Dowdell 2016 Table S1. Oligonucleotide primers used for B. burgdorferi B31 lipoprotein amplification.

TIGR ORF	GenBank Genome Coordinates	Genome Locus	Plasmid	Fwd Cloning Primer	Sequence (5' to 3')	Length (bp)	Ta (°C)	Rev Cloning Primer	Sequence (5' to 3')	Length (bp)	Ta (°C)	PCR Expression Amplicon (bp)	PCR Screen Amplicon (bp)	Start Codon/ORF Modification	PCR and Cloning Specifics/Comments
BB_0028	AE000783.1:26399..27448	C	pSC1015	BB0028-fwd	ACCTGCATATGAAACAAAAATACGAAAAC	29	53	BB0028-rev	ATCAGCCCGGGTTCTTTAGTTAATTTTCTGTTTTC	35	54	1066	1186		
BB_0141	AE000783.1:141979..142935	C	pSC1024	BB0141-fwd	ACCTGCATATGAATTTGATTTTTAATATTAATTTAT	36	52	BB0141-rev	ATCAGCCCGGGAATATTGCTTTCGGCTG	28	54	970	1090	LM to M	43°C Ta, 39 cycles
BB_0144	AE000783.1:144586..145458	C	pSC1021	BB0144-fwd	ACCTGCATATGTATAAATTATTTTTATTTTTTTATTAT	37	50	BB0144-rev	ATCAGCCCGGGATCAAATAAGGTCTTATATTTTTC	35	52	889	1009		44°C Ta, 39 cycles
BB_0155	AE000783.1:156462..157598	C	pSC1035	BB0155-fwd	ACCTGCATATGAAAAAACACTATAAAGCTC	30	54	BB0155-rev	ATCAGCCCGGGTAATTTTAATAATGCATTTAAATTCC	37	53	1153	1273		
BB_0158	AE000783.1:158628..159344	C	pSC1037	BB0158-fwd	ACCTGCATATGGTATTTAGAACATATAAAC	30	51	BB0158-rev	ATCAGCCCGGGTATATCTTCAAATAAATCTCCAG	34	53	733	853		
BB_0171	AE000783.1:173529..174116	C	pSC1048	BB0171-fwd	ACCTGCATATGGGACGAAACTTTTTAG	27	54	BB0171-rev	ATCAGCCCGGGCCAATCTTCTTTTGGAACAG	31	56	604	724	V to M	
BB_0193	AE000783.1:190719..191459	C	pSC1041	BB0193-fwd	ACCTGCATATGTCTGGCCCTAAAAAAC	27	57	BB0193-rev	ATCAGCCCGGGTTGTTTATAAATGTTAAATTCATATTG	38	54	757	877		
BB_0213	AE000783.1:218425..219078	C	pSC1047	BB0213-fwd	ACCTGCATATGCAGAGCGGATTAAA	25	55	BB0213-rev	ATCAGCCCGGGGCCAACTTTAAAAAAAAGATT	32	53	670	790		
BB_0215	AE000783.1:219797..220639	C	pSC1030	BB0215-fwd	ACCTGCATATGAAAAAAGTTATTATCTTAATTTT	34	52	BB0215-rev	ATCAGCCCGGGTGTTTTTATCCCTAAAAAGC	31	53	856	976	LM to M	
BB_0224	AE000783.1:228864..229148	C	pSC1045	BB0224-fwd	ACCTGCATATGCCTGGAAGAAAGG	24	54	BB0224-rev	ATCAGCCCGGGATTGTATTGGTAATTAAAGCA	32	53	301	421		
BB_0227	AE000783.1:231621..232322	C	pSC1027	BB0227-fwd	ACCTGCATATGCTAAATCCAAGAACAA	27	54	BB0227-rev	ATCAGCCCGGGTTTTACAAATTGTGCTATTTC	32	52	718	838		
BB_0298	AE000783.1:306625..307317	C	pSC1029	BB0298-fwd	ACCTGCATATGAAAATTTTGTGGTTAATAA	30	52	BB0298-rev	ATCAGCCCGGGCTTCAAATTACTCATGATCC	31	53	709	829		
BB_0323	AE000783.1:328032..329165	C	pSC1032	BB0323-fwd	TGAATATAAAGAATAAATTAATATCGC	27	54	BB0323-rev	ATCAGCCCGGGTTTGGCAGGAATTATTATCTTC	33	56	1141	1261		Fwd-blunt primer
BB_0324	AE000783.1:329262..329621	C	pSC1019	BB0324-fwd	ACCTGCATATGAAAAAGCTAATATTACTAAAC	32	53	BB0324-rev	ATCAGCCCGGGTTTTTTATTATATTTTCTATTTTATTTAAT	39	50	376	496		
BB_0328	AE000783.1:334919..336508	C	pSC1004	BB0328-2-fwd	ACCTGCATATGAAATATATAAAAATAGCCTTAATGC	36	57	BB0328-rev	ATCAGCCCGGGTTTTTTAGTTTTAATATCTTCATATAAAT	40	53	1588	1708		
BB_0329	AE000783.1:336629..338215	C	pSC1006	BB0329-fwd	ACCTGCATATGAAATTACAAAGGTCATTATTTTTA	35	56	BB0329-rev	ATCAGCCCGGGTTTATTTTTTAATTTTAGCTGAGATA	37	53	1603	1723		
BB_0330	AE000783.1:338358..339983	C	pSC1007	BB0330-fwd	ACCTGCATATGAGCTTTAATAAAACTAAAAAAATC	35	56	BB0330-rev	ATCAGCCCGGGATTATGTTTTGCATTTTTAATTGG	35	55	1642	1762		
BB_0352	AE000783.1:361188..362321	C	LP50N	BB0352_2_fwd	AGCTCGGTACCCTAAACATAGAAAGTATAAAATCAAATAAAC	42	60	BB0352_2_rev	TGAGCCCCCGGGATTTTTATTTTTTTTTAGATTATTAGCTTTAG	44	61	1304	1424		Cloned using native promoter (~150bp upstream of ATG codon)
BB_0365	AE000783.1:373567..374151	C	pSC1001	BB0365-fwd	ACCTGCATATGTATAAAAATGGTTTTTTTAAAAAC	35	55	BB0365-rev	ATCAGCCCGGGATTCGTTAACATAGGTGAAATTTT	35	57	601	721		
BB_0382	AE000783.1:391932..392957	C	pSC1022	BB0382-fwd	ACCTGCATATGAGAATTGTAATTTTTATATTCG	33	54	BB0382-rev	ATCAGCCCGGGTAACTTTAATATTTGTTTTATAAAAAT	38	51	1042	1162		
BB_0384	AE000783.1:394105..395166	C	pSC1036	BB0384-fwd	ACCTGCATATGTTTAAAAGATTTATTTTTATTAC	34	51	BB0384-rev	ATCAGCCCGGGTAACTTTGATTTAAATAAATCAAATG	37	53	1078	1198	L to M	
BB_0385	AE000783.1:395481..396563	C	pSC1031	BB0385-fwd	ACCTGCATATGTATTATGAGATCTATTTTTTG	32	52	BB0385-rev	ATCAGCCCGGGATTTTCCATTTGCAAAACA	30	53	1099	1219	V to M	
BB_0398	AE000783.1:409416..410447	C	pSC1034	BB0398-fwd	ACCTGCATATGAATCTATTGGTCAAAATTG	30	54	BB0398-rev	ATCAGCCCGGGTTTTTTACCTAAATACACGC	31	53	1048	1168		
BB_0456	AE000783.1:475606..476211	C	pSC1049	BB0456-fwd	ACCTGCATATGAAGCAAAAATTAAGTTG	28	52	BB0456-rev	ATCAGCCCGGGAATTCCAGGCGATAAAAC	29	54	622	742		
BB_0460	AE000783.1:481344..482057	C	pSC1028	BB0460-fwd	ACCTGCATATGAAAACTAGAATAATCATTTTTC	33	53	BB0460-rev	ATCAGCCCGGGAGACTGAGAGTGAAGG	27	52	730	850	V to M	
BB_0475	AE000783.1:494150..494542	C	pSC1046	BB0475-fwd	ACCTGCATATGATGAAAGCTCAAAAATTTA	30	54	BB0475-rev	ATCAGCCCGGGTTGTTTTTCAAAAATGTATAATG	34	52	409	529		
BB_0536	AE000783.1:544586..547387	C	pSC1044	BB0536-fwd	TGAATTATCAAAGAATTAAGAATTATTG	28	55	BB0536-rev	ATCAGCCCGGGTTCAGGTATTAGCAATATTTCTG	34	56	2809	2929		Fwd-blunt primer
BB_0542	AE000783.1:552440..553018	C	pSC1026	BB0542-fwd	ACCTGCATATGGATAATTTAAATAGTATAAATAGT	35	52	BB0542-rev	ATCAGCCCGGGACTCTTAAGAATAGAAGAAAC	32	52	595	715	L to M	
BB_0628	AE000783.1:658898..659623	C	pSC1023	BB0628-fwd	ACCTGCATATGAGAAAGTGTTTTGTTAG	28	53	BB0628-rev	ATCAGCCCGGGATAAACTAATCTAAGTTTTATTGG	35	52	742	862		
BB_0652	AE000783.1:690885..692645	C	pSC1043	BB0652-fwd	ACCTGCATATGAAAAAAGGATCTAAGC	27	52	BB0652-rev	ATCAGCCCGGGATTACTCTTTGCATATTTTGAAC	34	55	1777	1897		
BB_0664	AE000783.1:702283..702966	C	pSC1033	BB0664-fwd	ATAATCATATGTTACATAATACAATGC	27	56	BB0664-rev	ATCAGCCCGGGTTGGGCTTTGATTTCTTG	29	55	700	820		
BB_0689	AE000783.1:730632..731099	C	pSC1016	BB0689-fwd	ACCTGCATATGAAAAAATTGATTATAATTTTTAC	34	52	BB0689-rev	ATCAGCCCGGGATTCTTATATTTTCTTTTTCCAA	34	52	484	604		
BB_0758	AE000783.1:800996..801778	C	pSC1039	BB0758-fwd	ACCTGCATATGCTGCAAAAAAGTATGG	27	55	BB0758-rev	ATCAGCCCGGGATTGATAACTATTTTTTGAGG	32	51	799	919	V to M	
BB_0806	AE000783.1:850994..852514	C	pSC1038	BB0806-fwd	TGAAATTTGTTTTGAATAATTTATTTAAAG	30	56	BB0806-rev	ATCAGCCCGGGTAACTGTTTTTTAATATTTTCATC	35	52	1528	1648		Fwd-blunt primer
BB_0823	AE000783.1:867743..868114	C	pSC1042	BB0823-fwd	ACCTGCATATGAATACAAAAACATTATATTTAATA	35	52	BB0823-rev	ATCAGCCCGGGTTTAGAATGATCAATTATTAAATTG	36	52	388	508		
BB_0832	AE000783.1:880267..881091	C	pSC1020	BB0832-fwd	ACCTGCATATGTTAAAAACATTAACAAAAATA	32	52	BB0832-rev	ATCAGCCCGGGGGTTTGAATATTTGAAGCTAG	32	54	841	961		
BB_0844	AE000783.1:903929..904900	C	pSC1040	BB0844-fwd	ACCTGCATATGAAAAAAAAAAATTTATCAATTTAC	35	53	BB0844-rev	ATCAGCCCGGGTTTACTCGTCTCTAAAAAATC	32	53	988	1108		
BB_A03	AE000790.1:1397..1906	lp54	pSC1066	BBA03-fwd	ACCTGCATATGAAAAAAACGATTATTGTATT	31	52	BBA03-rev	ATCAGCCCGGGTATAGTGTCTTTAAGTTTATTAAGT	36	53	526	646	L to M	
BB_A04	AE000790.1:1981..2829	lp54	pSC1059	BBA04-fwd	ACCTGCATATGAAAAGAGTCATTGTATCC	29	54	BBA04-rev	ATCAGCCCGGGGTTAATTAACGAATTAAATGC	32	51	865	985	I to M	
BB_A05	AE000790.1:2939..4192	lp54	pSC1056	BBA05-fwd	ACCTGCATATGAATAAAATAGGAATTGCAT	30	53	BBA05-rev	ATCAGCCCGGGACGCCTGCTAATCTCTTTTA	31	58	1270	1390		
BB_A07	AE000790.1:4603..5091	lp54	pSC1061	BBA07-fwd	ACCTGCATATGTGTGGGAGACGTATG	26	57	BBA07-rev	ATCAGCCCGGGAAACGAAGCAGATGCATC	29	57	505	625	V to M	
BB_A14	AE000790.1:8793..9158	lp54	pSC1068	BBA14-fwd	ACCTGCATATGCAAATTAAAAATTTCCCC	29	54	BBA14-rev	ATCAGCCCGGGAGGTATATTTTTTGAGTATTTTTTG	36	54	382	502	L to M	
BB_A15	lp54/AE000790.1:9393..10214	lp54	pSC1000										958		described in Schulze RJ *et al* **Mol Microbiol** (2010)
BB_A16	lp54/AE000790.1:10224..11114	lp54	pSC1009	BBA16-fwd	ACCTGCATATGAGATTATTAATAGGATTTGC	31	54	BBA16-rev	ATCAGCCCGGGTTTTAAAGCGTTTTTAAGCTC	32	55	907	1027	Fixed internal stop codon to restore full-length B31 OspB (trunc. in B31-A3)	
BB_A24	lp54/AE000790.1:15937..16512	lp54	pSC1008	BBA24-fwd	ACCTGCATATGATTAAATGTAATAATAAAACTTTT	35	53	BBA24-rev	ATCAGCCCGGGGTTATTTTTGCATTTTTCATCAG	34	55	592	712		
BB_A32	AE000790.1:20654..20848	lp54	pSC1065	BBA32-fwd	ACCTGCATATGAGAATTACCGGTCTTC	27	55	BBA32-rev	ATCAGCCCGGGAAGCTTTCTGTTTCTACG	29	54	211	331		
BB_A33	AE000790.1:21023..21562	lp54	pSC1054	BBA33-fwd	ACCTGCATATGAAGAGATATATTTATGTATATATC	35	52	BBA33-rev	ATCAGCCCGGGTTTTTGAATTAGTGCTAAAGC	32	54	556	676		
BB_A34	AE000790.1:21620..23209	lp54	pSC1055	BBA34-fwd	ACCTGCATATGATAATAAAAAAAAGAGGAC	30	52	BBA34-rev	ATCAGCCCGGGTTCTTCTATAGGTTTTATTTCTG	34	53	1606	1726		
BB_A36	AE000790.1:23710..24351	lp54	pSC1063	BBA36-fwd	ACCTGCATATGATGCAAAGGATAAGTATT	29	53	BBA36-rev	ATCAGCCCGGGAACATTTCCATAATTTTTCAAA	33	52	658	778	L to M	
BB_A57	AE000790.1:38097..39341	lp54	pSC1053	BBA57-fwd	ACCTGCATATGAACGGCAAGCTTAG	25	55	BBA57-rev	ATCAGCCCGGGTTGATAATTTTTTTCTACCAATAA	35	53	1261	1381	L to M	
BB_A59	AE000790.1:39809..40048	lp54	pSC1057	BBA59-fwd	ACCTGCATATGGTTAAAAAAATAATATTTATTTC	34	51	BBA59-rev	ATCAGCCCGGGATTGCTCTGCTCACTCTC	29	58	256	376		
BB_A62	AE000790.1:42203..42409	lp54	pSC1052	BBA62-fwd	ACCTGCATATGACAAAATTAATGTACGC	28	54	BBA62-rev	ATCAGCCCGGGCTTTTTCATTGACTTTGTC	30	52	223	343		
BB_A64	AE000790.1:42560..43483	lp54	pSC1060	BBA64-fwd	ACCTGCATATGAAGGATAACATTTTGAAA	29	52	BBA64-rev	ATCAGCCCGGGCTGAATTGGAGCAAGAATA	30	54	940	1060	I to M	
BB_A65	AE000790.1:43621..44469	lp54	pSC1064	BBA65-fwd	ACCTGCATATGAATAAAATAAAATTATCAATATTAAT	37	51	BBA65-rev	ATCAGCCCGGGATTATTATTAAATTTAAATAATGTGTC	38	51	865	985	L to M	
BB_A68	AE000790.1:46409..47164	lp54	pSC1062	BBA68-fwd	ACCTGCATATGAAAAAAGCCAAACTAAATAT	31	54	BBA68-rev	ATCAGCCCGGGGTAAAAGGCAGGTTTTAAAG	31	54	772	892	L to M	
BB_A69	AE000790.1:47412..48203	lp54	pSC1058	BBA69-fwd (=BBA68-fwd)	ACCTGCATATGAAAAAAGCCAAACTAAATAT	31	54	BBA69-rev	ATCAGCCCGGGATAAAAGGCAGATTGTAAAG	31	53	808	928	L to M	
BB_A72	AE000790.1:49789..50031	lp54	pSC1067	BBA72-fwd	ACCTGCATATGCATAAGGAGAGTGTT	26	54	BBA72-rev	ATCAGCCCGGGTTCATTTTTCTGATCTTTTAAC	33	52	259	379		
BB_B08	AE000792.1:5888..6517	cp26	pSC1014	BBB08-fwd	ACCTGCATATGAAAAAAAAGTTTAATTTTATTTTTC	36	54	BBB08-rev	ATCAGCCCGGGTTGTAAAAATTTTTCAATTGC	32	52	646	766		44°C Ta, 39 cycles
BB_B09	AE000792.1:6677..7714	cp26	pSC1051	BBB09-fwd	ACCTGCATATGAAATACCTTAAAAACATTTC	31	53	BBB09-rev	ATCAGCCCGGGAAATTTATGCCTACTTGATTG	32	54	1054	1174		
BB_B16	cp26/AE000792.1:12014..13606	cp26	LP3N	BBB16_2_fwd	AGCTCGGTACCAGATCAATTATTTTGCTTATTTAATG	37	59	BBB16_2_rev	TGAGCCCCCGGGTTTAATTGGTTTTATTTCAGAT	34	63	1763	1883		Cloned using native promoter (~150bp upstream of ATG codon)
BB_B19	cp26/AE000792.1:16903..17535	cp26	pSC1002	BBB19-fwd	ACCTGCATATGAAAAAGAATACATTAAGTGC	31	55	BBB19-rev	ATCAGCCCGGGAGGTTTTTTTGGACTTTCTGC	32	59	649	769		
BB_B25	AE000792.1:21339..21851	cp26	pSC1025	BBB25-fwd	ACCTGCATATGAAATACTGTTTTTCTTTG	29	52	BBB25-rev	ATCAGCCCGGGTAAAATTTTGTTTTTAAATGCAT	34	52	529	649		
BB_B27	AE000792.1:22603..23154	cp26	pSC1018	BBB27-fwd	ACCTGCATATGAAGAAGTTTTTAATATCCG	30	54	BBB27-rev	ATCAGCCCGGGAGTTAAAAACTTTTGAGTATATAT	36	52	568	688		
BB_C10	AE000791.1:6281..6808	cp9	pSC1087	BBC10-fwd	ACCTGCATATGCAAAAAATAAACATAGC	28	52	BBC10-rev	ATCAGCCCGGGATCTTCTTCAAGATATTTTATTATAC	37	53	544	664		
BB_D10	AE000793.1:5876..6454	lp17	pSC1088	BBD10-fwd	ACCTGCATATGAATTCAAAATTTATTTTAAAG	32	51	BBD10-rev	ATCAGCCCGGGACTGCCACCAAGTAATTTAAC	32	58	595	715		
BB_E04	AE000785.1:4719..4859	lp25	pSC1091	BBE04-fwd	AATGACATATGAAAAACCCCAAATCAA	27	54	BBE04-rev	GAGCCCCCGGGATTTTGGTTATTTTCTGGA	30	63	157	277	L to M	
BB_E08	AE000785.1:6555..6701	lp25	pSC1089	BBE08-fwd	ACCTGCATATGCAAAAAAATGTTTATTG	28	54	BBE08-rev	GAGCCCCCGGGTAAAACAAAATTTGATAAGCA	32	62	163	283		
BB_E31	AE000785.1:21946..22677	lp25	pSC1090	BBE31-fwd	TGAAATACCATATAATCGTAAG	22	52	BBE31-rev	ATCAGCCCGGGAAGGTTGCTTATTGACAA	29	53	739	859		Fwd-blunt primer
BB_F01	AE000794.1:467..1465	lp28-1	pSC1093	BBF01-fwd	ACCTGCATATGAAATTATTAAAAATATTTATGTGTG	36	54	BBF01-rev	ATCAGCCCGGGACTTAAACCCTTTACACTT	30	53	1015	1135	L to M	
BB_F20	AE000794.1:10698..10991	lp28-1	pSC1092	BBF20-fwd	ACCTGCATATGAACAAAAAATTTTCTATTTC	31	52	BBF20-rev	ATCAGCCCGGGGTTGCTTTTGCAATATGAA	30	54	310	430		
BB_G01	AE000786.1:116..1009	lp28-2	pSC1095	BBG01-fwd	ACCTGCATATGAGAAAAAGTTTGTTTTTAT	30	52	BBG01-rev	ATCAGCCCGGGTTTTTTATTGAGACTTTCTAAAAC	35	54	910	1030		
BB_G25	AE000786.1:22273..22659	lp28-2	pSC1094	BBG25-fwd	ACCTGCATATGAAAAATTTAAAGACAAAAATT	32	52	BBG25-rev	ATCAGCCCGGGTCTTCTGCTGTATTTTTTG	30	52	403	523		
BB_H01	AE000784.1:273..467	lp28-3	pSC1099	BBH01-fwd	ACCTGCATATGAACAAATTATTGATATTCAT	31	52	BBH01-rev	ATCAGCCCGGGGTAATAATGGTTGAACGTG	30	53	211	331		ORF identical to BB_Q89
BB_H06	AE000784.1:2260..2970	lp28-3	pSC1098	BBH06-fwd	ACCTGCATATGAAAAAAAGTTTTTTATCAAT	31	52	BBH06-rev	ATCAGCCCGGGTAATAAAGTTTGCTTAATAGCT	33	53	727	847		
BB_H18	AE000784.1:12105..13220	lp28-3	pSC1096	BBH18-fwd	ACCTGCATATGAAAATGAAGGAGAAGCG	28	57	BBH18-rev	ATCAGCCCGGGTAGGCTAATACCAATTCG	29	52	1132	1252	L toM	
BB_H32	AE000784.1:21470..22219	lp28-3	pSC1097	BBH32-fwd	ACCTGCATATGAAATATAATACGATTATAAGC	32	52	BBH32-rev	ATCAGCCCGGGAAGGGTATATATTAAAATTATCTCG	36	54	766	886		
BB_H37	AE000784.1:25433..26371	lp28-3	pSC1100	BBH37-fwd	ACCTGCATATGATTAAGGGAAAGGAGAG	28	55	BBH37-rev	ATCAGCCCGGGAGACTTACTTAAAGCATTTTTTG	34	55	955	1075	L to M	
BB_I14	AE000789.1:6159..6272	lp28-4	pSC1107	BBI14-fwd	AATGACATATGAAAAACAAAATAATTTTATG	31	50	BBI14-rev	GAGCCCCCGGGGTTTTTTATTTTATCAGCATG	32	63	130	250		
BB_I16	AE000789.1:7183..8538	lp28-4	pSC1102	BBI16-fwd	ACCTGCATATGAAATACCACATAATTACA	29	52	BBI16-rev	ATCAGCCCGGGAAGTTTATATTTTGACACTATAAG	3	52	1372	1492		
BB_I28	AE000789.1:17302..17874	lp28-4	pSC1101	BBI28-fwd	ACCTGCATATGAAATGCCATATAATTGC	28	53	BBI28-rev	ATCAGCCCGGGAATCCGACAGATCTGG	27	53	589	709		
BB_I29	AE000789.1:18518..19183	lp28-4	pSC1108	BBI29-fwd	ACCTGCATATGAAAAACAACATAATTTTATG	31	52	BBI29-rev	ATCAGCCCGGGATTCGGCAGTGATAATATG	30	54	682	802		
BB_I36	AE000789.1:22095..22931	lp28-4	pSC1104	BBI36-fwd	ACCTGCATATGAAAAACTTTAAATTAAATACTATT	35	52	BBI36-rev	ATCAGCCCGGGATCAGCTTGATCTAGTAGAT	31	54	853	973	L to M	
BB_I38	AE000789.1:23159..23995	lp28-4	pSC1105	BBI38-fwd (=BBI36-fwd)	ACCTGCATATGAAAAACTTTAAATTAAATACTATT	35	52	BBI38-rev (=BBI36-rev)	ATCAGCCCGGGATCAGCTTGATCTAGTAGAT	31	54	853	973	L to M	
BB_I39	AE000789.1:24223..25089	lp28-4	pSC1106	BBI39-fwd	ACCTGCATATGAAAAACTTTAAATTAAATATTATTAA	3	52	BBI39-rev	ATCAGCCCGGGATCAGCTTGGTTTAGTAG	29	52	883	1003		
BB_I42	AE000789.1:26360..26914	lp28-4	pSC1103	BBI42-fwd	ACCTGCATATGAGGATTTTGGTTGG	25	54	BBI42-rev	ATCAGCCCGGGTGTAGGTAAAATAGGAACTG	31	53	571	691		
BB_J01	AE000787.1:482..667	lp38	pSC1121	BBJ01-fwd	ACCTGCATATGAAATACCATATAATCGTAAG	31	53	BBJ01-rev	ATCAGCCCGGGTCCTGCACTAGCTGTTTC	29	58	202	322		
BB_J09	lp38/ AE000787.1:6089..6862	lp38	pSC1011	BBJ09-fwd	ACCTGCATATGAAAAAATTAATAAAAATACTACTG	35	53	BBJ09-rev	ATCAGCCCGGGAGTATTTAACAAGGCCACAAC	32	58	790	910		
BB_J34	AE000787.1:25337..26407	lp38	pSC1119	BBJ34-fwd	ACCTGCATATGATAAAAGGCAATACGT	27	53	BBJ34-rev	ATCAGCCCGGGTTTATCTTTATTTTTAGGCTTAAC	35	53	1087	1207		
BB_J36	AE000787.1:26995..28053	lp38	pSC1118	BBJ36-fwd	ACCTGCATATGAAAAGGAAAAGCAATATATG	31	55	BBJ36-rev	ATCAGCCCGGGAAGCGCAACTTTTTTATAAAC	32	55	1075	1195		
BB_J41	AE000787.1:29905..30771	lp38	pSC1120	BBJ41-fwd	ACCTGCATATGAAAAACCTTAAATTAAATATTATT	35	52	BBJ41-rev	ATCAGCCCGGGATCAGCTTGGTTTAGTAGAT	31	55	883	1003	L to M	
BB_J47	AE000787.1:34905..35591	lp38	pSC1122	BBJ47-fwd	TGAGGAATATTAGCAATTGTATC	23	56	BBJ47-rev	ATCAGCCCGGGGTAAGAACTATTCTCCTTTTC	32	53	694	814		Fwd-blunt primer
BB_K01	AE000788.1:188..1081	lp36	pSC1117	BBK01-fwd	ACCTGCATATGAGAAAAAGTTTGTTTTTAT	30	52	BBK01-rev	ATCAGCCCGGGTTTTTTATTGAGACTTTCTAAAAC	35	54	910	1030		
BB_K07	AE000788.1:5288..6040	lp36	pSC1110	BBK07-fwd	ACCTGCATATGAGTAAACTAATATTGGC	28	52	BBK07-rev	ATCAGCCCGGGATTATTAAAGCACAAATGTATG	33	52	769	889		
BB_K12	AE000788.1:7335..8033	lp36	pSC1111	BBK12-fwd (=BBK07-fwd)	ACCTGCATATGAGTAAACTAATATTGGC	28	52	BBK12-rev	ATCAGCCCGGGGCTTAAAGTTGTCAATGTT	30	53	715	835		
BB_K19	AE000788.1:12602..13237	lp36	pSC1113	BBK19-fwd	ACCTGCATATGAAAAAATATATTATCAATTTAAGT	35	52	BBK19-rev	ATCAGCCCGGGATTGTTAGGTTTTTCTTTTCC	32	54	652	772	L to M	
BB_K32	AE000788.1:20389..21453	lp36	pSC1116	BBK32-fwd	ACCTGCATATGAAAAAAGTTAAAAGTAAATATTTG	35	54	BBK32-rev	ATCAGCCCGGGGTACCAAACGCCATTCTTG	30	58	1081	1201		
BB_K48	AE000788.1:30719..31585	lp36	pSC1112	BBK48-fwd	ACCTGCATATGAATTTAATTAATAAATTATTTATTCTA	38	51	BBK48-rev	ATCAGCCCGGGTCTAGAGTCCATATCTTGC	30	54	883	1003	V to M	
BB_K50	AE000788.1:33081..34079	lp36	pSC1109	BBK50-fwd	ACCTGCATATGAATTTAATAATTAAAGTGATGTTG	35	55	BBK50-rev (=BBK48-rev)	ATCAGCCCGGGTCTAGAGTCCATATCTTGC	30	54	1015	1135		
BB_K52	AE000788.1:34595..35443	lp36	pSC1115	BBK52-fwd	ACCTGCATATGAAAAAGAACATATATATTTTG	32	51	BBK52-rev	ATCAGCCCGGGTTCATCAGTAAAAAGTTTTAATT	34	52	865	985		
BB_K53	AE000788.1:35868..36422	lp36	pSC1114	BBK53-fwd	ACCTGCATATGAGGATTTTGGTTGG	25	5	BBK53-rev	ATCAGCCCGGGTGTAGGTAAAATAGAAACTGG	32	54	571	691		
BB_L28	AE001580.1:17205..17651	cp32-8	pSC1083	BBL28-fwd	ACCTGCATATGAAAATCATCAACATATTATT	31	52	BBL28-rev	ATCAGCCCGGGGGAACCGTTGCATGTAG	28	57	463	583		
BB_L39	AE001580.1:26370..26903	cp32-8	pSC1081	BBL39-fwd	TGGAGAAATTTATGAATAAGAA	22	52	BBL39-rev	ATCAGCCCGGGTTTTAAATTTCTTTTAAGCTCTTC	35	54	541	661		Fwd-blunt primer
BB_L40	AE001580.1:26931..28067	cp32-8	pSC1082	BBL40-fwd	ACCTGCATATGAATAAAAAAACAATTATTATTTG	34	53	BBL40-rev	ATCAGCCCGGGATCTTCTTCATCATAATTATCC	33	52	1152	1272		
BB_M27	AE001578.1:16593..17075	cp32-6	pSC1077	BBM27-fwd	TGAGAAATAAAAACATATTTAAATT	25	52	BBM27-rev	ATCAGCCCGGGATTAGTGCCCTCTTCGAG	29	57	490	610		ORF identical to BB_P27
BB_M28	AE001578.1:17247..17696	cp32-6	pSC1076	BBM28-fwd	ACCTGCATATGAAAATCATCAACATATTATT	31	52	BBM28-rev	ATCAGCCCGGGGGAACCACCATTGTTGC	28	58	466	586		
BB_M38	AE001578.1:26245..27015	cp32-6	pSC1075	BBM38-fwd	ACCTGCATATGGAGCAACTTATGAATAAG	29	55	BBM38-rev	ATCAGCCCGGGTTCTTTTTTATTAGAATCTTTAGAT	36	52	787	907		
BB_N28	AE001581.1:17302..17730	cp32-9	pSC1086	BBN28-fwd	ACCTGCATATGAAAATTATCAACATATTATTTTG	34	53	BBN28-rev	ATCAGCCCGGGTTGCTGAGCTTGGCAG	27	58	445	565		
BB_N38	AE001581.1:26210..26770	cp32-9	pSC1084	BBN38-fwd	TGAATAAGAAAATGAAAATGTT	22	52	BBN38-rev	ATCAGCCCGGGTTTTAAATTTTTTTTAAGCACTTC	35	53	568	688		Fwd-blunt primer
BB_N39	AE001581.1:26798..27829	cp32-9	pSC1085	BBN39-fwd	ACCTGCATATGAATAAAAAAACATTGATTATT	32	52	BBN39-rev	ATCAGCCCGGGCTGACTGTCACTGATGTATC	31	56	1048	1168		
BB_O28	AE001579.1:17245..17667	cp32-7	pSC1080	BBO28-fwd	ACCTGCATATGAAAATTATCAACATATTATTTTG	34	53	BBO28-rev	ATCAGCCCGGGATTGCAGGTAGCAGTTGC	29	60	439	559		
BB_O39	AE001579.1:26152..26841	cp32-7	pSC1078	BBO39-fwd	ACCTGCATATGAATAAGAAAATGAAAATGTT	31	53	BBO39-rev	ATCAGCCCGGGTTCTTTTTTATCTTCTTCTATTC	34	52	706	826		
BB_O40	AE001579.1:26893..27984	cp32-7	pSC1079	BBO40-fwd	ACCTGCATATGAATAAAAAAATATTGATTATTTTTG	36	53	BBO40-rev	ATCAGCCCGGGATATGAATTACTATCCTCAATG	33	52	1108	1228		
BB_P27	AE001575.1:16578..17060	cp32-1	pSC1071	BBP27-fwd	TGAGAAATAAAAACATATTTAAATT	25	52	BBP27-rev	ATCAGCCCGGGATTAGTGCCCTCTTCGAG	29	57	490	610		Fwd-blunt primer
BB_P28	AE001575.1:17232..17678	cp32-1	pSC1069	BBP28-fwd	ACCTGCATATGAAAATCATCAACATATTATT	31	52	BBP28-rev	ATCAGCCCGGGGGACCCATTGCCGCAG	27	62	463	583		
BB_P38	cp32-1/ AE001575.1:26247..26768	cp32-1	pSC1010	BBP38-fwd	TGAATAAGAAAATGAAAATGTTTAT	25	54	BBP38-rev	ATCAGCCCGGGTTTTAAATTTCTTTTAAGCTCTTC	35	54	529	649		Fwd-blunt primer
BB_P39	AE001575.1:26796..27932	cp32-1	pSC1070	BBP39-fwd	ACCTGCATATGAATAAAAAAACAATTATTATTTG	34	52	BBP39-rev	ATCAGCCCGGGATCTTCTTCATCATAATTATCC	33	52	1153	1273		
BB_Q03	AE001584.1:856..1407	lp56	pSC1125	BBQ03-fwd	ACCTGCATATGAGGATTTTGGTTGG	25	54	BBQ03-rev	ATCAGCCCGGGTAAAATTTTTCCATTAATTGTATTT	36	52	568	688		
BB_Q05	AE001584.1:2744..3496	lp56	pSC1124	BBQ05-fwd	TGAAATACTATATATGTGTGT	21	51	BBQ05-rev	ATCAGCCCGGGAAGGTTACTTATTGAAAATATCTG	35	54	760	880		Fwd-blunt primer
BB_Q35	AE001584.1:20844..21455	lp56	pSC1127	BBQ35-fwd	ACCTGCATATGAAAATCATCAACATATTATT	31	52	BBQ35-rev	ATCAGCCCGGGGTTTTGCCAATTAGCTG	28	53	628	748		
BB_Q46	AE001584.1:29559..29654	lp56	pSC1123	BBQ46-fwd	AATGACATATGATTAAAAATGTAATTTATATTTTAC	36	51	BBQ46-rev	GAGCCCCCGGGTCCTACAATCCAAATTTTG	30	64	112	232	L to M	
BB_Q47	AE001584.1:29937..30974	lp56	pSC1126	BBQ47-fwd	ACCTGCATATGAATAAAAAAAATGAAAATATTTATT	35	52	BBQ47-rev	ATCAGCCCGGGCTGACTGTAACTGATGTATC	31	54	1054	1174		
BB_Q89	AE001584.1:52532..52726	lp56	pSC1128	BBQ89-fwd	ACCTGCATATGAACAAATTATTGATATTCAT	31	52	BBQ89-rev	ATCAGCCCGGGGTAATAATGGTTGAACGTG	30	53	211	331		ORF identical to BB_H01
BB_R28	AE001577.1:17103..17525	cp32-4	pSC1074	BBR28-fwd	ACCTGCATATGAAAATTATCAACATATTATTTTG	34	53	BBR28-rev	ATCAGCCCGGGTGAATTTTTGCACGTACTAC	31	56	439	559		
BB_R40	AE001577.1:25865..25969	cp32-4	pSC1073	BBR40-fwd	ACCTGCATATGAATAAGAAAATGAAAAATTTA	32	53	BBR40-rev	GAGCCCCCGGGGCCAATACTTTGCTCATC	29	68	121	241		
BB_R42	cp32-4/ AE001577.1:26853..27527	cp32-4	pSC1012	BBR42-fwd	ACCTGCATATGAATAAAAAAATAAAAATGTTTATT	35	52	BBR42-rev	ATCAGCCCGGGTTCTTTTTTACCTTCTACAGTTTC	35	57	691	811		
BB_S30	AE001576.1:17803..18249	cp32-3	pSC1072	BBS30-fwd	ACCTGCATATGAAAATCATCAACATATTATTT	32	53	BBS30-rev	ATCAGCCCGGGGCCACCATTATTGCAGTT	29	57	463	583		
BB_S41	cp32-3/ AE001576.1:26708..27298	cp32-3	pSC1013	BBS41-fwd	ACCTGCATATGAATAAGAAAATGAAAAATTTAAT	34	53	BBS41-rev	ATCAGCCCGGGTTTTTTATCTTCTATATTTTGAGG	35	52	607	727		

Abbreviations: C: chromosome; cp: circular plasmid; lp: linear plasmid; bp: base pairs; Ta: annealing temperature

Supporting Table S2. Detailed peptide and spectral counts for proteins detected by MudPIT analyses of B. burgdorferi B31-A3 spirochetes subjected or not to proteolytic surface shaving

Two replicate B. burgdorferi B31-A3 spirochetes samples subjected to proteinase-K as well as two untreated control samples were analyzed by MudPIT.
The MS/MS datasets were searched against a protein database downloaded from the Spirochete Genome Browser, which contains accession numbers of all putative B. burgdorferi B31 ORFs (http://sgb.leibniz-fli.de/cgi/list.pl?ssi=free&c_sid=yes&sid=24&srt=ltg&.submit=Go).
Exactly redundant sequences were removed from this database, leaving 1559 non-redundant Bb proteins. After adding usual contaminants and randomizing each protein entry, the total search space was 3472 amino acid sequences. The MS dataset was searched for Methionine oxidation as a differential modification.

Combining all 4 runs, proteins had to be identified with at least 2 tryptic peptides of at least 7 amino acid long and/or 2 spectral counts. Proteins that were subsets of others were removed using the parsimony option in DTASelect on the proteins detected after merging all runs. Proteins that were identified by the same set of peptides (including at least one peptide unique to such protein group to distinguish between isoforms) were grouped together, and one accession number was arbitrarily considered as representative of each protein group. Half-tryptic peptides were allowed for the proteinase-K treated individual runs but did not contribute to establishing the master list of identified proteins ("ALL" columns).

In each analysis, the following parameters are specified for each protein:
- Peptide counts (columns end with _P);
- Total spectral counts (_S);
- Spectral counts for peptides shared between protein isoforms (_sS);
- Peptide counts for peptides uniquely matching the protein (_uDP);
- Spectral counts for peptides uniquely matching the protein (_uS);
- Spectral counts distributed according to the spectral count contribution of peptides unique to each isoform (_dS);
- Sequence coverage as a percentage (_SC);
- Distributed Normalized Spectral Abundance Factors (_dNSAF), calculated based on distributed spectral counts and protein length.

The number of times a protein is detected across replicates is listed in the "Detected # Out of" columns.
dNSAF are averaged across replicate runs ("dNSAF AVG" columns).
Summary statistics on False Discovery Rates (FDR, %) are calculated at the bottom of the table.

A total of 621 proteins (excluding contaminants) were detected, including 83 listed in Table 1. Each of the detected proteins was subjected to prediction algorithms to detect potential signal peptidases I & II cleavage sites (LipoP1.0), signal peptide (SignalP4.1), and transmembrane domains (TMHMM2.0).
For all detected proteins, the difference in sequence coverage (% of protein sequence covered by detected peptides, merging peptides from the 2 replicates analyzed for each condition) observed between the proteinase K-treated and control samples were calculated. The ratio in average dNSAF values measured in the control and proteinase K-treated samples were also calculated.
The proteins were grouped based on their known or predicted location:
51 were tested to be surface ("S") proteins, 4 were localized to the outer membrane ("P-OM"), and 28 were localized to the inner membrane ("P-IM"). An additional 10 proteins were predicted to contain a signal peptidase II cleavage site by LipoP1.0 ("SpII"), while another 63 were predicted to contain a signal peptide by LipoP1.0 ("SpI") and/or SignalP4.1. Another 100 proteins were predicted to contain at least 1 transmembrane domain by TMHMM 2.0, but no signal peptide ("TM"), while the remaining 365 proteins were most likely cytoplasmic ("CYT").

The complete MudPIT mass spectrometry dataset (raw files, peak files, search files, as well as DTASelect result files) can be obtained from the MassIVE database via ftp://MSV000080434@massive.ucsd.edu (password ASD06166) and from the ProteomeXchange repository under accession number PXD005617.

