Supplementary Materials for

Repurposing a macromolecular machine: Architecture and evolution of the F7 chemosensory system

Davi R. Ortega[1], Poorna Subramanian[1], Petra Mann[2], Andreas Kjaer[1,†], Songye Chen[1], Kylie J. Watts[3], Sahand Pirbadian[4], David A. Collins[5], Romain Kooger[6], Marina G. Kalyuzhnaya[5], Simon Ringgaard[2], Ariane Briegel[7*], Grant J. Jensen[1,8*]

Correspondence to: jensen@caltech.edu, a.briegel@biology.leidenuniv.nl

This PDF file includes:

Materials and Methods
Figs. S1 to S4
Tables S1 to S9
Captions for Datasets S1 to S2

Other Supplementary Materials for this manuscript include the following:

Datasets S1 to S2

Materials and Methods

Strains and growth conditions

Vibrio cholerae

Strain list and construction:
Wild-type: *Vibrio cholerae* C6706
Strain PM6: *Δvca1088*
Strain PM7: *Δvca1093*, *Δvca1094*, *Δvca1095* (ΔF7)
Strain PM18: *Δvca1092*

V. cholerae deletion strains were generated using standard allele exchange (*47*) with the plasmids listed below.

Plasmid for deletion of *vca1093*, *vca1094* and *vca1095*:
Plasmid pPM045 was constructed by PCR amplification of the up- and down-stream regions of *vca1093* and *vca1095*, respectively. PCR1 was performed with primers ccccctctagaaattggctaatccctcctaaactc / aatcttgcgcagttgttccatatc and C6706 chromosomal DNA as template. PCR2 was performed with primers gatatggaacaactgcgcaagatt cgcttaagcaccactgccgaa / ccccctctagacatcatcaaattcgtcgtcatgc and C6706 chromosomal DNA as template. A third PCR was then performed using primers ccccctctagaaattggctaatccctcctaaactc / ccccctctagacatcatcaaattcgtcgtcatgc and PCR1 and PCR2 as template. The product from PCR3 was then digested with XbaI and ligated into the equivalent site of plasmid pCVD442 (*47*) resulting in plasmid pPM045.

Plasmid for deletion of *vca1092*
Plasmid pPM051 was constructed by PCR amplification of the up- and down-stream regions of *vca1092*. PCR1 was performed with primers ccccctctagaacggttgtcttgatcttgagtgc / aacaaactggggcacaacctg and C6706 chromosomal DNA as template. PCR2 was performed with primers caggttgtgccccagtttgttatgcataaagcaccgataaatcagg/ ccccctctagaattgccttgctgatctttgaccc and C6706 chromosomal DNA as template. A third PCR was then performed using primers Ccccc tctaga acggttgtcttgatcttgagtgc / ccccctctagaattgccttgctgatctttgaccc and PCR1 and PCR2 as template. The product from PCR3 was then digested with XbaI and ligated into the equivalent site of plasmid pCVD442 resulting in plasmid pPM051.

Plasmid for deletion of *vca1088*
Plasmid pSR1228 was constructed by PCR amplification of the up- and down-stream regions of *vca1088*. PCR1 was performed with primers ccccctctagaaagccaatgtagggtttgtgcag / tatcgccgttattttgtgttttctcg and C6706 chromosomal DNA as template. PCR2 was performed with primers cgagaaaacacaaaataacggcgataaaccgtgggggattggctg / ccccctctagatgcgataatgtgcctgtactttg and C6706 chromosomal DNA as template. A third PCR was then performed using primers ccccctctagaaagccaatgtagggtttgtgcag / ccccctctagatgcgataatgtgcctgtactttg and PCR1 and PCR2 as template. The product from PCR3 was then digested with XbaI and ligated into the equivalent site of plasmid pCVD442 resulting in plasmid pSR1228.

During plasmid and strain construction, *V. cholerae* and *E. coli* were grown at 37°C in LB medium or on LB agar plates containing antibiotics in the following concentrations: 200 mg/mL

streptomycin; 50 mg/mL kanamycin; 100 mg/mL ampicillin; 50 mg/mL carbenicillin; and 20 mg/mL chloramphenicol for *E. coli*, and 5 mg/mL for *V. cholerae*.

For cryo-ET microscopy *V. cholerae* cells were grown as described previously (*16*): after growth in LB medium for 24 hours at 30°C with shaking, 150 µl cell suspension was diluted into 2 ml Ca-HEPES buffer and grown for an additional 16 hours with shaking at 30°C.

Pseudomonas aeruginosa

The *P. aeruginosa* mutant strains imaged in this study were acquired from the transposon mutant collection from the University of Washington, Table S4. Wild-type *P. aeruginosa* PAO1 and a PAO1 *aer2* deletion mutant [PAO1047](*30*) were imaged in this study. Cells were grown in MOPS-based nitrogen starvation medium for ~24 hours at 30°C with shaking. MOPS-based minimal medium limited nitrogen(*48*): 43mM NaCl, 50mM MOPS (from 1M stock of MOPS/NaMOPS pH 7.2), 40 mM Sodium Succinate, 1mM $MgSO_4$, 2.2mM KCl, 0.1mM CaCl, 10µM $FeNH_4SO_4$*7H_20, 1 mM NH_4Cl, 1.25mM NaH_2PO_4.

Shewanella oneidensis

For imaging the chemosensory systems, *Shewanella oneidensis* MR-1 wild-type cells were cultured using continuous flow bioreactors (chemostats) or batch cultures as previously described(*20*).

Methylomicrobium alcaliphilum

For imaging intracellular structures wild type *M. alcaliphilum* $20Z^R$ cells were grown in a modified nitrate mineral salts medium(*49*) with a final pH of 9.0 consisting of: 9.9mM KNO_3, 0.8mM $MgSO_4$ x 7 H_2O, 13.6µM $CaCl_2$ x 2 H_2O, 0.5M g*L^{-1} NaCl, 2mM KH_2PO_4, 2mM Na_2HPO_4, 22.5mM $NaHCO_3$, 2.5mM Na_2CO_3 along with trace elements 13.4 µM Na_2EDTA, 7.2µM $FeSO_4$ x 7 H_2O, 4.8µM $CuSO_4$ x 5 H_2O, 1 µM $ZnSO_4$ x7 H_2O, 0.9 µM Na_2O_4W x $2H_2O$, 0.8 µM $CoCl_2$ x 6 H_2O, 0.5µM H_3BO_3, 0.2 µM $MnCl_2$ x 4 H_2O, 0.2µM $NiCl_2$ x 6 H_2O, 0.2µM Na_2MoO_4 x 2 H_2O. Cultures were grown at 30°C in septated bottles containing 20% CH_4 headspace. Cell samples for cryo-ET preparations were taken at mid-exponential phase, at a cell density of OD_{600} = 0.5.

Electron cryotomography

Cells were prepared for electron cryotomography as described previously(*50*) . Images were collected using either an FEI Polara 300 keV field emission gun microscope or an FEI TITAN Krios 300 keV field emission gun microscope with lens aberration correction (FEI Hillsboro, OR). Both microscopes were equipped with Gatan imaging filers and 'K2 summit' counting electron detector cameras (Gatan, Pleasanton, CA). The data collection software used to collect the tilt series was UCSFtomo (*51*). The cumulative electron dose was 160 e^-/A^2 or less for each individual tilt series. CTF correction, frame alignment and SIRT reconstruction were done using the IMOD software package (*52*). The tomograms used in this study are available in the Electron Tomography Database – Caltech (*53*) and their identifiers can be found in Table S5.

1D electron density profiles

To measure the distance between the inner membrane (IM) and the CheA/CheW base plate, we used a custom script written in Node.js that takes as input the tomogram and the model points

that delineate the inner membrane using 3dmod. The script calculates the average pixel value in profiles running perpendicular to the model points but in the same plane as the model points were collected. These averaged profiles are output in a JSON formatted file. The script and instructions for installation and use are available in a GitLab repository at https://gitlab.com/daviortega/sideview-profile-average. To visualize the profile we used the ObservableHQ notebook located at https://beta.observablehq.com/@daviortega/generic-notebook-to-analyse-1d-averaged-electron-density-p. For each profile, we measure the distance between the peaks corresponding to the electron density of the IM, the CheA/CheW baseplate and the intermediate layers when possible, in pixels. The measurement uncertainty was estimated as the expanded uncertainty using k = 2 as a coverage factor propagated from the uncertainty in determining the center of each peak in pixels, as recommended by (*54*). The values reported in nanometers were calculated by multiplying the measurement and uncertainty by the pixel size for each tomogram.

