b|e|i RESOURCES

SUPPORTING INFECTIOUS DISEASE RESEARCH

Master Clone List for NR-19280

Yersinia pestis Strain KIM Gateway® Clone Set, Recombinant in *Escherichia coli*, Plates 1-43

Catalog No. NR-19280

Table 1: *Yersinia pestis* Gateway® Clone, Plate 1 (UYPVA), NR-19597[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38250	A01	NTL02YP3655	transcriptional activator of nhaA	900	AAM87251.1	3.90531915
38268	A02	NTL02YP0999	apbA protein	912	AAM84595.1	6.01785714
38344	A03	NTL02YP3653	putative regulator	939	AAM87249.1	5.6680286
38375	A04	NTL02YP3668	homoserine kinase	951	AAM87264.1	5.57214934
38386	A05	NTL02YP1006	cytochrome o ubiquinol oxidase subunit II	957	AAM84602.1	5.45937813
38408	A06	NTL02YP2211	suppressor of htrB, heat shock protein	963	AAM85807.1	5.40877368
38447	A07	NTL02YP3649	penicillin tolerance protein	978	AAM87245.1	5.34086444
38477	A08	NTL02YP0988	thiamin-monophosphate kinase	990	AAM84584.1	6.8223301
36045	A09	NTL02YP3670	hypothetical protein	159	AAM87266.1	4.53266332
36094	A10	NTL02YP3672	hypothetical protein	174	AAM87268.1	4.72429907
36136	A11	NTL02YP1000	hypothetical protein	189	AAM84596.1	5.25327511
36241	A12	NTL02YP2577	hypothetical protein	225	AAM86173.1	3.88301887
36280	B01	NTL02YP4086	membrane-bound ATP synthase, F0 sector, subunit c	240	AAM87682.1	4.79285714
36342	B02	NTL02YP3654	30S ribosomal subunit protein S20	264	AAM87250.1	3.86513158
36362	B03	NTL02YP2570	hypothetical protein	270	AAM86166.1	5.40322581
38504	B04	NTL02YP2573	putative ABC transporter permease	996	AAM86169.1	6.65444015
38516	B05	NTL02YP0234	putative heat shock protein	1002	AAM83830.1	2.08445298
38780	B06	NTL02YP0985	bifunctional pyrimidine deaminase/reductase	1110	AAM84581.1	6.64173913
38843	B07	NTL02YP2567	putative hemolysin	1140	AAM86163.1	6.50169492
38933	B08	NTL02YP3656	Na+/H antiporter, pH dependent	1185	AAM87252.1	6.04244898
36435	B10	NTL02YP0995	exonuclease VII, small subunit	297	AAM84591.1	3.96142433
36474	B11	NTL02YP2568	hypothetical protein	309	AAM86165.1	4.90830946
36516	B12	NTL02YP2566	putative alpha helix protein	324	AAM86162.1	6.35714286
36671	C01	NTL02YP3648	hypothetical protein	381	AAM87244.1	5.58194774
36779	C02	NTL02YP0987	transcription termination L factor	417	AAM84583.1	5.97592998
36804	C03	NTL02YP4080	membrane-bound ATP synthase, F1 sector, epsilon-subunit	423	AAM87676.1	5.95464363
36893	C04	NTL02YP4088	membrane-bound ATP synthase	450	AAM87684.1	5.99387755
36885	C05	NTL02YP0984	hypothetical protein	450	AAM84580.1	5.97755102
36951	C06	NTL02YP3674	hypothetical protein	468	AAM87270.1	5.96456693
36966	C07	NTL02YP4085	membrane-bound ATP synthase, F0 sector, subunit b	471	AAM87681.1	5.98238748
37033	C08	NTL02YP2837	pH 6 Antigen fimbrial subunit	492	AAM86433.1	4.9943609
39239	C09	NTL02YP1002	putative transport protein	1371	AAM84598.1	5.897236
39255	C10	NTL02YP4079	N-acetyl glucosamine-1-phosphate uridyltransferase	1377	AAM87675.1	6.22582922
39275	C11	NTL02YP3661	putative proline/betaine transporter	1389	AAM87257.1	6.28551435
39356	C12	NTL02YP0997	putative oxidoreductase	1452	AAM84593.1	6.13739946
39397	D01	NTL02YP2569	exonuclease I	1494	AAM86164.1	5.74380704
39453	D02	NTL02YP4083	membrane-bound ATP synthase, F1 sector, alpha-subunit	1542	AAM87679.1	6.03539823
39637	D03	NTL02YP0993	1-deoxyxylulose-5-phosphate synthase	1860	AAM84589.1	5.79
37095	D04	NTL02YP3651	prolipoprotein signal peptidase (SPase II)	510	AAM87247.1	5.98363636

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37137	D07	NTL02YP0986	riboflavin synthase, beta chain	531	AAM84582.1	7.13309982
37150	D08	NTL02YP3650	probable FKBX-type 16KD peptidyl-prolyl cis-trans isomerase	534	AAM87246.1	7.14111498
37153	D09	NTL02YP4084	membrane-bound ATP synthase, F1 sector, delta-subunit	534	AAM87680.1	5.81707317
37182	D10	NTL02YP3677	hypothetical protein	543	AAM87273.1	6.79588336
37326	D11	NTL02YP3662	putative molybdochetalase	588	AAM87258.1	4.11464968
37341	D12	NTL02YP0983	hypothetical protein	594	AAM84579.1	6.5
37346	E01	NTL02YP0998	4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis enzyme	597	AAM84594.1	6.80376766
39687	E02	NTL02YP4090	hypothetical protein	1971	AAM87686.1	5.23421183
39692	E03	NTL02YP1005	cytochrome o ubiquinol oxidase subunit I	1992	AAM84601.1	5.41043307
39880	E04	NTL02YP3652	isoleucine tRNA synthetase	2817	AAM87248.1	5.18340917
37392	E05	NTL02YP1004	cytochrome o ubiquinol oxidase subunit III	615	AAM84600.1	6.79236641
37505	E06	NTL02YP3676	phosphoglyceromutase 2	648	AAM87272.1	6.71511628
37581	E07	NTL02YP4089	glucose-inhibited division protein	672	AAM87685.1	6.77668539
37634	E08	NTL02YP0982	hypothetical protein	696	AAM84578.1	6
38027	E10	NTL02YP4087	membrane-bound ATP synthase, F0 sector, subunit a	825	AAM87683.1	7.01040462
38031	E11	NTL02YP2575	putative enzyme of sugar metabolism	828	AAM86171.1	7.58410138
38136	E12	NTL02YP4082	membrane-bound ATP synthase, F1 sector, gamma-subunit	864	AAM87678.1	6.4170354
36859	F01	NTL02YPB0035	low calcium response protein R	441	NP_857749.1	4.97505198
36995	F02	NTL02YPD0056	unknown	477	NP_857841.1	4.98646035
37053	F04	NTL02YPB0010	secreted effector protein	498	NP_857725.1	4.98698885
37081	F05	NTL02YPB0038	secretion chaperone	507	NP_857752.1	5.96160878
37203	F06	NTL02YPB0047	yopK targeting protein	549	NP_857759.1	4.72665535
37213	F07	NTL02YPB0063	putative resolvase	552	NP_857768.1	4.79898649
37329	F08	NTL02YPA0007	hypothetical protein	588	NP_857644.2	4.79936306
37385	F09	NTL02YPA0003	tail fiber assembly protein G	609	NP_857640.2	4.38983051
36165	F10	NTL02YPB0049	hypothetical protein	198	NP_954879.1	3.94117647
36196	F11	NTL02YPE0007	hypothetical protein	207	NP_857909.1	4.80161943
36344	G01	NTL02YPB0012	needle complex major subunit	264	NP_857727.1	3.90131579
37458	G03	NTL02YPD0049	unknown	633	NP_857833.1	4.80089153
37523	G04	NTL02YPB0024	needle complex export protein	654	NP_857738.1	4.78530259
37543	G05	NTL02YPB0055	secreted effector protein	660	NP_857762.1	4.78857143
37565	G06	NTL02YPB0006	needle complex assembly protein	666	NP_857721.1	4.78328612
37761	G07	NTL02YPB0008	needle complex inner membrane lipoprotein	735	NP_857723.1	4.38193548
37909	G10	NTL02YPB0022	needle complex export protein	786	NP_857736.1	3.99031477
37932	G11	NTL02YPA0076	hypothetical protein	795	NP_857699.2	5.63353293
37998	H01	NTL02YPB0018	transcriptional regulator	816	NP_857733.1	5.62149533
36391	H02	NTL02YPB0030	secretion and targeting control protein	279	NP_857744.1	3.80877743
36420	H03	NTL02YPB0036	low calcium response protein G	288	NP_857750.1	3.99085366
36440	H04	NTL02YPB0054	yKCD1p58 hypothetical protein	297	NP_954882.1	5.7537092
38040	H07	NTL02YPA0050	hypothetical protein	831	NP_857682.2	5.57520092
38195	H08	NTL02YPB0029	secretion control protein	882	NP_857743.1	4.23318872
38297	H09	NTL02YPB0025	needle complex export protein	924	NP_857739.1	2.93568465
38413	H10	NTL02YPB0051	plasmid-partitioning control protein	963	NP_857761.2	3.53938185
38424	H11	NTL02YPB0046	secreted effector protein	969	NP_857758.1	3.60951437

Table 2: *Yersinia pestis* Gateway® Clone, Plate 3 (UYPVC), NR-19599[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37892	A01	NTL02YP0041	putative transposase	783	AAM83637.1	4.63791009
38232	A02	NTL02YP2052	hypothetical protein	894	AAM85648.1	3.91755889
38295	A03	NTL02YP2076	putative transcriptional regulator LYSR-type	924	AAM85672.1	5.44190871
37778	A04	NTL02YP2559	putative oxidoreductase	741	AAM86155.1	5.73751601
37798	A05	NTL02YP0373	uroporphyrinogen III synthase	750	AAM83969.1	3.97974684
37813	A06	NTL02YP0345	chaperone	756	AAM83941.1	4.78894472
37917	A07	NTL02YP0348	glutamine cyclotransferase	792	AAM83944.1	5.09254808
37953	A08	NTL02YP3642	putative structural protein	801	AAM87238.1	4.10107015
38007	A09	NTL02YP3635	S-adenosylmethionine-6-N,N-adenosyl (rRNA) dimethyltransferase	819	AAM87231.1	5.61233993
38001	A10	NTL02YP0342	putative pilus chaperone, PapD family	819	AAM83938.1	3.98719441
38016	A11	NTL02YP3646	dihydrodipicolinate reductase	822	AAM87242.1	5.64617169
38048	A12	NTL02YP3631	putative DNA binding protein	834	AAM87227.1	4.61098398
38074	B01	NTL02YP2558	putative isomerase	843	AAM86154.1	5.60588901
36049	B02	NTL02YP1470	hypothetical protein	162	AAM85066.1	1.98514851
36059	B03	NTL02YP0351	hypothetical protein	165	AAM83947.1	4.88780488
36082	B04	NTL02YP2556	hypothetical protein	171	AAM86152.1	1.98578199
36135	B05	NTL02YP0377	hypothetical protein	189	AAM83973.1	7.72925764
36151	B06	NTL02YP1469	hypothetical protein	195	AAM85065.1	3.97446809
36259	B07	NTL02YP2527	hypothetical protein	234	AAM86123.1	2
36284	B08	NTL02YP1468	conserved protein	243	AAM85064.1	2.98233216
36386	B09	NTL02YP2519	hypothetical protein	279	AAM86115.1	3.85893417
36396	B10	NTL02YP2526	hypothetical protein	282	AAM86122.1	3.85403727
36434	B11	NTL02YP0349	peptidyl-prolyl cis-trans isomerase C	297	AAM83945.1	3.95252226
38154	B12	NTL02YP3637	diadenosine tetraphosphatase	870	AAM87233.1	4.64725275
38159	C01	NTL02YP1436	putative NAGC-like transcriptional regulator	873	AAM85032.1	8.52135816
38191	C02	NTL02YP2550	hypothetical protein	882	AAM86146.1	3.9197397
38244	C03	NTL02YP1433	putative acetylneuraminate lyase	900	AAM85029.1	8.22978723
38273	C04	NTL02YP1432	hypothetical protein	915	AAM85028.1	8.29528796
38422	C05	NTL02YP1464	cysteine synthase A, O-acetylserine sulfhydrolase A	969	AAM85060.1	7.83448959
38479	C06	NTL02YP1477	putative reductase	990	AAM85073.1	5.31456311
38540	C07	NTL02YP3634	pyridoxine biosynthesis protein	1008	AAM87230.1	5.2471374
38583	C08	NTL02YP1466	cell division protein	1026	AAM85062.1	3.82551595
38771	C09	NTL02YP3616	hypothetical protein	1104	AAM87212.1	5.02272727
38819	C10	NTL02YP1435	putative membrane protein	1128	AAM85031.1	4.32106164
36442	C11	NTL02YP2525	hypothetical protein	300	AAM86121.1	3.87352941
36481	C12	NTL02YP2524	hypothetical protein	312	AAM86120.1	6.82954545
36586	D01	NTL02YP1476	hypothetical protein	351	AAM85072.1	3.99232737
36612	D02	NTL02YP3609	hypothetical protein	360	AAM87205.1	3.9675
36627	D03	NTL02YP3614	hypothetical protein	366	AAM87210.1	3.99507389
36653	D04	NTL02YP3613	hypothetical protein	375	AAM87209.1	3.98554217
36661	D05	NTL02YP3636	hypothetical protein	378	AAM87232.1	3.98564593
36769	D06	NTL02YP1430	hypothetical protein	414	AAM85026.1	5.5
36780	D07	NTL02YP1428	hypothetical protein	417	AAM85024.1	3.97374179
36942	D08	NTL02YP3638	hypothetical protein	465	AAM87234.1	3.99405941
36959	D09	NTL02YP1437	hypothetical protein	471	AAM85033.1	3.99021526
38830	D10	NTL02YP0372	uroporphyrinogen III methylase	1134	AAM83968.1	4.93867121
38854	D11	NTL02YP2555	L-lactate dehydrogenase	1146	AAM86151.1	4.7529511

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38902	D12	NTL02YP0343	conserved hypothetical protein	1173	AAM83939.1	5.48227535
38968	E01	NTL02YP3645	carbamoyl-phosphate synthetase, glutamine (small) subunit	1203	AAM87241.1	4.84231698
38990	E02	NTL02YP0371	hemY protein	1221	AAM83967.1	4.53291039
39005	E03	NTL02YP1475	putative manganese transport system permease	1230	AAM85071.1	3.98031496
39074	E04	NTL02YP2557	hypothetical protein	1278	AAM86153.1	2.50227618
39086	E05	NTL02YP0352	putative ATP-dependent RNA helicase	1287	AAM83948.1	5.39939714
39104	E06	NTL02YP2546	putative membrane permease of ABC transporter	1293	AAM86142.1	5.20780195
36993	E07	NTL02YP3641	hypothetical protein	477	AAM87237.1	3.9787234
37010	E08	NTL02YP3640	dihydrofolate reductase type I	483	AAM87236.1	3.82600382
37026	E09	NTL02YP2560	hypothetical protein	489	AAM86156.1	4.95463138
37022	E10	NTL02YP0369	hypothetical protein	489	AAM83965.1	3.97920605
37082	E11	NTL02YP0136	putative transposase	510	AAM83732.1	4.79272727
37088	F01	NTL02YP1461	PTS system, glucose-specific IIA component	510	AAM85057.1	4
37084	F02	NTL02YP0223	putative transposase	510	AAM83819.1	3.98909091
37136	F03	NTL02YP0346	fimbrial protein (precursor)	531	AAM83942.1	4.79334501
37167	F04	NTL02YP2548	nucleoprotein/polynucleotide-associated enzyme	540	AAM86144.1	4.82758621
39194	F05	NTL02YP2551	putative inner membrane permease	1341	AAM86147.1	5.23171615
39207	F06	NTL02YP1458	putative kinase sensor protein	1350	AAM85054.1	5.09856115
39216	F07	NTL02YP2518	hypothetical protein	1356	AAM86114.1	4.91475645
39241	F08	NTL02YP2554	argininosuccinate synthetase	1371	AAM86150.1	4.41034727
39248	F09	NTL02YP3612	hypothetical protein	1374	AAM87208.1	5.2241867
39278	F10	NTL02YP0368	putative amino acid/amine symporter	1392	AAM83964.1	
39299	F11	NTL02YP2561	putative transport protein	1401	AAM86157.1	4.37890354
39313	F12	NTL02YP1473	glutamate tRNA synthetase, catalytic subunit	1416	AAM85069.1	4.88667582
39328	G01	NTL02YP2552	hypothetical protein	1431	AAM86148.1	5.00747791
39513	G02	NTL02YP3611	hypothetical protein	1638	AAM87207.1	4.70441001
39577	G03	NTL02YP1462	PEP-protein phosphotransferase system enzyme I	1728	AAM85058.1	4.45588235
37280	G04	NTL02YP1460	hypothetical protein	576	AAM85056.1	3.97727273
37387	G05	NTL02YP1471	hypothetical protein	612	AAM85067.1	4.80521472
37406	G06	NTL02YP3615	hypothetical protein	618	AAM87211.1	4.79331307
37449	G07	NTL02YP2547	response regulator	630	AAM86143.1	4.79701493
37518	G08	NTL02YP2522	hypothetical protein	654	AAM86118.1	3.83285303
37595	G09	NTL02YP3643	hypothetical protein	678	AAM87239.1	4.81615599
37638	G10	NTL02YP2549	hypothetical protein	696	AAM86145.1	3.99320652
37655	G11	NTL02YP1434	putative enzyme	702	AAM85030.1	4
37756	G12	NTL02YP1465	cysZ protein	735	AAM85061.1	4.37935484
37766	H01	NTL02YP2521	hypothetical protein	738	AAM86117.1	4
38179	H02	NTL02YP1439	putative transcriptional regulator	879	AAM85035.1	4.8759521
38197	H03	NTL02YP0338	positive regulator for ilvC	885	AAM83934.1	5.9675676
38214	H04	NTL02YP2538	putative transcriptional regulator	888	AAM86134.1	4.5948276
38213	H05	NTL02YP2512	PTS enzyme IID, mannose-specific	888	AAM86108.1	4.5765086
38427	H06	NTL02YP1452	hypothetical protein	972	AAM85048.1	4.1758893
38555	H07	NTL02YP3628	hypothetical protein	1014	AAM87224.1	4.1185958
36000	H08	NTL02YP2516	hypothetical protein	150	AAM86112.1	3.9157895
36064	H09	NTL02YP2530	hypothetical protein	165	AAM86126.1	2.795122

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36108	H10	NTL02YP2509	hypothetical protein	180	AAM86105.1	3.9681818
36189	H11	NTL02YP1451	hypothetical protein	207	AAM85047.1	1.8825911

Table 3: *Yersinia pestis* Gateway® Clone, Plate 4 (UYPVD), NR-19600[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36443	A01	NTL02YP2534	hypothetical protein	300	AAM86130.1	3.2
38615	A03	NTL02YP1441	thiosulfate binding periplasmic protein of sulfate/thiosulfate ABC	1038	AAM85037.1	4.40445269
38697	A04	NTL02YP0359	dTDP-glucose 4,6-dehydratase	1074	AAM83955.1	4.43716338
38707	A05	NTL02YP0356	putative transport protein	1080	AAM83952.1	4.38035714
38725	A07	NTL02YP0364	TDP-Fuc4NAc:lipid II Fuc4NAc transferase	1086	AAM83960.1	4.28419183
38741	A08	NTL02YP0360	glucose-1-phosphate thymidylyltransferase	1092	AAM83956.1	6.97173145
38754	A09	NTL02YP0355	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase	1098	AAM83951.1	6.46924429
38760	A10	NTL02YP3598	3-isopropylmalate dehydrogenase	1098	AAM87194.1	2.36906854
38801	A11	NTL02YP1444	ATP-binding component of sulfate permease A protein	1119	AAM85040.1	3.83951682
38923	A12	NTL02YP3601	putative efflux protein	1182	AAM87197.1	3.22094926
38926	B01	NTL02YP0357	UDP-N-acetyl glucosamine -2-epimerase	1185	AAM83953.1	2.29714286
36519	B02	NTL02YP0353	thioredoxin 1	327	AAM83949.1	4.9346049
36538	B03	NTL02YP3619	hypothetical protein	333	AAM87216.1	5.58713137
36678	B04	NTL02YP2529	putative regulator	387	AAM86125.1	3.99297424
36866	B05	NTL02YP3624	hypothetical protein	444	AAM87220.1	4.23760331
36904	B06	NTL02YP1421	cytochrome c-type protein	456	AAM85017.1	5.83669355
36915	B07	NTL02YP1425	hypothetical protein	459	AAM85021.1	3.44088176
36923	B08	NTL02YP0337	hypothetical protein	462	AAM83933.1	5.53984064
37002	B09	NTL02YP0336	hypothetical protein	483	AAM83932.1	2
38970	B10	NTL02YP1456	putative membrane protein, possible efflux component	1206	AAM85052.1	3.89486356
38969	B11	NTL02YP0362	putative regulator	1206	AAM83958.1	2.92857143
38999	C01	NTL02YP1450	putative aminotransferase	1227	AAM85046.1	3.78768745
39010	C02	NTL02YP1446	hypothetical protein	1233	AAM85042.1	4.0494894
39031	C03	NTL02YP2540	galactoside permease (M protein)	1245	AAM86136.1	4.10116732
39040	C04	NTL02YP0363	putative cytochrome	1257	AAM83959.1	4.52505783
39047	C05	NTL02YP0354	transcription termination factor Rho polarity suppressor	1260	AAM83950.1	5.24538462
39052	C06	NTL02YP0358	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	1263	AAM83954.1	3.42747506
39227	C07	NTL02YP0365	TDP-Fuc4NAc:lipidII transferase	1365	AAM83961.1	3.67544484
39287	C08	NTL02YP2508	putative transport protein	1395	AAM86104.1	3.68850174
39344	C09	NTL02YP0341	hypothetical protein	1443	AAM83937.1	5.96358732
37072	C10	NTL02YP2545	hypothetical protein	507	AAM86141.1	7.4095064
37116	C11	NTL02YP3625	hypothetical protein	519	AAM87221.1	6.72271914
37114	C12	NTL02YP2517	hypothetical protein	519	AAM86113.1	6.5706619
37236	D01	NTL02YP3627	hypothetical protein	561	AAM87223.1	5.83361065
37265	D02	NTL02YP2514	hypothetical protein	570	AAM86110.1	2.72622951
37368	D03	NTL02YP3600	isopropylmalate isomerase subunit	603	AAM87196.1	4.79160187

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37402	D04	NTL02YP1422	cytochrome c-type protein	618	AAM85018.1	5.80243161
37421	D05	NTL02YP3630	hypothetical protein	621	AAM87226.1	2
37430	D06	NTL02YP1423	hypothetical protein	624	AAM85019.1	2.80120482
37535	D07	NTL02YP2543	yersiniabactin biosynthesis component	657	AAM86139.1	5.13629842
37608	D08	NTL02YP1457	transcriptional regulator in 2-component system	684	AAM85053.1	2
39366	D09	NTL02YP1453	putative permease	1461	AAM85049.1	3.47368421
39381	D10	NTL02YP0339	ketol-acid reductoisomerase	1479	AAM83935.1	3.9526004
39405	D11	NTL02YP3599	3-isopropylmalate isomerase (dehydratase) subunit	1500	AAM87195.1	2.36168831
39418	D12	NTL02YP3626	hypothetical protein	1512	AAM87222.1	4.29381443
39438	E01	NTL02YP1449	hypothetical protein	1530	AAM85045.1	3.98917197
39455	E02	NTL02YP1448	putative sensor kinase	1545	AAM85044.1	5.56845426
39499	E03	NTL02YP3604	putative ABC transport system thiamine permease protein	1620	AAM87200.1	3.11385542
39572	E04	NTL02YP2532	putative ABC transporter	1719	AAM86127.1	3.15747584
39629	E05	NTL02YP3623	hypothetical protein	1845	AAM87219.1	5.76976127
37752	E06	NTL02YP3605	putative ATP-binding component of a transport system	732	AAM87201.1	5.27072539
37773	E07	NTL02YP0366	probable UDP-N-acetyl-D-mannosaminuronic acid transferase	741	AAM83962.1	3.76568502
37789	E08	NTL02YP3629	hypothetical protein	744	AAM87225.1	6.37372449
37848	E09	NTL02YP3606	hypothetical protein	768	AAM87202.1	6.24752475
37925	E10	NTL02YP0361	hypothetical protein	795	AAM83957.1	2.17964072
37984	E11	NTL02YP2535	hypothetical protein	813	AAM86131.1	4.56740914
38043	E12	NTL02YP1442	inner membrane permease T of sulfate/thiosulfate ABC	834	AAM85038.1	4.56750572
38065	F01	NTL02YP2511	PTS enzyme IIC, mannose-specific	840	AAM86107.1	2.33181818
38096	F02	NTL02YP2533	hypothetical protein	852	AAM86129.1	1.98654709
37960	F03	NTL02YP2502	putative 2-oxo-hept-3-ene-1,7-dioate hydratase	804	AAM86098.1	3.78672986
38042	F04	NTL02YP1379	hypothetical protein	834	AAM84975.1	4.37070938
38119	F05	NTL02YP2505	putative 3,4-dihydroxyphenylacetate 2,3-dioxygenase	858	AAM86101.1	4.63028953
38139	F06	NTL02YP1398	hypothetical protein	867	AAM84994.1	4.51157663
38185	F07	NTL02YP0327	hypothetical protein	882	AAM83923.1	6.59761388
38201	F08	NTL02YP2482	putative resistance protein, exporter	885	AAM86078.1	2
36061	F09	NTL02YP1412	hypothetical protein	165	AAM85008.1	-
36268	F10	NTL02YP1401	hypothetical protein	237	AAM84997.1	2.94945848
36361	F11	NTL02YP2485	DNA polymerase III, theta subunit	270	AAM86081.1	3.70645161
36385	F12	NTL02YP1416	hypothetical protein	279	AAM85012.1	3
36489	G01	NTL02YP0297	repressor of all met genes but metF	318	AAM83893.1	-
36604	G02	NTL02YP2481	hypothetical protein	357	AAM86077.1	3.79093199
38278	G03	NTL02YP0315	activator, hydrogen peroxide-inducible genes	918	AAM83911.1	6.73695198
38307	G04	NTL02YP0289	1,4-dihydroxy-2-naphthoate octaprenyltransferase	930	AAM83885.1	6.80721649
38372	G05	NTL02YP2486	putative proline iminopeptidase	951	AAM86082.1	6.96367306
38423	G06	NTL02YP3594	probable transcriptional activator for leuABCD operon	969	AAM87190.1	5.81863231
38487	G07	NTL02YP0326	putative ABC transporter permease protein	993	AAM83922.1	4.51597289

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38517	G08	NTL02YP0332	branched-chain amino-acid aminotransferase	1002	AAM83928.1	5.38387716
38547	G09	NTL02YP3589	transcriptional repressor of fru operon and others	1011	AAM87185.1	5.46146527
38631	G10	NTL02YP1383	phosphoribosylaminoimidazole synthetase	1044	AAM84979.1	4.12730627
38668	G11	NTL02YP1395	lipoprotein-34	1062	AAM84991.1	3.48366606
36792	G12	NTL02YP1392	hypothetical protein	420	AAM84988.1	6.56521739
36798	H01	NTL02YP0328	hypothetical protein	423	AAM83924.1	2.99352052
36908	H02	NTL02YP3588	hypothetical protein	456	AAM87184.1	2
36918	H03	NTL02YP2480	hypothetical protein	459	AAM86076.1	4.55310621
36914	H04	NTL02YP1387	putative oxidoreductase	459	AAM84983.1	4.77154309
36946	H05	NTL02YP0296	hypothetical protein	468	AAM83892.1	2
36971	H06	NTL02YP1399	hypothetical protein	474	AAM84995.1	4.89688716
36970	H07	NTL02YP1393	bacterioferritin comigratory protein	474	AAM84989.1	5.5
36991	H08	NTL02YP2507	putative regulator	477	AAM86103.1	2
38677	H09	NTL02YP1389	putative permease	1065	AAM84985.1	3.3520362
38818	H10	NTL02YP1403	N-succinyl-diaminopimelate deacylase	1128	AAM84999.1	3.38955479
38885	H11	NTL02YP2479	flagellar biosynthesis protein	1161	AAM86075.1	4.05578684
38898	H12	NTL02YP0304	acetylornithine deacetylase	1170	AAM83900.1	3.97355372

Table 4: *Yersinia pestis* Gateway® Clone, Plate 5 (UYPVE), NR-19601[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38938	A01	NTL02YP1411	putative enzyme	1188	AAM85007.1	5.758957655
39177	A02	NTL02YP0290	heat shock protein, ATPase subunit	1332	AAM83886.1	4.674198251
39183	A03	NTL02YP0316	putative oxidoreductase	1335	AAM83878.1	4.088
39233	A04	NTL02YP2500	hypothetical 4-hydroxyphenylacetate permease	1368	AAM86096.1	4.575284091
39294	A05	NTL02YP2506	putative 5-carboxy-2-hydroxymuconate semialdehyde dehydrogenase	1398	AAM86102.1	4.448539638
37121	A07	NTL02YP0291	heat shock protein, proteasome-related peptidase subunit	525	AAM83887.1	3.808849558
37194	A08	NTL02YP2483	hypothetical protein	546	AAM86079.1	2.093856655
37190	A09	NTL02YP1381	spermidine N1-acetyltransferase	546	AAM84977.1	2.817406143
37198	A10	NTL02YP1413	hypothetical protein	549	AAM85009.1	2.797962649
37310	A11	NTL02YP1414	hypothetical protein	585	AAM85010.1	3.7408
37352	A12	NTL02YP0300	putative transposase	600	AAM83896.1	1.9875
37397	B01	NTL02YP0309	secreted hemophore	618	AAM83905.1	1.981762918
39454	B02	NTL02YP0329	putative 2-component regulator	1545	AAM83925.1	4.23533123
39473	B03	NTL02YP3597	2-isopropylmalate synthase	1563	AAM87193.1	4.134747349
39472	B04	NTL02YP2499	putative component B of 4-hydroxyphenylacetic acid-hydroxylase	1563	AAM84984.1	3.84404242
39479	B05	NTL02YP1388	hypothetical protein	1578	AAM84761.1	5.563658838
39543	B06	NTL02YP1410	putative sulfatase	1674	AAM85006.1	4.127187865
39601	B07	NTL02YP3592	acetolactate synthase III, large subunit	1782	AAM87188.1	3.885839737
39616	B08	NTL02YP3593	putative fatty acid biosynthesis protein	1806	AAM87189.1	4.503791983
39650	B09	NTL02YP0333	dihydroxyacid dehydratase	1899	AAM83929.1	5.090252708
39669	B10	NTL02YP2045	RNase II, mRNA degradation	1935	AAM85641.1	4.259240506
37469	B11	NTL02YP1382	phosphoribosylglycinamide formyltransferase 1	639	AAM84978.1	3.72017673

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37474	B12	NTL02YP0301	putative transposase	642	AAM83897.1	5.089442815
37498	C01	NTL02YP0317	hypothetical protein	648	AAM83913.1	3.763081395
37538	C02	NTL02YP1384	uracil phosphoribosyltransferase	660	AAM84980.1	1.801428571
37551	C03	NTL02YP1417	nitrate/nitrite response regulator	663	AAM85013.1	1.995732575
37591	C04	NTL02YP1402	hypothetical protein	678	AAM84998.1	3.380222841
37636	C05	NTL02YP1391	hypothetical protein	696	AAM84987.1	3.362771739
37688	C06	NTL02YP1397	phosphoribosylaminoimidazole-succinocarboxamide synthetase	714	AAM84993.1	3.75994695
37706	C07	NTL02YP1386	putative DNA replication factor	720	AAM84982.1	2
37740	C08	NTL02YP0314	peroxiredoxin family protein	732	AAM83910.1	6.67357513
37855	C09	NTL02YP2011	hypothetical protein	771	AAM85607.1	4.628853268
37864	C10	NTL02YP0933	putative amidotransferase	774	AAM84529.1	4.626535627
37863	C11	NTL02YP0911	hypothetical protein	774	AAM84507.1	9.843980344
37939	D01	NTL02YP2042	putative transaldolase	798	AAM85638.1	3.721957041
37958	D02	NTL02YP2040	L-ribulose-5-phosphate 4-epimerase	804	AAM85636.1	5.79028436
38117	D03	NTL02YP2030	hypothetical protein	858	AAM85626.1	4.599109131
38113	D04	NTL02YP0938	Na-translocating NADH ubiquinone oxidoreductase, gamma chain	858	AAM84534.1	1.944320713
35948	D05	NTL02YP0925	hypothetical protein	120	AAM84521.1	2.9875
36033	D06	NTL02YP0916	hypothetical protein	159	AAM84512.1	2
36105	D07	NTL02YP0935	hypothetical protein	180	AAM84531.1	2.845454545
36117	D08	NTL02YP0915	hypothetical protein	183	AAM84511.1	3.950672646
36219	D09	NTL02YP2039	osmotically inducible lipoprotein	216	AAM85635.1	4.96484375
36218	D10	NTL02YP2012	hypothetical protein	216	AAM85608.1	4.93359375
36217	D11	NTL02YP2001	hypothetical protein	216	AAM85597.1	4
36306	D12	NTL02YP2026	hypothetical protein	252	AAM85622.1	6.52739726
38255	E01	NTL02YP1998	oligopeptide ABC transporter permease protein	906	AAM85594.1	7.261099366
38266	E02	NTL02YP0946	probable LysR-type transcriptional regulatory protein	912	AAM84542.1	6.441176471
38332	E03	NTL02YP2020	putative enzyme	936	AAM85616.1	7.111680328
38361	E04	NTL02YP0943	hypothetical protein	948	AAM84539.1	6.737854251
38440	E05	NTL02YP2029	positive transcriptional regulator for cysteine regulon	975	AAM85625.1	6.608866995
38522	E06	NTL02YP2000	ATP-binding protein of oligopetide ABC transporter	1002	AAM85596.1	4.41074856
38521	E07	NTL02YP1999	ATP-binding protein of oligopetide ABC transporter	1002	AAM85595.1	4.419385797
38609	E09	NTL02YP2022	hypothetical protein	1035	AAM85618.1	3.349767442
38639	E10	NTL02YP2025	putative protease	1047	AAM85621.1	4.480220791
36438	E11	NTL02YP2006	hypothetical protein	297	AAM85602.1	2
36485	E12	NTL02YP2014	hypothetical protein	315	AAM85610.1	4
36515	F01	NTL02YP2034	hypothetical protein	324	AAM85630.1	5.313186813
36521	F02	NTL02YP2038	hypothetical protein	327	AAM85634.1	5.811989101
36528	F03	NTL02YP2043	hypothetical protein	330	AAM85639.1	6.043243243
36563	F04	NTL02YP0910	hypothetical protein	342	AAM84506.1	2
36650	F05	NTL02YP2002	hypothetical protein	375	AAM85598.1	7.638554217
36731	F06	NTL02YP0950	transcriptional regulator of cryptic csgA gene for	402	AAM84546.1	6.846153846
36753	F07	NTL02YP2027	hypothetical protein	408	AAM85623.1	1.997767857
36913	F08	NTL02YP0948	guanine-hypoxanthine phosphoribosyltransferase	459	AAM84544.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38689	F09	NTL02YP0944	damage-inducible protein P putative tRNA synthetase	1071	AAM84540.1	4.335733573
38715	F10	NTL02YP0942	hypothetical protein	1083	AAM84538.1	4.261798753
38767	F11	NTL02YP0951	gamma-glutamate kinase	1104	AAM84547.1	4.212412587
38813	F12	NTL02YP2008	putative transposase	1125	AAM85604.1	4.182832618
38900	G01	NTL02YP2035	putative heat shock protein	1170	AAM85631.1	4.410743802
38956	G02	NTL02YP0912	putative permease, major facilitator superfamily	1200	AAM84508.1	3.292741935
38994	G03	NTL02YP0941	Na-translocating NADH ubiquinone oxidoreductase, beta chain	1224	AAM84537.1	4.039556962
39027	G04	NTL02YP0937	Na-translocating NADH ubiquinone oxidoreductase:subunit B	1242	AAM84533.1	4.070202808
39058	G05	NTL02YP0949	hypothetical protein	1266	AAM84545.1	3.951761103
36947	G06	NTL02YP0913	hypothetical protein	468	AAM84509.1	3.998031496
37117	G07	NTL02YP0955	putative biotin synthesis protein	522	AAM84551.1	4.428825623
37122	G08	NTL02YP0957	shikimate kinase II	525	AAM84553.1	3.732743363
37155	G09	NTL02YP0909	regulator of plasmid mcrB operon (microcin B17	537	AAM84505.1	3.814558059
37178	G10	NTL02YP2010	hypothetical protein	543	AAM85606.1	3.794168096
37298	G11	NTL02YP0932	phosphoheptose isomerase	582	AAM84528.1	2.781350482
37322	G12	NTL02YP0956	hypothetical protein	588	AAM84552.1	3.792993631
37334	H01	NTL02YP2023	cob(I)alamin adenolsyltransferase	591	AAM85619.1	2
37367	H02	NTL02YP2032	GTP cyclohydrolase II	603	AAM85628.1	7.152410575
37361	H03	NTL02YP0940	hypothetical protein	603	AAM84536.1	3.782270607
37416	H04	NTL02YP2021	hypothetical protein	621	AAM85617.1	2
39091	H05	NTL02YP2017	tryptophan synthase, beta protein	1287	AAM85613.1	3.854559156
39222	H06	NTL02YP0936	Na-translocating NADH ubiquinone oxidoreductase:subunit A	1362	AAM84532.1	4.514265335
39289	H07	NTL02YP0914	putative glutamyl-tRNA(gln) amidotransferase subunit A	1398	AAM84510.1	4.337969402
39326	H08	NTL02YP2018	N-(5-phosphoribosyl)anthranilate isomerase	1428	AAM85614.1	4.08106267
39365	H09	NTL02YP0945	aminoacyl-histidine dipeptidase (peptidase D)	1461	AAM84541.1	4.2751499
39490	H10	NTL02YP0947	hypothetical protein	1605	AAM84543.1	4.041337386
39512	H11	NTL02YP1996	oligopeptide ABC transporter periplasmic binding protein	1638	AAM85592.1	4.190107271
39606	H12	NTL02YP0926	putative membrane protein, C-terminal part of adhesin	1791	AAM84522.1	4.592572365

Table 5: *Yersinia pestis* Gateway® Clone, Plate 6 (UYPVF), NR-19602[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37445	A01	NTL02YP0939	Na^+-translocating NADH ubiquinone oxidoreductase	630	AAM84535.1	2
37501	A02	NTL02YP2013	putative outer membrane protein	648	AAM85609.1	3.80232558
37516	A03	NTL02YP0920	putative permease of ABC transporter	654	AAM84516.1	3.38040346
37549	A04	NTL02YP0934	hypothetical protein	663	AAM84530.1	3.42247511
37568	A05	NTL02YP0919	putative inner membrane permease of ABC transporter	669	AAM84515.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37764	A06	NTL02YP2037	orotidine-5-phosphate decarboxylase	738	AAM85633.1	3.76478149
37792	A07	NTL02YP0930	hypothetical protein	747	AAM84526.1	6.12579416
37791	A08	NTL02YP0921	glutamine transport ATP-binding protein	747	AAM84517.1	2
37821	A09	NTL02YP0953	hypothetical protein	759	AAM84549.1	7.61827284
37823	A10	NTL02YP2007	energy transducer	759	AAM85603.1	5.40801001
37830	A11	NTL02YP2033	membrane bound non-essential phosphatidylglycerophosphate phosphatase	762	AAM85629.1	7.1084788
37645	A12	NTL02YP2466	cell-distal portion of basal-body rod	699	AAM86062.1	5.69012179
37743	B01	NTL02YP0899	hypothetical protein	732	AAM84495.1	1.99870466
37742	B02	NTL02YP0897	hypothetical protein	732	AAM84493.1	2.9857513
37748	B03	NTL02YP2465	basal-body outer-membrane L (lipopolysaccharide layer) ring protein	732	AAM86061.1	6.75
37800	B04	NTL02YP0904	hypothetical protein	750	AAM84500.1	4.15949367
37836	B05	NTL02YP2472	putative flagella basal body P-ring formation protein	765	AAM86068.1	3.79627329
37862	B06	NTL02YP0889	hypothetical protein	774	AAM84485.1	4.16953317
35984	B10	NTL02YP3560	hypothetical protein	147	AAM87156.1	1.98395722
36023	B11	NTL02YP1987	hypothetical protein	156	AAM85583.1	2.82653061
36028	B12	NTL02YP3556	hypothetical protein	156	AAM87152.1	3.85714286
36081	C01	NTL02YP2473	hypothetical protein	171	AAM86069.1	1.98578199
36090	C02	NTL02YP2476	hypothetical protein	174	AAM86072.1	5.89252336
36112	C03	NTL02YP3565	hypothetical protein	180	AAM87161.1	3.84090909
36210	C04	NTL02YP1372	hypothetical protein	213	AAM84968.1	6.43873518
36240	C05	NTL02YP2458	hypothetical protein	225	AAM86054.1	2.66037736
37980	C06	NTL02YP0887	hypothetical protein	813	AAM84483.1	4.64712778
37981	C07	NTL02YP1377	phosphate-specific transport component	813	AAM84973.1	4.59554513
38033	C08	NTL02YP3575	cell division protein	828	AAM87171.1	4.60023041
38054	C09	NTL02YP1983	hypothetical protein	837	AAM85579.1	6.63968073
38184	C10	NTL02YP3554	negative regulator of exu regulon, exuT, uxaAC	879	AAM87150.1	1.99673558
38228	C11	NTL02YP0879	hypothetical protein	894	AAM84475.1	5.21199143
38289	C12	NTL02YP3576	D-alanine-D-alanine ligase B	921	AAM87172.1	6.16961498
38335	D01	NTL02YP3572	UDP-3-O-acyl N-acetylglucosamine deacetylase	936	AAM87168.1	6.48360656
38353	D02	NTL02YP2463	flagellar biosynthesis protein	945	AAM86059.1	5.49238579
38389	D03	NTL02YP1979	putative transcriptional regulator	957	AAM85575.1	6.13640923
38525	D04	NTL02YP2459	putative transcriptional regulator	1002	AAM86055.1	6.22072937
36296	D05	NTL02YP0882	30S ribosomal subunit protein S16	249	AAM84478.1	3.96193772
36408	D06	NTL02YP3563	hypothetical protein	285	AAM87159.1	3.8
36456	D07	NTL02YP2474	anti-FliA factor	303	AAM86070.1	7.52186589
36467	D08	NTL02YP3561	hypothetical protein	306	AAM87157.1	6.04913295
36473	D09	NTL02YP1984	acid shock protein	309	AAM85580.1	7.42120344
36514	D10	NTL02YP1982	hypothetical protein	324	AAM85578.1	4.31043956
36562	D11	NTL02YP0901	hypothetical protein	342	AAM84497.1	4.14397906
36575	D12	NTL02YP0885	50S ribosomal subunit protein L19	348	AAM84481.1	3.98453608
36602	E01	NTL02YP1989	hypothetical protein	357	AAM85585.1	3.97732997
36680	E02	NTL02YP3568	7,8-dihydro-8-oxoguanine-triphosphatase	387	AAM87164.1	2
36689	E03	NTL02YP3558	hypothetical protein	390	AAM87154.1	5.87674419
38552	E04	NTL02YP2460	flagellar biosynthesis protein, hook-filament junction protein	1014	AAM86056.1	6.46110057

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38703	E08	NTL02YP0890	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	1077	AAM84486.1	4.40107431
38784	E09	NTL02YP2464	homolog of Salmonella P-ring of flagella basal	1110	AAM86060.1	2.93478261
38806	E10	NTL02YP0891	chorismate mutase-T	1122	AAM84487.1	4.18932874
38867	E11	NTL02YP3573	tubulin-like GTP-binding protein and GTPase	1152	AAM87169.1	4.05536913
38916	E12	NTL02YP0906	hypothetical protein	1182	AAM84502.1	1.74549918
39045	F01	NTL02YP3574	ATP-binding cell division protein	1257	AAM87170.1	4.64687741
39081	F02	NTL02YP0878	conserved hypothetical protein	1284	AAM84474.1	4.71676737
39092	F03	NTL02YP2468	hook protein	1287	AAM86064.1	4.78824416
36743	F04	NTL02YP2470	cell-proximal portion of basal-body rod protein	405	AAM86066.1	5.83820225
36766	F05	NTL02YP3564	hypothetical protein	411	AAM87160.1	7.94235033
36774	F06	NTL02YP2471	cell-proximal portion of basal-body rod protein	414	AAM86067.1	6.30396476
36800	F07	NTL02YP2477	flagellar protein	423	AAM86073.1	6.61987041
36846	F08	NTL02YP0905	putative thioredoxin-like protein	438	AAM84501.1	5.79079498
36864	F09	NTL02YP2475	flagellar biosynthesis protein	444	AAM86071.1	2
36934	F10	NTL02YP0896	putative yhbH sigma 54 modulator	465	AAM84492.1	8.04554455
36972	F11	NTL02YP1986	putative cytochrome	474	AAM85582.1	1.8151751
37009	F12	NTL02YP3559	hypothetical protein	483	AAM87155.1	2
39130	G03	NTL02YP3553	transport of hexuronates	1305	AAM87149.1	6.57695167
39218	G04	NTL02YP0902	phosphatidylserine synthase	1359	AAM84498.1	4.62115797
39221	G05	NTL02YP0880	GTP-binding export factor	1362	AAM84476.1	7.04707561
39303	G06	NTL02YP1978	putative D-arabinitol dehydrogenase	1404	AAM85574.1	4.4432133
39359	G07	NTL02YP3551	altronate oxidoreductase	1452	AAM87147.1	3.31903485
39396	G08	NTL02YP3550	altronate hydrolase	1491	AAM87146.1	4.22403658
39432	G09	NTL02YP3577	UDP-N-acetyl-muramate:alanine ligase	1524	AAM87173.1	3.98976982
39446	G10	NTL02YP0907	putative membrane translocase	1536	AAM84503.1	3.70748731
39470	G11	NTL02YP1373	putative membrane translocase	1536	AAM84503.1	4.356875
39536	G12	NTL02YP2462	flagellar biosynthesis protein, hook-filament junction protein 1	1665	AAM86058.1	4.10791789
37145	H01	NTL02YP3571	hypothetical protein	531	AAM87167.1	8.12259194
37144	H02	NTL02YP3549	hypothetical protein	531	AAM87145.1	1.92994746
37149	H03	NTL02YP3570	hypothetical protein	534	AAM87166.1	2.76132404
37230	H04	NTL02YP0883	hypothetical protein	561	AAM84479.1	4.80199667
37304	H05	NTL02YP3555	hypothetical protein	582	AAM87151.1	1.70418006
37371	H06	NTL02YP1980	acyl carrier protein phosphodiesterase	606	AAM85576.1	6.54489164
37488	H07	NTL02YP1995	putative channel protein	645	AAM85591.1	2.77080292
37594	H08	NTL02YP2469	basal-body rod modification protein	678	AAM86065.1	6.59610028
37596	H09	NTL02YP0888	putative anaerobic c4-dicarboxylate transport protein	681	AAM84484.1	3.7295423
37646	H10	NTL02YP3557	hypothetical protein	699	AAM87153.1	5.34912043
37896	H11	NTL02YP2449	flagellar biosynthesis protein	783	AAM86045.1	6.54556501
38023	H12	NTL02YP2447	flagellar biosynthesis protein	825	AAM86043.1	6.71676301