Known (Table 1) and/or predicated subcellular location	Locus	Proteins In Group	Description	B31A3_Control_merged-SeqCov (%)	B31A3_ProK_merged-SeqCov (%)	DiffSeqCov (Control - ProK) (%)	B31A3_Cntl-Ti dNSAF AVG	B31A3_Cntl-Ti Detected # Out of 2	B31A3_PK-Ti dNSAF AVG	B31A3_PK-Ti Detected # Out of 2	B31A3_Cntl-Ti: B31A3_PK-Ti	B31A3_Control_1_P	B31A3_Control_1_S	B31A3_Control_1_uS	B31A3_Control_1_uDP	B31A3_Control_1_sS	B31A3_Control_1_dS	B31A3_Control_1_SC	B31A3_Control_1_dNSAF	B31A3_Control_2_P	B31A3_Control_2_S	B31A3_Control_2_uS	B31A3_Control_2_uDP	B31A3_Control_2_sS	B31A3_Control_2_dS	B31A3_Control_2_SC	B31A3_Control_2_dNSAF	B31A3_ProK_1_P	B31A3_ProK_1_S	B31A3_ProK_1_uS	B31A3_ProK_1_uDP	B31A3_ProK_1_sS	B31A3_ProK_1_dS	B31A3_ProK_1_SC	B31A3_ProK_1_dNSAF	B31A3_ProK_2_P	B31A3_ProK_2_S	B31A3_ProK_2_uS	B31A3_ProK_2_uDP	B31A3_ProK_2_sS	B31A3_ProK_2_dS	B31A3_ProK_2_SC	B31A3_ProK_2_dNSAF	ALL_y2_P	ALL_y2_S	ALL_y2_uS	ALL_y2_uDP	ALL_y2_sS	ALL_y2_dS	ALL_y2_SC	ALL_y2_dNSAF	Length	MW	pI
S	BB_0158	BB_0158	antigen	68.49	23.53	-44.96	0.00243	2	0.00024	2	10.3447	15	65	65	15	0	65	55.5	0.00202	17	90	90	17	0	90	65.6	0.00285	4	8	8	4	0	8	23.5	0.0004	2	2	2	2	0	2	8.82	6.9E-05	21	165	165	21	0	165	68.5	0.0015	238	27262	6.7
S	BB_0213	BB_0213	predicted coding region BB0213	9.22	11.52	2.3	0.0001	1	8.4E-05	2	1.21429	2	3	3	2	0	3	9.22	0.0001	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.23	5.5E-05	2	3	3	2	0	3	11.5	0.00011	4	6	6	4	0	6	18	6E-05	217	25760	6.6
S	BB_0689	BB_0689	predicted coding region BB0689	58.06	9.68	-48.38	0.00105	2	5.3E-05	1	19.8679	8	34	34	8	0	34	46.5	0.00162	4	10	10	4	0	10	35.5	0.00049	X	X	X	X	X	X	X	X	1	1	1	1	0	1	9.68	5.3E-05	11	45	45	11	0	45	58.1	0.00063	155	17971	9.2
S	BB_A04	BB_A04	antigen	16.31	0	-16.31	5.3E-05	1	0	0	∞	X	X	X	X	X	X	X	X	2	2	2	2	0	2	16.3	5.3E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	16.3	1.5E-05	282	31848	9.2
S	BB_A07	BB_A07	chpAI protein	40.12	0	-40.12	0.00016	2	0	0	∞	1	2	2	1	0	2	9.26	9.1E-05	3	5	5	3	0	5	40.1	0.00023	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	7	7	3	0	7	40.1	9.3E-05	162	18589	9
S	BB_A14	BB_A14	conserved hypothetical protein	19.01	8.26	-10.75	0.00012	2	0.0002	1	0.62626	1	1	1	1	0	1	9.92	6.1E-05	3	3	3	3	0	3	19	0.00019	1	2	2	1	0	2	8.26	0.0002	X	X	X	X	X	X	X	X	3	6	6	3	0	6	19	0.00011	121	13950	9.6
S	BB_A15	BB_A15	outer surface protein A (ospA)	90.11	66.3	-23.81	0.21792	2	0.00333	2	65.4221	84	7192	7192	84	0	7192	90.1	0.19461	111	8753	8753	111	0	8753	90.1	0.24123	13	88	88	13	0	88	48	0.00385	18	94	94	18	0	94	53.5	0.00281	116	####	####	116	0	####	90.1	0.12776	273	29367	8.7
S	BB_A16	BB_A16	outer surface protein B (ospB)	38.51	22.97	-15.54	0.05408	2	0.00029	2	185.842	25	1920	1915	25	5	1915	38.5	0.04779	25	2375	2375	25	0	2375	38.5	0.06037	4	11	11	4	0	11	21.6	0.00044	4	5	5	4	0	5	17.6	0.00014	31	4310	4310	31	0	4310	38.5	0.0315	296	31717	9
S	BB_A24	BB_A24	decorin binding protein A (dbpA)	53.93	30.89	-23.04	0.00126	2	0.00021	2	5.95261	6	14	14	6	0	14	39.3	0.00054	10	50	50	10	0	50	53.4	0.00197	2	4	4	2	0	4	17.3	0.00025	3	4	4	3	0	4	25.1	0.00017	11	72	72	11	0	72	53.9	0.00082	191	21214	8.8
S	BB_A57	BB_A57	predicted coding region BBA57	7.73	2.17	-5.56	1.8E-05	2	2.9E-05	1	0.62069	1	1	1	1	0	1	7.25	1.8E-05	1	1	1	1	0	1	7.73	1.8E-05	1	1	1	1	0	1	2.17	2.9E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	7.73	1E-05	414	47424	5.3
S	BB_A59	BB_A59	lipoprotein	72.15	29.11	-43.04	0.01054	2	0.00359	2	2.93378	6	142	142	6	0	142	63.3	0.01328	7	82	82	7	0	82	72.2	0.00781	6	12	12	6	0	12	29.1	0.00182	6	52	52	6	0	52	29.1	0.00537	8	285	285	8	0	285	72.2	0.00781	79	8995	4.5
S	BB_A64	BB_A64	antigen	25.41	6.19	-19.22	0.00024	2	3.9E-05	1	6.23077	5	9	9	5	0	9	21.8	0.00022	5	11	11	5	0	11	24.8	0.00027	1	1	1	1	0	1	6.19	3.9E-05	X	X	X	X	X	X	X	X	8	20	20	8	0	20	25.4	0.00014	307	34952	9.2
S	BB_A68	BB_A68	predicted coding region BBA68	64.54	32.27	-32.27	0.00628	2	0.00026	2	24.3566	32	260	260	32	0	260	61.4	0.00765	33	164	164	33	0	164	61.4	0.00492	3	4	4	3	0	4	12.8	0.00019	6	10	10	6	0	10	28.7	0.00033	44	436	436	44	0	436	64.5	0.00376	251	29173	8.2
S	BB_A69	BB_A69	predicted coding region BBA69	73	0	-73	0.00334	2	0	0	∞	26	130	130	26	0	130	65.4	0.00365	25	106	106	25	0	106	66.2	0.00303	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	36	236	236	36	0	236	73	0.00194	263	30487	8.9
S	BB_B08	BB_B08	predicted coding region BBB08	24.4	31.58	7.18	0.00046	2	0.00077	2	0.60523	2	14	14	2	0	14	20.6	0.00049	3	12	12	3	0	12	24.4	0.00043	3	9	9	3	0	9	19.1	0.00051	5	26	26	5	0	26	31.6	0.00102	5	51	51	5	0	51	40.7	0.00053	209	24620	8
S	BB_B19	BB_B19	outer surface protein C (ospC)	74.76	30.48	-44.28	0.00333	2	0.00042	2	7.86288	16	127	127	16	0	127	71.9	0.00447	14	61	61	14	0	61	62.4	0.00219	2	6	6	2	0	6	21	0.00034	4	13	13	4	0	13	30.5	0.00051	20	207	207	20	0	207	74.8	0.00213	210	22341	8.3
S	BB_B25	BB_B25	predicted coding region BBB25	9.41	9.41	0	8.7E-05	1	0.00017	2	0.5241	1	2	2	1	0	2	9.41	8.7E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	9.41	0.00014	1	4	4	1	0	4	9.41	0.00019	1	8	8	1	0	8	9.41	0.0001	170	20119	9
S	BB_D10	BB_D10	conserved hypothetical protein	38.54	22.4	-16.14	0.00044	2	0.00024	2	1.83471	4	19	19	4	0	19	31.3	0.00073	2	4	4	2	0	4	14.1	0.00016	3	3	3	3	0	3	22.4	0.00019	1	7	7	1	0	7	12	0.0003	7	33	33	7	0	33	49	0.00037	192	22705	9
S	BB_E31	BB_E31	antigen	46.5	0	-46.5	0.00072	2	0	0	∞	9	24	24	9	0	24	37.5	0.00073	8	23	23	8	0	23	39.9	0.00071	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	12	47	47	12	0	47	46.5	0.00042	243	28153	9.2
S	BB_F20	BB_F20	conserved hypothetical protein	17.53	9.28	-8.25	0.00027	2	0.00015	2	1.83562	2	5	5	2	0	5	17.5	0.00038	1	2	2	1	0	2	8.25	0.00016	1	1	1	1	0	1	9.28	0.00012	2	2	2	2	0	2	9.28	0.00017	3	10	10	3	0	10	17.5	0.00022	97	11057	9.2
S	BB_G01	BB_G01	predicted coding region BBG01	74.07	16.5	-57.57	0.005	2	6.8E-05	2	73.4853	23	305	208	21	97	258	65.7	0.00642	22	146	137	19	9	141	63.3	0.00357	2	2	2	2	0	2	6.73	8E-05	2	3	1	1	2	2	9.76	5.5E-05	30	453	347	27	106	398	74.1	0.0029	297	34556	8.8
S	BB_H06	BB_H06	predicted coding region BBH06	68.64	69.07	0.43	0.01284	2	0.01728	2	0.74327	17	404	404	17	0	404	64.4	0.01265	14	409	409	14	0	409	50	0.01304	9	371	371	9	0	371	54.7	0.01879	14	456	456	14	0	456	65.3	0.01577	20	1639	1639	20	0	1639	68.6	0.01503	236	27162	7.1
S	BB_H18	BB_H18	predicted coding region BBH18	21.56	7.28	-14.28	0.00019	2	3.2E-05	1	5.9375	5	15	15	5	0	15	21.6	0.0003	2	4	4	2	0	4	6.47	8.1E-05	1	1	1	1	0	1	7.28	3.2E-05	X	X	X	X	X	X	X	X	6	19	19	6	0	19	21.6	0.00011	371	42627	9.3
S	BB_H32	BB_H32	antigen	27.71	10.44	-17.27	0.00061	2	7.3E-05	2	8.35616	9	36	36	9	0	36	27.7	0.00107	1	5	5	1	0	5	4.42	0.00015	1	1	1	1	0	1	4.02	4.8E-05	2	3	3	2	0	3	10.4	9.8E-05	9	41	41	9	0	41	27.7	0.00036	249	28804	9
S	BB_H37	BB_H37	predicted coding region BBH37	72.44	18.91	-53.53	0.00641	2	0.0001	2	62.2039	34	311	303	33	8	311	68.9	0.00736	33	226	226	33	0	226	67.6	0.00545	3	4	4	3	0	4	12.8	0.00015	2	2	2	2	0	2	14.1	5.2E-05	42	543	535	41	8	543	72.4	0.00377	312	35332	8.6
S	BB_I16	BB_I16	predicted coding region BBI16	26.16	0	-26.16	0.00062	2	0	0	∞	5	14	14	5	0	14	17.5	0.00023	4	61	61	4	0	61	15.7	0.00102	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	8	75	75	8	0	75	26.2	0.00036	451	54321	8.1
S	BB_I29	BB_I29	predicted coding region BBI29	72.4	43.89	-28.51	0.00291	2	0.00033	2	8.93865	20	99	99	20	0	99	63.8	0.00331	20	74	74	20	0	74	72.4	0.00252	6	10	10	6	0	10	35.8	0.00054	2	3	3	2	0	3	18.6	0.00011	28	186	186	28	0	186	72.4	0.00182	221	25586	8.5
S	BB_I36	BB_I36	antigen	71.22	4.32	-66.9	0.0037	2	4.3E-05	1	85.9302	27	265	7	2	258	182	69.4	0.00483	26	135	6	3	129	94.6	66.2	0.00256	1	2	0	0	2	1	4.32	4.3E-05	X	X	X	X	X	X	X	X	34	402	13	3	389	260	71.2	0.00202	278	32186	8.7
S	BB_I38	BB_I38	predicted coding region BBI38	64.75	4.32	-60.43	0	0	4.3E-05	1	0	25	258	0	0	258	0	63	X	23	129	0	0	129	0	59.4	X	1	2	0	0	2	1	4.32	4.3E-05	X	X	X	X	X	X	X	X	32	390	1	1	389	20	73	0.00016	278	32209	8.9
S	BB_I39	BB_I39	predicted coding region BBI39	77.08	15.28	-61.8	0.01636	2	0.00029	1	56.2096	41	793	709	37	84	792	70.1	0.02032	51	475	434	48	41	474	77.1	0.01239	3	7	7	3	0	7	15.3	0.00029	X	X	X	X	X	X	X	X	58	1275	1150	53	125	1273	77.1	0.00957	288	32964	9.4
S	BB_J09	BB_J09	outer surface protein D (ospD)	88.33	50.58	-37.75	0.06896	2	0.00301	2	22.8934	47	2656	2656	47	0	2656	85.6	0.07634	62	2103	2103	62	0	2103	85.6	0.06157	9	107	107	9	0	107	35.4	0.00498	12	33	33	12	0	33	44	0.00105	70	4884	4884	70	0	4884	90.7	0.04112	257	28434	5.4
S	BB_J34	BB_J34	predicted coding region BBJ34	78.09	4.49	-73.6	0.00328	2	2.3E-05	1	142.696	31	245	245	31	0	245	75	0.00508	24	70	70	24	0	70	62.6	0.00148	X	X	X	X	X	X	X	X	1	1	1	1	0	1	4.49	2.3E-05	39	316	316	39	0	316	78.1	0.00192	356	39650	5.5
S	BB_J36	BB_J36	predicted coding region BBJ36	65.06	0	-65.06	0.0008	2	0	0	∞	17	52	52	17	0	52	55.1	0.00109	10	24	24	10	0	24	39.8	0.00051	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	20	76	76	20	0	76	65.1	0.00047	352	39540	8.9
S	BB_K01	BB_K01	predicted coding region BBK01	78.79	9.43	-69.36	0.00535	2	5.5E-05	1	97.2909	31	290	193	29	97	240	66	0.00596	43	191	182	40	9	187	77.1	0.00474	X	X	X	X	X	X	X	X	2	3	1	1	2	2	9.43	5.5E-05	51	484	378	48	106	433	78.8	0.00316	297	34140	9
S	BB_K07	BB_K07	predicted coding region BBK07	9.2	0	-9.2	0.0001	2	0	0	∞	1	5	5	1	0	5	9.2	0.00015	1	2	2	1	0	2	9.2	6E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	7	7	1	0	7	9.2	6.1E-05	250	27758	7.3
S	BB_K19	BB_K19	predicted coding region BBK19	66.35	16.11	-50.24	0.00611	2	0.00015	2	39.915	17	245	245	17	0	245	62.1	0.00858	17	102	102	17	0	102	61.6	0.00364	1	2	2	1	0	2	11.4	0.00011	2	5	5	2	0	5	16.1	0.00019	20	354	354	20	0	354	66.4	0.00363	211	24326	8.1
S	BB_K50	BB_K50	immunogenic protein P37	44.28	16.27	-28.01	0.00057	2	5.5E-05	2	10.4182	9	24	24	9	0	24	30.4	0.00053	12	27	27	12	0	27	37.4	0.00061	1	1	1	1	0	1	3.31	3.6E-05	2	3	3	2	0	3	13	7.4E-05	15	54	54	15	0	54	44.3	0.00035	332	37314	8.2
S	BB_L28	BB_L28	mlpH	14.19	0	-14.19	0.0001	1	0	0	∞	X	X	X	X	X	X	X	X	1	2	2	1	0	2	14.2	0.0001	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	14.2	2.9E-05	148	16626	7.8
S	BB_L39	BB_L39;BB_P38	erpN	69.49	48.59	-20.9	0.00813	2	0.00075	2	10.869	17	247	247	17	0	247	65	0.01031	19	140	140	19	0	140	69.5	0.00595	1	1	1	1	0	1	7.34	6.8E-05	6	31	31	6	0	31	48.6	0.00143	21	419	419	21	0	419	69.5	0.00512	177	20106	6.1
S	BB_M27	BB_M27;BB_P27	revA	37.5	13.13	-24.37	0.00035	2	0.00038	2	0.928	5	11	11	5	0	11	29.4	0.00051	2	4	4	2	0	4	24.4	0.00019	2	8	8	2	0	8	13.1	0.0006	3	3	3	3	0	3	13.1	0.00015	7	26	26	7	0	26	37.5	0.00035	160	17921	8.5
S	BB_N38	BB_N38	erpP	53.23	8.06	-45.17	0.00169	2	4.4E-05	1	38.4773	11	70	70	11	0	70	53.2	0.00278	8	15	15	8	0	15	46.8	0.00061	X	X	X	X	X	X	X	X	1	1	1	1	0	1	8.06	4.4E-05	13	86	86	13	0	86	53.2	0.001	186	20689	8.3
S	BB_N39	BB_N39	erpQ	37.03	0	-37.03	0.00025	2	0	0	∞	8	13	13	8	0	13	37	0.00028	4	10	10	4	0	10	15.7	0.00022	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	9	23	23	9	0	23	37	0.00015	343	39348	5
S	BB_O40	BB_O40	erpM	9.37	9.37	0	4.1E-05	1	6.7E-05	1	0.61194	1	2	0	0	2	0	3.86	X	1	2	2	1	0	2	5.51	4.1E-05	X	X	X	X	X	X	X	X	2	3	2	1	1	3	9.37	6.7E-05	2	7	4	1	3	4.8	9.37	2.9E-05	363	41843	5.1
S	BB_P28	BB_P28	mlpA	32.43	12.84	-19.59	0.00026	2	8.1E-05	1	3.16049	3	11	3	2	8	5.18	20.3	0.00026	3	5	5	3	0	5	24.3	0.00025	1	1	1	1	0	1	12.8	8.1E-05	X	X	X	X	X	X	X	X	7	17	9	6	8	12	32.4	0.00018	148	16413	6
S	BB_P39	BB_P39	erpB	17.99	17.99	0	9.8E-05	2	9.5E-05	1	1.03158	4	8	6	3	2	8	18	0.00016	1	2	2	1	0	2	10.3	4E-05	2	3	3	2	0	3	14.3	9.5E-05	1	1	0	0	1	0	3.7	X	5	14	11	4	3	13.2	22	7.6E-05	378	43636	4.9
S	BB_Q05	BB_Q05	antigen	7.2	11.2	4	0.00012	1	9.8E-05	1	1.22449	X	X	X	X	X	X	X	X	1	4	4	1	0	4	7.2	0.00012	X	X	X	X	X	X	X	X	2	3	3	2	0	3	11.2	9.8E-05	3	7	7	3	0	7	18.4	6.1E-05	250	28941	5.8
S	BB_Q35	BB_Q35	mlpJ	26.11	16.75	-9.36	0.00013	2	0.00007	2	1.82857	2	6	6	2	0	6	19.7	0.00022	1	1	1	1	0	1	6.4	3.7E-05	1	1	1	1	0	1	9.36	5.9E-05	1	2	2	1	0	2	7.39	8E-05	4	8	8	4	0	8	30.5	8.5E-05	203	23578	5.5
S	BB_R28	BB_R28	mlpD	15.71	10.71	-5	0.00018	1	0.00017	1	1.06433	2	10	2	1	8	3.45	15.7	0.00018	X	X	X	X	X	X	X	X	1	2	2	1	0	2	10.7	0.00017	X	X	X	X	X	X	X	X	2	12	4	1	8	5.33	15.7	8.2E-05	140	15862	7.2
S	BB_R42	BB_R42	erpY	16.96	0	-16.96	3.3E-05	2	0	0	∞	1	1	1	1	0	1	7.59	3.3E-05	1	1	1	1	0	1	9.38	3.4E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	17	1.9E-05	224	25416	8.1
S	BB_S30	BB_S30	mlpC	31.76	12.16	-19.6	0.00036	2	5.5E-05	1	6.54545	4	14	6	3	8	10.4	31.8	0.00052	1	4	4	1	0	4	18.9	0.0002	X	X	X	X	X	X	X	X	1	1	1	1	0	1	12.2	5.5E-05	4	19	11	3	8	14.7	31.8	0.00021	148	16731	6
S	BB_S41	BB_S41	erpG	20.41	0	-20.41	7.6E-05	2	0	0	∞	1	1	1	1	0	1	20.4	3.8E-05	2	3	3	2	0	3	20.4	0.00012	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	4	4	2	0	4	20.4	4.4E-05	196	22049	5.5
P-OM	BB_0028	BB_0028	predicted coding region BB0028	78.22	75.36	-2.86	0.00763	2	0.01096	2	0.69645	20	390	390	20	0	390	70.2	0.00826	23	325	325	23	0	325	73.1	0.00701	20	291	291	20	0	291	60.7	0.00997	32	511	511	32	0	511	75.4	0.01195	33	1487	1487	33	0	1487	78.2	0.00922	349	39705	8.8
P-OM	BB_0324	BB_0324	predicted coding region BB0324	44.54	45.38	0.84	0.00113	2	0.00164	2	0.68888	7	19	19	7	0	19	36.1	0.00118	6	17	17	6	0	17	44.5	0.00107	3	8	8	3	0	8	29.4	0.0008	11	36	36	11	0	36	45.4	0.00247	13	80	80	13	0	80	53.8	0.00145	119	13898	9.5
P-OM	BB_0460	BB_0460	predicted coding region BB0460	30.8	19.41	-11.39	0.00058	2	0.00029	2	2.01742	7	29	29	7	0	29	27.9	0.0009	3	8	8	3	0	8	10.6	0.00025	5	10	10	5	0	10	19.4	0.0005	1	2	2	1	0	2	3.38	6.9E-05	8	49	49	8	0	49	30.8	0.00045	237	28191	8.9
P-OM	BB_A62	BB_A62	lipoprotein	50	38.24	-11.76	0.01946	2	0.03279	2	0.59354	15	233	233	15	0	233	50	0.02531	11	123	123	11	0	123	50	0.01361	13	158	158	13	0	158	38.2	0.02777	16	315	315	16	0	315	38.2	0.0378	17	799	799	17	0	799	50	0.02542	68	7763	8.1
P-IM	BB_0141	BB_0141	membrane fusion protein (mtrC)	35.85	39.62	3.77	0.00052	2	0.00089	2	0.58876	11	38	38	11	0	38	35.9	0.00088	4	7	7	4	0	7	19.5	0.00017	9	33	33	9	0	33	36.2	0.00124	6	21	21	6	0	21	28.3	0.00054	14	99	99	14	0	99	41.8	0.00067	318	35174	9
P-IM	BB_0144	BB_0144	glycine betaine	85.86	80	-5.86	0.01684	2	0.02123	2	0.79348	16	636	636	16	0	636	70.3	0.0162	25	674	674	25	0	674	85.9	0.01749	23	475	475	23	0	475	65.2	0.01958	32	813	813	32	0	813	75.9	0.02288	30	2533	2533	30	0	2533	85.9	0.0189	290	33263	5.4
P-IM	BB_0193	BB_0193	predicted coding region BB0193	12.6	9.76	-2.84	9.1E-05	2	4.1E-05	2	2.21951	2	2	2	2	0	2	9.76	6E-05	1	4	4	1	0	4	2.85	0.00012	1	1	1	1	0	1	4.88	4.9E-05	1	1	1	1	0	1	4.88	3.3E-05	3	8	8	3	0	8	12.6	7E-05	246	28882	9.5
P-IM	BB_0215	BB_0215	phosphate ABC transporter	78.93	70.71	-8.22	0.01114	2	0.01069	2	1.04199	23	483	483	23	0	483	76.1	0.01274	20	355	355	20	0	355	65.4	0.00954	20	320	320	20	0	320	70.7	0.01366	16	265	265	16	0	265	63.6	0.00772	29	1416	1416	29	0	1416	78.9	0.01094	280	31250	8
P-IM	BB_0227	BB_0227	predicted coding region BB0227	60.52	60.52	0	0.00262	2	0.00462	2	0.56713	13	98	98	13	0	98	57.5	0.00311	13	66	66	13	0	66	46.8	0.00213	12	94	94	12	0	94	57.5	0.00482	16	126	126	16	0	126	60.5	0.00441	17	379	379	17	0	379	60.5	0.00352	233	27491	6
P-IM	BB_0298	BB_0298	conserved hypothetical protein	46.52	62.17	15.65	0.0005	2	0.00137	2	0.36623	8	19	19	8	0	19	35.7	0.00061	4	12	12	4	0	12	32.6	0.00039	13	40	39	13	1	39	46.5	0.00203	7	20	20	7	0	20	27	0.00071	19	91	90	19	1	90	67.8	0.00085	230	26497	6.3
P-IM	BB_0323	BB_0323	predicted coding region BB0323	33.16	23.08	-10.08	0.00018	2	0.00037	2	0.47326	9	16	16	9	0	16	33.2	0.00031	1	2	2	1	0	2	3.45	4E-05	5	12	12	5	0	12	17.2	0.00038	4	17	17	4	0	17	11.4	0.00037	11	47	47	11	0	47	36.6	0.00027	377	44151	9.3
P-IM	BB_0328	BB_0328	oligopeptide ABC transporter	79.21	80.34	1.13	0.02577	2	0.04506	2	0.57189	49	1344	1329	48	15	1344	68.1	0.01877	79	2304	2292	78	12	2304	79.2	0.03277	64	1751	1739	62	12	1751	75.2	0.03957	109	3277	3237	107	40	3277	80.3	0.05055	86	8042	7971	85	71	8042	83.4	0.03289	529	60629	6
P-IM	BB_0329	BB_0329	oligopeptide ABC transporter	79.17	75.95	-3.22	0.01643	2	0.01749	2	0.93968	39	1013	1013	39	0	1013	66.7	0.01417	44	1312	1312	44	0	1312	76.9	0.0187	46	836	834	45	2	835	65	0.01889	51	1047	1037	49	10	1041	73.7	0.01608	56	4113	4113	56	0	4113	79.2	0.01685	528	60663	5.8
P-IM	BB_0330	BB_0330	oligopeptide ABC transporter	87.06	76.52	-10.54	0.03246	2	0.03527	2	0.92027	58	1888	1888	58	0	1888	82.3	0.02578	77	2814	2814	77	0	2814	85.6	0.03914	71	1958	1956	70	2	1957	69.3	0.04325	71	1813	1803	69	10	1809	71.7	0.02729	89	8330	8330	89	0	8330	87.1	0.03332	541	62368	9.1
P-IM	BB_0365	BB_0365	lipoprotein LA7	82.99	82.99	0	0.03976	2	0.07003	2	0.56775	13	1017	1017	13	0	1017	81.4	0.03873	24	1052	1052	24	0	1052	83	0.0408	25	1480	1480	25	0	1480	69.1	0.09119	27	1162	1162	27	0	1162	82	0.04888	25	4660	4660	25	0	4660	83	0.05197	194	21866	5.8
P-IM	BB_0382	BB_0382	basic membrane protein B (bmpB)	68.91	61	-7.91	0.00563	2	0.00483	2	1.16411	16	173	173	16	0	173	61.9	0.00375	18	340	340	18	0	340	64.5	0.0075	15	174	174	15	0	174	61	0.0061	13	149	149	13	0	149	59.8	0.00357	21	836	836	21	0	836	68.9	0.0053	341	37593	5.2
P-IM	BB_0384	BB_0384	basic membrane protein C (bmpC)	11.05	16.43	5.38	5.3E-05	2	0.00012	2	0.44538	1	2	2	1	0	2	5.67	4.2E-05	1	3	3	1	0	3	5.38	6.4E-05	3	5	5	3	0	5	6.52	0.00017	2	3	3	2	0	3	9.92	6.9E-05	5	12	12	5	0	12	17.6	7.4E-05	353	39824	9.1
P-IM	BB_0385	BB_0385	basic membrane protein D (bmpD)	82.78	85	2.22	0.02891	2	0.03253	2	0.88881	32	779	779	32	0	779	81.4	0.01599	43	2002	2002	43	0	2002	82.8	0.04184	30	775	775	30	0	775	74.7	0.02573	54	1735	1735	54	0	1735	85	0.03933	47	5245	5245	47	0	5245	83.3	0.03152	360	39705	5.4
P-IM	BB_0398	BB_0398	predicted coding region BB0398	0	2.92	2.92	0	0	0.00007	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	2.92	7E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	2.92	1.3E-05	343	40586	7.5
P-IM	BB_0456	BB_0456	predicted coding region BB0456	6.97	15.92	8.95	3.7E-05	1	0.0003	1	0.12458	1	1	1	1	0	1	6.97	3.7E-05	X	X	X	X	X	X	X	X	3	5	5	3	0	5	15.9	0.0003	X	X	X	X	X	X	X	X	3	6	6	3	0	6	15.9	6.5E-05	201	23584	8.3
P-IM	BB_0542	BB_0542	predicted coding region BB0542	21.88	36.46	14.58	0.00088	2	0.0007	2	1.25899	6	20	20	6	0	20	21.9	0.00077	3	25	25	3	0	25	11.5	0.00098	2	8	8	2	0	8	11.5	0.0005	6	21	21	6	0	21	36.5	0.00089	8	74	74	8	0	74	40.1	0.00083	192	22219	7.9
P-IM	BB_0628	BB_0628	conserved hypothetical protein	0	13.28	13.28	0	0	0.00022	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	13.3	9.9E-05	2	10	10	2	0	10	9.96	0.00034	3	12	12	3	0	12	13.3	0.00011	241	27490	5.6
P-IM	BB_0652	BB_0652	protein-export membrane protein (s	13.65	38.23	24.58	0.00012	2	0.00068	2	0.17768	4	9	9	4	0	9	10.2	0.00011	3	10	10	3	0	10	10.4	0.00013	11	21	21	11	0	21	22.5	0.00043	15	67	67	15	0	67	34.5	0.00093	19	105	105	19	0	105	35.8	0.00039	586	65028	8.9
P-IM	BB_0664	BB_0664	predicted coding region BB0664	34.36	59.91	25.55	0.00107	1	0.00154	2	0.69831	6	33	33	6	0	33	34.4	0.00107	X	X	X	X	X	X	X	X	10	55	55	10	0	55	59.9	0.0029	3	5	5	3	0	5	22	0.00018	10	93	93	10	0	93	59.9	0.00089	227	26510	5.1
P-IM	BB_0806	BB_0806	predicted coding region BB0806	24.7	18.77	-5.93	0.00024	2	0.0002	2	1.21717	10	31	31	10	0	31	24.7	0.00045	2	2	2	2	0	2	6.52	3E-05	4	12	12	4	0	12	14.2	0.00028	4	7	7	4	0	7	12.7	0.00011	11	52	52	11	0	52	27.1	0.00022	506	58284	6.7
P-IM	BB_0832	BB_0832	predicted coding region BB0832	8.03	17.15	9.12	2.7E-05	1	3.7E-05	2	0.72973	1	1	1	1	0	1	8.03	2.7E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	8.03	4.4E-05	1	1	1	1	0	1	9.12	3E-05	2	2	2	2	0	2	8.03	1.6E-05	274	31119	9.6
P-IM	BB_A03	BB_A03	outer membrane protein	78.11	75.15	-2.96	0.02125	2	0.03024	2	0.70278	19	510	510	19	0	510	72.2	0.02229	25	454	454	25	0	454	78.1	0.02021	32	610	610	32	0	610	72.8	0.04314	24	359	359	24	0	359	69.2	0.01733	29	1881	1881	29	0	1881	85.8	0.02408	169	19222	5.4
P-IM	BB_A05	BB_A05	antigen	16.07	4.08	-11.99	4.4E-05	2	2.4E-05	2	1.83333	2	4	4	2	0	4	7.67	7.1E-05	1	1	1	1	0	1	8.39	1.8E-05	1	1	1	1	0	1	3.36	2.9E-05	1	1	1	1	0	1	3.84	2E-05	3	5	5	3	0	5	16.1	2.6E-05	417	48842	9.1
P-IM	BB_A34	BB_A34	oligopeptide ABC transporter	7.56	17.2	9.64	4.3E-05	2	5.8E-05	2	0.74138	3	20	3	1	17	3.04	7.56	4.2E-05	3	19	3	1	16	3.02	7.56	4.3E-05	4	15	3	2	12	3.02	10.4	6.8E-05	5	44	3	2	41	3.04	12.7	4.7E-05	4	89	11	2	78	11.1	12.5	4.5E-05	529	60993	5.7
P-IM	BB_B16	BB_B16	oligopeptide ABC transporter	76.04	75.47	-0.57	0.01758	2	0.02878	2	0.61077	47	1185	1181	46	4	1183	65.1	0.01649	51	1315	1311	50	4	1315	72.6	0.01867	47	1367	1367	47	0	1367	70.4	0.03083	72	1736	1735	71	1	1736	71.5	0.02673	67	5555	5548	66	7	5555	76	0.02268	530	60766	6.5
P-IM	BB_B27	BB_B27	predicted coding region BBB27	10.93	8.74	-2.19	8.1E-05	1	6.5E-05	1	1.24615	1	2	2	1	0	2	10.9	8.1E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	8.74	6.5E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	19.7	3.5E-05	183	21551	9.5

Known (Table 1) and/or predicated subcellular location	Locus	Proteins In Group	Description	B31A3_Control_merged-SeqCov (%)	B31A3_ProK_merged-SeqCov (%)	DiffSeqCov (Control - ProK) (%)	B31A3_Cntl-Ti dNSAF AVG	B31A3_Cntl-Ti Detected # Out of 2	B31A3_PK-Ti dNSAF AVG	B31A3_PK-Ti Detected # Out of 2	B31A3_Cntl-Ti: B31A3_PK-Ti	B31A3_Control_1_P	B31A3_Control_1_S	B31A3_Control_1_uS	B31A3_Control_1_uDP	B31A3_Control_1_sS	B31A3_Control_1_dS	B31A3_Control_1_SC	B31A3_Control_1_dNSAF	B31A3_Control_2_P	B31A3_Control_2_S	B31A3_Control_2_uS	B31A3_Control_2_uDP	B31A3_Control_2_sS	B31A3_Control_2_dS	B31A3_Control_2_SC	B31A3_Control_2_dNSAF	B31A3_ProK_1_P	B31A3_ProK_1_S	B31A3_ProK_1_uS	B31A3_ProK_1_uDP	B31A3_ProK_1_sS	B31A3_ProK_1_dS	B31A3_ProK_1_SC	B31A3_ProK_1_dNSAF	B31A3_ProK_2_P	B31A3_ProK_2_S	B31A3_ProK_2_uS	B31A3_ProK_2_uDP	B31A3_ProK_2_sS	B31A3_ProK_2_dS	B31A3_ProK_2_SC	B31A3_ProK_2_dNSAF	ALL_y2_P	ALL_y2_S	ALL_y2_uS	ALL_y2_uDP	ALL_y2_sS	ALL_y2_dS	ALL_y2_SC	ALL_y2_dNSAF	Length	MW	pI
P	BB_0536	BB_0536	zinc protease	67.31	65.17	-2.14	0.00669	2	0.00993	2	0.67335	59	581	581	59	0	581	60.7	0.0046	71	1088	1088	71	0	1088	61.1	0.00877	53	512	512	53	0	512	52.7	0.00656	97	1525	1521	97	4	1521	64.6	0.0133	100	3634	3634	100	0	3634	71.7	0.00843	933	108458	6.3
SpII	BB_0383	BB_0383	basic membrane protein A (bmpA)	86.73	79.94	-6.79	0.04097	2	0.05328	2	0.76891	34	1434	1432	34	2	1432	77.9	0.0312	43	2286	2286	43	0	2286	86.7	0.05074	43	1691	1691	43	0	1691	75.5	0.05963	59	1950	1950	59	0	1950	74.9	0.04694	49	7220	7213	49	7	7213	86.7	0.04604	339	36968	5.3
SpII	BB_0639	BB_0639	spermidine/putrescine ABC transpo	81.9	76.72	-5.18	0.01661	2	0.01806	2	0.91971	34	630	630	34	0	630	70.1	0.01337	40	918	918	40	0	918	81.6	0.01985	43	644	644	43	0	644	70.7	0.02212	53	597	597	53	0	597	72.7	0.014	58	2714	2714	58	0	2714	83.9	0.01687	348	40681	5.9
SpII	BB_0840	BB_0840	predicted coding region BB0840	32.16	27.7	-4.46	0.00033	2	0.00021	2	1.59903	13	36	36	13	0	36	32.2	0.00049	4	12	12	4	0	12	13.2	0.00017	3	7	7	3	0	7	10.6	0.00016	9	17	17	9	0	17	27.7	0.00026	16	70	70	16	0	70	36.6	0.00028	538	62131	8.9
SpII	BB_A25	BB_A25	decorin binding protein B (dbpB)	20.32	9.63	-10.69	0.00016	2	5.4E-05	2	2.94444	2	6	6	2	0	6	10.7	0.00024	2	2	2	2	0	2	15.5	8E-05	1	1	1	1	0	1	9.63	6.4E-05	1	1	1	1	0	1	9.63	4.4E-05	3	10	10	3	0	10	20.3	0.00012	187	20398	9.6
SpII	BB_A60	BB_A60	surface lipoprotein P27	79.42	9.75	-69.67	0.00236	2	7.3E-05	2	32.3425	14	62	62	14	0	62	48.4	0.00165	26	113	113	26	0	113	78	0.00307	2	2	2	2	0	2	9.75	8.6E-05	1	2	2	1	0	2	5.42	5.9E-05	31	178	178	31	0	178	79.4	0.00139	277	32444	9.1
SpII	BB_A66	BB_A66	antigen	0	3.89	3.89	0	0	0.00004	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.89	4E-05	1	2	2	1	0	2	3.89	1.1E-05	411	45874	9.2
SpII	BB_A73	BB_A73	antigen	6.08	0	-6.08	5.1E-05	1	0	0	∞	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.08	5.1E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.08	1.5E-05	296	34647	8.9
SpII	BB_J08	BB_J08	predicted coding region BBJ08	2.29	10.46	8.17	0	0	5.3E-05	1	0	1	8	0	0	8	0	2.29	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	10.5	5.3E-05	2	10	2	1	8	2.03	12.8	1.4E-05	306	34640	8.9
SpII	BB_K47	BB_K47	predicted coding region BBK47	51.22	0	-51.22	0.0005	2	0	0	∞	12	37	12	5	25	30.8	45.4	0.00069	10	19	5	3	14	13.6	40.9	0.00031	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	16	56	15	5	41	41.4	51.2	0.00027	328	37091	5.9
SpII	BB_K49	BB_K49	predicted coding region BBK49	45.92	0	-45.92	0.00018	2	0	0	∞	10	29	4	3	25	10.3	39.6	0.00023	9	15	2	2	13	5.43	37.2	0.00012	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	15	44	6	4	38	16.6	45.9	0.00011	331	37658	6.2
SpI	BB_0016	BB_0016	glpE protein (glpE)	28.8	9.6	-19.2	8.9E-05	2	0.00036	2	0.2493	2	2	2	2	0	2	16.8	0.00012	1	1	1	1	0	1	12	6E-05	1	2	2	1	0	2	9.6	0.00019	1	8	8	1	0	8	9.6	0.00052	3	13	13	3	0	13	28.8	0.00023	125	14557	10
SpI	BB_0019	BB_0019	predicted coding region BB0019	27.06	15.88	-11.18	0.00026	2	0.00038	2	0.69129	3	8	8	3	0	8	22.9	0.00035	3	4	4	3	0	4	20.6	0.00018	3	6	6	3	0	6	15.9	0.00042	4	7	7	4	0	7	15.9	0.00034	5	22	22	5	0	22	27.1	0.00028	170	19274	6.1
SpI	BB_0027	BB_0027	predicted coding region BB0027	17.92	32.08	14.16	0.00222	2	0.00433	2	0.51236	1	3	3	1	0	3	7.08	0.0001	2	122	122	2	0	122	17.9	0.00433	3	19	19	3	0	19	28.3	0.00107	6	197	197	6	0	197	32.1	0.00758	5	339	339	5	0	339	32.1	0.00346	212	23865	9.1
SpI	BB_0031	BB_0031	signal peptidase I (lepB-2)	4.6	19.94	15.34	2.3E-05	1	0.00014	2	0.16912	1	1	1	1	0	1	4.6	2.3E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	10.4	0.00015	3	5	5	3	0	5	15	0.00013	5	10	10	5	0	10	24.5	6.6E-05	326	38481	8.9
SpI	BB_0032	BB_0032	predicted coding region BB0032	17.14	34.9	17.76	0.00018	2	0.00051	2	0.35756	7	16	16	7	0	16	15.7	0.00024	4	8	8	4	0	8	14.1	0.00012	12	26	26	12	0	26	28.2	0.00063	12	23	23	12	0	23	24.5	0.00038	20	72	72	20	0	72	35.7	0.00032	490	57590	9.3
SpI	BB_0034	BB_0034	predicted coding region BB0034	32.96	51.4	18.44	0.0115	2	0.03218	2	0.35736	13	215	215	13	0	215	33	0.00887	11	336	336	11	0	336	33	0.01412	16	468	468	16	0	468	46.4	0.03125	23	726	726	23	0	726	48	0.0331	14	1699	1699	14	0	1699	37.4	0.02054	179	19104	8.6
SpI	BB_0038	BB_0038	predicted coding region BB0038	3.17	9.5	6.33	2.9E-05	1	0.00012	1	0.24576	1	2	2	1	0	2	3.17	2.9E-05	X	X	X	X	X	X	X	X	3	5	5	3	0	5	9.5	0.00012	X	X	X	X	X	X	X	X	4	7	7	4	0	7	12.7	3E-05	505	59024	6.7
SpI	BB_0058	BB_0058	predicted coding region BB0058	10.06	15.7	5.64	5.6E-05	1	0.00013	1	0.42748	4	5	5	4	0	5	10.1	5.6E-05	X	X	X	X	X	X	X	X	6	11	11	6	0	11	11.9	0.0002	3	5	5	3	0	5	5.64	6.2E-05	10	21	21	10	0	21	18.3	6.9E-05	656	76395	7.9
SpI	BB_0063	BB_0063	predicted coding region BB0063	12.54	20.9	8.36	7.8E-05	2	0.00042	2	0.18483	2	5	5	2	0	5	9.55	0.00011	1	2	2	1	0	2	2.99	4.5E-05	4	10	10	4	0	10	20.9	0.00036	3	20	20	3	0	20	16.7	0.00049	6	37	37	6	0	37	28.4	0.00024	335	37306	8.8
SpI	BB_0087	BB_0087	L-lactate dehydrogenase (ldh)	42.41	40.51	-1.9	0.00045	2	0.00124	2	0.35858	10	35	33	10	2	33	39.6	0.00077	3	5	5	3	0	5	17.1	0.00012	4	11	11	4	0	11	22.2	0.00042	12	80	80	12	0	80	40.5	0.00207	18	131	131	18	0	131	49.4	0.0009	316	34901	6.9
SpI	BB_0126	BB_0126	predicted coding region BB0126	64.53	66.5	1.97	0.00502	2	0.01015	2	0.49468	14	119	119	14	0	119	58.1	0.00433	13	154	154	13	0	154	57.6	0.00571	10	120	120	10	0	120	56.7	0.00707	20	329	329	20	0	329	66.5	0.01323	20	715	715	20	0	715	64.5	0.00762	203	23595	5.3
SpI	BB_0142	BB_0142	predicted coding region BB0142	42.73	46.36	3.63	0.00137	2	0.00554	2	0.2468	15	113	113	15	0	113	38.2	0.0019	12	49	49	12	0	49	29.3	0.00084	9	178	178	9	0	178	28.4	0.00484	26	337	337	26	0	337	46.4	0.00625	29	622	622	29	0	622	45.5	0.00306	440	50847	8.7
SpI	BB_0159	BB_0159	predicted coding region BB0159	11.16	16.52	5.36	0.00013	2	0.00013	2	1.06349	1	1	1	1	0	1	6.25	3.3E-05	2	7	7	2	0	7	11.2	0.00024	1	2	2	1	0	2	6.7	0.00011	2	4	4	2	0	4	9.82	0.00015	4	12	12	4	0	12	11.2	0.00012	224	25805	9.1
SpI	BB_0202	BB_0202	hemolysin	3.88	10.68	6.8	1.8E-05	1	8.7E-05	1	0.2069	1	1	1	1	0	1	3.88	1.8E-05	X	X	X	X	X	X	X	X	3	3	3	3	0	3	10.7	8.7E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	7.77	1.6E-05	412	46391	9.2
SpI	BB_0204	BB_0204	Lambda CII stability-governing prot	25.39	30.03	4.64	0.00028	2	0.00065	2	0.42813	4	10	10	4	0	10	13	0.00023	7	14	14	7	0	14	21.1	0.00033	4	7	7	4	0	7	12.1	0.00026	11	41	41	11	0	41	26.9	0.00104	12	71	71	12	0	71	27.9	0.00048	323	37194	9.6
SpI	BB_0209	BB_0209	predicted coding region BB0209	11.37	10.59	-0.78	0.00015	1	9.5E-05	2	1.52632	2	5	5	2	0	5	11.4	0.00014	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.67	9.4E-05	2	3	3	2	0	3	9.02	9.6E-05	4	10	10	4	0	10	15.3	8.5E-05	255	30055	8.4
SpI	BB_0210	BB_0210	surface-located membrane protein	34.32	40.13	5.81	0.001	2	0.00181	2	0.55132	29	98	98	29	0	98	25.4	0.00065	29	201	201	29	0	201	29.2	0.00135	24	114	114	24	0	114	21.2	0.00122	54	332	330	54	2	330	38	0.00241	62	733	733	62	0	733	44.5	0.00142	1119	128086	9.2
SpI	BB_0236	BB_0236	predicted coding region BB0236	3.59	12.72	9.13	1.1E-05	1	7.2E-05	2	0.15278	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.59	1.1E-05	4	6	6	4	0	6	12.7	0.00011	1	3	3	1	0	3	3.59	3.7E-05	4	10	10	4	0	10	12.7	3.2E-05	668	75351	8.7
SpI	BB_0237	BB_0237	acid-inducible protein (act206)	31.29	31.29	0	0.00024	2	0.00053	2	0.44592	6	22	22	6	0	22	20	0.00031	6	11	11	6	0	11	13.8	0.00016	3	7	7	3	0	7	7.68	0.00016	11	57	57	11	0	57	28.8	0.00089	15	83	83	15	0	83	34.6	0.00034	521	59737	9.2
SpI	BB_0238	BB_0238	predicted coding region BB0238	0	11.83	11.83	0	0	6.1E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	4.58	9.1E-05	1	1	1	1	0	1	7.25	3.1E-05	2	3	3	2	0	3	11.8	2.5E-05	262	30379	8.3
SpI	BB_0259	BB_0259	predicted coding region BB0259	35.55	36.36	0.81	0.00024	2	0.00041	2	0.5878	14	40	40	14	0	40	28.2	0.0004	5	8	8	5	0	8	12.8	8.2E-05	16	43	43	16	0	43	34.1	0.0007	5	11	11	5	0	11	13.4	0.00012	23	97	97	23	0	97	44.9	0.00028	737	86337	9
SpI	BB_0261	BB_0261	predicted coding region BB0261	17.83	26.52	8.69	0.00012	2	0.00028	2	0.4306	5	12	12	5	0	12	13.7	0.00019	3	3	3	3	0	3	10.7	4.9E-05	4	10	10	4	0	10	12	0.00026	12	17	17	12	0	17	26.5	0.0003	14	41	41	14	0	41	31.1	0.00019	460	54024	9.4
SpI	BB_0265	BB_0265	predicted coding region BB0265	0	29.48	29.48	0	0	0.0002	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	11	6.9E-05	2	7	7	2	0	7	18.5	0.00033	3	8	8	3	0	8	29.5	0.0001	173	20158	8.3
SpI	BB_0276	BB_0276	flagellar biosynthesis protein (fliZ)	8.17	19.71	11.54	3.6E-05	1	0.0002	1	0.18367	1	1	1	1	0	1	8.17	3.6E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	4	5	5	4	0	5	19.7	0.0002	4	5	5	4	0	5	13	5.2E-05	208	24405	5.9
SpI	BB_0315	BB_0315	predicted coding region BB0315	16.23	10.09	-6.14	0.00016	1	0.00014	1	1.13287	4	5	5	4	0	5	16.2	0.00016	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	4	4	1	0	4	10.1	0.00014	4	9	9	4	0	9	16.2	8.5E-05	228	26880	9.4
SpI	BB_0319	BB_0319	exported protein (tpn38b)	72.57	69.43	-3.14	0.00237	2	0.00441	2	0.53661	15	100	100	15	0	100	62.6	0.00211	14	122	122	14	0	122	58.6	0.00262	12	74	74	12	0	74	50.9	0.00253	28	270	270	28	0	270	69.4	0.0063	25	552	552	25	0	552	72.6	0.00341	350	40130	8
SpI	BB_0336	BB_0336	P26	0	9.56	9.56	0	0	0.00255	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	79	79	1	0	79	5.58	0.00376	2	41	41	2	0	41	9.56	0.00133	1	2	2	1	0	2	3.98	1.7E-05	251	29765	6.8
SpI	BB_0359	BB_0359	carboxyl-terminal protease (ctp)	59.16	61.26	2.1	0.00151	2	0.00392	2	0.38511	23	127	127	23	0	127	51	0.00198	21	66	66	21	0	66	48	0.00105	21	171	171	21	0	171	38.5	0.0043	32	206	206	32	0	206	59.4	0.00354	37	562	562	37	0	562	61.1	0.00256	475	53542	8.3
SpI	BB_0368	BB_0368	glycerol-3-phosphate dehydrogena	39.39	44.08	4.69	0.00201	2	0.00359	2	0.55955	8	133	133	8	0	133	35.8	0.00271	6	63	63	6	0	63	29.8	0.00131	7	129	129	7	0	129	32	0.00425	11	130	130	11	0	130	44.1	0.00292	13	455	455	13	0	455	49.6	0.00271	363	40697	6.2
SpI	BB_0393	BB_0393	ribosomal protein L11 (rplK)	32.87	41.96	9.09	0.00026	2	0.00034	2	0.77679	2	4	4	2	0	4	21	0.00021	2	6	6	2	0	6	23.8	0.00032	4	6	6	4	0	6	42	0.0005	1	3	3	1	0	3	11.9	0.00017	4	18	18	4	0	18	39.9	0.00027	143	15168	10
SpI	BB_0395	BB_0395	preprotein translocase subunit (sec	19.64	19.64	0	0.00047	2	0.00054	2	0.85478	2	4	4	2	0	4	19.6	0.00053	1	3	3	1	0	3	19.6	0.0004	1	1	1	1	0	1	19.6	0.00021	3	6	6	3	0	6	19.6	0.00087	3	14	14	3	0	14	19.6	0.00054	56	6695	9.2
SpI	BB_0405	BB_0405	predicted coding region BB0405	53.2	66.01	12.81	0.00553	2	0.02236	2	0.2474	19	137	137	19	0	137	50.7	0.00499	19	164	164	19	0	164	47.8	0.00608	9	255	255	9	0	255	27.1	0.01502	31	739	739	31	0	739	66	0.02971	27	1252	1252	27	0	1252	56.7	0.01334	203	22252	5.2
SpI	BB_0406	BB_0406	predicted coding region BB0406	38.42	38.92	0.5	0.00154	2	0.00234	2	0.65841	6	43	43	6	0	43	35	0.00156	7	41	41	7	0	41	32	0.00152	6	14	14	6	0	14	32	0.00082	9	96	96	9	0	96	35.5	0.00386	9	191	191	9	0	191	38.4	0.00204	203	22800	8.3
SpI	BB_0418	BB_0418	predicted coding region BB0418	32.46	40.35	7.89	0.00119	2	0.00229	2	0.52035	8	48	48	8	0	48	26	0.00104	10	61	61	10	0	61	26.3	0.00134	9	27	27	9	0	27	25.7	0.00094	20	152	152	20	0	152	40.4	0.00363	15	280	280	15	0	280	39.8	0.00177	342	38773	9
SpI	BB_0420	BB_0420	sensory transduction histidine kina	0	4.89	4.89	0	0	1.6E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	1.34	1.6E-05	3	3	3	3	0	3	3.55	1.6E-05	3	4	4	3	0	4	3.61	5.8E-06	1494	172818	8.1
SpI	BB_0504	BB_0504	conserved hypothetical protein	11.18	22.75	11.57	4.4E-05	2	0.00023	2	0.19214	3	4	4	3	0	4	8.63	5.8E-05	1	2	2	1	0	2	2.55	3E-05	5	10	10	5	0	10	12.9	0.00023	7	14	14	7	0	14	16.7	0.00022	11	28	28	11	0	28	23.9	0.00012	510	58003	7.2
SpI	BB_0537	BB_0537	conserved hypothetical protein	18.22	33.64	15.42	0.00023	2	0.00034	2	0.66082	4	8	8	4	0	8	18.2	0.00028	3	5	5	3	0	5	18.2	0.00018	1	2	2	1	0	2	5.14	0.00011	7	15	15	7	0	15	33.6	0.00057	9	30	30	9	0	30	33.6	0.0003	214	24700	9.3
SpI	BB_0543	BB_0543	predicted coding region BB0543	46.33	56.88	10.55	0.00718	2	0.01361	2	0.5273	8	175	175	8	0	175	46.3	0.00593	9	244	244	9	0	244	46.3	0.00842	14	82	82	14	0	82	56.9	0.0045	23	607	607	23	0	607	56.9	0.02272	13	1006	1006	13	0	1006	50.9	0.00998	218	24388	5.2
SpI	BB_0546	BB_0546	predicted coding region BB0546	59.09	48.95	-10.14	0.00242	2	0.00209	2	1.16211	15	99	99	15	0	99	48.3	0.00256	18	87	87	18	0	87	59.1	0.00229	10	24	24	10	0	24	34.6	0.001	18	111	111	18	0	111	49	0.00317	22	318	318	22	0	318	59.1	0.00241	286	32430	9.4
SpI	BB_0575	BB_0575	CTP synthase (pyrG)	17.64	29.27	11.63	0.0001	2	0.0004	2	0.25743	6	14	14	6	0	14	15	0.00019	1	1	1	1	0	1	2.63	1.4E-05	8	19	19	8	0	19	19.1	0.00043	9	25	25	9	0	25	24.6	0.00038	13	59	59	13	0	59	31.1	0.00024	533	59398	8
SpI	BB_0588	BB_0588	pfs protein (pfs-2)	20.75	5.66	-15.09	0.00011	1	3.1E-05	1	3.6129	3	4	4	3	0	4	20.8	0.00011	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.66	3.1E-05	3	4	4	3	0	4	20.8	3.3E-05	265	29088	9.3
SpI	BB_0603	BB_0603	membrane-associated protein p66	48.38	57.93	9.55	0.00159	2	0.00494	2	0.32165	21	117	117	21	0	117	34.1	0.0014	25	146	146	25	0	146	44.3	0.00178	18	107	107	18	0	107	37.5	0.00207	39	591	591	39	0	591	53.2	0.0078	41	927	927	41	0	927	63.1	0.00325	618	68172	6.3
SpI	BB_0646	BB_0646	predicted coding region BB0646	54.74	48.32	-6.42	0.00068	2	0.00178	2	0.37892	8	14	14	8	0	14	31.2	0.00032	13	45	45	13	0	45	43.4	0.00104	11	28	28	11	0	28	40.4	0.00102	16	102	102	16	0	102	44	0.00255	21	178	178	21	0	178	54.7	0.00118	327	37596	9.5
SpI	BB_0668	BB_0668	flagellar filament outer layer protein	0	16.57	16.57	0	0	5.8E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	9.01	7E-05	2	2	2	2	0	2	7.56	4.7E-05	3	3	3	3	0	3	12.8	1.9E-05	344	38835	8.1
SpI	BB_0714	BB_0714	predicted coding region BB0714	13.98	21.74	7.76	0.00012	2	0.00022	2	0.52727	3	6	6	3	0	6	14	0.00014	1	4	4	1	0	4	4.04	9.3E-05	3	5	5	3	0	5	10.9	0.00019	4	10	10	4	0	10	13.4	0.00025	6	25	25	6	0	25	21.7	0.00017	322	38625	7.3
SpI	BB_0739	BB_0739	predicted coding region BB0739	0	23.59	23.59	0	0	0.00014	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	4	4	1	0	4	7.69	0.00025	1	1	1	1	0	1	15.9	4.2E-05	2	5	5	2	0	5	23.6	5.5E-05	195	23102	8.1
SpI	BB_0744	BB_0744	antigen	0	1.57	1.57	0	0	3.4E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	1.57	3.4E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	1.57	6.2E-06	700	79929	5.3
SpI	BB_0751	BB_0751	predicted coding region BB0751	71.15	70.03	-1.12	0.00397	2	0.00806	2	0.49268	32	225	225	32	0	225	65.6	0.00466	28	156	156	28	0	156	64.2	0.00329	22	146	145	22	1	145	60.5	0.00485	35	493	493	35	0	493	70	0.01127	44	1019	1018	44	1	1018	71.2	0.00617	357	41901	6.5
SpI	BB_0776	BB_0776	predicted coding region BB0776	55.08	47.59	-7.49	0.00142	2	0.00192	2	0.73852	4	37	37	4	0	37	35.3	0.00146	6	34	34	6	0	34	38	0.00137	3	19	19	3	0	19	17.7	0.00121	7	60	60	7	0	60	47.6	0.00262	12	144	144	12	0	144	57.8	0.00167	187	21522	9.1
SpI	BB_0795	BB_0795	outer membrane protein	41.9	56.76	14.86	0.00133	2	0.00234	2	0.56899	30	177	177	30	0	177	36.9	0.00159	27	117	117	27	0	117	34.5	0.00107	18	69	69	18	0	69	28.6	0.001	41	377	370	41	7	370	54.6	0.00368	49	735	735	49	0	735	58.3	0.00194	821	94568	6.4
SpI	BB_0796	BB_0796	predicted coding region BB0796	0	10.81	10.81	0	0	8.8E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	10.8	8.8E-05	1	2	2	1	0	2	10.8	2.3E-05	185	21446	8.3
SpI	BB_0811	BB_0811	predicted coding region BB0811	0	6.82	6.82	0	0	2.1E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	4.69	2.5E-05	1	1	1	1	0	1	2.13	1.7E-05	2	2	2	2	0	2	6.82	9.2E-06	469	53095	8.6
SpI	BB_0838	BB_0838	predicted coding region BB0838	29.14	36.47	7.33	0.00025	2	0.00044	2	0.56787	13	32	32	13	0	32	15.1	0.00021	17	45	45	17	0	45	20.7	0.0003	11	22	22	11	0	22	14.6	0.00023	32	92	92	32	0	92	33.5	0.00066	37	183	183	37	0	183	40.8	0.00035	1146	134380	8.5
SpI	BB_A52	BB_A52	outer membrane protein	17.44	24.56	7.12	0.00008	1	0.0003	2	0.26667	X	X	X	X	X	X	X	X	2	3	3	2	0	3	17.4	8E-05	5	10	10	5	0	10	24.6	0.00043	2	6	6	2	0	6	6.76	0.00017	4	18	18	4	0	18	24.2	0.00014	281	33103	8.7
SpI	BB_B24	BB_B24	predicted coding region BBB24	13.1	7.14	-5.96	4.4E-05	1	0.00014	1	0.30986	1	1	1	1	0	1	13.1	4.4E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	7.14	0.00014	X	X	X	X	X	X	X	X	2	3	3	2	0	3	20.2	3.9E-05	168	20116	9.9
SpI	BB_E09	BB_E09	protein p23	13.24	0	-13.24	0.00021	1	0	0	∞	2	8	8	2	0	8	13.2	0.00021	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	8	8	2	0	8	13.2	6E-05	287	34057	6.8
SpI	BB_E16	BB_E16	predicted coding region BBE16	5.34	20.87	15.53	3.7E-05	1	0.00023	2	0.1588	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.34	3.7E-05	4	6	6	4	0	6	20.9	0.00035	2	3	3	2	0	3	13.6	0.00012	5	10	10	5	0	10	26.2	0.00011	206	24534	9.3
SpI	BB_F24	BB_F24	conserved hypothetical protein	38.98	36.22	-2.76	0.00034	2	0.00056	2	0.59609	7	20	20	7	0	20	39	0.00058	2	3	3	2	0	3	7.87	8.9E-05	6	15	15	6	0	15	18.9	0.00071	5	13	13	5	0	13	33.1	0.00042	11	51	51	11	0	51	42.1	0.00043	254	29653	8.7
SpI	BB_J29	BB_J29;BB_J43	predicted coding region BBJ29	0	4.64	4.64	0	0	4.7E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	4.64	4.7E-05	1	2	2	1	0	2	4.64	1.3E-05	345	40963	5
SpI	BB_K45	BB_K45	immunogenic protein P37	58.71	13.23	-45.48	0.00374	2	0.00035	1	10.7752	19	158	158	19	0	158	51.9	0.00377	18	153	153	18	0	153	56.1	0.00371	3	9	9	3	0	9	13.2	0.00035	X	X	X	X	X	X	X	X	28	320	320	28	0	320	58.7	0.00223	310	35323	9.5
SpI	BB_M26	BB_M26	conserved hypothetical protein	24.37	25.21	0.84	0.00017	1	7.6E-05	2	2.18421	2	3	2	1	1	2.67	24.4	0.00017	X	X	X	X	X	X	X	X	2	2	0	0	2	0.83	25.2	8.4E-05	1	2	0	0	2	1	9.24	6.9E-05	4	7	2	1	5	5	34.5	9.1E-05	119	13880	9.1
SpI	BB_P26	BB_P26	conserved hypothetical protein	15.13	22.69	7.56	0	0	5.1E-05	2	0	1	1	0	0	1	0	15.1	X	X	X	X	X	X	X	X	X	1	1	0	0	1	0.33	15.1	3.3E-05	1	1	1	1	0	1	22.7	6.9E-05	2	3	1	1	2	1.5	22.7	2.7E-05	119	13880	9.2
SpI	BB_Q33	BB_Q33	conserved hypothetical protein	22.69	25.21	2.52	8.3E-05	1	7.6E-05	2	1.09211	2	2	1	1	1	1.33	22.7	8.3E-05	X	X	X	X	X	X	X	X	2	2	0	0	2	0.83	25.2	8.4E-05	1	2	0	0	2	1	9.24	6.9E-05	4	6	1	1	5	2.5	32.8	4.5E-05	119	13877	9.1
TM	BB_0006	BB_0006	conserved hypothetical integral me	8.56	22.46	13.9	0.00014	2	0.00074	2	0.1886	1	11	11	1	0	11	6.15	0.00022	2	3	3	2	0	3	8.56	6E-05	4	12	12	4	0	12	15.5	0.00038	6	50	50	6	0	50	22.5	0.00109	7	76	76	7	0	76	24.9	0.00044	374	42911	9.4
TM	BB_0039	BB_0039	predicted coding region BB0039	43	69.6	26.6	0.00041	2	0.00182	2	0.22467	17	43	43	17	0	43	41.4	0.00064	3	12	12	3	0	12	5.8	0.00018	29	113	113	29	0	113	64.8	0.0027	16	57	57	16	0	57	34.4	0.00093	37	219	219	37	0	219	71.4	0.00095	500	58503	9.1
TM	BB_0044	BB_0044	predicted coding region BB0044	18.05	17.29	-0.76	5.7E-05	1	0.00025	1	0.23265	X	X	X	X	X	X	X	X	1	1	1	1	0	1	18.1	5.7E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	17.3	0.00025	3	5	5	3	0	5	24.8	8.1E-05	133	16053	4.9
TM	BB_0054	BB_0054	predicted coding region BB0054	34.4	34.4	0	0.00146	2	0.00186	2	0.78273	7	29	29	7	0	29	34.4	0.00171	7	20	20	7	0	20	34.4	0.0012	4	11	11	4	0	11	32	0.00105	8	41	41	8	0	41	34.4	0.00268	8	99	99	8	0	99	34.4	0.00171	125	14015	4.9
TM	BB_0104	BB_0104	periplasmic serine protease DO (ht	14.91	40.58	25.67	0.00016	2	0.0007	2	0.22869	5	15	15	5	0	15	14.9	0.00023	2	6	6	2	0	6	7.04	9.3E-05	14	48	48	14	0	48	35.4	0.00119	7	13	13	7	0	13	17.4	0.00022	17	82	82	17	0	82	40.6	0.00037	483	53104	9.1
TM	BB_0106	BB_0106	predicted coding region BB0106	3.51	7.03	3.52	3.3E-05	2	0.00011	2	0.3	1	4	4	1	0	4	3.51	5.2E-05	1	1	1	1	0	1	3.51	1.3E-05	2	5	5	2	0	5	7.03	0.00011	2	8	8	2	0	8	3.51	0.00011	3	18	18	3	0	18	7.03	6.8E-05	569	67849	9
TM	BB_0140	BB_0140	acriflavine resistance protein (acrB)	5.79	29.25	23.46	1.8E-05	2	0.00019	2	0.09326	1	2	2	1	0	2	1.83	1.4E-05	2	3	3	2	0	3	3.96	2.2E-05	6	11	11	6	0	11	11	0.00013	15	33	33	15	0	33	24.7	0.00026	17	48	48	17	0	48	26.9	0.0001	1036	115439	8.2
TM	BB_0203	BB_0203	Lambda CII stability-governing prot	32.48	28.94	-3.54	0.00038	2	0.00086	2	0.44496	5	15	15	5	0	15	22.2	0.00036	4	17	17	4	0	17	21.5	0.00041	2	21	21	2	0	21	9	0.00081	7	35	35	7	0	35	28.9	0.00092	9	88	88	9	0	88	32.5	0.00061	311	35825	5.3
TM	BB_0240	BB_0240	glycerol uptake facilitator (glpF)	7.48	7.48	0	0.00003	1	0.00053	2	0.05682	X	X	X	X	X	X	X	X	1	1	1	1	0	1	7.48	3E-05	1	4	4	1	0	4	7.48	0.00019	2	27	27	2	0	27	7.48	0.00087	2	32	32	2	0	32	7.48	0.00027	254	27195	7.6
TM	BB_0257	BB_0257	cell division protein	0	14.61	14.61	0	0	0.0001	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	5.97	4.6E-05	4	15	15	4	0	15	12.1	0.00016	3	14	14	3	0	14	11.1	3.8E-05	787	90269	5.8
TM	BB_0263	BB_0263	signal peptidase I (lepB-3)	8.33	8.33	0	4.4E-05	1	0.00006	2	0.73333	1	1	1	1	0	1	8.33	4.4E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	8.33	7.1E-05	1	1	1	1	0	1	8.33	4.9E-05	1	3	3	1	0	3	8.33	3.9E-05	168	19837	9.6
TM	BB_0268	BB_0268	conserved hypothetical protein	35.85	37.74	1.89	0.00026	2	0.00079	2	0.32614	4	8	8	4	0	8	22	0.00037	2	3	3	2	0	3	20.1	0.00014	4	8	8	4	0	8	23.9	0.0006	6	19	19	6	0	19	33.3	0.00098	9	38	38	9	0	38	40.3	0.00052	159	18344	5.7
TM	BB_0271	BB_0271	flagellar biosynthesis protein (flhA)	17.93	32.14	14.21	0.00024	2	0.00069	2	0.34307	6	29	29	6	0	29	17.7	0.00031	6	15	15	6	0	15	11.5	0.00016	10	26	26	10	0	26	18.7	0.00045	18	79	79	18	0	79	29.3	0.00092	19	146	146	19	0	146	31	0.00045	697	76969	5.2
TM	BB_0279	BB_0279	flagellar protein (fliL)	62.92	63.48	0.56	0.01364	2	0.0184	2	0.74138	7	199	199	7	0	199	51.7	0.00826	12	450	450	12	0	450	62.9	0.01902	14	238	238	14	0	238	56.2	0.01598	15	454	454	15	0	454	43.3	0.02081	15	1310	1310	15	0	1310	73.6	0.01592	178	20060	5.4
TM	BB_0280	BB_0280	flagellar motor rotation protein B (m	41.54	43.08	1.54	0.00079	2	0.00272	2	0.28876	6	36	36	6	0	36	31.9	0.00102	6	19	19	6	0	19	21.2	0.00055	9	87	87	9	0	87	31.9	0.004	10	46	46	10	0	46	36.5	0.00144	12	188	188	12	0	188	52.7	0.00156	260	29206	6.1
TM	BB_0281	BB_0281	flagellar motor rotation protein A (m	15.77	50.38	34.61	0.00033	2	0.00088	2	0.37472	3	13	13	3	0	13	12.3	0.00037	3	10	10	3	0	10	11.2	0.00029	5	15	15	5	0	15	25.8	0.00069	8	34	34	8	0	34	43.9	0.00107	8	71	71	8	0	71	40.4	0.00059	260	28354	5.3
TM	BB_0286	BB_0286	flagellar protein (flbB)	40.1	40.58	0.48	0.00029	2	0.0011	2	0.2602	4	12	12	4	0	12	35.8	0.00043	2	4	4	2	0	4	16.4	0.00015	7	15	15	7	0	15	33.3	0.00087	6	34	34	6	0	34	40.1	0.00134	10	65	65	10	0	65	47.3	0.00068	207	24579	6.3
TM	BB_0332	BB_0332	oligopeptide ABC transporter	13.07	13.73	0.66	0.00017	2	0.00043	2	0.39394	4	12	12	4	0	12	13.1	0.00029	1	2	2	1	0	2	4.25	4.9E-05	2	9	9	2	0	9	7.84	0.00035	4	19	19	4	0	19	13.1	0.00051	6	42	42	6	0	42	13.7	0.0003	306	34061	9.8
TM	BB_0353	BB_0353	predicted coding region BB0353	3.34	4.67	1.33	1.2E-05	1	5.4E-05	1	0.22222	1	1	1	1	0	1	3.34	1.2E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	4	4	3	0	4	4.67	5.4E-05	4	5	5	4	0	5	8.01	1.8E-05	599	71260	9
TM	BB_0354	BB_0354	predicted coding region BB0354	0	6.65	6.65	0	0	5.8E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.47	6.9E-05	1	2	2	1	0	2	3.18	4.7E-05	2	4	4	2	0	4	6.65	2.5E-05	346	41138	9.2
TM	BB_0362	BB_0362	prolipoprotein diacylglyceryl transfe	15.85	21.04	5.19	0.0005	2	0.0011	2	0.45281	3	27	27	3	0	27	15.9	0.00061	2	17	17	2	0	17	12.2	0.00039	3	25	25	3	0	25	15.9	0.00091	6	52	52	6	0	52	21	0.00129	4	108	108	4	0	108	21	0.00071	328	37595	8.9
TM	BB_0401	BB_0401	glutamate transporter	0	6.75	6.75	0	0	4.1E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	6.75	4.1E-05	2	2	2	2	0	2	6.75	1.1E-05	400	45713	9.5
TM	BB_0469	BB_0469	signal peptidase II (lsp)	0	23.53	23.53	0	0	0.00029	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	8.24	0.00014	2	9	9	2	0	9	23.5	0.00043	1	10	10	1	0	10	8.24	0.00013	170	19976	9.8
TM	BB_0498	BB_0498	preprotein translocase subunit (sec	4.84	13.36	8.52	7.7E-05	2	0.00018	2	0.42778	3	7	7	3	0	7	4.84	0.00012	1	2	2	1	0	2	1.61	3.5E-05	6	9	9	6	0	9	11.8	0.00025	3	6	6	3	0	6	7.6	0.00011	9	24	24	9	0	24	13.4	0.00012	434	48610	9.7
TM	BB_0526	BB_0526	predicted coding region BB0526	12.52	5.44	-7.08	0.00016	1	0.00004	2	3.95	6	13	13	6	0	13	12.5	0.00016	X	X	X	X	X	X	X	X	1	2	2	1	0	2	2.14	3.9E-05	2	3	3	2	0	3	3.29	4E-05	9	18	18	9	0	18	18	6.4E-05	607	70953	8.6
TM	BB_0539	BB_0539	conserved hypothetical integral me	22.41	10.78	-11.63	0.00069	2	0.00053	2	1.31238	7	27	27	7	0	27	10.8	0.00086	5	16	16	5	0	16	22.4	0.00052	2	4	4	2	0	4	7.33	0.00021	7	24	24	7	0	24	10.8	0.00084	9	71	71	9	0	71	22.4	0.00066	232	25708	9.2
TM	BB_0563	BB_0563	predicted coding region BB0563	16.57	25.97	9.4	0.0007	2	0.00128	2	0.55051	2	9	9	2	0	9	9.94	0.00037	3	25	25	3	0	25	16.6	0.00104	3	10	10	3	0	10	16	0.00066	5	42	42	5	0	42	26	0.00189	5	86	86	5	0	86	26	0.00103	181	19824	9.9
TM	BB_0597	BB_0597	methyl-accepting chemotaxis prote	20.54	36.46	15.92	0.00018	2	0.00083	2	0.21282	11	31	31	11	0	31	18	0.00031	1	4	4	1	0	4	2.59	4.1E-05	11	56	56	11	0	56	18.6	0.00091	20	67	67	20	0	67	34.6	0.00074	24	153	153	24	0	153	34.6	0.00045	735	84570	5.6
TM	BB_0600	BB_0600	predicted coding region BB0600	2.51	9.27	6.76	1.4E-05	1	5.9E-05	2	0.23729	1	1	1	1	0	1	2.51	1.4E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.47	2.3E-05	2	6	6	2	0	6	5.79	9.5E-05	4	8	8	4	0	8	11.8	3.3E-05	518	60479	6.6
TM	BB_0602	BB_0602	chaperonin	10.8	14.4	3.6	4.5E-05	2	0.00018	2	0.25281	1	2	2	1	0	2	6	5.9E-05	1	1	1	1	0	1	4.8	3E-05	1	2	2	1	0	2	6	9.6E-05	3	8	8	3	0	8	14.4	0.00026	4	13	13	4	0	13	19.2	0.00011	250	29473	9.2
TM	BB_0604	BB_0604	L-lactate permease (lctP)	10.4	10.4	0	0.00019	2	0.00052	2	0.35441	4	24	24	4	0	24	10.4	0.00035	1	1	1	1	0	1	4.4	1.5E-05	3	15	15	3	0	15	10.4	0.00036	4	42	42	4	0	42	10.4	0.00069	4	82	82	4	0	82	10.4	0.00035	500	53680	9.2
TM	BB_0645	BB_0645	PTS system	4.86	24.51	19.65	0.0001	1	0.00015	2	0.70345	X	X	X	X	X	X	X	X	1	7	7	1	0	7	4.86	0.0001	3	5	5	3	0	5	9.53	0.00012	8	11	11	8	0	11	22.8	0.00017	7	21	21	7	0	21	16.7	8.8E-05	514	55843	9
TM	BB_0651	BB_0651	conserved hypothetical protein	55.24	35.24	-20	0.01146	2	0.02018	2	0.5681	4	115	115	4	0	115	31.4	0.00809	8	207	207	8	0	207	55.2	0.01483	5	164	164	5	0	164	35.2	0.01867	5	279	279	5	0	279	32.4	0.02168	8	761	761	8	0	761	55.2	0.01568	105	11840	9.6
TM	BB_0653	BB_0653	protein-export membrane protein (s	0	19.4	19.4	0	0	0.00016	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	7.69	0.00012	5	7	7	5	0	7	19.4	0.00019	5	10	10	5	0	10	19.4	7.2E-05	299	34057	9
TM	BB_0674	BB_0674	predicted coding region BB0674	0	3.45	3.45	0	0	4.7E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.45	4.7E-05	1	2	2	1	0	2	3.45	1.2E-05	348	41679	9.5
TM	BB_0680	BB_0680	methyl-accepting chemotaxis prote	13.81	24.83	11.02	9.8E-05	1	0.00022	2	0.45161	6	10	10	6	0	10	13.8	9.8E-05	X	X	X	X	X	X	X	X	9	15	15	9	0	15	17.9	0.00024	10	18	18	10	0	18	20.3	0.0002	15	42	42	15	0	42	25.2	0.00012	753	84579	5.1
TM	BB_0681	BB_0681	methyl-accepting chemotaxis prote	14.94	18.55	3.61	8.2E-05	2	0.00017	2	0.4881	6	10	10	6	0	10	12.9	0.00012	3	4	4	3	0	4	8.96	4.7E-05	4	7	7	4	0	7	5.82	0.00013	8	16	16	8	0	16	15.1	0.00021	13	35	35	13	0	35	23.4	0.00012	636	71460	5.9
TM	BB_0709	BB_0709	conserved hypothetical protein	46.65	53.35	6.7	0.00059	2	0.0013	2	0.45119	8	24	24	8	0	24	34.4	0.00052	9	30	30	9	0	30	37.9	0.00066	7	31	31	7	0	31	32.1	0.00108	16	64	64	16	0	64	47.2	0.00152	16	148	148	16	0	148	53.4	0.00093	343	39462	9
TM	BB_0729	BB_0729	glutamate transporter (gltP)	7.56	6.7	-0.86	9.6E-05	1	0.00025	2	0.39184	3	6	6	3	0	6	7.56	9.6E-05	X	X	X	X	X	X	X	X	2	6	6	2	0	6	4.1	0.00015	5	19	19	5	0	19	6.7	0.00033	6	31	31	6	0	31	10.4	0.00014	463	49621	9.6
TM	BB_0753	BB_0753	membrane spanning protein	6.97	15.57	8.6	6.2E-05	1	0.00021	2	0.29952	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.97	6.2E-05	1	3	3	1	0	3	6.97	0.00015	2	8	8	2	0	8	15.6	0.00027	2	13	13	2	0	13	15.6	0.00012	244	27646	9