Bioinformatics resources and software packages

All sequences in this study were collected in the MiST database (*55*), domain architecture predictions from PFAM(*56*) were selected from SeqDepot (*57*), and 3D atomic models were taken from the Protein Data Bank (PDB) (*58*). Domain architecture prediction was performed with CD-VIST (http://cdvist.zhulinlab.org/)(*25*). We used CD-HIT v4.6 to reduce redundancy in unaligned sequences(*59*). Multiple sequence alignments were performed with the algorithm L-INS-I from the package MAFFT v7.305b (*60*). We used Gblocks v 0.91b (*61*) to eliminate poorly aligned columns in multiple sequence alignments. To perform sequence alignments with structural information we used STRAT from the MultiSeq (*62*) tool for VMD v1.9.3 (*63*) which in turn was used to visualize and manipulate 3D structures. Homology modeling was performed using MODELLER v9.17 (*64*). Secondary structure predictions were performed with JNet Structure Predictions(*65*) in the Jalview(*66*) software, which was also used to visualize multiple sequence alignments. Similarity searches for sequences were conducted using BLAST v2.7.1+ (*67*) and HMMER v3.1b2 (*68*). Phylogenetic reconstructions were performed using RAxML v8.2.10(*69*). To collapse branches with low support in phylogenetic trees we used TreeCollapseCL4 (*70*). Tomograms and model points were manipulated using 3dmod v4.9.9 (*52*).

Protein domain architecture prediction

The domain architecture of the C-termini of chemoreceptors are poorly conserved among members of this protein family(*71*). Further, protein domains commonly appearing in this region, such as HAMP(*72*) and PAS(*26*), are so diverse that in several instances predictive models have difficulty identifying them. To address this problem we used CD-VIST on the two Aer2-like receptors without known domain architectures from *S. oneidensis* and *M. alcaliphilum* with TMHMM prediction, skipping HMMER3 and RPSBLAST steps, but adding three consecutive HHSEARCH steps against the PDB database with HHBLITS using uniclust30 at different thresholds for minimum probability: 60%, 40% and 20%. Analyzing the CD-VIST domain coverage we predicted that *S. oneidensis*'s Aer2-like receptor has a PAS-PAS-HAMP-HAMP-MCPsignal domain architecture, similar to *V. cholerae* and that the *M. alcaliphilum*'s Aer2-like receptor has a HAMP-PAS-HAMP-HAMP-MCPsignal domain architecture. We further enhanced our confidence in this predictions by aligning the Aer2-like sequences to the sequence of the templates used to produce the homology models.

Homology modeling
To build homology models for the Aer2-like receptors in *V. cholerae*, *P. aeruginosa*, *S. oneidensis* and *M. alcaliphilum* we used several crystal structures available in the Protein Data Bank (PDB), Table S6. The files used in this process are described in Table S7 and can be found in the Supplementary Dataset S1.

First we built a homology model with two HAMPs followed by the MCPSignal domain that we name 2H+S. For that we used the structures 3ZX6 and the second HAMP of 4I3M to form a chimeric template. We manually aligned the structures of the templates against the Aer2 in *P. aeruginosa* (PA1076) and performed a multiple sequence alignment using L-INS_I and MultiSeq. To construct the homology model of this structure, we use MODELLER with the following parameters: a.library_schedule = autosched.slow, a.max_var_iterations = 1000, a.repeat_optimization = 100 and a.max_molpdf = 1e6. To make sure that the connection between both HAMPs remained the same, we added a restraint in both chains A and B from residues 359 to 385. We built 100 homology models with these parameters and chose the one with the lowest DOPE score.

Next, to add a PAS domain to this structure, we used the 3VOL and 4HI4 structures. First we aligned chain B of 3VOL with the 2H+S homology model produced in the previous step. We noticed that this alignment produced clashes between the PAS domains. To overcome this obstacle, we used chains B and D in the 4HI4 structure as a model for the dimerization of the two PAS domains. We aligned chain B of 4HI4 to the 3VOL structure using the residues QWTDRT and then manually manipulated the dimer of PAS to be positioned in line with the 2H+S model to build the next homology model: P+2H+S. Sequence alignment was performed as described before against the sequence of Aer2 in *P. aeruginosa* (PA1076). This homology model was used as the basis of the complete homology models of all the Aer2-like receptors.

To build the homology model of Aer2 in *P. aeruginosa* (PA1076), we used the P+2H+S model together with the 4I3M structure. For that we manually aligned the structures to build the template. However, there is a 13 residue region unresolved in both structures (R156 – G169) but predicted to be alpha helical. We assume that these two structures then are around 2.2 nm apart and took that into consideration while positioning the structures. Finally the homology model was built using MODELLER with the parameters described above and with a restraint to force alpha helical conformation between residues 140 to 181.

To build the homology model of the Aer2-like receptor in *V. cholerae* (VCA1092) we used the P+2H+S model together with 4HI4. The sequences of the templates and VCA1092 aligned pretty well with only a minor gap in the residues ELLRD, also predicted to be alpha helical. We aligned the end of chain B of the already aligned 4HI4 used in the P+2H+S model to the beginning of chain A of P+2H+P using STAMP and manually adjusted the position of the structures using VMD. The homology model was constructed with MODELLER and we imposed a restraint to force alpha helical conformation between residues 21 to 43 (C terminal) and 151 to 171 (unresolved gap).

To build the homology model of the Aer2-like receptor in *S. oneidensis* (SO_2123) we used the VCA1092 model since they have the same domain architecture. The sequences of the templates and SO_2123 also aligned pretty well with only a minor gap in the residues ESIDA, also predicted to be alpha helical. The C-terminus of the sequence is also predicted to be alpha helical up to the residue PHE7. We aligned the end of chain B of the already aligned 4HI4 used in the P+2H+S model to the beginning of chain A of P+2H+P using STAMP and manually adjusted the position the structures using VMD. The homology modeling was performed with MODELLER and we imposed a restraint to force alpha helical conformation between residues 21 to 43 (C terminal) and 151 to 171 (unresolved gap).

To build the homology model of the Aer2-like receptor in *M. alcaliphilum* (MEALZ_2872) we used the P+2H+S model and the 4I3M structure. To find out which of the 3 HAMPs in the 4I3M structure is most closely related to the C-terminal HAMP of MEALZ_2872 we used BLAST to find HAMP sequences in the *Pseudomonas* group similar to each of the HAMPs in the 4I3M and to the C-terminal HAMP of MEALZ_2872. We aligned the sequences using L-INS-I and perform a phylogenetic reconstruction using RAxML with -m PROTGAMMAIAUTO -p 1234555 -x 9876545 -f a -N 100 as parameters. Tree nodes were collapsed to a certainty score of 50. The phylogenetic analysis showed that the C-terminal HAMP of MEALZ_2872 is closely related to the second HAMP of 4IM3. We truncated the 4IM3 structure to contain only the second HAMP and aligned an extended helix connecting to the third HAMP with the PAS domain of the P+2H+S model. We used this alignment to place the HAMP at the right position and deleted the extended helix. These structures were used as a template for the MEALZ_2872 homology model built with MODELLER as described above and with restraints to force alpha helical conformation in residues 194 to 216, 255 to 270 and 721 to 728.

Chemotaxis system classification

Relevant protein sequences of chemotaxis components were classified using HMMER and the hidden Markov models previously published (*9*). The model with highest score was used to assign chemotaxis components to classes.

F7 system identification in γ-Proteobacteria.

To estimate how widespread F7 systems are in γ-Proteobacteria, we randomly picked 310 genomes from γ-Protebacteria from MiST. From those, we selected the CheA protein sequences and then classified them using HMMs provided by the authors of (*9*). The CheA proteins classified as F7 systems belonged to 176 genomes. Table S8 list all 310 genomes and marks the presence of the F7 systems in the 176 genomes.

