

1 Supplementary Information

2 3 **The ligand-binding domain of a chemoreceptor from *Comamonas testosteroni* has a** 4 **previously unknown homotrimeric structure**

5 Running title: trimeric structure of MCP2201LBD

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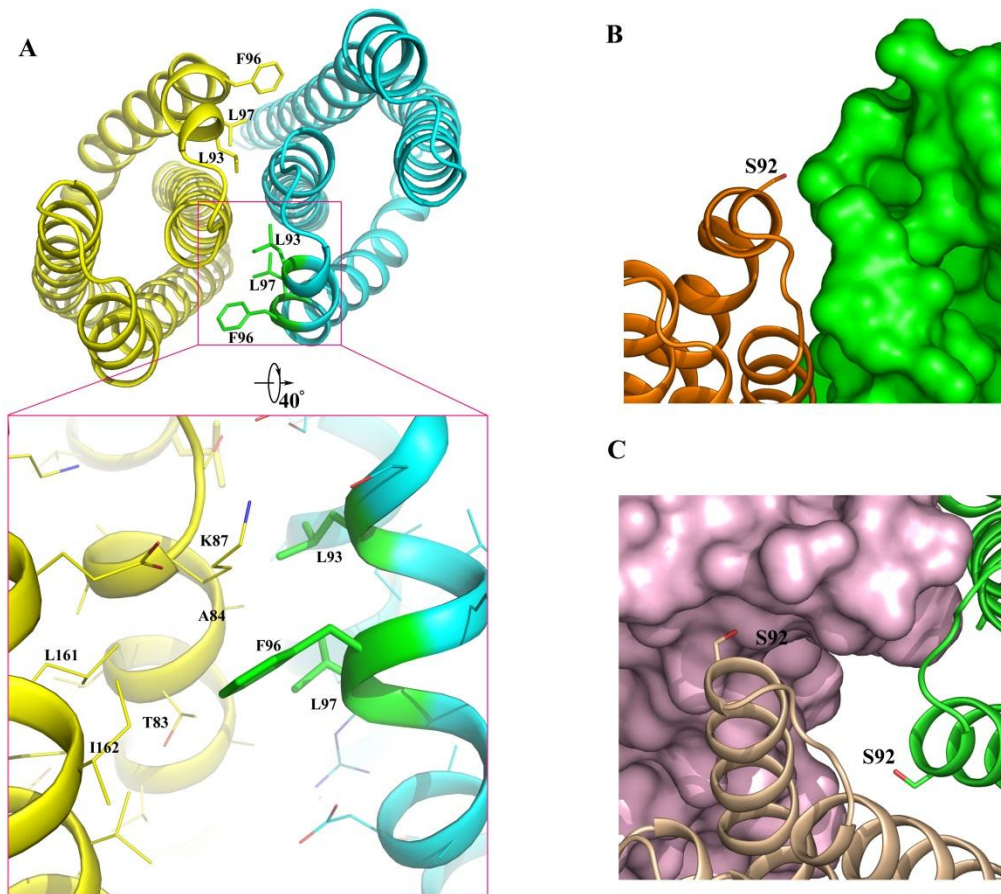
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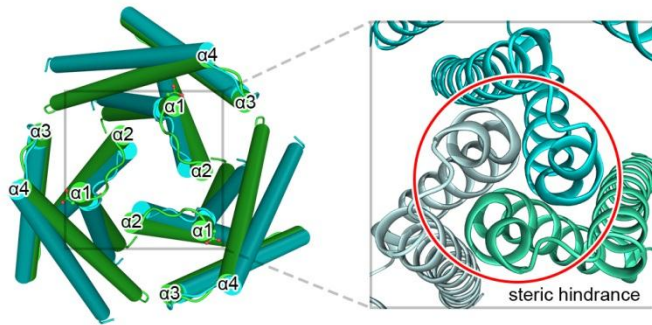


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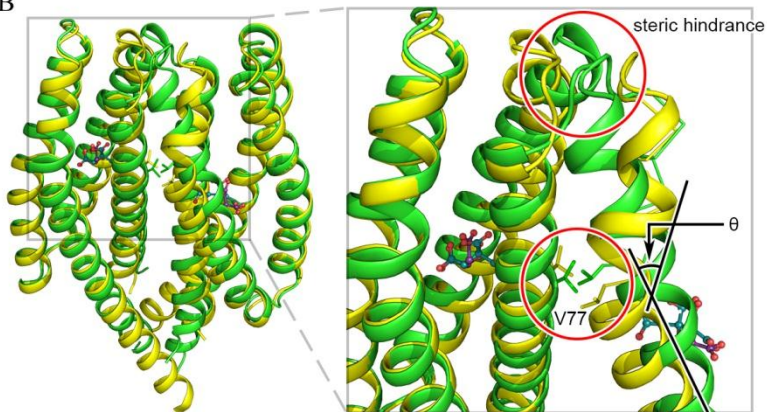
28 **Figure S1. Locations of residues L93, F96, L97 and S92 at dimer and/or trimer interface.** (A)
 29 A top view and enlargement of apo dimer structure of MCP2201 LBD show that residue L93,
 30 F96 and L97 do not pack against any hydrophobic residue of the other protomer. The locations of
 31 these residues in trimeric interface are shown in Figure 3D. (B) Residue S92 locates at the apo
 32 dimer interface, yet is solvent accessible. (C) S92 occupies in the trimer interface the full space
 33 where cannot tolerate amino acid residues with large side chain. Different chains are shown in
 34 different colors.
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A



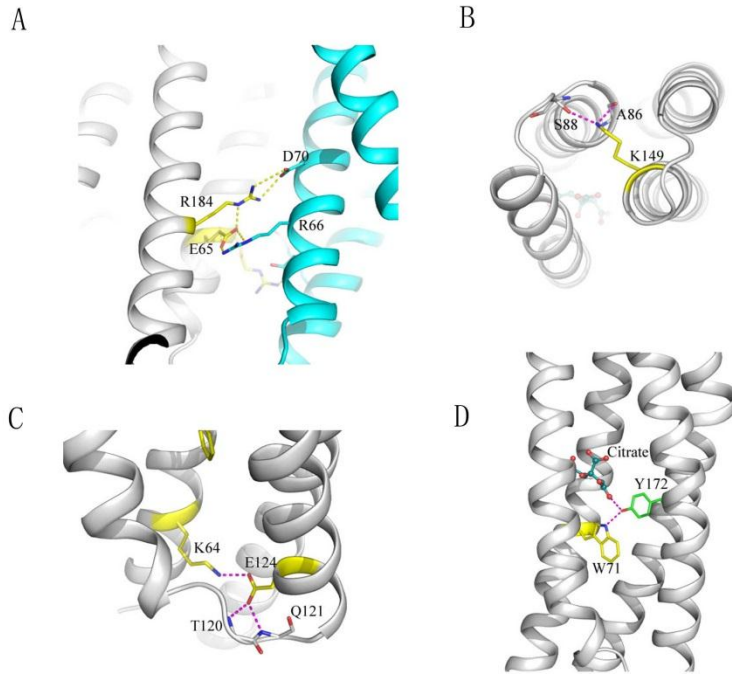
B



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39 **Figure S2. Steric hindrance observed in the modelled ligand-free trimer and citrate-bound**
40 **dimer.** (A) Three ligand-free (cyan) LBD protomers are superposed into citrate-bound (green)
41 TOM, displaying significant steric hindrance (ringed by red circles) in the trimer interface. Three
42 protomers of ligand-free LBD are distinguished by colors in the enlarged views. (B) Two citrate-
43 bound (green) LBD protomers are superposed into ligand-free (yellow) LBD dimer, displaying
44 significant steric hindrance (ringed by red circles) in the dimeric interface.

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262 **Figure S4. A close inspection of conserved residues E65, R66, D70 (A), K149 (B), E124 (C)**
 263 **and W71 (D).**
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Table S1. Data Collection and Refinement Statistics.

| | MCP2201LBD (ligand-free) | MCP2201LBD-citrate complex 1 | MCP2201LBD-citrate complex 2 |
|--|--------------------------|------------------------------|------------------------------|
| Data collection | | | |
| Space group | P 1 2 ₁ 1 | H 3 | H 3 |
| Cell dimensions | | | |
| a, b, c (Å) | 64.78, 105.03, 91.07 | 49.40, 49.40, 406.34 | 48.86, 48.86, 376.15 |
| α , β , γ (°) | 90.00, 90.95, 90.00 | 90.00, 90.00, 120.00 | 90.00, 90.00, 120.00 |
| Resolution (Å) | 55.13–2.80 (2.95–2.80) | 45.15–2.50 (2.64–2.50) | 42.05–2.50 (2.60–2.50) |
| R_{merge} | 0.107 (0.643) | 0.152 (0.291) | 0.126 (0.557) |
| R_{meas} | 0.126 (0.753) | 0.187 (0.384) | 0.148 (0.663) |
| R_{pim} | 0.066 (0.389) | 0.107 (0.248) | 0.075 (0.353) |
| I/σ(I) | 7.7 (2.3) | 4.3 (2.2) | 6.6 (2.3) |
| CC_{1/2} | 0.994 (0.700) | 0.953 (0.791) | 0.987 (0.762) |
| Completeness (%) | 99.5 (99.8) | 94.5 (94.0) | 95.7 (92.2) |
| Redundancy | 3.6 (3.7) | 2.3 (1.9) | 3.3 (3.0) |
| Refinement | | | |
| Resolution (Å) | 55.13–2.80 | 45.15–2.50 | 42.05–2.50 |
| No. reflections | 28676 | 12091 | 10730 |
| R_{work}/R_{free} | 0.224 / 0.285 | 0.203 / 0.256 | 0.184 / 0.245 |
| No. Non-H atoms | | | |
| Protein | 8363 | 2167 | 2231 |
| Ligand/ion | - | 36 | 36 |
| Water | - | 95 | 60 |
| B factors | | | |
| Protein | 68.6 | 37.0 | 53.1 |
| Ligand/ion | - | 51.3 | 54.6 |
| Water | - | 35.8 | 47.6 |
| R.m.s. deviations | | | |
| Bond lengths (Å) | 0.009 | 0.007 | 0.008 |
| Bond angles (°) | 1.321 | 0.983 | 1.019 |
| Ramachandran plot | | | |
| Favored | 96.87% | 96.09% | 97.58% |
| Allowed | 3.13% | 3.91% | 2.42% |
| Outliers | 0% | 0% | 0% |

Values in parentheses refer to the highest resolution shell.

