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Title	Genome sequence reveals that <i>Pseudomonas fluorescens</i> F113 possesses a large and diverse array of systems for rhizosphere function and host interaction
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F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_0319	CDS	+	382794..382997	67		YafQ toxin protein	Pseudomonas sp. GM30	ZP_10679031.1	5E-36	54	67
PSF113_0322	CDS	-	384297..385454	385		hypothetical protein	Pseudomonas sp. GM21	ZP_10700790.1	0	346	385
PSF113_0453	CDS	-	539485..540699	404		Major facilitator family transporter	Pseudomonas sp. GM84	ZP_10605236.1	0	321	404
PSF113_0454	CDS	-	543300..543497	65		hypothetical protein	Pseudomonas sp. GM48	ZP_10664277.1	2E-28	54	64
PSF113_0738	CDS	-	894478..895422	314	motD	MotD	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10438812.1	1E-107	174	261
PSF113_0739	CDS	-	895419..896243	274	motC	Flagellar motor rotation protein MotA	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10438813.1	2E-163	234	274
PSF113_0740	CDS	+	896563..897615	350	fliC2	Flagellar biosynthesis protein FliC	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10438814.1	0	327	350
PSF113_0741	CDS	+	897798..901226	1142		TPR domain protein,putative component of TonB system	Bordetella petrii DSM 12804	YP_001631626.1	0	512	1111
PSF113_0743	CDS	-	902625..903317	230	fliA2	RNA polymerase sigma factor for flagellar operon	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439966.1	3E-141	197	230
PSF113_0745	CDS	-	903997..906291	764	flhF2	Flagellar biosynthesis protein FlhF	Azotobacter vinelandii DJ	YP_002799937.1	0	380	753
PSF113_0747	CDS	-	908378..909547	389	flhB	Flagellar biosynthesis protein FlhB	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439969.1	0	332	386
PSF113_0748	CDS	-	909651..910553	300	motB2	Flagellar motor rotation protein MotB	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439970.1	5E-175	242	280
PSF113_0749	CDS	-	910550..911434	294	motA2	Flagellar motor rotation protein MotA	Enterobacteriaceae bacterium 9_2_54FAA	ZP_07950070.1	8E-118	173	281
PSF113_0750	CDS	-	911674..912240	188	flhC	Flagellar transcriptional activator FlhC	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439972.1	9E-126	175	187
PSF113_0751	CDS	-	912244..912486	80	flhD	FlhD	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439973.1	9E-46	73	80
PSF113_0753	CDS	-	913278..913592	104	fliS2	FliS2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439975.1	5E-55	90	104
PSF113_0754	CDS	-	913704..915113	469	fliD2	Flagellar hook-associated protein FliD	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439976.1	0	376	453
PSF113_0755	CDS	-	915302..915622	106	fliE2	FliE2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439977.1	2E-49	84	104
PSF113_0756	CDS	+	915882..917606	574	fliF2	Flagellar M-ring protein FliF	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439978.1	0	465	577
PSF113_0757	CDS	+	917615..918601	328	fliG2	Flagellar motor switch protein FliG	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439979.1	0	303	328
PSF113_0758	CDS	+	918594..919316	240	fliH2	FliH2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439980.1	5E-112	164	219
PSF113_0760	CDS	+	920733..921203	156	fliJ2	FliJ2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439982.1	5E-81	125	155
PSF113_0761	CDS	+	921659..922600	313	fliK2	FliK2	Polaromonas sp. CF318	ZP_10562011.1	2E-21	51	98
PSF113_0762	CDS	+	922724..923197	157	fliL2	FliL2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439984.1	1E-54	103	156
PSF113_0763	CDS	+	923201..924253	350	fliM2	Flagellar motor switch protein FliM	Azotobacter vinelandii DJ	YP_002799578.1	0	270	350
PSF113_0764	CDS	+	924246..924716	156	fliN2	FliN2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439986.1	1E-65	119	159
PSF113_0765	CDS	+	924770..925135	121	fliO2	FliO2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439987.1	2E-35	75	112
PSF113_0766	CDS	+	925132..925902	256	fliP2	Flagellar biosynthesis protein FliP	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439988.1	8E-135	210	226
PSF113_0767	CDS	+	925928..926197	89	fliQ2	FliQ2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439989.1	3E-52	84	89

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_0768	CDS	+	926203..926991	262	fliR2	FliR2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439990.1	4E-150	235	262
PSF113_0769	CDS	-	927134..928330	398	flgL2	FlgL2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439991.1	0	352	398
PSF113_0770	CDS	-	928357..929967	536	flgK2	FlgK2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439992.1	0	462	535
PSF113_0771	CDS	-	930110..931072	320	flgJ2	FlgJ2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439993.1	2E-170	240	303
PSF113_0772	CDS	-	931072..932226	384	flgI2	Flagellar P-ring protein FlgI	Azotobacter vinelandii DJ	YP_002799569.1	0	262	350
PSF113_0773	CDS	-	932238..932882	214	flgH2	Flagellar L-ring protein FlgH	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439995.1	2E-123	184	213
PSF113_0774	CDS	-	932942..933724	260	flgG2	Flagellar basal-body rod protein FlgG	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439996.1	4E-180	247	260
PSF113_0775	CDS	-	933756..934502	248	flgF2	Flagellar basal-body rod protein FlgF	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439997.1	2E-151	216	241
