Supplementary Information

Repurposing a chemosensory macromolecular machine

Ortega D. R. et al.
Supplementary Discussion

Our results also shed light on the biological function of CheD. CheD is thought to interact with chemoreceptors in an adaptation mechanism together with CheC and CheY\(^1\), but more recent results showed that CheD from *Bacillus subtilis* is able to deamidate chemoreceptors *in vitro* without CheC\(^2\). Our results provide two further pieces of evidence supporting the idea that CheD is able to perform a biological role independently of CheC. First, the ancestral F7 system included cheD but not cheC. Second, cheD co-evolved with the ancestral F7 cheY (it was lost in the same evolutionary step), pointing to a functional link.

A recent study in *Comamonas testosteroni*, an organism with a stage 4 F7 system, shows that the kinase CheA is able to phosphorylate both the ancient CheY as well as the recently acquired CheY-F6-like\(^3\). Deletion of the CheY-F6-like protein completely abolished chemotaxis response, while the deletion of CheY-F7 only partially affected it. The study further shows that CheY-F7 has a much faster auto-dephosphorylation rate than CheY-F6-like. The authors interpreted these results such that the CheY-F6-like is the primary response regulator, and CheY-F7 may act as a phosphate sink. These conclusions are based on previous work in organisms with multiple CheY genes per chemosensory cluster.

However, because CheY-F7 in stages 1 and 2 is the sole response regulator of the system, we hypothesize that it plays a major role in the control of a yet-unknown cellular process, at least in stages 1 and 2. The rapid auto-dephosphorylation does not necessarily imply a phosphate sink as the main biological function of this CheY. Thus, in the intermediate stages of the extant \(\beta\)-Proteobacteria, including the system in *C. testosteroni*, the CheY-F7 may retain both the older unknown function as well as its new role in the control of the flagellar motor.

On the other hand, the immediate loss of McpA and adjacent genes from stage 1 to 3, might indicate the loss of the original F7 function. If this were true, why would the system keep a conserved response regulator (cheY) for a lost function? One hypothesis is that the original CheY and CheD might be serving in an auxiliary feedback loop in addition to the canonical CheB/CheR adaptation mechanism in stages 3 and 4. This could compensate response time of the flagellar control as the system acquired mutations to accommodate the new components and function,
providing flexibility. In the stage 5, the system evolved to perform optimum response without the need of CheY/CheD adaptation mechanism, resulting in loss of these components in that stage.

Imaging four $\gamma$-Proteobacteria with both F6 and F7 systems by cryo-ET, we observed that the arrays formed by different chemosensory systems were both separate and structurally distinct. This is consistent with previous studies showing physical separation of the arrays from different chemosensory gene clusters in *V. cholerae* (F6 and F9 systems $^4$) and *P. aeruginosa* (F6 and F7 systems$^5$). It is also consistent with experiments in *E. coli* showing that engineered chemoreceptors with additional heptads cannot form arrays with shorter, native chemoreceptors, likely because of a large physical mismatch in the CheA/CheW layers$^6$.

In all cases, we observed that the F7 arrays in non-enteric $\gamma$-Proteobacteria were membrane-associated, but it remains unclear how this is achieved. In other arrays, N-terminal hydrophobic alpha-helices of chemoreceptors mediate membrane insertion. Aer2-like receptors in *V. cholerae*, *P. aeruginosa* and *S. oneidensis*, however, lack any predicted transmembrane regions. The *M. alcaliphilum* Aer2-like receptor has two small fragments of transmembrane regions (10 and 14 residues), but these are likely too short to attach the receptor to the membrane. One possibility is that the receptors are post-translationally modified for membrane attachment. Another possibility is that another protein serves as a membrane anchor. Our work ruled out one such candidate – the McpA receptor in the same gene cluster; $\Delta$mcpA F7 arrays were still attached to the membrane.

One of the most striking features of the F7 arrays in non-enteric $\gamma$-Proteobacteria was the presence of additional density layers between the CheA/CheW baseplate and the IM. Based on our homology models of the receptors, we propose that these layers correspond to domain features (Fig. 2B). The L2 layer matched the PAS domain present in Aer2-like receptors in all four species. The fainter (possibly less-ordered) L3 layer in *V. cholerae* and *S. oneidensis* matched the additional PAS domain in the Aer2-like receptors from these species. This suggests that PAS domains might mediate intra- and inter-trimer interactions, potentially contributing to cooperativity in the signaling array. The L1 layer matched the junction between the HAMP and signaling domains, which is puzzling because this chemoreceptor region is predicted to have low molecular density$^7$. It is unlikely that this density is produced by another known chemotaxis protein. For example
CheR, that binds the chemoreceptor in that area, is not expected to have enough abundance to generate a visible density layer\textsuperscript{8,9}. Furthermore, previous cryo-ET of \textit{in vitro} preparations containing only \textit{E. coli} CheA, CheW and Tsr showed a similar layer in that region, suggesting one or more of these proteins alone is responsible for the L1 layer\textsuperscript{10}. Similarly, the L3 layer in \textit{P. aeruginosa} F7 array appears to be located between 2 HAMP domains. Interestingly, both \textit{P. aeruginosa} L3 and the L1 layer in all organisms coincide with a coupling double alpha-helix linker between two four-helical bundles. However, the composition of these layers remains unclear.

Another mystery is the function of the F7 chemosensory array in non-enteric \textgamma-Proteobacteria. Flagellar motility in these organisms is controlled by the F6 chemosensory system\textsuperscript{11–13}, which is expressed under a variety of conditions. In contrast, the \textit{P. aeruginosa} and \textit{V. cholerae} F7 system is only expressed when cells are grown in stressful conditions such as into late stationary phase, induced by the stress-related sigma factor RpoS\textsuperscript{5,14,15}. Expression of the F7 system in different conditions has not been studied in \textit{S. oneidensis} or \textit{M. alcaliphilum}, but both organisms live in unique and challenging environments which may be poorly mimicked by laboratory growth; \textit{S. oneidensis} is a facultative anaerobe adapted to changing environments\textsuperscript{16} and \textit{M. alcaliphilum} is a haloalkaliphilic methanotroph\textsuperscript{17}. While we did not test different growth conditions for \textit{M. alcaliphilum}, we did observe that formation of F7 arrays in \textit{S. oneidensis} was dependent on culture conditions. Another clue is that both \textit{P. aeruginosa} and \textit{V. cholerae} are capable of sensing oxygen, which binds to the PAS-heme domains of Aer2 receptors to activate signaling\textsuperscript{18,19}. We therefore favor the working model that the older F7 systems are part of an emergency response system activated by stress conditions, perhaps related to the availability of oxygen. The McpA receptor may also be an important mediator of this response. McpA has no sensory domain, but has been implicated in taxis toward trichloroethylene\textsuperscript{20}. A previous study in \textit{P. aeruginosa} showed that McpA physically co-localizes with F6 system proteins\textsuperscript{5}. Here we find that despite being part of the F6 system, McpA co-evolved with the F7 system, suggesting that McpA may bridge the two systems to provide additional inputs to the flagellar control system in response to stress.
Supplementary Figure 1: Phylogeny of CheA, CheB and CheR concatenated alignments of F7 and F8 systems and gene neighborhood of 15 genes up and downstream from CheA. The inlet shows a CheABR tree with additional sequences from F1 systems. The tree is rooted by the common ancestor between F1 systems and the F7/F8 systems.
Supplementary Figure 2: Phylogenetic profile of the F7 and F6 systems in g-Proteobacteria shows that only organisms with F7 stage 1 (red) or stage 2 (green) systems also has F6 systems. Organisms with F7 stage 5 (blue) does not have F6 systems. Note that the distribution of stage 1 and stage 2 are mixed in the non-enteric group. Genomes with empty circles were genomes included in this part of the research but not in the analysis of classifying the F7 systems.
Supplementary Figure 3: Protein domain architecture of chemoreceptors in the gene cluster of stage 3 and 4 of F7 systems shows the high incidence of receptors with transmembrane regions and periplasmic sensory domains (TarH, Cache superfamily, 4HB-MCP_1).
Supplementary Figure 4: Sequence logo of the C-terminal of McpA-like sequences.

Supplementary Figure 5: Phylogenetic tree of Aer2-like receptors and McpA-like receptors.

The tags in the tips are built using the name of the organism and the locus of the receptor. Tips with red dots belong to chemoreceptors from stage 1 and green to stage 2. The only exception to the monophyletic distribution of Aer2-like receptors were in *V. cholerae*, where an addition to the Aer2 homolog, a second, orphan 36H receptor (VC0098) was likely introduced by a recent lateral gene transfer from *Marinomonas*. Genomes with empty circles were genomes included in this part of the research but not in the analysis of classifying the F7 systems.
**Supplementary Figure 6:** The 1D electron density profile is a collapse of a 3D sub-volume. For each model point (red), the algorithm extends a profile perpendicular to the model points (blue). Then, it averages the intensity of the pixels perpendicular to the profile in the slices above and below (green). The final 1D profile is an average of the profiles calculated for each pixel of the model point.
Supplementary Tables

Supplementary Table 1: Presence and absence of the chemosensory arrays in imaged strains of *V. cholerae, P. aeruginosa, S. oneidensis*, and *M. alcaliphilum*.

|                          | Imaged cell poles | Short array | Tall array |
|--------------------------|-------------------|-------------|------------|
| **Vibrio cholerae**      |                   |             |            |
| Wild-type C6706          | 29                | 20          | 7          |
| Δmcp (VCA1088)           | 20                | 19          | 5          |
| ΔF7 cheW, cheW, cheA (VCA1093, VCA1094, VCA1095) | 29 | 18 | 0 |
| Δmcp (Aer2/VCA1092)      | 27                | 24          | 0          |
| **Pseudomonas aeruginosa** |                  |             |            |
| Wild -type PAO1          | 16                | 7           | 5          |
| ΔF6 cheW                 | 15                | 8           | 6          |
| Δmcp ‘mcpA’ (PAO180)     | 8                 | 4           | 2          |
| ΔF7 cheW (PAO177)        | 33                | 12          | 0          |
| ΔF7 cheA (PAO 178)       | 34                | 24          | 0          |
| Δmcp ‘aer2’, ‘mcpB’ (PAO176) | 21       | 11          | 0          |
| **Shewanella oneidensis MR-1** |                |             |            |
| Chemostat growth         | 29                | 20          | 7          |
| Batch culture growth      | 29                | 18          | 0          |
| **Methylomicrobium alcaliphilum 20Z** |          |             |            |
| Wild-type                | 8                 | 5           | 2          |
### Supplementary Table 2: Chemosensory gene clusters in the genomes of *V. cholerae*, *P. aeruginosa*, *S. oneidensis* and *M. alcaliphilum*.

