	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)
	Average Spectral Counts across all the proteins			**9.96**		**9.3**		**8.01**				**9.71**		**8.82**		**9.72**				
Inner membrane proteins																				
Q02UQ2	Putative chemotaxis transducer OS=Pseudomonas ae	0	2	**0.2**	10	**1.1**	4	**0.5**	**0.6**	**0.4**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.08**
Q02UD7	Sulfate transport protein CysA OS=Pseudomonas aer	1	1	**0.1**	1	**0.1**	1	**0.1**	**0.1**	**0.0**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Q02IZ1	Probable transglycolase OS=Pseudomonas aeruginos	2	12	**1.2**	11	**1.2**	10	**1.2**	**1.2**	**0.0**	1	**0.1**	5	**0.6**	7	**0.7**	**0.5**	**0.3**	**0.4**	**0.02**
Q02P75	Putative iron transport system substrate-binding prot	3	3	**0.3**	4	**0.4**	2	**0.2**	**0.3**	**0.1**	0	**0.0**	1	**0.1**	1	**0.1**	**0.1**	**0.1**	**0.2**	**0.02**
Q02DZ6	Phosphate ABC transporter, ATP-binding protein OS=	4	1	**0.1**	1	**0.1**	1	**0.1**	**0.1**	**0.0**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Q02DR7	Putative uncharacterized protein OS=Pseudomonas a	6	1	**0.1**	1	**0.1**	1	**0.1**	**0.1**	**0.0**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Q02F63	Putative uncharacterized protein OS=Pseudomonas a	7	2	**0.2**	3	**0.3**	2	**0.2**	**0.3**	**0.1**	0	**0.0**	0	**0.0**	1	**0.1**	**0.0**	**0.1**	**0.1**	**0.01**
Q02QD0	Putative ATP-dependent helicase OS=Pseudomonas a	8	3	**0.3**	4	**0.4**	5	**0.6**	**0.5**	**0.2**	0	**0.0**	2	**0.2**	1	**0.1**	**0.1**	**0.1**	**0.2**	**0.04**
Q02TI8	Putative uncharacterized protein OS=Pseudomonas a	10	2	**0.2**	1	**0.1**	2	**0.2**	**0.2**	**0.1**	1	**0.1**	0	**0.0**	0	**0.0**	**0.0**	**0.1**	**0.2**	**0.05**
Periplasmic proteins																				
Q02TC6	Putative tail length determination protein OS=Pseudo	0	2	**0.2**	1	**0.1**	1	**0.1**	**0.1**	**0.0**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.01**
Q02I29	D-alanyl-D-alanine-endopeptidase OS=Pseudomonas	1	6	**0.6**	9	**1.0**	4	**0.5**	**0.7**	**0.2**	1	**0.1**	3	**0.3**	2	**0.2**	**0.2**	**0.1**	**0.3**	**0.04**
Q02UB6	Polyamine transport protein OS=Pseudomonas aerug	2	56	**5.6**	36	**3.9**	28	**3.5**	**4.3**	**1.1**	14	**1.4**	23	**2.6**	14	**1.4**	**1.8**	**0.7**	**0.4**	**0.03**
Q02PL1	Putative D-alanyl-D-alanine carboxypeptidase OS=Ps	2	2	**0.2**	3	**0.3**	1	**0.1**	**0.2**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.02**
Q02EI0	Putative periplasmic monofunctional chorismate muta	2	11	**1.1**	9	**1.0**	12	**1.5**	**1.2**	**0.3**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Q02PI4	Putative soluble lytic transglycosylase OS=Pseudomo	3	4	**0.4**	10	**1.1**	4	**0.5**	**0.7**	**0.4**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.04**
Q02N84	Putative periplasmic spermidine/putrescine-binding p	3	23	**2.3**	16	**1.7**	9	**1.1**	**1.7**	**0.6**	1	**0.1**	5	**0.6**	4	**0.4**	**0.4**	**0.2**	**0.2**	**0.02**
Q02TF9	Putative binding protein component of ABC transport	3	18	**1.8**	16	**1.7**	9	**1.1**	**1.6**	**0.4**	2	**0.2**	1	**0.1**	2	**0.2**	**0.2**	**0.1**	**0.1**	**0.00**
