	Average Spectral Counts across all the proteins			**9.96**		**9.3**		**8.01**	**9.1**	**1.0**		**9.71**		**8.82**		**9.72**	**9.4**	**0.5**		
	Description	**# cys**	WT-1	**WT-1 normalized**	WT-2	**WT-2 normalized**	WT-3	**WT-3 normalized**	**average**	**sd**	dsbA-1	**dsbA-1 normalized**	dsbA-2	**dsbA-2 normalized**	dsbA-3	**dsbA-3 normalized**	**average**	**sd**	**ratio**	**p (t student)**
Periplasmic proteins																				
Q02LZ0	Putative binding protein component of ABC	**0**	185	**18.6**	142	**15.3**	176	**22.0**	**18.6**	**3**	250	**25.7**	289	**32.8**	306	**31.5**	**30.0**	**4**	**1.6**	**0.02**
Q02QE7	Putative ABC-type phosphate/phosphonate	**0**	120	**12.0**	94	**10.1**	91	**11.4**	**11.2**	**1**	136	**14.0**	187	**21.2**	194	**20.0**	**18.4**	**4**	**1.6**	**0.03**
Q02JH8	Glutaminase-asparaginase OS=Pseudomona	**0**	169	**17.0**	169	**18.2**	108	**13.5**	**16.2**	**2**	132	**13.6**	221	**25.1**	151	**15.5**	**18.1**	**6**	**1.1**	**0.65**
Q02JX6	Sulfate-binding protein of ABC transporter (	**0**	65	**6.5**	51	**5.5**	52	**6.5**	**6.2**	**1**	93	**9.6**	132	**15.0**	105	**10.8**	**11.8**	**3**	**1.9**	**0.03**
Q02JH9	Gamma-glutamyltranspeptidase OS=Pseud	**0**	47	**4.7**	49	**5.3**	36	**4.5**	**4.8**	**0**	71	**7.3**	75	**8.5**	73	**7.5**	**7.8**	**1**	**1.6**	**0.00**
Q02ID4	Protein tolB OS=Pseudomonas aeruginosa (	**0**	41	**4.1**	34	**3.7**	33	**4.1**	**4.0**	**0**	64	**6.6**	71	**8.0**	73	**7.5**	**7.4**	**1**	**1.9**	**0.00**
Q02UA2	Putative binding protein component of ABC	**0**	40	**4.0**	27	**2.9**	29	**3.6**	**3.5**	**1**	71	**7.3**	63	**7.1**	69	**7.1**	**7.2**	**0**	**2.0**	**0.00**
Q02IA4	Putative uncharacterized protein OS=Pseud	**0**	29	**2.9**	19	**2.0**	31	**3.9**	**2.9**	**1**	19	**2.0**	50	**5.7**	47	**4.8**	**4.2**	**2**	**1.4**	**0.38**
Q02UD4	Sulfate-binding protein OS=Pseudomonas a	**0**	22	**2.2**	15	**1.6**	21	**2.6**	**2.1**	**1**	26	**2.7**	27	**3.1**	41	**4.2**	**3.3**	**1**	**1.5**	**0.10**
Q02L09	Molybdate-binding periplasmic protein mod	**0**	20	**2.0**	13	**1.4**	10	**1.2**	**1.6**	**0**	16	**1.6**	18	**2.0**	20	**2.1**	**1.9**	**0**	**1.2**	**0.25**
Q02RT2	Putative TRAP-type C4-dicarboxylate transp	**0**	13	**1.3**	5	**0.5**	8	**1.0**	**0.9**	**0**	17	**1.8**	14	**1.6**	15	**1.5**	**1.6**	**0**	**1.7**	**0.04**
Q02ME5	Putative glycerophosphoryl diester phospho	**0**	11	**1.1**	7	**0.8**	7	**0.9**	**0.9**	**0**	15	**1.5**	16	**1.8**	15	**1.5**	**1.6**	**0**	**1.8**	**0.01**
Q02G61	Putative C4-dicarboxylate-binding protein O	**0**	21	**2.1**	11	**1.2**	12	**1.5**	**1.6**	**0**	9	**0.9**	14	**1.6**	12	**1.2**	**1.2**	**0**	**0.8**	**0.36**
Q02FW5	Putative periplasmic binding protein OS=Ps	**0**	5	**0.5**	4	**0.4**	4	**0.5**	**0.5**	**0**	11	**1.1**	5	**0.6**	11	**1.1**	**0.9**	**0**	**2.0**	**0.07**
Q02FT3	Putative uncharacterized protein OS=Pseud	**0**	9	**0.9**	4	**0.4**	3	**0.4**	**0.6**	**0**	5	**0.5**	11	**1.2**	5	**0.5**	**0.8**	**0**	**1.3**	**0.56**
Q02G64	Catalase OS=Pseudomonas aeruginosa (str	**0**	0	**0.0**	3	**0.3**	0	**0.0**	**0.1**	**0**	3	**0.3**	11	**1.2**	7	**0.7**	**0.8**	**0**	**7.1**	**0.09**