|                     | Classification | Alternative name in literature | Function                        | Gene cluster          |
|---------------------|----------------|---------------------------------|----------------------------------|-----------------------|
| *Vibrio cholerae*   |                |                                 |                                  |                       |
| Cluster I           | F9             | -                               | Unknown                          | VC1394-VC1405         |
| Cluster II          | F6             | -                               | Chemotaxis                       | VC2059-VC2064         |
| Cluster III         | F7             | -                               | Unknown                          | VCA1090-VCA1095       |
| *Pseudomonas aeruginosa* |            |                                 |                                  |                       |
| Cluster I/V         | F6             | Che I                           | Chemotaxis                       | PA1457-PA1464         |
| Cluster II          | F7             | Che II                          | Unknown                          | PA0173-PA0180         |
| Cluster III         | ACF            | Wsp                             | Biofilm formation                | PA3703-PA3708         |
| Cluster IV          | TFP            | Chp                             | Twitching motility               | PA0410-PA0415         |
| *Shewanella oneidensis* |            |                                 |                                  |                       |
| Cluster I           | F7             | CheA-1                          | Unknown                          | SO_2117-SO_2126       |
| Cluster II          | F6             | CheA-3                          | Chemotaxis                       | SO_3200-SO_3209       |
| *Methylomicrobium alcaliphilum* | |                          |                                  |                       |
| Cluster I           | F7             | -                               | Unknown                          | MEALZ_2869-MEALZ_2879 |
| Cluster II          | F8             | -                               | Unknown                          | MEALZ_2939-MEALZ_2942 |
| Cluster III         | F6             | -                               | Unknown                          | MEALZ_3148-MEALZ_3158 |
Supplementary Table 3: Number of cells and sub-tomograms used to generate averages shown in Figure 2.

|                      | Cells (tomograms) | Sub-tomograms | Pixel size (nm) |
|----------------------|-------------------|---------------|-----------------|
| *P. aeruginosa*      | 5                 | 1113          | 0.64            |
| *V. cholerae*        | 6                 | 265           | 1.3             |
| *S. oneidensis*      | 5                 | 327           | 1               |
| *M. alcaliphilum*    | 2                 | 1448          | 1               |

Supplementary Table 4: Locations of electron density layers in arrays. Distances are measured from the CheA/CheW baseplate in nanometers. Uncertainties reported are the expanded standard uncertainty.

| Layers (F7)       | *V. cholerae*     | *P. aeruginosa* | *S. oneidensis* | *M. alcaliphilum* |
|-------------------|-------------------|-----------------|-----------------|-------------------|
| Inner membrane (IM)| 38.4±1.9 nm       | 40.3±1.8 nm     | 35.5±2.7 nm     | 35.1±2.8 nm       |
| Layer 3 (L3)      | 29.5±1.9 nm       | 30.7±1.8 nm     | 30.7±4.3 nm     | -                 |
| Layer 2 (L2)      | 24.8±1.9 nm       | 24.0±1.8 nm     | 24.0±2.7 nm     | 25.3±4.4 nm       |
| Layer 1 (L1)      | 17.5±1.9 nm       | 17.9±2.9 nm     | 17.3±2.7 nm     | 17.4±4.4 nm       |
| Signaling Layer (SL)| -               | 7.0±1.8 nm     | 6.7±4.3 nm     | 7.5±2.8 nm       |

Supplementary Table 5: *P. aeruginosa* strains

| Strain name | PA ORF | Gene               |
|-------------|--------|--------------------|
| PW1307      | PA0178 | CheA F7 system     |
| PW1305      | PA0177 | CheW F7 system     |
| PW1312      | PA0180 | MCPA               |
| PW3654      | PA1464 | CheW F6 system     |

Supplementary Table 6: Cryo-Electron Tomograms used in this study available on ETDB. Tomograms can be found on ETDB by the Open Index Protocol id (OIP id).

