Table 1 Annotation of virulence factors in Y148 based on the VFDB database.

Jul_22-1685871124								
VFclass	**Virulence factors**	**Related genes**	**Y148 (Prediction)**	**P.aeruginosa LESB58**	**P.aeruginosa PA7**	**P.aeruginosa PAO1**	**P.fluorescens Pf-5**	**P.mendocina ymp**
			contig_1 (contig_1)	**chromosome (NC_011770)**	**chromosome (NC_009656)**	**chromosome (NC_002516)**	**chromosome (NC_004129)**	**chromosome (NC_009439)**
	Flagella	flaG	-	PLES_42281	PSPA7_4278	PA1093	PFL_1630	Pmen_2834
		fleN	orf05952	PLES_39591	PSPA7_3873	PA1454	PFL_1666	Pmen_2806
		fleQ	orf05682	PLES_42241	PSPA7_4274	PA1097	PFL_1634	Pmen_2829
		fleR	orf05684	PLES_42221	PSPA7_4272	PA1099	PFL_1636	Pmen_2827
		fleS	orf05683	PLES_42231	PSPA7_4273	PA1098	PFL_1635	Pmen_2828
		flgA	orf02080	PLES_17141	PSPA7_1780	PA3350	PFL_4483	Pmen_2853
		flgB	orf05650	PLES_42441	PSPA7_4300	PA1077	PFL_4480	Pmen_2850
		flgC	orf05652	PLES_42431	PSPA7_4299	PA1078	PFL_4479	Pmen_2849
		flgD	orf05653	PLES_42421	PSPA7_4298	PA1079	PFL_4478	Pmen_2848
		flgE	orf05654	PLES_42411	PSPA7_4297	PA1080	PFL_4477	Pmen_2847
		flgF	orf05655	PLES_42401	PSPA7_4296	PA1081	PFL_1613	Pmen_2846
		flgG	orf05656	PLES_42391	PSPA7_4295	PA1082	PFL_1614	Pmen_2845
		flgH	orf05657	PLES_42381	PSPA7_4294	PA1083	PFL_1615	Pmen_2844
		flgI	orf05658	PLES_42371	PSPA7_4293	PA1084	PFL_1616	Pmen_2843
		flgJ	orf05659	PLES_42361	PSPA7_4292	PA1085	PFL_1617	Pmen_2842
		flgK	orf05660	PLES_42351	PSPA7_4291	PA1086	PFL_1618	Pmen_2841
		flgL	orf05661	PLES_42341	PSPA7_4290	PA1087	PFL_1619	Pmen_2840
		flgM	orf02081	PLES_17131	PSPA7_1779	PA3351	PFL_4484	Pmen_2854
		flgN	orf02082	PLES_17121	PSPA7_1778	PA3352	PFL_4485	Pmen_2855
		flhA	orf05950	PLES_39611	PSPA7_3875	PA1452	PFL_1664	Pmen_2808
		flhB	orf05947	PLES_39641	PSPA7_3878	PA1449	PFL_1654	Pmen_2809
		flhF	orf05951	PLES_39601	PSPA7_3874	PA1453	PFL_1665	Pmen_2807
		fliA	orf05953	PLES_39581	PSPA7_3872	PA1455	PFL_1667	Pmen_2805
		fliC	orf05675	PLES_42291	PSPA7_4279	PA1092	PFL_1629	Pmen_2835
		fliD	orf05677	PLES_42271	PSPA7_4277	PA1094	PFL_1631	Pmen_2833
		fliE	orf05685	PLES_42211	PSPA7_4271	PA1100	PFL_1637	Pmen_2826
		fliF	orf05686	PLES_42201	PSPA7_4270	PA1101	PFL_1638	Pmen_2825
		fliG	orf05687	PLES_42191	PSPA7_4269	PA1102	PFL_1639	Pmen_2824
		fliH	orf05688	PLES_42181	PSPA7_4268	PA1103	PFL_1640	Pmen_2823
		fliI	orf05689	PLES_42171	PSPA7_4267	PA1104	PFL_1641	Pmen_2822
		fliJ	orf05690	PLES_42161	PSPA7_4266	PA1105	PFL_1642	Pmen_2821
		fliK	orf05938	PLES_39721	PSPA7_3888	PA1441	PFL_1646	Pmen_2817

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
Adherence		fliL	orf05940	PLES_39711	PSPA7_3885	PA1442	PFL_1647	Pmen_2816
		fliM	orf05941	PLES_39701	PSPA7_3884	PA1443	PFL_1648	Pmen_2815
