

Supplementary Figures and Text

8 hrs

EAR28894.1 (100%), 59,234.6 Da
hypothetical protein PTD2_07619 [Pseudoalteromonas tunicata D2]
134 exclusive unique peptides, 222 exclusive unique spectra, 701 total spectra, 541/579 amino acids (93% coverage)

MEIMFKKTL	ALAITGVSV	ANAADVKT	TATTAVLQQT	AIGTAKAHAK	GTALGASGVF
GTAADATNSA	NCKALAAAFYG	VSLTKADGTA	AHAVAADGSG	GDVATFADGS	GRELTTVHTT
AANACLATVK	PVLSTTAAKD	GLEYTQATAL	EIKPVIIVAGI	GGYKAEDTLLT	FQFSGAKLDL
TKTTAPSIIV	AAAGQAGAGV	TFDILDITDS	QIRFTVKATT	PANDFVRGNG	ILELSNIFLD
STGLAATTSV	MVNSFGTNTS	GTKFDESTAA	TIVSLLPQYT	TEVTTLLLDAD	IDVVGKDRQQF
ANNLTADVLA	VKHTKNPTSA	NVLVPANTTY	VVTGDFSWAY	APSVDTNKKDG	KLSSAELMAA
NVAVLAGGDD	TVKSLALNAT	NTELTIVTNI	VGAALDATNT	ITFNVPGYDS	GKGTNPMISV
QDFTVKVDTM	SDKSVGSKAV	NMPSLAKTAA	GTWKLNGSVV	VVPYVPPFGPA	TQPILRHTNA
GTQTGDITVR	YMVEGVHTAW	QSLAAAGIKD	AKPGVRDMLG	LVTDALKGEG	YDSTTTGFKV
ALEVVTNVP	KDVFVYGGAK	ITAEGQDRIH	LGTFKTNVN		

26 hrs

EAR28894.1 (100%), 59,234.6 Da
hypothetical protein PTD2_07619 [Pseudoalteromonas tunicata D2]
223 exclusive unique peptides, 360 exclusive unique spectra, 852 total spectra, 543/579 amino acids (94% coverage)

MEIMFKKTL	ALAITGVSV	ANAADVKT	TATTAVLQQT	AIGTAKAHAK	GTALGASGVF
GTAADATNSA	NCKALAAAFYG	VSLTKADGTA	AHAVAADGSG	GDVATFADGS	GRELTTVHTT
AANACLATVK	PVLSTTAAKD	GLEYTQATAL	EIKPVIIVAGI	GGYKAEDTLLT	FQFSGAKLDL
TKTTAPSIIV	AAAGQAGAGV	TFDILDITDS	QIRFTVKATT	PANDFVRGNG	ILELSNIFLD
STGLAATTSV	MVNSFGTNTS	GTKFDESTAA	TIVSLLPQYT	TEVTTLLLDAD	IDVVGKDRQQF
ANNLTADVLA	VKHTKNPTSA	NVLVPANTTY	VVTGDFSWAY	APSVDTNKKDG	KLSSAELMAA
NVAVLAGGDD	TVKSLALNAT	NTELTIVTNI	VGAALDATNT	ITFNVPGYDS	GKGTNPMISV
QDFTVKVDTM	SDKSVGSKAV	NMPSLAKTAA	GTWKLNGSVV	VVPYVPPFGPA	TQPILRHTNA
GTQTGDITVR	YMVEGVHTAW	QSLAAAGIKD	AKPGVRDMLG	LVTDALKGEG	YDSTTTGFKV
ALEVVTNVP	KDVFVYGGAK	ITAEGQDRIH	LGTFKTNVN		

42 hrs

EAR28894.1 (100%), 59,234.6 Da
hypothetical protein PTD2_07619 [Pseudoalteromonas tunicata D2]
212 exclusive unique peptides, 343 exclusive unique spectra, 888 total spectra, 536/579 amino acids (93% coverage)

MEIMFKKTL	ALAITGVSV	ANAADVKT	TATTAVLQQT	AIGTAKAHAK	GTALGASGVF
GTAADATNSA	NCKALAAAFYG	VSLTKADGTA	AHAVAADGSG	GDVATFADGS	GRELTTVHTT
AANACLATVK	PVLSTTAAKD	GLEYTQATAL	EIKPVIIVAGI	GGYKAEDTLLT	FQFSGAKLDL
TKTTAPSIIV	AAAGQAGAGV	TFDILDITDS	QIRFTVKATT	PANDFVRGNG	ILELSNIFLD
STGLAATTSV	MVNSFGTNTS	GTKFDESTAA	TIVSLLPQYT	TEVTTLLLDAD	IDVVGKDRQQF
ANNLTADVLA	VKHTKNPTSA	NVLVPANTTY	VVTGDFSWAY	APSVDTNKKDG	KLSSAELMAA
NVAVLAGGDD	TVKSLALNAT	NTELTIVTNI	VGAALDATNT	ITFNVPGYDS	GKGTNPMISV
QDFTVKVDTM	SDKSVGSKAV	NMPSLAKTAA	GTWKLNGSVV	VVPYVPPFGPA	TQPILRHTNA
GTQTGDITVR	YMVEGVHTAW	QSLAAAGIKD	AKPGVRDMLG	LVTDALKGEG	YDSTTTGFKV
ALEVVTNVP	KDVFVYGGAK	ITAEGQDRIH	LGTFKTNVN		

68 hrs

EAR28894.1 (100%), 59,234.6 Da
hypothetical protein PTD2_07619 [Pseudoalteromonas tunicata D2]
269 exclusive unique peptides, 488 exclusive unique spectra, 1417 total spectra, 540/579 amino acids (93% coverage)

MEIMFKKTL	ALAITGVSV	ANAADVKT	TATTAVLQQT	AIGTAKAHAK	GTALGASGVF
GTAADATNSA	NCKALAAAFYG	VSLTKADGTA	AHAVAADGSG	GDVATFADGS	GRELTTVHTT
AANACLATVK	PVLSTTAAKD	GLEYTQATAL	EIKPVIIVAGI	GGYKAEDTLLT	FQFSGAKLDL
TKTTAPSIIV	AAAGQAGAGV	TFDILDITDS	QIRFTVKATT	PANDFVRGNG	ILELSNIFLD
STGLAATTSV	MVNSFGTNTS	GTKFDESTAA	TIVSLLPQYT	TEVTTLLLDAD	IDVVGKDRQQF
ANNLTADVLA	VKHTKNPTSA	NVLVPANTTY	VVTGDFSWAY	APSVDTNKKDG	KLSSAELMAA
NVAVLAGGDD	TVKSLALNAT	NTELTIVTNI	VGAALDATNT	ITFNVPGYDS	GKGTNPMISV
QDFTVKVDTM	SDKSVGSKAV	NMPSLAKTAA	GTWKLNGSVV	VVPYVPPFGPA	TQPILRHTNA
GTQTGDITVR	YMVEGVHTAW	QSLAAAGIKD	AKPGVRDMLG	LVTDALKGEG	YDSTTTGFKV
ALEVVTNVP	KDVFVYGGAK	ITAEGQDRIH	LGTFKTNVN		

Figure S1. LC-MS/MS coverage of the EAR28894 protein. Identified peptides mapped across the entirety of the sequence, with the exception of an N-terminal segment consisting of the first 13-27 amino acid residues. Residues highlighted in green represent chemical modifications (e.g., deamidation, oxidation).

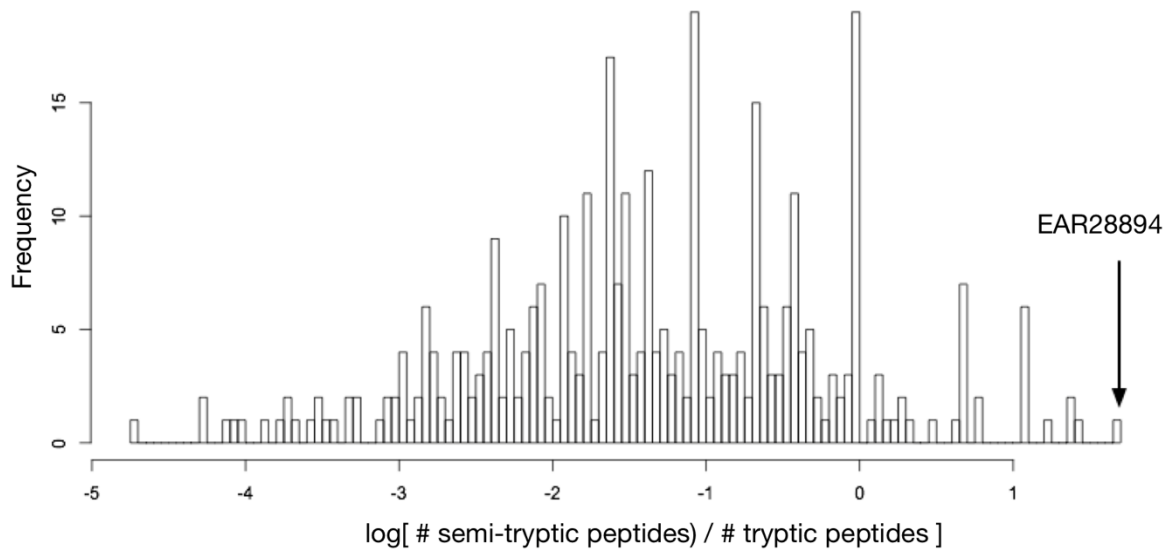


Figure S2. Ratio of semi-tryptic to tryptic peptides across all proteins in LC-MS/MS data. EAR28894 deviates from all other proteins in this regard, and therefore is likely to be most heavily processed by non-trypsin proteases.