| Jensen Lab id | OIP id                                                                 | Organism    |
|--------------|------------------------------------------------------------------------|-------------|
| ab2015-06-02-1| 6cefe7c25e66ce42e4e2440490a68845a5513037717bc9e096c48fd83b47ae9cd        | *Vibrio cholerae* |
| ab2015-06-02-2| 98d93b8c8e390eb6c200fc2d30c9626cb1a7c140cd30a60eddb3a179a8226b           | *Vibrio cholerae* |
| Jensen Lab id   | OIP id                                                                 | Organism          |
|----------------|-------------------------------------------------------------------------|-------------------|
| ab2015-06-02-3 | 39a5d8490ee3823eaf785268aba1593d3be05bf8b66cc0292d0c247bb7b0a6ba       | Vibrio cholerae  |
| ab2015-06-02-5 | 2620f1ee27c5e63853bb3f3d09796b19d7bd91fbd5781daa892d68fb31be735        | Vibrio cholerae  |
| ab2015-06-02-6 | 9ba344e00d31084d2aef8a799f3089e46ead3b2a02c0e73c5852337f67121fc         | Vibrio cholerae  |
| ab2015-06-02-7 | 1e00525c41a9faa849b9fd686b70757a6f25a9ceacb6e951b6eef99006f09          | Vibrio cholerae  |
| ab2015-06-02-8 | 3cb8dc276fb373a99af2ee54301fcb0989eb0037b9c3c2bd21f8e035f0f9b215         | Vibrio cholerae  |
| ab2015-06-02-9 | 5739b1525b6a0e906de41a8e024e0b502f964e19193feeeda1a62ced0e41b5d5d17    | Vibrio cholerae  |
| ab2015-06-02-10| 7e869e97212b3df06a7f0dec5f77ef3836c1ec4787f1cbe677da60aca3bda727       | Vibrio cholerae  |
| ab2015-06-02-11| 8329b3a0b5373c89d5280c42ca8aabb19a38a6ee03e5910275b82776f8745fa         | Vibrio cholerae  |
| ab2015-06-02-12| de04da0f550b2f37da40847e13b637877ed6994bb5d8d0c24c87ad9f3cf52924        | Vibrio cholerae  |
| ab2015-06-02-13| 4caf0202a48c92372ca3a24101d9c5e2b446fadbf80109b5d071509811fa3aa         | Vibrio cholerae  |
| ab2015-06-02-14| b2f7be0de38a1eb8d0eab4d8493616c9122931ec0490e1bb5b45474a032098f        | Vibrio cholerae  |
| ab2015-06-02-15| bd8198a02bd6692981104ff1b15a243f4705433876cb56c784db8f91378e00          | Vibrio cholerae  |
| ab2015-06-02-16| 87c29d70069315af599618c344d80bf2fc48f44c0057002798241842b5b5c9          | Vibrio cholerae  |
| ab2015-06-02-17| 066cf7fae820b463b2e7405a9078e97b6de9910587458df904759d75f4ed2c          | Vibrio cholerae  |
| ab2015-06-02-18| 82fdc6778793542fad9bfe7c18a6fa972dc3bf230b2e108aa53a5807811bdad7       | Vibrio cholerae  |
| ab2015-06-02-20| 2524250ba11140c386c211aa14d164a166926ee9ca7af566aeeedbbaba29856c48    | Vibrio cholerae  |
| ab2015-06-02-21| 95a8202f59bdcfc9814f417aa40b3c355fc6f12cb147784d1d1665d8ccce8221       | Vibrio cholerae  |
| ab2015-06-02-22| 09443b1917375d027553f4c2029dc847c654efdb2e5a3df0c5938a9afaa1a9          | Vibrio cholerae  |
| Jensen Lab id | OIP id                                      | Organism        |
|--------------|---------------------------------------------|-----------------|
| ab2015-06-02-23 | 453536f21d3074fd3f6fcae6d834c6e37335f46 6611e2f1842c6beb8e7e7681e | Vibrio cholerae |
| ab2015-06-02-24 | 03ab91b142bf62ed9c21e1da4b17e25d7c7b7 0cbd6a25481342d9736f2a2290 | Vibrio cholerae |
| ab2015-06-02-25 | 8853ea7d7f6da168b62b9db8694ad82dfa23c 9b00eafb3f71b025f20cb3ab4d | Vibrio cholerae |
| ab2015-06-02-26 | 8770f212cedc32db61a0e0b8a40a5ea1ec42c 31bceda0c4919b86dcde7246b | Vibrio cholerae |
| ab2015-06-02-27 | e1b34b3df7aa6367398901bfb96d5a003759a 2dd71a473e45a43d598e7792d9 | Vibrio cholerae |
| ab2015-06-02-29 | 08324bf01302bd1bd972045548218ff3e317aea e74602363e66a187c52e234be | Vibrio cholerae |
| ab2015-06-02-30 | 2eda58ca01240b7486bda36c36e36217918c8 9fc1361dada13e9ad95af4271 | Vibrio cholerae |
| ab2015-06-02-31 | 6b6bb8a7f2127c66174756b85d4bf0efde943c bfc305e40a3330181009bd893e | Vibrio cholerae |
| ab2015-06-02-32 | 61c8ec9a912eb1bceda440939a48d46e99128f feca99578b16e0e2031f4a22 | Vibrio cholerae |
| ab2015-06-03-1  | 1979f4babc9f5fa49c4644f3f40df46cbf2b82399 e8137db7799b9e030bc8455 | Vibrio cholerae |
| ab2015-06-03-2  | 544970e8e49ff409d461730c89757fdebee6fff3 64c1c604d355bc522c88df0f12 | Vibrio cholerae |
| ab2015-06-03-3  | e87e0b6e154e5dfe0c120ce92e6400764ae249 64aa592553e49de6187b7fbb57 | Vibrio cholerae |
| ab2015-06-03-4  | 20d581e5578e3156dd96496119c1296494e0 62deecf45634c79f19f3313686b | Vibrio cholerae |
| ab2015-06-03-5  | 10c8a0be7b87bd95eb2d8573e782a856e493 b65735a0b290c0a772092d2efc | Vibrio cholerae |
| ab2015-06-03-6  | 0c1b01aa1ed45fcba7d17500c4829f9480924fa 210f9706d6a1a5da9d4dc1477 | Vibrio cholerae |
| ab2015-06-03-7  | 21482339f240527367c699214ba438d2b9a7a c6376d611f2d69e6e8c10d41d039 | Vibrio cholerae |
| ab2015-06-03-8  | 453a055bdf6eb8d65f2154f51a568cfc3f58c36 aa445f6be7a820cd3963e9 | Vibrio cholerae |
| ab2015-06-03-9  | faed3ad56cb4667d1986bb9a7869a4a9da0a9 e2d016dbb6d823e1f5f1cc149 | Vibrio cholerae |
| Jensen Lab id | OIP id | Organism |
|--------------|--------|----------|
| ab2015-06-03-10 | 1c8abd7e25085ccce2ce38fb25ff51ac70ddfc88cad18322406467298bfaa3e | Vibrio cholerae |
| ab2015-06-03-11 | 920321536f97c55c300ad77d279265973442bd4ec0e7286a952d134ec384b42 | Vibrio cholerae |
| ab2015-06-03-12 | 9262dbfb593f79bf0cf9ac6f9125326ed755dd3e4edc569b68b0fc279f84d8d | Vibrio cholerae |
| ab2015-06-03-13 | 72b627c7010d0ea37a8aa011925069437195c51f77e5adcf41f6a8330e75cc65 | Vibrio cholerae |
| ab2015-06-03-14 | 223d692a658a507a7085c75f8c757b05c1cf1d2ee8e352a1db4371f2062e3ec4 | Vibrio cholerae |
| ab2015-06-03-15 | c55cf52f955579f23cda1c2244e2b64315f8fbb490f106899cf327a87a99512 | Vibrio cholerae |
| ab2015-06-03-16 | b59e667fadb1914c70ad191dad31a30a87ba416e8de4877000d1f6cb52869601 | Vibrio cholerae |
| ab2015-06-03-17 | 067ac5b8ce49df5e254c958a0e6b6fd601de877847f17d8db6c76f2b30d882 | Vibrio cholerae |
| ab2015-06-03-18 | c9dd866db34f7ed34af143d2a879e5b28035fce2a4392aceb54f7824ceec0e37 | Vibrio cholerae |
| ab2015-06-03-19 | fabd724070997b695534be1bc4ad91faa2b2c82876f66da65aeeee18eb39ca29 | Vibrio cholerae |
| ab2015-06-03-20 | 34ff16d0af7ba6cfbe49df20981049070d2b9b9f5a1919896a839eb62dc86a8 | Vibrio cholerae |
| ab2015-06-03-21 | 4440060c9b511b30ec0b7c123b3891a3823a77a8393437862aa534392e0be26 | Vibrio cholerae |
| ab2015-06-03-22 | 48c976b5ec236342fdd4aefe521086e3657da4a45c4afad6003edeb44a5e8275 | Vibrio cholerae |
| ab2015-06-03-23 | 1c1669ab1c51ec5655f2fc7e1296de6494c1c68785e7f4a7ce0cc651d2125c9 | Vibrio cholerae |
| ab2015-06-03-24 | aa070936e1ae30b373bc2d2aed88f1576cd3ed6766dcb992f1200e46aeaebe | Vibrio cholerae |
| ab2015-06-03-25 | d84b38c0f3c63be65666a28afa8900aeac8991b29dad0b539585fbc3b96c | Vibrio cholerae |
| ab2015-06-03-26 | f38ac8c272b532e7dd3e3da38b1fff38f42385a2aa55872da24bf10720544ba | Vibrio cholerae |
| ab2015-06-03-27 | 9d8070fbab0e5bfdd555544219789104f5dcbda613d24385c416cccd3c3158 | Vibrio cholerae |
| Jensen Lab id | OIP id                                                | Organism               |
|--------------|------------------------------------------------------|------------------------|
| ab2015-06-03-28 | bd0aa53c9bb4904c623c2304b5ca71f3e7dbbb15fdbe2eb481dbdb01d561986 | Vibrio cholerae        |
| ab2015-06-03-29 | 81345eefbcb7600a9f57a2f556a10f3a20a6845df3ca51cc1d679664ee8e21f | Vibrio cholerae        |
| ab2015-06-04-5  | e95c286a1ca5b5b3b3b5bf0a318a30c627623d2b63b68c9991db337ae48e8c2 | Vibrio cholerae        |
| ab2015-06-04-6  | 79b0258243f18a1752dac35aa7e0bff1a711f791ddd0379c184e05d9d1c5dd86 | Vibrio cholerae        |
| ab2015-06-04-7  | 6b8f4ae3d17ab82176fe1bb2c79c55d5ce757c5355323bbadc84d17a5a6f75dd | Vibrio cholerae        |
| ab2015-06-04-8  | 18fca4c49057b64129c9dbd0f9c8be7562fcee4d5ff21a449b1fd79a5e910f8 | Vibrio cholerae        |
| ab2015-06-04-9  | a950ed3ce23097a99fda4d949f5353bca9f5ce3cd7a49d5f3d08d668a989 | Vibrio cholerae        |
| ab2015-06-04-10 | 275fd79f1fb013309e3dc4a22c607ab406b6b2a16489a508c3490ede71dac93 | Vibrio cholerae        |
| ab2015-06-04-11 | eadc30e57abcbceba8e69544d43debdb4d71392ef20f168d9a5659a2dc877a9 | Vibrio cholerae        |
| ab2015-06-04-12 | 82b9550d3ebda9a078ece5cea3cfd02ceece6dd01115d8b2b558d5b5c073f9dd | Vibrio cholerae        |
| ab2015-06-04-13 | 204dea6006208b691ae45b1aa8a62421894c0956a5d5bf6aa8a3e75253345d | Vibrio cholerae        |
| ab2015-06-04-14 | 7504bd89df0bdf83ed926065c92df7b57db0072ebb740cfe9c957f1d5c4c81 | Vibrio cholerae        |
| ab2015-06-04-15 | 7b4aafbf390105748d85295198579497fd0d6712da0eb1900e6c2436cf6617349 | Vibrio cholerae        |
| ab2015-06-04-16 | c9ff6e5934554670fe2166f28de7ad17f453696c914b4ca1e3f0e7e009f0a4 | Vibrio cholerae        |
| ab2015-06-04-17 | 095901997ad173f1a9cf5804cd7f92e2c95ee7b44be14b1a1f9e94ed74e6a85d | Vibrio cholerae        |
| ab2015-06-04-18 | 2f236dac0a263b2e3278aef8ab2aad6c7ace83bde857c6916683146369424e93 | Vibrio cholerae        |
| ab2015-06-04-19 | b4daca6e8f77b714d0f1faac2b7dc9933c4617d736b0a8ef29e9e1056c0214f8 | Vibrio cholerae        |
| ab2015-06-04-20 | ed95dd31b7e3a97a2bedc0e8985ad471dad7c7447a7070d5d5b37b8f259da41a | Vibrio cholerae        |
| Jensen Lab id  | OIP id                                                                 | Organism               |
|----------------|------------------------------------------------------------------------|------------------------|
| ab2015-06-04-21 | a41257cc5f1d3c4a84cd9645921671bff4e5b58de593872740a35172f4d102a5       | Vibrio cholerae        |
| ab2015-06-04-22 | 863a029fcd72521b29fa7417a13b2df4420fccc9491a090eab79c7c7d727514        | Vibrio cholerae        |
| ab2015-06-04-23 | c63ed39ab954f5d93ec80607005b54739f6940f8e317c3ea88d951b0e63ed82        | Vibrio cholerae        |
| ab2015-06-04-24 | 5f040233e108f1d0d81448d4b7c44476947e2075742fd79ad2f0d0ad9f686fa        | Vibrio cholerae        |
| ab2015-06-04-25 | 9a31271d398507a3e7cb0694927dbda47043f35bf8171cbdf56df5896c7e060        | Vibrio cholerae        |
| ab2015-06-04-26 | 687d83b774894a40bf9f35c54e0e50d2e11613d6260723ac83573e3fd6c55b309      | Vibrio cholerae        |
| ab2015-06-04-27 | 5cc452dfbe2e22d0d2102b010e926f7c97355c0c209148f049292cf3b910de          | Vibrio cholerae        |
| ab2015-06-04-28 | 49fb9f6a24a7d07799479b844a0ed91a204f95afa28a8d59561b858d9a4d19      | Vibrio cholerae        |
| ab2015-06-04-29 | 388ed8a6ca9fdab947246fd283023b21353f166c6e41949320a028cea2f1a          | Vibrio cholerae        |
| ab2015-06-04-30 | 92c05f4866a31ee526ba1cd95d513c9d0063e794554cd1246514abc1e8c9395        | Vibrio cholerae        |
| ab2015-06-04-31 | 60d87f38e11916f13cf6345b22f0b5fc567d6ecba651e7ed98c1ba23faca1a27      | Vibrio cholerae        |
| ab2015-06-04-32 | 2b200698dc60f223c28d33d12a2eeed4bfb6808399563791bf228fda34936e        | Vibrio cholerae        |
| ab2015-05-29-38 | 71b7016135114ee9988af24a00ae627349d8610625a8925152e418ce042cb8          | Pseudomonas aeruginosa |
| ab2015-05-29-39 | 3bc9419d595c592ff177294ce8b038f5c4a40287cc1d2ff95ab43e42e22c5b5        | Pseudomonas aeruginosa |
| ab2015-05-29-40 | baf59323b4cd6b20e471b0587f4349bb437cc89fba137eb726c76d2b35996859       | Pseudomonas aeruginosa |
| ab2015-05-29-41 | 375ec06c3542bc3d33e7ec94c751bd1669ffee998a44cc8b8948ddc246dbd02517     | Pseudomonas aeruginosa |
| ab2015-05-29-42 | dda73882e77f151644b4d9fc73810f58c0789cf5ebd5c464108940e978d3913        | Pseudomonas aeruginosa |
| ab2015-05-29-43 | e01db4daa89125bfae9539157ab0d459e9a10b53148d17af60eb3afadf667e37       | Pseudomonas aeruginosa |
| Jensen Lab id  | OIP id                                                                 | Organism            |
|---------------|------------------------------------------------------------------------|---------------------|
| ab2015-05-29-38 | 71b7016135114ee9988af24a00aec627349d8610625a8925152e418ce042cb8       | Pseudomonas aeruginosa |
| ab2015-05-29-39 | 9ff1533aa7d28d3d64439293ea263ca3ce6a6101f19c7367426d9a3bba3773e6       | Pseudomonas aeruginosa |
| ab2015-05-29-40 | c5f0fc46599f6ee48fe23a59fc1d752cd64ab4031c3846fb85d078a88bfa5c        | Pseudomonas aeruginosa |
| ab2015-05-29-41 | fe52314687302e52d76a76292a84a8e7730dac37451c7026621190f2185cd7df       | Pseudomonas aeruginosa |
| ab2015-05-29-42 | fc8e9658e5fe5d5e30364f389fc123f4754537bd6a5132fb71b2af99aa02e7a2      | Pseudomonas aeruginosa |
| ab2015-05-29-43 | 433cf08b0ab2269a91f4e946b17c551e8a92a30c8c5214bc8384072c8915bb5        | Pseudomonas aeruginosa |
| ab2015-05-29-44 | 9162280a2e505e7a74c03de6202f084eb4b83882453525539fd87da3905d77c       | Pseudomonas aeruginosa |
| ab2015-05-29-45 | 9db03886a5482eb6fcdad84cd7abf0ddad7bdc4a3d741d971cc9dd3a2c378cda2      | Pseudomonas aeruginosa |
| ab2015-05-29-46 | 31ee1b22c3f010a3a31df973be75ff1a126069e78fbb1db3d0cd3985330d          | Pseudomonas aeruginosa |
| ab2015-05-29-47 | 799edd343b37e6df51118d39052ad7241e7c05238266bc7779c1ab9227f8a4c        | Pseudomonas aeruginosa |
| ab2015-05-29-48 | 70225551790f3a513cffe5e1f0971b3844f1c985e4f3e3b57579dd349aecd1          | Pseudomonas aeruginosa |
| ab2015-05-29-49 | 76bc18f739812662c22ae910f2e1a2bc7ac72f9c79ee19df0493c60be7f6711        | Pseudomonas aeruginosa |
| ab2015-05-29-50 | 2f3db7b47e7d42594be348214e07578d7ea1f08a10f8cd937bec3abb8692c6aa       | Pseudomonas aeruginosa |
| ab2015-05-29-51 | dbe07cf9023a7c8d67cea0f6bc02eeaa93f5c2e60453ca2aa4685d8e3a535654       | Pseudomonas aeruginosa |
| ab2015-05-29-52 | 8861e2f49e3b2155f99422428acb7ca764c5c22352dd6f5c411d89daaa99c8c        | Pseudomonas aeruginosa |
| ab2015-05-29-53 | 8bbe069df1ecaef06813ea816ded484d908679412e938d42afbb30e0f47747          | Pseudomonas aeruginosa |
| ab2015-05-29-54 | 87be5d5a167d3c23ad2126bc4d72844c0ed6af2848768fd1bb764ad0a05355b        | Pseudomonas aeruginosa |
| ab2015-05-29-55 | 975a50a6ac4a0a1ce1913d3f339c433b73ba15a3a8eef22b3768a9327e1ca5a21      | Pseudomonas aeruginosa |
| Jensen Lab id   | OIP id                                                                 | Organism                        |
|----------------|------------------------------------------------------------------------|---------------------------------|
| ab2015-05-29-56| d0799bdb371912d4370d6226ae8263e1f9bf419e49c42c16514c657f11105f37       | *Pseudomonas aeruginosa*        |
| ab2015-05-29-57| dfd11ff2b7b5261968452f994235bece1d208b793fc7768b883163fa0cad72c      | *Pseudomonas aeruginosa*        |
| ab2015-05-29-58| 06dc2aa14271a7d5c79c6e112a3aeacc8c643246c659fab33b3bbb01febe25356   | *Pseudomonas aeruginosa*        |
| ab2015-05-29-59| f92bcce7b8dac999467e57653d9e3ab40172618fc09fb5806e64040e8a3410f5     | *Pseudomonas aeruginosa*        |
| ab2015-05-29-60| bd0b6b93ba4f3528fe3f78a789dd847ee83a6d4b08c6652053e72ae6b897b         | *Pseudomonas aeruginosa*        |
| ab2015-05-29-61| 37d4d1c6d5229a5db3700596859b305aea3a4606d7362ba176424c9217ebf28       | *Pseudomonas aeruginosa*        |
| ab2015-05-29-62| 4e059367636fa821409e894b49151556c01d65ebe01eca3e44fdec6531adc7       | *Pseudomonas aeruginosa*        |
| ab2014-010-14-1 | b9d6746d36ee7943e0eb19c929921460080c78b36755b8d6748820c842ae76       | *Pseudomonas aeruginosa*        |
| ab2014-010-14-10| c8c1989c09901dd7a257d86497a713e85a761edd2209efe0d8784d228e5b3585     | *Pseudomonas aeruginosa*        |
| ab2014-010-14-11| 18ec447aac947d6ed610084fbb9e808bdb761bf68919b853ac4946632d6c6e50     | *Pseudomonas aeruginosa*        |
| ab2014-010-14-12| 58c0a2aab1b8f0322fcc4b93838458a820fc8db74f716b53ba166aee26be92001   | *Pseudomonas aeruginosa*        |
| ab2014-010-14-13| 9e8108ef3cf66406b628ec973b10079ef0ca5781a05ca1a875ed6decc2fe02     | *Pseudomonas aeruginosa*        |
| ab2014-010-14-14| 7935084f249ec5bc222b38951cd369dab76cfa95a769d42d0eb1312cc5bb50c     | *Pseudomonas aeruginosa*        |
| ab2014-010-14-15| 51b27c3cf74ce394c1d54773bd1a7d15d3379f5c8db4aa2f899dbdaa6d71251     | *Pseudomonas aeruginosa*        |
| ab2014-010-14-17| 76f7220c7323438d65b7d4334916e9aadb0be04be1b662615be1ad312407c6      | *Pseudomonas aeruginosa*        |
| ab2014-010-14-22| 797a818bb2e811f5ed0d6d22bd6db158fabbcd22e8bfc7f1010ad265af8897      | *Pseudomonas aeruginosa*        |
| ab2014-010-14-23| 32a5ff8d6dda8584aaafec4883226c8463c2e9a08ce553c969ca698fedef9       | *Pseudomonas aeruginosa*        |
| ab2014-010-14-3 | 2c11ded42bcc0cd87dc67464247187c3c82d71742a8b50f346516a958361706a     | *Pseudomonas aeruginosa*        |
| Jensen Lab id | OIP id                                                                 | Organism                      |
|---------------|------------------------------------------------------------------------|-------------------------------|
| ab2014-010-14-4 | 20cd19c0fa4b3e32b33075348be5ab3102def5 083ce6fd7ac55b01ac0cb5835       | *Pseudomonas aeruginosa*      |
| ab2014-010-14-5 | 3e6133278fc31ba361c1cd7c95c081a822d972 3dc3b7f3549870510a422e2522     | *Pseudomonas aeruginosa*      |
| ab2014-010-14-6 | 3cbeac672c18cd66252b47d650ec124b17baf5 19849a6844fab4af70fbbea1       | *Pseudomonas aeruginosa*      |
| ab2014-010-14-8 | cb237b8021a9e653613163394c11258bb3b72 fe0972a977765c18478e5d43c2      | *Pseudomonas aeruginosa*      |
| ab2014-010-14-9 | 8bf9ec4e43a3e6bd11c44bb6d341d138e14b41 c7766e6e21a81a17d399c1c69c2     | *Pseudomonas aeruginosa*      |
| sc2014-02-14-1  | ecf996b6c698beb104f0c84bda7955a48c7ed b6049ce2b9256cb31e2b85b0         | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-1  | 37a38f6896b2fb3379eaa9776e69ccef45da a011b009f9cf498a04ab5b6e           | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-3  | 82c7e7111f000b9de9be253c966a0d87b3b5 85cf47a4e3ada52b7a90ae362f          | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-6  | c807ab328c5bd06874ad4f9fb731f4d888f238 94d00cafed1089f98407ed99          | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-7  | 9a62dfe3b6bed92f6bd03916b1fe055c1abd7 d4d2f781348c01ae89c45d5           | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-8  | 6e0a323a040374567356e08c438fd42806aef 88c731f05e2d9e13684d940ae8        | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-9  | 9e82ba83f3538f16f9942ea4216cd7fe20ebcc 1c82ed3dbaa8f7e34bdc3a1e9         | *Methylomicrobium alcaliphylum* |
| sc2014-02-12-12 | 262660a13b3cd4b6cc7e4ac73b739ddccbb23d9 3df8d54d138ae911af40f95480      | *Methylomicrobium alcaliphylum* |