PSF113_0776	CDS	-	934515..935663	382	flgE2	Flagellar hook protein FlgE	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439998.1	0	343	382
PSF113_0777	CDS	-	935746..936423	225	flgD2	FlgD2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10439999.1	3E-126	204	225
PSF113_0778	CDS	-	936427..936834	135	flgC2	Flagellar basal-body rod protein FlgC	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10440000.1	5E-89	130	135
PSF113_0779	CDS	-	936850..937263	137	flgB2	FlgB2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10440001.1	8E-82	124	137
PSF113_0780	CDS	+	937426..938136	236	flgA2	FlgA2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10440002.1	1E-99	149	207
PSF113_0781	CDS	+	938322..938519	65	flgM2	FlgM2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10440003.1	1E-15	39	59
PSF113_0782	CDS	+	938559..938990	143	flgN2	FlgN2	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10440004.1	4E-65	104	137
PSF113_0810	CDS	-	980757..981017	86	higB2	HigB	Delftia acidovorans SPH-1	YP_001562241.1	2E-31	56	79
PSF113_0811	CDS	-	981310..982338	342		transcriptional regulator, AraC family	Pseudomonas putida S16	YP_004700345.1	1E-156	213	246
PSF113_0812	CDS	+	982497..983366	289		putative solute-binding component of ABC transporter	Pseudomonas putida S16	YP_004700348.1	0	255	290
PSF113_0816	CDS	+	985574..987001	475		Aspartyl-tRNA(Asn)amidotransferase subunit A @ Glutamyl-tRNA(Gln) amidotransferase subunit A	Acidovorax sp. CF316	ZP_10391513.1	0	267	457
PSF113_0819	CDS	-	989330..990913	527		Phytoene dehydrogenase-related protein	Agrobacterium radiobacter K84	YP_002546768.1	0	326	526
PSF113_0822	CDS	+	992664..993443	259		3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	Burkholderia sp. H160	ZP_03263858.1	3E-125	177	257
PSF113_0824	CDS	+	994800..995816	338		Possible gluconolactonase	Pseudomonas fluorescens SBW25	YP_002871579.1	0	270	338
PSF113_0825	CDS	+	995845..997128	427		Histidinol dehydrogenase(EC 1.1.1.23)	Methylobacterium nodulans ORS 2060	YP_002499446.1	0	284	425
PSF113_0826	CDS	+	997128..997880	250		3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	Runella slithyiformis DSM 19594	YP_004654053.1	4E-63	117	258
PSF113_0827	CDS	+	997891..998322	143		Glyoxalase/bleomycin resistance protein/dioxygenase	Burkholderia sp. H160	ZP_03263855.1	2E-47	73	128
PSF113_0831	CDS	+	1001695..1003137	480		Carbohydrate-selective porin	Pseudomonas fluorescens SBW25	YP_002871586.1	0	303	457
PSF113_0832	CDS	+	1003152..1003895	247		3-oxoacyl-[acyl-carrier protein] reductase	Burkholderia sp. H160	ZP_03263843.1	4E-79	130	244
PSF113_0992	CDS	-	1194081..1194440	119		Mobile element protein	Pseudomonas syringae pv. japonica str. M301072	ZP_16685788.1	3E-79	117	119
PSF113_0994	CDS	-	1195993..1197582	529		lysogenic conversion protein	Pseudomonas putida BIRD-1	YP_005932322.1	7E-69	154	527
PSF113_0999	CDS	-	1201927..1202331	134		hypothetical protein	Pseudomonas fluorescens Q8r1-96	ZP_17669922.1	1E-85	124	133
PSF113_1038	CDS	+	1240087..1240362	91		hypothetical protein	Pseudomonas syringae pv. aesculi str. NCPPB 3681	ZP_06459090.1	2E-54	80	91
PSF113_1170	CDS	+	1390188..1390769	193		dockerin type 1 protein	Pseudomonas chlororaphis O6	ZP_10174710.1	2E-107	158	193

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_1178	CDS	+	1396691..1397128	145		prophage tail fimber assembly protein	<i>Pseudomonas chlororaphis</i> subsp. aureofaciens 30-84	EJL08081.1	8E-09	25	37
PSF113_1188	CDS	-	1403843..1404490	215	rfaZ	RfaZ	<i>Pseudomonas avellanae</i> BPIC 631	ZP_16386226.1	2E-95	135	215
PSF113_1463	CDS	+	1686804..1687034	76		hypothetical protein	<i>Pseudomonas</i> sp. GM79	ZP_10612532.1	2E-41	63	76
PSF113_1539	CDS	+	1796727..1797500	257		Glucose-1-phosphate cytidyltransferase (EC 2.7.7.33)	<i>Pseudomonas</i> sp. GM60	ZP_10641967.1	0	245	257
PSF113_1540	CDS	+	1797482..1798564	360		Similar to CDP-glucose 4,6-dehydratase (EC 4.2.1.45)	<i>Pseudomonas</i> sp. GM74	ZP_10629261.1	0	318	360
PSF113_1541	CDS	+	1798561..1799121	186		dTDP-4-dehydrorhamnose 3,5-epimerase	<i>Pseudomonas</i> sp. GM80	ZP_10606112.1	1E-123	170	186
PSF113_1542	CDS	+	1799121..1799990	289		UDP-glucose 4-epimerase	<i>Pseudomonas</i> sp. GM80	ZP_10606111.1	5E-169	233	284
PSF113_1543	CDS	+	1799980..1801050	356		C-methyltransferase	<i>Pseudomonas</i> sp. GM74	ZP_10629265.1	0	291	356
PSF113_1544	CDS	+	1801066..1801803	245		Cephalosporin hydroxylase	<i>Pseudomonas fluorescens</i> R124	ZP_18345414.1	5E-128	170	239
PSF113_1547	CDS	+	1805812..1806972	386		DegT/DnrJ/EryC1/StrS aminotransferase	<i>Pseudomonas</i> sp. GM17	ZP_10708182.1	0	320	386
PSF113_1548	CDS	+	1806979..1807680	233		N-Acetylneuraminate cytidyltransferase	<i>Pseudomonas</i> sp. GM50	ZP_10649148.1	7E-141	199	231
PSF113_1549	CDS	+	1807677..1809182	501		Pseudaminic acid cytidyltransferase (EC 2.7.7.43)	<i>Pseudomonas fluorescens</i> R124	ZP_18345418.1	0	379	501
PSF113_1550	CDS	+	1809175..1810227	350		N-acetylneuraminate synthase (EC 2.5.1.56)	<i>Pseudomonas</i> sp. GM80	ZP_10606103.1	0	312	350
PSF113_1552	CDS	+	1811395..1812726	443		Conserved domain protein	<i>Pseudomonas</i> sp. GM25	ZP_10688563.1	0	288	430
PSF113_1553	CDS	+	1812723..1812992	89		hypothetical protein	<i>Pseudomonas</i> sp. GM102	ZP_10594708.1	1E-25	49	84
