## **Supporting Information**

## Kojima et al. 10.1073/pnas.0800308105

Vibrio alginolyticus Vibrio parahaemolyticus Vibrio cholerae Vibrio vulnificus Vibrio fischeri Idiomarina loihiensis Pseudomonas aeruginosa

Vibrio alginolyticus Vibrio parahaemolyticus Vibrio cholerae Vibrio vulnificus Vibrio fischeri Idiomarina loihiensis Pseudomonas aeruginosa

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| -21      MKKWLITSGVFELFSTSSFAVMGKRYVATPQQSQTEMVNITPLECUVHPIPSF6         1      MNKWLITSGVMESLISANSYAVMGKRYVATPQQSQTEMVNITPLECUVHPIPSF6         1      MNKWVITSLFAISMESASVASALEVRYVATPQQSQTEMVNITPLECUVHPIPSF6         1      MNKWVITSLFAISMESASVASALEVRYVATPQQSQTEMVNITPLECUVHPIPNYG         1      MKKKILITSGVUTTFASLEVAAMTKRYIATPQQSQTEMVNITPLECUVHPIPNYG         1      MKKKILITSGVUTTFASLEVAAMTKRYIATPQQSQTEMVNISPLECUVHPIPNYG         1      MKKKILITSGVUTTFASLEVAAMTKRYIATPQQSQTEMVNISPLECULHPIPNYG         1      MKKIFVTSALLVSFLIATPVLA-NKNYVAKPEQSKITMLENSPLECULHNIPNYG         1      MKNIPMUTAVSASLLLSQAQANSVRHYSANLDNSAUQTSEKNRLACEMEHETPRYG         1      MKNIPMUTAVSASLLLPFLLSSLPALAVTFQTRLESVEIKVEGDQ-FECLSOPVANFG         36       DAVISSRANKKINLDFELKMRRPMGETRNVSLISMPPPNR26EHADRITINLKFFKQFDQY         57       DAVISSRANKKINLDFELKMRRPMGDTRNVSLYSMPPVR26EHADRITINLKFFKQFDQY         59       DAEISSRAGKKINLDFELKMRRPMGETRNVSLISMPPVR26EHADRITINLKFFKQFDGY         50       ASGTSSYNKKMNLDFELKMRRPMGTRNVSLISMPPVR26EHADRITINLKFFKQFDGY         50       DAEISSRAGKKINLDFELKMRRPMGETRNVSLISMPPVR26EHADRITINLKFFKQFDGY         50       SAGTSSYNKKMNLDFELKMRRPMGETRNVSLISMPPVR26EHADRITINLKFFKQFDGY         51       VGEVRRGEQATFRLKPEAQWLGRGSATLLAAAPVR2QGDINLGQVSIGSGEVPF         68       m1 <th>35<br/>56<br/>58<br/>55<br/>58<br/>50<br/>95<br/>116<br/>116<br/>118<br/>118<br/>108</th>   | 35<br>56<br>58<br>55<br>58<br>50<br>95<br>116<br>116<br>118<br>118<br>108                             |
|--|---|
| 1      MNKWLITSGVMLSLLSANSYAVMGKRYVATPQQSQLBHVVNTPLEQUIVHPIPSTG         1      MNKWVITSLFATSMLSASVASALEVRYVATPQQSQLBHVVNTPLEQUIVHPIPSTG         1      MNKWVITSLFATSMLSASVASALEVRYVATPQQSQLBHVVNTPLEQUIVHPIPSTG         1      MKKWVITSLFATSMLSASVASALEVRYVATPQQSQLBHVVNTPLEQUIVHPIPNYG         1      MKKWLITSGVMLSLLSANSYAVMGKRYVATPQQSQLBHVVNTPLEQUIVHPIPNYG         1      MKKWLITSGVMLSLSASVASALEVRYVATPQQSQLBHVVNTPLEQUIVHPIPNYG         1      MKNWPMLTAVSASLLUSFLTATPVLA-NKNYVARPQQSQLBHVVNTPLEQUIVHPIPNYG         1      MKNWPMLTAVSASLLUSGQQQANSVRHYSANLDNSAUQISEKNRLAGEMEHEIPRYG         1      MKNWPMLTAVSASLLLSGQQQANSVRHYSANLDNSAUQISEKNRLAGEMEHEIPRYG         1      MQPRLLLIPFLLSSLPALAVTFQTRLESVEJKVEGDQ-FECKLSQPVANF3         6       DAVISSRASKKINLDFELKMRRPMGETRNVSLISMPPPNRPQEHADRITNLKFFKQFDGY         7       DAEISSRAGKKINLDFELKMRRPMGETRNVSLISMPPPNRPQEADRITNLKFFKQFDGY         8      MKNWPMGETRAVSLISMPPPNRPGEADARTINLKFFKQFDGY         9       DAEISSRAGKKINLDFELKMRRPMGETRNVSLISMPPPNRPGEADARTINLKFFKQFDGY         9       DAEISSRAGKKINLDFELKMRRPMGETRAVSLISMPPPNRPGEADARTINLKFFKQFDGY         9       DAEISSRAGKKINLDFELKMRRPMGETRAVSLISMPPPNRPGEADARTINLKFFKQFDGY         9       KVRQSESSYNKKMNLDFELKMRRPMGETRAVSLISMPPPNRQCGESSYRICAMQLYKQFDGE         9       KVRQSESSYRELNIRMKVEMOKLPDSYGVSAIESVPPNQCGESSYRICAMQLYKQFDGE         9       KVRQS   | 95<br>56<br>58<br>55<br>58<br>50<br>95<br>116<br>116<br>118<br>118<br>108                             |