		fliN	orf05942	PLES_39691	PSPA7_3883	PA1444	PFL_1649	Pmen_2814
		fliO	orf05943	PLES_39681	PSPA7_3882	PA1445	PFL_1650	Pmen_2813
		fliP	orf05944	PLES_39671	PSPA7_3881	PA1446	PFL_1651	Pmen_2812
		fliQ	orf05945	PLES_39661	PSPA7_3880	PA1447	PFL_1652	Pmen_2811
		fliR	orf05946	PLES_39651	PSPA7_3879	PA1448	PFL_1653	Pmen_2810
		fliS	orf05680	PLES_42261	PSPA7_4276*	PA1095	PFL_1632	Pmen_2831
		fliT	orf05681	PLES_42251	PSPA7_4275	PA1096	PFL_1633	Pmen_2830
		motA	orf04400	PLES_53401	PSPA7_5683	PA4954	PFL_0555	Pmen_0624
		motB	orf04401	PLES_53391	PSPA7_5682	PA4953	PFL_0556	Pmen_0625
		motC	orf05958	PLES_39531	PSPA7_3866	PA1460	PFL_1672	Pmen_2800
		motD	orf05959	PLES_39521	PSPA7_3865	PA1461	PFL_1673	Pmen_2799
		motY	orf02242	PLES_15071	PSPA7_1621	PA3526	PFL_4854	Pmen_1393
	LPS O-antigen (P. aeruginosa)	--	orf01872; orf01873; orf01875; orf01876; orf01877; orf01878; orf01879; orf04353	PLES_19081; PLES_19091; PLES_19101; PLES_19111; PLES_19121; PLES_19131; PLES_19141; PLES_19151; PLES_19161; PLES_19171; PLES_19181	PSPA7_1969; PSPA7_1970; PSPA7_1971; PSPA7_1972; PSPA7_1973; PSPA7_1974; PSPA7_1975; PSPA7_1976; PSPA7_1977; PSPA7_1978; PSPA7_1979; PSPA7_1980; PSPA7_1981; PSPA7_1982; PSPA7_1983; PSPA7_1984; PSPA7_1985; PSPA7_1986	PA3141; PA3142; PA3143; PA3144; PA3145; PA3146; PA3147; PA3148; PA3149; PA3150; PA3151; PA3152; PA3153; PA3154; PA3155; PA3156; PA3157; PA3158; PA3159; PA3160	-	-
		fimT	-	PLES_49321	PSPA7_5189	PA4549	-	Pmen_0963
		fimU	orf04823	PLES_49331	PSPA7_5190	PA4550	-	Pmen_0962
		fimV	orf01846	PLES_19441	PSPA7_2018	PA3115	PFL_2069	Pmen_2718
		pilA	orf04850	PLES_49071	PSPA7_5161	PA4525	PFL_5287	Pmen_0777

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
	Type IV pili biosynthesis	pilB	orf04849	PLES_49091	PSPA7_5162	PA4526	-	Pmen_0775
		pilC	orf04848	PLES_49101	PSPA7_5163	PA4527	PFL_5288	Pmen_0774
		pilD	orf04847	PLES_49111	PSPA7_5164	PA4528	PFL_5289	Pmen_0773
		pilE	orf04818	PLES_49391	PSPA7_5196	PA4556	PFL_5311	Pmen_0957
		pilF	orf02544	PLES_11691	PSPA7_1309	PA3805	PFL_4956	Pmen_3502
		pilM	orf04301	PLES_54341	PSPA7_5781	PA5044	PFL_0445	Pmen_0542
		pilN	orf04302	PLES_54331	PSPA7_5780	PA5043	PFL_0446	Pmen_0543
		pilO	orf04303	PLES_54321	PSPA7_5779	PA5042	PFL_0447	Pmen_0544
		pilP	orf04304	PLES_54311	PSPA7_5778	PA5041	PFL_0448	Pmen_0545
		pilQ	orf04305	PLES_54301	PSPA7_5777	PA5040	PFL_0449	Pmen_0546
		pilR	orf04826	PLES_49301	PSPA7_5187	PA4547	PFL_5309	Pmen_0965
		pilS	orf04827	PLES_49291	PSPA7_5186	PA4546	-	Pmen_0966
		pilT	orf03327	PLES_03931	PSPA7_0495	PA0395	PFL_5837	Pmen_4149
		pilU	orf03326	PLES_03941	PSPA7_0496	PA0396	-	Pmen_4148
		pilV	orf04824	PLES_49341	PSPA7_5191	PA4551	-	Pmen_0961
		pilW	orf04822	PLES_49351	PSPA7_5192	PA4552	-	Pmen_0960
