

Supplementary Information

Socialization of *Providencia stuartii* enables resistance to environmental insults.

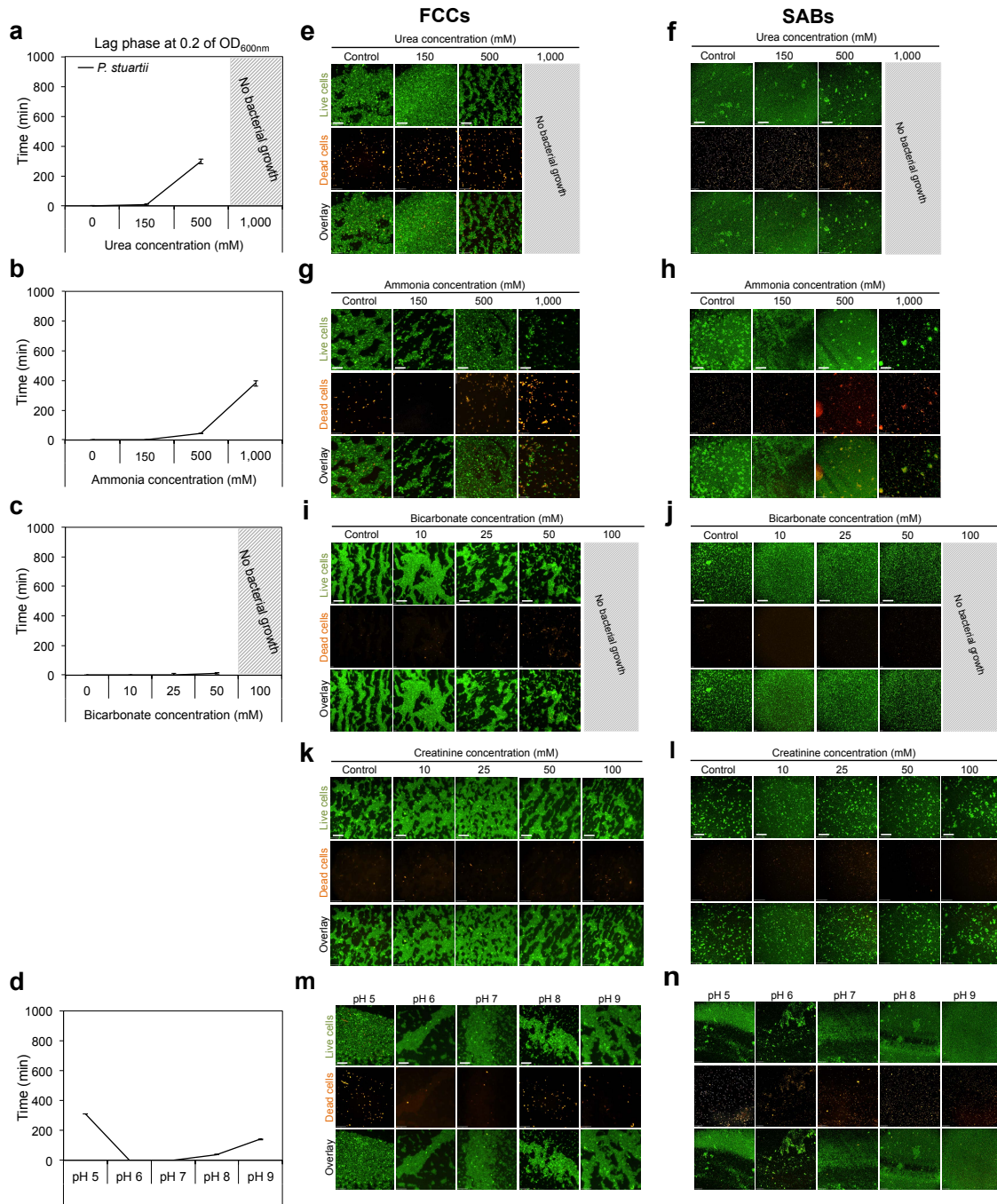
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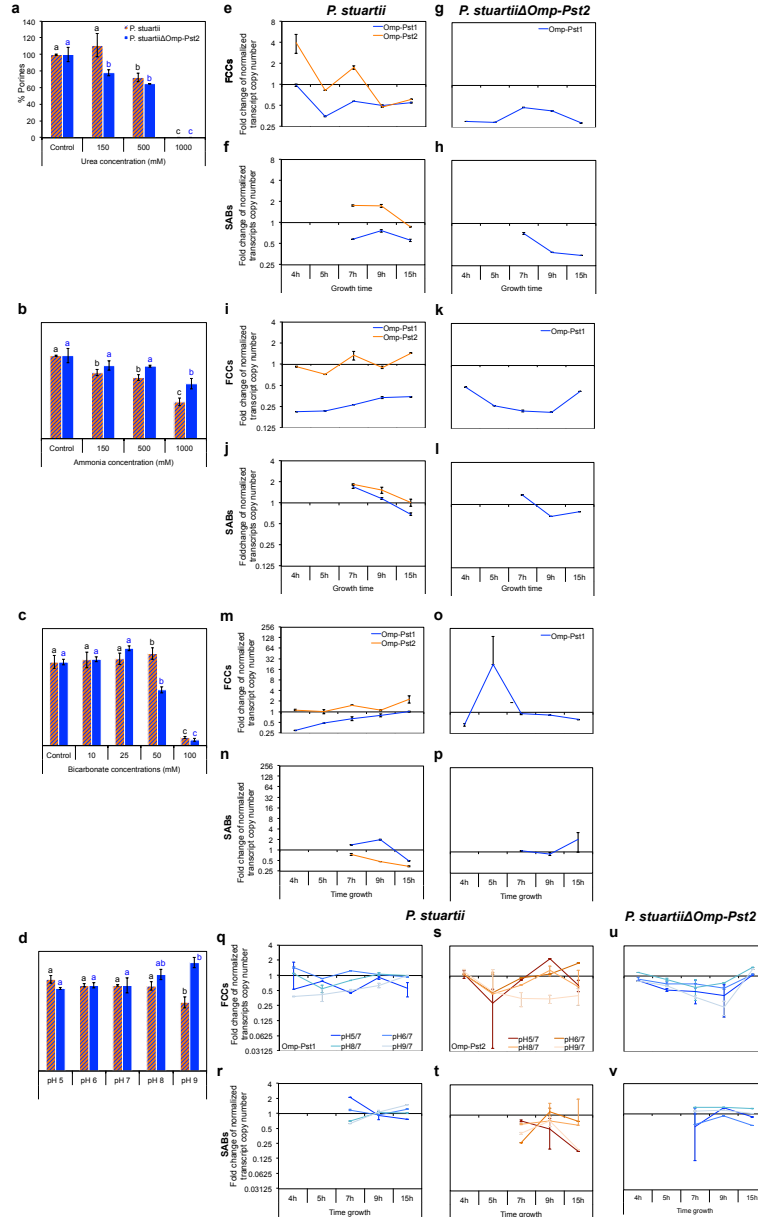
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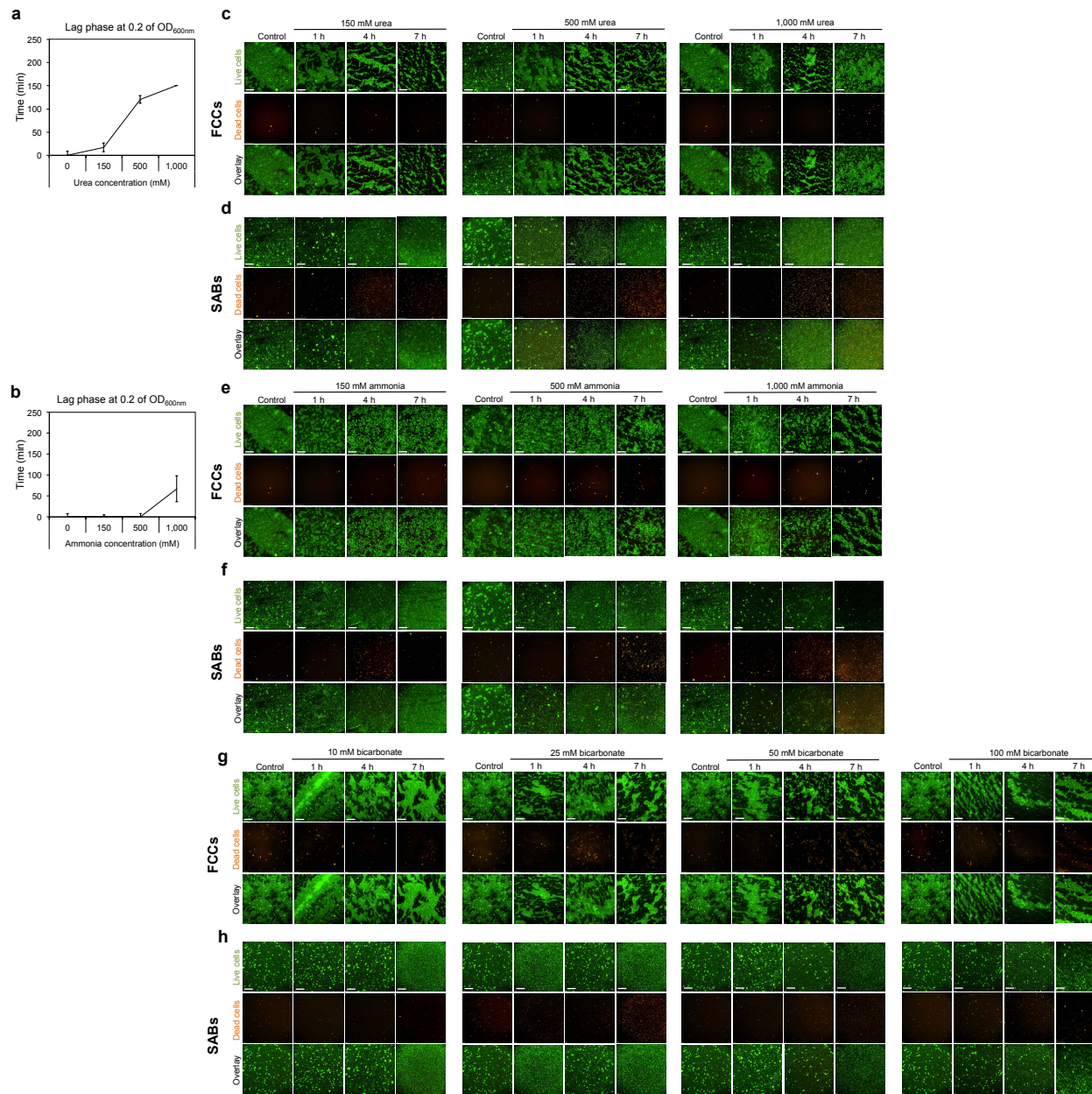
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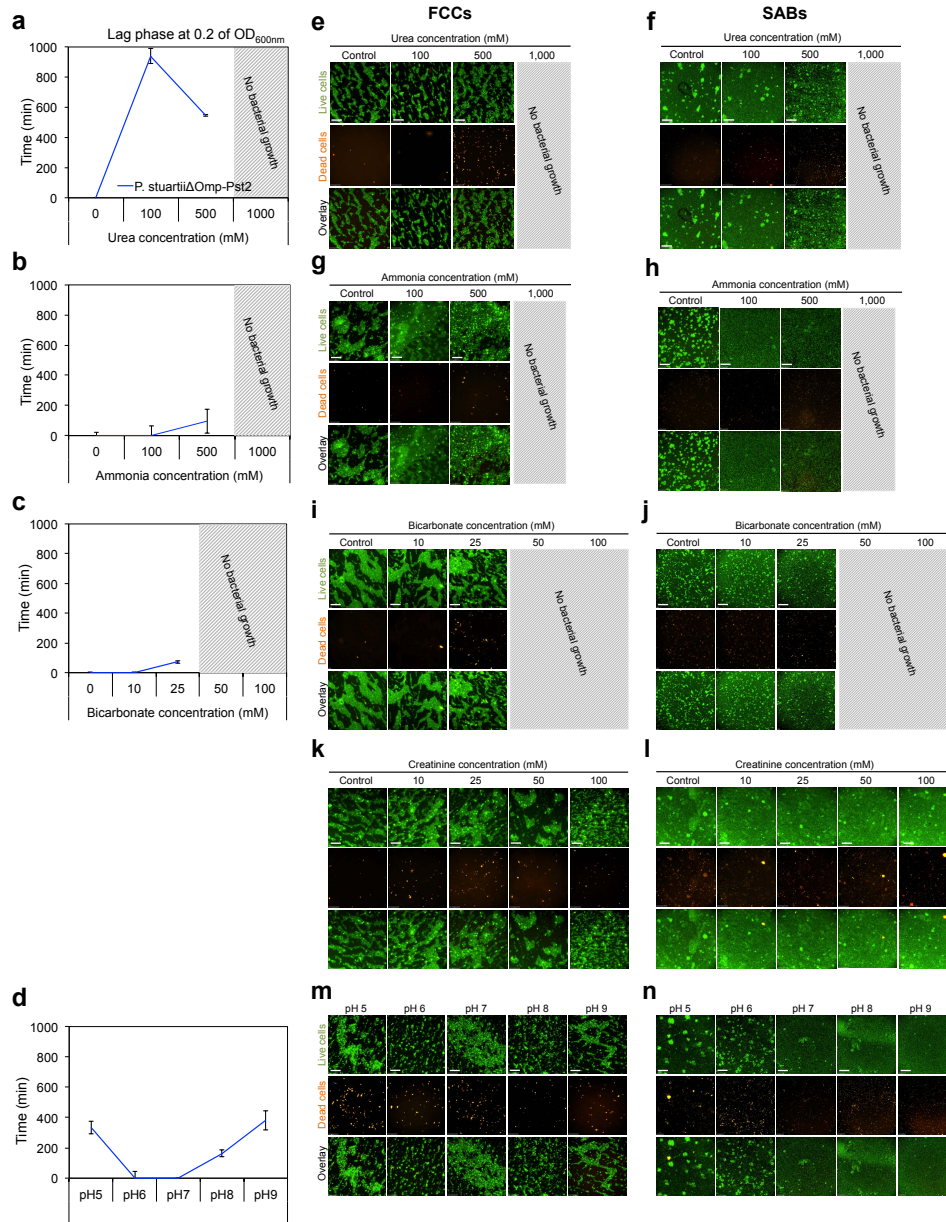
Supplementary Figure S1. *P. stuartii* is highly resistant to catabolites present in the urinary tract. (a-d) The overall impact of environmental cues on *P. stuartii* growth was monitored by determining, at increasing concentrations of the cues or pH, the lag time before reaching an optical density of 0.2 at 600 nm. Panels a, b, c, and d show results for urea, ammonia, bicarbonate and for different pH, respectively. All measurements were performed in triplicates; errors bars outline standard deviations from the average. Grey-hatched rectangles indicate concentrations at which bacteria were unable to grow. (e-n) Epifluorescence microscopy was used to monitor FCC (e,g,i,k,m) and SAB formation (f,h,j,l,n) in the presence of urea (e,f), ammonium (g,h), bicarbonate (i,j), creatinine (k,l) and at various pH (m,n). All bacteria are labelled by the permeant DNA stain Syto9 (green channel), but only dead cells are labelled by propidium iodide (red channel). For each condition, an overlay of the two channels is shown. Grey-hatched rectangles indicate concentrations at which bacteria were unable to grow. Scale bars correspond to 50 and 200 μ m in FCC and SAB micrographs, respectively.