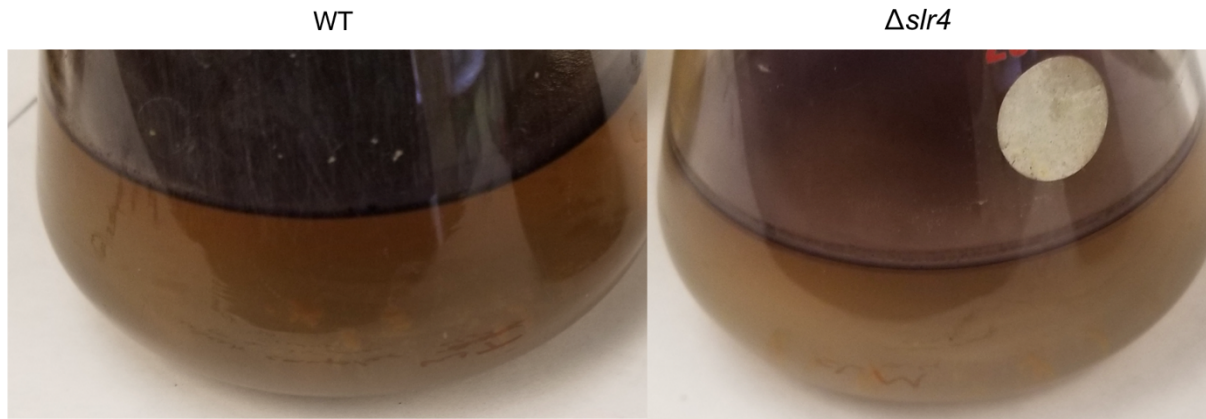


Figure S3. Pellicle biofilms formed by the WT vs $\Delta slr4$ mutant strain. Liquid cultures were grown for 8 hours (shaking) in liquid Difco marine broth media, followed by 72 hours of static (non-shaking) incubation.

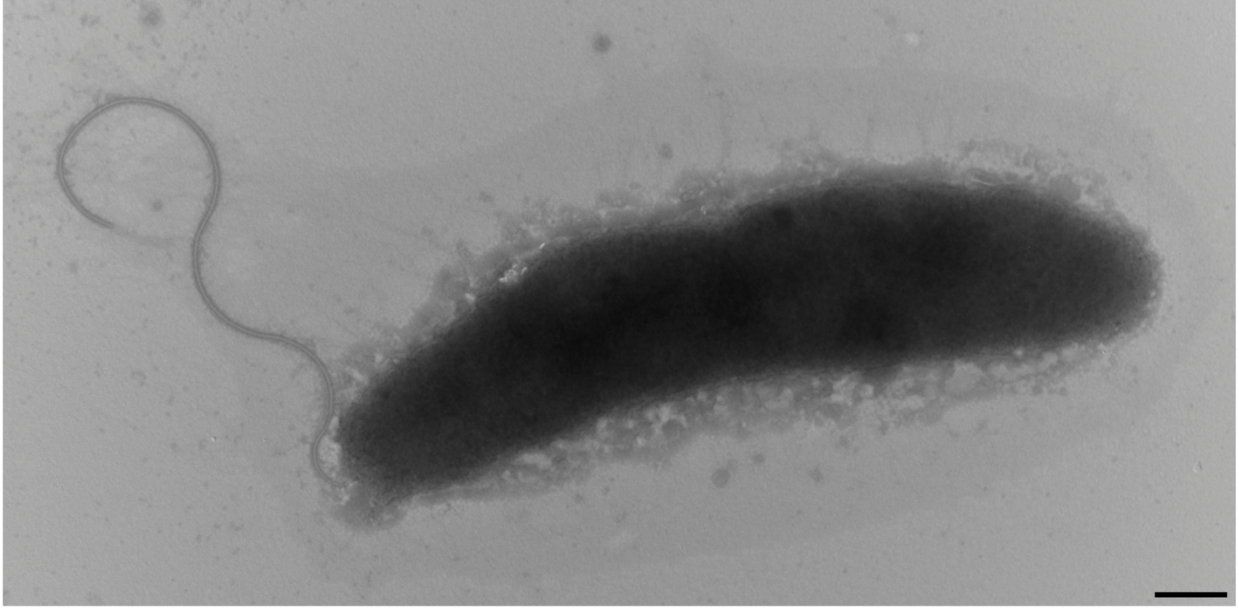


Figure S4. TEM micrograph of a *P. tunicata* cell revealing the presence of a putative outermost capsular layer. Scale bar = 500 nm.

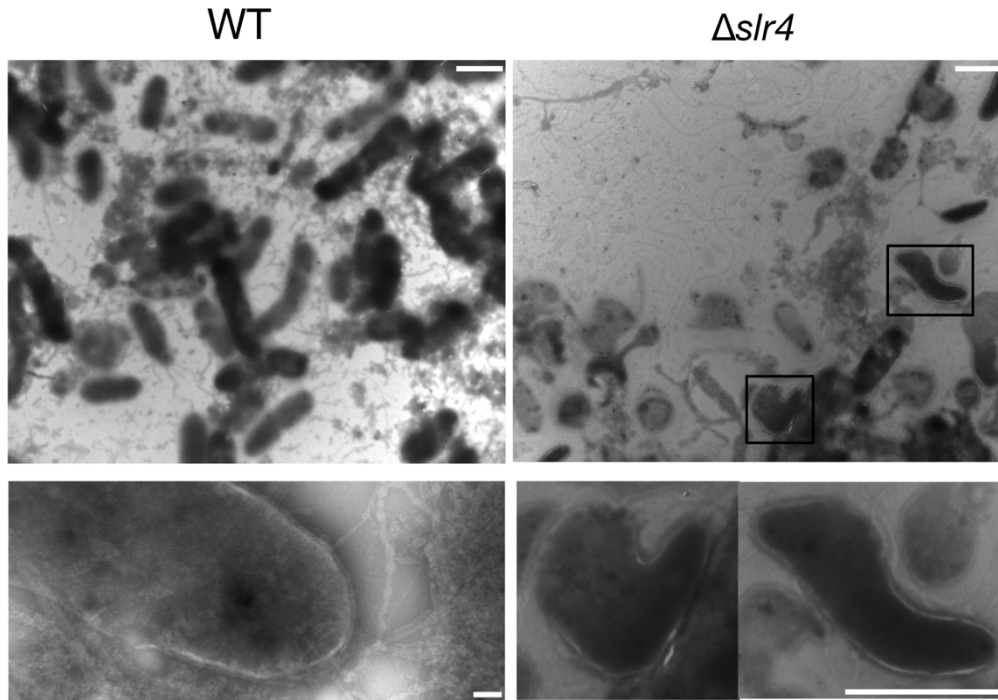


Figure S5. TEM micrographs of 48-hr pellicle biofilms (WT versus $\Delta slr4$ mutant strain). Top left – dense cell clusters in the WT strain interconnected by biofilm matrix material. Bottom left – a WT cell within a biofilm with extracellular biofilm matrix including fibrous structures coated by S-layer material. Top right – image taken from a $\Delta slr4$ biofilm showing a sparser cell distribution that is not connected by S-layer associated matrix material. Bottom right – two examples from the image above of deformed cell shapes. Scale bars are 2 microns, with the exception of the bottom left image where it is 100 nm.