		pilX	orf04821	PLES_49361	PSPA7_5193	PA4553	-	Pmen_0959
		pilY1	orf04820	PLES_49371	PSPA7_5194	PA4554	PFL_5312	Pmen_0958
		pilY2	orf04819	PLES_49381	PSPA7_5195	PA4555	-	-
		pilZ	orf01684	PLES_21031	PSPA7_2201	PA2960	-	Pmen_1635
	Type IV pili twitching motility related proteins	chpA	orf03309	PLES_04111	PSPA7_0513	PA0413	PFL_5823	Pmen_0408
		chpB	orf03308	PLES_04121	PSPA7_0514	PA0414	-	Pmen_0409
		chpC	orf03307	PLES_04131	PSPA7_0515	PA0415	PFL_5822	Pmen_0410
		chpD	orf03306	PLES_04141	PSPA7_0516	PA0416	-	-
		chpE	orf03305	PLES_04151	PSPA7_0517	PA0417	-	Pmen_0661
		pilG	orf03314	PLES_04061	PSPA7_0508	PA0408	PFL_5827	Pmen_0403
		pilH	orf03313	PLES_04071	PSPA7_0509	PA0409	PFL_5826	Pmen_0404
		pilI	orf03312	PLES_04081	PSPA7_0510	PA0410	PFL_5825	Pmen_0405
		pilJ	orf03311	PLES_04091	PSPA7_0511	PA0411	PFL_5824	Pmen_0406
		pilK	orf03310	PLES_04101	PSPA7_0512	PA0412	-	Pmen_0407
		phzA1	orf02989	PLES_07171	PSPA7_0888	PA4210	-	-
		phzA2	orf00499	PLES_34251	PSPA7_3385	PA1899	-	-
		phzB1	orf02990	PLES_07161	PSPA7_0888	PA4211	-	-
		phzB2	orf00500	PLES_34241	PSPA7_3384	PA1900	-	-
		phzC1	orf00501; orf02991	PLES_07151	PSPA7_0887	PA4212	-	-
		phzC2	-	PLES_34231	PSPA7_3383	PA1901	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
Antimicrobial activity	Phenazines biosynthesis	phzD1	orf00502; orf02992	PLES_07141	PSPA7_0886	PA4213	-	-
		phzD2	-	PLES_34221	PSPA7_3382	PA1902	-	-
		phzE1	orf00503; orf02993	PLES_07131	PSPA7_0885	PA4214	-	-
		phzE2	-	PLES_34211	PSPA7_3381	PA1903	-	-
		phzF1	orf00504; orf02994	PLES_07121	PSPA7_0884	PA4215	-	-
		phzF2	-	PLES_34201	PSPA7_3380	PA1904	-	-
		phzG1	-	PLES_07111	PSPA7_0883	PA4216	-	-
		phzG2	orf00505; orf02995	PLES_34191	PSPA7_3379	PA1905	-	-
		phzH	orf03684	PLES_00521	-	PA0051	-	-
		phzM	orf02987	PLES_07181	PSPA7_0889	PA4209	-	-
		phzS	orf02996	PLES_07101	PSPA7_0881	PA4217	-	-
Antiphagocytosis	Alginate biosynthesis	alg44	orf02257	PLES_14911	PSPA7_1603	PA3542	PFL_1022	Pmen_1029
		alg8	orf02256	PLES_14921	PSPA7_1604	PA3541	PFL_1023	Pmen_1030
		algA	orf02267	PLES_14821	PSPA7_1594	PA3551	PFL_1013	Pmen_1020
		algC	orf04010	PLES_57171	PSPA7_6098	PA5322	PFL_6054	Pmen_4379
		algD	orf02255	PLES_14931	PSPA7_1605	PA3540	PFL_1024	Pmen_1031
		algE	orf02259	PLES_14891	PSPA7_1601	PA3544	PFL_1020	Pmen_1027
		algF	orf02266	PLES_14831	PSPA7_1595	PA3550	PFL_1014	Pmen_1021
		algG	orf02260	PLES_14881	PSPA7_1600	PA3545	PFL_1019	Pmen_1026
		algI	orf02264	PLES_14851	PSPA7_1597	PA3548	PFL_1016	Pmen_1023
		algJ	orf02265	PLES_14841	PSPA7_1596	PA3549	PFL_1015	Pmen_1022
		algK	orf02258	PLES_14901	PSPA7_1602	PA3543	PFL_1021	Pmen_1028
		algL	orf02262	PLES_14861	PSPA7_1598	PA3547	PFL_1017	Pmen_1024
		algX	orf02261	PLES_14871	PSPA7_1599	PA3546	PFL_1018	Pmen_1025