Phylogenetic tree of F7 systems in Proteobacteria

To build a tree of the F7 and F8 systems in Proteobacteria we used a concatenated alignment of the protein sequences of CheA, CheB and CheR, as previously described (*9*). We first collected every CheA belonging to these two classes from 1152 Proteobacteria genomes in MiST (547 from F7 class and 168 from F8 class) and used CD-HIT to eliminate redundancy at the 85% identity level (201 from F7 class and 119 from F8 class). To find CheB and CheR proteins that confidently function with the selected CheAs, we searched for genes that code for these proteins in the range of 10 genes upstream and downstream from each *cheA* gene. Conflicts of multiple or missing *cheB*, *cheR*, or *cheA* genes within that range were manually resolved or the system was

removed from the dataset. At this stage the dataset contained 272 protein sequences of CheAs, CheBs and CheRs. We aligned each protein individually with L-INS-I from MAFFT. We used Jalview to examine the alignment and removed 10 sequences for not being complete genes and re-aligned the sequences with L-INS-I. The final dataset had 262 sequences from 246 genomes. For each protein family, we used Gblocks to remove alignment positions with low information. The Gblock parameters were: b3=8 -b4=10 b5=h. The resulting alignments of the protein sequences of CheA, CheB and CheR were concatenated into a single alignment with 698 columns. We used RAxML with parameters -m PROTGAMMAIAUTO -f d -d -N 25 with different seeds 10 times and 3 partitions set to evolutionary model AUTO with boundaries 1-312, 313-559 and 560-698 to accommodate possible differences in the evolutionary models selected for CheA, CheB and CheR sequences. We selected the tree with best maximum likelihood score. We also ran 1000 rapid bootstrap on the same alignment with the parameters -m PROTGAMMAIAUTO -p 1234555 -x 9876545 -f a -N 1000. We mapped these bootstrap values to the best tree and used TreeCollapseCL4 to collapse nodes with less than 50% uncertainty to polytomies. We also mapped the CheA gene neighborhoods (15 genes up and downstream) to the CheABR tree using custom scripts written in Python to produce Fig. S1. BLAST all vs. all to all CheAs and selected neighboring genes was used to loosely define homologous sets of proteins with at least 10E-40 E-value and query coverage of 95% to any member of the set. As an exception to this rule, the anti-signa factor antagonists were selected with the threshold of 1E-5 and query coverage of 50%. Homologs of relevant proteins are highlighted in different colors. We manually selected representatives of relevant genes neighboring CheA for major branches relevant to this study for display in Fig. 3.

Phylogenetic profiles of F6 and F7 systems

We first selected the genomes of the organisms we imaged: *Methylomicrobium alcaliphilum*, *20Z*, *Pseudomonas aeruginosa PAO1*, *Shewanella oneidensis MR-1*, *Vibrio cholerae O1 biovar El Tor str. N1696*. In order to perform phylogenetic profiling of the chemotaxis systems in γ-Proteobacteria, we added 162 genomes from this class and 10 genomes from β-Proteobacteria as an outgroup, for a total of 176 genomes (Table S9). The number of selected genomes is coincidently the same as the number of genomes from γ-Proteobacteria with F7 systems described above but only a fraction of genomes are present in both sets. To build the organism tree we used the same procedure as described in (*73*) with the difference that the final concatenated alignment served as an input to RAxML to generate 164 inferences with the parameters -m PROTGAMMAIAUTO -p 12345 -f d -d -N 164. Chemotaxis proteins from these genomes were classified as described above and mapped onto the organism tree to produce Fig. S2.

Domain architecture prediction of chemoreceptors present in stage 3 and 4 F7 systems

We selected the protein sequences of chemoreceptors present in the gene neighborhood used to build Fig. S1 and use CDVIST to predict the domain architecture using TMHMM, HMMER3 against Pfam 30.0 database. The results are shown in Fig. S3.

Identification of Aer2-like and McpA-like receptors

We first collected all 3389 chemoreceptors from the 176 genomes used to build the phylogenetic profiles. We defined a protein as a chemoreceptor if it contained the MCPsignal PFAM domain. Then we grouped them in clusters of orthologous groups using the same technique described in

(*18*). To pick Aer2-like receptors we used an E-value of 1E-135 and selected all 144 receptors present in the same group as the Aer2 (PA1076) from *P. aeruginosa*. From those, we removed 6 receptors from the β-Proteobacteria outgroup, 5 that were not classified as 36H receptors and 3 other sequences that did not seem to align well with the group. The final set of Aer2-like receptors had 130 Aer2-like receptors and was aligned using L-INS-I and manually inspected with Jalview. Chemoreceptor families and subfamilies are prone to have diverse C-terminal domain architectures so following the procedure in (*71*) we manually trimmed the sequences to only contain the regions common to all receptors. This final alignment was used to build a phylogenetic tree with RAxML. We built 200 independent inferences with parameters -m PROTGAMMAILG -p 1234555 -f d -d -N 200 and 1000 rapid bootstrap trees with -m PROTGAMMAILG -p 1234555 -x 9876545 -f a -N 1000. Bootstrap scores were mapped to the tree with best maximum likelihood from the 200 independent inferences. Nodes were collapsed to polytomies at 50% uncertainty using TreeCollapseCL4. The same procedure was executed to make the tree of McpA-like receptors but with an E-value threshold of 1E-30. The McpA-like cluster was defined as the one containing McpA from *P. aeruginosa* (PA0180). There were 40 McpAs in the final dataset. Both trees are displayed in Fig. S4.

Phylogenetic tree of CheY

The CheY protein comprises a single domain, known in the PFAM database as Response Regulator (Response_reg). However, this domain appears in several other proteins as well. In order to select proteins with one and only one response regulator domain, we collected the domain architecture information from PFAM v30 and predicted transmembrane regions by TMHMM from SeqDepot for all sequences from the 246 genomes and used Regular Architecture (https://www.npmjs.com/package/regarch) to filter only single CheY domains with the following rule:

```
{
   "patterns": [
      {
         "npos": [
            {
               "count": "{0}"
               "name": "TM",
               "resource": "tmhmm2",
            }
         ],
         "pos": [
            {
               "name": "^",
               "resource": "regarch"
            },
            {
               "name": "Response_reg",
               "resource": "pfam30"
            },
            {
```

```
                "name": "$",
                "resource": "regarch"
            }
        ]
    }
  ]
}
```

This pattern selected 4941 sequences. We then used the same clustering techniques described for Aer2-like and McpA-like receptors with an E-value threshold of 10E-30 and selected the largest group, with 1394 sequences. This group contains the known CheYs of the model organisms in this study and others. We aligned this dataset with L-INS-I and manually removed 3 sequences that were highly divergent using Jalview. We built the tree with 500 rapid bootstraps with RAxML and searched for the best tree of this set with the parameters -m PROTGAMMALG -p 1234555 -x 9876545 -f a -N 500. Finally we collapsed nodes with less than 50% support into polytomies using TreeCollapseCL4 to produce Fig. 4.