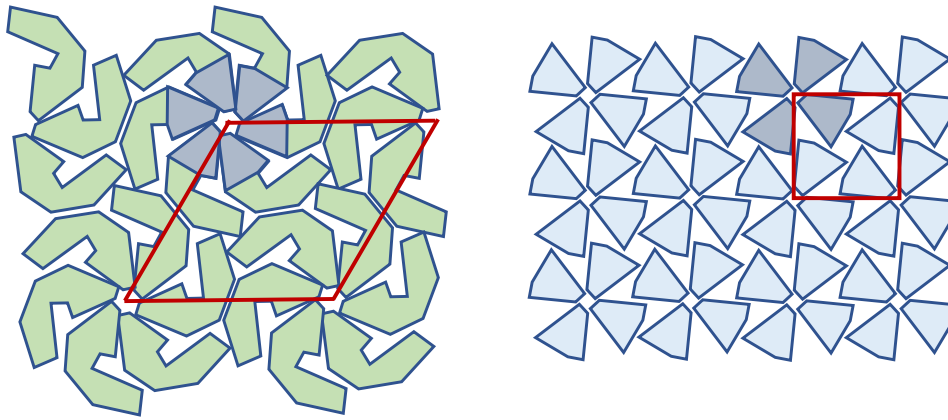


Figure S6. Hypothetical model of Slr4 S-layer lattice assembly (right) compared to *rsaA* S-layer assembly (left). A smaller (truncated) S-layer subunit relative to *rsaA* could alter inter-subunit interactions to result in a four-fold symmetric pattern (right) instead of a six-fold hexagonal symmetry (left). The model is consistent with the top-down view of a square lattice as observed in Figs. 3 and 4, as well as the side-view showing V-shaped cups as shown in Fig. 4.

Table S1. Top proteins identified by LC-MS/MS.

Accession	-10lgP	Cov. (%)	#Pept ides	#Unique	P T M	Avg. Mass (kDa)	Description
EAR28894.1	468.71	93	111	110	Y	59235	hypothetical protein PTD2_07619
EAR29208.1	170.89	20	12	12	Y	68830	hypothetical protein PTD2_09189
EAR29563.1	133.95	8	3	3	Y	60109	flagellin
EAR27917.1	104.01	5	4	4	N	103265	TonB-dependent outer membrane receptor
EAR28105.1	75.5	6	3	3	N	61087 139223	30S ribosomal subunit protein S1
EAR30644.1	56.2	0	2	2	Y	8	fibronectin type III domain protein
EAR27255.1	53.86	2	2	1	N	67577	putative lipoprotein
EAR28194.1	50.54	3	2	2	N	82187	TonB-dependent receptor
EAR26551.1	48.39	3	2	2	Y	105969	sensor histidine kinase/response regulator
EAR27983.1	44.82	3	1	1	N	63152	putative orphan protein

Table S2. Supporting peptides for EAR28894 identification by LC-MS/MS.

Peptide	-10lgP	Mass	L	ppm	m/z	z	RT	F	Scan	#Spec	Start	End	PTM
R.YMVEGVHTAWQS LAAAGIK.D	119.18	2031.025	19	-7.4	1016.512	2	20.76	2	3156	9	491	509	
K.DGLEYTQATALEI KPVIVAGIGGYK.A	117.52	2605.4	25	-8.2	1303.697	2	22.33	2	3432	45	140	164	
R.YM(+15.99)VEGVH TAWQSLAAAGIK.D	111.23	2047.02	19	-5.9	683.3431	3	20.02	2	3018	5	491	509	1
R.DMLGLVTDALKG EGYDSTTTGFK.V	107.36	2418.162	23	-4.7	1210.083	2	24.78	2	3863	13	517	539	
R.HTNAGTQTGDITV R.Y	104.91	1469.722	14	-6.2	735.8639	2	11.4	2	1422	4	477	490	
K.GTNPMISVQDFTV K.V	100.89	1535.765	14	-4.9	768.8862	2	20.01	2	3017	4	413	426	
K.ADGTAAHVAAD GSGGDVATFADGSG R.E	97.12	2403.069	27	-7.9	802.0238	3	14.93	2	2057	9	86	112	
R.DM(+15.99)LGLVT DALKGEGYDSTTTG FK.V	92.65	2434.157	23	-6.5	1218.078	2	20.99	2	3197	6	517	539	1
R.QQFAN(+.98)NLTA DVLAVK.H	91.34	1631.852	15	-6.5	816.9279	2	19.91	2	Ta	3	298	312	2
K.VALEVVTNVPSK DVFVYGGAK.I	90.54	2191.189	21	-7.8	1096.593	2	19.65	2	2941	18	540	560	
K.GTNPM(+15.99)ISV QDFTVK.V	88.79	1551.76	14	-6.3	776.8825	2	18.42	2	2717	3	413	426	1
A.TALEIKPVIVAGIG GYK.A	88.03	1728.019	17	-8.1	865.0095	2	19.96	2	3005	2	148	164	
R.YMVEGVHTAWQ(+ +98)SLAAAGIK.D	88	2032.009	19	-3.6	1017.008	2	21.43	2	3275	3	491	509	2
K.LSSAELMAANVA VLAGDDTVK.S	87.8	2131.083	22	-5.6	1066.543	2	22.34	2	3433	4	352	373	
K.DGLEYTQ(+.98)AT ALEIKPVIVAGIGGY K.A	87.28	2606.384	25	10.3	652.61	4	22.38	2	3441	12	140	164	2
R.QQFANNLTADVL AVK.H	84.32	1630.868	15	-3.8	816.4381	2	20.18	2	3053	4	298	312	
K.TSVTATTAVLQQT AIGTAK.A	83.11	1861.016	19	-7.8	931.5078	2	18.03	2	2646	3	28	46	
R.DMLGLVTDALK.G K.AEDTLTFQFSGAK .L	83.06	1174.627	11	-5.3	588.3175	2	23.81	2	3689	7	517	527	
K.ALAAFYGVSLTK. A	82.59	1413.678	13	-4.9	707.8427	2	19.86	2	2984	31	165	177	
K.LSSAELM(+15.99) AANVAVLAGGDDT VK.S	82.53	1239.686	12	-6.6	620.8463	2	19.91	2	2993	2	74	85	
R.ELTTVHTTAANAC (+57.02)LATVKPVLS TTAAK.D	81.88	2147.078	22	0.2	1074.546	2	19.61	2	2933	4	352	373	1
R.Q(+.98)QFANNLTA DVLAVK.H	81.48	2768.474	27	-5.8	693.1218	4	16.99	2	2429	5	113	139	3
K.DRQQFANNLTAD VLAVK.H	81.46	1631.852	15	-6.5	816.9279	2	20.55	2	3119	2	298	312	2
K.LNGSVVVVPPYVPP GPATQPILR.H	80.18	1901.996	17	-4.4	952.001	2	19.83	2	2976	4	296	312	
K.LN(+.98)GSVVVPP YVFPGPATQPILR.H	79.7	2322.31	22	3.3	775.1131	3	23.76	2	3680	3	455	476	
K.VALEVVTNVPSK. D	79.29	2323.294	22	-4.5	775.4351	3	24.08	2	3738	7	455	476	2
T.ALEIKPVIVAGIGG YK.A	78.86	1254.718	12	-3.7	419.2451	3	16.45	2	2334	13	540	551	
K.GTALGASGVFGT AADATNSANCKA.L Y.MVEGVHTAWQSL AAAGIK.D	77.2	1626.971	16	-5.8	543.3278	3	19.84	2	2979	4	149	164	
R.HTN(+.98)AGTQTG DITVR.Y	76.07	2154.001	24	-5.8	719.0035	3	17.55	2	2553	4	51	74	
K.TTAPSTVAAAGQ AGAGVTFDILDITDS QIR.F	75.15	1867.961	18	-2.8	934.9854	2	20.84	2	3171	2	492	509	
H.AVAADGSGGDVA TFADGSGRE	74.87	1470.706	14	-5.4	736.3564	2	11.78	2	1499	3	477	490	2
A.ANACLATVKPVL STTAAK.D	74.7	3059.577	31	-8.3	1020.858	3	25.6	2	4007	17	183	213	
R.IHLGTFK.T	74.54	1779.802	20	-7.6	890.9016	2	14.95	2	2061	2	93	112	
	73.72	1757.971	18	-6.2	879.9873	2	15.75	2	2208	4	122	139	
	71.1	814.4701	7	0.2	408.2424	2	14.68	2	2009	5	569	575	