	Alginate regulation	algP/algR3	orf04082	PLES_56471	PSPA7_5998	PA5253	PFL_5995	Pmen_0287
		algQ	orf04079	PLES_56491	PSPA7_6001	PA5255	PFL_5997	Pmen_0285
		algR	orf04073	PLES_56551	PSPA7_6007	PA5261	PFL_6003	Pmen_0279
		algU	orf05206	PLES_45811	PSPA7_4757	PA0762	PFL_1448	Pmen_1467
		algW	orf04933	PLES_48251	PSPA7_5018	PA4446	PFL_0933	Pmen_0888
		algZ	orf04072	PLES_56561	PSPA7_6008	PA5262	-	Pmen_0278
		mucA	orf05207	PLES_45801	PSPA7_4756	PA0763	PFL_1449	Pmen_1468
		mucB	orf05208	PLES_45791	PSPA7_4755	PA0764	PFL_1450	Pmen_1469
		mucC	orf05209	PLES_45781	PSPA7_4754	PA0765	-	Pmen_1470
		mucD	orf05210	PLES_45771	PSPA7_4753	PA0766	PFL_1451	Pmen_1471
		mucE	orf02799	PLES_09431	PSPA7_1072	PA4033	-	-
		mucP	orf02372	PLES_13861	PSPA7_1490	PA3649	PFL_1183	Pmen_3046

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
Biosurfactant	Rhamnolipid biosynthesis	rhlA	orf02214	PLES_15331	PSPA7_1647	PA3479	-	-
		rhlB	orf02213	PLES_15341	PSPA7_1648	PA3478	-	-
		rhlC	orf05719	PLES_41891	-	PA1130	-	-
Enzyme	Hemolytic phospholipase C	plcH	orf05294	PLES_44741	PSPA7_4676	PA0844	-	-
	Non-hemolytic phospholipase C	plcN	orf02047	PLES_17461	PSPA7_1801	PA3319	PFL_3126	-
	Phospholipase C	plcB	orf03714	PLES_00251	PSPA7_0027	PA0026	-	-
	Phospholipase D	pldA	-	-	-	PA3487	-	-
	Achromobactin biosynthesis and transport	acsA	-	-	PSPA7_3092	-	-	-
		acsB	-	-	PSPA7_3089	-	-	-
		acsC	-	-	-	-	-	-
		acsD	-	-	PSPA7_3094	-	-	-
		cbrA	-	-	-	-	-	-
		cbrB	-	-	-	-	-	-
		cbrC	-	-	-	-	-	-
		cbrD	-	-	-	-	-	-
	Pyochelin receptor	fptA	orf03000	PLES_07061	PSPA7_0879	PA4221	PFL_2293	-
	Pyochelin	pchA	orf03010	PLES_06961	PSPA7_0869	PA4231	PFL_3488	-
		pchB	orf03009	PLES_06971	PSPA7_0870	PA4230	PFL_3489	-
		pchC	orf03008	PLES_06981	PSPA7_0871	PA4229	PFL_3490	-
		pchD	orf03007	PLES_06991	PSPA7_0872	PA4228	PFL_3496	-
		pchE	orf03005	PLES_07011	PSPA7_0874	PA4226	PFL_3493	-
		pchF	orf03004	PLES_07021	PSPA7_0875	PA4225	PFL_3492	-
		pchG	orf03003	PLES_07031	PSPA7_0876	PA4224	-	-
		pchH	orf03002	PLES_07041	PSPA7_0877	PA4223	PFL_3495	-
		pchI	orf03001	PLES_07051	PSPA7_0878	PA4222	PFL_3494	-
		pchR	orf03006	PLES_07001	PSPA7_0873	PA4227	PFL_3497	-
	Pyoverdine receptors	fpvA	orf01044	PLES_28981; PLES_29011; PLES_29041	PSPA7_2861	PA2398	PFL_2391	Pmen_4556
		pvdA	orf01031	PLES_29161	PSPA7_2874	PA2386	PFL_4079	Pmen_2871
		pvdD	-	PLES_28971	-	PA2399	PFL_4094	-

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			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
Iron uptake	Pyoverdine	pvdE	orf01042	PLES_28991; PLES_29021; PLES_29051	PSPA7_2862	PA2397	PFL_4091	-
		pvdF	orf01041	PLES_29061	PSPA7_2863	PA2396	PFL_4090	-
		pvdG	orf01081	PLES_28701	PSPA7_2828	PA2425	-	-
		pvdH	orf01059	PLES_28831	PSPA7_2846	PA2413	PFL_4179	Pmen_2868