| 1      WNKWLITSUFAISMLSAVASALEVRYVATPQOSTUMATNIPLE CRUVHPIPNYC         1      WNKWLITSGLVLTTFASLPLAAMTKRYIATPQOSQUEWVMISPLE CRUVHPIPNYC         1      WKKIFYTSALLVSFLIATPVLA-NKNYVAKPQOSTUMATNIPLE CRUVHPIPNYC         1      WKKIFYTSALLVSFLIATPVLA-NKNYVAKPQOSTUMATNIPLE CRUVHPIPNYC         1      WKNIPMLTAVSASULLI SGQAQANSVRHYSANLONSAUQISEKNRLACEMEHEIPRYC         1      MKNIPMLTAVSASULLI SGQAQANSVRHYSANLONSAUQISEKNRLACEMEHEIPRYC         3      MKNIPMLTAVSASULLI SGQAQANSVRHYSANLONSAUQISEKNRLACEMEHEIPRYC         36       DAVISSRNNKKINLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         57       DAVISSRNKKINLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         58       ALESSRNGKKINLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         59       DAFISSRNGKKINLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         59       DAFISSRNGKKINLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         50       DAFISSRNGKKINLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         50       SACISSYNKKMNLDFELKMRRPMGETRNVSLISMPPPNROCEHADRITNLKFFKQFDQY         50       KVRTQSEASKELNLRMKNEMQKLPDSYGVSAIESVPPNQOCESSYRIGMQU/VKQDQFGY         51       VGEVRRGEQATFRLKPEAQWLGRGSATLLAAAPPWROCQGDNLGQVSIGSGEVPF         68       m1   | 95<br>58<br>58<br>58<br>58<br>50<br>95<br>116<br>116<br>118<br>118<br>118<br>108                      |
| 1  | 56<br>58<br>55<br>58<br>50<br>95<br>116<br>116<br>118<br>115<br>118<br>108                            |
| 1      MKKIFUTSALLVSFLITATIVAL-NKNYTARVEOSALTUNENSPLECUSINTIPANG         1      MKKI-FUTSALLVSFLITATIVAL-NKNYTARVEOSALTUNENSPLECUSINTIPANG         1      MKNIPMI_TAVSASLLL_SGQAQANSVRHYSANLDNSAVQISEKNRLAGEMEHEIPRYG         1      MKNIPMI_TAVSASLLL_SGQAQANSVRHYSANLDNSAVQISEKNRLAGEMEHEIPRYG         1      MKNIPMI_TAVSASLLL_SGQAQANSVRHYSANLDNSAVQISEKNRLAGEMEHEIPRYG         1      MQPRLLLPFLLSSLPALAVTFQTRLESVE#KVEGDQ-FECKLSQPVANF3         6       DAVISSRAVKKINLDFELKMRRPMGETRNVSLISMPPPUR2GEHADRITNLKFFKQFDGY         5       DAVISSRASKKINLDFELKMRRPMGETRNVSLISMPPPVR2GEHADRITNLKFFKQFDGY         5       DAVISSRASKKINLDFELKMRRPMGETRNVSLISMPPPVR2GEANDRITNLKFFKQFDGY         50       DAVISSRASKKINLDFELKMRRPMGETRNVSLISMPPPVR2GEANDRITNLKFFKQFDGY         50       DAVISSRASKKINLDFELKMRRPMGETRNVSLISMPPPVR2GEANDRITNLKFFKQFDGY         50       SAGISSYNKKMNLDFELKMRRPMGETRAVSLISMPPPR02GESSYNKICMQLYKQFDGE         50       KVR2QSESSYNKKMNLDFELKMRRPMGETRAVNLYSMPAR/M20GAESMLNLKFFKQFDGY         50       KVR2QSESSYNKKMNLDFELKMRRPMGETRAVNLYSMPAR/M20GAESSNRICMQLYKQFDGE         51       VGEVRRAGEQATFRLKPEAQNLGRGSATLLAAAPPWR2QGDINLGQVSIGSGEVPF         68       m1       89       810       m2  | 95<br>58<br>50<br>116<br>116<br>118<br>115<br>118<br>108  |
