative small secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3546 PE=4 SV=1	12	2	3	2	196	20.4	4.94	9.27
Q9I0X7	Putative stress response protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3727 PE=4 SV=1	36	8	14	8	194	20.2	5.87	39.48
Q9AK40	Putative sugar ABC transporter ATP-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4886 PE=4 SV=1	9	3	3	3	537	57.5	5.52	10.22
Q9AK39	Putative sugar ABC transporter integral membrane protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4887 PE=3 SV=1	7	4	7	4	374	39.3	7.06	24.42
Q8CK39	Putative sugar hydrolase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1065 PE=3 SV=1	6	4	5	4	756	83.4	5.67	17.11
Q9ZBQ1	Putative sugar transporter OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5878 PE=3 SV=1	8	5	8	5	472	50.4	6.35	14.8
Q9RDN3	Putative sugar-binding receptor OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2404 PE=4 SV=1	16	4	5	4	369	39.6	5.44	17.72
Q9FCI0	Putative sulfurylase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5178 PE=4 SV=1	10	3	3	3	392	42.6	4.75	7.97
Q9XWV4	Putative tellurium resistance protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4277 PE=4 SV=1	24	3	4	3	191	20.3	4.65	14.26
Q9I2A3	Putative thiodoxin OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5419 PE=4 SV=1	8	2	3	2	318	33.6	4.60	7.84
Q9XA42	Putative transcriptional regulator OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3571 PE=1 SV=1	11	2	3	2	224	24.7	6.16	1.99
Q9K4D9	Putative transferase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5365 PE=4 SV=1	5	2	2	2	434	46.3	7.91	5.59
Q9X7V0	Putative transferase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6755 PE=4 SV=1	12	2	4	2	227	24.4	9.60	10.68
Q9KZM0	Putative transport protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3024 PE=4 SV=1	15	3	4	3	326	34.2	5.91	13.9
Q9I109	Putative uracyl permease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1450 PE=4 SV=1	6	2	2	2	478	49.2	7.96	4.03
Q9KY50	Putative zinc metalloprotease SCOS695 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5695 PE=3 SV=1	22	7	10	7	430	46.2	6.29	29.28
Q9I286	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=pdxS PE=3 SV=1	7	7	12	7	303	32.2	5.25	45.79
Q9I299	Pyruvate kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5423 PE=3 SV=1	5	2	2	2	476	51.1	5.71	5.75
Q9RI40	Pyruvate, phosphate dikinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0208 PE=3 SV=1	6	4	5	4	898	95.9	5.08	13.06
Q9KYX2	Ribosome hibernation promoting factor OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=hpf PE=3 SV=1	13	2	3	2	254	27.9	7.61	11.56
Q9I1G6	Rod shape-determining protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2611 PE=3 SV=1	8	2	2	2	343	36.5	5.94	5.93
Q9RI68	Sec-independent protein translocase protein Taa OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=taa PE=3 SV=1	45	2	2	2	95	10.0	9.52	3.05
Q9F3K5	Secreted protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5260 PE=4 SV=1	18	3	5	3	320	33.4	5.31	14.68
Q9I0I2	Serine/threonine protein kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4775 PE=4 SV=1	5	3	4	3	717	74.1	6.46	4.96
Q69874	Signal recognition particle protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=fnh PE=3 SV=1	5	2	2	2	550	59.2	9.25	2.07
Q9ZBP9	Signal recognition particle receptor FtsY OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ftsY PE=3 SV=1	28	10	13	10	412	43.6	4.89	40.95
Q04943	Signal transduction histidine-protein kinase AfsQ2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=afsq2 PE=3 SV=1	7	3	4	3	535	57.4	5.35	14.28
050503	Solute-binding protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6009 PE=4 SV=1	73	26	63	26	371	39.2	5.48	194.56
Q9KY55	Succinate-CoA ligase [ADP-forming] subunit alpha OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=sucD PE=3 SV=1	11	2	2	2	294	30.2	5.71	5.85
Q9KY56	Succinate-CoA ligase [ADP-forming] subunit beta OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=sucC1 PE=3 SV=1	6	2	3	2	394	41.6	4.89	9.36