		pvdI	orf01046; orf01047; orf01264	PLES_28951	PSPA7_2859	PA2402	PFL_4093	-
		pvdJ	orf01045	PLES_28961	PSPA7_2860	PA2400	-	-
		pvdL	orf01080	PLES_28711	PSPA7_2829	PA2424	PFL_4189	-
		pvdM	orf01038	PLES_29091	PSPA7_2866	PA2393	PFL_4087	-
		pvdN	orf01039	PLES_29081	PSPA7_2865	PA2394	PFL_4088	-
		pvdO	orf01040	PLES_29071	PSPA7_2864	PA2395	PFL_4089	-
		pvdP	orf01037	PLES_29101	PSPA7_2868	PA2392	PFL_4086	-
		pvdQ	orf01030	PLES_29171	PSPA7_2876	PA2385	PFL_2902	-
		pvdS	orf01082	PLES_28691	PSPA7_2827	PA2426	PFL_4190	Pmen_2873
		pvdY	orf01083	PLES_28681	PSPA7_2826	PA2427	PFL_4191	-
	Yersiniabactin	fyuA	-	-	-	-	-	-
		irp1	-	-	-	-	-	-
		irp2	-	-	-	-	-	-
		irp3	-	-	-	-	-	-
		irp4	-	-	-	-	-	-
		irp5	-	-	-	-	-	-
		ybtA	-	-	-	-	-	-
		ybtP	-	-	-	-	-	-
		ybtQ	-	-	-	-	-	-
Protease	Alkaline protease	aprA	orf05844	PLES_40631	PSPA7_4143	PA1249	PFL_2483	-
	Elastase	lasA	orf00467	PLES_34521	PSPA7_3417	PA1871	-	-
		lasB	orf02449	PLES_12581	PSPA7_1397	PA3724	-	-
	Protease IV	prpL	orf02951	PLES_07521	PSPA7_0919	PA4175	-	-
Quorum sensing	Acylhomoserine lactone synthase	hdtS	orf03734	PLES_00041	PSPA7_0005	PA0005	PFL_0011	Pmen_0011
	N-(3-oxo-dodecanoyl)-L-	lasI	orf05928	PLES_39821	PSPA7_3897	PA1432	-	-
		lasR	orf05926	PLES_39841	PSPA7_3898	PA1430	-	-
	N-(3-oxo-hexanoyl)-	ahlI	-	-	-	-	-	-
		ahlR	-	-	-	-	-	-

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			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
	N-(butanoyl)-L-homoserine	rhlI	orf02211	PLES_15361	PSPA7_1650	PA3476	-	-
		rhlR	orf02212	PLES_15351	PSPA7_1649	PA3477	-	-
Regulation	GacS/GacA two-component system	gacA	orf01248	PLES_26021	PSPA7_2613	PA2586	PFL_3563	Pmen_2375
		gacS	orf05383	PLES_43881	PSPA7_4582	PA0928	PFL_4451	Pmen_1730
	Harpins	hopP1	-	-	-	-	-	-
		hrpA1	-	-	-	-	-	-
		hrpA2	-	-	-	-	-	-
		hrpK1	-	-	-	-	-	-
		hrpW1	-	-	-	-	-	-
		hrpZ1	-	-	-	-	-	-
	Hcp secretion island-1 encoded type VI secretion system (H-T6SS)	--	orf03665	PLES_00721	PSPA7_0142	PA0071	PFL_6075	Pmen_2310
		--	orf03664	PLES_00731	PSPA7_0143	PA0072	PFL_6076	Pmen_2311
		--	orf03663	PLES_00741	PSPA7_0144	PA0073	PFL_6077	Pmen_2312
		--	orf03660	PLES_00771	PSPA7_0147	PA0076	PFL_6080	Pmen_2315
		--	orf03658	PLES_00791	PSPA7_0149	PA0078	PFL_6082	Pmen_2317
		--	orf03657	PLES_00801	PSPA7_0150	PA0079	PFL_6083	Pmen_2318
		--	orf03656	PLES_00811	PSPA7_0151	PA0080	PFL_6084	Pmen_2319
		--	orf03653	PLES_00831	PSPA7_0154	PA0082	PFL_6086	Pmen_2321
		--	orf03652	PLES_00841	PSPA7_0155	PA0083	PFL_6087	Pmen_2322
		--	orf03651	PLES_00851	PSPA7_0156	PA0084	PFL_6088	Pmen_2323
		--	orf03649	PLES_00871	PSPA7_0158	PA0086	-	Pmen_2327
		--	orf03648	PLES_00881	PSPA7_0159	PA0087	PFL_6090	Pmen_2328
		--	orf03647	PLES_00891	PSPA7_0160	PA0088	PFL_6091	Pmen_2329
		--	orf03646	PLES_00901	PSPA7_0161	PA0089	PFL_6092	Pmen_2330