PSF113_1581	CDS	-	1838167..1840368	733		hypothetical protein	<i>Pseudomonas viridiflava</i> UASWS0038	ZP_11289897.1	2E-92	167	369
PSF113_1647	CDS	+	1913982..1915241	419	matE	MatE	<i>Pseudomonas aeruginosa</i> UCBPP-PA14	YP_790024.1	2E-148	234	412
PSF113_1651	CDS	+	1918441..1919535	364		glycosyl hydrolase bnr repeat-containing protein	<i>gamma</i> proteobacterium HTCC2207	ZP_01225182.1	2E-80	132	342
PSF113_1652	CDS	+	1919557..1921701	714		putative zinc-binding dehydrogenase	<i>Ralstonia solanacearum</i> CFBP2957	YP_003748271.1	0	487	686
PSF113_1653	CDS	+	1921710..1923356	548		Heparinase II/III-like	<i>Pseudomonas aeruginosa</i> UCBPP-PA14	YP_790028.1	0	360	547
PSF113_1654	CDS	+	1923359..1924543	394		hypothetical protein	<i>Pseudomonas</i> sp. GM67	ZP_10634475.1	0	257	388
PSF113_1657	CDS	+	1926872..1928065	397		acyltransferase 3	<i>Pseudomonas</i> sp. GM55	ZP_10643050.1	3E-160	235	398
PSF113_1759	CDS	-	2049894..2050790	298		Transcriptional regulator, LysR family	<i>Pseudomonas</i> sp. GM60	ZP_10636446.1	2E-171	242	295
PSF113_1760	CDS	+	2050894..2051742	282		ThiJ/Pfpl family protein	<i>Pseudomonas</i> sp. GM67	ZP_10634853.1	3E-142	200	279
PSF113_1793	CDS	+	2090217..2090471	84	iacP	IacP	<i>Pseudomonas</i> sp. GM49	ZP_10654481.1	0,000001	21	37
PSF113_1800	CDS	+	2095052..2095618	188	orgA	OrgA	<i>Pseudomonas fluorescens</i> Q2-87	ZP_17084184.1	5E-89	138	182
PSF113_1925	CDS	-	2257555..2258784	409		Mobile element protein	<i>Pseudomonas</i> sp. GM79	ZP_10618130.1	0	280	349
PSF113_1937	CDS	+	2271783..2272937	384		hypothetical protein	<i>Burkholderia phymatum</i> STM815	YP_001863389.1	7E-36	108	307
PSF113_2025	CDS	-	2368301..2369224	307		Inositol transport system sugar-binding protein	<i>Pseudomonas fluorescens</i> SS101	ZP_17665903.1	0	259	307
PSF113_2026	CDS	-	2369273..2370427	384		Protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin	<i>Pseudomonas fragi</i> A22	ZP_10850286.1	0	274	382
PSF113_2027	CDS	-	2370424..2371272	282		Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	<i>Pseudomonas</i> sp. GM78	ZP_10624378.1	0	271	282
PSF113_2028	CDS	+	2371397..2372422	341		dna-binding protein	<i>Pseudomonas</i> sp. M47T1	ZP_10148580.1	0	310	341
PSF113_2029	CDS	-	2372432..2373499	355	pnpD2	Alcohol dehydrogenase (EC 1.1.1.1)	<i>Pseudomonas</i> sp. GM78	ZP_10623894.1	0	333	354
PSF113_2030	CDS	-	2373504..2373917	137		hypothetical protein	<i>Pseudomonas</i> sp. GM79	ZP_10616321.1	8E-91	127	137
PSF113_2031	CDS	-	2373956..2374801	281	pcpA	PcpA	<i>Pseudomonas</i> sp. GM79	ZP_10616322.1	0	261	281
PSF113_2032	CDS	+	2374972..2375886	304		transcriptional regulator, LysR family	<i>Pseudomonas</i> sp. GM79	ZP_10616323.1	0	303	304
PSF113_2034	CDS	+	2377611..2379047	478		Permeases of the major facilitator superfamily	<i>Pantoea</i> sp. GM01	ZP_10556988.1	0	267	475
PSF113_2035	CDS	+	2379125..2380021	298		Catechol 1,2-dioxygenase 1 (EC 1.13.11.1)	<i>Pseudomonas</i> sp. GM79	ZP_10616326.1	0	291	298
PSF113_2036	CDS	+	2380211..2380945	244		Xylose isomerase domain protein TIM barrel	<i>Pseudomonas</i> sp. GM79	ZP_10616327.1	0	288	290
PSF113_2037	CDS	+	2381014..2382009	331		Myo-inositol 2-dehydrogenase (EC 1.1.1.18)	<i>Pseudomonas</i> sp. GM78	ZP_10623887.1	0	313	331
PSF113_2038	CDS	+	2382059..2383150	363		NADH-dependent dehydrogenase	<i>Pseudomonas</i> sp. GM78	ZP_10623886.1	0	356	363

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PSF113_2042	CDS	+	2387126..2387428	100		stress responsive alpha-beta barrel domain protein	Burkholderia sp. H160	ZP_03269771.1	3E-36	60	97
PSF113_2145	CDS	+	2513232..2513567	111		acetyltransferase, GNAT family	Pseudomonas mandelii JR-1	ZP_11108873.1	7E-55	83	107
PSF113_2225	CDS	-	2599711..2600664	317		endonuclease/exonuclease/phosphatase family	Pseudomonas aeruginosa PA7	YP_001348249.1	8E-35	103	312
PSF113_2260	CDS	+	2638804..2639544	246	azlC3	AzIC	Pseudomonas sp. GM60	ZP_10639841.1	6E-134	189	213
PSF113_2261	CDS	+	2639541..2639867	108		branched-chain amino acid transport	Pseudomonas sp. GM67	ZP_10632735.1	2E-54	99	108
PSF113_2274	CDS	+	2657055..2658269	404		Response regulator receiver domain protein	Nitrosospira multiformis ATCC 25196	YP_411242.1	6E-131	201	401
PSF113_2442	CDS	-	2850226..2851224	332		perosamine synthase	Pseudomonas sp. GM17	ZP_10709575.1	1E-154	229	293
PSF113_2443	CDS	-	2851215..2851724	169		hypothetical protein	Pseudomonas sp. GM17	ZP_10709576.1	7E-107	155	169
PSF113_2445	CDS	-	2862223..2863581	452		hypothetical protein	Nitrolancetus hollandicus Lb	ZP_10246177.1	2E-91	204	472
PSF113_2447	CDS	-	2867162..2867848	228		hypothetical protein	Pseudomonas fragi A22	ZP_10849905.1	12	38	123
PSF113_2448	CDS	-	2868202..2868537	111		hypothetical protein	Nitrolancetus hollandicus Lb	ZP_10246176.1	2E-09	37	107
PSF113_2449	CDS	-	2868865..2869620	251		iron ABC transporter ATP-binding protein	Pseudomonas sp. GM67	ZP_10632022.1	1E-164	231	251
PSF113_2450	CDS	-	2869614..2870675	353	fecD	Iron(III) dicitrate transport system permease protein FecD (TC 3.A.1.14.1)	Pseudomonas mandelii JR-1	ZP_11114318.1	0	325	352
PSF113_2451	CDS	-	2870672..2871859	395		periplasmic binding protein	Pseudomonas sp. GM49	ZP_10655015.1	0	339	395
PSF113_2453	CDS	-	2874435..2875412	325		Fe2+-dicitrate sensor,membrane component	Pseudomonas sp. GM41(2012)	ZP_10670704.1	0	278	325
PSF113_2454	CDS	-	2875413..2875946	177		RNA polymerase sigma-70 factor, ECF subfamily	Pseudomonas sp. GM41(2012)	ZP_10670703.1	6E-112	157	171