Known (Table 1) and/or predicated subcellular location	Locus	Proteins In Group	Description	B31A3_Control_merged-SeqCov (%)	B31A3_ProK_merged-SeqCov (%)	DiffSeqCov (Control - ProK) (%)	B31A3_Cntl-Ti dNSAF AVG	B31A3_Cntl-Ti Detected # Out of 2	B31A3_PK-Ti dNSAF AVG	B31A3_PK-Ti Detected # Out of 2	B31A3_Cntl-Ti: B31A3_PK-Ti	B31A3_Control_1_P	B31A3_Control_1_S	B31A3_Control_1_uS	B31A3_Control_1_uDP	B31A3_Control_1_sS	B31A3_Control_1_dS	B31A3_Control_1_SC	B31A3_Control_1_dNSAF	B31A3_Control_2_P	B31A3_Control_2_S	B31A3_Control_2_uS	B31A3_Control_2_uDP	B31A3_Control_2_sS	B31A3_Control_2_dS	B31A3_Control_2_SC	B31A3_Control_2_dNSAF
TM	BB_0783	BB_0783	predicted coding region BB0783	19.29	28.17	8.88	0.0003	2	0.00036	2	0.83611	4	27	27	4	0	27	12.4	0.00051	2	5	5	2	0	5	12.9	9.5E-05
TM	BB_0789	BB_0789	cell division protein (ftsH)	20.03	27.39	7.36	8.7E-05	2	0.00041	2	0.21481	6	11	11	6	0	11	15.7	0.00013	2	4	4	2	0	4	7.98	4.7E-05
TM	BB_0824	BB_0824	predicted coding region BB0824	18.58	28.96	10.38	0.00018	2	0.01161	2	0.01576	2	5	5	2	0	5	10.4	0.0002	2	4	4	2	0	4	13.1	0.00016
TM	BB_0843	BB_0843	conserved hypothetical integral me	3.53	3.53	0	5.4E-05	2	0.00017	2	0.32143	1	6	6	1	0	6	3.32	9.2E-05	1	1	1	1	0	1	3.53	1.6E-05
TM	BB_B22	BB_B22	conserved hypothetical protein	5.99	14.19	8.2	0.00012	2	0.00025	2	0.45635	2	9	9	2	0	9	5.99	0.00015	1	5	5	1	0	5	1.77	8.3E-05
TM	BB_B28	BB_B28	predicted coding region BBB28	55.56	57.97	2.41	0.00143	2	0.00214	2	0.66651	21	121	121	21	0	121	55.6	0.00216	10	38	38	10	0	38	28.3	0.00069
TM	BB_B29	BB_B29	PTS system	52.95	49.08	-3.87	0.00713	2	0.02108	2	0.33805	26	677	677	26	0	677	42.3	0.00923	33	362	362	33	0	362	53	0.00503
TM	BB_D15	BB_D15	conserved hypothetical protein	20.71	6.43	-14.28	0.00027	2	8.5E-05	1	3.11765	4	7	7	4	0	7	14.3	0.00037	2	3	3	2	0	3	15	0.00016
TM	BB_J27	BB_J27	predicted coding region BBJ27	11.19	7.3	-3.89	0.00011	1	4.9E-05	2	2.20408	3	6	6	3	0	6	11.2	0.00011	X	X	X	X	X	X	X	X
TM	BB_K13	BB_K13	conserved hypothetical protein	14.71	43.7	28.99	9.5E-05	1	0.00103	1	0.09232	X	X	X	X	X	X	X	X	2	3	3	2	0	3	14.7	9.5E-05
TM	BB_0252	BB_0252	conserved hypothetical integral me	7.56	8.6	1.04	5.8E-05	2	0.00016	2	0.35802	4	8	8	4	0	8	7.56	7.7E-05	1	4	4	1	0	4	2.35	3.9E-05
TM	BB_0091	BB_0091	V-type ATPase	2.8	22.53	19.73	3.6E-05	1	0.00047	2	0.07742	1	3	3	1	0	3	2.8	3.6E-05	X	X	X	X	X	X	X	X
TM	BB_0408	BB_0408	PTS system	32.48	35.84	3.36	0.00173	2	0.00458	2	0.37656	30	186	186	30	0	186	31.7	0.0022	22	104	104	22	0	104	30.4	0.00125
TM	BB_0629	BB_0629	PTS system	28.12	35.46	7.34	0.00031	2	0.0009	2	0.3456	10	20	20	10	0	20	24.3	0.00024	9	32	32	9	0	32	21.3	0.00038
TM	BB_B04	BB_B04	PTS system	7	10.84	3.84	0.00013	2	0.00092	2	0.14597	2	9	9	2	0	9	5.87	0.00015	3	7	7	3	0	7	7	0.00012
TM	BB_0071	BB_0071	predicted coding region BB0071	4.08	11.84	7.76	1.5E-05	2	0.00017	2	0.08721	1	1	1	1	0	1	2.04	1.5E-05	1	1	1	1	0	1	2.04	1.5E-05
TM	BB_0333	BB_0333	oligopeptide ABC transporter	20.92	23.5	2.58	0.00019	2	0.00138	2	0.13881	5	13	13	5	0	13	20.6	0.00028	2	5	5	2	0	5	10.9	0.00011
TM	BB_0145	BB_0145	glycine betaine	5.02	5.02	0	9.9E-05	1	0.00008	1	1.2375	1	4	4	1	0	4	5.02	9.9E-05	X	X	X	X	X	X	X	X
TM	BB_0118	BB_0118	zinc protease	26.32	32.27	5.95	0.00049	2	0.00129	2	0.37664	8	25	25	8	0	25	19.9	0.00042	9	32	32	9	0	32	21.7	0.00055
TM	BB_0170	BB_0170	predicted coding region BB0170	20.23	30.21	9.98	0.00017	2	0.00051	2	0.3432	7	25	25	7	0	25	18.5	0.00027	3	7	7	3	0	7	6.89	7.7E-05
TM	BB_0442	BB_0442	inner membrane protein	8.27	16.18	7.91	5.5E-05	2	0.00013	2	0.41353	2	5	5	2	0	5	4.78	6.8E-05	1	3	3	1	0	3	3.49	4.1E-05
TM	BB_0157	BB_0157	predicted coding region BB0157	10.14	10.14	0	0.00011	2	0.0003	1	0.36486	1	2	2	1	0	2	10.1	0.00011	1	2	2	1	0	2	10.1	0.00011
TM	BB_0217	BB_0217	phosphate ABC transporter	5.18	18.6	13.42	2.3E-05	1	0.00035	2	0.06571	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.18	2.3E-05
TM	BB_0380	BB_0380	Mg2+ transport protein (mgtE)	4.19	10.13	5.94	4.9E-05	1	0.00004	2	1.225	2	3	3	2	0	3	4.19	4.9E-05	X	X	X	X	X	X	X	X
TM	BB_0416	BB_0416	pheromone shutdown protein (traB	39.11	31.68	-7.43	0.00067	2	0.00066	2	1.0136	16	49	49	16	0	49	36.9	0.0009	8	24	24	8	0	24	16.8	0.00045
TM	BB_0766	BB_0766	colicin V production protein	8.64	8.64	0	0.00037	1	0.0001	1	3.61386	1	8	8	1	0	8	8.64	0.00036	X	X	X	X	X	X	X	X
TM	BB_0453	BB_0453	conserved hypothetical protein	0	25.36	25.36	0	0	0.00044	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
TM	BB_0595	BB_0595	predicted coding region BB0595	0	11.06	11.06	0	0	0.00012	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
TM	BB_A01	BB_A01	conserved hypothetical protein	7.45	0	-7.45	4.6E-05	2	0	0	∞	1	1	1	1	0	1	7.45	4.6E-05	1	1	1	1	0	1	6.21	4.7E-05
TM	BB_0075	BB_0075	predicted coding region BB0075	19.4	26.87	7.47	0.00027	2	0.00028	2	0.97122	6	18	18	6	0	18	15.4	0.00028	4	16	16	4	0	16	9.17	0.00026
TM	BB_0134	BB_0134	predicted coding region BB0134	4.71	3.93	-0.78	1.9E-05	1	3.1E-05	1	0.6129	1	1	1	1	0	1	4.71	1.9E-05	X	X	X	X	X	X	X	X
TM	BB_0137	BB_0137	long-chain-fatty-acid CoA ligase	32.86	50.79	17.93	0.00046	2	0.00143	2	0.32008	15	64	64	15	0	64	29.8	0.00075	6	14	14	6	0	14	13.7	0.00017
TM	BB_0291	BB_0291	flagellar basal-body rod protein (fliF	30.4	40.42	10.02	0.00039	2	0.00067	2	0.57808	14	40	40	14	0	40	26.2	0.00052	6	19	19	6	0	19	19.7	0.00025
TM	BB_0596	BB_0596	methyl-accepting chemotaxis prote	8.67	29.51	20.84	6.2E-05	1	0.00038	2	0.1623	4	6	6	4	0	6	8.67	6.2E-05	X	X	X	X	X	X	X	X
TM	BB_0752	BB_0752	predicted coding region BB0752	35.26	48.8	13.54	0.00035	2	0.00153	2	0.2279	11	28	28	11	0	28	30.9	0.00041	4	19	19	4	0	19	15.9	0.00028
TM	BB_E19	BB_E19	conserved hypothetical protein	0	15.87	15.87	0	0	0.00013	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
TM	BB_U09	BB_U09	conserved hypothetical protein	11.32	26.42	15.1	0.00014	2	0.00047	2	0.29747	1	2	2	1	0	2	11.3	0.00014	1	2	2	1	0	2	11.3	0.00014
TM	BB_0067	BB_0067	peptidase	5.07	13.01	7.94	3.8E-05	2	0.00025	2	0.15139	2	4	4	2	0	4	5.07	5E-05	1	2	2	1	0	2	2.03	2.5E-05
TM	BB_0174	BB_0174	predicted coding region BB0174	5.65	5.65	0	2.5E-05	1	9.4E-05	2	0.26596	1	1	1	1	0	1	5.65	2.5E-05	X	X	X	X	X	X	X	X
TM	BB_0260	BB_0260	predicted coding region BB0260	51.63	57.86	6.23	0.00084	2	0.00265	2	0.31571	13	59	59	13	0	59	51.6	0.00129	5	17	17	5	0	17	23.4	0.00038
TM	BB_0326	BB_0326	predicted coding region BB0326	1.83	11.6	9.77	1.6E-05	1	4.1E-05	2	0.39024	1	2	2	1	0	2	1.83	1.6E-05	X	X	X	X	X	X	X	X
TM	BB_0345	BB_0345	predicted coding region BB0345	50.25	50.75	0.5	0.00072	2	0.00154	2	0.46662	17	44	43	17	1	43	50.3	0.0008	4	34	34	4	0	34	12.6	0.00064
TM	BB_0593	BB_0593	long-chain-fatty-acid CoA ligase	51.94	58.6	6.66	0.00161	2	0.00485	2	0.33141	28	189	189	28	0	189	50.9	0.00216	14	90	90	14	0	90	29.9	0.00105
TM	BB_0665	BB_0665	predicted coding region BB0665	8.78	17.55	8.77	2.3E-05	1	0.00011	2	0.21698	1	1	1	1	0	1	8.78	2.3E-05	X	X	X	X	X	X	X	X
TM	BB_0757	BB_0757	ATP-dependent Clp protease prote	14.08	40.29	26.21	0.00014	1	0.00031	2	0.45981	2	4	4	2	0	4	14.1	0.00014	X	X	X	X	X	X	X	X
TM	BB_G33	BB_G33	conserved hypothetical protein	14.29	21.43	7.14	2.8E-05	1	0.00035	2	0.07977	7	53	0	0	53	1	14.3	2.8E-05	4	28	0	0	28	0	8.65	X
TM	BB_H13	BB_H13	conserved hypothetical protein	17.12	23.42	6.3	0.00186	1	0.001	2	1.87048	7	56	5	1	51	56	17.1	0.00186	4	28	0	0	28	0	10.4	X
TM	BB_K40	BB_K40	conserved hypothetical protein	35.87	38.59	2.72	0.00168	2	0.00696	2	0.24083	6	59	59	6	0	59	28.8	0.00237	3	24	24	3	0	24	27.2	0.00098
TM	BB_L27	BB_L27	bdrP	38.66	47.94	9.28	0.00072	2	4.5E-05	2	16.0222	10	63	0	0	63	3	30.4	0.00011	8	38	1	1	37	34.2	31.4	0.00133
TM	BB_L35	BB_L35	bdrO	16.67	32.81	16.14	0.00014	2	0.00032	1	0.44582	4	12	2	1	10	6.8	16.7	0.00026	2	6	0	0	6	0.67	8.33	2.6E-05
TM	BB_M34	BB_M34	bdrK	14.86	30.18	15.32	5.6E-05	2	0.00047	2	0.11915	2	5	1	1	4	2.33	11.7	7.8E-05	2	4	0	0	4	1	6.76	3.4E-05
TM	BB_N27	BB_N27	bdrR	27.32	36.08	8.76	3.2E-05	1	2.4E-05	2	1.33333	8	53	0	0	53	0.83	27.3	3.2E-05	4	28	0	0	28	0	11.9	X
TM	BB_N34	BB_N34	bdrQ	12.85	22.91	10.06	4.2E-05	1	9.5E-05	1	0.44211	2	5	0	0	5	0	8.94	X	2	4	0	0	4	1	8.38	4.2E-05
TM	BB_O27	BB_O27	bdrN	27.8	41.46	13.66	1.2E-05	2	2.3E-05	2	0.52174	8	56	0	0	56	0.33	24.4	1.2E-05	6	34	0	0	34	0.33	18.5	1.2E-05
TM	BB_O34	BB_O34	bdrM	18.95	28.95	10	4.7E-05	2	9.4E-05	2	0.5	3	6	1	1	5	2.07	15.3	8E-05	2	6	0	0	6	0.33	7.89	1.3E-05
TM	BB_P34	BB_P34	bdrA	23.81	20.48	-3.33	5.3E-05	2	0.00019	2	0.28495	4	8	0	0	8	0.5	18.1	1.8E-05	2	6	2	1	4	2.47	9.52	8.9E-05
TM	BB_Q34	BB_Q34	bdrW	22.27	58.4	36.13	5.2E-05	2	0.00283	2	0.01837	8	59	0	0	59	3	19.3	9.3E-05	5	30	0	0	30	0.33	12.6	1.1E-05
TM	BB_R27	BB_R27	bdrH	34.09	42.61	8.52	2.5E-05	2	0.00316	1	0.00791	8	53	0	0	53	0.83	30.1	3.5E-05	5	30	0	0	30	0.33	17.1	1.4E-05
TM	BB_S29	BB_S29	bdrF	23.92	38.76	14.84	8.8E-05	1	0.00104	2	0.08502	8	58	0	0	58	2.5	21.5	8.8E-05	6	33	0	0	33	0	20.1	X
TM	BB_S37	BB_S37	bdrE	37.76	49.49	11.73	0.00146	2	0.00592	2	0.24645	6	60	56	5	4	59.8	33.2	0.00225	6	18	14	5	4	17.3	34.2	0.00066
CYT	BB_0002	BB_0002	beta-N-acetylhexosaminidase	0	13.45	13.45	0	0	6.4E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0003	BB_0003	predicted coding region BB0003	2.64	14.76	12.12	2.5E-05	2	0.00026	2	0.09728	1	2	2	1	0	2	2.64	3.3E-05	1	1	1	1	0	1	2.64	1.7E-05
CYT	BB_0005	BB_0005	tryptophanyl-tRNA synthetase (trsA	23.51	23.51	0	8.4E-05	2	0.00049	2	0.17143	4	6	6	4	0	6	23.5	0.00013	2	2	2	2	0	2	10.2	4.3E-05
CYT	BB_0007	BB_0007	predicted coding region BB0007	0	6.32	6.32	0	0	5.7E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0009	BB_0009	predicted coding region BB0009	20.96	41.02	20.06	0.00027	2	0.0008	2	0.33543	5	17	17	5	0	17	21	0.00038	3	7	7	3	0	7	12.6	0.00016
CYT	BB_0011	BB_0011	predicted coding region BB0011	5.38	12.54	7.16	2.6E-05	1	0.00017	2	0.15029	1	1	1	1	0	1	5.38	2.6E-05	X	X	X	X	X	X	X	X
CYT	BB_0015	BB_0015	uridine kinase (udk)	19.32	27.05	7.73	0.00016	2	0.00033	2	0.49846	2	5	5	2	0	5	19.3	0.00018	1	4	4	1	0	4	9.18	0.00015
CYT	BB_0020	BB_0020	pyrophosphate--fructose 6-phospha	40.72	51.17	10.45	0.0005	2	0.00104	2	0.48456	13	55	55	13	0	55	34.8	0.00073	7	20	20	7	0	20	23.2	0.00027
CYT	BB_0022	BB_0022	Holliday junction DNA helicase (ruv	0	5.48	5.48	0	0	4.7E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0023	BB_0023	Holliday junction DNA helicase (ruv	0	29.95	29.95	0	0	0.00021	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0025	BB_0025	conserved hypothetical protein	0	19.75	19.75	0	0	0.00013	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0026	BB_0026	methylenetetrahydrofolate dehydrog	36.04	32.79	-3.25	0.00038	1	0.0002	2	1.90099	8	16	16	8	0	16	36	0.00038	X	X	X	X	X	X	X	X
CYT	BB_0035	BB_0035	DNA topoisomerase IV (parC)	0	6.23	6.23	0	0	2.6E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0042	BB_0042	phosphate transport system regula	52.02	54.71	2.69	0.00063	2	0.00087	2	0.73064	10	28	28	10	0	28	48.4	0.00093	6	10	10	6	0	10	39.9	0.00034
CYT	BB_0045	BB_0045	P115 protein	0	4.52	4.52	0	0	0.00003	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0049	BB_0049	predicted coding region BB0049	33.33	0	-33.33	0.00171	2	0	0	∞	2	14	14	2	0	14	33.3	0.00265	1	4	4	1	0	4	33.3	0.00077
CYT	BB_0055	BB_0055	triosephosphate isomerase	50.2	48.62	-1.58	0.0009	2	0.00103	2	0.87317	10	46	46	10	0	46	50.2	0.00134	5	15	15	5	0	15	26.9	0.00045
CYT	BB_0056	BB_0056	phosphoglycerate kinase (pgk)	76.59	77.86	1.27	0.00131	2	0.00256	2	0.5133	23	104	104	23	0	104	67.9	0.00195	15	35	35	15	0	35	50.1	0.00067
CYT	BB_0057	BB_0057	glyceraldehyde 3-phosphate dehyd	73.43	77.91	4.48	0.00255	2	0.00456	2	0.56009	22	143	143	22	0	143	70.5	0.00315	19	87	87	19	0	87	66.9	0.00195
CYT	BB_0059	BB_0059	hemolysin (tlyC)	16.99	18.53	1.54	0.00016	2	0.00062	2	0.25528	3	10	10	3	0	10	17	0.00029	1	1	1	1	0	1	8.88	2.9E-05
CYT	BB_0061	BB_0061	thioredoxin (trxA)	70.94	71.79	0.85	0.00041	2	0.00045	2	0.92601	5	9	9	5	0	9	70.9	0.00057	2	4	4	2	0	4	35	0.00026
CYT	BB_0064	BB_0064	methionyl-tRNA formyltransferase (	17.95	30.13	12.18	0.00023	2	0.00041	2	0.55774	4	11	11	4	0	11	17.3	0.00026	3	8	8	3	0	8	14.1	0.00019
CYT	BB_0065	BB_0065	polypeptide deformylase (def)	22.09	40.7	18.61	0.00039	1	0.00034	2	1.13824	2	9	9	2	0	9	22.1	0.00039	X	X	X	X	X	X	X	X
CYT	BB_0068	BB_0068	conserved hypothetical protein	33.11	44.03	10.92	0.00023	2	0.0006	2	0.3796	7	16	16	7	0	16	28.7	0.0004	2	2	2	2	0	2	9.22	5.1E-05
CYT	BB_0070	BB_0070	conserved hypothetical protein	14.38	14.38	0	7.3E-05	2	0.0002	2	0.37056	1	2	2	1	0	2	14.4	9.7E-05	1	1	1	1	0	1	14.4	4.9E-05
CYT	BB_0074	BB_0074	peptide chain release factor 2 (prfB	9.77	6.61	-3.16	6.4E-05	1	6.9E-05	1	0.92754	2	3	3	2	0	3	9.77	6.4E-05	X	X	X	X	X	X	X	X
CYT	BB_0084	BB_0084	aminotransferase (nifS)	41.47	55.45	13.98	0.00019	2	0.00052	2	0.37476	10	21	21	10	0	21	41.5	0.00037	1	1	1	1	0	1	6.16	1.8E-05
CYT	BB_0086	BB_0086	conserved hypothetical protein	0	6.65	6.65	0	0	3.2E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0088	BB_0088	GTP-binding membrane protein (le	18.78	17.89	-0.89	3.3E-05	2	0.00011	2	0.31132	1	2	2	1	0	2	5.01	2.6E-05	3	3	3	3	0	3	13.8	4E-05
CYT	BB_0089	BB_0089	predicted coding region BB0089	11.42	12.96	1.54	9.1E-05	2	0.00022	2	0.40625	2	7	7	2	0	7	11.4	0.00016	1	1	1	1	0	1	4.94	2.3E-05
CYT	BB_0092	BB_0092	V-type ATPase	7.35	0	-7.35	7.2E-05	1	0	0	∞	1	2	2	1	0	2	7.35	7.2E-05	X	X	X	X	X	X	X	X
CYT	BB_0093	BB_0093	V-type ATPase	13.13	35.02	21.89	6.8E-05	2	0.00046	2	0.1488	3	6	6	3	0	6	13.1	0.0001	2	2	2	2	0	2	7.83	3.5E-05
CYT	BB_0094	BB_0094	V-type ATPase	17.06	37.93	20.87	0.0002	2	0.00107	2	0.18446	3	11	11	3	0	11	6.72	0.00015	6	18	18	6	0	18	16.9	0.00025
CYT	BB_0095	BB_0095	predicted coding region BB0095	17.13	33.7	16.57	0.00033	1	0.00075	2	0.436	3	8	8	3	0	8	17.1	0.00033	X	X	X	X	X	X	X	X
CYT	BB_0096	BB_0096	V-type ATPase	28.5	42	13.5	0.00056	2	0.00588	2	0.09481	3	22	22	3	0	22	28.5	0.00081	2	8	8	2	0	8	22.5	0.0003
CYT	BB_0101	BB_0101	asparaginyl-tRNA synthetase (asnS	11.37	8.37	-3	0.00013	1	7.7E-05	1	1.64935	3	8	8	3	0	8	11.4	0.00013	X	X	X	X	X	X	X	X
CYT	BB_0103	BB_0103	predicted coding region BB0103	55.33	62.94	7.61	0.00104	2	0.00138	2	0.75273	8	44	44	8	0	44	55.3	0.00165	4	11	11	4	0	11	36.6	0.00042
CYT	BB_0105	BB_0105	methionine aminopeptidase (map)	5.98	5.98	0	5.9E-05	1	3.3E-05	1	1.78788	1	2	2	1	0	2	5.98	5.9E-05	X	X	X	X	X	X	X	X
CYT	BB_0107	BB_0107	N-utilization substance protein B (n	7.59	38.62	31.03	0.0002	1	0.00022	1	0.9148	1	4	4	1	0	4	7.59	0.0002	X	X	X	X	X	X	X	X
CYT	BB_0109	BB_0109	acetyl-CoA C-acetyltransferase (fad	47.74	50.25	2.51	0.00043	2	0.00092	2	0.46514	15	46	43	15	3	43	47.7	0.0008	2	3	3	2	0	3	12.8	5.7E-05
CYT	BB_0110	BB_0110	predicted coding region BB0110	11.89	25.77	13.88	0.00026	2	0.0004	2	0.66582	4	13	13	4	0	13	11.9	0.00021	2	19	19	2	0	19	7.27	0.00031
CYT	BB_0111	BB_0111	replicative DNA helicase (dnaB)	6.81	9.89	3.08	3.2E-05	1	0.00011	2	0.30189	2	2	2	2	0	2	6.81	3.2E-05	X	X	X	X	X	X	X	X
CYT	BB_0112	BB_0112	ribosomal protein L9 (rplI)	14.45	32.95	18.5	0.00017	2	0.00056	2	0.3059	1	7	7	1	0	7	5.2	0.0003	1	1	1	1	0	1	9.25	4.3E-05
CYT	BB_0113	BB_0113	ribosomal protein S18 (rpsR)	0	12.5	12.5	0	0	0.00021	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0115	BB_0115	ribosomal protein S6 (rpsF)	0	23.74	23.74	0	0	0.00027	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
CYT	BB_0121	BB_0121	ribosome releasing factor (frr)	20.11	20.11	0	8.1E-05	2	0.00036	2	0.225	1	1	1	1	0	1	14.7	4E-05	3	3	3	3	0	3	20.1	0.00012
CYT	BB_0122	BB_0122	translation elongation factor TS (tsf	41.22	40.5	-0.72	0.00054	2	0.00129	2	0.42203	9	36	36	9	0	36	36.6	0.00095	4	5	5	4	0	5	22.9	0.00013
CYT	BB_0123	BB_0123	ribosomal protein S2 (rpsB)	80.38	75	-5.38	0.00533	2	0.00721	2	0.7387	28	260	260	28	0	260	73.5	0.00739	19	113	113	19	0	113	66.2	0.00327
CYT	BB_0125	BB_0125	predicted coding region BB0125	58.33	42.92	-15.41	0.00127	2	0.00101	2	1.25893	10	57	57	10	0	57	50.4	0.00175	9	25	25	9	0	25	51.3	0.00078
CYT	BB_0128	BB_0128	cytidylate kinase (cmk-1)	10.41	30.32	19.91	6.7E-05	1	0.0001	2	0.67	2	2	2	2	0	2	10.4	6.7E-05	X	X	X	X	X	X	X	X
CYT	BB_0130	BB_0130	predicted coding region BB0130	3.53	3.53	0	0.00003	1	3.2E-05	1	0.9375	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.53	3E-05
CYT	BB_0131	BB_0131	recA protein (recA)	34.25	38.08	3.83	0.00022	2	0.0006	2	0.37584	7	15	15	7	0	15	34.3	0.0003	3	7	7	3	0	7	18.1	0.00014
CYT	BB_0132	BB_0132	transcription elongation factor (greA	39.96	52.83	12.87	0.00061	2	0.00206	2	0.29669	31	105	105	31	0	105	39.1	0.00086	13	43	43	13	0	43	20.9	0.00036
CYT	BB_0133	BB_0133	predicted coding region BB0133	23.89	49.04	25.15	0.00021	2	0.00073	2	0.29019	5	14	14	5	0	14	16.2	0.00033	2	4	4	2	0	4	7.64	9.6E-05
CYT	BB_0135	BB_0135	histidyl-tRNA synthetase (hisS)	17.51	23.19	5.68	0.00011	2	0.00018	2	0.6	6	12	12	6	0	12	17.5	0.00019	1	1	1	1	0	1	2.84	1.6E-05
CYT	BB_0146	BB_0146	glycine betaine	20.16	26.34	6.18	0.00015	2	0.00062	2	0.24071	5	12	12	5	0	12	20.2	0.00024	1	3	3	1	0	3	6.45	6.1E-05