268 **Table S2. Strains and plasmids used in this study**

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| Strains/plasmids | Relevant genotype or description | Source |
|-------------------------------|--|-------------------------------|
| Strains | | |
| <i>Comamonas testosteroni</i> | | |
| CNB-1 | | (Wu <i>et al.</i> , 2006) |
| CNB-1Δ20 | All putative chemoreceptor genes were disrupted in strain CNB-1 | (Ni <i>et al.</i> , 2013) |
| <i>Escherichia coli</i> | | |
| DH5α | F ϕ80d <i>lacZ</i> ΔM15 Δ (<i>lacZYA-argF</i>) U169 <i>recA1 endA1 hsdR17</i> (r _K ⁻ m _K ⁺) <i>supE44 λ- thi-1 gyrA96 relA1 phoA</i> ; host for DNA manipulations | (Hanahan, 1983) |
| BL21(DE3) | F <i>ompT hsdS_B</i> (r _B ⁻ m _B ⁻) <i>gal dcm</i> (DE3) | Novagen |
| Plasmids | | |
| pBBR1MCS-2 | Km ^r , <i>lacPOZ</i> ' broad host vector with R type conjugative origin | (Kovach <i>et al.</i> , 1995) |
| pBBR1MCS2-MCP2201 | Carries MCP2201 as well as its upstream 150 bp DNA, used for chemotaxis assays | (Ni <i>et al.</i> , 2013) |
| pBBR1MCS2-MCP2201-R81A | Carries MCP2201 with R81A mutation | This work |
| pBBR1MCS2-MCP2201-T104A | Carries MCP2201 with T104A mutation | This work |
| pBBR1MCS2-MCP2201-T108A | Carries MCP2201 with T108A mutation | This work |
| pBBR1MCS2-MCP2201-R135A | Carries MCP2201 with R135A mutation | This work |
| pBBR1MCS2-MCP2201-Y138A | Carries MCP2201 with Y138A mutation | This work |
| pBBR1MCS2-MCP2201-R142A | Carries MCP2201 with R142A mutation | This work |
| pBBR1MCS2-MCP2201-Y172A | Carries MCP2201 with Y172A mutation | This work |
| pBBR1MCS2-MCP2201-L93R | Carries MCP2201 with L93R mutation | This work |
| pBBR1MCS2-MCP2201-F96A | Carries MCP2201 with F96A mutation | This work |
| pBBR1MCS2-MCP2201-L97A | Carries MCP2201 with L97A mutation | This work |
| pBBR1MCS2-MCP2201-S88A | Carries MCP2201 with R81A mutation | This work |
| pBBR1MCS2-MCP2201-D90A | Carries MCP2201 with D90A mutation | This work |
| pBBR1MCS2-MCP2201-S92W | Carries MCP2201 with S92W mutation | This work |
| pBBR1MCS2-MCP2201-S92R | Carries MCP2201 with S92R mutation | This work |
| pBBR1MCS2-MCP2201-S73A | Carries MCP2201 with S73A mutation | This work |
| pBBR1MCS2-MCP2201-F96C-His | Carries MCP2201 with F96C mutation and a C-terminal His-tag, used for TMEA crosslinking | This work |
| pET28a | | |
| pET28a- <i>mcp2201</i> LBD | pET28a derivative for expression of MCP2201LBD, spanning residues Q46-T203 and used for citrate-bound structure determination and other assays. | (Ni <i>et al.</i> , 2013) |
| pET22b | | |
| pET22b- <i>mcp2201</i> LBD | pET22b derivative for expression of MCP2201LBD, spanning residues M57-T203 and used for apo form structure determination. | This work |

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272 **Dataset S1. Protein sequences of MCP2201 orthologs.**273 **Protein sequences of MCP2201 orthologs.** NCBI accession numbers are shown.

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275 >Comamonas_testosteroni_1 |WP_041744100.1 methyl-accepting chemotaxis
276 protein [Comamonas testosteroni]
277 MRLTKLNIGARLGLGFVAVLAFVAVITVIGIWLHLSVGKATQQMMQEPLTKERLISDWNSNVSVAVARTTA
278 IAKSSDASLVQFLAADAATAKSTANVLKQIEPLITQPAEREILDKIMQVRKTYIASRDKVSQKADGMAE
279 EAESTLINSYVPAAQGYLKLGLGELLNLQRASLDAKAAEVEQIESSRTYFLVLALLALAIGTVSAWRLTQG
280 ITAPLKHAVSVARRVADGDLTARIHVSSSDETGQLMQALHDMNTSLDRLVGVQVRQGTDSIATASGQIAAGN
281 HDLSARTEEQASSLQQTAAASMEQLTSTVKQNADNASQANQLALSASDVAVKGGMVVSQVVEITMGAISQSSR
282 KISDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSAAEAAKEIKQLIQASVTKVEE
283 GSAQVSQAGQTMDEIVSSVQRVTDIMGEITAASHEQTSQIEQINRAVAEMDLVTQQNAALVEESTAAAQSM
284 QQQTSDLQMVSVFRLKSA
285 >Comamonas_terrigena_1 |WP_066535939.1 HAMP domain-containing protein
286 [Comamonas terrigena]
287 MNFSKFNIGARLGLGFVAVLAFVAVITAIGMQLHLSVGKATQQMMQEPLTKERLISDWNSNVSVAVARTTA
288 IAKSSDASLVFPLAADAATAKGTADV LKQIEPLISLPAEREIMDKIMAIRKTYIASRDKVSQKAEGLSE
289 EAEATLVNAFVPAAQGYLKLSELLSLQRSGLDAKAAEVQAIENTSQTYFVILAVLALAIGAVSAWRLTQG
290 ITAPLRNAVTVARRVADGDLSTDIRVTGTDETGQLLQALHDMNASLGRLVGVQVRQGTDSIATASSQIASGN
291 HDLSSRTEEQASSLQQTAAASMEQLTSTVKQNADNASQANQLALSASDVAVKGGLVVSQVVEITMGAISTSSK
292 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSAAEAAKEIKQLIQASVDKVEE
293 GSLQVSQAGQTMDEIVSSVQRVTDIMGEITAASQEQTSGIEQINRAVAEMDLVTQQNAALVEESTAAAQSM
294 QQQTGDLQMVSVFRLKHA
295 >Rhodoferrax_ferrireducens_1 |WP_011464516.1 methyl-accepting chemotaxis
296 protein [Rhodoferrax ferrireducens]
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298 AVAKSSDPSLVPPFFSTNAAEITKSTSAALLKQIEPLLSQEEKDLFSKVSDVRKAYLSSRDQVTKLKADGQA
299 DEANRLLESTYIPAADNYMMLVSEFLGLQRKNLDAKAVEISGIETTSRNYLVALAALVLTFGVICAWLLTV
300 GITGPLTNAVAVARRVADGDLATDIQTEGKDETAQLLQALSAMKDNLARIVGNVVRQSGEGVATASAEIAQG
301 NNDLSARTEQQASALEETAASMEELSATVRQNADNARQANQLAQSASTVAIKGGEVVSQVVEITMKGINDSS
302 KKISDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSADA AKEIKGLINDSVQRVE
303 QGSTLVQDQAGVTMTEVSSIRRVTDIMGEISAASTEQSQGVAQVSEAVTQMDQVTQQNAALVEEMAAAASS
304 LKSQAQELVGTVSVFKLSQSQGAGLPDSSAPQRTSRVRSAPAPAPAPAARKLGNTPAKPAIRAKPDSLAAAP
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306 >Rhodoferrax_fermentans_1 |WP_078366276.1 HAMP domain-containing protein
307 [Rhodoferrax fermentans]
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310 EEAYSILEKDYLPADGYMMLVGEFLAVQRKNLDTRAQEMADIERSRNL LALAVSALALGALCAWLLTV
311 GITGPLKNSLAVATRVAEGDLSADIQVVGQDETAQLLQALSTMKNQLAGIVSHVRQGSQGVSVASAEIAQG
312 NNNLSERTEQQASALEETAASMEELSATVRQNADNARQANQLAQSASTVAIQGGEVNVQVATMKGINDSS
313 RKIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSADA AKEIKSLITDSVQRVE
314 QGTALVDQAGVTMAEVVSSIRR VNDIMGEISAASTEQSQGVAQISEAVTHMDQATQQNAALVEEMAAAASS
315 LKSQAQELVEVVS VFKLSANSQMG
316 >Noviherbaspirillum_massiliense_1 |WP_019143412.1 methyl-accepting
317 chemotaxis protein [Noviherbaspirillum massiliense]
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319 VAKSSDPALSPFFAKDAAASAKSSSDLIKQIEPLLSPEEKELFAKIMEIRKAYTAGRDGVMMLKADGQAE
320 EANSMLKKNYLPVSAAYQDQVRDFLDMQRKSLDAMAKEIDSTATTSRKLLIALAALVTAFGAIFAWLLTTG
321 ITAPLQKAVLAVRRVANGDLSRSVEVESSDETGQLLQALKDMNGSLARMVSTVRHGVDIAISTASSEIATGN
322 QDLSRTEQQASSLEETASSMEELTSTVKQNADNARQANQLAVSASAVAGKGGQVVAQVVDTMASISDSSK
323 KIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRLAQRSA AAKEIKVLIDDSVGNVAA
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327 protein [Noviherbaspirillum humi]
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330 EEANALLDKSYLPAAEAYQATVAEFVTAQRDYLDKLAADIAVIKQESRNRVILLALLCVAIGVASAWWLTR
331 SITRPMRNALAVARRVADGDLTGRVEIESSDEVGQLQALQALKDMNNNLQRIVSDIRGGTDTIATASSQIASG

