

TABLE S1 Identity of open reading frames (*orf*) present in the *erm*(44)-containing prophage ϕ JW4341-pro of *Staphylococcus xylosus* JW4341 (GenBank/EMBL acc. no. HG796218) with genes present in the GenBank, January 2014, as well as identity to putative domains.

GenBank Designation	Gene Location and Orientation			ExPASy PROSITE Motif (http://prosite.expasy.org/)	NCBI Superfamilies/ Multi-domains (http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi)	NCBI pBLAST result (http://blast.ncbi.nlm.nih.gov/Blast.cgi)	Accession number of highest identity pBLAST alignment to gene	Identity with gene / Coverage with gene (in percent) of pBLAST alignment
	Start	End	Orientation					
<i>orf1</i>	2482	3519	-	no hit	INT_P4[cd00801]	<i>S. equorum</i> Phage integrase	WP_002512109	79/100
<i>orf2</i>	3576	4244	-	PS51257 PROKAR_LIPOPROTEIN Prokaryotic membrane lipoprotein lipid	no hit	hypothetical protein [<i>Staphylococcus carnosus</i> subsp. <i>carnosus</i>]	YP_002634606	39/99
<i>orf3</i>	4296	4919	-	no hit	DUF4352[cl13117]	hypothetical protein [<i>Staphylococcus epidermidis</i>]	WP_002503297	67/83
<i>orf4</i>	5129	5572	-	no hit	DUF955[cl01076]	hypothetical protein [<i>Staphylococcus aureus</i>]	WP_000281659	47/99
<i>orf5</i>	5574	5903	-	PS50943 HTH_CROC1 Cro/C1-type HTH	-HTH_XRE [cd00093] -HipB[COG1396]	Cro/CI family transcriptional regulator [<i>Staphylococcus aureus</i> subsp. <i>aureus</i> COL]	YP_185761	67/95
<i>orf6</i>	6081	6320	+	PS50943 HTH_CROC1 Cro/C1-type HTH	HTH_XRE[cd00093]	Cro/CI family transcriptional regulator [<i>Staphylococcus caprae</i>]	WP_002453556	97/66
<i>orf7</i>	6322	7041	+	no hit	- ORF6C[cl11181] -Phage_pRha super family[cl10713]	Rha family transcriptional regulator [<i>Staphylococcus xylosus</i>] (Phage_pRha)	WP_017722683	53/68
<i>orf8</i>	7153	8004	-	no hit	DUF4393[cl16812]	hypothetical protein StauST398-1_0049 [<i>Staphylococcus</i> phage StauST398-1]	YP_008059022	56/99
<i>orf9</i>	8099	8416	+	no hit	DUF771[cl09962]	hypothetical protein, <i>S. equorum</i> , <i>Staphylococcus</i> phage 2638A	WP_002512120	67/100
<i>orf10</i>	9152	9775	+	no hit	DUF1071[cl05727]	putative topoisomerase [<i>Staphylococcus</i> phage phiRS7]	WP_002482931	89/99

<i>orf11</i>	9772	10221	+	PS50935 SSB Single-strand binding (SSB) domain	Ssb[COG0629]	single-stranded DNA-binding protein [<i>Staphylococcus xylosus</i>]	WP_017722690	93/100
<i>orf12</i>	10233	10898	+	no hit	DUF968[cl18484]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722691	97/100
<i>orf13</i>	10899	11405	+	no hit	HTH_36 super family[cl18666]	hypothetical protein SPTP3103_gp20 [<i>Staphylococcus</i> phage tp310-3]	YP_001429982	79/92
<i>orf14</i>	11630	12403	+	no hit	- AAA[cd00009] -PRK08116 [PRK08116]	DNA replication protein DnaC [<i>Staphylococcus capitis</i>]	WP_002470008	82/92
<i>orf15</i>	12795	13199	+	no hit	DUF1064 [pfam06356]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722696	99/100
<i>orf16</i>	13392	13742	+	no hit	PVL_ORF50 super family[cl06686]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722698	72/100
<i>orf17</i>	13743	14285	+	no hit	no hit	phage protein [<i>Staphylococcus equorum</i>]	WP_002512134	44/100
<i>orf18</i>	14356	14712	+	PS50830 TNASE_3 Thermonuclease domain	SNc super family[cl00140]	hypothetical protein [<i>Staphylococcus</i> sp. AL1]	WP_019469733	77/95
<i>orf19</i>	14705	15016	+	no hit	NTP-PPase_u3[cd11540]	hypothetical protein phiRS7_0056 [<i>Staphylococcus</i> phage phiRS7]	AGW43792	99/92
<i>orf20</i>	15083	15418	-	no hit	Tic20 super family[cl15809]	hypothetical protein [<i>Staphylococcus</i> sp. HGB0015]	WP_016425416	56/95
<i>orf21</i>	15916	16164	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722718	99/100
<i>orf22</i>	16223	16621	+	no hit	no hit	hypothetical protein phiRS7_0061 [<i>Staphylococcus</i> phage phiRS7]	AGW43797	63/99
<i>orf23</i>	16817	17539	+	no hit	-HNHc[cd00085] -COG4639 [COG4639] -McrA[COG1403]	HNH endonuclease [<i>Staphylococcus xylosus</i>]	WP_017722720	98/100
<i>orf24</i>	17638	17946	+	no hit	Terminase_4 super family[cl01525]	Terminase [<i>Staphylococcus xylosus</i>]	WP_017722721	100/100
<i>orf25</i>	17936	19630	+	no hit	COG4626 [COG4626]	terminase [<i>Staphylococcus xylosus</i>]	WP_017722722	100/100
<i>orf26</i>	19634	20905	+	no hit	portal_HK97[TIGR01537]	portal protein [<i>Staphylococcus xylosus</i>]	WP_017722723	99/97
<i>orf27</i>	20856	21626	+	no hit	S14_ClpP_1[cd07016]	peptidase [<i>Staphylococcus xylosus</i>]	WP_017722724	98/100
<i>orf28</i>	21642	22817	+	no hit	Phage_capsid super	phage capsid protein	WP_017722725	87/100