Locus	B31A3_ProK_1_P	B31A3_ProK_1_S	B31A3_ProK_1_uS	B31A3_ProK_1_uDP	B31A3_ProK_1_sS	B31A3_ProK_1_dS	B31A3_ProK_1_SC	B31A3_ProK_1_dNSAF	B31A3_ProK_2_P	B31A3_ProK_2_S	B31A3_ProK_2_uS	B31A3_ProK_2_uDP	B31A3_ProK_2_sS	B31A3_ProK_2_dS	B31A3_ProK_2_SC	B31A3_ProK_2_dNSAF	ALL_y2_P	ALL_y2_S	ALL_y2_uS	ALL_y2_uDP	ALL_y2_sS	ALL_y2_dS	ALL_y2_SC	ALL_y2_dNSAF	Length	MW	pI
BB_0783	3	8	8	3	0	8	14	0.00024	7	23	23	7	0	23	25.6	0.00048	10	63	63	10	0	63	32.7	0.00035	394	45766	8.4
BB_0789	9	16	16	9	0	16	26	0.0003	10	40	40	10	0	40	16.6	0.00051	15	69	69	15	0	69	24.4	0.00023	639	70802	8.3
BB_0824	4	124	124	4	0	124	23.5	0.0081	7	339	339	7	0	339	29	0.01512	5	42	42	5	0	42	18.6	0.0005	183	21175	8.8
BB_0843	2	6	6	2	0	6	3.53	0.00015	3	11	11	3	0	11	3.53	0.00019	3	24	24	3	0	24	3.53	0.00011	482	52856	8.4
BB_B22	3	4	4	3	0	4	8.2	0.00011	4	22	22	4	0	22	10.6	0.0004	5	39	39	5	0	39	12	0.00019	451	48977	8.5
BB_B28	17	45	45	17	0	45	56.3	0.0013	20	151	151	20	0	151	52.7	0.00298	27	355	355	27	0	355	59.7	0.00186	414	49380	8.6
BB_B29	28	861	861	28	0	861	32.5	0.01899	46	1539	1539	46	0	1539	48.3	0.02317	42	3112	3112	42	0	3112	53	0.01242	542	58938	8.6
BB_D15	1	1	1	1	0	1	6.43	8.5E-05	X	X	X	X	X	X	X	X	5	11	11	5	0	11	20.7	0.00017	140	16635	9.7
BB_J27	1	2	2	1	0	2	3.16	5.8E-05	2	2	2	2	0	2	7.3	4E-05	3	10	10	3	0	10	11.2	5.3E-05	411	46456	5.8
BB_K13	X	X	X	X	X	X	X	X	9	30	30	9	0	30	43.7	0.00103	10	33	33	10	0	33	44.5	0.0003	238	27221	9.2
BB_0252	6	18	18	6	0	18	8.6	0.00028	2	4	4	2	0	4	4.56	4.3E-05	7	33	33	7	0	33	10.8	9.3E-05	767	86971	9.6
BB_0091	9	20	20	9	0	20	20.2	0.00039	12	40	40	12	0	40	19.1	0.00054	13	62	62	13	0	62	22.2	0.00022	608	69125	8.3
BB_0408	20	262	262	20	0	262	26.2	0.00501	33	318	318	33	0	318	32.8	0.00415	41	863	863	41	0	863	38.1	0.00299	625	67130	7.5
BB_0629	11	23	23	11	0	23	25.4	0.00044	28	104	104	28	0	104	35.5	0.00136	31	178	178	31	0	178	36.4	0.00062	626	67805	8.9
BB_B04	5	23	23	5	0	23	10.8	0.00062	4	66	66	4	0	66	9.71	0.00122	4	49	49	4	0	49	7	0.00024	443	48761	8.1
BB_0071	3	10	10	3	0	10	5.71	0.00024	3	6	6	3	0	6	8.37	1E-04	5	9	9	5	0	9	11.6	4E-05	490	58164	9.3
BB_0333	4	23	23	4	0	23	15.5	0.00079	9	84	84	9	0	84	22.9	0.00196	12	125	125	12	0	125	25.8	0.00077	349	39418	9.2
BB_0145	1	2	2	1	0	2	5.02	8E-05	X	X	X	X	X	X	X	X	1	6	6	1	0	6	5.02	4.3E-05	299	33735	9
BB_0118	9	29	29	9	0	29	25.2	0.00079	12	96	96	12	0	96	26.5	0.00179	18	180	180	18	0	180	35.7	0.00089	437	49741	9.2
BB_0170	10	34	34	10	0	34	23.3	0.0006	9	35	35	9	0	35	22	0.00042	14	94	94	14	0	94	32.3	0.0003	682	78475	8.8
BB_0442	4	6	6	4	0	6	10.9	0.00013	3	9	9	3	0	9	8.64	0.00014	6	22	22	6	0	22	13.6	8.8E-05	544	64002	8.9
BB_0157	X	X	X	X	X	X	X	X	1	5	5	1	0	5	10.1	0.0003	1	9	9	1	0	9	10.1	0.00014	138	15595	9.6
BB_0217	4	11	11	4	0	11	18.6	0.0004	4	12	12	4	0	12	18.6	0.0003	4	24	24	4	0	24	18.6	0.00016	328	36113	9.3
BB_0380	1	1	1	1	0	1	1.76	2.6E-05	2	3	3	2	0	3	8.37	5.4E-05	4	7	7	4	0	7	12.6	3.3E-05	454	50747	5.1
BB_0416	8	14	14	8	0	14	24	0.00041	10	45	45	10	0	45	21.3	0.00091	23	128	128	23	0	128	41.6	0.00069	404	45678	9.3
BB_0766	X	X	X	X	X	X	X	X	1	2	2	1	0	2	8.64	0.0001	1	10	10	1	0	10	8.64	0.00013	162	18716	9.1
BB_0453	1	1	1	1	0	1	4.29	4.3E-05	8	29	29	8	0	29	25.4	0.00085	8	30	30	8	0	30	25.4	0.00023	280	32302	8.6
BB_0595	X	X	X	X	X	X	X	X	3	3	3	3	0	3	11.1	0.00012	3	3	3	3	0	3	11.1	3.1E-05	208	24003	9.8
BB_A01	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	7.45	2.7E-05	161	17887	9.5
BB_0075	1	2	2	1	0	2	2.99	5.1E-05	13	29	29	13	0	29	26.9	0.0005	16	63	63	16	0	63	33.5	0.00029	469	54638	9.2
BB_0134	1	1	1	1	0	1	3.93	3.1E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	8.64	1.1E-05	382	44325	9.3
BB_0137	25	74	74	25	0	74	42.5	0.0014	23	113	113	23	0	113	44.6	0.00146	29	261	261	29	0	261	47	0.0009	630	70763	8.8
BB_0291	15	32	32	15	0	32	35.2	0.00067	19	46	46	19	0	46	29.7	0.00066	27	135	135	27	0	135	41	0.00051	569	65134	5.5
BB_0596	6	17	17	6	0	17	13.2	0.00028	13	42	42	13	0	42	28.4	0.00048	14	64	64	14	0	64	28.3	0.00019	715	80470	7.6
BB_0752	12	60	60	12	0	60	36.9	0.00143	19	100	100	19	0	100	39.2	0.00163	28	207	207	28	0	207	54	0.00089	502	57435	8.7
BB_E19	X	X	X	X	X	X	X	X	2	4	4	2	0	4	15.9	0.00013	2	4	4	2	0	4	15.9	3.4E-05	252	29282	8.6
BB_U09	3	5	5	3	0	5	26.4	0.00056	1	5	5	1	0	5	10.4	0.00038	2	11	11	2	0	11	21.7	0.00022	106	12136	8.7
BB_0067	1	1	1	1	0	1	3.04	2E-05	6	35	35	6	0	35	13	0.00048	6	42	42	6	0	42	13	0.00015	592	67627	6.4
BB_0174	1	2	2	1	0	2	5.65	7.9E-05	1	4	4	1	0	4	5.65	0.00011	1	7	7	1	0	7	5.65	5E-05	301	34488	9
BB_0260	13	36	36	13	0	36	41.8	0.00128	28	166	166	28	0	166	55.5	0.00402	24	252	252	24	0	252	60.2	0.00162	337	39145	4.4
BB_0326	3	3	3	3	0	3	4.94	3.9E-05	3	6	5	3	1	5	6.66	4.4E-05	5	10	10	5	0	10	8.27	2.3E-05	931	107524	5
BB_0345	8	42	42	8	0	42	25.9	0.00126	17	89	89	17	0	89	46	0.00182	27	209	208	27	1	208	63.8	0.00113	398	46456	5.8
BB_0593	31	341	341	31	0	341	52.6	0.00632	29	267	267	29	0	267	49.6	0.00338	43	881	881	43	0	881	64.2	0.00296	645	72887	9
BB_0665	3	5	5	3	0	5	17.6	0.00019	1	1	1	1	0	1	8.78	2.6E-05	2	6	6	2	0	6	12.5	4.1E-05	319	37381	8.6
BB_0757	4	8	8	4	0	8	23.8	0.00046	3	4	4	3	0	4	21.8	0.00016	5	15	15	5	0	15	34	0.00016	206	23206	7.9
BB_G33	7	27	2	2	25	10.3	21.4	0.00046	11	103	2	1	101	7.77	14.7	0.00024	11	191	4	2	187	30.7	24.4	0.00025	266	30587	5.5
BB_H13	6	26	1	1	25	5.17	19.8	0.00028	12	113	12	2	101	46.6	23.4	0.00171	10	203	18	2	185	133	23	0.00129	222	25840	5.6
BB_K40	5	109	109	5	0	109	33.2	0.00708	10	154	154	10	0	154	38.6	0.00683	8	338	338	8	0	338	35.9	0.00397	184	21564	6.2
BB_L27	11	48	0	0	48	0.33	35.1	2.1E-05	22	180	0	0	180	1.67	47.9	7E-05	15	226	1	1	225	12.3	55.2	0.00014	194	22421	5.2
BB_L35	6	77	0	0	77	0	26	X	7	156	1	1	155	7.6	28.7	0.00032	5	38	3	2	35	5.9	31.8	6.7E-05	192	22050	6.6
BB_M34	5	18	2	1	16	11.5	22.1	0.00062	7	20	4	2	16	8.7	27	0.00032	6	44	20	3	24	40.5	30.2	0.00039	222	25444	5.3
BB_N27	10	46	0	0	46	0.33	30.9	2.1E-05	19	164	0	0	164	0.67	36.1	2.8E-05	11	188	0	0	188	0.83	43.8	9.3E-06	194	22294	5.2
BB_N34	2	6	0	0	6	0	8.38	X	4	9	1	1	8	2.07	22.9	9.5E-05	3	23	0	0	23	0	12.9	X	179	20714	5.5
BB_O27	12	50	0	0	50	0.33	36.6	1.9E-05	21	174	0	0	174	0.67	41.5	2.7E-05	12	211	0	0	211	0.33	43.4	3.5E-06	205	23698	5.4
BB_O34	3	5	1	1	4	1.83	12.1	0.00012	4	13	1	1	12	1.67	24.7	7.2E-05	5	29	2	2	27	3.26	19	3.7E-05	190	21974	5.2
BB_P34	3	4	1	1	3	2.17	11	0.00012	4	14	4	2	10	6.4	16.7	0.00025	6	32	7	2	25	12.7	27.1	0.00013	210	24118	5.4
BB_Q34	11	50	0	0	50	0	28.2	X	23	177	4	3	173	82.5	58.4	0.00283	13	212	3	1	209	29.4	28.6	0.00027	238	27307	5.2
BB_R27	6	27	0	0	27	0	21.6	X	16	121	17	4	104	68.1	42.6	0.00316	11	193	0	0	193	0.83	34.1	1E-05	176	20350	5.3
BB_S29	10	48	3	1	45	35.5	31.6	0.00203	19	170	0	0	170	1	35.9	3.9E-05	12	208	3	1	205	33.3	26.8	0.00034	209	24109	5.2
BB_S37	10	82	10	6	72	80.5	40.8	0.00491	11	175	24	6	151	166	45.9	0.00693	9	310	292	8	18	309	40.8	0.00341	196	22652	6.1
BB_0002	2	3	3	2	0	3	7.6	0.0001	1	1	1	1	0	1	5.85	2.4E-05	1	2	2	1	0	2	3.51	1.3E-05	342	38465	8.7
BB_0003	6	10	10	6	0	10	14.5	0.00026	5	14	14	5	0	14	13	0.00025	7	27	27	7	0	27	14.8	0.00013	454	52012	6.8
BB_0005	6	18	18	6	0	18	19.3	0.00061	6	16	16	6	0	16	21.5	0.00037	8	40	40	8	0	40	32	0.00025	353	40419	9.1
BB_0007	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.32	5.7E-05	1	2	2	1	0	2	6.32	1.5E-05	285	33538	7.3
BB_0009	5	9	9	5	0	9	13.5	0.00032	12	52	52	12	0	52	38	0.00127	12	83	83	12	0	83	41	0.00054	334	38543	9.3
BB_0011	2	4	4	2	0	4	12.5	0.00017	2	6	6	2	0	6	5.38	0.00018	3	11	11	3	0	11	12.5	8.5E-05	279	32820	9.3
BB_0015	1	1	1	1	0	1	7.73	5.8E-05	3	15	15	3	0	15	27.1	0.00059	3	25	25	3	0	25	27.1	0.00026	207	24006	7.6
BB_0020	21	58	58	21	0	58	51.2	0.00125	11	56	56	11	0	56	28.1	0.00082	25	186	186	25	0	186	57.5	0.00073	555	62477	6.6
BB_0022	X	X	X	X	X	X	X	X	1	2	2	1	0	2	5.48	4.7E-05	1	2	2	1	0	2	5.48	1.2E-05	347	39006	5.3
BB_0023	2	5	5	2	0	5	12.7	0.0003	2	3	3	2	0	3	25.9	0.00012	2	3	3	2	0	3	10.2	3.3E-05	197	22688	8.1
BB_0025	1	1	1	1	0	1	8.64	4.9E-05	3	6	6	3	0	6	19.8	0.0002	2	5	5	2	0	5	14.8	4.5E-05	243	27034	5.5
BB_0026	5	7	7	5	0	7	27.3	0.00027	2	5	5	2	0	5	9.42	0.00013	10	26	26	10	0	26	46.8	0.00018	308	34032	8.9
BB_0035	1	2	2	1	0	2	2.24	3.8E-05	1	1	1	1	0	1	3.99	1.3E-05	1	2	2	1	0	2	2.24	6.9E-06	626	72042	8.5
BB_0042	8	20	20	8	0	20	54.7	0.00107	8	18	18	8	0	18	43.5	0.00066	14	75	75	14	0	75	58.3	0.00073	223	25980	5.1
BB_0045	X	X	X	X	X	X	X	X	2	3	3	2	0	3	4.52	3E-05	1	2	2	1	0	2	2.2	5.3E-06	819	95857	5.7
BB_0049	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	18	18	2	0	18	33.3	0.001	39	4343	9
BB_0055	9	27	27	9	0	27	48.6	0.00128	7	24	24	7	0	24	43.1	0.00077	13	111	111	13	0	111	60.1	0.00095	253	27759	6.2
BB_0056	24	95	95	24	0	95	74.1	0.00289	21	107	107	21	0	107	59.8	0.00222	34	341	341	34	0	341	84.2	0.00188	393	42346	6.8
BB_0057	16	87	87	16	0	87	58.2	0.0031	26	247	247	26	0	247	72.8	0.00602	30	562	562	30	0	562	80.3	0.00363	335	36255	8
BB_0059	3	13	13	3	0	13	14.7	0.0006	3	20	20	3	0	20	17	0.00063	5	42	42	5	0	42	25.1	0.00035	259	29769	5.4
BB_0061	4	6	6	4	0	6	59	0.00061	3	4	4	3	0	4	35	0.00028	8	22	22	8	0	22	75.2	0.00041	117	13467	4.8
BB_0064	5	11	11	5	0	11	20.2	0.00042	7	15	15	7	0	15	26	0.00039	10	45	45	10	0	45	35.3	0.00031	312	35107	8.9
BB_0065	3	5	5	3	0	5	30.8	0.00035	2	7	7	2	0	7	16.9	0.00033	3	18	18	3	0	18	33.7	0.00023	172	19922	7.4
BB_0068	5	15	15	5	0	15	28.7	0.00061	6	21	21	6	0	21	23.6	0.00058	12	52	52	12	0	52	54.3	0.00038	293	33278	7.1
BB_0070	1	3	3	1	0	3	14.4	0.00023	1	3	3	1	0	3	14.4	0.00016	1	9	9	1	0	9	14.4	0.00013	153	16765	9.7
BB_0074	1	2	2	1	0	2	6.61	6.9E-05	X	X	X	X	X	X	X	X	2	5	5	2	0	5	9.77	3.1E-05	348	40269	8.2
BB_0084	10	22	22	10	0	22	44.8	0.00062	9	21	21	9	0	21	40.8	0.00041	17	65	65	17	0	65	60	0.00033	422	48125	8.5
BB_0086	X	X	X	X	X	X	X	X	2	2	2	2	0	2	6.65	3.2E-05	2	2	2	2	0	2	6.65	8.5E-06	511	57238	9.1
BB_0088	1	1	1	1	0	1	2.68	2.1E-05	6	13	13	6	0	13	17.9	0.00019	8	19	19	8	0	19	25	7.4E-05	559	62901	5.8
BB_0089	3	6	6	3	0	6	13	0.00022	3	9	9	3	0	9	11.4	0.00023	3	21	21	3	0	21	11.4	0.00014	324	38100	9.2
BB_0092	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	7.35	2.1E-05	204	24026	9.9
BB_0093	5	12	12	5	0	12	12.7	0.00033	11	31	31	11	0	31	35	0.00058	13	49	49	13	0	49	30	0.00024	434	48026	5.9
BB_0094	10	35	35	10	0	35	27.4	0.00076	18	93	93	18	0	93	36.3	0.00138	16	154	154	16	0	154	37	0.0006	551	61620	5.3
BB_0095	4	7	7	4	0	7	19.9	0.00046	6	23	23	6	0	23	33.7	0.00104	6	38	38	6	0	38	33.7	0.00045	181	21662	6.1
BB_0096	7	129	129	7	0	129	40	0.00771	8	99	99	8	0	99	36.5	0.00404	8	256	256	8	0	256	42	0.00277	200	22851	7.3
BB_0101	2	3	3	2	0	3	8.37	7.7E-05	X	X	X	X	X	X	X	X	5	11	11	5	0	11	19.7	5.1E-05	466	53600	8
BB_0103	6	18	18	6	0	18	46.7	0.00109	9	40	40	9	0	40	62.9	0.00166	10	113	113	10	0	113	67.5	0.00124	197	23277	6.4
BB_0105	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.98	3.3E-05	1	3	3	1	0	3	5.98	2.6E-05	251	27711	8
BB_0107	1	2	2	1	0	2	7.59	0.00016	3	5	5	3	0	5	38.6	0.00028	3	11	11	3	0	11	38.6	0.00016	145	16808	5
BB_0109	12	55	55	12	0	55	33.7	0.00165	7	9	9	7	0	9	32.4	0.00018	19	110	104	19	6	104	60.3	0.00057	398	42940	7.3
BB_0110	2	2	2	2	0	2	8.59	5.3E-05	9	41	41	9	0	41	25.8	0.00074	9	72	72	9	0	72	23.8	0.00034	454	53411	9
BB_0111	2	4	4	2	0	4	6.81	0.00011	3	6	6	3	0	6	9.89	0.00011	3	12	12	3	0	12	9.89	5.7E-05	455	51662	6.7
BB_0112	5	8	8	5	0	8	27.8	0.00055	5	12	12	5	0	12	26.6	0.00057	7	27	27	7	0	27	31.8	0.00034	173	19959	9.5
BB_0113	1	2	2	1	0	2	12.5	0.00025	1	2	2	1	0	2	12.5	0.00017	1	4	4	1	0	4	12.5	9E-05	96	11614	10.2
BB_0115	2	5	5	2	0	5	23.7	0.00043	1	2	2	1	0	2	13	0.00012	2	7	7	2	0	7	23.7	0.00011	139	16437	9.5
BB_0121	4	7	7	4	0	7	14.7	0.00045	3	6	6	3	0	6	17.4	0.00027	6	17	17	6	0	17	25.5	0.0002	184	21539	8.6
BB_0122	11	39	39	11	0	39	36.2	0.00167	10	33	31	10	2	31	32.3	0.00091	17	113	113	17	0	113	46.2	0.00088	279	31304	8.2
BB_0123	23	165	165	23	0	165	60.4	0.00759	31	218	218	31	0	218	67.3	0.00684	40	747	747	40	0	747	80.4	0.00622	260	29676	7.4
BB_0125	5	20	20	5	0	20	30.4	0.001	8	30	30	8	0	30	42.9	0.00102	15	132	132	15	0	132	61.7	0.00119	240	27129	8.4
BB_0128	3	3	3	3	0	3	25.3	0.00016	1	1	1	1	0	1	4.98	3.7E-05	4	5	5	4	0	5	20.4	4.9E-05	221	25602	9
BB_0130	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.53	3.2E-05	1	2	2	1	0	2	3.53	1.7E-05	255	29972	9.2
BB_0131	7	20	20	7	0	20	27.7	0.00065	7	24	24	7	0	24	32.3	0.00054	11	66	66	11	0	66	46	0.00039	365	39949	7.4
BB_0132	35	168	168	35	0	168	40.4	0.00223	46	208	208	46	0	208	47.6	0.00188	57	517	517	57	0	517	54.4	0.00124	901	105315	6.4
BB_0133	8	14	14	8	0	14	31.5	0.00053	12	36	36	12	0	36	46.2	0.00094	14	68	68	14	0	68	49	0.00047	314	37176	6.1
BB_0135	6	10	10	6	0	10	20.8	0.00026	3	5	5	3	0	5	5.25	8.9E-05	12	28	28	12	0	28	29.5	0.00013	457	52849	8.5
BB_0146	6	16	16	6	0	16	15.1	0.00051	6	33	33	6	0	33	23.9	0.00072	10	63	63	10	0	63	31.5	0.00037	372	42481	8.7

Known (Table 1) and/or predicated subcellular location	Locus	Proteins In Group	Description	B31A3_Control_merged-SeqCov (%)	B31A3_ProK_merged-SeqCov (%)	DiffSeqCov (Control - ProK) (%)	B31A3_Cntl-Ti dNSAF AVG	B31A3_Cntl-Ti Detected # Out of 2	B31A3_PK-Ti dNSAF AVG	B31A3_PK-Ti Detected # Out of 2	B31A3_Cntl-Ti: B31A3_PK-Ti	B31A3_Control_1_P	B31A3_Control_1_S	B31A3_Control_1_uS	B31A3_Control_1_uDP	B31A3_Control_1_sS	B31A3_Control_1_dS	B31A3_Control_1_SC	B31A3_Control_1_dNSAF	B31A3_Control_2_P	B31A3_Control_2_S	B31A3_Control_2_uS	B31A3_Control_2_uDP	B31A3_Control_2_sS	B31A3_Control_2_dS	B31A3_Control_2_SC	B31A3_Control_2_dNSAF	B31A3_ProK_1_P	B31A3_ProK_1_S	B31A3_ProK_1_uS	B31A3_ProK_1_uDP	B31A3_ProK_1_sS	B31A3_ProK_1_dS	B31A3_ProK_1_SC	B31A3_ProK_1_dNSAF	B31A3_ProK_2_P	B31A3_ProK_2_S	B31A3_ProK_2_uS	B31A3_ProK_2_uDP	B31A3_ProK_2_sS	B31A3_ProK_2_dS	B31A3_ProK_2_SC	B31A3_ProK_2_dNSAF	ALL_y2_P	ALL_y2_S	ALL_y2_uS	ALL_y2_uDP	ALL_y2_sS	ALL_y2_dS	ALL_y2_SC	ALL_y2_dNSAF	Length	MW	pI
CYT	BB_0147	BB_0147	flagellar filament 41 kDa core protei	35.12	48.21	13.09	0.00041	2	0.001	2	0.408	8	33	33	8	0	33	35.1	0.00073	3	4	4	3	0	4	12.5	9E-05	15	48	48	15	0	48	48.2	0.00171	5	12	12	5	0	12	22.6	0.00029	14	88	88	14	0	88	47	0.00057	336	35765	5.7
CYT	BB_0149	BB_0149	flagellar hook-associated protein 2 (	3.46	8.57	5.11	1.7E-05	2	2.7E-05	2	0.62963	1	1	1	1	0	1	1.8	1.1E-05	1	2	2	1	0	2	1.65	2.3E-05	1	1	1	1	0	1	3.16	1.8E-05	2	3	3	2	0	3	5.41	3.7E-05	3	5	5	3	0	5	6.02	1.6E-05	665	74718	5.5
CYT	BB_0151	BB_0151	N-acetylglucosamine-6-phosphate (	45.14	52.62	7.48	0.00085	2	0.0018	2	0.47339	11	51	51	11	0	51	41.2	0.00094	7	41	41	7	0	41	30.2	0.00077	13	91	91	13	0	91	43.1	0.00271	13	44	44	13	0	44	37.7	0.0009	20	222	222	20	0	222	55.1	0.0012	401	44203	7
CYT	BB_0153	BB_0153	superoxide dismutase (sodA)	42.52	52.34	9.82	0.0003	2	0.00069	2	0.43504	2	3	3	2	0	3	8.41	0.0001	5	14	14	5	0	14	34.1	0.00049	2	2	2	2	0	2	12.6	0.00011	9	33	33	9	0	33	52.3	0.00126	11	48	48	11	0	48	69.2	0.00049	214	24929	6.7
CYT	BB_0154	BB_0154	preprotein translocase subunit (sec	9.9	17.02	7.12	9.9E-05	1	0.00033	1	0.29819	7	12	12	7	0	12	9.9	9.9E-05	X	X	X	X	X	X	X	X	11	25	25	11	0	25	17	0.00033	X	X	X	X	X	X	X	X	15	36	36	15	0	36	21.8	8.7E-05	899	102086	7.8
CYT	BB_0163	BB_0163	predicted coding region BB0163	12.2	18.73	6.53	0.00007	2	0.00015	2	0.46667	4	8	8	4	0	8	9.45	0.0001	2	3	3	2	0	3	4.47	3.9E-05	2	3	3	2	0	3	7.39	6.2E-05	7	17	17	7	0	17	15.3	0.00024	9	31	31	9	0	31	20.6	0.00012	582	67952	8.8
CYT	BB_0168	BB_0168	dnaK suppressor	45.6	48	2.4	0.00248	2	0.00277	2	0.8961	7	80	80	7	0	80	45.6	0.00473	2	4	4	2	0	4	27.2	0.00024	10	45	45	10	0	45	48	0.0043	5	19	19	5	0	19	40	0.00124	11	148	148	11	0	148	58.4	0.00256	125	14547	8.4
CYT	BB_0176	BB_0176	methanol dehydrogenase regulator	52.52	56.68	4.16	0.00054	2	0.0014	2	0.3871	11	36	36	11	0	36	51.3	0.00079	5	13	13	5	0	13	35.9	0.00029	12	37	37	12	0	37	37.1	0.00131	18	61	61	18	0	61	55.5	0.00148	23	144	144	23	0	144	64.4	0.00092	337	37779	7.5
CYT	BB_0178	BB_0178	glucose inhibited division protein A	15.79	29.98	14.19	0.0001	2	0.00027	2	0.3797	5	11	11	5	0	11	15.8	0.00013	1	6	6	1	0	6	5.9	7.2E-05	5	19	19	5	0	19	16.3	0.00036	6	13	13	6	0	13	20.9	0.00017	11	49	49	11	0	49	32.1	0.00017	627	70821	8.4
CYT	BB_0179	BB_0179	thiophene and furan oxidation prote	4.31	10.13	5.82	0.00004	2	6.1E-05	2	0.65574	1	2	2	1	0	2	4.31	3.2E-05	1	3	3	1	0	3	4.31	4.9E-05	2	2	2	2	0	2	5.82	5.2E-05	1	4	4	1	0	4	4.31	7E-05	3	11	11	3	0	11	10.1	5.1E-05	464	51606	5.6
CYT	BB_0180	BB_0180	flagellar protein	8.54	28.66	20.12	0.00023	1	0.00055	2	0.40614	1	5	5	1	0	5	8.54	0.00023	X	X	X	X	X	X	X	X	1	7	7	1	0	7	8.54	0.00051	4	12	12	4	0	12	28.7	0.0006	4	24	24	4	0	24	28.7	0.00032	164	19437	8.8
CYT	BB_0181	BB_0181	flagellar hook-associated protein (flg	9.73	13.72	3.99	3.5E-05	2	8.3E-05	2	0.42169	3	5	5	3	0	5	9.73	5.9E-05	1	1	1	1	0	1	3.35	1.2E-05	4	8	8	4	0	8	10.4	0.00015	1	1	1	1	0	1	3.35	1.3E-05	7	15	15	7	0	15	20.1	5.2E-05	627	70575	5.8
CYT	BB_0182	BB_0182	flagellar hook-associated protein 3 (	17.69	21.46	3.77	0.00019	1	0.00017	2	1.10345	4	11	11	4	0	11	17.7	0.00019	X	X	X	X	X	X	X	X	6	11	11	6	0	11	21.5	0.00031	2	2	2	2	0	2	5.42	3.8E-05	8	24	24	8	0	24	29.3	0.00012	424	47226	5.9
CYT	BB_0183	BB_0183	conserved hypothetical protein	42.31	51.54	9.23	0.00028	1	0.00054	2	0.52206	3	5	5	3	0	5	42.3	0.00028	X	X	X	X	X	X	X	X	4	5	5	4	0	5	37.7	0.00046	3	10	10	3	0	10	42.3	0.00063	5	20	20	5	0	20	51.5	0.00033	130	15203	7.4
CYT	BB_0185	BB_0185	conserved hypothetical protein	17.51	5.99	-11.52	0.0001	1	3.8E-05	1	2.68421	2	3	3	2	0	3	17.5	0.0001	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.99	3.8E-05	2	4	4	2	0	4	17.5	4E-05	217	24323	8.6
CYT	BB_0187	BB_0187	predicted coding region BB0187	18.6	18.6	0	8.6E-05	1	9.5E-05	1	0.90526	1	1	1	1	0	1	18.6	8.6E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	18.6	9.5E-05	1	2	2	1	0	2	18.6	5E-05	86	10224	8.9
CYT	BB_0188	BB_0188	ribosomal protein L20 (rplT)	6.96	13.91	6.95	6.4E-05	1	0.00028	2	0.22776	1	1	1	1	0	1	6.96	6.4E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	13.9	0.00021	2	5	5	2	0	5	13.9	0.00035	3	8	8	3	0	8	20.9	0.00015	115	13469	11.4
CYT	BB_0190	BB_0190	translation initiation factor 3 (infC)	9.68	26.88	17.2	0.00004	1	0.00032	1	0.12461	1	1	1	1	0	1	9.68	4E-05	X	X	X	X	X	X	X	X	3	5	5	3	0	5	26.9	0.00032	X	X	X	X	X	X	X	X	3	6	6	3	0	6	26.9	7E-05	186	21534	9.8
CYT	BB_0194	BB_0194	conserved hypothetical protein	7.81	11.9	4.09	5.5E-05	1	5.3E-05	2	1.03774	1	2	2	1	0	2	7.81	5.5E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	4.09	4.4E-05	1	2	2	1	0	2	7.81	6.1E-05	2	5	5	2	0	5	11.9	4E-05	269	30986	7
CYT	BB_0195	BB_0195	cell division control protein 27	53.3	59.37	6.07	0.00195	2	0.00353	2	0.55212	22	145	145	22	0	145	52.2	0.00283	15	54	54	15	0	54	43.5	0.00107	14	142	116	14	26	116	47	0.00366	18	158	158	18	0	158	45.9	0.0034	26	489	489	26	0	489	61.7	0.00279	379	44124	7.1
CYT	BB_0198	BB_0198	guanosine-3'	1.8	4.05	2.25	1.1E-05	1	7.2E-05	1	0.15278	1	1	1	1	0	1	1.8	1.1E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	4.05	7.2E-05	X	X	X	X	X	X	X	X	3	5	5	3	0	5	4.05	1.6E-05	667	77763	8.6
CYT	BB_0200	BB_0200	D-alanine--D-alanine ligase (ddlA)	33.43	53.93	20.5	0.0007	2	0.00191	2	0.3663	8	40	40	8	0	40	33.4	0.00083	7	27	27	7	0	27	29.8	0.00057	10	51	51	10	0	51	41	0.00171	10	92	92	10	0	92	37.6	0.00211	15	210	210	15	0	210	57.6	0.00128	356	40223	5.3
CYT	BB_0201	BB_0201	UDP-N-acetylmuramoylalanyl-D-glu	16.34	5.91	-10.43	5.1E-05	2	5.1E-05	2	1	4	6	6	4	0	6	12	8.7E-05	1	1	1	1	0	1	4.33	1.5E-05	1	3	3	1	0	3	3.35	7.1E-05	1	2	2	1	0	2	2.56	3.2E-05	5	12	12	5	0	12	16.3	5.1E-05	508	57149	6.7
CYT	BB_0207	BB_0207	UTP--glucose-1-phosphate uridylylt	0	19.42	19.42	0	0	8.8E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	0	1	1	0	5.76	X	2	3	3	2	0	3	13.7	8.8E-05	3	4	4	3	0	4	19.4	3.1E-05	278	32221	9.1
CYT	BB_0218	BB_0218	phosphate ABC transporter	38.46	45	6.54	0.00024	2	0.0007	2	0.34914	6	12	12	6	0	12	29.2	0.00034	2	5	5	2	0	5	22.3	0.00014	7	18	18	7	0	18	25.8	0.00083	8	18	18	8	0	18	38.9	0.00056	13	53	53	13	0	53	50.4	0.00044	260	29431	6.8
CYT	BB_0220	BB_0220	alanyl-tRNA synthetase (alaS)	13.3	19.87	6.57	6.3E-05	2	0.00014	2	0.44056	1	1	1	1	0	1	2.69	1.2E-05	5	9	9	5	0	9	13.3	0.00011	3	4	4	3	0	4	5.89	8E-05	5	15	15	5	0	15	15.5	0.00021	9	29	29	9	0	29	19.9	0.00011	594	67774	6.7
CYT	BB_0222	BB_0222	glucose-6-phosphate 1-dehydroger	0	10.64	10.64	0	0	0.0001	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	10.6	0.0001	2	3	3	2	0	3	10.6	2.8E-05	235	27198	6.4
CYT	BB_0226	BB_0226	seryl-tRNA synthetase (serS)	23.29	17.65	-5.64	0.00014	2	0.0003	2	0.47458	7	10	10	7	0	10	23.3	0.00017	2	6	6	2	0	6	9.41	0.00011	3	8	8	3	0	8	7.06	0.00023	5	19	19	5	0	19	15.5	0.00036	11	43	43	11	0	43	29.9	0.00022	425	48787	6.7
CYT	BB_0228	BB_0228	conserved hypothetical protein	1.65	4.84	3.19	2.3E-05	1	2.9E-05	2	0.7931	1	3	3	1	0	3	1.65	2.3E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	2.88	2.5E-05	3	4	4	3	0	4	3.6	3.4E-05	3	8	8	3	0	8	3.6	1.8E-05	971	112959	8
CYT	BB_0229	BB_0229	ribosomal protein L31 (rpmE)	0	25.93	25.93	0	0	0.0003	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	25.9	0.0003	X	X	X	X	X	X	X	X	2	2	2	2	0	2	25.9	5.3E-05	81	9301	9.9
CYT	BB_0230	BB_0230	transcription termination factor Rho	33.2	44.47	11.27	0.0003	2	0.00049	2	0.61807	13	40	40	13	0	40	31.5	0.00057	2	2	2	2	0	2	6.99	2.9E-05	13	29	29	13	0	29	36.1	0.00067	11	19	19	11	0	19	24.5	0.0003	25	89	89	25	0	89	50.1	0.00037	515	57625	8.3
CYT	BB_0231	BB_0231	conserved hypothetical protein	0	14.81	14.81	0	0	0.00044	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	5	5	1	0	5	14.8	0.00044	X	X	X	X	X	X	X	X	1	5	5	1	0	5	14.8	8E-05	135	14963	7.7
CYT	BB_0232	BB_0232	hbbU protein	10.19	10.19	0	6.8E-05	1	0.00011	1	0.61261	1	1	1	1	0	1	10.2	6.8E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	10.2	0.00011	X	X	X	X	X	X	X	X	1	2	2	1	0	2	10.2	4E-05	108	12686	10.1
CYT	BB_0233	BB_0233	ribosomal protein S20 (rpsT)	11.21	0	-11.21	0.00021	1	0	0	∞	2	3	3	2	0	3	11.2	0.00021	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	11.2	6.1E-05	107	12595	10.9
CYT	BB_0235	BB_0235	conserved hypothetical protein	11.96	18.21	6.25	0.00013	2	0.00032	2	0.41772	4	7	7	4	0	7	12	0.00014	2	6	6	2	0	6	4.62	0.00012	5	14	14	5	0	14	16	0.00045	3	8	8	3	0	8	6.79	0.00018	8	35	35	8	0	35	21.2	0.00021	368	41488	6.9
CYT	BB_0239	BB_0239	deoxyguanosine/deoxyadenosine k	46.83	60	13.17	0.00127	2	0.00409	2	0.31008	8	54	54	8	0	54	38.5	0.00195	6	16	16	6	0	16	38.1	0.00059	5	91	91	5	0	91	42.4	0.00531	7	72	72	7	0	72	44.9	0.00287	13	233	233	13	0	233	73.7	0.00246	205	24117	5.5
CYT	BB_0241	BB_0241	glycerol kinase (glpK)	39.92	42.32	2.4	0.0005	2	0.00057	2	0.86865	11	50	50	11	0	50	36.7	0.00074	8	17	17	8	0	17	31.5	0.00026	10	24	24	10	0	24	37.1	0.00057	11	35	35	11	0	35	35.9	0.00057	17	124	124	17	0	124	44.9	0.00054	501	55606	7.4
CYT	BB_0243	BB_0243	glycerol-3-phosphate dehydrogena	66.22	56.55	-9.67	0.00304	2	0.00616	2	0.49294	29	148	148	29	0	148	53.9	0.00207	37	280	280	37	0	280	61.1	0.004	21	85	85	21	0	85	45.5	0.00193	45	671	671	45	0	671	55.6	0.01039	52	1152	1152	52	0	1152	67.2	0.00473	527	60251	8.8
CYT	BB_0248	BB_0248	oligoendopeptidase F (pepF)	12.03	23.9	11.87	7.5E-05	1	0.00013	2	0.59055	4	6	6	4	0	6	12	7.5E-05	X	X	X	X	X	X	X	X	5	5	5	5	0	5	13.7	0.0001	6	11	11	6	0	11	17.3	0.00015	10	21	21	10	0	21	22.9	7.7E-05	590	69723	7.3
CYT	BB_0251	BB_0251	leucyl-tRNA synthetase (leuS)	38.21	35.12	-3.09	0.00038	2	0.0004	2	0.9375	22	64	64	22	0	64	31.4	0.00056	8	21	21	8	0	21	19.1	0.00019	16	33	33	16	0	33	32	0.00047	11	34	34	11	0	34	22.3	0.00033	31	147	147	31	0	147	44.8	0.00038	840	98158	9
CYT	BB_0253	BB_0253	ATP-dependent protease LA (lon-1	0	6.7	6.7	0	0	0.00004	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	4	4	3	0	4	6.7	5.9E-05	1	2	2	1	0	2	2.48	2E-05	1	2	2	1	0	2	2.98	5.4E-06	806	90710	9.3
CYT	BB_0264	BB_0264	heat shock protein 70 (dnaK-1)	8.15	39.51	31.36	0.00003	1	0.00029	2	0.10453	2	2	2	2	0	2	8.15	3E-05	X	X	X	X	X	X	X	X	9	14	14	9	0	14	31.4	0.00034	5	14	14	5	0	14	18.9	0.00023	10	27	27	10	0	27	35.2	0.00012	491	54945	5.2
CYT	BB_0267	BB_0267	conserved hypothetical protein	17.19	35.33	18.14	0.00015	1	0.0002	2	0.755	7	13	13	7	0	13	17.2	0.00015	X	X	X	X	X	X	X	X	8	11	11	8	0	11	21.8	0.00021	9	15	15	9	0	15	23.5	0.00019	16	39	39	16	0	39	40.4	0.00013	634	70753	5.7
CYT	BB_0269	BB_0269	ATP-binding protein (ylxH-1)	7.12	21.02	13.9	2.5E-05	1	0.00047	2	0.05285	1	1	1	1	0	1	7.12	2.5E-05	X	X	X	X	X	X	X	X	4	22	22	4	0	22	13.9	0.00089	2	2	2	2	0	2	7.12	5.5E-05	6	25	25	6	0	25	21	0.00018	295	32783	8
CYT	BB_0270	BB_0270	flagellar-associated GTP-binding pr	25.77	48.97	23.2	0.00016	2	0.00078	2	0.20871	5	9	9	5	0	9	23.2	0.00017	3	8	8	3	0	8	9.79	0.00016	8	25	22	8	3	22	36.3	0.00068	12	42	42	12	0	42	41.5	0.00088	18	84	84	18	0	84	54.1	0.00047	388	44369	8.3
CYT	BB_0278	BB_0278	flagellar motor switch protein (fliM)	38.07	55.11	17.04	0.00046	2	0.00055	2	0.84058	11	33	33	11	0	33	33	0.00069	4	11	11	4	0	11	17.1	0.00024	6	10	10	6	0	10	31.3	0.00034	13	33	33	13	0	33	53.1	0.00077	16	81	81	16	0	81	48	0.0005	352	39284	5.4
CYT	BB_0288	BB_0288	flagellum-specific ATP synthase (fli	39.45	32.11	-7.34	0.00027	2	0.00042	2	0.64539	12	22	22	12	0	22	39.5	0.00037	4	10	10	4	0	10	13.3	0.00017	3	9	9	3	0	9	8.26	0.00025	11	32	32	11	0	32	32.1	0.0006	16	68	68	16	0	68	43.8	0.00034	436	48382	5.3
CYT	BB_0289	BB_0289	flagellar assembly protein (fliH)	12.75	21.24	8.49	9.7E-05	2	0.00035	2	0.27557	2	6	6	2	0	6	7.19	0.00014	1	2	2	1	0	2	5.56	4.9E-05	2	3	3	2	0	3	9.48	0.00012	6	22	22	6	0	22	21.2	0.00059	5	31	31	5	0	31	19.6	0.00022	306	35190	5
CYT	BB_0290	BB_0290	flagellar motor switch protein (fliG-2	0	6.1	6.1	0	0	4.7E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.1	4.7E-05	1	2	2	1	0	2	6.1	1.3E-05	344	39007	4.9
CYT	BB_0295	BB_0295	heat shock protein (hslU)	26.37	48.35	21.98	0.00039	2	0.00114	2	0.34296	12	31	31	12	0	31	25.9	0.0005	8	17	17	8	0	17	21.5	0.00028	15	57	57	15	0	57	29.7	0.0015	20	44	44	20	0	44	40	0.00079	27	147	147	27	0	147	46.6	0.0007	455	51883	7.9
CYT	BB_0296	BB_0296	heat shock protein (hslV)	9.34	19.23	9.89	4.1E-05	1	0.00018	2	0.23034	1	1	1	1	0	1	9.34	4.1E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	9.89	0.00013	2	5	5	2	0	5	19.2	0.00022	2	8	8	2	0	8	19.2	9.5E-05	182	19637	8.1
CYT	BB_0299	BB_0299	cell division protein (ftsZ)	65.35	62.62	-2.73	0.00061	2	0.00102	2	0.5918	17	49	49	17	0	49	59.4	0.0009	6	17	17	6	0	17	30	0.00032	11	31	31	11	0	31	44.6	0.00092	19	56	56	19	0	56	56.7	0.00113	21	140	140	21	0	140	65.4	0.00075	404	42972	4.9
CYT	BB_0300	BB_0300	cell division protein (ftsA)	24.7	27.12	2.42	0.00014	2	0.00042	2	0.33962	6	13	13	6	0	13	17.2	0.00023	2	3	3	2	0	3	11.9	5.5E-05	7	17	17	7	0	17	17.9	0.00049	9	18	18	9	0	18	24.5	0.00036	11	42	42	11	0	42	34.1	0.00022	413	45036	6.6
CYT	BB_0304	BB_0304	UDP-N-acetylmuramoylalanyl-D-glu	3.66	15.73	12.07	1.6E-05	1	6.1E-05	2	0.2623	1	1	1	1	0	1	3.66	1.6E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.66	5.2E-05	3	4	4	3	0	4	15.7	7E-05	2	6	6	2	0	6	8.19	2.8E-05	464	53446	7.9
CYT	BB_0306	BB_0306	conserved hypothetical protein	4.05	18.24	14.19	2.5E-05	1	5.4E-05	2	0.46296	X	X	X	X	X	X	X	X	1	1	1	1	0	1	4.05	2.5E-05	2	2	2	2	0	2	9.8	8.1E-05	1	1	1	1	0	1	8.45	2.8E-05	4	4	4	4	0	4	18.2	2.9E-05	296	34382	9
CYT	BB_0309	BB_0309	predicted coding region BB0309	6.18	6.18	0	2.9E-05	1	0.00014	1	0.21014	1	1	1	1	0	1	6.18	2.9E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	6.18	0.00014	X	X	X	X	X	X	X	X	3	4	4	3	0	4	12.4	3.3E-05	259	29977	9.2
CYT	BB_0312	BB_0312	purine-binding chemotaxis protein (	34.09	34.09	0	0.00034	2	0.00117	2	0.28779	3	12	12	3	0	12	31.8	0.0005	2	4	4	2	0	4	26.1	0.00017	2	14	14	2	0	14	23.9	0.00095	3	30	30	3	0	30	34.1	0.00139	5	60	60	5	0	60	44.3	0.00074	176	20020	5.1
CYT	BB_0314	BB_0314	octaprenyl-diphosphate synthase (i	5.19	9.22	4.03	2.2E-05	1	7.1E-05	1	0.30986	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.19	2.2E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	9.22	7.1E-05	1	3	3	1	0	3	5.19	1.9E-05	347	39992	9.6
CYT	BB_0318	BB_0318	methylgalactoside ABC transporter	0	5.14	5.14	0	0	0.00005	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.14	5E-05	1	3	3	1	0	3	5.14	1.3E-05	486	56532	9
CYT	BB_0325	BB_0325	predicted coding region BB0325	2.71	14.91	12.2	0.00002	1	0.00011	2	0.18349	1	1	1	1	0	1	2.71	2E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	8.4	0.00013	2	4	4	2	0	4	6.5	8.8E-05	5	9	9	5	0	9	17.6	5.3E-05	369	42782	6
CYT	BB_0327	BB_0327	glycerol-3-phosphate O-acyltransfe	0	9.4	9.4	0	0	0.0001	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	5.7	0.00012	2	3	3	2	0	3	9.4	8.2E-05	3	6	6	3	0	6	9.4	4.4E-05	298	34764	8.4
CYT	BB_0334	BB_0334	oligopeptide ABC transporter	35.86	42.76	6.9	0.00113	2	0.00277	2	0.40788	11	55	55	11	0	55	29.3	0.0014	7	33	33	7	0	33	23.8	0.00086	14	79	79	14	0	79	42.8	0.00326	12	81	81	12	0	81	34.1	0.00228	17	247	247	17	0	247	46.2	0.00184	290	32665	7.6
CYT	BB_0335	BB_0335	oligopeptide ABC transporter	27.24	38.7	11.46	0.00021	2	0.00065	2	0.31994	6	11	11	6	0	11	27.2	0.00025	4	7	7	4	0	7	18.6	0.00016	6	22	22	6	0	22	18	0.00081	11	19	19	11	0	19	38.7	0.00048	11	58	58	11	0	58	38.7	0.00039	323	37100	9.3
CYT	BB_0337	BB_0337	enolase (eno)	19.4	42.26	22.86	8.6E-05	2	0.0005	2	0.17304	4	5	5	4	0	5	14.6	8.5E-05	2	5	5	2	0	5	4.85	8.7E-05	4	8	8	4	0	8	16.9	0.00022	13	41	41	13	0	41	42.3	0.00077	16	59	59	16	0	59	46.4	0.00029	433	47290	5.5
CYT	BB_0338	BB_0338	ribosomal protein S9 (rpsI)	0	19.12	19.12	0	0	0.00024	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	4	4	2	0	4	19.1	0.00024	2	4	4	2	0	4	19.1	6.4E-05	136	15417	10.9
CYT	BB_0339	BB_0339	ribosomal protein L13 (rplM)	6.85	7.53	0.68	5.1E-05	1	0.00029	2	0.17647	1	1	1	1	0	1	6.85	5.1E-05	X	X	X	X	X	X	X	X	1	5	5	1	0	5	7.53	0.00041	1	3	3	1	0	3	7.53	0.00017	2	9	9	2	0	9	14.4	0.00013	146	16694	10.1
CYT	BB_0341	BB_0341	glu-tRNA amidotransferase	23.92	31.55	7.63	0.0002	2	0.00057	2	0.34974	7	18	18	7	0	18	23.9	0.00027	3	8	8	3	0	8	12	0.00012	8	25	25	8	0	25	22.7	0.00062	9	31	31	9	0	31	26.4	0.00052	11	79	79	11	0	79	34.6	0.00035	485	54521	6.6
CYT	BB_0342	BB_0342	glu-tRNA amidotransferase	44.96	48.59	3.63	0.00065	2	0.00102	2	0.64138	14	66	66	14	0	66	33.5	0.00098	8	21	21	8	0	21	22.6	0.00032	13	46	46	13	0	46	34.7	0.00111	18	56	56	18	0	56	39.1	0.00092	27	188	188	27	0	188	53.8	0.00082	496	55545	5.7
CYT	BB_0348	BB_0348	pyruvate kinase (pyk)	10.9	17.82	6.92	4.6E-05	1	0.00012	2	0.37398	3	3	3	3	0	3	10.9	4.6E-05	X	X	X	X	X	X	X	X	3	5	5	3	0	5	14.7	0.00013	4	7	7	4	0	7	12.6	0.00012	9	15	15	9	0	15	23.1	6.8E-05	477	53032	7.2
CYT	BB_0350	BB_0350	ribosomal protein L28 (rpmB)	0	9.78	9.78	0	0	0.00017	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	9.78	0.00026	1	1	1	1	0	1	9.78	8.9E-05	1	3	3	1	0	3	9.78	7.1E-05	92	10176	11
CYT	BB_0351	BB_0351	predicted coding region BB0351	34.29	46.74	12.45	0.00038	2	0.0027	2	0.14005	9	31	31	9	0	31	21.5	0.00044	7	22	22	7	0	22	19.2	0.00032	13	149	149	13	0	149	28.2	0.00341	20	127	127	20	0	127	43.3	0.00199	22	318	318	22	0	318	51.3	0.00132	522	60867	8.4
CYT	BB_0355	BB_0355	transcription factor	12.35	24.07	11.72	6.9E-05	2	0.00044	2	0.15826	1	2	2	1	0	2	12.4	9.1E-05	1	1	1	1	0	1	12.4	4.6E-05	2	5	5	2	0	5	24.1	0.00037	2	10	10	2	0	10	24.1	0.0005	1	13	13	1	0	13	12.4	0.00017	162	19020	6.6
CYT	BB_0361	BB_0361	ATP-binding protein (ylxH-2)	5.79	16.58	10.79	1.9E-05	1	0.00012	2	0.15574	1	1	1	1	0	1	5.79	1.9E-05	X	X	X	X	X	X	X	X	4	5	5	4	0	5	16.6	0.00016	2	4	4	2	0	4	6.58	8.6E-05	5	10	10	5	0	10	22.4	5.7E-05	380	42911	9.2
CYT	BB_0364	BB_0364	conserved hypothetical protein	17.46	21.43	3.97	0.00012	2	0.00022	2	0.52679	1	2	2	1	0	2	6.35	0.00012	1	2	2	1	0	2	11.1	0.00012	1	2	2	1	0	2	7.94	0.00019	2	4	4	2	0	4	21.4	0.00026	4	10	10	4	0	10	38.9	0.00017	126	13974	8.6
CYT	BB_0366	BB_0366	aminopeptidase I (yscI)	24.67	34.93	10.26	0.00013	2	0.00025	2	0.51984	2	4	4	2	0	4	11.8	6.5E-05	5	12	12	5	0	12	20.3	0.0002	3	5	5	3	0	5	16.2	0.00013	7	21	21	7	0	21	26.2	0.00037	10	42	42	10	0	42	35.2	0.0002	458	51500	6
CYT	BB_0367	BB_0367	predicted coding region BB0367	60.87	51.09	-9.78	0.00162	2	0.0018	2	0.89839	5	24	24	5	0	24	52.2	0.00193	6	16	16	6	0	16	60.9	0.00131	2	25	25	2	0	25	37	0.00325	2	4	4	2	0	4	35.9	0.00035	6	69	69	6	0	69	60.9	0.00162	92	10636	5.6
CYT	BB_0369	BB_0369	ATP-dependent Clp protease	3.67	5.24	1.57	1.9E-05	2	5.3E-05	2	0.35849	2	3	3	2	0	3	3.67	2.9E-05	1	1	1	1	0	1	2.23	9.9E-06	1	2	2	1	0	2	2.23	3.1E-05	2	7	7	2	0	7	5.24	7.5E-05	3	13	13	3	0	13	6.68	3.7E-05	763	88906	8
CYT	BB_0370	BB_0370	tyrosyl-tRNA synthetase (tyrS)	16.3	17.78	1.48	0.00013	2	0.00015	2	0.85333	4	12	12	4	0	12	16.3	0.00022	1	2	2	1	0	2	4.94	3.7E-05	2	4	4	2	0	4	6.17	0.00012	5	9	9	5	0	9	15.3	0.00018	6	23	23	6	0	23	21.2	0.00012	405	46363	8.9
CYT	BB_0371	BB_0371	glycyl-tRNA synthetase (glyS)	16.18	30.11	13.93	7.6E-05	2	0.00023	2	0.32618	1	1	1	1	0	1	2.25	1.7E-05	4	8	8	4	0	8	13.9	0.00014	1	1	1	1	0	1	2.25	2.7E-05	10	24	24	10	0	24	30.1	0.00044	13	34	34	13	0	34	34.2	0.00017	445	52210	7.1
CYT	BB_0372	BB_0372	glutamyl-tRNA synthetase (gltX)	52.65	47.35	-5.3	0.00064	2	0.0008	2	0.79551	18	48	48	18	0	48	46.5	0.00072	13	36	36	13	0	36	33.9	0.00055	14	35	35	14	0	35	30.2	0.00085	14	45	45	14	0	45	32.7	0.00075	30	163	163	30	0	163	57.4	0.00072	490	56752	8.8
CYT	BB_0374	BB_0374	predicted coding region BB0374	10.82	18.21	7.39	3.9E-05	2	0.00014	2	0.27273	1	2	2	1	0	2	5.8	3.9E-05	1	2	2	1	0	2	5.01	4E-05	3	7	7	3	0	7	18.2	0.00022	1	3	3	1	0	3	6.6	6.5E-05	5	14	14	5	0	14	29	8E-05	379	43457	8.6
CYT	BB_0375	BB_0375	pfs protein (pfs-1)	0	13.08	13.08	0	0	6.9E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	13.1	6.9E-05	2	2	2	2	0	2	13.1	1.8E-05	237	26586	7.6
CYT	BB_0376	BB_0376	S-adenosylmethionine synthetase (	45.66	54.59	8.93	0.00056	2	0.00103	2	0.54439	13	48	48	13	0	48	45.4	0.0009	5	11	11	5	0	11	24.7	0.00021	10	29	29	10	0	29	45.7	0.00088	15	56	56	15	0	56	46.4	0.00117	22	144	144	22	0	144	56.9	0.00079	392	43070	8.6
CYT	BB_0381	BB_0381	conserved hypothetical protein	12.21	32.21	20	0.00016	2	0.00036	2	0.45682	3	14	14	3	0	14	9.26	0.00022	2	7	7	2	0	7	9.68	0.00011	8	19	19	8	0	19	23.4	0.00048	6	14	14	6	0	14	18.5	0.00024	11	54	54	11	0	54	32.2	0.00025	475	55786	7.3
CYT	BB_0386	BB_0386	ribosomal protein S7 (rpsG)	22.29	49.04	26.75	0.00028	1	0.00089	2	0.31579	2	6	6	2	0	6	22.3	0.00028	X	X	X	X	X	X	X	X	5	18	18	5	0	18	41.4	0.00137	2	8	8	2	0	8	22.3	0.00042	6	32	32	6	0	32	49	0.00044	157	18252	10.1
CYT	BB_0388	BB_0388	DNA-directed RNA polymerase (rpo	0.94	14.89	13.95	1.1E-05	1	0.00012	2	0.09091	1	2	2	1	0	2	0.94	1.1E-05	X	X	X	X	X	X	X	X	11	17	17	11	0	17	11.8	0.00015	8	16	16	8	0	16	8.5	9.5E-05	15	35	35	15	0	35	15.8	5.5E-05	1377	154657	8
CYT	BB_0389	BB_0389	DNA-directed RNA polymerase (rpo	31.34	39.39	8.05	0.00018	2	0.00084	2	0.21445	14	27	27	14	0	27	19	0.00017	12	29	29	12	0	29	21.1	0.00019	21	58	58	21	0	58	23.7	0.0006	31	154	154	31	0	154	34.4	0.00109	40	263	263	40	0	263	41.7	0.00049	1155	129624	6.1
CYT	BB_0390	BB_0390	ribosomal protein L7/L12 (rplL)	58.06	89.52	31.46	0.00788	2	0.01273	2	0.61905	11	183	183	11	0	183	54.8	0.0109	11	80	80	11	0	80	58.1	0.00485	7	92	92	7	0	92	45.2	0.00887	10	252	252	10	0	252	89.5	0.01658	14	540	540	14	0	540	58.1	0.00942	124	12904	4.7
CYT	BB_0391	BB_0391	ribosomal protein L10 (rplJ)	59.52	49.4	-10.12	0.00372	2	0.00701	2	0.53126	10	152	152	10	0	152	54.8	0.00668	6	17	17	6	0	17	37.5	0.00076	4	115	115	4	0	115	36.3	0.00818	8	120	120	8	0	120	48.8	0.00583	13	404	404	13	0	404	64.9	0.0052	168	18679	9.6
CYT	BB_0392	BB_0392	ribosomal protein L1 (rplA)	37.17	50.44	13.27	0.00044	2	0.00121	2	0.36469	6	23	23	6	0	23	30.5	0.00075	2	4	4	2	0	4	6.64	0.00013	12	39	39	12	0	39	50.4	0.00206	3	10	10	3	0	10	15.5	0.00036	14	76	76	14	0	76	55.3	0.00073	226	25668	9.6
CYT	BB_0394	BB_0394	transcription antitermination factor (	50.54	39.67	-10.87	0.00075	2	0.00156	2	0.47848	8	32	32	8	0	32	50.5	0.00128	2	5	5	2	0	5	10.9	0.0002	3	22	22	3	0	22	19.6	0.00143	9	38	38	9	0	38	39.7	0.00169	12	97	97	12	0	97	56.5	0.00114	184	21216	8.2
CYT	BB_0397	BB_0397	predicted coding region BB0397	7.45	0	-7.45	7.9E-05	1	0	0	∞	1	3	3	1	0	3	7.45	7.9E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	3	3	1	0	3	7.45	2.3E-05	282	32983	8
CYT	BB_0402	BB_0402	prolyl-tRNA synthetase (proS)	44.26	46.11	1.85	0.00053	2	0.00097	2	0.54892	17	48	48	17	0	48	43.7	0.00073	9	22	22	9	0	22	28.5	0.00034	10	26	26	10	0	26	27.1	0.00064	16	78	78	16	0	78	38.1	0.0013	25	172	172	25	0	172	52.9	0.00076	488	56311	8.2
CYT	BB_0404	BB_0404	predicted coding region BB0404	0	22.46	22.46	0	0	0.00012	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	22.5	0.00012	1	2	2	1	0	2	22.5	3.1E-05	138	16257	10.4
CYT	BB_0407	BB_0407	mannose-6-phosphate isomerase (	25.54	30.38	4.84	0.00031	2	0.00044	2	0.70776	5	19	19	5	0	19	21.2	0.00038	5	12	12	5	0	12	25.5	0.00024	6	15	15	6	0	15	28.2	0.00048	7	18	18	7	0	18	24.2	0.00039	11	64	64	11	0	64	34.7	0.00037	372	42840	5.6
CYT	BB_0417	BB_0417	adenylate kinase (adk)	21.33	16.59	-4.74	0.00042	1	0.00021	2	2	4	12	12	4	0	12	21.3	0.00042	X	X	X	X	X	X	X	X	2	4	4	2	0	4	11.4	0.00023	2	5	5	2	0	5	5.21	0.00019	5	19	19	5	0	19	21.3	0.00019	211	24099	9.2
CYT	BB_0419	BB_0419	response regulatory protein (rrp-1)	8.14	20.52	12.38	2.4E-05	1	9.9E-05	2	0.24242	1	1	1	1	0	1	8.14	2.4E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	7.17	3.9E-05	3	6	6	3	0	6	20.5	0.00016	3	8	8	3	0	8	20.5	5.6E-05	307	35074	7
CYT	BB_0421	BB_0421	hydrolase	14.34	22.22	7.88	0.00025	2	0.00022	2	1.1713	3	14	14	3	0	14	14.3	0.00037	2	5	5	2	0	5	14.3	0.00013	3	6	6	3	0	6	12.5	0.00026	3	6	6	3	0	6	14.3	0.00018	5	31	31	5	0	31	22.2	0.00024	279	32154	5.6
CYT	BB_0426	BB_0426	predicted coding region BB0426	33.16	50.27	17.11	0.00036	2	0.00098	2	0.36419	4	11	11	4	0	11	33.2	0.00043	2	7	7	2	0	7	23.5	0.00028	2	13	13	2	0	13	21.9	0.00083	8	26	26	8	0	26	50.3	0.00113	9	57	57	9	0	57	50.3	0.00066	187	21918	7.3
CYT	BB_0429	BB_0429	predicted coding region BB0429	23.26	23.26	0	0.00032	2	0.00038	1	0.83421	2	7	7	2	0	7	23.3	0.0004	1	4	4	1	0	4	10.9	0.00023	X	X	X	X	X	X	X	X	2	6	6	2	0	6	23.3	0.00038	2	17	17	2	0	17	23.3	0.00029	129	14696	9
CYT	BB_0435	BB_0435	DNA gyrase	4.44	22.84	18.4	4.6E-05	2	0.00024	2	0.19247	2	7	7	2	0	7	4.44	6.4E-05	2	3	3	2	0	3	4.44	2.8E-05	8	16	16	8	0	16	13.7	0.00024	8	24	24	8	0	24	16.9	0.00024	12	50	50	12	0	50	22.8	0.00013	810	91379	7.3
CYT	BB_0436	BB_0436	DNA gyrase	37.09	50.55	13.46	0.00074	2	0.00128	2	0.57399	21	100	100	21	0	100	35.4	0.00116	10	27	27	10	0	27	19.4	0.00032	21	69	69	21	0	69	41.3	0.00129	23	100	100	23	0	100	39.6	0.00128	33	293	293	33	0	293	47.3	0.00099	639	72057	7
CYT	BB_0438	BB_0438	DNA polymerase III	5.19	8.31	3.12	1.9E-05	1	0.00016	1	0.12258	1	1	1	1	0	1	5.19	1.9E-05	X	X	X	X	X	X	X	X	3	5	5	3	0	5	8.31	0.00016	X	X	X	X	X	X	X	X	4	6	6	4	0	6	13.5	3.4E-05	385	44614	5.6
CYT	BB_0439	BB_0439	conserved hypothetical protein	0	19.19	19.19	0	0	0.00024	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	19.2	0.00024	X	X	X	X	X	X	X	X	1	2	2	1	0	2	19.2	4.4E-05	99	11229	9
CYT	BB_0443	BB_0443	spoIIIJ-associtated protein (jag)	3.72	8.26	4.54	6.2E-05	1	0.00011	2	0.57407	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.72	6.2E-05	1	3	3	1	0	3	4.55	0.00015	2	2	2	2	0	2	8.26	6.7E-05	3	7	7	3	0	7	12	6.3E-05	242	28267	9.4
CYT	BB_0444	BB_0444	nucleotide sugar epimerase	63.94	65.07	1.13	0.00141	2	0.00306	2	0.46156	23	100	100	23	0	100	55.2	0.00208	11	35	35	11	0	35	39.2	0.00074	18	99	99	18	0	99	49.3	0.00333	22	121	121	22	0	121	62.8	0.00278	33	345	345	33	0	345	75.2	0.0021	355	40183	7.8
CYT	BB_0445	BB_0445	fructose-bisphosphate aldolase (fba	31.2	44.01	12.81	0.0002	2	0.00043	2	0.46154	3	8	8	3	0	8	18.4	0.00016	4	11	11	4	0	11	26.5	0.00023	7	8	8	7	0	8	35.9	0.00027	11	26	26	11	0	26	44	0.00059	13	53	53	13	0	53	49	0.00032	359	39981	6.5
CYT	BB_0449	BB_0449	conserved hypothetical protein	0	12.37	12.37	0	0	0.00017	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	12.4	0.00017	1	2	2	1	0	2	12.4	4.5E-05	97	11591	9.6
CYT	BB_0459	BB_0459	predicted coding region BB0459	6.65	11.47	4.82	5.1E-05	1	0.00011	2	0.47664	2	3	3	2	0	3	6.65	5.1E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	9.17	8.2E-05	2	7	7	2	0	7	6.65	0.00013	3	13	13	3	0	13	11.5	6.5E-05	436	51774	5.4
CYT	BB_0462	BB_0462	conserved hypothetical protein	43.64	38.18	-5.46	0.00074	2	0.00402	2	0.18512	5	13	13	5	0	13	43.6	0.00087	4	9	9	4	0	9	20	0.00062	6	61	61	6	0	61	38.2	0.00663	6	19	19	6	0	19	38.2	0.00141	10	102	102	10	0	102	43.6	0.00201	110	12479	6.7
CYT	BB_0466	BB_0466	ABC transporter	0	14.8	14.8	0	0	6.6E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.05	4.3E-05	1	3	3	1	0	3	9.75	8.8E-05	2	4	4	2	0	4	14.8	3.1E-05	277	31476	9.1
CYT	BB_0467	BB_0467	conserved hypothetical protein	10.04	14.85	4.81	9.7E-05	1	0.00014	2	0.68794	2	3	3	2	0	3	10	9.7E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	10	0.0001	3	5	5	3	0	5	10.9	0.00018	3	9	9	3	0	9	10.9	8.5E-05	229	26948	8.8
CYT	BB_0472	BB_0472	UDP-N-acetylglucosamine 1-carbox	3.39	7.69	4.3	3.3E-05	1	6.3E-05	2	0.52381	1	2	2	1	0	2	3.39	3.3E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	4.98	0.00011	1	1	1	1	0	1	2.71	1.8E-05	2	5	5	2	0	5	6.11	2.4E-05	442	48497	8.6
CYT	BB_0476	BB_0476	translation elongation factor TU (tuf	71.32	66.83	-4.49	0.00686	2	0.015	2	0.4572	33	661	661	33	0	661	67.3	0.01218	13	82	82	13	0	82	39.7	0.00154	30	874	874	30	0	874	61.6	0.02605	21	194	194	21	0	194	61.9	0.00395	39	1804	1804	39	0	1804	73.1	0.00973	401	44330	6.1
CYT	BB_0477	BB_0477	ribosomal protein S10 (rpsJ)	52.43	40.78	-11.65	0.00134	2	0.00297	2	0.45295	5	12	12	5	0	12	40.8	0.00086	5	25	25	5	0	25	51.5	0.00183	9	47	47	9	0	47	40.8	0.00545	2	6	6	2	0	6	29.1	0.00048	10	88	88	10	0	88	52.4	0.00185	103	11766	10
CYT	BB_0478	BB_0478	ribosomal protein L3 (rplC)	27.67	29.61	1.94	7.2E-05	2	0.00066	2	0.10942	3	3	3	3	0	3	21.4	0.00011	1	1	1	1	0	1	6.31	3.7E-05	4	22	22	4	0	22	29.6	0.00128	1	1	1	1	0	1	9.71	4E-05	6	27	27	6	0	27	42.2	0.00028	206	22212	10
CYT	BB_0479	BB_0479	ribosomal protein L4 (rplD)	0	21.05	21.05	0	0	0.00019	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	4	4	2	0	4	16.3	0.00023	2	4	4	2	0	4	12.4	0.00016	3	8	8	3	0	8	21.1	8.3E-05	209	23492	10.2