332 NLDLSSRTEQQASSLEETASSMEELTSTVKQSDNARQANQLALSASEVAGRGGAVVTQVVSTMASINESS
333 RKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSANAAKEIKTLISDSVEKVD
334 DGARLVDQAGATMNEIVESVRRVSDIIGEITAASEEQRVGIEQINQAIVQMDQVTQQNASLVEQAAAAAEA
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336 WEEF
337 >Duganella_1 |WP_082507153.1 MULTISPECIES: HAMP domain-containing
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341 EQANETFEEKTYRPAQAQYQALVQDLLSMQRGKIDTIGKEIDISISANSRSLTLVAVLAVAFVAVCAVYVLTG
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343 NQDLSARTEQQAASLEETASSMEELTSTVKQADNARQANQLAGAAASVARKGGSVSEVVTMESIDASS
344 RKIVDIITVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSAAAAKEIKELIGDSVEKVN
345 AGTRLVSDAGNTMEEIVSSVQRVSDIISEITAASAEQSSGIDEVYKAVGQMDQVTQQNAALVEEAAAAAES
346 MQNQASNLADVVSFKVR
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348 partial [Pelomonas sp. KK5]
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350 ARSSDASLVKFFAEDAAASTKSSQALAEKIDALITEPDEKRLFDELAQTRKRYVAARDAITKLKADGKDDE
351 ALKQLDQAFVPAARDYERLMQALLDYQRKVIDSTAQEIDAIAARSRTMLIALAVVIGIGALVAWRISLGI
352 TRPLAHAVTAARRVADGDLTGRFDDTRLGEDETGQLLALRDMNGSLERIVSEVREGTDTMSTASVEIATG
353 TTDLSSRTEQQASALQQTAAATMEQLTGTVRQADNAAQASQLAASASEVASRGGTVVAQVVDTMGAISQAS
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356 protein [Massilia eurypsychrophila]
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358 AIAKSSDVS LVPFFAANAALTTKGTAEVTKKLEPLLVTD AEEKKAYGDAMAVRKYTLASRDQVTRLKAEGKP
359 EEAEDVLTKVYLPAAESYQALVARFLAVQRQNLDSMKGQIEESRDAAQTRVVVLAALSLLCGIAFAWWLTV
360 GITAPVRRAVASARRVADGDLTEDIQVTSTDELGQLQALKDMNANLLKIVRDIRTGTDEMATASEIAAG
361 NLDLSSRTEQQAASIEETASSMEELTSTVKQADNARQANQLAMQANVLTNEASSVATEGGAVVAQVVRTMADITSS
362 KKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAAEVRTLAQRSASAAKEIKGLIDDSVDKVD
363 TGSTLVQKAGATMGQIVSSVQRVTDIMAEITAASREQSAGIEEVNRAIAQMDQVTQQNAALVEESAAAAGS
364 MHDQATGLARAVSAFKLGMEPVAAQTAPRAPVAARAAKPALAAPMRRPRLPAAGDEWEQF
365 >Acidovorax_sp._NA3_1 |WP_094097023.1 HAMP domain-containing protein
366 [Acidovorax sp. NA3]
367 MKNLKIGTRLGGGFALVVLVMMMTTIGLWRLQTV AQATHNMTQQPLAMERMISDWYRYVYSAVRRTSAIV
368 KSTDPSLGAFFAEDAAMSTRESGKLQDQIEPLLSSPAEKELWVTIKKARVTYLSSRDQAVKAKADGQLEEA
369 DRTLNQAF LPAAEKYMALIQQLLDLQRASIDTTAKDIQAVYAQSRMWLMLLCTLAVVAGGLCAWWLTRGII
370 RPLSDAVRVARAVADNDLTTTVQVHSRDETGQLMQALQDMNTSLAQVVGVRVRSGETGIATASNQIDAGNQD
371 LSSRTEQQASSLEETAASMEELTSTVKQADNARQANQLAASASQVAVQGGQVSNVVGTM SAINTSSRKI
372 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRS LAQRSAAAAKDIKTLIDDSVGKVD EGT
373 QQVAEAGKTMEAIIVDSVKRVTDIMAEIAAASQEQSAGIDQVHQAISQMDQVTQQNAALVEEAAAATGSLKA
374 QAAQLSQAVSVFRIAGQPEARIAAPQRTAPRPVAAPTRTSPPPSTPCHRPAALQRPASKPRQPPLPRSAA
375 RTTGNPSEPRARRVRAHAPPDKTPILIAACAYE
376 >Herbaspirillum_chlorophenolicum_1 |WP_050468456.1 methyl-accepting
377 chemotaxis protein [Herbaspirillum chlorophenolicum]
378 MSYFANMKIGKRLALGF AFILVAACVVAFS IWRLHGIAGATAAMMQPLTKERLVSDWYRTIHTSVRRTT
379 AIAKSTDP SLAAFFAEDAAISTKLSTEQQAIEALLSSDAEKAVFDKLSAVRKDYIKYRDAISKAKADGQV
380 DEVEKILSGPYNAAAKGYLDLLQQLLNVRAGIDQIAQDIQGIYEQSRNMLLALGALLFVLGWLFAWRLAV
381 GITRPLERAVDVAETVAAGDLTMQVDAHLASRRDETGKLLHALQAMTGNLARIVGQVRS GDTAISTASREI
382 ASGNLDLSARTERQAGSLEETASAMEELTSTVHQADNARQANQLAASASAVAQQGGEVVSQV VSTMGSIN
383 ESSRKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRS LAQRSAAAAKEIKGLIDDSVA
384 KVG TGSQLVGQAGSTMDQVVASVRHVADIVGEITAASSEQSDGIGQVNLAITEMDQTTQQNAALVEQAAAA
385 AEAMQEQAARLSEVVSQFKLGS AHEQQVANAAEPVLAAPRPSR NITPERAALGH
386 >Noviherbaspirillum_sp._Root189_1 |WP_057292684.1 methyl-accepting
387 chemotaxis protein [Noviherbaspirillum sp. Root189]

388 MFANLKIGHRLALGFAGALAFSVVITGNSLWKMNEVSAQVQSMTESPLSKERYTADWSRNI STAVARTTAV
389 AKSSDPSLSTFFAADTAATMKSTSEVLKLEVLSSDEEKTFLGKIVETRKS YTA YRDAVFKLKAEGKADE
390 ANQVLEANYLPAAKNYQDLVAQFLNLQRGQLNEDAANIKETQIAARNQMIALSALVILFGIGCAWWLTVGI
391 TGPLRNAVAARRVADGDLGSEIDVTSSDETQGLLHALRDMNANLRTTVTRVRQGTDTIATASNQIAAGNQ
392 DLSARTEQQASSLEETASSMEELTSTVRQNADNARQANQLADAASQVAAKGGGEVIGEVVGTMGQINASARK
393 IVDI IAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLAQRSASAAKEIKGLIEASVDQVDAG
394 SMLVNQAGKTMADIVDSVRRVTDIMGEITAASQEQTSGIEQINQAITQMDVDTQQNASLVEEAAAASEAMQ
395 QQAAELARVVSFKIDGENVPSSFVDVPAIIPRAGTAVAQKSTRTLKVRHASSVTSATPVPERRSFSKIRD
396 NKDGDWEEF
397 >Achromobacter_1 |WP_088595591.1 MULTISPECIES: HAMP domain-containing
398 protein [Achromobacter]
399 MLKNMRIGARLALGFIVLALAILITGISLWRLSTVAAATRAMELPLAKERMTNDWANYVLVIGITRTTAI
400 AKSSDPTLAGFLASGATEGTRASLEIMKKLEPLIQDTDEKAVYQKIMDTRGGYVAARDAIMKFKGEGKADE
401 ADKIFLSTFQPASVNYSKLLAEFVEVQRKRLDTHAAHIQEI DHDSRQQLIILAILATAFGALCAWVLRGI
402 TQPLAKALTAARRVADGDLGSEITVHGRDETQGLLEALQAMNGNLRNIVGQVRGGTDSIATAAREIAAGNL
403 DLSSRTEEQASSLSETAATMEQMTVTVKQNADNARQANQLAVSASEVASRGGAVVSQVVGTTMSSINESR
404 IVDI IGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRS LAQRSATAAKDIKQLISDSVAKVDSG
405 SQLVSQAGATMDEIVESVKRVTDIMGEISAATHEQTGSIEQINLAI AQMEQVTQQNAALVEEAAAASGAMQ
406 DQTSTLAQLVSVFRLAQGSAEQAVARLQANAQAGTHEAGGYVALPA
407 >Pelomonas_1 |WP_056270509.1 MULTISPECIES: methyl-accepting chemotaxis
408 protein [Pelomonas]
409 MTKLSIGKRLAAGFALVLAACVIAVAAWRLASTAAATRQMMDEPLAKERLISDWSRNINSGVRRRTMAIA
410 KSSDASLVELFKEDAAQSTKSSGEMQEKLKGLIRSPDEQKLFDAVGEARKVYLLDSRDLTQLKKGDAEDA
411 EKLLMEVFPVPGSKVYLARMQEFLDHQRKRIDQTAADIDAANGTGRMLLGLI GLAMLAVGIAAAWRITRSIT
412 LPLAAANELAERVADGNLMRSGAGAVAGSDEIGQLQTTLRMRRETL SQAIGSIRDSAESIGTASAEIASGN
413 QDLSARTEKAASSLEQTASAMEELTGTVHQSAAGQANSLAVSASVAQRGGDVVAQVVHTMDEINASSR
414 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRS LAGRSADAKEIKGLIGSSVERVDA
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417 >Duganella_zoogloeoides_1 |WP_019922517.1 HAMP domain-containing
418 protein [Duganella zoogloeoides]
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420 AIARSTDASLATYFADEAKSSARSSEYQKKIEELITEPDEKELFARIGAQRKIYLSRDEL SKFKADGDL
421 EQAQRVFDTVFVPGTAKYQALIADLLKMQRARIDATAAHIDGVADSSRNLLLVL AALMLAFGVLCAWLLTS
422 GITGPLRAAVVAARRVASGDLTGHIIDDRGTDETSQLLGALKEMNASLLGIVAEVRS GTDHITTSSTEIAEG
423 NQDLSRTEQQAGALEETASSMEELTSVVKHNADNARQANQLAASASQVAVKGGQVVSQVVD TMDSSINES
424 RRIVDI IAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKQLIGDSVDKVN
425 QGSKLVADAGATMDDIVSSVARVSDIITEITAATTEQSAGINEV NQAIGSMDAVTQQNAALVEQAAAAAES
426 MQQQAAVLAQAVAVFKVEGVAYQSRPGARPRKALQIT
427 >Herbaspirillum_1 |WP_079214426.1 MULTISPECIES: HAMP domain-containing
428 protein [Herbaspirillum]
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431 EEATRILDKVFPASNAYQEAMRQLVELQRKEIDATAKEIDEIAAKSRTLIMVLEALILLGLVVCARYLTL
432 GITRPLGTAVDISRVAEGDLSSDVQVKSDETQGLLQSLKDMNVSLRGIVSNVRNGTDTIT TASAIEAAG
433 NLDLSSRTEEQASSLEETASAMEELISTVRQNADNARQASQLAVSASEVAEQGGGVVSQVVD TMGAINESS
434 RKIVDI ISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRS LAQRSASAAKEIKELINDSVEKVG
435 NGSRLVEQAGATMSEVVNSVRRVTDIVSEISAASAEQTTGIEQVNHAI TQMDQVTQQNAALVEEAAAAAAS
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437 >Duganella_sp._HH101_1 |WP_070272075.1 HAMP domain-containing protein
438 [Duganella sp. HH101]
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441 DEAEKVFTNVFRPGSTSYQTLMQELLKMQRAKIDATAVHIDEVAASSRNLLYVLALLVLA FAVSSWLLTT
442 GITGPLQQAVTAARRVAGGDLTGHIIDDSARDETQGLLSALKEMNASLLGIVTEVRS GTDHITTSSEIAAG
443 NQDLSRTEQQAGALEETASSMEELTSTVKHNADNARQANQLAASAAQVAVKGGQVVSQVVD TMSINQSS
444 RKIVDI IAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKTLIGDSVEKVN