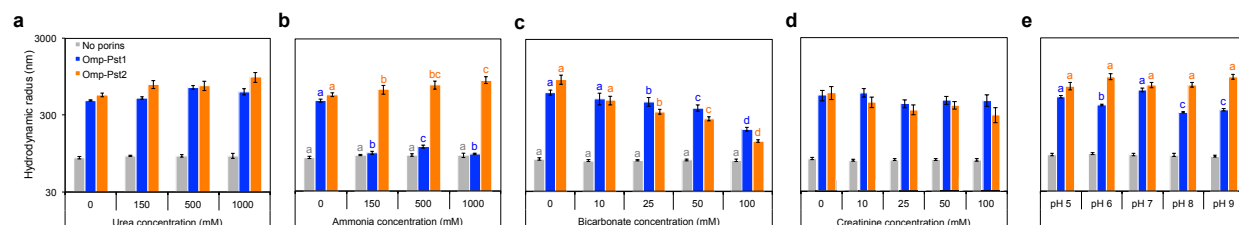
Supplementary Figure S2. Regulation of porin expression in the presence of environmental cues is more pronounced in FCC than SAB, and sometimes opposed. (a-d) Porin abundance in the OM of *P. stuartii* FCC and SAB cells grown in presence of increasing concentrations of urea (panel a), ammonia (b), bicarbonate (c) and to various pH (d) was evaluated by image processing of digitized SDS-PAGE gels using ImageJ. Plots show percent increase or decrease in porin abundance in the OM, after normalization of intensity counts from porin bands of exposed bacteria by those of unexposed bacteria. All measurements were performed in triplicates; errors bars outline standard deviations from the average. Different letters above the bars indicate significant differences (p < 0.05; ANOVA followed by post-hoc Tukey HSD test; see statistical indicators in Supplementary Table S1). **(e-v)** Immediate changes in the expression of Omp-Pst1 (blue) and Omp-Pst2 (orange) in WT *P. stuartii* or *P. stuartii*ΔOmp-Pst2 FCCs and SABs cells were monitored by RT-qPCR following 30 min incubation with 500 mM of urea (panels e, f and g, h, respectively), 500 mM ammonia (i, j and k, l), to 50 mM bicarbonate (m, n and o, p), or to pH variation (q, r, s, t and u, v). For each growth time point, we report the ratio of normalized transcript copy numbers between cells exposed and not exposed (control) to the cues. All measurements were performed in triplicates; errors bars outline standard deviations from the average. Different letters above the bars indicate significant differences (p < 0.05; ANOVA followed by post-hoc Tukey HSD test; see statistical indicators in Supplementary Table S2).