Known (Table 1) and/or predicated subcellular location	Locus	Proteins In Group	Description	B31A3_Control_merged-SeqCov (%)	B31A3_ProK_merged-SeqCov (%)	DiffSeqCov (Control - ProK) (%)	B31A3_Cntl-Ti dNSAF AVG	B31A3_Cntl-Ti Detected # Out of 2	B31A3_PK-Ti dNSAF AVG	B31A3_PK-Ti Detected # Out of 2	B31A3_Cntl-Ti: B31A3_PK-Ti	B31A3_Control_1_P	B31A3_Control_1_S	B31A3_Control_1_uS	B31A3_Control_1_uDP	B31A3_Control_1_sS	B31A3_Control_1_dS	B31A3_Control_1_SC	B31A3_Control_1_dNSAF
CYT	BB_0481	BB_0481	ribosomal protein L2 (rplB)	5.05	13.72	8.67	5.3E-05	1	0.00017	1	0.30636	1	2	2	1	0	2	5.05	5.3E-05
CYT	BB_0482	BB_0482	ribosomal protein S19 (rpsS)	16.3	36.96	20.66	0.00008	1	0.00078	1	0.10256	1	1	1	1	0	1	16.3	8E-05
CYT	BB_0484	BB_0484	ribosomal protein S3 (rpsC)	3.07	19.11	16.04	0.00005	1	8.9E-05	2	0.5618	1	2	2	1	0	2	3.07	5E-05
CYT	BB_0485	BB_0485	ribosomal protein L16 (rplP)	9.42	18.84	9.42	5.5E-05	1	0.00032	2	0.17241	X	X	X	X	X	X	X	X
CYT	BB_0487	BB_0487	ribosomal protein S17 (rpsQ)	8.33	11.9	3.57	0.00018	1	0.00014	1	1.26056	X	X	X	X	X	X	X	X
CYT	BB_0488	BB_0488	ribosomal protein L14 (rplN)	0	12.9	12.9	0	0	0.00031	2	0	X	X	X	X	X	X	X	X
CYT	BB_0490	BB_0490	ribosomal protein L5 (rplE)	39.56	62.64	23.08	0.001	2	0.00224	2	0.44519	6	37	37	6	0	37	35.2	0.0015
CYT	BB_0492	BB_0492	ribosomal protein S8 (rpsH)	15.91	28.03	12.12	0.00011	2	0.00048	2	0.2314	1	3	3	1	0	3	15.2	0.00017
CYT	BB_0493	BB_0493	ribosomal protein L6 (rplF)	5.56	26.67	21.11	4.2E-05	1	0.00038	2	0.11082	X	X	X	X	X	X	X	X
CYT	BB_0494	BB_0494	ribosomal protein L18 (rplR)	19.33	40.34	21.01	0.00012	1	0.00052	2	0.238	1	2	2	1	0	2	19.3	0.00012
CYT	BB_0495	BB_0495	ribosomal protein S5 (rpsE)	14.55	16.97	2.42	0.00013	1	0.00021	2	0.64423	2	3	3	2	0	3	14.6	0.00013
CYT	BB_0496	BB_0496	ribosomal protein L30 (rpmD)	0	36.63	36.63	0	0	0.00058	2	0	X	X	X	X	X	X	X	X
CYT	BB_0497	BB_0497	ribosomal protein L15 (rplO)	21.38	21.38	0	0.00013	2	0.00035	2	0.36888	1	3	3	1	0	3	15.9	0.00015
CYT	BB_0500	BB_0500	ribosomal protein S13 (rpsM)	0	22.4	22.4	0	0	0.00039	1	0	X	X	X	X	X	X	X	X
CYT	BB_0501	BB_0501	ribosomal protein S11 (rpsK)	0	38.06	38.06	0	0	0.00054	2	0	X	X	X	X	X	X	X	X
CYT	BB_0502	BB_0502	DNA-directed RNA polymerase (rpo	43.48	46.96	3.48	0.00142	2	0.0044	2	0.32213	12	109	109	12	0	109	43.5	0.00233
CYT	BB_0503	BB_0503	ribosomal protein L17 (rplQ)	7.32	26.02	18.7	0.00006	1	0.00033	2	0.18462	1	1	1	1	0	1	7.32	6E-05
CYT	BB_0505	BB_0505	conserved hypothetical protein	0	8.02	8.02	0	0	3.8E-05	2	0	X	X	X	X	X	X	X	X
CYT	BB_0509	BB_0509	predicted coding region BB0509	14.56	17.18	2.62	0.00013	2	0.00021	2	0.64563	5	11	11	5	0	11	14.1	0.00019
CYT	BB_0513	BB_0513	phenylalanyl-tRNA synthetase	5.3	4.17	-1.13	4.2E-05	1	4.6E-05	1	0.91304	2	3	3	2	0	3	5.3	4.2E-05
CYT	BB_0514	BB_0514	phenylalanyl-tRNA synthetase	26.68	33.57	6.89	9.9E-05	2	0.00043	2	0.23239	5	9	9	5	0	9	19.4	0.00012
CYT	BB_0518	BB_0518	heat shock protein 70 (dnaK-2)	49.13	43.78	-5.35	0.00126	2	0.0012	2	1.04829	18	84	84	18	0	84	38.3	0.00098
CYT	BB_0519	BB_0519	grpE protein (grpE)	57.22	50.27	-6.95	0.00094	2	0.00187	2	0.50161	9	23	23	9	0	23	45.5	0.00091
CYT	BB_0521	BB_0521	predicted coding region BB0521	35.33	36.67	1.34	0.00022	2	0.00084	2	0.26422	3	6	6	3	0	6	24.7	0.0003
CYT	BB_0522	BB_0522	NH(3)-dependent NAD+ synthetase	18.47	40.09	21.62	0.00047	2	0.00088	2	0.53281	4	12	12	4	0	12	18.5	0.0004
CYT	BB_0527	BB_0527	conserved hypothetical protein	4.96	15.65	10.69	2.9E-05	1	0.00011	2	0.26852	X	X	X	X	X	X	X	X
CYT	BB_0528	BB_0528	aldose reductase	30.16	37.14	6.98	0.00023	2	0.00039	2	0.57252	4	11	11	4	0	11	26	0.00026
CYT	BB_0533	BB_0533	phnP protein (phnP)	0	12.65	12.65	0	0	6.5E-05	1	0	X	X	X	X	X	X	X	X
CYT	BB_0534	BB_0534	exodeoxyribonuclease III (exoA)	7.45	17.25	9.8	2.9E-05	1	0.00021	2	0.13615	1	1	1	1	0	1	7.45	2.9E-05
CYT	BB_0538	BB_0538	conserved hypothetical protein	0	14.39	14.39	0	0	0.00012	1	0	X	X	X	X	X	X	X	X
CYT	BB_0540	BB_0540	translation elongation factor G (fus-	35.79	24.24	-11.55	0.00031	2	0.00024	2	1.28926	14	31	31	14	0	31	27.4	0.00033
CYT	BB_0541	BB_0541	predicted coding region BB0541	9.72	25	15.28	0.0001	1	0.0005	1	0.20683	1	1	1	1	0	1	9.72	0.0001
CYT	BB_0544	BB_0544	phosphoribosyl pyrophosphate syn	6.4	7.88	1.48	0.00016	1	2.5E-05	2	6.56	2	9	9	2	0	9	6.4	0.00016
CYT	BB_0545	BB_0545	xylulokinase (xylB)	0	6.61	6.61	0	0	5.4E-05	1	0	X	X	X	X	X	X	X	X
CYT	BB_0550	BB_0550	flagellar protein (flaJ)	8.97	37.93	28.96	5.2E-05	1	0.00038	2	0.13867	X	X	X	X	X	X	X	X
CYT	BB_0551	BB_0551	chemotaxis response regulator (che	15.04	18.05	3.01	8.4E-05	2	0.00012	1	0.68293	1	1	1	1	0	1	8.27	5.6E-05
CYT	BB_0556	BB_0556	predicted coding region BB0556	0	5.54	5.54	0	0	0.00012	1	0	X	X	X	X	X	X	X	X
CYT	BB_0557	BB_0557	phosphocarrier protein HPr (ptsH-2	17.44	30.23	12.79	0.00018	1	0.00029	1	0.61404	X	X	X	X	X	X	X	X
CYT	BB_0558	BB_0558	phosphoenolpyruvate-protein phos	0	7.5	7.5	0	0	7.1E-05	1	0	X	X	X	X	X	X	X	X
CYT	BB_0559	BB_0559	PTS system	70.9	56.08	-14.82	0.00113	2	0.00146	2	0.77266	6	26	26	6	0	26	54.5	0.00102
CYT	BB_0560	BB_0560	heat shock protein 90 (htpG)	38	41.38	3.38	0.00052	2	0.00081	2	0.64118	20	63	63	20	0	63	35.1	0.00072
CYT	BB_0561	BB_0561	phosphogluconate dehydrogenase	31.9	21.34	-10.56	0.00023	2	0.00024	2	0.95851	10	26	26	10	0	26	30	0.00041
CYT	BB_0562	BB_0562	predicted coding region BB0562	12.22	18.33	6.11	0.00042	2	0.00036	2	1.14958	2	9	9	2	0	9	12.2	0.00037
CYT	BB_0566	BB_0566	predicted coding region BB0566	26.21	15.53	-10.68	0.00011	2	0.00035	2	0.31034	1	2	2	1	0	2	15.5	0.00014
CYT	BB_0567	BB_0567	chemotaxis histidine kinase (cheA-	28.99	22.41	-6.58	0.00012	2	0.0002	2	0.61692	11	22	22	11	0	22	26.5	0.00023
CYT	BB_0568	BB_0568	protein-glutamate methylesterase (	4.42	11.43	7.01	3.9E-05	1	0.0002	2	0.19118	X	X	X	X	X	X	X	X
CYT	BB_0569	BB_0569	predicted coding region BB0569	11.36	23.56	12.2	9.4E-05	2	0.00041	2	0.22871	5	11	11	5	0	11	11.4	0.00014
CYT	BB_0570	BB_0570	chemotaxis response regulator (che	54.84	45.16	-9.68	0.00049	1	0.00086	1	0.56659	X	X	X	X	X	X	X	X
CYT	BB_0572	BB_0572	glycosyl transferase (lgtD)	24.86	22.35	-2.51	0.00018	2	0.00027	2	0.65185	7	15	15	7	0	15	21.8	0.00031
CYT	BB_0573	BB_0573	ABC transporter	36.67	40.37	3.7	0.00077	2	0.00096	2	0.80249	6	34	34	6	0	34	29.6	0.00093
CYT	BB_0578	BB_0578	methyl-accepting chemotaxis prote	21.85	20.31	-1.54	0.00013	1	0.00022	2	0.6129	6	7	7	6	0	7	21.9	0.00013
CYT	BB_0579	BB_0579	DNA polymerase III	13.7	25.06	11.36	8.6E-05	2	0.00025	2	0.34127	9	20	20	9	0	20	9.04	0.00013
CYT	BB_0581	BB_0581	DNA recombinase (recG)	6.27	15.01	8.74	4.3E-05	1	9.1E-05	2	0.47253	3	5	4	3	1	4	6.27	4.3E-05
CYT	BB_0582	BB_0582	carboxypeptidase	5.34	12.98	7.64	5.6E-05	1	9.1E-05	1	0.61538	1	2	2	1	0	2	5.34	5.6E-05
CYT	BB_0585	BB_0585	UDP-N-acetylmuramoylalanine--D-g	10.86	11.09	0.23	3.3E-05	1	0.00011	2	0.29464	X	X	X	X	X	X	X	X
CYT	BB_0587	BB_0587	methionyl-tRNA synthetase (metG)	24.52	28.47	3.95	0.00017	2	0.00035	2	0.47309	10	23	23	10	0	23	19.2	0.00023
CYT	BB_0594	BB_0594	arginyl-tRNA synthetase (argS)	38.41	37.06	-1.35	0.00027	2	0.00043	2	0.6338	14	31	31	14	0	31	31.1	0.00039
CYT	BB_0601	BB_0601	serine hydroxymethyltransferase (g	7.91	4.32	-3.59	0.00016	1	0.00002	1	7.95	2	9	9	2	0	9	7.91	0.00016
CYT	BB_0606	BB_0606	conserved hypothetical protein	37.42	29.45	-7.97	0.00023	2	0.00076	2	0.29712	5	9	9	5	0	9	37.4	0.00041
CYT	BB_0608	BB_0608	aminoacyl-histidine dipeptidase (pe	21.85	24.58	2.73	0.00017	2	0.00025	2	0.65737	3	8	8	3	0	8	9.87	0.00012
CYT	BB_0610	BB_0610	trigger factor (tig)	20.04	26.65	6.61	0.00012	2	0.00017	2	0.72781	4	7	7	4	0	7	16.7	0.00011
CYT	BB_0612	BB_0612	ATP-dependent Clp protease	46.28	41.4	-4.88	0.00085	2	0.00105	2	0.80725	16	69	69	16	0	69	44.7	0.00119
CYT	BB_0613	BB_0613	ATP-dependent protease LA (lon-2	17.59	23.25	5.66	0.00005	2	0.00035	2	0.14164	6	9	9	6	0	9	12.4	8.2E-05
CYT	BB_0615	BB_0615	ribosomal protein S4 (rpsD)	11	28.71	17.71	3.6E-05	1	0.00058	2	0.06239	X	X	X	X	X	X	X	X
CYT	BB_0617	BB_0617	predicted coding region BB0617	0	17.21	17.21	0	0	0.00023	2	0	X	X	X	X	X	X	X	X
CYT	BB_0618	BB_0618	cytidine deaminase (cdd)	33.12	9.74	-23.38	9.6E-05	2	5.3E-05	1	1.81132	2	3	3	2	0	3	20.8	0.00014
CYT	BB_0619	BB_0619	conserved hypothetical protein	5.76	10.3	4.54	2.2E-05	1	5.5E-05	2	0.4	1	1	1	1	0	1	5.76	2.2E-05
CYT	BB_0621	BB_0621	4-methyl-5(b-hydroxyethyl)-thiazole	15.22	17.93	2.71	0.00016	1	0.00019	2	0.86559	2	4	4	2	0	4	15.2	0.00016
CYT	BB_0622	BB_0622	acetate kinase (ackA)	11.86	15.01	3.15	0.00018	1	0.00011	2	1.6729	3	10	10	3	0	10	11.9	0.00018
CYT	BB_0627	BB_0627	vacuolar X-prolyl dipeptidyl aminop	5.2	26.71	21.51	1.7E-05	1	0.00022	2	0.07834	1	1	1	1	0	1	5.2	1.7E-05
CYT	BB_0630	BB_0630	1-phosphofructokinase (fruK)	51.47	58.63	7.16	0.00059	2	0.00082	2	0.71255	6	16	16	6	0	16	37.1	0.00039
CYT	BB_0636	BB_0636	glucose-6-phosphate 1-dehydroger	11.3	30.33	19.03	0.00007	2	0.00035	2	0.2	4	8	8	4	0	8	11.3	0.00012
CYT	BB_0642	BB_0642	spermidine/putrescine ABC transp	17.58	17	-0.58	0.00019	2	0.00011	2	1.73874	5	13	13	5	0	13	17.6	0.00028
CYT	BB_0644	BB_0644	conserved hypothetical protein	24.57	28.45	3.88	0.00037	2	0.00032	2	1.1358	4	18	18	4	0	18	24.6	0.00057
CYT	BB_0647	BB_0647	ferric uptake regulation protein (fur)	10.8	5.11	-5.69	8.4E-05	1	5.7E-05	2	1.47368	1	2	2	1	0	2	10.8	8.4E-05
CYT	BB_0649	BB_0649	heat shock protein (groEL)	36.51	51.01	14.5	0.00027	2	0.0011	2	0.24292	10	29	29	10	0	29	27.7	0.00039
CYT	BB_0650	BB_0650	predicted coding region BB0650	37.5	25	-12.5	0.00023	2	0.00038	2	0.61436	3	6	6	3	0	6	26.8	0.0004
CYT	BB_0654	BB_0654	predicted coding region BB0654	12.11	25.26	13.15	7.8E-05	1	0.0003	2	0.26174	3	4	4	3	0	4	12.1	7.8E-05
CYT	BB_0655	BB_0655	heat shock protein (dnaJ-2)	0	16.67	16.67	0	0	0.00022	1	0	X	X	X	X	X	X	X	X
CYT	BB_0658	BB_0658	phosphoglycerate mutase (gpmA)	17.79	21.74	3.95	0.00018	1	0.00025	2	0.71429	3	6	6	3	0	6	17.8	0.00018
CYT	BB_0659	BB_0659	lysyl-tRNA synthetase	6.14	10.17	4.03	7.1E-05	1	8.4E-05	2	0.84524	2	5	5	2	0	5	6.14	7.1E-05
CYT	BB_0669	BB_0669	chemotaxis histidine kinase (cheA-2	23.61	26.39	2.78	0.00012	2	0.00045	2	0.25664	10	20	20	10	0	20	16.8	0.00017
CYT	BB_0670	BB_0670	purine-binding chemotaxis protein (	21.89	56.65	34.76	0.00012	2	0.00045	2	0.26622	5	11	11	5	0	11	17.2	0.00017
CYT	BB_0671	BB_0671	chemotaxis operon protein (cheX)	68.94	72.05	3.11	0.0025	2	0.0049	2	0.51082	11	48	48	11	0	48	59.6	0.0022
CYT	BB_0673	BB_0673	conserved hypothetical protein	0	7.6	7.6	0	0	0.00014	1	0	X	X	X	X	X	X	X	X
CYT	BB_0675	BB_0675	predicted coding region BB0675	0	13.94	13.94	0	0	0.00011	1	0	X	X	X	X	X	X	X	X
CYT	BB_0676	BB_0676	phosphoglycolate phosphatase (gp	17.73	47.27	29.54	0.00015	2	0.00079	2	0.19314	2	5	5	2	0	5	11.4	0.00017
CYT	BB_0677	BB_0677	ribose/galactose ABC transporter	7.84	10.26	2.42	4.9E-05	2	7.9E-05	2	0.62025	2	3	3	2	0	3	7.84	4.1E-05
CYT	BB_0683	BB_0683	3-hydroxy-3-methylglutaryl-CoA syn	42.01	44.96	2.95	0.00101	2	0.00172	2	0.58765	17	99	99	17	0	99	39.6	0.0018
CYT	BB_0685	BB_0685	3-hydroxy-3-methylglutaryl-CoA red	0	3.25	3.25	0	0	5.5E-05	1	0	X	X	X	X	X	X	X	X
CYT	BB_0687	BB_0687	phosphomevalonate kinase	7.26	13.88	6.62	0.00012	1	0.00013	2	0.87313	1	5	5	1	0	5	7.26	0.00012
CYT	BB_0690	BB_0690	neutrophil activating protein (napA)	39.68	68.78	29.1	0.00155	2	0.00928	2	0.1667	4	15	15	4	0	15	31.2	0.00059
CYT	BB_0691	BB_0691	translation elongation factor G (fus-	11.51	14.05	2.54	0.00005	2	0.00015	2	0.33333	3	6	6	3	0	6	6.58	6.6E-05
CYT	BB_0693	BB_0693	xylose operon regulatory protein (xy	8.71	2.99	-5.72	7.3E-05	1	0.00002	1	3.65	2	4	4	2	0	4	8.71	7.4E-05
CYT	BB_0694	BB_0694	signal recognition particle protein (f	46.98	35.57	-11.41	0.00033	2	0.00046	2	0.71552	11	29	29	11	0	29	32	0.00048
CYT	BB_0696	BB_0696	conserved hypothetical protein	50	41.46	-8.54	0.00128	2	0.001	2	1.26992	4	12	12	4	0	12	41.5	0.00108
CYT	BB_0698	BB_0698	tRNA (guanine-N1)-methyltransfera	0	6.69	6.69	0	0	0.0001	1	0	X	X	X	X	X	X	X	X
CYT	BB_0702	BB_0702	lipopolysaccharide biosynthesis-rela	34.97	33.74	-1.23	0.00018	2	0.0003	2	0.61279	4	6	6	4	0	6	35	0.00027
CYT	BB_0704	BB_0704	acyl carrier protein	48.75	35	-13.75	0.00028	2	0.00061	2	0.46053	2	3	3	2	0	3	48.8	0.00028
CYT	BB_0705	BB_0705	ribonuclease III (rnc)	46.34	47.56	1.22	0.00291	2	0.00751	2	0.38735	8	97	97	8	0	97	41.5	0.00291
CYT	BB_0707	BB_0707	predicted coding region BB0707	13.16	14.64	1.48	0.00013	1	0.00015	2	0.87582	5	11	11	5	0	11	13.2	0.00013
CYT	BB_0712	BB_0712	RNA polymerase sigma-70 factor (r	16.8	19.65	2.85	8.8E-05	2	0.00015	2	0.60274	5	11	11	5	0	11	14.9	0.00013
CYT	BB_0713	BB_0713	conserved hypothetical protein	8.7	8.3	-0.4	8.8E-05	1	0.0002	2	0.44221	2	3	3	2	0	3	8.7	8.8E-05
CYT	BB_0715	BB_0715	rod shape-determining protein (mre	53.74	57.89	4.15	0.0011	2	0.00381	2	0.28849	16	89	89	16	0	89	53.7	0.00182
CYT	BB_0720	BB_0720	threonyl-tRNA synthetase (thrZ)	8.26	14.46	6.2	6.4E-05	1	0.0001	2	0.64	2	5	5	2	0	5	8.26	6.4E-05
CYT	BB_0725	BB_0725	conserved hypothetical protein	15.21	33.84	18.63	8.5E-05	2	0.00021	2	0.3972	2	4	4	2	0	4	15.2	0.00011
CYT	BB_0726	BB_0726	ATP-binding protein (ylxH-3)	22.6	17.65	-4.95	0.00021	1	0.00041	2	0.50244	5	9	9	5	0	9	22.6	0.00021
CYT	BB_0727	BB_0727	pyrophosphate--fructose 6-phospha	70.98	68.3	-2.68	0.00192	2	0.00246	2	0.77999	30	142	142	30	0	142	68.3	0.00234
CYT	BB_0733	BB_0733	predicted coding region BB0733	7.97	10.87	2.9	0.00008	1	0.00014	2	0.57554	2	3	3	2	0	3	7.97	8E-05
CYT	BB_0734	BB_0734	conserved hypothetical protein	3.56	5.64	2.08	2.2E-05	1	7.3E-05	1	0.30137	X	X	X	X	X	X	X	X
CYT	BB_0737	BB_0737	histidine phosphokinase/phophatas	0	8.06	8.06	0	0	5.4E-05	2	0	X	X	X	X	X	X	X	X
CYT	BB_0738	BB_0738	valyl-tRNA synthetase (valS)	23.31	21.26	-2.05	0.00017	2	0.00019	2	0.90374	11	34	34	11	0	34	18.7	0.00029
CYT	BB_0741	BB_0741	chaperonin (groES)	32.26	52.69	20.43	0.00016	2	0.00039	2	0.40816	2	3	3	2	0	3	19.4	0.00024
CYT	BB_0742	BB_0742	ABC transporter	0	9.73	9.73	0	0	0.00005	2	0	X	X	X	X	X	X	X	X
CYT	BB_0749	BB_0749	predicted coding region BB0749	36.28	62.79	26.51	0.0004	1	0.00044	2	0.89367	8	23	23	8	0	23	36.3	0.0004
CYT	BB_0754	BB_0754	ABC transporter	50.49	49.51	-0.98	0.00095	2	0.00126	2	0.75316	13	46	46	13	0	46	50.5	0.0011
CYT	BB_0760	BB_0760	predicted coding region BB0760	31.45	41.13	9.68	0.00072	2	0.00205	2	0.35251	2	10	10	2	0	10	29.8	0.0006