Q9XAJ1	SURF1-like protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3611 PE=3 SV=1	13	3	4	3	278	30.3	4.64	9.09
Q9X908	Thymidylate kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tmk PE=3 SV=1	3	3	3	3	1089	115.7	5.52	7.6
Q88019	Transaldolase 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tal1 PE=3 SV=1	19	5	6	4	381	40.4	4.79	20.77
Q9XAC0	Transaldolase 2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tal2 PE=3 SV=1	21	6	8	5	372	40.6	5.05	28.37
Q88019	Transketolase B OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO663 PE=3 SV=1	4	4	6	4	698	74.5	5.68	15.65
Q8CJC8	Translation initiation factor IF-2 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=ihf2 PE=3 SV=1	4	4	4	4	1033	105.6	9.47	8.39
Q9AC47	Transport permease protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1929 PE=3 SV=1	7	2	2	2	795	27.5	6.57	2.84
Q8X7V2	Transport permease protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6757 PE=3 SV=1	17	5	9	5	309	34.1	9.60	21.13
Q9I047	UDP-glucose 4-epimerase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2988 PE=3 SV=1	17	4	5	4	326	34.4	5.15	17.31
Q9RIZ8	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0167 PE=4 SV=1	26	5	10	5	294	31.0	6.00	30.29
Q9RI48	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0198 PE=4 SV=1	10	2	2	2	288	30.8	7.21	7.16
Q9RI46	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0200 PE=4 SV=1	29	8	14	8	301	32.2	6.33	40.26
Q9S1P4	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0247 PE=4 SV=1	8	2	2	2	341	35.9	4.61	6.06
Q9I2K3	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO0705 PE=4 SV=1	10	2	2	2	272	30.6	5.16	6.57
Q9K3Q9	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1089 PE=4 SV=1	29	12	18	12	467	52.9	5.07	43.06
Q8CK29	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1407 PE=4 SV=1	6	7	9	7	1553	167.1	5.48	23.76
Q9X819	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2161 PE=3 SV=1	47	4	7	4	118	12.4	4.46	22.59
Q9RDK4	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2582 PE=3 SV=1	6	3	4	3	402	43.9	6.39	6.15
Q8CJY0	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2999 PE=4 SV=1	14	18	21	18	1653	183.6	5.43	51.28
Q9X8L7	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3353 PE=4 SV=1	48	6	7	6	126	13.3	7.08	19.05
Q9XAJ4	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3608 PE=4 SV=1	15	2	2	2	169	17.1	5.15	5.95
Q9X856	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3659 PE=4 SV=1	17	2	3	2	178	20.4	4.51	7.08
Q9XA19	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3845 PE=4 SV=1	9	3	4	3	515	54.3	4.89	6.26
Q9X8U0	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO3904 PE=4 SV=1	6	2	3	2	373	42.9	8.63	8.61
Q9KZW4	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4137 PE=4 SV=1	28	4	5	4	206	23.2	4.60	16.58
Q9I0P7	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4244 PE=4 SV=1	6	3	5	3	652	70.8	5.35	11.13
Q9I0N9	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO4252 PE=4 SV=1	19	3	4	3	149	16.5	4.92	14.75
Q9Z560	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5519 PE=4 SV=1	19	5	6	5	308	34.5	6.07	10.33

Q9ZB12	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6482 PE=4 SV=1	40	4	8	4	147	16,1	5,00	23,15
Q88016	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO6660 PE=4 SV=1	8	2	2	2	311	33,9	5,94	4,96
Q9K4M1	Uncharacterized protein OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO7293 PE=4 SV=1	14	2	2	2	225	23,8	6,90	6,06
Q9FC4	UPF0182 protein SC05204 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5204 PE=3 SV=2	59	63	147	63	1000	109,5	5,97	496,62
Q9AK76	Uracil phosphoribosyltransferase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=sup PE=3 SV=2	14	2	2	2	211	22,9	5,44	5,5
O69981	Vitamin B12-dependent ribonucleotide reductase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=nrdI PE=2 SV=1	13	9	15	9	967	105,2	5,50	34,61
Q9RI56	Zinc metalloprotease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO1652 PE=3 SV=1	28	9	16	9	374	39,8	5,97	47,52
O50511	Zinc protease OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO5837 PE=4 SV=1	6	2	2	2	450	49,0	4,83	6,29