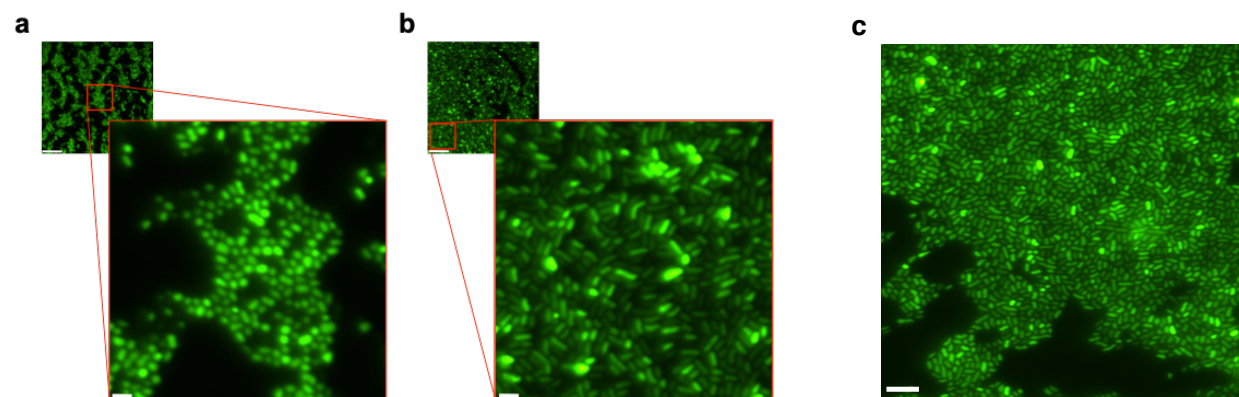
Supplementary Figure S3. FCC and SAB cells are generally more resistant than their planktonic counterparts. (a-b) Recovery of preformed *P. stuartii* FCC and SAB cells after sudden exposure to urea (a) or ammonia (b) was monitored by determining, at increasing concentrations of these, the lag time before reaching an optical density of 0.2 at 600 nm. All measurements were performed in triplicates; error bars outline standard deviations from the average. (e-h) Epifluorescence microscopy was used to monitor FCC (e,g,i,k,m) and SAB survival and recovery (f,h,j,l,n) in presence of increasing concentrations of urea (panels c and d, respectively), ammonia (e, f), and bicarbonate (g, h). All bacteria are labelled by the permeant DNA stain Syto9 (green channel), but only dead cells are labelled by propidium iodide (red channel). For each condition, an overlay of the two channels is shown. Grey-hatched rectangles indicate concentrations at which bacteria were unable to grow. Scale bars correspond to 50 and 200 μ m in FCC and SAB micrographs, respectively. Note that preformed *P. stuartii* FCC and SAB generally resist better to the cues than their developing counterparts, as illustrated by survival of FCC and SAB at 1 M urea and 100 mM bicarbonate, where new cells do not grow (Supplementary Fig. 1). An exception is ammonium, which disrupts SAB formed in its absence although preformed FCC survive and new FCC and SAB can form (Supplementary Fig. 1).



Supplementary Figure S4. Omp-Pst2 benefits resistance of *P. stuartii* to its pathophysiological environment. (a-d) The contribution of Omp-Pst2 in adapting to high concentration of urea (a), ammonia (b), bicarbonate (c) or to different pHs (d) was evaluated on the *P. stuartii*ΔOmp-Pst2 strain by determining, at increasing concentrations of the cues or pH, the lag time before reaching an optical density of 0.2 at 600 nm, and comparing results to the wild-type (Supplementary Fig. 1). All measurements were performed in triplicates; errors bars outline standard deviations from the average. Grey-hatched rectangles indicate concentrations at which bacteria were unable to grow. (e-n) Epifluorescence microscopy was used to monitor FCC (e,g,i,k,m) and SAB formation (f,h,j,l,n) by *P. stuartii*ΔOmp-Pst2 cells in the presence of urea (e,f), ammonium (g,h), bicarbonate (i,j), creatinine (k,l) and at various pH (m,n). All bacteria are labelled by the permeant DNA stain Syto9 (green channel), but only dead cells are labelled by propidium iodide (red channel). For each condition, an overlay of the two channels is shown. Grey-hatched rectangles indicate concentrations at which bacteria were unable to grow. Scale bars correspond to 50 and 200 μm in FCC and SAB micrographs, respectively.



Supplementary Figure S5. Omp-Pst1 and Omp-Pst2 self-association into DOT can be challenged by environmental cues. LDAO-solubilized Omp-Pst1 (blue) and Omp-Pst2 (orange) were reconstituted in ~50-nm radius LUV, in presence of increasing concentrations of urea (a), ammonia (b), bicarbonate (c), creatinine (d) or at various pH (e), and after 24 h incubation with biobeads, the hydrodynamic radius of proteoliposomes was measured by DLS. The hydrodynamic radii of LUVs incubated at with the cues but without porin were also measured (grey). Different letters above the bars indicate significant differences ($p < 0.05$; ANOVA followed by post-hoc Tukey HSD test; see statistical indicators in Supplementary Table S3).



Supplementary Figure S6. The orientation of *P. stuartii* cells differs in native FCC and in FCC formed in presence of environmental cues. Close-up views of FCCs developed in the presence of urea (a) and ammonia (b), showing "standing" and "seated" orientations of cells, respectively. (c) Unexposed FCC feature cells in the standing orientation. Epifluorescence microscopy was used to image FCC cells post-labelling by the permeant DNA stain Syto9 (green channel). The scale bars in the small and large panels are 50 µm and 5 µm, respectively.

Supplementary Table S1 – Statistical analysis from SDS-PAGE gels experiments on porin abundance in OMs. All experiments were conducted for at least three biologically independent replicates. Technical replicates were averaged to produce replicate means that were subsequently used for analysis. Mean values were compared within and between groups using one-way ANOVA followed by Tukey's post hoc for two-two comparisons. Differences were considered statistically significant if $p < 0.05$ (True).

GLM – SDS-PAGE Gels

All statistic parameters – *P. stuartii*:

Generalized Linear Model Regression Results

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Dep. Variable:      Y      No. Observations:      39
Model:              GLM    Df Residuals:          35
Model Family:       Gamma  Df Model:            3
Link Function:      inverse_power  Scale:          0.20020
Method:             IRLS   Log-Likelihood:      inf
Date:               Thu, 14 Feb 2019  Deviance:        212.99
Time:               16:59:38  Pearson chi2:    7.01
No. Iterations:     8        Covariance Type:    nonrobust
=====

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	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.4455	0.395	1.129	0.259	-0.328	1.219
Urea	4.854e-05	1.21e-05	4.011	0.000	2.48e-05	7.23e-05
Ammonium	1.704e-05	6.75e-06	2.524	0.012	3.81e-06	3.03e-05
Urea:Ammonium	8.351e-16	7.63e-16	1.094	0.274	-6.61e-16	2.33e-15
pH	0.0362	0.057	0.638	0.523	-0.075	0.147
Urea:pH	0.0003	8.47e-05	4.011	0.000	0.000	0.001
Ammonium:pH	0.0001	4.73e-05	2.524	0.012	2.67e-05	0.000
Urea:Ammonium:pH	0	0	nan	nan	0	0

Bicarbonate – *P. stuartii*:

Generalized Linear Model Regression Results

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=====
Dep. Variable:      Y      No. Observations:      15
Model:              GLM    Df Residuals:          13
Model Family:       Gamma  Df Model:            1
Link Function:      inverse_power  Scale:          0.29338
Method:             IRLS   Log-Likelihood:    -136.43
Date:               Mon, 20 May 2019  Deviance:        5.1540
Time:               09:29:53  Pearson chi2:    3.81
No. Iterations:     7        Covariance Type:    nonrobust
=====

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	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0001	3.41e-05	4.046	0.000	7.11e-05	0.000
Concentration	3.294e-06	1.26e-06	2.606	0.009	8.17e-07	5.77e-06

All statistic parameters – *P. stuartii*ΔOmp-Pst2:

Generalized Linear Model Regression Results

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=====
Dep. Variable:      Values  No. Observations:      39
Model:              GLM    Df Residuals:          35
Model Family:       Gamma  Df Model:            3
Link Function:      inverse_power  Scale:          0.19051
Method:             IRLS   Log-Likelihood:      inf
Date:               Mon, 20 May 2019  Deviance:        212.67
Time:               09:37:42  Pearson chi2:    6.67
No. Iterations:     8        Covariance Type:    nonrobust
=====

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	coef	std err	z	P> z	[0.025	0.975]
Intercept	1.2797	0.498	2.572	0.010	0.305	2.255
Urea	0.0041	0.001	4.534	0.000	0.002	0.006
Ammonia	0.0005	0.000	1.670	0.095	-9.18e-05	0.001
pH	-0.0586	0.069	-0.855	0.392	-0.193	0.076

Bicarbonate – *P. stuartii*ΔOmp-Pst2:

Generalized Linear Model Regression Results

Dep. Variable:	Y	No. Observations:	15
Model:	GLM	Df Residuals:	13
Model Family:	Gamma	Df Model:	1
Link Function:	inverse_power	Scale:	0.31456
Method:	IRLS	Log-Likelihood:	-133.53
Date:	Mon, 20 May 2019	Deviance:	7.3202
Time:	09:30:46	Pearson chi2:	4.09
No. Iterations:	7	Covariance Type:	nonrobust

	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0001	3.93e-05	3.569	0.000	6.33e-05	0.000
Concentration	7.247e-06	2.08e-06	3.491	0.000	3.18e-06	1.13e-05

2-2 comparison (Tukey) – *P. stuartii*

Urea condition:

Multiple Comparison of Means - Tukey HSD,FWER=0.05

group1	group2	meandiff	lower	upper	reject
0	150	0.1542	-0.1792	0.4876	False
0	500	-0.3759	-0.7093	-0.0425	True
0	1000	-1.3651	-1.6985	-1.0317	True
150	500	-0.5301	-0.8635	-0.1966	True
150	1000	-1.5193	-1.8527	-1.1858	True
500	1000	-0.9892	-1.3226	-0.6558	True

Ammonia condition:

Multiple Comparison of Means - Tukey HSD,FWER=0.05

group1	group2	meandiff	lower	upper	reject
0	150	-0.2778	-0.4343	-0.1212	True
0	500	-0.3618	-0.5183	-0.2052	True
0	1000	-0.7592	-0.9157	-0.6026	True
150	500	-0.084	-0.2405	0.0726	False
150	1000	-0.4814	-0.6379	-0.3248	True
500	1000	-0.3974	-0.5539	-0.2408	True

Bicarbonate condition:

Multiple Comparison of Means - Tukey HSD,FWER=0.05

group1	group2	meandiff	lower	upper	reject
0	10	975.8383	211.0188	1740.6579	True
0	25	756.3667	-8.4529	1521.1862	False
0	50	780.3097	15.4901	1545.1292	True
0	100	-4409.2103	-5174.0299	-3644.3908	True
10	25	-219.4717	-984.2912	545.3479	False
10	50	-195.5287	-960.3482	569.2909	False
10	100	-5385.0487	-6149.8682	-4620.2291	True
25	50	23.943	-740.8765	788.7625	False
25	100	-5165.577	-5930.3965	-4400.7575	True
50	100	-5189.52	-5954.3395	-4424.7005	True

pH condition:

Multiple Comparison of Means - Tukey HSD,FWER=0.05

group1	group2	meandiff	lower	upper	reject
5	6	-0.0942	-0.2838	0.0954	False
5	7	-0.0976	-0.2871	0.092	False
5	8	-0.1051	-0.2947	0.0844	False
5	9	-0.3684	-0.558	-0.1788	True
6	7	-0.0034	-0.1929	0.1862	False
6	8	-0.0109	-0.2005	0.1786	False
6	9	-0.2742	-0.4638	-0.0846	True
7	8	-0.0076	-0.1972	0.182	False

7	9	-0.2708	-0.4604	-0.0813	True
8	9	-0.2632	-0.4528	-0.0737	True

2-2 comparison (Tukey) – <i>P. stuartii</i> ΔOmp-Pst2					
Urea condition:					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
=====					
group1	group2	meandiff	lower	upper	reject

0	150	-0.2351	-0.4253	-0.045	True
0	500	-0.3753	-0.5654	-0.1851	True
0	1000	-1.0683	-1.2585	-0.8782	True
150	500	-0.1401	-0.373	0.0928	False
150	1000	-0.8332	-1.0661	-0.6003	True
500	1000	-0.6931	-0.926	-0.4602	True
Ammonia condition:					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
=====					
group1	group2	meandiff	lower	upper	reject

0	150	-0.1283	-0.3409	0.0842	False
0	500	-0.135	-0.3475	0.0775	False
0	1000	-0.3613	-0.5738	-0.1487	True
150	500	-0.0066	-0.2669	0.2536	False
150	1000	-0.2329	-0.4932	0.0274	False
500	1000	-0.2263	-0.4865	0.034	False
Bicarbonate condition:					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
=====					
group1	group2	meandiff	lower	upper	reject

0	10	346.731	-289.3837	982.8457	False
0	25	154.9093	-481.2053	791.024	False
0	50	-2002.9833	-2639.098	-1366.8687	True
0	100	-4633.1367	-5269.2513	-3997.022	True
10	25	-191.8217	-827.9363	444.293	False
10	50	-2349.7143	-2985.829	-1713.5997	True
10	100	-4979.8677	-5615.9823	-4343.753	True
25	50	-2157.8927	-2794.0073	-1521.778	True
25	100	-4788.046	-5424.1607	-4151.9313	True
50	100	-2630.1533	-3266.268	-1994.0387	True
pH condition:					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
=====					
group1	group2	meandiff	lower	upper	reject

5	6	0.0374	-0.2237	0.2985	False
5	7	0.0388	-0.1744	0.252	False
5	8	0.1749	-0.0862	0.436	False
5	9	0.3246	0.0635	0.5857	True
6	7	0.0014	-0.2118	0.2146	False
6	8	0.1375	-0.1236	0.3986	False
6	9	0.2872	0.0261	0.5483	True
7	8	0.1361	-0.0771	0.3493	False
7	9	0.2858	0.0726	0.499	True
8	9	0.1497	-0.1114	0.4108	False

Supplementary Table S2 – Statistical analysis from RT-qPCR experiments on porin expression into FCCs and SABs. All experiments were conducted for at least three biologically independent replicates. Technical replicates were averaged to produce replicate means that were subsequently used for analysis. Mean values were compared within and between groups using one-way ANOVA followed by Tukey's post hoc for two-two comparisons. Differences were considered statistically significant if $p < 0.05$ (True).

GLM – RTqPCR – *P. stuartii*

Parameter correlations: Urea - Omp-Pst1

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	88			
Model:	GLM	Df Residuals:	80			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.22000			
Method:	IRLS	Log-Likelihood:	-1032.9			
Date:	Tue, 21 May 2019	Deviance:	19.302			
Time:	15:24:28	Pearson chi2:	17.6			
No. Iterations:	7	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	1.976e-05	4.34e-06	4.553	0.000	1.13e-05	2.83e-05
C(Phenotype) [T.Floating]	-5.015e-06	4.73e-06	-1.060	0.289	-1.43e-05	4.26e-06
Time	-5.654e-07	3.72e-07	-1.518	0.129	-1.3e-06	1.64e-07
C(Phenotype) [T.Floating]:Time	1.242e-07	4.13e-07	0.301	0.763	-6.85e-07	9.33e-07
Urea	-8.492e-09	3.04e-08	-0.279	0.780	-6.81e-08	5.11e-08
C(Phenotype) [T.Floating]:Urea	1.565e-08	3.27e-08	0.478	0.632	-4.85e-08	7.98e-08
Time:Urea	3.323e-09	3.17e-09	1.049	0.294	-2.89e-09	9.53e-09
C(Phenotype) [T.Floating]:Time:Urea	-1.773e-09	3.47e-09	-0.511	0.609	-8.57e-09	5.03e-09

Parameter correlations: Urea - Omp-Pst2

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	88			
Model:	GLM	Df Residuals:	80			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.78223			
Method:	IRLS	Log-Likelihood:	-881.32			
Date:	Tue, 21 May 2019	Deviance:	56.367			
Time:	15:25:17	Pearson chi2:	62.6			
No. Iterations:	8	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0001	4.72e-05	2.651	0.008	3.26e-05	0.000
C(Phenotype) [T.Floating]	8.957e-05	7.12e-05	1.257	0.209	-5e-05	0.000
Time	-4.41e-06	3.91e-06	-1.127	0.260	-1.21e-05	3.26e-06
C(Phenotype) [T.Floating]:Time	-1.412e-06	6.45e-06	-0.219	0.827	-1.4e-05	1.12e-05
Urea	-1.312e-07	1.32e-07	-0.995	0.320	-3.9e-07	1.27e-07
C(Phenotype) [T.Floating]:Urea	-9.149e-08	2.12e-07	-0.431	0.666	-5.08e-07	3.25e-07
Time:Urea	6.08e-09	1.15e-08	0.530	0.596	-1.64e-08	2.86e-08
C(Phenotype) [T.Floating]:Time:Urea	1.064e-08	2.18e-08	0.488	0.625	-3.21e-08	5.33e-08