PSF113_2455	CDS	-	2876015..2877241	408		Multidrug resistance protein B	Pseudomonas sp. GM67	ZP_10632028.1	0	331	403
PSF113_2468	CDS	-	2889865..2895588	1907		hypothetical protein	Pseudomonas sp. GM41(2012)	ZP_10667339.1	3E-23	187	654
PSF113_2571	CDS	-	3027075..3028190	371		Phenylpropionate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit	Pseudomonas aeruginosa ATCC 700888	ZP_15626210.1	0	273	364
PSF113_2574	CDS	-	3030979..3031806	275		transcriptional regulatory protein	Burkholderia sp. Ch1-1	ZP_10031946.1	2E-41	85	267
PSF113_2578	CDS	-	3035847..3036497	216		hypothetical protein	Leptosphaeria maculans JN3	XP_003840512.1	2E-30	79	225
PSF113_2580	CDS	-	3039138..3040232	364		bnr domain-containing protein	Pseudomonas fluorescens Q8r1-96	ZP_17671118.1	4E-91	170	358
PSF113_2583	CDS	+	3043484..3044029	181		hypothetical protein	Sphingobium sp. SYK-6	YP_004834889.1	2E-45	76	160
PSF113_2584	CDS	+	3044049..3044504	151		aromatic-ring-hydroxylating dioxygenase beta subunit	Sphingobium sp. SYK-6	YP_004835931.1	6E-27	59	147
PSF113_2585	CDS	+	3044563..3045504	313		NmrA-like protein	Frankia sp. QA3	ZP_10309179.1	3E-105	172	299
PSF113_2605	CDS	-	3065028..3065993	321	pdtC	PdtC, QsbA	Pseudomonas sp. GM102	ZP_10599892.1	0	287	321
PSF113_2607	CDS	+	3068150..3069193	347	ptdP	PtdP, QbsJ	Pseudomonas sp. GM102	ZP_10599890.1	0	278	343
PSF113_2608	CDS	+	3069190..3070482	430	ampG2	AmpG	Pseudomonas sp. GM50	ZP_10650419.1	2E-174	309	407
PSF113_2609	CDS	+	3070641..3072908	755		Methionine ABC transporter ATP-binding protein	Ralstonia solanacearum GMI1000	NP_521762.1	0	537	808
PSF113_2610	CDS	+	3072932..3075454	840		Putrescine aminotransferase (EC 2.6.1.82)	Serratia sp. AS12	YP_004500188.1	0	433	852
PSF113_2611	CDS	+	3075828..3076871	347	pdtF	Sulfur carrier protein adenyllyltransferase ThiF	Pseudomonas sp. GM102	ZP_10599886.1	0	308	347
PSF113_2612	CDS	+	3076893..3077300	135	pdtG	PdtG, QsbD	Pseudomonas sp. GM50	ZP_10650423.1	1E-79	117	134
PSF113_2613	CDS	+	3077372..3077644	90	pdtH	PdtH, QsbE	Pseudomonas sp. GM102	ZP_10599884.1	7E-50	78	90
PSF113_2614	CDS	+	3077729..3079582	617		hypothetical protein	Pseudomonas sp. TJI-51	ZP_08143500.1	0	298	547
PSF113_2615	CDS	+	3079579..3081228	549	pdtJ	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	Ralstonia solanacearum Po82	YP_006032419.1	0	378	548
PSF113_2616	CDS	+	3081267..3082442	391	pdtO	PdtO	Pseudomonas sp. GM50	ZP_10650427.1	0	344	391
PSF113_2617	CDS	+	3082439..3083644	401		hypothetical protein	Pseudomonas sp. GM50	ZP_10650428.1	0	334	402
PSF113_2618	CDS	+	3083641..3084723	360		unsaturated glucuronyl hydrolase	Pseudomonas sp. GM102	ZP_10599879.1	2E-150	242	366
PSF113_2736	CDS	+	3218181..3219521	446	tolC	TolC	Pseudomonas mendocina ymp	YP_001186218.1	7E-167	258	432
PSF113_2750	CDS	+	3234170..3234487	105		transcriptional regulator	Pseudomonas sp. GM74	ZP_10629848.1	2E-64	100	105
PSF113_2751	CDS	+	3234480..3235751	423	hipA2	HIP A PROTEIN	Pseudomonas fluorescens WH6	ZP_07776376.1	0	398	419
PSF113_2752	CDS	+	3236163..3237206	347		Dihydroflavonol-4-reductase (EC 1.1.1.219)	Pseudomonas sp. HYS	ZP_11261341.1	0	254	347
PSF113_2865	CDS	+	3375210..3375602	130		putative translation initiation inhibitor protein	Novosphingobium sp. AP12	ZP_10744851.1	7E-82	116	130
PSF113_2866	CDS	+	3375665..3376489	274		Saccharopine dehydrogenase	Pseudomonas sp. GM24	ZP_10694342.1	4E-87	124	168

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_2875	CDS	+	3385596..3386573	325		probable transcription regulator PA3771	Pseudomonas chlororaphis O6	ZP_10175621.1	0	269	325
PSF113_2876	CDS	+	3386711..3387586	291	qbdB	QbdB	Pseudomonas sp. GM17	ZP_10712333.1	0	263	291
PSF113_2877	CDS	+	3387609..3388772	387		Permeases of the major facilitator superfamily	Pseudomonas aeruginosa 138244	ZP_11915370.1	9E-139	261	351
PSF113_2878	CDS	+	3388807..3389919	370		Deacetylases, including yeast histone deacetylase and acetoin utilization protein	Pseudomonas aeruginosa PAb1	ZP_06877188.1	0	270	365
PSF113_3032	CDS	-	3583921..3584643	240		hypothetical protein	Pseudomonas mandelii JR-1	ZP_11110187.1	8E-151	208	239
PSF113_3033	CDS	-	3584806..3585750	314		hypothetical protein	Pseudomonas viridiflava UASWS0038	ZP_11286954.1	2E-87	159	317
PSF113_3034	CDS	-	3585747..3587411	554		hypothetical protein	Pseudomonas viridiflava UASWS0038	ZP_11286953.1	0	302	566
PSF113_3036	CDS	-	3589239..3589994	251		cobalamin biosynthetic protein	Pseudomonas protegens Pf-5	YP_259560.1	8E-93	139	239
PSF113_3123	CDS	-	3682946..3684298	450		serine protease,subtilase family	Arsenophonus nasoniae	CBA74876.1	1E-108	204	430
PSF113_3132	CDS	-	3692953..3694023	356		putative exported protein	Rhizobium leguminosarum bv. trifolii WSM1325	YP_002976281.1	0	244	329
PSF113_3136	CDS	-	3696580..3697176	198		twin-arginine translocation pathway signal	Pseudomonas sp. GM24	ZP_10691545.1	7E-129	178	194
PSF113_3151	CDS	-	3712292..3714682	796		Ferrichrome-iron receptor	Halomonas boliviensis LC1	ZP_09186870.1	0	464	661
PSF113_3153	CDS	-	3715768..3716166	132		RNA polymerase sigma-70 factor, ECF subfamily	Pseudomonas sp. GM80	ZP_10608172.1	5E-85	128	132
PSF113_3157	CDS	-	3717668..3718996	442		periplasmic serine protease	Pseudomonas sp. GM67	ZP_10632736.1	5E-28	64	151
PSF113_3298	CDS	-	3889413..3889667	84		putative membrane protein	Pseudomonas sp. GM102	ZP_10597742.1	2E-44	75	84