445 QGSKLVADAGLTMDEIVSSVHRVSDIITEITAASTEQSAGINEVYQAIIGAMDGVTQQNAALVEEAAAAAES
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447 >Pelomonas_puraquae_1 |WP_088484898.1 HAMP domain-containing protein
448 [Pelomonas_puraquae]
449 MIKLSIGKRLAAGFALVVLVLAGFVIALAVWRLDATAAATRQMMAEPLAKERLISDWSRNINAGVRRRTMAIA
450 KSSDASLVELFKEDQAQSTKSSGEMQEKLKGLIRSPEEQALFDVAVGKARKVYIDSRDQIVKLLKDGQAEAA
451 DKVFNDFVAPGAKVYLERMQEFLDHQRKEIDETAAGINSSNSSGRTVLLSLGVLILALGAGAAWHTTRSIT
452 VPLAAANELAERVADGNLMRSGQGMAARADEIGQLQTTLRMRRETLAQTIGSIRDSAESIGTASSEIASGN
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454 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRSLAGRSADAKEIKSLIGSSVERVEA
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461 DEANKIFETVFRPGTAKYQELIAELLKMQRAKIDAAAQHIEDVASSSRNLLYVLATLVLAFGVTSAWLLTT
462 GITRPLQEAUVVARRVASGDLTAHIDDSARDETGQLLSALKEMNASLLGIVTEVRQGTGHEHITISSTEIAQG
463 NQDLRRTEQQAGALEETASSMEELTSTVKHNADNARQANQLATSAAQVAVKGGEVVAQVVGTMD SINQSS
464 SKIVDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVATEVRNLAQRSAGAAKEIKALIGDSVEKVN
465 LGSKLVADAGTTMDEIVASVHKVSDMISEITAASSEQSAGINEVNQAIIGSMDAVTQQNAALVEQAAAAAES
466 MQQQAAALAQAVSVFKVEDTLRLSHREALAKPAVAQRKQLQITRS
467 >Cupriavidus_1 |WP_017511610.1 MULTISPECIES: methyl-accepting
468 chemotaxis protein [Cupriavidus]
469 MKNLGIGVRLGIGFGVLLLLSTFMTVLGVLRLLEDVAGRTHAMMQPLAKERIVSDWYRLMYASVRRTTAIT
470 RSSDPSLGQFFAAETKTSAETIAAMRDKIKPMLTSDAEKASFERILVVRNPNYNSRDKIAKLKQDGQAEDA
471 VKVLENEFVPAGDAYLAEIQKLLDIQRTSIDATAEEINRIYESARNGLIALGVIALAIGVAFAWWLTIGIT
472 RPLHRAVGFARTVAAGDLTGRIDVDSRDETGQLLALREMNIENILGIVKEVRKGTGTEAIATGTSQIAAGNTD
473 LSQRTEQQASSLQETASSMEELTSIVRQNASAKQASGLAVNASDVATQGGEVVGVVHTMDEINAASRKV
474 VEIISVIEGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRSLAQRSATAAKEIKALIGDSADRVERGS
475 QLVAQAGQTMEEIVSAVKRVTDIMGEISAASVEQSAGIEQVNQAVTQMDTQVTTQQNAALVEQAAAAAGSLEE
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477 >Massilia_sp._9096_1 |WP_036173002.1 methyl-accepting chemotaxis
478 protein [Massilia_sp. 9096]
479 MKNLNIGARLSLGFGLVLAFTLLMTAIGIFQMRVADATRDMMTVPLTKERLVSDWYRRIHTSVTRTTAIA
480 RSADPSLGAFFAEQTAVSTREVTTELQKKVEPLLDTPQEKQALARIAAARKPYLALRDAMTALKKDGKAEAA
481 QQMLVQQFQAGAEYLASLSDFLDLQREAINRRTGEVDALYQHNRSVLLGMGLAVLAFGAACAWWLTTRGIV
482 VPLNRAVEIAVSVANNDLRSDIEVSSRDETGRLLGALKTMNAGLARIVGQVRSQTTQIATASSEIIVGNLD
483 LSSRTEQQASALEETAASMEELTSTVKQADNARQANQLALSASAVAVRGGEVVGVVDTMEAINAASRKI
484 VDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRTLAQRSASAAKEIKALIGDSVKGIDAGS
485 QLVQSAGTTMAEVVTSIQRVTDIMGEITSASAEQSSGIEQVNRAIADMDGVTQQNAALVEQASAAAAAMQD
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487 >Bordetella_sp._N_1 |WP_057651873.1 methyl-accepting chemotaxis protein
488 [Bordetella_sp. N]
489 MLKMNKIGARLALGFGLVLAFLALAMLITGMSLWRLSTVANATRAMELPLAKERMTNDWANYVLVGITRRTTAI
490 AKSTDTSLAPFFAGDAAEGTRASLEIMKKLEPLIQDTDEKAVYKIMDVRGGYVNARDYIMKLGEGKAE
491 ANKIFLSTFPASVGYSKLLAEFVDVQRKRLDLDAAHIQEIQESRQQLIILALLALAFGATCAWLLTRGI
492 TRPLASALDAARRVADGDLSSSEIKVHGRDETGQLLEALQGMNGNLRNIVGQVRGGTDSIATAAREIAAGNL
493 DLSSRTEEQASSLSETAATMEQMTVTVKQADNARQANQLAMSASEVASRGGAVVSQVVGTTMSSINSSRR
494 IVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSATAAKDIKQLISDSVAKVDSG
495 SQLVQAGATMDEIVESVKRVTDIMGEISAATHEQTGSIEQINLAIQMEQVTQQNAALVEEAAAAASGAMQ
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497 >Bordetella_genomosp._10_1 |WP_094853882.1 HAMP domain-containing
498 protein [Bordetella_genomosp. 10]
499 MLKMNKIGARLALGFGLVLAFLALIAAIGLWRLSGVADATRAMELPLAKERMTNDWANFVLVGITRRTSAI
500 AKSTDPSSLSSFFARDASEGTRISLEIMKKLEPLIQAEDEKAVYQKIMEVVRVGYVNARDAIMKLGEGKAE
501 ASQIFQSTFLPASVGYSKLLAEFVGVQRKRLDQDAHIQQIAGESRHQLIVLAILVLAFGAVCAWLLTRGI