| 1      MKR1-PVT3ALLV3FLATPVL4-INAN VARECQANTITUEROFLICATESINATIAN         1      MKNINPWTTAVSASLILLS GOQANSVRHV3SAILDUNGAQUESKRRLAGENHEIERRYG         1      MKNINPWTTAVSASLILLS GOQANSVRHV3SAILDUNGAQUESKRRLAGENHEIERRYG         1      MQPRLLLIPFLLSSLPåLAVTFQTRLESVEUKVEGDQ-FECRLSQPVANFG         A       A5       A6       A7       A8         36       DAV SSSRANKKINLDFELKMRRPMGETRNVSLISMPPPRR2GEHADRITINLKFFKQFDGY         57       DAS SSRASKKINLDFELKMRRPMGETRNVSLISMPPPRR2GEHADRITINLKFFKQFDGY         58       DAFESSRASKKIVLDFELKMRRPMGETRNVSLISMPPPRR2GECADRITINLOFFKQFDGY         59       DAFESSRASKKIVLDFELKMRRPMGETRNVSLISMPPPRR2GECADRITINLKFFQFNGY         59       SAGESSYNKKMUDFELKMRRPMGETRAVNLVSMPAR/MCDCAESMLNLKFFKQFDGY         50       KVRFQSEASKELNLRMKMEMQKLPDSYGVSAIESVPPR/QCCESSYRIGMQUYKQFDGE         50       VGEFVRRGEQATFRLKPEAQWLGRGSATLLAAAPPWR2QCDINLGQVSIGSGEVPF         68       m1       69       A10       m2       MotY-N  | 95<br>58<br>50<br>116<br>116<br>118<br>115<br>118<br>108  |
| 1  | 95<br>50<br>116<br>116<br>118<br>115<br>118<br>108  |
| β4     β5     β6     β7     β3       36     DAV SSRANKKINLDFELKMRRPMGETRNVSLISMPPPURPGEHADRITNLKFFKQFDGY       57     DAV SSRASKKINLDFELKMRRPMGETRNVSLISMPPPURPGEHADRITNLKFFKQFDGY       57     DAV SSRASKKINLDFELKMRRPMGETRNVSLISMPPPURPGEADRITNLKFFKQFDGY       57     DAE SSRAGKKINLDFELKMRRPMGETRNVSLISMPPPURPGEADRITNLKFFKQFDGY       59     DAE SSRAGKKINLDFELKMRRPMGETRNVSLISMPPPURPGEADRITNLKFFKQFDGY       59     DAE SSRAGKKINLDFELKMRRPMGETRNVSLISMPPPURPGEADRITNLKFFKQFDGY       59     SKRESKINLDFELKMRRPMGETRAVSLISMPPPURPGEADRITNLKFFKQFDGY       50     SKRESKINLDFELKMRRPMGETRAVSLISMPPPURPGEADRITNLKFFKQFDGY       51     VGEQERSKELNLRMKMEMOKLPDSYGVSAIESVPPN0.026ESSVRIGMOLVKQFDGE       51     VGEQEVRRGEQATFRLKPEAQNLGGGSATLLAAAPPURPQQGDINLGQVSIGSGEVPF       68     m1     89     810     m2   | 95<br>116<br>118<br>115<br>118<br>108   |
| β4         β5         β6         β7         β8           36         DAV SSRANKKINLDFELKMRRPMGETRNVSLISMPPPMRPCEHADRITNLKFFKQFDQY           57         DAV SSRASKKINLDFELKMRRPMGETRNVSLISMPPPMRPCEHADRITNLKFFKQFDQY           57         DAE SSRAGKKINLDFELKMRRPMGTRNVSLISMPPPMRPCEADRITNLKFFKQFDQY           59         DAE SSRAGKKINLDFELKMRRPMGTRNVSLISMPPPMRPCEADRITNLKFFKQFDQY           50         SAG SSRASKKINLDFELKMRRPMGTRNVSLISMPPPMRPCEADRITNLKFFKQFDQY           50         SAG SSRAKKNLDFELKMRRPMGTRNVSLISMPPPMRPCEADRITNLKFFKQFDQY           56         SAQ SSYANKKMNLDFELKMRRPMGETRAVNLYSMPARIMPCGAESMLNLKFFKQFDQY           57         VKROSEBSKELNLRMKMEMOKLPDSYGVSAIESVPPRMQ20ESSYRICAMQLYKQFDGE           51         VGEVRRGEQATFRLKPEAQWLGRGSATLLAAAPPWRCQGDINLGQVSIGSGEVPF           68         m1         89         810         m2         MolY-N   | 95<br>116<br>118<br>118<br>115<br>118<br>108  |
| 36 DAVESSRANKKINLDFELKMRRPMGETRNVSLISMPPPURPGEHADRITINLKFFKQFDGY<br>57 DAVESSRASKKINLDFELKMRRPMGETRNVSLISMPPPURPGEHADRITINLKFFKQFDGY<br>59 DAESSRASKKIVLDFELKMRRPMGTRNVSLISMPPURPGEADRITINLGFFKQFDGY<br>59 DAESSRASKKIVLDFELKMRRPMGETRAVSLISMPPORPGEADRITINLKFFQQFNGY<br>56 SAQESSYNKKMILDFELKMRRPMGETRAVSLISMPPORPGEADRITINLKFFQQFNGY<br>56 SAQESSYNKKMILDFELKMRRPMGETRAVSLISMPPORPGEADRITINLKFFQQFNGY<br>56 SAQESSYNKKMILDFELKMRRPMGETRAVSLISMPPORPGEADRITINLKFFQQFNGY<br>56 SAQESSYNKKMILDFELKMRRPMGETRAVSLISMPPORPGESSYRIGMQLYKQFDGE<br>51 VGEVRRGEQATFRLKPEAQWLGRGSATLLAAAPPWRCQGDINLGQVSIGSGEVPF   | 95<br>116<br>116<br>118<br>115<br>118<br>108  |
