



	<i>L. interrogans</i>	<i>L. noguchii</i>	<i>L. kirschneri</i>	<i>L. alstonii</i>	<i>L. weilii</i>	<i>L. alexanderi</i>	<i>L. borgpetersenii</i>	<i>L. santarosai</i>	<i>L. kmetyi</i>	<i>L. fainei</i>	<i>L. broomii</i>	<i>L. wolffii</i>	<i>L. licerasiae</i>	<i>L. inadai</i>	<i>L. wolbachii</i>	<i>L. yamagatae</i>	<i>L. vanthielii</i>	<i>L. terpstuae</i>	<i>L. meyeri</i>	<i>L. biflexa</i>
<i>L. interrogans</i>																				
<i>L. noguchii</i>	96																			
<i>L. kirschneri</i>	97	96																		
<i>L. alstonii</i>	81	80	81																	
<i>L. weilii</i>	82	81	82	82																
<i>L. alexanderi</i>	81	80	81	83	97															
<i>L. borgpetersenii</i>	81	80	82	82	92	94														
<i>L. santarosai</i>	81	81	81	82	90	90	89													
<i>L. kmetyi</i>	78	76	78	78	79	79	78	76												
<i>L. fainei</i>	48	47	48	48	48	48	46	47	48											
<i>L. broomii</i>	47	46	47	46	47	47	45	45	46	92										
<i>L. wolffii</i>	49	49	48	48	47	47	45	47	47	68	69									
<i>L. licerasiae</i>	46	47	46	46	48	48	47	46	47	69	69	80								
<i>L. inadai</i>	46	47	46	46	47	47	45	46	46	92	94	69	70							
<i>L. wolbachii</i>	34	34	34	35	34	34	34	35	35	37	36	36	35	37						
<i>L. yamagatae</i>	35	35	35	33	35	35	35	36	33	35	35	35	34	37	80					
<i>L. vanthielii</i>	33	33	34	34	34	33	33	35	35	37	36	36	33	36	98	79				
<i>L. terpstuae</i>	33	33	33	33	34	34	34	35	34	36	36	36	34	37	93	80	93			
<i>L. meyeri</i>	34	34	34	35	35	35	34	34	33	37	36	35	33	36	92	77	93	90		
<i>L. biflexa</i>	36	36	36	33	35	35	35	35	35	33	35	37	34	35	81	87	79	80	78	

Figure S1. Amino acid sequence identities of LIC1111 from 20 different *Leptospira* strains. The image was generated comparing the sequence of the protein encoded by LIC11112 from *L. interrogans* serovar Copenhageni with other 20 species (pathogenic, intermediate and saprophytic). Similarity is shown in red above 80%, in yellow between 50% and 80% and in green below 50%.

	<i>L. interrogans</i>	<i>L. noguchii</i>	<i>L. kirschneri</i>	<i>L. alstonii</i>	<i>L. weilii</i>	<i>L. alexanderi</i>	<i>L. borgpetersenii</i>	<i>L. santarosai</i>	<i>L. kmetyi</i>	<i>L. fainei</i>	<i>L. broomii</i>	<i>L. wolffii</i>	<i>L. licerasiae</i>	<i>L. inadai</i>	<i>L. wolbachii</i>	<i>L. yamagatae</i>	<i>L. vanthielii</i>	<i>L. terpstuae</i>	<i>L. meyeri</i>	<i>L. biflexa</i>
<i>L. interrogans</i>																				
<i>L. noguchii</i>	98																			
<i>L. kirschneri</i>	99	98																		
<i>L. alstonii</i>	91	93	92																	
<i>L. weilii</i>	92	93	92	96																
<i>L. alexanderi</i>	88	89	88	91	90															
<i>L. borgpetersenii</i>	88	89	89	90	89	95														
<i>L. santarosai</i>	88	89	89	91	89	93	93													
<i>L. kmetyi</i>	91	92	91	94	92	92	92	92												
<i>L. fainei</i>	78	79	78	78	78	77	78	78	80											
<i>L. broomii</i>	78	79	78	78	78	76	78	77	80	99										
<i>L. wolffii</i>	77	78	77	77	78	75	76	75	78	87	87									
<i>L. licerasiae</i>	76	78	77	75	78	73	75	73	76	84	84	90								
<i>L. inadai</i>	77	79	78	78	77	76	77	77	79	99	99	86	84							
<i>L. wolbachii</i>	61	60	61	61	61	60	60	60	61	60	60	60	62	60						
<i>L. yamagatae</i>	61	60	60	61	61	60	60	60	61	60	60	59	61	60	95					
<i>L. vanthielii</i>	61	60	61	61	61	60	60	60	61	60	60	60	62	60	100	95				
<i>L. terpstuae</i>	61	60	61	61	61	60	60	60	61	60	60	60	62	60	99	95	99			
<i>L. meyeri</i>	60	60	60	61	60	60	60	60	60	59	59	59	61	59	99	95	99	99		
<i>L. biflexa</i>	60	60	60	60	61	60	60	60	60	59	59	59	61	59	96	97	96	96	96	