PSF113_3302	CDS	+	3892671..3892844	57		hypothetical protein	Pseudomonas fluorescens Pf0-1	YP_348753.1	9E-28	51	53
PSF113_3303	CDS	+	3893476..3894552	358		putative membrane protein	Pseudomonas stutzeri DSM 10701	YP_006522558.1	5E-171	254	330
PSF113_3305	CDS	+	3897288..3898403	371		ABC-type multidrug transport system, permease component	Pseudomonas stutzeri A1501	YP_001170635.1	0	273	371
PSF113_3306	CDS	-	3898507..3898764	85		Acetate kinase	Rhodanobacter sp. 2APBS1	ZP_08953387.1	2E-16	44	78
PSF113_3308	CDS	+	3900162..3902099	645		hypothetical protein	Xanthomonas campestris pv. campestris str. ATCC 33913	NP_636148.1	0	321	642
PSF113_3309	CDS	+	3902096..3903097	333		putative membrane protein	Pseudomonas stutzeri TS44	ZP_14470735.1	3E-143	202	322
PSF113_3310	CDS	+	3903240..3904277	345		Threonine dehydrogenase and related Zn-dependent dehydrogenases	Celeribacter baekdonensis B30	ZP_11133190.1	0	251	344
PSF113_3311	CDS	+	3904883..3906370	495		Membrane protein	Pseudomonas sp. Ag1	ZP_10475632.1	0	384	455
PSF113_3313	CDS	-	3906857..3908554	565		Sulfate permease	Pseudomonas entomophila L48	YP_609791.1	0	464	561
PSF113_3350	CDS	-	3943406..3944590	394		3-ketoacyl-CoA thiolase(EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Pseudomonas sp. HYS	ZP_11258811.1	0	315	394
PSF113_3352	CDS	+	3945924..3947576	550		Histidine kinase, HAMP region:Bacterial chemotaxis sensory transducer precursor	Pseudomonas stutzeri TS44	ZP_14470700.1	0	372	549
PSF113_3353	CDS	-	3947629..3947958	109		putative MarR family transcriptional regulator	Pseudomonas sp. GM21	ZP_10695694.1	7E-57	87	108
PSF113_3355	CDS	-	3948810..3952373	1187		Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits	Chromobacterium violaceum ATCC 12472	NP_899973.1	0	694	1138
PSF113_3356	CDS	+	3952747..3954417	556		Anaerobic dehydrogenases,typically selenocysteine-containing	Pseudomonas stutzeri TS44	ZP_14470659.1	0	413	547
PSF113_3363	CDS	+	3960840..3961766	308		Quinone oxidoreductase(EC 1.6.5.5)	Pseudomonas sp. GM21	ZP_10695681.1	0	292	308
PSF113_3365	CDS	+	3962878..3963765	295	cysB3	Cys regulon transcriptional activator CysB	Pseudomonas sp. GM21	ZP_10695680.1	0	264	295
PSF113_3366	CDS	+	3963931..3964968	345	ditL	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase (EC 4.1.1.45)	Pseudomonas aeruginosa 2192	ZP_04934604.1	0	279	337
PSF113_3367	CDS	-	3965013..3965858	281		3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	Pseudomonas sp. GM21	ZP_10695668.1	0	268	281
PSF113_3368	CDS	+	3966280..3967941	553		putative exported protein	Pseudomonas aeruginosa 2192	ZP_04934658.1	0	368	555
PSF113_3370	CDS	+	3969429..3970559	376		glycosyl hydrolase	Pseudomonas sp. GM21	ZP_10695665.1	0	319	376
PSF113_3372	CDS	+	3973174..3974145	323		Lactoylglutathione lyase-related lyase	Glaciicola sp. 4H-3-7+YE-5	YP_004432635.1	0	247	320
PSF113_3373	CDS	+	3974142..3974960	272		Enoyl-CoA hydratase (EC 4.2.1.17)	Pseudomonas sp. GM21	ZP_10695662.1	6E-168	253	272
PSF113_3375	CDS	+	3975905..3977509	534		Beta-carotene ketolase(EC 1.14.-.-)	Marinobacter adhaerens HP15	YP_005883709.1	0	420	529

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_3376	CDS	-	3977567..3978232	221		transcriptional regulator, TetR family	Pseudomonas sp. GM21	ZP_10695659.1	7E-150	208	221
PSF113_3377	CDS	+	3978415..3979692	425	ditQ	Cytochrome P450	Marinobacter adhaerens HP15	YP_005883710.1	0	273	418
PSF113_3378	CDS	+	3979743..3980774	343		hypothetical protein	Pseudomonas mendocina DLHK	ZP_15951229.1	0	302	343
PSF113_3380	CDS	+	3981696..3982997	433		Permeases of the major facilitator superfamily	Pseudomonas sp. GM21	ZP_10695655.1	0	382	433
PSF113_3381	CDS	+	3983021..3983371	116		hypothetical protein	Pseudomonas sp. GM21	ZP_10695654.1	3E-74	106	116
PSF113_3382	CDS	-	3983428..3984261	277		short-chain dehydrogenase reductase sdr	Herbaspirillum sp. CF444	ZP_10722646.1	9E-87	136	275
PSF113_3383	CDS	-	3984344..3985579	411	ethA	Ferredoxin reductase	Pseudomonas stutzeri TS44	ZP_14470697.1	0	341	411
PSF113_3384	CDS	-	3985600..3985920	106		Ferredoxin, 2Fe-2S	Pseudomonas sp. GM21	ZP_10695651.1	2E-68	99	106
PSF113_3385	CDS	-	3985954..3987216	420		major facilitator superfamily mfs_1	Pseudomonas aeruginosa 2192	ZP_04934635.1	0	323	398
PSF113_3386	CDS	+	3987569..3987805	78	ditA3	DitA3	Pseudomonas abietaniphila	AAD21062.1	2E-37	60	77
PSF113_3387	CDS	+	3987851..3988615	254	ditB	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)	Pseudomonas sp. GM21	ZP_10695648.1	2E-173	242	252
PSF113_3388	CDS	+	3988677..3989627	316	ditC	2,3-dihydroxybiphenyl 1,2-dioxygenase (EC 1.13.11.39)	Pseudomonas aeruginosa 2192	ZP_04934631.1	0	263	301
PSF113_3389	CDS	+	3989629..3990513	294	ditD	Fumarylacetoacetate hydrolase family protein	Pseudomonas sp. GM21	ZP_10695646.1	0	259	294
PSF113_3390	CDS	+	3990548..3990832	94	ditE	DitE	Pseudomonas sp. GM21	ZP_10695645.1	5E-42	73	83
PSF113_3391	CDS	+	3990897..3991682	261	ditR	Transcriptional regulator, lclR family	Bordetella bronchiseptica Bbr77	CCN03081.1	7E-43	85	235
PSF113_3392	CDS	-	3991692..3992882	396	ditF	3-ketoacyl-CoA thiolase(EC 2.3.1.16)	Marinobacter adhaerens HP15	YP_005883727.1	0	305	382
PSF113_3393	CDS	-	3992882..3993280	132		hypothetical protein	Pseudomonas sp. GM21	ZP_10695642.1	5E-87	124	132
PSF113_3394	CDS	+	3993420..3994121	233	ditG	DitG	Pseudomonas sp. GM21	ZP_10695641.1	6E-150	217	233