**Supplementary Table 7:** Atomic models used to produce the homology models used in this work

| Domain(s) | PDB code | Reference |
|-----------|----------|----------|
| HAMP(*A. fulgidus*) + MCP_Signal(*E. coli*) | 3ZX6     | 21       |
| PAS(*P. aeruginosa*)                | 4HI4     | 22       |
| PAS + HAMP (*P. aeruginosa*)        | 3VOL     | 23       |
| Domain(s)                     | PDB code | Reference |
|------------------------------|----------|-----------|
| 3xHAMP (P. aeruginosa)       | 4I3M     | 24        |

**Supplementary Table 8**: Relevant files used to build the homology models produced in this work

| File                        | Type             | Description                                                                 |
|-----------------------------|------------------|-----------------------------------------------------------------------------|
| 3XZ6_4I3M.pir               | Sequence alignment | Sequence alignment used to build the 2H+S homology model                    |
| 3XZ6_4I3M_74.pdb            | 3D atomic model  | Best homology model from 2H+S                                               |
| 4HI4_BD.pdb                 | 3D atomic model  | chains B and D of 4HI4 aligned with 2H+S model                              |
| 3XZ6_4I3M_4HIH.pir          | Sequence alignment | Sequence alignment used to build the P+2H+S homology model                  |
| 3XZ6_4I3M_4HIH_99.pdb       | 3D atomic model  | Best homology model from P+2H+S                                              |
| 4I3M.bio.pos.pdb            | 3D atomic model  | Model of 4I3M positioned against 3XZ6_4I3M_4HIH_99.pdb to build the model for Aer2 (PA0176) |
| 3XZ6_4I3M_4HI4_4I3M.pir     | Sequence alignment | Sequence alignment used to build the model for Aer2 (PA0176)              |
| Aer2Pa_3HAMP_PAS_2HAMP.B99990041.pdb | 3D atomic model | Best Aer2 (PA0176) homology model                                             |
| 3XZ6_4I3M_4HI4_4HI4.pir     | Sequence alignment | Sequence alignment used to build the model for Aer2-like (VCA1092)         |
| VCA1092.B999900035.pdb      | 3D atomic model  | Best Aer2-like (VCA1092) homology model                                     |
| 3XZ6_4I3M_4HI4_4HI4_SO.pir  | Sequence alignment |                                                                           |
| File                                      | Type                        | Description                                                                 |
|-------------------------------------------|-----------------------------|-----------------------------------------------------------------------------|
| SO_2123.B99990017.pdb                     | 3D atomic model             | used to build the model for Aer2-like (SO_2123)                             |
| hamp_sequence_for_MEALZ.linsi.fa          | Sequence alignment          | Best Aer2-like (SO_2123) homology model                                    |
| RAxML_bipartitionns_50coll.hamp_sequence_for_MEALZ.linsi.rec.tree | Phylogenetic Tree           | Sequence alignment of HAMP domains in the group of Pseudomonas group similar to the 3 HAMPs in 4I3M and the C-terminal HAMP of MEALZ_2872 |
| 4I3M.bio.HAMP2.withtail4alignment.pdb     | 3D atomic model             | Model of the second HAMP of 4I3M with part of the helix connecting to the third HAMP. |
| 4I3M.bio.HAMP2.alnMEALZ.pdb               | 3D atomic model             | Model of the second HAMP of 4I3M without part of the helix connecting to the third HAMP. |
| 3ZX6_4I3M_4HI4_HAMP2_MEALZ.pir            | 3D atomic model             | Sequence alignment used to build the model for Aer2-like (MEALZ_2872)       |
| MEALZ_2872_wHAMP.B99990020.pdb           | 3D atomic model             | Best Aer2-like (MEALZ_2872) homology model                                  |

