SUPPORTING INFORMATION

Structure and Catalytic Mechanism of LigI: Insight into the Amidohydrolase Enzymes of cog3618 and Lignin Degradation[†]

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Table S1: Predicted LigI genes inferred from homology

GI	Organism	Locus Tag	Max ID (NCBI)
351731544	*Acidovorax radicis N35*	AradN_010100017295	55%
365086078	*Acidovorax sp. NO-1*	KYG_01097	55%
222082169	*Agrobacterium radiobacter K84*	Arad_8733	54%
220914096	*Arthrobacter chlorophenolicus A6*	Achl_3359	54%
359777281	*Arthrobacter globiformis NBRC 12137*	ARGLB_069_00110	55%
116662338	*Arthrobacter sp. FB24*	Arth_4374	51%
329849573	*Asticcacaulis biprosthecum C19*	ABI_24670	55%
119898830	*Azoarcus sp. BH72*	azo2539	56%
356881461	*Azospirillum brasilense Sp245*	AZOBR_p310190	56%
148254161	*Bradyrhizobium sp. BTAi1*	BBta_2700	55%
146339359	*Bradyrhizobium sp. ORS 278*	BRADO2340	53%
365275495	*Bradyrhizobium sp. ORS 285*	BRAO285_120005	55%
302383231	*Brevundimonas subvibrioides ATCC 15264*	Bresu_2121	74%
186472070	*Burkholderia phymatum STM815*	Bphy_3206	53%
341614854	*Citromicrobium sp. JLT1363*	CJLT1_010100007853	76%
264678878	*Comamonas testosteroni CNB-2*	CtCNB1_2743	54%
299532407	*Comamonas testosteroni S44*	CTS44_16478	55%
260222182	*Curvibacter putative symbiont of Hydra magnipapillata*	Csp_F37800	51%
160899880	*Delftia acidovorans SPH-1*	Daci_4447	56%
333913324	*Delftia sp. Cs1-4*	DelCs14_1671	56%
333913996	*Delftia sp. Cs1-4*	DelCs14_2357	55%
90415600	*gamma proteobacterium HTCC2207*	GB2207_09791	58%
254514232	*gamma proteobacterium NOR5-3*	NOR53_1796	58%
254514752	*gamma proteobacterium NOR5-3*	NOR53_1336	51%
332530760	*Hylemonella gracilis ATCC 19624*	HGR_12477	55%
357394384	*Kitasatospora setae KM-6054*	KSE_75150	55%
171060305	*Leptothrix cholodnii SP-6*	Lcho_3635	53%
83309353	*Magnetospirillum magneticum AMB-1*	amb0254	55%
23016548	*Magnetospirillum magnetotacticum MS-1*	Magn03011001	56%
326794128	*Marinomonas mediterranea MMB-1*	Marme_0834	54%
333906780	*Marinomonas posidonica IVIA-Po-181*	Mar181_0382	51%
152997937	*Marinomonas sp. MWYL1*	Mmwyl1_3940	53%
84688103	*Maritimibacter alkaliphilus HTCC2654*	RB2654_21003	56%
87200832	*Novosphingobium aromaticivorans DSM 12444*	Saro_2819	83%
359400972	*Novosphingobium pentaromativorans US6-1*	NSU_3632	84%
334145621	*Novosphingobium sp. PP1Y*	PP1Y_Mpl10379	83%
121604930	*Polaromonas naphthalenivorans CJ2*	Pnap_2029	54%
91790158	*Polaromonas sp. JS666*	Bpro_4322	55%
328544470	*Polymorphum gilvum SL003B-26A1*	SL003B_2852	57%
109900186	*Pseudoalteromonas atlantica T6c*	Patl_3887	52%
325002752	*Pseudonocardia sp. P1*	PseP1_010100028491	52%
337280123	*Ramlibacter tataouinensis TTB310*	Rta_24780	55%
88799839	*Reinekea blandensis MED297*	MED297_02915	54%
116248946	*Rhizobium leguminosarum bv. viciae 3841*	pRL120277	55%
254461538	*Rhodobacteraceae bacterium HTCC2083*	RB2083_2129	57%
356667492	*Rhodococcus opacus PD630*	OPAG_07973	56%
89899146	*Rhodoferax ferrireducens T118*	Rfer_0332	54%
115522775	*Rhodopseudomonas palustris BisA53*	RPE_0749	55%

91975464	*Rhodopseudomonas palustris BisB5*	RPD_0984	56%
316936167	*Rhodopseudomonas palustris DX-1*	Rpdx1_4875	55%
86748000	*Rhodopseudomonas palustris HaA2*	RPB_0874	54%
192293539	*Rhodopseudomonas palustris TIE-1*	Rpal_5181	54%
334343380	*Sphingobium chlorophenolicum L-1*	Sphch_3897	53%
113473776	*Sphingomonas sp. KA1*	pCAR3_098	83%
291452252	*Streptomyces albus J1074*	SSHG_02545	56%
357409779	*Streptomyces flavogriseus ATCC 33331*	Sfla_0533	51%
291436208	*Streptomyces ghanaensis ATCC 14672*	SSFG_01312	54%
329937281	*Streptomyces griseoaurantiacus M045*	SGM_2372	55%
302559216	*Streptomyces griseoflavus Tu4000*	SSRG_02731	53%
359151387	*Streptomyces sp. S4*	StrS4_010100031750	56%
344997778	*Streptomyces sp. SirexAA-E*	SACTE_0140	54%
345015780	*Streptomyces violaceusniger Tu 4113*	Strvi_8545	51%
239820758	*Variovorax paradoxus S110*	Vapar_6113	56%
121607172	*Verminephrobacter eiseniae EF01-2*	Veis_0169	53%
260767376	*Vibrio furnissii CIP 102972*	VFA_000428	57%
153831912	*Vibrio harveyi HY01*	A1Q_3973	53%