Q02SA0	Putative uncharacterized protein OS=Pseud	**0**	140	**14.1**	83	**8.9**	95	**11.9**	**11.6**	**3**	117	**12.0**	174	**19.7**	148	**15.2**	**15.7**	**4**	**1.3**	**0.20**
Q02Q40	Peptidyl-prolyl cis-trans isomerase OS=Pseu	**1**	125	**12.6**	8	**0.9**	84	**10.5**	**8.0**	**6**	130	**13.4**	166	**18.8**	142	**14.6**	**15.6**	**3**	**2.0**	**0.13**
Q02HR8	Serine protease MucD OS=Pseudomonas ae	**1**	129	**13.0**	147	**15.8**	111	**13.9**	**14.2**	**1**	73	**7.5**	188	**21.3**	135	**13.9**	**14.2**	**7**	**1.0**	**0.99**
Q02EU1	Putative amino acid ABC transporter, peripla	**1**	64	**6.4**	72	**7.7**	49	**6.1**	**6.8**	**1**	57	**5.9**	114	**12.9**	87	**9.0**	**9.2**	**4**	**1.4**	**0.30**
Q02FY7	Ferric iron-binding periplasmic protein HitA	**1**	53	**5.3**	41	**4.4**	32	**4.0**	**4.6**	**1**	56	**5.8**	52	**5.9**	90	**9.3**	**7.0**	**2**	**1.5**	**0.12**
Q02T21	Putative 3-carboxymuconate cyclase OS=Ps	**1**	22	**2.2**	14	**1.5**	20	**2.5**	**2.1**	**1**	39	**4.0**	40	**4.5**	27	**2.8**	**3.8**	**1**	**1.8**	**0.05**
Q02EJ8	Probable c4-dicarboxylate-binding protein C	**1**	38	**3.8**	23	**2.5**	23	**2.9**	**3.1**	**1**	27	**2.8**	36	**4.1**	36	**3.7**	**3.5**	**1**	**1.2**	**0.45**
Q02IA7	Putative uncharacterized protein OS=Pseud	**1**	3	**0.3**	3	**0.3**	1	**0.1**	**0.2**	**0**	6	**0.6**	9	**1.0**	13	**1.3**	**1.0**	**0**	**4.0**	**0.03**
Q02I29	D-alanyl-D-alanine-endopeptidase OS=Pseu	**1**	6	**0.6**	9	**1.0**	4	**0.5**	**0.7**	**0**	1	**0.1**	3	**0.3**	2	**0.2**	**0.2**	**0**	**0.3**	**0.04**
Q02L92	Binding protein component of ABC ribose tr	**1**	9	**0.9**	10	**1.1**	9	**1.1**	**1.0**	**0**	12	**1.2**	14	**1.6**	11	**1.1**	**1.3**	**0**	**1.3**	**0.14**
Q02U53	Probable gamma-glutamyltranspeptidase O	**1**	12	**1.2**	6	**0.6**	6	**0.7**	**0.9**	**0**	6	**0.6**	11	**1.2**	4	**0.4**	**0.8**	**0**	**0.9**	**0.74**
Q02U41	Putative zinc protease OS=Pseudomonas ae	**1**	4	**0.4**	4	**0.4**	5	**0.6**	**0.5**	**0**	3	**0.3**	14	**1.6**	3	**0.3**	**0.7**	**1**	**1.5**	**0.59**
Q02P18	Acyl-CoA thioesterase I OS=Pseudomonas a	**1**	22	**2.2**	19	**2.0**	13	**1.6**	**2.0**	**0**	26	**2.7**	26	**2.9**	37	**3.8**	**3.1**	**1**	**1.6**	**0.04**
Q02IP1	Branched-chain amino acid transport protei	**2**	296	**29.7**	264	**28.4**	278	**34.7**	**30.9**	**3**	334	**34.4**	356	**40.4**	448	**46.1**	**40.3**	**6**	**1.3**	**0.07**
Q02I48	Arginine/ornithine binding protein AotJ OS=	**2**	245	**24.6**	172	**18.5**	180	**22.5**	**21.9**	**3**	286	**29.5**	272	**30.8**	323	**33.2**	**31.2**	**2**	**1.4**	**0.01**
Q02JI3	Putative binding protein component of ABC	**2**	269	**27.0**	195	**21.0**	140	**17.5**	**21.8**	**5**	187	**19.3**	200	**22.7**	272	**28.0**	**23.3**	**4**	**1.1**	**0.71**
Q02TG9	Peptidyl-prolyl cis-trans isomerase OS=Pseu	**2**	94	**9.4**	72	**7.7**	84	**10.5**	**9.2**	**1**	107	**11.0**	163	**18.5**	154	**15.8**	**15.1**	**4**	**1.6**	**0.06**
Q02TP7	Nitrite reductase OS=Pseudomonas aerugin	**2**	281	**28.2**	214	**23.0**	209	**26.1**	**25.8**	**3**	47	**4.8**	272	**30.8**	92	**9.5**	**15.0**	**14**	**0.6**	**0.26**
Q02UB7	Polyamine transport protein OS=Pseudomo	**2**	93	**9.3**	99	**10.6**	71	**8.9**	**9.6**	**1**	72	**7.4**	102	**11.6**	115	**11.8**	**10.3**	**2**	**1.1**	**0.69**
