

Table S1: Raw spectral counts

Identified proteins	Accession	MW	ClpC ^{trap}		Empty vector	
	Number	kDa	Exp1	Exp2	Exp1	Exp2
ATP-dependent Clp protease, ATP-binding subunit ClpC	A6QEH7	91	5028	5652	49	0
6-phosphofructokinase GN=pfkA	A6QHN3	35	1484	3580	1847	3059
50S ribosomal protein L3 GN=rpLC	A6QJ92	24	849	1253	873	1378
Elongation factor Tu GN=tuf	A6QEK0	43	506	789	552	987
50S ribosomal protein L2 GN=rpLB	A6QJ89	30	500	581	516	880
DNA-binding response regulator SrrA GN=srrA	A6QH40	28	435	820	424	796
Formate acetyltransferase GN=pfIB	A6QDK2	85	413	314	94	307
FtsK/SpoIIIE (DNA translocase stage III) family protein GN=NWMN_1634	A6QHS4	145	376	1858	514	1726
ATP-dependent Clp protease, ATP-binding subunit ClpB GN=NWMN_0845	A6QFI5	98	363	462	112	361
Pyruvate kinase GN=pykA	A6QHN2	63	331	361	84	260
Elongation factor G GN=fusA	A6QEI9	77	289	127	37	96
Phosphomevalonate kinase GN=mvaK2	A6QEP5	40	263	571	376	586
Probable inorganic polyphosphate/ATP-NAD kinase GN=ppnK	A6QFL7	31	188	439	360	424
30S ribosomal protein S2 GN=rpsB	A6QGF6	29	180	153	36	84
Iron-regulated surface determinant protein A GN=isdA	A6QG31	39	159	271	267	361
Chaperone protein DnaK GN=dnaK	A6QHC3	66	158	315	33	59
FeS assembly protein SufB GN=sufB	A6QFC9	53	142	105	48	57
30S ribosomal protein S19 GN=rpsS	A6QJ88	11	128	175	296	264
Probable malate:quinone oxidoreductase 2 GN=mqo2	A6QK94	56	127	137	57	144
Elastin-binding protein ebpS GN=ebpS	A6QH29	53	126	143	213	330
Diaminopimelate decarboxylase GN=sbnH	A6QDA7	46	122	119	115	180
30S ribosomal protein S12 GN=rpsL	A6QEI7	15	122	64	92	70
Bifunctional autolysin GN=atl	A6QFR2	137	117	185	55	122
DNA-directed RNA polymerase subunit beta GN=rpoB	A6QEJ4	133	111	469	40	184
Zn-binding lipoprotein adcA-like protein GN=NWMN_2306	A6QJP6	61	106	190	197	381
Pyruvate dehydrogenase E1 component, beta subunit GN=phdB	A6QFV0	35	102	56	39	20
Asparagine--tRNA ligase GN=asnS	A6QH05	49	99	53	39	76
Alkaline shock protein 23 GN=NWMN_2086	A6QJ26	19	98	120	54	67
GMP synthase [glutamine-hydrolyzing] GN=guaA	A6QE71	58	96	73	34	63
ATP-dependent Clp protease, ATP-binding subunit ClpL	A6QK38	78	92	270	37	128
Putative uncharacterized protein GN=NWMN_1462	A6QHA2	41	92	140	144	110
UvrB/UvrC motif domain protein GN=NWMN_0485	A6QEH5	19	85	126	69	109
Glucosamine-fructose-6-phosphate aminotransferase, isomerizing GN=glmS	A6QIZ6	66	84	97	17	41
Iron uptake regulatory protein GN=NWMN_1406	A6QH46	17	83	174	106	237
Bifunctional purine biosynthesis protein PurH GN=purH	A6QFT1	54	81	103	71	220
Putative uncharacterized protein GN=NWMN_0811	A6QFF1	44	80	51	14	37
DNA-directed RNA polymerase subunit beta' GN=rpoC	A6QEJ5	135	75	329	30	157
50S ribosomal protein L5 GN=rpLE	A6QJ80	20	75	71	12	44
Peptidase M20/M25/M40 family protein GN=NWMN_2230	A6QJH0	41	74	112	109	92
Pyruvate dehydrogenase E1 component, alpha subunit GN=phdA	A6QFU9	41	73	46	22	6
Zinc and cobalt transport repressor protein GN=NWMN_2049	A6QIY9	12	71	173	76	177
Putative uncharacterized protein GN=NWMN_0123	A6QDG3	273	68	802	40	461

Glutamate synthase, large subunit GN=gltB	A6QEC6	166	65	146	135	337
30S ribosomal protein S4 GN=rpsD	A6QHQ3	23	65	87	22	69
50S ribosomal protein L16 GN=rplP	A6QJ85	16	63	327	59	304
ATP synthase subunit beta GN=atpD	A6QIU7	51	63	129	42	100
DNA gyrase subunit A GN=gyrA	A6QD45	100	63	29	0	69
Naphthoate synthase GN=memB	A6QFQ5	30	62	37	16	26
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex GN=pdhC	A6QFV1	46	61	84	78	79
Ferritin GN=NWMN_1831	A6QIC1	20	60	21	15	25
Formate dehydrogenase homolog GN=NWMN_2210	A6QJF0	111	59	112	1	32
Cell division protein ftsA GN=ftsA	A6QG85	53	59	89	22	58
Protein RecA GN=recA	A6QGI4	38	58	150	16	26
L-lactate dehydrogenase 2 GN=ldh2	A6QK89	34	58	53	24	43
50S ribosomal protein L6 GN=rplF	A6QJ77	20	57	57	9	47
Putative uncharacterized protein GN=NWMN_0275	A6QDW5	30	57	40	36	47
Transcriptional regulatory protein walR GN=walR	A6QD57	27	55	129	66	146
Ribonucleoside-diphosphate reductase GN=nrdE	A6QF40	82	55	97	27	58
Putative uncharacterized protein GN=NWMN_0364	A6QE54	21	54	77	33	42
L-lactate dehydrogenase 1 GN=ldh1	A6QDL6	35	54	16	7	3
Glycosyl transferase, group 1 family protein GN=NWMN_0527	A6QEL7	58	53	44	199	123
60 chaperonin GN=groL	A6QIM7	58	50	104	11	33
Ribosome maturation factor RimM GN=rimM	A6QGD9	19	50	96	101	213
Cell division protein SepF GN=sepF	A6QG89	21	49	87	48	113
SsrA-binding protein GN=smpB	A6QF90	18	49	63	30	93
RNAIII-activating protein TRAP GN=NWMN_1726	A6QI16	20	49	41	56	77
Cobalamin synthesis protein, P47K family protein GN=NWMN_0656	A6QEZ6	35	49	32	31	60
Dak phosphatase GN=NWMN_1136	A6QGC6	61	48	21	0	13
Tyrosine recombinase xerD GN=xerD	A6QH45	34	47	159	34	95
Acetyltransferase, GNAT family protein GN=NWMN_2419	A6QK09	11	46	99	96	79
Acetate kinase GN=ackA	A6QHP5	44	46	67	14	21
30S ribosomal protein S3 GN=rpsC	A6QJ86	24	45	146	26	88
Glycerophosphoryl diester phosphodiesterase GN=glpQ	A6QFH0	35	45	63	14	98
Isochorismatase family protein GN=NWMN_1856	A6QIE6	21	44	81	89	104
Ribose-phosphate pyrophosphokinase GN=prs	A6QEF3	35	44	70	4	31
Zinc-specific metalloregulatory protein GN=NWMN_1457	A6QH97	16	44	43	48	38
2-oxoglutarate dehydrogenase E1 component GN=odhA	A6QGW6	105	44	4	32	83
Translation initiation factor IF-3 GN=infC	A6QHL4	20	43	29	20	30
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B GN=gatB	A6QIC7	54	42	47	4	23
S1 RNA binding domain protein GN=NWMN_1969	A6QIQ9	81	41	4	4	14
Glutamyl-tRNA(Gln) amidotransferase subunit A GN=gatA	A6QIC8	53	40	113	6	33
DNA polymerase III subunit beta GN=dnaN	A6QD42	42	40	44	4	19
Phosphosugar-binding transcriptional regulator RpiR family protein GN=NWMN_2217	A6QJF7	33	39	437	109	160
ATP synthase subunit alpha GN=atpA	A6QIU9	55	38	52	48	78
Enolase GN=eno	A6QF85	47	38	28	21	13
FeS assembly ATPase SufC GN=sufC	A6QFC5	28	37	76	8	17
Chaperone protein DnaJ GN=dnaJ	A6QHC2	42	34	80	6	8