Table 6: *Yersinia pestis* Gateway® Clone, Plate 7 (UYPVG), NR-19603[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38135	A01	NTL02YP1369	putative permease of ABC transporter	864	AAM84965.1	3.571902655
38156	A02	NTL02YP0277	hypothetical protein	873	AAM83873.1	4.589266156
38401	A03	NTL02YP2452	hypothetical protein	960	AAM86048.1	5.389
36066	A04	NTL02YP3526	hypothetical protein	165	AAM87122.1	4.643902439
36277	A05	NTL02YP1354	hypothetical protein	240	AAM84950.1	4.857142857
38494	A06	NTL02YP2438	flagellar motor switch protein	993	AAM86034.1	3.315585673
38524	A07	NTL02YP2444	flagellar motor switch protein	1002	AAM86040.1	3.182341651
38577	A08	NTL02YP2453	putative permease of ABC transporter	1023	AAM86049.1	5.066792098
38602	A09	NTL02YP3546	hypothetical protein	1029	AAM86517.1	3.543498597
38793	A10	NTL02YP1363	ATP hydrolase of ABC transporter	1116	AAM84959.1	3.37283737
38804	A11	NTL02YP3521	ATP-binding component of sn-glycerol 3-phosphate transport system	1119	AAM87117.1	6.33649698
38945	A12	NTL02YP3542	putative enzyme	1191	AAM87138.1	3.170593014
36494	B01	NTL02YP2436	basal-body component	318	AAM86032.1	4.717877095
36517	B02	NTL02YP3535	hypothetical protein	324	AAM87131.1	4.799450549
36617	B03	NTL02YP0267	hypothetical protein	363	AAM83863.1	4
36672	B04	NTL02YP1357	hypothetical protein	384	AAM84953.1	5.125
36783	B05	NTL02YP2445	flagellar motor switch protein	417	AAM86041.1	6.407002188
36832	B06	NTL02YP3528	hypothetical protein	432	AAM87124.1	2.987288136
36877	B07	NTL02YP2441	flagellar fliJ protein	447	AAM86037.1	5.706365503
36883	B08	NTL02YP3523	hypothetical protein	447	AAM87119.1	6.739219713
39033	B09	NTL02YP3518	putative solute-binding periplasmic protein of ABC transporter	1245	AAM87114.1	2.577431907
39185	B10	NTL02YP1362	putative membrane protein	1335	AAM84958.1	6.52
39201	B11	NTL02YP0273	hypothetical protein	1347	AAM83869.1	5.085075703
39212	B12	NTL02YP2442	flagellar hook-length control protein	1353	AAM86038.1	3.91959799
36911	C01	NTL02YP0265	hypothetical protein	459	AAM83861.1	4.488977956
36990	C02	NTL02YP2435	hypothetical protein	477	AAM86031.1	
36999	C03	NTL02YP1349	hypothetical protein	480	AAM84945.1	4.646153846
37021	C04	NTL02YP0258	transcriptional repressor	489	AAM83854.1	5.958412098
37094	C05	NTL02YP3544	hypothetical protein	510	AAM87140.1	5.747272727
37087	C06	NTL02YP1353	hypothetical protein	510	AAM84949.1	6.850909091
37158	C07	NTL02YP2446	flagellar biosynthesis protein	537	AAM86042.1	5.341421144
37161	C08	NTL02YP3524	hypothetical protein	537	AAM87120.1	5.294627383
37183	C09	NTL02YP0274	hypothetical protein	546	AAM83870.1	2.389078498
37267	C10	NTL02YP3540	hypothetical protein	570	AAM87136.1	2.770491803
37264	C11	NTL02YP2443	flagellar biosynthesis	570	AAM86039.1	3.118032787
39285	C12	NTL02YP1356	hypothetical protein	1395	AAM84952.1	3.083623693
39290	D01	NTL02YP1359	putative permease, major facilitator superfamily	1398	AAM84955.1	4.0472879
39404	D02	NTL02YP3539	hypothetical protein	1500	AAM87135.1	3.388961039
39518	D03	NTL02YP2454	ATP binding protein of ABC transporter for	1644	AAM86050.1	3.400831354
39555	D04	NTL02YP3532	putative hemolysin activator protein	1689	AAM87128.1	4.893001735
39581	D05	NTL02YP3538	hypothetical protein	1734	AAM87134.1	3.182638106
39658	D06	NTL02YP2432	hypothetical protein	1914	AAM86028.1	5.579836233
39379	D07	NTL02YP1371	putative divalent cation transporter	1476	AAM84967.1	3.700527704
37389	D08	NTL02YP2434	putative DNA repair enzyme	612	AAM86030.1	5.559815951
37420	D09	NTL02YP3527	hypothetical protein	621	AAM87123.1	5.881996974
37472	D10	NTL02YP3533	hypothetical protein	639	AAM87129.1	6.539027982
37481	D11	NTL02YP3534	putative tellurite resistance protein	642	AAM87130.1	6.486803519
37633	D12	NTL02YP0269	hypothetical protein	696	AAM83865.1	5.248641304

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37661	E01	NTL02YP3536	hypothetical protein	702	AAM87132.1	2.772237197
37705	E02	NTL02YP1358	transcriptional response regulatory protein (sensor BaeS)	720	AAM84954.1	3.786842105
37714	E03	NTL02YP1347	hypothetical protein	723	AAM84943.1	7.374836173
37840	E04	NTL02YP0272	putative membrane protein	768	AAM83868.1	3.082920792
37950	E05	NTL02YP2421	putative periplasmic cysteine-binding ABC transport protein	801	AAM86017.1	3.084423306
38006	E06	NTL02YP3516	putative inner membrane permease protein of ABC	819	AAM87112.1	3.61233993
38100	E07	NTL02YP0240	putative ATP-binding component of a transport system	855	AAM83836.1	3.475977654
38118	E08	NTL02YP2413	putative cytochrome	858	AAM86009.1	3.638084633
38346	E09	NTL02YP0248	putative AraC-like regulator	942	AAM83844.1	6.387983707
35976	E10	NTL02YP3504	hypothetical protein	138	AAM87100.1	2.971910112
36043	E11	NTL02YP3496	hypothetical protein	159	AAM87092.1	4.969849246
36320	E12	NTL02YP1324	hypothetical protein	258	AAM84920.1	5.953020134
38474	F01	NTL02YP0231	putative permease of ABC transporter	990	AAM83827.1	3.177669903
38568	F02	NTL02YP2423	putative 1-aminocyclopropane-1-carboxylate deaminase	1020	AAM86019.1	3.413207547
38652	F03	NTL02YP3510	conserved hypothetical protein	1050	AAM87106.1	3.110091743
38783	F04	NTL02YP2426	putative flagellin	1110	AAM86022.1	6.477391304
38817	F05	NTL02YP1330	hypothetical protein	1128	AAM84926.1	3.48630137
38824	F06	NTL02YP0249	putative oxidoreductase	1131	AAM83845.1	3.230572161
38855	F07	NTL02YP0242	hypothetical protein	1149	AAM83838.1	3.419680404
36400	F08	NTL02YP3498	hypothetical protein	282	AAM87094.1	4
36425	F09	NTL02YP3492	hypothetical protein	291	AAM87088.1	5.864048338
36441	F10	NTL02YP1321	hypothetical protein	300	AAM84917.1	4
36458	F11	NTL02YP3501	hypothetical protein	303	AAM87097.1	3.982507289
36483	F12	NTL02YP3497	hypothetical protein	312	AAM87093.1	3.980113636
36550	G01	NTL02YP3509	hypothetical protein	336	AAM87105.1	4
36547	G02	NTL02YP2417	hypothetical protein	336	AAM86013.1	4
36670	G03	NTL02YP3503	hypothetical protein	381	AAM87099.1	4.990498812
36722	G04	NTL02YP2428	repressor of class 3a and 3b operons	399	AAM86024.1	4
36746	G05	NTL02YP3502	hypothetical protein	405	AAM87098.1	5.973033708
38872	G06	NTL02YP2412	hypothetical protein	1155	AAM86008.1	2.538912134
38913	G07	NTL02YP2409	conserved hypothetical protein	1179	AAM86005.1	3.404429861
38918	G08	NTL02YP1333	putative dehydrogenase	1182	AAM84929.1	3.076923077
38952	G09	NTL02YP1327	hypothetical protein	1197	AAM84923.1	5.895715441
39108	G10	NTL02YP0235	hypothetical protein	1296	AAM83831.1	3.105538922
39213	G11	NTL02YP0237	putative transporter	1356	AAM83833.1	6.399713467
36773	G12	NTL02YP2429	repressor of class 3a and 3b operons	414	AAM86025.1	6.136563877
36797	H01	NTL02YP0254	hypothetical protein	423	AAM83850.1	5.622030238
36822	H02	NTL02YP1326	nucleoside diphosphate kinase	429	AAM84922.1	4.914712154
36882	H03	NTL02YP3505	hypothetical protein	447	AAM87101.1	5.921971253
36930	H04	NTL02YP3493	hypothetical protein	462	AAM87089.1	6.902390438
36998	H05	NTL02YP1342	hypothetical protein	480	AAM84938.1	5.926923077
37061	H06	NTL02YP0247	putative inner membrane permease	504	AAM83843.1	6.564338235
37100	H08	NTL02YP3494	hypothetical protein	513	AAM87090.1	6.963833635
37107	H09	NTL02YP3515	hypothetical protein	516	AAM87111.1	2.82733813
39298	H10	NTL02YP2427	filament capping protein	1401	AAM86023.1	3.731436502
39322	H11	NTL02YP2408	symporter of D-alanine, D-serine, and glycine	1425	AAM86004.1	2.965870307

Table 7: *Yersinia pestis* Gateway® Clone, Plate 8 (UYPVH), NR-19604[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39436	A01	NTL02YP3512	putative membrane protein	1527	AAM87108.1	3.733886407
39459	A02	NTL02YP1339	IMP dehydrogenase	1548	AAM84935.1	3.558564232
39652	A04	NTL02YP3511	hypothetical protein	1902	AAM87107.1	3.779608651
37296	A05	NTL02YP0244	hypothetical protein	582	AAM83840.1	7.45659164
37555	A06	NTL02YP2420	putative ABC transporter permease for cystine	663	AAM86016.1	2.806543385
37649	A07	NTL02YP0245	putative deoxyribose-phosphate aldolase	702	AAM83841.1	2.684636119
37700	A08	NTL02YP3500	hypothetical protein	717	AAM87096.1	5.739762219
37717	A09	NTL02YP2425	alternative sigma factor 28	723	AAM86021.1	6.52948886
37801	A10	NTL02YP1328	putative fimbrial biogenesis protein	750	AAM84924.1	5.373417722
37832	A11	NTL02YP2419	putative ATP-binding component of ABC transport system	762	AAM86015.1	5.347880299
37924	A12	NTL02YP0252	hypothetical protein	795	AAM83848.1	3.102994012
37263	B01	NTL02YP2385	hypothetical protein	570	AAM85981.1	2.793442623
37309	B02	NTL02YP1301	outer membrane protein X	585	AAM84897.1	2.8224
37434	B03	NTL02YP3480	hypothetical protein	624	AAM87076.1	2.796686747
37534	B04	NTL02YP2404	putative 2-component transcriptional regulator	657	AAM86000.1	2.797704448
37584	B05	NTL02YP1306	hypothetical protein	675	AAM84902.1	2.808391608
37726	B06	NTL02YP0214	putative transcriptional regulator	726	AAM83810.1	2.808093995
37780	B07	NTL02YP3484	hypothetical protein	741	AAM87080.1	6.882202305
37865	B08	NTL02YP1309	putative ATP synthase beta subunit	774	AAM84905.1	3.633906634
36088	B10	NTL02YP1304	hypothetical protein	174	AAM84900.1	4
37956	B11	NTL02YP1308	suppressor protein	804	AAM84904.1	3.645734597
38005	B12	NTL02YP3482	bacitracin resistance protein	819	AAM87078.1	3.076833527
38028	C01	NTL02YP0218	hypothetical protein	828	AAM83814.1	3.632488479
38099	C02	NTL02YP0227	hypothetical protein	855	AAM83823.1	3.079329609
38285	C03	NTL02YP0210	methylase for 50S ribosomal subunit protein L11	921	AAM83806.1	3.825182102
38400	C04	NTL02YP2398	putative transposase	960	AAM85994.1	4.722
38551	C05	NTL02YP2380	putative periplasmic solute-binding protein of ABC transporter	1014	AAM85976.1	4.95540797
38575	C06	NTL02YP1307	hypothetical protein	1023	AAM84903.1	3.335841957
36247	C08	NTL02YP2401	hypothetical protein	228	AAM85997.1	3.981343284
36281	C09	NTL02YP0208	hypothetical protein	243	AAM83804.1	3.96819788
36311	C10	NTL02YP2406	hypothetical protein	255	AAM86002.1	4.949152542
36383	C11	NTL02YP2393	putative phage protein	276	AAM85989.1	3.537974684
36410	C12	NTL02YP0222	cold shock-like protein	288	AAM83818.1	5.93597561
36416	D01	NTL02YP2394	hypothetical protein	288	AAM85990.1	4
36433	D02	NTL02YP0212	site-specific DNA inversion stimulation factor	297	AAM83808.1	3.985163205
36463	D03	NTL02YP2395	hypothetical protein	306	AAM85991.1	6.176300578
36470	D04	NTL02YP0221	cold shock-like protein	309	AAM83817.1	3.558739255
38601	D05	NTL02YP3486	putative O-sialoglycoprotein endopeptidase	1029	AAM87082.1	3.64546305
38685	D06	NTL02YP1292	hypothetical protein	1068	AAM84888.1	3.084837545
38705	D07	NTL02YP2388	hypothetical protein	1077	AAM85984.1	5.397493286
38878	D08	NTL02YP1302	MFS (major facilitator superfamily) transporter	1158	AAM84898.1	3.316360601
38907	D09	NTL02YP0225	hypothetical protein	1176	AAM83821.1	3.394736842
38922	D10	NTL02YP3479	hypothetical protein	1182	AAM87075.1	4.023731588

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38942	D11	NTL02YP1298	dihydropteridine reductase	1191	AAM84894.1	3.34037368
39061	D12	NTL02YP2379	putative periplasmic solute-binding protein of ABC transporter	1269	AAM85975.1	3.057295646
36512	E01	NTL02YP1313	putative regulator	324	AAM84909.1	4.266483516
36546	E02	NTL02YP1317	[2FE-2S] ferredoxin, electron carrer protein	336	AAM84913.1	3.861702128
36557	E03	NTL02YP1295	regulatory protein P-II for glutamine synthetase	339	AAM84891.1	4.82585752
36568	E04	NTL02YP3491	hypothetical protein	342	AAM87087.1	5.12565445
36571	E05	NTL02YP2405	hypothetical protein	345	AAM86001.1	3.836363636
36611	E06	NTL02YP2391	putative phage protein	360	AAM85987.1	5.315
36616	E07	NTL02YP0224	hypothetical protein	363	AAM83820.1	4.163771712
36621	E08	NTL02YP3483	putative kinase	363	AAM87079.1	3.533498759
36709	E09	NTL02YP2392	hypothetical protein	396	AAM85988.1	4.327981651
36838	E10	NTL02YP2383	hypothetical protein	435	AAM85979.1	4.877894737
39200	E11	NTL02YP0226	hypothetical protein	1347	AAM83822.1	4.330209084
39226	E12	NTL02YP0215	putative metabolite transport protein, permease	1365	AAM83811.1	3.834163701
39280	F01	NTL02YP1303	hypothetical protein	1392	AAM84899.1	3.802374302
39364	F02	NTL02YP0209	sodium/pantothenate symporter	1461	AAM83805.1	5.00799467
39501	F03	NTL02YP1294	putative NH3-dependent NAD(+) synthetase	1623	AAM84890.1	2.992182802
39586	F04	NTL02YP3488	DNA primase	1749	AAM87084.1	2.885969816
39668	F05	NTL02YP1316	heat shock protein	1935	AAM84912.1	3.351392405
36844	F06	NTL02YP0216	putative decarboxylase	438	AAM83812.1	6.441422594
36876	F07	NTL02YP2397	putative transposase	447	AAM85993.1	4.784394251
36968	F08	NTL02YP0219	putative outer membrane receptor	474	AAM83815.1	4.501945525
36983	F09	NTL02YP0213	hypothetical protein	477	AAM83809.1	1.992263056
37083	F10	NTL02YP0206	acetyl CoA carboxylase, BCCP subunit	510	AAM83802.1	2
37124	F11	NTL02YP1315	hypothetical protein	525	AAM84911.1	5.111504425
37201	F12	NTL02YP2402	phosphatidylglycerophosphate synthetase	549	AAM85593.1	4.23089983
37209	G01	NTL02YP2407	putative outer membrane protein	552	AAM86003.1	2.817567568
37521	G02	NTL02YP3059	putative transport system permease protein	654	AAM86655.1	4.716138329
37539	G03	NTL02YP1971	putative transport ATPase	660	AAM85567.1	2.771428571
37635	G04	NTL02YP1284	hypothetical protein	696	AAM84880.1	3.495923913
37676	G05	NTL02YP3062	hypothetical protein	708	AAM86658.1	2.779411765
37708	G06	NTL02YP3050	hypothetical protein	720	AAM86646.1	2.773684211
37746	G07	NTL02YP1278	pyridoxine biosynthesis	732	AAM84874.1	5.752590674
37838	G08	NTL02YP3048	DNA polymerase III, epsilon subunit	765	AAM86644.1	5.624844721
37854	G09	NTL02YP1962	putative carboxypeptidase	771	AAM85558.1	6.371146732
37897	G10	NTL02YP3053	hypothetical protein	783	AAM86649.1	2.582017011
36168	G12	NTL02YP3067	hypothetical protein	201	AAM86663.1	4.975103734
36279	H01	NTL02YP3046	hypothetical protein	240	AAM86642.1	2.95
36447	H02	NTL02YP0184	hypothetical phage protein	303	AAM83780.1	5.259475219
37915	H03	NTL02YP3077	UDP-N-acetylglucosamine acetyltransferase	789	AAM86673.1	1.998793727
37962	H04	NTL02YP3055	putative aldose reductase	804	AAM86651.1	3.097156398
37996	H05	NTL02YP3060	putative lipoprotein	816	AAM86656.1	3.324766355
38063	H06	NTL02YP1282	hypothetical protein	840	AAM84878.1	3.640909091
38077	H07	NTL02YP3051	probable hydroxyacylglutathione hydrolase	843	AAM86647.1	4.988674972

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38164	H08	NTL02YP0179	putative transcriptional regulator	876	AAM83775.1	3.177947598
38207	H09	NTL02YP1283	putative regulator	888	AAM84879.1	4.581896552
38265	H10	NTL02YP0178	putative transcriptional regulator LYSR-type	912	AAM83774.1	4.961134454
38331	H11	NTL02YP1966	hypothetical protein	936	AAM85562.1	5.095286885

Table 8: *Yersinia pestis* Gateway® Clone, Plate 9 (UYPVI), NR-19605[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36700	A01	NTL02YP3054	hypothetical protein	393	AAM86650.1	3.967667436
36724	A02	NTL02YP3072	hypothetical protein	399	AAM86668.1	3
36756	A03	NTL02YP3061	colanic acid synthesis regulator	408	AAM86657.1	3.995535714
36761	A04	NTL02YP0185	hypothetical phage protein	411	AAM83781.1	3.458980044
38402	A05	NTL02YP3073	acetyl CoA carboxylase, carboxytransferase component, alpha subunit	960	AAM86669.1	5.051
38439	A06	NTL02YP1961	putative muconate cycloisomerase I	975	AAM85557.1	3.916256158
38605	A08	NTL02YP3058	ATP-binding component of a transporter	1032	AAM86654.1	3.572761194
38629	A09	NTL02YP0200	regulator of penicillin binding protein 3	1044	AAM83796.1	3.519372694
38650	A10	NTL02YP1974	fermentative D-lactate dehydrogenase, NAD-dependent	1050	AAM85570.1	4.386238532
38688	A11	NTL02YP0869	DNA-dependent ATPase, DNA- and ATP-dependent coprotease	1071	AAM84465.1	5.96669667
38752	A12	NTL02YP3042	hypothetical protein	1095	AAM86638.1	6.449339207
38925	B01	NTL02YP0203	putative reductase	1185	AAM83799.1	3.266938776
36771	B02	NTL02YP1972	hypothetical protein	414	AAM85568.1	4.533039648
36820	B03	NTL02YP0874	hypothetical protein	429	AAM84470.1	2.886993603
36857	B04	NTL02YP3065	hypothetical protein	441	AAM86661.1	3.702702703
36898	B05	NTL02YP1973	heat shock protein	453	AAM85569.1	2.914807302
37020	B06	NTL02YP0197	rod shape-determining protein	489	AAM83793.1	3.988657845
37104	B07	NTL02YP0876	hypothetical protein	516	AAM84472.1	5.588129496
37241	B08	NTL02YP0870	regulator, OraA protein	564	AAM84466.1	6.240066225
38932	B09	NTL02YP3076	tetraacyldisaccharide-1-P sythetase	1185	AAM86672.1	5.342857143
39265	B10	NTL02YP3071	cell cycle protein	1383	AAM86667.1	3.598735067
39348	B11	NTL02YP0191	PmbA/TldD family protein	1446	AAM83787.1	3.721399731
39358	B12	NTL02YP3052	transcriptional regulator for nitrite reductase (cytochrome c552)	1452	AAM86648.1	3.754021448
39463	C01	NTL02YP1286	putative periplasmic binding transport protein	1554	AAM84882.1	3.618569636
39486	C02	NTL02YP0875	gamma-glutamate-cysteine ligase	1599	AAM84471.1	3.812690665
39539	C03	NTL02YP1958	transcriptional regulator of aroF, aroG, tyrA and	1668	AAM85554.1	3.760538642
37255	C05	NTL02YP3057	putative phosphatase	567	AAM86653.1	5.561779242
37251	C06	NTL02YP0873	putative phosphatase	567	AAM84469.1	6.546952224
37282	C07	NTL02YP1960	thiol peroxidase	576	AAM85556.1	5.321428571
37289	C08	NTL02YP1288	hypothetical protein	579	AAM84884.1	2.802907916
37395	C12	NTL02YP3066	hypothetical protein	615	AAM86662.1	2.839694656
38116	D01	NTL02YP1928	N-ethylmaleimide reductase	858	AAM85524.1	3.628062361
38126	D02	NTL02YP1937	pyridoxal kinase 2 / pyridoxine kinase	861	AAM85533.1	3.613762486
38162	D03	NTL02YP3018	succinyl-CoA synthetase, alpha subunit	873	AAM86614.1	3.380065717

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38192	D04	NTL02YP3028	hypothetical protein	882	AAM86624.1	1.60845987
38188	D05	NTL02YP0845	probable 3-hexulose-6-phosphate isomerase	882	AAM84441.1	4.590021692
38222	D06	NTL02YP1945	homolog of *Salmonella* peptide transport permease protein	891	AAM85541.1	5.175080559
38293	D07	NTL02YP0855	anaerobic dimethyl sulfoxide reductase subunit C	924	AAM84451.1	1.613070539
38352	D08	NTL02YP0866	putative transcriptional regulator	945	AAM84462.1	3.665989848
38418	D09	NTL02YP1946	peptide ABC transport inner membrane permease protein	966	AAM85542.1	4.588469185
36246	D10	NTL02YP1951	phage shock protein B	228	AAM85547.1	3
36285	D11	NTL02YP1953	phage shock protein	243	AAM85549.1	3
36340	D12	NTL02YP1939	hypothetical protein	264	AAM85535.1	3.740131579
36407	E01	NTL02YP3031	hypothetical protein	285	AAM86627.1	5.270769231
36449	E02	NTL02YP0858	cytochrome b(562)	303	AAM84454.1	3.78425656
36462	E03	NTL02YP0842	hypothetical protein	306	AAM84438.1	2.75433526
38481	E04	NTL02YP3041	hypothetical protein	990	AAM86637.1	4.178640777
38475	E05	NTL02YP0847	putative inner membrane permease protein of ABC transporter	990	AAM84443.1	3.355339806
38493	E06	NTL02YP1944	putative ATP-binding protein of peptide ABC transport system	993	AAM85540.1	3.343659245
38766	E07	NTL02YP0850	putative solute-binding periplasmic protein of ABC transporter	1104	AAM84446.1	3.277972028
38852	E08	NTL02YP0863	sugar (D-ribose?) transport system permease protein	1146	AAM84459.1	4.3153457
38870	E09	NTL02YP1933	hypothetical protein	1155	AAM85529.1	4.09958159
36580	E10	NTL02YP3024	succinate dehydrogenase, hydrophobic subunit	348	AAM86620.1	3.75
36590	E11	NTL02YP3030	small membrane protein A	351	AAM86626.1	4
36737	E12	NTL02YP3013	hypothetical protein	402	AAM86609.1	4
36873	F01	NTL02YP1957	hypothetical protein	447	AAM85553.1	1.310061602
36872	F02	NTL02YP1927	lactoylglutathione lyase	447	AAM85523.1	4.72073922
36948	F03	NTL02YP1932	putative outer membrane protein	468	AAM85528.1	3.214566929
38894	F04	NTL02YP3019	succinyl-CoA synthetase, beta subunit	1167	AAM86615.1	3.186412593
38996	F05	NTL02YP3020	2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase E2 component)	1224	AAM86616.1	3.201740506
39292	F07	NTL02YP1954	putative enzyme	1398	AAM85550.1	3.621696801
39320	F08	NTL02YP0865	hypothetical protein	1425	AAM84461.1	3.899658703
37160	F10	NTL02YP3032	hypothetical protein	537	AAM86628.1	3.109185442
37240	F11	NTL02YP0857	cytochrome b(561)	564	AAM84453.1	3.612582781
37333	F12	NTL02YP1940	hypothetical protein	591	AAM85536.1	4.624405705
39394	G01	NTL02YP3037	hypothetical protein	1491	AAM86633.1	3.577400392
39420	G02	NTL02YP0848	putative ATP-binding protein of ABC transport system	1515	AAM84444.1	3.760771704
39430	G03	NTL02YP0862	putative ATP-binding protein of ABC transport system	1524	AAM84458.1	3.598465473
39464	G04	NTL02YP1941	putative transport protein	1554	AAM85537.1	3.669385194
39475	G05	NTL02YP3017	cytochrome d terminal oxidase, polypeptide subunit I	1569	AAM86613.1	3.840894966
39523	G06	NTL02YP1947	peptide-binding periplasmic protein of peptide ABC transport	1647	AAM85543.1	4.643746295

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39594	G07	NTL02YP3023	succinate dehydrogenase, flavoprotein subunit	1767	AAM86619.1	3.715550636
37398	G08	NTL02YP0854	anaerobic dimethyl sulfoxide reductase subunit B	618	AAM84450.1	3.914893617
37517	G09	NTL02YP1935	pyridoxinephosphate oxidase	654	AAM85531.1	4.063400576
37562	G10	NTL02YP1950	phage shock protein A	666	AAM85546.1	5.009915014
37698	G11	NTL02YP3022	succinate dehydrogenase, iron sulfur protein	717	AAM86618.1	1.780713342
37853	G12	NTL02YP0852	L-ribulose-5-phosphate 4-epimerase	771	AAM84448.1	6.731196054
37973	H01	NTL02YP0851	transcriptional regulator	810	AAM84447.1	6.616470588
38058	H02	NTL02YP3002	phosphoglyceromutase 1	837	AAM86598.1	5.380843786
38131	H03	NTL02YP2995	repressor of molybdate ABC transporter genes	861	AAM86590.1	5.1809101
38254	H04	NTL02YP1891	hypothetical protein	906	AAM85487.1	5.21141649
38261	H05	NTL02YP0812	ATP-sulfurylase, subunit 2	909	AAM84408.1	5.208640674
38296	H06	NTL02YP2979	putative structural protein	924	AAM86575.1	5.425311203
38321	H07	NTL02YP1919	putative transcriptional regulator LYSR-type	933	AAM85515.1	4.952723535
38456	H08	NTL02YP1889	putative sugar transferase	984	AAM85485.1	4.482421875
38512	H09	NTL02YP0832	putative transcriptional regulator	999	AAM84428.1	4.931665063
38511	H10	NTL02YP0823	RNA polymerase, sigma S (sigma38) factor	999	AAM84419.1	6.111645813
36017	H11	NTL02YP2993	hypothetical protein	153	AAM86589.1	5.683937824
36042	H12	NTL02YP2994	hypothetical protein	159	AAM86591.1	2.869346734

Table 9: *Yersinia pestis* Gateway® Clone, Plate 10 (UYPVJ), NR-19606[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36121	A01	NTL02YP1895	hypothetical protein	183	AAM85491.1	2
36187	A02	NTL02YP0835	hypothetical protein	207	AAM84431.1	3.700404858
36204	A03	NTL02YP2978	hypothetical protein	210	AAM86574.1	4.648
36290	A04	NTL02YP2980	hypothetical protein	246	AAM86576.1	2.982517483
36499	A05	NTL02YP0816	hypothetical protein	321	AAM84412.1	2.980609418
36548	A06	NTL02YP3001	putative starvation-inducible protein	336	AAM86597.1	3.643617021
36544	A07	NTL02YP0815	putative cytochrome oxidase subunit	336	AAM84411.1	4.14893617
36561	A08	NTL02YP0834	transcriptional repressor of chromosomal ars operon	342	AAM84430.1	2
38519	A09	NTL02YP0822	lipoprotein	1002	AAM84418.1	3.453934741
38537	A10	NTL02YP2988	putative isomerase	1005	AAM86584.1	3.133971292
38561	A11	NTL02YP2998	UDP-galactose-4-epimerase	1017	AAM86594.1	3.522232734
38556	A12	NTL02YP1897	lipoate-protein ligase A	1017	AAM85493.1	3.487228004
38585	B02	NTL02YP1920	transcriptional repressor for pur regulon, glyA, glnB	1026	AAM85516.1	3.422138837
38619	B03	NTL02YP2986	biotin synthetase	1038	AAM86582.1	2.833951763
38638	B04	NTL02YP1898	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tryptophan repressible)	1047	AAM85494.1	4.890524379
38646	B05	NTL02YP0819	putative hydrogenase subunit	1050	AAM84415.1	3.503669725
38658	B06	NTL02YP3003	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	1053	AAM86599.1	3.464775846

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38657	B07	NTL02YP2999	galactose-1-phosphate uridylyltransferase	1053	AAM86595.1	5.774931382
38671	B08	NTL02YP3006	quinolinate synthetase	1062	AAM86602.1	4.999092559
36619	B09	NTL02YP1893	hypothetical protein	363	AAM85489.1	3.17866005
36626	B10	NTL02YP1923	hypothetical protein	366	AAM85519.1	2
36721	B11	NTL02YP1904	hypothetical protein	399	AAM85500.1	2
36781	B12	NTL02YP1903	hypothetical protein	417	AAM85499.1	2
36935	C01	NTL02YP1896	lipoprotein	465	AAM85492.1	2
37097	C02	NTL02YP0811	hypothetical protein	513	AAM84407.1	6.640144665
38678	C03	NTL02YP1910	hypothetical protein	1065	AAM85506.1	5.352036199
38734	C04	NTL02YP0829	putative dihydroxyacetone kinase	1089	AAM84425.1	3.336581045
38857	C05	NTL02YP0827	putative dehydrogenase	1149	AAM84423.1	3.308662742
38858	C06	NTL02YP1901	hypothetical protein	1149	AAM85497.1	6.002523129
38863	C07	NTL02YP1917	cyclopropane fatty acyl phospholipid synthase	1152	AAM85513.1	3.341442953
38866	C08	NTL02YP3000	galactokinase	1152	AAM86596.1	3.291107383
38865	C09	NTL02YP2985	8-amino-7-oxononanoate synthase	1152	AAM86581.1	3.323825503
38964	C10	NTL02YP1918	putative transport protein	1203	AAM85514.1	3.249396621
39011	C11	NTL02YP1908	hypothetical protein	1233	AAM85504.1	3.184603299
39079	C12	NTL02YP2987	7,8-diaminopelargonic acid synthetase	1281	AAM86583.1	3.358819076
37321	D01	NTL02YP0806	superoxide dismutase precursor (Cu-Zn)	588	AAM84402.1	4.839171975
37415	D02	NTL02YP1921	superoxide dismutase, iron	621	AAM85517.1	3.444780635
37440	D03	NTL02YP0821	L-isoaspartate protein carboxylmethyltransferase type II	627	AAM84417.1	2.796101949
37575	D04	NTL02YP0807	hypothetical protein	672	AAM84403.1	6.203651685
37582	D05	NTL02YP0830	hypothetical protein	675	AAM84426.1	4.548251748
37685	D06	NTL02YP2982	putative ATP-binding protein of ABC transporter	711	AAM86578.1	2.776298269
37730	D07	NTL02YP3005	nucleoside/purine/pyrimidine transporter	726	AAM86601.1	3.775456919
37769	D08	NTL02YP2983	dethiobiotin synthetase	738	AAM86579.1	3.228791774
39110	D09	NTL02YP0805	enolase	1296	AAM84401.1	2.574850299
39245	D10	NTL02YP1915	putative transport protein	1374	AAM85511.1	3.873408769
39256	D11	NTL02YP0837	cytochrome C peroxidase	1380	AAM84433.1	3.629577465
39312	D12	NTL02YP1914	pyruvate kinase I	1413	AAM85510.1	3.641431521
39414	E01	NTL02YP1905	hypothetical protein	1512	AAM85501.1	3.754510309
39422	E02	NTL02YP0813	ATP-sulfurylase, subunit 1	1518	AAM84409.1	5.122593068
39468	E03	NTL02YP2996	ATP-binding component of molybdate transport system	1557	AAM86592.1	2.987476518
39509	E04	NTL02YP0804	CTP synthetase	1638	AAM84400.1	3.161501788
39535	E05	NTL02YP1892	hypothetical protein	1665	AAM85488.1	3.651612903
39642	E06	NTL02YP0809	sulfite reductase (NADPH), flavoprotein beta subunit	1881	AAM84405.1	5.246746486
37834	E07	NTL02YP0820	survival protein	765	AAM84416.1	1.971428571
37852	E08	NTL02YP0836	hypothetical protein	771	AAM84432.1	3.622688039
37866	E09	NTL02YP1906	putative ATP-binding component of a transport system	774	AAM85502.1	4.506142506
37922	E11	NTL02YP2992	molybdate-binding periplasmic protein of molybdate ABC transporter	792	AAM86588.1	3.286057692
37961	E12	NTL02YP2984	biotin biosynthesis protein	804	AAM86580.1	5.648104265
37977	F01	NTL02YP3007	hypothetical protein	810	AAM86603.1	3.637647059
38014	F02	NTL02YP2989	putative phosphatase	822	AAM86585.1	3.792343387
37928	F04	NTL02YP0787	ATP-binding component of hydroxymate-dependent iron ABC transporter	795	AAM84383.1	5.508982036

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38030	F05	NTL02YP2377	putative permease	828	AAM85973.1	5.918202765
38047	F06	NTL02YP3453	hypothetical protein	834	AAM87049.1	6.598398169
38070	F07	NTL02YP0803	hypothetical protein	843	AAM84399.1	6.966024915
38069	F08	NTL02YP0795	hypothetical protein	843	AAM84391.1	5.997734994
38124	F09	NTL02YP3465	regulator of lacZ	858	AAM87061.1	3.636971047
38165	F10	NTL02YP0783	probable regulator for maltose metabolism	876	AAM84379.1	2.77510917
36201	F11	NTL02YP2370	hypothetical protein	210	AAM85966.1	4.72
36437	F12	NTL02YP1883	hypothetical protein	297	AAM85479.1	3.913946588
38223	G01	NTL02YP2376	ATP-binding component of transport system for maltose	891	AAM85972.1	3.932330827
38218	G02	NTL02YP1272	hypothetical protein	891	AAM84868.1	1.992481203
38235	G03	NTL02YP3450	putative AraC-type regulatory protein	894	AAM87046.1	4.549250535
38269	G04	NTL02YP1276	GTP-binding protein	912	AAM84872.1	8.298319328
38399	G05	NTL02YP2360	AraC-type transcriptional regulator for yersiniabactin uptake and	960	AAM85956.1	4.992
38513	G06	NTL02YP1274	leader peptidase (signal peptidase I)	999	AAM84870.1	3.327237729
38672	G07	NTL02YP3447	TonB complex protein	1062	AAM87043.1	3.316696915
38704	G08	NTL02YP1885	vitamin B12 transport permease protein	1077	AAM85481.1	3.111011638
36436	G09	NTL02YP1881	integration host factor (IHF), alpha subunit	297	AAM85478.1	3
36566	G10	NTL02YP2375	hypothetical protein	342	AAM85971.1	3.827225131
36609	G11	NTL02YP0792	hypothetical protein	360	AAM84388.1	3.895
36673	G12	NTL02YP1882	hypothetical protein	384	AAM85477.1	2
36816	H01	NTL02YP3466	putative enzyme	426	AAM87062.1	3
36831	H02	NTL02YP3446	TonB-complex protein	432	AAM87042.1	5.199152542
36903	H03	NTL02YP1271	sigma-E factor, negative regulatory protein	456	AAM84867.1	3.629032258
36916	H04	NTL02YP1884	hypothetical protein	459	AAM85480.1	5.661322645
36976	H05	NTL02YP3443	hypothetical protein	474	AAM87039.1	3
36997	H06	NTL02YP0778	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	480	AAM84374.1	5.580769231
37008	H07	NTL02YP3473	hypothetical protein	483	AAM87069.1	1.984703633
38733	H08	NTL02YP0788	solute-binding periplasmic protein of hydroxamate-dependent iron ABC	1089	AAM84384.1	5.141718335
38868	H09	NTL02YP0780	putative tRNA synthetase	1155	AAM84376.1	4.29707113
38880	H10	NTL02YP3451	putative oxidoreductase	1158	AAM87047.1	3.641068447
38887	H11	NTL02YP3470	putative synthetase/amidase	1161	AAM87066.1	1.716069942
38983	H12	NTL02YP3448	cystathionine beta-lyase (beta-cystathionase)	1212	AAM87044.1	2.694089457

Table 10: *Yersinia pestis* Gateway® Clone, Plate 11 (UYPVK), NR-19607[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39044	A01	NTL02YP3475	putative transport	1257	AAM87071.1	3.194294526
39077	A02	NTL02YP0790	glutamate-1-semialdehyde aminotransferase	1281	AAM84386.1	3.878122634
39305	A03	NTL02YP3468	outer membrane channel protein	1404	AAM87064.1	3.707063712
39323	A04	NTL02YP3456	suppressor of ftsI	1425	AAM87052.1	3.632764505
37197	A05	NTL02YP0782	dnaK suppressor protein	549	AAM84378.1	1.994906621
37220	A06	NTL02YP1886	vitamin B12-binding periplasmic protein of vitamin B12	555	AAM85482.1	2.796638655

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37221	A07	NTL02YP2368	hypothetical protein	555	AAM85964.1	5.490756303
37278	A08	NTL02YP0784	hypothetical protein	576	AAM84380.1	2.805194805
37279	A09	NTL02YP1268	RNA polymerase, sigma-E factor	576	AAM84864.1	2.784090909
37300	A10	NTL02YP2369	hypothetical protein	582	AAM85965.1	2.762057878
37318	A11	NTL02YP3464	hypothetical protein	585	AAM87060.1	2.8096
37317	A12	NTL02YP3461	modulator of drug activity B	585	AAM87057.1	2.6848
37456	B01	NTL02YP3467	hypothetical protein	633	AAM87063.1	2.757800892
37522	B02	NTL02YP3472	3,4 dihydroxy-2-butanone-4-phosphate synthase	654	AAM87068.1	3.587896254
37533	B03	NTL02YP2364	yersiniabactin thioesterase	657	AAM85960.1	3.292682927
39350	B04	NTL02YP3476	putative kinase	1446	AAM87072.1	1.432032301
39378	B05	NTL02YP0779	poly(A) polymerase I	1476	AAM84375.1	3.682717678
39427	B06	NTL02YP0797	deoxyguanosine triphosphate triphosphohydrolase	1521	AAM84393.1	3.779628443
39469	B07	NTL02YP3445	hypothetical protein	1557	AAM87041.1	3.71884784
39612	B08	NTL02YP1273	GTP-binding elongation factor	1800	AAM84869.1	3.883695652
39649	B09	NTL02YP3463	DNA topoisomerase IV subunit B	1896	AAM87059.1	10.29442149
37526	B10	NTL02YP1269	sigma-E factor, negative regulatory protein	657	AAM84865.1	4.262553802
37548	B11	NTL02YP0794	hypothetical protein	663	AAM84390.1	3.544807966
37557	B12	NTL02YP3449	hypothetical protein	663	AAM87045.1	4.536273115
37598	C01	NTL02YP1275	RNase III, ds RNA	681	AAM84871.1	6
37607	C02	NTL02YP0781	hypothetical protein	684	AAM84377.1	2.306629834
37751	C03	NTL02YP3458	1-acyl-sn-glycerol-3-phosphate acyltransferase	732	AAM87045.1	5.251295337
37745	C04	NTL02YP1277	recO protein	732	AAM84873.1	1.998704663
37829	C05	NTL02YP1887	ATP-binding component of vitamin B12 transport system	762	AAM85483.1	5.182044888
37860	C06	NTL02YP3442	hypothetical protein	771	AAM87038.1	5.803945746
37822	C07	NTL02YP1266	putative enzyme	759	AAM84862.1	4.921151439
37859	C08	NTL02YP3422	flagellar biosynthesis protein	771	AAM87018.1	3.218249075
37857	C09	NTL02YP2335	putative DEOR-type transcriptional regulator	771	AAM85931.1	3.085080148
37873	C10	NTL02YP1254	putative lactam utilization protein	777	AAM84850.1	2.651162791
37887	C11	NTL02YP3424	putative flagellar biosynthetic protein	780	AAM87020.1	3.407317073
37985	C12	NTL02YP3440	hypothetical protein	813	AAM87036.1	5.82883939
38073	D01	NTL02YP2345	putative citrate lyase	843	AAM85941.1	3.621744054
38107	D02	NTL02YP3436	hypothetical protein	855	AAM87032.1	5.530726257
38150	D03	NTL02YP2340	hypothetical protein	870	AAM85936.1	6.235164835
36180	D04	NTL02YP2331	hypothetical protein	204	AAM85927.1	3.995901639
36554	D05	NTL02YP0173	hypothetical protein	339	AAM83769.1	4.200527704
38236	D06	NTL02YP2344	putative transcriptional regulator LYSR-type	897	AAM85940.1	6.395944504
38249	D07	NTL02YP3420	hypothetical protein	900	AAM87016.1	5.813829787
38330	D08	NTL02YP0176	putative membrane protein	936	AAM83772.1	5.012295082
38329	D09	NTL02YP0159	aspartate carbamoyltransferase, catalytic subunit	936	AAM83755.1	5.792008197
38376	D10	NTL02YP0163	repressor of treA,B,C	954	AAM83759.1	4.967806841
38505	D11	NTL02YP3428	hypothetical protein	996	AAM87024.1	2.838803089
38576	D12	NTL02YP2334	putative glutaminase	1023	AAM85930.1	3.483537159
38600	E01	NTL02YP3419	response regulator of ato, ornithine decarboxylase antizyme	1029	AAM87015.1	5.29373246

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38613	E02	NTL02YP1249	hypothetical protein	1038	AAM84845.1	3.43135436
36669	E03	NTL02YP3418	hypothetical protein	381	AAM87014.1	3.698337292
36694	E04	NTL02YP0167	cytochrome b(562)	393	AAM83763.1	3.877598152
36776	E05	NTL02YP3421	hypothetical protein	414	AAM87017.1	4.883259912
36772	E06	NTL02YP2330	periplasmic protein	414	AAM85926.1	4.262114537
36790	E07	NTL02YP1256	hypothetical protein	420	AAM84852.1	5.426086957
36802	E08	NTL02YP3434	hypothetical protein	423	AAM87030.1	2
36807	E09	NTL02YP0161	hypothetical protein	426	AAM83757.1	4.650214592
36892	E10	NTL02YP3437	hypothetical protein	450	AAM87033.1	4.285714286
36954	E11	NTL02YP0160	aspartate carbamoyltransferase, regulatory subunit	471	AAM83756.1	2
36967	E12	NTL02YP0172	putative ribonuclease	474	AAM83768.1	4.461089494
38777	F01	NTL02YP3430	putative adhesin	1107	AAM87026.1	3.39581517
38829	F02	NTL02YP0174	succinate-semialdehyde dehydrogenase	1134	AAM83770.1	5.348381601
38833	F03	NTL02YP3425	putative flagellar biosynthetic protein	1134	AAM87021.1	3.10988075
38941	F04	NTL02YP2337	putative aminotransferase	1188	AAM85933.1	3.238599349
39015	F05	NTL02YP3438	hypothetical protein	1233	AAM87034.1	3.056559309
39054	F06	NTL02YP2355	putative prophage integrase	1263	AAM85951.1	3.923254029
39073	F07	NTL02YP2341	putative major facilitator superfamily (MFS) transport protein	1278	AAM85937.1	3.025796662
39094	F08	NTL02YP3439	putative secretion NTP hydrolase	1287	AAM87035.1	3.713639789
39128	F09	NTL02YP2356	anthranilate synthase	1305	AAM85952.1	4.005947955
39166	F10	NTL02YP2347	putative Coenzyme A transferase	1323	AAM85943.1	3.556859868
39169	F11	NTL02YP1265	ATP-dependent RNA helicase	1326	AAM84861.1	6.043923865
36974	F12	NTL02YP2343	hypothetical protein	474	AAM85939.1	4.441634241
36982	G01	NTL02YP0162	hypothetical protein	477	AAM83758.1	2
37004	G02	NTL02YP1246	hypothetical protein	483	AAM84842.1	5.391969407
37189	G03	NTL02YP1251	putative carboxylase	546	AAM84847.1	4.42662116
37214	G04	NTL02YP0170	putative alpha helix protein	555	AAM83766.1	4.134453782
37233	G05	NTL02YP2342	hypothetical protein	561	AAM85938.1	2.81530782
37262	G06	NTL02YP2350	putative fimbrial precursor	570	AAM85946.1	2.813114754
37294	G07	NTL02YP3427	hypothetical protein	579	AAM87023.1	2.783521809
37347	G08	NTL02YP1257	conserved hypothetical protein	597	AAM84853.1	2.814756672
37364	G09	NTL02YP1241	ATPase of high-affinity potassium transport system, C-chain	603	AAM84837.1	2.768273717
37432	G10	NTL02YP2338	putative oxidoreductase	624	AAM85934.1	2.792168675
39190	G11	NTL02YP0169	PmbA/TldD family protein	1341	AAM83765.1	3.095582911
39209	G12	NTL02YP2353	hypothetical protein	1350	AAM85949.1	1.58705036
39361	H01	NTL02YP2329	putative integral membrane protein	1455	AAM85925.1	2.371237458
39369	H02	NTL02YP1248	deoxyribodipyrimidine photolyase (photoreactivation)	1464	AAM84843.1	3.585106383
39440	H03	NTL02YP2336	L-asparagine permease	1530	AAM85932.1	3.144585987
39510	H04	NTL02YP1267	quinolinate synthetase, B protein	1638	AAM84863.1	3.592967819
39514	H05	NTL02YP2333	putative transport protein	1641	AAM85929.1	5.334919691
39661	H06	NTL02YP2332	putative integral membrane protein	1920	AAM85928.1	3.657142857
39677	H07	NTL02YP0175	hypothetical protein	1956	AAM83771.1	3.143787575
37491	H08	NTL02YP2351	putative pilin chaperone	645	AAM85947.1	3.22189781
37499	H09	NTL02YP1258	putative pyrrolidone-carboxylate peptidase	648	AAM84854.1	4.203488372
37508	H10	NTL02YP2346	putative transcriptional regulator	651	AAM85942.1	7.149059334
37525	H11	NTL02YP1263	putative accessory protein for YplA	657	AAM84859.1	4.901004304
37680	H12	NTL02YP1259	uracil-DNA-glycosylase	711	AAM84855.1	2.399467377

