

TABLE 1

Identification of proteins in *A. radioresistens* S13, grown on acetate, benzoate and phenol.^(a) corresponding to Fig. 2, ^b theoretical pI; ^c theoretical mass). Results of *De Novo* sequencing are underlined, while those obtained by peptide mass fingerprinting (PMF) are indicated in **bold**

Spot n. ^a	Location	Annotation UniprotKB	UniprotKB code	Sequence coverage	score	Identified peptides (<u>De Novo sequencing</u> /PMF)	pI ^b	Mass (kDa) ^c
4s	Soluble proteome	Carboxy-terminal Protease for Penicilling-binding protein (Tsp)	Q6FEN	22%	77.0	R.QLATLVDR.Q R.QHYLNMR.L K.AFYEVLGEL.K K.TVAEQQDYWR.K K.EEDLAKQK.A R.QTTLQLEGIGVSIRPER.G K.IETIVEGGPASK.S R.RAGTEYR.S K.NVEGIHDLR.N R.NNPGGSLEEVAR.M K.LVDIYDEEFGER.K K.WDTIPTAPFK.R R.EGSIQPYVTK.L	8.11	80.36

5s	Soluble proteome	30S Ribosomal protein S2	Q6FA53	55%	68.0	M.ADYNVSMR.D K.MRQYIFGAR.N R.QYIFGAR.N K.IHIINLEHTVPALNDALNFANQLASK.K R.AGQPYVDH.W R.WLGGMLTNWK.T K.NMGGLPDALFVIDVDHEAIAIK.E K.NLGIPVIGIVDTNSNPDNVDYVIPGNDDAIR.A K.EYAQSQANAQAKGEEAPAASEA.-	9.00	27.52
6s	Soluble proteome	Glutaminase/Asparaginase	Q6FAL6	21%	24.0	K.ELLTAR.K R.VPQGFVLR.N K..LLTALALTQTR.D K.NIVPTLTELQQR.G K.RFNNTSEFNIEIK.G R.NAEQPDDKYNWVVAHDLNPQK.A	8.53	37.92

7s	Soluble proteome	Soluble Pyridine Nucleotide Transhydrogenase	Q6FA50	23%	124.0	R.EQGVLIR.H K.IDIYHGR.A R.QTVSSIIR.Y R.VAALNGLNR.L K.ADAILWCNGR.S K.IPYEVGQASFR.H K.VIQQQVDTHSR.F K.LLSYLDDEIADALSYHLR.E K.YFIETTFNYPTMAEAYR.V K.TEQELTEEKIPYEVGQASFR.H	6.63	52.55
8s	Soluble proteome	Pseudouridine (ψ) Synthase (TruB)	Q6FDU7	30%	66.0	R.YMEEVIAAGR.V R.IEPGDEL.R.I R.KVQFQIEDEIR.R R.VLIYYKPEGEICSR.N R.LDINSTGLLLFTNDGELANR.L R.LMHPSNEIER.E R.VMGEVTPQIR.Q R.RLFESQGLK.V	9.79	35.98
9s	Soluble proteome	ATP Synthase Gamma Chain	Q6FFK1	23%	133.0	R.YMVERPVK.R R.VGYIIVSSDR.G K.VVQHVQQQR.E R.RAQERMAQGRPYAENMHR.V R.YIESMVYQGVINIACEQSAR.M	9.23	32.05