K.FDESTAATIVSLLP QYTTEVTLLDADI DVGKDR.Q	70.58	3696.862	34	-5.9	1233.287	3	30.27	2	4799	18	264	297
K.NPITSANVLVPAN(+98)TTYVVTGDFS WAYAPSVDTNK.D	70.2	3499.678	33	-2.1	1167.564	3	23.2	2	3585	1	316	348 2
K.LSSAELMAAN(+98)VAVLAGGDDTVK.S	70.11	2132.067	22	-4	711.6935	3	22.34	2	3434	1	352	373 2
R.GNGILELSNIFLDS TGLAATTSVMVNSF GTNTSGTK.F	68.95	3616.793	36	-5.8	1206.598	3	30.13	2	4775	4	228	263
N.AC(+57.02)LATVK PVLSTTAAK.D	68.72	1629.912	16	-4.3	544.3091	3	15.44	2	2147	4	124	139 3
R.QQ(+98)FANNLTA DVLAVK.H	68.34	1631.852	15	-6.5	816.9279	2	20.58	2	3125	1	298	312 2
K.AVNMPSLAKTAA GTWKLNGSVVVVP YVFPGPATQPILR.H	67.65	3949.165	38	-5.7	988.2929	4	24.14	2	3749	3	439	476
A.TTSVMVNSFSGTNT SGTK.F	67.28	1730.815	17	-7.9	866.4077	2	15.57	2	2172	2	247	263
R.ELTTVHTTAAAC (+57.02).L	66.89	1387.64	13	-5.7	694.8234	2	12.19	2	1575	2	113	125 3
K.FDESTAATIVSLLP Q(+98)YTTEVTLL DADIDVGKDR.Q	65.37	3697.846	34	-2.4	1233.62	3	30.34	2	4811	5	264	297 2
R.HTNAGTQGDITV RYMVEGVHTAWQS LAAAGIK.D	65.29	3482.737	33	-2	697.5532	5	24.95	2	3895	5	477	509
K.SLALNATNELTI VTN(+98)IVGAALD ATN(+98)ITTFNVP YDSGK.G	65.16	3981.011	39	3.6	1328.016	3	33.66	2	5375	2	374	412 2
D.GTAAHAVAADGS GGDVATFADGSGR. E	64.86	2217.005	25	-4.8	740.0052	3	14.56	2	1985	4	88	112
K.SLALNATNELTI VTN(+98)IVGAALD ATNTITFNVPYDS GK.G	64.42	3980.027	39	-8.4	1327.672	3	34.23	2	5471	1	374	412 2
K.NPITSANVLVPANT TYVVTGDFSWAYA PSVDTNK.D	64.3	3498.694	33	-6.7	1167.231	3	23.25	2	3594	2	316	348
K.ATTPAN(+98)DFV R.G	63.73	1091.525	10	-3.4	546.7678	2	13.32	2	1769	4	218	227 2
K.TAAGTWK.L	63.26	733.3759	7	-3.9	367.6938	2	10.43	2	1257	1	448	454
K.DVFVYGGAK.I K.DRQQFAN(+98)N LTADVLAVK.H	62.78	954.481	9	-3.9	478.2459	2	15.63	2	2183	2	552	560
L.GLVTDALKGEGY DSTTTGFK.V	62.56	1902.98	17	-6.8	952.4907	2	19.23	2	2867	1	296	312 2
K.AVNMPSLAKTAA GTWKLN(+98)GSVV VVPYVFPGPATQPIL R.H	62.38	2059.011	20	-7.4	1030.505	2	24.75	2	3857	2	520	539
D.GSGGDVATFADG SGR.E	61.37	3950.149	38	1.1	988.5457	4	24.17	2	3755	1	439	476 2
K.TAAGTWKLNGSV VVVPYVFPGPATQPI LR.H	60.93	1352.596	15	-7.6	677.2999	2	13.8	2	1850	2	98	112
K.GTNPMSVQ(+98) DFTVK.V	60.92	3037.675	29	-6.8	1013.559	3	23.78	2	3684	3	448	476
60.66	1536.749	14	-4	769.3789	2	20.63	2	3133	2	413	426 2	
K.PVIVAGIGYK.A N.GSVVVVPYVFPGP ATQPILR.H	60.45	1072.628	11	-7.3	537.3174	2	17.27	2	2490	2	154	164
C.LATVKPVLSTTAA K.D	60.23	2095.183	20	-7.2	1048.591	2	23.46	2	3629	4	457	476
R.HTNAGTQ(+98)TG DITVRYMVEGVHTA WQSLAAAGIK.D	59.96	1398.845	14	-5.3	700.4259	2	14.29	2	1938	4	126	139
A.AGQAGAGVTFDIL DITDSQIR.F	59.69	3483.721	33	-1.1	871.9364	4	24.94	2	3893	1	477	509 2
K.NPITSANVLVPANT TYVVTGDFSWAYA PSVDTNKDGK.L	59.53	2147.086	21	-3.5	1074.546	2	23.66	2	3663	4	193	213
K.VALEVVTNVP DVF.V	58.83	3798.838	36	-3.3	1267.282	3	22.42	2	3449	2	316	351
58.61	1615.882	15	-11	808.9395	2	20.41	2	3095	2	540	554	

K.SLALNATNELTI VTNIVGAALDATNT ITFNVPGYDSGK.G D.ATNTITFNVPGYD SGK.G	58.31	3979.043	39	-7.8	1327.344	3	33.45	2	5339	5	374	412
R.QQFANN(+.98)LTA DVLAVK.H	57.54	1683.81	16	-7.7	842.906	2	18.43	2	2718	2	397	412
N.ACLATVKPVLSTT AAK.D	57.49	1631.852	15	-3.1	544.9562	3	19.97	2	3007	1	298	312 2
K.AVNMPSLAK.T A.HAVAADGSGGDV ATFADGSGR.E	57.04	1572.891	16	-7.2	787.447	2	15.05	2	2079	4	124	139
F.GPATQPILR.H V.VVPYVFPGPATQP ILR.H	56.55	929.5004	9	-5.3	310.8391	3	15.31	2	2125	3	439	447
R.DM(+15.99)LGLVT DALK.G	55.12	1916.861	21	-2.9	639.9592	3	14.06	2	1896	3	92	112
K.LN(+.98)GSVVVVP YVFPGPATQ(+.98)PI LR.H	54.83	951.5501	9	-7.8	476.7786	2	13.55	2	1809	2	468	476
R.DMLGLVTDALKEG EGYD.S	54.53	1752.993	16	-11	877.494	2	26.21	2	4112	1	461	476
V.TDALKGEGYDST TTGFK.V	54.41	1190.622	11	-3.5	596.316	2	19.54	2	2921	1	517	527 1
L.PQYTTTEVTLLDA DIDVGKDR.Q	54.03	2324.278	22	3.9	582.079	4	24.15	2	3752	4	455	476 2
V.EGVHTAWQSLAA AGIK.D	53.73	1695.803	16	-10.3	848.8998	2	25.56	2	4001	2	517	532
L.EVVTVNPSKDVVFV YGGAK.I	53.2	1789.837	17	-5.7	895.9207	2	24.82	2	3872	1	523	539
K.DAKPGVR.D R.YMVEGVHTAWQS LAAAGIKDAKPGVR .D	52.08	2349.17	21	-7.6	1175.583	2	29.93	2	4741	2	277	297
K.ATTPANDFVR.G	51.6	1637.853	16	-5.4	819.9291	2	20.86	2	3175	1	494	509
V.PFGPATQPILR.H K.DRQ(+.98)QFANN LTADVLAVK.H	51.3	1907.999	18	-6.5	955.0007	2	19.73	2	2958	2	543	560
A.LEVVTVNPSK.D K.AVN(+.98)MPSLA K.T	50.41	741.4133	7	-0.5	248.1449	3	5.63	2	415	3	510	516
K.GEGYDSTTTGFK. V	50.16	2754.428	26	-4.4	689.6111	4	19.1	2	2844	2	491	516
N.NLTADVLAVK.H V.PYVFPGPATQPILR .H	50.01	1090.541	10	-1.8	364.5202	3	14.2	2	1922	4	218	227
R.ELTTVHTTAAN.A	49.77	1195.671	11	-5.3	598.8397	2	23.85	2	3698	3	466	476
K.VDTMSDK.S	49.75	1902.98	17	-6.8	952.4907	2	19.29	2	2877	1	296	312 2
K.ITAEGQDR.I K.LN(+.98)GSVVVVP YVFPGPA.T	49.66	1084.613	10	-4	543.3115	2	16.52	2	2346	1	542	551
K.PVLSTTAAK.D R.YMVEGVHTAWQS .L	49.63	930.4844	9	3.3	466.251	2	14.94	2	2060	1	439	447 2
K.AVNM(+15.99)PSL AKTAAGTWKLNLS VVVVPYVFPGPATQ PILR.H	49.62	1261.546	12	-5.1	631.7772	2	13.02	2	1718	2	528	539
N.AGTQTDITVR.Y K.TTAPSITVAAAGQ (+.98)AGAGVTFDIL DITDSQIR.F	49.32	1042.602	10	-7.3	522.3046	2	17.91	2	2623	2	303	312
K.AVN(+.98)MPSLA K.T	48.9	1554.856	14	-6.9	778.4298	2	26.27	2	4122	4	463	476
K.AVNM(+15.99)PSL AKTAAGTWKLNLS VVVVPYVFPGPATQ PILR.H	48.88	1156.572	11	-0.4	579.2932	2	11.49	2	1445	2	113	123
R.YMVEGVHTAWQ(+ +.98)SLAAAGIKDAK PGVR.D	48.07	794.348	7	-4	398.1797	2	7.75	2	803	2	427	433
K.LN(+.98)GSVVVVP YVFPGPA.T	48.07	794.348	7	-4	398.1797	2	7.75	2	803	2	427	433
K.PVLSTTAAK.D R.YMVEGVHTAWQS .L	47.35	888.4301	8	-0.9	445.2219	2	8.25	2	888	3	561	568
K.AVNM(+15.99)PSL AKTAAGTWKLNLS VVVVPYVFPGPATQ PILR.H	46.99	1614.866	16	-8.8	808.433	2	24.49	2	3810	2	455	470 2
N.AGTQTDITVR.Y K.TTAPSITVAAAGQ (+.98)AGAGVTFDIL DITDSQIR.F	46.9	886.5123	9	-4.6	444.2614	2	11.61	2	1469	2	131	139
K.AVN(+.98)MPSLA K.T	46.07	1406.629	12	-3.2	704.3195	2	17.23	2	2481	1	491	502
K.AVNM(+15.99)PSL AKTAAGTWKLNLS VVVVPYVFPGPATQ PILR.H	45.14	3965.16	38	-7.2	992.2901	4	23.28	2	3599	1	439	476 1
N.AGTQTDITVR.Y K.TTAPSITVAAAGQ (+.98)AGAGVTFDIL DITDSQIR.F	44.77	1117.573	11	-4.3	559.7913	2	12.11	2	1560	2	480	490
K.AVN(+.98)MPSLA K.T	44.21	3060.562	31	5	1021.2	3	46.37	2	7513	4	183	213 2
R.YMVEGVHTAWQ(+ +.98)SLAAAGIKDAK PGVR.D	44.14	945.4954	9	-4.3	473.7529	2	11.52	2	1451	2	439	447 1
K.AVNM(+15.99)PSL AKTAAGTWKLNLS VVVVPYVFPGPATQ PILR.H	43.22	2755.412	26	6.1	552.093	5	19.08	2	2841	1	491	516 2

