

**Table 1**

**Identification of J strain proteins by LC-MS/MS.** Protein identified by a liquid chromatography (LC) separation (reversed-phase HPLC) coupled with a tandem mass spectrometry (MS/MS) by searching *M. hyopneumoniae* strain J protein databases using MASCOT search engine.

Accession number <sup>1</sup>	Protein description <sup>2</sup>	MASCOT score <sup>3</sup>	Sequence coverage (%)	COG <sup>4</sup>
gi 71893362 ref YP_278808.1	glucose-inhibited division protein A	16	3.3	D
gi 71893368 ref YP_278814.1	hypothetical protein MHJ_0009	252	10.8	S
gi 71893370 ref YP_278816.1	heat shock protein	172	20.0	O
gi 71893373 ref YP_278819.1	fructose-bisphosphate aldolase	288	49.1	G
gi 71893387 ref YP_278833.1	isoleucyl-tRNA synthetase	78	12.2	J
gi 71893390 ref YP_278836.1	glyceraldehyde 3-phosphate dehydrogenase	476	37.8	G
gi 71893407 ref YP_278853.1	ATP synthase gamma chain	23	6.0	C
gi 71893408 ref YP_278854.1	ATP synthase subunit B	230	30.1	C
gi 71893411 ref YP_278857.1	elongation factor Ts	79	22.1	J
gi 71893422 ref YP_278868.1	molecular chaperone DnaK	1508	38.5	O
gi 71893426 ref YP_278872.1	bacterial nucleoid DNA-binding protein	272	43.8	L
gi 71893430 ref YP_278876.1	elongation factor EF-2	161	19.1	K
gi 71893431 ref YP_278877.1	30S ribosomal protein S7	46	24.4	J
gi 71893437 ref YP_278883.1	NADH oxidase	940	35.2	R
gi 71893438 ref YP_278884.1	thymidine phosphorylase	85	24.4	F
gi 71893439 ref YP_278885.1	purine-nucleoside phosphorylase	239	22.0	F

gi 71893450 ref YP_278896.1	hypothetical protein MHJ_0091	42	17.0	S
gi 71893452 ref YP_278898.1	thiol peroxidase	242	38.4	O
gi 71893454 ref YP_278900.1	thioredoxin reductase	367	27.5	O
gi 71893457 ref YP_278903.1	ATP-dependent protease binding protein	144	16.6	O
gi 71893458 ref YP_278904.1	triosephosphate isomerase	13	9.0	G
gi 71893462 ref YP_278908.1	P97 paralog 1	258	18.8	S
gi 71893463 ref YP_278909.1	DNA gyrase subunit B	166	16.3	L
gi 71893464 ref YP_278910.1	6-phosphofructokinase	101	20.2	G
gi 71893467 ref YP_278913.1	adenine phosphoribosyltransferase	861	52.1	F
gi 71893468 ref YP_278914.1	pyruvate dehydrogenase E1-alpha subunit	1149	41.2	C
gi 71893469 ref YP_278915.1	pyruvate dehydrogenase	1731	55.4	C
gi 71893472 ref YP_278918.1	hypothetical protein MHJ_0115	29	35.4	S
gi 71893476 ref YP_278922.1	50S ribosomal protein L20	30	25.6	J
gi 71893479 ref YP_278925.1	pyruvate kinase	102	26.7	G
gi 71893482 ref YP_278928.1	aminopeptidase	48	4.0	G
gi 71893484 ref YP_278930.1	50S ribosomal protein L21	138	17.0	J
gi 71893485 ref YP_278931.1	50S ribosomal protein L27	29	36.9	J
gi 71893486 ref YP_278932.1	lipase-esterase	86	13.2	R
gi 71893489 ref YP_278935.1	L-lactate dehydrogenase	290	45.1	C
gi 71893490 ref YP_278936.1	hypothetical protein MHJ_0134	56	3.0	S