| 57 DAV SSRASKKINLDFELKMRRPMGETRNVSLISMPPP WRDCEHADRITNLKFFKQFDGY<br>57 DAE SSRASKKINLDFELKMRRPMGDTRNVSLVSMPPP WRDCEGADRITNLOFFKQFDGY<br>59 DAE SSRASKKIVLDFELKMRRPMGETRNVSLISMPPPM WRDCASANDITNLKFFKQFDGY<br>56 SACTSSYNKKMNDFELKMRRPMGETRAVNLVSMPANM COGASSMLNLKFFKQFDGY<br>59 KVROSESSKELNLRMKHEMQKLPDSYGVSATESVPPR QZCESSYRICHMQLYKQFDGE<br>51 VGEVRRAGEQATFRLKPEAQWLGRGSATLLAAAPPWRDQGDINLGQVSIGSGEVPF   | 116<br>116<br>118<br>115<br>118<br>108  |
| 57 DAE SSRAGKKINLDFELKMRRPMGDTRNVSLVSMPPVMRDCEGADRITNLOFFKOFDGY<br>59 DAE SSRASKKIVLDFELKMRRPMGETRNVSLISMPPPTMRPCENADRITNIKFFQPFNGY<br>56 SACTSSYTNIKMNLDFELKMNRPMGETRAVNLVSMPARIMPCDCAESMLNLKFFKOFDGY<br>59 KVRFQSEQSKELNLRMKMEMOKLPDSYGVSAIESVPPRIOPCESSYRIGNMQLYKQFDGE<br>51 VGEFVRRGEQATFRLKPEAQWLGRGSATLLAAAPPWRDQGDINLGQVSIGSGEVPF<br>88 m1 89 810 m2 MotY-N   | 116<br>118<br>115<br>118<br>108   |
| 59 DAE SSRASKI VLDFELKWRRPMGETRIVSLISMPPPMRZCENADRITIVIKFFQFNG<br>56 SACESSYNKKMILDFELKWRRPMGETRIVSLISMPPPMZCENADRITIVIKFFQFNG<br>59 KVRFQSEASKELNLPMKWEMQKLPDSYGVSAIESVPPMQQCESSYRIGMQLYKQFDGE<br>51 VGEVRRGEQATFRLKPEAQWLGRGSATLLAAAPPMR2QGDINLGQVSIGSGEVPF<br>88 m1 89 810 m2 MotY-N  | 118<br>115<br>118<br>108  |
| 56 SAQESSYENKKMILDEELKMIREPMGETRAVNLVSMPAR/MCODAESMLNLKFFKQFDGY<br>59 KVRTQSEASKELNLRMKMEMQKLPDSYGVSAIESVPPR/QCOCESSYRIGMQLYKQFDGE<br>51 VGEFVRRAGEQATFRLKPEAQWLGRGSATLLAAAPPWR2QQGDINLGQVSIGSGEVPF  | 115<br>118<br>108   |
| 59 KNCSCESSVRIGHAMMED ELEMANDED ELAMADE SALA AND ODDAE SMILLAR F KODGE<br>51 VGEEVRRAGEQAT FRLKPEAQWLGRGSAT LAAAPPWR CQGDINLGQVSIGSGEVPF<br>88 gr1 89 810 gr2 MotY-N   | 113<br>118<br>108   |
| 51 VGETVRAGEGATFRLKPEAQWLGRGSATLLAAAPPWR2QGDINLGQVSIGSGEVPF  | 108   |
|  | 100   |
| 68 a1 69 610 a2 MotY-N   |   |
|  |   |
|  | 154   |
|  | 175   |
| 117 VGQQTAWG-1LSELEKGRTPTFSTQDWQSRDQRIEWALSSVLFQSKMAFSLQTANLLKT  | 175   |
| 117 IGGQTAWS-LLSELEKGRYPTFSYQDWQSRDQRIEVALSSVLFQQPYNEFSLQISKLLPY   | 175   |
| 119 VGGQTAWG-ILSELEKGRYPTFSYQDWQSRDQRIEVALSAVLFQQKYNVFSUCVANLLPY   | 177   |
| 116 VGGPTAWS-MLAELESGREPTETYADWQSPKQMLEVALSPVLLQEQYNVESMCLANLLPY   | 174   |
| 119 LQKQLAWT-LLSELEKGRYPTFFYDDWYNNRDQVAVSLSSVNFRRTYDDFMSCVNALLPF   | 177   |
| 109 NSSQQQAGRLLTGLLEGRSPLVRHRTWQGDRLEVRLLPAREASVYSQYQAGIAKILPV   | 166   |
| MotY-C<br>611 ac3 612 ac4  |   |
|  | 212   |
|  | 234   |
|  | 234   |
|  | 200   |
|  | 200   |
|  | 200   |
| 178 SEDDIATIVLNHEADSE-KUILSSQRKUKQISDILQVDNELELVLVDATIDSLGARGPNU   | 230   |
|  |   |
| TOL MERGAVERGARENDEL-VENDARAVEDTERGFEVENDESTIKTERDOUSONKFINK   | 225   |
|  | 225   |
|  | 225   |
| α         β13         β14           214         SLSERTAESLRDYFOSL GLPEDRIOVOGYGKRRETADVGSPIGKDKNEFVUISUGRTOV-<br>235         SLSERTAESLRDYFOSL GLPEDRIOVOGYGKRRETADVGTPIGKDKNEFVUISUGRTOV-   | 225<br>272<br>293   |
| α4         β13         β14           214         SLSERRAESLRDYFOSL CLPEDRIOVOGYCKRRCTAD/GSPIGKDK/RF/VISL/GRTQV-<br>235         SLSERRAESLRDYFOSL CLPEDRIOVOGYCKRRCTAD/GSPIGKDK/RF/VISL/GRTQV-<br>236           235         SLSERRAESLRDYFOSL CLPEDRIOVOGYCKRRCTAD/GSPIGKDK/RF/VISL/GRTQV-<br>236         NLSEGRAPU RF/FKSTRI PEDRIOVOGYCKRRCTAD/GSPIGKDK/RF/VISL/GRTQV-<br>236   | 225<br>272<br>293<br>294  |