502 TRPLASAVDAARRVAEGDLSSEIVIHGRDETGQLLLALQAMNGNLRDIVGQVRGGTDSIATAAREIAAGNL
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505 SQLVVSQAGATMDEIVESVKRVTDIMGEISAATHEQTGSIEQINLAIQAQMEQVTQQNAALVEEAAAASGAMQ
506 DQTATLAQLVSVFRITQDAAAKRVPRLAGAVQEIEEFAAMPA
507 >Massilia_sp._Root351_1 |WP_057154754.1 methyl-accepting chemotaxis
508 protein [Massilia sp. Root351]
509 MSMLSNIIRIGKRLALGFVILALSVAITGISIWRLHEVANATRAMMEVPLAKERMISDWSSKIDS AIRRTT
510 AIARSSDPSLVGFFFADEAKKSSAVSAELQKKIEALVDEDEKELFNRIQEQRKIYLSRDKVTKLKAEGALE
511 EAEAHFSNVFAPGAAAYQNLMAELLRQGRKIDAI AVEIENGADTSRKL LIALTALV LALGVVCSWLLTAS
512 ITRPLGQALDAARRVAAGDLTGTIRVSGSDETGQLLALQDMNALLNIVMQVRSQTAEIETSSTEIAAGN
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514 KIVDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRTLAQRSAAAAKEIKELIGDSVDKVNQ
515 GGKLVADAGATMEDIVSSVHRVSTIITEITTASKEQSAGIDEVYKAIGEMDQVTQQNAALVEQAAAAESM
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517 >Pelomonas_sp._Root1217_1 |WP_057299221.1 methyl-accepting chemotaxis
518 protein [Pelomonas sp. Root1217]
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533 LSQRTEEQASSLQQTAA SMEELTSIVRQ NADNAKQASALAVNASEIAAKGGDVADKVAETMEEINGASKKV
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548 protein [Cupriavidus pauculus]
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552 RPLHRAVG FARTVAAGDLTSRIEVD SRDETGQLLDALREMNENILGIVQEVRTGTDAIATGTSQIAAGNTD
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554 VDII SVIEGIAFQTNILALNAAVEAARAGEQGRGFVAVGAGEVRSQAQRSAATAAKEIKALIGDSADRVERGS
555 QLVAQAGQTM EQIVSAVKRVTDIMGEISAASAEQSAGIEQVNQAVTQMDT VTTQQNAALVEQAAAAAGSLEE
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561 NKVLEAEFVPAGDAYLGEIQKLLDIQRESIDSTAEENRIYQRTARNGLIALGIVALAIGVAFAWWLTIGIT
562 RPLHRAVGFARTVAAGDLTSRIDSSTDETGQLLDALREMNDNILGIVREVRNGTESIATGTSQIAAGNTD
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589 [Ralstonia pickettii]
590 MQFISNMRIKRLALGFAVVLAFSIVITAIWIWRLDSASTATREMMNEPLLKERLMGDWYANLAAGIRRTI
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592 EEAQRILDQVFPANAYQDTMRQLVEVQRRTIDAAAKKIDADSARSRTLLMVLEGLILTMGIAFAYFLTL
593 SITRPLHAAVGIASRVAEGDLSTVVAQSTDETGRLLQALADMTAQLVGTVGSIRVASESVAGAAGQIAAG
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595 KKIAEITGMIEGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSQAQRSAATAKEIKELIEASTGKVQ
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603 GIVRPLRTAVDIARKVADGDLTAQIDASAKDETGQLLLALKDMNTSLNIVSEVRSRGTDSIATSSTQIAAG
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606 AGSMLVAQAGSTMNDIVDSVQRVSDIITEITAASSEQSVGIDEINRAIGQMDAVTQNAALVEESAAAAES
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612 EAANDVFEXTFVPAAAKYQKMLDLLEHQRASIDATARDIDEVAKTSRNLTLAVLALGFGVVCWLLTM
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616 AGSMLVAQAGSTMNDIVDSVQRVSDIITEITAASSEQSVGIDEINRAIGQMDAVTQQNAALVEESAAAAES
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619 [Acidovorax avenae]
620 MRNLPIGARLGAGFAMVLGLMALMTVFGLWRLQSV AQATHDMTQQPLANERMISDWYRYVDSAARRTTAIV
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622 DRLLTQVYLPATKEYVALIQKLLDLQRADIDATAAHIQDIHAQSRLLLAVLGLLALALGAACAVWLTRGIV
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625 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVGEVRLASRSAAAADIKTLIGDSVSRVDEGS
626 SQVAEAGRTMDEIVQNVQRVNDLVAEISAASEEQSRGIDQVHQAVSQMDQVTQQNAALVEEAAAATGSLKA
627 QAAQLSQAVSVFRI PAGMQAAAAAPASAVAPSTRHAPGLAPVRAISGAVRASAHVAPRPVPARTPAAPQAL
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629 >Rugamonas_rubra_1 |WP_093391227.1 HAMP domain-containing protein
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631 MNTFKNMSIGTRLGLGFLILALAMLITGISVWRLQNLSDATRAMMEVPLAKERMISDWYSKIDSAIRRTT
632 AIARSSDQSLVAYFADEAKASSAVSAEYQKKVEALVVDPEKELFGRIGEQRKIYLSRRDQVAKFKAAGQL
633 EEADAVFLKVFAPGSTAYLGLMQELLKMRGKIDATAQRIEAVAAQSRLLLLVLAALVLAFLGALCSWLLTT
634 GITRPLATAVQAARRVAEGDLTGHIIEVRSRDETGQLLQALQHMNASLLSIVSQVRSRGTGTEHIASSSTQIAAG
635 NLDLSQRTEEQASLEETASSMEELTSTVKHNADNARQANQLAASAAQVAVKGGAVVAQVVGTMESINSAS
636 KKIVDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKALIGDSVEQVN
637 QGGRLVADAGATMQEIVASVHRVSDIITEITAASTEQSAGIDEVYRAIGQMDSVTQQNAALVEQSAAAAEA
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639 >Herbaspirillum_sp._HZ10_1 |WP_088752409.1 HAMP domain-containing
640 protein [Herbaspirillum sp. HZ10]
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644 GITRPLERAVNAAESVAAGDLTTRIDADLAARRDETGKLLHALQAMTDNLARIVGQVRSRGTDAIATASREI
645 AGNLDLSARTERQAGSLEETASAMEELTSTVHQADNARQANQLAASASSVAQGGVVSQVVTMGMSIN
646 ESSRKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSASAAKEIKGLIDDSVA
647 KVGSGSELVGRAGSTMGEVVASVRHVADIVGEITAASREQSDGISQVNLAITEMDQTTQQNAALVEQAAAA
648 AEAMQEQAARLSEVVSQFKLAAQEAQAYAVPLGRPAVDITPELPAQR
649 >Massilia_1 |WP_047823722.1 MULTISPECIES: methyl-accepting chemotaxis
650 protein [Massilia]
651 MGLVANIKIGKRLGLGFALILAMTVAISAVGAWRMNKIADKTKAMMAVPLAKERLITDWYTLNFASIRRTA
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653 AEEAARILDKEFTPAQKYQDLLQDLVNMQRSTSMNDTAGAIDVNADSSSTNLIMILCACAVALGSVISWMLT
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655 GNLDLSSRTEEQAGALEETAASMEELTTTVRQNADNARQANQLAIAASAVATQGGAVVGEVITTMGAINDS
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662 MNLLRNVSIGVRLGLGFVILLFSMVIITGISVWRLHVDVATATRTMMEQPLAKERYISDWYGRIDSAVRRTI
663 AIARSSDTSLSGYFAEESKVSSASSAELQKKIEALIDLPEKAMFAGLLEQRKVYISSRDQVYKLGESQV
664 EAANDVFEKTFVPAAAKYQKMQDQDLLEHQRASIDTTAREIDAVANTSRNLLLVLAVLALAFGVVCAWVLT
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670 >Cupriavidus_gilardii_1 |WP_053823517.1 methyl-accepting chemotaxis
671 protein [Cupriavidus gilardii]

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673 KSSDPTLGAFFANETKHSVKAIADLRDKIEPLLSTDAEKQAFQTILRVREPYNASRDKITKLKQEGLTDEA
674 NTVLEKEFVPAGDAYLGEIQKLLDIQRASIDATARDINAVYQTARNRLIGLGVLVLAIGIAFAVWLTRGIT
675 RPLHRAVHIARTVAAGDLSARIDVDSKDETGQLLQALAEMNGNLLRIVNEVRLGTEAIATGTSQISVGNTD
676 LSQRTEEQAASLQETASSMEQLTSIVRQNADNAKQASRLAVDASDIAVKGGTVVGQVVDTMDEIHGASKKV
677 TDIIAVIESIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSQAQRSAATAAKEIKSLIDDSAERVEKGS
678 QLVSEAGQTMEEIVGAVKRVTDIMGEISAASAEQSAGIEQVNQAVTQMDTVTQQNAALVEQAAAAAGSLEE
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681 protein [Herbaspirillum lusitanum]
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685 GITRPIINSAVTISRVAEGDLTSDVQVGSKDETGQLLQALQDMNISLRGIVSNVRTGTDTIATASSEIAAG
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687 RKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSQAQRSAATAAKEIKVLINDSVEKVG
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690 >Janthinobacterium_sp._GW456P_1 |WP_086153639.1 HAMP domain-containing
691 protein [Janthinobacterium sp. GW456P]
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693 AIARSSDTTLGAYFAEEAKQSSVVSSELQKKIEALISSPEEKELFRLVSEQRKVYLDRAQVSKLKADGQE
694 AEAFAFGQIFVPGSTKYLKVVNDMLQHQQRASIDTTAREIDDVAKTSRNLTLAVLALGFGVVCALLTT
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700 [Duganella sp. CF517]
701 MNMLENISIGKRLAFGFTVILAFAMLITGIVSWRQLQGVASATADMMQVPLAKERLIGDWSSNIDSARRTT
702 AIARSTDTTLGYPYFADEAKASSAKSSDYQKKIEALITDADEKDLFARIGEQRKIYLSREKLTKLKAAGEL
703 EESNKVFESVFRPCTAAYQALVGDLLKMQRAKIDATAANIDAVAASSRNLLYVLAALVLTFGVVCALLTT
704 GIVRPLREAVVARRVASGDLTGHDASARDETGQLLAALKEMNASLLGIVTEVRSRGTDHITTSSEIAAG
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706 KRIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKALIGDSVDKVN
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709 >Ralstonia_sp._NFACC01_1 |WP_092969169.1 HAMP domain-containing protein
710 [Ralstonia sp. NFACC01]
711 MQLIRNMGIGKRLAFGFVVLAFSVVITAIWRLDNAATATRMMNEPLLKERLIGDWYANLVVGIRRTI
712 AVAKSADPTLGPYFAQEAASSKASGEYQKKVEALLSTEEKTLFAKIGELRKGYSARDAINAAKASGNP
713 DEAQRVLDQVFPANAYQDIMRQLLEVQRRSIDDIAKDIDASAAKSRTLLMVLEGLILALGLVFAYFLTV
714 SITRPLHVAVGIASRVAAGDLSVAAANSKDETGKLLQALADMTQQLVGTVGSIRVATESVAGAAGQIAAG
715 NMDLSTRTEQQAASIEETAASSTELTEAVKRNAENARQATS LAASAREMTEAGRVEVTAMVQTVSEVSTAS
716 KKIAEITGLIEGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSQAQRASGAAKEVKELIEASTGKVE
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718 MQEQSGNLRRAVSVFRLGAG
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728 LGSKLVADAGSTMGEIVASVQKVSMDISEITAASSEQSAGINEVNOAILSMDAVTQQNAALVEEAAAAAES
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731 protein [Herbaspirillum frisingense]
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778 EAEAHFKNVFAPGAAAYQGLMAELLQRQRSKIDAIGLEIERGADASRSL LIALTALVLVFGVVC SWLLTVG
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788 NQVLEKEFVPAGDAYLAEIQKLLDIQRGSIDATAREVDGIYVARNLSIALGVVLAIGIAFSVWLTVGIT
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830 ERLLTQVYMPATKAYVALIQKLLDLQRDIDATAAHIQDIHAQSRLLLTVLGLLALALGAACALWLTRGIV
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841 DEAKVVFENTFVPGSAKFQKFVQDLLLHQRASIDATAHDIDTMAITSRNLLLGLAVLALAFGTVCALLTT
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849 MNILGNMNIGKRLTLGFAIILAFSVVVAGMSLWRLEQVSSATREMMSDPLKTERIMGDWYTNLSSGIRRTL
850 AIAKSSDPSLGPYFAAEAAESTRSSTEYQKAVEKLLVTPREKELFQKIGEQRKIYLSRRDQIVKLKAEGKV
851 DEAMQLLDKTFVPAALYQQLMRDMVDLQRKIDIDDTAKEIDDIAAQSRVLILVLEGLILLGLIVLARYLTL
852 GITKPLHTAVTVSRKVAEGDLAQVQVSTRDETQQLLQSLRDMNDSLRGIVTNRVTGTDITSTASSEIAAG
853 NLDLSSRTEQQASSLEETASAMEELISTRQONADNARQASQLAHSASAVAEQGGGVVNVQVDTMGAINASS
854 RKIVEIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSASAQKEIKELINDSVEKVD
855 DGSRLVEQAGNTMQEVVSSVRRVTDIVAEISAASAEQTSGLIEQINLAITQMDQVTQQNAALVEEAAAAAES
856 MQNQAGQLMQMVSFRLSEGEPPVVRREIDVTPGTPLPG
857 >Acidovorax_cattleyae_1 |WP_092839683.1 HAMP domain-containing protein
858 [Acidovorax cattleyae]
859 MRNLSIGTRLAGGFALVGLMALMTTFGLWRLQSVQATHAMTQQPLANERMISDWYRYVDSAAARRTTAIV
860 KSSDPSLAFFAEDSAMTTRESARLVEKIEPQLDSPEEKAVWADIKARTAYLASRDQAVKAKAEGRADEA
861 ERLLTQVYLPATKAYVALIQQLLDLQRRDIDATAAHIQDIHAQSRLLLIVLGLLALALGAACAVWLTRGIV
862 RPLSEAVRVARAVAASDLTSHVTVSADETGQLLQALKDMNKSLAQVVGVRVAGTDSIATASNEIDGGNQD
863 LSSRTEEQASSLQQTAAAMEQLTSTVRHNADNARQASQLASSAAGTAARGGQVVAGVVDTMGAIHSSRKI
864 SDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRALAGRSAAAADIKALIGDSVSRVAEGS
865 SQVEEAGRTMDEIVQSVQRVNDLVAEISAASEEQSRGIDQVHQAVSQMDQVTQQNAALVEEAAAATGSLKA
866 QAGQLSQAVSVFRIIPAGTQQAQAAVAPAMDP SARHVPVGPPTPARAASGAVRAPAPVAPPRPAPARPPAAAQ
867 ALPRTAAPAAATAPKASRGSDDDWETF
868 >Acidovorax_sp._Leaf160_1 |WP_056665002.1 methyl-accepting chemotaxis
869 protein [Acidovorax sp. Leaf160]
870 MNNLKIGARLGGGFALVLMMLMFTAAGVWRLHTVAQATSEMTQQPLANERMISDWYRYVYSAARRTSAIV
871 KSSDPSLQGFFAADIATTTKEAAQLQORIEPLLDSAEEKALWGEIQKARTLYLSSRDQAVKAKADQAEAA
872 DRLLTQVFLPATDQYALIQRLLDMQRGSIDATARDIDNVFRQSRWLILLGTAALALGAACAWWLTRGIV
873 RPLSQAVRVARAVASSDLTSQVTVSSTDETQQLLQALKDMNASLAQVVGVRVRSMTDSIATASGQIDAGNQD
874 LSSRTEEQASALEETAASMEELTSTVKQNAENARQANQLAASASQTAAQGGQVVAGVVDTMKGINDSSRKI
875 SDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRALAQRSASAADIKGLIGDSVAKVEEGS
876 QQVAQAGRTMDNLVQSVQRVSDLVAEISAASQEQSAGIDQVHQAVSQMDSVTQQNAALVEEAAAATGSLKS
877 QASQLAAAVSVFRIDAGSQAAAQALRAAAATASVAPVAPRAVTALQRAPAVAAPAPRPAAPAAAAPAAKAAA
878 HPAASRLAPPKPRAAATPPSPAARGSDDDWETF
879 >Polaromonas_sp._OV174_1 |WP_092007234.1 HAMP domain-containing protein
880 [Polaromonas sp. OV174]
881 MSLKLNKIGMRLGLGFLAMLLMAFIAGIGIWRLQTVADATRDMMELPLAKERMISDWSRLVYVGVTRTSA
882 VAKSSDPSLAFFAKDSAASSLEASAFKLEPLLTSDAEKAGMQAMQDKRKPVAARDAIYKAKAAGDSE
883 EAARLIEVYLPFGASYQSALQDLVDLQRKSIDGMAGHVDELAQASRTLMGVLGLLATVFGVVCALLTRSI
884 TQPLSQALKLAETVASGDLSSSTIVVNSRDETQQLMQALKAMNDSLAKLVGEVRQGTDTIATASGQIAAGNQ
885 DLSSRTEEQASSLEETAASMEELTSTVKQNADNARQANQLAVSASSVAVKGGSVVSVQVVDTMGSINASSRK
886 IVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAAEVRNLAQRSAAAQKEIKTLIDDSVSKVEEG
887 SSQVAEAGKTMDEIVDSVKRVTDIMAEITAASSEQTSGLIEQINQAITQMDQVTQQNAALVEEAAAAAQSLQ
888 EQASGLSQVSVFKLDGAQAQPIHVAQARRAMPARSAKPGAAPRQPPTLKPAIAAPAAAAGDWETF
889 >Cupriavidus_sp._SK-3_1 |WP_035861449.1 methyl-accepting chemotaxis
890 protein [Cupriavidus sp. SK-3]
891 MKNLIGVRLGIGFGVLLSTFMTVFSVMGLHEVAQRTHDMMQPLAKERVVSDWYRLMHTSVRRTTAVA
892 RSSDPGLGAFFAAETKGSVEAIAALRDKIEPMLSSEAEEKAAFQTIQAVRKPYNDSRDKITKLKEEGSTDEA
893 NRVLEAEFVPAGNAYLAEIQKLLDIQRTSIDTTAQHINGIYETTRNRLIVLGLLVLAIGVAFSLWLTIGIT
894 QPLHRAVGFARKVAAGDLTSRIDVDSKDETQQLLQALNEMNGNILRIVTQVVRTGTESIAGTSQIAAGNTD
895 LSQRTEEQASSLQQTASSMEELTSIVRQONADNAKQASSLAVNASEIAVRGGEVVGQVVDTMDEINGASRKV
896 VDIIAVIEGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSLAQRSATAAKEIKTLIGDSAERVEKGS