Q02EL2	Putative ABC transporter, periplasmic aminc	**2**	64	**6.4**	52	**5.6**	40	**5.0**	**5.7**	**1**	86	**8.9**	87	**9.9**	87	**9.0**	**9.2**	**1**	**1.6**	**0.00**
Q02KV3	Putative binding protein component of ABC	**2**	44	**4.4**	51	**5.5**	35	**4.4**	**4.8**	**1**	41	**4.2**	71	**8.0**	50	**5.1**	**5.8**	**2**	**1.2**	**0.43**
Q02MS5	Thiol:disulfide interchange protein DsbG OS	**2**	23	**2.3**	16	**1.7**	18	**2.2**	**2.1**	**0**	14	**1.4**	30	**3.4**	26	**2.7**	**2.5**	**1**	**1.2**	**0.53**
Q02EE7	Putative iron ABC transporter, periplasmic ir	**2**	3	**0.3**	7	**0.8**	5	**0.6**	**0.6**	**0**	17	**1.8**	18	**2.0**	24	**2.5**	**2.1**	**0**	**3.7**	**0.00**
Q02R82	Polyamine ABC transporter protein OS=Pse	**2**	16	**1.6**	9	**1.0**	10	**1.2**	**1.3**	**0**	17	**1.8**	14	**1.6**	27	**2.8**	**2.0**	**1**	**1.6**	**0.14**
Q02TP8	Cytochrome c-551 OS=Pseudomonas aerug	**2**	20	**2.0**	17	**1.8**	21	**2.6**	**2.2**	**0**	14	**1.4**	23	**2.6**	16	**1.6**	**1.9**	**1**	**0.9**	**0.59**
Q02UB6	Polyamine transport protein OS=Pseudomo	**2**	56	**5.6**	36	**3.9**	28	**3.5**	**4.3**	**1**	14	**1.4**	23	**2.6**	14	**1.4**	**1.8**	**1**	**0.4**	**0.03**
Q02KL7	Periplasmic beta-glucosidase OS=Pseudom	**2**	13	**1.3**	14	**1.5**	12	**1.5**	**1.4**	**0**	9	**0.9**	22	**2.5**	12	**1.2**	**1.6**	**1**	**1.1**	**0.82**
Q02EI0	Putative periplasmic monofunctional chorisr	**2**	11	**1.1**	9	**1.0**	12	**1.5**	**1.2**	**0**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0**	**0.0**	**0.00**
Q02S25	Putative amino acid ABC transporter OS=Ps	**2**	16	**1.6**	15	**1.6**	13	**1.6**	**1.6**	**0**	8	**0.8**	17	**1.9**	9	**0.9**	**1.2**	**1**	**0.8**	**0.33**
Q02SS4	Cephalosporinase OS=Pseudomonas aerugi	**2**	4	**0.4**	5	**0.5**	9	**1.1**	**0.7**	**0**	9	**0.9**	14	**1.6**	10	**1.0**	**1.2**	**0**	**1.7**	**0.18**
Q02ET5	Putative binding protein component of ABC	**2**	14	**1.4**	9	**1.0**	8	**1.0**	**1.1**	**0**	19	**2.0**	0	**0.0**	12	**1.2**	**1.1**	**1**	**0.9**	**0.92**
Q02UC2	Probable periplasmic polyamine binding pro	**2**	11	**1.1**	9	**1.0**	8	**1.0**	**1.0**	**0**	4	**0.4**	7	**0.8**	6	**0.6**	**0.6**	**0**	**0.6**	**0.02**
Q02TQ7	Putative c-type cytochrome OS=Pseudomor	**2**	31	**3.1**	27	**2.9**	25	**3.1**	**3.0**	**0**	15	**1.5**	30	**3.4**	21	**2.2**	**2.4**	**1**	**0.8**	**0.29**
Q02F96	Azurin OS=Pseudomonas aeruginosa (strain	**3**	85	**8.5**	102	**11.0**	43	**5.4**	**8.3**	**3**	45	**4.6**	91	**10.3**	102	**10.5**	**8.5**	**3**	**1.0**	**0.94**
Q02MY1	Thiol peroxidase OS=Pseudomonas aerugin	**3**	23	**2.3**	24	**2.6**	16	**2.0**	**2.3**	**0**	20	**2.1**	18	**2.0**	23	**2.4**	**2.2**	**0**	**0.9**	**0.52**
Q02HR6	Negative regulator for alginate biosynthesis	**3**	6	**0.6**	9	**1.0**	4	**0.5**	**0.7**	**0**	13	**1.3**	18	**2.0**	18	**1.9**	**1.7**	**0**	**2.5**	**0.01**
Q02QW4	Cyclohexadienyl dehydratase OS=Pseudom	**3**	16	**1.6**	11	**1.2**	10	**1.2**	**1.3**	**0**	1	**0.1**	8	**0.9**	3	**0.3**	**0.4**	**0**	**0.3**	**0.03**
Q02N84	Putative periplasmic spermidine/putrescine-	**3**	23	**2.3**	16	**1.7**	9	**1.1**	**1.7**	**1**	1	**0.1**	5	**0.6**	4	**0.4**	**0.4**	**0**	**0.2**	**0.02**
Q02TF9	Putative binding protein component of ABC	**3**	18	**1.8**	16	**1.7**	9	**1.1**	**1.6**	**0**	2	**0.2**	1	**0.1**	2	**0.2**	**0.2**	**0**	**0.1**	**0.00**