K.SLALNATNELTI VTNIVGAALDATN(+ .98)TITFN(+.98)VPG YDSGK.G	43.18	3981.011	39	3.6	1328.016	3	33.59	2	5363	1	374	412	2
T.PAN(+.98)DFVR.G L.ATVKPVLSTTAAK .D	42.92	818.3922	7	1.5	410.204	2	13.36	2	1776	2	221	227	2
T.TPANDFVR.G E.VVTNVPSKDFV YGGAK.I	41.7	918.4559	8	-7.9	460.2316	2	14.13	2	1908	1	220	227	
V.VPYVFPGPATQPI LR.H	41.56	1778.957	17	-9.1	890.4775	2	19.76	2	2964	1	544	560	
G.SVVVVPYVFPGPA TQPILR.H	41.44	1653.924	15	-12.5	827.959	2	26.24	2	4117	1	462	476	
T.VKPVLSTTAAK.D V.ALEVVTNVPSKD VFVYGGAK.I	41.16	2038.162	19	-5.9	1020.082	2	23.55	2	3645	2	458	476	
K.VALEVVTN(+.98) VPSKDFVYGGAK.I	40.8	1113.676	11	-2.1	372.2318	3	11.76	2	1495	2	129	139	
R.GNGILELSNIFLDS TGLAATTSVM(+15.9 9)VNSFGTN(+.98)TS GTK.F	40.62	2092.12	20	-9.6	1047.057	2	19.74	2	2960	1	541	560	
G.GDVATFADGSGR. E	40.6	2192.173	21	-3.4	1097.09	2	21.73	2	3326	4	540	560	2
D.GLEYTQATALEIK PVIVAGIGGYK.A	40.27	3633.772	36	-0.2	1817.893	2	27.88	2	4394	1	228	263	1; 2
K.LNGSVVVVPYVFP GPATQ(+.98)PILR.H	39.83	1151.521	12	-8.4	576.7628	2	13.59	2	1815	1	101	112	
M.ISVQDFTVK.V	39.54	2490.373	24	-2.3	831.1298	3	21.76	2	3331	2	141	164	
T.PANDFVR.G	39.43	2323.294	22	1.3	581.8315	4	23.86	2	3699	1	455	476	2
N.PMISVQDFTVK.V R.FTVKATTPANDFV R.G	39.06	1035.56	9	-4.1	518.7852	2	17.83	2	2609	2	418	426	
N.PM(+15.99)ISVQDF TVK.V	37.85	817.4082	7	-3.1	409.7101	2	14.13	2	1907	1	221	227	
N.IFLDSTGLAATTS VMVNSFGTNTSGTK .F	37.77	1263.653	11	-6.5	632.8298	2	20.09	2	3035	2	416	426	
R.YM(+15.99)VEGVH TAWQS.L	37.52	1565.82	14	-7.5	783.9115	2	16.27	2	2300	1	214	227	
K.VALEVVTNVPSK D.V	37.07	1279.648	11	-2.5	640.8298	2	18.61	2	2753	1	416	426	1
R.YMVEGVHTAWQS LAA.A	36.89	2719.337	27	-6.2	907.4474	3	23.66	2	3662	1	237	263	
K.ITAEGQ(+.98)DR.I	35.71	1422.624	12	-6.5	712.3146	2	16.29	2	2304	1	491	502	1
A.TQPILR.H	35.24	1369.745	13	-6.3	685.8755	2	16.63	2	2366	1	540	552	
K.LDLTK.T V.VVVPYVFPGPATQ PILR.H	35.01	1661.787	15	-6.7	831.8953	2	20.16	2	3048	2	491	505	
K.TTAPSITVAAAGQ AGAGVTFDILDITDS Q(+.98)IR.F	34.15	889.4141	8	-1	445.7139	2	8.79	2	979	1	561	568	2
A.TTPANDFVR.G R.GNGILELSNIFLDS TGLAATTSVM(+15.9 9)VN(+.98)SFGTNTS GTK.F	33.85	726.4388	6	-3.5	364.2254	2	12.07	2	1553	2	471	476	
A.NAC(+57.02)LATV KPVLSTTAAK.D	33.84	588.3483	5	-7.5	295.1792	2	11.95	2	1529	2	178	182	
N.VAVLAGDDTVK .S	33.75	1852.061	17	-7.2	927.0311	2	26.2	2	4111	1	460	476	
R.ELTTVHTAANA. C	32.91	3060.562	31	5	1021.2	3	46.71	2	7569	3	183	213	2
D.TLTFQFSGAK.L	32.67	1019.504	9	-4.7	510.7567	2	13.85	2	1859	1	219	227	
D.VLAVK.H V.PSKDFVYGGAK. I	32.26	3633.772	36	-5.9	1212.257	3	27.87	2	4392	1	228	263	1; 2
	32.25	1743.955	17	-6	872.9797	2	15.66	2	2191	1	123	139	3
	31.78	1143.614	12	-9.1	572.8088	2	14.06	2	1895	2	362	373	
	31.73	1227.61	12	-5.2	614.8088	2	12.26	2	1587	1	113	124	
	31.72	1098.571	10	-7.2	550.2888	2	18.03	2	2645	2	168	177	
	31.7	528.3635	5	-3.2	265.1882	2	10.56	2	1281	1	308	312	
	31.19	1266.661	12	-11.4	634.3304	2	19.72	2	2957	1	549	560	