General stress protein-like protein GN=NWMN_1632	A6QHS2	18	33	72	21	43
RNA-metabolising metallo-beta-lactamase GN=NWMN_1184	A6QGH4	63	33	42	29	37
30S ribosomal protein S7 GN=rpsG	RS7	18	33	17	4	22
Putative uncharacterized protein GN=NWMN_0078	A6QDB8	26	32	121	22	141
2-dehydropantoate 2-reductase GN=panE	A6QK87	32	32	80	70	77
Putative uncharacterized protein GN=NWMN_0601	A6QEU1	35	32	38	26	41
Putative uncharacterized protein GN=NWMN_0526	A6QEL6	57	32	34	118	86
Staphylococcal accessory gene regulator A GN=agrA	A6QIN6	28	31	55	10	29
Sigma 54 modulation protein GN=NWMN_0721	A6QF61	22	31	46	15	28
Iron-containing alcohol dehydrogenase GN=adhE	A6QDD4	95	31	28	2	60
Inosine-5'-monophosphate dehydrogenase GN=guaB	A6QE70	53	30	77	5	19
Uracil phosphoribosyltransferase GN=upp	A6QEJ8	23	30	31	9	24
Nitroreductase family protein GN=NWMN_0373	A6QE63	29	30	4	19	28
Septation ring formation regulator EzrA GN=ezrA	A6QHQ1	66	29	55	18	65
30S ribosomal protein S1 GN=rpsA	A6QH25	43	29	36	13	20
ATP-dependent Clp protease proteolytic subunit GN=clpP	A6QF76	22	29	34	10	11
30S ribosomal protein S10 GN=rpsJ	A6QJ93	12	29	27	18	27
Putative uncharacterized protein GN=NWMN_0545	A6QEN5	14	28	108	29	119
Staphopain thiol proteinase GN=sspB	A6QID7	44	28	79	49	68
Ferredoxin--NADP reductase GN=NWMN_2274	A6QJL4	38	28	35	63	47
UPF0358 protein NWMN_0977 GN=NWMN_0977	A6QFW7	10	28	16	28	35
30S ribosomal protein S5 GN=rpsE	A6QJ75	17	27	95	21	68
Putative uncharacterized protein GN=NWMN_1735	A6QI25	114	27	43	11	52
Serine-protein kinase rsbW GN=rsbW	A6QIR1	18	27	40	11	17
Polyribonucleotide nucleotidyltransferase GN=pnp	A6QGH3	77	27	19	3	14
UPF0365 protein NWMN_1476 GN=NWMN_1476	A6QHB6	35	26	84	16	85
Putative ATP:guanido phosphotransferase NWMN_0486 GN=NWMN_0486	A6QEH6	39	26	44	15	2
Amidophosphoribosyltransferase GN=purF	A6QFS8	54	26	4	23	115
Quinol oxidase polypeptide II QoxA GN=qoxA	A6QF50	42	25	81	14	51
UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 GN=murA	A6QIU4	45	25	79	5	14
Putative uncharacterized protein GN=NWMN_2250	A6QJJ0	16	25	78	22	55
30S ribosomal protein S8 GN=rpsH	A6QJ78	15	25	28	9	4
Proline--tRNA ligase GN=proS	A6QGG3	64	25	28	7	21
Ferrichrome ABC transporter lipoprotein GN=NWMN_2078	A6QJ18	37	25	20	3	16
50S ribosomal protein L19 GN=rplS	A6QGE1	13	25	19	20	34
Dehydrogenase family protein GN=NWMN_2201	A6QJE1	41	25	11	0	0
Small GTP-binding protein domain:GTP-binding protein TypA GN=NWMN_0974	A6QFW4	69	25	8	0	7
Translation initiation factor IF-2 GN=infB	A6QGG8	78	24	81	33	93
Putative uncharacterized protein GN=NWMN_0079	A6QDB9	29	24	35	45	82
L-asparaginase GN=ansA	A6QH27	36	24	32	18	76
Glycosyl transferase, group 1 family protein GN=NWMN_0906	A6QFP6	57	24	13	56	40
Fumarylacetoacetate hydrolase family protein GN=NWMN_0839	A6QFH9	33	24	6	5	0
Glycosyl transferase group 2 family protein GN=NWMN_0192	A6QDN2	66	23	28	24	22
Cell division protein ftsZ GN=ftsZ	A6QG86	41	22	82	15	37
50S ribosomal protein L13 GN=rplM	A6QJ60	16	22	45	22	66

Amino acid ABC transporter, amino acid-binding protein GN=NWMN_2313	A6QJQ3	29	22	30	11	25
ABC transporter ATP-binding protein GN=NWMN_1303	A6QGU3	60	22	19	3	17
Fructose specific permease GN=fruA	A6QF09	69	21	32	19	56
Lipoyl synthase GN=lipA	A6QFD6	35	21	28	8	14
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase GN=fabZ	A6QIU3	16	21	10	8	4
Transcriptional regulator AraC family protein GN=NWMN_2281	A6QJM1	82	20	70	36	59
Putative uncharacterized protein GN=NWMN_1621	A6QHR1	46	20	40	21	49
Arginine--tRNA ligase GN=argS	A6QER9	62	20	0	8	8
Acetoin utilization protein AcuC GN=acuC	A6QHR8	45	20	26	15	13
Aldehyde dehydrogenase family protein GN=NWMN_2026	A6QIW6	52	19	81	10	49
GTP-sensing transcriptional pleiotropic repressor CodY	A6QGF5	29	19	49	11	16
Putative uncharacterized protein GN=NWMN_1631	A6QHS1	55	19	45	16	16
Putative uncharacterized protein GN=NWMN_2507	A6QK97	18	19	20	22	28
Sucrose-6-phosphate hydrolase GN=scrB	A6QIN8	58	19	19	18	24
Putative uncharacterized protein GN=NWMN_1861	A6QIF1	7	19	0	3	0
Carbamoyl-phosphate synthase large chain GN=carB	A6QGA4	117	18	119	4	112
Putative uncharacterized protein GN=NWMN_0814	A6QFF4	14	18	87	43	103
Putative uncharacterized protein GN=NWMN_1119	A6QGA9	66	18	39	13	43
50S ribosomal protein L1 GN=rplA	A6QEJ0	25	18	32	7	13
Transcriptional regulator SarA GN=sarA	A6QES8	15	18	10	5	11
Glyceraldehyde 3-phosphate dehydrogenase 1 GN=gapA	A6QF81	36	17	39	0	0
Phosphosugar-binding transcriptional regulator GN=NWMN_2225	A6QJG5	30	17	36	27	37
Serine protease HtrA GN=htrA	A6QFN2	87	17	27	25	95
Alkyl hydroperoxide reductase subunit C GN=ahpC	A6QE62	21	17	27	20	32
Putative uncharacterized protein GN=NWMN_0047	A6QD87	43	17	25	23	26
Foldase protein prsA GN=prsA	A6QI23	36	17	21	3	15
Aspartate--tRNA ligase GN=aspS	A6QHH2	67	17	7	0	5
DNA gyrase subunit B GN=gyrB	A6QD44	73	17	49	6	28
ATP-dependent zinc metalloprotease FtsH GN=ftsH	A6QEG3	78	17	35	26	176
Transketolase GN=tkt	A6QGP4	72	16	9	1	0
MarR family regulatory protein GN=NWMN_2286	A6QJM6	17	16	6	2	4
50S ribosomal protein L29 GN=rpmC	A6QJ84	9	16	4	4	8
Xanthine phosphoribosyltransferase GN=xpt	A6QE68	21	16	60	7	12
Pseudouridine synthase GN=NWMN_0878	A6QFL8	33	15	53	27	40
Bifunctional protein pyrR GN=pyrR	A6QG99	20	15	44	0	10
FeS assembly protein SufD GN=sufD	A6QFC6	49	15	32	4	16
50S ribosomal protein L14 GN=rplN	A6QJ82	13	15	22	8	14
Glucose-6-phosphate 1-dehydrogenase GN=zwf	A6QH52	57	15	16	3	4
2-C-methyl-D-erythritol 4-phosphate cytidyltransferase 1 GN=ispD1	A6QDM5	27	8	11	0	0
2-C-methyl-D-erythritol 4-phosphate cytidyltransferase 2 GN=ispD2	A6QDM9	27	3	2	0	1
Iron compound ABC transporter, iron compound-binding protein GN=NWMN_2185	A6QJC5	34	15	13	4	10
Alanine--tRNA ligase GN=alaS	A6QHF9	99	15	10	2	20
Probable siderophore biosynthesis protein SbnA GN=sbnA	A6QDA0	36	15	35	10	33