| α4         β13         β14           214         SLSER RESLROYFOSI CLPEDRI OVOGYCKRE TAD/GSPIGKDK/REVISI GRTQV-           235         SLSER RESLROYFOSI CLPEDRI OVOGYCKRE TAD/GSPIGKDK/REVISI GRTQV-           236         NLSEO/REVISI CLPEDRI OVOGYCKRE TAD/GSPIGKDK/REVISI GRTQV-           237         NLSEO/REVISI CLPEDRI OVOGYCKRE TAD/GSPIGKDK/REVISI GRTQV-           237         NLSEO/REVISI CLPEDRI OVOGYCKRE TAD/GSPIGKDK/REVISI GRTQV-   | 225<br>272<br>293<br>294<br>295   |
| col         β13         β14           214         SLSERAESLROYFOLGUEDRIOVOGYOKRRETAD/GSPIGKDKNEFVISLGRTOV-           235         SLSERAESLROYFOLGUEDRIOVOGYOKRRETAD/GSPIGKDKNEFVISLGRTOV-           236         NLSEQAEVLREYFKSIGLPEDRIOVOGYOKRRETAD/GSPIGKDKNEFVISLGRTOV-           237         NLSERAESLROYFOLGUEDRIOVOGYOKRRETAD/GSPIGKDKNEFVISLGRTOV-           238         NLSEQAEVLREYFKSIGLPEDRIOVOGYOKRRETAD/ASPIGKDKNEFVISLGRTOV-           234         OVSERAESLROYFKALGUEDRIOVOGYOKRRETAD/ASPIGKDKNEFVISLGRTOV-           234         OVSERAESLROYFKALGUEDRIOVOGYOKRRETAD/ASPIGKDKNEFVISLGRTOV-   | 225<br>272<br>293<br>294<br>295<br>292  |
| ave         regregeneration  | 225<br>272<br>293<br>294<br>295<br>292<br>292   |
| α.4         β13         β14           214         SLSERRESLROYFOSL CLPEORIOVOGYOKRR TADUGSDUSKURKETWISL         614           214         SLSERRESLROYFOSL CLPEORIOVOGYOKRR TADUGSDUSKURKETWISLORTOV-           235         SLSERRESLROYFOSL CLPEORIOVOGYOKRR TADUGSDUSKURKETWISLORTOV-           236         NLSEOREVLREYFRSTCLEPEORIOVOGYOKRR TADUGSDUSKURKETWISLORTOV-           237         NLSEOREVLREYFRSTCLEPEORIOVOGYOKRR TADUASPTIGKKINGTVISLORTOV-           238         PUSERRALLKLOVFESTCLEPEORIOVOGYOKRR TADUASPTIGKKINGTVISLORTOV-           239         NLSEOREVLREYFRSTCLEPEORIOVOGYOKRR TADUASPTIGKKINGTVISLORTOV-           234         QVSERRALLKLOVFESTCLEPADRICVIS/GERGTADUATPTIGKKINGTVISLORTITICAR           237         ELTEORIKETOOFFVERCIDAERIKTVAN GERGTADUATPTIGKKINGTVUSTLORTITICAR           238         ELTEORIKETOOFFVERCIDAERIKTVAN GERGTADUATPTIGKKINGTVUSTLORTITICAR           239         ELTEORIKETOOFFVERCIDAERIKTVAN GERGTADUATPTIGKKINGTVUSTLORTITICAR           230         ELTEORIKETOOFFVERCIDAERIKTVAN GERGTADUATPTIGKKINGTVUSTLORTITICAR           237         ELTEORIKETOOFFVERCIDAERIKTVAN GERGTADUATPTIGKKINGTVUSTLORKKETUNGTKETKUSTLORTITICAR           238         ELTEORIKETWENTENGTERENKINGTVUSTLORKKETUNGTKETKUSTLORTITICAR           239         ELTEORIKETWENTENGTERENKINGKETKETKUSTLORTITICAR           240         ERTENNAN           251         ELTEORIKETKAN GERGTADUATERAN  <   | 225<br>272<br>293<br>294<br>295<br>292<br>296<br>296  |
| c4         β13         β14           214         SLSERRAESLRDYFOSL CLPERFLOVOGY GKRR TADXGSPIGKDKTRFVTSLGRTOV-           235         SLSERRAESLRDYFOSL CLPERFLOVOGY GKRR TADXGSPIGKDKTRFVTSLGRTOV-           236         NLSEQRAEVLREYFKST CLPERFLOVOGY GKRR TADXGSPIGKDKTRFVTSLGRTOV-           237         NLSERRAESLRDYFFKST CLPERFLOVOGY GKRR TADXGTPIGKDKTRFVTSLGRTOV-           238         QVSERRALELPEDFLOVOGY GKRR TADXASPIGKDKTRFVTSLGRTOV-           239         DLSRRAESLRDYFKST CLPEDFLOVOGY GKRR TADXASPIGKDKTRFVTSLGRTSTGV-           231         DLSRRAESLRDYFKAL CLPEDFLOVOGY GKRR TADXASPIGKDKTRFVTSLGRTSTGV-           232         QVSERRALKLONYFEST CLPADRTRVHSYGERR TADXATPIGKNKTRFVTSLGRTSTI-           236         DLSRRALAVQEYLKSNOVPESQTNVRFYGERVLVSTORETURQTTRFVTVH SCRTTI-  | 272<br>293<br>294<br>295<br>292<br>296<br>285   |