**Supplementary Table 9**: 310 randomly selected non-redundant γ-Proteobacteria genomes used in this work. The presence of an F7 system is indicated.
| Genome                                           | has F7 |
|-------------------------------------------------|--------|
| Acidithiobacillus caldus SM-1                   | no     |
| Acidithiobacillus ferrivorans SS3               | no     |
| Acidithiobacillus sp. GGI-221                   | no     |
| Acidithiobacillus thiooxidans ATCC 19377        | no     |
| Acinetobacter baumannii AB5075                  | no     |
| Acinetobacter bereziniae LMG 1003                | no     |
| Acinetobacter calcoaceticus RUH2202             | no     |
| Acinetobacter haemolyticus ATCC 19194           | no     |
| Acinetobacter johnsonii SH046                   | no     |
| Acinetobacter junii SH205                       | no     |
| Acinetobacter lwofii SH145                      | no     |
| Acinetobacter nosocomialis Ab22222              | no     |
| Acinetobacter oleivorans DR1                    | no     |
| Acinetobacter parvus DSM 16617 = CIP 108168     | no     |
| Acinetobacter radioresistens DSM 6976 = NBRC 102413 | no     |
| Acinetobacter sp. NCTC 10304                    | no     |
| Acinetobacter ursingii DSM 16037 = CIP 107286   | no     |
| Aeromonas aquariorum AAK1                       | no     |
| Aeromonas caviae Ae398                          | no     |
| Aeromonas hydrophila SSU                        | no     |
| Aeromonas media WS                               | no     |
| Aeromonas salmonicida subsp. salmonicida A449   | no     |
| Aeromonas veronii AER397                        | no     |
| Alcanivorax borkumensis SK2                     | no     |
| Alcanivorax dieselolei B5                       | yes    |
| Alcanivorax hongdengensis A-11-3                | no     |
| Genome                                         | has F7 |
|------------------------------------------------|--------|
| *Alcanivorax pacificus W11-5*                  | yes    |
| *Alcanivorax sp. DG881*                        | no     |
| *Aliivibrio salmonicida LF11238*               | no     |
| *Alischewanella aestuarii B11*                 | no     |
| *Alischewanella agri BL06*                     | no     |
| *Alischewanella jeotgali KCTC 22429*           | no     |
| *Alkalilimnicola ehrlichii MLHE-1*             | no     |
| *Allochromatium vinosum DSM 180*               | yes    |
| *Alteromonadales bacterium TW-7*               | yes    |
| *Alteromonas mediterrana MED64*                | no     |
| *Alteromonas sp. SN2*                          | yes    |
| *Azotobacter vinelandii DJ*                    | yes    |
| *Beggiatoa alba B18LD*                         | yes    |
| *Beggiatoa sp. SS*                             | yes    |
| *Cardiobacterium hominis ATCC 15826*           | no     |
| *Cardiobacterium valvarum F0432*               | no     |
| *Cellvibrio japonicus Ueda107*                 | no     |
| *Cellvibrio sp. BR*                            | yes    |
| *Chromohalobacter salexigens DSM 3043*         | yes    |
| *Citrobacter freundii 4_7_47CFAA*             | yes    |
| *Citrobacter koseri ATCC BAA-895*             | yes    |
| *Citrobacter rodentium ICC168*                | yes    |
| *Citrobacter sp. 30_2*                        | yes    |
| *Citrobacter youngae ATCC 29220*              | yes    |
| *Colwellia psychrerythraea 34H*                | no     |
| *Cronobacter sakazakii ES15*                   | yes    |
| Genome                                      | has F7 |
|---------------------------------------------|--------|
| Cronobacter turicensis z3032                | yes    |
| Dichelobacter nodosus VCS1703A              | no     |
| Dickeya dadantii Ech703                     | yes    |
| Dickeya zeae Ech1591                        | yes    |
| Ectothiorhodospira sp. PHS-1                | yes    |
| Edwardsiella ictaluri 93-146                | yes    |
| Edwardsiella tarda ATCC 23685               | yes    |
| Endoriftia persephone 'Hot96_1+Hot96_2'    | no     |
| Enhydrobacter aerosaccus SK60               | no     |
| Enterobacter asburiae LF7a                  | yes    |
| Enterobacter cancerogenus ATCC 35316        | yes    |
| Enterobacter cloacae subsp. cloacae GS1     | yes    |
| Enterobacter hormaechei ATCC 49162          | yes    |
| Enterobacter radicincitans DSM 16656        | yes    |
| Enterobacter sp. 638                        | yes    |
| Enterobacteriaceae bacterium 9_2_54FAA      | yes    |
| Erwinia amylovora CFBP1430                  | yes    |
| Erwinia billingiae Eb661                   | yes    |
| Erwinia pyrifoliae Ep1/96                   | yes    |
| Erwinia sp. Ejp617                          | yes    |
| Erwinia tasmaniensis Et1/99                 | yes    |
| Escherichia albertii TW11588                 | yes    |
| Escherichia coli KTE229                     | yes    |
| Escherichia fergusonii ECD227               | yes    |
| Escherichia hermannii NBRC 105704           | yes    |
| Escherichia sp. TW09276                     | yes    |
| Genome                                      | has F7 |
|--------------------------------------------|--------|
| *Ferrimonas balearica DSM 9799*           | no     |
| *Floribacter dumoffii Tex-KL*              | no     |
| *Frateuria aurantia DSM 6220*              | yes    |
| *Gallaecimonas xiamenensis 3-C-1*          | yes    |
| *Glaciecola agarifytica NO2*               | yes    |
| *Glaciecola arctica BSs20135*              | no     |
| *Glaciecola chathamensis S18K6*            | yes    |
| *Glaciecola lipolytica E3*                 | no     |
| *Glaciecola mesophila KMM 241*             | no     |
| *Glaciecola nitratireducens FR1064*        | yes    |
| *Glaciecola pallidula DSM 14239 = ACAM 615*| yes    |
| *Glaciecola polaris LMG 21857*             | no     |
| *Glaciecola psychrophila 170*              | no     |
| *Glaciecola sp. 4H-3-7+YE-5*               | yes    |
| *Grimontia hollisae CIP 101886*            | yes    |
| *Grimontia sp. AK16*                      | yes    |
| *Hafnia alvei ATCC 51873*                  | yes    |
| *Hahella chejuensis KCTC 2396*             | yes    |
| *Halomonas boliviensis LC1*                | yes    |
| *Halomonas elongata DSM 2581*              | yes    |
| *Halomonas sp. GFAJ-1*                     | yes    |
| *Halomonas titanicae BH1*                  | yes    |
| *Halorhodospira halophila SL1*             | yes    |
| *Halothiobacillus neapolitanus c2*         | no     |
| *Hydrocarboniphaga effusa AP103*           | yes    |
| *Idiomarina loihiensis L2TR*               | no     |
| Genome                                                                 | has F7 |
|-----------------------------------------------------------------------|-------|
| Idiomarina xiamenensis 10-D-4                                         | no    |
| Kangiella koreensis DSM 16069                                         | no    |
| Klebsiella aerogenes KCTC 2190                                        | yes   |
| Klebsiella pneumoniae subsp. pneumoniae HS11286                        | no    |
| Legionella drancourtii LLAP12                                          | yes   |
| Legionella longbeachae NSW150                                         | no    |
| Legionella pneumophila subsp. pneumophila                              | no    |
| Listonella anguillarum M3                                             | yes   |
| Marichromatium purpuratum 984                                         | yes   |
| Marinobacter adhaerens HP15                                            | no    |
| Marinobacter algicola DG893                                            | no    |
| Marinobacter hydrocarbonoclasticus ATCC 49840                         | no    |
| Marinobacter hydrocarbonoclasticus VT8                                | no    |
| Marinobacter manganoxydans MnI7-9                                     | no    |
| Marinobacter santoriniensis NKSG1                                     | no    |
| Marinobacter sp. ELB17                                                | no    |
| Marinobacterium stanieri S30                                           | yes   |
| Marinomonas mediterranea MMB-1                                        | yes   |
| Marinomonas posidonae IVIA-Po-181                                     | no    |
| Marinomonas sp. MWYL1                                                 | yes   |
| Methylobacter tundripaludum SV96                                      | yes   |
| Methylomicrobium album BG8                                             | yes   |
| Methylomicrobium alcalophilum 20Z                                      | yes   |
| Methylomonas methanica MC09                                            | yes   |
| Methylophaga aminisulfidivorans MP                                     | yes   |
| Genome                                      | has F7 |
|---------------------------------------------|--------|
| *Methylophaga frappieri*                    | no     |
| *Methylophaga lonarensis MPL*               | no     |
| *Methylophaga thiooxydans DMS010*           | no     |
| *Moraxella macaceae 0408225*                | no     |
| *Morganella morganii subsp. morganii KT*    | yes    |
| *Moritella sp. PE36*                        | yes    |
| *Nitrosoccus halophilus Nc 4*               | no     |
| *Nitrosoccus oceani ATCC 19707*             | no     |
| *Nitrosoccus watsonii C-113*                | no     |
| *Oceanimonas sp. GK1*                       | no     |
| *Pantoea agglomerans 299R*                  | yes    |
| *Pantoea ananatis LMG 20103*                | yes    |
| *Pantoea sp. aB*                            | yes    |
| *Pantoea stewartii subsp. stewartii DC283*  | yes    |
| *Pantoea vagans C9-1*                       | yes    |
| *Pectobacterium atrosepticum SCRI1043*      | yes    |
| *Pectobacterium carotovorum subsp. brasiliensis PBR1692* | yes |
| *Pectobacterium sp. SCC3193*                | yes    |
| *Pectobacterium wasabiae CFBP 3304*         | yes    |
| *Photobacterium damselae subsp. damselae CIP 102761* | no |
| *Photobacterium leiognathi subsp. mandapamensis svers.1.1.* | no |
| *Photobacterium profundum SS9*              | no     |
| *Photobacterium sp. AK15*                   | no     |
| *Photorhabdus asymbiotica*                  | yes    |
| *Photorhabdus luminescens subsp. laumondii TTO1* | yes |
| *Proteus mirabilis WGLW6*                   | yes    |
| Genome                                                         | has F7 |
|---------------------------------------------------------------|--------|
| Proteus penneri ATCC 35198                                   | yes    |
| Providencia alcalifaciens DSM 30120                           | yes    |
| Providencia burhodogranatiae DSM 19968                       | yes    |
| Providencia rettgeri Dmelm                                 | no     |
| Providencia rustigianii DSM 4541                             | yes    |
| Providencia stuartii ATCC 25827                              | yes    |
| Pseudoalteromonas arctica A 37-1-2                           | no     |
| Pseudoalteromonas atlantica T6c                              | no     |
| Pseudoalteromonas citrea NCIMB 1889                          | yes    |
| Pseudoalteromonas haloplanktis ANT/505                       | yes    |
| Pseudoalteromonas luteoviolacea B = ATCC 29581               | yes    |
| Pseudoalteromonas marina mano4                               | yes    |
| Pseudoalteromonas piscicida JCM 20779                        | yes    |
| Pseudoalteromonas rubra ATCC 29570                           | yes    |
| Pseudoalteromonas sp. Bsw20308                               | yes    |
| Pseudoalteromonas spongiae UST010723-006                     | yes    |
| Pseudoalteromonas undina NCIMB 2128                          | yes    |
| Pseudomonas aeruginosa LESB58                                 | yes    |
| Pseudomonas avellanae BPIC 631                               | no     |
| Pseudomonas brassicacearum subsp. brassicacearum NFM421      | no     |
| Pseudomonas denitrificans ATCC 13867                         | yes    |
| Pseudomonas entomophila L48                                  | no     |
| Pseudomonas extremaustralis 14-3 substr. 14-3b                | no     |
| Pseudomonas fluorescens F113                                  | no     |
| Pseudomonas fragi A22                                        | no     |
| Pseudomonas fulva 12-X                                       | no     |
| Genome                                      | has F7 |
|---------------------------------------------|--------|
| *Pseudomonas fuscovaginae UPB0736*         | no     |
| *Pseudomonas geniculata N1*                | yes    |
| *Pseudomonas mendocina ymp*                | no     |
| *Pseudomonas monteilii SB3078*             | no     |
| *Pseudomonas poae RE*1-1-14*               | no     |
| *Pseudomonas protegens CH40*               | no     |
| *Pseudomonas pseudoalcaligenes KF707*      | yes    |
| *Pseudomonas psychrotolerans L19*          | no     |
| *Pseudomonas putida GB-1*                  | no     |
| *Pseudomonas resinovorans NBRC 106553*     | yes    |
| *Pseudomonas sp. TKP*                      | no     |
| *Pseudomonas stutzeri KOS6*                | no     |
| *Pseudomonas syringae pv. phaseolicola 1448A* | no     |
| *Pseudomonas viridiflava UASWS0038*        | no     |
| *Pseudoxanthomonas spadix BD-a59*          | no     |
| *Pseudoxanthomonas suwonensis 11-1*        | yes    |
| *Psychrobacter arcticus 273-4*             | no     |
| *Psychrobacter cryohalolentis K5*          | no     |
| *Psychrobacter sp. PRwf-1*                 | no     |
| *Psychromonas sp. CNPT3*                   | no     |
| *Rahnella aquatilis CIP 78.65 = ATCC 33071* | yes    |
| *Rahnella sp. Y9602*                       | yes    |
| *Rheinheimera nanhaiensis E407-8*          | no     |
| *Rheinheimera sp. A13L*                    | no     |
| *Rhodanobacter fulvus Jip2*                | yes    |
| *Rhodanobacter sp. 116-2*                  | no     |
| Genome                                              | has F7 |
|----------------------------------------------------|--------|
| *Rhodanobacter spathiphylli B39*                  | no     |
| *Rhodanobacter thiooxydans LCS2*                   | yes    |
| *Saccharophagus degradans 2-40*                    | yes    |
| *Salinisphaera shabanensis E1L3A*                  | yes    |
| *Salmonella bongori N268-08*                       | yes    |
| *Salmonella enterica subsp. enterica serovar Gallinarum str. 9184* | yes    |
| *Serratia liquefaciens ATCC 27592*                 | yes    |
| *Serratia marcescens VGH107*                       | yes    |
| *Serratia odorifera 4Rx13*                         | yes    |
| *Serratia plymuthica S13*                          | yes    |
| *Serratia proteamaculans 568*                      | yes    |
| *Serratia sp. AS13*                                | yes    |
| *Shewanella amazonensis SB2B*                      | yes    |
| *Shewanella baltica OS155*                         | yes    |
| *Shewanella benthica KT99*                         | yes    |
| *Shewanella denitrificans OS217*                   | no     |
| *Shewanella frigidimarina NCIMB 400*               | no     |
| *Shewanella halifaxensis HAW-EB4*                  | no     |
| *Shewanella loihica PV-4*                          | yes    |
| *Shewanella oneidensis MR-1*                       | yes    |
| *Shewanella pealeana ATCC 700345*                  | no     |
| *Shewanella piezotolerans WP3*                     | no     |
| *Shewanella putrefaciens CN-32*                    | no     |
| *Shewanella sediminis HAW-EB3*                     | yes    |
| *Shewanella sp. MR-4*                              | yes    |
| *Shewanella violacea DSS12*                        | yes    |
| Genome                                      | has F7 |
|---------------------------------------------|--------|
| *Shewanella woodyi* ATCC 51908              | yes    |
| *Shigella boydii* CDC 3083-94               | yes    |
| *Shigella dysenteriae* 1617                 | no     |
| *Shigella flexneri* 4343-70                 | yes    |
| *Shigella sonnei* Ss046                    | yes    |
| *Shigella sp. D9*                          | yes    |
| *Simiduia agarivorans* SA1 = DSM 21679      | yes    |
| *Stenotrophomonas maltophilia* K279a        | yes    |
| *Stenotrophomonas sp. SKA14*                | yes    |
| *Teredinibacter turnerae* T7901             | yes    |
| *Thalassolituus oleivorans* MIL-1           | yes    |
| *Thioalkalimicrobium aerophilum* AL3        | yes    |
| *Thioalkalivibrio sp. K90mix*               | no     |
| *Thioalkalivibrio sulfidophilus* HL-EbGr7   | no     |
| *Thiocapsa marina* 5811                     | no     |
| *Thiocystis violascens* DSM 198              | yes    |
| *Thiomicrospira crunogena* XCL-2            | yes    |
| *Thiorhodococcus drewsii* AZ1               | yes    |
| *Thiorhodospira sibirica* ATCC 700588       | yes    |
| *Thiorhodovibrio* sp. 970                   | no     |
| *Thiothrix nivea* DSM 5205                   | no     |
| *Vibrio alginolyticus* 40B                  | no     |
| *Vibrio anguillarum* 775                    | yes    |
| *Vibrio brasiliensis* LMG 20546             | yes    |
| *Vibrio campbellii* CAIM 519 = NBRC 15631   | no     |
| *Vibrio caribbenthicus* ATCC BAA-2122       | no     |
| Genome                                      | has F7 |
|---------------------------------------------|--------|
| *Vibrio cholerae* HC-23A1                   | no     |
| *Vibrio coralliilyticus* ATCC BAA-450       | yes    |
| *Vibrio fischeri* MJ11                      | no     |
| *Vibrio furnissii* CIP 102972               | yes    |
| *Vibrio harveyi* 1DA3                       | no     |
| *Vibrio ichthyoenteri* ATCC 700023          | no     |
| *Vibrio metschnikovii* CIP 69.14            | no     |
| *Vibrio mimicus* MB451                      | yes    |
| *Vibrio nigripulchritudo* ATCC 27043        | yes    |
| *Vibrio ordalii* ATCC 33509                 | yes    |
| *Vibrio orientalis* CIP 102891 = ATCC 33934| yes    |
| *Vibrio parahaemolyticus* O1:Kuk str. FDA_R31| no   |
| *Vibrio rotiferianus* DAT722                | no     |
| *Vibrio scophthalmi* LMG 19158              | no     |
| *Vibrio shilonii* AK1                       | no     |
| *Vibrio sinaloensis* DSM 21326              | yes    |
| *Vibrio sp.* HENC-01                        | no     |
| *Vibrio splendidus* ATCC 33789              | no     |
| *Vibrio tubiashii* NCIMB 1337 = ATCC 19106 | yes    |
| *Vibrio vulnificus* MO6-24/O                | yes    |
| *Vibrionales bacterium* SWAT-3               | no     |
| *Wohlfahrthimonas chitiniclastica* SH04     | no     |
| *Xanthomonas albilineans* GPE PC73          | yes    |
| *Xanthomonas axonopodis* pv. malvacearum str. GSPB2388 | yes |
| *Xanthomonas campestris* pv. musacearum NCPPB 4381 | yes |
| *Xanthomonas citri* subsp. citri Aw12879    | yes    |
| Genome                                           | has F7 |
|------------------------------------------------|--------|
| Xanthomonas fuscans subsp. aurantifolii str. ICPB 10535 | yes    |
| Xanthomonas gardneri ATCC 19865                  | yes    |
| Xanthomonas oryzae pv. oryzicola BLS256         | yes    |
| Xanthomonas perforans 91-118                    | yes    |
| Xanthomonas sacchari NCPPB 4393                  | yes    |
| Xanthomonas translucens DAR61454                 | yes    |
| Xanthomonas vesicatoria ATCC 35937              | yes    |
| Xenorhabdus bovienii SS-2004                    | yes    |
| Xenorhabdus nematophila ATCC 19061              | yes    |
| Xylella fastidiosa Temecula1                    | no     |
| Yersinia aldovae ATCC 35236                      | yes    |
| Yersinia bercovieri ATCC 43970                   | yes    |
| Yersinia enterocolitica subsp. palearctica Y11  | yes    |
| Yersinia frederiksenii ATCC 33641               | yes    |
| Yersinia intermedia ATCC 29909                   | yes    |
| Yersinia kristensenii ATCC 33638                 | yes    |
| Yersinia mollaretii ATCC 43969                   | yes    |
| Yersinia pestis PY-16                           | yes    |
| Yersinia pseudotuberculosis PB1/+               | yes    |
| Yersinia rohdei ATCC 43380                      | yes    |
| Yersinia ruckeri ATCC 29473                     | yes    |
| Yokenella regensburgei ATCC 43003               | yes    |
| endosymbiont of Riftia pachyptila (vent Ph05)   | yes    |
| gamma proteobacterium HdN1                      | no     |