Figure S2. Amino acid sequence identities of LIC11037 from 20 different *Leptospira* strains. The image was generated comparing the sequence of the protein encoded by LIC11112 from *L. interrogans* serovar Copenhageni with other 20 species (pathogenic, intermediate and saprophytic). Similarity is shown in red above 80%, in yellow between 50% and 80% and in green below 50%.

	<i>L. interrogans</i>	<i>L. noguchii</i>	<i>L. kirshneri</i>	<i>L. alstonii</i>	<i>L. weilii</i>	<i>L. alexanderi</i>	<i>L. borgpetersenii</i>	<i>L. santarosai</i>	<i>L. kmetyi</i>	<i>L. fainei</i>	<i>L. broomii</i>	<i>L. wolffii</i>	<i>L. licherasiae</i>	<i>L. inadai</i>	<i>L. wolbachii</i>	<i>L. yanagawae</i>	<i>L. vanthiellii</i>	<i>L. terpstae</i>	<i>L. meyeri</i>	<i>L. biflexa</i>
<i>L. interrogans</i>																				
<i>L. noguchii</i>	91																			
<i>L. kirshneri</i>	93	93																		
<i>L. alstonii</i>	83	84	84																	
<i>L. weilii</i>	83	83	85	92																
<i>L. alexanderi</i>	83	84	84	89	96															
<i>L. borgpetersenii</i>	84	84	84	89	92	94														
<i>L. santarosai</i>	79	83	85	87	86	86	85													
<i>L. kmetyi</i>	81	81	82	82	82	82	82	77												
<i>L. fainei</i>	57	56	58	56	55	55	58	57	59											
<i>L. broomii</i>	54	56	53	53	54	54	54	56	57	93										
<i>L. wolffii</i>	55	56	56	55	57	55	57	57	58	69	70									
<i>L. licherasiae</i>	54	55	56	56	53	54	56	55	54	65	64	73								
<i>L. inadai</i>	59	56	54	54	54	53	53	56	55	92	95	72	63							
<i>L. wolbachii</i>	37	37	37	37	37	37	36	37	37	37	38	39	38	38						
<i>L. yanagawae</i>	37	36	36	35	37	37	37	37	36	38	38	38	38	37	76					
<i>L. vanthiellii</i>	37	36	36	37	36	36	37	37	36	38	38	38	38	38	95	77				
<i>L. terpstae</i>	38	37	37	37	37	37	37	38	36	37	39	39	38	39	91	76	90			
<i>L. meyeri</i>	38	37	37	37	37	37	37	37	37	38	39	39	37	39	86	75	86	88		
<i>L. biflexa</i>	37	36	36	35	36	36	35	36	36	37	38	38	38	38	74	80	75	74	73	

Figure S3. Amino acid sequence identities of LIC20144 from 20 different *Leptospira* strains. The image was generated comparing the sequence of the protein encoded by LIC11112 from *L. interrogans* serovar Copenhageni with other 20 species (pathogenic, intermediate and saprophytic). Similarity is shown in red above 80%, in yellow between 50% and 80% and in green below 50%.