		clpV1	orf03645	PLES_00911	PSPA7_0162	PA0090	PFL_6093	Pmen_2331
		fha1	orf03655	PLES_00821	PSPA7_0152	PA0081	PFL_6085	Pmen_2320
		hcp1	orf03650	PLES_00861	PSPA7_0157	PA0085	PFL_6089	Pmen_2324
		icmF1	orf03659	PLES_00781	PSPA7_0148	PA0077	PFL_6081	Pmen_2316
		ppkA	orf03662	PLES_00751	PSPA7_0145	PA0074	PFL_6078	Pmen_2313
		pppA	orf03661	PLES_00761	PSPA7_0146	PA0075	PFL_6079	Pmen_2314
		vgrG1	orf01367; orf03640; orf03644	PLES_00921	PSPA7_0163	PA0091	PFL_6094	-
	P. aeruginosa TTSS translocated effectors	exoS	orf02583	PLES_11331	-	PA3841	-	-
		exoT	orf03692	PLES_00451	-	PA0044	-	-
		exoU	-	-	-	-	-	-
		exoY	orf00804	PLES_31341	-	PA2191	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
	P. aeruginosa TTSS	exsA	orf00298	PLES_36161	-	PA1713	-	-
		exsB	orf00297	PLES_36171	-	PA1712	-	-
		exsC	orf00295	PLES_36181	-	PA1710	-	-
		exsD	orf00299	PLES_36151	-	PA1714	-	-
		exsE	orf00296	-	-	PA1711	-	-
		pcr1	orf00284	PLES_36281	-	PA1699	-	-
		pcr2	orf00285	PLES_36271	-	PA1700	-	-
		pcr3	orf00286	PLES_36261	-	PA1701	-	-
		pcr4	orf00287	PLES_36251	-	PA1702	-	-
		pcrD	orf00288	PLES_36241	-	PA1703	-	-
		pcrG	orf00290	PLES_36221	-	PA1705	-	-
		pcrH	orf00292	-	-	PA1707	-	-
		pcrR	orf00289	PLES_36231	-	PA1704	-	-
		pcrV	orf00291	PLES_36211	-	PA1706	-	-
		popB	orf00293	PLES_36201	-	PA1708	-	-
		popD	orf00294	PLES_36191	-	PA1709	-	-
		popN	orf00283	PLES_36291	-	PA1698	-	-
		pscB	orf00300	PLES_36141	-	PA1715	-	-
		pscC	orf00301	PLES_36131	-	PA1716	-	-
		pscD	orf00302	PLES_36121	-	PA1717	-	-
		pscE	-	PLES_36111	-	PA1718	-	-
		pscF	orf00303	PLES_36101	-	PA1719	-	-
		pscG	orf00304	PLES_36091	-	PA1720	-	-
		pscH	orf00305	PLES_36081	-	PA1721	-	-
		pscI	orf00306	PLES_36071	-	PA1722	-	-
		pscJ	orf00307	PLES_36061	-	PA1723	-	-
		pscK	orf00308	PLES_36051	-	PA1724	-	-
		pscL	orf00309	PLES_36041	-	PA1725	-	-
		pscN	orf00282	PLES_36301	-	PA1697	-	-
		pscO	orf00280	PLES_36311	-	PA1696	-	-
		pscP	orf00281	-	-	PA1695	-	-
		pscQ	orf00278	PLES_36321	-	PA1694	-	-
		pscR	orf00279	PLES_36331	-	PA1693	-	-
		pscS	orf00277	PLES_36341	-	PA1692	-	-
		pscT	orf00276	PLES_36351	-	PA1691	-	-
		pscU	orf00275	PLES_36361	-	PA1690	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
Secretion system		avrB2	-	-	-	-	-	-
		avrB3	-	-	-	-	-	-
		avrB4-1	-	-	-	-	-	-
		avrB4-2	-	-	-	-	-	-
		avrD1	-	-	-	-	-	-
		avrE1	-	-	-	-	-	-
		avrPto1	-	-	-	-	-	-
		avrRpm1	-	-	-	-	-	-
		avrRps4	-	-	-	-	-	-
		hopA1	-	-	-	-	-	-
		hopAA1'	-	-	-	-	-	-
		hopAA1-1	-	-	-	-	-	-
		hopAA1-2	-	-	-	-	-	-
		hopAA1	-	-	-	-	-	-
		hopAB1	-	-	-	-	-	-
		hopAB2	-	-	-	-	-	-
		hopAB3'	-	-	-	-	-	-
		hopAC1	-	-	-	-	-	-
		hopAC	-	-	-	-	-	-
		hopAD1	-	-	-	-	-	-
		hopAE1	-	-	-	-	-	-
		hopAF1	-	-	-	-	-	-
		hopAG1	-	-	-	-	-	-