Locus	B31A3_Control_2_P	B31A3_Control_2_S	B31A3_Control_2_uS	B31A3_Control_2_uDP	B31A3_Control_2_sS	B31A3_Control_2_dS	B31A3_Control_2_SC	B31A3_Control_2_dNSAF	B31A3_ProK_1_P	B31A3_ProK_1_S	B31A3_ProK_1_uS	B31A3_ProK_1_uDP	B31A3_ProK_1_sS	B31A3_ProK_1_dS	B31A3_ProK_1_SC	B31A3_ProK_1_dNSAF	B31A3_ProK_2_P	B31A3_ProK_2_S	B31A3_ProK_2_uS	B31A3_ProK_2_uDP	B31A3_ProK_2_sS	B31A3_ProK_2_dS	B31A3_ProK_2_SC	B31A3_ProK_2_dNSAF	ALL_y2_P	ALL_y2_S	ALL_y2_uS	ALL_y2_uDP	ALL_y2_sS	ALL_y2_dS	ALL_y2_SC	ALL_y2_dNSAF	Length	MW	pI
BB_0481	X	X	X	X	X	X	X	X	3	4	4	3	0	4	13.7	0.00017	X	X	X	X	X	X	X	X	3	5	5	3	0	5	14.4	3.9E-05	277	30591	10.5
BB_0482	X	X	X	X	X	X	X	X	2	6	6	2	0	6	37	0.00078	X	X	X	X	X	X	X	X	2	7	7	2	0	7	37	0.00016	92	10410	10.2
BB_0484	X	X	X	X	X	X	X	X	2	3	3	2	0	3	10.2	0.00012	2	2	2	2	0	2	8.87	5.6E-05	4	6	6	4	0	6	17.1	4.4E-05	293	33142	10
BB_0485	1	1	1	1	0	1	9.42	5.5E-05	2	6	6	2	0	6	18.8	0.00052	1	2	2	1	0	2	18.8	0.00012	3	9	9	3	0	9	28.3	0.00014	138	15568	10.6
BB_0487	1	2	2	1	0	2	8.33	0.00018	1	1	1	1	0	1	11.9	0.00014	X	X	X	X	X	X	X	X	2	3	3	2	0	3	20.2	7.7E-05	84	9852	10
BB_0488	X	X	X	X	X	X	X	X	1	3	3	1	0	3	12.9	0.00029	1	5	5	1	0	5	12.9	0.00033	1	8	8	1	0	8	12.9	0.00014	124	13656	10.1
BB_0490	3	12	12	3	0	12	13.7	0.0005	7	54	54	7	0	54	62.1	0.00355	4	21	21	4	0	21	26.4	0.00094	9	124	124	9	0	124	67	0.00147	182	20416	9.5
BB_0492	1	1	1	1	0	1	15.9	5.7E-05	5	10	10	5	0	10	28	0.00091	1	1	1	1	0	1	15.2	6.2E-05	6	15	15	6	0	15	28	0.00025	132	14814	9.9
BB_0493	1	1	1	1	0	1	5.56	4.2E-05	5	8	8	5	0	8	24.4	0.00053	5	5	5	5	0	5	22.8	0.00023	7	14	14	7	0	14	32.2	0.00017	180	19938	9.8
BB_0494	X	X	X	X	X	X	X	X	2	9	9	2	0	9	30.3	0.0009	2	2	2	2	0	2	21	0.00014	2	12	12	2	0	12	30.3	0.00022	119	13722	10.4
BB_0495	X	X	X	X	X	X	X	X	2	3	3	2	0	3	17	0.00022	3	4	4	3	0	4	17	0.0002	3	6	6	3	0	6	14.6	7.9E-05	165	17779	10.4
BB_0496	X	X	X	X	X	X	X	X	3	7	7	3	0	7	36.6	0.00083	1	4	4	1	0	4	9.9	0.00032	3	11	11	3	0	11	36.6	0.00024	101	11765	11.4
BB_0497	2	2	2	2	0	2	21.4	0.0001	2	5	5	2	0	5	21.4	0.00041	3	5	5	3	0	5	21.4	0.00028	3	15	15	3	0	15	21.4	0.00022	145	16039	10.5
BB_0500	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	6	6	2	0	6	22.4	0.00039	2	6	6	2	0	6	22.4	0.0001	125	14078	10.8
BB_0501	X	X	X	X	X	X	X	X	3	10	10	3	0	10	38.1	0.00089	1	3	3	1	0	3	8.96	0.00018	3	13	13	3	0	13	38.1	0.00021	134	14307	10.3
BB_0502	3	23	23	3	0	23	16.8	0.0005	12	192	192	12	0	192	43.2	0.00665	14	91	91	14	0	91	40.9	0.00215	18	407	407	18	0	407	51.9	0.00255	345	38685	5.4
BB_0503	X	X	X	X	X	X	X	X	4	6	6	4	0	6	26	0.00058	1	1	1	1	0	1	17.1	6.6E-05	5	8	8	5	0	8	33.3	0.00014	123	14500	11
BB_0505	X	X	X	X	X	X	X	X	1	1	1	1	0	1	2.67	4.6E-05	1	1	1	1	0	1	5.73	3.1E-05	2	2	2	2	0	2	8.02	1.7E-05	262	29138	8.3
BB_0509	2	4	4	2	0	4	7.4	7.2E-05	5	9	9	5	0	9	14.8	0.00026	4	8	8	4	0	8	10	0.00016	9	32	32	9	0	32	22.2	0.00017	419	48742	9.2
BB_0513	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	4.17	4.6E-05	3	6	6	3	0	6	7.2	2.5E-05	528	59952	7
BB_0514	3	6	6	3	0	6	12	8E-05	4	13	13	4	0	13	12.4	0.00027	10	40	40	10	0	40	31.5	0.00058	12	68	68	12	0	68	34.3	0.00026	566	65174	5.2
BB_0518	17	130	130	17	0	130	37	0.00154	14	75	75	14	0	75	26.5	0.00141	17	77	77	17	0	77	37	0.00099	36	366	366	36	0	366	60	0.00125	635	69276	5.3
BB_0519	10	24	24	10	0	24	56.2	0.00097	6	25	25	6	0	25	33.7	0.0016	13	49	49	13	0	49	50.3	0.00214	19	121	121	19	0	121	63.6	0.0014	187	21939	8.7
BB_0521	2	3	3	2	0	3	22.7	0.00015	3	13	13	3	0	13	30.7	0.00104	5	12	12	5	0	12	36.7	0.00065	6	34	34	6	0	34	41.3	0.00049	150	17209	7.9
BB_0522	2	16	16	2	0	16	13.5	0.00054	3	11	11	3	0	11	19.4	0.00059	9	32	32	9	0	32	34.2	0.00118	11	71	71	11	0	71	45.1	0.00069	222	25094	5.8
BB_0527	1	1	1	1	0	1	4.96	2.9E-05	1	2	2	1	0	2	10.7	9.1E-05	2	4	4	2	0	4	15.7	0.00012	2	7	7	2	0	7	15.7	5.8E-05	262	29823	5.5
BB_0528	3	8	8	3	0	8	16.5	0.00019	3	5	5	3	0	5	13	0.00019	8	23	23	8	0	23	33.3	0.0006	10	47	47	10	0	47	42.5	0.00032	315	36754	9
BB_0533	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	12.7	6.5E-05	2	2	2	2	0	2	12.7	1.7E-05	253	28965	7.8
BB_0534	X	X	X	X	X	X	X	X	3	5	5	3	0	5	17.3	0.00023	1	6	6	1	0	6	7.45	0.00019	3	12	12	3	0	12	17.3	0.0001	255	29756	5.3
BB_0538	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	14.4	0.00012	1	2	2	1	0	2	14.4	3.3E-05	132	14929	5.9
BB_0540	12	27	27	12	0	27	28.1	0.00029	7	13	13	7	0	13	14	0.00022	8	22	22	8	0	22	16.9	0.00026	20	91	91	20	0	91	35.8	0.00028	693	77573	5.6
BB_0541	X	X	X	X	X	X	X	X	1	3	3	1	0	3	25	0.0005	X	X	X	X	X	X	X	X	2	4	4	2	0	4	34.7	0.00012	72	8385	6.1
BB_0544	X	X	X	X	X	X	X	X	1	1	1	1	0	1	4.19	2.9E-05	1	1	1	1	0	1	3.69	2E-05	3	11	11	3	0	11	10.6	5.9E-05	406	45749	7.7
BB_0545	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	6.61	5.4E-05	2	3	3	2	0	3	6.61	1.4E-05	454	51364	8.1
BB_0550	1	1	1	1	0	1	8.97	5.2E-05	1	5	5	1	0	5	13.1	0.00041	4	6	6	4	0	6	37.9	0.00034	4	12	12	4	0	12	37.9	0.00018	145	16655	9.2
BB_0551	1	2	2	1	0	2	6.77	0.00011	X	X	X	X	X	X	X	X	1	2	2	1	0	2	18.1	0.00012	3	5	5	3	0	5	33.1	8.1E-05	133	15177	8.8
BB_0556	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.54	0.00012	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.54	2.2E-05	289	34463	9
BB_0557	1	2	2	1	0	2	17.4	0.00017	X	X	X	X	X	X	X	X	1	3	3	1	0	3	30.2	0.00028	2	5	5	2	0	5	47.7	0.00013	86	9386	5.5
BB_0558	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	5	5	3	0	5	7.5	7.1E-05	3	5	5	3	0	5	7.5	1.9E-05	573	64596	5.2
BB_0559	9	31	31	9	0	31	40.7	0.00123	5	16	16	5	0	16	41.8	0.00101	8	44	44	8	0	44	53.4	0.0019	13	113	113	13	0	113	71.4	0.00129	189	20781	5.4
BB_0560	11	28	28	11	0	28	22.9	0.00032	14	37	37	14	0	37	23.4	0.00068	24	75	75	24	0	75	34.9	0.00094	37	203	203	37	0	203	48.3	0.00068	650	75424	6.9
BB_0561	1	3	3	1	0	3	1.94	4.9E-05	9	18	18	9	0	18	21.3	0.00046	1	1	1	1	0	1	1.51	1.8E-05	15	48	48	15	0	48	36	0.00022	464	52558	7
BB_0562	2	11	11	2	0	11	12.2	0.00046	1	2	2	1	0	2	6.67	0.00013	5	13	13	5	0	13	18.3	0.00059	4	34	34	4	0	34	18.3	0.00041	180	19773	9.1
BB_0566	1	1	1	1	0	1	10.7	7.3E-05	2	3	3	2	0	3	15.5	0.00035	X	X	X	X	X	X	X	X	3	6	6	3	0	6	26.2	0.00013	103	11837	4.8
BB_0567	2	2	2	2	0	2	3.92	2.1E-05	4	11	11	4	0	11	10.9	0.00018	9	19	19	9	0	19	20.3	0.00022	15	53	53	15	0	53	35.3	0.00016	714	79390	5.1
BB_0568	1	2	2	1	0	2	4.42	3.9E-05	3	7	7	3	0	7	11.4	0.00022	4	9	9	4	0	9	11.4	0.00019	3	16	16	3	0	16	7.79	9E-05	385	42691	9.3
BB_0569	1	4	4	1	0	4	2.71	5.1E-05	8	18	18	8	0	18	14.8	0.00036	9	33	33	9	0	33	18.8	0.00046	12	66	66	12	0	66	23.6	0.00024	590	68054	5.1
BB_0570	3	8	8	3	0	8	54.8	0.00049	X	X	X	X	X	X	X	X	3	13	13	3	0	13	45.2	0.00086	5	21	21	5	0	21	61.3	0.00037	124	13726	5.6
BB_0572	2	2	2	2	0	2	9.22	4.2E-05	3	8	8	3	0	8	11.5	0.00027	5	12	12	5	0	12	18.4	0.00027	12	37	37	12	0	37	31.6	0.00022	358	42106	8.9
BB_0573	3	22	22	3	0	22	20.4	0.00061	6	23	23	6	0	23	30	0.00102	6	30	30	6	0	30	32.6	0.00091	8	109	109	8	0	109	40.4	0.00087	270	30699	8.6
BB_0578	X	X	X	X	X	X	X	X	5	8	8	5	0	8	17.2	0.00025	5	9	9	5	0	9	18	0.00019	9	23	23	9	0	23	23.9	0.00013	389	44575	5.7
BB_0579	4	7	7	4	0	7	6.12	4.5E-05	11	25	25	11	0	25	15.3	0.00026	13	35	35	13	0	35	18	0.00025	25	81	81	25	0	81	27.6	0.00015	1161	132367	6.7
BB_0581	X	X	X	X	X	X	X	X	5	7	7	5	0	7	13.4	0.00012	3	5	5	3	0	5	3.79	5.9E-05	8	15	14	8	1	14	16.2	4.4E-05	686	79044	7.3
BB_0582	X	X	X	X	X	X	X	X	2	2	2	2	0	2	13	9.1E-05	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.34	2.5E-05	262	30676	9.2
BB_0585	2	2	2	2	0	2	10.9	3.3E-05	1	3	3	1	0	3	2.66	8E-05	2	8	8	2	0	8	8.43	0.00014	4	13	13	4	0	13	16.2	6.2E-05	451	51069	8.7
BB_0587	4	10	10	4	0	10	8.31	0.0001	10	27	27	10	0	27	20.3	0.00044	9	24	24	9	0	24	16.6	0.00027	17	80	80	17	0	80	29.2	0.00024	734	85214	8.8
BB_0594	5	12	12	5	0	12	11.5	0.00015	11	23	23	11	0	23	26.9	0.00047	10	28	28	10	0	28	23.4	0.00039	25	93	93	25	0	93	49.9	0.00034	591	67637	9.1
BB_0601	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	4.32	2E-05	2	10	10	2	0	10	7.91	5.2E-05	417	45881	7.6
BB_0606	1	1	1	1	0	1	12.3	4.6E-05	4	14	14	4	0	14	18.4	0.00103	4	10	10	4	0	10	29.5	0.0005	8	33	33	8	0	33	48.5	0.00044	163	18141	9.3
BB_0608	4	13	13	4	0	13	17.4	0.00021	3	5	5	3	0	5	11.3	0.00013	6	22	22	6	0	22	24.6	0.00038	7	48	48	7	0	48	26.5	0.00022	476	53577	5.5
BB_0610	2	8	8	2	0	8	7.71	0.00013	2	4	4	2	0	4	6.83	0.00011	5	13	13	5	0	13	19.8	0.00023	10	32	32	10	0	32	32.4	0.00015	454	52906	5.1
BB_0612	5	29	29	5	0	29	18.8	0.00051	19	59	59	19	0	59	41.4	0.00164	7	24	24	7	0	24	18.6	0.00046	22	181	181	22	0	181	48.8	0.00091	430	47601	7.9
BB_0613	2	2	2	2	0	2	5.17	1.9E-05	9	31	31	9	0	31	14	0.00046	11	25	25	11	0	25	19.7	0.00025	20	67	67	20	0	67	30.1	0.00018	813	92312	6.6
BB_0615	1	1	1	1	0	1	11	3.6E-05	5	12	12	5	0	12	28.7	0.00069	5	12	12	5	0	12	23	0.00047	6	23	23	6	0	23	28.7	0.00024	209	24084	10.3
BB_0617	X	X	X	X	X	X	X	X	2	2	2	2	0	2	17.2	0.0002	1	4	4	1	0	4	14.8	0.00027	2	6	6	2	0	6	17.2	0.00011	122	14613	5.5
BB_0618	1	1	1	1	0	1	12.3	4.9E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	9.74	5.3E-05	4	5	5	4	0	5	33.1	7E-05	154	17548	8.2
BB_0619	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.03	3.6E-05	2	3	3	2	0	3	9.7	7.4E-05	1	3	3	1	0	3	5.76	2E-05	330	37377	5.5
BB_0621	X	X	X	X	X	X	X	X	2	3	3	2	0	3	16.3	0.00019	2	4	4	2	0	4	17.9	0.00018	3	9	9	3	0	9	23.9	0.00011	184	19884	5.2
BB_0622	X	X	X	X	X	X	X	X	3	6	6	3	0	6	15	0.00017	1	2	2	1	0	2	5.33	4E-05	4	18	18	4	0	18	17.2	9.4E-05	413	46211	9.2
BB_0627	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.07	2.8E-05	5	21	21	5	0	21	23.6	0.00041	5	22	22	5	0	22	23.6	0.00011	423	47384	7.6
BB_0630	6	32	32	6	0	32	35.8	0.00078	9	21	21	9	0	21	47.2	0.00082	13	31	31	13	0	31	58.3	0.00082	13	87	87	13	0	87	58	0.00061	307	33595	6.9
BB_0636	1	1	1	1	0	1	2.72	1.6E-05	6	15	15	6	0	15	21.1	0.00038	9	19	19	9	0	19	26.8	0.00032	11	43	43	11	0	43	30.3	0.00019	478	56113	8.1
BB_0642	1	5	5	1	0	5	4.03	0.00011	1	1	1	1	0	1	2.31	3.4E-05	4	8	8	4	0	8	17	0.00019	7	26	26	7	0	26	25.9	0.00016	347	39580	6.7
BB_0644	1	5	5	1	0	5	7.33	0.00016	3	3	3	3	0	3	14.2	0.00015	4	14	14	4	0	14	22	0.00049	7	40	40	7	0	40	37.9	0.00037	232	25644	7
BB_0647	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.11	6.8E-05	1	1	1	1	0	1	5.11	4.6E-05	1	2	2	1	0	2	10.8	2.5E-05	176	20206	8.1
BB_0649	6	10	10	6	0	10	19.5	0.00014	15	65	65	15	0	65	36	0.00143	18	51	51	18	0	51	43.3	0.00076	27	151	151	27	0	151	62.4	0.0006	545	58952	5.2
BB_0650	1	1	1	1	0	1	24.1	6.7E-05	2	5	5	2	0	5	25	0.00053	1	3	3	1	0	3	13.4	0.00022	4	15	15	4	0	15	37.5	0.00029	112	13024	6.8
BB_0654	X	X	X	X	X	X	X	X	4	8	8	4	0	8	14.7	0.00025	7	16	16	7	0	16	22.1	0.00034	7	27	27	7	0	27	25.3	0.00015	380	45402	6.8
BB_0655	X	X	X	X	X	X	X	X	3	5	5	3	0	5	16.7	0.00022	X	X	X	X	X	X	X	X	2	4	4	2	0	4	9.78	3.1E-05	276	31404	9.5
BB_0658	X	X	X	X	X	X	X	X	4	9	9	4	0	9	21.7	0.00043	1	2	2	1	0	2	4.74	6.5E-05	5	17	17	5	0	17	26.1	0.00015	253	28943	6.8
BB_0659	X	X	X	X	X	X	X	X	3	7	6	3	1	6	10.2	0.00014	1	2	2	1	0	2	4.03	3.1E-05	3	13	13	3	0	13	8.06	5.4E-05	521	60938	8.4
BB_0669	5	7	7	5	0	7	10.9	6.1E-05	9	34	34	9	0	34	17.5	0.00047	17	46	46	17	0	46	25.9	0.00043	22	107	107	22	0	107	30.2	0.00027	864	98353	5
BB_0670	3	4	4	3	0	4	14	6.5E-05	8	13	13	8	0	13	32.8	0.00033	11	32	32	11	0	32	43.4	0.00056	16	59	59	16	0	59	50	0.00027	466	53061	4.9
BB_0671	9	60	60	9	0	60	66.5	0.0028	12	61	61	12	0	61	66.5	0.00453	15	104	104	15	0	104	72.1	0.00527	16	272	272	16	0	272	74.5	0.00366	161	17614	4.5
BB_0673	X	X	X	X	X	X	X	X	1	2	2	1	0	2	7.6	0.00014	X	X	X	X	X	X	X	X	1	2	2	1	0	2	7.6	2.5E-05	171	20537	9.3
BB_0675	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	4	4	3	0	4	13.9	0.00011	1	2	2	1	0	2	4.18	1.5E-05	287	33637	9
BB_0676	2	4	4	2	0	4	12.7	0.00014	6	16	16	6	0	16	36.4	0.00087	6	19	19	6	0	19	35.5	0.0007	8	43	43	8	0	43	46.8	0.00042	220	24984	5.9
BB_0677	1	4	4	1	0	4	2.99	5.6E-05	2	3	3	2	0	3	7.84	6.7E-05	3	6	6	3	0	6	10.3	9.1E-05	3	16	16	3	0	16	10.3	6.5E-05	536	60390	9.2
BB_0683	5	12	12	5	0	12	18.9	0.00022	17	93	93	17	0	93	38.8	0.00273	12	35	35	12	0	35	31.5	0.0007	25	239	239	25	0	239	45	0.00127	407	46029	6.3
BB_0685	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.25	5.5E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.25	1E-05	431	48922	8.6
BB_0687	X	X	X	X	X	X	X	X	2	3	3	2	0	3	10.7	0.00011	2	6	6	2	0	6	10.4	0.00015	3	14	14	3	0	14	13.9	9.6E-05	317	35260	7.2
BB_0690	10	63	63	10	0	63	39.7	0.00251	13	47	47	13	0	47	52.9	0.00297	24	361	361	24	0	361	68.8	0.01559	22	475	475	22	0	475	68.8	0.00544	189	22414	5.5
BB_0691	2	3	3	2	0	3	8.07	3.4E-05	3	10	10	3	0	10	7.62	0.00018	5	10	10	5	0	10	11.1	0.00012	7	28	28	7	0	28	18.8	9.1E-05	669	75057	5.8
BB_0693	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	2.99	2E-05	3	5	5	3	0	5	11.7	2.7E-05	402	46082	7
BB_0694	7	11	11	7	0	11	26.6	0.00019	9	19	19	9	0	19	20.8	0.00051	12	23	23	12	0	23	32.9	0.00042	22	81	81	22	0	81	50.3	0.00039	447	49695	9.5
BB_0696	5	16	16	5	0	16	50	0.00147	3	9	9	3	0	9	19.5	0.00131	2	7	7	2	0	7	39	0.0007	5	44	44	5	0	44	50	0.00116	82	9253	8.1
BB_0698	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.69	0.0001	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.69	1.8E-05	239	27179	7.9
BB_0702	1	2	2	1	0	2	9.2	9.2E-05	3	4	4	3	0	4	33.7	0.00029	3	6	6	3	0	6	33.7	0.0003	5	18	18	5	0	18	47.2	0.00024	163	19016	9.1
BB_0704	1	3	3	1	0	3	23.8	0.00028	1	2	2	1	0	2	11.3	0.0003	3	9	9	3	0	9	35	0.00092	3	14	14	3	0	14	60	0.00038	80	9334	4.3
BB_0705	5	95	95	5	0	95	32.5	0.00291	8	204	204	8	0	204	47.2	0.00991	8	154	154	8	0	154	44.7	0.00511	11	550	550	11	0	550	52	0.00484	246	27942	6.1
BB_0707	X	X	X	X	X	X	X	X	4	6	6	4	0	6	6.09	0.00012	6	14	14	6	0	14	11.5	0.00019	10	31	31	10	0	31	20.9	0.00011	608	71684	6.4
BB_0712	2	4	4	2	0	4	4.44	4.8E-05	7	10	10	7	0	10	14.1	0.00019	4	8	8	4	0	8	7.61	0.0001	14	33	33	14	0	33	29.5	0.00011	631	73643	5.3
BB_0713	X	X	X	X	X	X	X	X	2	5	5	2	0	5	8.3	0.00024	2	5	5	2	0	5	5.14	0.00016	4	13	13	4	0	13	11.9	0.00011	253	29838	5.6
BB_0715	4	18	18	4	0	18	18.6	0.00038	17	49	49	17	0	49	49.9	0.00162	20	265	265	20	0	265	57.9	0.00599	21	408	408	21	0	408	53.7	0.00245	361	39755	7.8
BB_0720	X	X	X	X	X	X	X	X	6	9	9	6	0	9	14.5	0.00019	1	1	1	1	0	1	1.89	1.4E-05	6	13	13	6	0	13	16.9	4.8E-05	581	68172	6.9
BB_0725	1	2	2	1	0	2	7.22	5.7E-05	4	6	6	4	0	6	21.3	0.00027	2	5	5	2	0	5	12.6	0.00016	6	17	17	6	0	17	33.8	0.00014	263	29883	5.3
BB_0726	X	X	X	X	X	X	X	X	5	16	16	5	0	16	17.7	0.00059	2	9	9	2	0	9	11.8	0.00023	8	34	34	8	0	34	28.2	0.00023	323	36067	9.1
BB_0727	18	89	89	18	0	89	53.6	0.00149	18	71	71	18	0	71	51.1	0.00189	27	166	166	27	0	166	65	0.00302	39	459	459	39	0	459	72.5	0.00222	448	49887	7.5
BB_0733	X	X	X	X	X	X	X	X	2	3	3	2	0	3	10.9	0.00013	1	5	5	1	0	5	7.25	0.00015	3	11	11	3	0	11	15.2	8.6E-05	276	31386	9.1
BB_0734	1	1	1	1	0	1	3.56	2.2E-05	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.64	7.3E-05	2	4	4	2	0	4	9.2	2.6E-05	337	38280	9.7
BB_0737	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.88	3.6E-05	2	3	3	2	0	3	8.06	7.3E-05	1	2	2	1	0	2	3.88	1.3E-05	335	38667	8.5
BB_0738	4	6	6	4	0	6	8.23	5.2E-05	7	13	13	7	0	13	15.7	0.00018	7	21	21	7	0	21	12.1	0.0002	17	74	74	17	0	74	28	0.00018	875	101865	7
BB_0741	1	1	1	1	0	1	12.9	8.1E-05	1	2	2	1	0	2	8.6	0.00026	4	6	6	4	0	6	52.7	0.00053	4	12	12	4	0	12	52.7	0.00028	93	10313	7.2
BB_0742	X	X	X	X	X	X	X	X	3	4	4	3	0	4	6.55	8.5E-05	1	1	1	1	0	1	3.19	1.4E-05	3	4	4	3	0	4	6.55	1.5E-05	565	64391	6.1
BB_0749	X	X	X	X	X	X	X	X	6	12	12	6	0	12	26.1	0.00033	16	29	29	16	0	29	53.3	0.00055	18	60	60	18	0	60	65.6	0.0003	430	49352	4.7
BB_0754	11	33	33	11	0	33	31.1	0.0008	10	23	23	10	0	23	36.3	0.00089	16	62	62	16	0	62	48.9	0.00164	24	164	164	24	0	164	64.1	0.00115	309	35183	9
BB_0760	2	14	14	2	0	14	20.2	0.00085	4	5	5	4	0	5	28.2	0.00048	7	55	55	7	0	55	38.7	0.00362	6	79	79	6	0	79	31.5	0.00138	124	14129	6.2

Known (Table 1) and/or predicated subcellular location	Locus	Proteins In Group	Description	B31A3_Control_merged-SeqCov (%)	B31A3_ProK_merged-SeqCov (%)	DiffSeqCov (Control - ProK) (%)	B31A3_Cntl-Ti dNSAF AVG	B31A3_Cntl-Ti Detected # Out of 2	B31A3_PK-Ti dNSAF AVG	B31A3_PK-Ti Detected # Out of 2	B31A3_Cntl-Ti: B31A3_PK-Ti	B31A3_Control_1_P	B31A3_Control_1_S	B31A3_Control_1_uS	B31A3_Control_1_uDP	B31A3_Control_1_sS	B31A3_Control_1_dS	B31A3_Control_1_SC	B31A3_Control_1_dNSAF	B31A3_Control_2_P	B31A3_Control_2_S	B31A3_Control_2_uS	B31A3_Control_2_uDP	B31A3_Control_2_sS	B31A3_Control_2_dS	B31A3_Control_2_SC	B31A3_Control_2_dNSAF	B31A3_ProK_1_P	B31A3_ProK_1_S	B31A3_ProK_1_uS	B31A3_ProK_1_uDP	B31A3_ProK_1_sS	B31A3_ProK_1_dS	B31A3_ProK_1_SC	B31A3_ProK_1_dNSAF	B31A3_ProK_2_P	B31A3_ProK_2_S	B31A3_ProK_2_uS	B31A3_ProK_2_uDP	B31A3_ProK_2_sS	B31A3_ProK_2_dS	B31A3_ProK_2_SC	B31A3_ProK_2_dNSAF	ALL_y2_P	ALL_y2_S	ALL_y2_uS	ALL_y2_uDP	ALL_y2_sS	ALL_y2_dS	ALL_y2_SC	ALL_y2_dNSAF	Length	MW	pI
CYT	BB_0763	BB_0763	response regulatory protein (rrp-2)	7.06	3.53	-3.53	6.5E-05	1	3.6E-05	1	1.80556	2	4	4	2	0	4	7.06	6.5E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.53	3.6E-05	3	6	6	3	0	6	10.6	2.9E-05	453	51529	7
CYT	BB_0767	BB_0767	UDP-N-acetylglucosamine--N-acety	0	6.34	6.34	0	0	2.8E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.58	3.3E-05	1	1	1	1	0	1	2.75	2.2E-05	2	2	2	2	0	2	6.34	1.2E-05	363	41118	9.8
CYT	BB_0768	BB_0768	pyridoxal kinase (pdxK)	7.58	7.58	0	5.6E-05	1	9.1E-05	1	0.61538	1	2	2	1	0	2	7.58	5.6E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	7.58	9.1E-05	X	X	X	X	X	X	X	X	1	4	4	1	0	4	7.58	3.3E-05	264	30121	7.4
CYT	BB_0769	BB_0769	sialoglycoprotease (gcp)	13.87	17.34	3.47	0.00013	1	0.00019	2	0.66321	4	6	6	4	0	6	13.9	0.00013	X	X	X	X	X	X	X	X	2	3	3	2	0	3	6.94	0.0001	4	12	12	4	0	12	13.9	0.00028	8	21	21	8	0	21	27.8	0.00013	346	38486	8.5
CYT	BB_0777	BB_0777	adenine phosphoribosyltransferase	56.25	54.55	-1.7	0.00126	2	0.0026	2	0.48596	10	50	50	10	0	50	56.3	0.0021	2	10	10	2	0	10	15.9	0.00043	8	54	54	8	0	54	47.7	0.00367	7	33	33	7	0	33	38.1	0.00153	12	147	147	12	0	147	65.9	0.00181	176	20173	7.1
CYT	BB_0778	BB_0778	ribosomal protein L21 (rplU)	11.65	30.1	18.45	7.3E-05	1	0.00033	2	0.21922	X	X	X	X	X	X	X	X	1	1	1	1	0	1	11.7	7.3E-05	2	3	3	2	0	3	27.2	0.00035	2	4	4	2	0	4	24.3	0.00032	4	8	8	4	0	8	30.1	0.00017	103	12180	9.5
CYT	BB_0782	BB_0782	conserved hypothetical protein	0	14.08	14.08	0	0	0.00052	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	9	9	2	0	9	14.1	0.00052	X	X	X	X	X	X	X	X	2	9	9	2	0	9	14.1	9.5E-05	206	23768	8.5
CYT	BB_0784	BB_0784	conserved hypothetical protein	0	5.88	5.88	0	0	0.0003	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.88	0.0003	X	X	X	X	X	X	X	X	1	3	3	1	0	3	5.88	5.5E-05	119	13754	5.2
CYT	BB_0785	BB_0785	stage V sporulation protein G	47.42	40.21	-7.21	0.00211	2	0.00225	2	0.93434	6	39	39	6	0	39	45.4	0.00297	3	16	16	3	0	16	32	0.00124	5	12	12	5	0	12	40.2	0.00148	4	36	36	4	0	36	29.9	0.00303	8	103	103	8	0	103	47.4	0.0023	97	11196	9.1
CYT	BB_0786	BB_0786	general stress protein (ctc)	45.79	45.33	-0.46	0.00072	2	0.00091	2	0.78831	7	19	19	7	0	19	40.2	0.00066	5	22	22	5	0	22	29.4	0.00077	4	12	12	4	0	12	26.2	0.00067	7	30	30	7	0	30	45.3	0.00114	11	83	83	11	0	83	59.4	0.00084	214	24041	8.3
CYT	BB_0797	BB_0797	DNA mismatch repair protein (mutS	0	2.67	2.67	0	0	1.9E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	0.93	2.8E-05	1	1	1	1	0	1	1.74	9.5E-06	2	3	3	2	0	3	2.67	7.5E-06	862	99749	6.4
CYT	BB_0800	BB_0800	N-utilization substance protein A (n	25.31	30.5	5.19	0.00038	2	0.0007	2	0.53912	10	22	22	10	0	22	25.3	0.00034	4	27	27	4	0	27	15.6	0.00042	5	28	28	5	0	28	16.8	0.00069	7	42	42	7	0	42	19.5	0.00071	14	103	103	14	0	103	39.8	0.00046	482	54817	4.9
CYT	BB_0801	BB_0801	translation initiation factor 2 (infB)	0	6.46	6.46	0	0	3.7E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	4	4	3	0	4	6.46	3.7E-05	1	2	2	1	0	2	1.25	4.9E-06	882	97796	9.2
CYT	BB_0802	BB_0802	ribosome-binding factor A (rbfA)	0	7.87	7.87	0	0	0.00038	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	4	4	1	0	4	7.87	0.00038	X	X	X	X	X	X	X	X	1	4	4	1	0	4	7.87	6.8E-05	127	14441	9.9
CYT	BB_0804	BB_0804	ribosomal protein S15 (rpsO)	0	29.55	29.55	0	0	0.00025	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	10.2	0.00041	1	1	1	1	0	1	19.3	9.3E-05	2	3	3	2	0	3	10.2	7.4E-05	88	10217	10.3
CYT	BB_0805	BB_0805	polyribonucleotide nucleotidyltransf	1.39	8.31	6.92	0.00001	1	0.00003	2	0.33333	X	X	X	X	X	X	X	X	1	1	1	1	0	1	1.39	1E-05	3	3	3	3	0	3	5.96	5E-05	1	1	1	1	0	1	2.35	1.1E-05	3	3	3	3	0	3	7.34	9E-06	722	80063	6
CYT	BB_0817	BB_0817	UDP-N-acetylmuramate--alanine lig	11.11	23.08	11.97	0.0001	2	0.0003	2	0.35017	2	3	3	2	0	3	6.41	4.7E-05	3	10	10	3	0	10	11.1	0.00016	5	11	11	5	0	11	13.3	0.00028	8	18	18	8	0	18	23.1	0.00031	8	42	42	8	0	42	23.1	0.00019	468	53480	6.5
CYT	BB_0818	BB_0818	conserved hypothetical protein	22.22	19.79	-2.43	0.00018	2	0.0002	2	0.91837	4	11	11	4	0	11	15.3	0.00028	2	3	3	2	0	3	11.1	7.8E-05	3	4	4	3	0	4	11.1	0.00017	3	8	8	3	0	8	13.5	0.00023	8	26	26	8	0	26	33	0.0002	288	33324	5.3
CYT	BB_0819	BB_0819	cytidylate kinase (cmk-2)	8.89	15.56	6.67	0.00017	1	5.6E-05	2	2.98214	X	X	X	X	X	X	X	X	1	4	4	1	0	4	8.89	0.00017	1	1	1	1	0	1	8.89	6.6E-05	1	1	1	1	0	1	6.67	4.5E-05	2	6	6	2	0	6	15.6	7.2E-05	180	21066	6.4
CYT	BB_0820	BB_0820	predicted coding region BB0820	75.76	75.76	0	0.00074	2	0.0041	2	0.17938	2	5	5	2	0	5	56.1	0.00056	3	8	8	3	0	8	75.8	0.00091	5	18	18	5	0	18	75.8	0.00326	6	40	40	6	0	40	75.8	0.00495	5	70	70	5	0	70	75.8	0.00229	66	7579	5.3
CYT	BB_0831	BB_0831	xylose operon regulatory protein (xy	6.03	16.83	10.8	2.3E-05	1	0.00019	2	0.11979	1	1	1	1	0	1	6.03	2.3E-05	X	X	X	X	X	X	X	X	3	6	6	3	0	6	16.8	0.00023	2	6	6	2	0	6	10.8	0.00016	3	13	13	3	0	13	16.8	8.9E-05	315	34455	5.7
CYT	BB_0833	BB_0833	isoleucyl-tRNA synthetase (ileS)	28.02	35.22	7.2	0.00029	2	0.0006	2	0.48911	21	57	57	21	0	57	26.2	0.0004	8	25	25	8	0	25	13.1	0.00018	18	55	55	18	0	55	20.7	0.00063	23	72	72	23	0	72	27.4	0.00056	35	206	206	35	0	206	37.9	0.00043	1042	122332	8.6
CYT	BB_0835	BB_0835	phosphomannomutase (cpsG)	0	10.53	10.53	0	0	4.6E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	4.04	6.3E-05	2	2	2	2	0	2	6.49	2.9E-05	4	5	5	4	0	5	10.5	1.9E-05	570	66009	9.2
CYT	BB_0836	BB_0836	excinuclease ABC	0	4.31	4.31	0	0	3.6E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	4.31	3.6E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	4.31	6.4E-06	673	77567	6.9
CYT	BB_0837	BB_0837	excinuclease ABC	3.79	3.37	-0.42	2.3E-05	1	3.8E-05	1	0.60526	3	3	3	3	0	3	3.79	2.3E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	3.37	3.8E-05	X	X	X	X	X	X	X	X	5	6	6	5	0	6	7.16	1.4E-05	950	105796	8.2
CYT	BB_0841	BB_0841	arginine deiminase (arcA)	4.15	7.07	2.92	3.6E-05	2	0.00002	1	1.8	1	2	2	1	0	2	4.15	3.6E-05	1	2	2	1	0	2	4.15	3.7E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	7.07	2E-05	1	4	4	1	0	4	4.15	2.1E-05	410	46844	5.8
CYT	BB_0842	BB_0842	ornithine carbamoyltransferase	11.89	27.13	15.24	4.5E-05	1	7.4E-05	2	0.60811	1	2	2	1	0	2	11.9	4.5E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	8.84	7.3E-05	2	3	3	2	0	3	18.3	7.5E-05	4	7	7	4	0	7	27.1	4.6E-05	328	36583	6.7
CYT	BB_0852	BB_0852	predicted coding region BB0852	9.39	26.9	17.51	1.9E-05	2	0.00019	1	0.10215	1	1	1	1	0	1	3.55	1.9E-05	1	1	1	1	0	1	5.84	1.9E-05	X	X	X	X	X	X	X	X	7	9	9	7	0	9	26.9	0.00019	7	11	11	7	0	11	26.9	6E-05	394	46241	7
CYT	BB_A13	BB_A13	conserved hypothetical protein	29.79	12.77	-17.02	0.00048	2	0.00093	1	0.51125	3	7	7	3	0	7	21.3	0.00037	2	11	11	2	0	11	29.8	0.00059	2	11	11	2	0	11	12.8	0.00093	X	X	X	X	X	X	X	X	4	29	29	4	0	29	29.8	0.00045	141	16104	5.4
CYT	BB_A20	BB_A20	conserved hypothetical protein	14.4	21.6	7.2	0.00016	2	0.00029	2	0.56597	2	10	10	2	0	10	11.2	0.0003	1	1	1	1	0	1	9.6	3E-05	2	10	10	2	0	10	9.6	0.00048	3	3	3	3	0	3	18.4	9.8E-05	3	23	23	3	0	23	14.4	0.0002	250	28946	8.7
CYT	BB_A21	BB_A21	conserved hypothetical protein	0	24.31	24.31	0	0	0.00018	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	4	4	3	0	4	24.3	0.00018	2	3	3	2	0	3	16.6	3.6E-05	181	21816	9.5
CYT	BB_A39	BB_A39	predicted coding region BBA39	0	6.15	6.15	0	0	0.00012	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.15	0.00012	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.15	2.2E-05	195	22696	8
CYT	BB_A43	BB_A43	conserved hypothetical protein	10.48	0	-10.48	0.00012	1	0	0	∞	1	2	2	1	0	2	10.5	0.00012	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	10.5	3.5E-05	124	14356	4.8
CYT	BB_A45	BB_A45	conserved hypothetical protein	0	13.97	13.97	0	0	0.00018	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	4	4	2	0	4	14	0.00018	2	4	4	2	0	4	14	4.8E-05	179	21338	7.4
CYT	BB_A76	BB_A76	thymidylate synthase-complementi	12.08	18.49	6.41	8.4E-05	1	0.00023	2	0.36522	2	3	3	2	0	3	12.1	8.4E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	6.42	9E-05	3	12	12	3	0	12	18.5	0.00037	4	17	17	4	0	17	18.5	0.00014	265	31277	8.3
CYT	BB_B03	BB_B03	predicted coding region BBB03	0	9.58	9.58	0	0	5.8E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	9.58	8E-05	1	2	2	1	0	2	5.35	3.6E-05	3	5	5	3	0	5	9.58	2.4E-05	449	54295	9.6
CYT	BB_B05	BB_B05	PTS system	0	20.87	20.87	0	0	8.7E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	20.9	0.0001	1	1	1	1	0	1	9.57	7.1E-05	2	2	2	2	0	2	20.9	3.8E-05	115	13188	6.7
CYT	BB_B07	BB_B07	outer surface protein	46.03	39.73	-6.3	0.00089	1	0.00093	2	0.95601	14	44	44	14	0	44	46	0.00089	X	X	X	X	X	X	X	X	14	46	46	14	0	46	34.5	0.00151	7	16	16	7	0	16	20.3	0.00036	22	105	105	22	0	105	52.3	0.00062	365	41916	8.1
CYT	BB_B12	BB_B12	conserved hypothetical protein	5.93	23.72	17.79	2.9E-05	1	0.00107	2	0.02703	1	1	1	1	0	1	5.93	2.9E-05	X	X	X	X	X	X	X	X	4	14	14	4	0	14	17.4	0.00066	4	46	46	4	0	46	19.4	0.00148	4	24	24	4	0	24	20.6	0.00021	253	29474	8.7
CYT	BB_B17	BB_B17	IMP dehydrogenase (guaB)	0	3.71	3.71	0	0	2.5E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	3.71	3E-05	1	1	1	1	0	1	3.71	2E-05	1	2	2	1	0	2	3.71	1.1E-05	404	43768	8.3
CYT	BB_B18	BB_B18	GMP synthase (guaA)	36.93	36.74	-0.19	0.00046	2	0.00069	2	0.66136	14	50	50	14	0	50	34.9	0.0007	5	15	15	5	0	15	15.7	0.00021	13	29	29	13	0	29	29.4	0.00066	14	47	47	14	0	47	34.1	0.00073	26	141	141	26	0	141	48.3	0.00058	528	60206	8.6
CYT	BB_D18	BB_D18	conserved hypothetical protein	23.64	4.55	-19.09	0.00013	1	0.00011	1	1.22936	3	4	4	3	0	4	23.6	0.00013	X	X	X	X	X	X	X	X	1	2	2	1	0	2	4.55	0.00011	X	X	X	X	X	X	X	X	3	6	6	3	0	6	23.6	5.9E-05	220	25729	9.4
CYT	BB_D22	BB_D22	conserved hypothetical protein	22.47	22.47	0	0.00025	2	0.00025	2	1	1	3	3	1	0	3	18	0.00025	2	3	3	2	0	3	22.5	0.00025	1	1	1	1	0	1	22.5	0.00013	1	4	4	1	0	4	18	0.00037	2	11	11	2	0	11	22.5	0.00027	89	10331	9.5
CYT	BB_E02	BB_E02	predicted coding region BBE02	1.88	6.34	4.46	1.2E-05	1	5.6E-05	2	0.21429	1	2	2	1	0	2	1.88	1.2E-05	X	X	X	X	X	X	X	X	3	10	10	3	0	10	4.23	9.4E-05	2	3	3	2	0	3	2.11	1.9E-05	4	13	13	4	0	13	4.93	2.2E-05	1277	150979	7.1
CYT	BB_E17	BB_E17	predicted coding region BBE17	0	20.12	20.12	0	0	0.00011	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	10.7	7.1E-05	2	3	3	2	0	3	20.1	0.00014	2	4	4	2	0	4	20.1	5.1E-05	169	20092	6.7
CYT	BB_E22	BB_E22	pyrazinamidase/nicotinamidase (pr	25.28	28.65	3.37	0.00019	2	0.00026	2	0.71648	4	8	8	4	0	8	25.3	0.00033	1	1	1	1	0	1	10.1	4.2E-05	2	3	3	2	0	3	15.7	0.0002	5	7	7	5	0	7	28.7	0.00032	7	19	19	7	0	19	35.4	0.00023	178	20480	8.5
CYT	BB_G07	BB_G07	conserved hypothetical protein	15.26	20.53	5.27	0.00004	1	0.00013	1	0.31746	X	X	X	X	X	X	X	X	1	1	1	1	0	1	15.3	4E-05	2	2	2	2	0	2	20.5	0.00013	X	X	X	X	X	X	X	X	2	3	3	2	0	3	20.5	3.4E-05	190	22990	9.9
CYT	BB_G08	BB_G08	stage 0 sporulation protein J (spoO	19.61	17.65	-1.96	0.00017	2	0.0001	2	1.70588	2	10	10	2	0	10	14.5	0.00029	1	2	2	1	0	2	5.1	5.9E-05	1	3	3	1	0	3	5.49	0.00014	2	2	2	2	0	2	12.2	6.4E-05	4	17	17	4	0	17	22.8	0.00014	255	29260	8.9
CYT	BB_H28	BB_H28	conserved hypothetical protein	26.69	29.48	2.79	0.00034	2	0.00045	2	0.76563	5	16	14	4	2	15.2	26.3	0.00045	2	8	8	2	0	8	13.9	0.00024	4	9	7	3	2	8.56	21.1	0.00041	5	15	15	5	0	15	22.3	0.00049	8	48	44	7	4	46.1	33.9	0.0004	251	29360	8
CYT	BB_H29	BB_H29	conserved hypothetical protein	7.18	20.1	12.92	7.2E-05	1	0.00026	2	0.27376	X	X	X	X	X	X	X	X	1	2	2	1	0	2	7.18	7.2E-05	1	1	1	1	0	1	6.7	5.7E-05	4	12	12	4	0	12	13.4	0.00047	5	15	15	5	0	15	20.1	0.00016	209	25034	9.5
CYT	BB_I21	BB_I21	conserved hypothetical protein	5.2	3.6	-1.6	0.00003	1	9.6E-05	1	0.3125	1	1	1	1	0	1	5.2	3E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.6	9.6E-05	X	X	X	X	X	X	X	X	2	3	3	2	0	3	8.8	2.6E-05	250	28694	8.9
CYT	BB_J17	BB_J17	conserved hypothetical protein	37.96	39.18	1.22	0.00026	2	0.00038	2	0.67632	6	16	16	6	0	16	26.5	0.00048	1	1	1	1	0	1	11.4	3.1E-05	3	6	6	3	0	6	18	0.00029	3	14	14	3	0	14	21.2	0.00047	9	37	37	9	0	37	50.6	0.00033	245	28606	8.9
CYT	BB_J45	BB_J45	predicted coding region BBJ45	0	13.33	13.33	0	0	0.0001	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	3	3	2	0	3	13.3	0.0001	2	3	3	2	0	3	13.3	2.7E-05	240	25946	7
CYT	BB_K21	BB_K21	conserved hypothetical protein	23.69	39.36	15.67	0.00032	1	0.00053	2	0.60112	4	12	10	3	2	10.8	23.7	0.00032	X	X	X	X	X	X	X	X	2	4	2	1	2	2.44	9.64	0.00012	6	29	29	6	0	29	36.1	0.00095	7	45	41	6	4	42.9	39.4	0.00037	249	29091	8.8
CYT	BB_L32	BB_L32	plasmid partition protein	4.88	20.33	15.45	0.00006	1	8.6E-05	2	0.69767	1	2	2	1	0	2	4.88	6E-05	X	X	X	X	X	X	X	X	2	4	2	1	2	2.67	15.5	0.00013	2	4	1	1	3	1.27	8.13	4.2E-05	3	10	10	3	0	10	20.3	8.8E-05	246	28594	7.9
CYT	BB_M02	BB_M02;BB_O02	hypothetical protein	8.7	6.96	-1.74	6.4E-05	1	3.5E-05	1	1.82857	1	2	2	1	0	2	8.7	6.4E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	6.96	3.5E-05	1	2	2	1	0	2	8.7	1.9E-05	230	26692	8.2
CYT	BB_M22	BB_M22	conserved hypothetical protein	0	20.37	20.37	0	0	9.1E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	0	0	1	0	6.3	X	2	3	2	1	1	3	14.1	9.1E-05	2	3	2	1	1	2.67	14.1	2.1E-05	270	30679	5.2
CYT	BB_M24	BB_M24;BB_N24	blyB	8.7	16.52	7.82	0.00013	1	7.1E-05	1	1.80282	1	2	2	1	0	2	8.7	0.00013	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	16.5	7.1E-05	2	3	3	2	0	3	25.2	5.6E-05	115	13189	5.3
CYT	BB_O25	BB_O25	conserved hypothetical protein	29.73	29.73	0	0.0002	1	0.00039	2	0.51786	1	2	0	0	2	0	13.5	X	1	3	3	1	0	3	16.2	0.0002	1	2	2	1	0	2	16.2	0.00022	2	9	7	1	2	7.74	29.7	0.00057	2	16	12	1	4	13.3	29.7	0.00026	111	12994	9.3
CYT	BB_O32	BB_O32	plasmid partition protein	4.42	21.29	16.87	5.9E-05	1	0.00025	2	0.236	1	2	2	1	0	2	4.42	5.9E-05	X	X	X	X	X	X	X	X	3	7	7	3	0	7	21.3	0.00034	1	5	5	1	0	5	10.8	0.00016	3	14	14	3	0	14	21.3	0.00012	249	28693	8.6
CYT	BB_P03	BB_P03;BB_S03	hypothetical protein	8.65	9.19	0.54	0.00004	1	6.5E-05	1	0.61538	1	1	1	1	0	1	8.65	4E-05	X	X	X	X	X	X	X	X	1	1	1	1	0	1	9.19	6.5E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	17.8	2.3E-05	185	20003	5.6
CYT	BB_P06	BB_P06	conserved hypothetical protein	29.32	19.44	-9.88	0.00012	2	8.1E-05	2	1.44444	5	9	6	3	3	8.25	29.3	0.00019	1	2	2	1	0	2	6.79	4.6E-05	2	3	3	2	0	3	12.4	0.00011	2	2	2	2	0	2	13.9	5E-05	6	16	13	4	3	14.8	36.4	9.9E-05	324	36721	6
CYT	BB_P22	BB_P22	conserved hypothetical protein	0	21.4	21.4	0	0	8.8E-05	1	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	2	2	1	1	1	2	12.2	8.8E-05	1	1	0	0	1	0	9.23	X	2	2	1	1	1	1.33	15.1	1.1E-05	271	30647	5.2
CYT	BB_P25	BB_P25	conserved hypothetical protein	32.43	32.43	0	0.0002	1	0.00108	2	0.18519	2	3	1	1	2	3	32.4	0.0002	X	X	X	X	X	X	X	X	2	11	11	2	0	11	18.9	0.00118	3	14	12	2	2	13.3	32.4	0.00098	3	28	24	2	4	26.7	32.4	0.00052	111	12908	9.4
CYT	BB_P32	BB_P32	plasmid partition protein	34.15	24.8	-9.35	7.6E-05	2	8.5E-05	2	0.89412	2	3	3	2	0	3	24.4	9E-05	1	2	2	1	0	2	9.76	6.1E-05	1	2	2	1	0	2	4.88	9.7E-05	2	3	2	1	1	2.17	19.9	7.2E-05	5	10	9	4	1	9.26	44.3	8.1E-05	246	28639	9
CYT	BB_P33	BB_P33	conserved hypothetical protein	14.36	9.41	-4.95	3.7E-05	1	5.9E-05	1	0.62712	1	1	1	1	0	1	9.41	3.7E-05	1	2	0	0	2	0	4.95	X	1	1	1	1	0	1	9.41	5.9E-05	X	X	X	X	X	X	X	X	2	4	2	1	2	3	14.4	3.2E-05	202	24207	9.5
CYT	BB_Q08	BB_Q08	plasmid partition protein	4.35	9.88	5.53	5.8E-05	1	9.4E-05	1	0.61702	1	2	2	1	0	2	4.35	5.8E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	9.88	9.4E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	14.2	3.4E-05	253	29610	6.4
CYT	BB_Q13	BB_Q13	conserved hypothetical protein	24.38	11.11	-13.27	4.3E-05	2	0.00011	2	0.40952	3	5	2	1	3	2.75	17.6	6.3E-05	1	1	1	1	0	1	6.79	2.3E-05	2	5	5	2	0	5	11.1	0.00018	1	1	1	1	0	1	4.32	2.5E-05	4	12	9	2	3	10.2	24.4	6.8E-05	324	36806	6.3
CYT	BB_Q40	BB_Q40	plasmid partition protein	3.98	10.36	6.38	5.9E-05	1	0.00033	2	0.17665	1	2	2	1	0	2	3.98	5.9E-05	X	X	X	X	X	X	X	X	2	6	4	1	2	5.33	3.98	0.00025	3	13	10	2	3	12.7	10.4	0.00041	2	16	16	2	0	16	10.4	0.00014	251	29206	9
CYT	BB_Q41	BB_Q41	conserved hypothetical protein	15.59	8.06	-7.53	0.00012	1	6.4E-05	1	1.89063	X	X	X	X	X	X	X	X	2	3	1	1	2	3	15.6	0.00012	1	1	1	1	0	1	8.06	6.4E-05	X	X	X	X	X	X	X	X	2	3	1	1	2	1.5	15.6	1.7E-05	186	22091	9.3
CYT	BB_R33	BB_R33	plasmid partition protein	44.62	38.65	-5.97	0.00038	1	0.00039	2	0.97704	9	14	13	9	1	13	44.6	0.00038	X	X	X	X	X	X	X	X	4	11	11	4	0	11	27.5	0.00052	3	8	8	3	0	8	22.3	0.00026	10	33	33	10	0	33	49.8	0.00028	251	29666	8
CYT	BB_R34	BB_R34	conserved hypothetical protein	5.52	16.57	11.05	0	0	0.00009	1	0	X	X	X	X	X	X	X	X	1	2	0	0	2	0	5.52	X	X	X	X	X	X	X	X	X	2	2	2	2	0	2	16.6	9E-05	2	3	1	1	2	1.5	12.7	1.8E-05	181	21948	9.6
CYT	BB_S35	BB_S35	plasmid partition protein	10.57	21.54	10.97	0.0002	2	0.00037	2	0.52674	3	6	6	3	0	6	10.6	0.00018	2	7	7	2	0	7	10.6	0.00021	2	8	8	2	0	8	10.6	0.00039	5	11	10	4	1	10.8	21.5	0.00036	4	27	26	3	1	26.7	15.9	0.00024	246	28658	8
CYT	BB_U05	BB_U05	plasmid partition protein	0	4.2	4.2	0	0	7.7E-05	2	0	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	1	0	2	4.2	9.1E-05	1	2	2	1	0	2	4.2	6.2E-05	1	4	4	1	0	4	4.2	3.3E-05	262	30536	8.8
CYT	BB_U06	BB_U06	conserved hypothetical protein	12	12	0	3.7E-05	2	0.00012	1	0.30833	1	1	1	1	0	1	12	3.7E-05	1	1	1	1	0	1	9	3.8E-05	1	2	2	1	0	2	12	0.00012	X	X	X	X	X	X	X	X	2	4	4	2	0	4	12	4.3E-05	200	24239	9.6
255	Contamina	Contaminant_INT-	BSA	27.68	4.94		0.00018	2	5.4E-05	1	3.38889	12	24	24	12	0	24	25.2	0.00029	3	6	6	3	0	6	7.41	7.4E-05	X	X	X	X	X	X	X	X	2	4	4	2	0	4	4.94	5.4E-05	13	33	33	13	0	33	27.7	0.00012	607	69271	6.1
302	Contamina	Contaminant_gi|7	lysyl endopeptidase (EC 3.4.21.50)	32.71	32.34		0.00014	2	0.00026	2	0.53053	2	3	3	2	0	3	16.4	8.2E-05	4	7	7	4	0	7	16.4	0.0002	3	7	7	3	0	7	25.7	0.00031	3	7	7	3	0	7	23.1	0.00021	6	21	21	6	0	21	32.7	0.00017	269	27961	6.7
386	Contamina	Contaminant_KEF	no description	6.53	7.31		7.8E-05	1	0.00012	2	0.67241	3	7	6	2	1	6.75	6.53	7.8E-05	X	X	X	X	X	X	X	X	3	7	7	3	0	7	5.44	0.00013	2	8	8	2	0	8	4.35	0.0001	6	22	21	5	1	21.6	9.49	7.3E-05	643	65494	6.6
402	Contamina	Contaminant_KEF	no description	16.86	27.82		6.9E-05	2	0.00038	2	0.1811	5	7	7	5	0	7	12.3	8.7E-05	2	4	4	2	0	4	9.11	5.1E-05	8	33	33	8	0	33	25.5	0.00067	5	7	7	5	0	7	17.4	9.6E-05	10	50	50	10	0	50	28.3	0.00018	593	59519	5.2
479	Contamina	Contaminant_NRL	owl|| Immunoglobulin g1 (igg1) (mo	1.87	8.18		3.5E-05	1	3.7E-05	2	0.94595	1	2	2	1	0	2	1.87	3.5E-05	X	X	X	X	X	X	X	X	1	2	2	1	0	2	3.5	5.6E-05	1	1	1	1	0	1	4.67	1.9E-05	1	2	2	1	0	2	1.87	1E-05	428	46852	8.9
480	Contamina	Contaminant_KEF	no description	1.63	5.59		3.4E-05	1	1.9E-05	1	1.78947	1	2	2	1	0	2	1.63	3.4E-05	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	1	0	1	5.59	1.9E-05	1	2	2	1	0	2	1.63	1E-05	429	47927	5.5
490	Contamina	Contaminant_KEF	no description	10.85	9.92		0.00003	2	9.9E-05	2	0.30303	3	3	2	2	1	2.25	6.51	2.6E-05	2	3	3	2	0	3	4.34	3.5E-05	5	10	10	5	0	10	9.92	0.00019	1	1	1	1	0	1	1.86	1.3E-05	7	17	16	6	1	16.4	14.6	5.5E-05	645	65865	8
533	Contamina	Contaminant_KEF	no description	3.7	11.09		1.2E-05	1	3.2E-05	2	0.375	1	1	1	1	0	1	3.7	1.2E-05	X	X	X	X	X	X	X	X	2	2	2	2	0	2	7.07	3.8E-05	1	2	2	1	0	2	4.02	2.6E-05	3	4	4	3	0	4	12.4	1.4E-05	622	61987	5.2
			Total Distributed SpC														####								####								####								####								####					
			Total Peptides									3655								2763								3227								4211								6646										
			Total Proteins																500								396								535								548								628			
			Total Contaminant Protein Distributed SpC														48								20								61								31								150						
			Total Contaminant Peptides									27								11								22								16								46										
			Total Contaminant Proteins																8								4								6								8								8			
				AVG	SDV																																																	
			Spectra FDR (%)	**0.15**	**0.10**												0.07								0.1								0.15								0.29								0.13						
			Peptides FDR (%)	**0.26**	**0.08**							0.16								0.29								0.34								0.24								0.29										
			Proteins FDR (%)	**1.52**	**0.33**														1.1858								1.9802								1.4733								1.4388								2.4845			
			SHUFFLED_SpC														13								20								20								58								94						
			SHUFFLED_Pep									6								8								11								10								19										
			SHUFFLED_Protein																6								8								8								8								16			
	SHUFFLED_BB_0342		FALSE POSITIVE									1	2	2	X	0	2	2.42	X	1	9	9	X	0	9	2.42	X	1	4	4	X	0	4	2.42	X	1	39	39	X	0	39	2.42	X	1	54	54	X	0	54	2.42	X	496	55545	5.7
	SHUFFLED_BB_0512		FALSE POSITIVE									X	X	X	X	X	X	X	X	1	1	1	X	0	1	1.39	X	2	6	6	X	0	6	1.48	X	3	7	7	X	0	7	2.54	X	2	2	2	X	0	2	2.72	X	2166	254243	4.8
	SHUFFLED_BB_0128		FALSE POSITIVE									1	1	1	X	0	1	8.14	X	1	2	2	X	0	2	8.14	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	3	3	X	0	3	8.14	X	221	25602	9
	SHUFFLED_BB_0399		FALSE POSITIVE									1	3	3	X	0	3	5.94	X	1	1	1	X	0	1	5.94	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	4	4	X	0	4	5.94	X	219	25544	9.3
	SHUFFLED_BB_D14		FALSE POSITIVE									1	2	2	X	0	2	4.32	X	1	2	2	X	0	2	4.32	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	4	4	X	0	4	4.32	X	370	44198	10
	SHUFFLED_BB_0849		FALSE POSITIVE									1	3	3	X	0	3	51.5	X	X	X	X	X	X	X	X	X	1	1	1	X	0	1	51.5	X	X	X	X	X	X	X	X	X	2	4	4	X	0	4	51.5	X	33	4050	9.8
	SHUFFLED_BB_G10		FALSE POSITIVE									X	X	X	X	X	X	X	X	1	1	1	X	0	1	1.28	X	1	1	1	X	0	1	2.09	X	X	X	X	X	X	X	X	X	2	2	2	X	0	2	3.37	X	1098	123862	8.4
	SHUFFLED_BB_0395		FALSE POSITIVE									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	X	0	2	25	X	1	2	2	X	0	2	25	X	1	4	4	X	0	4	25	X	56	6695	9.2
	SHUFFLED_BB_0787		FALSE POSITIVE									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	X	0	1	10.1	X	1	2	2	X	0	2	9.04	X	1	2	2	X	0	2	9.04	X	188	21250	9.5
	SHUFFLED_BB_0625		FALSE POSITIVE									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	3	4	4	X	0	4	8.75	X	1	1	1	X	0	1	3.01	X	1	2	2	X	0	2	2.3	X	697	79335	9.4
	SHUFFLED_BB_H09		FALSE POSITIVE									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	1	1	X	0	1	0.78	X	1	2	2	X	0	2	1.49	X	1	2	2	X	0	2	1.49	X	1278	150872	8.1
	SHUFFLED_BB_0757		FALSE POSITIVE									1	2	2	X	0	2	7.28	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	X	0	2	7.28	X	206	23206	7.9
	SHUFFLED_BB_S23		FALSE POSITIVE									X	X	X	X	X	X	X	X	1	2	2	X	0	2	37.3	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	X	0	2	37.3	X	67	7478	9.9
	SHUFFLED_BB_0043		FALSE POSITIVE									X	X	X	X	X	X	X	X	1	2	2	X	0	2	5.78	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	X	0	2	5.78	X	346	40531	6.6
	SHUFFLED_BB_J08		FALSE POSITIVE									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	3	3	X	0	3	7.52	X	1	3	3	X	0	3	7.52	X	306	34640	8.9
	SHUFFLED_BB_0028		FALSE POSITIVE									X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	1	2	2	X	0	2	4.3	X	1	2	2	X	0	2	4.3	X	349	39705	8.8