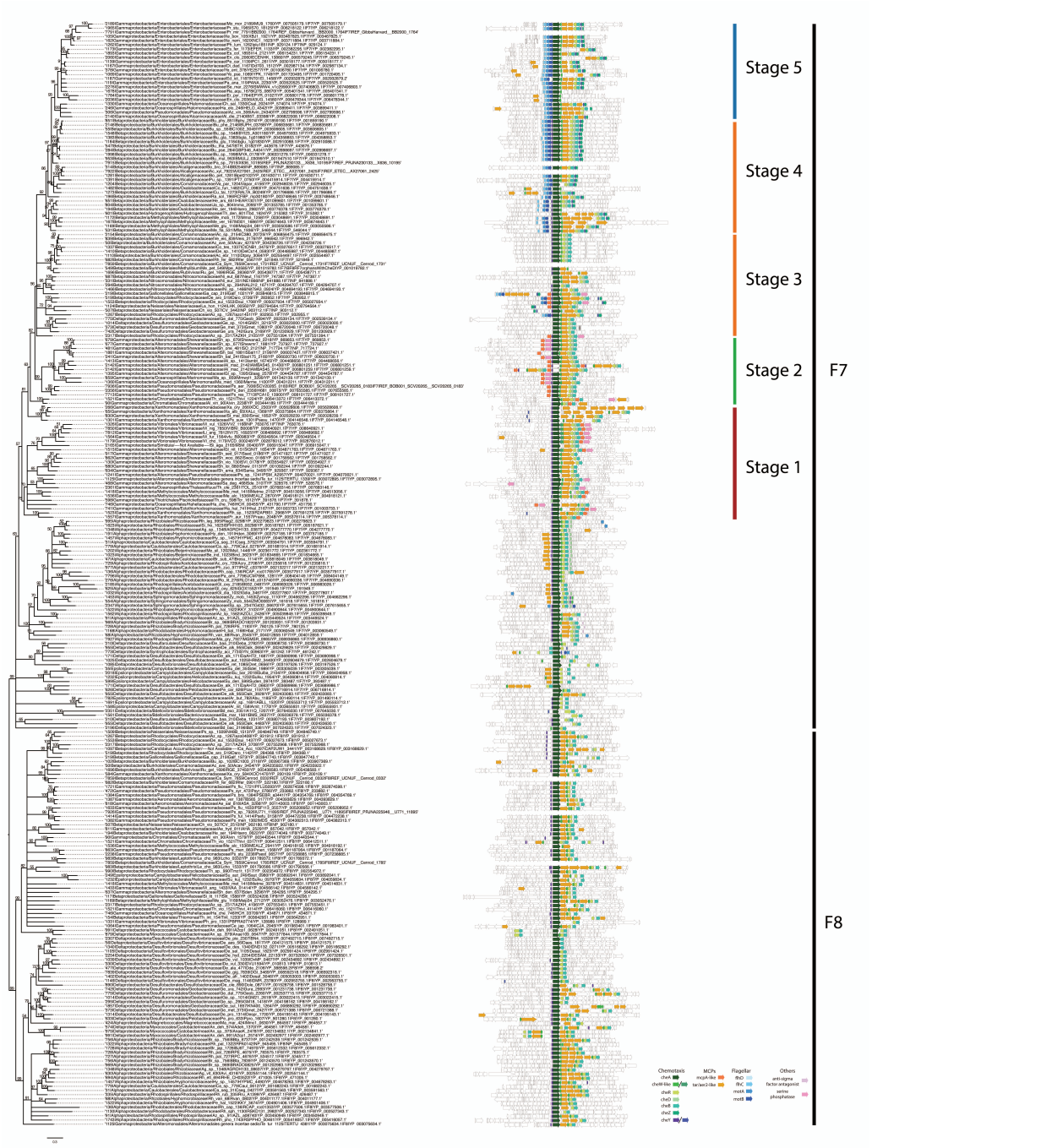

Fig. S1.

Phylogeny of CheA, CheB and CheR concatenated alignments of F7 and F8 systems and gene neighborhood of 15 genes up and downstream from CheA.

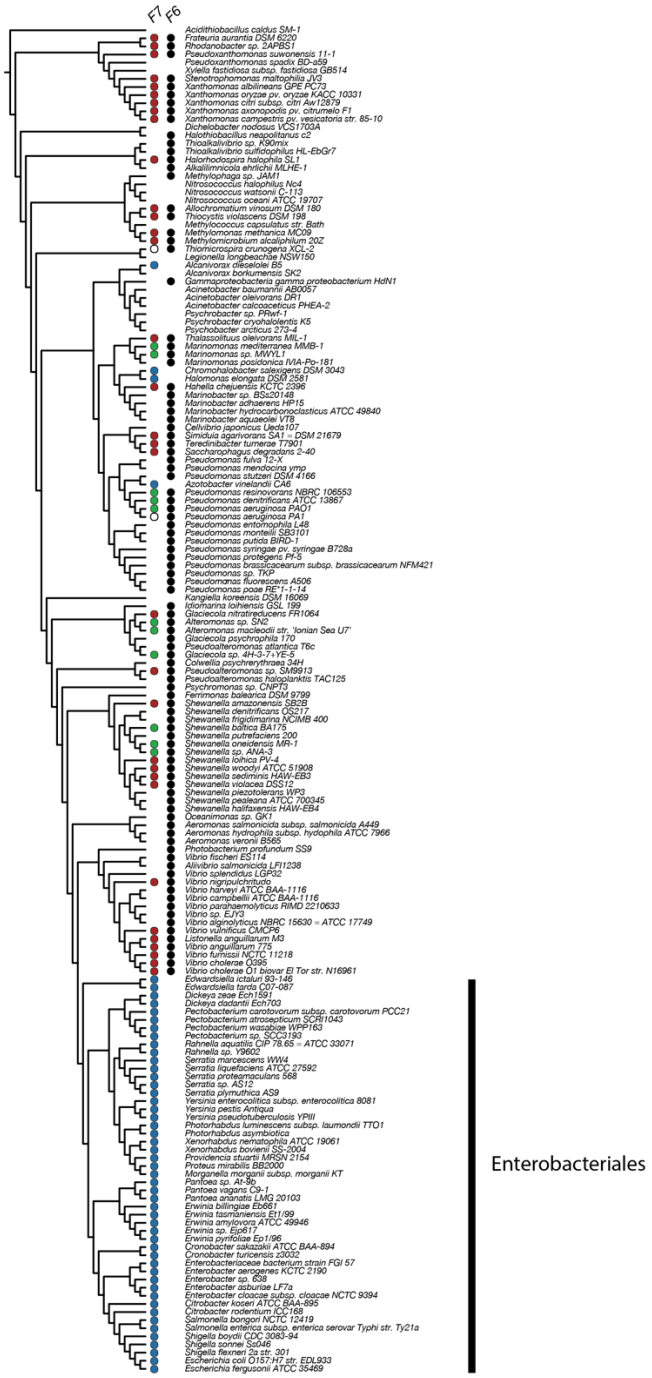

Fig. S2.

Phylogenetic profile of the F7 and F6 systems in γ-Proteobacteria shows that only organisms with stage 1 (red) and from stage 2 (green) has F6 systems but not from stage 5 (blue). Note that the distribution of stage 1and 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.

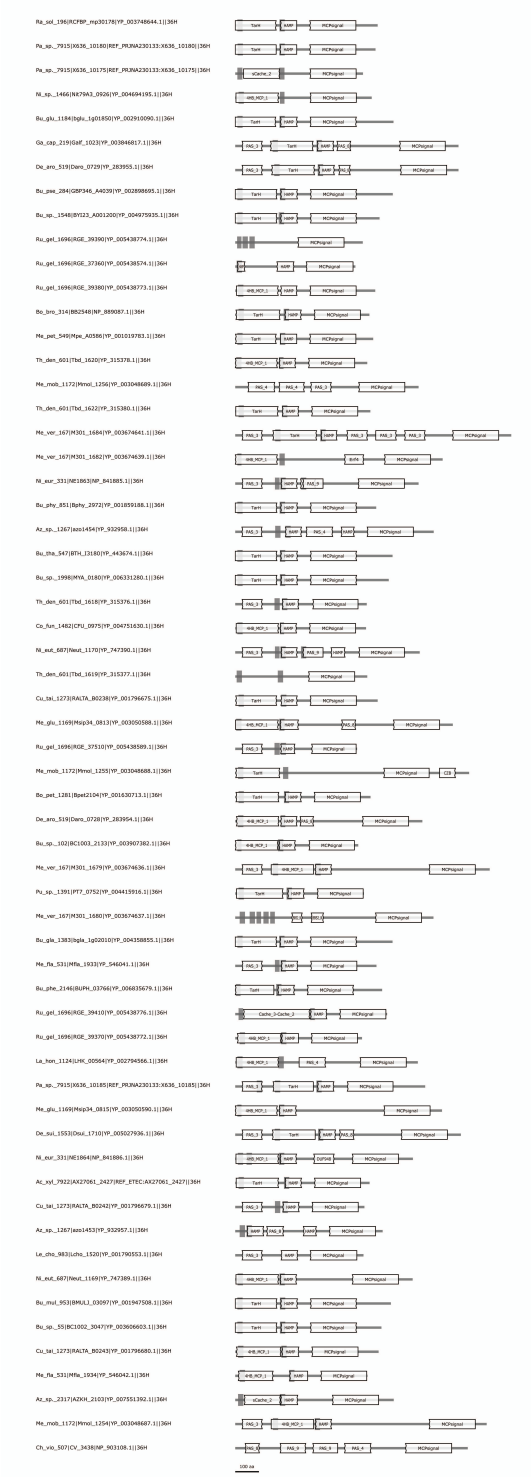

Fig. S3.