gi 71893491 ref YP_278937.1	peptide chain release factor 1	68	7.0	J
gi 71893500 ref YP_278946.1	hypothetical protein MHJ_0144	73	23.8	S
gi 71893501 ref YP_278947.1	trigger factor	312	27.7	O
gi 71893513 ref YP_278959.1	phosphopentomutase	48	3.0	G
gi 71893521 ref YP_278967.1	30S ribosomal protein S11	70	34.3	J
gi 71893522 ref YP_278968.1	30S ribosomal protein S13	99	15.3	J
gi 71893528 ref YP_278974.1	50S ribosomal protein L15	42	17.2	J
gi 71893531 ref YP_278977.1	50S ribosomal protein L6	284	33.5	J
gi 71893532 ref YP_278978.1	30S ribosomal protein S8	83	16.0	J
gi 71893534 ref YP_278980.1	50S ribosomal protein L5	130	23.3	J
gi 71893535 ref YP_278981.1	50S ribosomal protein L24	87	15.0	J
gi 71893541 ref YP_278987.1	50S ribosomal protein L22	58	22.4	J
gi 71893542 ref YP_278988.1	30S ribosomal protein S19	52	28.9	J
gi 71893543 ref YP_278989.1	50S ribosomal protein L2	248	33.0	J
gi 71893545 ref YP_278991.1	50S ribosomal protein L4	74	18.0	J
gi 71893546 ref YP_278992.1	50S ribosomal protein L3	58	18.7	J
gi 71893550 ref YP_278996.1	protein P97	1638	6.5	S
gi 71893551 ref YP_278997.1	protein P102	693	15.5	S
gi 71893558 ref YP_279004.1	cell division protein	149	24.6	O
gi 71893559 ref YP_279005.1	lysyl-tRNA synthetase	109	8.0	J

gi 71893560 ref YP_279006.1	hydrolase of the HAD family	28	12.0	R
gi 71893564 ref YP_279010.1	oligopeptide ABC transporter system permease	127	16.9	E
gi 71893566 ref YP_279012.1	oligopeptide ABC transporter ATP-binding protein	55	16.7	E
gi 71893567 ref YP_279013.1	oligopeptide ABC transporter ATP-binding protein	39	18.6	E
gi 71893568 ref YP_279014.1	hypothetical protein MHJ_0212	424	19.0	S
gi 71893569 ref YP_279015.1	lipoprotein	106	14.6	S
gi 71893571 ref YP_279017.1	ribonucleotide-diphosphate reductase alpha subunit	160	21.5	F
gi 71893572 ref YP_279018.1	hypothetical protein MHJ_0216	106	36.7	S
gi 71893573 ref YP_279019.1	ribonucleotide-diphosphate reductase beta subunit	64	34.0	F
gi 71893574 ref YP_279020.1	serine hydroxymethyltransferase	14	8.0	E
gi 71893575 ref YP_279021.1	methylmalonate-semialdehyde dehydrogenase	86	22.7	C
gi 71893579 ref YP_279025.1	myo-inositol catabolism protein	25	16.0	G
gi 71893589 ref YP_279035.1	protein-export membrane protein	29	12.0	N
gi 71893592 ref YP_279038.1	hypothetical protein MHJ_0236	45	25.0	S
gi 71893595 ref YP_279041.1	TRSE-like protein	23	2.0	N
gi 71893598 ref YP_279044.1	phosphopyruvate hydratase	313	37.9	G
gi 71893599 ref YP_279045.1	seryl-tRNA synthetase	39	21.0	J
gi 71893600 ref YP_279046.1	hypothetical protein MHJ_0244	62	33.0	S
gi 71893601 ref YP_279047.1	triacylglycerol lipase	26	23.0	R
gi 71893602 ref YP_279048.1	lipoate-protein ligase A	100	17.7	H