Table 11: *Yersinia pestis* Gateway® Clone, Plate 12 (UYPVL), NR-19608[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37710	A01	NTL02YP3431	putative chaperone	720	AAM87027.1	5.125
37777	A02	NTL02YP2354	putative pilin chaperone	741	AAM85950.1	5.717029449
37793	A03	NTL02YP1250	hypothetical protein	747	AAM84846.1	6.08386277
37750	A04	NTL02YP3404	putative flagellar rod protein	732	AAM87000.1	5.961139896
37788	A05	NTL02YP3415	hypothetical protein	744	AAM87011.1	5.257653061
37895	A06	NTL02YP0143	hypothetical protein	783	AAM83739.1	6.267314702
38000	A07	NTL02YP0144	putative ATP-binding component of ABC transport system	819	AAM83740.1	6.806752037
36085	A08	NTL02YP0154	probable sigma-54 modulation protein	174	AAM83750.1	3.943925234
36106	A09	NTL02YP1228	hypothetical protein	180	AAM84824.1	4.968181818
36336	A10	NTL02YP0139	hypothetical protein	264	AAM83735.1	4.963815789
36350	A11	NTL02YP3411	hypothetical protein	267	AAM87007.1	4.605863192
36403	A12	NTL02YP2316	hypothetical protein	285	AAM85912.1	1.969230769
36430	B01	NTL02YP3400	hypothetical protein	294	AAM86996.1	3.526946108
36446	B02	NTL02YP0140	hypothetical protein	303	AAM83736.1	5.551020408
36486	B03	NTL02YP2324	putative cytochrome precursor	315	AAM85920.1	-
38435	B04	NTL02YP0145	hypothetical protein	975	AAM83741.1	4.673891626
38696	B05	NTL02YP0146	putative isomerase	1074	AAM83742.1	2.999102334
36577	B06	NTL02YP1231	PEP-dependent phosphotransferase IIA component for cellobiose, arbutin	348	AAM84827.1	-
36576	B07	NTL02YP1229	PEP-dependent phosphotransferase enzyme IV for cellobiose, arbutin	348	AAM84825.1	5.961340206
36716	B08	NTL02YP0131	30S ribosomal subunit protein S9	399	AAM83727.1	6.047835991
36739	B09	NTL02YP0134	hypothetical protein	405	AAM83730.1	4.959550562
36762	B10	NTL02YP1226	hypothetical protein	411	AAM84822.1	4.024390244
36815	B11	NTL02YP3412	hypothetical protein	426	AAM87008.1	5.510729614
36814	B12	NTL02YP3408	flagellar biosynthesis protein, cell-proximal portion of basal-body	426	AAM87004.1	2.993562232
36821	C01	NTL02YP1238	conserved hypothetical protein	429	AAM84834.1	3.987206823
38731	C02	NTL02YP0137	protease	1089	AAM83733.1	3.270150576
38762	C03	NTL02YP2314	sodium-calcium/proton antiporter	1101	AAM85910.1	2.439088519
38842	C04	NTL02YP0133	hypothetical protein	1140	AAM83729.1	2.754237288
38912	C05	NTL02YP3401	putative flagella basal body protein	1176	AAM86997.1	2.246710526
38908	C06	NTL02YP1225	putative potassium channel	1176	AAM84821.1	2.446546053
38975	C07	NTL02YP3394	lateral flagellin	1206	AAM86990.1	2.439004815
38989	C08	NTL02YP2322	outer membrane protein	1218	AAM85918.1	4.76073132
39051	C09	NTL02YP0138	UDP-N-glucosamine 1-carboxyvinyltransferase	1263	AAM83734.1	4.047582502
36880	C10	NTL02YP3396	hypothetical protein	447	AAM86992.1	5.821355236
36949	C11	NTL02YP2318	inner membrane protein	468	AAM85914.1	4.147637795
37012	C12	NTL02YP0128	hypothetical protein	486	AAM83724.1	4.595057034
37036	D01	NTL02YP0155	phosphotransferase system enzyme IIA	495	AAM83751.1	4.510280374
37141	D03	NTL02YP2325	putative thioredoxin-family protein	531	AAM85921.1	5.234676007
37154	D04	NTL02YP0684	putative transposase	537	AAM84280.1	6.244367418
37171	D05	NTL02YP1235	negative modulator of initiation of replication	543	AAM84831.1	6.173241852
37239	D06	NTL02YP0149	hypothetical protein	564	AAM83745.1	4.162251656
39223	D07	NTL02YP1230	PEP-dependent phosphotransferase enzyme II for cellobiose, arbutin	1362	AAM84826.1	3.165477889
39224	D08	NTL02YP3399	putative flagellar hook-associated protein	1362	AAM86995.1	3.14764622
39240	D09	NTL02YP2308	hypothetical protein	1371	AAM85904.1	5.432317505

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39247	D10	NTL02YP2319	hypothetical protein	1374	AAM85915.1	5.622347949
39277	D11	NTL02YP0135	serine endoprotease	1392	AAM83731.1	3.696927374
39330	D12	NTL02YP0152	RNA polymerase, sigma(54 or 60) factor	1434	AAM83748.1	3.421302578
39352	E01	NTL02YP2312	multi modular putative transcriptional regulator; also putative	1449	AAM85908.1	3.001343183
39424	E02	NTL02YP2309	putative aldehyde dehydrogenase	1518	AAM85905.1	3.103979461
39515	E03	NTL02YP3417	putative flagellar M ring protein	1641	AAM87013.1	2.95240928
39550	E04	NTL02YP1236	phosphoglucomutase	1686	AAM84832.1	3.211471611
37238	E05	NTL02YP0148	hypothetical protein	564	AAM83744.1	6.105960265
37248	E06	NTL02YP0150	hypothetical protein	567	AAM83746.1	1.815485997
37269	E07	NTL02YP0142	hypothetical protein	573	AAM83738.1	2.804241436
37446	E08	NTL02YP1239	regulator of kdp operon (transcriptional effector)	630	AAM84835.1	2.785074627
37473	E09	NTL02YP0130	regulator of transcription stringent starvation protein A	642	AAM83726.1	1.804985337
37537	E10	NTL02YP3406	putative flagellar assembly protein	657	AAM87002.1	2.738880918
37550	E11	NTL02YP1221	urease accessory protein	663	AAM84817.1	4.780938834
37613	E12	NTL02YP1220	urease accessory protein	687	AAM84816.1	4.635488308
37842	F01	NTL02YP1192	hypothetical protein	768	AAM84788.1	2
37900	F04	NTL02YP0685	putative transposase	786	AAM84281.1	5.468523002
37965	F05	NTL02YP1213	putative ATP-binding protein of ABC transport system	807	AAM84809.1	2
37964	F06	NTL02YP1212	putative permease of ABC transporter	807	AAM84808.1	2.598583235
38095	F07	NTL02YP2295	hypothetical protein	852	AAM85891.1	3.507847534
38233	F08	NTL02YP2304	putative histidine degradation enzyme	894	AAM85900.1	3.358672377
38227	F09	NTL02YP0111	putative transcriptional regulator LYSR-type	894	AAM83707.1	3.950749465
35987	F10	NTL02YP0112	hypothetical protein	150	AAM83708.1	2.973684211
36130	F11	NTL02YP1193	hypothetical protein	186	AAM84789.1	2
36267	F12	NTL02YP1204	glutaredoxin-like protein	237	AAM84800.1	3.981949458
36287	G01	NTL02YP3386	hypothetical protein	243	AAM86982.1	3.96819788
38292	G03	NTL02YP0107	putative acetyltransferase	924	AAM83703.1	4.760373444
38371	G04	NTL02YP2279	hypothetical protein	951	AAM85875.1	5.16851665
38409	G05	NTL02YP2292	putative oxidoreductase	963	AAM85888.1	2
38426	G06	NTL02YP1202	ribonucleoside-diphosphate reductase 2, beta chain, frag	972	AAM84798.1	4.869565217
38454	G07	NTL02YP1211	putative permease of ABC transporter	984	AAM84807.1	4.614257813
38502	G08	NTL02YP2307	hypothetical protein	996	AAM85903.1	2.448841699
38531	G09	NTL02YP1199	solute-binding periplasmic protein of high-affinity glycine betaine/proline	1005	AAM84795.1	2.733971292
38560	G10	NTL02YP2296	putative nucleotide di-P-sugar epimerase or dehydratase	1017	AAM85892.1	3.122043519
38571	G11	NTL02YP3389	putative transcription repressor	1020	AAM86985.1	3.198113208
36378	G12	NTL02YP0100	RNA polymerase, omega subunit	276	AAM83696.1	-
36545	H01	NTL02YP1206	hypothetical protein	336	AAM84802.1	3.835106383
36592	H02	NTL02YP0117	hypothetical protein	354	AAM83713.1	4.223350254
36641	H03	NTL02YP1205	acid shock protein	372	AAM84801.1	5.405339806
36662	H04	NTL02YP0118	hypothetical protein	381	AAM83714.1	2.833729216
36726	H05	NTL02YP3378	hypothetical protein	399	AAM86974.1	2
36740	H06	NTL02YP1208	hypothetical protein	405	AAM84804.1	2.997752809
38599	H08	NTL02YP3391	hypothetical protein	1029	AAM86987.1	4.036482694
38782	H09	NTL02YP2293	hypothetical protein	1110	AAM85889.1	4.008695652

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38891	H10	NTL02YP1200	permease of high-affinity ABC transport system for	1167	AAM84796.1	3.072908036
38940	H11	NTL02YP2289	hypothetical protein	1188	AAM85885.1	3.147394137

Table 12: *Yersinia pestis* Gateway® Clone, Plate 13 (UYPVM), NR-19609[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38984	A01	NTL02YP0104	sodium/glutamate symporter	1215	AAM83700.1	2.364143426
39114	A02	NTL02YP2303	putative imidazolonepropionase	1296	AAM85899.1	3.035928144
39153	A03	NTL02YP1201	ATP-binding component of high affinity transport system	1317	AAM84797.1	3.020633751
39195	A04	NTL02YP3384	hypothetical protein	1341	AAM86980.1	5.769732078
36887	A05	NTL02YP1207	hypothetical protein	450	AAM84803.1	5
36938	A06	NTL02YP2288	hypothetical protein	465	AAM85884.1	5.516831683
36989	A07	NTL02YP1217	urease (urea amidohydrolase) beta subunit	477	AAM84813.1	5.061895551
37003	A08	NTL02YP1195	hypothetical protein	483	AAM84791.1	5.244741874
37132	A09	NTL02YP1189	flavodoxin 1	528	AAM84785.1	6.424295775
37166	A10	NTL02YP2297	hypothetical protein	540	AAM85893.1	2.655172414
37272	A11	NTL02YP2300	hypothetical protein	573	AAM85896.1	2
37315	A12	NTL02YP2290	hypothetical protein	585	AAM85886.1	2
37330	B01	NTL02YP0120	hypothetical protein	591	AAM83716.1	6.171156894
39315	B04	NTL02YP0127	glutamate synthase, small subunit	1419	AAM83723.1	5.602467443
39318	B05	NTL02YP1187	hypothetical protein	1422	AAM84783.1	3.55745554
39321	B06	NTL02YP2301	putative chlorohydrolase	1425	AAM85897.1	3.509897611
39337	B07	NTL02YP0105	putative transport protein, symporter	1437	AAM83701.1	3.055517942
39478	B08	NTL02YP1210	putative substrate-binding periplasmic protein of ABC transporter	1578	AAM84806.1	3.725587145
39530	B09	NTL02YP3380	hypothetical protein	1659	AAM86976.1	3.416715715
39564	B10	NTL02YP0098	putative enzyme	1704	AAM83694.1	2.844036697
37471	B11	NTL02YP2282	hypothetical protein	639	AAM85878.1	2.787923417
37515	B12	NTL02YP0123	sigma cross-reacting protein 27A (SCRP-27A)	654	AAM83719.1	2
37514	C01	NTL02YP0108	putative transposase	654	AAM83704.1	4.220461095
37540	C02	NTL02YP2281	hypothetical protein	660	AAM85877.1	2.717142857
37600	C03	NTL02YP2280	putative oxidoreductase	681	AAM85876.1	4
37626	C04	NTL02YP0102	putative RNA methylase	693	AAM83698.1	1.993178718
37668	C05	NTL02YP1214	putative ATP-binding protein of ABC transport system	705	AAM84810.1	6.201342282
37664	C06	NTL02YP0113	hypothetical protein	705	AAM83709.1	5.684563758
37724	C07	NTL02YP0122	putative peptidoglycan enzyme	726	AAM83718.1	6.451697128
37844	C08	NTL02YP2302	putative repressor	768	AAM85898.1	5.870049505
37893	C09	NTL02YP0085	lipopolysaccharide core biosynthesis glycosyl transferase	783	AAM83681.1	5.365735115
37979	C11	NTL02YP4069	putative amino acid ABC transport system permease	810	AAM87665.1	4.843529412
37971	C12	NTL02YP0088	formamidopyrimidine DNA glycosylase	810	AAM83683.1	1.778823529
38109	D01	NTL02YP4071	putative solute-binding periplasmic protein precursor for ABC	855	AAM87667.1	3.596648045

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38130	D02	NTL02YP2960	putative inner membrane permease of ABC transporter	861	AAM86556.1	1.728079911
38132	D03	NTL02YP0096	putative alpha helix protein	864	AAM83692.1	1.717920354
38216	D04	NTL02YP4075	inner membrane permease	888	AAM87671.1	5.297413793
36206	D05	NTL02YP4041	hypothetical protein	210	AAM87637.1	4.884
38314	D07	NTL02YP2971	hypothetical protein	930	AAM86567.1	5.534020619
38313	D08	NTL02YP2961	putative solute-binding protein of ABC transporter	930	AAM86557.1	5.522680412
38334	D09	NTL02YP2968	penicillin-binding protein 7	936	AAM86564.1	5.295081967
38355	D10	NTL02YP2970	putative regulator protein	945	AAM86566.1	8.76751269
38383	D11	NTL02YP4052	putative ornithine cyclodeaminase	954	AAM87648.1	4.875251509
38433	D12	NTL02YP4076	inner membrane permease	972	AAM87672.1	5.306324111
38443	E01	NTL02YP0080	ADP-L-glycero-D-mannoheptose-6-epimerase	978	AAM83676.1	4.44302554
38472	E02	NTL02YP0083	heptosyl transferase I	990	AAM83679.1	4.75631068
38582	E03	NTL02YP0078	threonine dehydrogenase	1026	AAM83674.1	3.074108818
36534	E04	NTL02YP1871	hypothetical protein	333	AAM85467.1	6.597855228
36560	E05	NTL02YP4050	hypothetical protein	339	AAM87646.1	2.683377309
36596	E06	NTL02YP2965	hypothetical protein	354	AAM86561.1	4.799492386
36601	E07	NTL02YP1876	50S ribosomal subunit protein L20	357	AAM85472.1	2.906801008
36613	E08	NTL02YP4061	RNase P	360	AAM87657.1	5.3625
36777	E09	NTL02YP4049	heat shock protein	414	AAM87645.1	5.610132159
36919	E10	NTL02YP2974	molybdopterin converting factor, subunit 2	459	AAM86570.1	5.573146293
36953	E11	NTL02YP0092	deoxyuridinetriphosphatase	471	AAM83688.1	2
36975	E12	NTL02YP2958	hypothetical protein	474	AAM86554.1	4.871595331
36996	F01	NTL02YP0086	putative enzyme of lipopolysaccharide synthesis	480	AAM83682.1	1.986538462
38589	F02	NTL02YP2977	molybdopterin biosynthesis protein A	1026	AAM86573.1	4.110694184
38620	F03	NTL02YP4051	threonine dehydratase	1038	AAM87647.1	3.977736549
38628	F04	NTL02YP4077	periplasmic phosphate-binding protein	1041	AAM87673.1	3.0453284
38701	F05	NTL02YP0082	ADP-heptose--lps heptosyltransferase II	1077	AAM83678.1	1.552372426
38764	F06	NTL02YP4058	DNA polymerase III, beta-subunit	1101	AAM87654.1	5.752848379
38769	F07	NTL02YP2963	hypothetical protein	1104	AAM86559.1	2.753496504
38853	F08	NTL02YP1182	N-acetylglucosamine-6-phosphate deacetylase	1146	AAM84778.1	2.783305228
38960	F09	NTL02YP4065	hypothetical protein	1200	AAM87661.1	2.508064516
39026	F10	NTL02YP0079	2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)	1242	AAM83675.1	4.610764431
39059	F11	NTL02YP1181	transcriptional repressor of nag (N-acetylglucosamine) operon	1266	AAM84777.1	2.539050536
39118	F12	NTL02YP2957	putative Leu/Ile/Val/Thr binding protein of ABC transporter	1299	AAM86553.1	1.289768484
37007	G01	NTL02YP2976	molybdopterin biosynthesis protein C	483	AAM86572.1	4.739961759
37079	G02	NTL02YP4048	heat shock protein	507	AAM87644.1	6.906764168
37168	G03	NTL02YP2966	putative adenylate cyclase	540	AAM86562.1	2
37344	G04	NTL02YP0093	putative transcriptional regulator	597	AAM83689.1	6.481946625
37423	G05	NTL02YP4066	hypothetical protein	621	AAM87662.1	2.80484115
37425	G06	NTL02YP0097	hypothetical protein	624	AAM83693.1	2.484939759
37495	G07	NTL02YP4042	hypothetical protein	645	AAM87638.1	2.776642336
37497	G08	NTL02YP0094	orotate phosphoribosyltransferase	648	AAM83690.1	2.646802326
37542	G09	NTL02YP4040	putative outer membrane protein	660	AAM87636.1	4.517142857
37554	G10	NTL02YP1869	murein transglycosylase E	663	AAM85465.1	6.674253201

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39176	G11	NTL02YP0091	flavoprotein affecting synthesis of DNA and pantothenate	1332	AAM83687.1	6.358600583
39230	G12	NTL02YP4064	GTP-binding protein	1365	AAM87660.1	2.527402135
39242	H01	NTL02YP4046	alanine-alpha-ketoisovalerate	1371	AAM87642.1	3.66335932
39272	H02	NTL02YP0084	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	1386	AAM83680.1	5.726507714
39302	H03	NTL02YP4059	DNA biosynthesis protein	1401	AAM87655.1	3.595419847
39497	H04	NTL02YP2956	putative branched chain inner membrane permease of	1617	AAM86552.1	3.736873868
39516	H05	NTL02YP4063	60 kDa inner-membrane protein	1641	AAM87658.1	3.668649613
39531	H06	NTL02YP4047	putative membrane/transport protein	1659	AAM87643.1	2.928193055
39534	H07	NTL02YP1179	asparagine synthetase B	1665	AAM84775.1	3.426392962
39571	H08	NTL02YP2967	D-lactate dehydrogenase, FAD protein	1716	AAM86563.1	2.648063781
37566	H09	NTL02YP0090	DNA repair protein	669	AAM83686.1	6.094499295
37574	H10	NTL02YP4068	putative phosphatase	669	AAM87664.1	6.088857546
37573	H11	NTL02YP4053	putative transposase	669	AAM87649.1	4.007052186
37580	H12	NTL02YP4072	hypothetical protein	672	AAM87668.1	1.903089888

Table 13: *Yersinia pestis* Gateway® Clone, Plate 14 (UYPVN), NR-19610[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37684	A01	NTL02YP2973	hypothetical protein	711	AAM86569.1	1.853529
37690	A02	NTL02YP1870	hypothetical protein	714	AAM85466.1	4.795756
37692	A03	NTL02YP0095	RNase PH	717	AAM83691.1	5.577279
37722	A04	NTL02YP4073	negative regulator for pho regulon	723	AAM87669.1	5.178244
37772	A05	NTL02YP4070	putative glutamate/aspartate ABC transport system permease protein	738	AAM87666.1	2.750643
37804	A06	NTL02YP1180	N-acetylglucosamine metabolism protein	753	AAM84776.1	6.423707
38102	A07	NTL02YP0776	pantothenate synthetase	855	AAM84372.1	1.796648
38121	A08	NTL02YP2952	hypothetical protein	858	AAM86027.1	3.351893
38125	A09	NTL02YP4026	formate dehydrogenase formation protein	858	AAM87622.1	1.760579
38133	A10	NTL02YP0777	3-methyl-2-oxobutanoate hydroxymethyltransferase	864	AAM84373.1	6.410398
38168	A11	NTL02YP1863	hypothetical protein	876	AAM85459.1	6.131004
38190	A12	NTL02YP1839	heat shock protein, integral membrane protein	882	AAM85435.1	4.842733
38200	B01	NTL02YP1866	permease for iron and manganese ABC transporter	885	AAM85462.1	6.201081
38220	B02	NTL02YP1855	putative inner membrane permease of oligogalacturonide ABC	891	AAM85451.1	4.831364
38231	B03	NTL02YP1865	permease for iron and manganese ABC transporter	894	AAM85461.1	6.024625
36212	B04	NTL02YP1864	hypothetical protein	213	AAM85460.1	3.956522
36324	B05	NTL02YP2931	hypothetical protein	258	AAM86527.1	2.969799
36348	B06	NTL02YP2944	hypothetical protein	267	AAM86540.1	5.680782
36541	B07	NTL02YP4029	hypothetical protein	333	AAM87625.1	4.884718
36540	B08	NTL02YP4018	hypothetical protein	333	AAM87614.1	4.86059
36555	B09	NTL02YP0773	hypothetical protein	339	AAM84369.1	3.98153
36574	B10	NTL02YP0767	hypothetical protein	348	AAM84363.1	5.719072
36587	B11	NTL02YP1859	putative pectin degradation protein	351	AAM85455.1	4.974425

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38260	B12	NTL02YP0764	hypothetical protein	909	AAM84360.1	5.926238
38277	C01	NTL02YP4037	glycine tRNA synthetase, alpha subunit	915	AAM87633.1	5.608377
38301	C02	NTL02YP0771	putative ATP-binding component of ABC transport system	927	AAM84367.1	5.672182
38316	C03	NTL02YP4023	formate dehydrogenase formation protein	930	AAM87619.1	5.362887
38319	C04	NTL02YP0770	putative carbonic anhdrase	933	AAM84366.1	3.475848
38432	C05	NTL02YP4025	formate dehydrogenase-O, iron-sulfur subunit	972	AAM87621.1	4.784585
38437	C06	NTL02YP0766	spermidine synthase putrescine aminopropyltransferase	975	AAM84362.1	4.717241
38463	C07	NTL02YP1854	putative inner membrane permease of oligogalacturonide ABC	987	AAM85450.1	4.098345
38553	C08	NTL02YP2955	putative inner membrane permease of ABC transporter	1014	AAM86551.1	2.431689
36606	C09	NTL02YP4031	hypothetical protein	357	AAM87627.1	5.433249
36663	C10	NTL02YP0775	aspartate 1-decarboxylase	381	AAM84371.1	3.95962
36943	C11	NTL02YP4019	putative transposase	465	AAM87615.1	5.889109
36950	C12	NTL02YP2949	hypothetical protein	468	AAM86545.1	4.785433
36994	D01	NTL02YP4030	hypothetical protein	477	AAM87626.1	5.93617
37180	D03	NTL02YP2935	hypothetical protein	543	AAM86531.1	2.653516
37177	D04	NTL02YP1840	putative fimbrial protein	543	AAM85436.1	5.614065
37187	D05	NTL02YP0769	hypoxanthine phosphoribosyltransferase	546	AAM84365.1	2.726962
37200	D06	NTL02YP1850	hypothetical protein	549	AAM5446.1	2.689304
38821	D07	NTL02YP1853	ABC transporter, ATP-binding protein	1128	AAM85449.1	2.873288
38892	D08	NTL02YP1846	putative oligogalacturonide lyase	1167	AAM85442.1	2.146645
38899	D09	NTL02YP1843	putative fimbrial component	1170	AAM85439.1	5.736364
38911	D10	NTL02YP2930	ribonucleoside-diphosphate reductase 1, beta subunit, B2	1176	AAM86526.1	2.797697
38948	D11	NTL02YP2933	hypothetical protein	1194	AAM86529.1	2.777958
38979	D12	NTL02YP2934	tyrosine-specific transport system protein	1209	AAM86530.1	2.760608
39064	E01	NTL02YP4033	mannitol-1-phosphate dehydrogenase	1269	AAM87629.1	2.811306
39102	E02	NTL02YP1852	putative solute-binding periplasmic protein of oligogalacturonide ABC	1293	AAM85448.1	3.540885
39186	E03	NTL02YP2943	putative symporter	1335	AAM86539.1	3.490909
39232	E04	NTL02YP1845	putative transport protein	1368	AAM85441.1	2.46875
37219	E05	NTL02YP1862	putative regulator of yfeABCD	555	AAM85458.1	2
37223	E06	NTL02YP4032	repressor for mtl	555	AAM87628.1	2.647059
37235	E07	NTL02YP2932	ecotin, serine protease inhibitor	561	AAM86528.1	2.663894
37276	E08	NTL02YP4038	3-methyl-adenine DNA glycosylase I	573	AAM87634.1	3.502447
37561	E09	NTL02YP1861	putative phosphatase	666	AAM85457.1	5.784703
37589	E10	NTL02YP4024	formate dehydrogenase, cytochrome B556 (FDO) subunit	675	AAM87620.1	6.896503
37733	E11	NTL02YP4035	hypothetical protein	726	AAM87631.1	6.241514
37737	E12	NTL02YP2928	3-demethylubiquinone-9 3-methyltransferase	729	AAM86524.1	6.016905
37833	F01	NTL02YP2953	ATP-binding component of ABC transporter	762	AAM86549.1	6.512469
39291	F02	NTL02YP1849	putative symporter	1398	AAM85445.1	3.133519
39297	F03	NTL02YP0756	aromatic amino acid transport protein	1401	AAM84352.1	5.244969
39314	F04	NTL02YP2951	putative aromatic-L-amino-acid decarboxylase	1416	AAM86547.1	3.415522
39325	F05	NTL02YP0760	lipoamide dehydrogenase (NADH) component of 2-oxodehydrogenase and	1428	AAM84356.1	3.387602

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39538	F06	NTL02YP1856	putative pectate lyase	1668	AAM85452.1	2.890515
39667	F07	NTL02YP4034	PTS system mannitol-specific enzyme IIABC components	1932	AAM87630.1	5.509128
39674	F08	NTL02YP4028	methyl-accepting chemotaxis protein II	1950	AAM87624.1	3.305025
37881	F09	NTL02YP1841	probable pilin chaperone	780	AAM85437.1	3.281707
37919	F10	NTL02YP1847	putative regulator	792	AAM85443.1	4.260817
37927	F11	NTL02YP0765	S-adenosylmethionine decarboxylase	795	AAM84361.1	5.833533
37957	F12	NTL02YP1844	putative pilin chaperone	804	AAM85440.1	3.208531
37969	G01	NTL02YP1857	2-deoxy-D-gluconate 3-dehydrogenase	807	AAM85453.1	6.067296
38057	G02	NTL02YP2954	hypothetical ABC transporter ATP-binding protein	837	AAM86550.1	3.200684
38051	G03	NTL02YP0757	transcriptional regulator for pyruvate dehydrogenase complex	837	AAM84353.1	5.881414
38094	G04	NTL02YP1848	putative regulator	852	AAM85444.1	3.232063
38105	G05	NTL02YP2950	putative thiosulfate sulfurtransferase	855	AAM86546.1	3.231285
38034	G06	NTL02YP4008	putative chaperone	828	AAM87604.1	3.28341
38359	G07	NTL02YP3993	ferric anguibactin transport system permease protein	945	AAM87589.1	3.126904
38381	G08	NTL02YP1819	hypothetical protein	954	AAM85415.1	5.696177
38480	G09	NTL02YP1828	hypothetical protein	990	AAM85424.1	3.147573
36298	G10	NTL02YP1822	hypothetical protein	249	AAM85418.1	3
38507	G11	NTL02YP4004	xylose binding periplasmic protein of ABC transport	996	AAM87600.1	5.920849
38538	G12	NTL02YP0731	ornithine carbamoyltransferase 1	1008	AAM84327.1	6.105916
38598	H03	NTL02YP2915	hypothetical protein	1029	AAM86510.1	3.08232
38749	H04	NTL02YP0738	hypothetical protein	1095	AAM84334.1	2.899559
36623	H05	NTL02YP3997	hypothetical protein	363	AAM87593.1	2
36827	H06	NTL02YP0732	hypothetical protein	432	AAM84328.1	4.279661
36837	H07	NTL02YP1818	hypothetical protein	435	AAM85414.1	4.974737
36912	H08	NTL02YP0730	hypothetical protein	459	AAM84326.1	4.977956
37001	H09	NTL02YP2908	hypothetical protein	480	AAM86504.1	2.75
37078	H11	NTL02YP3998	putative transposase	507	AAM87594.1	4.694698
38951	H12	NTL02YP4002	inner membrane permease of D-xylose ABC transporter	1194	AAM87598.1	2.928687

Table 14: *Yersinia pestis* Gateway® Clone, Plate 15 (UYPVO), NR-19611[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39006	A01	NTL02YP1820	putative alanine racemase	1230	AAM85416.1	2.522047244
39072	A02	NTL02YP3990	hypothetical protein	1275	AAM87586.1	4.137642586
39109	A03	NTL02YP0740	putative prophage P4 integrase	1296	AAM84336.1	3.214071856
37112	A04	NTL02YP1836	hypothetical protein	519	AAM85432.1	2
37176	A05	NTL02YP1832	hypothetical protein	543	AAM85428.1	4.212692967
37204	A06	NTL02YP0754	regulates ampC	552	AAM84350.1	2
37273	A07	NTL02YP2924	hypothetical protein	573	AAM86520.1	7.106035889
37312	A08	NTL02YP1831	hypothetical protein	585	AAM85427.1	2
37328	A09	NTL02YP4017	hypothetical protein	588	AAM87613.1	2
37450	A10	NTL02YP2906	putative epimerase/aldolase	630	AAM86502.1	4.63880597
37464	A11	NTL02YP4009	putative outer membrane usher protein	636	AAM87605.1	2
37494	A12	NTL02YP4011	putative fimbrial-like protein	645	AAM87607.1	4.827737226

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39146	B01	NTL02YP2907	hypothetical protein	1314	AAM86503.1	1.259970458
39362	B02	NTL02YP4006	xylulokinase	1455	AAM87602.1	3.068227425
39445	B03	NTL02YP4003	putative ATP-binding protein of xylose ABC transport	1533	AAM87599.1	3.77813096
39467	B04	NTL02YP0751	putative integral membrane protein	1557	AAM84347.1	3.507201002
37520	B05	NTL02YP2925	positive response regulator for colanic capsule biosynthesis	654	AAM86521.1	2.786743516
37588	B06	NTL02YP4013	putative transposase	675	AAM87609.1	4.825174825
37720	B07	NTL02YP2909	putative phage repressor protein cI	723	AAM86505.1	1.766710354
37806	B08	NTL02YP1830	putative pilus assembly chaperone	753	AAM85426.1	6.078184111
37779	B10	NTL02YP2888	putative regulator	741	AAM86484.1	2.768245839
37884	B11	NTL02YP2889	hypothetical protein	780	AAM86485.1	10.1695122
38062	C01	NTL02YP0706	putative sugar transport permease	840	AAM84302.1	6.207954545
36214	C02	NTL02YP2882	hypothetical protein	213	AAM86478.1	5.656126482
36253	C03	NTL02YP2881	hypothetical protein	231	AAM86477.1	5.778597786
36258	C04	NTL02YP1790	hypothetical protein	234	AAM85386.1	7.598540146
36334	C05	NTL02YP2891	hypothetical protein	261	AAM86487.1	4.6910299
38210	C06	NTL02YP1794	proton conductor component of motor	888	AAM85390.1	8.298491379
38259	C07	NTL02YP0727	putative ATP-binding component of dipeptide transport system	909	AAM84323.1	3.753424658
38500	C08	NTL02YP0698	putative collagenase	996	AAM84294.1	1.941119691
38637	C09	NTL02YP1788	putative oxidoreductase	1047	AAM85384.1	3.149034039
38655	C10	NTL02YP1812	protein methylesterase	1053	AAM85407.1	3.43915828
36618	C11	NTL02YP1797	hypothetical protein	363	AAM85393.1	3.977667494
36636	C12	NTL02YP2900	hypothetical protein	369	AAM86496.1	5.875305623
36652	D01	NTL02YP2890	hypothetical protein	375	AAM86486.1	6.089156627
36745	D02	NTL02YP2899	hypothetical protein	405	AAM86495.1	3.878651685
36752	D03	NTL02YP1801	hypothetical protein	408	AAM85397.1	4
38748	D04	NTL02YP0707	ATP-binding component of sn-glycerol 3-phosphate transport system	1095	AAM84303.1	3.364757709
38840	D05	NTL02YP2892	hypothetical protein	1137	AAM86488.1	3.294817332
38991	D06	NTL02YP0703	hypothetical protein	1221	AAM84299.1	2.981760508
36836	D07	NTL02YP0724	anaerobic ribonucleotide reductase activating protein	435	AAM84320.1	-
36888	D08	NTL02YP1785	putative regulator	450	AAM85381.1	4
37048	D09	NTL02YP1799	positive regulator of CheA protein activity	498	AAM85395.1	3.890334572
37050	D10	NTL02YP2884	hypothetical protein	498	AAM86480.1	1.992565056
37070	D11	NTL02YP0700	hypothetical protein	507	AAM84296.1	5.66179159
37147	D12	NTL02YP1787	hypothetical protein	534	AAM85383.1	2.81184669
37311	E01	NTL02YP1793	regulator of flagellar biosynthesis	585	AAM85389.1	6.344
37348	E02	NTL02YP2894	hypothetical protein	597	AAM86490.1	1.778649922
39371	E03	NTL02YP2887	6-phospho-beta-glucosidase A	1464	AAM86483.1	3.440824468
39398	E04	NTL02YP2897	hypothetical protein	1494	AAM86493.1	3.31029987
39493	E05	NTL02YP1809	methyl-accepting chemotaxis protein IV, peptide sensor receptor	1611	AAM85405.1	2.898849182
39567	E06	NTL02YP3986	putative urocanase	1707	AAM87582.1	3.849456211
39683	E07	NTL02YP0702	hypothetical protein	1971	AAM84298.1	4.755345599
37468	E08	NTL02YP0710	hypothetical protein	639	AAM84306.1	7.008836524
37487	E09	NTL02YP1814	chemotactic response CheY protein phophatase	645	AAM85410.1	2.8
37558	E10	NTL02YP3981	response regulator	663	AAM87577.1	2.832147937

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37694	E11	NTL02YP0726	dipeptide ABC transporter, ATP binding protein	717	AAM84322.1	6.678996037
37703	E12	NTL02YP0715	ATP-binding component of phosphonate ABC transporter	720	AAM84311.1	5.268421053
38022	F01	NTL02YP2257	hypothetical protein	825	AAM85853.1	3.068208092
38039	F02	NTL02YP2264	hypothetical protein	831	AAM85860.1	2
38038	F03	NTL02YP2252	possible protoporphyrinogen oxidase	831	AAM85848.1	2.621125144
38072	F04	NTL02YP2266	hypothetical protein	843	AAM85862.1	3.610419026
38104	F05	NTL02YP2249	2-dehydro-3-deoxyphosphooctulonate aldolase	855	AAM85845.1	3.605586592
38115	F06	NTL02YP1778	putative oxidoreductase	858	AAM85374.1	6.765033408
38173	F07	NTL02YP3377	hypothetical protein	876	AAM86973.1	6.197598253
38178	F08	NTL02YP1172	putative magnesium and cobalt efflux protein	879	AAM84768.1	6.163220892
38242	F09	NTL02YP0697	hypothetical protein	900	AAM84293.1	5.054255319
36011	F10	NTL02YP1173	hypothetical protein	153	AAM84769.1	3.953367876
36089	F11	NTL02YP2272	hypothetical protein	174	AAM85868.1	5.859813084
36093	F12	NTL02YP3345	hypothetical protein	174	AAM86941.1	3.953271028
36182	G01	NTL02YP3355	hypothetical protein	204	AAM86951.1	3.954918033
38256	G02	NTL02YP2276	hypothetical protein	906	AAM85872.1	5.559196617
38279	G03	NTL02YP1170	solute-binding periplasmic protein of glutamate/aspartate ABC transporter	918	AAM84766.1	4.897703549
38324	G04	NTL02YP2278	hypothetical protein	933	AAM85873.1	4.816032888
38419	G05	NTL02YP2258	phosphoribosylpyrophosphate synthetase	966	AAM85854.1	5.880715706
38659	G07	NTL02YP0692	putative enzyme	1056	AAM84288.1	3.384124088
38699	G08	NTL02YP2275	hypothetical protein	1074	AAM85871.1	5.400359066
38719	G09	NTL02YP2253	peptide chain release factor RF-1	1083	AAM85849.1	2.893143366
38744	G10	NTL02YP2269	hypothetical protein	1092	AAM85865.1	3.248233216
36216	G11	NTL02YP1783	hypothetical protein	216	AAM85379.1	3.96484375
36373	G12	NTL02YP2259	hypothetical protein	273	AAM85855.1	3.728434505
36388	H01	NTL02YP3367	hypothetical protein	279	AAM86963.1	4.833855799
36479	H02	NTL02YP0691	hypothetical protein	312	AAM84287.1	4.914772727
36537	H03	NTL02YP3365	hypothetical protein	333	AAM86961.1	4.587131367
36620	H04	NTL02YP2273	hypothetical protein	363	AAM85869.1	5.171215881
36633	H05	NTL02YP0690	hypothetical protein	369	AAM84286.1	5.66992665
38743	H06	NTL02YP2261	putative GTP-binding protein	1092	AAM85857.1	3.438162544
38787	H07	NTL02YP1175	putative ATP-binding protein in pho regulon	1113	AAM84771.1	3.391153513
38881	H08	NTL02YP0694	acridine efflux pump	1161	AAM84290.1	2.665278934
39014	H09	NTL02YP3357	possible peptidase	1233	AAM86953.1	3.177533386
39075	H10	NTL02YP3346	putative drug efflux protein	1278	AAM86942.1	3.89908953
39155	H11	NTL02YP2254	glutamyl-tRNA reductase	1317	AAM85850.1	3.822402358
39204	H12	NTL02YP3374	hypothetical protein	1347	AAM86970.1	3.82408075

Table 15: *Yersinia pestis* Gateway® Clone, Plate 16 (UYPVP), NR-19612[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36931	A01	NTL02YP0678	hypothetical protein	465	AAM84274.1	5.932673
36961	A02	NTL02YP2274	hypothetical protein	471	AAM85870.1	3
36969	A03	NTL02YP1174	hypothetical protein	474	AAM84770.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37056	A04	NTL02YP1166	putative alpha helical protein	501	AAM84762.1	7.120148
37325	A06	NTL02YP3349	hypothetical protein	588	AAM86945.1	2.818471
37604	A07	NTL02YP3341	putative transposase	681	AAM86937.1	2
39308	A08	NTL02YP0696	putative outer membrane protein, efflux pump	1407	AAM84292.1	2.959917
39334	A09	NTL02YP3340	putative carbohydrate symporter permease	1434	AAM86936.1	2.717775
39387	A10	NTL02YP3356	hypothetical protein	1485	AAM86952.1	3.339672
39395	A11	NTL02YP3348	putative enterotoxin-like protein	1491	AAM86944.1	3.598955
39409	A12	NTL02YP0679	transcription pausing L factor	1506	AAM84275.1	2.980595
39449	B01	NTL02YP1176	hypothetical protein	1539	AAM84772.1	3.553515
39480	B02	NTL02YP1171	apolipoprotein N-acyltransferase	1587	AAM84582.1	2.808851
39598	B03	NTL02YP3375	ATP-binding cassette transporter A	1773	AAM86971.1	3.341975
39600	B04	NTL02YP3376	ATP-binding protein	1776	AAM86972.1	3.849119
39621	B05	NTL02YP3354	partial leucine-rich repeat protein	1818	AAM86950.1	3.827234
39644	B06	NTL02YP3351	partial leucine-rich repeat protein	1881	AAM86947.1	3.766268
37631	B07	NTL02YP2270	putative 2-component transcriptional regulator	693	AAM85866.1	2.695771
37637	B08	NTL02YP2267	hypothetical protein	696	AAM85863.1	2.798913
37734	B09	NTL02YP1167	ATP-binding protein of glutamate/aspartate transport system	729	AAM84763.1	6.386216
37847	B10	NTL02YP3373	thioesterase	768	AAM86969.1	5.153465
37918	C01	NTL02YP1169	glutamate/aspartate ABC transport system inner membrane permease	792	AAM84765.1	6.528846
37976	C02	NTL02YP2250	putative transcriptional regulator	810	AAM85846.1	3.603529
37787	C03	NTL02YP3329	putative transcriptional activator	744	AAM86925.1	7.118622
37815	C04	NTL02YP2219	hypothetical protein	756	AAM85815.1	6.052764
37846	C05	NTL02YP3306	hypothetical protein	768	AAM86902.1	5.950495
37959	C06	NTL02YP2225	hypothetical protein	804	AAM85821.1	3.593602
37983	C07	NTL02YP2227	putative copper homeostasis protein	813	AAM85823.1	5.550996
37992	C08	NTL02YP2223	hypothetical protein	816	AAM85819.1	4.398364
37989	C09	NTL02YP1136	putative myo-inositol catabolism protein iolB	816	AAM84732.1	3.635514
38037	C10	NTL02YP2241	putative phosphodiesterase	831	AAM85837.1	3.304248
38045	C11	NTL02YP3331	hypothetical protein	834	AAM86927.1	3.613272
36010	C12	NTL02YP1150	hypothetical protein	153	AAM84746.1	2
36122	D01	NTL02YP2247	hypothetical protein	183	AAM85843.1	4.627803
36119	D02	NTL02YP1142	hypothetical protein	183	AAM84738.1	3.950673
36179	D03	NTL02YP1137	hypothetical protein	204	AAM84733.1	5.79918
36209	D04	NTL02YP1154	hypothetical protein	213	AAM84750.1	6.474308
36257	D05	NTL02YP1148	hypothetical protein	234	AAM84744.1	2.850365
38141	D06	NTL02YP2242	putative ABC transporter permease	867	AAM85838.1	3.246968
38171	D07	NTL02YP2246	hypothetical protein	876	AAM85842.1	6.046943
38309	D08	NTL02YP1130	putative periplasmic solute-binding protein of ABC transporter	930	AAM84726.1	5.023711
38416	D09	NTL02YP1152	lipoate biosynthesis protein A	966	AAM84748.1	5.767396
38415	D10	NTL02YP1143	hypothetical protein	966	AAM84739.1	5.199801
38430	D11	NTL02YP2226	putative enzyme	972	AAM85822.1	5.41502
38593	D12	NTL02YP1132	D-ribose high-affinity transport system	1029	AAM84728.1	3.272217
38607	E01	NTL02YP1163	DNA polymerase III, delta subunit	1035	AAM84759.1	3.422326
38718	E02	NTL02YP2244	putative ABC transporter periplasmic binding protein	1083	AAM85840.1	3.089938

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38694	E03	NTL02YP3335	aerobactin synthetase (subunit alpha)	1071	AAM86931.1	4.227723
36319	E04	NTL02YP1151	hypothetical protein	258	AAM84747.1	1.969799
36325	E05	NTL02YP3310	putative transposase	258	AAM86906.1	2.966443
36338	E06	NTL02YP1155	hypothetical protein	264	AAM84751.1	3.973684
36387	E07	NTL02YP3305	putative transposase	279	AAM86901.1	2.971787
36413	E08	NTL02YP1140	conserved hypothetical protein	288	AAM84736.1	5.579268
36549	E09	NTL02YP3309	putative transposase	336	AAM86905.1	3.930851
36645	E10	NTL02YP3324	hypothetical protein	372	AAM86920.1	2.07767
36683	E11	NTL02YP1149	hypothetical protein	390	AAM84745.1	2
36688	E12	NTL02YP3313	hypothetical protein	390	AAM86909.1	5.167442
38716	F01	NTL02YP1157	rlpA lipoprotein	1083	AAM84753.1	3.197685
38786	F02	NTL02YP1158	rod shape-determining membrane protein	1113	AAM84754.1	3.336513
38792	F03	NTL02YP3332	hypothetical protein	1113	AAM86928.1	3.277537
38837	F04	NTL02YP1133	conserved hypothetical protein	1137	AAM84729.1	3.114698
38871	F05	NTL02YP2240	putative transcriptional regulator	1155	AAM85836.1	1.521339
38961	F06	NTL02YP1156	D-alanyl-D-alanine carboxypeptidase, fraction A	1203	AAM84752.1	3.202735
38972	F07	NTL02YP2236	putative permease	1206	AAM85832.1	3.250401
39252	F08	NTL02YP3330	hypothetical protein	1377	AAM86926.1	3.701482
39434	F09	NTL02YP1128	putative aldehyde dehydrogenase	1527	AAM84724.1	3.749202
39448	F10	NTL02YP2233	putative virulence factor	1536	AAM85829.1	3.071066
39456	F11	NTL02YP2662	hypothetical protein	1545	AAM86258.1	3.685804
36711	F12	NTL02YP3325	hypothetical protein	396	AAM86921.1	5.974771
36708	G01	NTL02YP2224	hypothetical protein	396	AAM85820.1	5.931193
36958	G02	NTL02YP1160	hypothetical protein	471	AAM84756.1	4.309198
37030	G03	NTL02YP1146	putative cold-shock protein	492	AAM84742.1	2
37066	G04	NTL02YP2663	hypothetical protein	504	AAM86259.1	6.683824
37119	G05	NTL02YP2218	Holliday junction nuclease	522	AAM85814.1	4
37232	G06	NTL02YP2238	putative oxidoreductase component	561	AAM85834.1	2.810316
37283	G07	NTL02YP2228	hypothetical protein	576	AAM85824.1	2.795455
39508	G08	NTL02YP2232	putative hemolysin activator protein	1635	AAM85828.1	3.423284
39585	G09	NTL02YP3337	aerobactin synthetase (subunit beta)	1749	AAM86933.1	3.428731
39610	G10	NTL02YP2222	aspartate tRNA synthetase	1797	AAM85818.1	3.769733
39648	G11	NTL02YP1159	peptidoglycan synthetase, penicillin-binding protein 2	1896	AAM84755.1	3.245351
37401	G12	NTL02YP1145	putative regulatory protein	618	AAM84741.1	2.50304
37429	H01	NTL02YP1164	rlpB lipoprotein	624	AAM84760.1	2.641566
37463	H02	NTL02YP3308	hypothetical protein	636	AAM86904.1	2.807692
37511	H03	NTL02YP3328	putative N-acylhomoserine lactone synthase	651	AAM86924.1	2.709117
37628	H04	NTL02YP1162	hypothetical protein	693	AAM84758.1	2.799454
37654	H05	NTL02YP1153	lipoate biosynthesis protein	702	AAM84749.1	2.397574
37616	H06	NTL02YP2196	cell division inhibitor	687	AAM85792.1	2.790922
37630	H07	NTL02YP2193	putative isomerase	693	AAM85789.1	6.687585
37709	H08	NTL02YP3292	hypothetical protein	720	AAM86888.1	3.897368
37739	H09	NTL02YP3281	hypothetical protein	729	AAM86877.1	2.621586
37810	H10	NTL02YP2202	hypothetical protein	753	AAM85798.1	2.754098