897 QLVGQAGHTMEEIVGAVKRVTDIMGEISAASAEQSAGIEQVNQAVTQMDTQNAALVEQAAAAAGSLEE
898 QAQRLQAVSSFRLVAA
899 >Massilia_sp._NR_4-1_1 |WP_050408258.1 methyl-accepting chemotaxis
900 protein [Massilia sp. NR 4-1]
901 MNALNHISIGKRLAIGFAVILAFCLITGIGMWRLQOVAQATKMMETPLAKERMISDWHSRIDSAIRRTT
902 AIARSSDQSLGAYFAEESKASSAASAEQKKIEDLLQDEDEKALFAKSMEQRKVYLSRRDQVAKLKSAGEL
903 EPAQEVFEKTFVPGAAKYQSLVQDLLKMQREKIDATARHIEGIAINSRTLLLVLVSVLVLGFGAVCAWLLTV
904 GITAPLSRAVDAARRVASGDLGQIDVAGSDETQQLLQALKDMNQSLLNIVTEVRNGTDSINTSSSEIAAG
905 NQDLSSRTEEQASALEETASSMEELTSTVRQNADNARQANQLASAAASVAVRGGSVVTVNVGTMESINESS
906 RKIVDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSASAAKEIKELIGDSVEKVN
907 QGSKLVAEAGSTMEEIVASVHRVSDIISEITAASSEQSVGIEEVSRAIGQMDQVTQNAALVEESAAAAES
908 MQHQAHSLAQVVSFVNVGQMGKPALRLGR
909 >Cupriavidus_basilensis_1 |WP_006163414.1 methyl-accepting chemotaxis
910 protein [Cupriavidus basilensis]
911 MKNLIGVRLGIGFGVLLSTLMTVFSILGLQDVASHTHMMQPLAKERVSDWYRLMHTSVRRTTAVA
912 RSSDPSLGTFFAAETKGSVDAIAALRDKLEPMLTSDAEKAAFKTIQTVRKPYNESRDKITKLKEAGQTDEA
913 NQVLDSEFVPAGNAYLAEIQKLLDIQRASIDQ TALAINIYLSARNRLIALGVLVLAIGVAFSAWLTAGIT
914 APLHRAVGFARKVASGDLTSHIRSDSKDETQQLLRALGDMNGNILRIVTQVVRTGTESI ASGTSQIAAGNTD
915 LSQRTEEQASSLQETASSMEELTSIVRQNADNAKQASSLAVNASEIAVKGGMVVGVVDTMQEINGASRKV
916 ADIIAVIEGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSATAAKEIKSLIGDSVERVEKGS
917 QLVTTAGQTMDEIVGAVKRVTDIMGEISAASAEQSAGIEQVNQAVTQMDTQNAALVEQAAAAAGSLEE
918 QAQRLKEAVSTFRLVAA
919 >Herbaspirillum_seropedicae_1 |WP_069374298.1 HAMP domain-containing
920 protein [Herbaspirillum seropedicae]
921 MNIIIGNMNIQRRLTLGFALILTFSSIIAGIGLWRLDHVAQATREMMAEPLKTERLMADWYTNLVAGIRRTI
922 AIAKSSDPALGPYFAAEVAASSKSSGEYQKQVEALLSTPEEKALFQKIGELRKLYLSSRDEINKAKAAGNT
923 EEAMRILDQVFPNATAYQDTMRKLVDFQRKEMDDTAREIDATAAKSRTLILVLEGLILLGGVVFARYLTL
924 GITKPLHRAVDVSRVAEGDLSSEIAVTSRDETQQLLQSLKDMNQSLRGIVSNVRSRGTDTISTASSEIAAG
925 NLDLSSRTEEQASSLAETASAMEELIIVRQNADNARQASQLANSASAVAEQGGGVVSQVVDTMGAINASS
926 RKIVDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSASAAKEIKELINDSVGKVD
927 DGSRLVEQAGNTMQEVVSSVRRVTDIVAEISAASTEQTHGIEQINLAITQMDQVTQNAALVEEAAAAAAS
928 MQTQAGRLMQMVSFRLSEREPLVRREIDVTPSSPVLQ
929 >Massilia_sp._Leaf139_1 |WP_056332738.1 methyl-accepting chemotaxis
930 protein [Massilia sp. Leaf139]
931 MGFISNIKIGKRLGLGFALILAMTVLIACAGIWRLENEVADATRMMMAAPLTKERLITDWYSLNFASIRRTA
932 AIVKSTDPALGPYFKEDAAASVKKAAELLKEIEPLIAGDAEKALFAKILEQRKLYSASRDGAVKAKAAGNE
933 EEAAKLLDEKFTPAASKLYQELLHELVMQRTSIDATAKAIDASAGRSTTIIAALTAVAVLLGAALSWLLTN
934 GITRPIRDALELAETVAGGDLTRNIDASAKDETGALLRALRHMNDSLKIVTQVRNGTDTIATGSAEISAG
935 NLDLSARTEQQAGALEETAASMEELTTTVRQNADNARQANQLSIAASEVAAQGGAVVGQVITTMGSINESS
936 RKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSASAAKEIKVLIGDSVDKVD
937 VGAKLVDQAGATMEQVVSIRRVTDIMAEITHASQEQTGGIEQVNQAIGQMDQVTQNAALVEEAAAAAGS
938 MQDQAAKLAQVVSFVFLSGPALGAPAVASARTAVPARALARSAPAVRVAKAAPAKAPARVSEDEWETF
939 >Oxalobacteraceae_bacterium_IMCC9480_1 |WP_040727868.1 methyl-accepting
940 chemotaxis protein, partial [Oxalobacteraceae bacterium IMCC9480]
941 MIPQFIRDLTIGKRLGLGFVLLMLSMATTAIGITRLNAVASATRELLKEPLATERLVSDWNRNISAGVRR
942 TSAIARSSDPSLATFFAEDQASSTKNSSELQKAIGERMRTVREKAVFAEVGELRKVYLSRRDQIVALKKEG
943 KLDEANQLLDQFTFPAKKNYLIKIDELQGEERRQIDQTAIDIEASYEAGRNLMLILAVVMLIQGVLVSWLL
944 SRSITGPLANAVRFAREVASGNLTATIHSRRRDESGQLTDALQTMVTNLSTLVTVGRIATDNI SVSAQQIA
945 SGNADLSNRTEQASSLEETASSMEELTSTVRQNADHAQQATQLAVVASGVAVRGGAVVRQVVTMAAIND
946 SSRKIVDIIG
947 >Acidovorax_ebreus_1 |WP_012655282.1 methyl-accepting chemotaxis
948 protein [Acidovorax ebreus]
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950 KSTDPSLQGFFAADTATSTRESAELQKRIETLLTSEEEKALWADIQKARVTYLSSRDQAVKAKAEGQLEEA
951 ERLLTQVYLPATDQYVALIQRLLDMQRSRIDATAQGINVYTYGQSRLLVIVLGVGLGAGALCAWWLTRGIT
952 RPLAQAVQVARAVAANDLTSRVQVDSRDETQQLLQALQEMNASLSQVVARVRSRGTGDIATASSQLDAGNQD
953 LSSRTEEQASSLQETAASMEELTSTVRQNADNARQANQLASSAAQTATQGGQVAVGVVQTMGAINASSRKI