gi 71893604 ref YP_279050.1	DNA polymerase III subunits gamma and tau	14	5.0	L
gi 71893605 ref YP_279051.1	hypothetical protein MHJ_0249	56	27.0	S
gi 71893610 ref YP_279056.1	hypoxanthine-guanine phosphoribosyltransferase	132	21.9	F
gi 71893614 ref YP_279060.1	DNA ligase	13	5.0	L
gi 71893620 ref YP_279066.1	P97 paralog 2	36	16.0	S
gi 71893621 ref YP_279067.1	phenylalanyl-tRNA synthetase alpha chain	26	15.0	J
gi 71893622 ref YP_279068.1	phenylalanyl-tRNA synthetase beta subunit	152	23.1	J
gi 71893628 ref YP_279074.1	CTP synthetase	49	17.2	F
gi 71893639 ref YP_279085.1	hypothetical protein MHJ_0283	65	23.1	S
gi 71893643 ref YP_279089.1	30S ribosomal protein S6	148	19.1	J
gi 71893644 ref YP_279090.1	hypothetical protein MHJ_0288	95	20.5	S
gi 71893650 ref YP_279096.1	permease	15	2.0	G
gi 71893700 ref YP_279146.1	hypothetical protein MHJ_0347	26	21.0	S
gi 71893701 ref YP_279147.1	P60-like lipoprotein	42	8.1	S
gi 71893706 ref YP_279152.1	amino acid permease	20	4.0	E
gi 71893715 ref YP_279161.1	lipoprotein	168	11.4	S
gi 71893721 ref YP_279167.1	Lppt protein	628	24.0	S
gi 71893722 ref YP_279168.1	hypothetical protein MHJ_0369	452	22.6	S
gi 71893724 ref YP_279170.1	PTS system enzyme IIB component	201	14.0	G
gi 71893726 ref YP_279172.1	hypothetical protein MHJ_0373	1042	43.1	S

gi 71893727 ref YP_279173.1	lipoprotein	494	24.3	S
gi 71893733 ref YP_279179.1	thioredoxin	174	30.9	O
gi 71893755 ref YP_279201.1	hypothetical protein MHJ_0404	18	6.0	S
gi 71893760 ref YP_279206.1	methionine--tRNA ligase	40	14.0	J
gi 71893765 ref YP_279211.1	asparaginyl-tRNA synthetase	99	10.7	J
gi 71893767 ref YP_279213.1	ATP-dependent helicase PcrA	177	19.5	L
gi 71893768 ref YP_279214.1	hypothetical protein MHJ_0417	67	15.0	S
gi 71893769 ref YP_279215.1	Holliday junction DNA helicase motor protein	19	4.0	L
gi 71893777 ref YP_279223.1	transketolase	288	28.0	G
gi 71893779 ref YP_279225.1	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	19	7.3	J
gi 71893787 ref YP_279233.1	3-hexulose-6-phosphate synthase	172	22.1	G
gi 71893793 ref YP_279239.1	hypothetical protein MHJ_0442	16	3.0	S
gi 71893796 ref YP_279242.1	hypothetical protein MHJ_0445	175	15.6	S
gi 71893803 ref YP_279249.1	acyl carrier protein phosphodiesterase	73	14.9	I
gi 71893807 ref YP_279253.1	50S ribosomal protein L1	197	45.9	J
gi 71893808 ref YP_279254.1	50S ribosomal protein L11	128	32.9	J
gi 71893812 ref YP_279258.1	leucyl aminopeptidase	128	32.7	E
gi 71893814 ref YP_279260.1	hypothetical protein MHJ_0463	127	15.7	S
gi 71893816 ref YP_279262.1	hypothetical protein MHJ_0465	32	15.4	S
gi 71893820 ref YP_279266.1	phosphoenolpyruvate-protein phosphotransferase	248	36.7	G

gi 71893826 ref YP_279272.1	ATP synthase subunit B	127	18.3	C
gi 71893827 ref YP_279273.1	ATP synthase subunit A	46	2.9	C
gi 71893830 ref YP_279276.1	hypothetical protein MHJ_0479	31	9.7	S
gi 71893831 ref YP_279277.1	hypothetical protein MHJ_0480	85	12.2	S
gi 71893837 ref YP_279283.1	hypothetical protein MHJ_0486	78	13.0	S
gi 71893838 ref YP_279284.1	phosphoglycerate kinase	252	22.3	G
gi 71893842 ref YP_279288.1	mannose-6-phosphate isomerase	154	40.4	G
gi 71893844 ref YP_279290.1	P216 surface protein	2746	46.5	S
gi 71893845 ref YP_279291.1	P76 membrane protein precursor	1931	30.4	S
gi 71893854 ref YP_279300.1	dihydrolipoamide acetyltransferase	269	23.5	C
gi 71893855 ref YP_279301.1	dihydrolipoamide dehydrogenase	271	10.2	C
gi 71893856 ref YP_279302.1	acetate kinase	290	26.4	C
gi 71893857 ref YP_279303.1	phosphate acetyltransferase	316	28.7	C
gi 71893862 ref YP_279308.1	46K surface antigen precursor	514	42.0	S
gi 71893873 ref YP_279319.1	oligoendopeptidase F	122	18.1	E
gi 71893875 ref YP_279321.1	elongation factor Tu	1178	55.2	J
gi 71893876 ref YP_279322.1	heat shock ATP-dependent protease	437	22.4	O
gi 71893879 ref YP_279325.1	deoxyribose-phosphate aldolase	219	33.0	F
gi 71893880 ref YP_279326.1	DNA gyrase subunit A	125	20.5	L
gi 71893883 ref YP_279329.1	glucose-6-phosphate isomerase	96	5.8	G