I.HLGTFK.T	31.06	701.386	6	-3.1	351.6992	2	14.66	2	2005	2	570	575
R.GNGILELSNIFLDS												
TGLAATTSVM(+15.99)VNSFGTNTSGTK.F	30.98	3632.788	36	-7.2	1211.928	3	27.78	2	4376	1	228	263 1
K.AEDTLTFQ(+.98)FSGAK.L	30.85	1414.662	13	9.7	708.345	2	25.55	2	3999	3	165	177 2
T.TPAN(+.98)DFVR.G	29.92	919.4399	8	-1.2	460.7267	2	13.37	2	1778	1	220	227 2
V.ALEVVTNVPSK.D	29.52	1155.65	11	-1.4	578.8314	2	16.56	2	2354	2	541	551
G.SGGDVATFADGS												
GR.E	28.96	1295.574	14	-11.1	648.7872	2	13.77	2	1845	1	99	112
H.TNAGTQTGDITVR												
.Y	28.86	1332.663	13	-6.2	667.3348	2	12.41	2	1614	1	478	490
R.ELTTVHTTAA.N	28.71	1042.53	10	-4.7	522.2696	2	12.13	2	1564	1	113	122
R.DM(+15.99)LGLVT												
DALKGEGYD.S	27.7	1711.798	16	-8.4	856.8988	2	21.26	2	3246	1	517	532 1
K.ITAEGQDRIHLGT												
FK.T	27.54	1684.89	15	-4.1	422.228	4	15.54	2	2167	1	561	575
R.YM(+15.99)VEGVH												
TAWQ.S	26.46	1335.592	11	-11.9	668.7952	2	16.49	2	2341	1	491	501 1
A.TVKPVLSTTAAK.												
D	26.23	1214.723	12	-9.6	608.3632	2	14.35	2	1949	1	128	139
K.NPTSANVLPANT												
TY.V	26.21	1560.778	15	-11.4	781.3875	2	17.88	2	2619	1	316	330
T.NPMISVQDFTVK.												
V	26.19	1377.696	12	-7.5	689.8502	2	20.05	2	3026	1	415	426
K.TSVTATTAVLQQT												
AIGTAKAHA.K	26.18	2140.149	22	-10	714.3831	3	17.72	2	2588	1	28	49
K.ADGTAAHAVAAD												
.G	25.95	1068.484	12	-4.9	535.2464	2	9.71	2	1134	1	86	97
D.ILDITDSQIR.F	25.55	1172.64	10	-7	587.3232	2	17.34	2	2502	1	204	213
R.HTN(+.98)AGTQ(+.												
98)TGDITVR.Y	25.35	1471.69	14	-0.1	736.8524	2	12.34	2	1601	1	477	490 2
K.GTNPM(+15.99)ISV												
Q(+.98)DFTVK.V	23.46	1552.744	14	-2.9	777.3771	2	18.9	2	2809	1	413	426 1; 2
V.FVYGGAK.I	22.94	740.3857	7	-5.8	371.198	2	15.66	2	2190	1	554	560
R.ELTTVHTTAAN(+.												
98)AC(+57.02).L	22.87	1388.624	13	8.2	695.3251	2	12.27	2	1589	1	113	125 2; 3

* L = Length; F = Fraction; 1 - Oxidation (M); 2 - Deamidation (NQ); 3 - Carbamidomethylation

Table S3. Niche analysis of species/genomes with detected EAR28894 (Slr4) homologs.

Protein sequence (accession #)	Species	Marine	Host-associated	Fresh water	Habitat description	Reference/Source
WP_055732151.1	<i>Agarivorans gilvus</i>	Yes	Yes		Seaweed	https://www.ncbi.nlm.nih.gov/pubmed/20363930
WP_026972292.1	<i>Aliagarivorans marinus</i>	Yes			Seawater	https://www.dsmz.de/catalogues/details/culture/DSM-23064.html
WP_026957844.1	<i>Aliagarivorans taiwanensis</i>	Yes			Seawater	https://www.ncbi.nlm.nih.gov/pubmed/19567569
WP_091340846.1	<i>Alkalimonas amylolytica</i>	No		Yes	Lake Chahannor in China	https://www.ncbi.nlm.nih.gov/pubmed/14986177
WP_124748942.1	<i>Alteromonas facilis</i>	Yes	Yes		Isolated from a sea cucumber culture pond in China	https://www.ncbi.nlm.nih.gov/pubmed/30528643
WP_046556214.1	<i>Arsukibacterium ikkense</i>	Yes			Isolated from the alkaline, low-saline ikaite columns in the Ikka Fjord, SW Greenland	https://www.ncbi.nlm.nih.gov/pubmed/16790334
WP_085282491.1	<i>Colwellia chukchiensis</i>	Yes			Isolated from seawater samples from the Chukchi Sea in the Arctic Ocean	https://www.ncbi.nlm.nih.gov/pubmed/20495042
WP_085298075.1	<i>Colwellia mytili</i>	Yes	Yes		Isolated from the mussel <i>Mytilus edulis</i> from the South Sea in Korea	https://www.ncbi.nlm.nih.gov/pubmed/27902189
WP_118961217.1	<i>Colwellia sp. RSH04</i>	Yes			Seawater	https://www.ebi.ac.uk/biosamples/samples/SAMN09916314
WP_057830656.1	<i>Colwellia sp. TT2012</i>	Yes			Marine sediment, Pacific Ocean: the Tonga Trench	https://www.ncbi.nlm.nih.gov/nucleotide/LJYX00000000.1
RLB69876.1	<i>Deltaproteobacteria bacterium</i>	Yes			marine sediment hydrothermal vent sediments from dive 4571_4 depth 0-3 cm	https://www.ncbi.nlm.nih.gov/protein/RLB69876.1
PCH94196.1,PC159289.1	<i>Gammaproteobacteria bacterium</i>	Yes			mediterranean seawater-France	https://www.uniprot.org/taxonomy/1805126
WP_040521162.1, WP_070111740.1	<i>Glaciecola punicea</i>	Yes			isolated from sea-ice cores collected from coastal areas of eastern Antarctica	https://ijs.microbiologyresearch.org/content/journal/ijsem/10.1099/00207713-48-4-1213
GAB56998.1, PTB83247.1, PTB83248.1, PTB84530.1, PTB85125.1, PTB85126.1, RUO41646.1, RUO41647.1, RUO41648.1	<i>Glaciecola punicea ACAM 611</i>	Yes			Antarctic sea ice	https://jlb.asm.org/content/194/12/3267
WP_133538702.1	<i>Idiomarina aestuarii</i>	Yes			isolation of the type strain from shallow coastal seawater.	https://ijs.microbiologyresearch.org/content/journal/ijsem/10.1099/ijms.0.022970-0
WP_126834469.1	<i>Idiomarina aquatica</i>	Yes			Isolated from salterns	https://ijs.microbiologyresearch.org/content/journal/ijsem/10.1099/ijsem.0.000619
WP_126834469.1	<i>Idiomarina aquimaris</i>	Yes	Yes		isolated from the reef-building coral <i>Isopora palifera</i>	https://ijs.microbiologyresearch.org/content/journal/ijsem/10.1099/ijms.0.035592-0
KFZ29179.1, WP_034731676.1	<i>Idiomarina atlantica</i>	Yes			isolated from the deep sea sediment of the North Atlantic Ocean	https://link.springer.com/article/10.1007%2Fs10482-014-0337-7