954 SDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRLAQRSAAAAKDIKGLIGDSVAKVEEGS
955 HQVEEAGRTMDAIVQSVQRVSDLVAEITAASQEESAGIEQVHQAITQMDQVTQQNAALVEEATAATGSLKA
956 QAGQLAQAVSVFRVEGLQAAQTATATATAAAAAPAPLRPPAPATTTTTTTKPPAAARTLAAPARPPAAAKAAP
957 ATARHSDDDWEAF
958 >Massilia_putida_1 |WP_075792765.1 HAMP domain-containing protein
959 [Massilia putida]
960 MGFVANMKIGRRLGLGFALILAMTVAIAVIGAWRLTEVAGSTRAMMAVPLTKERLITDWYGLNFASIRRTA
961 AIVKSTDPPLGAYFKDDSAASVKRAAELLKQIEPLIAASGPEHDLFARILEQRKAYSASRDGAVKAKADGN
962 AEEAARILDQGFTPAAQQYQGLLQDLVAMQRASMDATAAIDANATASTRILIVVFSTCALLLGAVASWLLT
963 RGIVLPIRAAVAVAETVAAGDLTRTIEAHTHDETGALLRALRHMNDSLGVIVSQVRGGTDTIATASREISA
964 GNLDLSSRTEQQAGALEETAASMEELTTTVRQNADNARQANQLAISASEIATQGGAVVGEVVTMGINAS
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966 NAGTKLVDRAGATMSDVVDSIRKVSIVAEITSATQEQTGGIEQVNQAIGQMDHVTQQNAALVEEAAAAA
967 SMQDQAAKLAEVVSVFKLERGHSALPVPALPRAALRAPAAVR
968 >Massilia_sp._LC238_1 |WP_036214233.1 methyl-accepting chemotaxis
969 protein [Massilia sp. LC238]
970 MGFISNIRIGRRLGLGFAVILAMTLLIIVAGISRMNDVAASTRDMMAVPLTKERLITDWYSLNFASIRRTA
971 AIVKSADPELGPYFKEDAAAASVKKAAELLKQIEPLIAGEKEKALFAKILEQRKTYASRDGAVKAKADGNA
972 EEAARILEQGFTPAAQKYQDLLHELVLVQRSSIDQTAKAIDESARHNSTVIVSVAAGAVLLGAALSWLLTT
973 GITRPIHAAVQAAETVASGDLTGHIKADTKDETGALLRALRNMNDSLKIVSEVRSMTDTIATGSAEISAG
974 NFDLSARTEQQAGALEETAASMEELTTTVRQNADNARQANQLAITASSVALDAGNVVGVVITTMGSINDSS
975 KKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRLAQRSAAAAKEIKTLIGDSVEKVE
976 AGTRLVDQGTMEQVVTSIRRVTDIMAEIASASQEQTGGIEQVNQAIGQMDQVTQQNAALVEESAAAAAS
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979 [Massilia sp. PDC64]
980 MGLIANMKIGRRLGLGFALILAMTVAIAAVGAWRLNEVADSTKAMMAVPLTKERLITDWYGLNFASIRRTA
981 AIVKSNDPPLGYPYFKEDAAAASVKKAAELLKQIEPLIAASGPEHDLFAQIVEQRKVYSASRDGAVKAKADGN
982 ADEAARILDQSFPTAAEKYQRLQLDLVAMQRTSMDATAAIDANAMASTRLIAIFSSCALLLGAIASWLLT
983 RGIVLPIRAAVAVAETVASGDLTHTIEAHTQDETGALLRALRHMNDSLGVIVGVQVRGGTDTIATASREISA
984 GNLDLSSRTEQQAGALEETAASMEELTTTVRQNADNARQANQLAIAASEIATQGGAVVGEVVTMGINAS
985 ANRIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSQAQRSAAAAKEIKDLIAASTANV
986 DAGTKLVQAGATMEQVVDSIRRVTDIMGEITSATQEQTGGIEQVNQAIGQMDQVTQQNAALVEEAAAAA
987 SMQEQAAKLAEVVGVFKVERGFSLAAPVAAPVARPALPRASAPAPAPKRPVKRAAPVAAGDWEFF
988 >Janthinobacterium_sp._PC23-8_2 |WP_094444369.1 HAMP domain-containing
989 protein [Janthinobacterium sp. PC23-8]
990 MNLLRDVSI GMRLLGLGFAGILLFSILITGISVLRHLNVATDTRLMMEQPLAKERYISDWYKIDSGIRRTA
991 AIARSSDTTLGAFFADEAKASSVVSSELQKKIEALLSTPEEKEMFRQISEMRKAYIISRQIYKMKKDGQF
992 DEAKVVFDA AFLPGSAKFLKVTQDLLQYQRTSIDATAHDI DAMAVASRNL LCLAVLALAFGGVCAWLLTT
993 SIVHPLRAAVSVARRVAAGDLTAQIDASAQDETGQLLLALKDMNASLLRIVGEVRSMTDSIATSSTQIAAG
994 NQDLSRTEQQAGSLEETASSMEELTSTVKQNADNARQANQLAASAAQVAVKGGEVVAQVVGTMESINSSS
995 NKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKALIGASVEQVN
996 AGSMLVAQAGSTMNDIVASVQRVSDIITEITAASSEQSVGIDEINRAIGQMDAVTQQNAALVEEAAAAAES
997 MQNQAHLKLAEVVSVFKLDELSALR
998 >Massilia_sp._Root335_1 |WP_056443095.1 methyl-accepting chemotaxis
999 protein [Massilia sp. Root335]
1000 MGFLANMNI AKRLGVGFALVGLTLVIATAAVWRLNAIADATRMMMAVPLAKERMLTEWHMQTFAAVRRRTA
1001 AIVKSTDPPLVEFFKADGVKTATRSTELVKQIEPLLDGPEEHALFNRIVELRKAYTDSKVKAIKARADGDA
1002 EAAERILNQEYVPTSDAYEGKQGGEMVKMQQDRIDAIARKIDNANRNSARMIIVLAGVAVLFGAICAWLLAR
1003 AIVDPIRQAVDVAEKVAGGDLTQRIDATGTGETAALLRALRHMNDGLSVIVSQVRSGTDTIATASAEISAG
1004 NMDLSSRTEQQAGSLGTTASTVEQLTGTVRQNADNARQASQLSIAASDIIVQGGAVVDQVVQTMGAINSSS
1005 KKIVDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRLAQRSAAAAKEIKQLIVDSVGKVE
1006 DGTKLVQAGMTMSEVVDSIRKVSIVAEIASASGEQSTGIEQVNRAIAEMDSSTQHNAALVEESAAAATA
1007 LRDQADKLAEVVSLFHLSTQAAAAPKAVAAPARAPARAVVPPV PARAGAGKPAPGRAAAAAAEWDTF
1008 >Collimonas_sp._OK242_1 |WP_092353905.1 HAMP domain-containing protein
1009 [Collimonas sp. OK242]