Quinol oxidase polypeptide I QoxB GN=qoxB	A6QFR9	75	15	68	17	83
Putative uncharacterized protein GN=NWMN_1479	A6QHB9	51	15	22	0	16
Transcription termination-antitermination factor GN=nusA	A6QGG6	44	14	21	2	15
RNA polymerase sigma factor GN=sigA	A6QHA4	42	14	17	0	4
Acriflavin resistance protein GN=NWMN_2162	A6QJA2	115	14	5	8	30
50S ribosomal protein L25 GN=rplY	A6QEF4	24	14	31	4	22
Nitrate reductase, alpha subunit GN=narG	A6QJN7	140	14	193	22	168
UPF0348 protein NWMN_0989 GN=NWMN_0989	A6QFX9	45	13	109	36	74
Excinuclease ABC subunit A GN=uvrA	A6QF67	105	13	36	4	21
Holo-[acyl-carrier-protein] synthase GN=acpS	A6QIR6	14	13	35	26	34
Thioesterase superfamily protein GN=NWMN_1816	A6QIA6	20	13	33	7	55
Universal stress protein family protein GN=NWMN_1600	A6QHP0	15	13	27	12	19
DNA-directed RNA polymerase subunit alpha GN=rpoA	A6QJ66	35	13	13	0	0
Ribonucleotide-diphosphate reductase beta chain GN=nrdF	A6QF41	38	13	11	2	9
D-isomer specific 2-hydroxyacid dehydrogenase family protein GN=NWMN_2205	A6QJE5	35	13	1	1	0
Probable manganese transport protein MntH GN=mntH	A6QFW1	50	13	7	12	16
Transcription termination factor Rho GN=rho	A6QIW5	50	12	42	0	13
Site-specific recombinase GN=NWMN_0592	A6QET2	21	12	27	3	31
Signal peptidase IB GN=spsB	A6QFH6	22	12	19	8	15
ATP synthase subunit delta GN=atpH	A6QIV0	20	12	10	11	13
Putative uncharacterized protein GN=NWMN_1336	A6QGX6	31	12	9	0	4
Peptide deformylase 1 GN=pdf1	A6QFU7	21	12	3	17	13
Sigma factor sigB regulation protein GN=rsbU	A6QIR3	38	11	50	3	8
GTP pyrophosphokinase GN=relA	A6QHH6	85	11	27	11	24
Putative uncharacterized protein GN=NWMN_2088	A6QJ28	21	11	23	15	27
50S ribosomal protein L22 GN=rplV	A6QJ87	13	11	11	4	10
PTS system glucose-specific EIICBA component GN=ptsG	A6QDH3	74	11	20	7	18
Para-aminobenzoate synthase component II GN=pabA	A6QF22	22	11	10	8	13
Putative uncharacterized protein GN=NWMN_0956	A6QFU6	63	10	44	6	21
ATP-dependent protease ATPase subunit HslU GN=hslU	A6QGF4	52	10	29	1	18
50S ribosomal protein L21 GN=rplU	A6QHI9	11	10	19	13	17
Ferrichrome ABC transporter lipoprotein GN=NWMN_0705	A6QF45	38	10	17	4	8
Clumping factor A GN=clfA	Q53653	97	10	17	0	10
30S ribosomal protein S17 GN=rpsQ	A6QJ83	10	10	14	3	20
Alcohol dehydrogenase GN=adh1	A6QER7	36	10	9	2	0
Lytic regulatory protein GN=NWMN_2051	A6QIZ1	41	10	6	4	10
Protein translocase subunit SecA 1 GN=secA1	A6QF62	96	10	56	4	72
50S ribosomal protein L15 GN=rplO	A6QJ73	16	10	6	7	18
Phosphomethylpyrimidine kinase GN=thiD	A6QEN3	30	10	27	0	8
Pyruvate oxidase GN=poxB	A6QK28	64	10	29	6	40
3-oxoacyl-[acyl-carrier protein] reductase GN=fabG	A6QGD1	26	10	8	6	10
Transcription factor fapR GN=fapR	A6QGC8	22	9	39	18	47
Putative uncharacterized protein GN=NWMN_0685	A6QF25	27	9	31	1	19
Putative uncharacterized protein GN=NWMN_1645	A6QHT5	16	9	26	5	14
Succinyl-CoA ligase [ADP-forming] subunit beta GN=sucC	A6QGE5	42	9	22	0	0
UPF0298 protein NWMN_0985 GN=NWMN_0985	A6QFX5	10	9	20	3	16
ATP synthase subunit b GN=atpF	A6QIV1	20	9	18	5	12
Lipoprotein GN=NWMN_0782	A6QFC2	30	9	16	5	14

Nuclease sbcCD subunit C GN=sbcC	A6QGP8	117	9	15	0	7
Transcription antitermination protein NusG GN=nusG	P0C1S3	21	9	12	4	3
Biotin carboxylase subunit of acetyl-CoA carboxylase GN=accC	A6QH71	50	9	11	0	4
Putative uncharacterized protein GN=NWMN_0651	A6QEZ1	27	9	7	6	4
RNA pseudouridylate synthase GN=NWMN_1742	A6QI32	31	9	2	0	5
Putative uncharacterized protein GN=NWMN_1679	A6QHW9	35	9	0	0	3
Putative uncharacterized protein GN=NWMN_1654	A6QHU4	21	9	21	4	30
50S ribosomal protein L31 type B GN=rpME2	A6QIW4	10	9	4	0	4
Aldo/keto reductase family protein GN=NWMN_0672	A6QF12	32	9	0	0	0
tRNA-specific 2-thiouridylase MnmA GN=mnmA	A6QHG3	42	9	6	4	0
6-carboxy-5,6,7,8-tetrahydropterin synthase GN=NWMN_0680	A6QF20	16	8	32	7	26
Allophanate hydrolase subunit 2 GN=NWMN_0686	A6QF26	38	8	25	8	5
Ribonuclease Z GN=rnz	A6QH51	35	8	15	7	27
Putative uncharacterized protein GN=NWMN_2037	A6QIX7	43	8	13	18	2
Putative uncharacterized protein GN=NWMN_2356	A6QUJ6	17	8	10	2	3
4-amino-4-deoxychorismate lyase GN=pabC	A6QF24	24	8	9	7	14
Siderophore compound ABC transporter binding protein GN=sirA	A6QD99	37	8	9	5	7
(Dimethylallyl)adenosine tRNA methylthiotransferase MiaB GN=miaB	A6QGJ1	59	8	14	0	12
Phosphoglycerate kinase GN=pgk	A6QF82	43	8	12	3	0
Putative uncharacterized protein GN=NWMN_1102	A6QG92	24	8	6	0	0
50S ribosomal protein L17 GN=rpLQ	A6QJ65	14	8	13	7	14
CTP synthase GN=pyrG	A6QIX1	60	8	8	4	10
Lysine--tRNA ligase GN=lysS	A6QEG9	59	8	30	3	16
Alkyl hydroperoxide reductase subunit F GN=ahpF	A6QE61	55	8	20	0	3
Ribonuclease Y GN=rny	A6QGI5	59	8	29	9	26
DNA mismatch repair protein MutS GN=mutS	A6QGJ4	100	8	13	2	9
30S ribosomal protein S16 GN=rpsP	A6QGD8	10	8	11	4	4
Catabolite control protein A GN=ccpA	A6QHR9	36	8	15	0	3
Pantothenate synthetase GN=panC	A6QK85	31	8	2	0	2
Tyrosine recombinase XerC GN=xerC	A6QGF2	35	7	72	3	19
Transcriptional regulator CtsR GN=ctsR	A6QEH4	18	7	29	2	8
Accessory secretory protein Asp1 GN=NWMN_2551	A6QKE1	61	7	24	17	34
Putative uncharacterized protein GN=NWMN_0632	A6QEX2	24	7	11	1	6
DNA repair protein RecN GN=recN	A6QH65	64	7	11	0	4
Putative uncharacterized protein GN=NWMN_1730	A6QI20	13	7	10	1	4
Putative uncharacterized protein GN=NWMN_0299	A6QDY9	21	7	9	1	12
Serine-aspartate repeat-containing protein E GN=sdrE	O86489	127	7	2	9	1
2-isopropylmalate synthase GN=leuA	A6QIQ3	56	7	1	11	15
Methionyl-tRNA formyltransferase GN=fmt	A6QGB6	34	7	0	0	0
2-oxoisovalerate dehydrogenase, E2 component GN=NWMN_1421	A6QH61	47	7	12	4	3
Phosphoribosylformylglycinamide synthase 2 GN=purL	A6QFS7	80	7	38	0	59
Pur operon repressor GN=purR	A6QEE9	30	7	30	4	2
Uridylate kinase GN=pyrH	A6QGF8	26	7	10	1	2
Hydrolase GN=NWMN_0584	A6QES4	31	7	7	0	0
Putative uncharacterized protein GN=NWMN_2087	A6QJ27	9	7	5	0	3
Formate--tetrahydrofolate ligase GN=fhs	A6QHR5	60	7	7	3	14