RUO53158.1,WP_126763865.1,WP_126763868.1,WP_126763869.1	<i>Idiomarina halophila</i>	Yes		isolated from the sediment of the solar saltern pond located in Gomso, Republic of Korea	https://www.microbiologyresearch.org/docs/erver/fulltext/ijsem/65/4/1268_ijs000094.pdf
RUO56263.1,WP_126771356.1,WP_126771358.1,WP_126771362.1	<i>Idiomarina homiensis</i>	Yes		isolated from seashore sand in Korea	https://www.microbiologyresearch.org/docs/erver/fulltext/ijsem/56/9/2229.pdf
RUO62606.1,WP_126753970.1	<i>Idiomarina insulalsae</i>	Yes		isolated from a sea salt evaporation pond on the Island of Sal in the Cape Verde Archipelago	https://pdf.sciencedirectassets.com/273235/1-s2.0-S0723202009X00068/1-s2.0-S072320200900085X/main.pdf
WP_026861598.1,WP_126775152.1	<i>Idiomarina sediminum</i>	Yes		isolated from the soil of a sea salt evaporation pond	https://www.microbiologyresearch.org/docs/erver/fulltext/ijsem/60/1/1.pdf
HAD47721.1	<i>Idiomarina sp.</i>	Yes		marine metagenome	https://www.ncbi.nlm.nih.gov/pubmed/30148503
MBG23301.1	<i>Idiomarinaceae bacterium</i>	Yes		marine metagenome from a Mediterranean Sea water sample	https://www.ncbi.nlm.nih.gov/pubmed/29337314
WP_088331539.1	<i>Lacimicrobium sp. SS2-24</i>	Yes	Yes	sediment from sea cucumber culture	https://www.ncbi.nlm.nih.gov/nucleotide/N1WW00000000.1
WP_031571199.1	<i>Pararheinheimera texasensis</i>	No	Yes	USA: Spring Lake; San Marcos; Texas	http://gtdb.ecogenomic.org/genomes?gid=GCF_000711985.1
MBU77382.1	<i>Pseudoalteromonas nadaceae bacterium</i>	Yes		marine metagenome from a South Atlantic Ocean water sample	https://www.ncbi.nlm.nih.gov/pubmed/29337314
WP_077536094.1	<i>Pseudoalteromonas aliena</i>	Yes		Sea of Japan, Pacific Ocean	https://www.ncbi.nlm.nih.gov/pubmed/15388692
WP_010361438.1	<i>Pseudoalteromonas citrea</i>	Yes		Marine	https://www.ncbi.nlm.nih.gov/pubmed/12190022/
WP_091983032.1	<i>Pseudoalteromonas denitrificans</i>	Yes		Marine	https://doi.org/10.1248/bpb.22.532
SFC52264.1	<i>Pseudoalteromonas denitrificans DSM 6059</i>	Yes		Marine	https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?lvl=0&id=43656 , https://www.microbiologyresearch.org/docs/erver/fulltext/ijsem/37/4/ij3-37-4-416.pdf
KID36130.1	<i>Pseudoalteromonas elyakovii</i>	Yes		isolated from marine environments	https://www.microbiologyresearch.org/docs/erver/fulltext/ijsem/53/1/125.pdf
CCQ10312.1	<i>Pseudoalteromonas luteoviolacea B = ATCC 29581</i>	Yes		Marine	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3593315/
WP_010368594.1,WP_045962959.1,WP_045987911.1,WP_088531627.1,WP_117332793.1	<i>Pseudoalteromonas piscicida</i>	Yes		found in the marine environment	https://www.ncbi.nlm.nih.gov/pubmed/28363962
WP_119852593.1	<i>Pseudoalteromonas profundus</i>	Yes		isolated from a deep-sea seamount	https://www.ncbi.nlm.nih.gov/pubmed/27493151
WP_022946007.1	<i>Pseudoalteromonas ruthenica</i>	Yes	Yes	isolated from marine invertebrates	https://www.microbiologyresearch.org/docs/erver/fulltext/ijsem/52/1/0520235a.pdf
WP_130050461.1	<i>Pseudoalteromonas shioyasakiensis</i>	Yes		isolated from Pacific Ocean sediment	https://www.ncbi.nlm.nih.gov/pubmed/24021728
MAD02172.1	<i>Pseudoalteromonas sp.</i>	Yes		marine metagenome from a Pacific Ocean water sample	https://www.ncbi.nlm.nih.gov/pubmed/29337314
MBD58444.1	<i>Pseudoalteromonas sp.</i>	Yes		marine metagenome from an Indian Ocean water sample	https://www.ncbi.nlm.nih.gov/pubmed/29337314

WP_042150686.1	<i>Pseudoalteromonas</i> sp. '520P1 No. 412'	Yes		Marine	https://mra.asm.org/content/2/6/e01346-14
WP_042150686.1	<i>Pseudoalteromonas</i> sp. '520P1 No. 423'	Yes		Marine	https://mra.asm.org/content/2/6/e01346-14
WP_069020791.1	<i>Pseudoalteromonas</i> sp. BMB	Yes	Yes	Isolated from gut of comb jelly	https://www.uniprot.org/proteomes/UP000094131
WP_130151616.1	<i>Pseudoalteromonas</i> sp. CO133X	Yes	Yes	Octocoral	https://onlinelibrary.wiley.com/doi/full/10.1002/jobm.201800087
WP_130151616.1	<i>Pseudoalteromonas</i> sp. CO302Y	Yes	Yes	Octocoral host-associated	https://onlinelibrary.wiley.com/doi/full/10.1002/jobm.201800087
WP_130126916.1	<i>Pseudoalteromonas</i> sp. CO342X	Yes		(Muricea sp.), Panama: Coiba National Park	https://www.ncbi.nlm.nih.gov/nuccore/1577351741
WP_099029058.1	<i>Pseudoalteromonas</i> sp. GCY	Yes		Isolated from Northern Yellow Sea	https://www.ncbi.nlm.nih.gov/nuccore/NZ_NHNM00000000.1
WP_095726933.1	<i>Pseudoalteromonas</i> sp. HM-SA03	Yes	Yes	Source (marine), Host (Hapalochlaena), Location (Australia: Moreton Bay)	https://www.ncbi.nlm.nih.gov/nuccore/NZ_NSDG00000000.1
WP_125251093.1	<i>Pseudoalteromonas</i> sp. J010	Yes	Yes	Isolated from surface of crustose coralline alga	https://www.ncbi.nlm.nih.gov/nuccore/NZ_RDBW00000000.1
WP_086997608.1	<i>Pseudoalteromonas</i> sp. JB197	No		Isolated from cheese rind	https://www.ncbi.nlm.nih.gov/nuccore/NZ_NRGZ00000000.1
WP_119861005.1	<i>Pseudoalteromonas</i> sp. MSK9-3	Yes		Isolated from surface saline water	https://www.ncbi.nlm.nih.gov/nuccore/NZ_MIET00000000.1
WP_017217139.1	<i>Pseudoalteromonas</i> sp. NJ631	Yes	Yes	Isolation source (ocean), host - Hymeniacion perleve (marine sponge)	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AKXJ00000000.1
WP_128731076.1	<i>Pseudoalteromonas</i> sp. PS5	Yes	Yes	Isolated from (host: Neogoniolithon solubile), USA: reef near Looe Key	https://www.ncbi.nlm.nih.gov/nuccore/NZ_RCSQ00000000.1
WP_053910113.1	<i>Pseudoalteromonas</i> sp. SW0106-04	Yes		Seawater (Indian Ocean)	https://www.ebi.ac.uk/biosamples/samples/SAMD00039894

WP_105171055.1	<i>Pseudoalteromonas sp. T1lg24</i>	Yes			Isolated from sea water (sediment depth)	https://www.ncbi.nlm.nih.gov/nucleotide/NC_000000000.1
WP_024611180.1	<i>Pseudoalteromonas sp. TB64</i>	Yes	Yes		Isolated from a sponge, Antarctica	https://www.ncbi.nlm.nih.gov/nucleotide/NC_000000000.1
WP_010561144.1, WP_100912554.1	<i>Pseudoalteromonas spongiae</i>	No	Yes	Yes	isolated from the surface of the sponge <i>Mycale adhaerens</i> in Hong Kong waters	https://www.ncbi.nlm.nih.gov/pubmed/16014487
WP_009838156.1, WP_119081635.1	<i>Pseudoalteromonas tunicata</i>	Yes			Marine organism originally isolated from tunicates	https://www.ncbi.nlm.nih.gov/pubmed/9828422
WP_086744222.1	<i>Pseudoalteromonas ulvae</i>	Yes	Yes		Isolated from surface of marine alga	https://www.ncbi.nlm.nih.gov/pubmed/11491351
WP_134053939.1	<i>Rheinheimera aquimaris</i>	Yes			isolated from seawater of the East Sea in Korea	https://www.ncbi.nlm.nih.gov/pubmed/17625162
WP_019674711.1	<i>Rheinheimera perlucida</i>	Yes			Isolated from surface water from Baltic Sea	https://www.ncbi.nlm.nih.gov/pubmed/16957117
WP_132584183.1	<i>Rheinheimera sp. D18</i>	Yes			Isolated from yellow sea (China)	https://www.ncbi.nlm.nih.gov/nucleotide/NC_0037745.1
WP_127697655.1	<i>Rheinheimera sp. KYPC3</i>	No		Yes	Isolated from freshwater stream	http://link.springer.com/443.webvpn.jxust.edu.cn/article/10.1007%2Fs00203-019-01657-5
WP_068063761.1	<i>Rheinheimera sp. SA_1</i>	No		Yes	isolated from "iron backwash sludge of a waterworks in Germany"	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4991719/