Q02PI4	Putative soluble lytic transglycosylase OS=F	**3**	4	**0.4**	10	**1.1**	4	**0.5**	**0.7**	**0**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0**	**0.0**	**0.04**
Q02FA5	Putative binding protein component of ABC	**3**	4	**0.4**	4	**0.4**	4	**0.5**	**0.4**	**0**	6	**0.6**	7	**0.8**	6	**0.6**	**0.7**	**0**	**1.5**	**0.02**
Q02DL1	Putative zinc ABC transporter, periplasmic z	**3**	8	**0.8**	3	**0.3**	6	**0.7**	**0.6**	**0**	3	**0.3**	1	**0.1**	5	**0.5**	**0.3**	**0**	**0.5**	**0.18**
Q02PZ6	Putative binding protein component of ABC	**4**	197	**19.8**	173	**18.6**	152	**19.0**	**19.1**	**1**	148	**15.2**	254	**28.8**	176	**18.1**	**20.7**	**7**	**1.1**	**0.72**
Q02G90	Cytochrome c551 peroxidase OS=Pseudom	**4**	94	**9.4**	79	**8.5**	60	**7.5**	**8.5**	**1**	28	**2.9**	105	**11.9**	36	**3.7**	**6.2**	**5**	**0.7**	**0.48**
Q02GU1	Putative binding protein component of ABC	**4**	67	**6.7**	67	**7.2**	47	**5.9**	**6.6**	**1**	25	**2.6**	40	**4.5**	41	**4.2**	**3.8**	**1**	**0.6**	**0.02**
Q02GU5	Putative binding protein component of ABC	**4**	62	**6.2**	66	**7.1**	46	**5.7**	**6.4**	**1**	25	**2.6**	32	**3.6**	38	**3.9**	**3.4**	**1**	**0.5**	**0.01**
Q02DL9	Cytochrome c4 OS=Pseudomonas aeruginos	**4**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0**	3	**0.3**	6	**0.7**	9	**0.9**	**0.6**	**0**		**0.02**
Q02DY4	Putative glycine betaine/L-proline ABC trans	**4**	23	**2.3**	18	**1.9**	10	**1.2**	**1.8**	**1**	3	**0.3**	6	**0.7**	6	**0.6**	**0.5**	**0**	**0.3**	**0.02**
Q02GU4	Putative binding protein component of ABC	**4**	13	**1.3**	12	**1.3**	12	**1.5**	**1.4**	**0**	5	**0.5**	7	**0.8**	3	**0.3**	**0.5**	**0**	**0.4**	**0.01**

Q02E45	Putative binding protein component of ABC	4	24	2.4	13	1.4	12	1.5	1.8	1	1	0.1	8	0.9	2	0.2	0.4	0	0.2	0.03
Q02ER3	Putative ABC transporter, periplasmic substr	4	11	1.1	8	0.9	5	0.6	0.9	0	1	0.1	1	0.1	0	0.0	0.1	0	0.1	0.01
Q02RL0	Thiol:disulfide interchange protein DsbC OS	4	5	0.5	6	0.6	5	0.6	0.6	0	6	0.6	5	0.6	8	0.8	0.7	0	1.1	0.43
Q02JC8	Glutathione peroxidase OS=Pseudomonas a	4	8	0.8	7	0.8	1	0.1	0.6	0	4	0.4	9	1.0	3	0.3	0.6	0	1.0	0.95
Q02NB6	Monomeric isocitrate dehydrogenase OS=P	4	32	3.2	58	6.2	42	5.2	4.9	2	21	2.2	33	3.7	41	4.2	3.4	1	0.7	0.23
Q02GT9	Putative binding protein component of ABC	5	35	3.5	33	3.5	31	3.9	3.6	0	7	0.7	10	1.1	10	1.0	1.0	0	0.3	0.00
Q02NA8	Thioredoxin reductase OS=Pseudomonas a	5	9	0.9	14	1.5	11	1.4	1.3	0	11	1.1	10	1.1	15	1.5	1.3	0	1.0	0.97
Q02E40	Phosphomannomutase AlgC OS=Pseudomo	7	13	1.3	23	2.5	15	1.9	1.9	1	20	2.1	23	2.6	23	2.4	2.3	0	1.2	0.28
Q02QM9	Nitrous-oxide reductase OS=Pseudomonas	11	102	10.2	73	7.8	62	7.7	8.6	1	7	0.7	74	8.4	18	1.9	3.7	4	0.4	0.12
Q02T53	Catalase OS=Pseudomonas aeruginosa (str	1	81	8.1	110	11.8	70	8.7	9.6	2	49	5.0	69	7.8	70	7.2	6.7	1	0.7	0.11
Outer membrane proteins																				
Q02IZ8	PhoP/Q and low Mg2+ inducible outer mem	0	8	0.8	10	1.1	5	0.6	0.8	0	9	0.9	11	1.2	31	3.2	1.8	1	2.1	0.26
Q02IC0	Basic amino acid, basic peptide and imipen	0	19	1.9	17	1.8	10	1.2	1.7	0	11	1.1	6	0.7	23	2.4	1.4	1	0.8	0.65
Q02JX7	Putative mucoidy inhibitor A OS=Pseudomo	0	3	0.3	4	0.4	4	0.5	0.4	0	3	0.3	15	1.7	6	0.6	0.9	1	2.1	0.34