Putative uncharacterized protein GN=NWMN_0976	A6QFW6	19	7	8	1	3
Putative uncharacterized protein GN=NWMN_1504	A6QHE4	48	6	33	34	27
Carboxyl-terminal protease GN=ctpA	A6QGX2	55	6	10	14	20
Putative uncharacterized protein GN=NWMN_0191	A6QDN1	66	6	10	6	6
Lipoprotein GN=NWMN_0428	A6QEB8	30	6	5	4	1
Putative uncharacterized protein GN=NWMN_2063	A6QJ03	35	6	5	8	0
Putative uncharacterized protein GN=NWMN_0272	A6QDW2	21	6	8	0	0
Teichoic acid biosynthesis protein D GN=tagD	A6QEV1	16	6	8	3	8
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase GN=murG	A6QGX0	40	6	18	0	2
Methicillin resistance protein FemA GN=femA	A6QGS6	49	6	11	5	3
Cysteine synthase GN=NWMN_0475	A6QEG5	33	6	14	0	1
2-oxoisovalerate dehydrogenase, E1 component, beta subunit GN=NWMN_1422	A6QH62	36	6	13	0	1
UPF0042 nucleotide-binding protein NWMN_0733 GN=NWMN_0733	A6QF73	35	6	6	1	4
S-adenosylmethionine synthase GN=metK	A6QHX0	44	6	28	4	7
ATP-dependent Clp protease ATP-binding subunit ClpX	A6QHK8	46	6	18	8	11
Bifunctional protein Fold GN=fold	A6QFS2	31	6	13	0	1
Inositol-1-monophosphatase family protein GN=NWMN_0973	A6QFW3	30	6	11	0	4
UPF0637 protein NWMN_0972 GN=NWMN_0972	A6QFW2	24	6	9	4	5
Chromosome partition protein Smc GN=smc	A6QGD4	137	5	61	0	15
Phosphoribosylaminoimidazole-succinocarboxamide synthase GN=purC	A6QFS5	27	5	18	0	4
50S ribosomal protein L10 GN=rplJ	A6QEJ1	18	5	15	0	13
ABC transporter ATP-binding protein GN=NWMN_0613	A6QEV3	64	5	10	8	26
30S ribosomal protein S13 GN=rpsM	A6QJ68	14	5	10	2	10
Pyruvate carboxylase GN=pycA	A6QFW9	129	5	8	0	0
SbnI protein GN=sbnI	A6QDA8	30	5	5	9	18
Oligopeptide permease, peptide-binding protein GN=opp1A	A6QJV4	60	5	2	5	2
Peptide methionine sulfoxide reductase MsrA 2 GN=msrA	A6QGX5	21	5	2	0	1
Putative uncharacterized protein GN=NWMN_0576	A6QER6	20	5	9	0	8
50S ribosomal protein L30 GN=rpmD	A6QJ74	7	5	6	8	10
Glucokinase GN=glk	A6QH91	35	5	7	0	0
Enoyl-[acyl-carrier-protein] reductase [NADPH] GN=NWMN_0881	A6QFM1	28	5	13	5	1
Oxidoreductase GN=NWMN_0657	A6QEZ7	35	5	0	5	9
Putative uncharacterized protein GN=NWMN_0119	A6QDF9	38	5	6	4	0
Redox-sensing transcriptional repressor rex GN=rax	A6QIP3	24	5	8	0	2
Trigger factor GN=tig	A6QHK9	49	5	2	3	5
Putative uncharacterized protein GN=NWMN_1135	A6QGC5	13	5	7	4	11
50S ribosomal protein L27 GN=rpmA	A6QHI7	10	5	4	0	4
Phage cI-like repressor GN=NWMN_1921	A6QIL1	27	5	4	1	1
Putative uncharacterized protein GN=NWMN_1820	A6QIB0	10	5	2	0	0
50S ribosomal protein L4 GN=rplD	A6QJ91	22	5	12	7	17
50S ribosomal protein L35 GN=rpmI	A6QHL3	8	5	7	5	12
Universal stress protein family protein GN=NWMN_1604	A6QHP4	18	5	28	3	20
Isocitrate dehydrogenase [NADP] GN=citC	A6QHM7	46	5	10	0	0
Anaerobic ribonucleoside-triphosphate reductase GN=nrdD	A6QKA5	70	5	24	12	11