		hopAG	-	-	-	-	-	-
		hopAH1	-	-	-	-	-	-
		hopAH2-1	-	-	-	-	-	-
		hopAH2-2	-	-	-	-	-	-
		hopAH2	-	-	-	-	-	-
		hopAI1'	-	-	-	-	-	-
		hopAI1	-	-	-	-	-	-
		hopAJ1	-	-	-	-	-	-
		hopAJ2	-	-	-	-	-	-
		hopAK1	-	-	-	-	-	-
		hopAM1-1	-	-	-	-	-	-
		hopAM1-2	-	-	-	-	-	-
		hopAN1	-	-	-	-	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
	P. syringae TTSS effectors	hopAO1	-	-	-	-	-	-
		hopAP1	-	-	-	-	-	-
		hopAQ1	-	-	-	-	-	-
		hopAS1'	-	-	-	-	-	-
		hopAS1	-	-	-	-	-	-
		hopAT1'	-	-	-	-	-	-
		hopAT1	-	-	-	-	-	-
		hopAU1	-	-	-	-	-	-
		hopAV1	-	-	-	-	-	-
		hopAW1	-	-	-	-	-	-
		hopB1	-	-	-	-	-	-
		hopC1	-	-	-	-	-	-
		hopD1	-	-	-	-	-	-
		hopD	-	-	-	-	-	-
		hopE1	-	-	-	-	-	-
		hopF2	-	-	-	-	-	-
		hopF3	-	-	-	-	-	-
		hopG1	-	-	-	-	-	-
		hopH1	-	-	-	-	-	-
		hopI1	-	-	-	-	-	-
		hopJ1	-	-	-	-	-	-
		hopK1	-	-	-	-	-	-
		hopL1	-	-	-	-	-	-
		hopM1'	-	-	-	-	-	-
		hopM1	-	-	-	-	-	-
		hopN1	-	-	-	-	-	-
		hopO1-1	-	-	-	-	-	-
		hopO1-3'	-	-	-	-	-	-
		hopP1-2	-	-	-	-	-	-
		hopQ1-1	-	-	-	-	-	-
		hopQ1-2	-	-	-	-	-	-
		hopQ1	-	-	-	-	-	-
		hopR1	-	-	-	-	-	-
		hopS1'	-	-	-	-	-	-
		hopS2	-	-	-	-	-	-
		hopT1-1	-	-	-	-	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
		hopT1-2	-	-	-	-	-	-
		hopT2	-	-	-	-	-	-
		hopU1	-	-	-	-	-	-
		hopV1	-	-	-	-	-	-
		hopW1-1	-	-	-	-	-	-
		hopW1-2	-	-	-	-	-	-
		hopX1	-	-	-	-	-	-
		hopY1	-	-	-	-	-	-
		hopZ3	-	-	-	-	-	-
	P. syringae TTSS	hrcC	-	-	-	-	-	-
		hrcJ	-	-	-	-	-	-
		hrcN	-	-	-	-	-	-
		hrcQa	-	-	-	-	-	-
		hrcQb	-	-	-	-	-	-
		hrcR	-	-	-	-	-	-
		hrcS	-	-	-	-	-	-
		hrcT	-	-	-	-	-	-
		hrcU	-	-	-	-	-	-
		hrcV	-	-	-	-	-	-
		hrpB	-	-	-	-	-	-
		hrpD	-	-	-	-	-	-
		hrpE	-	-	-	-	-	-
		hrpF	-	-	-	-	-	-
		hrpG	-	-	-	-	-	-
		hrpJ	-	-	-	-	-	-
		hrpL	-	-	-	-	-	-
		hrpO	-	-	-	-	-	-
		hrpP	-	-	-	-	-	-
		hrpQ	-	-	-	-	-	-
		hrpR	-	-	-	-	-	-
		hrpS	-	-	-	-	-	-
		hrpT	-	-	-	-	-	-
		hrpV	-	-	-	-	-	-
		shcA	-	-	-	-	-	-
		shcE	-	-	-	-	-	-
		shcF	-	-	-	-	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
		shcM	-	-	-	-	-	-
		shcN	-	-	-	-	-	-
		shcS1	-	-	-	-	-	-
		shcS2	-	-	-	-	-	-
		shcV	-	-	-	-	-	-
Toxin	Exolysin	exlA	-	-	PSPA7_4642	-	PFL_4237*	-
		exlB	-	-	PSPA7_4641	-	PFL_4236	-
	Exotoxin A (ETA)	toxA	orf05739	PLES_41711	-	PA1148	-	-
	Hydrogen cyanide production	hcnA	orf00806	PLES_31321	PSPA7_3103	PA2193	PFL_2577	-
		hcnB	orf00807	PLES_31311	PSPA7_3102	PA2194	PFL_2578	-
		hcnC	orf00808	PLES_31301	PSPA7_3101	PA2195	PFL_2579	-
	Phytotoxin coronatine	--	-	-	-	-	-	-
		cfa1	-	-	-	-	-	-
		cfa2	-	-	-	-	-	-
		cfa3	-	-	-	-	-	-
		cfa4	-	-	-	-	-	-
		cfa5	-	-	-	-	-	-
		cfa6	-	-	-	-	-	-
		cfa7	-	-	-	-	-	-
		cfa8	-	-	-	-	-	-
		cfa9	-	-	-	-	-	-
		cfl	-	-	-	-	-	-
		cmaA	-	-	-	-	-	-
		cmaB	-	-	-	-	-	-
		cmaC	-	-	-	-	-	-
		cmaD	-	-	-	-	-	-
		cmaE	-	-	-	-	-	-
		cmaT	-	-	-	-	-	-
		cmaU	-	-	-	-	-	-