PHS21107.1	<i>Robiginitomaculum</i> sp.	Yes		from Antarctic seawater	http://www.bacterio.net/robiginitomaculum.html
WP_109338879.1	<i>Salinimonas</i> sp. HMF8227	Yes		Isolated from saltern in South Korea	https://www.ncbi.nlm.nih.gov/nucleotide/CP029347.1
WP_119977519.1	<i>Shewanella algidipiscicola</i>	Yes	Yes	isolated from marine fish of the Danish Baltic Sea	https://www.ncbi.nlm.nih.gov/pubmed/17267977
WP_059744161.1	<i>Shewanella frigidimarina</i>	Yes		Isolated from Antarctic coastal areas	https://www.ncbi.nlm.nih.gov/pubmed/11837303
WP_108947122.1	<i>Shewanella halifaxensis</i>	Yes		Isolated from marine sediment	https://www.ncbi.nlm.nih.gov/pubmed/16403888
WP_115405978.1	<i>Shewanella putrefaciens</i>	Yes	Yes	Associated with spoiled fish	https://www.ncbi.nlm.nih.gov/pubmed/2641275
WP_012143353.1	<i>Shewanella sediminis</i>	Yes		Isolated from marine sediment	https://www.ncbi.nlm.nih.gov/pubmed/16014474
WP_076411007.1	<i>Shewanella</i> sp. UCD-KL12	Yes	Yes	Isolated from seagrass	https://www.ncbi.nlm.nih.gov/pubmed/28360178
WP_028771745.1	<i>Shewanella waksmanii</i>	Yes	Yes	Marine strain isolated from sipuncula	https://www.ncbi.nlm.nih.gov/pubmed/13130035
WP_044830703.1	<i>Thalassomonas actiniarum</i>	Yes	Yes	Isolated from marine animals	https://www.ncbi.nlm.nih.gov/pubmed/19329588/
WP_044836570.1	<i>Thalassomonas viridans</i>	Yes		isolated from oysters off the Mediterranean coast	https://www.ncbi.nlm.nih.gov/pubmed/11491324
WP_115999569.1, WP_116007234.1, WP_116007235.1, WP_116014431.1	<i>Thalassotalea euphylliae</i>	Yes	Yes	Isolated from coral	https://www.ncbi.nlm.nih.gov/pubmed/27582443
WP_074500610.1	<i>Thalassotalea</i> sp. PP2-459	Yes	Yes	Isolated from clam larvae in shellfish hatchery in Spain	https://www.ncbi.nlm.nih.gov/pubmed/23743010

WP_074191941.1	<i>Vibrio antiquarius</i>	Yes		Isolated from deep sea hydrothermal vent	https://www.pnas.org/content/112/21/E2813
WP_104968991.1	<i>Vibrio diabolicus</i>	Yes	Yes	Isolated from a deep-sea hydrothermal vent annelid worm	https://www.ncbi.nlm.nih.gov/pubmed/9336897
WP_005434363.1	<i>Vibrio harveyi</i>	Yes	Yes	Pathogen of marine vertebrates and invertebrates	https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1472-765X.2006.01989.x
WP_038864853.1, WP_045422135.1	<i>Vibrio jasicida</i>	Yes	Yes	Isolated from marine vertebrates and invertebrates	https://www.ncbi.nlm.nih.gov/pubmed/21984666
WP_088881413.1	<i>Vibrio rotiferianus</i>	Yes	Yes	Marine pathogen	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3133291/
WP_095760150.1	<i>Vibrio sp. V1B</i>	Yes	Yes	Isolated from gut of saltwater clam	https://www.ncbi.nlm.nih.gov/pubmed/29051252

Table S4. Oligos used for plasmid construction

Oligo ID	Sequence
JC467	TCAGTTTCATGAACTTGGAGAATGCTGCAGTAAGCAACCGCTAAGTTTAAGTAGT
JC468	ACTACTTAACTTAGCGGTTGCTTACTGCAGCATTCTCCAAGTTTCATGAACTGA
JC470	CGGCAGGCTTAACTTGCTGCGTT
JC491	GCGGGATCCAAACAATTATTTTAGGTGGTTTAATTAG
JC492	GCGCAAGCTTGCCGATTAATGGACCAAGTGTCAAC

Supplementary Text

>Protein PTD2_07619 (EAR28894)

MEIMFKKTLALAITGVSVAANAAVVKTSTATTAVLQOTAIGTAKAHAKGTALGASGVFGTAADATNSANCKALAA
FYGVSLTKADGTAHAVAADGSGGDVATFADGSGRELTTVHTTAANACLATVKPVLSTTAAKDGLEYTQATALEIKP
VIVAGIGGYKAEDTLTFQFSGAKLDLTKTTAPSITVAAAGQAGAGVTFDILDITDSQIRFTVKATTPANDFVRNGI
LELSNIFLDSTGLAATTSVMVNSFGTNTSGTKFDESTAATIVSLLPQYTTTEVTTLLDADIDVGKDRQQFANNLTADV
LAVKHTKNPTSANVLPANTTYVVVTGDFSWAYAPSVDTNKDGKLSAELMAANVAVLAGGDDTVKSLALNATNTELT
IVTNIVGAALDATNTITFNVPGYDSGKGTNPMISVQDFTVKVDTMSDKSVGSKAVNMPSLAKTAAGTWKLNGSVVVV
PYVPFGPATQPIRLRHTNAGTQTGDITVRYMVEGVHTAWQSLAAAGIKDAKPGVRDMLGLVTDALKEGYDSTTTGFK
VALEVVTNVPKDVVYGGAKITAEGQDRIHLGTFKTNVN

>PTD2_07619 (EAR28894) deletion/replacement

MHQ

>PTD2_07619 (EAR28894) gene

ATGGAAATTATGTTCAAGAAAACCTACTACTAGCACTAGCAATTACTGGTGTCTTCTGTAGCAGCTAATGCAGCTGTGGT
AAAAACAAGCGTAACAGCAACTACTGCTGTTTTACAACAACAGCAATTGGTACTGCTAAAGCTCACGCTAAAGGTA
CTGCTCTAGGTGCTTCTGGTGTGTTCCGGTACAGCTGCAGATGCAACAAATTCAGCTAACTGTAAAGCATTAGCTGCT
TTTTATGGTGTTCATTAATAAGCTGATGGTACAGCTGCTCACGCTGTTGCTGCTGATGGTTCAGGTGGCGACGT
AGCTACTTTTGTGCTGATGGTTCAGGTGCTGAATTAACAACAGTACACACTACAGCTGCTAATGCTTGTCTTGCAACTG
TTAAACCAGTCTTTCTACTACCGCTGCTAAAGATGGTCTTGAGTACACTCAAGCTACAGCACTGAAATTAACCA
GTTATTGTTGCTGGTATCCGGTGGTTACAAAGCTGAAGATACGTTAACGTTCCAATCTCTGGCGCTAAATTAGATTT
AATAAACAACACTGCTCCATCTATTACTGTTGCAGCAGCTGGTCAAGCTGGTGTGCTGGTGTGACATTTGATATCCTTG
ATATCACTGATTACAAAATTCGTTTCACCGTTAAAGCAACTACTCCAGCGAATGATTTTTGTTTCGTGGTAACGGTATT
TTAGAATTAAGCAACATCTTCCTAGATTCTACAGGTCTTGCTGCTACTACTTCTGTAATGGTTAATTCTTTTGGTAC
TAATACATCAGGTACTAAATTTGATGAATCAACAGCTGCAACGATTGTATCTTTACTTCCACAATACACTACAGAAG
TAACTACGTTACTTGTATGCAGATATCGATGTAGGTAAAGATCGTCAACAATTTGCTAACAACCTAACAGCTGATGTT
TTAGCTGTTAAACACACTAAAAACCAACATCTGCTAACGTATTAGTTCCTGCTAATAACAACCTTATGTTGTTACTGG
TGATTTCTCTTGGGCTTATGCGCCAAGCGTAGATACAAACAAGATGGCAAATTATCTTCAGCTGAGTTAATGGCTG
CGAATGTTGCTGTTTTAGCTGGTGGTGTATGATACAGTTAAGTCTTTAGCTCTTAATGCTACAAACACTGAATTAACA
ATTGTTACTAATATTGTTGGTGTGCTGCATTAGATGCAACTAACACTATTACATTCAATGTTCCAGGCTATGATTCAGG
TAAAGGCACTAACCAATGATTTCTGTTCAAGATTTTCACGGTTAAAGTTGATACTATGTCTGATAAATCAGTTGGTA
GCAAAGCTGTAAACATGCCATCACTTGCTAAAACAGCAGCTGGTACATGGAAATTAATGGTTCTGTTGTTGTTGTT
CCTTATGTTCCATTTGGTCCAGCTACACAACCAATTTTACGCCACACTAATGCTGGTACACAAACCTGGTGTATACAC
AGTTCGTTACATGGTTGAAGGTGTTACACTGCATGGCAATCACTTGCAGCAGCTGGCATCAAAGATGCAAAACCTG
CCGTACGTGATATGTTAGGCTAGTAACTGACGCACCTAAAGGTGAAGGTTATGACTCTACAACACTACTGGCTTCAAA
GTAGCTTTAGAAGTTGTAACCTAACGTTCTTCAAAGACGTGTTTCGTATACGGCGGCGCTAAAATCACTGCTGAAGG
TCAAGATCGTATCCATTTAGGTACTTTCAAACCTAACGTAAACTAA

> PTD2_07619 (EAR28894) deletion/replacement

ATGCTGCAGTAA