<i>L. interrogans</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAEN	NPGNSGGPAIQD
<i>L. noguchii</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAEN	NPGNSGGPAIQD
<i>L. kirshneri</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAEN	NPGNSGGPAIQD
<i>L. alstonii</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAES	NPGNSGGPAIQD
<i>L. weilii</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAES	NPGNSGGPAIQD
<i>L. alexanderi</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAES	NPGNSGGPAIQD
<i>L. borgpetersenii</i>	LIGNKKILTNAHVVSN	AHDCDLAVLEAES	NPGNSGGPAIQD
<i>L. santarosai</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAES	NPGNSGGPAIQD
<i>L. kmetyi</i>	LIGNKRILTNAHVVSN	AHDCDLAVLEAES	NPGNSGGPAIQD
<i>L. fainei</i>	LIGKKRILTNAHVVSN	AHDCDLAILEAED	NPGNSGGPAIQG
<i>L. broomii</i>	LIGKKRILTNAHVVSN	AHDCDLAILEAED	NPGNSGGPAIQD
<i>L. wolffii</i>	LIGNKRILTNAHVVISN	AHDCDLAVLEAED	NPGNSGGPAIQN
<i>L. licherasiae</i>	LIGNKRILTNAHVVISN	AHDCDLAVLEAED	NPGNSGGPAIQN
<i>L. inadai</i>	LIGKKRILTNAHVVSN	AHDCDLALLEAED	NPGNSGGPAIQD
<i>L. wolbachii</i>	LISKNRILTNAHVVSN	AHDCDLALLEVSD	NPGNSGGPALQN
<i>L. yanagawae</i>	IISKNRILTNAHVVSN	AHDCDLAILEVPD	NPGNSGGPALQD
<i>L. vanthiellii</i>	LISKNRILTNAHVVSN	AHDCDLALLEVSD	NPGNSGGPALQN
<i>L. terpstae</i>	LISKNRILTNAHVVSN	AHDCDLALLEVSD	NPGNSGGPALQN
<i>L. meyeri</i>	LISKNRILTNAHVVSN	AHDCDLALLEVSD	NPGNSGGPALQE
<i>L. biflexa</i>	IIAKNRILTNAHVVSN	AHDCDLAILEVPD	NPGNSGGPALQN

Figure S4. Alignment of the LIC20143 of *L. interrogans* serovar Copenhageni with other *Leptospira* species. Alignment was done using the PROMALS3D tool, which aligns the sequences considering the amino acid sequence and protein domains. The amino acids Histidine (H), Aspartic acid (D) and Serine (S)—highlighted—are present in all 20 species of *Leptospira* selected in this study and represent the residues essential to the catalytic activity.