LipoP1.0 (http://www.cbs.dtu.dk/services/LipoP/)					TMHMM2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/)				SignalP4.1 gram- predictions (http://www.cbs.dtu.dk/services/SignalP/)												Table 1																			
Location	Score	Margin	Cleavage	Pos+2	ExpAA	First60	PredHel	Topology	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	SignalP4.1 Consensus	Dmaxcut	Networks-used	Protein Name	Consens. Loc.	His-tag Loc.	dNSAF-pK/ dNSAF+pK	Previous Location	References for Prev. Loc. (PMID)	Predicted MW (kDa)	Observed M.W. (kDa)	Paralogous Family (Casjens 2000)	Number of Paralogs	Comments	in vivo Differential Expression				Immunogenicity	Tn mutant
CYT	-0.20091				0.12	0.11	0	o	0.174	33	0.321	25	0.882	17	0.734	0.515	N	0.57	SignalP-noTM	S2	S	S	10.3447			27	27	S2	44								+
CYT	-0.20091				0.2	0.2	0	o	0.183	20	0.331	20	0.841	3	0.654	0.483	N	0.57	SignalP-noTM		S	S	1.21429			26	26			low dNSAF ratio for S							–
CYT	-0.20091	1.77444			1.26	1.26	0	o	0.149	19	0.316	19	0.802	13	0.672	0.483	N	0.57	SignalP-noTM		S	S	19.8679	S	16368984	18	17					+					+§
SpII	2.49438	2.69529	14-15	N	0.16	0.02	0	o	0.143	22	0.229	22	0.735	1	0.377	0.298	N	0.57	SignalP-noTM	S2	S	S	"			32	33	S2	44					+		+	+
SpII	2.91333	3.11424	19-20	K	2.79	2.79	0	o	0.13	26	0.192	11	0.466	2	0.384	0.263	N	0.51	SignalP-TM	ChpAI	S	S	"	S	20421380	18	21					+			+	+
SpII	5.73099	3.27118	19-20	S	23.83	23.76	0	o	0.336	25	0.528	25	0.907	5	0.849	0.679	Y	0.57	SignalP-noTM		S	S†	0.62626			14	14	OrfD	143	low dNSAF ratio for S, due to pK resistance				+		+
SpII	19.6863	17.8708	16-17	K	0.1	0.1	0	o	0.164	24	0.336	19	0.807	18	0.725	0.518	N	0.57	SignalP-noTM	OspA	S	S	65.4221	S	6192088	29	31	OspAB	53		+		+		+	–
SpII	18.4788	13.5055	15-16	A	0.04	0.04	0	o	0.187	22	0.373	20	0.854	10	0.784	0.566	N	0.57	SignalP-noTM	OspB	S	S	185.842	S	6735474	32	34	OspAB	53		+		+	+	+	+
SpII	3.28639	3.4873	24-25	G	15.85	15.85	1	i12-31o	0.155	31	0.239	31	0.681	13	0.483	0.329	N	0.51	SignalP-TM	DbpA	S	S	5.95261	S	9573101	21	21						+		+	+
SpII	10.826	7.2885	22-23	N	0.65	0.65	0	o	0.516	28	0.66	28	0.947	19	0.852	0.75	Y	0.57	SignalP-noTM		S	S	0.62069	S	23303811	47	56								+	+
SpII	7.63463	7.83554	16-17	S	20.28	20.28	1	i7-26o	0.147	20	0.232	20	0.635	2	0.439	0.309	N	0.51	SignalP-TM		S	S	2.93378			9	18					+		+	+	+
SpII	9.13705	9.33796	27-28	S	19.44	19.4	1	o10-32i	0.151	35	0.219	33	0.411	26	0.256	0.233	N	0.51	SignalP-TM	P35	S	S	6.23077	S	16368984	34	32	P35	54						+	+
SpII	7.09235	0.72531	29-30		13.86	13.86	1	i7-29o	0.248	38	0.441	27	0.934	21	0.873	0.644	Y	0.57	SignalP-noTM	CRASP-1	S	S	24.3566	S	14607842	29	27	P35	54							+
SpII	3.20834	1.30831	24-25	A	15.61	15.61	1	i7-29o	0.135	36	0.261	27	0.629	19	0.485	0.344	N	0.51	SignalP-TM		S	S	"	S	16368984	30	31	P35	54					+		+
SpII	3.71991	3.92082	17-18	N	22.51	22.27	1	i5-27o	0.119	56	0.217	15	0.61	6	0.483	0.315	N	0.51	SignalP-TM		S	S	0.60523			25	27			low dNSAF ratio for S, is protein pK resistant?							+
SpII	20.6353	12.9424	18-19	N	0.6	0.6	0	o	0.364	24	0.532	24	0.946	2	0.804	0.66	Y	0.57	SignalP-noTM	OspC	S	S	7.86288	S	1560779	22	22					+			+	+
SpII	1.0607	1.26161	13-14	S	4.37	1.66	0	o	0.176	23	0.348	23	0.887	3	0.734	0.529	N	0.57	SignalP-noTM		S	S†	0.5241			19	18			low dNSAF ratio for S, due to pK resistance				+		+
SpII	3.92093	4.12184	18-19	Q	15.18	15.06	1	i5-24o	0.232	26	0.31	26	0.591	5	0.449	0.361	N	0.51	SignalP-TM		S	S	1.83471			23	21			low dNSAF ratio for S							+
SpII	6.13534	6.33825	17-18	N	0.43	0.42	0	o	0.233	18	0.408	18	0.844	16	0.713	0.552	N	0.57	SignalP-noTM	P35	S	S	"	S	21695244	28	27	P35	60			+				–
SpII	13.7282	5.76274	21-22	D	17.8	17.8	0	o	0.337	30	0.489	30	0.939	19	0.834	0.651	Y	0.57	SignalP-noTM		S	S	1.83562			11	14										+
SpII	10.917	6.37393	17-18	N	0.05	0.05	0	o	0.16	23	0.327	23	0.883	16	0.7	0.502	N	0.57	SignalP-noTM		S	S	73.4853			35	31	BB_0844	12						+		+
SpII	4.24522	4.44613	18-19	D	0.71	0.71	0	o	0.284	19	0.448	19	0.872	2	0.748	0.589	Y	0.57	SignalP-noTM	CRASP-2	S	S	0.74327	S	16925556	27	26	CRASP-2		low dNSAF ratio for S					+	+
SpII	7.6072	7.80811	24-25	D	18.61	18.61	1	i12-30o	0.11	29	0.144	13	0.248	9	0.217	0.171	N	0.51	SignalP-TM		S	S	5.9375			43	43										+
SpII	8.91217	9.11308	17-18	N	1.87	1.62	0	o	0.268	24	0.372	24	0.829	2	0.582	0.47	N	0.57	SignalP-noTM	P35	S	S	8.35616			29	22	P35	60							+
SpII	4.9518	3.1493	26-27	N	0.62	0.62	0	o	0.173	32	0.336	32	0.815	25	0.611	0.465	N	0.57	SignalP-noTM		S	S	62.2039			33	37	BB_0844	12						+		+
SpII	2.14854	2.34945	16-17	R	0.3	0.18	0	o	0.233	23	0.319	23	0.741	2	0.467	0.389	N	0.57	SignalP-noTM	VraA	S	S	"	S	11179306	54	75	P35	60								na
SpII	10.0931	8.21577	17-18	T	0.25	0.25	0	o	0.48	23	0.612	23	0.929	19	0.789	0.695	Y	0.57	SignalP-noTM		S	S	8.93865			26	27	P35	60		+		+	+			na
SpII	5.99472	2.10954	29-30		18.04	18.04	1	i9-31o	0.212	27	0.435	27	0.952	25	0.869	0.639	Y	0.57	SignalP-noTM	P35	S	S	85.9302			32	37	P35	54								na
SpII	5.79867	1.77267	29-30		18.04	18.04	1	i9-31o	0.212	27	0.434	27	0.952	25	0.867	0.638	Y	0.57	SignalP-noTM		S	S	0			32	38	P35	54						+		na
SpII	7.64303	1.76749	33-34		5.63	5.63	0	o	0.196	27	0.415	27	0.925	25	0.855	0.622	Y	0.57	SignalP-noTM		S	S	56.2096			33	37	P35	54						+		na
SpII	18.2273	9.15461	19-20	V	0.57	0.57	0	o	0.445	24	0.626	24	0.963	16	0.899	0.754	Y	0.57	SignalP-noTM	OspD	S	S	22.8934	S	1398980	28	29								+	+
SpII	10.1531	7.10112	18-19	K	3.33	3.22	0	o	0.228	24	0.363	24	0.778	4	0.596	0.472	N	0.57	SignalP-noTM		S	S	142.696			40	41	CRASP-2	92						+		+
SpII	19.2032	12.8461	19-20	K	9.27	9.25	0	o	0.166	25	0.355	25	0.927	5	0.827	0.577	Y	0.57	SignalP-noTM		S	S	"			40	35	CRASP-2	92								+
SpII	12.2834	8.03962	17-18	N	0.09	0.09	0	o	0.186	23	0.365	23	0.911	16	0.747	0.544	N	0.57	SignalP-noTM		S	S	97.2909			34	38	BB_0844	12						+		+
SpII	10.8843	11.0852	15-16	K	0.02	0.02	0	o	0.211	21	0.373	21	0.756	13	0.595	0.478	N	0.57	SignalP-noTM		S	S	"	S	19776192	28	31	BB_K07	59						+		+
SpI	5.64382	2.39322	21-22		6.08	6	0	o	0.445	22	0.59	22	0.946	1	0.826	0.701	Y	0.57	SignalP-noTM		S	S	39.915			24	30								+	+
SpII	13.8444	14.0453	19-20	K	0.07	0.06	0	o	0.158	25	0.29	21	0.857	2	0.679	0.473	N	0.57	SignalP-noTM	P37	S	S	10.4182			37	46	P37	75								+
SpII	17.6345	17.8354	17-18	N	0.17	0.17	0	o	0.287	21	0.489	21	0.911	14	0.83	0.649	Y	0.57	SignalP-noTM	MlpH	S	S	"			17	19	Mlp	113								–
SpII	9.64826	9.84917	23-24	K	11.39	11.39	0	o	0.116	30	0.257	27	0.763	21	0.511	0.351	N	0.51	SignalP-TM	ErpN	S	S	10.869	S	11283278	20	19	ErpA	162	identical to BB_P38/ErpA					+	+
SpII	9.09726	3.80779	19-20	K	1.69	1.67	0	o	0.371	25	0.467	25	0.893	4	0.68	0.567	N	0.57	SignalP-noTM	RevA	S	S	0.928	S	11500397	18	nd	Rev	63	low dNSAF ratio for S; native protein is resitant to pK				+	+	+
SpII	12.6696	12.132	19-20	K	7.39	7.39	0	o	0.139	26	0.314	26	0.892	15	0.777	0.532	N	0.57	SignalP-noTM	ErpP	S	S	38.4773	S	11283278	21	20	ErpA	162						+	+
SpII	12.5726	6.71201	17-18	K	4.54	4.54	0	o	0.513	23	0.613	23	0.84	3	0.75	0.677	Y	0.57	SignalP-noTM	ErpQ	S	S	"	S	11283278	39	55	ErpB	163						+	–
SpII	16.0992	12.6387	17-18	K	13.9	13.9	1	i5-24o	0.587	23	0.627	23	0.813	3	0.693	0.658	Y	0.57	SignalP-noTM	ErpM	S	S	0.61194	S	11283278	42	40	ErpB	163	low dNSAF ratio for S					+	+
SpII	15.779	14.4238	17-18	N	0.13	0.13	0	o	0.377	23	0.547	23	0.926	14	0.825	0.678	Y	0.57	SignalP-noTM	MlpA	S	S	3.16049			16	19	Mlp	113					+		–
SpII	9.72242	9.92333	17-18	K	2.97	2.97	0	o	0.304	23	0.446	23	0.843	20	0.664	0.548	N	0.57	SignalP-noTM	ErpB	S	S	1.03158	S	11283278	44	61	ErpB	163	low dNSAF ratio for S					+	+	–
SpII	11.9569	12.1578	15-16	N	0.03	0.03	0	o	0.219	22	0.383	22	0.852	12	0.705	0.534	N	0.57	SignalP-noTM	P35	S	S	1.22449			29	30	P35	60	low dNSAF ratio for S					+		na
SpII	13.9058	12.6473	17-18	N	0.02	0.02	0	o	0.29	23	0.461	23	0.893	14	0.761	0.602	Y	0.57	SignalP-noTM	MlpJ	S	S	1.82857			24	21	Mlp	113						+	na
SpII	16.0924	16.2933	17-18	N	0.42	0.42	0	o	0.287	21	0.492	21	0.911	14	0.847	0.659	Y	0.57	SignalP-noTM	MlpD	S	S	1.06433			16	16	Mlp	113	low dNSAF ratio for S					+	+
SpII	15.325	15.5259	19-20	K	0.11	0.11	0	o	0.166	24	0.339	23	0.832	5	0.737	0.526	N	0.57	SignalP-noTM	ErpY	S	S	"	S	11283278	25	27	ErpG	164						+	+
SpII	16.4935	16.6944	17-18	N	0.17	0.17	0	o	0.287	21	0.489	21	0.912	14	0.831	0.65	Y	0.57	SignalP-noTM	MlpC	S	S	6.54545			17	16	Mlp	113						+	+
SpII	13.7184	9.54449	19-20	K	2.04	2.04	0	o	0.22	27	0.405	25	0.885	21	0.784	0.584	Y	0.57	SignalP-noTM	ErpG	S	S	"	S	25864455	22	23	ErpG	164					+	+	+
SpII	5.96399	2.81488	24-25	S	21.23	21.11	1	i13-35o	0.202	33	0.269	33	0.588	11	0.383	0.311	N	0.51	SignalP-TM		P-OM	S	0.69645	P-OM	22519960	40	38			Multiple OM to	TA		TP	VT	VP		–
CYT	-0.20091				0.43	0.3	0	o	0.172	19	0.31	19	0.709	11	0.551	0.423	N	0.57	SignalP-noTM		P-OM	P-OM	0.68888	P-OM	22519960	14	16										+
SpII	3.51557	3.07065	16-17	S	0.24	0.24	0	o	0.225	28	0.364	24	0.869	15	0.706	0.525	N	0.57	SignalP-noTM		P-OM	P-OM	2.01742			28	29			dNSAF ratio close to 2.0 but P-OM			+		+	+
SpII	10.5911	7.66563	17-18	E	2.62	2.62	0	o	0.125	20	0.323	20	0.91	16	0.835	0.563	N	0.57	SignalP-noTM	Lp6.6	P-OM	P-OM	0.59354	P-OM	9009290	8	13				+		+	+		+
SpII	7.64539	7.8463	25-26	V	10.71	10.69	0	o	0.143	28	0.254	28	0.6	24	0.327	0.281	N	0.51	SignalP-TM	BesA	P-IM	P-IM	0.58876			35	39										+
SpII	5.79043	5.99134	15-16	D	0.02	0.01	0	o	0.112	41	0.195	11	0.453	1	0.393	0.268	N	0.51	SignalP-TM	ProX	P-IM	P-IM	0.79348			33	32										+§
SpII	3.75044	3.95135	19-20	K	0.38	0.25	0	o	0.138	22	0.239	22	0.591	1	0.404	0.316	N	0.57	SignalP-noTM		P-IM	P-IM	2.21951			29	28			dNSAF ratio close to 2.0 but P-IM							–
SpII	10.8726	11.0735	19-20	K	0.09	0.09	0	o	0.179	21	0.368	21	0.881	1	0.773	0.558	N	0.57	SignalP-noTM	PstS	P-IM	P-IM	1.04199			31	30								+	–
SpII	3.91814	4.11905	22-23	T	1.03	0.98	0	o	0.118	29	0.251	11	0.757	3	0.637	0.432	N	0.57	SignalP-noTM		P-IM	P-IM	0.56713	P-OM	20398211	27	26			likely mislocalized previously (Shiyong)							–
CYT	-0.20091				0.15	0.01	0	o	0.142	22	0.185	11	0.44	2	0.357	0.249	N	0.51	SignalP-TM		P-IM	P-IM	0.36623	P	16368984	26	26										–
SpII	12.336	12.5369	20-21	K	4.27	4.27	0	o	0.259	23	0.418	23	0.874	19	0.719	0.559	N	0.57	SignalP-noTM		P-IM	P-IM	0.47326	P-OM	19754308	44	14								+	–
SpII	11.5375	8.80608	23-24	I	17.25	17.23	1	i9-26o	0.281	29	0.25	29	0.383	8	0.239	0.246	N	0.51	SignalP-TM	OppA-1	P-IM	P-IM	0.57189	S	9393787	60	59	OppA	37						+	+
SpII	6.2305	6.43141	18-19	N	0.09	0.06	0	o	0.174	25	0.219	25	0.558	3	0.359	0.271	N	0.51	SignalP-TM	OppA-2	P-IM	P-IM	0.93568	S	9296108; 971	61	60	OppA	37						+	+
SpII	18.2895	13.8965	27-28	N	3.67	3.62	0	o	0.245	30	0.457	30	0.935	21	0.818	0.627	Y	0.57	SignalP-noTM	OppA-3	P-IM	P-IM	0.92027			62	57	OppA	37							+
SpII	14.3539	14.5548	21-22	T	2.83	2.76	0	o	0.166	22	0.367	22	0.912	4	0.83	0.585	Y	0.57	SignalP-noTM	IpLA7	P-IM	P-IM	0.56775	P-IM	17464050	22	21				+		+		+	+
SpII	2.54014	2.74105	14-15	F	0.62	0.49	0	o	0.151	20	0.201	20	0.384	1	0.3	0.237	N	0.51	SignalP-TM	BmpB	P-IM	P-IM	1.16411	S	18166585	38	34	Bmp	36	likely mislocalized previously; only done by IFA without proper subsurface c							–
SpII	11.0722	8.94558	16-17	F	0.9	0.18	0	o	0.172	17	0.354	17	0.927	1	0.764	0.547	N	0.57	SignalP-noTM	BmpC	P-IM	P-IM	0.44538			40	39	Bmp	36							+
CYT	-0.20091	0.75525			2.78	2.64	0	o	0.213	47	0.206	47	0.375	38	0.158	0.188	N	0.57	SignalP-TM	BmpD	P-IM	P-IM	0.88881			37	38	Bmp	36						+	–
SpII	4.42185	4.62276	19-20	N	0.07	0.07	0	o	0.199	26	0.35	26	0.872	1	0.672	0.501	N	0.57	SignalP-noTM		P-IM	P-IM	0			41	36										–
SpI	1.618	1.53405	23-24		0.01	0.01	0	o	0.485	24	0.476	24	0.752	1	0.505	0.49	N	0.57	SignalP-noTM		P-IM	P-IM	0.12458			24	23										+
CYT	-0.20091				21.06	20.72	1	i13-35o	0.135	37	0.142	37	0.209	35	0.119	0.134	N	0.51	SignalP-TM		P-IM	P-IM	1.25899			22	19					+					+§
SpII	9.14224	7.4993	16-17	S	0.96	0.96	0	o	0.33	22	0.524	22	0.936	1	0.857	0.68	Y	0.57	SignalP-noTM		P-IM	P-IM	0			27	26										–
SpII	3.72874	2.90054	17-18	L	131.52	22.3	6	i7-29o413	0.133	27	0.18	11	0.486	1	0.32	0.232	N	0.51	SignalP-TM	SecD	P-IM	nd	0.17768			65	nd			not detected by His-tag but seems to be P by MudPIT; supporte					+		–
CYT	-0.20091	2.15595			22.27	22.27	1	i7-29o	0.105	37	0.139	11	0.295	1	0.185	0.156	N	0.51	SignalP-TM		P-IM	P-IM	0.69831			26	28										–
SpII	2.28024	2.48115	21-22	L	3.86	3.32	0	o	0.149	28	0.301	28	0.88	8	0.715	0.496	N	0.57	SignalP-noTM		P-IM	P-IM	1.21717			58	53										–
SpII	3.23021	3.43112	17-18	A	3.24	3.21	0	o	0.157	30	0.286	23	0.819	2	0.711	0.486	N	0.57	SignalP-noTM		P-IM	P-IM	0.72973			31	27										–
SpII	7.67847	7.87938	16-17	K	0.03	0.03	0	o	0.218	24	0.345	24	0.766	17	0.579	0.455	N	0.57	SignalP-noTM		P-IM	P-IM	0.70278	S	22851744	19	17			likely mislocalized previously by IFA, but looks like it's resistant t					+		+
SpII	10.2964	10.4973	17-18	K	0.04	0.04	0	o	0.115	21	0.196	21	0.44	2	0.35	0.253	N	0.51	SignalP-TM	S1	P-IM	P-IM	1.83333	P	19822648	49	52										+
SpII	9.18653	0.86594	18-19	S	1.48	1.47	0	o	0.454	24	0.558	24	0.827	19	0.705	0.627	Y	0.57	SignalP-noTM	OppAV	P-IM	P-IM	0.74138	P	21628523	61	59	OppA	37					+	+	+
SpII	8.22842	8.42933	21-22	V	0.44	0.39	0	o	0.156	26	0.199	26	0.453	6	0.305	0.238	N	0.51	SignalP-TM	OppAIV	P-IM	P-IM	0.61077	P-IM	16468989	61	58	OppA	37						+	+
SpII	1.02816	1.22907	15-16	S	15.65	14.01	1	i5-22o	0.156	23	0.213	23	0.496	2	0.321	0.253	N	0.51	SignalP-TM		P-IM	P-IM	1.24615	P-OM	20398211	22	21			high dNSAF for P protein; likely mislocalized previously							+

LipoP1.0 (http://www.cbs.dtu.dk/services/LipoP/)					TMHMM2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/)				SignalP4.1 gram- predictions (http://www.cbs.dtu.dk/services/SignalP/)											Table 1															
Location	Score	Margin	Cleavage	Pos+2	ExpAA	First60	PredHel	Topology	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	SignalP4.1 Consensus	Dmaxcut	Networks-used	Protein Name	Consens. Loc.	His-tag Loc.	dNSAF-pK/ dNSAF+pK	Previous Location	References for Prev. Loc. (PMID)	Predicted MW (kDa)	Observed M.W. (kDa)	Paralogous Family (Casjens 2000)	Number of Paralogs	Comments	in vivo Differential Expression				Immunogenicity	Tn mutant
SpII	8.10693	8.30784	22-23	V	6.29	6.08	0	o	0.14	27	0.308	27	0.93	6	0.769	0.525	N	0.57	SignalP-noTM		P	nd	0.67335			108	nd			not detected by His-tag but seems to be P by MudPIT						+
SpII	8.99542	9.19633	17-18	S	0.09	0.08	0	o	0.117	21	0.18	11	0.376	1	0.335	0.237	N	0.51	SignalP-TM																	
SpII	3.06746	3.26837	15-16	T	1.32	1.29	0	o	0.15	19	0.324	19	0.854	15	0.682	0.492	N	0.57	SignalP-noTM																	
SpII	4.2231	3.46124	20-21	A	15.07	14.16	1	i7-26o	0.294	26	0.374	26	0.667	16	0.471	0.41	N	0.51	SignalP-TM																	
SpII	9.30329	9.5042	20-21	S	14.73	14.66	1	i7-26o	0.325	32	0.316	32	0.555	16	0.354	0.33	N	0.51	SignalP-TM																	
SpII	4.50329	4.7042	16-17	D	0.18	0.18	0	o	0.129	23	0.269	23	0.733	13	0.515	0.384	N	0.57	SignalP-noTM																	
SpII	5.8237	4.71367	18-19	T	0.05	0.05	0	o	0.365	24	0.534	24	0.894	5	0.815	0.666	Y	0.57	SignalP-noTM																	
SpII	8.21198	4.46474	20-21	S	0.1	0.04	0	o	0.221	28	0.389	28	0.897	8	0.78	0.573	Y	0.57	SignalP-noTM																	
SpII	1.0979	1.29881	13-14	N	0	0	0	o	0.135	19	0.23	19	0.513	12	0.356	0.289	N	0.57	SignalP-noTM																	
SpII	2.89632	3.09723	24-25	S	4.49	4.49	0	o	0.111	41	0.211	18	0.535	7	0.412	0.286	N	0.51	SignalP-TM																	
SpII	2.89632	3.09723	24-25	S	4.49	4.49	0	o	0.111	41	0.211	18	0.535	7	0.412	0.286	N	0.51	SignalP-TM																	
CYT	-0.20091	0.7911			20.14	20.14	1	i5-24o	0.101	22	0.104	11	0.219	1	0.094	0.101	N	0.51	SignalP-TM																	
SpI	4.37766	4.57857	19-20		47.81	6.09	2	o101-123i	0.181	18	0.252	18	0.609	1	0.398	0.306	N	0.51	SignalP-TM																	
CYT	-0.20091	1.13792			44.36	20.47	1	i5-27o	0.168	26	0.271	26	0.518	19	0.342	0.298	N	0.51	SignalP-TM																	
CYT	-0.20091				22.47	20.44	1	i41-63o	0.111	66	0.182	43	0.465	35	0.18	0.181	N	0.51	SignalP-TM																	
CYT	-0.20091				21.58	21.53	1	i26-48o	0.107	52	0.094	66	0.098	62	0.069	0.085	N	0.51	SignalP-TM																	
SpI	15.9425	15.7446	21-22		80.26	30.03	4	i5-22o48-6	0.815	22	0.796	22	0.883	18	0.796	0.796	Y	0.51	SignalP-TM																	
CYT	-0.20091				18.29	17.81	1	i20-37o	0.158	37	0.139	11	0.26	1	0.191	0.158	N	0.51	SignalP-TM																	
TMH	1.64252	1.84343			4.87	4.4	0	o	0.202	20	0.404	20	0.894	1	0.834	0.606	Y	0.57	SignalP-noTM																	
CYT	-0.20091	0.88261			21.27	21.26	1	i29-48o	0.115	43	0.108	19	0.135	18	0.116	0.111	N	0.51	SignalP-TM																	
SpI	8.56896	8.76987	22-23		15.16	14.15	1	i7-25o	0.442	23	0.452	23	0.695	19	0.447	0.45	N	0.57	SignalP-noTM																	
CYT	-0.20091				21.8	21.78	1	i7-29o	0.122	30	0.117	11	0.219	1	0.131	0.122	N	0.51	SignalP-TM																	
CYT	-0.20091	2.28398			18.53	18.06	1	i25-42o	0.174	48	0.141	38	0.172	3	0.104	0.127	N	0.51	SignalP-TM																	
SpI	0.58978	0.7907	21-22		0.04	0	0	o	0.217	22	0.378	22	0.865	16	0.639	0.501	N	0.57	SignalP-noTM																	
SpI	2.35272	2.55363	23-24		72.8	25.39	3	o5-27i84-1	0.316	24	0.294	24	0.399	19	0.243	0.275	N	0.51	SignalP-TM																	
CYT	-0.20091				22.88	22.88	1	i7-29o	0.114	37	0.123	11	0.197	1	0.152	0.134	N	0.51	SignalP-TM																	
CYT	-0.20091				18.72	18.67	1	i13-30o	0.268	28	0.199	28	0.25	26	0.149	0.181	N	0.51	SignalP-TM																	
SpI	5.29273	4.51561	26-27		22.84	22.84	1	i7-29o	0.177	27	0.194	11	0.493	5	0.376	0.261	N	0.51	SignalP-TM																	
SpI	2.17122	2.37213	19-20		7.24	7.24	0	o	0.397	20	0.447	20	0.592	11	0.441	0.445	N	0.51	SignalP-TM																	
SpI	2.55115	2.75206	19-20		151.14	42.54	7	i5-22o27-4	0.189	20	0.329	20	0.801	1	0.618	0.436	N	0.51	SignalP-TM																	
SpI	0.86999	1.0709	26-27		20.01	20.01	1	i11-33o	0.222	27	0.256	27	0.395	25	0.234	0.248	N	0.51	SignalP-TM																	
CYT	-0.20091	2.54838			20.51	20.5	1	i21-43o	0.138	47	0.163	47	0.282	38	0.157	0.161	N	0.51	SignalP-TM																	
CYT	-0.20091				21.42	21.4	1	i2-24o	0.12	27	0.106	27	0.19	1	0.087	0.099	N	0.51	SignalP-TM																	
CYT	-0.20091				19.96	19.96	1	i2-21o	0.132	22	0.099	60	0.116	48	0.072	0.089	N	0.51	SignalP-TM																	
SpI	9.34817	9.54908	22-23		38.49	16.57	2	i5-22o61-8	0.497	21	0.616	21	0.867	1	0.772	0.689	Y	0.57	SignalP-noTM																	
CYT	-0.20091				19.51	19.06	1	o4-26i	0.11	20	0.198	16	0.494	6	0.401	0.273	N	0.51	SignalP-TM																	
CYT	-0.20091	0.43378			29.19	22.04	1	i5-27o	0.102	36	0.123	11	0.24	2	0.146	0.131	N	0.51	SignalP-TM																	
CYT	-0.20091				16.24	16.2	1	i5-27o	0.323	22	0.284	22	0.376	1	0.276	0.281	N	0.51	SignalP-TM																	
SpI	1.76265	1.96356	23-24		22.66	22.66	1	i7-29o	0.213	29	0.25	29	0.552	3	0.333	0.281	N	0.51	SignalP-TM																	
CYT	-0.20091				21.14	17.07	1	i7-26o	0.161	32	0.227	22	0.409	12	0.319	0.261	N	0.51	SignalP-TM																	
SpI	0.02495	0.22587	19-20		0.23	0.09	0	o	0.455	20	0.524	20	0.726	16	0.616	0.567	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.87	22.87	1	i30-52o	0.101	22	0.092	22	0.117	20	0.076	0.086	N	0.51	SignalP-TM																	
SpI	5.36826	5.56917	18-19		45.88	20.17	0	o	0.254	20	0.404	20	0.792	18	0.579	0.468	N	0.51	SignalP-TM																	
SpI	6.89647	7.09738	23-24		37.7	11.87	0	o	0.643	24	0.761	24	0.942	9	0.884	0.819	Y	0.57	SignalP-noTM																	
SpI	0.83733	1.03825	20-21		0.58	0	0	o	0.244	21	0.441	21	0.893	14	0.781	0.601	Y	0.57	SignalP-noTM																	
SpI	3.89671	4.09762	26-27		49.65	20.44	2	o4-26i714	0.152	27	0.22	11	0.588	1	0.496	0.322	N	0.51	SignalP-TM																	
CYT	-0.20091				22.15	22.15	1	i2-24o	0.104	24	0.096	59	0.166	1	0.082	0.091	N	0.51	SignalP-TM																	
CYT	-0.20091				0.91	0.91	0	o	0.287	23	0.474	23	0.905	9	0.821	0.637	Y	0.57	SignalP-noTM																	
SpI	7.06226	7.26317	23-24		43.43	18.48	0	o	0.488	24	0.415	24	0.485	7	0.373	0.4	N	0.51	SignalP-TM																	
CYT	-0.20091				22.93	22.93	1	i13-35o	0.213	43	0.188	43	0.227	7	0.14	0.171	N	0.51	SignalP-TM																	
CYT	-0.20091	0.86214			18.36	18.28	1	i7-29o	0.115	29	0.16	11	0.318	8	0.27	0.201	N	0.51	SignalP-TM																	
CYT	-0.20091				20.29	12.29	0	o	0.49	24	0.607	24	0.937	15	0.779	0.688	Y	0.57	SignalP-noTM																	
SpI	1.68761	1.88852	21-22		16.83	14.61	1	i5-22o	0.418	22	0.599	22	0.941	17	0.849	0.716	Y	0.57	SignalP-noTM																	
CYT	-0.20091				19.1	18.35	1	i5-23o	0.22	26	0.165	26	0.26	1	0.126	0.151	N	0.51	SignalP-TM																	
SpI	7.11219	7.3131	22-23		0.47	0.31	0	o	0.69	23	0.78	23	0.945	21	0.894	0.833	Y	0.57	SignalP-noTM																	
CYT	-0.20091	0.37555			41.99	22.12	1	i7-29o	0.321	40	0.212	40	0.214	36	0.083	0.165	N	0.51	SignalP-TM																	
SpI	1.0601	1.26101	21-22		1.91	1.9	0	o	0.719	22	0.668	22	0.885	18	0.6	0.636	Y	0.57	SignalP-noTM																	
SpI	6.85167	7.05258	22-23		10.2	10.19	0	o	0.513	23	0.605	23	0.888	1	0.776	0.686	Y	0.57	SignalP-noTM																	
CYT	-0.20091				16.28	16.28	1	i36-53o	0.108	60	0.105	36	0.136	35	0.09	0.1	N	0.51	SignalP-TM																	
SpI	6.26253	6.46344	23-24		2.05	1.97	0	o	0.393	22	0.588	22	0.949	4	0.9	0.735	Y	0.57	SignalP-noTM																	
CYT	-0.20091	1.60177			23.01	18.77	1	i7-24o	0.236	23	0.2	23	0.281	20	0.193	0.198	N	0.51	SignalP-TM																	
CYT	-0.20091	0.36912			21.66	21.65	1	i7-29o	0.304	27	0.192	27	0.258	3	0.138	0.172	N	0.51	SignalP-TM																	
SpI	2.84501	3.04592	17-18		1.35	1.35	0	o	0.709	18	0.791	18	0.957	17	0.851	0.819	Y	0.57	SignalP-noTM																	
SpI	5.38267	5.58358	29-30		20.27	19.52	1	i13-32o	0.539	30	0.667	30	0.913	26	0.787	0.724	Y	0.57	SignalP-noTM																	
SpI	3.86015	4.06106	20-21		18.52	18.52	1	i7-26o	0.469	21	0.455	21	0.61	5	0.474	0.462	N	0.51	SignalP-TM																	
SpI	0.99128	1.19219	42-43		22.77	21.84	1	i20-42o	0.132	43	0.175	43	0.325	37	0.163	0.171	N	0.51	SignalP-TM																	
CYT	-0.20091				16.48	16.42	1	i5-22o	0.11	30	0.14	14	0.263	9	0.203	0.164	N	0.51	SignalP-TM																	
CYT	-0.20091				18.31	18.05	1	o4-21i	0.141	25	0.137	25	0.267	1	0.14	0.138	N	0.51	SignalP-TM																	
CYT	-0.20091				14.35	14.31	1	i9-31o	0.154	25	0.114	25	0.119	20	0.092	0.106	N	0.51	SignalP-TM																	
SpI	8.33176	8.53267	21-22		27.97	19.04	1	i7-26o	0.412	22	0.372	22	0.567	6	0.414	0.387	N	0.51	SignalP-TM																	
CYT	-0.20091	2.10156			20.58	20.58	1	i20-42o	0.141	49	0.15	11	0.261	1	0.236	0.182	N	0.51	SignalP-TM																	
SpI	6.80286	4.32924	25-26		9.88	9.88	0	o	0.381	23	0.604	23	0.975	20	0.954	0.768	Y	0.57	SignalP-noTM																	
SpI	5.71245	3.78786	25-26		12.77	12.77	1	i7-24o	0.423	23	0.637	23	0.98	20	0.953	0.786	Y	0.57	SignalP-noTM																	
SpI	6.73934	4.32574	25-26		10.29	10.29	0	o	0.381	23	0.604	23	0.976	20	0.954	0.769	Y	0.57	SignalP-noTM																	
TMH	0.64404	0.84495			177.43	27.39	8	i30-52o56	0.13	51	0.118	11	0.191	2	0.143	0.127	N	0.51	SignalP-TM																	
TMH	2.01493	2.21584			22.56	22.54	1	i25-47o	0.122	53	0.115	11	0.186	2	0.131	0.121	N	0.51	SignalP-TM																	
TMH	0.6806	0.88151			20.13	20.13	1	i12-29o	0.165	29	0.152	29	0.272	28	0.159	0.155	N	0.51	SignalP-TM																	
TMH	16.0599	16.2608			43.33	24.46	2	i9-31o57-7	0.141	31	0.107	31	0.147	1	0.068	0.093	N	0.51	SignalP-TM																	
TMH	0.6698	0.87072			23.02	22.33	1	i13-35o	0.245	47	0.174	47	0.261	5	0.149	0.165	N	0.51	SignalP-TM																	
TMH	5.63675	5.83766			20.04	20.02	1	i21-40o	0.11	41	0.118	20	0.214	17	0.135	0.124	N	0.51	SignalP-TM																	
TMH	0.00889	0.2098			280.52	21.75	13	i7-29o338	0.187	30	0.138	30	0.254	2	0.123	0.133	N	0.51	SignalP-TM																	
TMH	0.478	0.67891			23	23	1	i13-35o	0.381	31	0.129	31	0.114	5	0.056	0.102	N	0.51	SignalP-TM																	
TMH	13.1699	10.5466			133.02	35.42	6	i13-35o56	0.13	29	0.157	41	0.265	28	0.185	0.167	N	0.51	SignalP-TM																	
TMH	20.6023	20.8032			98.11	43.69	4	o10-39i46	0.151	26	0.149	26	0.238	14	0.154	0.15	N	0.51	SignalP-TM																	
TMH	1.54316	1.74407			22.85	22.85	1	i12-34o	0.11	37	0.165	11	0.38	2	0.27	0.204	N	0.51	SignalP-TM																	
TMH	13.639	13.8399			42.92	42.81	2	i13-35o40	0.118	26	0.124	11	0.183	1	0.159	0.137	N	0.51	SignalP-TM																	
TMH	3.78933	3.99024			160.5	37.1	8	i21-42o46	0.148	43	0.087	11	0.101	67	0.076	0.083	N	0.51	SignalP-TM																	
TMH	1.51692	1.71783			22.69	22.69	1	o30-52i	0.106	36	0.101	64	0.117	56	0.067	0.088	N	0.51	SignalP-TM																	
TMH	0.0504	0.25131			20.29	20.19	1	o25-44i	0.106	41	0.095	12	0.118	11	0.091	0.094	N	0.51	SignalP-TM																	
TMH	11.7254	11.9263			85.89	42.5	4	i7-29o34-5	0.143	49	0.129	49	0.187	8	0.11	0.122	N	0.51	SignalP-TM																	
TMH	12.5761	12.777			22.74	22.73	1	i13-35o	0.105	35	0.132	11	0.315	1	0.159	0.142	N	0.51	SignalP-TM																	
TMH	7.31385	5.50741			133.38	21.97	6	i9-31o100	0.123	33	0.181	33	0.516	28	0.191	0.184	N	0.51	SignalP-TM																	
TMH	20.5694	20.7703			139.17	34.85	6	i7-29o49-7	0.143	31	0.118	11	0.191	1	0.135	0.124	N	0.51	SignalP-TM																	
TMH	7.03381	7.23472			141.82	27.26	6	i40-62o84	0.103	56	0.13	23	0.219	12	0.155	0.139	N	0.51	SignalP-TM																	
TMH	1.95465	2.15556			132.01	26.16	5	o15-34i55	0.11	46	0.109	46	0.142	37	0.066	0.093	N	0.51	SignalP-TM																	
TMH	7.19592	7.39683			202.34	43.04	9	i7-26o36-5	0.407	33	0.144	33	0.224	3	0.084	0.121	N	0.51	SignalP-TM																	
TMH	0.72801	0.92892			81.25	19.92	4	i7-24o72-9	0.133	31	0.131	11	0.226	3	0.179	0.149	N	0.51	SignalP-TM																	
TMH	3.98936	4.19027			211.63	21.08	10	i20-39o71	0.11	70	0.109	12	0.152	7	0.124	0.115	N	0.51	SignalP-TM																	
TMH	1.12165	1.32256			21.14	21.09	1	i7-26o	0.105	28	0.113	11	0.216	2	0.12	0.116	N	0.51	SignalP-TM																	
TMH	7.59655	7.79746			147.63	30	7	i21-38o48	0.284	39	0.307	39	0.464	35	0.197	0.266	N	0.51	SignalP-TM																	
TMH	0.67129	0.8722			68.86	32.27	3	o15-32i44	0.191	33	0.187	33	0.241	28	0.169	0.18	N	0.51	SignalP-TM																	
TMH	3.54446	3.74537			46.44	21.77	2	o17-39i32	0.145	37	0.123	13	0.197	9	0.157	0.136	N	0.51	SignalP-TM																	
TMH	8.66899	7.79124			45.91	22.57	2	i9-31o436	0.138	27	0.12	11	0.208	2	0.143	0.129	N	0.51	SignalP-TM																	
TMH	18.8917	19.0926			53.04	37.97	3	i7-24o28-4	0.192	24	0.107	11	0.177	1	0.11	0.108	N	0.51	SignalP-TM																	
TMH	5.91255	6.11346			280.82	43.1	13	o4-23i28-4	0.118	30	0.096	11	0.148	3	0.092	0.095	N	0.51	SignalP-TM																	
TMH	11.3557	11.5566			232.38	27.44	10	o15-37i58	0.137	37	0.137	37	0.225	7	0.156	0.144	N	0.51	SignalP-TM																	
TMH	0.30932	0.51023			20.59	20.45	1	o20-39i	0.128	45	0.138	11	0.244	3	0.197	0.16	N	0.51	SignalP-TM																	
TMH	5.30133	5.50224			130.76	21.82	6	i13-35o13	0.122	34	0.15	11	0.283	5	0.242	0.184	N	0.51	SignalP-TM																	
TMH	1.5384	1.73931			119.22	41.55	6	i5-22o37-5	0.104	22	0.103	11	0.143	3	0.107	0.104	N	0.51	SignalP-TM																	
TMH	10.0546	10.2555			44.17	23.36	2	o10-32i35	0.13	30	0.106	67	0.19	1	0.087	0.099	N	0.51	SignalP-TM																	
TMH	10.5171	5.64673			53.4	23.62	2	o10-32i32	0.159	29	0.147	11	0.333	2	0.214	0.172	N	0.51	SignalP-TM																	
TMH	2.52213	2.72304			21.97	21.78	1	i9-31o	0.263	33	0.187	33	0.246	31	0.106	0.157	N	0.51	SignalP-TM																	
TMH	1.99117	2.19208			199.82	42.25	9	o4-26i38-5	0.111	27	0.112	38	0.163	34	0.08	0.1	N	0.51	SignalP-TM																	
TMH	9.6323	9.83321			135.77	27.49	6	i26-48o58	0.105	26	0.095	11	0.126	65	0.096	0.096	N	0.51	SignalP-TM																	