Q02SN3	Outer membrane protein OprG OS=Pseudo	0	13	1.3	5	0.5	6	0.7	0.9	0	3	0.3	9	1.0	7	0.7	0.7	0	0.8	0.59
Q02TD7	Putative tail length determinator protein OS	0	12	1.2	8	0.9	7	0.9	1.0	0	3	0.3	6	0.7	7	0.7	0.6	0	0.6	0.08
Q02IM0	Putative uncharacterized protein OS=Pseud	1	12	1.2	7	0.8	6	0.7	0.9	0	12	1.2	14	1.6	6	0.6	1.1	0	1.3	0.49
Q02IH6	Putative lipoprotein OS=Pseudomonas aeru	1	3	0.3	1	0.1	3	0.4	0.3	0	2	0.2	14	1.6	9	0.9	0.9	1	3.5	0.19
Q02TY5	Major intrinsic multiple antibiotic resistance	1	22	2.2	24	2.6	11	1.4	2.1	1	4	0.4	43	4.9	17	1.7	2.3	2	1.1	0.84
Q02G51	Putative uncharacterized protein OS=Pseud	2	0	0.0	10	1.1	8	1.0	0.7	1	3	0.3	90	10.2	60	6.2	5.6	5	8.0	0.17
Q02EX7	Type 4 fimbrial biogenesis outer membrane	2	27	2.7	32	3.4	22	2.7	3.0	0	22	2.3	27	3.1	26	2.7	2.7	0	0.9	0.42
Q02RC0	Putative outer membrane antigen OS=Pseu	2	1	0.1	2	0.2	1	0.1	0.1	0	6	0.6	14	1.6	8	0.8	1.0	1	6.9	0.04
Q02KR8	Major porin and structural outer membrane	4	60	6.0	43	4.6	33	4.1	4.9	1	23	2.4	59	6.7	54	5.6	4.9	2	1.0	0.97
Q02L18	Staphylolytic protease preproenzyme LasA (	4	23	2.3	27	2.9	17	2.1	2.4	0	2	0.2	5	0.6	5	0.5	0.4	0	0.2	0.00
Q02TC1	Putative phage-related protein, tail compon	4	8	0.8	7	0.8	8	1.0	0.9	0	2	0.2	4	0.5	3	0.3	0.3	0	0.4	0.01
Q02LJ1	Putative cysteine proteases OS=Pseudomor	8	40	4.0	23	2.5	22	2.7	3.1	1	11	1.1	27	3.1	16	1.6	1.9	1	0.6	0.20
Q02DR8	Putative uncharacterized protein OS=Pseud	8	33	3.3	31	3.3	23	2.9	3.2	0	1	0.1	3	0.3	1	0.1	0.2	0	0.1	0.00
Q02GC2	Type 4 fimbrial biogenesis protein PilY1 OS=	11	1	0.1	2	0.2	0	0.0	0.1	0	17	1.8	40	4.5	18	1.9	2.7	2	25.8	0.05
Inner membrane proteins																				
Q02DK4	Putative ABC transporter, periplasmic bindir	0	165	16.6	105	11.3	143	17.9	15.2	3	174	17.9	265	30.0	240	24.7	24.2	6	1.6	0.09
Q02Q88	Periplasmic tail-specific protease OS=Pseud	0	153	15.4	137	14.7	108	13.5	14.5	1	119	12.3	186	21.1	172	17.7	17.0	4	1.2	0.40
Q02GV2	Putative membrane protein OS=Pseudomor	0	5	0.5	7	0.8	6	0.7	0.7	0	34	3.5	87	9.9	50	5.1	6.2	3	9.2	0.04
Q02RB9	Putative outer membrane protein OmpH OS	0	29	2.9	13	1.4	7	0.9	1.7	1	23	2.4	27	3.1	12	1.2	2.2	1	1.3	0.58
Q02UB0	Putative uncharacterized protein OS=Pseud	0	26	2.6	13	1.4	9	1.1	1.7	1	19	2.0	25	2.8	8	0.8	1.9	1	1.1	0.84
Q02G23	Putative pili assembly chaperone OS=Pseuc	0	5	0.5	6	0.6	4	0.5	0.5	0	12	1.2	7	0.8	13	1.3	1.1	0	2.0	0.03
Q02UQ2	Putative chemotaxis transducer OS=Pseudo	0	2	0.2	10	1.1	4	0.5	0.6	0	0	0.0	0	0.0	0	0.0	0.0	0	0.0	0.08
Q02E74	Nitrogen regulatory protein PII OS=Pseudo	0	13	1.3	17	1.8	8	1.0	1.4	0	15	1.5	15	1.7	10	1.0	1.4	0	1.0	0.89
Q02SG8	Soluble lytic transglycosylase B OS=Pseudo	0	17	1.7	13	1.4	5	0.6	1.2	1	9	0.9	15	1.7	12	1.2	1.3	0	1.0	0.92
Q02SF1	Putative Mg2+ and Co2+ transporter CorC	0	7	0.7	8	0.9	2	0.2	0.6	0	3	0.3	3	0.3	4	0.4	0.4	0	0.6	0.25
Q02IH0	Putative Zn-dependent protease OS=Pseud	1	26	2.6	12	1.3	15	1.9	1.9	1	18	1.9	30	3.4	27	2.8	2.7	1	1.4	0.27
Q02H96	Putative uncharacterized protein OS=Pseud	1	18	1.8	8	0.9	8	1.0	1.2	1	16	1.6	22	2.5	11	1.1	1.8	1	1.4	0.34
Q02EN2	Putative carboxyl-terminal protease OS=Ps	1	11	1.1	12	1.3	7	0.9	1.1	0	7	0.7	12	1.4	10	1.0	1.0	0	1.0	0.82
Q02SG0	Putative murein transglycosylase OS=Pseuc	2	26	2.6	20	2.2	20	2.5	2.4	0	25	2.6	33	3.7	31	3.2	3.2	1	1.3	0.11