Ferrichrome transport ATP-binding protein fhuA GN=fhuA	A6QEV6	29	5	3	6	2
30S ribosomal protein S20 GN=rpsT	A6QHC8	9	5	17	2	12
Ribosomal RNA small subunit methyltransferase H GN=rsmH	A6QG79	36	5	7	0	3
Flavoheмоprotein GN=NWMN_0175	A6QDL5	43	0	11	0	0
65 membrane protein GN=NWMN_1872	A6QIG2	66	4	12	8	34
Penicillin-binding protein 3 GN=pbpC	A6QH95	77	4	9	5	24
Putative uncharacterized protein GN=NWMN_0369	A6QE59	24	4	8	1	4
Phenylalanine--tRNA ligase beta subunit GN=pheT	A6QG40	89	4	3	0	9
2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase GN=mendD	A6QFQ3	63	4	1	2	8
Branched-chain-amino-acid aminotransferase GN=ilvE	A6QEK6	40	4	2	2	0
Penicillin binding protein 2 GN=pbpB	A6QH01	80	4	21	5	39
ABC transporter permease protein GN=NWMN_0691	A6QF31	56	4	0	2	1
Putative uncharacterized protein GN=NWMN_1127	A6QGB7	50	4	7	7	0
Putative uncharacterized protein GN=NWMN_0270	A6QDW0	10	4	9	8	26
50S ribosomal protein L28 GN=rpmB	A6QGC4	7	4	8	2	13
1-acyl-sn-glycerol-3-phosphate acyltransferase GN=plsC	A6QHR0	23	4	13	2	5
UDP-N-acetylenolpyruvylglucosamine reductase GN=murB	A6QF47	34	4	0	0	0
Threonine--tRNA ligase GN=thrS	A6QHL6	74	4	57	0	22
33 chaperonin GN=hsI0	A6QEG4	32	4	8	5	2
Staphylococcal accessory regulator R GN=sarR	A6QJD5	14	4	3	0	3
Chorismate synthase GN=aroC	A6QH17	43	4	1	1	0
Staphylococcal tandem lipoprotein GN=lpl9nm	A6QEA2	31	4	2	2	0
Putative uncharacterized protein GN=NWMN_1648	A6QHT8	46	4	16	12	16
50S ribosomal protein L18 GN=rplR	A6QJ76	13	4	12	4	20
Putative uncharacterized protein GN=NWMN_2511	A6QKA1	22	4	3	0	0
Putative uncharacterized protein GN=NWMN_0737	A6QF77	34	4	6	0	3
Cell cycle protein GpsB GN=gpsB	A6QGZ6	13	4	20	0	2
Uridine kinase GN=udk	A6QHF2	24	4	6	0	4
Deoxyribose-phosphate aldolase 1 GN=dra	A6QDC2	23	4	3	1	0
Putative uncharacterized protein GN=NWMN_1324	A6QGW4	30	4	7	2	16
Putative uncharacterized protein GN=NWMN_0355	A6QE45	41	4	31	3	15
Superoxide dismutase GN=sodA	A6QH96	23	4	9	0	12
Putative uncharacterized protein GN=NWMN_0274	A6QDW4	33	4	20	7	11
Putative uncharacterized protein GN=NWMN_2270	A6QJL0	23	4	10	4	4
Dihydrolipoyl dehydrogenase GN=pdhD	A6QFV2	49	4	122	4	6
Ornithine cyclodeaminase GN=sbnB	A6QDA1	38	4	6	0	3
NADH-dependent flavin oxidoreductase Oye family protein GN=NWMN_0315	A6QE05	45	3	8	14	0
Polyribonucleotide nucleotidyltransferase GN=NWMN_0470	A6QEG0	15	3	8	3	10
Putative uncharacterized protein GN=NWMN_1187	A6QGH7	49	3	2	0	0
ABC transporter, ATP-binding protein GN=NWMN_0343	A6QE33	32	3	2	1	2
Protein GlcT GN=glcT	A6QGR0	33	3	32	1	15
Propeptide, PepSY amd peptidase M4 GN=NWMN_1639	A6QHS9	12	3	4	0	0
D-isomer specific 2-hydroxyacid dehydrogenase GN=NWMN_0801	A6QFE1	35	3	31	14	19
UPF0154 protein NWMN_1255 GN=NWMN_1255	A6QGP5	11	3	3	2	0
Putative uncharacterized protein GN=NWMN_1746	A6QI36	22	3	5	0	5
Sortase A, peptide LPXTG peptidoglycan transferase GN=srtA	A6QK16	24	3	5	1	2

Holliday junction ATP-dependent DNA helicase RuvA GN=ruvA	A6QHI4	22	3	4	2	1
Acetyltransferase, GNAT family protein GN=NWMN_2468	A6QK58	19	3	4	0	0
Putative uncharacterized protein GN=NWMN_0495	A6QEI5	20	3	1	0	0
Putative uncharacterized protein GN=NWMN_0187	A6QDM7	66	3	11	2	8
Transaldolase GN=NWMN_1672	A6QHW2	26	3	1	0	0
Putative uncharacterized protein GN=NWMN_2164	A6QJA4	30	3	4	2	3
Glycerol uptake operon antiterminator regulatory protein GN=glpP	A6QGJ6	20	3	5	0	8
Putative uncharacterized protein GN=NWMN_1265	A6QGQ5	11	3	2	0	0
Serine acetyltransferase GN=cysE	A6QEI1	24	3	5	4	5
Putative uncharacterized protein GN=NWMN_0284	A6QDX4	21	3	5	0	0
50S ribosomal protein L20 GN=rplT	A6QHL2	14	3	13	0	8
Putative uncharacterized protein GN=NWMN_2352	A6QJU2	28	3	4	4	9
Methicillin resistance expression factor FemB GN=femB	A6QGS7	50	3	11	0	0
Fructosamine kinase family protein GN=NWMN_2487	A6QK77	33	3	8	3	8
Putative uncharacterized protein GN=NWMN_2283	A6QJM3	13	3	23	5	23
Glycerol kinase GN=glpK	A6QGJ8	56	3	28	0	8
ATP synthase gamma chain GN=atpG	A6QIU8	32	3	5	5	14
Putative uncharacterized protein GN=NWMN_2045	A6QIY5	53	3	12	6	9
Hydrolase GN=NWMN_1210	A6QGK0	35	3	4	0	10
Capsular polysaccharide synthesis enzyme CapB GN=capB	A6QDD6	26	3	8	0	6
Putative uncharacterized protein GN=NWMN_0948	A6QFT8	20	3	26	0	17
Penicillin-binding protein 1 GN=pbpA	A6QG81	83	3	1	2	35
Peptidase M20/M25/M40 family protein GN=NWMN_1644	A6QHT4	53	3	4	1	6
HPr kinase/phosphorylase GN=hprK	A6QF68	34	3	7	0	0
Aspartate transaminase GN=NWMN_1871	A6QIG1	48	3	4	0	1
Preprotein translocase component SecDF GN=secDF	A6QHH9	84	3	5	6	14
Pyrimidine nucleoside phosphorylase GN=pdp	A6QIY0	46	3	26	2	7
Bifunctional protein GlmU GN=gcaD	A6QEF2	49	3	6	4	11
ABC transporter, ATP-binding protein GN=NWMN_2412	A6QK02	26	3	3	1	5
Glycerol-3-phosphate dehydrogenase [NAD(P)+] GN=gpsA	A6QH23	36	3	8	0	0
SpoU rRNA Methylase family protein GN=NWMN_1048	A6QG38	27	3	6	0	2
Alkylhydroperoxidase AhpD family protein GN=NWMN_2371	A6QJW1	16	3	5	0	6
Aerobic glycerol-3-phosphate dehydrogenase GN=glpD	A6QGJ9	64	3	38	17	42
Putative uncharacterized protein GN=NWMN_0954	A6QFU4	24	3	4	0	0
Abortive infection protein family protein GN=NWMN_2236	A6QJH6	47	3	5	4	12
5' nucleotidase family protein GN=NWMN_0894	A6QFN4	58	3	3	0	6
ATP-binding Mrp/Nbp35 family protein GN=NWMN_2067	A6QJ07	38	3	10	0	0
Single-stranded DNA-binding protein GN=NWMN_0358	A6QE48	19	0	4	0	0
D-3-phosphoglycerate dehydrogenase GN=serA	A6QHQ7	58	2	22	2	15
Probable manganese-dependent inorganic pyrophosphatase GN=ppaC	A6QIE7	34	2	9	1	1
Ribosomal RNA large subunit methyltransferase H GN=rlmH	A6QD63	18	2	8	0	4
Uroporphyrinogen decarboxylase GN=hemE	A6QI15	39	2	5	0	2
Hippurate hydrolase GN=hipO	A6QGU9	43	2	10	15	2
Preprotein translocase, YajC subunit GN=NWMN_1540	A6QHI0	10	2	9	0	4
DNA polymerase III, alpha subunit GN=dnaE	A6QHN7	123	2	4	0	5
Alanine racemase 1 GN=alr2	A6QGV0	41	2	3	5	3
GTPase obg GN=obg	A6QHI6	47	2	19	1	8