Table 16: *Yersinia pestis* Gateway® Clone, Plate 17 (UYPVQ), NR-19613[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37905	A01	NTL02YP2215	inner membrane permease of zinc ABC transporter	786	AAM85811.1	4.204600484
37941	A02	NTL02YP2178	putative phage antirepressor	798	AAM85774.1	3.081145585
35960	A03	NTL02YP2183	hypothetical protein	126	AAM85779.1	2
36018	A05	NTL02YP3302	hypothetical protein	153	AAM86898.1	3.968911917
36024	A06	NTL02YP2180	hypothetical protein	156	AAM85776.1	2.974489796
36200	A07	NTL02YP2181	hypothetical protein	210	AAM85777.1	5.872
36304	A08	NTL02YP1117	hypothetical protein	252	AAM84713.1	2
36359	A09	NTL02YP2198	cell division topological specificity factor	270	AAM85794.1	3.738709677
38015	A10	NTL02YP3282	putative pyrroline-5-carboxylate reductase	822	AAM86878.1	3.554524362
38103	A11	NTL02YP1127	conserved hypothetical protein	855	AAM84723.1	6.54301676
38204	A12	NTL02YP3278	hypothetical protein	885	AAM86874.1	5.644324324
38229	B01	NTL02YP1105	putative transcriptional regulator LYSR-type	894	AAM84701.1	5.880085653
38308	B02	NTL02YP1098	putative phosphatidate cytidiltransferase	930	AAM84694.1	4.884536082
38391	B03	NTL02YP2213	solute-binding periplasmic protein for zinc ABC transporter	957	AAM85809.1	5.311935807
38404	B04	NTL02YP3300	periplasmic binding protein for ABC transporter	960	AAM86896.1	8.169
38489	B05	NTL02YP1106	putative oxidoreductase	993	AAM84702.1	3.485963214
38535	B06	NTL02YP2216	Holliday junction helicase subunit A	1005	AAM85812.1	3.475598086
36375	B07	NTL02YP3294	hypothetical protein	273	AAM86890.1	3.808306709
36450	B08	NTL02YP1122	putative regulator	303	AAM84718.1	3.973760933
36457	B09	NTL02YP3284	hypothetical protein	303	AAM86880.1	5.959183673
36471	B10	NTL02YP1115	hypothetical protein	309	AAM84711.1	5.853868195
36523	B11	NTL02YP3291	hypothetical protein	327	AAM86887.1	3.931880109
36570	B12	NTL02YP2204	hypothetical protein	345	AAM85800.1	5.451948052
36579	C01	NTL02YP2205	possible chaperone	348	AAM85801.1	6.399484536
36637	C02	NTL02YP3304	putative transposase	369	AAM86900.1	5.621026895
36685	C03	NTL02YP2184	hypothetical protein	390	AAM85780.1	3.802325581
36734	C04	NTL02YP1119	hypothetical protein	402	AAM84715.1	4.746606335
38570	C05	NTL02YP3298	putative permease of ABC transporter	1020	AAM86894.1	2.923584906
38586	C07	NTL02YP2209	hypothetical protein	1026	AAM85805.1	5.237335835
38739	C08	NTL02YP3295	membrane-bound lytic murein transglycosylase C	1089	AAM86891.1	3.056687334
38736	C09	NTL02YP2194	putative transglycosylase	1089	AAM85790.1	2.657218778
38759	C10	NTL02YP3279	hypothetical protein	1098	AAM86875.1	2.585237258
38785	C11	NTL02YP3296	putative solute-binding periplasmic protein of ABC transporter	1110	AAM86892.1	3.634782609
38850	C12	NTL02YP3286	putative oxidase	1143	AAM86882.1	5.634826712
38883	D01	NTL02YP2199	RNase D	1161	AAM85795.1	2.159034138
36854	D02	NTL02YP1120	hypothetical protein	441	AAM84716.1	5.553014553
36875	D03	NTL02YP2192	hypothetical protein	447	AAM85788.1	4.104722793
36874	D04	NTL02YP2187	putative phage nin-region protein	447	AAM85783.1	4.425051335
37044	D05	NTL02YP1093	hypothetical protein	498	AAM84689.1	4.650557621
37138	D07	NTL02YP1111	hypothetical protein	531	AAM84707.1	4.65323993
37215	D08	NTL02YP1126	hypothetical protein	555	AAM84722.1	4.630252101
37222	D09	NTL02YP3283	putative resistance protein	555	AAM86879.1	4.638655462
37245	D10	NTL02YP2182	putative phage protein	564	AAM85778.1	4.437086093
37270	D11	NTL02YP1118	hypothetical protein	573	AAM84714.1	4.644371941
39023	D12	NTL02YP2191	putative transposase	1239	AAM85787.1	1.738076622

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39036	E01	NTL02YP3293	adenine glycosylase	1248	AAM86889.1	5.562111801
39161	E02	NTL02YP1101	putative enzyme	1320	AAM84697.1	4.580147059
39346	E03	NTL02YP2210	pyruvate kinase II, glucose stimulated	1443	AAM85806.1	3.643964936
39403	E04	NTL02YP3299	putative ATP-binding component of ABC transport system	1500	AAM86895.1	3.026623377
39588	E06	NTL02YP1100	hypothetical protein	1764	AAM84696.1	3.033259424
39660	E07	NTL02YP1116	putative autotransporter	1917	AAM84712.1	3.0148186
39653	E08	NTL02YP2203	putative enzyme	1905	AAM85799.1	2.743958869
37285	E09	NTL02YP3289	hypothetical protein	576	AAM86885.1	1.998376623
37363	E10	NTL02YP1097	probable enzyme	603	AAM84693.1	5.085536547
37373	E11	NTL02YP2201	putative outer membrane protein	606	AAM85797.1	2
37372	E12	NTL02YP2186	putative phage ninG-like protein	606	AAM85782.1	4
37462	F01	NTL02YP3303	hypothetical protein	636	AAM86899.1	6.133136095
37479	F02	NTL02YP2207	2-keto-3-deoxygluconate 6-phosphate aldolase/2-keto-4-hydroxyglutarate aldolase	642	AAM85803.1	4.384164223
37490	F03	NTL02YP2188	putative DNA methyltransferase	645	AAM85784.1	4.468613139
37579	F04	NTL02YP3285	putative ribosomal protein	672	AAM86881.1	4.262640449
37599	F05	NTL02YP2217	Holliday junction helicase subunit B	681	AAM85813.1	3.79889043
37431	F06	NTL02YP1767	hypothetical protein	624	AAM85363.1	4.575301205
37441	F07	NTL02YP1773	hypothetical protein	627	AAM85369.1	5.257871064
37451	F08	NTL02YP3938	50S ribosomal subunit protein L3	630	AAM87534.1	5.273134328
37454	F09	NTL02YP1770	hypothetical protein	633	AAM85366.1	5.23922734
37569	F10	NTL02YP1081	acyl-CoA thioesterase I	669	AAM84677.1	5.550070522
37576	F11	NTL02YP1766	transcriptional regulatory protein	672	AAM85362.1	5.825842697
37612	F12	NTL02YP1082	putative ATP-binding component of a transport system	687	AAM84678.1	5.127922971
37647	G01	NTL02YP3943	30S ribosomal subunit protein S3	699	AAM87539.1	6.292286874
37658	G02	NTL02YP2862	hypothetical protein	702	AAM86458.1	5.588948787
37675	G03	NTL02YP2872	16S pseudouridylate 516 synthase	708	AAM86468.1	4.657754011
36148	G04	NTL02YP3946	50S ribosomal subunit protein L29	192	AAM87542.1	1.961206897
36208	G05	NTL02YP1091	hypothetical protein	213	AAM84687.1	3.936758893
36406	G06	NTL02YP2875	50S ribosomal subunit protein L25	285	AAM86471.1	2.987692308
36459	G07	NTL02YP3940	50S ribosomal subunit protein L23	303	AAM87536.1	1.895043732
37713	G08	NTL02YP1087	hypothetical protein	723	AAM84683.1	3.770642202
37872	G09	NTL02YP1080	putative oxidoreductase	777	AAM84676.1	2
38017	G10	NTL02YP3976	dehydroshikimate reductase	822	AAM87572.1	5.032482599
38026	G11	NTL02YP3941	50S ribosomal subunit protein L2	825	AAM87537.1	2.537572254
38148	G12	NTL02YP1079	putative thioredoxin-like protein	870	AAM84675.1	1.824175824
38272	H01	NTL02YP1078	putative protease	915	AAM84674.1	5.719371728
38364	H02	NTL02YP3970	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase	948	AAM87566.1	5.686234818
38421	H03	NTL02YP2851	putative dehydrogenase	966	AAM86447.1	4.137176938
38458	H04	NTL02YP2861	hypothetical protein	984	AAM86457.1	5.391601563
38484	H05	NTL02YP3963	RNA polymerase, alpha subunit	990	AAM87559.1	2.82815534
36468	H06	NTL02YP3950	30S ribosomal subunit protein S14	306	AAM87546.1	2.959537572
36488	H07	NTL02YP3948	50S ribosomal subunit protein L24	315	AAM87544.1	2.977464789
36539	H08	NTL02YP3942	50S ribosomal subunit protein L22	333	AAM87538.1	4.967828418
36572	H09	NTL02YP2869	hypothetical protein	345	AAM86465.1	3.571428571
36595	H10	NTL02YP2874	hypothetical protein	354	AAM86470.1	2.984771574
36597	H11	NTL02YP3954	50S ribosomal subunit protein L18	354	AAM87550.1	2.987309645
36646	H12	NTL02YP3947	50S ribosomal subunit protein L14	372	AAM87543.1	3.927184466

Table 17: *Yersinia pestis* Gateway® Clone, Plate 18 (UYPVR), NR-19614[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38597	A01	NTL02YP2867	putative transport system permease protein	1029	AAM86463.1	1.517306
38676	A02	NTL02YP1084	phosphoribosylaminoimidazole carboxylase, CO(2)-fixing subunit	1065	AAM84680.1	1.743891
38763	A03	NTL02YP2866	putative transport system permease protein	1101	AAM86462.1	2.658195
38795	A04	NTL02YP1771	hypothetical protein	1116	AAM85367.1	2.50173
38848	A05	NTL02YP2850	hypothetical protein	1143	AAM86446.1	2.262891
38947	A06	NTL02YP2857	mannonate hydrolase	1194	AAM86453.1	7.576985
38958	A07	NTL02YP2871	bicyclomycin resistance protein transmembrane protein	1200	AAM86467.1	2.98629
36702	A08	NTL02YP3951	30S ribosomal subunit protein S8, and regulator	393	AAM87547.1	2.979215
36767	A09	NTL02YP3944	50S ribosomal subunit protein L16	411	AAM87540.1	3.43459
36786	A10	NTL02YP3945	hypothetical protein	417	AAM87541.1	3.503282
36803	A11	NTL02YP3967	mechanosensitive channel protein	423	AAM87563.1	2
36842	A12	NTL02YP3965	putative transcriptional regulator	435	AAM87561.1	3.981053
36841	B01	NTL02YP3957	50S ribosomal subunit protein L15	435	AAM87553.1	4.684211
36871	B02	NTL02YP1772	putative phosphohydrolase	447	AAM85368.1	2
36978	B03	NTL02YP3973	hypothetical protein	474	AAM87569.1	6.136187
37037	B04	NTL02YP1088	peptidyl-prolyl cis-trans isomerase B	495	AAM84684.1	2
39125	B07	NTL02YP1774	isocitrate dehydrogenase, specific for $NADP^+$	1305	AAM85370.1	3.577695
39182	B08	NTL02YP3958	putative ATPase subunit of translocase	1332	AAM87554.1	3.338192
39254	B09	NTL02YP3968	potassium uptake protein	1377	AAM87564.1	3.804517
39258	B10	NTL02YP1769	adenylosuccinate lyase	1380	AAM85365.1	3.714789
39327	B11	NTL02YP1089	cysteine tRNA synthetase	1431	AAM84685.1	3.662814
39360	B12	NTL02YP1765	sensor protein PhoQ	1455	AAM85361.1	3.664883
39375	C01	NTL02YP2858	putative oxidoreductase	1473	AAM86454.1	3.658295
39502	C02	NTL02YP2868	putative ATP-binding component of a transport system	1626	AAM86464.1	3.342737
39511	C03	NTL02YP1777	aerotaxis sensor receptor, flavoprotein	1638	AAM85373.1	2.800954
39587	C04	NTL02YP2873	putative ATP-dependent helicase	1758	AAM86469.1	3.354283
37123	C05	NTL02YP1085	phosphoribosylaminoimidazole carboxylase, catalytic subunit	525	AAM84681.1	2.817699
37169	C06	NTL02YP3949	50S ribosomal subunit protein L5	540	AAM87545.1	2.817241
37237	C07	NTL02YP3974	putative DNA topoisomerase	561	AAM87570.1	2.815308
37320	C08	NTL02YP3975	hypothetical protein	585	AAM87571.1	2.8128
37375	C09	NTL02YP3939	50S ribosomal subunit protein L4	606	AAM87535.1	2
37422	C10	NTL02YP3962	30S ribosomal subunit protein S4	621	AAM87558.1	6.155825
37760	C11	NTL02YP3926	hypothetical protein	735	AAM87522.1	5.180645
37911	C12	NTL02YP1760	putative NAGC-like transcriptional regulator	789	AAM85356.1	5.501809
37914	D01	NTL02YP2828	ATP-binding protein of iron/siderophore ABC transporter	789	AAM86424.1	5.47889
38013	D02	NTL02YP2836	pH 6 Antigen chaperone protein	822	AAM86432.1	2.585847
38067	D03	NTL02YP3925	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	840	AAM87521.1	2
38160	D04	NTL02YP2832	putative transcriptional regulator LYSR-type	873	AAM86428.1	1.874042
38182	D05	NTL02YP1741	putative shikimate 5-dehydrogenase	879	AAM85337.1	5.274211
36072	D06	NTL02YP1761	hypothetical protein	168	AAM85357.1	2.947115

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36144	D07	NTL02YP0652	hypothetical protein	192	AAM84249.1	3.887931
36152	D08	NTL02YP1750	hypothetical protein	195	AAM85346.1	3.961702
36235	D09	NTL02YP3921	hypothetical protein	222	AAM87517.1	4.118321
36251	D10	NTL02YP3922	hypothetical protein	228	AAM87518.1	4.958955
36380	D11	NTL02YP0661	putative regulator for maltose metabolism	276	AAM84257.1	4.702532
38203	D12	NTL02YP2834	endonuclease IV	885	AAM86430.1	2.03027
38341	E01	NTL02YP2841	fructose-1-phosphate kinase	939	AAM86437.1	5.346272
38337	E02	NTL02YP0660	malate dehydrogenase	939	AAM84256.1	5.319714
38461	E03	NTL02YP0666	hypothetical protein	987	AAM84262.1	5.024343
38514	E04	NTL02YP2844	putative permease	999	AAM86440.1	1.599615
38684	E05	NTL02YP0668	sensor protein for basR	1068	AAM84264.1	3.437726
38774	E06	NTL02YP2833	hypothetical protein	1107	AAM86429.1	3.027899
36419	E07	NTL02YP3929	hypothetical protein	288	AAM87525.1	3.771341
36428	E08	NTL02YP0672	hypothetical protein	294	AAM84268.1	2.979042
36484	E09	NTL02YP3937	30S ribosomal subunit protein S10	312	AAM87533.1	2.977273
36543	E10	NTL02YP0677	protein export - membrane protein	336	AAM84273.1	3.601064
36594	E11	NTL02YP1742	hypothetical protein	354	AAM85338.1	3.893401
36600	E12	NTL02YP0654	hypothetical protein	357	AAM84250.1	4.093199
36608	F01	NTL02YP0664	50S ribosomal subunit protein L21	360	AAM84260.1	5.57
36629	F02	NTL02YP3928	hypothetical protein	366	AAM87524.1	3.975369
36657	F03	NTL02YP3931	30S ribosomal subunit protein S12	375	AAM87527.1	5.828916
36681	F04	NTL02YP3930	hypothetical protein	387	AAM87526.1	2
36713	F05	NTL02YP3927	hypothetical protein	396	AAM87523.1	3.720183
36730	F06	NTL02YP0662	hypothetical protein	402	AAM84258.1	3.988688
38800	F07	NTL02YP0656	fructose-bisphosphatase	1119	AAM84252.1	5.289905
38832	F08	NTL02YP2842	PTS system, fructose-specific IIA/fpr component	1134	AAM86438.1	3.042589
38901	F09	NTL02YP2830	solute-binding periplasmic protein of iron/siderophore ABC transporter	1170	AAM86426.1	4.541322
38903	F10	NTL02YP0667	putative GTP-binding factor	1173	AAM84263.1	2.483924
38909	F11	NTL02YP1764	hypothetical protein	1176	AAM85360.1	2.448191
38935	F12	NTL02YP3934	protein chain elongation factor EF-Tu	1185	AAM87530.1	5.213061
38963	G01	NTL02YP1757	hypothetical protein	1203	AAM85353.1	5.671762
36770	G03	NTL02YP1752	hypothetical protein	414	AAM85348.1	3.471366
36906	G04	NTL02YP1743	hypothetical protein	456	AAM85339.1	4.15121
36965	G05	NTL02YP3932	30S ribosomal subunit protein S7	471	AAM87528.1	2.982387
36957	G06	NTL02YP0659	repressor of Arg regulon	471	AAM84255.1	2.984344
36977	G07	NTL02YP3936	bacterioferrin	474	AAM87532.1	3.515564
36986	G08	NTL02YP0671	transcription elongation factor	477	AAM84267.1	4.709865
37059	G09	NTL02YP2838	putative membrane protein	501	AAM86434.1	2
37159	G10	NTL02YP2843	hypothetical protein	537	AAM86439.1	5.214905
37175	G11	NTL02YP1748	hypothetical protein	543	AAM85344.1	2
39191	G12	NTL02YP0676	mrsA protein	1341	AAM84272.1	1.724837
39262	H01	NTL02YP0657	putative ligase	1383	AAM84253.1	5.189037
39332	H02	NTL02YP1739	PTS system, glucose-specific IIBC component	1434	AAM85335.1	4.037992
39351	H03	NTL02YP0670	D-alanyl-D-alanine carboxypeptidase, fraction B	1449	AAM84266.1	5.696441
39416	H04	NTL02YP2831	lysine-specific permease	1512	AAM86427.1	3.701031
39477	H05	NTL02YP2845	putative ABC transporter	1575	AAM86441.1	4.814241
39582	H06	NTL02YP0651	hypothetical protein	1737	AAM84247.1	5.185706
39618	H07	NTL02YP3920	K$^+$ efflux NEM-activable K$^+$/H$^+$ antiporter	1809	AAM87516.1	3.905895

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39671	H08	NTL02YP0674	integral membrane peptidase, cell division protein	1944	AAM84270.1	3.25504
37212	H09	NTL02YP3919	putative NAD(P)H oxidoreductase	552	AAM87515.1	6.445946
37253	H10	NTL02YP1754	hypothetical protein	567	AAM85350.1	4.672158
37261	H11	NTL02YP1751	hypothetical protein	570	AAM85347.1	2
37275	H12	NTL02YP3918	hypothetical protein	573	AAM87514.1	2.980424

Table 18: *Yersinia pestis* Gateway® Clone, Plate 19 (UYPVS), NR-19615[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37281	A01	NTL02YP1744	hypothetical protein	576	AAM85340.1	5.03409091
37327	A02	NTL02YP3923	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)	588	AAM87519.1	4.61624204
37467	A03	NTL02YP0650	peptide methionine sulfoxide reductase	639	AAM84246.1	5.32253314
37475	A04	NTL02YP0673	cell division protein	642	AAM84269.1	2.63489736
37492	A05	NTL02YP2839	putative regulator	645	AAM86435.1	2
37547	A06	NTL02YP0669	transcriptional regulatory protein, member of 2-component regulatory	663	AAM84265.1	2.69274538
37670	A07	NTL02YP1758	putative ATP-binding component of a transport system	705	AAM85354.1	2.77852349
37849	A08	NTL02YP3912	taurine ATP-binding component of ABC transport system	768	AAM87508.1	4.63613861
37968	A10	NTL02YP1734	4-amino-4-deoxychorismate lyase	807	AAM85330.1	1.3175915
37970	A11	NTL02YP3890	putative nitrite transporter	807	AAM87486.1	8.6635183
37993	A12	NTL02YP2813	hypothetical protein	816	AAM86409.1	2
38025	B01	NTL02YP2822	putative lipoprotein	825	AAM86418.1	7.1132948
38108	B02	NTL02YP3913	taurine ABC transport system inner membrane permease	855	AAM87509.1	3.4726257
38144	B03	NTL02YP3914	taurine dioxygenase	867	AAM87510.1	2
35944	B04	NTL02YP2818	hypothetical protein	117	AAM86414.1	2
36048	B05	NTL02YP0632	hypothetical protein	162	AAM84228.1	-
36244	B06	NTL02YP0638	30S ribosomal subunit protein S18	228	AAM84234.1	3.97761194
36274	B07	NTL02YP3908	hypothetical protein	237	AAM87504.1	2.70036101
38258	B08	NTL02YP3907	probable phosphoribulokinase	906	AAM87503.1	5.77484144
38312	B09	NTL02YP2823	putative iron/ascorbate-dependent oxidoreductase	930	AAM86419.1	3.06907216
38311	B10	NTL02YP1729	malonyl-CoA-[acyl-carrier-protein] transacylase	930	AAM85325.1	3.61134021
38370	B11	NTL02YP1728	3-oxoacyl-[acyl-carrier-protein] synthase III	951	AAM85324.1	5.9283552
38420	B12	NTL02YP2803	putrescine permease of ABC transporter	966	AAM86399.1	2
38451	C01	NTL02YP3915	putative LPS biosynthetic enzyme	981	AAM87511.1	4.20763957
38465	C02	NTL02YP2821	ATP-binding component of ATP transporter	987	AAM86417.1	4.59493671
38584	C04	NTL02YP1722	hypothetical protein	1026	AAM85318.1	5.76360225
36487	C05	NTL02YP2809	hypothetical protein	315	AAM86405.1	4.74366197
36697	C06	NTL02YP0637	30S ribosomal subunit protein S6	393	AAM84233.1	3.99076212
36759	C07	NTL02YP3905	hypothetical protein	408	AAM87501.1	3.97767857
36834	C08	NTL02YP3906	hypothetical protein	432	AAM87502.1	3.98305085
36828	C09	NTL02YP1717	hypothetical protein	432	AAM85312.1	5.29449153

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36895	C10	NTL02YP0639	50S ribosomal subunit protein L9	453	AAM84235.1	3.98377282
36901	C11	NTL02YP0641	hypothetical protein	456	AAM84237.1	5.24395161
36940	C12	NTL02YP2801	hypothetical protein	465	AAM86397.1	4.68118812
38627	D01	NTL02YP3888	tryptophan tRNA synthetase	1041	AAM87484.1	2.84181314
38636	D02	NTL02YP1718	dihydro-orotase	1047	AAM85314.1	6.33854646
38742	D03	NTL02YP1735	putative thymidylate kinase	1092	AAM85035.1	5.37102473
38827	D04	NTL02YP2800	putative enzyme	1131	AAM86396.1	4.96242528
38831	D05	NTL02YP2804	ATP-binding component of putrescine ABC transport system	1134	AAM86400.1	4.66950596
38934	D06	NTL02YP3895	permease (major facilitator superfamily)	1185	AAM87491.1	4.68734694
39002	D08	NTL02YP2806	periplasmic putrescine-binding protein of putrescine ABC transporter	1227	AAM86402.1	2.20599842
39007	D09	NTL02YP3902	acetylornithine delta-aminotransferase	1230	AAM87498.1	2.91968504
36985	D10	NTL02YP0628	hypothetical protein	477	AAM84224.1	5.56673114
37017	D11	NTL02YP2807	putative sensory transduction regulator	486	AAM86403.1	4.39543726
37126	D12	NTL02YP1724	hypothetical protein	525	AAM85320.1	6.18584071
37287	E01	NTL02YP3901	p-aminobenzoate synthetase, component II	576	AAM87497.1	5.60876623
37358	E02	NTL02YP3899	peptidyl-prolyl cis-trans isomerase A	600	AAM87495.1	2
37379	E03	NTL02YP1723	hypothetical	609	AAM85319.1	2.55007704
37413	E04	NTL02YP0643	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase (rotamase)	621	AAM84239.1	2.75189107
37457	E05	NTL02YP3904	cyclic AMP receptor protein	633	AAM87500.1	2.78008915
39028	E06	NTL02YP1732	3-oxoacyl-[acyl-carrier-protein] synthase II	1242	AAM85328.1	3.17550702
39117	E07	NTL02YP2819	D-alanyl-D-alanine carboxypeptidase penicillin-binding protein 6	1299	AAM86415.1	1.42419716
39141	E08	NTL02YP3894	cytosine deaminase	1311	AAM87490.1	6.08068098
39148	E09	NTL02YP3898	phospho-beta-glucosidase	1314	AAM87494.1	5.23190547
39452	E10	NTL02YP3900	hypothetical protein	1542	AAM87496.1	2.517067
39541	E11	NTL02YP0631	putative acyl coenzyme A dehydrogenase	1674	AAM84227.1	4.59043174
39553	E12	NTL02YP2812	putative transport protein	1689	AAM86408.1	6.70098323
37470	F02	NTL02YP1736	thymidylate kinase	639	AAM85332.1	2
37466	F03	NTL02YP0647	hypothetical protein	639	AAM84243.1	6.65243004
37509	F04	NTL02YP2825	hypothetical protein	651	AAM86421.1	2.78147612
37560	F05	NTL02YP0644	hypothetical protein	666	AAM84240.1	2
37578	F06	NTL02YP2820	putative transport system permease protein	672	AAM86416.1	6.37921348
37577	F07	NTL02YP2815	putative deoxyribose-phosphate aldolase	672	AAM86411.1	5.2008427
37719	F08	NTL02YP2826	putative transferase	723	AAM86422.1	6.1965924
37758	F09	NTL02YP1730	3-oxoacyl-[acyl-carrier-protein] reductase	735	AAM85326.1	6.49677419
37776	F10	NTL02YP0642	hypothetical protein	741	AAM84238.1	4.75928297
37775	F11	NTL02YP0630	hypothetical protein	741	AAM84226.1	4.7631242
38186	F12	NTL02YP0612	phosphatidylserine decarboxylase	882	AAM84208.1	5.23861171
38302	G01	NTL02YP2798	putative ftsH proteinase activity modulator	927	AAM86394.1	6.13547053
38340	G02	NTL02YP1688	hypothetical protein	939	AAM85284.1	6.39836568
38347	G03	NTL02YP0621	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase	942	AAM84217.1	5.50203666
38448	G04	NTL02YP1703	hypothetical protein	981	AAM85299.1	5.73163565
38510	G05	NTL02YP0610	putative lysyl-tRNA synthetase	999	AAM84206.1	5.78344562
38530	G06	NTL02YP0626	putative protease specific for phage lambda cII	1005	AAM84222.1	2.72822967
36008	G07	NTL02YP0624	hypothetical protein	153	AAM84220.1	5.93782383

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36307	G08	NTL02YP2795	hypothetical protein	252	AAM86391.1	3.9760274
36322	G09	NTL02YP1693	hypothetical protein	258	AAM85290.1	6.77852349
38533	G10	NTL02YP1698	hypothetical protein	1005	AAM85294.1	3.24976077
38569	G11	NTL02YP2778	putative arylsulfatase	1020	AAM86374.1	3.30849057
38588	G12	NTL02YP2780	putative nucleotide di-P-sugar epimerase or dehydratase	1026	AAM86376.1	3.53377111
38592	H01	NTL02YP0603	hypothetical protein	1029	AAM84199.1	6.04583723
38622	H02	NTL02YP1683	putative lacI-family transcriptional regulator	1041	AAM85279.1	2.97132285
38661	H03	NTL02YP1687	hypothetical protein	1056	AAM85283.1	2.99817518
38726	H04	NTL02YP1711	putative transport protein	1086	AAM85307.1	2.34369449
38740	H05	NTL02YP3882	3-dehydroquinate synthase	1089	AAM87478.1	5.26660762
38794	H06	NTL02YP1714	sarcosine oxidase-like protein	1116	AAM85310.1	5.76816609
36427	H07	NTL02YP0600	GroES protein	294	AAM84196.1	3.9760479
36460	H08	NTL02YP0622	putative host factor I for bacteriophage Q	306	AAM84218.1	4.62716763
36599	H09	NTL02YP0606	fumarate reductase, anaerobic, membrane anchor polypeptide	357	AAM84202.1	3.98992443
36699	H10	NTL02YP2794	hypothetical protein	393	AAM86390.1	1.98383372
36696	H11	NTL02YP0607	fumarate reductase, anaerobic, membrane anchor polypeptide	393	AAM84203.1	4.84526559
36742	H12	NTL02YP1709	hypothetical protein	405	AAM85305.1	5.16404494

Table 19: *Yersinia pestis* Gateway® Clone, Plate 20 (UYPVT), NR-19616[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36925	A01	NTL02YP0605	suppresses groEL, may be chaperone	462	AAM84201.1	3.98406
36956	A02	NTL02YP0618	hypothetical protein	471	AAM84214.1	3.98434
37120	A03	NTL02YP3881	shikimate kinase I	522	AAM87477.1	5.65836
38816	A04	NTL02YP3880	putative transport portein	1125	AAM87476.1	3.29099
38839	A05	NTL02YP2796	hypothetical	1137	AAM86392.1	3.33985
39048	A07	NTL02YP0625	putative protease specific for phage lambda cII	1260	AAM84221.1	3.50923
39070	A08	NTL02YP1690	hypothetical protein	1275	AAM85286.1	6.44106
39089	A09	NTL02YP0623	putative GTP binding subunit for protease of lambda cII repressor	1287	AAM84219.1	5.69706
39120	A10	NTL02YP0597	anaerobic C-4-dicarboxylate symporter	1302	AAM84193.1	4.0462
39137	A11	NTL02YP0627	adenylosuccinate synthetase	1311	AAM84223.1	2.8416
37186	A12	NTL02YP0599	hypothetical protein	546	AAM84195.1	5.21502
37217	B01	NTL02YP1699	hypothetical protein	555	AAM85295.1	5.63529
37234	B02	NTL02YP2783	putative chorismate mutase	561	AAM86379.1	5.62063
37284	B03	NTL02YP2781	putative enzyme	576	AAM86377.1	2.79221
37476	B04	NTL02YP1713	hypothetical protein	642	AAM85309.1	6.1129
37625	B05	NTL02YP3886	D-ribulose-5-phosphate 3-epimerase	690	AAM87482.1	6.48493
37627	B06	NTL02YP0615	hypothetical protein	693	AAM84211.1	6.2442
39203	B07	NTL02YP1696	hypothetical protein	1347	AAM85292.1	3.61788
39301	B08	NTL02YP2790	hypothetical protein	1401	AAM86386.1	3.71409
39338	B09	NTL02YP0598	aspartate ammonia-lyase (aspartase)	1437	AAM84194.1	3.5369
39393	B10	NTL02YP2779	putative dTDP-glucose enzyme	1491	AAM86375.1	5.42325
39419	B11	NTL02YP0617	hypothetical protein	1515	AAM84213.1	1.9254
39521	B12	NTL02YP0601	GroEL protein	1647	AAM84197.1	3.51097

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39623	C01	NTL02YP0609	fumarate reductase, anaerobic, flavoprotein subunit	1824	AAM84205.1	3.36749
37753	C02	NTL02YP3887	phosphoglycolate phosphatase	732	AAM87483.1	6.00518
37755	C03	NTL02YP0608	fumarate reductase, anaerobic, iron-sulfur protein subunit	735	AAM84204.1	5.93677
37763	C04	NTL02YP1704	putative transcriptional activator protein	738	AAM85300.1	6.28663
37883	C05	NTL02YP2784	ATP-binding component of 3rd arginine transport system	780	AAM86380.1	2.7878
37944	C06	NTL02YP2791	putative ABC transport protein	798	AAM86387.1	6.27446
38021	C07	NTL02YP1686	putative inner membrane permease of ABC transporter	825	AAM85282.1	3.02428
37563	C09	NTL02YP3276	hypothetical protein	666	AAM86872.1	5.66997
37660	C10	NTL02YP3239	putative oxidoreductase	702	AAM86835.1	4.58491
37659	C11	NTL02YP3234	catabolic regulation response regulator	702	AAM86830.1	5.93396
37677	C12	NTL02YP3270	DNA-specific endonuclease I	708	AAM86866.1	5.47193
37683	D01	NTL02YP2159	putative phage tail protein	711	AAM85755.1	5.98136
37736	D02	NTL02YP2174	hypothetical protein	729	AAM85770.1	4.82055
37886	D03	NTL02YP3265	hypothetical protein	780	AAM86861.1	4.79756
38009	D04	NTL02YP0582	positive regulator for rhaBAD operon	822	AAM84178.1	5.17285
35963	D05	NTL02YP3244	hypothetical protein	126	AAM86840.1	1.96988
35969	D06	NTL02YP1680	hypothetical protein	132	AAM85276.1	1.97674
38078	D07	NTL02YP3258	putative actin	843	AAM86854.1	1.66478
38153	D08	NTL02YP3260	putative transport protein	870	AAM86856.1	1.61429
38158	D09	NTL02YP0583	positive regulator for rhaRS operon	873	AAM84179.1	1.62432
38288	D10	NTL02YP2164	hypothetical protein	921	AAM85760.1	4.25598
38393	D11	NTL02YP3257	replication initiation inhibitor	957	AAM86853.1	4.94483
38562	D12	NTL02YP3263	D-erythrose 4-phosphate dehydrogenase	1017	AAM86859.1	2.81835
36282	E01	NTL02YP0595	hypothetical protein	243	AAM84191.1	3.85866
36310	E02	NTL02YP2168	hypothetical protein	255	AAM85764.1	3.98305
36347	E03	NTL02YP0586	hypothetical protein	267	AAM84182.1	4.40391
36349	E04	NTL02YP3236	hypothetical protein	267	AAM86832.1	3.97394
36448	E05	NTL02YP0587	putative transposase	303	AAM84183.1	3.77843
36480	E06	NTL02YP2163	hypothetical protein	312	AAM85759.1	4.52557
36565	E07	NTL02YP2161	putative phage tail protein	342	AAM85757.1	4.17801
36607	E08	NTL02YP0596	divalent cation tolerance protein	360	AAM84192.1	3.9875
36660	E09	NTL02YP3253	hypothetical protein	378	AAM86849.1	5.16986
38758	E10	NTL02YP3248	aminomethyltransferase of glycine cleavage system	1098	AAM86844.1	2.78998
38770	E11	NTL02YP3240	hypothetical protein	1104	AAM86836.1	2.30944
38789	E12	NTL02YP2172	hypothetical protein	1113	AAM85768.1	1.57676
38904	F01	NTL02YP2148	hypothetical protein	1173	AAM85744.1	3.12366
38914	F02	NTL02YP3250	2-octaprenyl-6-methoxyphynol hydroxylase	1179	AAM86846.1	3.01723
38971	F03	NTL02YP2170	hypothetical protein	1206	AAM85766.1	3.12279
36755	F05	NTL02YP2165	hypothetical protein	408	AAM85761.1	1.93973
36793	F06	NTL02YP2150	putative phage tail protein	420	AAM85746.1	5.30217
36801	F07	NTL02YP3277	hypothetical protein	423	AAM86873.1	4.91145
36808	F08	NTL02YP0588	hypothetical protein	426	AAM84184.1	2.99142
36813	F09	NTL02YP3235	hypothetical protein	426	AAM86831.1	4.85622
36830	F10	NTL02YP2157	hypothetical protein	432	AAM85753.1	5.11441
36848	F11	NTL02YP3245	hypothetical protein	438	AAM86841.1	2
36890	F12	NTL02YP2176	hypothetical protein	450	AAM85772.1	1.99388

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37143	G01	NTL02YP3238	hypothetical protein	531	AAM86834.1	3.13485
37208	G02	NTL02YP2155	hypothetical protein	552	AAM85751.1	2.82264
37224	G03	NTL02YP0592	electron transport protein	558	AAM84188.1	6.4097
37226	G04	NTL02YP2169	hypothetical protein	558	AAM85765.1	2.83779
39053	G06	NTL02YP0578	L-rhamnose isomerase	1263	AAM84174.1	3.95165
39147	G07	NTL02YP3251	proline aminopeptidase P II	1314	AAM86847.1	3.88109
39198	G08	NTL02YP3255	D-3-phosphoglycerate dehydrogenase	1344	AAM86851.1	3.05058
39316	G09	NTL02YP3233	catabolite repression sensor kinase for PhoB	1419	AAM86829.1	3.52776
39341	G10	NTL02YP3249	hypothetical protein	1437	AAM86845.1	5.09072
39604	G11	NTL02YP0594	thiol:disulfide interchange protein	1788	AAM84190.1	3.96444
39690	G12	NTL02YP3267	biosynthetic arginine decarboxylase	1980	AAM86863.1	3.62376
39693	H01	NTL02YP3264	transketolase 1 isozyme	1995	AAM86860.1	3.70319
37246	H02	NTL02YP3269	hypothetical protein	564	AAM86865.1	2
37293	H03	NTL02YP3252	hypothetical protein	579	AAM86848.1	2.81906
37313	H04	NTL02YP2166	hypothetical protein	585	AAM85762.1	2.7904
37332	H05	NTL02YP0590	hypothetical protein	591	AAM84186.1	2.80983
37350	H06	NTL02YP3254	putative ligase	597	AAM86850.1	2.79906
37405	H07	NTL02YP3259	hypothetical protein	618	AAM86855.1	2.81155
37417	H08	NTL02YP2154	putative phage tail protein	621	AAM85750.1	2.77458
37455	H09	NTL02YP2158	hypothetical protein	633	AAM85754.1	2
37478	H10	NTL02YP2173	hypothetical protein	642	AAM85769.1	2.40762
37536	H11	NTL02YP3256	ribosephosphate isomerase	657	AAM86852.1	2.7977
38106	H12	NTL02YP3183	tagatose-bisphosphate aldolase 2	855	AAM86779.1	3.58659

Table 20: *Yersinia pestis* Gateway® Clone, Plate 21 (UYPVU), NR-19617[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38127	A01	NTL02YP2118	hypothetical protein	861	AAM85714.1	3.59267481
38326	A02	NTL02YP3227	peptide chain release factor RF-2	933	AAM86823.1	3.47687564
38323	A03	NTL02YP2137	putative regulator	933	AAM85733.1	5.95272354
38390	A04	NTL02YP2099	hypothetical protein	957	AAM85695.1	5.96389168
38534	A05	NTL02YP2131	glyceraldehyde-3-phosphate dehydrogenase A	1005	AAM85727.1	3.5492823
35997	A06	NTL02YP2124	hypothetical protein	150	AAM85720.1	3.95263158
36181	A07	NTL02YP3217	hypothetical protein	204	AAM86813.1	3.70081967
36398	A08	NTL02YP3224	hypothetical protein	282	AAM86820.1	5.77950311
36466	A09	NTL02YP3211	hypothetical protein	306	AAM86807.1	2.9017341
38546	A10	NTL02YP3198	D-ribose high-affinity transport system protein	1011	AAM86794.1	4.04852521
38559	A11	NTL02YP2127	cytoplasmic L-asparaginase I	1017	AAM85723.1	3.52034059
38558	A12	NTL02YP2114	Hnr protein	1017	AAM85353.1	3.0756859
38579	B01	NTL02YP3199	putative periplasmic binding protein precursor	1023	AAM86795.1	5.75634995
38640	B03	NTL02YP2123	selenophosphate synthase	1047	AAM85719.1	3.06071757
38721	B04	NTL02YP3185	hypothetical protein	1083	AAM86781.1	2.79252004
38776	B05	NTL02YP3196	putative transport ATP-binding protein	1107	AAM86792.1	3.26503923
38849	B06	NTL02YP3210	hypothetical protein	1143	AAM86806.1	2.772612
38861	B07	NTL02YP3188	transcriptional repressor of the lac operon	1149	AAM86784.1	3.47182506
38965	B08	NTL02YP2139	hypothetical protein	1203	AAM85735.1	3.21962993

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36465	B09	NTL02YP3205	hypothetical protein	306	AAM86801.1	4.63872832
36482	B10	NTL02YP3190	hypothetical protein	312	AAM86786.1	7.13352273
36536	B11	NTL02YP3213	hypothetical protein	333	AAM86809.1	2
36603	B12	NTL02YP2145	hypothetical protein	357	AAM85741.1	3.78589421
36644	C01	NTL02YP3221	hypothetical protein	372	AAM86817.1	4.97572816
36658	C02	NTL02YP2129	hypothetical protein	378	AAM85725.1	5.61961722
36677	C03	NTL02YP2120	hypothetical protein	387	AAM85716.1	2
36725	C04	NTL02YP3220	hypothetical protein	399	AAM86816.1	1.9977221
36754	C05	NTL02YP2112	DNA-binding protein HLP-II (HU, BH2, HD, NS)	408	AAM85708.1	2.97767857
36782	C06	NTL02YP2104	hypothetical protein	417	AAM85700.1	2
36823	C07	NTL02YP2108	putative transposase	429	AAM85704.1	2
38966	C08	NTL02YP3192	hypothetical protein	1203	AAM86788.1	3.20675784
39057	C09	NTL02YP3195	putative periplasmic binding protein	1263	AAM86791.1	3.92018419
39134	C10	NTL02YP3194	putative malF-type permease	1308	AAM86223.1	3.74035608
39133	C11	NTL02YP3186	putative hexuronate transporter transmembrane protein	1308	AAM86782.1	3.86424332
39162	C12	NTL02YP2135	hypothetical protein	1320	AAM85731.1	3.81911765
39181	D01	NTL02YP3189	putative outer membrane protein	1332	AAM86785.1	3.7638484
39246	D02	NTL02YP2113	putative UDP-glucose dehydrogenase	1374	AAM85709.1	3.76520509
39281	D03	NTL02YP2103	putative arginine/ornithine antiporter	1392	AAM85699.1	3.72346369
36960	D04	NTL02YP2130	hypothetical protein	471	AAM85726.1	2
37115	D05	NTL02YP3200	hypothetical protein	519	AAM86796.1	2.81753131
37207	D06	NTL02YP2125	hypothetical protein	552	AAM85721.1	2
37292	D07	NTL02YP3184	hypothetical protein	579	AAM86780.1	2.80129241
37303	D08	NTL02YP3231	flavodoxin 2	582	AAM86827.1	2.84565916
37335	D09	NTL02YP2111	thymidine kinase	591	AAM85707.1	2.8177496
37502	D10	NTL02YP2128	hypothetical protein	648	AAM85724.1	2.79215116
37603	D11	NTL02YP3203	hypothetical protein	681	AAM86799.1	2.79750347
37699	D12	NTL02YP3229	protein disulfide isomerase II	717	AAM86825.1	2.65785997
39286	E01	NTL02YP2100	pyridine nucleotide transhydrogenase, beta subunit	1395	AAM85696.1	5.76445993
39389	E02	NTL02YP3182	hypothetical protein	1488	AAM86778.1	3.3841623
39401	E03	NTL02YP2107	putative carboxypeptidase	1500	AAM85703.1	3.5987013
39435	E04	NTL02YP2101	pyridine nucleotide transhydrogenase, alpha subunit	1527	AAM85697.1	3.71346522
39447	E05	NTL02YP2141	putative sporulation protein	1536	AAM85737.1	3.70685279
39451	E06	NTL02YP3197	ATP-binding component of D-ribose high-affinity transport system	1539	AAM86793.1	3.709943
39670	E07	NTL02YP2134	hypothetical protein	1935	AAM85730.1	3.65316456
37707	E08	NTL02YP2143	negative regulator for fad regulon, and positive	720	AAM85739.1	2.78421053
37808	E09	NTL02YP2116	formyltetrahydrofolate deformylase	753	AAM85712.1	3.64943253
37807	E10	NTL02YP2098	transcriptional regulation of aerobic and anaerobic respiration and osmotic balance	753	AAM85694.1	5.73518285
37845	E11	NTL02YP3207	hypothetical protein	768	AAM86803.1	6.65717822
37856	E12	NTL02YP2133	hypothetical protein	771	AAM85729.1	3.6350185
37885	F01	NTL02YP3206	hypothetical protein	780	AAM86802.1	2.64756098
37904	F03	NTL02YP2146	hypothetical protein	786	AAM85742.1	5.78571429
37940	F04	NTL02YP2138	hypothetical protein	798	AAM85374.1	3.57398568