Q02QW4	Cyclohexadienyl dehydratase OS=Pseudomonas aeru	3	16	**1.6**	11	**1.2**	10	**1.2**	**1.3**	**0.2**	1	**0.1**	8	**0.9**	3	**0.3**	**0.4**	**0.4**	**0.3**	**0.03**
Q02GU4	Putative binding protein component of ABC transpor	4	13	**1.3**	12	**1.3**	12	**1.5**	**1.4**	**0.1**	5	**0.5**	7	**0.8**	3	**0.3**	**0.5**	**0.2**	**0.4**	**0.01**
Q02DY4	Putative glycine betaine/L-proline ABC transporter, pe	4	23	**2.3**	18	**1.9**	10	**1.2**	**1.8**	**0.5**	3	**0.3**	6	**0.7**	6	**0.6**	**0.5**	**0.2**	**0.3**	**0.02**
Q02E45	Putative binding protein component of ABC dipeptide	4	24	**2.4**	13	**1.4**	12	**1.5**	**1.8**	**0.6**	1	**0.1**	8	**0.9**	2	**0.2**	**0.4**	**0.4**	**0.2**	**0.03**
Q02ER3	Putative ABC transporter, periplasmic substrate-bindi	4	11	**1.1**	8	**0.9**	5	**0.6**	**0.9**	**0.2**	1	**0.1**	1	**0.1**	0	**0.0**	**0.1**	**0.1**	**0.1**	**0.01**
Q02GT9	Putative binding protein component of ABC dipeptid	5	35	**3.5**	33	**3.5**	31	**3.9**	**3.6**	**0.2**	7	**0.7**	10	**1.1**	10	**1.0**	**1.0**	**0.2**	**0.3**	**0.00**
Q02S18	Putative amino-acid ABC transporter binding protei O	5	4	**0.4**	4	**0.4**	5	**0.6**	**0.5**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Outer membrane proteins																				
Q02L18	Staphylolytic protease preproenzyme LasA OS=Pseud	4	23	**2.3**	27	**2.9**	17	**2.1**	**2.4**	**0.4**	2	**0.2**	5	**0.6**	5	**0.5**	**0.4**	**0.2**	**0.2**	**0.00**
Q02TC1	Putative phage-related protein, tail component OS=P	4	8	**0.8**	7	**0.8**	8	**1.0**	**0.9**	**0.1**	2	**0.2**	4	**0.5**	3	**0.3**	**0.3**	**0.1**	**0.4**	**0.01**
Q02DR8	Putative uncharacterized protein OS=Pseudomonas a	8	33	**3.3**	31	**3.3**	23	**2.9**	**3.2**	**0.3**	1	**0.1**	3	**0.3**	1	**0.1**	**0.2**	**0.1**	**0.1**	**0.00**
Extracellular proteins																				
Q02IF1	ExoU OS=Pseudomonas aeruginosa (strain UCBPP-P	0	14	**1.4**	25	**2.7**	25	**3.1**	**2.4**	**0.9**	0	**0.0**	5	**0.6**	1	**0.1**	**0.2**	**0.3**	**0.1**	**0.02**
Q02KJ9	Translocator protein PopB OS=Pseudomonas aerugin	0	8	**0.8**	18	**1.9**	12	**1.5**	**1.4**	**0.6**	0	**0.0**	4	**0.5**	1	**0.1**	**0.2**	**0.2**	**0.1**	**0.03**
Q02KK0	Translocator outer membrane protein PopD OS=Pseu	0	4	**0.4**	11	**1.2**	7	**0.9**	**0.8**	**0.4**	0	**0.0**	1	**0.1**	1	**0.1**	**0.1**	**0.1**	**0.1**	**0.03**
Q02KJ7	Type III secretion protein PcrV OS=Pseudomonas aer	0	3	**0.3**	7	**0.8**	6	**0.7**	**0.6**	**0.3**	0	**0.0**	1	**0.1**	0	**0.0**	**0.0**	**0.1**	**0.1**	**0.02**
Q02M97	Chitinase OS=Pseudomonas aeruginosa (strain UCBP	1	24	**2.4**	28	**3.0**	17	**2.1**	**2.5**	**0.5**	12	**1.2**	13	**1.5**	8	**0.8**	**1.2**	**0.3**	**0.5**	**0.01**
Q02GR5	Type IV pilin structural subunit OS=Pseudomonas aer	2	4	**0.4**	4	**0.4**	4	**0.5**	**0.4**	**0.1**	0	**0.0**	1	**0.1**	3	**0.3**	**0.1**	**0.2**	**0.3**	**0.03**
Q02PA2	Putative aminopeptidase OS=Pseudomonas aerugino	6	33	**3.3**	42	**4.5**	17	**2.1**	**3.3**	**1.2**	3	**0.3**	3	**0.3**	3	**0.3**	**0.3**	**0.0**	**0.1**	**0.01**
Q02I11	Chitin-binding protein CbpD OS=Pseudomonas aerug	8	173	**17.4**	122	**13.1**	73	**9.1**	**13.2**	**4.1**	24	**2.5**	32	**3.6**	25	**2.6**	**2.9**	**0.6**	**0.2**	**0.01**