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).

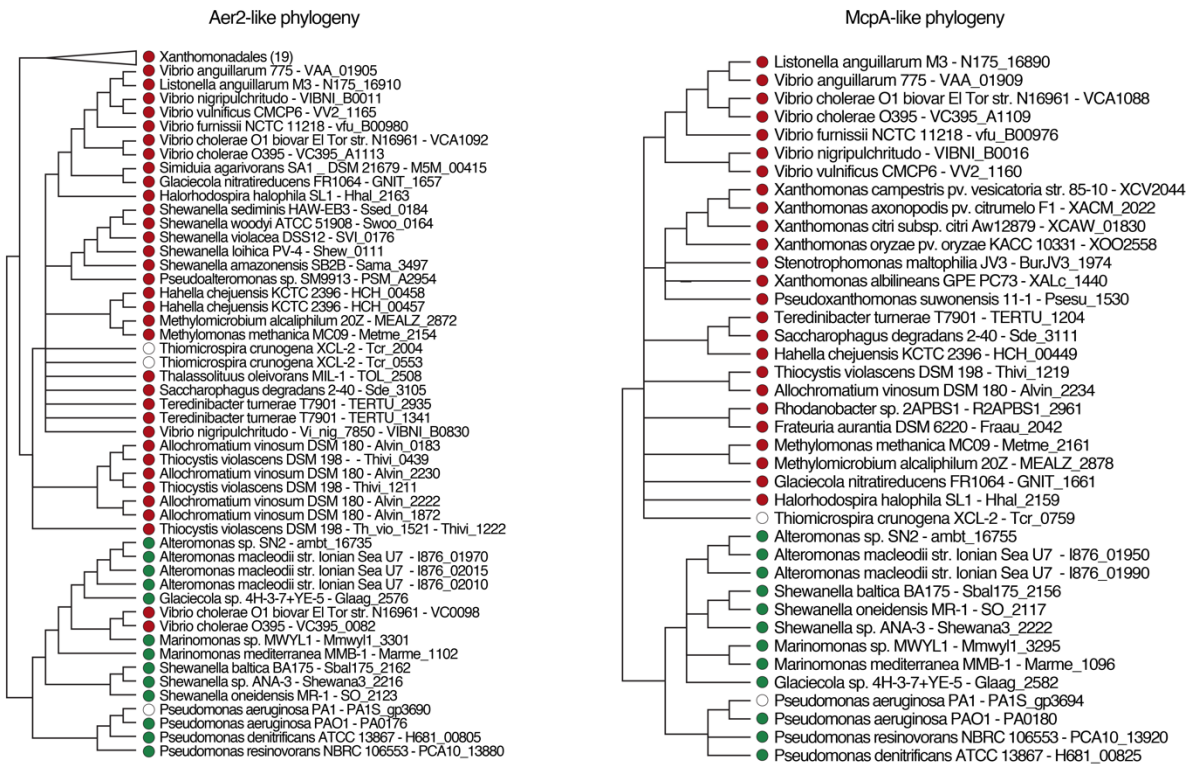

Fig. S4.

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. cholera*, 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.

Table S1.

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

Table S2.

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

Table S3.

Locations of electron density layers in arrays. Distances are measured from the CheA/CheW baseplate in nanometers. Uncertainties reported are the expanded standard uncertainty.hemosensory gene clusters in the genomes of *V. cholerae*, *P. aeruginosa*, *S. oneidensis* and *M. alcaliphilum*.

Layer	***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

Table S4.

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

Table S5.

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	6cef7c25e66ce42e4e2440490a68845a55130377f7bc9e096c48fd83b47ae9cd	*Vibrio cholerae*
ab2015-06-02-2	98d93b8c8e390eb6c200fc2d30c9626cb1a7c140cd930a60eddb3a179aa8226b	*Vibrio cholerae*
ab2015-06-02-3	39a5d8490ee3823eaf785268aba1593d3be05b8bf6cc029d2e0c247bb7b0a6ba	*Vibrio cholerae*
ab2015-06-02-5	2620f1ee27c5e63853bb3f3d09796b19d7bd91fbdb5781daa892d68fb31be735	*Vibrio cholerae*
ab2015-06-02-6	9ba344e00d31084d2aef8a799f3089e46ead3b28a02c0e73c5852337f67121fc	*Vibrio cholerae*
ab2015-06-02-7	1e00525c41a9faaa849befd686b70757a6f25a9ceacbcde951b6eeef99006f09	*Vibrio cholerae*
ab2015-06-02-8	3cb8dc276fb373a99af2ee54301fcb0989eb0037b9c3c2bd21f8e035f0f98215	*Vibrio cholerae*
ab2015-06-02-9	5739b1525b6a0e906de41a8e024e0b502f964e19193feed1a62ced0e41b5dc17	*Vibrio cholerae*
ab2015-06-02-10	7e869e97212b3df06af70decf577ef3836c1ec4787f1cbe677da60aca3bda727	*Vibrio cholerae*
ab2015-06-02-11	8329b3a0b5373c89d5280c42ca8aabb19a38a6ee03e5910275b82776ff8745fa	*Vibrio cholerae*
ab2015-06-02-12	de04da0f550b2f37d4a0847e13b637877ed6994bb5d8d0c24c87ad9f3cf52924	*Vibrio cholerae*
ab2015-06-02-13	4caf0202a48c92372ca3a24101d9c5e2b446fadbf80109b5d0710598a11fa3aa	*Vibrio cholerae*
ab2015-06-02-14	b2f7beb0de38a1eb8d0eab4d8493616c9122931ec0490e1bb5b45474a032098f	*Vibrio cholerae*
ab2015-06-02-15	bd8198a02bd66929811014f1b15a243f4705433876cb56c784bdc8fb91378c00	*Vibrio cholerae*
ab2015-06-02-16	87c298d70069315af599618c344d80bf2fc48f44c0057002798241842b58b5c9	*Vibrio cholerae*
ab2015-06-02-17	066cf7fae820b463b2e7405a9078e97b6de9910587458dfd904759d75fb4ed2c	*Vibrio cholerae*

Jensen Lab id	OIP id	Organism
ab2015-06-02-18	82fdc6778793542fad9bfe7c18a6fa972dc3bf230b2e108aa53a5807811bdad7	*Vibrio cholerae*
ab2015-06-02-20	2524250ba11140c386c211aa14d164a166926ee9ca7af5566eedbbba29856c48	*Vibrio cholerae*
ab2015-06-02-21	95a8202f59bdcfc9814f417aa40b3c355fc6f12cb147784d1d1665d8ccce8221	*Vibrio cholerae*
ab2015-06-02-22	09443b1917375d0f2755c3f4c2029dc847c654efdb2e5a3df0c5938a9afaa1a9	*Vibrio cholerae*
ab2015-06-02-23	453536f21d3074fd3f6fcae6d834c6e37335f466611e2f1842c6beb8ee77681e	*Vibrio cholerae*
ab2015-06-02-24	03ab91b142bf62ed9c21e1da4b17e25d7c73b70cbd6a25481342d9736f2a2290	*Vibrio cholerae*
ab2015-06-02-25	8853aea7df6d8a168b62b9db8694ad82dfa23c9b00eafb3f71b025f20cb34abd	*Vibrio cholerae*
ab2015-06-02-26	8770b212ceddc32db6f1ae0b8a40a5eaa1ec42c31bceda0c4919b86dcde7246b	*Vibrio cholerae*
ab2015-06-02-27	e1b34b3df7aa6367398010bf8b96d5a003759a2dd71a473e45a43d598e779d29	*Vibrio cholerae*
ab2015-06-02-29	08324bf01302b1db927045548218ff3e317aeae74602363e669a187c52e234be	*Vibrio cholerae*
ab2015-06-02-30	2eda58ca01240b7486bda36c36e36217918c89fcb1361ddda13eeda95afc4271	*Vibrio cholerae*
ab2015-06-02-31	6b6b8ba7f2127c66614756b85d4bb0efde943cbfc305e40a3330181009bd893e	*Vibrio cholerae*
ab2015-06-02-32	61c86c9a912eb1bcada440939a48d46e99128ffeca99578b16e00e22031f4a22	*Vibrio cholerae*
ab2015-06-03-1	197f9f4bbc9f5fa49c4644f3f40df46cbf2b82399e8137db7799b9e030bc8455	*Vibrio cholerae*
ab2015-06-03-2	544970e8e49ff409d4f61730c89757fdbee6fff364c1c604d355bc522c8d0f12	*Vibrio cholerae*
ab2015-06-03-3	e87e0b6e154e5dfec0120ce92e6400764ae24964aa592553e49de6187b7ffb57	*Vibrio cholerae*
ab2015-06-03-4	20d581e5578e3156ddf96496119c1296494e062deecf45634c79f19f331368b6	*Vibrio cholerae*
ab2015-06-03-5	10c8a0be7b87b3d95eb2d8573e782a856e493b65735aab290c0a772092d2ecfc	*Vibrio cholerae*