30S ribosomal protein S11 GN=rpsK	A6QJ67	14	2	22	4	36
Putative uncharacterized protein GN=NWMN_2209	A6QJE9	17	2	4	0	0
Iron compound ABC transporter, iron compound-binding protein GN=NWMN_0581	A6QES1	33	2	4	0	0
Dihydrolipoamide succinyltransferase E2 component of 2-oxoglutarate dehydrogenase complex GN=sucB	A6QGW5	47	2	7	0	0
Capsular polysaccharide type 5 biosynthesis protein cap5A GN=cap5A	P95695	25	2	6	0	12
DNA polymerase GN=polA	A6QHM3	99	2	5	1	35
ABC transporter ATP-binding protein GN=NWMN_1867	A6QIF7	33	2	0	0	6
Amino acid ABC transporter, permease protein GN=NWMN_2312	A6QJQ2	26	2	4	0	0
Putative uncharacterized protein GN=NWMN_2434	A6QK24	37	2	6	0	1
Transcriptional regulator LysR family protein GN=NWMN_2441	A6QK31	34	2	72	9	32
Protein esaA GN=esaA	P0C049	115	2	5	0	17
Zinc-containing alcohol dehydrogenase superfamily protein GN=NWMN_2272	A6QJL2	37	2	5	1	0
Glutamate dehydrogenase GN=gudB	A6QFG8	47	2	10	6	0
Putative uncharacterized protein GN=NWMN_1317	A6QGV7	44	2	8	1	0
DNA polymerase III polC-type GN=polC	A6QGG4	163	2	28	0	5
Serine/threonine-protein kinase PrkC GN=prkC	A6QGC0	74	2	0	5	15
GTPase Der GN=der	A6QH24	49	2	5	2	2
Tyrosine--tRNA ligase GN=tyrS	A6QHR2	48	2	3	0	1
30S ribosomal protein S6 GN=rpsF	A6QE47	12	2	8	6	16
30S ribosomal protein S9 GN=rpsI	A6QJ59	15	2	5	3	3
Putative uncharacterized protein GN=NWMN_1612	A6QHQ2	17	2	2	0	2
Phage cI-like repressor GN=NWMN_0994	A6QFY4	27	2	1	3	6
DNA-binding response regulator VraR GN=vraR	A6QIB2	24	2	8	2	3
Amino acid ABC transporter, ATP-binding protein GN=NWMN_2311	A6QJQ1	27	2	5	0	7
Putative uncharacterized protein GN=NWMN_0958	A6QFU8	24	2	2	2	5
Phosphopantothencysteine decarboxylase GN=coaBC	A6QGB1	44	2	3	1	0
Oligoendopeptidase F GN=NWMN_0870	A6QFL0	70	2	3	1	4
MarR family regulatory protein GN=NWMN_0655	A6QEZ5	17	2	7	0	5
Putative uncharacterized protein GN=NWMN_2335	A6QJS5	25	2	13	5	17
Putative uncharacterized protein GN=NWMN_1381	A6QH21	22	2	3	0	0
NAD-dependent epimerase/dehydratase GN=NWMN_2375	A6QJW5	25	2	2	0	0
DNA polymerase III gamma subunit GN=dnaX	A6QED2	63	2	16	0	5
ATP-dependent RNA helicase DEAD box family protein GN=NWMN_1985	A6QIS5	57	2	17	0	13
Glucose-6-phosphate isomerase GN=pgi	A6QFH3	50	2	3	0	2
Protein SprT-like GN=NWMN_1968	A6QIQ8	18	2	20	6	16
Chromosomal replication initiator protein DnaA GN=dnaA	A6QD41	52	2	14	0	5
Thiol-disulphide oxidoreductase, DCC family protein GN=NWMN_2044	A6QIY4	16	2	8	3	8
Glutamate-1-semialdehyde 2,1-aminomutase 2 GN=hemL2	A6QI46	47	2	6	0	0
Serine hydroxymethyltransferase GN=glyA	A6QIV7	45	2	7	0	7
Staphylococcal respiratory response protein SrrB GN=srrB	A6QH39	66	2	0	0	8
Putative uncharacterized protein GN=NWMN_2285	A6QJM5	14	0	8	3	4
50S ribosomal protein L23 GN=rplW	A6QJ90	11	0	5	1	6

Phosphoribosylformylglycinamide cyclo-ligase GN=purM	A6QFS9	37	0	7	0	0
Assimilatory nitrite reductase [NAD(P)H], large subunit GN=nirB	A6QJP0	89	0	0	0	13
Cardiolipin synthase 1 GN=cls1	A6QGM0	57	0	1	0	5
Nitric oxide synthase oxygenase GN=NWMN_1852	A6QIE2	42	0	1	4	3
Aldo/keto reductase family protein GN=NWMN_1408	A6QH48	33	0	14	0	18
Putative uncharacterized protein GN=NWMN_0375	A6QE65	36	0	24	2	23
Putative uncharacterized protein GN=NWMN_2332	A6QJS2	26	1	3	0	4
Protein nrdI GN=nrdI	A6QF39	15	1	2	0	4
Molybdenum ABC transporter, periplasmic molybdate-binding protein GN=modA	A6QJB9	29	1	14	0	10
Signal recognition particle protein GN=ffh	A6QGD7	51	1	13	0	16
Putative uncharacterized protein GN=NWMN_0522	A6QEL2	21	1	3	2	0
Homoserine dehydrogenase GN=metL	A6QGN0	47	1	4	0	1
Adapter protein mecA GN=mecA	A6QFK8	28	1	8	0	0
Putative uncharacterized protein GN=NWMN_2282	A6QJM2	16	1	7	0	4
Putative uncharacterized protein GN=NWMN_2002	A6QIU2	19	1	5	0	0
Putative uncharacterized protein GN=NWMN_1430	A6QH70	13	1	4	0	1
ATP synthase epsilon chain GN=atpC	A6QIU6	15	1	0	2	3
ABC transporter ATP-binding protein GN=NWMN_1459	A6QH99	29	1	7	0	6
Putative TrmH family tRNA/rRNA methyltransferase GN=NWMN_0494	Q9AGT0	27	1	5	0	2
Putative uncharacterized protein GN=NWMN_2405	A6QJZ5	27	1	2	0	0
Isoleucine--tRNA ligase GN=ileS	A6QG93	105	1	6	0	0
Phosphoenolpyruvate-protein phosphotransferase GN=NWMN_0950	A6QFU0	63	1	11	0	10
Replicative DNA helicase GN=dnaB	A6QD55	53	1	9	0	5
Peptide chain release factor 3 GN=prfC	A6QFN0	60	1	21	0	13
Pseudouridine synthase GN=NWMN_1646	A6QHT6	27	1	18	6	17
Succinate dehydrogenase flavoprotein subunit GN=sdhA	A6QG51	66	1	2	0	9
Fructose-bisphosphate aldolase GN=fbaA	A6QIW9	31	1	3	0	0
Putative uncharacterized protein GN=NWMN_0615	A6QEV5	30	0	0	0	3
D-alanine-activating DltD protein GN=dltD	A6QFE6	45	0	4	0	0
Siderophore biosynthesis lucC family protein GN=sbnF	A6QDA5	72	0	0	0	5
Putative uncharacterized protein GN=NWMN_0874	A6QFL4	23	0	3	0	0
Riboflavin biosynthesis protein ribF GN=ribF	A6QGH1	37	0	2	0	0
Lactose phosphotransferase system repressor GN=lacR	A6QJ40	29	0	16	8	15
Dihydropteroate synthase chain A GN=folP	A6QEG6	29	0	7	0	2
Secretory antigen SsaA GN=NWMN_2199	A6QJD9	29	0	8	0	0
Glutamine synthetase GN=glnA	A6QGK7	51	0	4	0	0
Probable glycine dehydrogenase [decarboxylating] subunit 2 GN=gcvPB	A6QH79	55	0	22	0	2
Putative uncharacterized protein GN=NWMN_1848	A6QID8	13	0	3	0	3
Oxidoreductase family protein GN=NWMN_0321	A6QE11	38	0	11	0	0
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG GN=mnmG	A6QKK1	70	0	3	0	0
Phage integrase GN=int	A6QIA4	41	0	2	0	0
Tryptophanyl-tRNA synthetase GN=trpS	A6QFK6	37	0	3	0	0
Putative Holliday junction resolvase GN=NWMN_1517	A6QHF7	16	0	4	0	0
Putative uncharacterized protein GN=NWMN_0641	A6QEY1	33	0	9	0	0