<i>L. interrogans</i>	ISGNRILTNA H VVSNSY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGR
<i>L. noguchii</i>	ISGNRILTNA H VVSNSY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGK
<i>L. kirshneri</i>	ISGNRILTNA H VVSNSY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGR
<i>L. alstonii</i>	ISGNRILTNA H VVSNSGY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGK
<i>L. weillii</i>	ISGNRILTNA H VVSNSGY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGK
<i>L. alexanderi</i>	ISGNRILTNA H VVISNSY	FLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGK
<i>L. borgpetersenii</i>	ISGNRILTNA H VVSNSNY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQSGK
<i>L. santarosai</i>	ISGNRILTNA H VVSDSSY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGK
<i>L. kmetyi</i>	IAGNRILTNA H VVSNSGY	YLGFD C DLAILKVEE	VNANIIPGY S GGPAIQNGK
<i>L. fainei</i>	IQGNRILTNA H VVAESKF	FLGFD C DLALLKVED	VTANILPGY S GGPAIQNGK
<i>L. broomii</i>	IQGNRILTNA H VVAESKF	FLGFD C DLALLKVED	VTANILPGY S GGPAIQNGQ
<i>L. wolffii</i>	VAGNRILTNA H VISESKY	FLGFD C DLALIKVED	VGANILPGY S GGPAIQNGK
<i>L. licherasiae</i>	IAGNRILTNA H VISESKY	FIGFD C DLALISVED	VGANILPGY S GGPAIQNGK
<i>L. inadai</i>	IQGNRILTNA H VVAESKF	FLGFD C DLALLKVAD	VTANILPGY S GGPAVQNGQ
<i>L. wolbachii</i>	LPNQITILTNA H VVRDAKR	FIGYD C DLALLQVAD	ITANIQPGN S GGPAVQNGK
<i>L. yanagawae</i>	LPNQITILTNA H VVRDAKR	YIGYD C DLALLQVND	ISANIQPGN S GGPAVQNGK
<i>L. vanthielli</i>	LPNQITILTNA H VVRDAKR	FIGYD C DLALLQVTD	ITANIQPGN S GGPAVQNGK
<i>L. terpstae</i>	LSNQITILTNA H VVRDAKR	FIGYD C DLALLQVTD	ITANIQPGN S GGPAVQNGK
<i>L. meyeri</i>	LPNQITILTNA H VVRDAKR	YIGYD C DLALLQVND	INANIQPGN S GGPAVQNGK
<i>L. biflexa</i>	LPNQITILTNA H VVRDAKR	FIGYD C DLALLQVND	ISANIQPGN S GGPAVQNGK

Figure S5. Alignment of the LIC1112 of *L. interrogans* serovar Copenhageni with other *Leptospira* species. Alignment was done using the PROMALS3D tool, which aligns the sequences considering the amino acid sequence and protein domains. The amino acids Histidine (H), Aspartic acid (D) and Serine (S)—highlighted—are present in all 20 species of *Leptospira* selected in this study and represent the residues essential to the catalytic activity.

<i>L. interrogans</i>	VHEKGYIVTNY H VIED	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. noguchii</i>	VHEKGYIVTNY H VIED	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. kirshneri</i>	VHEKGYIVTNY H VIED	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. alstonii</i>	VHEKGYIVTNY H VIEG	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. weilii</i>	VHEKGYIVTNY H VIEG	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. alexanderi</i>	VHEKGYIVTNY H VIEG	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. borgpetersenii</i>	VHEKGYIVTNY H VIEG	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. santarosai</i>	VHEKGYIVTNY H VIEG	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. kmetyi</i>	VHEKGYIVTNY H VIEG	HERA D IALLKIRE	NPGS S GGPLLNI
<i>L. fainei</i>	IHEKGYIVTN F H VIEG	HERA D ISLLKIRE	NPGS S GGPLLNI
<i>L. broomii</i>	IHEKGYIVTN F H VIEG	HERA D ISLLKIRE	NPGS S GGPLLNI
<i>L. wolffii</i>	IHEKGYIVTN F H VIQD	HERA D IALLKIKE	NPGS S GGPLLNI
<i>L. licerasiae</i>	IHEKGYVVTN F H VISD	HERA D IALLKIKE	NPGS S GGPLLNI
<i>L. inadai</i>	IHEKGYIATN F H VIEG	HERA D ISLLKIRE	NPGS S GGPLLNI
<i>L. wolbachii</i>	IDERGFVVTNY H VIKN	HERA D IALLKIPS	NPGS S GGPLLNI
<i>L. yanagawe</i>	IDERGFVVTNY H VIKN	HERA D IALLKIPS	NPGS S GGPLLNI
<i>L. vanthiellii</i>	–	HERA D IALLKIPS	NPGS S GGPLLNI
<i>L. terpstrae</i>	IDERGFVVTNY H VIKN	HERA D IALLKIPS	NPGS S GGPLLNI
<i>L. meyeri</i>	IDERGFVVTNY H VIKN	HERA D IALLKIPS	NPGS S GGPLLNI
<i>L. biflexa</i>	IDERGFVVTNY H VIKN	HERA D IALLKIPS	NPGS S GGPLLNI