gi 71893886 ref YP_279332.1	ribosome recycling factor	34	9.8	J
gi 71893908 ref YP_279354.1	PTS system galactitol-specific enzyme IIB component	28	13.2	G
gi 71893920 ref YP_279366.1	hypothetical protein MHJ_0571	17	1.9	S
gi 71893921 ref YP_279367.1	dihydrolipoamide dehydrogenase	89	23.3	C
gi 71893934 ref YP_279380.1	translation initiation factor IF-2	20	4.0	J
gi 71893937 ref YP_279383.1	glycerol-3-phosphate dehydrogenase	18	6.8	R
gi 71893941 ref YP_279387.1	ATP-binding protein	171	21.9	L
gi 71893944 ref YP_279390.1	phosphoglyceromutase	93	22.2	G
gi 71893952 ref YP_279398.1	hypothetical protein MHJ_0603	14	5.0	S
gi 71893954 ref YP_279400.1	inorganic pyrophosphatase	43	10.8	C
gi 71893955 ref YP_279401.1	ABC transporter xylose-binding lipoprotein	575	34.2	R
gi 71893956 ref YP_279402.1	sugar ABC transporter ATP-binding protein	88	13.5	R
gi 71893966 ref YP_279412.1	DNA-directed RNA polymerase beta' subunit	143	23.3	K
gi 71893968 ref YP_279414.1	50S ribosomal protein L7/L12	94	24.0	J
gi 71893971 ref YP_279417.1	lipoprotein	51	13.2	S
gi 71893972 ref YP_279418.1	DNA adenine methylase	23	2.0	L
gi 71893979 ref YP_279425.1	5'-nucleotidase precursor	101	19.7	F
gi 71893984 ref YP_279430.1	O-sialoglycoprotein endopeptidase	101	25.2	O
gi 71893985 ref YP_279431.1	transcription antitermination protein NusG	25	4.0	K
gi 71893998 ref YP_279444.1	30S ribosomal protein S9	26	24.2	J



gi 71893999 ref YP_279445.1	50S ribosomal protein L13	30	13.2	J
gi 71894003 ref YP_279449.1	glucose-inhibited division protein B	17	12.0	M
gi 71894004 ref YP_279450.1	prolipoprotein p65	1431	37.2	S
gi 71894005 ref YP_279451.1	ABC transporter ATP-binding protein P115-like	108	20.1	D
gi 71894010 ref YP_279456.1	hypothetical protein MHJ_0662	896	20.2	S
gi 71894011 ref YP_279457.1	adhesin like-protein P146	1015	21.7	S
gi 71894015 ref YP_279461.1	transcription elongation factor	59	32.5	K
gi 71894021 ref YP_279467.1	hypothetical protein MHJ_0673	183	10.6	S

<sup>1</sup> CDS access number in the NCBI database (<http://www.ncbi.nlm.nih.gov>).

<sup>2</sup> Protein identification according to NCBI database (<http://www.ncbi.nlm.nih.gov>).

<sup>3</sup> MASCOT score is  $-10 \times \log(P)$ , where  $P$  is the probability that the observed match is a random event.

<sup>4</sup> COG database functional classes: (J) Translation, ribosomal structure and biogenesis, (K) Transcription, (L) DNA replication, recombination and repair, (D) Cell division and chromosome partitioning, (O) Posttranslational modification, protein turnover, chaperones, (M) Cell envelope biogenesis, outer membrane, (N) Cell motility and secretion, (C) Energy production and conversion, (G) Carbohydrate transport and metabolism, (E) Amino acid transport and metabolism, (F) Nucleotide transport and metabolism, (H) Coenzyme metabolism, (I) Lipid metabolism, transport and catabolism, (R) General function prediction only, and (S) Function unknown.