Q02TJ3	Putative uncharacterized protein OS=Pseudomonas a	9	28	**2.8**	19	**2.0**	22	**2.7**	**2.5**	**0.4**	0	**0.0**	2	**0.2**	0	**0.0**	**0.1**	**0.1**	**0.0**	**0.00**
Q02L61	Putative halovibrin OS=Pseudomonas aeruginosa (str	10	2	**0.2**	5	**0.5**	4	**0.5**	**0.4**	**0.2**	0	**0.0**	1	**0.1**	1	**0.1**	**0.1**	**0.1**	**0.2**	**0.04**
Non cytoplasmic proteins																				
Q02K64	Putative uncharacterized protein OS=Pseudomonas a	2	30	**3.0**	20	**2.2**	32	**4.0**	**3.1**	**0.9**	8	**0.8**	13	**1.5**	19	**2.0**	**1.4**	**0.6**	**0.5**	**0.06**
Q02ES8	Putative uncharacterized protein OS=Pseudomonas a	2	2	**0.2**	1	**0.1**	2	**0.2**	**0.2**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.01**
Q02E70	Phosphorylcholine phosphatase OS=Pseudomonas ae	2	5	**0.5**	5	**0.5**	4	**0.5**	**0.5**	**0.0**	3	**0.3**	2	**0.2**	1	**0.1**	**0.2**	**0.1**	**0.4**	**0.01**
Q02IK9	Putative uncharacterized protein OS=Pseudomonas a	2	10	**1.0**	6	**0.6**	7	**0.9**	**0.8**	**0.2**	0	**0.0**	1	**0.1**	0	**0.0**	**0.0**	**0.1**	**0.0**	**0.00**
Q02GG4	Putative uncharacterized protein OS=Pseudomonas a	2	11	**1.1**	6	**0.6**	4	**0.5**	**0.7**	**0.3**	0	**0.0**	0	**0.0**	1	**0.1**	**0.0**	**0.1**	**0.0**	**0.02**
Q02PL9	Putative carboxypeptidase OS=Pseudomonas aerugin	3	19	**1.9**	17	**1.8**	12	**1.5**	**1.7**	**0.2**	0	**0.0**	1	**0.1**	2	**0.2**	**0.1**	**0.1**	**0.1**	**0.00**
Q02QQ2	Putative uncharacterized protein OS=Pseudomonas a	3	1	**0.1**	3	**0.3**	2	**0.2**	**0.2**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.03**
Q02E92	Putative ABC-type amino acid transporter OS=Pseud	3	5	**0.5**	4	**0.4**	2	**0.2**	**0.4**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.01**
Q02KQ9	Putative uncharacterized protein OS=Pseudomonas a	3	4	**0.4**	3	**0.3**	4	**0.5**	**0.4**	**0.1**	0	**0.0**	2	**0.2**	1	**0.1**	**0.1**	**0.1**	**0.3**	**0.02**
Q02PL8	Putative hydrolase OS=Pseudomonas aeruginosa (str	4	23	**2.3**	18	**1.9**	21	**2.6**	**2.3**	**0.3**	2	**0.2**	8	**0.9**	7	**0.7**	**0.6**	**0.4**	**0.3**	**0.00**
Q02ST2	Putative periplasmic protein OS=Pseudomonas aerug	4	4	**0.4**	3	**0.3**	2	**0.2**	**0.3**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Q02P64	Putative uncharacterized protein OS=Pseudomonas a	4	8	**0.8**	6	**0.6**	5	**0.6**	**0.7**	**0.1**	0	**0.0**	1	**0.1**	2	**0.2**	**0.1**	**0.1**	**0.2**	**0.00**
Q02H56	Putative uncharacterized protein OS=Pseudomonas a	6	12	**1.2**	7	**0.8**	5	**0.6**	**0.9**	**0.3**	0	**0.0**	1	**0.1**	2	**0.2**	**0.1**	**0.1**	**0.1**	**0.02**
Q02F52	Putative uncharacterized protein OS=Pseudomonas a	6	3	**0.3**	4	**0.4**	1	**0.1**	**0.3**	**0.2**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.03**
Q02IE4	Putative uncharacterized protein OS=Pseudomonas a	7	3	**0.3**	2	**0.2**	3	**0.4**	**0.3**	**0.1**	0	**0.0**	0	**0.0**	0	**0.0**	**0.0**	**0.0**	**0.0**	**0.00**
Q02KZ1	Fatty acyl cis-trans isomerase OS=Pseudomonas aeru	8	10	**1.0**	7	**0.8**	13	**1.6**	**1.1**	**0.4**	0	**0.0**	1	**0.1**	2	**0.2**	**0.1**	**0.1**	**0.1**	**0.02**