**Supplementary Table 10**: Genomes used in phylogenetic profiles.
### Genomes imaged in this study

- *Methylmicrobium alcalophilum* 20Z
- *Pseudomonas aeruginosa PAO1*
- *Shewanella oneidensis* MR-1
- *Vibrio cholerae* O1 biovar El Tor str. N16961

### Gamma-Proteobacteria

- *Acinetobacter baumannii* AB0057
- *Acinetobacter calcoaceticus* PHEA-2
- *Acinetobacter oleivorans* DR1
- *Aeromonas hydrophila* subsp. *hydrophila* ATCC 7966
- *Aeromonas salmonicida* subsp. *salmonicida* A449
- *Aeromonas veronii* B565
- *Alcanivorax borkumensis* SK2
- *Alcanivorax dieselolei* B5
- *Aliivibrio salmonicida* LFI1238
- *Alkalilimnicola ehrlichii* MLHE-1
- *Allochromatium vinosum* DSM 180
- *Alteromonas macleodii* str. *'Ionian Sea U7'*
- *Alteromonas sp.* SN2
- *Azotobacter vinelandii* CA6
- *Cellvibrio japonicus* Ueda107
- *Chromohalobacter salexigens* DSM 3043
- *Citrobacter koseri* ATCC BAA-895
- *Citrobacter rodentium* ICC168
- *Colwellia psychrerythraea* 34H
- *Cronobacter sakazakii* ATCC BAA-894
- *Cronobacter turicensis* z3032
| **Gamma-Proteobacteria** |
|--------------------------|
| *Dichelobacter nodosus* VCS1703A |
| *Dickeya dadantii* Ech703 |
| *Dickeya zeae* Ech1591 |
| *Edwardsiella ictaluri* 93-146 |
| *Edwardsiella tarda* C07-087 |
| *Enterobacter aerogenes* KCTC 2190 |
| *Enterobacter asburiae* LF7a |
| *Enterobacter cloacae subsp. cloacae* NCTC 9394 |
| *Enterobacter sp.* 638 |
| *Enterobacteriaceae bacterium* strain FGI 57 |
| *Erwinia amylovora* ATCC 49946 |
| *Erwinia billingiae* Eb661 |
| *Erwinia pyrifoliae* Ep1/96 |
| *Erwinia sp.* Ejp617 |
| *Erwinia tasmaniensis* Et1/99 |
| *Escherichia coli* O157:H7 str. EDL933 |
| *Escherichia fergusonii* ATCC 35469 |
| *Ferrimonas balearica* DSM 9799 |
| *Frateruria aurantia* DSM 6220 |
| *Gammaproteobacteria gamma proteobacterium* HdN |
| *Glaciecola nitratireducens* FR1064 |
| *Glaciecola psychrophila* 170 |
| *Glaciecola sp.* 4H-3-7+YE-5 |
| *Hahella chejuensis* KCTC 2396 |
| *Halomonas elongata* DSM 2581 |
| *Halorhodospira halophila* SL1 |
| **Gamma-Proteobacteria** |
|--------------------------|
| *Halothiobacillus neapolitanus c2* |
| *Herminiimonas arsenicoxydans* |
| *Idiomarina loihiensis GSL 199* |
| *Kangiella koreensis DSM 16069* |
| *Legionella longbeachae NSW150* |
| *Listonella anguillarum M3* |
| *Marinobacter adhaerens HP15* |
| *Marinobacter aquaeolei VT8* |
| *Marinobacter hydrocarbonoclasticus ATCC 49840* |
| *Marinobacter sp. BSs20148* |
| *Marinomonas mediterranea MMB-1* |
| *Marinomonas posidonica IVIA-Po-181* |
| *Marinomonas sp. MWYL1* |
| *Methylococcus capsulatus str. Bath* |
| *Methylomonas methanica MC09* |
| *Methylophaga sp. JAM1* |
| *Morganella morganii subsp. morganii KT* |
| *Nitrosococcus halophilus Nc4* |
| *Nitrosococcus oceani ATCC 19707* |
| *Nitrosococcus watsonii C-113* |
| *Oceanimonas sp. GK1* |
| *Pantoea ananatis LMG 20103* |
| *Pantoea sp. At-9b* |
| *Pantoea vagans C9-1* |
| *Pectobacterium atrosepticum SCRI1043* |
| *Pectobacterium carotovorum subsp. carotovorum PCC21* |
| **Gamma-Proteobacteria** |
|--------------------------|
| *Pectobacterium sp. SCC3193* |
| *Pectobacterium wasabiae WPP163* |
| *Photobacterium profundum SS9* |
| *Photorhabdus asymbiotica* |
| *Photorhabdus luminescens subsp. laumondii TTO1* |
| *Proteus mirabilis BB2000* |
| *Providencia stuartii MRSN 2154* |
| *Pseudoalteromonas atlantica T6c* |
| *Pseudoalteromonas haloplanktis TAC125* |
| *Pseudoalteromonas sp. SM9913* |
| *Pseudomonas aeruginosa PA1* |
| *Pseudomonas brassicacearum subsp. brassicacearum NFM421* |
| *Pseudomonas denitrificans ATCC 13867* |
| *Pseudomonas entomophila L48* |
| *Pseudomonas fluorescens A506* |
| *Pseudomonas fulva 12-X* |
| *Pseudomonas mendocina ymp* |
| *Pseudomonas monteilii SB3101* |
| *Pseudomonas poae RE*1-1-14* |
| *Pseudomonas protegens Pf-5* |
| *Pseudomonas putida BIRD-1* |
| *Pseudomonas resinovorans NBRC 106553* |
| *Pseudomonas sp. TKP* |
| *Pseudomonas stutzeri DSM 4166* |
| *Pseudomonas syringae pv. syringae B728a* |
| *Pseudoxanthomonas spadix BD-a59* |
### Gamma-Proteobacteria