Q02DZ3	Putative phosphate ABC transporter, peripla	2	17	1.7	10	1.1	6	0.7	1.2	0	20	2.1	21	2.4	19	2.0	2.1	0	1.8	0.04
Q02IZ1	Probable transglycolase OS=Pseudomonas	2	12	1.2	11	1.2	10	1.2	1.2	0	1	0.1	5	0.6	7	0.7	0.5	0	0.4	0.02
Q02MY7	Putative uncharacterized protein OS=Pseud	2	21	2.1	11	1.2	10	1.2	1.5	1	2	0.2	7	0.8	19	2.0	1.0	1	0.7	0.42
Q02QG5	Cytochrome P450 OS=Pseudomonas aerugi	2	5	0.5	4	0.4	3	0.4	0.4	0	6	0.6	7	0.8	14	1.4	1.0	0	2.2	0.11
Q02EP9	GTP-binding protein TypA/BipA OS=Pseudo	2	12	1.2	9	1.0	8	1.0	1.1	0	6	0.6	4	0.5	12	1.2	0.8	0	0.7	0.31
Q02S55	Putative binding protein component of ABC	2	3	0.3	3	0.3	1	0.1	0.2	0	4	0.4	8	0.9	5	0.5	0.6	0	2.4	0.09
Q02L27	Putative exported oxidoreductase OS=Pseu	3	14	1.4	9	1.0	14	1.7	1.4	0	9	0.9	14	1.6	8	0.8	1.1	0	0.8	0.47
Q02FV9	Putative metal-binding protein OS=Pseudor	4	1	0.1	2	0.2	0	0.0	0.1	0	28	2.9	44	5.0	32	3.3	3.7	1	35.4	0.01
Q02QX0	Putative uncharacterized protein mrp OS=P	4	10	1.0	20	2.2	8	1.0	1.4	1	3	0.3	10	1.1	14	1.4	1.0	1	0.7	0.45
Q02PC8	3-oxoacyl-[acyl-carrier-protein] synthase 2	5	9	0.9	18	1.9	15	1.9	1.6	1	15	1.5	10	1.1	18	1.9	1.5	0	1.0	0.89
Q02UT9	Alkyl hydroperoxide reductase subunit F OS	5	4	0.4	6	0.6	5	0.6	0.6	0	1	0.1	3	0.3	5	0.5	0.3	0	0.6	0.17
Q02Q87	Putative quinone oxidoreductase OS=Pseuc	6	4	0.4	7	0.8	7	0.9	0.7	0	4	0.4	2	0.2	8	0.8	0.5	0	0.7	0.45
Q02MH2	Putative aldehyde dehydrogenase OS=Pseu	7	3	0.3	5	0.5	5	0.6	0.5	0	8	0.8	14	1.6	12	1.2	1.2	0	2.5	0.04
Q02F59	Putative uncharacterized protein fimX OS=F	8	9	0.9	4	0.4	3	0.4	0.6	0	2	0.2	1	0.1	4	0.4	0.2	0	0.4	0.16
Q02K68	Succinate dehydrogenase (A subunit) OS=F	10	11	1.1	13	1.4	15	1.9	1.5	0	3	0.3	11	1.2	24	2.5	1.3	1	0.9	0.87
Q02K69	Succinate dehydrogenase (B subunit) OS=F	11	5	0.5	8	0.9	6	0.7	0.7	0	5	0.5	9	1.0	17	1.7	1.1	1	1.6	0.35
Q02QG1	Putative non-ribosomal peptide synthetase	12	7	0.7	23	2.5	12	1.5	1.6	1	13	1.3	29	3.3	52	5.3	3.3	2	2.1	0.24
Q02IG1	Probable coenzyme A ligase OS=Pseudomo	12	9	0.9	18	1.9	11	1.4	1.4	1	5	0.5	16	1.8	21	2.2	1.5	1	1.1	0.88
Extracellular proteins																				
Q02IR1	Flagellar capping protein FliD OS=Pseudom	0	6	0.6	8	0.9	16	2.0	1.2	1	63	6.5	58	6.6	69	7.1	6.7	0	5.8	0.00
Q02IQ9	Flagellin type B OS=Pseudomonas aeruginc	0	41	4.1	39	4.2	14	1.7	3.4	1	25	2.6	30	3.4	34	3.5	3.2	1	0.9	0.83
Q02GL8	Pyocin S5 OS=Pseudomonas aeruginosa (st	0	36	3.6	34	3.7	29	3.6	3.6	0	10	1.0	29	3.3	18	1.9	2.1	1	0.6	0.08
Q02IQ3	Flagellar hook-associated protein 1 FlgK OS	0	1	0.1	0	0.0	0	0.0	0.0	0	12	1.2	18	2.0	27	2.8	2.0	1	60.3	0.01
Q02IF1	ExoU OS=Pseudomonas aeruginosa (strain	0	14	1.4	25	2.7	25	3.1	2.4	1	0	0.0	5	0.6	1	0.1	0.2	0	0.1	0.02
Q02KJ9	Translocator protein PopB OS=Pseudomona	0	8	0.8	18	1.9	12	1.5	1.4	1	0	0.0	4	0.5	1	0.1	0.2	0	0.1	0.03
Q02KK0	Translocator outer membrane protein PopD	0	4	0.4	11	1.2	7	0.9	0.8	0	0	0.0	1	0.1	1	0.1	0.1	0	0.1	0.03
Q02KJ7	Type III secretion protein PcrV OS=Pseudo	0	3	0.3	7	0.8	6	0.7	0.6	0	0	0.0	1	0.1	0	0.0	0.0	0	0.1	0.02

Q02GG5	Putative uncharacterized protein OS=Pseud	0	17	1.7	26	2.8	12	1.5	2.0	1	15	1.5	17	1.9	8	0.8	1.4	1	0.7	0.33
Q02UZ4	Putative uncharacterized protein OS=Pseud	1	1	0.1	3	0.3	4	0.5	0.3	0	17	1.8	17	1.9	26	2.7	2.1	0	6.9	0.00