PSF113_3395	CDS	+	3994127..3995116	329	ditH	Fumarylacetoacetate hydrolase family protein	Pseudomonas mendocina DLHK	ZP_15951247.1	0	276	325
PSF113_3396	CDS	+	3995231..3996631	466	ditA1	Large subunit naph/bph dioxygenase	Pseudomonas aeruginosa 2192	ZP_04934639.1	0	318	465
PSF113_3397	CDS	+	3996721..3997296	191	ditA2	Biphenyl dioxygenase beta subunit (EC 1.14.12.18)	Pseudomonas sp. GM21	ZP_10695638.1	2E-127	181	191
PSF113_3398	CDS	-	3997382..3998122	246		hypothetical protein	Pseudomonas sp. GM21	ZP_10695637.1	2E-134	208	244
PSF113_3399	CDS	+	3998224..3999024	266	ditI	Putative short-chain dehydrogenase/reductase (EC 1.1.1.100)	Pseudomonas sp. GM21	ZP_10695636.1	0	261	266
PSF113_3400	CDS	-	3999151..4000782	543	ditJ	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	Frankia sp. EUN1f	ZP_06413672.1	2E-177	257	528
PSF113_3401	CDS	+	4000967..4001698	243	ditK	DitK	Pseudomonas sp. GM21	ZP_10695634.1	4E-137	192	196
PSF113_3402	CDS	+	4002263..4003096	277	ditL2	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase (EC 4.1.1.45)	Pseudomonas sp. GM21	ZP_10695633.1	0	265	277
PSF113_3403	CDS	+	4003096..4003947	283	ditM	Fumarylacetoacetate hydrolase family protein	Pseudomonas sp. GM21	ZP_10695632.1	0	269	283
PSF113_3404	CDS	+	4003961..4004863	300	ditN	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	Pseudomonas sp. GM21	ZP_10695631.1	0	289	300
PSF113_3405	CDS	+	4004860..4006035	391	ditO	3-ketoacyl-CoA thiolase(EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Burkholderia xenovorans LB400	YP_555845.1	0	283	389
PSF113_3407	CDS	+	4006680..4007957	425	ditQ2	Cytochrome P450	Glaciecola sp. 4H-3-7+YE-5	YP_004432599.1	0	302	424
PSF113_3408	CDS	+	4008071..4009378	435		BarH	Glaciecola sp. 4H-3-7+YE-5	YP_004432600.1	0	345	435
PSF113_3409	CDS	+	4009615..4010637	340		FadE30	Pseudomonas mendocina DLHK	ZP_15951261.1	0	280	322
PSF113_3410	CDS	+	4010637..4011710	357		Acyl-CoA dehydrogenase,short-chain specific	Pseudomonas sp. GM21	ZP_10696717.1	0	319	357
PSF113_3411	CDS	+	4011707..4012507	266		Enoyl-CoA hydratase (EC 4.2.1.17)	Pseudomonas sp. GM21	ZP_10696716.1	0	258	266
PSF113_3412	CDS	+	4012550..4013674	374		Acyl-CoA dehydrogenase,short-chain specific (EC 1.3.99.2)	Pseudomonas aeruginosa 2192	ZP_04934607.1	0	344	374
PSF113_3413	CDS	+	4013699..4014250	183		Glutathione peroxidase(EC 1.11.1.9)	Pseudomonas sp. GM21	ZP_10696714.1	6E-115	159	183
PSF113_3414	CDS	+	4014253..4015113	286		Pantoate--beta-alanine ligase (EC 6.3.2.1)	Pseudomonas sp. GM21	ZP_10696713.1	2E-168	231	286
PSF113_3415	CDS	+	4015202..4016059	285		methyl-accepting chemotaxis protein	Pseudomonas sp. GM21	ZP_10696712.1	0	256	285
PSF113_3416	CDS	+	4016066..4017271	401		major facilitator superfamily transporter	Pseudomonas sp. GM21	ZP_10696710.1	0	362	401
PSF113_3439	CDS	+	4050097..4051026	309	pnpR	Transcriptional regulator, LysR family	Pseudomonas sp. Ny2402	ACZ51387.1	0	263	308
PSF113_3440	CDS	+	4051143..4051637	164	pnpC1	PnpC1	Pseudomonas sp. GM78	ZP_10624263.1	4E-107	149	164

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_3441	CDS	+	4051691..4052710	339	pnpC2	FIG00454641: hypothetical protein	Burkholderia sp. CCGE1002	YP_003609571.1	0	271	339
PSF113_3442	CDS	+	4052805..4054268	487	pnpD	Aldehyde dehydrogenase(EC 1.2.1.3)	Burkholderia ambifaria AMMD	YP_777096.1	0	394	488
PSF113_3443	CDS	+	4054277..4055344	355	pnpF	Alcohol dehydrogenase (EC 1.1.1.1)	Pseudomonas sp. WBC-3	ABU50914.1	0	327	355
PSF113_3444	CDS	+	4055420..4056292	290	dio1	Dio1	Pseudomonas sp. WBC-3	ABU50913.1	0	247	290
PSF113_3445	CDS	+	4056296..4056607	103	yciL	YciL	Pseudomonas sp. GM78	ZP_10624268.1	1E-60	90	103
PSF113_3446	CDS	+	4056609..4056956	115	pnpX2	PnpX2	Pseudomonas sp. GM78	ZP_10624269.1	2E-63	91	111
PSF113_3450	CDS	-	4060077..4060928	283	hpcE	HpcE	Bradyrhizobium sp. WSM471	ZP_09649218.1	5E-95	150	281
PSF113_3451	CDS	+	4061690..4062052	120		4-hydroxyphenylacetate 3-monooxygenase reductase component	Granulibacter bethesdensis CGDNIH1	YP_744202.1	1E-33	58	112
PSF113_3452	CDS	-	4062156..4062659	167		carboxymuconolactone decarboxylase	Alicyclophilus denitrificans BC	YP_004128766.1	2E-65	107	165
PSF113_3456	CDS	+	4066299..4067786	495		3-(3-hydroxy-phenyl)propionate hydroxylase	Agrobacterium vitis S4	YP_002539780.1	0	314	488
PSF113_3457	CDS	+	4067890..4068525	211		arylmalonate decarboxylase	Novosphingobium sp. Rr 2-17	ZP_10362077.1	2E-70	114	207
PSF113_3459	CDS	+	4070563..4070994	143		putative exported protein	Agrobacterium vitis S4	YP_002539772.1	2E-44	75	139
PSF113_3460	CDS	-	4071116..4071901	261		mhp operon transcriptional activator	Agrobacterium vitis S4	YP_002539763.1	3E-66	107	253
PSF113_3463	CDS	+	4074715..4075464	249		carboxymuconolactone decarboxylase	Agrobacterium vitis S4	YP_002539775.1	1E-71	114	213
PSF113_3466	CDS	+	4077150..4077575	141		carboxymuconolactone decarboxylase	Agrobacterium vitis S4	YP_002539778.1	1E-55	88	137
PSF113_3467	CDS	+	4077610..4078158	182		Biphenyl-2,3-diol 1,2-dioxygenase	Novosphingobium sp. Rr 2-17	ZP_10362079.1	6E-56	86	171
PSF113_3469	CDS	+	4079513..4079845	110		nucleic-acid-binding protein containing a zn-ribbon	Novosphingobium sp. Rr 2-17	ZP_10362075.1	1E-27	50	80
PSF113_3476	CDS	-	4087478..4088362	294	ligR	Transcriptional regulator ligR, LysR family	Pseudomonas putida W619	YP_001748333.1	2E-141	201	288