| Species Name                                      | Strain/Reference                  |
|--------------------------------------------------|-----------------------------------|
| *Pseudoxanthomonas suwonensis* 11-1               |                                   |
| *Psychrobacter arcticus* 273-4                   |                                   |
| *Psychrobacter cryohalolentis* K5                |                                   |
| *Psychrobacter sp. PRwf-1*                       |                                   |
| *Psychromonas sp. CNPT3*                         |                                   |
| *Rahnella aquatilis* CIP 78.65 = ATCC 33071      |                                   |
| *Rahnella sp. Y9602*                            |                                   |
| *Rhodanobacter sp. 2APBS1*                       |                                   |
| *Saccharophagus degradans* 2-40                  |                                   |
| *Salmonella bongori* NCTC 12419                  |                                   |
| *Salmonella enterica subsp. enterica serovar Typhi str. Ty21a* |               |
| *Serratia liquefaciens* ATCC 27592               |                                   |
| *Serratia marcescens* WW4                        |                                   |
| *Serratia plymuthica* AS9                        |                                   |
| *Serratia proteamaculans* 568                    |                                   |
| *Serratia sp. AS12*                              |                                   |
| *Shewanella amazonensis* SB2B                    |                                   |
| *Shewanella baltica* BA175                       |                                   |
| *Shewanella denitrificans* OS217                 |                                   |
| *Shewanella frigidimarina* NCIMB 400             |                                   |
| *Shewanella halifaxensis* HAW-EB4                 |                                   |
| *Shewanella loihica* PV-4                        |                                   |
| *Shewanella pealeana* ATCC 700345                |                                   |
| *Shewanella piezotolerans* WP3                   |                                   |
| *Shewanella putrefaciens* 200                     |                                   |
| *Shewanella sediminis* HAW-EB3                    |                                   |
| **Gamma-Proteobacteria** |
|--------------------------|
| *Shewanella sp. ANA-3* |
| *Shewanella violacea DSS12* |
| *Shewanella woodyi ATCC 51908* |
| *Shigella boydii CDC 3083-94* |
| *Shigella flexneri 2a str. 301* |
| *Shigella sonnei Ss046* |
| *Simiduia agarivorans SA1 = DSM 21679* |
| *Stenotrophomonas maltophilia JV3* |
| *Teredinibacter turnerae T7901* |
| *Thalassolituus oleivorans MIL-1* |
| *Thioalkalivibrio sp. K90mix* |
| *Thioalkalivibrio sulfidophilus HL-EbGr7* |
| *Thiocystis violascens DSM 198* |
| *Thiomicrospira crunogena XCL-2* |
| *Vibrio alginolyticus NBRC 15630 = ATCC 17749* |
| *Vibrio anguillarum 775* |
| *Vibrio campbellii ATCC BAA-1116* |
| *Vibrio cholerae O395* |
| *Vibrio fischeri ES114* |
| *Vibrio furnissii NCTC 11218* |
| *Vibrio harveyi ATCC BAA-1116* |
| *Vibrio nigripulchritudo* |
| *Vibrio parahaemolyticus RIMD 2210633* |
| *Vibrio splendidus LGP32* |
| *Vibrio vulnificus CMCP6* |
### Gamma-Proteobacteria

| Organism Identifier        | Locus       | Accession          | Pentapeptide |
|---------------------------|-------------|--------------------|--------------|
| Xanthomonas albilineans GPE PC73 |             |                    |              |
| Xanthomonas axonopodis pv. citrulmo F1 |             |                    |              |
| Xanthomonas campestris pv. vesicatoria str. 85-10 | | | |
| Xanthomonas citri subsp. citri Aw12879 | | | |
| Xanthomonas oryzae pv. oryzae KACC 10331 | | | |
| Xenorhabdus bovienii SS-2004 | | | |
| Xenorhabdus nematophila ATCC 19061 | | | |
| Xylella fastidiosa subsp. fastidiosa GB514 | | | |
| Yersinia enterocolitica subsp. enterocolitica 8081 | | | |
| Yersinia pestis Antiqua | | | |
| Yersinia pseudotuberculosis YPIII | | | |

### Beta-Proteobacteria

| Organism Identifier        | Locus       | Accession          | Pentapeptide |
|---------------------------|-------------|--------------------|--------------|
| A chromobacter xylosoxidans NBRC 15126 = ATCC 27061 | | | |
| Acidithiobacillus caldus SM-1 | | | |
| Bordetella pertussis 18323 | | | |
| Candidatus Accumulibacter phosphatis clade IIA str. UW-1 | | | |
| Collimonas fungivorans Ter331 | | | |
| Gallionella capsiferriformans ES-2 | | | |
| Janthinobacterium sp. Marseille | | | |
| Ralstonia pickettii 12J | | | |
| Ralstonia solanacearum Po82 | | | |
| Variovorax paradoxus S110 | | | |