Q02M97	Chitinase OS=Pseudomonas aeruginosa (str	1	24	2.4	28	3.0	17	2.1	2.5	0	12	1.2	13	1.5	8	0.8	1.2	0	0.5	0.01
Q02IX1	Pyocin killing protein OS=Pseudomonas aer	1	22	2.2	27	2.9	11	1.4	2.2	1	5	0.5	10	1.1	11	1.1	0.9	0	0.4	0.06
Q02E95	Secreted protein Hcp OS=Pseudomonas aer	1	0	0.0	1	0.1	0	0.0	0.0	0	3	0.3	1	0.1	11	1.1	0.5	1	14.5	0.20
Q02P97	Putative hydrolase OS=Pseudomonas aerug	3	7	0.7	8	0.9	2	0.2	0.6	0	3	0.3	6	0.7	4	0.4	0.5	0	0.8	0.56
Q02RJ6	Elastase LasB OS=Pseudomonas aeruginosa	4	93	9.3	89	9.6	44	5.5	8.1	2	48	4.9	70	7.9	69	7.1	6.7	2	0.8	0.41
Q02TE3	Putative tail fiber protein OS=Pseudomonas	5	11	1.1	20	2.2	9	1.1	1.5	1	4	0.4	11	1.2	11	1.1	0.9	0	0.6	0.29
Q02PA2	Putative aminopeptidase OS=Pseudomonas	6	33	3.3	42	4.5	17	2.1	3.3	1	3	0.3	3	0.3	3	0.3	0.3	0	0.1	0.01
Q02SZ7	Pvds-regulated endoprotease, lysyl class OS	7	9	0.9	13	1.4	13	1.6	1.3	0	8	0.8	10	1.1	5	0.5	0.8	0	0.6	0.16
Q02I11	Chitin-binding protein CbpD OS=Pseudomo	8	173	17.4	122	13.1	73	9.1	13.2	4	24	2.5	32	3.6	25	2.6	2.9	1	0.2	0.01
Q02TJ3	Putative uncharacterized protein OS=Pseud	9	28	2.8	19	2.0	22	2.7	2.5	0	0	0.0	2	0.2	0	0.0	0.1	0	0.0	0.00
Non cytoplasmic proteins																				
Q02RZ5	Putative ABC-type transport protein, peripla	0	106	10.6	49	5.3	44	5.5	7.1	3	107	11.0	106	12.0	103	10.6	11.2	1	1.6	0.09
Q02GY8	Putative toluene tolerance protein OS=Pseu	0	58	5.8	33	3.5	40	5.0	4.8	1	54	5.6	80	9.1	58	6.0	6.9	2	1.4	0.18
Q02PB4	Electron transfer flavoprotein alpha-subunit	0	63	6.3	93	10.0	57	7.1	7.8	2	56	5.8	61	6.9	46	4.7	5.8	1	0.7	0.19
Q02V61	Putative lysin domain OS=Pseudomonas ae	0	20	2.0	15	1.6	24	3.0	2.2	1	43	4.4	68	7.7	49	5.0	5.7	2	2.6	0.03
Q02UA7	Putative uncharacterized protein OS=Pseud	0	28	2.8	21	2.3	18	2.2	2.4	0	40	4.1	48	5.4	51	5.2	4.9	1	2.0	0.01
Q02NC5	Putative secretion system protein OS=Pseu	0	28	2.8	27	2.9	13	1.6	2.4	1	48	4.9	51	5.8	31	3.2	4.6	1	1.9	0.06
Q02S91	Putative uncharacterized protein OS=Pseud	0	36	3.6	32	3.4	22	2.7	3.3	0	41	4.2	43	4.9	37	3.8	4.3	1	1.3	0.06
Q02Q81	Putative ABC transporter, periplasmic substr	0	11	1.1	11	1.2	10	1.2	1.2	0	24	2.5	25	2.8	16	1.6	2.3	1	2.0	0.03
Q02GQ6	Putative uncharacterized protein OS=Pseud	0	13	1.3	6	0.6	6	0.7	0.9	0	19	2.0	20	2.3	13	1.3	1.9	0	2.1	0.05
Q02PP4	Putative uncharacterized protein OS=Pseud	0	13	1.3	14	1.5	13	1.6	1.5	0	13	1.3	18	2.0	16	1.6	1.7	0	1.1	0.43
Q02IS9	Putative dehydrogenase OS=Pseudomonas	0	2	0.2	2	0.2	0	0.0	0.1	0	6	0.6	11	1.2	5	0.5	0.8	0	5.7	0.05
Q02DG3	Putative periplasmic transport protein OS=P	0	14	1.4	13	1.4	11	1.4	1.4	0	13	1.3	13	1.5	14	1.4	1.4	0	1.0	0.58
Q02EM8	Putative ABC-type amino acid transport pro	0	10	1.0	8	0.9	9	1.1	1.0	0	9	0.9	12	1.4	13	1.3	1.2	0	1.2	0.26
Q02RT9	Putative membrane or periplasmic protein C	0	6	0.6	4	0.4	0	0.0	0.3	0	7	0.7	8	0.9	5	0.5	0.7	0	2.1	0.16
Q02SA7	Probable ABC-type taurine transporter, peri	0	9	0.9	1	0.1	3	0.4	0.5	0	6	0.6	4	0.5	9	0.9	0.7	0	1.4	0.49
Q02I15	Putative uncharacterized protein OS=Pseud	0	3	0.3	5	0.5	3	0.4	0.4	0	3	0.3	9	1.0	5	0.5	0.6	0	1.5	0.40
Q02GY1	Putative uncharacterized protein OS=Pseud	0	2	0.2	3	0.3	5	0.6	0.4	0	3	0.3	9	1.0	5	0.5	0.6	0	1.6	0.40
Q02NU4	Carboxypeptidase G2 OS=Pseudomonas ae	0	6	0.6	3	0.3	4	0.5	0.5	0	5	0.5	6	0.7	4	0.4	0.5	0	1.1	0.62