					family[cl12304]	[<i>Staphylococcus xylosus</i>]		
<i>orf29</i>	22890	23177	+	no hit	-head tail connector gp6[cd08054]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722726	97/100
<i>orf30</i>	23363	23518	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722727	96/94
<i>orf31</i>	23511	23936	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722728	97/100
<i>orf32</i>	23933	24328	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722729	96/100
<i>orf33</i>	24361	24993	+	no hit	Phage_tail super family[cl12297]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722730	99/99
<i>orf34</i>	25089	25619	+	no hit	Big_2 super family[cl02708]	tail protein [<i>Staphylococcus xylosus</i>]	WP_017722731	99/100
<i>orf35</i>	25687	26037	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722732	97/100
<i>orf36</i>	26330	32643	+	no hit	tape_meas_TP901 [TIGR01760]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722734	89/99
<i>orf37</i>	32657	33493	+	no hit	Sipho_tail super family[cl17486]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722735	98/100
<i>orf38</i>	34352	35089	+	no hit	Prophage_tail super family [cl12123]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722736	94/97
<i>orf39</i>	35684	38314	+	no hit	-Peptidase_G2 super family [cl13409] -Pectate_lyase_3 [pfam12708]	hypothetical protein [<i>Staphylococcus simiae</i>]	WP_002462649	72/99
<i>orf40</i>	38326	39834	+	no hit	-DUF2479 [pfam10651] -PRK13460 [PRK13460]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722739.	82/100
<i>orf41</i>	39846	40250	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722740	87/95
<i>orf42</i>	40441	40752	+	no hit	no hit	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_002512170	46/89
<i>orf43</i>	40804	41115	+	no hit	Phage_holin_5 super family[cl06138]	hypothetical protein [<i>Staphylococcus xylosus</i>]	WP_017722743	84/88

<i>orf44</i>	41169	42536	+	PS50911 CHAP CHAP domain	-SH3_5 super family[cl17964] -PGRP super family[cl02712] -CHAP super family[cl17642]	hypothetical protein [<i>Staphylococcus equorum</i>]	WP_002512172	72/100
<i>orf44</i>	43396	44298	+	no hit	BCCT super family[cl00569]	hypothetical protein [<i>Staphylococcus xylosus</i>]	YP_001096319	77/99
<i>orf46</i>	44342	45022	+	no hit	BCCT super family[cl00569]	hypothetical protein [<i>Staphylococcus xylosus</i>]	YP_001096319	76/95
<i>orf47</i>	46038	46562	+	no hit	no hit	membrane protein [<i>Staphylococcus xylosus</i>]	WP_017722449	90/100
<i>orf48</i>	47035	47448	-	PS01031 HSP20 Heat shock hsp20 proteins family	IbpA[COG0071]	hypothetical protein [<i>Staphylococcus lentus</i>]	WP_016998738	50/95
<i>orf49</i>	47875	48252	+	PS01031 HSP20 Heat shock hsp20 proteins family	ACD_sHsps-like[cd06464]	heat-shock protein [<i>Staphylococcus delphini</i>]	WP_019166846	36/95
<i>orf 50</i>	48428	48475	+	no hit	no hit	Erm(44) leader peptide 1 [<i>Staphylococcus xylosus</i>]	CDL65149	100/100
<i>orf 51</i>	48503	48556	+	no hit	no hit	Erm(44) leader peptide 2 [<i>Staphylococcus xylosus</i>]	CDL65150	100/100
<i>orf 52</i> [<i>erm(44)</i>]	48617	49348	+	PS01131 Ribosomal RNA adenine dimethylases signature	AdoMet_MTases super family [cl17173]	23S rRNA methylase for macrolide-lincosamide-streptogramin B resistance [<i>Staphylococcus xylosus</i>]	CDL65151	100/100
<i>orf53</i>	51804	52001	+	PS50943 HTH_CROC1 Cro/C1-type HTH domain	HTH_XRE [cd00093]	DNA-binding protein [<i>Virgibacillus halodenitrificans</i>]	WP_019376599	65/92
<i>orf54</i>	51970	52248	+	no hit	Pep_deformylase super family [cl00234]	peptide deformylase [<i>Bacillus</i> sp. 10403023]	WP_010676498	52/90
<i>orf55</i>	52226	52564	+	no hit	Pep_deformylase super family [cl00234]	peptide deformylase [<i>Bacillus fordii</i>]	WP_018705992	63/100
<i>orf56</i>	53780	54976	-	no hit	KefB super family[cl10482]	Kef-type K+ transport system, membrane component [<i>Propionibacterium acidipropionici</i> ATCC 4875]	YP_006981026	56/99