Parameter correlations: Ammonia - Omp-Pst1

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	89			
Model:	GLM	Df Residuals:	81			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.18900			
Method:	IRLS	Log-Likelihood:	-1039.4			
Date:	Tue, 21 May 2019	Deviance:	15.403			
Time:	15:26:44	Pearson chi2:	15.3			
No. Iterations:	7	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	1.976e-05	4.02e-06	4.913	0.000	1.19e-05	2.76e-05
C(Phenotype) [T.Floating]	-5.015e-06	4.39e-06	-1.143	0.253	-1.36e-05	3.58e-06
Time	-5.654e-07	3.45e-07	-1.638	0.101	-1.24e-06	1.11e-07
C(Phenotype) [T.Floating]:Time	1.242e-07	3.82e-07	0.325	0.745	-6.25e-07	8.74e-07

Ammonium	-2.697e-08	1.19e-08	-2.259	0.024	-5.04e-08	-3.57e-09
C(Phenotype) [T.Floating]:Ammonium	8.771e-08	2.01e-08	4.364	0.000	4.83e-08	1.27e-07
Time:Ammonium	1.78e-09	1.11e-09	1.601	0.109	-3.99e-10	3.96e-09
C(Phenotype) [T.Floating]:Time:Ammonium	-4.559e-09	1.8e-09	-2.530	0.011	-8.09e-09	-1.03e-09

Parameter correlations: Ammonia - Omp-Pst2

Generalized Linear Model Regression Results

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Dep. Variable:      Y      No. Observations:      89
Model:              GLM      Df Residuals:          81
Model Family:      Gamma      Df Model:              7
Link Function:      inverse_power      Scale:          0.74485
Method:              IRLS      Log-Likelihood:        -869.64
Date:              Tue, 21 May 2019      Deviance:          51.910
Time:              15:27:33      Pearson chi2:         60.3
No. Iterations:      8      Covariance Type:      nonrobust
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	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0001	4.61e-05	2.717	0.007	3.49e-05	0.000
C(Phenotype) [T.Floating]	8.957e-05	6.95e-05	1.289	0.198	-4.67e-05	0.000
Time	-4.41e-06	3.82e-06	-1.155	0.248	-1.19e-05	3.07e-06
C(Phenotype) [T.Floating]:Time	-1.412e-06	6.29e-06	-0.225	0.822	-1.37e-05	1.09e-05
Ammonium	1.805e-07	2.8e-07	0.644	0.520	-3.69e-07	7.3e-07
C(Phenotype) [T.Floating]:Ammonium	4.068e-07	4.24e-07	0.961	0.337	-4.23e-07	1.24e-06
Time:Ammonium	-5.772e-09	2.3e-08	-0.251	0.802	-5.08e-08	3.93e-08
C(Phenotype) [T.Floating]:Time:Ammonium	-3.723e-08	3.37e-08	-1.106	0.269	-1.03e-07	2.87e-08

Parameter correlations: Bicarbonate - Omp-Pst1

Generalized Linear Model Regression Results

```

=====
Dep. Variable:      Values      No. Observations:      48
Model:              GLM      Df Residuals:          40
Model Family:      Gamma      Df Model:              7
Link Function:      inverse_power      Scale:          0.28273516624
Method:              IRLS      Log-Likelihood:        -618.86
Date:              Fri, 05 Jul 2019      Deviance:          12.855
Time:              13:51:13      Pearson chi2:         11.3
No. Iterations:      8
=====

```

	coef	std err	z	P> z	[95.0% Conf. Int.]
Intercept	1.779e-05	4.1e-06	4.341	0.000	9.76e-06 2.58e-05
C(Phenotypes) [T.Floating]	-1.118e-05	4.31e-06	-2.591	0.010	-1.96e-05 -2.72e-06
Time	-1.128e-06	2.75e-07	-4.098	0.000	-1.67e-06 -5.88e-07
C(Phenotypes) [T.Floating]:Time	8.29e-07	2.97e-07	2.791	0.005	2.47e-07 1.41e-06
Cconditions	-1.554e-08	9.83e-09	-1.581	0.114	-3.48e-08 3.73e-09
C(Phenotypes) [T.Floating]:Cconditions	3.568e-08	1.16e-08	3.063	0.002	1.29e-08 5.85e-08
Time:Cconditions	1.162e-09	6.73e-10	1.728	0.084	-1.56e-10 2.48e-09
C(Phenotypes) [T.Floating]:Time:Cconditions	-2.541e-09	8.11e-10	-3.133	0.002	-4.13e-09 -9.51e-10

Parameter correlations: Bicarbonate - Omp-Pst2

Generalized Linear Model Regression Results

```

=====
Dep. Variable:      Values      No. Observations:      48
Model:              GLM      Df Residuals:          40
Model Family:      Gamma      Df Model:              7
Link Function:      inverse_power      Scale:          0.350373625544
Method:              IRLS      Log-Likelihood:        -516.90
Date:              Fri, 05 Jul 2019      Deviance:          15.804
Time:              14:02:51      Pearson chi2:         14.0
No. Iterations:      7
=====

```

	coef	std err	z	P> z	[95.0% Conf. Int.]
Intercept	2.502e-05	2.08e-05	1.204	0.229	-1.57e-05 6.58e-05
C(Phenotypes) [T.Floating]	-3.345e-05	2.65e-05	-1.262	0.207	-8.54e-05 1.85e-05
Time	7.925e-07	2.01e-06	0.394	0.694	-3.15e-06 4.74e-06
C(Phenotypes) [T.Floating]:Time	7.57e-06	3.53e-06	2.143	0.032	6.48e-07 1.45e-05
Cconditions	-8.522e-08	9.79e-08	-0.870	0.384	-2.77e-07 1.07e-07
C(Phenotypes) [T.Floating]:Cconditions	1.389e-07	1.06e-07	1.312	0.190	-6.87e-08 3.46e-07
Time:Cconditions	1.602e-08	1.1e-08	1.452	0.146	-5.6e-09 3.76e-08
C(Phenotypes) [T.Floating]:Time:Cconditions	-2.859e-08	1.29e-08	-2.221	0.026	-5.38e-08 -3.36e-09

Parameter correlations: pH - Omp-Pst1

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	156			
Model:	GLM	Df Residuals:	148			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.29369			
Method:	IRLS	Log-Likelihood:	-1843.2			
Date:	Tue, 21 May 2019	Deviance:	47.729			
Time:	15:29:23	Pearson chi2:	43.5			
No. Iterations:	7	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	-3.249e-05	2.38e-05	-1.365	0.172	-7.91e-05	1.42e-05
C(Phenotype) [T.Floating]	3.936e-05	2.59e-05	1.522	0.128	-1.13e-05	9.01e-05
Time	3.894e-06	2.45e-06	1.593	0.111	-8.98e-07	8.69e-06
C(Phenotype) [T.Floating]:Time	-3.441e-06	2.61e-06	-1.317	0.188	-8.56e-06	1.68e-06
pH	7.667e-06	3.44e-06	2.227	0.026	9.2e-07	1.44e-05
C(Phenotype) [T.Floating]:pH	-5.688e-06	3.74e-06	-1.523	0.128	-1.3e-05	1.63e-06
Time:pH	-6.133e-07	3.43e-07	-1.786	0.074	-1.29e-06	5.97e-08
C(Phenotype) [T.Floating]:Time:pH	4.35e-07	3.67e-07	1.186	0.236	-2.84e-07	1.15e-06

Parameter correlations: pH - Omp-Pst2

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	155			
Model:	GLM	Df Residuals:	147			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.90306			
Method:	IRLS	Log-Likelihood:	-1510.8			
Date:	Tue, 21 May 2019	Deviance:	112.64			
Time:	15:28:36	Pearson chi2:	133.			
No. Iterations:	8	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	6.154e-05	0.000	0.222	0.825	-0.000	0.001
C(Phenotype) [T.Floating]	0.0002	0.000	0.511	0.609	-0.001	0.001
Time	2.285e-06	2.74e-05	0.083	0.934	-5.14e-05	5.6e-05
C(Phenotype) [T.Floating]:Time	-2.104e-05	3.64e-05	-0.578	0.563	-9.23e-05	5.03e-05
pH	1.1e-05	3.96e-05	0.278	0.781	-6.65e-05	8.85e-05
C(Phenotype) [T.Floating]:pH	-1.724e-05	5.17e-05	-0.334	0.739	-0.000	8.4e-05
Time:pH	-7.931e-07	3.88e-06	-0.204	0.838	-8.4e-06	6.82e-06
C(Phenotype) [T.Floating]:Time:pH	3.284e-06	5.26e-06	0.624	0.532	-7.02e-06	1.36e-05