PSF113_3477	CDS	-	4088390..4089316	308		3-hydroxyisobutyrate dehydrogenase-related beta-hydroxyacid dehydrogenase	Pseudomonas sp. M47T1	ZP_10149287.1	1E-113	192	282
PSF113_3479	CDS	-	4090410..4091126	238		Putative siderophore biosynthesis protein, related to 2-demethylmenaquinone methyltransferase	Serratia proteamaculans 568	YP_001478322.1	5E-127	177	235
PSF113_3480	CDS	-	4091123..4091857	244		FIG00959802: hypothetical protein	Pseudomonas syringae pv. aesculi str. NCPPB 3681	ZP_06460101.1	8E-168	223	244
PSF113_3481	CDS	+	4092011..4093234	407		Transcriptional regulator, LysR family	Pseudomonas sp. GM78	ZP_10623222.1	0	270	403
PSF113_3483	CDS	+	4094091..4095257	388		Lysophospholipase (EC 3.1.1.5)	Desulfurispirillum indicum S5	YP_004113620.1	3E-171	233	379
PSF113_3497	CDS	-	4109894..4111024	376		Multidrug resistance efflux pump	Agrobacterium sp. H13-3	YP_004280648.1	6E-143	216	363
PSF113_3498	CDS	-	4111098..4111544	148		putative membrane protein	Pseudomonas sp. GM18	ZP_10704146.1	2E-69	106	144
PSF113_3563	CDS	+	4185660..4186736	358	cheB3	Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61)	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10435492.1	0	287	354
PSF113_3573	CDS	-	4200744..4201667	307		Transcriptional regulator, LysR family	Pseudomonas sp. GM79	ZP_10614327.1	1E-145	206	300
PSF113_3574	CDS	-	4201701..4202675	324		Quinone oxidoreductase(EC 1.6.5.5)	Pseudomonas syringae pv. aceris str. M302273	ZP_16733109.1	3E-172	244	324
PSF113_3582	CDS	+	4212409..4213761	450		2-methylcitrate dehydratase	Alcanivorax dieselolei B5	YP_006821692.1	0	304	434
PSF113_3583	CDS	-	4213812..4215017	401	xis	Xis	Alcanivorax dieselolei B5	YP_006821700.1	1E-158	232	389
PSF113_3584	CDS	+	4215219..4216565	448		Citrate transporter	Pseudomonas mendocina NK-01	YP_004380609.1	0	264	423
PSF113_3586	CDS	+	4218078..4219106	342		D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	Pseudomonas sp. Ag1	ZP_10477217.1	5E-139	211	332
PSF113_3587	CDS	+	4219103..4220470	455		3-methylaspartate ammonia-lyase, glutamate mutase	Pseudomonas sp. Ag1	ZP_10477218.1	0	320	452
PSF113_3588	CDS	+	4220472..4220798	108		hypothetical protein	Pseudomonas sp. Ag1	ZP_10477219.1	2E-36	56	100
PSF113_3590	CDS	+	4221775..4223043	422		secretory lipase	Alcanivorax dieselolei B5	YP_006821703.1	1E-180	274	403
PSF113_3656	CDS	-	4302243..4303679	478		drug resistance mfs transporter	Burkholderia multivorans ATCC BAA-247	ZP_15919178.1	4E-159	264	437
PSF113_3660	CDS	+	4315325..4316173	282	lkcD	LkcD	Hahella chejuensis KCTC 2396	YP_434659.1	1E-97	149	283
PSF113_3663	CDS	+	4318277..4325512	2411	lkcF	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Hahella chejuensis KCTC 2396	YP_434656.1	2E-50	182	571
PSF113_3666	CDS	+	4329095..4330678	527	lkcJ	LkcJ	Pseudomonas sp. Ag1	ZP_10474276.1	0	433	525

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_4073	CDS	-	4801978..4802601	207		putative lipoprotein	Pseudomonas protegens Pf-5	YP_260543.1	1E-51	96	179
PSF113_4191	CDS	-	4918510..4918704	64		hypothetical protein	Pseudomonas sp. GM79	ZP_10614059.1	1E-32	58	64
PSF113_4279	CDS	+	5007641..5008678	345		DNA-cytosine methyltransferase (EC 2.1.1.37)	Pseudomonas syringae pv. tomato Max13	ZP_07234026.1	0	287	344
PSF113_4283	CDS	+	5013638..5014042	134		Gifsy-2 prophage protein	Pseudomonas fluorescens Bbc6R8	ZP_15597875.1	2E-43	71	97
PSF113_4290	CDS	-	5018559..5021138	859		Methyl-accepting chemotaxis protein	Pseudomonas sp. GM41(2012)	ZP_10670376.1	0	351	534
PSF113_4291	CDS	-	5021154..5021276	40		hypothetical protein	Pseudomonas syringae pv. syringae FF5	ZP_06500139.1	1E-08	23	40
PSF113_4292	CDS	-	5021239..5021565	108		hypothetical protein	Pseudomonas entomophila L48	YP_609626.1	1E-38	62	94
PSF113_4299	CDS	-	5027777..5027926	49		hypothetical protein	Pseudomonas fluorescens WH6	ZP_07773798.1	4E-18	34	49
PSF113_4300	CDS	-	5028086..5028649	187		Baseplate assembly protein V	Pseudomonas syringae pv. tomato K40	ZP_07255094.1	1E-108	152	187
PSF113_4301	CDS	-	5028646..5029170	174		hypothetical protein	Pseudomonas syringae pv. lachrymans str. M302278	ZP_16721365.1	6E-74	123	170
PSF113_4302	CDS	-	5029163..5029825	220		FIG00959540: hypothetical protein	Pseudomonas sp. GM17	ZP_10710365.1	3E-119	165	215
PSF113_4303	CDS	-	5029822..5030136	104		hypothetical protein	Pseudomonas putida GB-1	YP_001667445.1	6E-49	82	104
PSF113_4304	CDS	-	5030139..5031134	331		elements of external origin; phage-related functions and prophages	Pseudomonas mandelii JR-1	ZP_11109272.1	0	292	331
PSF113_4305	CDS	-	5031478..5031822	114		hypothetical protein	Pseudomonas mandelii JR-1	ZP_11112469.1	2E-64	99	114
PSF113_4306	CDS	-	5031819..5032979	386		Prophage Clp protease-like protein	Pseudomonas sp. GM74	ZP_10626716.1	0	324	383
PSF113_4307	CDS	-	5032976..5034457	493		FIG00963359: hypothetical protein	Pseudomonas syringae pv. actinidiae str. M302091	ZP_16713621.1	0	386	493
PSF113_4308	CDS	-	5034457..5034663	68		hypothetical protein	Pseudomonas sp. GM41(2012)	ZP_10670358.1	7E-39	63	68
PSF113_4309	CDS	-	5034665..5036677	670		Phage terminase, large subunit	Pseudomonas fulva 12-X	YP_004473518.1	0	430	606
PSF113_4310	CDS	-	5036682..5037284	200		terminase small subunit	Pseudomonas sp. GM41(2012)	ZP_10670356.1	2E-123	174	200
PSF113_4312	CDS	-	5038288..5038647	119		hypothetical protein	Pseudomonas fluorescens WH6	ZP_07773787.1	2E-66	100	119