| cd     β13     β14       214     SLSERRAESLRDYFOSL     GLPEDRIQVQGYGKRRPIADXGSPIGKDKNRFVVISLGRTQV-       235     SLSERRAESLRTYFESL     GLPEDRIQVQGYGKRRPIADXGSPIGKDKNRFVVISLGRTQV-       236     NLSEQRAEVLREYFKSL     GLPEDRIQVQGYGKRRPIADXASPIGKDKNRFVVISLGRTQV-       237     NLSERRAESLRDYFKAL     GLPEDRIQVQGYGKRRPIADXASPIGKDKNRFVVISLGRTQV-       238     VSERRALKLQNYFESL     GLPEDRIQVQGYGKRRPIADXASPIGKDKNRFVVISLGRTQV-       239     NLSERRAESLRDYFKAL     GLPEDRIQVQGYGKRRPIADXATPIGKDKNRFFVVISLGRTIL-       237     NLSERRAESLRDYFKAL     GLPEDRIQVGGYGKRRPIADXATPIGKDKNRFFVVISLGRTIL-       237     ELTEQRAKEIQQFFVERGIDAERIKTVAHGEDRVKSVDNEINRQINFFVISLGRTIL-       238     GLSRRRALAVQEYLKSNOVPESQINVRFYGERVFLVANSAANRARNAFVIVHSREAVV  | 272<br>293<br>294<br>295<br>292<br>296<br>285   |
| cd         β13         β14           214         SLSERRAESLRDYFOSLELPEDRIQVQQYGKRRTIADXGSPIGKDKNEFVISLGRTQV-           235         SLSERRAESLRTYFESLELPEDRIQVQQYGKRRTIADXGTPIGKDKNEFVISLGRTQV-           236         NLSEQRAEVLREYFKSIELPEDRIQVQQYGKRRTIADXGTPIGKDKNEFVISLGRTQV-           237         NLSEQRAEVLREYFKSIELPEDRIQVQQYGKRRTIADXASPIGKDKNEFVISLGRTQV-           238         QVSERRALKLQNYFESIELPEDRIQVQQYGKRRTIADXASPIGKDKNEFVISLGRTQI-           239         DLSRRAESLRDYFKSIELPEDRIQVQQYGKRRTIADXATPIGKNKNEFVISLGRTUI-           237         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKNEFVISLGRTUI-           238         QVSERRALKLQNYFESIELPADRIRVHSYGERRTIADXATPIGKNKNEFVISLGRTII-           239         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKNEFVISLGRTII-           239         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRTII-           231         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRTII-           238         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRTII-           239         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRTII-           231         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRTII-           232         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRTUIL           2331         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRVKSQDNEIDRQUXKEFVISLGRXHFVISLGRXHFVISLGRXHFVISLGRXHFVISLGRXHFVISLGRXHFVISLGR | 272<br>293<br>294<br>295<br>292<br>296<br>285<br>285  |
| c4     β13     β14       214     SLSERRAESLRDYFQSLGLPEDRIQVQQYGKRR2IAD/GSPIGKDKNRFVISLGRTQV-       235     SLSERRAESLRDYFQSLGLPEDRIQVQQYGKRR2IAD/ASPIGKDKNRFVISLGRTQV-       236     NLSEQRAEVLREYKSIGLPEDRIQVQQYGKRR2IAD/ASPIGKDKNRFVISLGRTQV-       237     NLSERRAESLDYFKSIGLPEDRIQVQQYGKRR2IAD/ASPIGKDKNRFVISLGRTQV-       237     SLSERRALKLQNYFESIGLPEDRIQVQQYGKRR2IAD/ASPIGKDKNRFVISLGRTQV-       237     SLSERRALKLQNYFESIGLPEDRIQVQQYGKRR2IAD/ASPIGKDKNRFVISLGRTID-       237     ELTEQRAKEIQQFFVERGIDAERIKTVAHGEDRVKSTDDEINRQINGFVISLGRTII-       237     ELTEQRAKEIQQFFVERGIDAERIKTVAHGEDRVKSTDDEINRQINGFVISLGRTII-       237     ELTEQRAKEIQQFFVERGIDAERIKTVAHGEDRVKSTDNEINRQINGFVISLGRTII-       236     LSRRRALAVQEYLKSNCVPESQINVRFYGERYJLVANNSAANRARNERVTVHSREAVV   | 272<br>293<br>294<br>295<br>292<br>296<br>285<br>272<br>272   |