GLM – RTqPCR – *P. stuartii*ΔOmp-Pst2

Parameter correlations: Urea

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	96			
Model:	GLM	Df Residuals:	88			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.20053			
Method:	IRLS	Log-Likelihood:	-1144.3			
Date:	Tue, 21 May 2019	Deviance:	19.798			
Time:	16:17:17	Pearson chi2:	17.6			
No. Iterations:	8	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	5.906e-06	2.35e-06	2.509	0.012	1.29e-06	1.05e-05
C(Phenotype) [T.Floating]	1.85e-06	2.72e-06	0.681	0.496	-3.48e-06	7.18e-06
Time	2.43e-07	2.34e-07	1.038	0.299	-2.16e-07	7.02e-07
C(Phenotype) [T.Floating]:Time	-7.038e-08	2.84e-07	-0.248	0.804	-6.26e-07	4.86e-07
Urea	-5.05e-08	2.39e-08	-2.115	0.034	-9.73e-08	-3.7e-09
C(Phenotype) [T.Floating]:Urea	6.131e-08	2.77e-08	2.215	0.027	7.06e-09	1.16e-07
Time:Urea	8.384e-09	2.96e-09	2.835	0.005	2.59e-09	1.42e-08
C(Phenotype) [T.Floating]:Time:Urea	-5.163e-09	3.54e-09	-1.459	0.144	-1.21e-08	1.77e-09

Parameter correlations: Ammonia

Generalized Linear Model Regression Results						
=====						
Dep. Variable:	Y	No. Observations:	96			
Model:	GLM	Df Residuals:	88			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.15986			
Method:	IRLS	Log-Likelihood:	-1145.4			
Date:	Tue, 21 May 2019	Deviance:	15.809			
Time:	16:18:11	Pearson chi2:	14.1			
No. Iterations:	7	Covariance Type:	nonrobust			
=====						
	coef	std err	z	P> z	[0.025	0.975]

Intercept	5.906e-06	2.1e-06	2.810	0.005	1.79e-06	1e-05
C(Phenotype) [T.Floating]	1.85e-06	2.43e-06	0.763	0.446	-2.91e-06	6.61e-06
Time	2.43e-07	2.09e-07	1.162	0.245	-1.67e-07	6.53e-07
C(Phenotype) [T.Floating]:Time	-7.038e-08	2.53e-07	-0.278	0.781	-5.67e-07	4.26e-07
Ammonium	-7.175e-09	7.82e-09	-0.918	0.359	-2.25e-08	8.14e-09
C(Phenotype) [T.Floating]:Ammonium	5.693e-08	1.47e-08	3.863	0.000	2.8e-08	8.58e-08
Time:Ammonium	5.944e-10	8.13e-10	0.731	0.465	-9.98e-10	2.19e-09
C(Phenotype) [T.Floating]:Time:Ammonium	-2.649e-09	1.48e-09	-1.785	0.074	-5.56e-09	2.59e-10
=====						

Parameter correlations: Bicarbonate

Generalized Linear Model Regression Results						
=====						
Dep. Variable:	Values	No. Observations:	48			
Model:	GLM	Df Residuals:	40			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	1.13895772977			
Method:	IRLS	Log-Likelihood:	-612.73			
Date:	Fri, 05 Jul 2019	Deviance:	30.400			
Time:	15:15:31	Pearson chi2:	45.6			
No. Iterations:	9					
=====						
	coef	std err	z	P> z	[95.0% Conf. Int.]	

Intercept	3.441e-05	1.61e-05	2.135	0.033	2.83e-06	6.6e-05
C(Phenotypes) [T.Floating]	-2.833e-06	1.91e-05	-0.148	0.882	-4.03e-05	3.46e-05
Time	-2.157e-06	1.09e-06	-1.988	0.047	-4.28e-06	-3e-08
C(Phenotypes) [T.Floating]:Time	1.842e-07	1.29e-06	0.143	0.886	-2.34e-06	2.71e-06
Cconditions	8.339e-09	4.73e-08	0.176	0.860	-8.43e-08	1.01e-07
C(Phenotypes) [T.Floating]:Cconditions	-5.474e-08	5.21e-08	-1.051	0.293	-1.57e-07	4.74e-08
Time:Cconditions	-7.075e-10	3.17e-09	-0.223	0.823	-6.92e-09	5.51e-09
C(Phenotypes) [T.Floating]:Time:Cconditions	4.06e-09	3.53e-09	1.149	0.250	-2.86e-09	1.1e-08
=====						

Parameter correlations: pH

Generalized Linear Model Regression Results						
=====						
Dep. Variable:	Y	No. Observations:	168			
Model:	GLM	Df Residuals:	160			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.21959			
Method:	IRLS	Log-Likelihood:	-2016.9			
Date:	Tue, 21 May 2019	Deviance:	34.902			
Time:	16:19:02	Pearson chi2:	35.1			
No. Iterations:	7	Covariance Type:	nonrobust			
=====						
	coef	std err	z	P> z	[0.025	0.975]

Intercept	1.953e-05	1.05e-05	1.856	0.063	-1.1e-06	4.02e-05
C(Phenotype) [T.Floating]	-9.239e-06	1.27e-05	-0.725	0.468	-3.42e-05	1.57e-05
Time	-2.693e-07	1.01e-06	-0.266	0.790	-2.25e-06	1.71e-06
C(Phenotype) [T.Floating]:Time	5.56e-07	1.27e-06	0.436	0.663	-1.94e-06	3.05e-06
pH	-1.726e-06	1.41e-06	-1.222	0.222	-4.49e-06	1.04e-06
C(Phenotype) [T.Floating]:pH	2.052e-06	1.73e-06	1.183	0.237	-1.35e-06	5.45e-06
Time:pH	6.412e-08	1.37e-07	0.469	0.639	-2.04e-07	3.32e-07
C(Phenotype) [T.Floating]:Time:pH	-1.241e-07	1.74e-07	-0.712	0.476	-4.66e-07	2.17e-07
=====						

2-2 comparison (Tukey) - Urea condition – *P. stuartii*

Omp-Pst1 porin – FCCs

Multiple Comparison of Means - Tukey HSD,FWER=0.05

=====						
group1	group2	meandiff	lower	upper	reject	
4h	0	500	16574.1498	-30452.3034	63600.6031	False
5h	0	500	-38902.0202	-69962.3523	-7841.6881	True
7h	0	500	-71189.8961	-123737.1743	-18642.618	True
9h	0	500	-63057.0912	-127634.1388	1519.9565	True
15h	0	500	-63286.2712	-114749.5456	-11822.9968	True
Omp-Pst2 porin – FCCs						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
=====						
group1	group2	meandiff	lower	upper	reject	
4h	0	500	6261.4946	1996.197	10526.7923	True
5h	0	500	-2134.6555	-12996.94	8727.629	False
7h	0	500	7521.8879	1598.1456	13445.6302	True
9h	0	500	-657.2522	-10717.0073	9402.5029	False
15h	0	500	-539.4299	-9813.6084	8734.7485	False
2-2 comparison (Tukey) - Urea condition – <i>P. stuartii</i> – According Time						
Omp-Pst1 porin – FCCs						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
=====						
group1	group2	meandiff	lower	upper	reject	
4	5	-69510.7473	-90915.2466	-48106.248	True	
4	7	-30288.1114	-51692.6107	-8883.6121	True	
4	9	-47009.2685	-68413.7677	-25604.7692	True	
4	15	-35263.6879	-56668.1872	-13859.1886	True	
5	7	39222.6359	17818.1367	60627.1352	True	
5	9	22501.4789	1096.9796	43905.9781	True	
5	15	34247.0594	12842.5601	55651.5587	True	
7	9	-16721.1571	-38125.6564	4683.3422	False	
7	15	-4975.5765	-26380.0758	16428.9228	False	
9	15	11745.5806	-9658.9187	33150.0798	False	
2-2 comparison (Tukey) – Ammonia condition – <i>P. stuartii</i>						
Omp-Pst1 porin – FCCs						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
=====						
group1	group2	meandiff	lower	upper	reject	
4H	0	500	-48214.2397	-94654.66	-1773.8194	True
5H	0	500	-35184.7269	-66101.6521	-4267.8018	True
7H	0	500	-80993.2267	-134113.1314	-27873.3221	True
9H	0	500	-54354.4792	-118532.4498	9823.4914	True
15H	0	500	-63325.4663	-115029.2888	-11621.6438	True
Omp-Pst1 porin – SABs						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
=====						
group1	group2	meandiff	lower	upper	reject	
7H	0	500	51763.2687	13226.7333	90299.804	True
9H	0	500	44588.3453	-2241.4323	91418.123	False
15H	0	500	122.8988	-69268.6729	69514.4706	False
2-2 comparison (Tukey) – Bicarbonate condition – <i>P. stuartii</i>						
Omp-Pst1 porin – FCCs						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
=====						
group1	group2	meandiff	lower	upper	reject	
4h	0	50	-252343.4867	-407839.5819	-96847.3915	True
5h	0	50	-54122.7379	-107260.2379	-985.2379	True
7h	0	50	-53049.4907	-161346.8928	55247.9113	False
9h	0	50	-37971.1624	-256101.1496	180158.8249	False
15h	0	50	5929.5254	-256043.3444	267902.3952	False