10s	Soluble proteome	Tolerance to colicins E2, E, A, and K, required for OM integrity (TolB)	B0VCX0	2%	61.0	<u>R.MNLPSEQGEVR.E</u>	8.81	46.40
14s	Soluble proteome	Putative uncharacterized protein (ACIAD2482)	Q6F9L4	3%	61.0	<u>K.ANDNQYLGQAALR.D</u>	6.20	39.51
15s	Soluble proteome	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (Ppiase)	Q6FFV0	11%	140	<u>K.DQLGYSYGYVMGR.T</u> <u>R.LLDGTVFDSSIAR.N</u>	9.05	24.92
16s	Soluble proteome	Phosphatidylserine decarboxylase	Q6F6W3	5%	40.0	<u>R.MVCLFDTELGR.M</u>	7.81	36.41
18s	Soluble proteome	Transcription elongation factor NusA	Q6FF41	2.4%	30.0	<u>K.LDMMLEEEYR.A + 2 Oxidation (M)</u>	4.51	55.30
20s	Soluble proteome	50S ribosomal protein L3	Q6F7R2	13.6%	279	<u>R.VTEAELEGR.E</u> <u>R.TQDATHGNSVSHR.V</u> <u>R.VTVQGLEIVSIDAER.S</u>	9.88	22.50
21s	Soluble proteome	tRNA 2-thiocytidine biosynthesis protein ttcA	Q6F8Q3	14%	168	<u>K.QPGFPEDVLPR.Y</u> <u>R.GSLYGFAQEIGATK.V</u> <u>R.LHSIFGALQNVSPSQLADR.D</u>	7.60	34.98
27s	Soluble proteome	Sulfate ABC transporter periplasmic substrate-binding protein (CysP)	Q6F9B2	3.9%	60.0	<u>K.DFLNVSYPTR.E</u>	9.53	36.88

1m	Membrane proteome	Transcription termination factor Rho	Q6F876	26%	288	K.IAEFMGLEGMAR.N R.SAAGSYLAGPDDIYVSPSQIR.R R.TGDTITGTIRPPK.E K.VNQINYDTPENSR.N R.GEVVASTFDESPAR.H K.DVVILLDSITR.L K.MDDVIYEEFK.G K.LLHPMDELAAMEFLDR.M	6.60	47.51
2m	Membrane proteome	Putative serine protease (DegP)	Q6F9B7	5%	113	R.SYLGVMLQDIDR.N K.MTQEELLQQQVPEILR.R	8.91	50.18
5m	Membrane proteome	D-ala-D-ala-carboxypeptidase; penicillin-binding protein 5	A3M7F9	11%	135	K.EFTFNGIK.Q K.YYPIYSEK.E K.GELTENEQVR.M R.NALLYTDPSVDGLK.T	7.02	38.1
7m	Membrane proteome	Sulfate adenylyl transferase (CysD)	Q6FDA0	21%	155	K.YQFDAAFGGAR.R K.QLEAESIHIRE.E K.LPFPLLHVDTGWK.F	7.96	18.5
9m	Membrane proteome	Protein involved in catabolism of external DNA	B2HZ48	8%	56	K.SGEFLTGIHR.L R.GLV MIDPPYELER.K	8.62	33.03
11m	Membrane proteome	Outer-membrane lipoproteins carrier protein (LolA)	Q6F8G3	9%	99	K.TVWIYD PDLQQAVR.Q K.TYYTLYPK.N	9.68	25.13

4m	Membrane proteome	Putative peptide import ATP-binding protein BMEII0863	Q8YBN6	2.7%	61	<u>HATVPPLASV</u>	9.36	36.71
10m	Membrane proteome	Xilose isomerase	Q64U20	2%	67	<u>EADSIETYEA</u>	5.07	49.02
12m	Membrane proteome	Phospholipid-binding protein with LysM domain	Q6FDT6	14%	164	<u>NADDIYPGKVL</u> <u>RHVAKVDD</u>	5.80	44.68
13m	Membrane proteome	Putative uncharacterized protein (peptide signal)	Q6FAQ8	17%	298	<u>KPVVIDAVINK</u> <u>SDFGIASYVPNV</u> <u>IGFNATTSE</u> <u>NSSVDVTI</u> <u>ITTEASVAK</u>	9.35	20.8
14m	Membrane proteome	Mobilization protein	Q6J2C2	2%	69	<u>TVIAHVEESH</u>	8.27	53.77