Jensen Lab id	OIP id	Organism
ab2015-06-03-6	0c1b01aa1ed45fcba7d17500c4829f9480924fa210f9706d6a1a5da9d4dc1477	*Vibrio cholerae*
ab2015-06-03-7	21482339f240527367c699214ba438d2b9a7ac6376d611f2d69e0f4c1d1d0039	*Vibrio cholerae*
ab2015-06-03-8	453a055bebf6eb8d65f2154f51a568cfc3f58c36aa445ff6be7a820c0d3963e9	*Vibrio cholerae*
ab2015-06-03-9	faed3ad567cb4667d1986bb9a7869a4a9da0a9e2d016dbb6d823e15f5d1cc149	*Vibrio cholerae*
ab2015-06-03-10	1c8abd7e25085ccccе2ce38fb25ff51ac70ddfc88cad18322406467298bfaa3e	*Vibrio cholerae*
ab2015-06-03-11	920321536f97c55c300ad77d279265973442bd4ec0e7286a95f2d134ec384b42	*Vibrio cholerae*
ab2015-06-03-12	9262dbfb593f79bf0c9cac6f9125326ede755dd3e4edc569b68b0fc279f84d8d	*Vibrio cholerae*
ab2015-06-03-13	72b627c7010d0ea37a8aa011925069437195c51f77e5adcf41f6a8330e75cc65	*Vibrio cholerae*
ab2015-06-03-14	223d692a658a507a7085c75f8c757b05c1cf1d2ee8e352a1db4371f2062e3ec4	*Vibrio cholerae*
ab2015-06-03-15	c55cf52f955779f23cda1c2244e2b64315f8fbb490f10689f9c32b7a87a99512	*Vibrio cholerae*
ab2015-06-03-16	b59e667fadb1914c70ad191dad31a30a87ba416e8de4877000d1f6cb52869601	*Vibrio cholerae*
ab2015-06-03-17	067ac5b8ce49dffe5254c958a0ef6bfd601de8778c47f17d8db6c76f2b03d882	*Vibrio cholerae*
ab2015-06-03-18	c9dd866db34f7ed34af143d2a879e5b28035fce2a4392aceb54f7824ceec0e37	*Vibrio cholerae*
ab2015-06-03-19	fabd724070997b695344be1bc4ad91faa2b2c82876f6bda65aeeee18eb39ca29	*Vibrio cholerae*
ab2015-06-03-20	34ff16d0af7b7a6cfbe49d20981049070d2b9b9f5a1919896a839eb62dc8c6a8	*Vibrio cholerae*
ab2015-06-03-21	4440060c9b511b30ec0b7c123b3891a3823a77a8393437862aa5344392e0be26	*Vibrio cholerae*
ab2015-06-03-22	48c976b5ec236342fdd4aefe521086e3657da4a45c4afad6003efdb44a5e8275	*Vibrio cholerae*
ab2015-06-03-23	1c1e69acb1c51ec5655f2fc7e1296de6494c1c68785e7f4a7ce0cc651d2125c9	*Vibrio cholerae*

Jensen Lab id	OIP id	Organism
ab2015-06-03-24	aa070936e1aee30b373bc2d2aed88f1576cd3ed6766dbc9f92f120be46aeeabe	*Vibrio cholerae*
ab2015-06-03-25	d84b38caf03c63be65666a628fa8f90aeaec8991ba29dad0b539585fbcf3b96c	*Vibrio cholerae*
ab2015-06-03-26	f38ac8c272b532e7dd3e3da38b1fff38f42385a2aa55872dda24bf10720544ba	*Vibrio cholerae*
ab2015-06-03-27	9d8070fbfbab0e5bfdd555544219789104fb5dcbda613d24385c416ccd3c3158	*Vibrio cholerae*
ab2015-06-03-28	bd0aaf3c9bb4904c623c2304b5ca71f3e7dbbbd15fdbe2eb481dbdb01d561986	*Vibrio cholerae*
ab2015-06-03-29	81345effbcb7600a9f57a2f556a10f3a20a6845df3ca51ccc1d67d964ee8e21f	*Vibrio cholerae*
ab2015-06-04-5	e95c286a1ca5b5b3b3b5bf0a318a30c627623d2b63b68c9991dab337ae48e8c2	*Vibrio cholerae*
ab2015-06-04-6	79b0258243f18a1752dac35aa7e0bff1a711f791ddd0379c184e05d9d1c5dd86	*Vibrio cholerae*
ab2015-06-04-7	6b8f4ae3d17ab82176fe1bb2c79c55d5ce757c5355323bbadc84d17a5a6f75dd	*Vibrio cholerae*
ab2015-06-04-8	18fca4c49057b64129c9dbd0f9c8be7562fcee4d5fff21a449b1fd79a5e910f8	*Vibrio cholerae*
ab2015-06-04-9	a9e50ed3ce23097a99fdaa4d949f5353bcba9f5ce3cd7a49d5f3df08d668a989	*Vibrio cholerae*
ab2015-06-04-10	275fbd79f1fb013309e3dc4a22c607ab406b6b2a16489a508c3490ede71dac93	*Vibrio cholerae*
ab2015-06-04-11	eadc30e57a5bbceba8e69544d43debdb4d71392ef20f16c8d9a5659a2dc877a9	*Vibrio cholerae*
ab2015-06-04-12	82b9550d3ebda9a078ece5cea3cfd02ceece06df9115d8b2d558d5b5c073f9dd	*Vibrio cholerae*
ab2015-06-04-13	204dea6006208b691ae45b1aa8a62421894c0d956a5d5bf6aaa8a3e75253345d	*Vibrio cholerae*
ab2015-06-04-14	7504bd89ddb0fd83ed926065c9d2cf7b57db0072ebb740cfefdc957f1d5c4c81	*Vibrio cholerae*
ab2015-06-04-15	7bc4afbf390105748d85295198579497fd0d6712da0eb190eec2436cf6617349	*Vibrio cholerae*
ab2015-06-04-16	c99f6e5934554670fe2166f2f8deb7ad17f453696c914b4ca1ea88f7e009f0a4	*Vibrio cholerae*