		corP	-	-	-	-	-	-
		corR	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-

VFclass	Virulence factors	Related genes	Y148 (Prediction)	P.aeruginosa LESB58	P.aeruginosa PA7	P.aeruginosa PAO1	P.fluorescens Pf-5	P.mendocina ymp
			contig_1 (contig_1)	chromosome (NC_011770)	chromosome (NC_009656)	chromosome (NC_002516)	chromosome (NC_004129)	chromosome (NC_009439)
	Phytotoxin phaseolotoxin	--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		--	-	-	-	-	-	-
		argD	-	-	-	-	-	-
		argK	-	-	-	-	-	-
		cysC1	-	-	-	-	-	-
		dcd2	-	-	-	-	-	-
	Phytotoxin syringomycin	syrB1	-	-	-	-	-	-
		syrB2	-	-	-	-	-	-
		syrC	-	-	-	-	-	-
		syrD	-	-	-	-	-	-
		syrE	-	-	-	-	-	-
		syrF	-	-	-	-	-	-
		syrP	-	-	-	-	-	-
	Phytotoxin syringopeptin	sypA	-	-	-	-	-	-
		sypB	-	-	-	-	-	-
		sypC	-	-	-	-	-	-
	TccC-type insecticidal toxins	--	-	-	-	-	-	-
	Table saved from VFDB (http://www.mgc.ac.cn/VFs/) [Tue Jul 22 08:53:24 2025]							

Note：Strains LESB58, PA7, PAO1, Pf-5 and ymp are the reference strains in the VFDB database.

Table 2 Annotation of virulence factors in Y148 based on the VFDB database.

Protein id	Contig id	Start	Stop	Strand	Element symbol	Element name	Scope	Type	Subtype	Class	Subclass	Method	Target length	Reference sequence length	% Coverage of reference	% Identity to reference	Alignment length	Closest reference accession	Closest reference name	HMM accession	HMM description
NA	contig_1	3E+06	3E+06	+	blaPDC-3	extended-spectrum class C beta-lactamase PDC-3	core	AMR	AMR	BETA-LACTAM	CEPHALOSPORIN	ALLELEX	397	397	100	100	397	WP_003121934.1	extended-spectrum class C beta-lactamase PDC-3	NA	NA
NA	contig_1	3E+06	3E+06	-	aph(3')-IIb	aminoglycoside O-phosphotransferase APH(3')-	core	AMR	AMR	AMINOGLYCOSIDE	KANAMYCIN	BLASTX	268	268	100	99.25	268	WP_003113011.1	aminoglycoside O-phosphotransferase APH(3')-	NA	NA
NA	contig_1	4E+06	4E+06	-	blaOXA-904	OXA-50 family oxacillin-hydrolyzing class D beta-lactamase OXA-904	core	AMR	AMR	BETA-LACTAM	BETA-LACTAM	ALLELEX	262	262	100	100	262	WP_003122322.1	OXA-50 family oxacillin-hydrolyzing class D beta-lactamase OXA-904	NA	NA
NA	contig_1	6E+06	6E+06	-	catB7	type B-4 chloramphenicol O-acetyltransferase	core	AMR	AMR	PHENICOL	CHLORAMPHENICOL	BLASTX	212	212	100	98.58	212	WP_003112709.1	type B-4 chloramphenicol O-acetyltransferase	NA	NA
NA	contig_1	6E+06	6E+06	-	oprD_V359L	Pseudomonas aeruginosa carbapenem resistant OprD	core	AMR	POINT	BETA-LACTAM	CARBAPENEM	POINTX	441	443	100	94.58	443	WP_003112576.1	outer membrane porin OprD	NA	NA
NA	contig_1	6E+06	6E+06	+	fosA	FosA family fosfomycin resistance glutathion	core	AMR	AMR	FOSFOMYCIN	FOSFOMYCIN	EXACTX	135	135	100	100	135	WP_003082280.1	FosA family fosfomycin resistance glutathione transferase	NA	NA