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37949	F05	NTL02YP2105	response transcriptional regulatory protein (RstB sensor)	801	AAM85701.1	6.2508918
37759	F06	NTL02YP2761	leucyl, phenylalanyl-tRNA-protein transferase	735	AAM86357.1	1.99354839
37929	F08	NTL02YP2090	hypothetical	795	AAM85686.1	6.56886228
38003	F09	NTL02YP2084	taurine ATP-binding component of a transport system	819	AAM85680.1	3.57974389
38012	F10	NTL02YP2083	putative inner membrane permease for ABC transporter	822	AAM85679.1	3.62180974
38060	F11	NTL02YP3847	protein of glp regulon	837	AAM87443.1	6.78563284
38194	F12	NTL02YP3867	hypothetical protein	882	AAM87463.1	6.26898048
36133	G01	NTL02YP3854	hypothetical protein	186	AAM87450.1	2
36159	G02	NTL02YP1674	hypothetical protein	198	AAM85270.1	5.74369748
36191	G03	NTL02YP2766	hypothetical protein	207	AAM86362.1	2.9757085
36202	G04	NTL02YP2777	hypothetical protein	210	AAM86373.1	5.352
38237	G05	NTL02YP2773	putative surface protein	897	AAM86369.1	6.08537887
38351	G06	NTL02YP3873	hypothetical protein	942	AAM87469.1	6.15580448
38348	G07	NTL02YP1664	putative transcriptional regulator LYSR-type	942	AAM85260.1	6.09775967
38362	G08	NTL02YP2771	putative enzyme	948	AAM86367.1	5.34311741
38492	G09	NTL02YP1662	D-ribose high-affinity transport system	993	AAM85258.1	9.67086157
38532	G10	NTL02YP1663	putative transcriptional regulator	1005	AAM85259.1	3.54545455
38557	G11	NTL02YP2080	repressor of galETK operon	1017	AAM85676.1	3.16461684
38604	H01	NTL02YP2082	putative solute-binding periplasmic protein of ABC transporter	1032	AAM85678.1	2.55317164
38666	H02	NTL02YP3179	hypothetical protein	1059	AAM86775.1	3.36214741
36227	H03	NTL02YP2762	protein chain initiation factor IF-1	219	AAM86358.1	5.78764479
36272	H04	NTL02YP2754	hypothetical protein	237	AAM86351.1	3.03249097
36305	H05	NTL02YP1672	hypothetical protein	252	AAM85268.1	4.08219178
36389	H06	NTL02YP3857	hypothetical protein	279	AAM87453.1	1.99059561
36493	H07	NTL02YP2093	acetolactate synthase I, valine sensitive, small subunit	318	AAM85689.1	5.61173184
36698	H08	NTL02YP1676	hypothetical protein	393	AAM85272.1	7.14318707
36741	H09	NTL02YP1675	hypothetical protein	405	AAM85271.1	2
36758	H10	NTL02YP3868	hypothetical protein	408	AAM87464.1	1.91517857
38693	H11	NTL02YP2775	putative enzyme	1071	AAM86371.1	3.20342034
38756	H12	NTL02YP1665	putative tartrate dehydrogenase	1098	AAM85261.1	3.35413005

Table 21: *Yersinia pestis* Gateway® Clone, Plate 22 (UYPVV), NR-19618[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38796	A01	NTL02YP2769	putative membrane protein	1116	AAM86365.1	3.292387543
39105	A02	NTL02YP2751	serine tRNA synthetase	1293	AAM86347.1	3.92348087
39113	A03	NTL02YP2079	putative chloride channel	1296	AAM85675.1	3.796407186
39333	A04	NTL02YP2086	putative virulence factor	1434	AAM85682.1	3.622116689
39342	A05	NTL02YP3838	glycogen synthase	1437	AAM87434.1	3.599187542
39380	A06	NTL02YP2096	alkaline phosphatase	1476	AAM85692.1	2.980870712
39411	A07	NTL02YP2085	AMP nucleosidase	1509	AAM85681.1	5.580374435
36833	A08	NTL02YP3843	hypothetical protein	432	AAM87439.1	4.911016949
36840	A09	NTL02YP3848	protein of glp regulon	435	AAM87444.1	6.134736842

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36973	A10	NTL02YP2081	hypothetical protein	474	AAM85677.1	3.982490272
37040	A11	NTL02YP2756	regulator protein	495	AAM86352.1	2
37090	B01	NTL02YP1670	hypothetical protein	510	AAM85266.1	2
37108	B02	NTL02YP3863	transcription elongation factor	516	AAM87459.1	2.84352518
37113	B03	NTL02YP2097	O-6-alkylguanine-DNA/cysteine-protein methyltransferase	519	AAM85693.1	2.792486583
37151	B04	NTL02YP3875	hypothetical protein	534	AAM87471.1	2.759581882
37195	B05	NTL02YP3871	hypothetical protein	546	AAM87467.1	2.805460751
39487	B06	NTL02YP3840	sn-glycerol-3-phosphate dehydrogenase (aerobic)	1599	AAM87436.1	2.954850519
39491	B07	NTL02YP3181	putative sulfatase	1608	AAM86777.1	3.563106796
39500	B08	NTL02YP3866	phosphoenolpyruvate carboxykinase	1620	AAM87462.1	3.386144578
39526	B09	NTL02YP2774	putative prismane	1653	AAM86370.1	4.156526875
39546	B10	NTL02YP1666	putative quarternary ammonium transport protein	1680	AAM85262.1	3.493604651
39549	B11	NTL02YP2092	acetolactate synthase I,valine-sensitive, large subunit	1683	AAM85688.1	3.308763784
39552	B12	NTL02YP1668	putative hemolysin activator protein	1689	AAM85264.1	3.526894158
39557	C01	NTL02YP2772	hypothetical protein	1692	AAM86368.1	6.020207852
39575	C02	NTL02YP2759	ATP-binding component of cytochrome-related transport	1725	AAM86355.1	3.363739377
39603	C03	NTL02YP2758	ATP-binding component of cytochrome-related transport	1785	AAM86354.1	3.901369863
37193	C04	NTL02YP1677	hypothetical protein	546	AAM85273.1	2.795221843
37286	C05	NTL02YP3851	hypothetical protein	576	AAM87447.1	2.826298701
37382	C06	NTL02YP2753	periplasmic protein	609	AAM86349.1	2.807395994
37443	C07	NTL02YP3876	hypothetical protein	627	AAM87472.1	2.818590705
37506	C08	NTL02YP3856	biotin biosynthesis protein	648	AAM87452.1	2.584302326
37606	C09	NTL02YP3869	putative phosphatase	681	AAM87465.1	6.769764216
37629	C10	NTL02YP2078	hypothetical protein	693	AAM85674.1	2.795361528
38020	C12	NTL02YP0577	rhamnulose-phosphate aldolase	825	AAM84173.1	5.719075145
38120	D01	NTL02YP2745	probable formate transporter	858	AAM86341.1	2
38137	D02	NTL02YP0561	4-hydroxybenzoate-octaprenyltransferase	867	AAM84157.1	3.310915105
38143	D03	NTL02YP3819	carbohydrate kinase	867	AAM87415.1	3.663726571
38281	D04	NTL02YP1660	putative solute binding protein of ABC transporter	918	AAM85256.1	5.124217119
38325	D05	NTL02YP2726	hypothetical protein	933	AAM86322.1	6.091469681
38339	D06	NTL02YP1656	hypothetical protein	939	AAM85252.1	6.362614913
38350	D07	NTL02YP3818	biphosphate aldolase	942	AAM87414.1	3.549898167
38358	D08	NTL02YP3816	D-ribose-binding periplasmic protein of ABC transporter	945	AAM87412.1	1.98680203
36037	D09	NTL02YP1639	hypothetical protein	159	AAM85235.1	3.929648241
36260	D10	NTL02YP2730	cold shock protein	234	AAM86326.1	4.795620438
36271	D11	NTL02YP2727	hypothetical protein	237	AAM86323.1	6.678700361
36317	D12	NTL02YP0556	hypothetical protein	258	AAM84152.1	2
36329	E01	NTL02YP1640	hypothetical protein	261	AAM85236.1	5.827242525
38366	E02	NTL02YP0550	putative tellurium resistance protein	951	AAM84146.1	3.641775984
38398	E03	NTL02YP1638	putative enzyme	960	AAM85234.1	5.956
38497	E04	NTL02YP3815	D-ribose high-affinity transport protein	993	AAM87411.1	3.494675702
38506	E05	NTL02YP3822	regulator of gluconate (gnt) operon	996	AAM87418.1	3.477799228
38543	E06	NTL02YP1641	hypothetical protein	1011	AAM85237.1	3.402473834
38611	E08	NTL02YP0566	hypothetical protein	1038	AAM84162.1	3.474025974

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38653	E09	NTL02YP0568	quinone oxidoreductase	1053	AAM84164.1	5.766697164
38709	E10	NTL02YP0570	alanine racemase 1	1080	AAM84166.1	3.391071429
38727	E11	NTL02YP2740	3-phosphoserine aminotransferase	1086	AAM86336.1	3.418294849
36490	E12	NTL02YP0575	hypothetical protein	318	AAM84171.1	4.75698324
36639	F01	NTL02YP0563	diacylglycerol kinase	372	AAM84159.1	5.951456311
36643	F02	NTL02YP2729	hypothetical protein	372	AAM86325.1	2
36655	F03	NTL02YP3832	hypothetical protein	375	AAM87428.1	2
36654	F04	NTL02YP3830	hypothetical protein	375	AAM87426.1	2
36747	F05	NTL02YP3827	hypothetical protein	405	AAM87423.1	2
36900	F06	NTL02YP0549	putative tellurium resistance protein	456	AAM84145.1	2
37064	F07	NTL02YP1650	dps protein	504	AAM85246.1	2
37068	F08	NTL02YP3825	gluconokinase 1	504	AAM87421.1	2
38751	F10	NTL02YP2742	putative outer membrane protein	1095	AAM86338.1	3.34185022
38772	F11	NTL02YP3829	aspartate-semialdehyde dehydrogenase	1104	AAM87425.1	3.448426573
38820	F12	NTL02YP1649	hypothetical protein	1128	AAM85245.1	3.098458904
38946	G01	NTL02YP0571	tyrosine aminotransferase	1194	AAM84167.1	3.174230146
39001	G02	NTL02YP1659	hypothetical protein	1227	AAM85255.1	3.089187056
39123	G03	NTL02YP1645	putative chemotaxis methyl-accepting transducer	1305	AAM85241.1	3.108550186
39158	G04	NTL02YP3824	high-affinity H+/gluconate symporter	1317	AAM87420.1	3.708179808
39180	G05	NTL02YP2739	5-enolpyruvylshikimate-3-phosphate synthetase	1332	AAM86335.1	3.050291545
39296	G06	NTL02YP0557	hypothetical protein	1401	AAM84153.1	2.970853574
37106	G07	NTL02YP2737	hypothetical protein	516	AAM86333.1	2.415467626
37111	G08	NTL02YP0565	putative regulator	519	AAM84161.1	2.821109123
37140	G09	NTL02YP1655	outer membrane protein X	531	AAM85251.1	2.826619965
37174	G10	NTL02YP1657	hypothetical protein	543	AAM85253.1	2.825042882
37319	H01	NTL02YP3828	hypothetical protein	585	AAM87424.1	6.7232
37308	H02	NTL02YP0551	putative tellurium resistance protein	585	AAM84147.1	2.8096
37465	H03	NTL02YP0553	hypothetical protein	639	AAM84149.1	2.804123711
37529	H04	NTL02YP1647	inner membrane permease	657	AAM85243.1	2.806312769
39307	H05	NTL02YP0569	replicative DNA helicase	1407	AAM84165.1	3.612992398
39329	H06	NTL02YP3837	glucose-1-phosphate adenylyltransferase	1431	AAM87433.1	1.39225017
39340	H07	NTL02YP2731	hypothetical protein	1437	AAM86327.1	5.680433311
39392	H08	NTL02YP1661	ATP-binding component of D-ribose high-affinity transport system	1491	AAM85257.1	3.548007838
39485	H09	NTL02YP3811	low-affinity inorganic phosphate transport protein	1596	AAM87407.1	3.371026895
39561	H10	NTL02YP3834	putative 2-component sensor protein	1698	AAM87430.1	2.881472957
39584	H11	NTL02YP2733	ATP-binding transport protein multicopy suppressor of htrB	1749	AAM86329.1	3.26607043
37609	H12	NTL02YP3817	conserved hypothetical protein	684	AAM87413.1	6.435082873

Table 22: *Yersinia pestis* Gateway® Clone, Plate 23 (UYPVW), NR-19619[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37632	A01	NTL02YP2738	cytidylate kinase	693	AAM86334.1	4.77353
37641	A02	NTL02YP3821	hypothetical protein	696	AAM87417.1	3.99049
37716	A03	NTL02YP1658	hypothetical protein	723	AAM85254.1	2.80603

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37715	A04	NTL02YP1646	ATP-binding component of glutamine high-affinity glutamine ABC	723	AAM85242.1	6.37615
37771	A05	NTL02YP3820	transcriptional regulatory protein	738	AAM87416.1	5.99229
37786	A06	NTL02YP1648	glutamine-binding periplasmic protein for high-affinity glutamine ABC	744	AAM85244.1	4.61224
37783	A07	NTL02YP0555	hypothetical protein	784	AAM84151.1	6.66709
37811	A08	NTL02YP2728	CTP:CMP-3-deoxy-D-manno-octulosonate transferase	753	AAM86324.1	6.69609
37875	A09	NTL02YP1651	putative enzyme	777	AAM85247.1	1.99633
38368	A10	NTL02YP1624	hypothetical protein	951	AAM85220.1	6.28254
38596	A12	NTL02YP2700	3-oxoacyl-[acyl-carrier-protein] synthase II	1029	AAM86296.1	3.37418
36016	B01	NTL02YP2711	hypothetical protein	153	AAM86307.1	-
36029	B02	NTL02YP3803	hypothetical protein	156	AAM87399.1	5.89796
36073	B03	NTL02YP2705	hypothetical protein	168	AAM86301.1	4.96154
36120	B04	NTL02YP1628	hypothetical protein	183	AAM85224.1	2
36141	B05	NTL02YP2725	hypothetical protein	189	AAM86321.1	-
36164	B06	NTL02YP3789	hypothetical protein	198	AAM87386.1	4.37395
36245	B07	NTL02YP1617	hypothetical protein	228	AAM85213.1	5.77239
36269	B08	NTL02YP1621	hypothetical protein	237	AAM85217.1	5.787
38708	B09	NTL02YP0543	hypothetical protein	1080	AAM84139.1	3.49732
38915	B10	NTL02YP0530	cystathionine beta-lyase (beta-cystathionase)	1182	AAM84126.1	5.68494
38973	B11	NTL02YP2716	aspartate aminotransferase	1206	AAM86312.1	3.2801
36454	B12	NTL02YP1612	NADH dehydrogenase I chain K	303	AAM85208.1	5.77551
36551	C01	NTL02YP3788	hypothetical protein	336	AAM87384.1	5.77128
36622	C02	NTL02YP3809	hypothetical protein	363	AAM87405.1	5.49628
36884	C03	NTL02YP3808	universal stress protein	447	AAM87404.1	5.79055
37024	C04	NTL02YP0541	hypothetical protein	489	AAM84137.1	4.90926
37052	C05	NTL02YP3796	hypothetical protein	498	AAM87392.1	2
37077	C06	NTL02YP3797	hypothetical protein	507	AAM87393.1	2
37105	C08	NTL02YP1626	hypothetical protein	516	AAM85222.1	5.78777
37157	C09	NTL02YP1619	gluconokinase 1	537	AAM85215.1	5.58579
39038	C10	NTL02YP2713	nicotinate phosphoribosyltransferase	1251	AAM86309.1	3.27653
39063	C11	NTL02YP3799	conserved hypothetical protein	1269	AAM87395.1	3.92131
39142	C12	NTL02YP0539	hypothetical protein	1314	AAM84135.1	3.85746
39167	D01	NTL02YP2723	mukF protein (killing factor KICB)	1323	AAM86319.1	3.16654
39189	D02	NTL02YP3806	putative secreted metalloprotease	1338	AAM87402.1	3.89042
39205	D03	NTL02YP3807	NADP-specific glutamate dehydrogenase	1347	AAM87403.1	3.81471
37173	D04	NTL02YP1610	NADH dehydrogenase I chain I	543	AAM85206.1	2
37185	D05	NTL02YP0538	orfX protein in hemin uptake locus	546	AAM84134.1	2.74573
37192	D06	NTL02YP1611	NADH dehydrogenase I chain J	546	AAM85207.1	7
37202	D07	NTL02YP2718	hypothetical protein	549	AAM86314.1	2.73005
37210	D08	NTL02YP2709	hypothetical protein	552	AAM86305.1	2.80574
37290	D09	NTL02YP2702	hypothetical protein	579	AAM86298.1	6.66882
37439	D10	NTL02YP0547	component in transcription antitermination	667	AAM84068.1	2.81109

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37486	D11	NTL02YP1631	hypothetical protein	645	AAM85227.1	2.76788
37503	D12	NTL02YP2717	hypothetical protein	648	AAM86313.1	2.75872
37507	E01	NTL02YP0537	orfY protein in hemin uptake locus	651	AAM84133.1	7.589
37611	E02	NTL02YP0531	ATP-binding protein of ABC transporter	687	AAM84127.1	2
37729	E03	NTL02YP1618	putative oxidoreductase	726	AAM85214.1	5.15274
39268	E04	NTL02YP3801	glutathione oxidoreductase	1383	AAM87397.1	3.31342
39370	E05	NTL02YP1615	NADH dehydrogenase I chain N	1464	AAM85211.1	2.9262
39443	E06	NTL02YP1614	NADH dehydrogenase I chain M	1533	AAM85210.1	3.74698
39547	E07	NTL02YP2703	paraquat-inducible protein B	1680	AAM86299.1	3.56221
37816	E08	NTL02YP2722	hypothetical protein	756	AAM86318.1	6.75879
37861	E09	NTL02YP3805	hypothetical protein	771	AAM87401.1	9.37731
37921	E11	NTL02YP2724	S-adenosylmethionine-dependent methyltransferase	792	AAM86320.1	6.09615
37945	E12	NTL02YP3792	CDP-diacylglycerol phosphotidylhydrolase	798	AAM87388.1	3.63842
37946	F01	NTL02YP0540	hypothetical protein	801	AAM84136.1	3.08086
38061	F02	NTL02YP0533	periplasmic binding protein	840	AAM84129.1	3.59318
38085	F03	NTL02YP3790	hypothetical protein	846	AAM87385.1	4.27991
38111	F04	NTL02YP0544	hypothetical protein	858	AAM84140.1	3.63252
37651	F05	NTL02YP0493	hypothetical protein	702	AAM84089.1	6.96765
37672	F06	NTL02YP3782	hypothetical protein	705	AAM87378.1	2.63758
37678	F07	NTL02YP0522	putative type III secretion system component	711	AAM84118.1	2.80559
37695	F08	NTL02YP1582	histidine ABC transporter, inner membrane permease	717	AAM85178.1	2
37774	F09	NTL02YP0490	endonuclease V (deoxyinosine 3endoduclease)	741	AAM84086.1	6.85275
37899	F11	NTL02YP0488	hypothetical protein	786	AAM84083.1	6.49516
37926	F12	NTL02YP0524	putative type III secretion system component	795	AAM84120.1	7.44551
37938	G01	NTL02YP1583	ATP-binding component of histidine ABC transport	798	AAM85179.1	2
37936	G02	NTL02YP0486	hypothetical protein	798	AAM84082.1	5.84845
36149	G03	NTL02YP0513	hypothetical protein	195	AAM84109.1	-
36211	G04	NTL02YP1590	hypothetical protein	213	AAM85186.1	4.74308
36221	G05	NTL02YP0511	putative type III secretion system component	219	AAM84107.1	2.95753
36231	G06	NTL02YP0509	putative type III secretion system component	222	AAM84105.1	4.72137
36295	G07	NTL02YP0512	hypothetical protein	249	AAM84108.1	4.87543
36379	G08	NTL02YP0492	DNA-binding protein HU-alpha (HU-2)	276	AAM84088.1	2
36393	G09	NTL02YP0523	putative type III secretion system component	282	AAM84119.1	1.98758
37972	G10	NTL02YP0497	putative transposase	810	AAM84093.1	2
38274	G11	NTL02YP1584	putative sugar nucleotide epimerase	915	AAM85180.1	5.22094
38290	G12	NTL02YP3780	putative endoglucanase	921	AAM87376.1	5.24246
38320	H01	NTL02YP1602	NADH dehydrogenase transcriptional regulator, LysR family	933	AAM85198.1	5.98458

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38357	H02	NTL02YP3787	ketodeoxygluconokinase	945	AAM87383.1	6.03756
38406	H03	NTL02YP0521	putative type III secretion system component	963	AAM84117.1	5.37488
38446	H04	NTL02YP1609	NADH dehydrogenase I chain H	978	AAM85205.1	6.03438
38488	H05	NTL02YP0500	hypothetical protein	993	AAM84096.1	3.55082
38590	H07	NTL02YP3778	putative ATP-binding component of dipeptide ABC transport	1026	AAM87374.1	5.23171
38626	H08	NTL02YP3779	putative ATP-binding component of dipeptide ABC trans	1041	AAM87375.1	3.605
38660	H09	NTL02YP1580	histidine-binding periplasmic protein of high-affinity histidine transport	1056	AAM85176.1	5.78467
36404	H10	NTL02YP2680	hypothetical protein	285	AAM86276.1	2
36478	H11	NTL02YP0502	hypothetical protein	312	AAM84098.1	5.9375
36530	H12	NTL02YP2679	putative sulfite reductase	330	AAM86275.1	2

Table 23: *Yersinia pestis* Gateway® Clone, Plate 24 (UYPVX), NR-19620[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36567	A01	NTL02YP2682	hypothetical protein	342	AAM86278.1	4.95026
36718	A02	NTL02YP0520	hypothetical protein	399	AAM84116.1	5.95216
36729	A03	NTL02YP0519	hypothetical protein	402	AAM84115.1	1.97738
36764	A04	NTL02YP2697	hypothetical protein	411	AAM86293.1	5.97118
36784	A05	NTL02YP2683	hypothetical protein	417	AAM86279.1	5.9628
36861	A06	NTL02YP1591	putative phosphotransferase system IIA component	444	AAM85187.1	5.76446
36879	A07	NTL02YP2687	hypothetical protein	447	AAM86283.1	2
36905	A08	NTL02YP1596	hypothetical protein	456	AAM85192.1	6.57661
38683	A09	NTL02YP0489	uroporphyrinogen decarboxylase	1068	AAM84085.1	2.61552
38746	A10	NTL02YP2691	outer membrane porin A	1092	AAM86287.1	3.447
38838	A11	NTL02YP1592	putative transcriptional regulator	1137	AAM85188.1	3.41886
38943	A12	NTL02YP2681	putative oxidoreductase	1191	AAM86277.1	3.26158
38962	B01	NTL02YP1595	acetate kinase	1203	AAM85191.1	3.19871
38998	B03	NTL02YP0508	putative type III secretion system component	1227	AAM84104.1	3.27624
39098	B04	NTL02YP3785	C4-dicarboxylic acids symporter	1290	AAM86729.1	7.06466
39101	B05	NTL02YP1601	putative aminotransferase	1293	AAM85197.1	3.22356
36939	B06	NTL02YP2685	methylglyoxal synthase	465	AAM86281.1	5.97228
37039	B07	NTL02YP2693	putative dehydrogenase	495	AAM86289.1	2
37046	B08	NTL02YP1597	hypothetical protein	498	AAM85193.1	2
37058	B09	NTL02YP1603	NADH dehydrogenase I chain A	501	AAM85199.1	2
37076	B10	NTL02YP3784	hypothetical protein	507	AAM87380.1	7.04022
37073	B11	NTL02YP2690	suppressor of lon	507	AAM86286.1	1.97989
37199	C01	NTL02YP1587	putative regulator	549	AAM85183.1	7.14771
37229	C02	NTL02YP0516	putative type III secretion system component	561	AAM84112.1	5.71381
37243	C03	NTL02YP1606	NADH dehydrogenase I chain E	564	AAM85202.1	2.83113
37324	C04	NTL02YP1586	hypothetical protein	588	AAM85182.1	2.77866
37323	C05	NTL02YP1579	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	588	AAM85175.1	4

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39273	C06	NTL02YP1607	NADH dehydrogenase I chain F	1386	AAM85203.1	3.78191
39406	C07	NTL02YP3786	hypothetical protein	1500	AAM87382.1	3.64935
39423	C08	NTL02YP1578	amidophosphoribosyltransferase PRPP amidotransferase	1518	AAM85174.1	3.73556
39476	C09	NTL02YP0507	putative secretin	1572	AAM84103.1	3.67928
39507	C10	NTL02YP0495	phosphoribosylaminoimidazolecarboxamide formyltransferase	1635	AAM84091.1	3.58806
39528	C11	NTL02YP0501	putative sodium/proline symporter	1656	AAM84097.1	3.5855
39574	C12	NTL02YP3783	pectate lyase	1719	AAM87379.1	8.12678
39609	D01	NTL02YP1605	NADH dehydrogenase I chain C, D	1797	AAM85201.1	5.15188
39647	D02	NTL02YP1599	putative ion transport protein	1893	AAM85195.1	3.7522
39681	D03	NTL02YP0503	acetyl CoA synthetase	1965	AAM84099.1	3.45686
37331	D04	NTL02YP0491	hypothetical protein	591	AAM84087.1	2.80349
37342	D05	NTL02YP1600	putative alpha helix protein	594	AAM85196.1	5.02839
37345	D06	NTL02YP0515	hypothetical protein	597	AAM84111.1	2.7551
37412	D07	NTL02YP0510	putative type III secretion system component	621	AAM84106.1	2.78971
37453	D08	NTL02YP0505	response regulator/transcription activator	633	AAM84101.1	2
37552	D09	NTL02YP1598	putative phosphatase	663	AAM85194.1	2.78947
37592	D10	NTL02YP1604	NADH dehydrogenase I chain B	678	AAM85200.1	2.77716
37602	D11	NTL02YP2684	hypothetical protein	681	AAM86280.1	6.2982
37615	D12	NTL02YP1581	histidine ABC transport system inner membrane permease	687	AAM85177.1	1.9945
37643	E01	NTL02YP1585	hypothetical protein	699	AAM85181.1	2
37916	E03	NTL02YP3174	putative permease protein	789	AAM86770.1	1.98914
36294	E04	NTL02YP0074	glutaredoxin 3	249	AAM83670.1	6.84429
36316	E05	NTL02YP0040	putative transposase	258	AAM83636.1	2
38276	E06	NTL02YP3149	putative type IV prepilin peptidase	915	AAM86745.1	3.66702
38306	E07	NTL02YP0032	periplasmic protein of mal regulon	930	AAM83628.1	5.5567
38373	E08	NTL02YP3163	hypothetical protein	951	AAM86759.1	6.27548
38392	E09	NTL02YP3152	hypothetical protein	957	AAM86748.1	5.71916
38394	E10	NTL02YP0061	hypothetical protein	960	AAM83657.1	6.222
38518	E11	NTL02YP0481	thiG protein	1002	AAM84077.1	3.3618
38564	E12	NTL02YP0072	glycerol-3-phosphate dehydrogenase (NAD+)	1020	AAM83668.1	3.61792
36847	F02	NTL02YP3155	putative general protein secretion protein	438	AAM86751.1	5.95816
36853	F03	NTL02YP0038	hypothetical protein	441	AAM83634.1	1.99376
36928	F04	NTL02YP3150	hypothetical protein	462	AAM86746.1	1.98008
36981	F05	NTL02YP0073	protein export molecular chaperone	477	AAM83669.1	5.96712
38642	F06	NTL02YP3156	putative general protein secretion protein	1047	AAM86752.1	3.35051
38674	F07	NTL02YP0069	O6-methylguanine-DNA methyltransferase transcription activator/repressor	1065	AAM83665.1	3.56742
38778	F08	NTL02YP0030	maltose ABC transporter ATP-binding protein	1110	AAM83626.1	3.50174
38798	F09	NTL02YP0047	hypothetical protein	1119	AAM83643.1	3.43917
38981	F11	NTL02YP0027	periplasmic maltose-binding protein	1212	AAM83623.1	3.27476
39107	F12	NTL02YP0052	putative transcriptional regulator	1296	AAM83643.1	6.3009
39119	G01	NTL02YP3171	putative tagatose 6-phosphate kinase 2	1299	AAM86767.1	4.04182
36992	G02	NTL02YP3145	hypothetical protein	477	AAM86741.1	4.53191
37019	G03	NTL02YP0065	putative solute-binding periplasmic protein of ABC transporter	489	AAM83661.1	5.96408

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37051	G04	NTL02YP3173	PTS family enzyme IIB component 2 (EIIB-AGA)	498	AAM86209.1	3.99071
37054	G05	NTL02YP0036	conserved hypothetical protein	501	AAM83632.1	2
37085	G06	NTL02YP0485	putative transcriptional regulator	510	AAM84081.1	6.36727
37109	G07	NTL02YP0035	hemolysin co-regulated protein	519	AAM83631.1	5.77818
37306	G08	NTL02YP0070	hypothetical protein	585	AAM83666.1	3.1152
37338	G09	NTL02YP3154	hypothetical protein	591	AAM86750.1	2.82092
37391	G10	NTL02YP0050	hypothetical protein	615	AAM83646.1	2.7771
39324	G11	NTL02YP0055	putative membrane pump protein	1428	AAM83651.1	3.75341
39343	G12	NTL02YP0031	maltose high-affinity receptor	1440	AAM83627.1	3.80203
39417	H01	NTL02YP3157	putative general secretion protein	1512	AAM86753.1	3.73582
39457	H02	NTL02YP0076	putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase	1548	AAM83672.1	3.78526
39466	H03	NTL02YP3169	hypothetical protein	1554	AAM86765.1	3.57842
39563	H05	NTL02YP3144	putative methyl-accepting chemotaxis protein	1701	AAM86740.1	3.00747
39662	H06	NTL02YP3158	putative general secretion protein	1923	AAM86754.1	3.63882
37461	H07	NTL02YP3143	hypothetical protein	636	AAM86739.1	2.54734
37671	H08	NTL02YP3146	hypothetical protein	705	AAM86742.1	2.78255
37686	H09	NTL02YP0054	hypothetical protein	714	AAM83650.1	2.40584
37790	H10	NTL02YP0048	ferredoxin-NADP reductase	747	AAM83644.1	6.64676
37839	H11	NTL02YP0051	triosephosphate isomerase	768	AAM83647.1	5.87252
37879	H12	NTL02YP3170	putative DEOR-type transcriptional regulator of aga operon	777	AAM86766.1	3.08568

Table 24: *Yersinia pestis* Gateway® Clone, Plate 25 (UYPVY), NR-19621[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37978	A02	NTL02YP3091	30S ribosomal subunit protein S2	810	AAM86687.1	2
38084	A03	NTL02YP3101	hypothetical protein	846	AAM86697.1	3.638826
38093	A04	NTL02YP3083	CDP-diglyceride synthetase	849	AAM86679.1	3.320585
38122	A05	NTL02YP3089	protein chain elongation factor EF-Ts	858	AAM86686.1	3.591314
38152	A06	NTL02YP3094	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	870	AAM8690.1	2.668132
38163	A07	NTL02YP3126	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase	873	AAM86722.1	2.786418
38283	A08	NTL02YP3108	positive regulator of gcv operon	918	AAM86704.1	6.289144
38298	A09	NTL02YP0008	ribokinase	927	AAM83604.1	5.462254
38305	A10	NTL02YP0013	homoserine transsuccinylase	930	AAM83609.1	5.224742
35942	A11	NTL02YP3771	hypothetical protein	114	AAM87367.1	1.974026
35974	A12	NTL02YP0018	hypothetical protein	138	AAM83614.1	3.949438
35986	B01	NTL02YP0014	hypothetical protein	150	AAM83610.1	3.947368
36125	B02	NTL02YP3109	hypothetical protein	183	AAM86705.1	3.955157
36169	B03	NTL02YP3086	hypothetical protein	201	AAM86682.1	4.585062
36174	B04	NTL02YP0009	hypothetical protein	204	AAM83605.1	5.807377
36364	B05	NTL02YP3763	hypothetical protein	270	AAM87359.1	5.9
36464	B06	NTL02YP2676	putative transposase	306	AAM86273.1	6.254335
36659	B07	NTL02YP3098	hypothetical protein	378	AAM86694.1	5.638756
38363	B08	NTL02YP3775	dipeptide transport system inner membrane permease	948	AAM87371.1	6.100202

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38466	B09	NTL02YP3139	positive regulator for lys	987	AAM86735.1	6.115871
38468	B10	NTL02YP3762	hypothetical protein	987	AAM87358.1	5.762415
38486	B11	NTL02YP0003	asparagine synthetase A	933	AAM83599.1	3.50242
38578	C01	NTL02YP3079	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	1023	AAM86675.1	3.575729
38625	C03	NTL02YP3131	hypothetical protein	1041	AAM86727.1	2.888992
38711	C04	NTL02YP3090	hypothetical protein	1080	AAM86685.1	1.801786
38747	C05	NTL02YP3137	repressor of galETK operon	1092	AAM86733.1	3.469081
38775	C06	NTL02YP3106	hypothetical protein	1107	AAM86702.1	3.450741
38886	C07	NTL02YP3140	MFS transporter	1161	AAM86736.1	3.412989
36750	C08	NTL02YP0024	hypothetical protein	408	AAM83620.1	5.962054
36749	C09	NTL02YP0012	hypothetical protein	408	AAM83608.1	5.979911
36787	C10	NTL02YP0007	D-ribose high-affinity transport system membrane-associated protein	420	AAM83603.1	2
36795	C11	NTL02YP3107	hypothetical protein	420	AAM86703.1	6.578261
36852	C12	NTL02YP0001	initiation of chromosome replication	441	AAM83597.1	2
36865	D01	NTL02YP3111	hypothetical protein	444	AAM86707.1	5.644628
36891	D02	NTL02YP3096	hypothetical protein	450	AAM86692.1	5.967347
36922	D03	NTL02YP0002	regulator for asnA, asnC and gidA	462	AAM83598.1	2
36964	D04	NTL02YP3122	hypothetical protein	471	AAM86718.1	2
38905	D05	NTL02YP3113	membrane-bound lytic murein transglycosylase A	1173	AAM86709.1	3.392415
38953	D06	NTL02YP3085	putative ATP-binding component of a transport system	1197	AAM86681.1	5.41633
38980	D07	NTL02YP3766	putative transposase	1209	AAM87362.1	3.329063
38993	D08	NTL02YP3134	putative resistance protein	1221	AAM86730.1	3.324346
39056	D09	NTL02YP3138	diaminopimelate decarboxylase	1263	AAM86734.1	4.025326
39062	D10	NTL02YP3115	putative amidase	1269	AAM86711.1	3.274255
39132	D11	NTL02YP0016	isocitrate lyase	1308	AAM83612.1	3.942878
39172	D12	NTL02YP3116	N-acetylglutamate synthase	1326	AAM86712.1	3.84041
39217	E01	NTL02YP3082	hypothetical protein	1356	AAM86678.1	1.281519
39225	E02	NTL02YP3770	regulator of uhpT	1362	AAM87366.1	6.651213
39229	E03	NTL02YP3102	hypothetical protein	1365	AAM86698.1	6.730249
37134	E05	NTL02YP3128	putative invasion protein	528	AAM86724.1	2.834507
37211	E06	NTL02YP3100	syd protein	552	AAM86696.1	6.194257
37227	E07	NTL02YP3087	ribosome releasing factor	558	AAM86683.1	1.994983
37228	E08	NTL02YP3765	molybdopterin-guanine dinucleotide biosynthesis protein B	558	AAM87361.1	2.82107
37266	E09	NTL02YP3124	hypothetical protein	570	AAM86720.1	6.790164
37337	E10	NTL02YP3080	automembrane protein H	591	AAM86676.1	3.087163
37383	E11	NTL02YP3123	hypothetical protein	609	AAM86719.1	2
37436	E12	NTL02YP3761	protein disulfide isomerase I	624	AAM87357.1	2.805723
37482	F01	NTL02YP3764	molybdopterin-guanine dinucleotide synthase	642	AAM87360.1	2
39271	F02	NTL02YP0022	aspartokinase III, lysine sensitive	1386	AAM83618.1	3.791024
39284	F03	NTL02YP3772	hypothetical protein	1392	AAM87368.1	3.898743
39319	F04	NTL02YP0010	putative permease	1425	AAM83606.1	3.734471
39462	F05	NTL02YP0005	putative 2-component regulator	1554	AAM83601.1	3.428482
39504	F06	NTL02YP0015	malate synthase A	1632	AAM83611.1	3.025718
39519	F07	NTL02YP0023	glucosephosphate isomerase	1647	AAM83619.1	3.413159
39576	F08	NTL02YP0017	isocitrate dehydrogenase kinase/phosphatase	1728	AAM83613.1	3.375566

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39605	F09	NTL02YP3773	hemolysin activator protein precursor	1788	AAM87369.1	4.492888
39679	F10	NTL02YP3117	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit	1959	AAM86713.1	10.63982
37620	F11	NTL02YP3129	methyl-directed mismatch repair protein	687	AAM86725.1	6.151307
37622	F12	NTL02YP0011	hypothetical protein	690	AAM83607.1	2
37731	G01	NTL02YP3088	uridylate kinase	726	AAM86684.1	2.792428
37770	G02	NTL02YP3769	sensor protein	738	AAM87365.1	2.775064
37825	G03	NTL02YP3084	hypothetical protein	759	AAM86680.1	5.305382
37869	G04	NTL02YP3097	hypothetical protein	774	AAM86693.1	3.627764
37913	G08	NTL02YP2666	putative 3-oxoacyl-acyl carrier protein reductase	792	AAM86266.1	5.412545
37920	G09	NTL02YP2670	putative 3-ketoacyl-acyl carrier protein reductase	832	AAM85802.1	5.677885
37967	G10	NTL02YP1560	putative structural protein	807	AAM85156.1	3.316411
38092	G11	NTL02YP2664	putative acyl transferase	849	AAM86260.1	3.073116
38149	G12	NTL02YP1559	murein DD-endopeptidase	870	AAM85155.1	3.564835
36510	H01	NTL02YP3728	PTS system fructose-like IIB component 1	321	AAM87324.1	4.290859
38542	H02	NTL02YP1571	putative enzyme	1011	AAM85167.1	3.414843
38665	H03	NTL02YP2643	hypothetical protein	1059	AAM86239.1	6.993631
38714	H04	NTL02YP3754	histidine protein kinase sensor for GlnG regulator	1080	AAM87350.1	3.161607
36632	H05	NTL02YP0476	50S ribosomal subunit protein L7/L12	369	AAM84072.1	2
36819	H06	NTL02YP0473	50S ribosomal subunit protein L11	429	AAM84069.1	5.974414
36962	H07	NTL02YP2642	hypothetical protein	471	AAM86238.1	5.972603
38735	H08	NTL02YP1558	chorismate synthase	1089	AAM85154.1	3.441984
38877	H09	NTL02YP3734	hypothetical protein	1155	AAM87330.1	2.521339
38927	H10	NTL02YP0470	protein chain elongation factor EF-Tu	1185	AAM84066.1	3.318367
38939	H11	NTL02YP1570	erythronate-4-phosphate dehyrogenase	1188	AAM85166.1	3.164495
38954	H12	NTL02YP3732	hypothetical protein	1197	AAM87328.1	3.280517

Table 25: *Yersinia pestis* Gateway® Clone, Plate 26 (UYPVZ), NR-19622[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39012	A01	NTL02YP2646	hypothetical protein	1233	AAM86242.1	3.26394
39157	A02	NTL02YP3745	hypothetical protein	1317	AAM87341.1	3.8703
37042	A03	NTL02YP0475	50S ribosomal subunit protein L10	498	AAM84071.1	5.80112
37089	A04	NTL02YP1577	membrane protein	510	AAM85173.1	6.11091
37139	A05	NTL02YP1566	fimbrial A protein precursor	531	AAM85162.1	2.7268
37162	A06	NTL02YP3731	hypothetical protein	537	AAM87327.1	2.79029
37302	A07	NTL02YP2639	hypothetical protein	582	AAM86235.1	3.10289
39263	A08	NTL02YP1575	dihydrofolate:folylpolyglutamate synthetase	1383	AAM85171.1	6.73928
39276	A09	NTL02YP3735	hypothetical protein	1389	AAM87331.1	3.6767
39336	A10	NTL02YP3753	glutamine synthetase	1434	AAM87349.1	3.60176
37339	B01	NTL02YP3751	putative phosphatase	591	AAM87347.1	2.79556
37388	B02	NTL02YP1556	hypothetical protein	612	AAM85152.1	2.7362
37624	B03	NTL02YP1573	hypothetical protein	690	AAM85169.1	7.55342
37795	B04	NTL02YP2674	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	747	AAM86270.1	2.38501
37858	B05	NTL02YP2668	putative enoyl-coa hydratase protein	771	AAM86264.1	5.59309

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37951	B07	NTL02YP2631	molybdopterin biosynthesis protein	801	AAM86227.1	7.28181
37966	B08	NTL02YP1533	hypothetical protein	807	AAM85129.1	3.61983
38075	B09	NTL02YP2625	putative esterase	843	AAM86221.1	3.08267
38088	B10	NTL02YP1532	hypothetical protein	849	AAM85127.1	3.61192
38151	B11	NTL02YP2623	putative transcriptional regulator LYSR-type	870	AAM86219.1	2.83516
38174	B12	NTL02YP3722	hypothetical protein	876	AAM87318.1	6.57533
38365	C01	NTL02YP0466	pantothenate kinase	951	AAM84062.1	6.24117
38396	C02	NTL02YP0465	biotin-[acetyl CoA carboxylase] holoenzyme synthetase	960	AAM84061.1	5.27
36262	C03	NTL02YP3710	hypothetical protein	234	AAM87306.1	3.9708
36328	C04	NTL02YP1530	hypothetical protein	261	AAM85126.1	2
36426	C05	NTL02YP3723	hypothetical protein	291	AAM87319.1	5.49245
36453	C06	NTL02YP1551	hypothetical protein	303	AAM85147.1	1.97668
38515	C07	NTL02YP3709	putative multidrug resistance protein	999	AAM87305.1	3.77478
38574	C08	NTL02YP0452	5-aminolevulinate dehydratase	1023	AAM84048.1	3.18438
38610	C10	NTL02YP0464	UDP-N-acetylenolpyruvoylglucosamine reductase	1038	AAM84059.1	3.33766
38729	C11	NTL02YP3726	PTS system fructose-like enzyme 2IIC component	1086	AAM87322.1	3.42185
38728	C12	NTL02YP3706	putative pectinesterase	1086	AAM87302.1	3.19893
38768	D01	NTL02YP2619	periplasmic D-galactose-binding ABC transport protein	1104	AAM86215.1	3.45979
38815	D02	NTL02YP3721	putative LACI-type transcriptional regulator	1125	AAM87317.1	6.12532
38864	D03	NTL02YP2622	putative transport protein	1152	AAM86218.1	3.34983
36542	D04	NTL02YP0451	hypothetical protein	336	AAM84047.1	4.9734
36564	D05	NTL02YP1536	hypothetical protein	342	AAM85132.1	1.99476
36581	D06	NTL02YP3707	hypothetical protein	348	AAM87303.1	3.99742
36625	D07	NTL02YP1535	hypothetical protein	366	AAM85131.1	2
36727	D08	NTL02YP3727	hypothetical protein	399	AAM87323.1	5.67426
36984	D09	NTL02YP0460	hypothetical protein	477	AAM84056.1	2
37000	D10	NTL02YP1534	hypothetical protein	480	AAM85130.1	2
37023	D11	NTL02YP0453	transcriptional activator	489	AAM83991.1	2
37035	D12	NTL02YP3724	putative glycoprotein/receptor	492	AAM87320.1	5.96617
37038	E01	NTL02YP1544	possible subunit of a heme lyase	495	AAM85140.1	2
38906	E02	NTL02YP3705	hemin storage system protein	1173	AAM87301.1	3.06183
38910	E03	NTL02YP2620	hypothetical protein	1176	AAM86216.1	3.24507
38959	E04	NTL02YP3712	lipopolysaccharide biosynthesis protein	1200	AAM87308.1	3.28548
39000	E06	NTL02YP1548	putative cytochrome c-type biogenesis protein	1227	AAM85144.1	3.10024
39017	E07	NTL02YP3711	hypothetical protein	1233	AAM87307.1	3.22702
39055	E08	NTL02YP2627	hypothetical protein	1263	AAM86223.1	4.01151
39066	E09	NTL02YP1550	long-chain fatty acid transport protein	1272	AAM85146.1	3.24162
39071	E10	NTL02YP2630	molybdopterin biosynthesis protein	1275	AAM86226.1	4.03726
39138	E11	NTL02YP1552	putative acyltransferase	1311	AAM85148.1	3.99556
39140	E12	NTL02YP2629	putative arylsulfatase activating enzyme	1311	AAM86225.1	3.77646
37071	F01	NTL02YP1539	hypothetical protein	507	AAM85135.1	2
37099	F03	NTL02YP1547	putative cytochrome c-type biogenesis protein	513	AAM85143.1	2
37146	F04	NTL02YP0462	protoporphyrin oxidase	534	AAM84058.1	2.82404
37163	F05	NTL02YP0448	hypothetical protein	540	AAM84044.1	2.81552

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37206	F06	NTL02YP1538	hypothetical protein	552	AAM85134.1	5.46284
37258	F07	NTL02YP0440	hypothetical protein	570	AAM84036.1	2.83934
37307	F08	NTL02YP0467	putative acetyltransferase	585	AAM84063.1	2
37433	F09	NTL02YP2635	hypothetical protein	624	AAM86231.1	2.78464
37519	F10	NTL02YP2633	hypothetical protein	654	AAM86229.1	2.81124
39184	F11	NTL02YP0458	proline dipeptidase	1335	AAM84054.1	3.93891
39234	F12	NTL02YP2636	hypothetical protein	1368	AAM86232.1	3.89063
39355	G01	NTL02YP0461	potassium uptake protein	1452	AAM84057.1	3.68097
39408	G02	NTL02YP0441	putative alpha helix chain	1506	AAM84037.1	3.55951
39426	G03	NTL02YP0454	putative oxidoreductase	1521	AAM84050.1	3.5663
39428	G04	NTL02YP2618	ATP-binding component of methyl-galactoside ABC transporter and	1521	AAM86214.1	3.5868
39506	G05	NTL02YP3713	putative kinase	1632	AAM87309.1	3.39773
39527	G06	NTL02YP3718	putative ATP-binding component of a transport system	1653	AAM87314.1	3.15535
39589	G07	NTL02YP2634	putative ATP-binding component of ABC transport system	1764	AAM86230.1	3.00554
39620	G08	NTL02YP0439	carbon starvation protein	1818	AAM84035.1	3.69699
37528	G09	NTL02YP1540	ATP binding protein of heme exporter A	657	AAM85136.1	2.79197
37546	G10	NTL02YP0446	hypothetical protein	663	AAM84042.1	2.79232
37570	G11	NTL02YP2628	putative ATP-binding ABC transporter protein	669	AAM86224.1	2.79126
37614	G12	NTL02YP1541	heme exporter protein B	687	AAM85137.1	2.36726
37650	H01	NTL02YP0443	hypothetical protein	702	AAM84039.1	1.81132
37696	H02	NTL02YP2621	GTP cyclohydrolase I	717	AAM86217.1	2.79128
37762	H03	NTL02YP1542	heme exporter protein C	738	AAM85138.1	6.42031
37782	H04	NTL02YP0455	ferrisiderophore reductase	744	AAM84051.1	2.42985
37814	H05	NTL02YP0442	COQ5 methyltransferase	756	AAM84038.1	6.5402
37874	H06	NTL02YP1549	lipoprotein precursor	777	AAM85145.1	6.61812
38157	H07	NTL02YP0436	putative carboxymethylenebutenolidase	873	AAM84032.1	3.65608
38224	H08	NTL02YP2589	glucose-1-phosphate uridylyltransferase	891	AAM86185.1	4.23738
38431	H09	NTL02YP3684	putative transposase	972	AAM87280.1	3.63142
38449	H10	NTL02YP3688	3-phosphoserine phosphatase	981	AAM87284.1	4.99412
36394	H11	NTL02YP1515	hypothetical protein	282	AAM85111.1	5.59938
36431	H12	NTL02YP3700	hypothetical protein	294	AAM87296.1	4.82335