LipoP1.0 (http://www.cbs.dtu.dk/services/LipoP/)					TMHMM2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/)				SignalP4.1 gram- predictions (http://www.cbs.dtu.dk/services/SignalP/)											Table 1																
Location	Score	Margin	Cleavage	Pos+2	ExpAA	First60	PredHel	Topology	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	SignalP4.1 Consensus	Dmaxcut	Networks-used	Protein Name	Consens. Loc.	His-tag Loc.	dNSAF-pK/ dNSAF+pK	Previous Location	References for Prev. Loc. (PMID)	Predicted MW (kDa)	Observed M.W. (kDa)	Paralogous Family (Casjens 2000)	Number of Paralogs	Comments	in vivo Differential Expression				Immunogenicity	Tn mutant
TMH	0.00747	0.20838			19.35	19.34	1	i5-23o	0.127	29	0.102	11	0.194	1	0.092	0.098	N	0.51	SignalP-TM																	
TMH	10.6611	6.06579			52.77	22.23	2	i21-43o11	0.113	44	0.174	22	0.431	19	0.27	0.21	N	0.51	SignalP-TM																	
TMH	5.96773	5.1117			47.48	21.94	1	i7-29o	0.153	21	0.227	21	0.582	2	0.39	0.287	N	0.51	SignalP-TM																	
TMH	5.22203	5.42294			251.25	22.65	12	i13-35o83	0.119	38	0.176	11	0.381	4	0.323	0.23	N	0.51	SignalP-TM																	
TMH	1.07298	1.27389			276.04	33.75	12	i23-45o50	0.108	39	0.112	70	0.157	65	0.101	0.108	N	0.51	SignalP-TM																	
TMH	3.32153	3.52244			43.66	40.6	2	o5-27I40-6	0.119	28	0.112	40	0.153	30	0.104	0.11	N	0.51	SignalP-TM																	
TMH	6.10431	5.07437			214.47	22.88	9	o20-42I75	0.174	43	0.168	43	0.243	16	0.157	0.164	N	0.51	SignalP-TM																	
TMH	2.28605	2.48696			42.85	35.45	2	o15-34I47	0.102	64	0.122	11	0.176	2	0.155	0.134	N	0.51	SignalP-TM																	
TMH	6.14452	4.95182			90.87	22.02	4	i19-41o27	0.134	33	0.141	18	0.232	8	0.194	0.161	N	0.51	SignalP-TM																	
TMH	2.20357	2.40448			20.11	20.1	1	o15-34i	0.134	32	0.124	32	0.186	30	0.108	0.118	N	0.51	SignalP-TM																	
CYT	-0.20091				256.62	20.63	12	i7-29o206	0.107	37	0.091	11	0.1	4	0.088	0.09	N	0.51	SignalP-TM																	
CYT	-0.20091				168.7	0	9	o308-325	0.106	18	0.141	18	0.23	1	0.178	0.158	N	0.57	SignalP-noTM																	
CYT	-0.20091				192.73	0	9	o297-319	0.109	20	0.102	36	0.12	27	0.098	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				190.93	0	9	o298-320	0.124	20	0.146	20	0.259	2	0.185	0.164	N	0.57	SignalP-noTM																	
CYT	-0.20091	0.57107			200.29	22.49	9	i33-55o79	0.102	64	0.103	11	0.132	1	0.109	0.106	N	0.51	SignalP-TM																	
CYT	-0.20091				157.63	1.36	7	i145-167	0.191	23	0.31	23	0.667	17	0.502	0.4	N	0.57	SignalP-noTM																	
CYT	-0.20091				138.65	22.06	7	i28-50o15	0.106	44	0.107	17	0.139	9	0.112	0.109	N	0.51	SignalP-TM																	
CYT	-0.20091				131.13	19.83	6	i42-64o68	0.112	25	0.086	25	0.107	70	0.07	0.08	N	0.51	SignalP-TM																	
CYT	-0.20091	0.00782			117.61	22.62	5	i7-29o102	0.122	30	0.097	61	0.108	1	0.066	0.085	N	0.51	SignalP-TM																	
CYT	-0.20091				109.89	21.45	5	i16-38o40	0.113	30	0.13	11	0.289	29	0.177	0.147	N	0.51	SignalP-TM																	
CYT	-0.20091	1.46371			124.08	20.91	5	i7-24o339	0.116	30	0.167	11	0.355	2	0.284	0.21	N	0.51	SignalP-TM																	
CYT	-0.20091	2.00927			81.11	33.92	4	o4-26I47-6	0.113	21	0.109	11	0.178	3	0.119	0.112	N	0.51	SignalP-TM																	
CYT	-0.20091				101.37	0	4	i122-144o	0.102	70	0.105	15	0.139	6	0.108	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				94.05	0	4	i282-299o	0.11	56	0.104	56	0.127	52	0.083	0.094	N	0.57	SignalP-noTM																	
CYT	-0.20091				87.85	0	4	o265-287i	0.121	45	0.11	45	0.128	35	0.098	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				81.76	37.33	4	i7-24o29-5	0.106	26	0.096	69	0.111	6	0.061	0.083	N	0.51	SignalP-TM																	
CYT	-0.20091				63.48	22.4	3	o15-36I78	0.099	45	0.092	62	0.092	56	0.056	0.078	N	0.51	SignalP-TM																	
CYT	-0.20091	2.58781			93.47	23.15	3	o28-50i62	0.164	27	0.164	27	0.239	16	0.169	0.166	N	0.51	SignalP-TM																	
CYT	-0.20091	0.75566			76.09	28.39	3	i45-62o67	0.157	20	0.271	20	0.578	15	0.446	0.336	N	0.51	SignalP-TM																	
CYT	-0.20091				44.73	0.06	2	i381-403o	0.147	27	0.253	23	0.605	20	0.438	0.34	N	0.57	SignalP-noTM																	
CYT	-0.20091				36.01	12.27	2	o43-60i15	0.133	64	0.123	64	0.181	1	0.115	0.119	N	0.57	SignalP-noTM																	
CYT	-0.20091				79.82	0	2	o331-352i	0.122	55	0.111	41	0.142	31	0.094	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091	1.14429			44.59	20.81	2	i25-44o47	0.128	51	0.139	13	0.199	10	0.183	0.155	N	0.51	SignalP-TM																	
CYT	-0.20091	1.26635			44.01	21.41	2	o15-33i30	0.128	21	0.138	21	0.245	2	0.166	0.148	N	0.51	SignalP-TM																	
CYT	-0.20091	1.08125			43.44	21.58	2	i7-29o473	0.113	54	0.141	11	0.264	1	0.2	0.163	N	0.51	SignalP-TM																	
CYT	-0.20091				40.22	0.4	2	i85-102o1	0.127	24	0.148	24	0.288	23	0.166	0.156	N	0.57	SignalP-noTM																	
CYT	-0.20091				41.59	9.35	2	i52-71o76	0.106	69	0.124	51	0.187	42	0.124	0.124	N	0.51	SignalP-TM																	
CYT	-0.20091				13.91	10.34	1	i44-66o	0.124	22	0.105	43	0.138	61	0.094	0.101	N	0.51	SignalP-TM																	
CYT	-0.20091	2.42188			42.7	5.15	1	i138-160o	0.168	19	0.304	19	0.796	1	0.546	0.418	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.2	0	1	o285-307i	0.111	48	0.106	21	0.134	15	0.104	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				23.03	0	1	i329-351o	0.101	43	0.102	66	0.115	57	0.089	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.6	0	1	i121-143o	0.167	56	0.121	56	0.142	8	0.098	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				27.68	0	1	i330-352o	0.104	26	0.102	30	0.143	2	0.094	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				19.72	0	1	o246-268i	0.105	39	0.138	22	0.235	11	0.162	0.149	N	0.57	SignalP-noTM																	
CYT	-0.20091				19.95	0	1	i92-111o	0.143	38	0.117	38	0.13	35	0.094	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.64	0	1	i239-261o	0.139	30	0.12	30	0.164	7	0.111	0.116	N	0.57	SignalP-noTM																	
CYT	-0.20091				23.15	0	1	o193-215i	0.155	30	0.127	30	0.134	7	0.102	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.32	0	1	o160-182i	0.115	43	0.11	59	0.143	51	0.101	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.69	0	1	o171-193i	0.122	41	0.121	20	0.195	1	0.132	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				21.55	0	1	o165-184i	0.101	27	0.106	11	0.143	5	0.11	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				20.25	0	1	i197-216o	0.104	28	0.118	11	0.171	1	0.137	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.69	0	1	o171-193i	0.122	41	0.121	20	0.195	1	0.132	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				19.78	0	1	i154-173o	0.102	28	0.106	40	0.127	2	0.098	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.69	0	1	o182-204i	0.122	41	0.121	20	0.195	1	0.132	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				20.18	0	1	i165-184o	0.103	28	0.12	11	0.181	5	0.141	0.13	N	0.57	SignalP-noTM																	
CYT	-0.20091				21.58	0	1	i183-205o	0.105	40	0.118	11	0.171	2	0.136	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.68	0	1	o215-237i	0.124	38	0.112	38	0.131	12	0.101	0.107	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.7	0	1	o153-175i	0.128	20	0.124	20	0.191	1	0.129	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				22.68	0	1	o186-208i	0.124	38	0.113	38	0.133	12	0.103	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				21.17	0	1	i169-188o	0.101	28	0.131	11	0.217	1	0.167	0.148	N	0.57	SignalP-noTM																	
CYT	-0.20091				10.57	9.24	0	o	0.162	22	0.225	22	0.479	21	0.302	0.253	N	0.51	SignalP-TM																	
CYT	-0.20091				3.46	0.59	0	o	0.109	69	0.11	11	0.159	2	0.12	0.114	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.39	0	0	o	0.107	30	0.136	11	0.227	2	0.185	0.159	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.09	0.05	0	o	0.121	29	0.111	51	0.134	39	0.1	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				13.16	13.15	0	o	0.111	37	0.107	46	0.142	36	0.085	0.099	N	0.51	SignalP-TM																	
CYT	-0.20091				0.66	0.12	0	o	0.114	36	0.122	11	0.208	1	0.145	0.133	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.55	0	0	o	0.103	22	0.123	15	0.204	12	0.144	0.133	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.92	0	0	o	0.104	34	0.123	17	0.176	11	0.152	0.137	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.108	18	0.107	30	0.129	27	0.101	0.104	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.22	2.22	0	o	0.314	37	0.263	37	0.351	32	0.178	0.223	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.09	0	0	o	0.101	54	0.114	11	0.164	1	0.13	0.121	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.01	0.01	0	o	0.122	21	0.123	21	0.156	12	0.117	0.121	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.11	21	0.111	21	0.141	14	0.11	0.111	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.101	37	0.103	68	0.117	62	0.088	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.68	0	0	o	0.117	22	0.183	22	0.426	18	0.282	0.23	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.139	39	0.125	11	0.201	2	0.155	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.26	20	0.219	20	0.263	3	0.205	0.212	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.1	0	0	o	0.102	20	0.133	11	0.223	1	0.176	0.153	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.07	0	0	o	0.12	40	0.111	11	0.164	3	0.129	0.12	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.13	60	0.116	60	0.115	52	0.091	0.104	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0.01	0	o	0.107	46	0.101	59	0.113	50	0.09	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.13	13	0.153	13	0.289	12	0.18	0.166	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.76	2.17	0	o	0.107	53	0.106	53	0.143	51	0.104	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.42	0.42	0	o	0.141	25	0.15	25	0.214	22	0.152	0.151	N	0.57	SignalP-noTM																	
CYT	-0.20091				33.83	7.17	0	o	0.207	22	0.294	22	0.708	4	0.489	0.386	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.1	39	0.103	39	0.12	34	0.091	0.097	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.4	0	0	o	0.1	58	0.12	11	0.178	3	0.146	0.132	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0	0	o	0.101	38	0.108	51	0.129	44	0.094	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.102	20	0.104	20	0.135	10	0.1	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091	0.75089			3.03	1.81	0	o	0.179	20	0.347	20	0.868	1	0.705	0.515	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.102	40	0.102	58	0.117	10	0.094	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0.05	0	o	0.171	41	0.144	11	0.271	3	0.203	0.172	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.79	0	0	o	0.11	29	0.106	12	0.132	6	0.113	0.109	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.11	25	0.119	25	0.147	14	0.127	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	59	0.097	70	0.108	44	0.088	0.093	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.111	21	0.126	11	0.214	6	0.167	0.146	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.84	0.83	0	o	0.125	62	0.128	11	0.225	2	0.156	0.141	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.01	0	o	0.106	24	0.196	20	0.519	12	0.324	0.256	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.118	25	0.107	25	0.132	24	0.08	0.094	N	0.57	SignalP-noTM																	
CYT	-0.20091				8.56	0.02	0	o	0.131	20	0.121	20	0.171	6	0.126	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091	1.6882			22.99	11.46	0	o	0.179	21	0.211	21	0.345	18	0.244	0.223	N	0.51	SignalP-TM																	
CYT	-0.20091				0.21	0	0	o	0.128	21	0.174	13	0.405	9	0.281	0.224	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.104	45	0.102	25	0.12	42	0.091	0.097	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.101	58	0.121	18	0.172	9	0.139	0.129	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.104	43	0.104	24	0.127	13	0.093	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.101	21	0.116	53	0.174	43	0.104	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.3	0	0	o	0.1	59	0.099	21	0.127	11	0.095	0.097	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.135	18	0.127	18	0.165	12	0.112	0.12	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.3	0.08	0	o	0.275	43	0.18	43	0.238	42	0.108	0.146	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0.05	0	o	0.108	45	0.136	50	0.259	44	0.117	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.55	0.16	0	o	0.107	32	0.111	32	0.128	21	0.105	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.1	0	0	o	0.101	37	0.099	11	0.114	1	0.097	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0	0	o	0.118	31	0.106	31	0.117	49	0.089	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.11	55	0.103	68	0.116	9	0.092	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.114	37	0.125	37	0.187	33	0.114	0.12	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.14	0.04	0	o	0.107	22	0.111	22	0.134	1	0.114	0.112	N	0.57	SignalP-noTM																	

LipoP1.0 (http://www.cbs.dtu.dk/services/LipoP/)					TMHMM2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/)				SignalP4.1 gram- predictions (http://www.cbs.dtu.dk/services/SignalP/)											Table 1																
Location	Score	Margin	Cleavage	Pos+2	ExpAA	First60	PredHel	Topology	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	SignalP4.1 Consensus	Dmaxcut	Networks-used	Protein Name	Consens. Loc.	His-tag Loc.	dNSAF-pK/ dNSAF+pK	Previous Location	References for Prev. Loc. (PMID)	Predicted MW (kDa)	Observed M.W. (kDa)	Paralogous Family (Casjens 2000)	Number of Paralogs	Comments	in vivo Differential Expression				Immunogenicity	Tn mutant
CYT	-0.20091				0.03	0	0	o	0.209	55	0.134	11	0.231	4	0.182	0.157	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.125	63	0.106	63	0.127	9	0.092	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.113	15	0.108	15	0.139	1	0.108	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.16	0	0	o	0.11	24	0.102	24	0.157	1	0.089	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.106	36	0.106	25	0.14	18	0.1	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0	0	o	0.111	31	0.106	31	0.138	22	0.097	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0	0	o	0.1	68	0.101	39	0.117	23	0.091	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.02	0	o	0.113	22	0.111	22	0.123	20	0.101	0.107	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.27	0.24	0	o	0.199	20	0.132	20	0.157	39	0.081	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091	2.45359			1.23	1.19	0	o	0.131	32	0.162	32	0.321	30	0.203	0.181	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.105	31	0.104	42	0.118	38	0.096	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0	0	o	0.107	33	0.107	48	0.14	1	0.101	0.104	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.12	0	0	o	0.114	53	0.11	20	0.145	12	0.108	0.109	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.103	58	0.122	46	0.225	40	0.098	0.111	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.34	0.02	0	o	0.14	29	0.184	29	0.353	23	0.216	0.199	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0.03	0	o	0.114	24	0.108	24	0.124	23	0.095	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.61	0.13	0	i	0.152	36	0.158	62	0.366	4	0.156	0.157	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.12	0	0	i	0.1	57	0.114	11	0.148	1	0.132	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.106	25	0.099	69	0.12	49	0.088	0.094	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.56	0	0	o	0.102	20	0.104	59	0.121	48	0.087	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0	0	o	0.104	20	0.101	29	0.116	24	0.089	0.095	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.14	0.01	0	o	0.116	39	0.124	39	0.173	32	0.115	0.12	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.29	0.04	0	o	0.121	35	0.123	53	0.223	45	0.103	0.114	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.105	20	0.119	20	0.167	10	0.135	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0.16	0	o	0.106	31	0.122	46	0.174	50	0.131	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.15	0.02	0	o	0.104	25	0.114	12	0.149	2	0.133	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.33	3.26	0	o	0.103	49	0.115	54	0.162	48	0.111	0.113	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0	0	o	0.103	21	0.098	67	0.113	8	0.092	0.095	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.25	0	0	o	0.123	46	0.107	20	0.166	1	0.11	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.111	32	0.131	11	0.21	2	0.171	0.15	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.105	50	0.108	28	0.133	23	0.101	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0.01	0	o	0.103	59	0.1	11	0.159	5	0.128	0.119	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.106	52	0.117	12	0.15	9	0.136	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.116	21	0.117	21	0.143	27	0.108	0.113	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.208	31	0.196	31	0.277	7	0.205	0.2	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.35	0.35	0	o	0.112	57	0.106	22	0.122	25	0.1	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.59	0	0	o	0.158	19	0.141	19	0.181	2	0.137	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.37	2.45	0	o	0.098	45	0.101	13	0.124	3	0.107	0.103	N	0.51	SignalP-TM																	
CYT	-0.20091				5.46	0	0	o	0.104	21	0.103	32	0.141	3	0.095	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.35	0	0	o	0.113	49	0.106	28	0.125	21	0.103	0.104	N	0.57	SignalP-noTM																	
CYT	-0.20091				4.21	2.59	0	o	0.133	44	0.131	44	0.167	50	0.111	0.122	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.01	0	o	0.129	21	0.149	21	0.235	18	0.185	0.166	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	25	0.101	34	0.112	27	0.083	0.092	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.46	0.09	0	o	0.107	49	0.104	11	0.145	1	0.108	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.26	0.01	0	o	0.107	39	0.12	39	0.183	4	0.134	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.106	10	0.108	43	0.124	37	0.085	0.097	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.08	0.01	0	o	0.1	43	0.112	22	0.181	39	0.118	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.127	24	0.105	24	0.12	57	0.087	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.128	39	0.126	39	0.158	29	0.103	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0	0	o	0.107	36	0.102	57	0.129	53	0.09	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.2	0.18	0	o	0.261	21	0.203	21	0.342	48	0.173	0.189	N	0.57	SignalP-noTM																	
CYT	-0.20091	1.59468			2.42	0.04	0	o	0.133	41	0.129	26	0.2	21	0.153	0.14	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.8	0	0	o	0.199	64	0.137	64	0.187	19	0.115	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.91	0	0	o	0.101	41	0.106	41	0.139	1	0.105	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.51	0	0	o	0.119	27	0.115	11	0.229	1	0.119	0.117	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.94	0.49	0	o	0.156	35	0.146	35	0.186	34	0.131	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.16	0.07	0	o	0.137	47	0.121	47	0.148	2	0.099	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.24	0.01	0	o	0.103	29	0.134	12	0.247	8	0.186	0.158	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.69	0	0	o	0.103	47	0.1	69	0.107	61	0.092	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.11	0.11	0	o	0.119	17	0.197	17	0.409	3	0.341	0.25	N	0.51	SignalP-TM																	
CYT	-0.20091				1.63	0	0	o	0.131	40	0.122	40	0.133	39	0.097	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.137	56	0.121	11	0.163	1	0.148	0.134	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0	0	o	0.115	36	0.126	22	0.186	7	0.148	0.136	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.12	50	0.107	25	0.114	22	0.097	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.15	0.02	0	i	0.113	24	0.155	11	0.334	2	0.239	0.195	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.117	49	0.118	11	0.192	3	0.136	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.139	24	0.132	53	0.199	37	0.139	0.135	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0	0	o	0.102	25	0.101	70	0.139	24	0.097	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.129	23	0.113	23	0.156	1	0.101	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	i	0.106	67	0.128	14	0.189	52	0.165	0.145	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.33	0	0	o	0.128	18	0.165	18	0.367	17	0.21	0.186	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.105	16	0.12	16	0.162	10	0.135	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				12.28	0.02	0	o	0.136	28	0.14	28	0.264	7	0.162	0.151	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.122	47	0.123	47	0.159	34	0.104	0.114	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.122	43	0.111	43	0.144	12	0.105	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.102	47	0.105	38	0.142	27	0.092	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				5.7	5.59	0	o	0.129	25	0.204	11	0.595	1	0.388	0.29	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.75	0.74	0	o	0.112	36	0.127	11	0.222	5	0.17	0.147	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.135	26	0.111	26	0.146	32	0.101	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.5	0.49	0	o	0.125	31	0.163	11	0.312	6	0.277	0.216	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.82	0	0	o	0.161	32	0.126	32	0.137	2	0.101	0.114	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.14	0.01	0	o	0.143	59	0.117	59	0.161	7	0.102	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.01	0	o	0.128	60	0.112	60	0.113	53	0.085	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				17.32	0	0	o	0.108	28	0.105	14	0.122	11	0.111	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.115	52	0.165	16	0.342	8	0.272	0.215	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.12	0	0	o	0.103	27	0.11	35	0.136	26	0.102	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.106	29	0.1	34	0.112	32	0.084	0.092	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0.17	0	o	0.161	39	0.159	51	0.276	46	0.109	0.136	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.11	0	0	o	0.11	44	0.105	11	0.125	6	0.113	0.109	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.21	0	0	o	0.138	37	0.113	37	0.121	36	0.093	0.104	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0.01	0	o	0.116	33	0.12	18	0.159	11	0.129	0.124	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0.04	0	o	0.271	22	0.403	22	0.722	11	0.582	0.487	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0.06	0	o	0.11	34	0.112	51	0.142	41	0.093	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				13.97	0.56	0	o	0.117	48	0.194	13	0.456	9	0.375	0.279	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.35	0	0	o	0.103	21	0.095	31	0.103	70	0.086	0.091	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.113	47	0.109	47	0.113	40	0.093	0.101	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.106	37	0.098	68	0.105	44	0.081	0.089	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.12	0.04	0	o	0.11	39	0.155	11	0.365	1	0.226	0.189	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.137	17	0.13	17	0.205	10	0.116	0.124	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.08	0.03	0	o	0.107	23	0.102	23	0.132	1	0.096	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0.02	0	o	0.105	36	0.11	41	0.132	35	0.105	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.38	0.02	0	o	0.11	56	0.136	11	0.259	2	0.185	0.159	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.105	39	0.105	26	0.127	20	0.101	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.1	0.02	0	o	0.111	46	0.099	46	0.104	15	0.09	0.095	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.107	56	0.1	32	0.13	6	0.095	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.22	0.01	0	o	0.139	18	0.144	18	0.244	1	0.155	0.149	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0	0	o	0.137	45	0.131	45	0.189	43	0.102	0.117	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.101	55	0.111	14	0.156	6	0.123	0.117	N	0.57	SignalP-noTM																	
CYT	-0.20091				13.02	2.05	0	o	0.109	63	0.1	63	0.117	49	0.087	0.094	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.105	29	0.122	11	0.187	4	0.152	0.136	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.18	0.01	0	o	0.102	42	0.121	11	0.219	1	0.135	0.128	N	0.57	SignalP-noTM																	
CYT	-0.20091				9.03	0	0	o	0.1	34	0.106	26	0.131	12	0.103	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.59	0.33	0	o	0.185	24	0.193	24	0.417	45	0.214	0.203	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.01	0	o	0.113	10	0.135	13	0.227	9	0.183	0.158	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.113	30	0.115	11	0.201	3	0.131	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0.03	0	o	0.105	20	0.126	17	0.177	16	0.151	0.138	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.07	0	0	o	0.104	31	0.11	57	0.139	48	0.108	0.109	N	0.57	SignalP-noTM																	

LipoP1.0 (http://www.cbs.dtu.dk/services/LipoP/)					TMHMM2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/)				SignalP4.1 gram- predictions (http://www.cbs.dtu.dk/services/SignalP/)											Table 1																	
Location	Score	Margin	Cleavage	Pos+2	ExpAA	First60	PredHel	Topology	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	SignalP4.1 Consensus	Dmaxcut	Networks-used	Protein Name	Consens. Loc.	His-tag Loc.	dNSAF-pK/ dNSAF+pK	Previous Location	References for Prev. Loc. (PMID)	Predicted MW (kDa)	Observed M.W. (kDa)	Paralogous Family (Casjens 2000)	Number of Paralogs	Comments	in vivo Differential Expression				Immunogenicity	Tn mutant
CYT	-0.20091				0.05	0	0	o	0.103	21	0.163	11	0.346	1	0.258	0.208	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.37	0.34	0	o	0.109	55	0.12	55	0.164	47	0.12	0.12	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.103	46	0.101	23	0.127	19	0.104	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.119	50	0.151	11	0.334	1	0.218	0.183	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.124	48	0.107	48	0.117	29	0.097	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.254	36	0.167	36	0.198	9	0.126	0.148	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.103	46	0.111	11	0.172	3	0.127	0.119	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.2	0	0	o	0.106	18	0.114	11	0.16	2	0.132	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.106	18	0.104	50	0.122	40	0.095	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.09	0	0	i	0.121	44	0.139	12	0.222	2	0.196	0.166	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.28	0.21	0	o	0.123	34	0.149	34	0.247	22	0.162	0.155	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.08	0.08	0	o	0.104	60	0.159	11	0.331	1	0.248	0.201	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	35	0.135	12	0.205	6	0.182	0.157	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.217	46	0.157	46	0.201	29	0.12	0.14	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.11	0.1	0	o	0.117	49	0.13	49	0.206	48	0.126	0.128	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.106	61	0.109	61	0.132	43	0.096	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.116	33	0.192	16	0.544	12	0.361	0.271	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.63	0.02	0	o	0.109	52	0.111	52	0.146	1	0.106	0.109	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.45	2.28	0	o	0.331	18	0.349	18	0.429	14	0.361	0.354	N	0.51	SignalP-TM																	
CYT	-0.20091				0.05	0	0	o	0.108	28	0.12	19	0.186	18	0.142	0.13	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.43	0	0	o	0.102	25	0.104	14	0.121	9	0.109	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.118	18	0.116	18	0.146	2	0.12	0.118	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.099	31	0.122	18	0.191	13	0.133	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0.15	0	o	0.109	9	0.112	51	0.144	43	0.103	0.107	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.2	0	0	o	0.102	53	0.103	53	0.137	38	0.089	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				5.88	1.75	0	o	0.446	22	0.285	22	0.392	19	0.169	0.231	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.02	0	o	0.108	29	0.153	11	0.298	1	0.227	0.188	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.1	0.02	0	o	0.124	30	0.166	30	0.386	25	0.202	0.183	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.101	62	0.134	11	0.248	3	0.178	0.155	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.104	24	0.121	22	0.188	14	0.133	0.127	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.15	36	0.115	36	0.144	1	0.099	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.108	42	0.104	42	0.107	35	0.089	0.097	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.12	0	0	o	0.127	22	0.136	11	0.273	20	0.181	0.157	N	0.57	SignalP-noTM																	
CYT	-0.20091				13.78	0.03	0	o	0.113	27	0.138	16	0.239	14	0.182	0.159	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0.03	0	o	0.131	30	0.145	15	0.274	9	0.203	0.172	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0	0	o	0.126	43	0.12	43	0.16	40	0.085	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.19	0.01	0	o	0.109	26	0.145	11	0.324	2	0.202	0.172	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.127	22	0.121	12	0.165	3	0.146	0.133	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.34	0	0	o	0.103	26	0.105	11	0.14	1	0.11	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.169	26	0.148	26	0.163	1	0.128	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				6.5	5.42	0	o	0.113	59	0.104	40	0.139	1	0.082	0.096	N	0.51	SignalP-TM																	
CYT	-0.20091				0.77	0.12	0	o	0.141	20	0.176	20	0.332	15	0.196	0.185	N	0.57	SignalP-noTM																	
CYT	-0.20091	1.51431			41.49	20.78	0	o	0.222	21	0.327	21	0.736	11	0.52	0.418	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0.03	0	o	0.222	60	0.15	60	0.128	5	0.09	0.122	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.07	0	0	o	0.107	70	0.101	37	0.111	33	0.087	0.095	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.94	0.01	0	o	0.139	22	0.134	22	0.189	17	0.131	0.132	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0	0	o	0.122	26	0.098	32	0.128	1	0.075	0.087	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.156	33	0.128	20	0.16	2	0.123	0.126	N	0.57	SignalP-noTM																	
CYT	-0.20091				12.98	0.02	0	o	0.237	26	0.23	26	0.392	19	0.192	0.212	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.46	0	0	o	0.118	33	0.117	33	0.14	20	0.113	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.12	0	0	o	0.108	36	0.18	11	0.444	4	0.346	0.258	N	0.57	SignalP-noTM																	
CYT	-0.20091				4.96	0	0	o	0.127	29	0.163	21	0.321	18	0.267	0.212	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.107	44	0.104	23	0.122	14	0.095	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.83	2.83	0	o	0.361	19	0.365	19	0.522	2	0.393	0.375	N	0.51	SignalP-TM																	
CYT	-0.20091				14.06	11.82	0	o	0.116	25	0.111	11	0.175	1	0.122	0.115	N	0.51	SignalP-TM																	
CYT	-0.20091				0.48	0.47	0	o	0.207	34	0.202	21	0.471	9	0.373	0.282	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.11	0.02	0	o	0.103	30	0.161	20	0.351	12	0.228	0.193	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.49	0	0	o	0.117	48	0.109	48	0.116	46	0.095	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0.09	0	o	0.119	24	0.149	43	0.349	37	0.155	0.152	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.101	33	0.105	20	0.122	11	0.107	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.104	28	0.104	35	0.145	27	0.101	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.92	0.81	0	o	0.113	34	0.161	21	0.361	2	0.244	0.2	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.08	0.05	0	o	0.106	57	0.12	11	0.196	3	0.141	0.13	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.104	28	0.158	11	0.37	1	0.235	0.194	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.22	0.02	0	o	0.109	29	0.121	11	0.207	2	0.145	0.132	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0	0	o	0.103	31	0.113	42	0.166	40	0.107	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.109	52	0.124	13	0.174	1	0.155	0.138	N	0.57	SignalP-noTM																	
CYT	-0.20091				6.48	0.01	0	o	0.119	31	0.117	31	0.167	8	0.101	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				8.04	0.06	0	o	0.14	25	0.203	25	0.457	1	0.332	0.263	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.12	40	0.114	40	0.156	1	0.103	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.31	0.02	0	o	0.133	58	0.114	11	0.149	2	0.13	0.121	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.27	0.06	0	o	0.109	40	0.125	22	0.202	3	0.155	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.31	1.28	0	o	0.102	46	0.111	28	0.134	18	0.108	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0.03	0	o	0.168	36	0.177	18	0.36	15	0.241	0.207	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.109	39	0.106	57	0.115	53	0.089	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.108	3	0.107	29	0.174	2	0.11	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.117	17	0.131	17	0.234	1	0.155	0.143	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0.02	0	o	0.107	35	0.125	40	0.172	33	0.124	0.125	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.105	43	0.105	68	0.117	56	0.097	0.101	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.124	67	0.106	22	0.134	13	0.1	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.21	0.21	0	o	0.188	39	0.137	39	0.113	36	0.09	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.8	0	0	o	0.115	20	0.106	41	0.121	35	0.087	0.097	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.07	0	0	o	0.111	21	0.114	21	0.13	15	0.107	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.43	0.27	0	o	0.117	30	0.115	30	0.231	49	0.1	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.2	0.2	0	o	0.265	20	0.259	20	0.382	19	0.261	0.259	N	0.51	SignalP-TM																	
CYT	-0.20091				0.56	0	0	o	0.123	25	0.125	11	0.195	1	0.155	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.75	0.64	0	o	0.124	31	0.157	18	0.322	15	0.217	0.186	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.23	0	0	o	0.157	36	0.115	36	0.112	11	0.089	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				4.16	0.08	0	o	0.121	30	0.151	17	0.34	16	0.224	0.185	N	0.57	SignalP-noTM																	
CYT	-0.20091				11.68	0.52	0	o	0.149	45	0.117	45	0.113	18	0.093	0.105	N	0.57	SignalP-noTM																	
CYT	-0.20091				18.5	1.03	0	o	0.113	22	0.11	22	0.146	1	0.108	0.109	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.02	0	o	0.105	46	0.112	11	0.194	1	0.117	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.61	0	0	o	0.109	33	0.108	12	0.141	12	0.117	0.112	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.83	0.03	0	o	0.137	33	0.189	33	0.384	29	0.209	0.199	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.136	45	0.118	13	0.16	8	0.132	0.124	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.106	22	0.107	32	0.145	69	0.095	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.01	0	o	0.119	26	0.179	11	0.396	1	0.316	0.243	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.23	0.04	0	o	0.112	39	0.106	39	0.127	1	0.099	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	53	0.107	69	0.122	65	0.095	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.36	0	0	o	0.109	49	0.127	22	0.197	18	0.152	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.57	0.25	0	o	0.115	22	0.188	18	0.432	10	0.32	0.237	N	0.51	SignalP-TM																	
CYT	-0.20091				0	0	0	o	0.101	27	0.102	11	0.121	2	0.105	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.099	39	0.104	37	0.127	30	0.095	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.71	0.39	0	o	0.135	51	0.131	12	0.212	4	0.171	0.15	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.35	0.03	0	o	0.155	37	0.13	37	0.144	33	0.103	0.117	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.16	0.05	0	o	0.113	21	0.174	11	0.409	1	0.292	0.229	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.48	0.03	0	o	0.123	24	0.133	11	0.212	1	0.175	0.153	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.08	0	0	o	0.106	42	0.107	69	0.138	2	0.101	0.104	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.51	0.18	0	o	0.103	62	0.158	11	0.311	2	0.249	0.201	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.21	0.19	0	o	0.13	40	0.138	40	0.171	28	0.131	0.135	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0.05	0	o	0.119	44	0.252	20	0.669	18	0.569	0.401	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.74	0.1	0	o	0.107	49	0.111	42	0.144	15	0.105	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.135	36	0.121	36	0.165	2	0.104	0.113	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.05	0.02	0	o	0.172	21	0.244	21	0.468	17	0.317	0.278	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.106	24	0.099	43	0.107	41	0.09	0.095	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.122	27	0.158	11	0.355	2	0.248	0.2	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0	0	o	0.104	47	0.113	31	0.177	45	0.107	0.11	N	0.57	SignalP-noTM																	

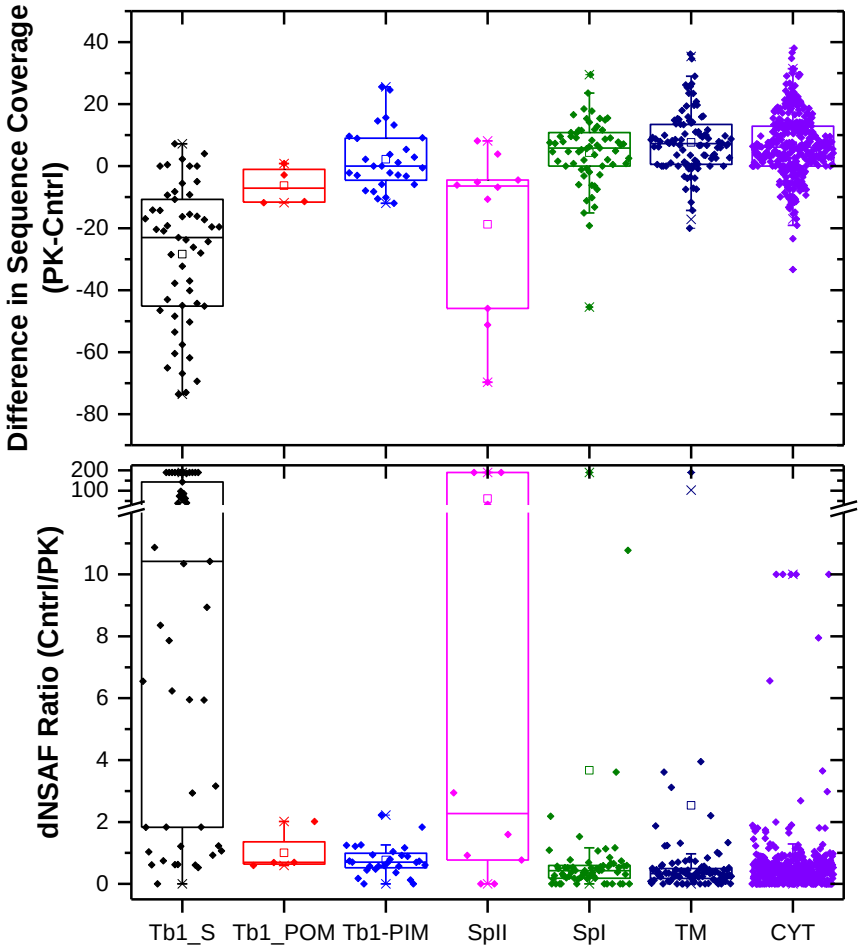
LipoP1.0 (http://www.cbs.dtu.dk/services/LipoP/)					TMHMM2.0 (http://www.cbs.dtu.dk/services/TMHMM-2.0/)				SignalP4.1 gram- predictions (http://www.cbs.dtu.dk/services/SignalP/)											Table 1																	
Location	Score	Margin	Cleavage	Pos+2	ExpAA	First60	PredHel	Topology	Cmax	pos	Ymax	pos	Smax	pos	Smean	D	SignalP4.1 Consensus	Dmaxcut	Networks-used	Protein Name	Consens. Loc.	His-tag Loc.	dNSAF-pK/ dNSAF+pK	Previous Location	References for Prev. Loc. (PMID)	Predicted MW (kDa)	Observed M.W. (kDa)	Paralogous Family (Casjens 2000)	Number of Paralogs	Comments	in vivo Differential Expression				Immunogenicity	Tn mutant
CYT	-0.20091				0.08	0	0	o	0.107	10	0.107	40	0.125	35	0.09	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				20.09	4.89	0	o	0.121	21	0.111	11	0.171	1	0.119	0.115	N	0.57	SignalP-noTM																	
CYT	-0.20091				7.65	7.65	0	o	0.202	39	0.275	39	0.577	29	0.35	0.31	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.39	0	0	o	0.111	32	0.116	32	0.158	29	0.099	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.25	0.08	0	i	0.117	40	0.135	11	0.207	8	0.183	0.158	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	31	0.101	65	0.11	5	0.094	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.03	2.72	0	o	0.122	58	0.135	11	0.236	1	0.183	0.158	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.77	0.61	0	o	0.111	53	0.103	59	0.116	52	0.088	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				4.13	4.13	0	i	0.113	36	0.138	20	0.282	15	0.17	0.153	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.02	0	o	0.111	37	0.144	11	0.301	1	0.198	0.17	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.3	0.25	0	o	0.125	36	0.136	36	0.263	32	0.159	0.146	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.107	45	0.104	31	0.121	56	0.101	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.94	0	0	o	0.109	54	0.112	16	0.156	31	0.124	0.118	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.105	33	0.157	11	0.303	3	0.25	0.201	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	i	0.105	43	0.108	43	0.139	39	0.095	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.34	0.06	0	o	0.143	32	0.148	41	0.342	39	0.146	0.147	N	0.57	SignalP-noTM																	
CYT	-0.20091				6.73	0.34	0	o	0.12	26	0.137	35	0.251	10	0.153	0.145	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.07	0.06	0	o	0.107	26	0.129	11	0.194	8	0.173	0.15	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0.01	0	o	0.122	38	0.117	12	0.162	1	0.134	0.125	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	i	0.119	38	0.106	38	0.106	64	0.093	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				13.23	0	0	o	0.112	42	0.126	11	0.249	1	0.154	0.139	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.89	0	0	o	0.104	51	0.111	11	0.159	3	0.124	0.117	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.3	0.15	0	o	0.107	66	0.103	35	0.141	2	0.102	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.11	0	0	o	0.162	19	0.158	19	0.198	11	0.134	0.146	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.128	47	0.107	11	0.145	2	0.112	0.11	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0	0	o	0.101	30	0.125	11	0.2	2	0.153	0.138	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.137	38	0.144	11	0.349	1	0.185	0.163	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.104	52	0.104	11	0.125	1	0.11	0.107	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0.03	0	o	0.105	29	0.108	60	0.149	1	0.098	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				16.35	1.55	0	o	0.153	47	0.205	47	0.43	35	0.223	0.214	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	66	0.107	24	0.129	17	0.105	0.106	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.105	55	0.107	44	0.121	15	0.099	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.17	0.17	0	o	0.114	32	0.132	20	0.185	1	0.162	0.146	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.25	0	0	o	0.106	46	0.114	46	0.146	39	0.11	0.112	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.06	0	0	o	0.122	29	0.108	29	0.155	1	0.09	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.1	0	0	o	0.101	32	0.101	32	0.121	3	0.097	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	i	0.387	22	0.206	22	0.136	20	0.104	0.158	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.19	0.19	0	o	0.108	36	0.121	28	0.193	23	0.14	0.13	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.5	0.33	0	o	0.104	21	0.151	21	0.257	9	0.215	0.181	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.1	0.01	0	o	0.122	50	0.131	50	0.27	49	0.118	0.124	N	0.57	SignalP-noTM																	
CYT	-0.20091				6.73	2.55	0	o	0.185	23	0.33	23	0.668	15	0.533	0.425	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.04	0.04	0	o	0.105	29	0.137	11	0.247	3	0.194	0.164	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.112	24	0.104	24	0.131	10	0.1	0.102	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.35	0	0	o	0.103	55	0.126	11	0.21	4	0.155	0.14	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.34	0.34	0	o	0.133	21	0.186	19	0.325	17	0.253	0.211	N	0.51	SignalP-TM																	
CYT	-0.20091				0.1	0	0	o	0.102	21	0.11	21	0.149	24	0.117	0.113	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.102	18	0.123	11	0.228	2	0.156	0.138	N	0.57	SignalP-noTM																	
CYT	-0.20091				2.82	2.81	0	o	0.116	44	0.182	11	0.397	3	0.325	0.249	N	0.57	SignalP-noTM																	
CYT	-0.20091				5.84	4.86	0	o	0.113	33	0.132	21	0.199	28	0.151	0.141	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	i	0.101	44	0.134	11	0.215	3	0.187	0.159	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.47	0.38	0	o	0.127	47	0.176	21	0.392	12	0.279	0.225	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.44	3.39	0	o	0.118	33	0.159	17	0.309	13	0.248	0.201	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.108	30	0.104	11	0.147	3	0.111	0.108	N	0.57	SignalP-noTM																	
CYT	-0.20091				3.89	3.89	0	o	0.111	33	0.156	21	0.274	13	0.221	0.186	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.22	1.2	0	o	0.146	29	0.178	29	0.311	13	0.22	0.198	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.1	43	0.109	45	0.135	13	0.096	0.103	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.121	45	0.107	22	0.134	14	0.094	0.101	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0.02	0	o	0.106	26	0.118	26	0.23	18	0.129	0.123	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0.01	0	o	0.252	21	0.26	21	0.483	19	0.258	0.259	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.96	0.78	0	o	0.134	47	0.167	24	0.343	23	0.219	0.191	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.03	0	0	o	0.101	54	0.104	69	0.112	61	0.092	0.098	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.01	0	0	o	0.111	66	0.105	66	0.127	40	0.093	0.099	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.121	45	0.107	22	0.134	14	0.094	0.101	N	0.57	SignalP-noTM																	
CYT	-0.20091	1.474			0.02	0.02	0	o	0.277	21	0.3	21	0.575	19	0.324	0.311	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.14	1.14	0	o	0.125	40	0.18	24	0.331	12	0.241	0.208	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	55	0.114	11	0.212	1	0.123	0.118	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.48	1.47	0	o	0.106	51	0.12	14	0.169	8	0.144	0.131	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.02	0	0	o	0.109	66	0.105	66	0.13	40	0.094	0.1	N	0.57	SignalP-noTM																	
CYT	-0.20091				1.52	1.5	0	o	0.132	33	0.178	24	0.346	23	0.242	0.208	N	0.57	SignalP-noTM																	
CYT	-0.20091				0	0	0	o	0.1	32	0.101	32	0.111	22	0.09	0.096	N	0.57	SignalP-noTM																	
CYT	-0.20091				6.8	6.69	0	o	0.101	33	0.107	11	0.142	1	0.115	0.11	N	0.51	SignalP-TM																	
CYT	-0.20091				0	0	0	o	0.1	21	0.115	35	0.146	29	0.113	0.114	N	0.57	SignalP-noTM																	
CYT	-0.20091				4.43	1.66	0	o	0.134	40	0.189	24	0.384	23	0.263	0.224	N	0.57	SignalP-noTM																	
CYT	-0.20091				8.38	8.36	0	o	0.106	32	0.182	13	0.415	9	0.332	0.252	N	0.57	SignalP-noTM																	
CYT	-0.20091				0.15	0	0	o	0.102	70	0.114	11	0.21	1	0.121	0.117	N	0.57	SignalP-noTM																	

Supporting Figure S1: **Statistical analyses of quantitative proteomics features for differently-located *B. burgdorferi* proteins**

A. For all proteins detected by MudPIT analysis (**Table S2**), the difference in sequence coverage (% of protein sequence covered by detected peptides) observed between the proteinase K-treated and control samples were calculated (DiffSeqCov). The ratio in average dNSAF values measured in the control and proteinase K-treated samples were also calculated (dNSAF ratio). The proteins were grouped based on their known or predicted location (7 categories as defined in **Table 1** and **Table S2**) and box-plots of the distribution in DiffSeqCov and dNSAF ratios were built.

B. The Mann−Whitney non-parametric U test was performed using OriginPro 9.1 to determine whether or not there were statistically significant differences between the distributions of the DiffSeqCov and dNSAF ratios parameters. The distributions of these parameters for proteins shown to be at the surface of *B. burgdorferi* B31-A3 cells ("S" proteins in Table 1) were systematically tested against the ranges of DiffSeqCov and dNSAF ratios for proteins shown (Table 1) or predicted to be localized elsewhere.

A



B

	x	y	Null Hypothesis	Alternative Hypothesis	U	Z	Exact Prob>U	Asymp. Prob>U
Difference in Sequence Coverage (PK - Control)	Table1_S	Table1_P-OM	F(x) >= G(y)	F(x) < G(y)	36	-2.12302	0.01495	0.01688
	Table1_S	Table1_P-IM	F(x) >= G(y)	F(x) < G(y)	137	-5.90927	3.88E-11	1.72E-09
	Table1_S	SpII	F(x) = G(y)	F(x) <> G(y)	177	-1.50985	0.13261	0.13108
	Table1_S	SpI	F(x) >= G(y)	F(x) < G(y)	227	-7.85903	4.82E-19	1.94E-15
	Table1_S	TM	F(x) >= G(y)	F(x) < G(y)	229	-9.13218	7.40E-27	3.36E-20
	Table1_S	CYT	F(x) >= G(y)	F(x) < G(y)	1044.5	-10.2737	5.09E-35	4.63E-25
	SpII	Table1_P-OM	F(x) = G(y)	F(x) <> G(y)	18	-0.21213	0.83916	0.832
	SpII	Table1_P-IM	F(x) >= G(y)	F(x) < G(y)	64	-2.50294	0.00523	0.00616
	SpII	SpI	F(x) >= G(y)	F(x) < G(y)	106	-3.34516	2.06E-04	4.11E-04
	SpII	TM	F(x) >= G(y)	F(x) < G(y)	122	-3.92613	8.60E-06	4.32E-05
	SpII	CYT	F(x) >= G(y)	F(x) < G(y)	550	-3.76887	2.33E-05	8.20E-05
	SpI	Table1_P-OM	F(x) <= G(y)	F(x) > G(y)	213	2.28908	0.00872	0.01104
	SpI	Table1_P-IM	F(x) = G(y)	F(x) <> G(y)	1072	1.62958	0.10298	0.10319
	SpI	TM	F(x) = G(y)	F(x) <> G(y)	2769	-1.29694	0.19494	0.19465
	SpI	CYT	F(x) = G(y)	F(x) <> G(y)	10690.5	-0.88955	0.37442	0.37371
	TM	Table1_P-OM	F(x) <= G(y)	F(x) > G(y)	359	2.68	0.00173	0.00368
	TM	Table1_P-IM	F(x) <= G(y)	F(x) > G(y)	1894	2.84539	0.00202	0.00222
	TM	CYT	F(x) = G(y)	F(x) <> G(y)	19291	0.87404	0.38255	0.3821
	CYT	Table1_P-OM	F(x) <= G(y)	F(x) > G(y)	1288	2.62773	0.00226	0.0043
	CYT	Table1_P-IM	F(x) <= G(y)	F(x) > G(y)	6603	2.57666	0.00473	0.00499
dNSAF Ratio (Control/PK)	Table1_S	Table1_P-OM	F(x) <= G(y)	F(x) > G(y)	175	2.35912	0.00712	0.00916
	Table1_S	Table1_P-IM	F(x) <= G(y)	F(x) > G(y)	1270	5.7011	2.78E-10	5.95E-09
	Table1_S	SpII	F(x) = G(y)	F(x) <> G(y)	300.5	0.88201	0.38061	0.37777
	Table1_S	SpI	F(x) <= G(y)	F(x) > G(y)	2969	7.77082	0	3.89E-15
	Table1_S	TM	F(x) <= G(y)	F(x) > G(y)	4763	8.70839	0	0
	Table1_S	CYT	F(x) <= G(y)	F(x) > G(y)	17343	10.01037	0	0
	SpII	Table1_P-OM	F(x) = G(y)	F(x) <> G(y)	29	1.20874	0.21578	0.22676
	SpII	Table1_P-IM	F(x) <= G(y)	F(x) > G(y)	204	2.10662	0.01664	0.01758
	SpII	SpI	F(x) <= G(y)	F(x) > G(y)	485.5	2.73533	2.50E-03	3.12E-03
	SpII	TM	F(x) <= G(y)	F(x) > G(y)	766.5	2.76717	2.22E-03	2.83E-03
	SpII	CYT	F(x) <= G(y)	F(x) > G(y)	2834	2.99067	9.97E-04	1.39E-03
	SpI	Table1_P-OM	F(x) >= G(y)	F(x) < G(y)	45	-2.13495	0.01464	0.01638
	SpI	Table1_P-IM	F(x) >= G(y)	F(x) < G(y)	526	-3.06138	9.60E-04	0.0011
	SpI	TM	F(x) = G(y)	F(x) <> G(y)	3433	0.96365	0.33578	0.33522
	SpI	CYT	F(x) = G(y)	F(x) <> G(y)	11447.5	-0.05475	0.95654	0.95634
	TM	Table1_P-OM	F(x) >= G(y)	F(x) < G(y)	62	-2.32492	0.00781	0.01004
	TM	Table1_P-IM	F(x) >= G(y)	F(x) < G(y)	755	-3.71601	7.23E-05	1.01E-04
	TM	CYT	F(x) = G(y)	F(x) <> G(y)	16786	-1.23175	0.21829	0.21804
	CYT	Table1_P-OM	F(x) >= G(y)	F(x) < G(y)	302	-2.02041	2.04E-02	2.17E-02
	CYT	Table1_P-IM	F(x) >= G(y)	F(x) < G(y)	3177	-3.34438	3.46E-04	4.12E-04