Jensen Lab id	OIP id	Organism
ab2015-06-04-17	095901997ad173f1a9cf5804cd7f92e2c95ee7bd4be14b1fa1fe94ed74e6a85d	*Vibrio cholerae*
ab2015-06-04-18	2f236dac0a263b2e3278aef8ab2aad6c7ace83bde857c6916683146369424e93	*Vibrio cholerae*
ab2015-06-04-19	b4daca6e8f77b714d01faac2b7dc9933c4617d736b0a6ef29eb9e1056c0214f8	*Vibrio cholerae*
ab2015-06-04-20	ed95dd31b7e3a97a2bedc0e8985ad471dad7c7447a7070d5d5b37b8f259da41a	*Vibrio cholerae*
ab2015-06-04-21	a41257cc5f1d3c4a84cd9645921671bff4e5b58de593872740a35172fd4102a5	*Vibrio cholerae*
ab2015-06-04-22	863a029fcd72521b29fa741b7a13b2df4420fcc9491a090eab709c7c7d727514	*Vibrio cholerae*
ab2015-06-04-23	c63edc39ab954f54d3ec80607005b54739f6940f8e317c3ea88d951b0e63ed82	*Vibrio cholerae*
ab2015-06-04-24	5f040233e108f1d0d81448d4b7c44476947e2075742fd79ad2f0d0adf9f686fa	*Vibrio cholerae*
ab2015-06-04-25	9a31271d398507a3e7cb0694927dbda47043f35bf8171cbd4f56df5896c7e060	*Vibrio cholerae*
ab2015-06-04-26	687d83b774894a40b9f35c54e0e50d2e11613d6260723ab83573e3fd6c55b309	*Vibrio cholerae*
ab2015-06-04-27	5cc452dfbe2e22d09dd2102b010e926f7c97355c0c209148f049292cf3b910de	*Vibrio cholerae*
ab2015-06-04-28	49ffb9f6a24a7d07799479b844a01ed91a204f95afa28a8d59561b858d9a4d19	*Vibrio cholerae*
ab2015-06-04-29	38f8ed8a6cba9fdab947246fd283023b21353f166c6e41f949320a028cea2f1a	*Vibrio cholerae*
ab2015-06-04-30	92c05f4866a31ee526bac1d95d513c9d0063e794554cdc124651fabc1e8c9395	*Vibrio cholerae*
ab2015-06-04-31	60d87f38e11916f13cf6345b22f0b5fc567d6ecba651e7ed98c1ba23faca1a27	*Vibrio cholerae*
ab2015-06-04-32	2b200698dc605f2234c28d33d12a2eeed4bfb6808399563791bf228fda34936e	*Vibrio cholerae*
ab2015-05-29-38	71b7016135114ee9988faf24a00aec627349d8610625a8925152e418ce042cb8	*Pseudomonas aeruginosa*
ab2015-05-29-33	3bc9419d595c59d2ffb177294ceb038f5c4a40287cc1d2ff95ab43e42e22c5b5	*Pseudomonas aeruginosa*

Jensen Lab id	OIP id	Organism
ab2015-05-29-34	baf59323b4cd6b20e471b0587f4349bb437cc89feba37eb726c76d2b35996859	*Pseudomonas aeruginosa*
ab2015-05-29-35	375ec0e6c3542bc3d33e7ec94c751bd1669ffe9984a4ccb8948ddc246bd02517	*Pseudomonas aeruginosa*
ab2015-05-29-36	dda73882e77f51644ba4d9fc73810f58c0789cf5ebd5c4c64108940c978d3913	*Pseudomonas aeruginosa*
ab2015-05-29-37	e0d1b4daa89125bfae9539157ab0d459e9a10b53148d17af60eb3afadf667e37	*Pseudomonas aeruginosa*
ab2015-05-29-38	71b7016135114ee9988faf24a00aec627349d8610625a8925152e418ce042cb8	*Pseudomonas aeruginosa*
ab2015-05-29-39	9ff1533aa7d28d3d64439293ea263ca3ce6a6101f19c7367426d9a3bba3773e6	*Pseudomonas aeruginosa*
ab2015-05-29-40	c5f0fcf46599f6ee48fe23a59fc1d752cd64ab4031c3846ffb85d078a8bfaf5c	*Pseudomonas aeruginosa*
ab2015-05-29-41	fe52314687302e52d76a76292a84a8e7730dac37451c7026621190f2185cd7df	*Pseudomonas aeruginosa*
ab2015-05-29-42	fc8e9658e5fe5d5e30364f389fc123f474537bda5132fb71b12af99aaf02e7a2	*Pseudomonas aeruginosa*
ab2015-05-29-43	433cf08b0ab2269a91f4e946b17c551e8a92a30c8c5214bc8384072fc8915b85	*Pseudomonas aeruginosa*
ab2015-05-29-44	9162280a2e505e7a74c03de6202f084eb4b83882453525539fdf87da3905d77c	*Pseudomonas aeruginosa*
ab2015-05-29-45	9db0388f6a5482eb6cad84cd7abf0ddad7bcd4a3d741d971cc9dd3a2c378cda2	*Pseudomonas aeruginosa*
ab2015-05-29-46	31eee1b22c3f3010a3a31df973be75ff1a126069e78bfbb1dbed30cd3985330d	*Pseudomonas aeruginosa*
ab2015-05-29-47	799edd343b37e6dff51118d39052ad7241e7c05238286bcc779c1ab9227f8a4c	*Pseudomonas aeruginosa*
ab2015-05-29-48	72025551790f3ada513cffe56e1f0971b3844f1c985e4f3e3b7579dd349aecd1	*Pseudomonas aeruginosa*
ab2015-05-29-49	76b1c8f739812662c22aee910f2e1a2bc7ac72f9c79ee19df0493c60be7f6711	*Pseudomonas aeruginosa*
ab2015-05-29-50	2f3db7b47e7d42594be348214e07578d7ea1f08a10f8cd937bec3abb8692c6aa	*Pseudomonas aeruginosa*
ab2015-05-29-51	dbe07cf9023a7c8d67cea0f6bc02eeaea93f5c2e60453ca2aa4685d8e3a53654	*Pseudomonas aeruginosa*

Jensen Lab id	OIP id	Organism
ab2015-05-29-52	8f861e2f49e3b2155f99422428acb7ca764c5c2 2352dd6f5c411d89daaa99c8c	*Pseudomonas aeruginosa*
ab2015-05-29-53	8bbc0699df1ecaeff06813ea816ded484d90867 9412e938d42afbb30e0f47747	*Pseudomonas aeruginosa*
ab2015-05-29-54	87be5d50a167d3c23ad2126bc4d72844c0ed6 af2848768fd1bb764ad0a05355b	*Pseudomonas aeruginosa*
ab2015-05-29-55	975a50a6ac4a0a1ce191d3f339c433b73ba15a 3a8eff22b3768a9327e1ca5a21	*Pseudomonas aeruginosa*
ab2015-05-29-56	d0799bdb371912d4370d6226ae8263e1f9bf4 19c49c42c16514c657f11f05f37	*Pseudomonas aeruginosa*
ab2015-05-29-57	dfd11ff2b7b5261968452f994235bece1d208b 793f0c7768b883163fa0cad72c	*Pseudomonas aeruginosa*
ab2015-05-29-58	06dc2aa14271a7d5c79c6e112a3aeacc8c6432 46c659fab33b3bbb01fbe25356	*Pseudomonas aeruginosa*
ab2015-05-29-59	f92bcceb78dac999467e57653d9e3ab4017261 8fc09fb5806e64040e8a3410f5	*Pseudomonas aeruginosa*
ab2015-05-29-60	bd0b6b93ba4f3528fe3f78a789dd847ee83a6d 4b08cd6e652053e72aefa6897b	*Pseudomonas aeruginosa*
ab2015-05-29-61	37d4d1c6d5229a5db3700596859b305aea3aa 460d67362ba176424c9217ebf28	*Pseudomonas aeruginosa*
ab2015-05-29-62	4e059367636fa821409e894b49151556c01d6 5ebe01eca3e4d4fedec6531adc7	*Pseudomonas aeruginosa*
ab2014-010-14-1	b9d6746d36ee7943e0eb19c9299214e60080c 78b367558d6748820c84c2aec76	*Pseudomonas aeruginosa*
ab2014-010-14-10	c8c1989c09901dd7a257d86497a713e85a761 edd2209efe0d8784d228e5b3585	*Pseudomonas aeruginosa*
ab2014-010-14-11	18ec447aac947d6ed610084fbb9e808bdb761b f68919b853ac4946632d6c6e50	*Pseudomonas aeruginosa*
ab2014-010-14-12	58c0a2aab1b8f0322fcc4b93838458a820fc8db 74f716b53ba166ae2cbe92001	*Pseudomonas aeruginosa*
ab2014-010-14-13	9e8108ef3cf66406b628ec973b10079efc0ca57 81a05ca1a875ed6fdecc2fe02	*Pseudomonas aeruginosa*
ab2014-010-14-14	7935084f249ec5bc222b38951cd369dab76cfa b95a769d42d0eb1312cc5bb50c	*Pseudomonas aeruginosa*
ab2014-010-14-15	51b27c3cf74ce394c1d54773bd1a7d15d3379f c8db4aa2f8b9dbdbaabdd71251	*Pseudomonas aeruginosa*