Table 26: *Yersinia pestis* Gateway® Clone, Plate 27 (UYPWA), NR-19623[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36850	A01	NTL02YP3701	DNA polymerase III, psi subunit	438	AAM87297.1	5
36924	A02	NTL02YP0420	hypothetical protein	462	AAM84016.1	5.591633
38587	A04	NTL02YP2617	inner membrane permease of galactoside ABC transporter	1026	AAM86213.1	3.572233
38603	A05	NTL02YP1508	hypothetical protein	1032	AAM85104.1	3.558769
38624	A06	NTL02YP2593	putative inner membrane permease of ABC transporter	1041	AAM86189.1	3.53469
38635	A07	NTL02YP3702	putative enzyme	1044	AAM87298.1	3.458487
38669	A08	NTL02YP1511	hypothetical protein	1062	AAM85106.1	2.553539
38691	A09	NTL02YP1509	hypothetical protein	1071	AAM85105.1	3.420342
38745	A10	NTL02YP2608	putative ABC transporter binding protein	1092	AAM86204.1	3.469965

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38773	A11	NTL02YP0421	hypothetical protein	1107	AAM84017.1	3.4551
38790	A12	NTL02YP2604	putative ATPase	1113	AAM86200.1	3.450997
37029	B01	NTL02YP0426	hypothetical protein	492	AAM84022.1	3.983083
37075	B02	NTL02YP3683	putative outer membrane protein	507	AAM87279.1	1.985375
37110	B04	NTL02YP0422	hypothetical protein	519	AAM84018.1	2.813953
37191	B05	NTL02YP1519	hypothetical protein	546	AAM85115.1	2.8157
37260	B06	NTL02YP1521	hypothetical protein	570	AAM85117.1	2
37301	B07	NTL02YP2596	putative siderophore biosynthetic protein	582	AAM86192.1	2.811897
37354	B08	NTL02YP1522	hypothetical protein	600	AAM85118.1	2.814063
37366	B09	NTL02YP1503	hypothetical protein	603	AAM85099.1	2.793157
38920	B11	NTL02YP2610	putative transport protein	1182	AAM86206.1	3.310147
39043	C01	NTL02YP2609	hypothetical protein	1257	AAM86205.1	4.046261
39068	C02	NTL02YP3695	hypothetical protein	1272	AAM87291.1	3.395579
39076	C03	NTL02YP3682	hypothetical protein	1278	AAM87278.1	3.820182
39116	C04	NTL02YP2597	putative siderophore biosynthetic protein	1299	AAM86193.1	3.342793
39135	C05	NTL02YP3693	putative transport system permease protein	1308	AAM87289.1	3.96365
39159	C06	NTL02YP0427	periplasmic binding protein	1320	AAM84023.1	3.458824
37381	C07	NTL02YP2602	2-deoxycytidine 5-triphosphate deaminase	609	AAM86198.1	2.802773
37396	C08	NTL02YP3697	hyperosmotically inducible periplasmic protein	615	AAM87293.1	2.789313
37435	C09	NTL02YP3681	hypothetical protein	624	AAM87277.1	2.793675
37556	C10	NTL02YP2607	hypothetical protein	663	AAM86203.1	2.853485
37545	C11	NTL02YP0423	hypothetical protein	663	AAM84019.1	2.802276
37601	C12	NTL02YP2603	uridine/cytidine kinase	681	AAM86199.1	2.790569
37639	D01	NTL02YP2612	putative membrane protein	696	AAM86208.1	7.153533
37662	D02	NTL02YP3689	hypothetical protein	702	AAM87285.1	4.101078
37732	D03	NTL02YP3690	purine-nucleoside phosphorylase	726	AAM87286.1	2.250653
37741	D04	NTL02YP0419	ATP-binding component of leucine transport	732	AAM84015.1	7.160622
39431	D05	NTL02YP1520	conserved hypothetical protein	1524	AAM85116.1	3.658568
39482	D07	NTL02YP3698	peptide chain release factor RF-3	1590	AAM87294.1	3.704908
39560	D08	NTL02YP2615	NAD-linked malate dehydrogenase (malic enzyme)	1698	AAM86211.1	3.310702
39643	D09	NTL02YP1512	hypothetical protein	1881	AAM85108.1	3.695992
39646	D10	NTL02YP2595	putative siderophore biosynthetic protein	1890	AAM86191.1	3.633161
37805	D11	NTL02YP1506	hypothetical protein	753	AAM85102.1	6.167718
37841	D12	NTL02YP0418	ATP-binding component of high-affinity branched-chain amino acid	768	AAM84014.1	2
37880	E01	NTL02YP1516	probable pilin chaperone	780	AAM85112.1	3.632927
37963	E03	NTL02YP0437	uridine phosphorylase	807	AAM84033.1	4.035419
37988	E04	NTL02YP3694	hypothetical protein	813	AAM87290.1	6.811254
37987	E05	NTL02YP3692	2-deoxyribose-5-phosphate aldolase	813	AAM87288.1	6.574443
38081	E06	NTL02YP0429	inner membrane permease	846	AAM84025.1	2
38087	E07	NTL02YP1496	hypothetical protein	849	AAM85092.1	3.24072
38110	E08	NTL02YP0412	RNA polymerase, sigma(32) factor	858	AAM84008.1	6.14588
38114	E09	NTL02YP1056	putative CDP-paratose synthetase	858	AAM84652.1	2
38177	E10	NTL02YP0389	outer membrane phospholipase A	879	AAM83985.1	6.394995
35965	E11	NTL02YP1483	hypothetical protein	129	AAM85080.1	2
36013	E12	NTL02YP1484	hypothetical protein	153	AAM85081.1	2.917098
36401	F01	NTL02YP1071	hypothetical protein	285	AAM84667.1	4.852308
36498	F02	NTL02YP0405	hypothetical protein	321	AAM84001.1	5.34903

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36704	F03	NTL02YP0402	hypothetical protein	396	AAM83998.1	2
36735	F04	NTL02YP1488	hypothetical protein	402	AAM85084.1	5.753394
36788	F05	NTL02YP0406	hypothetical protein	420	AAM84002.1	4.293478
36789	F06	NTL02YP1076	putative transcriptional regulator	420	AAM84512.1	5.521739
36845	F07	NTL02YP0414	hypothetical protein	438	AAM84010.1	6.307531
38438	F08	NTL02YP1480	glucokinase	975	AAM85076.1	5.854187
38509	F09	NTL02YP0386	magnesium and cobalt permease	999	AAM83982.1	4.662175
38648	F10	NTL02YP1499	ATP-binding protein of iron ABC transporter	1050	AAM85095.1	3.182569
38686	F11	NTL02YP2581	imidazoleglycerolphosphate dehydratase histidinol-phosphate phosphatase	1068	AAM86177.1	2.778881
36855	F12	NTL02YP1486	hypothetical protein	441	AAM85082.1	2
36886	G01	NTL02YP1077	hypothetical protein	450	AAM84673.1	1.987755
36955	G02	NTL02YP0388	hypothetical protein	471	AAM83984.1	1.927593
37025	G03	NTL02YP1072	hypothetical protein	489	AAM84668.1	1.994329
37125	G05	NTL02YP1498	hypothetical protein	525	AAM85094.1	2
37130	G06	NTL02YP0400	hypothetical protein	528	AAM83996.1	2.797535
37133	G07	NTL02YP1479	hypothetical protein	528	AAM85075.1	2
37353	G08	NTL02YP1485	putative cytochrome	600	AAM85079.1	2
38847	G09	NTL02YP1061	putative mannosyltransferase protein	1143	AAM84500.1	3.393068
38862	G11	NTL02YP1067	putative O-antigen chain length determinant	1152	AAM84663.1	3.390101
38982	G12	NTL02YP0395	hypothetical protein	1212	AAM83991.1	3.126997
38985	H01	NTL02YP1070	putative drug efflux protein	1215	AAM84666.1	1.633466
38987	H02	NTL02YP0384	hypothetical protein	1218	AAM83980.1	3.251987
39034	H03	NTL02YP1481	hypothetical protein	1248	AAM85077.1	3.195652
39082	H04	NTL02YP1057	putative O-antigen synthesis protein, WbyH	1284	AAM84653.1	3.889728
39087	H05	NTL02YP0417	inner membrane permease of high-affinity branched-chain amino	1287	AAM84013.1	6.182366
39100	H06	NTL02YP0398	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	1293	AAM83994.1	3.770443
39122	H07	NTL02YP1068	inosine-guanosine kinase	1305	AAM84664.1	3.976208
37394	H08	NTL02YP2586	phosphoribosyl-amp cyclohydrolase	615	AAM86182.1	2.79542
37404	H09	NTL02YP2582	hypothetical protein	618	AAM86178.1	2.574468
37411	H10	NTL02YP0392	putative homoserine/homoserine lactone efflux protein	621	AAM83988.1	2.783661
37410	H11	NTL02YP0391	threonine efflux protein	621	AAM83987.1	2.789713
37438	H12	NTL02YP0404	putative enzyme	627	AAM84000.1	2.794603

Table 27: *Yersinia pestis* Gateway® Clone, Plate 28 (UYPWB), NR-19624[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37527	A01	NTL02YP1489	putative lipoprotein	657	AAM85085.1	2.819225251
37567	A02	NTL02YP0410	ATP-binding component of a membrane-associated complex involved	669	AAM84006.1	2.78561354
37585	A03	NTL02YP1491	putative oxidoreductase component	675	AAM85087.1	7.427972028
37610	A04	NTL02YP0383	transcriptional regulator	687	AAM83979.1	6.722145805
37665	A05	NTL02YP0379	hypothetical protein	705	AAM83975.1	4.484563758

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39144	A06	NTL02YP1055	putative CDP-4-keto-6-deoxy-d-glucose-3-dehydrase	1314	AAM84651.1	3.993353028
39179	A07	NTL02YP2579	L-histidinal:NAD+ oxidoreductase	1332	AAM86175.1	3.970116618
39214	A08	NTL02YP1058	putative O-unit flippase-like protein	1356	AAM84654.1	3.655444126
39238	A09	NTL02YP0399	sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit	1371	AAM83995.1	4.812898653
39244	A10	NTL02YP1066	phosphomannomutase	1374	AAM84662.1	3.854314003
39311	A11	NTL02YP1064	mannose-1-phosphate guanyltransferase	1413	AAM84660.1	3.664143152
39367	A12	NTL02YP2587	gluconate-6-phosphate dehydrogenase	1461	AAM86183.1	3.692205197
39488	B01	NTL02YP1500	inner membrane permease of iron ABC transporter	1602	AAM85096.1	3.019488429
39532	B02	NTL02YP0409	cell division membrane protein	1662	AAM84005.1	3.299059929
39556	B03	NTL02YP1069	putative potassium efflux protein	1692	AAM84665.1	3.512124711
39628	B04	NTL02YP0390	ATP-dependent DNA helicase	1833	AAM83986.1	3.792845702
37687	B05	NTL02YP1060	putative glycosyltransferase	714	AAM84656.1	2.789124668
37693	B06	NTL02YP0381	putative phosphatase	717	AAM83977.1	2.788639366
37757	B07	NTL02YP1487	putative periplasmic protein	735	AAM85083.1	2.766451613
37785	B08	NTL02YP1065	putative glycosyltransferase	744	AAM84661.1	2
37877	B09	NTL02YP2585	imidazole glycerol phosphate synthase subunit imidazole glycerol	777	AAM86181.1	6.94369645
38019	B10	NTL02YP0378	diaminopimelate epimerase	825	AAM83974.1	2.640462428
38068	B11	NTL02YP0385	hypothetical protein	843	AAM83981.1	2
39839	B12	NTL02YP0824	methyl-directed mismatch repair protein	2556	AAM84420.1	13.06163328
39848	C01	NTL02YP3621	putative ATP-dependent protease	2604	AAM87217.1	7.574508321
39701	C02	NTL02YP2981	excision nuclease subunit B	2016	AAM86577.1	3.576361868
39702	C03	NTL02YP2320	hypothetical protein	2022	AAM85916.1	3.287099903
39707	C04	NTL02YP1455	putative ATP-binding component of a transport system	2037	AAM85051.1	3.189696678
39712	C05	NTL02YP2487	protease II	2052	AAM86083.1	3.643403442
39724	C06	NTL02YP0789	inner membrane permease of ABC transporter	2070	AAM84385.1	3.581516588
39855	C07	NTL02YP0871	alanyl-tRNA synthetase	2628	AAM84467.1	3.316341829
39862	C08	NTL02YP2031	aconitate hydrase 1	2673	AAM85627.1	3.871360118
39866	C09	NTL02YP0303	phosphoenolpyruvate carboxylase	2697	AAM83899.1	3.421629521
39870	C10	NTL02YP3569	preprotein translocase secretion protein	2715	AAM87165.1	3.57676951
39727	C12	NTL02YP0350	rep helicase, a single-stranded DNA dependent ATPase	2076	AAM83946.1	4.767958412
39728	D01	NTL02YP2478	flagellar biosynthesis protein	2079	AAM86074.1	3.589900897
39739	D02	NTL02YP0282	putative secretion ATPase	2115	AAM83878.1	3.432482599
39746	D03	NTL02YP2060	putative inner membrane permease	2139	AAM85656.1	11.06929784
39879	D04	NTL02YP3021	2-oxoglutarate dehydrogenase (decarboxylase component)	2808	AAM86617.1	3.044592697
39881	D05	NTL02YP0188	putative toxin subunit	2832	AAM83784.1	3.739206128
39894	D06	NTL02YP3543	putative ATP-binding transport component	2985	AAM87139.1	12.89322314
39772	D07	NTL02YP3617	hypothetical protein	2220	AAM87213.1	4.766814159
39778	D08	NTL02YP1375	putative inner membrane permease of high-affinity phosphate-specific	2250	AAM84971.1	5.083842795
39782	D09	NTL02YP1424	putative multimodular enzyme	2280	AAM85020.1	4.01637931
39792	D10	NTL02YP0786	peptidoglycan synthetase penicillin-binding protein 1B	2319	AAM84382.1	3.986011022
39793	D11	NTL02YP0181	putative toxin subunit	2325	AAM83777.1	3.706131078

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39798	E01	NTL02YP0124	aerobic respiration sensor-response protein histidine protein kinase/phosphatase	2337	AAM83720.1	3.433740008
39811	E02	NTL02YP1900	phosphoenolpyruvate synthase	2385	AAM85496.1	3.144329897
39818	E03	NTL02YP1325	hypothetical protein	2421	AAM84921.1	3.909386428
39821	E04	NTL02YP0298	aspartokinase II and homoserine dehydrogenase II	2436	AAM83894.1	3.980210016
39810	E05	NTL02YP1110	putative beta-glucosidase	2382	AAM84706.1	5.345582164
39814	E06	NTL02YP2095	hypothetical protein	2397	AAM85691.1	3.666393106
39822	E07	NTL02YP1083	putative oxidoreductase	2442	AAM84679.1	3.860999194
39832	E09	NTL02YP3839	glycogen phosphorylase	2520	AAM87435.1	3.88046875
39834	E10	NTL02YP0629	ribonuclease R	2535	AAM84225.1	2.778252427
39835	E11	NTL02YP1123	putative penicillin-binding protein	2538	AAM84719.1	3.723041117
39708	F02	NTL02YP3804	oligopeptidase A	2043	AAM87400.1	3.623619779
39716	F03	NTL02YP3191	possible beta-d-galactosidase	2061	AAM86787.1	3.654926226
39725	F04	NTL02YP4036	glycine tRNA synthetase, beta subunit	2070	AAM87632.1	3.740758294
39849	F05	NTL02YP0562	glycerol-3-phosphate acyltransferase	2607	AAM84158.1	3.680015111
39861	F06	NTL02YP0758	pyruvate dehydrogenase (decarboxylase component)	2664	AAM84354.1	2.321745562
39729	F07	NTL02YP0103	DNA helicase	2082	AAM83699.1	3.705937795
39731	F08	NTL02YP3218	putative phage DNA primase	2094	AAM86814.1	4.793345829
39741	F09	NTL02YP1838	carboxy-terminal protease for penicillin-binding protein 3	2121	AAM85434.1	3.227672374
39748	F10	NTL02YP0593	selenopolypeptide subunit of formate dehydrogenase H	2148	AAM84189.1	11.63711152
39868	F11	NTL02YP1792	$Mg2^+$ transport ATPase	2700	AAM85388.1	3.730656934
39869	F12	NTL02YP3849	positive regulator of mal regulon	2712	AAM87445.1	12.10792151
39882	G01	NTL02YP0572	excision nuclease subunit A	2884	AAM84168.1	3.44001387
39885	G02	NTL02YP1806	hypothetical protein	2877	AAM85402.1	2.412752828
39886	G03	NTL02YP3246	glycine decarboxylase	2880	AAM86842.1	13.59041096
39762	G04	NTL02YP3835	1,4-alpha-glucan branching enzyme	2184	AAM87431.1	11.4096223
39776	G05	NTL02YP3297	putative TonB-dependent outer membrane receptor	2238	AAM86893.1	3.319578578
39794	G06	NTL02YP3208	hypothetical protein	2325	AAM86804.1	4.090063425
39797	G07	NTL02YP3859	ferrous iron transport protein B	2334	AAM87455.1	4.094776748
39808	G08	NTL02YP3187	hypothetical protein	2379	AAM86783.1	3.339809839
39714	G09	NTL02YP2686	DNA helicase IV	2055	AAM86282.1	3.786634845
39730	G10	NTL02YP1563	putative peptidase	2091	AAM85159.1	2.788831534
36034	G11	NTL02YP1048	hypothetical protein	159	AAM84644.1	2
36069	G12	NTL02YP1040	hypothetical protein	168	AAM84636.1	2.985576923
36137	H01	NTL02YP1042	hypothetical protein	189	AAM84638.1	4
36178	H02	NTL02YP1031	haemolysin expression modulating protein	204	AAM84627.1	4.831967213
36370	H03	NTL02YP1015	DNA-binding protein HU-beta, NS1 (HU-1)	273	AAM84611.1	3.907348243
36511	H04	NTL02YP1033	putative ribosomal protein	324	AAM84629.1	7.008241758
36533	H05	NTL02YP1046	hypothetical protein	333	AAM84642.1	5.90080429
36556	H06	NTL02YP1026	nitrogen regulatory protein P-II 2	339	AAM84622.1	3.881266491
36593	H07	NTL02YP1037	hypothetical protein	354	AAM84633.1	2.972081218
39763	H08	NTL02YP3781	hypothetical protein	2187	AAM87377.1	3.684328693
39764	H09	NTL02YP0457	4-enzyme protein: 3-hydroxyacyl-CoA dehydrogenase 3-hydroxybutyryl-CoA epimerase; delta(3)-cis-delta(2)-trans-enoyl-CoA	2190	AAM84053.1	3.688340807
39768	H10	NTL02YP3164	hypothetical protein	2202	AAM86760.1	3.141837645

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39787	H11	NTL02YP0435	tetrahydropteroyltriglutamate methyltransferase	2292	AAM84031.1	4.114922813
39790	H12	NTL02YP2654	hypothetical protein	2301	AAM86250.1	3.979495942

Table 28: *Yersinia pestis* Gateway® Clone, Plate 29 (UYPWC), NR-19625[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39795	A01	NTL02YP1553	putative enzyme	2328	AAM85149.1	3.797719595
39799	A02	NTL02YP0425	hypothetical protein	2349	AAM84021.1	3.637086647
39802	A03	NTL02YP0403	zinc, lead, cadmium, and mercury transporting ATPase	2367	AAM83999.1	3.32322393
36664	A04	NTL02YP1043	putative gene 58	381	AAM84639.1	3.781472684
36869	A05	NTL02YP1017	hypothetical protein	447	AAM84613.1	5.702258727
36926	A06	NTL02YP1023	putative LRP-like transcriptional regulator	462	AAM84619.1	1.988047809
37188	A07	NTL02YP1030	hypothetical protein	546	AAM84626.1	2.83105802
37242	A08	NTL02YP1044	adenine phosphoribosyltransferase	564	AAM84640.1	2.791390728
37428	A09	NTL02YP1012	ATP-dependent proteolytic subunit of clpA-clpP serine protease	624	AAM84608.1	2.802710843
37485	A10	NTL02YP1050	adenylate kinase	645	AAM84646.1	2.764963504
39816	A11	NTL02YP1014	DNA-binding ATP-dependent protease La heat shock K-protein	2409	AAM84610.1	3.902409147
39820	A12	NTL02YP1494	putative oxidoreductase, major subunit	2433	AAM85090.1	3.565305297
39827	B01	NTL02YP2626	hypothetical protein	2478	AAM86222.1	3.83121525
39875	B02	NTL02YP1513	putative Clp ATPase	2751	AAM85109.1	2.632389824
39876	B03	NTL02YP0506	putative response regulator	2790	AAM84102.1	4.203533569
37902	B04	NTL02YP1053	putative glucose-1-phosphate cytidylyltransferase	786	AAM84649.1	4.960048426
38029	B05	NTL02YP1007	putative sugar hydrolase	828	AAM84603.1	3.657834101
38407	B06	NTL02YP1051	ferrochelatase	963	AAM84647.1	4.375872383
38478	B07	NTL02YP1052	putative CDP-6-deoxy-delta-3,4-glucoseen reductase	990	AAM84648.1	3.457281553
38621	B08	NTL02YP1022	putative cysteine synthase	1041	AAM84618.1	3.540240518
39065	B09	NTL02YP1013	ATP-dependent specificity component of clpP serine protease	1272	AAM84609.1	4.046493902
39112	B10	NTL02YP1027	probable ammonium transporter	1296	AAM84623.1	3.591317365
39888	B11	NTL02YP1074	cation-translocating ATPase	2886	AAM84670.1	12.62747779
39441	B12	NTL02YP1008	ampG protein	1533	AAM84604.1	3.348378894
39593	C01	NTL02YP1024	ATP-binding component of a transport system	1767	AAM84620.1	3.284449364
39631	C02	NTL02YP1025	putative ATP-binding component of a transport system	1851	AAM84621.1	3.619777895
39640	C03	NTL02YP1049	chaperone Hsp90, heat shock protein C 62.5	1875	AAM84645.1	3.765535248
39688	C04	NTL02YP1045	DNA polymerase III, tau and gamma subunits	1977	AAM84641.1	3.225086763
39713	C05	NTL02YP0517	putative type III secretion system component	2055	AAM84113.1	3.82673031
37247	C07	NTL02YPA0057	hypothetical protein	564	NP_857687.1	2.778145695
37424	C08	NTL02YPA0086	resolvase	621	NP_955505.1	2.801815431
37483	C09	NTL02YPA0022	hypothetical protein	642	NP_857661.1	2.790322581

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37496	C10	NTL02YPA0043	hypothetical protein	645	NP_857677.2	2.79270073
37513	C11	NTL02YPA0033	hypothetical protein	651	NP_857671.1	2.77568741
36236	D03	NTL02YPA0097	hypothetical protein	222	NP_955513.1	3.312977099
36252	D04	NTL02YPA0034	hypothetical protein	228	NP_955490.1	4.820895522
36265	D05	NTL02YPD0013	hypothetical protein	234	NP_857797.1	4.835766423
36264	D06	NTL02YPA0091	hypothetical protein	234	NP_955508.1	7.375912409
36293	D07	NTL02YPA0088	hypothetical protein	246	NP_955507.1	4.972027972
36313	D08	NTL02YPA0025	hypothetical protein	255	NP_955489.1	4.054237288
36352	D09	NTL02YPA0053	hypothetical protein	267	NP_955497.1	4.96742671
36351	D10	NTL02YPA0023	hypothetical protein	267	NP_857662.1	2
37648	D11	NTL02YPA0028	hypothetical protein	699	NP_857666.2	1.9932341
37723	D12	NTL02YPA0077	hypothetical protein	723	NP_955503.1	2.791612058
37754	E01	NTL02YPD0045	minor tail fiber protein L	732	NP_857829.1	2.769430052
37796	E02	NTL02YPA0013	hypothetical protein	747	NP_857650.1	5.872935197
37797	E03	NTL02YPD0009	hypothetical protein	747	NP_857793.1	6.660736976
37890	E05	NTL02YPA0002	transposase	780	NP_857639.1	6.141463415
37891	E07	NTL02YPA0099	hypothetical protein	780	NP_857712.1	3.630487805
38049	E08	NTL02YPD0036	hypothetical protein	834	NP_857820.1	3.080091533
38176	E09	NTL02YPA0019	hypothetical protein	876	NP_857656.1	6.447598253
36366	E10	NTL02YPD0042	hypothetical protein	270	NP_857826.1	2.74516129
36365	E11	NTL02YPA0063	hypothetical protein	270	NP_955499.1	5.390322581
36377	E12	NTL02YPA0040	hypothetical protein	273	NP_955491.1	5.916932907
36390	F01	NTL02YPA0030	hypothetical protein	279	NP_857668.1	3.962382445
36469	F03	NTL02YPA0069	hypothetical protein	306	NP_857696.1	7.277456647
36476	F04	NTL02YPA0081	hypothetical protein	309	NP_955504.1	4.696275072
36497	F05	NTL02YPA0012	hypothetical protein	318	NP_857649.1	3.991620112
36518	F06	NTL02YPD0063	hypothetical protein	324	NP_857847.1	-
38251	F07	NTL02YPD0026	hypothetical protein	900	NP_857810.1	3.324468085
38434	F08	NTL02YPA0090	partitioning protein	972	NP_857709.1	4.218379447
38471	F09	NTL02YPA0085	transposase	987	NP_857707.2	3.449853944
38508	F10	NTL02YPA0054	DNA polymerase I	996	NP_857684.2	5.516409266
38581	F11	NTL02YPA0041	hypothetical protein	1023	NP_955492.1	1.297271872
38700	G02	NTL02YPC0005	pesticin	1074	NP_857783.1	3.271992819
36552	G04	NTL02YPA0010	tail fiber protein M	336	NP_857647.1	4
36591	G06	NTL02YPD0085	hypothetical protein	351	NP_857870.1	2.979539642
36614	G07	NTL02YPD0015	hypothetical protein	360	NP_857799.2	2
36648	G08	NTL02YPD0032	hypothetical protein	372	NP_857816.1	4.13592233
36675	G09	NTL02YPD0039	hypothetical protein	384	NP_857823.1	3.867924528
36682	G10	NTL02YPA0064	hypothetical protein	387	NP_955500.1	3.81030445
36714	G11	NTL02YPA0080	hypothetical protein	396	NP_857703.2	3.188073395
36805	G12	NTL02YPA0031	hypothetical protein	423	NP_857669.2	2
36818	H01	NTL02YPC0004	pesticin immunity protein	426	NP_857782.1	2.991416309
36843	H02	NTL02YPD0035	hypothetical protein	435	NP_857819.1	3.816842105
36868	H03	NTL02YPA0058	hypothetical protein	444	NP_857688.1	4.681818182
38730	H04	NTL02YPA0039	hypothetical protein	1086	NP_857676.2	3.221136767
38761	H05	NTL02YPA0070	DNA ligase	1098	NP_857697.2	4.213532513
38978	H07	NTL02YP1114	putative transposase	1209	AAM84710.1	3.229783827
39022	H08	NTL02YPA0060	porphyrin biosynthetic enzyme	1236	NP_857690.1	1.077586207
39046	H09	NTL02YPA0021	hypothetical protein	1257	NP_857660.2	3.68234387
39295	H11	NTL02YPA0093	hypothetical protein	1398	NP_955510.1	3.696801113
39483	H12	NTL02YPA0020	hypothetical protein	1590	NP_857659.2	3.728834356

Table 29: *Yersinia pestis* Gateway® Clone, Plate 30 (UYPWD), NR-19626[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39893	A01	NTL02YPA0004	tail fiber protein	2937	NP_857641.2	3.620423245
36910	A02	NTL02YPD0031	unknown	456	NP_857815.1	3.864919355
36921	A03	NTL02YPA0016	hypothetical protein	459	NP_857653.2	2
36980	A05	NTL02YPA0056	hypothetical protein	474	NP_857686.2	2
36979	A06	NTL02YPA0015	hypothetical protein	474	NP_857652.2	2
37011	A07	NTL02YPA0035	hypothetical protein	483	NP_857672.2	3.399617591
37028	A08	NTL02YPD0068	putative endonuclease	489	NP_857853.1	-
37080	A09	NTL02YPA0100	antirestriction protein	507	NP_857713.1	2
37102	A11	NTL02YPA0065	F1 capsule antigen	513	NP_857692.1	2
39908	A12	NTL02YP0193	hypothetical protein	3192	AAM83789.1	3.814356436
39920	B01	NTL02YP3610	hypothetical protein	3495	AAM87206.1	3.863649222
39921	B02	NTL02YP3074	DNA polymerase III, alpha subunit	3516	AAM86670.1	3.819178853
39932	B03	NTL02YP2349	putative histidine protein kinase sensor	3852	AAM85945.1	3.279033916
39934	B04	NTL02YP1287	phosphoribosylformyl-glycineamide synthetase	3891	AAM84883.1	3.769015518
39899	B05	NTL02YP2088	putative virulence factor	3090	AAM85684.1	3.856230032
39902	B06	NTL02YP0695	acridine efflux pump	3126	AAM84291.1	3.859444093
39909	B07	NTL02YP2153	putative phage tail protein	3204	AAM85749.1	3.813810111
39914	B08	NTL02YP0611	putative periplasmic binding transport protein	3360	AAM84207.1	4.01
39919	B09	NTL02YP1756	transcription-repair coupling factor	3447	AAM85352.1	3.928018354
39935	B10	NTL02YP0653	hypothetical protein	3918	AAM84248.1	3.700353714
39936	B11	NTL02YP2755	cell division protein	3918	AAM86350.1	3.527286508
39898	B12	NTL02YP3708	putative multidrug resistance protein	3087	AAM87304.1	3.886152862
39900	C01	NTL02YP3165	putative chondroitin lyase	3114	AAM86761.1	3.350031706
39905	C02	NTL02YP1034	acridine efflux pump	3153	AAM84630.1	3.77857814
39915	C03	NTL02YP3120	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit	3372	AAM86716.1	4.003810082
39917	C04	NTL02YP1039	putative alpha helix protein	3420	AAM84635.1	3.970809249
39924	C05	NTL02YP1526	hypothetical protein	3579	AAM85122.1	3.808786958
39928	C06	NTL02YP0020	B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase, repressor of metE	3696	AAM83616.1	3.669432548
39940	C07	NTL02YP0478	RNA polymerase, beta prime subunit	4257	AAM84074.1	3.499650919
39941	C08	NTL02YP1323	putative autotransporter	4377	AAM84919.1	3.749151007
39942	C09	NTL02YP2721	kinesin-like cell division protein	4458	AAM86317.1	3.530680302
39943	C10	NTL02YP0183	putative toxin subunit	4551	AAM83779.1	3.693966456
39946	C11	NTL02YP2231	putative hemolysin	4731	AAM85827.1	3.6252358
37673	C12	NTL02YP1447	putative response regulator	708	AAM85043.1	4.588235294
36358	D01	NTL02YP0954	hypothetical protein	270	AAM84550.1	4
36667	D02	NTL02YP1378	hypothetical protein	381	AAM84974.1	3.990498812
36723	D03	NTL02YP2504	putative 5-carboxymethyl-2-hydroxymuconate isomerase	399	AAM86099.1	4
38089	D04	NTL02YP2024	putative oxidoreductase	849	AAM85620.1	3.811023622
36505	D05	NTL02YP3043	hypothetical protein	321	AAM86639.1	2.889196676
37013	D06	NTL02YP0288	2-heptaprenyl-1,4-naphthoquinone methyltransferase	486	AAM83884.1	4
38377	D07	NTL02YP0230	putative permease of ABC transporter	954	AAM83826.1	9.024144869
39150	D08	NTL02YP0283	putative secretion permease	1317	AAM83879.1	3.044215181
36455	D09	NTL02YP2036	hypothetical protein	303	AAM85632.1	6.113702624
38388	D10	NTL02YP1335	hypothetical protein	957	AAM84931.1	5.009027081

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38682	D11	NTL02YP0211	putative dehydrogenase	1068	AAM83807.1	7.203068592
36719	D12	NTL02YP1343	hypothetical protein	399	AAM84939.1	1.970387244
36520	E02	NTL02YP0376	hypothetical protein	327	AAM83972.1	4.506811989
36791	E03	NTL02YP1344	hypothetical protein	420	AAM84940.1	2
36894	E04	NTL02YP0205	putative dehydroquinase	453	AAM83801.1	3.997971602
36080	E05	NTL02YP1352	hypothetical protein	171	AAM84948.1	3
37093	E06	NTL02YP2424	hypothetical protein	510	AAM86020.1	1.998181818
36811	E08	NTL02YP1427	hypothetical protein	426	AAM85023.1	2
38380	E09	NTL02YP1320	enhanced serine sensitivity	954	AAM84916.1	5.302816901
37459	E10	NTL02YP1332	hypothetical protein	636	AAM84928.1	2.394970414
36086	E12	NTL02YP0187	hypothetical protein	174	AAM83783.1	3.864485981
38180	F01	NTL02YP1445	cysteine synthase B, O-acetylserine sulfhydrolase B	879	AAM85041.1	6.800870511
37063	F02	NTL02YP1418	ferredoxin-type protein	504	AAM85014.1	4.097426471
36249	F03	NTL02YP3529	hypothetical protein	228	AAM87125.1	5.973880597
36424	F04	NTL02YP3038	hypothetical protein	291	AAM86634.1	4.70694864
37014	F05	NTL02YP0335	hypothetical protein	486	AAM83931.1	-
37128	F06	NTL02YP3591	acetolactate synthase III, small subunit	525	AAM87187.1	6.617699115
36381	F07	NTL02YP1364	hypothetical protein	276	AAM84960.1	5.705696203
36146	F08	NTL02YP1337	hypothetical protein	192	AAM84933.1	2.974137931
36019	F09	NTL02YP3490	hypothetical protein	153	AAM87086.1	4.559585492
38503	F10	NTL02YP2455	putative solute-binding periplasmic protein	996	AAM86051.1	6.42953668
36145	F12	NTL02YP1314	hypothetical protein	192	AAM84910.1	3
36184	G01	NTL02YP0190	hypothetical protein	207	AAM83786.1	2
36492	G02	NTL02YP1934	hypothetical protein	318	AAM85530.1	3.522346369
36188	G03	NTL02YP1409	hypothetical protein	207	AAM85005.1	5.842105263
36040	G04	NTL02YP2531	hypothetical protein	159	AAM86128.1	-
36171	G06	NTL02YP3508	hypothetical protein	201	AAM87104.1	-
36160	G07	NTL02YP2399	hypothetical protein	198	AAM85995.1	3.966386555
36166	G08	NTL02YP0340	hypothetical protein	201	AAM83936.1	2
36706	G09	NTL02YP1346	hypothetical protein	396	AAM84942.1	3.986238532
36167	G10	NTL02YP1318	hypothetical protein	201	AAM84914.1	2
36157	G11	NTL02YP0220	hypothetical protein	198	AAM83816.1	2.983193277
38845	G12	NTL02YP3016	cytochrome d terminal oxidase, polypeptide subunit II	1140	AAM86612.1	5.346610169
36705	H01	NTL02YP1345	hypothetical protein	396	AAM84941.1	2.919724771
36183	H02	NTL02YP3513	hypothetical protein	204	AAM87110.1	2
36495	H03	NTL02YP3070	hypothetical protein	318	AAM86666.1	2
37912	H06	NTL02YP2315	PhoB-dependent, ATP-binding pho regulon component	789	AAM85911.1	3.616405308
36205	H07	NTL02YP3452	hypothetical protein	210	AAM87048.1	6.752
38142	H08	NTL02YP3435	hypothetical protein	867	AAM87031.1	4.942668137
36881	H10	NTL02YP3409	putative flagellar rod protein	447	AAM87005.1	6.648870637
36684	H12	NTL02YP1826	hypothetical protein	390	AAM85422.1	2

Table 30: *Yersinia pestis* Gateway® Clone, Plate 31 (UYPWE), NR-19627[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36624	A01	NTL02YP0808	putative 6-pyruvoyl tetrahydrobiopterin synthase	366	AAM84404.1	4.800493

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36301	A02	NTL02YP3460	hypothetical protein	249	AAM87056.1	2.802768
39615	A03	NTL02YP2313	nitrate/nitrite sensor	1806	AAM85909.1	4.02221
36867	A04	NTL02YP4045	hypothetical protein	444	AAM87641.1	3.96281
36933	A05	NTL02YP0752	prelipin peptidase dependent protein	465	AAM84348.1	1.89505
36856	A06	NTL02YP1894	hypothetical protein	441	AAM85490.1	3.997921
36399	A07	NTL02YP3474	hypothetical protein	282	AAM87070.1	3
35991	A08	NTL02YP1261	hypothetical protein	150	AAM84857.1	2
37669	A09	NTL02YP1219	urease accessory protein	705	AAM84815.1	2.78255
37843	A10	NTL02YP1198	conserved hypothetical protein	768	AAM84794.1	3.523515
36134	A11	NTL02YP3996	hypothetical protein	186	AAM87592.1	3
36902	A12	NTL02YP0826	ribose 5-phosphate isomerase B	456	AAM84422.1	5.195565
35990	B01	NTL02YP1247	hypothetical protein	150	AAM84844.1	3
38239	B02	NTL02YP0115	hypothetical protein	900	AAM83711.1	3.534043
38215	B03	NTL02YP2959	putative inner membrane permease of ABC transporter	888	AAM86555.1	3.545259
39377	B05	NTL02YP3999	hypothetical protein	1473	AAM87595.1	3.582948
37006	B06	NTL02YP1913	putative transposase	483	AAM85509.1	4
35958	B07	NTL02YP0801	hypothetical protein	126	AAM84397.1	1.981928
36527	B08	NTL02YP1224	hypothetical protein	330	AAM84820.1	2
36630	B09	NTL02YP0114	hypothetical protein	369	AAM83710.1	1.733496
35933	B10	NTL02YP1178	putative RNA	108	AAM84774.1	-
37062	B11	NTL02YP0733	hypothetical protein	504	AAM84329.1	2.998162
37043	B12	NTL02YP0818	hypothetical protein	498	AAM84414.1	2.239777
38270	C01	NTL02YP3462	putative transcriptional regulator LYSR-type	912	AAM87058.1	5.391807
38212	C02	NTL02YP2323	tellurite resistance	888	AAM85919.1	3.546336
35999	C03	NTL02YP2294	hypothetical protein	150	AAM85890.1	2
35979	C04	NTL02YP4060	50S ribosomal subunit protein L34	141	AAM87656.1	2.756906
36192	C05	NTL02YP2948	hypothetical protein	207	AAM86544.1	2
37640	C06	NTL02YP2991	inner membrane permease protein of molybdate ABC transport system	696	AAM86587.1	4.177989
36392	C07	NTL02YP0171	hypothetical protein	282	AAM83767.1	3.903727
38814	C08	NTL02YP2921	outer membrane protein 1b (Ibc)	1125	AAM86517.1	2.476395
37728	C09	NTL02YP0817	hypothetical protein	726	AAM84413.1	4.754569
38455	C10	NTL02YP1879	phenylalanine tRNA synthetase, alpha-subunit	984	AAM85475.1	6.34082
36870	C11	NTL02YP1188	negative regulator	447	AAM84784.1	2
36032	C12	NTL02YP0087	hypothetical protein	159	AAM83684.1	3
38797	D01	NTL02YP2938	putative outer membrane porin	1116	AAM86534.1	6.270761
39578	D03	NTL02YP0810	sulfite reductase, alpha subunit	1731	AAM84406.1	8.289102
38643	D05	NTL02YP3395	hypothetical protein	1047	AAM86991.1	3.423183
36084	D06	NTL02YP2964	hypothetical protein	171	AAM86560.1	2
38893	D07	NTL02YP2919	putative enzyme	1167	AAM86515.1	5.721624
37399	D08	NTL02YP0861	hypothetical protein	618	AAM84457.1	5.224924
38713	D09	NTL02YP3429	ferric enterobactin (enterochelin) binding protein	1080	AAM87025.1	5.8125
38717	D10	NTL02YP1223	putative nickel transport protein	1083	AAM84819.1	3.373108
35947	D11	NTL02YP0831	hypothetical protein	120	AAM84427.1	2.8375
36897	D12	NTL02YP1260	putative formate acetyltransferase	453	AAM84856.1	6.474645
37274	E01	NTL02YP3444	hypothetical protein	573	AAM87040.1	2.479608
36107	E04	NTL02YP1878	hypothetical protein	180	AAM85474.1	3.995455
37484	E05	NTL02YP0168	hypothetical protein	645	AAM83764.1	2.782482

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37092	E06	NTL02YP2298	hypothetical protein	510	AAM85894.1	3.258182
38056	E07	NTL02YP2945	putative inner membrane permease of ABC transport	837	AAM86541.1	6.213227
37691	E08	NTL02YP2326	ABC transporter ATP-binding protein	714	AAM85922.1	2.807692
38050	E09	NTL02YP0728	dipeptide transport system permease protein 2	837	AAM84324.1	3.22577
38702	E10	NTL02YP0739	hypothetical protein	1077	AAM84335.1	2.661594
37621	E11	NTL02YP3469	hypothetical protein	687	AAM87065.1	8.856946
37907	E12	NTL02YP3403	flagellar biosynthesis protein, cell-distal portion of basal-body	786	AAM86999.1	3.595642
37426	F01	NTL02YP0099	guanylate kinase	624	AAM83695.1	2.805723
38360	F02	NTL02YP0753	quinolinate phosphoribosyltransferase	948	AAM84349.1	7.687247
38805	F03	NTL02YP0742	hypothetical protein	1122	AAM84338.1	7.79346
37837	F04	NTL02YP2816	transcriptional repressor for deo operon, tsx, nupG	765	AAM86412.1	3.653416
36531	F05	NTL02YP2811	hypothetical protein	330	AAM86407.1	2
38732	F06	NTL02YP0585	rhamnose/proton symporter	1089	AAM84181.1	5.232064
36907	F08	NTL02YP2893	hypothetical protein	456	AAM86489.1	4.518145
39458	F09	NTL02YP1131	ATP-binding component of D-ribose high-affinity transport system	1548	AAM84727.1	3.684509
36690	F12	NTL02YP3879	hypothetical protein	390	AAM87475.1	3.981395
36987	G01	NTL02YP0721	phosphonate metabolism protein	477	AAM84317.1	3.452611
37101	G02	NTL02YP3971	peptide deformylase	513	AAM87567.1	2.166365
37295	G03	NTL02YP3910	hypothetical protein	579	AAM87506.1	4.600969
37571	G04	NTL02YP2787	arginine 3rd transport system permease protein	669	AAM86383.1	9.957687
37257	G05	NTL02YP3988	adenine phosphoribosyltransferase	567	AAM87584.1	2.823723
37384	G06	NTL02YP3334	aerobactin synthetase (subunit alpha)	609	AAM86930.1	1.8151
37129	G07	NTL02YP3953	hypothetical protein	525	AAM87549.1	3.444248
37644	G08	NTL02YP1706	putative membrane protein	699	AAM85302.1	8.484438
36640	G09	NTL02YP0716	hypothetical protein	372	AAM84312.1	4
39317	G10	NTL02YP3984	aromatic amino acid permease	1419	AAM87580.1	2.673749
37831	G11	NTL02YP2214	ATP-binding component of zinc ABC transport system	762	AAM85810.1	4.490025
36707	G12	NTL02YP1813	chemotaxis regulator	396	AAM85409.1	2.901376
36150	H01	NTL02YP1141	hypothetical protein	195	AAM84737.1	3.157447
35952	H02	NTL02YP3891	hypothetical protein	120	AAM87487.1	2
38248	H03	NTL02YP3230	site-specific recombinase	900	AAM86826.1	3.42234
36172	H04	NTL02YP3966	hypothetical protein	201	AAM87562.1	3
37906	H05	NTL02YP2792	putative ABC transport protein	786	AAM86388.1	4.858354
36744	H06	NTL02YP2886	hypothetical protein	405	AAM86482.1	2
39444	H07	NTL02YP3985	putative histidine ammonia-lyase	1533	AAM87581.1	3.262556
36736	H08	NTL02YP2251	hypothetical protein	402	AAM85847.1	-
36009	H09	NTL02YP1096	hypothetical protein	153	AAM84692.1	1.699482
37997	H10	NTL02YP3885	DNA adenine methylase	816	AAM87481.1	6.014019
35951	H11	NTL02YP3222	hypothetical protein	120	AAM86818.1	3
36318	H12	NTL02YP0665	50S ribosomal subunit protein L27	258	AAM84261.1	3.97651