UPF0753 protein NWMN_0419 GN=NWMN_0419	A6QEA9	103	0	8	0	18
30S ribosomal protein S15 GN=rpsO	A6QGH2	11	0	9	7	14
CamS sex pheromone cAM373 GN=camS	A6QID1	45	0	10	0	2
Aldehyde dehydrogenase GN=NWMN_1858	A6QIE8	52	0	31	6	22
Glycine betaine/L-proline transport ATP-binding subunit GN=opuCA	A6QJT7	46	0	13	0	0
Transcriptional regulator AraC family protein GN=NWMN_2198	A6QJD8	76	0	13	10	14
Putative uncharacterized protein GN=NWMN_0116	A6QDF6	28	0	10	0	8
DNA topoisomerase IV, A subunit GN=parC	A6QGQ8	91	0	4	0	15
ATP-dependent RNA helicase DEAD/DEAH box family protein GN=NWMN_1461	A6QHA1	51	0	10	2	5
D-alanine--D-alanine ligase GN=ddl	A6QIS7	40	0	8	0	0
Putative uncharacterized protein GN=NWMN_0264	A6QDV4	37	0	6	0	2
UDP-N-acetylmuramate--L-alanine ligase GN=murC	A6QHS3	49	0	15	1	5
Putative uncharacterized protein GN=NWMN_2243	A6QJI3	25	0	0	0	2
50S ribosomal protein L7/L12 GN=rpL	A6QEJ2	13	0	2	0	0
Tributyryl esterase GN=estA	A6QKB8	29	0	6	0	10
Putative uncharacterized protein GN=NWMN_0925	A6QFR5	46	0	2	5	1
UDP-N-acetylglucosamine 2-epimerase GN=capG	A6QDE1	43	0	5	0	0
Glyceraldehyde 3-phosphate dehydrogenase 2 GN=gapB	A6QHM0	37	0	6	0	0
Para-nitrobenzyl esterase chain A GN=NWMN_2350	A6QJU0	52	0	8	0	7
ABC transporter ATP-binding protein GN=NWMN_0603	A6QEU3	28	0	8	4	9
Urease subunit gamma GN=ureA	A6QJC8	11	0	8	4	13
Putative uncharacterized protein GN=NWMN_1924	A6QIL4	18	0	3	0	0
S-ribosylhomocysteine lyase GN=luxS	A6QIX8	18	0	1	4	9
Putative uncharacterized protein GN=NWMN_0671	A6QF11	51	0	3	1	8
Putative uncharacterized protein GN=NWMN_0520	A6QEL0	17	0	3	0	0
Peptidoglycan pentaglycine interpeptide biosynthesis protein GN=fmhB	A6QJA3	49	0	8	0	5
DNA translocase FtsK/SpoIIIE family protein GN=ftsK	A6QGH5	88	0	0	0	10
Ribose transcriptional repressor RbsR GN=rbsR	A6QDP5	37	0	18	6	7
Aspartate carbamoyltransferase GN=pyrB	A6QGA1	33	0	3	0	0
Cardiolipin synthase 2 GN=cls	A6QIT2	57	0	2	2	3
HTH-type transcriptional regulator SarS GN=sarS	A6QD96	30	0	3	1	1
Phosphate starvation-induced protein, PhoH homolog GN=phoH	A6QHB4	35	0	5	0	0
Transcriptional antiterminator BglG family protein GN=NWMN_2539	A6QKC9	73	0	9	0	16
Thioredoxin GN=trxA	A6QG47	11	0	3	0	4
Phage repressor GN=NWMN_1812	A6QIA2	24	0	6	0	0
Putative uncharacterized protein GN=NWMN_0267	A6QDV7	19	0	5	2	6
Putative uncharacterized protein GN=NWMN_0190	A6QDN0	38	0	4	0	2
Protein EssC GN=essC	P0C048	171	0	21	0	8
Ribonuclease R GN=rnr	A6QF89	90	0	0	1	9
Transcriptional regulator Fur family protein GN=NWMN_1753	A6QI43	17	0	9	3	17
GTPase Era GN=era	A6QHB0	34	0	4	0	0
UvrABC system protein B GN=uvrB	A6QF66	77	0	11	0	2
Cell-division initiation protein GN=divIC	A6QEF9	15	0	4	0	2
Putative uncharacterized protein GN=NWMN_1237	A6QGM7	33	0	3	2	11

CBS domain DNA-binding protein GN=NWMN_1599	A6QHN9	49	0	8	0	0
Putative uncharacterized protein GN=NWMN_0984	A6QFX4	35	0	7	0	3
Phage exonuclease GN=NWMN_1922	A6QIL2	36	0	10	2	3
Capsular polysaccharide synthesis enzyme CapC GN=capC	A6QDD7	29	0	7	0	0
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta GN=accD	A6QHN5	32	0	7	0	2
ATPase AAA family protein GN=NWMN_1529	A6QHG9	47	0	5	1	0
Choline dehydrogenase GN=betA	A6QK99	64	0	23	4	4
Transcription-repair coupling factor GN=mfd	A6QEF6	134	0	23	0	9
Putative uncharacterized protein GN=NWMN_0013	A6QD53	74	0	3	0	2
Dihydroorotate dehydrogenase GN=pyrD	A6QK78	40	0	2	0	0
N-acetylmuramoyl-L-alanine amidase domain protein GN=NWMN_2543	A6QKD3	69	0	9	0	7
ABC transporter, ATP-binding protein GN=NWMN_2353	A6QJU3	25	0	8	0	2
DNA replication and repair protein RecF GN=recF	A6QD43	42	0	5	0	0
Putative uncharacterized protein GN=NWMN_1098	A6QG88	26	0	2	0	0
Nitrite reductase transcriptional regulator NirR GN=nirR	A6QJP1	28	0	3	0	1
tRNA modification GTPase MnmE GN=mnmE	A6QKK2	51	0	10	0	2
Threonine dehydratase II GN=ilvA	A6QGY8	37	0	12	0	0
Putative uncharacterized protein GN=NWMN_0024	A6QD64	68	0	6	0	0
AraC family regulatory protein GN=NWMN_0636	A6QEX6	84	0	9	0	11
Serine--tRNA ligase GN=serS	A6QD48	49	0	2	0	0
Putative uncharacterized protein GN=NWMN_2591	A6QKI1	18	0	4	0	0
Alkaline phosphatase synthesis transcriptional regulatory protein GN=phoP	A6QHM6	27	0	6	0	0
Respiratory nitrate reductase, delta subunit GN=narJ	A6QJN5	23	0	4	0	5
RpiR family transcriptional regulator GN=NWMN_0137	A6QDH7	33	0	6	0	1
Superoxide dismutase GN=sodM	A6QDB7	23	0	3	0	3
ABC transporter, ATP-binding protein GN=NWMN_1954	A6QIP4	74	0	10	0	0
Phosphate acyltransferase GN=plsX	A6QGC9	35	0	4	0	0
PTS system, fructose-specific IIABC component GN=NWMN_2540	A6QKD0	70	0	54	9	55
Urease accessory protein UreE GN=ureE	A6QJD1	17	0	35	6	43
Leukocidin/hemolysin toxin family S subunit GN=lukS	A6QIL8	40	0	28	1	5
Competence transcription factor ComK homolog GN=comK	A6QFN5	23	0	20	2	7
DNA topoisomerase IV, B subunit GN=parE	A6QGQ7	74	0	18	0	3
Diapolycopene oxygenase GN=crtP	Q53589	57	0	18	0	0
Leukocidin/hemolysin toxin family F subunit GN=lukF	A6QIL7	39	0	17	0	3
Putative uncharacterized protein GN=NWMN_0273	A6QDW3	26	0	17	0	1
UDP-N-acetylmuramyl tripeptide synthetase GN=NWMN_1830	A6QIC0	49	0	16	3	7
Putative uncharacterized protein GN=NWMN_0046	A6QD86	88	0	16	0	6
Putative uncharacterized protein GN=NWMN_0201	A6QDP1	28	0	12	0	6
Capsular polysaccharide synthesis enzyme O-acetyl transferase CapH GN=capH	A6QDE2	23	0	11	0	3
30S ribosomal protein S14 GN=rpsN	A6QGN8	11	0	11	0	5
ATP-dependent DNA helicase GN=pcrA	A6QID3	84	0	10	0	4
Transcriptional repressor NrdR GN=nrdR	A6QHL9	18	0	10	0	2
Histidine--tRNA ligase GN=hisS	A6QHH3	48	0	9	4	0
Putative uncharacterized protein GN=NWMN_0011	A6QD51	37	0	9	0	6
Arginine repressor GN=argR	A6QH66	17	0	9	0	0