PSF113_4313	CDS	-	5038640..5040859	739		DNA primase, phage associated	Pseudomonas sp. GM80	ZP_10611520.1	0	623	739
PSF113_4314	CDS	-	5040849..5041076	75		C4-type zinc finger protein, DksA/TraR family	Pseudomonas syringae pv. lachrymans str. M302278	ZP_16721378.1	6E-33	58	75
PSF113_4315	CDS	-	5041069..5041587	172		FIG00958730: hypothetical protein	Pseudomonas syringae pv. lachrymans str. M302278	ZP_16721379.1	6E-109	153	172
PSF113_4319	CDS	+	5044275..5044859	194		hypothetical protein	Pseudomonas fluorescens Bbc6R8	ZP_15597836.1	5E-93	136	185
PSF113_4320	CDS	+	5044870..5045154	94		DNA-binding protein Roi-related protein	Pseudomonas protegens Pf-5	YP_259102.1	8E-54	83	94
PSF113_4321	CDS	+	5045313..5045642	109		transcriptional regulator	Pseudomonas protegens Pf-5	YP_259101.1	1E-60	92	108
PSF113_4322	CDS	+	5045686..5046102	138		hypothetical protein	Pseudomonas sp. GM74	ZP_10626698.1	2E-44	77	130
PSF113_4323	CDS	+	5046099..5046320	73		hypothetical protein	Pseudomonas fluorescens WH6	ZP_07773778.1	7E-27	51	73
PSF113_4324	CDS	+	5046317..5046859	180		metal dependent phosphohydrolase	Pseudomonas sp. GM41(2012)	ZP_10670343.1	1E-104	148	180
PSF113_4325	CDS	+	5047281..5048489	402		phage integrase	Pseudomonas extremaustralis 14-3 substr. 14-3b	ZP_10438956.1	0	267	336
PSF113_4501	CDS	-	5257976..5259292	438		hipa-like c-terminal domain protein	Pseudomonas putida LS46	ZP_15971311.1	0	277	438
PSF113_4845	CDS	+	5633910..5634398	162		RNA polymerase sigma-70 factor, ECF subfamily	Pseudomonas sp. GM60	ZP_10637073.1	4E-96	138	162
PSF113_4846	CDS	+	5634407..5635354	315		Iron siderophore sensor protein	Pseudomonas sp. GM78	ZP_10618249.1	5E-153	215	312
PSF113_4889	CDS	+	5680747..5680911	54		hypothetical protein	Pseudomonas brassicacearum subsp. brassicacearum NFM421	YP_004356144.1	1E-29	50	54
PSF113_4945	CDS	+	5740706..5740900	64		hypothetical protein	Pseudomonas sp. R81	ZP_11190749.1	3E-27	50	64
PSF113_4946	CDS	+	5741299..5742384	361		filamentation induced by cAMP protein fic	Pseudomonas syringae pv. avellanae str. ISPaVe037	ZP_17811982.1	0	334	361

F113 Locus	Type	Strand	Coordinates	Length (aa)	Gene	Function	Organism	Hit ACC	E-Value	Similarity	Alignment length
PSF113_5105	CDS	-	5915647..5916246	199		Transcriptional regulator, GntR family	<i>Pseudomonas syringae</i> pv. morsprunorum str. M302280	ZP_16662817.1	1E-123	172	199
PSF113_5106	CDS	+	5916647..5917816	389		Mn2+/Fe2+ transporter, NRAMP family	<i>Pseudomonas syringae</i> pv. oryzae str. 1_6	ZP_04586656.1	0	306	389
PSF113_5184	CDS	+	6003200..6005176	658		Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	<i>Pseudomonas</i> sp. GM17	ZP_10707280.1	0	594	661
PSF113_5185	CDS	+	6005173..6006546	457		Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	<i>Pseudomonas aeruginosa</i> ATCC 14886	ZP_15611258.1	2E-143	234	439
PSF113_5186	CDS	+	6006546..6009743	1065		Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)	<i>Pseudomonas stutzeri</i> DSM 4166	YP_005937550.1	0	927	1056
PSF113_5187	CDS	-	6009929..6010915	328		FIG00958850: hypothetical protein	<i>Pseudomonas fluorescens</i> BBc6R8	ZP_15603748.1	0	279	321
PSF113_5191	CDS	-	6013571..6016819	1082		COG0553: Superfamily II DNA/RNA helicases, SNF2 family	<i>Pseudomonas extremaustralis</i> 14-3 substr. 14-3b	ZP_10435057.1	0	1011	1082
PSF113_5192	CDS	-	6016819..6018447	542		putative; ORF located using Glimmer/Genemark	<i>Pectobacterium carotovorum</i> subsp. carotovorum PCC21	YP_006647908.1	5E-152	229	529
PSF113_5193	CDS	-	6018444..6019187	247		COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins	<i>Pseudomonas extremaustralis</i> 14-3 substr. 14-3b	ZP_10435055.1	5E-177	238	247
PSF113_5194	CDS	-	6019201..6021027	608		putative membrane protein	<i>Hafnia alvei</i> ATCC 51873	ZP_09376790.1	0	379	721
PSF113_5316	CDS	+	6149144..6149848	234		hypothetical protein	<i>Pseudomonas aeruginosa</i> PAO1	NP_254115.1	17	40	125
PSF113_5379	CDS	-	6220451..6220741	96		Cro-like protein	<i>Pseudomonas fluorescens</i>	ACT32384.1	5E-63	96	96
PSF113_5380	CDS	-	6220758..6220916	52		hypothetical protein	<i>Pseudomonas fluorescens</i>	ACT32385.1	3E-29	51	52
PSF113_5636	CDS	-	6504147..6505682	511		multidrug resistance efflux protein	<i>Bacillus cereus</i> BAG1X1-2	ZP_17364789.1	3E-163	261	500
PSF113_5637	CDS	-	6505682..6505957	91		hypothetical protein	<i>Photorhabdus asymbiotica</i>	YP_003040022.1	3E-10	29	84
PSF113_5638	CDS	-	6506559..6508595	678		4-amino-4-deoxychorismate synthase, amidotransferase component, aminase component	<i>Rhodococcus erythropolis</i> SK121	ZP_04383376.1	7E-176	302	673
PSF113_5640	CDS	-	6510201..6510953	250	prmC	PrmC	<i>Bacillus cereus</i> BAG1X1-2	ZP_17364784.1	2E-75	110	235
PSF113_5641	CDS	-	6511046..6512476	476	forZ	N-formimidoyl fortimicin A synthase	<i>Pseudomonas fluorescens</i> SBW25	YP_002871412.1	0	293	431
PSF113_5672	CDS	-	6543144..6543617	157		TonB-like protein	<i>Pseudomonas</i> sp. GM78	ZP_10618829.1	6E-46	80	158
PSF113_5730	CDS	+	6602672..6603031	119		Mobile element protein	<i>Pseudomonas syringae</i> pv. tomato str. DC3000	NP_793006.1	3E-79	117	119
PSF113_5813	CDS	+	6705413..6705991	192	tnpR	TnpR	<i>Pseudomonas putida</i>	CAB54047.1	4E-84	118	146
PSF113_5903	CDS	-	6824047..6825018	323	tctC2	Tricarboxylate transport protein TctC	<i>Pseudomonas</i> sp. S9	ZP_09711490.1	0	246	327