Table 31: *Yersinia pestis* Gateway® Clone, Plate 32 (UYPWF), NR-19628[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36071	A01	NTL02YP1725	50S ribosomal subunit protein L32	168	AAM85321.1	3.96634615
35935	A02	NTL02YP2782	hypothetical protein	111	AAM86378.1	2
38860	A04	NTL02YP2883	hypothetical protein	1149	AAM86479.1	2.55761144
37444	A05	NTL02YP0720	phosphonate metabolism protein	630	AAM84316.1	2.80447761
36309	A06	NTL02YP1147	cold shock protein	255	AAM84743.1	4.70169492
36254	A07	NTL02YP3288	hypothetical protein	231	AAM86884.1	3.50922509
36162	A08	NTL02YP2808	hypothetical protein	198	AAM86404.1	4.99579832
36026	A09	NTL02YP3202	hypothetical protein	156	AAM86798.1	1.82653061
36300	A10	NTL02YP2185	hypothetical protein	249	AAM85781.1	2
36605	A11	NTL02YP3960	30S ribosomal subunit protein S13	357	AAM87556.1	4.5138539
35938	A12	NTL02YP1708	hypothetical protein	114	AAM85304.1	2
35977	B01	NTL02YP0581	hypothetical protein	141	AAM84177.1	3.96132597
37656	B02	NTL02YP1807	hypothetical protein	702	AAM85403.1	5.4541779
37091	B03	NTL02YP2262	putative recombinase	510	AAM85858.1	1.99272727
36651	B04	NTL02YP2853	hypothetical protein	375	AAM86449.1	1.87710843
39124	B05	NTL02YP1749	respiratory NADH dehydrogenase	1305	AAM85345.1	6.97695167
36288	B06	NTL02YP1719	damage-inducible protein I	246	AAM85315.1	5.13286713
35983	B07	NTL02YP3241	hypothetical protein	147	AAM86838.1	1.75935829
36193	B08	NTL02YP3215	hypothetical protein	207	AAM86812.1	2
39021	B09	NTL02YP1800	putative resistance protein, transport	1236	AAM85396.1	2.95924765
37418	B10	NTL02YP2260	peptidyl-tRNA hydrolase	621	AAM85856.1	4.61422088
36674	B11	NTL02YP2860	hypothetical protein	384	AAM86456.1	2.6509434
39178	B12	NTL02YP0649	putative membrane protein	1332	AAM84245.1	7.59620991
36002	C01	NTL02YP2788	hypothetical protein	150	AAM86384.1	1.87894737
36273	C02	NTL02YP3212	hypothetical protein	237	AAM86808.1	1.99277978
38828	C04	NTL02YP3280	putative protein transport	1131	AAM86876.1	3.41844577
36692	C05	NTL02YP3964	50S ribosomal subunit protein L17	390	AAM87560.1	1.72093023
37131	C06	NTL02YP0655	inorganic pyrophosphatase	528	AAM84251.1	4.39612676
36092	C08	NTL02YP3271	hypothetical protein	174	AAM86867.1	4.87383178
35970	C09	NTL02YP3363	hypothetical protein	132	AAM86960.1	2.87209302
37016	C10	NTL02YP2658	hypothetical protein	486	AAM86254.1	3.98098859
36691	C12	NTL02YP3961	30S ribosomal subunit protein S11	390	AAM87557.1	2
38090	D01	NTL02YP2239	hypothetical protein	849	AAM85835.1	7.9583802
36917	D02	NTL02YP2179	putative phage endopeptidase Rz	459	AAM85775.1	2
38282	D03	NTL02YP2151	putative phage tail protein	918	AAM85747.1	8.02192067
36507	D04	NTL02YP3204	hypothetical protein	321	AAM86800.1	4.44875346
36020	D05	NTL02YP3717	hypothetical protein	153	AAM87313.1	4.65803109
39097	D06	NTL02YP3691	phosphopentomutase	1290	AAM87287.1	2.26240602
37767	D07	NTL02YP2584	N-(5-phospho-L-ribosyl-formimino)-5-amino-1-(5-phosphoribosyl)-4-imidazolecarboxamide isomerase	738	AAM86180.1	5.87275064
39789	D08	NTL02YP3307	hypothetical protein	2298	AAM86903.1	8.81565441
39126	D09	NTL02YP2106	sensor histidine protein kinase (RstA regulator)	1305	AAM85702.1	3.91226766
36055	D10	NTL02YP3130	hypothetical protein	162	AAM86726.1	4.81683168
39791	D11	NTL02YP2942	biodegradative arginine decarboxylase	2307	AAM86538.1	3.98380912
36936	D12	NTL02YP2115	hypothetical protein	465	AAM85711.1	1.86930693
38397	E02	NTL02YP0542	hypothetical protein	960	AAM84138.1	2.552
36502	E03	NTL02YP2647	putative transposase	321	AAM86243.1	4.84487535
36345	E04	NTL02YP0445	hypothetical protein	267	AAM84041.1	3.8762215

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39785	E05	NTL02YP3525	hypothetical protein	2286	AAM87121.1	8.54385211
37541	E06	NTL02YP3216	hypothetical protein	660	AAM86811.1	1.77428571
38280	E07	NTL02YP1568	hypothetical protein	918	AAM85164.1	5.29227557
36432	E08	NTL02YP3716	hypothetical protein	294	AAM87312.1	2.98502994
38378	E09	NTL02YP0411	cell division membrane protein	954	AAM84007.1	8.40945674
39833	E10	NTL02YP2321	putative outer membrane protein	2532	AAM85917.1	3.88569207
39807	E11	NTL02YP0554	hypothetical protein	2379	AAM84150.1	4.02232327
39580	E12	NTL02YP3228	ssDNA exonuclease	1734	AAM86824.1	3.24802706
36003	F01	NTL02YP3147	hypothetical protein	150	AAM86743.1	2.98421053
38520	F02	NTL02YP1557	putative adenine-specific methylase	1002	AAM85153.1	8.10460653
36452	F03	NTL02YP1543	heme exporter protein D	303	AAM85139.1	1.89212828
39831	F04	NTL02YP2835	outer membrane usher protein	2514	AAM86431.1	7.13586531
35929	F05	NTL02YP1654	hypothetical protein	105	AAM85250.1	3.9862069
36687	F06	NTL02YP3095	putative structural protein	390	AAM86691.1	3.98139535
36851	F07	NTL02YP3749	hypothetical protein	438	AAM87345.1	3.94560669
37826	F08	NTL02YP3846	repressor of the glp operon	759	AAM87442.1	2.62703379
37943	F09	NTL02YP2748	pyruvate formate lyase activating enzyme 1	798	AAM86344.1	2.79236277
36222	F10	NTL02YP0567	hypothetical protein	219	AAM84163.1	2.98455598
36812	F11	NTL02YP3132	hypothetical protein	426	AAM86728.1	4.9248927
38414	F12	NTL02YP1063	putative nucleotide di-P-sugar epimerase or dehydratase	966	AAM84659.1	3.41451292
36263	G01	NTL02YP3826	hypothetical protein	234	AAM87422.1	3.96350365
38002	G02	NTL02YP1634	putative enzyme	819	AAM85230.1	6.87776484
37340	G03	NTL02YP0019	repressor of aceBA operon	594	AAM83615.1	5.64353312
38548	G04	NTL02YP0393	lysophospholipase L(2)	1014	AAM83989.1	5.89278937
39715	G05	NTL02YP0558	hypothetical protein	2058	AAM84154.1	3.85033365
37718	G06	NTL02YP2689	hypothetical protein	723	AAM86285.1	4.62647444
36475	G07	NTL02YP3162	hypothetical protein	309	AAM86758.1	3
37127	G09	NTL02YP2672	putative myristoyl-acyl carrier dehydratase	525	AAM86268.1	5.61946903
39842	G11	NTL02YP3872	peptidoglycan synthetase penicillin-binding protein 1A	2580	AAM87468.1	3.7740458
36102	G12	NTL02YP2770	hypothetical protein	177	AAM86366.1	1.96313364
38618	H01	NTL02YP2743	periplasmic L-asparaginase II	1038	AAM86339.1	3.48144712
37923	H02	NTL02YP3092	methionine aminopeptidase	792	AAM86688.1	4.48197115
36303	H03	NTL02YP1038	hypothetical protein	252	AAM84634.1	2.73287671
37878	H04	NTL02YP2667	putative polyketide biosynthesis enoyl-coa hydratase	777	AAM86263.1	6.86780906
36529	H05	NTL02YP2678	hypothetical protein	330	AAM86274.1	2.97837838
37735	H06	NTL02YP1576	putative lipoprotein	729	AAM85172.1	4.58387516
38825	H07	NTL02YP0415	high-affinity leucine-specificleucine-specific-binding periplasmic protein of high-affinity branched-chain	1131	AAM84011.1	3.32536294
39726	H08	NTL02YP3358	putative OM receptor	2073	AAM86954.1	3.85660199
37868	H09	NTL02YP2653	hypothetical protein	774	AAM86249.1	4.42137592
39732	H11	NTL02YP3850	4-alpha-glucanotransferase (amylomaltase)	2097	AAM87446.1	3.81796912

Table 32: *Yersinia pestis* Gateway® Clone, Plate 33 (UYPWG), NR-19629[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39753	A01	NTL02YP2285	hypothetical protein	2163	AAM85881.1	3.757149342
39891	A02	NTL02YP0734	valine tRNA synthetase	2898	AAM84330.1	8.886997958
37642	A03	NTL02YP1019	hypothetical protein	699	AAM84615.1	6.364005413
36355	A04	NTL02YPD0007	hypothetical protein	267	AAC82669.1	3.986970684
36477	A05	NTL02YPA0094	hypothetical protein	309	NP_955511.1	2
38442	A06	NTL02YP2510	PTS enzyme IIAB, mannose-specific	975	AAM86106.1	3.480788177
38287	A07	NTL02YP1997	oligopeptide ABC transporter permease protein	921	AAM85593.1	8.299687825
39569	A09	NTL02YP2437	basal-body MS (membrane and supramembrane)-ring and collar	1713	AAM86033.1	3.350256703
39503	A10	NTL02YP1109	hypothetical protein	1629	AAM84705.1	1.151587777
37587	A11	NTL02YP2747	hypothetical protein	675	AAM86343.1	2
37818	A12	NTL02YP3105	5-3 exonuclease	756	AAM86701.1	2
37931	B01	NTL02YP3125	thymidylate synthetase	795	AAM86721.1	4.416766467
38882	B02	NTL02YP0927	putative membrane protein, N-terminal part of adhesin	1161	AAM84523.1	4.273105745
36327	B03	NTL02YP1281	hypothetical protein	261	AAM84877.1	3.983388704
38328	B04	NTL02YP0110	putative transferase	936	AAM83706.1	8.102459016
36710	B05	NTL02YP2418	hypothetical protein	396	AAM86014.1	4.151376147
36046	B06	NTL02YP0180	hypothetical protein	162	AAM83776.1	2.98019802
36100	B07	NTL02YP1926	hypothetical protein	177	AAM85522.1	2.820276498
36849	B08	NTL02YP3413	hypothetical protein	438	AAM87009.1	2
36022	B09	NTL02YP1985	hypothetical protein	156	AAM85581.1	2.979591837
36824	B10	NTL02YP3011	putative inner membrane protein	429	AAM86607.1	3.976545842
36035	B11	NTL02YP1380	hypothetical protein	159	AAM84976.1	3.804020101
37393	B12	NTL02YP2410	trp repressor binding protein	615	AAM86006.1	6.138931298
37448	C02	NTL02YP2467	cell-proximal portion of basal-body rod protein	630	AAM86063.1	6.217910448
38064	C03	NTL02YP1965	hypothetical protein	840	AAM85561.1	7.247727273
37986	C04	NTL02YP3454	conserved hypothetical protein	813	AAM87050.1	3.977725674
36079	C07	NTL02YP1305	hypothetical protein	171	AAM84901.1	2.938388626
37041	C10	NTL02YP3033	small protein B	495	AAM86629.1	3.934579439
37427	C11	NTL02YP0141	hypothetical protein	624	AAM83737.1	1.99246988
36243	C12	NTL02YP0081	hypothetical protein	228	AAM83677.1	1.985074627
37682	D01	NTL02YP1851	hypothetical protein	711	AAM85447.1	6.260985353
35992	D03	NTL02YP1264	hypothetical protein	150	AAM84860.1	2
36030	D04	NTL02YP4062	hypothetical protein	156	AAM87659.1	2
37386	D05	NTL02YP1431	hypothetical protein	612	AAM85027.1	6.231595092
38183	D06	NTL02YP2430	putative AraC-type regulatory protein	879	AAM86026.1	7.124047878
36109	D07	NTL02YP2969	hypothetical protein	180	AAM86565.1	3.468181818
36012	D08	NTL02YP1438	hypothetical protein	153	AAM85034.1	3.917098446
37349	D09	NTL02YP3075	RNAse HII	597	AAM86671.1	6.249607535
38410	D10	NTL02YP2339	putative LysR-type transcriptional regulator	963	AAM85935.1	5.956131605
37894	D11	NTL02YP0109	putative transposase	783	AAM83705.1	2.626974484
35993	D12	NTL02YP1420	hypothetical protein	150	AAM85016.1	6.9
36513	E01	NTL02YP1956	hypothetical protein	324	AAM85552.1	4.159340659
36588	E02	NTL02YP1875	protein chain initiation factor IF-3	351	AAM85471.1	5.204603581
38082	E03	NTL02YP0917	hypothetical protein	846	AAM84513.1	7.013544018
39237	E04	NTL02YP0263	rhsD protein	1371	AAM83859.1	5.123316797
38238	E05	NTL02YP3039	hypothetical protein	897	AAM86635.1	7.027748132

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38441	E06	NTL02YP2074	DNA-binding protein	975	AAM85670.1	5.772413793
36509	E07	NTL02YP3618	hypothetical protein	321	AAM87215.1	3.980609418
39410	E08	NTL02YP1365	putative transcriptional regulator	1506	AAM84961.1	6.611901682
36775	E09	NTL02YP3387	hypothetical protein	414	AAM86983.1	1.977973568
37802	E10	NTL02YP0711	phosphonate metabolism	753	AAM84307.1	6.196721311
35955	E11	NTL02YP3311	putative transposase	123	AAM86907.1	3.90797546
36041	E12	NTL02YP2870	hypothetical protein	159	AAM86466.1	3.713567839
39558	F01	NTL02YP3982	hypothetical protein	1692	AAM87578.1	7.355658199
35927	F02	NTL02YP0633	hypothetical protein	105	AAM84229.1	2.937931034
37250	F03	NTL02YP0604	elongation factor P (EF-P)	567	AAM84200.1	6.210873147
38374	F04	NTL02YP3336	acetyl CoA:N6-hydroxylsyine acetyl transferase	951	AAM86932.1	6.840565086
37034	F05	NTL02YP3317	hypothetical protein	492	AAM86913.1	3.994360902
36312	F06	NTL02YP2854	hypothetical protein	255	AAM86450.1	2.962711864
38189	F07	NTL02YP1572	pseudouridylate synthase I	882	AAM85168.1	6.809110629
39619	F08	NTL02YP2913	putative methyl-accepting chemotaxis transmembrane protein	1815	AAM86509.1	7.98328841
37360	F09	NTL02YP0699	hypothetical protein	603	AAM84295.1	5.216174184
36839	F10	NTL02YP3168	putative transposase	435	AAM86764.1	3.983157895
37553	F12	NTL02YP1824	putative transposase	663	AAM85420.1	3.992887624
38541	G01	NTL02YP3987	cysteine synthase	1008	AAM87583.1	6.417938931
36421	G02	NTL02YP2121	hypothetical protein	291	AAM85717.1	3.975830816
37510	G04	NTL02YP3327	hypothetical protein	651	AAM86923.1	6.176555716
36021	G06	NTL02YP3823	hypothetical protein	153	AAM87419.1	2
37172	G07	NTL02YP1561	putative transporting ATPase	543	AAM85157.1	6.283018868
37316	G08	NTL02YP2863	putative lipoprotein	585	AAM86459.1	6.2608
38294	G11	NTL02YP1784	hypothetical protein	924	AAM85380.1	3.228215768
38810	G12	NTL02YP2136	putative cobalt-nickel resistance (export) protein	1122	AAM85732.1	4.2616179
35980	H01	NTL02YP0487	hypothetical protein	144	AAM84084.1	4.983695652
38929	H02	NTL02YP0719	phosphonate metabolism protein	1285	AAM84315.1	6.229387755
36229	H03	NTL02YP3924	host factor for lysis of phiX174 infection	219	AAM87520.1	3.71042471
35939	H04	NTL02YP1712	hypothetical protein	114	AAM85308.1	2
39425	H05	NTL02YP3226	lysine tRNA synthetase	1518	AAM86822.1	7.718870347
35957	H09	NTL02YP0536	hemin uptake system component	126	AAM84132.1	2
36007	H10	NTL02YP0068	hypothetical protein	153	AAM83664.1	3.943005181
37164	H11	NTL02YP1529	hypothetical protein	540	AAM85125.1	2.972413793

Table 33: *Yersinia pestis* Gateway® Clone, Plate 34 (UYPWH), NR-19630[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36175	A01	NTL02YP0064	hypothetical protein	204	AAM83660.1	3.831967
37768	A02	NTL02YP2616	putative oxidoreductase	738	AAM86212.1	6.033419
38336	A03	NTL02YP0394	putative haloacid dehalogenase-like hydrolase	939	AAM83990.1	6.960163
38181	A04	NTL02YP1478	transcriptional regulator	879	AAM85074.1	5.225245
38338	A05	NTL02YP1054	putative CDP-D-glucose-4,6-dehydratase	939	AAM84650.1	7.39428
38044	A06	NTL02YP1492	putative membrane anchor protein for oxidoreductase	834	AAM85088.1	6.245995
39743	A07	NTL02YP3903	hypothetical protein	2121	AAM87499.1	7.467376

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36810	A08	NTL02YP1018	hypothetical protein	426	AAM84614.1	3.976395
38241	A09	NTL02YP0321	glutamate racemase	900	AAM83917.1	7.137234
36123	A10	NTL02YP2503	hypothetical protein	183	AAM86100.1	3
37181	A11	NTL02YP3040	hypothetical protein	543	AAM86636.1	5.698113
36239	A12	NTL02YP2374	hypothetical protein	225	AAM85970.1	3.826415
36860	B01	NTL02YP0132	50S ribosomal subunit protein L13	444	AAM83728.1	2
38342	B02	NTL02YP2946	putative ATP-binding component of ABC transporter	939	AAM86542.1	5.862104
38412	B03	NTL02YP3586	putative apolipoprotein	963	AAM87182.1	6.19342
36712	B04	NTL02YP3562	hypothetical protein	396	AAM87158.1	3.979358
36929	B06	NTL02YP3407	hypothetical protein	462	AAM87003.1	2.99004
37947	B07	NTL02YP1183	glucosamine-6-phosphate deaminase	801	AAM84779.1	6.653983
38322	B08	NTL02YP2067	transcriptional regulator for ara operon	933	AAM85662.1	6.535457
37231	B10	NTL02YP1289	hypothetical protein	561	AAM84885.1	5.517471
39193	B12	NTL02YP2311	acetylornithine delta-aminotransferase	1341	AAM85907.1	6.675597
37850	C01	NTL02YP0772	inner membrane permease of ABC transporter	771	AAM84368.1	7.203453
38271	C02	NTL02YP0960	possible NAGC-like transcriptional regulator	915	AAM84556.1	7.037696
39570	C03	NTL02YP1376	putative inner membrane permease of high-affinity phosphate-specific	1716	AAM84972.1	6.038724
38499	C04	NTL02YP0199	rod shape-determining protein	996	AAM83795.1	6.707529
38243	C05	NTL02YP1394	dihydrodipicolinate synthase	900	AAM84990.1	7.104255
37355	C07	NTL02YP1929	hypothetical protein	600	AAM85525.1	6.240625
37564	C08	NTL02YP3402	putative flagellar l-ring protein	666	AAM86998.1	5.902266
37437	C09	NTL02YP4027	superoxide dismutase, manganese	624	AAM87623.1	5.192771
38459	C11	NTL02YP3537	hypothetical protein	984	AAM87133.1	6.477539
36422	C12	NTL02YP2389	hypothetical protein	291	AAM85985.1	3.824773
39596	D01	NTL02YP3029	DNA repair protein	1770	AAM86625.1	6.51105
38134	D02	NTL02YP1262	putative extracellular phospholipase A	864	AAM84858.1	7.050885
39525	D03	NTL02YP1218	urease (urea amidohydrolase) alpha subunit	1653	AAM84814.1	6.431187
38053	D04	NTL02YP1858	5-keto-4-deoxyuronate isomerase	837	AAM85454.1	6.111745
39131	D05	NTL02YP3633	survival protein	1305	AAM87229.1	7.25948
38217	D06	NTL02YP0217	putative oxidoreductase	891	AAM83813.1	7.143931
39288	D07	NTL02YP4022	selenocysteine synthase: L-seryl-tRNA (Ser) selenium transferase	1395	AAM87618.1	7.149129
38467	D08	NTL02YP3519	putative repressor	987	AAM87115.1	4.8111
37400	D09	NTL02YP0868	hypothetical protein	618	AAM84464.1	5.092705
39439	D10	NTL02YP1930	hypothetical protein	1530	AAM85526.1	7.749682
36760	D11	NTL02YP0166	regulator of nucleoside diphosphate kinase	411	AAM83762.1	3.982262
36186	D12	NTL02YP0746	hypothetical protein	207	AAM84342.1	2.951417
39400	E02	NTL02YP0844	L-xylulose kinase, cryptic	1497	AAM84440.1	6.882238
37500	E04	NTL02YP1925	RNase T, degrades tRNA	648	AAM85521.1	4.818314
37744	E05	NTL02YP1255	hypothetical protein	732	AAM84851.1	6.187824
38563	E06	NTL02YP4043	putative dehydrogenase	1017	AAM87639.1	6.403974
36203	E07	NTL02YP2917	hypothetical protein	210	AAM86513.1	3.948
38310	E08	NTL02YP1426	coproporphyrinogen III oxidase	930	AAM85022.1	6.487629
37990	E09	NTL02YP1943	putative ATP-binding protein of peptide ABC transport	816	AAM85539.1	6.260514
38275	E10	NTL02YP1922	putative lipoprotein	915	AAM85518.1	6.387435

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37910	E11	NTL02YP0918	putative solute-binding protein of ABC transporter	789	AAM84514.1	6.25573
39306	E12	NTL02YP0268	hypothetical protein	1407	AAM83864.1	6.918452
37725	F01	NTL02YP0151	putative ATP-binding component of ABC transport system	726	AAM83747.1	5.886423
37531	F03	NTL02YP1916	riboflavin synthase, alpha chain	657	AAM85512.1	6.02439
38071	F04	NTL02YP1232	negative transcriptional regulator of cel operon	843	AAM84828.1	1.970555
36414	F05	NTL02YP1191	hypothetical protein	288	AAM84787.1	2
37889	F06	NTL02YP4074	ATP-binding component of high-affinity phosphate-specific ABC transport	780	AAM87670.1	7.030488
36291	F07	NTL02YP3068	hypothetical protein	246	AAM86664.1	3.583916
38476	F08	NTL02YP0860	putative solute-binding periplasmic protein of ABC transporter	990	AAM84456.1	6.425243
37667	F09	NTL02YP0814	adenosine 5-phosphosulfate kinase	705	AAM84410.1	6.216107
38221	F10	NTL02YP1867	ATP-binding protein for iron and manganese ABC	891	AAM85463.1	6.024705
37597	F11	NTL02YP0969	putative dehydrogenase	681	AAM84565.1	6.223301
37165	G01	NTL02YP2004	outer membrane protein X	540	AAM85600.1	6.25
36642	G02	NTL02YP1977	hypothetical protein	372	AAM85573.1	3.98301
36686	G03	NTL02YP3025	succinate dehydrogenase, cytochrome b556	390	AAM86621.1	3.97907
38004	G04	NTL02YP2997	hypothetical protein	819	AAM86593.1	6.740396
38284	G05	NTL02YP3410	putative flagellar protein	918	AAM87006.1	5.901879
36223	G06	NTL02YP0736	hypothetical protein	219	AAM84332.1	3.818533
38384	G07	NTL02YP0323	solute-binding periplasmic protein of ABC transporter	957	AAM83919.1	6.234704
38166	G08	NTL02YP1443	sulfate/thiosulfate permease	876	AAM85039.1	6.75655
38930	G09	NTL02YP0908	multidrug resistance secretion protein	1185	AAM84504.1	6.955102
39266	G10	NTL02YP3495	hypothetical protein	1383	AAM87091.1	7.569923
35924	G11	NTL02YP0793	hypothetical protein	102	AAM84389.1	2
38246	G12	NTL02YP2317	hypothetical protein	900	AAM85913.1	6.991489
38501	H01	NTL02YP0774	hypothetical protein	996	AAM84370.1	6.418919
38405	H02	NTL02YP3992	putative iron permease, ABC transporter	960	AAM87588.1	6.436
38498	H03	NTL02YP4012	hypothetical protein	993	AAM87608.1	6.453049
36357	H04	NTL02YP0683	30S ribosomal subunit protein S15	270	AAM84279.1	2
37343	H05	NTL02YP2237	hypothetical protein	594	AAM85833.1	5.539432
38097	H06	NTL02YP3193	putative malG type permease	852	AAM86789.1	6.180493
38035	H07	NTL02YP0438	hypothetical protein	831	AAM84034.1	5.311137
36988	H08	NTL02YP0735	DNA polymerase III, chi subunit	477	AAM84331.1	4.636364
39413	H09	NTL02YP0737	aminopeptidase A/I	1512	AAM84333.1	7.320876
36899	H10	NTL02YP2263	hypothetical protein	453	AAM85859.1	4.135903
39684	H11	NTL02YP1134	putative myo-inositol catabolism protein iolB	1971	AAM84730.1	6.871706
37812	H12	NTL02YP2847	putative ribose 5-phosphate isomerase A	753	AAM86443.1	6.189155

Table 34: *Yersinia pestis* Gateway® Clone, Plate 35 (UYPWI), NR-19631[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37374	A01	NTL02YP2814	hypothetical protein	606	AAM86410.1	6.219814241

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38464	A02	NTL02YP2732	putative enzyme	987	AAM86328.1	6.697176241
38896	A03	NTL02YP3177	putative deacetylase	1167	AAM86773.1	7.08036454
38663	A04	NTL02YP3719	putative ABC transport system permease protein	1056	AAM87315.1	7.100364964
38485	A05	NTL02YP3991	putative solute-binding iron ABC transport protein	990	AAM87587.1	6.257281553
37995	A06	NTL02YP2905	putative DEOR-type transcriptional regulator	816	AAM86501.1	7.205607477
37532	A07	NTL02YP2265	hypothetical protein	657	AAM85861.1	5.110473458
37982	A08	NTL02YP2197	cell division inhibitor	813	AAM85793.1	7.130128957
37652	A09	NTL02YP0636	hypothetical protein	702	AAM84232.1	3.547169811
37819	A10	NTL02YP3161	putative carbonic anhydrase	756	AAM86757.1	7.273869347
37414	A11	NTL02YP0748	putative DNA repair protein	621	AAM84344.1	5.889561271
37583	A12	NTL02YP1168	glutamate/aspartate inner membrane permease	675	AAM84764.1	5.784615385
37935	B01	NTL02YP0482	thiF protein	798	AAM84078.1	6.267303103
36261	B02	NTL02YP3133	hypothetical protein	234	AAM86729.1	2.959854015
36524	B03	NTL02YP3704	hypothetical protein	327	AAM87300.1	3.950953678
37674	B04	NTL02YP2268	hypothetical protein	708	AAM85864.1	6.201871658
38303	B05	NTL02YP3290	putative glutaminase	927	AAM86886.1	6.036194416
38425	B06	NTL02YP0663	octaprenyl diphosphate synthase	972	AAM84259.1	6.815217391
38091	B07	NTL02YP2594	putative ATP-binding component for iron transport system	849	AAM86190.1	6.997750281
37218	B08	NTL02YP1833	hypothetical protein	555	AAM85429.1	5.131092437
36098	B09	NTL02YP0723	hypothetical protein	177	AAM84319.1	1.995391705
37617	B10	NTL02YP2255	putative glutamyl-tRNA dehydrogenase	687	AAM85851.1	6.211829436
36372	B11	NTL02YP2195	hypothetical protein	273	AAM85791.1	2.955271566
38209	B12	NTL02YP1745	hypothetical protein	888	AAM85341.1	6.6875
38482	C01	NTL02YP3884	putative membrane protein	990	AAM87479.1	6.597087379
37820	C02	NTL02YP3178	2-deoxy-D-gluconate 3-dehydrogenase	756	AAM86774.1	5.738693467
38974	C03	NTL02YP3110	hypothetical protein	1206	AAM86706.1	8.012038523
37297	C04	NTL02YP0713	ATP-binding protein	582	AAM84309.1	6.15755627
38055	C05	NTL02YP2243	putative ABC transporter permease	837	AAM85839.1	7.007981756
36733	C06	NTL02YP1102	hypothetical protein	402	AAM84698.1	4.809954751
38369	C07	NTL02YP1697	hypothetical protein	951	AAM85293.1	6.898082745
38252	C08	NTL02YP0059	putative efflux permease protein	903	AAM83655.1	7.021208908
37142	C09	NTL02YP3078	(3R)-hydroxymyristol acyl carrier protein dehydratase	531	AAM86674.1	6.290718039
37954	C10	NTL02YP3980	hypothetical protein	801	AAM87576.1	3.730083234
36038	C11	NTL02YP2229	hypothetical protein	159	AAM85825.1	1.974874372
38167	C12	NTL02YP1685	putative inner membrane permease of ABC transporter	876	AAM85281.1	6.496724891
36250	D01	NTL02YP3860	ferrous iron transport protein A	228	AAM87456.1	3.839552239
38086	D02	NTL02YP0045	facilitator for glycerol uptake	849	AAM83641.1	7.14735658
35975	D03	NTL02YP2648	putative transposase	138	AAM86244.1	2.696629213
38300	D04	NTL02YP0416	high-affinity branched-chain amino acid ABC transport system	927	AAM84012.1	5.904860393
39042	D05	NTL02YP1823	hypothetical protein	1257	AAM85419.1	7.880493446
37504	D06	NTL02YP2902	hypothetical protein	648	AAM86498.1	5.546511628
39583	D07	NTL02YP2200	acyl-CoA synthetase	1740	AAM85796.1	6.932022472
37065	D08	NTL02YP1701	hypothetical protein	504	AAM85297.1	5.288602941
38356	D10	NTL02YP3750	tRNA processing exoribonuclease BN	945	AAM87346.1	6.507614213

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37908	D11	NTL02YP4014	putative transposase	786	AAM87610.1	6.694915254
36270	D12	NTL02YP1731	acyl carrier protein	237	AAM85327.1	2.826714801
37697	E01	NTL02YP2786	arginine 3rd transport system permease protein	717	AAM86382.1	6.207397622
36578	E02	NTL02YP1630	hypothetical protein	348	AAM85226.1	4.512886598
38453	E03	NTL02YP0058	6-phosphofructokinase I	984	AAM83654.1	5.78125
39627	E04	NTL02YP4010	putative membrane protein	1830	AAM87606.1	7.463636364
38112	E05	NTL02YP0717	ATP-binding component of phosphonate ABC transporter	858	AAM84313.1	6.722717149
39003	E06	NTL02YP3180	putative arylsulfatase regulator	1227	AAM86776.1	3.83504341
37689	E07	NTL02YP1837	putative transport system effector	714	AAM85433.1	2
37480	E08	NTL02YP2856	putative elongation factor	642	AAM86452.1	6.212609971
38483	E09	NTL02YP3916	hypothetical protein	990	AAM87512.1	6.733009709
39197	E10	NTL02YP2752	putative polynucleotide enzyme	1344	AAM86348.1	7.64234104
36806	E11	NTL02YP0043	putative transposase	426	AAM83639.1	3.909871245
37803	E12	NTL02YP0747	hypothetical protein	753	AAM84343.1	5.499369483
39611	F01	NTL02YP2879	putative sulfatase	1797	AAM86475.1	7.339684268
38450	F02	NTL02YP3909	hypothetical protein	981	AAM87505.1	4.675808031
37711	F03	NTL02YP3864	response regulator (sensor, EnvZ)	720	AAM87460.1	6.172368421
36785	F04	NTL02YP3160	hypothetical protein	417	AAM86756.1	3.912472648
36863	F05	NTL02YP2221	dATP pyrophosphohydrolase	444	AAM85817.1	3.991735537
38536	F06	NTL02YP2877	hypothetical protein	1005	AAM86473.1	6.206698565
38469	F07	NTL02YP3897	putative transcriptional regulator	987	AAM87493.1	5.642648491
39672	F08	NTL02YP2768	putative ATP-binding component of ABC transport system	1950	AAM86364.1	6.916080402
36363	F10	NTL02YP2637	hypothetical protein	270	AAM86233.1	3.948387097
39450	F11	NTL02YP2916	putative oligogalacturonide transporter	1539	AAM86512.1	4.928435719
37069	F12	NTL02YP3955	30S ribosomal subunit protein S5	504	AAM87551.1	6.297794118
36415	G01	NTL02YP1716	hypothetical protein	288	AAM85313.1	3.957317073
36585	G02	NTL02YP0034	hypothetical protein	351	AAM83630.1	3.992327366
37305	G03	NTL02YP3977	putative transferase	582	AAM87573.1	2.945337621
38123	G04	NTL02YP3201	hypothetical protein	858	AAM86797.1	6.189309577
38539	G05	NTL02YP3142	hypothetical protein	1008	AAM86738.1	6.55629771
37871	G06	NTL02YP0447	hypothetical protein	777	AAM84043.1	6.927784578
38395	G07	NTL02YP0387	hypothetical protein	960	AAM83983.1	5.75
38647	G08	NTL02YP1062	putative mannosyltransferase-like protein	1050	AAM84658.1	7.553211009
37544	G09	NTL02YP0408	hypothetical protein	663	AAM84004.1	6.223328592
37403	G10	NTL02YP1493	anaerobic dimethyl sulfoxide reductase subunit B	618	AAM85089.1	6.200607903
37781	G11	NTL02YP0401	hypothetical protein	744	AAM83997.1	6.178571429
37974	G12	NTL02YP1073	putative ligase	810	AAM84669.1	5.249411765
39933	H01	NTL02YP1981	helicase, ATP-dependent	3888	AAM85577.1	7.820519348
39836	H02	NTL02YP2089	putative virulence factor	2541	AAM85685.1	8.0414568
39850	H03	NTL02YP1842	putative usher protein	2613	AAM85438.1	3.49264983
39864	H04	NTL02YP2927	DNA gyrase, subunit A, type II topoisomerase	2676	AAM86523.1	7.859720177
39745	H05	NTL02YP0725	anaerobic ribonucleoside-triphosphate reductase	2139	AAM84321.1	6.88435062
39737	H06	NTL02YP3933	GTP-binding protein chain elongation factor EF-G	2109	AAM87529.1	8.083294556
39852	H07	NTL02YP2712	aminopeptidase N	2616	AAM86308.1	7.907756024

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39786	H08	NTL02YP2929	ribonucleoside diphosphate reductase 1, alpha subunit, B1	2289	AAM86525.1	3.374409618
36500	H09	NTL02YP1010	possible regulator of murein genes	321	AAM84606.1	3.648199446
39872	H10	NTL02YP3680	putative cation transport protein	2727	AAM87276.1	7.731839537
37524	H11	NTL02YP1036	acrAB operon repressor	657	AAM84632.1	5.169296987
38206	H12	NTL02YP1028	acyl-CoA thioesterase II	888	AAM84624.1	7.118534483

Table 35: *Yersinia pestis* Gateway® Clone, Plate 36 (UYPWJ), NR-19632[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39709	A01	NTL02YP0484	thiC protein	2046	AAM84080.1	7.85666347
39948	A03	NTL02YP1125	conserved hypothetical protein	6015	AAM84721.1	8.43699422

Table 36: *Yersinia pestis* Gateway® Clone, Plate 37 (UYPWK), NR-19633[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38262	A01	NTL02YP1003	protoheme IX farnesyltransferase	909	AAM84599.1	5.6796628
38286	A02	NTL02YP0994	geranyltranstransferase	921	AAM84590.1	5.75234131
36044	A03	NTL02YP3663	hypothetical protein	159	AAM87259.1	6.36180905
36397	A05	NTL02YP2563	hypothetical protein	282	AAM86160.1	5.95031056
38496	A06	NTL02YP3664	transaldolase B	993	AAM87260.1	5.27299129
39630	A07	NTL02YP0978	protein secretion, membrane protein	1848	AAM84574.1	5.68644068
39656	A08	NTL02YP3658	chaperone Hsp70	1911	AAM87254.1	4.72424398
37205	A09	NTL02YP1001	hypothetical protein	552	AAM84597.1	6.09628378
37888	A10	NTL02YP3666	hypothetical protein	780	AAM87262.1	7.56707317
38291	B02	NTL02YPB0040	secreted effector protein	921	NP_857754.1	3.90634755
38345	B03	NTL02YPC0007	plasminogen activator protease precursor	939	NP_857784.1	3.71092952
36598	B05	NTL02YPD0054	hypothetical protein	354	NP_857839.1	3.92385787
39050	B06	NTL02YPB0014	virulence protein	1260	NP_857729.1	5.39384615
39767	B07	NTL02YPB0070	protein kinase A	2199	NP_857776.1	4.18981688
38457	B08	NTL02YP2063	L-arabinose-binding periplasmic protein	984	AAM85659.1	3.6484375
35988	B09	NTL02YP0285	hypothetical protein	150	AAM83881.1	2.91052632
36226	B10	NTL02YP2492	hypothetical protein	219	AAM86089.1	3.66795367
36233	B11	NTL02YP2059	putative C-terminal fragment of inner membrane permease	222	AAM85655.1	3.85114504
38781	B12	NTL02YP1406	putative solute-binding periplasmic protein of ABC transporter	1110	AAM85002.1	4.9626087
39689	C01	NTL02YP2053	putative membrane protein	1980	AAM85649.1	4.50247525
38267	C02	NTL02YP0959	hypothetical protein	912	AAM84555.1	3.90336134
38066	C03	NTL02YP2520	putative enzyme	840	AAM86116.1	4.28068182
38779	C04	NTL02YP0374	porphobilinogen deaminase hydroxymethylbilane synthase	1110	AAM83970.1	3.25391304
38354	C07	NTL02YP2544	putative periplasmic binding protein of ABC transporter	945	AAM86140.1	2.50152284
38580	C08	NTL02YP3622	hypothetical protein	1023	AAM87218.1	3.33019755
36234	C09	NTL02YP2542	hypothetical protein	222	AAM86138.1	2
39442	C10	NTL02YP1440	sialic acid transporter	1533	AAM85036.1	3.21551176

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39533	C11	NTL02YP3602	solute-binding periplasmic protein of ABC transporter	1662	AAM87198.1	2.83901293
37870	C12	NTL02YP0306	acetylglutamate kinase	777	AAM83902.1	4.73684211
38196	D01	NTL02YP0299	5,10-methylenetetrahydrofolate reductase	885	AAM83895.1	5.3027027
36368	D02	NTL02YP0295	50S ribosomal subunit protein L31	273	AAM83891.1	4.67412141
38528	D03	NTL02YP0305	N-acetyl-gamma-glutamylphosphate reductase	1005	AAM83901.1	3.53971292
39174	D04	NTL02YP0311	secretion permease, type I secretion system	1329	AAM83907.1	4.66983199
39243	D05	NTL02YP0307	argininosuccinate lyase	1374	AAM83903.1	4.35785007
36299	D06	NTL02YP2041	hypothetical protein	249	AAM85637.1	4.84429066
39384	D09	NTL02YP2003	cardiolipin synthase	1482	AAM85599.1	3.82654402
39474	D10	NTL02YP2019	anthranilate synthase component I	1566	AAM85615.1	3.70547945
39633	D11	NTL02YP0929	putative adhesin system protein	1854	AAM84525.1	4.15100317
37937	D12	NTL02YP0884	tRNA (guanine-7-)-methyltransferase	798	AAM84480.1	6.46181384
36060	E01	NTL02YP0881	hypothetical protein	165	AAM84477.1	2
39335	E02	NTL02YP3552	uronate isomerase	1434	AAM87148.1	4.20352782
37934	E03	NTL02YP0270	hypothetical protein	798	AAM83866.1	6.99522673
37948	E04	NTL02YP1350	phosphomethylpyrimidine kinase	801	AAM84946.1	5.58263971
38219	E05	NTL02YP1355	hypothetical protein	891	AAM84951.1	6.33727175
36005	E06	NTL02YP3530	hypothetical protein	150	AAM87126.1	3.73157895
36143	E07	NTL02YP0261	hypothetical protein	192	AAM83857.1	4.40517241
36360	E08	NTL02YP2448	flagellar biosynthesis protein	270	AAM86044.1	4.78387097
38594	E09	NTL02YP1367	putative substrate-binding protein of ABC transporter	1029	AAM84963.1	3.05238541
38757	E10	NTL02YP2456	putative permease of ABC transporter	1098	AAM86052.1	3.56239016
38753	E11	NTL02YP0276	hypothetical protein	1098	AAM83872.1	3.49209139
36794	E12	NTL02YP2451	hypothetical protein	420	AAM86047.1	4.94130435
39145	F01	NTL02YP1366	4-aminobutyrate aminotransferase	1314	AAM84962.1	3.11299852
39149	F02	NTL02YP0275	hypothetical protein	1317	AAM83871.1	3.71849668
39163	F03	NTL02YP3547	Na/dicarboxylate symporter	1320	AAM87143.1	3
39202	F04	NTL02YP1368	putative permease of ABC transporter	1347	AAM84964.1	3.4888248
39210	F05	NTL02YP1370	putative heat shock protein	1353	AAM84966.1	3.92246949
39260	F06	NTL02YP3522	hypothetical protein	1380	AAM87118.1	3.21830986
39382	F07	NTL02YP2440	flagellum-specific ATP synthase	1479	AAM86036.1	3.00724161
37765	F08	NTL02YP2439	flagellar assembly protein	738	AAM86035.1	2.79434447
37794	F09	NTL02YP1351	hypothetical protein	747	AAM84947.1	6.68996188
37933	F10	NTL02YP0241	putative transport system permease protein of aliphatic	798	AAM83837.1	2.77804296
38193	F11	NTL02YP3517	putative inner membrane permease protein of ABC	882	AAM87113.1	5.76464208
38240	F12	NTL02YP0250	hypothetical protein	900	AAM83846.1	6.16170213
38317	G01	NTL02YP0246	putative ribokinase	933	AAM83842.1	5.56217883
38327	G02	NTL02YP3499	putative transcriptional regulators	933	AAM87095.1	6.22096608
36238	G03	NTL02YP1336	hypothetical protein	225	AAM84932.1	1.99622642
36177	G04	NTL02YP0238	putative DNA-damage inducible protein	204	AAM83834.1	2.97540984
38614	G05	NTL02YP1329	putative membrane protein	1038	AAM84925.1	3.42115028
38664	G06	NTL02YP0233	putative periplasmic binding protein of ABC transporter	1059	AAM83829.1	3.46587807
38834	G07	NTL02YP0243	solute-binding periplasmic protein of aliphatic sulfonates, ABC transporter	1137	AAM83839.1	3.48598131
39016	G08	NTL02YP3507	aspartate aminotransferase	1233	AAM87103.1	3.22466614

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39257	G10	NTL02YP1338	exonuclease VII, large subunit	1380	AAM84934.1	3.92957746
39388	G11	NTL02YP1334	putative GTP-binding factor	1488	AAM84930.1	3.66295812
39540	G12	NTL02YP0236	hypothetical protein	1671	AAM83832.1	3.03506721
37369	H01	NTL02YP0228	hypothetical protein	606	AAM83824.1	2.39628483
35961	H02	NTL02YP2400	hypothetical protein	126	AAM85996.1	2.73493976
35978	H03	NTL02YP2396	hypothetical protein	141	AAM85992.1	2.98895028
36015	H04	NTL02YP2384	hypothetical protein	153	AAM85980.1	3.75129534
36053	H05	NTL02YP2382	hypothetical protein	162	AAM85978.1	4.94554455
36155	H06	NTL02YP3485	hypothetical protein	195	AAM87081.1	4.77446809
37942	H07	NTL02YP2381	putative transcriptional regulator of the GntR family	798	AAM85977.1	2.78042959
38128	H08	NTL02YP2378	putative permease of ABC transporter	861	AAM85974.1	5.00887902
36232	H09	NTL02YP1300	hypothetical protein	222	AAM84896.1	1.98091603
39004	H10	NTL02YP1311	putative aminotransferase	1230	AAM84907.1	3.1023622
39025	H11	NTL02YP3481	tRNA nucleotidyl transferase	1239	AAM87077.1	2.94057858
39039	H12	NTL02YP1299	serine hydroxymethyltransferase	1254	AAM84895.1	3.76120556

Table 37: *Yersinia pestis* Gateway® Clone, Plate 38 (UYPWL), NR-19634[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36676	A01	NTL02YP1312	hypothetical protein	387	AAM84908.1	3.28337237
39231	A03	NTL02YP1293	putative 2-component transcriptional regulator	1368	AAM84889.1	3.39417614
39357	A04	NTL02YP1291	putative 2-component sensor protein	1452	AAM84887.1	2.20844504
39634	A05	NTL02YP2403	excinuclease ABC, subunit C	1854	AAM85999.1	3.44878564
39651	A06	NTL02YP3489	RNA polymerase, sigma(70) factor	1899	AAM87085.1	4.452295
37738	A07	NTL02YP3064	copper homeostasis protein (lipoprotein)	729	AAM86660.1	1.76462939
38147	A08	NTL02YP0192	putative carbon-nitrogen hydrolase	870	AAM83788.1	5.82527473
38349	A09	NTL02YP1968	hypothetical protein	942	AAM85564.1	5.21486762
36558	A10	NTL02YP1970	methylviologen resistance	339	AAM85566.1	2.35883905
36631	A11	NTL02YP0186	hypothetical protein	369	AAM83782.1	3.87775061
36666	A12	NTL02YP1279	CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase	381	AAM84875.1	3
38444	B01	NTL02YP0202	putative dehydrogenase	978	AAM83798.1	5.02259332
38549	B02	NTL02YP1964	hypothetical protein	1014	AAM85560.1	5.27514231
36941	B03	NTL02YP3049	RNase HI	465	AAM86645.1	1.98019802
39220	B04	NTL02YP3047	putative permease	1359	AAM86643.1	3.53395282
39374	B05	NTL02YP0194	cytoplasmic filament protein	1470	AAM83790.1	3.71721854
39496	B06	NTL02YP1963	putative transport periplasmic protein	1617	AAM85559.1	8.24743512
37408	B07	NTL02YP0204	hypothetical protein	621	AAM83800.1	2.77760968
38612	B08	NTL02YP0846	putative inner membrane permease protein of ABC	1038	AAM84442.1	3.35435993
38633	B09	NTL02YP1949	psp operon transcriptional activator	1044	AAM85545.1	3.50276753
38670	B10	NTL02YP1955	hypothetical protein	1062	AAM85551.1	3.33484574
38738	B11	NTL02YP3036	hypothetical protein	1089	AAM86632.1	3.06820195
36610	B12	NTL02YP1952	phage shock protein	360	AAM85548.1	2.9625
36829	C01	NTL02YP1931	transcriptional regulator for cryptic hemolysin	432	AAM85527.1	3.98728814
38921	C02	NTL02YP3010	membrane spanning protein	1182	AAM86606.1	3.18003273
38936	C03	NTL02YP0840	hypothetical protein	1188	AAM84436.1	3.2728013