Jensen Lab id	OIP id	Organism
ab2014-010-14-17	764f7220c7323438d65b7d4334916e9aadb0be04be1b662615be1ad1312407c6	*Pseudomonas aeruginosa*
ab2014-010-14-22	797a818b0722e811f5ed0d6d22bdfdb158fabbcd22e8bfc7f1010ad265af8897	*Pseudomonas aeruginosa*
ab2014-010-14-23	322a5ff8d6dda5854aaafec4883226c8463c2e9a08ce553c969ca6b98cfedef9	*Pseudomonas aeruginosa*
ab2014-010-14-3	2c11ded42bbc0cd87dc67464474187c3c82d71742a8b50f346516a958361706a	*Pseudomonas aeruginosa*
ab2014-010-14-4	20cd19c0fa4b3e32b33075348be5ab3102def5083cce6fd7ac55b01ac0cb5835	*Pseudomonas aeruginosa*
ab2014-010-14-5	3e6133278fc31ba361c1cd7c95c081a822d9723dc3b7f3549870510a422e2522	*Pseudomonas aeruginosa*
ab2014-010-14-6	3cbeac672c18cd66252b47d65f0ec124b17baf519849a6844fab4af70fbbcea1	*Pseudomonas aeruginosa*
ab2014-010-14-8	cb237b8021a9e653613163394c11258bb3b72fe09720a977596c18478e5d43c2	*Pseudomonas aeruginosa*
ab2014-010-14-9	8bf9ec4e43a3e6bd11c44bb6d341d138e14b41c776e66e21a8a17d399c1c69c2	*Pseudomonas aeruginosa*
sc2014-02-14-1	ecfe996b6c698beb104f0cf84bda7955a48c7edb6049ce2b9256cb3b1e2b85b0	*Methylomicrobium alcaliphylum*
sc2014-02-12-1	37a38f6896b2fbc3379ebba9976e69ccefd45daa011b009f9fc498f40ab5b68e	*Methylomicrobium alcaliphylum*
sc2014-02-12-3	82c7e7111fad00bd9de9be253c966a0d87b3b585cf47a4e3ada52b7a90ae362f	*Methylomicrobium alcaliphylum*
sc2014-02-12-6	c807ab328c5bd06874ad4f9fb731fafd888f23894d00cafed1089f988407ed99	*Methylomicrobium alcaliphylum*
sc2014-02-12-7	99a62dfe3b6bedf92f6bd93916b1fe055c1abd7d4d2f781348c01ae89c45dbd5	*Methylomicrobium alcaliphylum*
sc2014-02-12-8	6ce0a323a040374567356e08c438fd42806aef88c73f105e2d9e13684d940ae8	*Methylomicrobium alcaliphylum*
sc2014-02-12-9	9e828a83fb3538f1f6f9942ea4216cd7fe20ebcc1c82ed3dba8f7e34bdc3a1e9	*Methylomicrobium alcaliphylum*
sc2014-02-12-12	262b60a13fbcd486cc7c4ac73b739ddccb23d93cf8d5d4138ae911af40f95480	*Methylomicrobium alcaliphylum*

Table S6.
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	(*74*)
PAS(*P. aeruginosa*)	4HI4	(*22*)
PAS + HAMP (*P. aeruginosa*)	3VOL	(*75*)
3xHAMP (*P. aeruginosa*)	4I3M	(*76*)

Table S7.
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
3ZX6_4I3M_4HIH.pir	Sequence alignment	Sequence alignment used to build the P+2H+S homology model
3ZX6_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 3ZX6_4I3M_4HIH_99.pdb to build the model for Aer2 (PA0176)
3ZX6_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
3ZX6_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
3ZX6_4I3M_4HI4_4HI4_SO.pir	Sequence alignment used to build the model for Aer2-like (SO_2123)	

File	Type	Description
SO_2123.B99990017.pdb	3D atomic model	Best Aer2-like (SO_2123) homology model
hamp_sequence_for_MEALZ.linsi.fa	Sequence alignment	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
RAxML_bipartitions_50coll.hamp_sequence_for_MEALZ.linsi.rec.tree	Phylogenetic Tree	The tree with maximum likelihood based on hamp_sequence_for_MEALZ.linsi.fa
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	2\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	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

Table S8.

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 lwoffii 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

Genome	has F7
Alcanivorax dieselolei B5	yes
Alcanivorax hongdengensis A-11-3	no
Alcanivorax pacificus W11-5	yes
Alcanivorax sp. DG881	no
Aliivibrio salmonicida LFI1238	no
Alishewanella aestuarii B11	no
Alishewanella agri BL06	no
Alishewanella jeotgali KCTC 22429	no
Alkalilimnicola ehrlichii MLHE-1	no
Allochromatium vinosum DSM 180	yes
Alteromonadales bacterium TW-7	yes
Alteromonas mediterranea 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

Genome	has F7
Colwellia psychrerythraea 34H	no
Cronobacter sakazakii ES15	yes
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

Genome	has F7
Escherichia hermannii NBRC 105704	yes
Escherichia sp. TW09276	yes
Ferrimonas balearica DSM 9799	no
Fluoribacter dumoffii Tex-KL	no
Frateuria aurantia DSM 6220	yes
Gallaecimonas xiamenensis 3-C-1	yes
Glaciecola agarilytica 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

Genome	has F7
Hydrocarboniphaga effusa AP103	yes
Idiomarina loihiensis L2TR	no
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 posidonica IVIA-Po-181	no
Marinomonas sp. MWYL1	yes
Methylobacter tundripaludum SV96	yes
Methylococcus capsulatus str. Bath	no
Methylomicrobium album BG8	yes
Methylomicrobium alcaliphilum 20Z	yes

Genome	has F7
Methylomonas methanica MC09	yes
Methylophaga aminisulfidivorans MP	yes
Methylophaga frappieri	no
Methylophaga lonarensis MPL	no
Methylophaga thiooxydans DMS010	no
Moraxella macacae 0408225	no
Morganella morganii subsp. morganii KT	yes
Moritella sp. PE36	yes
Nitrosococcus halophilus Nc 4	no
Nitrosococcus oceani ATCC 19707	no
Nitrosococcus 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

Genome	has F7
Photorhabdus luminescens subsp. laumondii TTO1	yes
Proteus mirabilis WGLW6	yes
Proteus penneri ATCC 35198	yes
Providencia alcalifaciens DSM 30120	yes
Providencia burhodogranariea DSM 19968	yes
Providencia rettgeri Dmel1	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

Genome	has F7
Pseudomonas fragi A22	no
Pseudomonas fulva 12-X	no
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 CHA0	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

Genome	has F7
Rhodanobacter fulvus Jip2	yes
Rhodanobacter sp. 116-2	no
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

Genome	has F7
Shewanella sp. MR-4	yes
Shewanella violacea DSS12	yes
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 sulfidiphilus 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

Genome	has F7
Vibrio campbellii CAIM 519 = NBRC 15631	no
Vibrio caribbenthicus ATCC BAA-2122	no
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
Wohlfahrtiimonas chitiniclastica SH04	no
Xanthomonas albilineans GPE PC73	yes
Xanthomonas axonopodis pv. malvacearum str. GSPB2388	yes

Genome	has F7
Xanthomonas campestris pv. musacearum NCPPB 4381	yes
Xanthomonas citri subsp. citri Aw12879	yes
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

Table S9.
Genomes used in phylogenetic profiles.

Genomes imaged in this study
Methylomicrobium alcaliphilum 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

Gamma-Proteobacteria
Cronobacter turicensis z3032
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
Frateuria 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

Gamma-Proteobacteria
Halorhodospira halophila SL1
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

Gamma-Proteobacteria
Pectobacterium carotovorum subsp. carotovorum PCC21
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

Gamma-Proteobacteria
Pseudoxanthomonas spadix BD-a59
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

Gamma-Proteobacteria
Shewanella sediminis HAW-EB3
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 sp. EJY3
Vibrio splendidus LGP32

Gamma-Proteobacteria
Vibrio vulnificus CMCP6
Xanthomonas albilineans GPE PC73
Xanthomonas axonopodis pv. citrumelo 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
Achromobacter 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

Data S1. (separate file)
Files used to produce the homology models as described in Table S7.

Data S2. (separate file)
Phylogenetic trees in Figure 4, S1, S2 and S4.