Q02TG4	Putative uncharacterized protein OS=Pseud	0	3	0.3	3	0.3	1	0.1	0.2	0	3	0.3	10	1.1	2	0.2	0.5	1	2.2	0.37
Q02U25	Putative uncharacterized protein OS=Pseud	1	57	5.7	43	4.6	40	5.0	5.1	1	56	5.8	74	8.4	59	6.1	6.7	1	1.3	0.14
Q02GU6	Putative uncharacterized protein OS=Pseud	1	48	4.8	60	6.5	32	4.0	5.1	1	37	3.8	76	8.6	54	5.6	6.0	2	1.2	0.60
Q02P16	Putative ErfK/YbiS/YcfS/YnhG family protein	1	28	2.8	24	2.6	33	4.1	3.2	1	40	4.1	54	6.1	38	3.9	4.7	1	1.5	0.14
Q02RE7	Putative uncharacterized protein OS=Pseud	1	18	1.8	11	1.2	8	1.0	1.3	0	27	2.8	29	3.3	25	2.6	2.9	0	2.2	0.01
Q02UT4	Putative nucleoside 2-deoxyribosyltransfera	1	14	1.4	10	1.1	15	1.9	1.5	0	17	1.8	36	4.1	18	1.9	2.6	1	1.8	0.24
Q02PG7	Putative uncharacterized protein OS=Pseud	1	28	2.8	14	1.5	9	1.1	1.8	1	18	1.9	29	3.3	21	2.2	2.4	1	1.3	0.41
Q02MP9	Putative uncharacterized protein OS=Pseud	1	12	1.2	15	1.6	16	2.0	1.6	0	19	2.0	25	2.8	13	1.3	2.0	1	1.3	0.42
Q02TU5	Putative streptogramin lyase OS=Pseudomo	1	23	2.3	9	1.0	8	1.0	1.4	1	20	2.1	19	2.2	14	1.4	1.9	0	1.3	0.41
Q02HN1	Putative uncharacterized protein OS=Pseud	1	9	0.9	6	0.6	6	0.7	0.8	0	11	1.1	14	1.6	16	1.6	1.5	0	1.9	0.02
Q02HA1	Putative membrane protein OS=Pseudomon	1	7	0.7	2	0.2	2	0.2	0.4	0	4	0.4	4	0.5	9	0.9	0.6	0	1.5	0.41
Q02G99	Putative uncharacterized protein OS=Pseud	2	0	0.0	0	0.0	0	0.0	0.0	0	39	4.0	47	5.3	37	3.8	4.4	1		0.00
Q02G44	Putative lipoprotein OS=Pseudomonas aeru	2	16	1.6	10	1.1	9	1.1	1.3	0	7	0.7	27	3.1	18	1.9	1.9	1	1.5	0.43
Q02KA9	Putative uncharacterized protein OS=Pseud	2	10	1.0	12	1.3	11	1.4	1.2	0	12	1.2	20	2.3	16	1.6	1.7	1	1.4	0.20
Q02K64	Putative uncharacterized protein OS=Pseud	2	30	3.0	20	2.2	32	4.0	3.1	1	8	0.8	13	1.5	19	2.0	1.4	1	0.5	0.06
Q02G70	Putative uncharacterized protein OS=Pseud	2	0	0.0	2	0.2	1	0.1	0.1	0	8	0.8	17	1.9	8	0.8	1.2	1	10.5	0.04
Q02IK9	Putative uncharacterized protein OS=Pseud	2	10	1.0	6	0.6	7	0.9	0.8	0	0	0.0	1	0.1	0	0.0	0.0	0	0.0	0.00
Q02GG4	Putative uncharacterized protein OS=Pseud	2	11	1.1	6	0.6	4	0.5	0.7	0	0	0.0	0	0.0	1	0.1	0.0	0	0.0	0.02
Q02RU1	Putative peptidase OS=Pseudomonas aerug	2	8	0.8	4	0.4	4	0.5	0.6	0	4	0.4	9	1.0	6	0.6	0.7	0	1.2	0.64
Q02HQ5	Putative uncharacterized protein OS=Pseud	2	8	0.8	4	0.4	7	0.9	0.7	0	3	0.3	9	1.0	6	0.6	0.6	0	0.9	0.84
Q02JI5	Putative short-chain dehydrogenase OS=Ps	2	2	0.2	9	1.0	5	0.6	0.6	0	6	0.6	5	0.6	4	0.4	0.5	0	0.9	0.79
Q02SK2	Putative uncharacterized protein OS=Pseud	2	4	0.4	6	0.6	5	0.6	0.6	0	4	0.4	5	0.6	5	0.5	0.5	0	0.9	0.55
Q02IY6	Putative uncharacterized protein OS=Pseud	3	16	1.6	15	1.6	14	1.7	1.7	0	27	2.8	26	2.9	24	2.5	2.7	0	1.7	0.00
Q02PL9	Putative carboxypeptidase OS=Pseudomona	3	19	1.9	17	1.8	12	1.5	1.7	0	0	0.0	1	0.1	2	0.2	0.1	0	0.1	0.00
Q02FT6	Putative uncharacterized protein OS=Pseud	3	13	1.3	6	0.6	2	0.2	0.7	1	0	0.0	1	0.1	4	0.4	0.2	0	0.2	0.17
Q02PL8	Putative hydrolase OS=Pseudomonas aerug	4	23	2.3	18	1.9	21	2.6	2.3	0	2	0.2	8	0.9	7	0.7	0.6	0	0.3	0.00
Q02P64	Putative uncharacterized protein OS=Pseud	4	8	0.8	6	0.6	5	0.6	0.7	0	0	0.0	1	0.1	2	0.2	0.1	0	0.2	0.00
Q02H56	Putative uncharacterized protein OS=Pseud	6	12	1.2	7	0.8	5	0.6	0.9	0	0	0.0	1	0.1	2	0.2	0.1	0	0.1	0.02
Q02KZ1	Fatty acyl cis-trans isomerase OS=Pseudom	8	10	1.0	7	0.8	13	1.6	1.1	0	0	0.0	1	0.1	2	0.2	0.1	0	0.1	0.02