Omp-Pst2 porin – FCCs

Multiple Comparison of Means - Tukey HSD, FWER=0.05

	group1	group2	meandiff	lower	upper	reject
4h	0	50	6895.8395	-59887.8827	73679.5616	False
5h	0	50	345.2546	-17834.8625	18525.3718	False
7h	0	50	11245.2606	-8163.8192	30654.3404	False
9h	0	50	877.444	-9994.3841	11749.2721	False
15h	0	50	16834.8001	595.501	33074.0991	True

2-2 comparison (Tukey) – pH condition – *P. stuartii*

Omp-Pst1 porin – FCCs

4h:

Multiple Comparison of Means - Tukey HSD, FWER=0.05

group1	group2	meandiff	lower	upper	reject
5	6	30203.4498	-33493.5242	93900.4238	False
5	7	49864.7744	-2949.9663	102679.5152	False
5	8	18929.9289	-44767.0451	82626.9029	False
5	9	-5065.2398	-68762.2138	58631.7342	False
6	7	19661.3246	-33153.4161	72476.0654	False
6	8	-11273.5209	-74970.4949	52423.4531	False
6	9	-35268.6896	-98965.6636	28428.2843	False
7	8	-30934.8455	-83749.5863	21879.8952	False
7	9	-54930.0143	-107744.755	-2115.2735	True
8	9	-23995.1687	-87692.1427	39701.8052	False

5h:

Multiple Comparison of Means - Tukey HSD, FWER=0.05

group1	group2	meandiff	lower	upper	reject
5	6	4324.7478	-35825.5557	44475.0512	False
5	7	19422.9899	-13867.883	52713.8628	False
5	8	-9858.4211	-50008.7245	30291.8823	False
5	9	-15480.8529	-55631.1564	24669.4505	False
6	7	15098.2422	-18192.6308	48389.1151	False
6	8	-14183.1688	-54333.4722	25967.1346	False
6	9	-19805.6007	-59955.9041	20344.7027	False
7	8	-29281.411	-62572.2839	4009.4619	False
7	9	-34903.8429	-68194.7158	-1612.9699	True
8	9	-5622.4319	-45772.7353	34527.8716	False

7h:

Multiple Comparison of Means - Tukey HSD, FWER=0.05

group1	group2	meandiff	lower	upper	reject
5	6	83222.8583	9312.0111	157133.7054	True
5	7	77210.3097	15926.6727	138493.9467	True
5	8	37275.7864	-36635.0608	111186.6335	False
5	9	6370.9945	-67539.8527	80281.8416	False
6	7	-6012.5486	-67296.1855	55271.0884	False
6	8	-45947.0719	-119857.919	27963.7752	False
6	9	-76851.8638	-150762.7109	-2941.0167	True
7	8	-39934.5233	-101218.1603	21349.1136	False
7	9	-70839.3152	-132122.9522	-9555.6783	True
8	9	-30904.7919	-104815.639	43006.0552	False

Omp-Pst1 porin – SABs

7h:

Multiple Comparison of Means - Tukey HSD,FWER=0.05						
group1	group2	meandiff	lower	upper	reject	
5	6	-26759.8469	-78909.5474	25389.8536	False	
5	7	-33941.5292	-76521.5814	8638.5229	False	
5	8	-66739.4717	-118889.1722	-14589.7711	True	
5	9	-70736.6287	-122886.3292	-18586.9282	True	
6	7	-7181.6824	-49761.7345	35398.3698	False	
6	8	-39979.6248	-92129.3253	12170.0757	False	
6	9	-43976.7818	-96126.4823	8172.9187	False	
7	8	-32797.9424	-75377.9946	9782.1098	False	
7	9	-36795.0995	-79375.1516	5784.9527	False	
8	9	-3997.157	-56146.8576	48152.5435	False	

2-2 comparison (Tukey) - Urea condition – <i>P. stuartii</i> ΔOmp-Pst2						
Omp-Pst1 porin – FCCs						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
group1	group2	meandiff	lower	upper	reject	
4h	0	500	-48814.8603	-79244.6239	-18385.0967	True
5h	0	500	-79571.3733	-112223.3454	-46919.4013	True
7h	0	500	-84041.5601	-146780.2218	-21302.8985	True
9h	0	500	-80294.8613	-120605.1033	-39984.6194	True
15h	0	500	-66788.6326	-124584.7873	-8992.4779	True

Multiple Comparison of Means - Tukey HSD,FWER=0.05						
group1	group2	meandiff	lower	upper	reject	
7h	0	500	-51532.3838	-131390.0291	28325.2614	False
9h	0	500	-67561.3871	-143722.56	8599.7859	False
15h	0	500	-85432.9544	-138213.5268	-32652.382	True

2-2 comparison (Tukey) – Ammonia condition – <i>P. stuartii</i> ΔOmp-Pst2						
Omp-Pst1 porin – FCC						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
group1	group2	meandiff	lower	upper	reject	
4h	0	500	-40754.5817	-70288.9453	-11220.2181	True
5h	0	500	-79073.6582	-112314.5001	-45832.8162	True
7h	0	500	-104908.034	-169132.0224	-40684.0456	True
9h	0	500	-108527.7472	-148262.142	-68793.3525	True
15h	0	500	-21559.4458	-79543.416	36424.5245	True

2-2 comparison (Tukey) – pH condition – <i>P. stuartii</i> ΔOmp-Pst2						
Omp-Pst1 porin – FCC						
5h:						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
group1	group2	meandiff	lower	upper	reject	
5	6	17463.0878	-29975.2601	64901.4357	False	
5	7	61544.038	22810.7891	100277.2868	True	
5	8	31719.0228	-15719.3251	79157.3706	False	
5	9	11726.8916	-35711.4563	59165.2394	False	
6	7	44080.9502	5347.7013	82814.199	True	
6	8	14255.935	-33182.4129	61694.2828	False	
6	9	-5736.1962	-53174.5441	41702.1516	False	
7	8	-29825.0152	-68558.2641	8908.2336	False	

7	9	-49817.1464	-88550.3953	-11083.8976	True
8	9	-19992.1312	-67430.4791	27446.2167	False

7h:

```

Multiple Comparison of Means - Tukey HSD,FWER=0.05
=====
group1 group2  meandiff      lower      upper    reject
-----
5      6      25669.2245 -61218.4629  112556.9119 False
5      7      82700.2695  11756.7698  153643.7692  True
5      8      12770.8041 -74116.8833   99658.4916 False
5      9     -14547.9893 -101435.6767  72339.6981 False
6      7      57031.045  -13912.4547  127974.5447 False
6      8     -12898.4204 -99786.1078   73989.267  False
6      9     -40217.2138 -127104.9013  46670.4736 False
7      8     -69929.4654 -140872.9651  1014.0343  False
7      9     -97248.2588 -168191.7585 -26304.7591  True
8      9     -27318.7935 -114206.4809  59568.894  False

```

9h:

```

Multiple Comparison of Means - Tukey HSD,FWER=0.05
=====
group1 group2  meandiff      lower      upper    reject
-----
5      6      21948.695  -38626.9602   82524.3501 False
5      7      84516.5196  35056.7043  133976.3349  True
5      8      43319.6633 -17255.9918  103895.3184 False
5      9     -22639.6063 -83215.2615   37936.0488 False
6      7      62567.8246  13108.0093  112027.6399  True
6      8      21370.9683 -39204.6868   81946.6235 False
6      9     -44588.3013 -105163.9564  15987.3538 False
7      8     -41196.8563 -90656.6716   8262.959  False
7      9     -107156.1259 -156615.9412 -57696.3107  True
8      9     -65959.2696 -126534.9248 -5383.6145  True

```

Supplementary Table S3 – Statistical analysis from DLS experiments on porin propensity to self-associate in DOTs. All experiments were conducted for at least three biologically independent replicates. Technical replicates were averaged to produce replicate means that were subsequently used for analysis. Mean values were compared within and between groups using one-way ANOVA followed by Tukey's post hoc for two-two comparisons. Differences were considered statistically significant if $p < 0.05$ (True).