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39013	C04	NTL02YP3035	prophage CP4-57 integrase	1233	AAM86631.1	3.20974077
39078	C05	NTL02YP1942	hypothetical protein	1281	AAM85538.1	3.92127176
39080	C06	NTL02YP3026	citrate synthase	1281	AAM86622.1	3.24072672
39090	C07	NTL02YP1936	tyrosine tRNA synthetase	1287	AAM85532.1	3.52599849
37074	C08	NTL02YP3008	peptidoglycan-associated lipoprotein	507	AAM86604.1	1.80621572
37291	C09	NTL02YP3027	heat shock protein	579	AAM86623.1	3.76575121
39517	C10	NTL02YP0843	fumarase A	1644	AAM84439.1	2.58966746
37619	C11	NTL02YP3012	inner membrane protein	687	AAM86608.1	2.74140303
37679	C12	NTL02YP0856	putative oxidoreductase component	711	AAM84452.1	5.6045273
37901	D01	NTL02YP0841	methionine aminopeptidase	786	AAM84437.1	5.34987893
38343	D02	NTL02YP3004	putative transport system permease protein	939	AAM86600.1	5.50153218
37244	D03	NTL02YP1909	hypothetical protein	564	AAM85505.1	2.98509934
38710	D04	NTL02YP2990	ATP-binding component of molybdate transport	1080	AAM86586.1	3.375
39095	D05	NTL02YP0833	arsenical pump membrane protein	1290	AAM84429.1	3.37142857
39171	D06	NTL02YP1907	hypothetical protein	1326	AAM85503.1	3.01317716
37851	D07	NTL02YP0828	putative dehydrogenase	771	AAM84424.1	-
38011	D08	NTL02YP1899	hypothetical protein	822	AAM85495.1	9.64269142
37898	D09	NTL02YP3471	hypothetical protein	783	AAM87067.1	3.62332928
38046	D10	NTL02YP3441	hypothetical protein	834	AAM87037.1	2.83524027
36116	D11	NTL02YP0800	hypothetical protein	183	AAM84396.1	7.92376682
38387	D12	NTL02YP1270	regulates activity of sigma-E factor	957	AAM84866.1	2.99498495
38869	E01	NTL02YP1888	putative enzyme	1155	AAM85484.1	3.26610879
39304	E02	NTL02YP2357	hypothetical protein	1404	AAM85953.1	3.18698061
39345	E03	NTL02YP0791	putative channel transporter	1443	AAM84387.1	2.61564396
39349	E04	NTL02YP0798	periplasmic serine protease Do	1446	AAM84394.1	1.5013459
39461	E05	NTL02YP3455	hypothetical protein	1548	AAM87051.1	5.63350126
36004	E06	NTL02YP3426	hypothetical protein	150	AAM87022.1	3.99473684
36176	E07	NTL02YP0177	hypothetical protein	204	AAM83773.1	4
36302	E08	NTL02YP0158	hypothetical protein	252	AAM83754.1	5.92808219
36376	E09	NTL02YP3423	hypothetical protein	273	AAM87019.1	2.8913738
36367	E10	NTL02YP0157	phosphocarrier protein HPr-like NPr	273	AAM83753.1	3.72523962
36402	E11	NTL02YP1245	hypothetical protein	285	AAM84649.1	3.98153846
38367	E12	NTL02YP1253	putative carboxylase	951	AAM84849.1	5.30474268
39103	F01	NTL02YP2328	putative ABC inner membrane permease	1293	AAM85924.1	6.06826707
39354	F02	NTL02YP0164	PTS system enzyme IIBC	1452	AAM83760.1	3.56434316
39537	F03	NTL02YP0165	trehalase 6-P hydrolase	1668	AAM83761.1	4.28629977
37828	F05	NTL02YP1233	hypothetical protein	762	AAM84829.1	6.48254364
35937	F06	NTL02YP1237	hypothetical protein	114	AAM84833.1	1.99350649
36409	F07	NTL02YP0147	hypothetical protein	288	AAM83743.1	3.97256098
38304	F08	NTL02YP3398	hypothetical protein	927	AAM86994.1	5.24715615
38490	F09	NTL02YP1222	hypothetical protein	993	AAM84818.1	3.01161665
38554	F10	NTL02YP3397	hypothetical protein	1014	AAM86993.1	4.01612903
38656	F11	NTL02YP2310	hypothetical protein	1053	AAM85906.1	2.53705398
38992	F12	NTL02YP2327	putative integral membrane protein	1221	AAM85923.1	2.5852498
39196	G01	NTL02YP3414	flagellum-specific ATP synthase	1341	AAM87010.1	2.57639392
37103	G02	NTL02YP0129	stringent starvation protein B	516	AAM83725.1	6.54676259
39568	G03	NTL02YP0106	hypothetical protein	1710	AAM83702.1	2.73542857
38161	G04	NTL02YP2962	ATP-binding component of phosphonate transport	873	AAM86558.1	3.57940854

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38429	G05	NTL02YP1868	periplasmic-binding protein for iron and manganese ABC	972	AAM85464.1	4.87450593
39168	G06	NTL02YP4057	ssDNA and dsDNA binding protein	1323	AAM87653.1	3.04622157
39665	G08	NTL02YP1874	threonine tRNA synthetase	1929	AAM85470.1	2.96698832
36124	G09	NTL02YP2939	hypothetical protein	183	AAM86535.1	3.55605381
38875	G10	NTL02YP2947	putative ABC transport system inner membrane permease	1155	AAM86543.1	2.78075314
39347	G11	NTL02YP2936	catalase hydroperoxidase HPII(III)	1443	AAM86532.1	5.77275792
39542	H01	NTL02YP0768	hypothetical protein	1674	AAM84364.1	3.4369895
38101	H02	NTL02YP0755	regulates ampC	855	AAM84351.1	2.84469274
38315	H03	NTL02YP3989	hypothetical protein	930	AAM87585.1	4.06907216
38333	H04	NTL02YP2912	outer membrane protein 3b (a), protease VII	936	AAM86508.1	5.52459016
35941	H05	NTL02YP2910	hypothetical protein	114	AAM86506.1	-
36091	H06	NTL02YP2918	hypothetical protein	174	AAM86514.1	5.64018692
36278	H07	NTL02YP1827	hypothetical protein	240	AAM85423.1	1.98214286
38630	H08	NTL02YP0749	GMP reductase	1044	AAM84345.1	2.92435424
38645	H09	NTL02YP0729	putative transport system permease protein	1050	AAM84325.1	1.74311927
39008	H11	NTL02YP4015	proton motive force efflux pump protein	1230	AAM87611.1	3.14409449
39211	H12	NTL02YP1835	hypothetical protein	1353	AAM85431.1	3.15577889

Table 38: *Yersinia pestis* Gateway® Clone, Plate 39 (UYPWM), NR-19635[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39675	A01	NTL02YP2923	putative 2-component sensor protein	1953	AAM86519.1	3.03512293
37827	A02	NTL02YP3994	ATP-binding component of citrate-dependent iron(III) transport protein	759	AAM87590.1	5.156445557
36225	A04	NTL02YP1796	hypothetical protein	219	AAM85392.1	1.980694981
38187	A05	NTL02YP0718	phosphonate metabolism protein	882	AAM84314.1	5.479392625
38462	A06	NTL02YP1802	hypothetical protein	987	AAM85398.1	5.489776047
36444	A07	NTL02YP2898	hypothetical protein	300	AAM86494.1	3.723529412
38662	A08	NTL02YP2895	hypothetical protein	1056	AAM86491.1	3.464416058
38836	A09	NTL02YP0714	phosphonate metabolism protein	1137	AAM84310.1	3.31011045
39544	A10	NTL02YP1808	methyl-accepting chemotaxis protein I, serine sensor receptor	1674	AAM85404.1	3.339556593
37593	A11	NTL02YP1803	hypothetical protein	678	AAM85399.1	2.78551532
38172	A12	NTL02YP3353	partial leucine-rich repeat protein	876	AAM86949.1	6.054585153
38198	B01	NTL02YP0687	putative control proteins	885	AAM84283.1	2
35945	B02	NTL02YP3344	hypothetical protein	117	AAM86940.1	1.98089172
36057	B03	NTL02YP3370	hypothetical protein	162	AAM86966.1	3.955445545
36056	B04	NTL02YP3369	hypothetical protein	162	AAM86965.1	2.945544554
36103	B05	NTL02YP3368	hypothetical protein	177	AAM86964.1	4.695852535
38245	B06	NTL02YP2256	hypothetical protein	900	AAM85852.1	5.787234043
38436	B07	NTL02YP0682	tRNA pseudouridine 5S synthase	975	AAM84278.1	5.820689655
36194	B08	NTL02YP3360	hypothetical protein	207	AAM86956.1	2.417004049
38822	B09	NTL02YP3372	hypothetical protein	1128	AAM86968.1	3.108732877
38917	B10	NTL02YP1177	hypothetical protein	1182	AAM84773.1	3.251227496
39170	B11	NTL02YP1782	phosphoanhydride phosphorylase	1326	AAM85378.1	3.570278184
37271	C01	NTL02YP1779	hypothetical protein	573	AAM85375.1	2.528548124

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
35998	C02	NTL02YP2245	hypothetical protein	150	AAM85841.1	2.952631579
39494	C03	NTL02YP2234	putative virulence factor	1611	AAM85830.1	5.898243489
39579	C04	NTL02YP2230	arginine tRNA synthetase	1731	AAM85826.1	3.327498588
39607	C05	NTL02YP1139	putative ABC transporter, ATP-binding protein	1791	AAM84735.1	5.097214637
38138	C06	NTL02YP1092	5,10-methylene-tetrahydrofolate dehydrogenase	867	AAM84688.1	2.846747519
38230	C07	NTL02YP1107	hypothetical protein	894	AAM84703.1	5.485010707
39154	C09	NTL02YP2212	hypothetical protein	1317	AAM85808.1	1.258658806
36076	C10	NTL02YP3959	hypothetical protein	168	AAM87555.1	2.947115385
36113	C11	NTL02YP3956	50S ribosomal subunit protein L30	180	AAM87552.1	2.95
36197	C12	NTL02YP1086	hypothetical protein	210	AAM84682.1	2.944
36330	D01	NTL02YP1776	hypothetical protein	261	AAM85372.1	4.794019934
37952	D02	NTL02YP2859	regulator for uxu operon	801	AAM86455.1	4.83353151
38632	D03	NTL02YP1775	putative sucrose specific transcriptional regulator	1044	AAM85371.1	8.541512915
38811	D04	NTL02YP3972	hypothetical protein	1122	AAM87568.1	1.692771084
39099	D05	NTL02YP3969	hypothetical protein	1290	AAM87565.1	3.242105263
39376	D06	NTL02YP2864	hypothetical protein	1473	AAM86460.1	3.724388632
37152	D08	NTL02YP3952	50S ribosomal subunit protein L6	534	AAM87548.1	3.93902439
37975	D09	NTL02YP1738	hypothetical protein	810	AAM85334.1	3.02
38041	D10	NTL02YP0675	7,8-dihydropteroate synthase	834	AAM84271.1	3.421052632
38052	D11	NTL02YP1762	putative nicotinic acid mononucleotide:5,6-dimethylbenzimidazole (DMB) phosphoribosyltransferase	837	AAM85358.1	2.835803877
36207	D12	NTL02YP0648	hypothetical protein	213	AAM84244.1	2.95256917
36337	E01	NTL02YP0658	hypothetical protein	264	AAM84254.1	3.970394737
38617	E02	NTL02YP1747	hypothetical protein	1038	AAM85342.1	3.188311688
38737	E04	NTL02YP2846	putative permease	1089	AAM86442.1	4.313551816
39562	E05	NTL02YP2840	PTS system, fructose-specific IIBC transport protein	1701	AAM86436.1	2.970706491
36132	E06	NTL02YP2824	hypothetical protein	186	AAM86420.1	2.951327434
38649	E08	NTL02YP1737	DNA polymerase III, delta prime subunit	1050	AAM85333.1	1.760550459
38129	E10	NTL02YP2789	hypothetical protein	861	AAM86385.1	3.513873474
35964	E11	NTL02YP0613	hypothetical protein	129	AAM84209.1	3.840236686
36050	E12	NTL02YP1707	hypothetical protein	162	AAM85303.1	3
36139	F01	NTL02YP1691	hypothetical protein	189	AAM85287.1	3.825327511
38544	F02	NTL02YP1694	hypothetical protein	1011	AAM85289.1	5.712654615
38567	F03	NTL02YP1700	putative NAD(P)H-dependent xylose reductase	1020	AAM85296.1	2.879245283
38654	F04	NTL02YP0614	hypothetical protein	1053	AAM84210.1	1.76852699
37170	F05	NTL02YP0602	hypothetical protein	543	AAM84198.1	3.72212693
38809	F06	NTL02YP1710	hypothetical protein	1122	AAM85306.1	1.725473322
38808	F07	NTL02YP1689	hypothetical protein	1122	AAM85285.1	1.637693632
39018	F08	NTL02YP0616	hypothetical protein	1236	AAM84212.1	2.998432602
39035	F09	NTL02YP1692	putative transport protein	1248	AAM85288.1	2.430900621
37530	F10	NTL02YP1705	putative homoserine lactone synthase	657	AAM85301.1	4.18938307
39219	F11	NTL02YP1702	putative permease, major facilitator superfamily	1359	AAM85298.1	3.749106505
39331	F12	NTL02YP1682	phosphomannomutase	1434	AAM85278.1	3.187924016
39657	G01	NTL02YP0619	N-acetylmuramoyl-l-alanine amidase II	1914	AAM84215.1	5.498976459

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37817	G02	NTL02YP2785	arginine 3rd transport system periplasmic binding protein	756	AAM86381.1	5.791457286
37824	G03	NTL02YP2799	arginine 3rd transport system periplasmic binding protein	759	AAM86395.1	2
37749	G04	NTL02YP3274	hypothetical protein	732	AAM86870.1	6.347150259
37809	G05	NTL02YP2160	putative phage tail protein	753	AAM85756.1	5.752837327
37867	G06	NTL02YP2171	hypothetical protein	774	AAM85767.1	6.889434889
35982	G07	NTL02YP3273	hypothetical protein	144	AAM86869.1	3.972826087
36065	G08	NTL02YP3243	hypothetical protein	165	AAM86839.1	3.941463415
36074	G09	NTL02YP3272	hypothetical protein	168	AAM86868.1	1.951923077
36185	G10	NTL02YP0580	hypothetical protein	207	AAM84176.1	4.963562753
38403	G11	NTL02YP3275	glutathione synthetase	960	AAM86871.1	4.747
38550	H01	NTL02YP2152	hypothetical protein	1014	AAM85748.1	3.096774194
38712	H02	NTL02YP3261	fructose-bisphosphate aldolase, class II	1080	AAM86857.1	2.545535714
36508	H03	NTL02YP3266	hypothetical protein	321	AAM86862.1	4.988919668
36589	H04	NTL02YP2167	hypothetical protein	351	AAM85763.1	4.739130435
36679	H05	NTL02YP3247	glycine cleavage complex protein H	387	AAM86843.1	3.981264637
38750	H06	NTL02YP2156	putative phage antirepressor	1095	AAM85752.1	2.623788546
38807	H07	NTL02YP1681	inner membrane ABC transporter	1122	AAM85277.1	3.025817556
38889	H09	NTL02YP3262	phosphoglycerate kinase	1164	AAM86858.1	3.124584718
38957	H10	NTL02YP2147	putative aminotransferase	1200	AAM85743.1	3.200806452
39363	H11	NTL02YP0579	rhamnulokinase	1458	AAM84175.1	3.58411215
39402	H12	NTL02YP3232	inner membrane protein	1500	AAM86828.1	3.584415584

Table 39: *Yersinia pestis* Gateway® Clone, Plate 40 (UYPWN), NR-19636[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39664	A01	NTL02YP3242	hypothetical protein	1926	AAM86837.1	3.651577
37460	A02	NTL02YP2177	hypothetical protein	636	AAM85773.1	2.794379
38170	A03	NTL02YP2132	hypothetical protein	876	AAM85728.1	5.320961
39127	A07	NTL02YP2140	D-amino acid dehydrogenase subunit	1305	AAM85736.1	3.907063
39632	A08	NTL02YP2126	protease IV, a signal peptide peptidase	1851	AAM85722.1	3.322581
39663	A09	NTL02YP2122	DNA topoisomerase III	1926	AAM85718.1	3.129705
37991	A10	NTL02YP2119	exonuclease III	816	AAM85715.1	3.553738
35994	A12	NTL02YP1671	hypothetical protein	150	AAM85267.1	3.952632
36052	B01	NTL02YP2087	hypothetical protein	162	AAM85683.1	3.717822
36054	B02	NTL02YP2767	hypothetical protein	162	AAM86363.1	1.970297
36128	B03	NTL02YP3874	hypothetical protein	183	AAM87470.1	2.946188
36195	B04	NTL02YP3853	hypothetical protein	207	AAM87449.1	3.793522
38411	B05	NTL02YP2757	thioredoxin reductase	963	AAM86353.1	6.011964
36326	B06	NTL02YP3858	ferrous iron transport protein B	258	AAM87454.1	7.318792
36504	B07	NTL02YP2765	hypothetical protein	321	AAM86361.1	5.939058
37663	B08	NTL02YP3852	hypothetical protein	702	AAM87448.1	7.172507
38208	B09	NTL02YP1653	putative transmembrane subunit	888	AAM85249.1	5.862069
36405	B10	NTL02YP2735	integration host factor (IHF), beta subunit	285	AAM86331.1	4.861538
36418	B11	NTL02YP3831	hypothetical protein	288	AAM87427.1	6.539634
37047	B12	NTL02YP1652	hypothetical protein	498	AAM5248.1	2
38856	C01	NTL02YP0576	putative oxidoreductase	1149	AAM84172.1	3.267452
37376	C03	NTL02YP0564	regulator for SOS(lexA) regulon	609	AAM84160.1	2

Master Clone List for NR-19280

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39433	C04	NTL02YP3814	ATP-binding component of D-ribose high-affinity transport system	1524	AAM87410.1	2.872123
39545	C05	NTL02YP2736	30S ribosomal subunit protein S1	1674	AAM86332.1	2.229872
39599	C06	NTL02YP2744	hypothetical protein	1776	AAM86340.1	9.814978
39639	C07	NTL02YP2741	hypothetical protein	1869	AAM86337.1	3.337349
39691	C08	NTL02YP3836	glycosyl hydrolase, debranching enzyme	1989	AAM87432.1	5.214884
38491	C09	NTL02YP1623	putative LACI-type transcriptional regulator	993	AAM85219.1	3.493708
36070	C10	NTL02YP1629	hypothetical protein	168	AAM85225.1	2.995192
36356	C11	NTL02YP0527	hypothetical protein	270	AAM84123.1	4.967742
38826	C12	NTL02YP2715	putative outer membrane porin	1131	AAM86311.1	3.399658
38835	D01	NTL02YP0545	hypothetical protein	1137	AAM84141.1	3.316058
38841	D02	NTL02YP3798	hypothetical protein	1137	AAM87394.1	2.938828
39215	D03	NTL02YP1625	putative sugar transporter	1356	AAM85221.1	3.888252
38079	D06	NTL02YP3802	hypothetical protein	843	AAM87398.1	2
36077	D07	NTL02YP0514	hypothetical protein	171	AAM84110.1	1.985782
36346	D08	NTL02YP0496	putative transposase	267	AAM84092.1	5.807818
39041	D09	NTL02YP1588	conserved hypothetical protein	1257	AAM85184.1	4.093292
39136	D10	NTL02YP0494	phosphoribosylglycinamide synthetase	1311	AAM84090.1	3.933383
39151	D11	NTL02YP0504	glutamate-aspartate symport protein	1317	AAM84100.1	4.015475
37999	D12	NTL02YP0056	molybdate-binding periplasmic protein precursor	819	AAM83652.1	3.630966
38008	E01	NTL02YP0053	hypothetical protein	822	AAM83649.1	6.341067
38018	E02	NTL02YP0071	serine acetyltransferase	825	AAM83667.1	3.514451
38059	E03	NTL02YP3175	putative PTS permease protein	837	AAM86771.1	9.255416
38263	E04	NTL02YP3141	putative transcriptional regulator	909	AAM86737.1	6.10432
38264	E05	NTL02YP0025	inner membrane permease of maltose/maltodextran ABC transporter	912	AAM83621.1	6.290966
36095	E06	NTL02YP0062	hypothetical protein	177	AAM83658.1	2.986175
36266	E07	NTL02YP0029	hypothetical protein	237	AAM83625.1	2
36275	E08	NTL02YP0044	hypothetical protein	240	AAM83640.1	1.985714
38573	E09	NTL02YP0057	periplasmic sulfate-binding protein of sulfate/thiosulfate ABC transporter	1023	AAM83653.1	1.508937
36506	E10	NTL02YP3148	hypothetical protein	321	AAM86744.1	3.831025
36615	E11	NTL02YP0028	hypothetical protein	363	AAM83624.1	3.942928
36835	E12	NTL02YP0075	hypothetical protein	435	AAM83671.1	1.978947
36858	F01	NTL02YP3176	hypothetical protein	441	AAM86772.1	1.981289
38851	F02	NTL02YP0480	thiH protein	1146	AAM84076.1	3.477234
38895	F03	NTL02YP3172	putative tagatose-6-phosphate aldose/ketose isomerase	1167	AAM86768.1	3.004971
37055	F05	NTL02YP0049	hypothetical protein	501	AAM83645.1	1.974122
39250	F07	NTL02YP0067	probable sensor protein, histidine protein kinase	1377	AAM83663.1	3.882145
39383	F08	NTL02YP0037	hypothetical protein	1482	AAM83633.1	8.277267
37572	F09	NTL02YP3153	hypothetical protein	669	AAM86749.1	2.799718
37623	F10	NTL02YP0483	thiE protein	690	AAM84079.1	2.805479
37712	F11	NTL02YP0066	transcriptional regulator in 2-component system	723	AAM83662.1	2.757536
38253	F12	NTL02YP3777	dipeptide transport system permease protein 2	903	AAM87373.1	6.103924
39373	G01	NTL02YP0004	hypothetical protein	1467	AAM83600.1	3.743862
39492	G02	NTL02YP3774	periplasmic dipeptide transport protein of ABC transporter	1608	AAM87370.1	3.665049

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37903	G04	NTL02YP1569	putative transcriptional regulator	786	AAM85165.1	6.35109
38036	G05	NTL02YP1565	putative resistance protein	831	AAM85161.1	2.476464
38175	G06	NTL02YP3730	putative AraC-type regulatory protein	876	AAM87326.1	6.779476
36036	G07	NTL02YP1554	hypothetical protein	159	AAM85150.1	3.864322
36163	G08	NTL02YP3737	hypothetical protein	198	AAM87333.1	3
36332	G09	NTL02YP2652	hypothetical protein	261	AAM86248.1	2
36343	G10	NTL02YP3743	putative transposase	264	AAM87339.1	-
36395	G11	NTL02YP1562	hypothetical protein	282	AAM85158.1	6.242236
36503	G12	NTL02YP2673	hypothetical protein	321	AAM86269.1	4.68144
38616	H02	NTL02YP1567	cell division protein	1038	AAM85163.1	3.341373
38644	H03	NTL02YP3733	putative peptidase	1047	AAM87329.1	3.463661
38692	H04	NTL02YP1574	acetyl CoA carboxylase, carboxytransferase component, beta subunit	1071	AAM85170.1	3.942394
36717	H05	NTL02YP0471	preprotein translocase	399	AAM84067.1	1.979499
36757	H06	NTL02YP3729	PTS system fructose-like IIB component 2	408	AAM87325.1	6.082589
36963	H07	NTL02YP2649	hypothetical protein	471	AAM86245.1	1.978474
37027	H09	NTL02YP2665	hypothetical protein	489	AAM86261.1	1.984877
37032	H10	NTL02YP2657	hypothetical protein	492	AAM86253.1	1.994361
37031	H11	NTL02YP1555	hypothetical protein	492	AAM85151.1	1.74812
38995	H12	NTL02YP1564	3-oxoacyl-[acyl-carrier-protein] synthase I	1224	AAM85160.1	3.236551

Table 40: *Yersinia pestis* Gateway® Clone, Plate 41 (UYPWO), NR-19857[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39024	A01	NTL02YP2669	putative hydroxymethylglutar component in transcription antiterminationyl-coenzyme A synthase	1239	AAM86265.1	2.92728694
39085	A02	NTL02YP2671	putative beta-ketoacyl-acp synthase	1284	AAM86267.1	3.95241692
39173	A03	NTL02YP3741	putative methyltransferase	1326	AAM87337.1	3.83235725
37067	A04	NTL02YP2677	hypothetical protein	50 4	AAM86272.1	1.69301471
37184	A06	NTL02YP0472	component in transcription antitermination	546	AAM84068.1	2.8225256
37256	A07	NTL02YP3757	hypothetical protein	567	AAM87353.1	2.73311367
39261	A09	NTL02YP3756	O_2-independent coproporphyrinogen III oxidase	1380	AAM87352.1	6.72887324
39624	A10	NTL02YP3752	putative GTP-binding factor	1824	AAM87348.1	3.15343348
37512	A11	NTL02YP3758	hypothetical protein	651	AAM87354.1	2.78726483
37666	A12	NTL02YP0474	50S ribosomal subunit protein L1	705	AAM84070.1	2.78791946
37721	B01	NTL02YP3740	hypothetical protein	723	AAM87336.1	1.85321101
36138	B02	NTL02YP1531	hypothetical protein	189	AAM85128.1	5.88209607
38844	B04	NTL02YP2624	alcohol dehydrogenase class III formaldehyde dehydrogenase	1140	AAM86220.1	3.36610169
38888	B05	NTL02YP0456	thiolase I	1164	AAM83993.1	3.31893688
37252	B06	NTL02YP1546	disulfide oxidoreductase	567	AAM85142.1	2.82537068
39505	B07	NTL02YP0444	hypothetical protein	1632	AAM84040.1	
39685	B08	NTL02YP1545	cytochrome c-type biogenesis protein	1971	AAM85141.1	3.16260567
37605	B09	NTL02YP3714	putative transcriptional regulator, sorC family	681	AAM87310.1	6.23023578
38205	B10	NTL02YP0428	integral membrane protein, permease	888	AAM84024.1	2.27801724
38234	B11	NTL02YP2588	probably a UDP-gal transferase	894	AAM86184.1	6.30728051

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38318	B12	NTL02YP0433	hypothetical protein	933	AAM84029.1	6.57656732
38385	C01	NTL02YP0432	putative inner membrane permease	957	AAM84028.1	5.43831494
36058	C02	NTL02YP3696	hypothetical protein	162	AAM87292.1	3.85148515
36248	C04	NTL02YP2613	hypothetical protein	228	AAM86210.1	4.82089552
36628	C05	NTL02YP3703	hypothetical protein	366	AAM87299.1	3.34975369
36738	C06	NTL02YP3678	regulator for trp operon and aroH trp	402	AAM87274.1	3.61538462
36878	C07	NTL02YP2611	hypothetical protein	447	AAM86207.1	1.9835729
38623	C08	NTL02YP2592	putative permease for iron transport system	1041	AAM86188.1	3.42090657
38698	C09	NTL02YP0430	ATP-binding component	1074	AAM84026.1	3.48384201
37018	C10	NTL02YP3699	acyltransferase for 30S ribosomal subunit protein S18	486	AAM87295.1	1.98479087
37216	C11	NTL02YP1514	putative fimbrial protein	555	AAM85110.1	2.78991597
37378	C12	NTL02YP1518	putative fimbrial protein	609	AAM85114.1	2.81664099
38924	D01	NTL02YP3686	hypothetical protein	1182	AAM87282.1	3.32651391
39188	D02	NTL02YP1507	hypothetical protein	1338	AAM85103.1	3.59433962
37702	D03	NTL02YP0424	hypothetical protein	720	AAM84020.1	2.78289474
39208	D04	NTL02YP1523	hypothetical protein	1350	AAM85119.1	3.90215827
39267	D05	NTL02YP3687	probable ATP-dependent protease	1383	AAM87283.1	3.84680253
39495	D06	NTL02YP2600	putative membrane protein	1614	AAM86196.1	4.90749698
39673	D09	NTL02YP3679	soluble lytic murein transglycosylase	1950	AAM87275.1	3.38291457
37882	D10	NTL02YP2599	putative iron reductase	780	AAM86195.1	3.64634146
38247	D11	NTL02YP2578	ATP phosphoribosyltransferase	900	AAM86174.1	7.13404255
38299	D12	NTL02YP0380	site-specific recombinase	927	AAM83976.1	6.1540848
36118	E01	NTL02YP1075	hypothetical protein	183	AAM84671.1	4.85650224
38566	E02	NTL02YP1501	solute-binding periplasmic protein for iron ABC transporter	1020	AAM85097.1	1.8990566
39019	E03	NTL02YP1482	putative aminotransferase	1236	AAM85078.1	3.22805643
39823	E04	NTL02YP0931	putative acyl-CoA dehydrogenase	2448	AAM84527.1	3.82073955
39828	E05	NTL02YP3432	putative outer membrane usher protein	2481	AAM87028.1	3.84212614
39845	E06	NTL02YP0900	heat shock protein	2595	AAM84496.1	3.92409867
39696	E07	NTL02YP1890	putative transformylase	2004	AAM85486.1	3.08121331
39720	E08	NTL02YP2044	carbon starvation protein	2067	AAM85640.1	3.36877076
39721	E09	NTL02YP2457	putative oxidoreductase	2067	AAM86053.1	3.72567632
39851	E10	NTL02YP2028	DNA topoisomerase type I, omega protein	2616	AAM85624.1	4.09600904
39854	E11	NTL02YP0344	outer membrane usher protein FIMD precursor	2628	AAM83940.1	2.31896552
39858	E12	NTL02YP0903	hypothetical protein	2643	AAM84499.1	3.53633992
39863	F01	NTL02YP1993	CoA-linked acetaldehyde dehydrogenase	2676	AAM85589.1	3.08946981
39871	F02	NTL02YP1240	sensor for high-affinity potassium transport system	2727	AAM84836.1	2.64799422
39738	F04	NTL02YP2284	hypothetical protein	2112	AAM85880.1	5.21654275
39751	F05	NTL02YP1374	polyphosphate kinase	2151	AAM84970.1	3.01277955
39750	F06	NTL02YP1203	ribonucleoside-diphosphate reductase 2, alpha subunit	2151	AAM84799.1	4.36558649
39759	F07	NTL02YP2541	putative alpha-D-galactosidase	2181	AAM86137.1	3.02431337
39883	F08	NTL02YP0189	putative toxin subunit	2859	AAM83785.1	11.5001725
39887	F09	NTL02YP3477	adenylylating enzyme for glutamine synthetase	2883	AAM87073.1	14.0920287
39892	F10	NTL02YP3608	probable ATP-dependent RNA helicase	2907	AAM87204.1	3.27451646
39766	F11	NTL02YP0294	primosomal protein N	2199	AAM83890.1	3.2907548
39774	F12	NTL02YP3383	hypothetical protein	2226	AAM86979.1	3.05516328

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39775	G01	NTL02YP0802	(p)ppGpp synthetase I (GTP pyrophosphokinase)	2235	AAM84398.1	3.5221978
39779	G02	NTL02YP0859	catalase hydroperoxidase HPI(I)	2256	AAM84455.1	3.72430314
39800	G04	NTL02YP3620	hypothetical protein	2349	AAM87214.1	3.92967769
39805	G05	NTL02YP3607	DNA polymerase II	2370	AAM87203.1	3.46307054
39812	G06	NTL02YP1880	phenylalanine tRNA synthetase, beta-subunit	2388	AAM85476.1	3.70181219
39817	G07	NTL02YP4056	DNA gyrase subunit B, type II topoisomerase	2418	AAM87652.1	3.53254679
39837	G08	NTL02YP3893	nitrite reductase (NAD(P)H) subunit	2547	AAM87489.1	3.8971782
39717	G10	NTL02YP3896	hypothetical protein	2061	AAM87492.1	2.94145645
39718	G11	NTL02YP4044	alpha-amylase	2064	AAM87640.1	3.32224335
39840	G12	NTL02YP3813	hypothetical protein	2556	AAM87409.1	7.11325116
39841	H01	NTL02YP0589	hypothetical protein	2571	AAM84185.1	3.30141708
39843	H02	NTL02YP1165	leucine tRNA synthetase	2583	AAM84761.1	7.91955776
39846	H03	NTL02YP0762	aconitate hydrase B	2598	AAM84358.1	3.37642153
39736	H04	NTL02YP0101	(p)ppGpp synthetase II	2109	AAM83697.1	4.58026989
39749	H05	NTL02YP3870	putative dehydrogenase	2148	AAM87466.1	4.49040219
39755	H06	NTL02YP3301	ornithine decarboxylase isozyme	2163	AAM86897.1	3.40944167
39865	H07	NTL02YP0680	protein chain initiation factor IF-2	2679	AAM84276.1	2.35711659
39884	H08	NTL02YP2926	sensor for capsule biosynthesis	2874	AAM86522.1	4.28483185
39757	H09	NTL02YP1798	sensory transducer kinase	2172	AAM85394.1	3.44846293
39760	H10	NTL02YP2937	probably ATP-dependent helicase	2181	AAM86533.1	3.44394417
39769	H12	NTL02YP1112	hypothetical protein	2208	AAM84708.1	3.53291815

Table 41: *Yersinia pestis* Gateway® Clone, Plate 42 (UYPWP), NR-19858[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39770	A01	NTL02YP0686	polynucleotide phosphorylase	2214	AAM84282.1	3.490239574
39773	A03	NTL02YP3314	hypothetical protein	2223	AAM86910.1	3.641184269
39784	A04	NTL02YP2764	ATP-binding component of serine protease	2283	AAM86360.1	3.999139044
39788	A05	NTL02YP2734	hypothetical protein	2292	AAM86330.1	4.018439108
39801	A06	NTL02YP2746	formate acetyltransferase 1	2355	AAM86342.1	3.986221294
39722	A07	NTL02YP3746	hypothetical protein	2067	AAM87342.1	3.591362126
39744	A10	NTL02YP3136	putative reductase	2127	AAM86732.1	
39747	A11	NTL02YP2688	hypothetical protein	2139	AAM86284.1	3.294630564
39752	A12	NTL02YP1593	phosphotransacetylase	2154	AAM85189.1	4.318140383
39754	B01	NTL02YP2651	hypothetical protein	2163	AAM86246.1	6.816613709
39758	B02	NTL02YP3135	2-acyl-glycerophospho-ethanolamine acyltransferase	2178	AAM86731.1	3.663210099
36634	B03	NTL02YP1032	hypothetical protein	369	AAM84628.1	1.985330073
39777	B04	NTL02YP3127	PTS system enzyme I	2247	AAM86723.1	3.516834281
39780	B05	NTL02YP2590	putative outer membrane iron/siderophore receptor	2262	AAM86186.1	3.689834926
39813	B06	NTL02YP3081	hypothetical protein	2388	AAM86677.1	3.059719934
37118	B07	NTL02YP1029	glycoprotein/polysaccharide metabolism	522	AAM84625.1	2
37156	B08	NTL02YP1041	putative primosomal replication protein N	537	AAM84637.1	2.833622184
37288	B09	NTL02YP1009	putative polymerase/proteinase	579	AAM84605.1	2.79644588
37370	B10	NTL02YP1047	recombination and repair protein	606	AAM84643.1	2.815789474

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
39819	B11	NTL02YP2675	putative oxidoreductase	2430	AAM86271.1	3.642510121
39873	C01	NTL02YP3093	protein PII	2739	AAM86689.1	12.79057215
39874	C02	NTL02YP1608	NADH dehydrogenase I chain G	2745	AAM85204.1	11.18707361
38010	C03	NTL02YP1021	hypothetical protein	822	AAM84617.1	2.629930394
38937	C04	NTL02YP1035	acridine efflux pump	1188	AAM84631.1	3.060260586
39877	C05	NTL02YP3760	DNA polymerase I	2799	AAM87356.1	3.536456499
39889	C06	NTL02YP3119	protease III	2889	AAM86715.1	7.498463639
39565	C08	NTL02YP1020	hypothetical protein	1704	AAM84616.1	4.732224771
39645	C09	NTL02YP1016	putative protease maturation protein	1887	AAM84612.1	3.334717177
39704	C10	NTL02YP2605	methionine tRNA synthetase	2028	AAM86201.1	3.831237911
37559	C11	NTL02YPD0034	unknown	663	NP_857818.1	2.603129445
35985	C12	NTL02YPA0092	hypothetical protein	147	NP_955509.1	1.983957219
38680	D03	NTL02YPA0044	replication protein A	1065	NP_857678.1	3.40361991
39471	D04	NTL02YPA0029	hypothetical protein	1560	NP_857667.2	3.754375
39666	D05	NTL02YPA0038	exonuclease	1929	NP_857675.2	3.241239208
39804	D06	NTL02YPA0061	porphyrin biosynthetic enzyme	2367	NP_857691.2	4.007893644
39830	D07	NTL02YPA0066	F1 capsule protein	2502	NP_857693.1	3.833202203
39896	D08	NTL02YP1902	putative oxidase	3057	AAM85498.1	3.882789797
39897	D09	NTL02YP1360	hypothetical protein	3075	AAM84956.1	3.84847512
39906	D10	NTL02YP1361	hypothetical protein	3159	AAM84957.1	3.466395749
39913	D11	NTL02YP3520	hypothetical protein	3354	AAM87116.1	3.954331173
39901	D12	NTL02YP3347	integral transmembrane protein	3120	AAM86943.1	3.823101266
39911	E03	NTL02YP3794	putative autotransporter protein	3255	AAM87390.1	4.628528073
39912	E04	NTL02YP1695	hypothetical protein	3288	AAM85291.1	6.932992788
39929	E05	NTL02YP3118	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit	3726	AAM86714.1	3.157727031
39938	E06	NTL02YP0477	RNA polymerase, beta subunit	4029	AAM84073.1	6.707790612
39945	E08	NTL02YP0126	glutamate synthase, large subunit	4608	AAM83722.1	3.717082616
39622	E09	NTL02YP0310	secretion ATPase, Type I secretion system	1824	AAM83906.1	3.086909871
37390	E10	NTL02YP3659	hypothetical protein	612	AAM87255.1	2.36809816
35996	E11	NTL02YP2015	hypothetical protein	150	AAM85611.1	3.789473684
38445	E12	NTL02YP0898	suppressor of ftsH mutation	978	AAM84494.1	8.431237721
36439	F01	NTL02YP2528	hypothetical protein	297	AAM86124.1	3
38257	F02	NTL02YP2433	hypothetical protein	906	AAM86029.1	4.901691332
36321	F03	NTL02YP1463	phosphocarrier protein HPr	258	AAM85059.1	4.986577181
36063	F04	NTL02YP2431	hypothetical protein	165	AAM86027.1	2.83902439
36889	F06	NTL02YP2009	hypothetical protein	450	AAM85605.1	1.93877551
36075	F07	NTL02YP3545	hypothetical protein	168	AAM87142.1	2
35946	F08	NTL02YP0198	hypothetical protein	120	AAM83794.1	2
36158	F11	NTL02YP0260	hypothetical protein	198	AAM83856.1	1.907563025
35972	G01	NTL02YP2422	hypothetical protein	135	AAM86018.1	2.942857143
36039	G02	NTL02YP2461	hypothetical protein	159	AAM86057.1	1.658291457
36096	G03	NTL02YP0257	hypothetical protein	177	AAM83853.1	5.935483871
36129	G04	NTL02YP0872	carbon storage regulator	186	AAM84468.1	2
36461	G05	NTL02YP0838	hypothetical protein	306	AAM84434.1	3.979768786
36199	G06	NTL02YP1994	hypothetical protein	210	AAM85590.1	1.988
36335	G07	NTL02YP3069	hypothetical protein	261	AAM86665.1	2.956810631
38080	G08	NTL02YP0292	essential cell division protein	846	AAM83888.1	5.865688488
35967	G09	NTL02YP2005	hypothetical protein	129	AAM85601.1	-
36220	G10	NTL02YP3487	30S ribosomal subunit protein S21	216	AAM87083.1	4.78125
38473	G12	NTL02YP0125	hypothetical protein	990	AAM83721.1	7.024271845

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
36668	H01	NTL02YP1924	hypothetical protein	381	AAM85520.1	2.800475059
35943	H03	NTL02YP2277	hypothetical protein	117	AAM85874.1	-
39192	H04	NTL02YP0867	permease of major facilitator superfamily	1341	AAM84463.1	2.594496741
36228	H05	NTL02YP2941	hypothetical protein	219	AAM86537.1	2.648648649
38634	H07	NTL02YP3416	hypothetical protein	1044	AAM87012.1	3.061808118
36099	H08	NTL02YP1215	hypothetical protein	177	AAM84811.1	4.774193548
36140	H10	NTL02YP2283	hypothetical protein	189	AAM85879.1	2
36213	H11	NTL02YP1873	hypothetical protein	213	AAM85469.1	2
38949	H12	NTL02YP4000	putative integrase	1194	AAM87596.1	3.094003241

Table 42: *Yersinia pestis* Gateway® Clone, Plate 43 (UYPWQ), NR-19859[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
35971	A01	NTL02YP0825	hypothetical protein	135	AAM84421.1	-
35940	A02	NTL02YP2371	hypothetical protein	114	AAM85967.1	1.974025974
38955	A03	NTL02YP0750	putative integral membrane protein	1200	AAM84346.1	2.397580645
37747	A04	NTL02YP1804	hypothetical protein	732	AAM85400.1	2
36111	A05	NTL02YP3457	hypothetical protein	180	AAM87053.1	3.872727273
35949	A09	NTL02YP1815	hypothetical protein	120	AAM85411.1	2
36097	A10	NTL02YP0693	hypothetical protein	177	AAM84289.1	3.847926267
36068	A11	NTL02YP0712	hypothetical protein	168	AAM84308.1	2
36110	A12	NTL02YP3333	hypothetical protein	180	AAM86929.1	2.659090909
35930	B01	NTL02YP1746	hypothetical protein	105	AAM85343.1	-
35936	B02	NTL02YP1094	hypothetical protein	114	AAM84690.1	-
35966	B03	NTL02YP1755	hypothetical protein	129	AAM85351.1	2
35950	B04	NTL02YP2805	hypothetical protein	120	AAM86401.1	-
36198	B05	NTL02YP1811	hypothetical protein	210	AAM85408.1	-
35934	B06	NTL02YP3883	hypothetical protein	108	AAM87480.1	1.959459459
35962	B07	NTL02YP3223	hypothetical protein	126	AAM86819.1	2
35968	B08	NTL02YP1678	hypothetical protein	132	AAM85274.1	1.936046512
38890	B09	NTL02YP0708	hypothetical protein	1167	AAM84304.1	2.633802817
36333	B10	NTL02YP2878	hypothetical protein	261	AAM86474.1	3.857142857
39084	B11	NTL02YP1795	lateral flagellar motor protein	1284	AAM85391.1	3.879154079
36025	B12	NTL02YP2797	flagellar hook-length control protein	196	AAM86038.1	2
35995	C01	NTL02YP1780	hypothetical protein	150	AAM85376.1	2.731578947
38032	C03	NTL02YP3112	putative enzyme	828	AAM86708.1	10.54493088
36331	C04	NTL02YP2650	hypothetical protein	261	AAM86247.1	3.940199336
37005	C05	NTL02YP1504	hypothetical protein	483	AAM85100.1	2.992351816
36115	C06	NTL02YP0463	hypothetical protein	183	AAM84060.1	2.977578475
36417	C07	NTL02YP3738	hypothetical protein	288	AAM87334.1	4.951219512
36126	C09	NTL02YP3114	hypothetical protein	183	AAM86710.1	2
39826	C10	NTL02YP0853	anaerobic dimethyl sulfoxide reductase subunit A	2472	AAM84449.1	3.750398089
39803	C11	NTL02YP3343	hypothetical protein	2367	AAM86939.1	3.982135438
35953	C12	NTL02YP0060	putative transposase	123	AAM83656.1	-
35928	D01	NTL02YP1495	hypothetical protein	105	AAM85091.1	1.951724138
39636	D03	NTL02YP2719	putative amidase	1857	AAM86315.1	7.709541381
36369	D05	NTL02YP0407	hypothetical protein	273	AAM84003.1	5.837060703
36131	D06	NTL02YP1620	hypothetical protein	186	AAM85216.1	2.845132743
36083	D07	NTL02YP2760	hypothetical protein	171	AAM86356.1	-

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
38379	D08	NTL02YP0434	regulator for metE and metH	954	AAM84030.1	7.28470825
39867	D09	NTL02YP1975	hypothetical protein	2697	AAM85571.1	3.704420899
37148	D10	NTL02YP3159	hypothetical protein	534	AAM86755.1	2.796167247
36156	D11	NTL02YP3744	hypothetical protein	195	AAM87340.1	3.919148936
36006	D12	NTL02YP3715	hypothetical protein	150	AAM87311.1	2
37268	E01	NTL02YPD0010	unknown	570	NP_857794.1	2.954098361
39522	E03	NTL02YP1454	putative NADH oxidase	1647	AAM85050.1	9.998221695
39368	E04	NTL02YP0313	putative pyridine nucleotide-disulphide oxidoreductase	1464	AAM83909.1	4.95212766
36067	E06	NTL02YP0089	50S ribosomal subunit protein L33	168	AAM83685.1	3.9375
38225	E07	NTL02YP2940	putative transmembrane protein	891	AAM86536.1	5.216970999
39554	E08	NTL02YP3366	hypothetical protein	1689	AAM86962.1	5.327356854
39559	E09	NTL02YP2248	sulfate transporter	1698	AAM85844.1	6.859033372
39903	E10	NTL02YP1415	putative efflux pump	3132	AAM85011.1	5.195775536
39847	E12	NTL02YP0271	heat shock protein	2604	AAM83867.1	14.14447806
39860	F01	NTL02YP1834	hypothetical protein	2658	AAM85430.1	13.25277984
35973	F02	NTL02YP3015	hypothetical protein	135	AAM86611.1	1.977142857
36114	F03	NTL02YP4021	hypothetical protein	180	AAM87617.1	1.995454545
36286	F04	NTL02YP2911	putative virulence protein	243	AAM86507.1	2.96819788
36062	F05	NTL02YP1768	hypothetical protein	165	AAM85364.1	2.931707317
36809	F06	NTL02YP0709	hypothetical protein	426	AAM84305.1	4.798283262
37442	F08	NTL02YP2696	beta-hydroxydecanoyl thioester dehydrase	627	AAM86292.1	5.203898051
37876	F10	NTL02YP2387	putative transposase	777	AAM85983.1	3.982864137
36382	F11	NTL02YP1872	hypothetical protein	276	AAM85468.1	1.996835443
39115	F12	NTL02YP1319	putative peptidase	1299	AAM84915.1	7.060492905
36256	G01	NTL02YP1095	hypothetical protein	234	AAM84691.1	2.901459854
36491	G02	NTL02YP1161	hypothetical protein	318	AAM84757.1	3.762569832
36142	G03	NTL02YP2880	hypothetical protein	189	AAM86476.1	2.794759825

Table 43: *Yersinia pestis* Gateway® Clone, Plate 44 (UYPWR), NR-19860[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
37225	A02	NTL02YP1310	hypothetical protein	558	AAM84906.1	7.97993311
36374	A03	NTL02YP2390	hypothetical protein	273	AAM85986.1	5.750798722
36078	A06	NTL02YP0996	hypothetical protein	171	AAM84592.1	6.142180095
36763	A07	NTL02YP2574	hypothetical protein	411	AAM86170.1	7.982261641
37098	A08	NTL02YP0989	phosphatidylglycerophosphatase	513	AAM84585.1	2
39270	A11	NTL02YP4081	membrane-bound ATP synthase, F1 sector, beta-subunit	1383	AAM87677.1	1.218552354
38606	B01	NTL02YP0979	protein secretion, membrane protein	1035	AAM84575.1	6.48372093
37701	B02	NTL02YP3673	negative response regulator of genes in aerobic	717	AAM87269.1	6.188903567
38470	B03	NTL02YP4007	hypothetical protein	987	AAM87603.1	16.27458617
36154	B07	NTL02YP2562	hypothetical protein	195	AAM86158.1	3.914893617
39143	B08	NTL02YP0704	solute-binding periplasmic protein of ABC transporter	1314	AAM84300.1	20.70605613

[1] All information in this table was provided by J. Craig Venter Institute at the time of deposition. Please note that the locus tags have since been updated by JCVI and the corrected locus ID numbers can be obtained from the JCVI-CMR webpage using the locus search option and inputting the above locus IDs.

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