Siderophore biosynthesis lucA family protein GN=sbnE	A6QDA4	66	0	8	0	7
Folypolyglutamate synthase GN=folC	A6QHJ7	48	0	7	0	2
Putative uncharacterized protein GN=NWMN_1947	A6QIN7	35	0	7	0	0
Putative uncharacterized protein GN=NWMN_1351	A6QGZ1	133	0	7	0	4
Elongation factor 4 GN=lepA	A6QHC7	68	0	7	0	9
Putative uncharacterized protein GN=NWMN_1736	A6QI26	46	0	6	2	9
Putative uncharacterized protein GN=NWMN_0451	A6QEE1	28	0	6	2	2
Putative uncharacterized protein GN=NWMN_1322	A6QGW2	29	0	6	0	2
Putative uncharacterized protein GN=NWMN_1739	A6QI29	18	0	6	0	0
Type II pantothenate kinase GN=coaW	A6QIX4	29	0	6	0	0
Putative uncharacterized protein GN=NWMN_1855	A6QIE5	41	0	6	0	1
Ribonuclease 3 GN=rnc	A6QGD3	28	0	6	0	0
Teichoic acid translocation ATP-binding protein GN=tagH	A6QEU7	30	0	6	0	2
Carbamoyl-phosphate synthase small chain GN=pyrAA	A6QGA3	40	0	6	0	6
Glutamate racemase GN=murl	A6QG53	30	0	5	0	0
Aerobactin biosynthesis lucA/lucC family protein GN=NWMN_2080	A6QJ20	67	0	5	0	7
Oligopeptide ABC transporter, ATP-binding protein GN=NWMN_0143	A6QDI3	59	0	5	0	7
Putative uncharacterized protein GN=NWMN_0625	A6QEW5	17	0	5	0	5
DNA repair protein radA GN=radA	A6QEH8	50	0	5	0	2
Putative uncharacterized protein GN=NWMN_2223	A6QJG3	20	0	5	0	0
Cell division protein FtsQ GN=ftsQ	A6QG84	50	0	5	2	14
Glycine--tRNA ligase GN=glyQS	A6QHA8	54	0	5	2	3
Oxidoreductase GN=NWMN_1678	A6QHW8	31	0	5	0	0
Exonuclease GN=NWMN_1832	A6QIC2	21	0	5	0	2
Thymidylate kinase GN=tmk	A6QED6	24	0	5	0	0
Putative uncharacterized protein GN=NWMN_2553	A6QKE3	228	0	5	0	0
Putative uncharacterized protein GN=NWMN_0300	A6QDZ0	19	0	5	0	0
Octanoyltransferase LipM GN=lipM	A6QH77	32	0	5	0	3
Putative uncharacterized protein GN=NWMN_2035	A6QIX5	26	0	5	0	1
Peptidase M22, glycoprotease GN=NWMN_1958	A6QIP8	26	0	5	0	0
Putative uncharacterized protein GN=NWMN_1929	A6QIL9	48	0	5	0	0
4'-phosphopantetheinyl transferase superfamily protein GN=NWMN_0124	A6QDG4	25	0	5	0	2
Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase TrmFO GN=trmFO	A6QGF1	48	0	4	0	5
Putative uncharacterized protein GN=NWMN_0585	A6QES5	19	0	4	0	0
Putative uncharacterized protein GN=NWMN_0269	A6QDV9	10	0	4	0	5
Biofilm operon icaADBC HTH-type negative transcriptional regulator IcaR GN=icaR	A6QKF4	22	0	4	0	1
Putative pyruvate, phosphate dikinase regulatory protein GN=NWMN_1466	A6QHA6	31	0	4	0	0
Dehydrosqualene desaturase GN=crtN	O07855	57	0	4	0	0
Probable cell wall amidase lytH GN=NWMN_1534	A6QHH4	33	0	4	0	5
ATP-dependent DNA helicase RecG GN=recG	A6QGC7	78	0	4	0	0
Putative uncharacterized protein GN=NWMN_0987	A6QFX7	20	0	4	0	1
Putative uncharacterized protein GN=NWMN_1197	A6QGI7	30	0	4	4	5
67 Myosin-crossreactive streptococcal antigen homolog GN=NWMN_0050	A6QD90	68	0	3	0	0

Small heat shock protein Hsp20 GN=NWMN_2287	A6QJM7	16	0	3	1	0
Methionyl-tRNA synthetase GN=metS	A6QEE3	75	0	3	0	0
Truncated MHC class II analog protein GN=NWMN_2109	A6QJ49	15	0	3	0	0
Putative uncharacterized protein GN=NWMN_0376	A6QE66	26	0	3	0	0
Putative uncharacterized protein GN=NWMN_0775	A6QFB5	14	0	3	0	4
Putative uncharacterized protein GN=NWMN_0271	A6QDW1	30	0	3	0	0
Monooxygenase family protein GN=NWMN_2206	A6QJE6	42	0	3	0	0
Putative uncharacterized protein GN=NWMN_0666	A6QF06	18	0	3	0	0
Putative lipid kinase NWMN_0695 GN=NWMN_0695	A6QF35	34	0	3	0	0
Capsular polysaccharide biosynthesis protein CapM GN=capM	A6QDE7	21	0	3	0	1
ABC transporter, substrate-binding protein GN=NWMN_0173	A6QDL3	55	0	3	0	2
Undecaprenyl pyrophosphate synthetase GN=uppS	A6QGG0	30	0	3	0	0
Adenine phosphoribosyltransferase GN=apt	A6QHH7	19	0	3	0	0
Putative uncharacterized protein GN=NWMN_0422	A6QEB2	27	0	3	0	0
Putative uncharacterized protein GN=NWMN_0325	A6QE15	74	0	2	0	0
Putative uncharacterized protein GN=NWMN_0163	A6QDK3	28	0	2	0	2
Immunodominant antigen B GN=isaB	A6QKC7	19	0	2	0	0
Peptidase U32 family protein GN=NWMN_1513	A6QHF3	48	0	2	0	0
Potassium-transporting ATPase C chain GN=kdpC	A6QIS0	21	0	2	0	1
Putative uncharacterized protein GN=NWMN_0649	A6QEY9	21	0	2	0	0
Putative uncharacterized protein GN=NWMN_0809	A6QFE9	39	0	2	0	0
Ribonuclease BN GN=NWMN_1821	A6QIB1	46	0	2	3	0
Teichoic acid biosynthesis protein A GN=tagA	A6QEU6	29	0	2	0	0
tRNA (guanine-N(7)-)-methyltransferase GN=trmB	A6QHT1	25	0	2	0	3
Putative uncharacterized protein GN=NWMN_0575	A6QER5	51	0	2	2	0
Cytosol aminopeptidase GN=ampA	A6QFF2	54	0	2	0	2
Staphyloxanthin biosynthesis protein GN=NWMN_0218	A6QDQ8	33	0	1	3	6
Putative uncharacterized protein GN=NWMN_0222	A6QDR2	52	0	1	3	0
Putative uncharacterized protein GN=NWMN_2386	A6QJX6	110	0	0	0	3
MutS2 protein GN=mutS2	MUTS2	89	0	0	0	6
Membrane protein insertase YidC GN=yidC	A6QIT4	34	0	0	4	6
Putative uncharacterized protein GN=NWMN_0354	A6QE44	32	0	0	4	2
UPF0316 protein NWMN_1849 GN=NWMN_1849	A6QID9	23	0	0	2	3
N-acetyltransferase family protein GN=NWMN_2596	A6QKI6	30	0	0	1	4
Copper-exporting P-type ATPase A GN=copA	A6QK47	87	0	0	0	3
DNA topoisomerase GN=topA	A6QGF0	79	0	0	0	2
Putative uncharacterized protein GN=NWMN_1477	A6QHB7	26	0	0	0	2