GLM - DLS

Omp-Pst1 porin – All statistic parameters:

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	389			
Model:	GLM	Df Residuals:	381			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.097908			
Method:	IRLS	Log-Likelihood:	-1972.8			
Date:	Mon, 18 Mar 2019	Deviance:	33.696			
Time:	14:17:24	Pearson chi2:	37.3			
No. Iterations:	7	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0137	0.002	8.950	0.000	0.011	0.017
Cporin	-0.0130	0.002	-7.730	0.000	-0.016	-0.010
Urea	2.3e-07	6.93e-07	0.332	0.740	-1.13e-06	1.59e-06
Cporin:Urea	7.344e-07	8.34e-07	0.881	0.378	-9e-07	2.37e-06
Ammonium	3.751e-06	9.29e-07	4.036	0.000	1.93e-06	5.57e-06
Cporin:Ammonium	4.42e-06	1.36e-06	3.246	0.001	1.75e-06	7.09e-06
pH	-0.0007	0.000	-3.151	0.002	-0.001	-0.000
Cporin:pH	0.0012	0.000	5.136	0.000	0.001	0.002

Omp-Pst2 porin – All statistic parameters:

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	386			
Model:	GLM	Df Residuals:	378			
Model Family:	Gamma	Df Model:	7			
Link Function:	inverse_power	Scale:	0.36485			
Method:	IRLS	Log-Likelihood:	-2501.6			
Date:	Mon, 18 Mar 2019	Deviance:	123.99			
Time:	14:19:20	Pearson chi2:	138.			
No. Iterations:	8	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0066	0.001	4.551	0.000	0.004	0.010
Cporin	-0.0046	0.001	-3.105	0.002	-0.008	-0.002
Urea	4.958e-07	6.87e-07	0.722	0.470	-8.51e-07	1.84e-06
Cporin:Urea	-6.935e-07	6.79e-07	-1.022	0.307	-2.02e-06	6.36e-07
Ammonium	1.284e-05	1.92e-06	6.681	0.000	9.07e-06	1.66e-05
Cporin:Ammonium	-1.208e-05	1.82e-06	-6.651	0.000	-1.56e-05	-8.52e-06
pH	-0.0003	0.000	-1.475	0.140	-0.001	9.77e-05
Cporin:pH	0.0002	0.000	1.107	0.268	-0.000	0.001

Omp-Pst1 porin – Bicarbonate – All statistic parameters:

Generalized Linear Model Regression Results						
Dep. Variable:	Y	No. Observations:	96			
Model:	GLM	Df Residuals:	92			
Model Family:	Gamma	Df Model:	3			
Link Function:	inverse_power	Scale:	0.0066722			
Method:	IRLS	Log-Likelihood:	-380.86			
Date:	Sat, 20 Apr 2019	Deviance:	0.62057			
Time:	11:22:54	Pearson chi2:	0.614			
No. Iterations:	7	Covariance Type:	nonrobust			
	coef	std err	z	P> z	[0.025	0.975]
Intercept	0.0129	0.000	60.130	0.000	0.012	0.013
Bicarbonate	2.458e-06	4.09e-06	0.601	0.548	-5.56e-06	1.05e-05
Concentration	-0.0109	0.000	-50.047	0.000	-0.011	-0.010

Bicarbonate:Concentration	1.985e-05	4.23e-06	4.691	0.000	1.16e-05	2.81e-05
=====						
Omp-Pst1 porin – Bicarbonate:						
Generalized Linear Model Regression Results						
=====						
Dep. Variable:	Y	No. Observations:	96			
Model:	GLM	Df Residuals:	94			
Model Family:	Gamma	Df Model:	1			
Link Function:	inverse_power	Scale:	0.49076			
Method:	IRLS	Log-Likelihood:	-601.92			
Date:	Sat, 20 Apr 2019	Deviance:	56.351			
Time:	11:23:18	Pearson chi2:	46.1			
No. Iterations:	7	Covariance Type:	nonrobust			
=====						
	coef	std err	z	P> z	[0.025	0.975]

Intercept	0.0037	0.000	8.701	0.000	0.003	0.005
Bicarbonate	2.78e-05	1.06e-05	2.634	0.008	7.11e-06	4.85e-05
=====						

Omp-Pst2 porin – Bicarbonate – All statistic parameters:						
Generalized Linear Model Regression Results						
=====						
Dep. Variable:	Y	No. Observations:	50			
Model:	GLM	Df Residuals:	48			
Model Family:	Gamma	Df Model:	1			
Link Function:	inverse_power	Scale:	0.016299			
Method:	IRLS	Log-Likelihood:	-246.36			
Date:	Sat, 20 Apr 2019	Deviance:	0.76802			
Time:	11:34:22	Pearson chi2:	0.782			
No. Iterations:	18	Covariance Type:	nonrobust			
=====						
	coef	std err	z	P> z	[0.025	0.975]

Intercept	0.0013	3.89e-05	33.427	0.000	0.001	0.001
Bicarbonate	1.703e-05	1.17e-06	14.569	0.000	1.47e-05	1.93e-05
Concentration	0.0013	3.89e-05	33.427	0.000	0.001	0.001
Bicarbonate:Concentration	1.703e-05	1.17e-06	14.569	0.000	1.47e-05	1.93e-05
=====						

Omp-Pst2 porin – Bicarbonate:						
Generalized Linear Model Regression Results						
=====						
Dep. Variable:	Y	No. Observations:	50			
Model:	GLM	Df Residuals:	48			
Model Family:	Gamma	Df Model:	1			
Link Function:	inverse_power	Scale:	0.016299			
Method:	IRLS	Log-Likelihood:	-246.36			
Date:	Sat, 20 Apr 2019	Deviance:	0.76802			
Time:	11:35:15	Pearson chi2:	0.782			
No. Iterations:	6	Covariance Type:	nonrobust			
=====						
	coef	std err	z	P> z	[0.025	0.975]

Intercept	0.0026	7.79e-05	33.427	0.000	0.002	0.003
Bicarbonate	3.405e-05	2.34e-06	14.569	0.000	2.95e-05	3.86e-05
=====						

2-2 comparison (Tukey) – Ammonia condition						
Omp-Pst1 porin						
Multiple Comparison of Means - Tukey HSD,FWER=0.05						
=====						
group1	group2	meandiff	lower	upper	reject	

0	100	-226.57	-347.8389	-105.3011	True	
0	500	-207.49	-328.7589	-86.2211	True	
0	1000	-230.26	-351.5289	-108.9911	True	
100	500	19.08	-120.9493	159.1093	False	
100	1000	-3.69	-143.7193	136.3393	False	

500	1000	-22.77	-162.7993	117.2593	False
Omp-Pst2 porin					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
group1	group2	meandiff	lower	upper	reject
0	100	98.33	2.99	193.67	True
0	500	193.62	98.28	288.96	True
0	1000	308.39	205.411	411.369	True
100	500	95.29	-14.7991	205.3791	False
100	1000	210.06	93.2928	326.8272	True
500	1000	114.77	-1.9972	231.5372	False
2-2 comparison (Tukey) – Bicarbonate condition					
Omp-Pst1 porin					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
group1	group2	meandiff	lower	upper	reject
0	10	-57.92	-125.4145	9.5745	False
0	25	-71.63	-126.739	-16.521	True
0	50	-185.4	-240.509	-130.291	True
0	100	-260.72	-315.829	-205.611	True
10	25	-13.71	-81.2045	53.7845	False
10	50	-127.48	-194.9745	-59.9855	True
10	100	-202.8	-270.2945	-135.3055	True
25	50	-113.77	-168.879	-58.661	True
25	100	-189.09	-244.199	-133.981	True
50	100	-75.32	-130.429	-20.211	True
Omp-Pst2 porin					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
group1	group2	meandiff	lower	upper	reject
0	10	-116.89	-151.1648	-82.6152	True
0	25	-139.98	-174.2548	-105.7052	True
0	50	-221.96	-256.2348	-187.6852	True
0	100	-242.87	-277.1448	-208.5952	True
10	25	-23.09	-57.3648	11.1848	False
10	50	-105.07	-139.3448	-70.7952	True
10	100	-125.98	-160.2548	-91.7052	True
25	50	-81.98	-116.2548	-47.7052	True
25	100	-102.89	-137.1648	-68.6152	True
50	100	-20.91	-55.1848	13.3648	True
2-2 comparison (Tukey) – pH condition					
Omp-Pst1 porin					
Multiple Comparison of Means - Tukey HSD,FWER=0.05					
group1	group2	meandiff	lower	upper	reject
5	6	-110.6	-137.2876	-83.9124	True
5	7	14.73	-11.9576	41.4176	False
5	8	-192.42	-219.1076	-165.7324	True
5	9	-165.36	-192.0476	-138.6724	True
6	7	125.33	98.6424	152.0176	True
6	8	-81.82	-108.5076	-55.1324	True
6	9	-54.76	-81.4476	-28.0724	True
7	8	-207.15	-233.8376	-180.4624	True
7	9	-180.09	-206.7776	-153.4024	True
8	9	27.06	0.3724	53.7476	True