| cd     β13     β14       214     SLSERRAESLRDYFOSLGLPEDRIOVOGYGKRETADI.GSPIGKDKNRFVISLGRTOV-<br>235     SLSERRAESLRDYFOSLGLPEDRIOVOGYGKRETADI.GSPIGKDKNRFVISLGRTOV-<br>236       236     NLSEGRAEVLREYFKSIGLPEDRIOVOGYGKRETADI.ASPIGKDKNRFVISLGRTOV-<br>237     NLSERRAESLRDYFKALGLPEDRIOVOGYGKRETADI.ASPIGKDKNRFVISLGRTOV-<br>236       237     GUTEGRALKLONYFESIGLPEDRIVOVGYGKRETADI.ASPIGKDKNRFVISLGRTOV-<br>236     NLSERRAESLRDYFKALGLPEDRIVOVGYGKRETADI.ASPIGKDKNRFVISLGRTOV-<br>237       234     OVSERRALKLONYFESIGLPEDRIVVGYGKRETADI.ASPIGKDKNRFVISLGRSEV-<br>236     DLSRRALKLONYFESIGLPEDRIVVGYGKRETADI.ASPIGKDKNRFVISLGRSEV-<br>236       272  | 225<br>272<br>293<br>294<br>295<br>292<br>296<br>285<br>272<br>293<br>294                             |
| α4         β13         β14           214         SLSERRAESLRDYFQSL CLPEORIOVGOYGKRRTADUGSSPICKDKUREWISLGRTQV-           235         SLSERRAESLRDYFGSL CLPEORIOVGOYGKRRTADUGSSPICKDKUREWISLGRTQV-           236         NLSEOZAEVLREYFKSL CLPEORIOVGOYGKRRTADUASPICKDKUREWISLGRTQV-           237         NLSEOZAEVLREYFKSL CLPEORIOVGOYGKRRTADUASPICKDKUREWISLGRTQV-           236         NLSEOZAEVLREYFKSL CLPEORIOVGOYGKRRTADUASPICKDKUREWISLGRTQV-           237         NLSEOZAEVLREYFKSL CLPEORIOVGOYGKRRTADUASPICKDKUREWISLGRTQL-           238         QVSERRALKLQNYFESICLPADRIRVHSYGERRTADUASPICKDKUREWISLGRTUI-           237         ELTEOZAKEIQOFFVERCIDARBIKVHSYGERRTADUASPICKDKUREWISLGRTUI-           238         DLSRRALLAVQEYLKSNOVPESQUWRFYGERVELVANSAANRARNEWISVISLGRTUI-           239   | 225<br>272<br>293<br>294<br>295<br>292<br>296<br>285<br>272<br>293<br>294<br>295                      |
| α4         β13         β14           214         SLSER74ESLR0YF0SLGLPEDRIUV0GY0KRRTADUGSSNKLTNK           235         SLSER74ESLR0YF0SLGLPEDRIUV0GY0KRRTADUGSSNKLTNK           236         NLSE074EVLREYFKSLGLPEDRIUV0GY0KRRTADUGSPIGKDKNEFWISLGRT0V-           237         NLSE074EVLREYFKSLGLPEDRIUV0GY0KRRTADUGSPIGKDKNEFWISLGRT0V-           238         NLSE074EVLREYFKSLGLPEDRIUV0GY0KRRTADUASPIGKDKNEFWISLGRT0V-           239         DLSER74LLQUPFVERSIGLPEDRIUV0GY0KRRTADUASPIGKDKNEFWISLGRT0V-           237         NLSE074EVLREYFKSIGLPEDRIUV0GY0KRRT0ADUASPIGKDKNEFWISLGRT0VISLGRT0V-           237         NLSE074EVLREYFKSIGLPEDRIUV0GY0KRRT0ADUASPIGKDKNEFWISLGRT0VISLGRT0V-           240         VSER74LLQUPFVERGIGLEBRIKVHSVGERRTADUASPIGKDKNEFWISLGRTIII-           237         ELTE074KEIQ0FFVERGIDAERIKVHSVGERRTADUASPIGKDKNEFWISLGRTVISLGRSEV-           240         USER74LLQUPFVERGIDAERIKVHSVGERRTADUASPIGKDKNEFWISLGRVISLGRTUI-           250         LISR74LAVQEYLKSNOVPESONVRFYGERY2LVANSAANRAR74HVTVHSREAVV           272   | 272<br>293<br>294<br>295<br>292<br>296<br>285<br>272<br>293<br>293<br>293<br>295<br>292               |