### Supplementary Table 11: Aer2-like pentapeptide tethers:

| Organism Identifier | Locus     | Accession          | Pentapeptide |
|---------------------|-----------|--------------------|--------------|
| Al_mac_7736         | I876_01970 | YP_008194818.1     | DWEAF        |
| Al_mac_7736         | I876_02010 | YP_008194826.1     | EWETF       |
| Organism identifier | locus         | accession          | pentapeptide |
|---------------------|--------------|--------------------|--------------|
| Al_mac_7736         | I876_02015   | YP_008194827.1     | EWESF        |
| Al_sp._1413         | ambt_16735   | YP_004468654.1     | EWEAF        |
| Al_vin_90           | Alvin_0183   | YP_003442182.1     | QWEEEF       |
| Al_vin_90           | Alvin_1872   | YP_003443828.1     |              |
| Al_vin_90           | Alvin_2222   | YP_003444173.1     |              |
| Al_vin_90           | Alvin_2230   | YP_003444181.1     |              |
| Gl_nit_1515         | GNIT_1657    | YP_004871766.1     | EWKEEF       |
| Gl_sp._1395         | Glaag_2576   | YP_004434785.1     | EWESF        |
| Ha_che_746          | HCH_00457    | YP_431792.1        | DWEVF        |
| Ha_che_746          | HCH_00458    | YP_431793.1        | DWEVF        |
| Ha_hal_741          | Hhal_2163    | YP_001003729.1     | EWEEF        |
| Li_ang_7812         | N175_16910   | YP_008489689.1     | EWEEF        |
| Ma_med_1360         | Marme_1102   | YP_004312213.1     | DWEEF        |
| Ma_sp._859          | Mmwy11_3301  | YP_001342141.1     | GWEEF        |
| Me_alc_1536         | MEALZ_2872   | YP_004918123.1     | EWEEF        |
| Me_met_1418         | Metme_2154   | YP_004513058.1     | EWQDF        |
| Ps_aer_479          | PA0176       | NP_248866.1        | GWEEF        |
| Ps_aer_7891         | PA1S_gp3690  | REF_DMTMMU:PA1S_gp3690 | GWEEF   |
| Ps_den_2356         | H681_00805   | YP_007655583.1     | DWEEF        |
| Ps_res_7713         | PCA10_13880  | YP_008101725.1     | EWEEF        |
| Ps_sp._1241         | PSM_A2954    | YP_004070018.1     | EWEEF        |
| Ps_suw_1301         | Psusu_0059   | YP_004145153.1     | DWQEF        |
| Ps_suw_1301         | Psusu_1463   | YP_004146541.1     |              |
| Ps_suw_1301         | Psusu_1465   | YP_004146543.1     | EWAKF        |
| Ps_suw_1301         | Psusu_1466   | YP_004146544.1     | DWAEF        |
| Sa_deg_468          | Sde_3105     | YP_528574.1        | DWEDF        |
| Sh_ama_634          | Sama_3497    | YP_929369.1        | EWHEF        |
| Sh_bal_241          | Sbal175_2162 | YP_006020732.1     | EWEEF        |
| Sh_loi_680          | Shew_0111    | YP_001092242.1     | EWNEF        |
| Organism identifier | locus        | accession      | pentapeptide |
|---------------------|--------------|----------------|--------------|
| Sh_one_481          | SO_2123      | NP_717726.1    | EWEEF        |
| Sh_sed_917          | Ssed_0184    | YP_001471925.1 | EWNEF        |
| Sh_sp_679           | Shewana3_2216| YP_869851.1    | EWEDF        |
| Sh_vio_130          | SVI_0176     | YP_003554925.1 | EWNEF        |
| Sh_woo_862          | Swoo_0164    | YP_001758560.1 | EWNEF        |
| Si_agu_2165         | M5M_00415    | YP_006915050.1 | EWEEF        |
| St_mal_1491         | BurJV3_1158  | YP_004791716.1 | GWEEF        |
| St_mal_1491         | BurJV3_1903  | YP_004792454.1 | DWQEF        |
| St_mal_1491         | BurJV3_1904  | YP_004792455.1 | DWQEF        |
| St_mal_1491         | BurJV3_1908  | YP_004792459.1 | DWQEF        |
| St_mal_1491         | BurJV3_2459  | YP_004793006.1 |              |
| St_mal_1491         | BurJV3_3037  | YP_004793581.1 |              |
| St_mal_1491         | BurJV3_3580  | YP_004794119.1 |              |
| St_mal_1491         | BurJV3_3943  | YP_004794481.1 |              |
| Te_tur_1125         | TERTU_1341   | YP_003072897.1 | EWEDF        |
| Te_tur_1125         | TERTU_2935   | YP_003074319.1 |              |
| Th_cru_598          | Tcr_0553     | YP_390823.1    | DWSDF        |
| Th_cru_598          | Tcr_2004     | YP_392268.1    |              |
| Th_ole_2361         | TOL_2508     | YP_007683144.1 | EWEEF        |
| Th_vio_1521         | Thivi_0439   | YP_006412631.1 | QWEEF        |
| Th_vio_1521         | Thivi_1211   | YP_006413359.1 | DWEEF        |
| Th_vio_1521         | Thivi_1222   | YP_006413370.1 | EWSEF        |
| Vi_ang_1433         | VAA_01905    | YP_004577835.1 | EWEEF        |
| Vi_cho_1795         | VC395_0082   | YP_002818346.1 | EWESF        |
| Vi_cho_1795         | VC395_A1113  | YP_002822179.1 | EWEEF        |
| Vi_cho_319          | VC0098       | NP_229757.1    | EWESF        |
| Vi_cho_319          | VCA1092      | NP_233472.1    | EWEEF        |
| Vi_fur_1564         | vfu_B00980   | YP_005049501.1 | EWEEF        |
| Vi_nig_7850         | VIBNI_B0011  | YP_008640924.1 | EWEEF        |
| Organism identifier | locus     | accession     | pentapeptide |
|---------------------|-----------|---------------|--------------|
| Vi_nig_7850         | VIBNI_B0830 | YP_008641677.1 |              |
| Vi_vul_1326         | VV2_1165  | NP_763073.1   | EWEEF        |
| Xa_alb_65           | XALc_0649 | YP_003375155.1 | DWEEF        |
| Xa_alb_65           | XALc_1357 | YP_003375852.1 |              |
| Xa_alb_65           | XALc_1361 | YP_003375856.1 | QWRDF        |
| Xa_alb_65           | XALc_1362 | YP_003375857.1 | HWHEF        |
| Xa_alb_65           | XALc_1364 | YP_003375859.1 | QWQEF        |
| Xa_alb_65           | XALc_1365 | YP_003375860.1 | SWQEF        |
| Xa_alb_65           | XALc_1926 | YP_003376405.1 |              |
| Xa_alb_65           | XALc_2151 | YP_003376626.1 | NWQEF        |
| Xa_alb_65           | XALc_2152 | YP_003376627.1 | DWQEF        |
| Xa_alb_65           | XALc_2153 | YP_003376628.1 | DWQEF        |
| Xa_alb_65           | XALc_3131 | YP_003377604.1 |              |
| Xa_axo_1502         | XACM_0614 | YP_004850217.1 |              |
| Xa_axo_1502         | XACM_1288 | YP_004850870.1 | DWQDF        |
| Xa_axo_1502         | XACM_1685 | YP_004851263.1 |              |
| Xa_axo_1502         | XACM_1913 | YP_004851485.1 | NWQEF        |
| Xa_axo_1502         | XACM_1918 | YP_004851490.1 |              |
| Xa_axo_1502         | XACM_1920 | YP_004851492.1 | NWQEF        |
| Xa_axo_1502         | XACM_1921 | YP_004851493.1 | DWQEF        |
| Xa_axo_1502         | XACM_1922 | YP_004851494.1 |              |
| Xa_axo_1502         | XACM_1923 | YP_004851495.1 | SWQEF        |
| Xa_axo_1502         | XACM_1925 | YP_004851496.1 | NWAEF        |
| Xa_axo_1502         | XACM_1926 | YP_004851497.1 | DWSEF        |
| Xa_axo_1502         | XACM_1927 | YP_004851498.1 | QWQDF        |
| Xa_axo_1502         | XACM_1929 | YP_004851500.1 | QWQDF        |
| Xa_axo_1502         | XACM_1930 | YP_004851501.1 |              |
| Xa_axo_1502         | XACM_1932 | YP_004851503.1 | NWQEF        |
| Xa_axo_1502         | XACM_1933 | YP_004851504.1 | SWQEF        |
| Organism identifier | locus      | accession            | pentapeptide |
|--------------------|-----------|----------------------|--------------|
| Xa_axo_1502        | XACM_3051 | YP_004852602.1       |              |
| Xa_cam_666         | XCV0669   | YP_362400.1          |              |
| Xa_cam_666         | XCV1702   | YP_363433.1          |              |
| Xa_cam_666         | XCV1933   | YP_363664.1          | NWQEF        |
| Xa_cam_666         | XCV1938   | YP_363669.1          |              |
| Xa_cam_666         | XCV1939   | YP_363670.1          | NWQEF        |
| Xa_cam_666         | XCV1940   | YP_363671.1          | DWQEF        |
| Xa_cam_666         | XCV1941   | YP_363672.1          |              |
| Xa_cam_666         | XCV1942   | YP_363673.1          | SWQEF        |
| Xa_cam_666         | XCV1944   | YP_363675.1          | SWQEF        |
| Xa_cam_666         | XCV1945   | YP_363676.1          | NWAQE        |
| Xa_cam_666         | XCV1947   | YP_363678.1          | DWSEF        |
| Xa_cam_666         | XCV1948   | YP_363679.1          | QWQDF        |
| Xa_cam_666         | XCV1951   | YP_363682.1          | QWQDF        |
| Xa_cam_666         | XCV1952   | YP_363683.1          |              |
| Xa_cam_666         | XCV1954   | YP_363685.1          | NWQEF        |
| Xa_cam_666         | XCV1955   | YP_363686.1          | SWQEF        |
| Xa_cam_666         | XCV3261   | YP_364992.1          |              |
| Xa_cit_2353        | XCAW_02407| YP_007650389.1       |              |
| Xa_cit_2353        | XCAW_02490| YP_007650471.1       | DWQEF        |
| Xa_cit_2353        | XCAW_02492| YP_007650473.1       |              |
| Xa_cit_2353        | XCAW_02493| YP_007650474.1       | QWQDF        |
| Xa_cit_2353        | XCAW_02495| YP_007650476.1       | QWQDF        |
| Xa_cit_2353        | XCAW_02496| YP_007650477.1       | DWSEF        |
| Xa_cit_2353        | XCAW_02497| YP_007650478.1       | NWAQE        |
| Xa_cit_2353        | XCAW_02498| YP_007650479.1       | SWQEF        |
| Xa_cit_2353        | XCAW_02499| YP_007650480.1       | SWQEF        |
| Xa_cit_2353        | XCAW_02500| YP_007650481.1       |              |
| Xa_cit_2353        | XCAW_02501| YP_007650482.1       | NWQEF        |
| Organism identifier | locus   | accession       | pentapeptide |
|---------------------|---------|-----------------|--------------|
| Xa_cit_2353         | XCAW_02502 | YP_007650483.1 | NWQEF        |
| Xa_cit_2353         | XCAW_02504 | YP_007650485.1 |              |
| Xa_cit_2353         | XCAW_02508 | YP_007650489.1 | NWQEF        |
| Xa_cit_2353         | XCAW_03417 | YP_007651390.1 |              |
| Xa_cit_2353         | XCAW_03970 | YP_007651933.1 |              |
| Xa_cit_2353         | XCAW_04466 | YP_007652428.1 |              |
| Xa_ory_584          | XOO2840   | YP_201479.1     | DWAEF        |
| Xa_ory_584          | XOO2842   | YP_201481.6     | NWAEF        |
| Xa_ory_584          | XOO2844   | YP_201483.1     | SWQEF        |
| Xa_ory_584          | XOO2845   | YP_201484.1     |              |
| Xa_ory_584          | XOO2847   | YP_201486.1     | NWQDF        |
| Xa_ory_584          | XOO2848   | YP_201487.6     | DWQDF        |

**Supplementary Table 12: McpA-like C-terminal motif**

| Organism identifier | locus   | accession       | pentapeptide |
|---------------------|---------|-----------------|--------------|
| Al_mac_7736         | I876_01990 | YP_008194822.1 | DIELF-       |
| Al_mac_7736         | I876_01950 | YP_008194814.1 | EVELF-       |
| Al_sp._1413         | ambt_16755 | YP_004468658.1 | EVELF-       |
| Gl_sp._1395         | Glaag_2582 | YP_004434791.1 | DLELF-       |
| Ma_med_1360         | Marme_1096 | YP_004312207.1 | EIDLF-       |
| Ma_sp._859          | Mmwl1_3295 | YP_001342135.1 | DIDLF-       |
| Sh_sp._679          | Shewana3_2222 | YP_869857.1 | EIELF-       |
| Sh_one_481          | SO_2117   | NP_717720.2     | EIELF-       |
| Sh_bal_241          | Sbal175_2156 | YP_006020726.1 | EIELF-       |
| Ps_den_2356         | H681_00825 | YP_007655587.1 | EVELF-       |
| Ps_res_7713          | PCA10_13920 | YP_008101729.1 | EVELF-       |
| Ps_aer_479          | PA0180    | NP_248870.1     | EVELF-       |
| Ps_aer_7891         | PA1S_gp3694 | REF_DMTMMU:PA1S_gp3694 | EVELF- |
| Organism identifier | locus     | accession          | pentapeptide |
|---------------------|-----------|--------------------|--------------|
| Th_cru_598          | Tcr_0759  | YP_391029.1        | EIDLF-       |
| Ha_hal_741          | Hhal_2159 | YP_001003725.1     | DVELF-       |
| Gl Nit_1515         | GNIT_1661 | YP_004871770.1     | DIELF-       |
| Me_alc_1536         | MEALZ_2878| YP_004918129.1     | DIELF-       |
| Me_met_1418         | Metme_2161| YP_004513065.1     | DVELF-       |
| Fr_aur_1557         | Fraau_2042| YP_005378108.1     | DIDLF-       |
| Rh_sp._1523         | R2APBS1_2961| YP_007591271.1    | EIELF-       |
| Al_vin_90           | Alvin_2234| YP_003444185.1     | DIELF-       |
| Th_vio_1521         | Thivi_1219| YP_006413367.1     | DIELF-       |
| Ha_che_746          | HCH_00449 | YP_431784.1        | DIELF-       |
| Sa_deg_468          | Sde_3111  | YP_528580.1        | EIVLY-       |
| Te_tur_1125         | TERTU_1204| YP_003072781.1     | DIELYE       |
| Ps_suw_1301         | Psesu_1530| YP_004146608.1     | TVELF-       |
| Xa_alb_65           | XALc_1440 | YP_003375935.1     | TVELF-       |
| St_mal_1491         | BurJV3_1974| YP_004792525.1    | TVELF-       |
| Xa_ory_584          | XOO2558   | YP_201197.1        | TVELF-       |
| Xa_cit_2353         | XCAW_01830| YP_007649819.1     | TVELF-       |
| Xa_axo_1502         | XACM_2022 | YP_004851592.1     | TVELF-       |
| Xa_cam_666          | XCV2044   | YP_363775.1        | TVELF-       |
| Vi_vul_1326         | VV2_1160   | NP_763069.1        | EVELF-       |
| Vi_nig_7850         | VIBNI_B0016| YP_008640928.1    | EVELF-       |
| Vi_fur_1564         | vf_B00976  | YP_005049497.1     | EVELF-       |
| Vi_cho_1795         | VC395_A1109| YP_002822175.1    | EVELF-       |
| Vi_cho_319          | VCA1088   | NP_233469.1        | EVELF-       |
| Vi_ang_1433         | VAA_01909  | YP_004577831.1     | EVELF-       |
| Li_ang_7812         | N175_16890| YP_008489685.1     | EVELF-       |
Supplementary Note 1



Supplementary References

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