Figure S6. Alignment of the LIC11037 of *L. interrogans* serovar Copenhageni with other *Leptospira* species. Alignment was done using the PROMALS3D tool, which aligns the sequences considering the amino acid sequence and protein domains. The amino acids Histidine (H), Aspartic acid (D) and Serine (S)—highlighted—are present in all 20 species of *Leptospira*, except the Histidine that it is not present in *L. vanthiellii*, selected in this study and represent the residues essential to the catalytic activity.

Table S1. NCBI Accession IDs of all CDS for LIC11111, LIC11112, LIC20143, LIC20144 and LIC11037. They are displayed as follows: in red the pathogenic strains, in blue the intermediate ones and in green the saprophyte. All CDS were retrieved from the NCBI database through the Basic Local Alignment Search Tool (BLASTp).

NCBI Accession I.D.					
	LIC11111	LIC11112	LIC20143	LIC20144	LIC11037
<i>L. interrogans</i>	WP_000675215.1	WP_000039575.1	WP_000125234.1	WP_000944569.1	WP_001976240.1
<i>L. kirschneri</i>	WP_004765384.1	WP_004765506.1	WP_082293370.1	WP_004757632.1	EKO60201.1
<i>L. noguchii</i>	WP_017214502.1	WP_061247727.1	WP_004452497.1	WP_004449692.1	WP_002245775.1
<i>L. alstonii</i>	WP_020774559.1	WP_020774560.1	WP_061248069.1	WP_020772440.1	WP_020773847.1
<i>L. weilii</i>	WP_061222824.1	WP_003008403.1	WP_061222378.1	WP_061222350.1	WP_002996538.1
<i>L. alexanderi</i>	WP_078128092.1	WP_010578769.1	WP_078128700.1	WP_078128701.1	WP_078129293.1
<i>L. borgpetersenii</i>	EMO64919.1	EMO65007.1	WP_026054861.1	WP_002732170.1	EMO62864.1
<i>L. santarosai</i>	WP_004478972.1	WP_004491925.1	WP_076637811.1	WP_046943593.1	WP_016753804.1
<i>L. kmetyi</i>	WP_123179212.1	WP_100736899.1	WP_100756608.1	WP_123180574.1	WP_040913868.1
<i>L. fainei</i>	WP_016549290.1	WP_016549246.1	WP_016551179.1	WP_016551249.1	WP_016547636.1
<i>L. broomii</i>	WP_010570309.1	WP_010570308.1	WP_010568511.1	WP_010568510.1	WP_010570471.1
<i>L. wolffii</i>	WP_016544738.1	WP_01654468.1	WP_100758755.1	WP_135701288.1	WP_0165440.1
<i>L. licerasiae</i>	WP_008591953.1	WP_008592017.1	WP_008589276.1	WP_135667780.1	WP_008595422.1
<i>L. inadai</i>	WP_010411362.1	WP_010411360.1	WP_010409673.1	WP_010409676.1	WP_010411939.1
<i>L. wolbachii</i>	WP_015681858.1	WP_015680886.1	WP_015682936.1	WP_015682854.1	EOQ97072.1
<i>L. yanagawe</i>	WP_015677123.1	WP_039928164.1	WP_039929592.1	WP_015679341.1	WP_015678530.1
<i>L. biflexa</i>	WP_012390123.1	WP_012390124.1	WP_041770204.1	WP_012476598.1	WP_012387918.1
<i>L. vanthiellii</i>	WP_002988486.1	WP_002988746.1	WP_002980682.1	WP_002980637.1	EMY68206.1
<i>L. terpstrae</i>	WP_039937265.1	WP_002972837.1	WP_002975534.1	WP_002975543.1	WP_002973171.1
<i>L. meyeri</i>	WP_004786397.1	WP_020776352.1	WP_020777264.1	WP_004788280.1	EKJ86609.1



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