| cd         fl3         fl4           214         SLSERRAESLROYFOSL CLPEDRIOVOGYCKRF IADI GSPIGKDKNRFVISLGRTOV-           235         SLSERRAESLROYFOSL CLPEDRIOVOGYCKRF IADI GSPIGKDKNRFVISLGRTOV-           236         NLSEORAEVLREYFKSI CLPEDRIOVOGYCKRF IADI ASPIGKDKNRFVISLGRTOV-           237         NLSERRAESLROYFKAL CLPEDRIOVOGYCKRF IADI ASPIGKDKNRFVISLGRTOV-           238         NLSEORAEVLREYFKSI CLPEDRIOVOGYCKRF IADI ASPIGKDKNRFVISLGRTOV-           239         NLSERRAESLROYFKAL CLPEDRIOVOGYCKRF IADI ASPIGKDKNRFVISLGRTOV-           236         NLSERRAESLROYFKAL CLPEDRIOVOGYCKRF IADI ASPIGKDKNRFVISLGRTIV-           237         LETEORAKEIQQFFVERGIDAERIKTVAHGEDRIVKS DINEINROINREVISLGRTI           237         ELTEORAKEIQQFFVERGIDAERIKTVAHGEDRIVKS DINEINROINREVISLGRTIVOUTKPSSI           236         LSRRRALAVQEYLKSNCVPESOINVRFYGERYELVANNSAANRARNEVTVHSREAVV           272  | 225<br>272<br>293<br>294<br>295<br>292<br>296<br>285<br>272<br>293<br>294<br>295<br>295<br>295<br>298 |

**Fig. S1.** Multiple alignments of the MotY proteins from bacterial species with polar flagellum. Various structural features revealed by this study are indicated on top of the amino acid sequence of *Vibrio alginolyticus* MotY: red line,  $\alpha$ -helix; green line,  $\beta$ -structure. The secondary structural elements are labeled above the lines. The residues missing in the atomic model are indicated with magenta lines above the sequence. The blue boxes indicate the residues forming the intramolecular disulfide bridge. Arg-261, a well-conserved residue important for motility, is shown with the orange box. The N-terminal 21 signal-sequence residues of *V. alginolyticus* MotY are indicated with the black line above the sequence.

## Table S1. X-ray refinement statistics

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| Measurement              | Value               |
|--------------------------|---------------------|
| Resolution range, Å      | 41–2.85 (3.03–2.85) |
| Reflections working, no. | 9,699 (1,323)       |
| Reflections test, no.    | 953 (137)           |
| R <sub>w</sub> , %       | 29.0 (40.2)         |
| R <sub>free</sub> , %    | 31.2 (42.1)         |
| rmsd bond length, Å      | 0.012               |
| rmsd Bond angle, deg.    | 2.3                 |
| B-factors                |                     |
| Protein atoms, no.       | 55.3                |
| Solvent atoms, no.       | 45.6                |
| Ramachandran plot, %     |                     |
| Most favored             | 71.8                |
| Additionally allowed     | 25.5                |
| Generously allowed       | 2.8                 |
| Disallowed               | 0                   |
| Protein atoms, no.       | 2,003               |
| Solvent atoms, no.       | 12                  |
|                          |                     |

 $\text{Values in parentheses are for the highest-resolution shell. } \textit{R}_{w} = \Sigma \left\|\textit{Fo}\right| - \left|\textit{Fc}\right| / \Sigma \left|\textit{Fo}\right|; \textit{R}_{\text{free}} = \Sigma \left\|\textit{Fo}\right| - \left|\textit{Fc}\right| / \Sigma \left|\textit{Fo}\right|.$