1010 MKIANLKVGTMRGIGFAIILALS SVSTVIGISNLRQVAMATQQMMEKPLVKERLVS DWGLTTS AIVRTSL
1011 IVKSTDGSLATTF AEDIDASVKKGGELQKTLEPLLI SDAEKELFKS IMGLREKYQQAKVLAMKAKQDGNSE
1012 ESSRIYNDMFLPNAKNYKGLLDEL LSLQRKSIDQ TGREVAQLYSRSFNL MVLLGVLIVALGAVCAFLI SRS
1013 VTRPLGEAIKVAQTVASGNLSSRIEVKTT EETGQLMQALKDMNDSLLKVVGDV RIGTDTIATASGQIASGN
1014 QDLSSRTEQQASSLEETAASMEQLTGT VKQNADNARQANQLAVSASGVAVKGGGVVSQV VETMGSINTSAR
1015 KIVDIIIGVIDSIAFQTNILALNA AVEAARAGEQGRGFVAVASEVRNL AHRSAAAAKEIKALIDDSVEKVDI
1016 GVKLV DQAGTTMGEIVDSVKRVTDIMSEITA ASEEQTAGIEQVNQAIMQMDQVTQQNAALVEEAAAAAASL
1017 QDQAAHLVQVVSFNTGGMAESGGASSKTTNRLSPHAATSGRIA AVPR SARQA AVTNLKLPLKRVANVTAAT
1018 TADDEWATF
1019 >Brenneria_goodwinii_1 |WP_048638604.1 methyl-accepting chemotaxis
1020 protein [Brenneria goodwinii]
1021 MKNFRIGIRLAVGFGVLIVFSLVMLVSGVYQLRQIDQSTQRMMQEPLNKERLVADWFSVISASVQRSTAVA
1022 RSSDGLAELFAADNASATKES SARQE QFAKLVS SPEEKALFDKLSEVRQVYIRARDAISAANANGQREQA
1023 QQLFEQDFRPSRNYLDTLQALRDQQRATINQLGADISR NAGNGYLFLGIIIGLLITVAGSLLAWTFTRSIV
1024 RPLENALQITNAVAGGDL MHNVRGEGRDETAQLLHALQEMTIQLRTIVGEVRQGSESIAGASSQIAAGNLD
1025 LSSRTEEQSSALQETAAAEQLASTVRQNAENAKQANQLAQSTTGQAQAGGQLMNDVVQTMGAIDTSSRKI
1026 VDIIISVIDGIAFQTNILALNA AVEAARAGEQGRGFVAVAGEVRSLAQRSASAAKEIKELIDHSVQTVQTN
1027 RLVEQAGTSILDIVNGVRKVS DLVGEISSASQEQSLGIDQVNI AVNQMEQTTLQNAALVNEASAATQSLQQ
1028 QAEQLEQVVSFRLTEEQQISSSAAAASRSAPAATAPRAALALKPAADAKSAEGGWSSF
1029 >Pseudogulbenkiania_ferroxidans_1 |WP_008952658.1 methyl-accepting
1030 chemotaxis protein [Pseudogulbenkiania ferrooxidans]
1031 MRFKFNLTIVGQRLGVGFALVLSLLITIT ALGVWRLHEVALATQGMVQVPIAKERLVS DWYTNIVAGVRRST
1032 AVAISKDESLAQFFAEDQKYSTQQNNILQKQIEALLYLKEEQALFAEIRQKRQRF LQARDSMTNAKKAGRG
1033 ELAEQLFHSQFLPASKSYLEKMQAFLRLQRREVD SHARYVDGVYRESRIWMLILG VGAVLLGIIAAWA IAR
1034 SITRPLRQAIEVAYQVAAGDLTVKFKTCASDETGNLLRALGEMSDGLAKAVKRVRVQAE EEAANMTAQIASA
1035 SKQIAQRSQTQSTTAASTAVAVEQISTG IASISQRANQLLELTQAGHAQVQEGNRAMSLMEGEIRNTEQSV
1036 EDIAISVHKFVASVRSITDMTGQVKSIAEQTNLLALNA AIEAARAGEAGRGFAVVADEVKLA EESASSAC
1037 RIDEITATLNRQSTTVETFLKSGQHALHASRQYLD SVICVLSASGESVEQTSQEVMMV MATSVQGGQAEASQD
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1039 >Herbaspirillum_rubrisubalbicans_1 |WP_058896090.1 methyl-accepting
1040 chemotaxis protein [Herbaspirillum rubrisubalbicans]
1041 MNILGNMNI GKRLTLGFAVILAFSAVVA AISLWRLEQVASSTREMMNAPL KTERLVADWYTNV NAGIARTL
1042 AIAKSADASLGPFYFSKDVTASSKMSSEYQKQIQ TLLSTPEEKALFDKIGEQRKIYLSRDEI IKLKAAGNV
1043 EEAMRVL DKKVFPNAAVFQQLMRQLVDIQRKEMDESAMQID AISAQSHIIILVLEGLILL LGIVLARILT L
1044 GITKPLQNAV VVSRKVAAGDLSASVQVHSQDET GQLLQALKDMNDSL RGI VSNVRS GTDTI STASSEIATG
1045 NLDLSSRTEEQAGSLAETASAMEQLISTVRQ NADNARQASQLAQSASSVAEQGGGVVSRVVD TMGAINASS
1046 RKIVDIIIGVIDGIAFQTNILALNA AVEAARAGEQGRGFVAVASEVRSLAQRSASAAKEIKELIDHSVAKVG
1047 DGSRLVEQAGSTMQEVVSSVRHVTDIVAEI SAASAEQTNGIEQINLAI TQMDQVTQQNAALVEQAAAAAAS
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1049 >Herbaspirillum_rhizosphaerae_3 |WP_050475649.1 methyl-accepting
1050 chemotaxis protein [Herbaspirillum rhizosphaerae]
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1052 AIAKSSDPSLGAFFAEDAATSTKLSNEQQKALEALLTSDREKELFAQLSAVRKRYVAARDAITKAKTDGQV
1053 EEANRILEKVFVPEAKGYLDSLQQLLDLQRSS IDQIAAS IHELYMTRNLLI AFGVLLFVAGW MFAWRLAL
1054 SITRPLNQAVGIAETVAAGDLTSRIDTSRKDE TGKLLLALKTMNDNLQRIVGQVRS GTDTI ATASSEIATG
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1056 KKIVDIIISVIDGIAFQTNILALNA AVEAARAGEQGRGFVAVASEVRSLAQRSASAAKEIKELIDNSVQKVD
1057 SGSKLVEQAGATMTEVVASVRRVTDIVGEI SSASQE QSDGIEQVNRAIAQMD ESTQQNAALVEQAAAAAQS
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1060 >Herbaspirillum_hiltneri_3 |WP_053195617.1 methyl-accepting chemotaxis
1061 protein [Herbaspirillum hiltneri]
1062 MNFFANMNI SKRLNLGF AII LFS AIAVIALSIWRLHTVAETTQAMMEKPLAKERLVS DWYRTIHTSVRRTT
1063 AIAKSADPSLSAFFAEDAATATKLSNEQQKTLEGLLSSDKEKALFAQLATVRKSYIAARDAISKAKADGNV
1064 EEAARVLAKDFPAAAKGYLDSLQQLLDLQRSS IDDI AAGIHDHYTRSRNLLIACGALLFIAGWVFAWRLAL
1065 SIIIRPLKQALGIAETVAAGDLSSHIDTSRKDE TGKLLLALKTMNDNLQRIVGQVRS GTDTI ATASAEIASG
1066 NMDLSTRTEQQAGSLEETASAMEELTSTVKQ NADNARQANQLAVSASEVAVQGGSVVGVVDTMGAINASS

1067 KKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRS LAQRSASAAKEIKELISDSV DKVD
1068 SGSRLVEQAGATMAEVVASVRRVTDIVGEISSASQEQSTGIEEVNRAIAQMDESTQQNAALVEQAAAAAQS
1069 LQDQAATLTQVVGIFTLDSGHAVGNSAALAPAKPKPAIVATGAASVKSLPRKPMPI SAKTAVSAPAATPKR
1070 LPAAVSDDDWEQF
1071 >Acidovorax_sp._MR-S7_1 |WP_020226741.1 methyl-accepting chemotaxis
1072 protein [Acidovorax sp. MR-S7]
1073 MKNLNIGTRLGGGFALVLLMALMTAFGVWRLSAVAQATSDMTHQPLAVERMISDWYRYVYSAARRTTAIV
1074 KSTDPSLGEFFAAETATSTRESAELQKRIEGLLQRDEEKALWAEIQKARTGYLSSRDQAVKAKTEGRSEEA
1075 ERLLTQAYLPATEQYSALIQRLLDQMQRASIDATAQQIGATYAQSRRAWLIALGALGVALGAACAWWLTRGIT
1076 RPLAQAVQVARAVASSDLTSRPAPRASDETGQLLQALDDMNASLSQVVARVRQGADS IATASSQIDAGNQD
1077 LSSRTEEQASSLQQTAA SMEELTSTVRQNAENARQANQLASSASQTAAQGGQVVAGVQTMDAINASSRKI
1078 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRS LAQRSASAAAKDIKGLIGDSVTKVDEGS
1079 HQVAEAGRTMDAIVQSVQRVSDLVAEITAASQEQSAGIDQVHQAITMMDQVTQQNAALVEEATAATGALKA
1080 QAGDLASAVSVFRIEGGQSARAAAPAPRPAPAPIAARAAPAPAPVARPAAPKALAPVKAPAAARGTDDDWE
1081 SF
1082 >Janthinobacterium_sp._Marseille_1 |WP_011979309.1 methyl-accepting
1083 chemotaxis protein [Janthinobacterium sp. Marseille]
1084 MIFFSNMKIGARLMLGFGVVLALSIAIAADGIRQLHAVSAITRSMLELPIAKERMVSDWAAITKASIARTI
1085 GVAKSADPALAQFSAKFAADDSKQSMEEIIQKLEPLLNTDQEKELYAKILDVRKSF LAGREGVMKLTKEGKE
1086 AEA AKYFDTTFLPAADSFKNHFTFEFVELERKQMDAGTAQLSDVEAASTRQLMLLSAMPLAFGIFCAWRLTI
1087 GITRPLKTAVDAARRVAGGDLTNDIKAESKDECGQLLAALKDMNDGLQRIVGEVRLGTETITTTASNEIAAG
1088 NLDLSRTEQQASSLEETASSMEELTSTVKQNADNARQANQLAVSASEVALKGGDVVSQVVTMSSINESS
1089 RKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVATEVRS LAQRSASAAKEIKALIGDSV GKVD
1090 TGNKLVAEAGATMDEIVNSIRRVTDIMGEITAASQEQSAGIEQINQAIQMDHVTQQNASLVEEAAAAAES
1091 MQDQARKLGQVVGAFKLDNAQEANPPRASGVTRLAPKPAAGSAGLAVAAPLPQRRANGALPAGDEWEQF
1092 >Albidiferax_sp._OV413_1 |WP_092754252.1 HAMP domain-containing protein
1093 [Albidiferax sp. OV413]
1094 MPSFIAGLSVAKRLGLGFALVVLVSVITII FGISRLNAVAEAAQYMVASPIKTERIVSDWYRNIHTGVRRT
1095 GAI AKSNDPAVATYFAEDQAASTKSSSEFQKQVELLMDTDVEKTLFKQISEERKNYILVRDAILD LKKEGK
1096 AEEASQMLDQKFTPASKAYMSKMEELLNTQRKDI DDQSRTIQDSYATSRNLMVALGVVSVLLSIVIAWLLS
1097 GTITGPLAQASVIARQVASGDLTARIDTQRSDELGQLLTS LKTMQAGLVQV VANVRSGSES VATASAQIAE
1098 GNNDLSARTESQASALEQTAASMEELSSTVKQNADNARQANQLAMSASTVAIRGGEVVTQV VETMKGINES
1099 SRKISDIIQVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRS LAGRSAAEAAKEIKNLIGASVDRV
1100 AQGTALVDQAGSTMTEVVNSIRRVTDIMGEISAASNEQSLGVAQVGEAVTQMDQATQQNAALVEEMAAAA S
1101 SLRTQAQDLVQVVAVFKLGQHDGAQGLSLGFNR
1102 >Rhizobacter_gummiphilus_1 |WP_085752380.1 HAMP domain-containing
1103 protein [Rhizobacter gummiphilus]
1104 MNLSIGKRLALAFGLVLLLTAMITLLGLWRLQGTSQATAEMMAEPLTKERLIGDWYRNIQTGVRRTTAIV
1105 KSNDPALATFFAAEEKASSKASGEYQKSI EALLRTDEELALFKSISEHRKVYLSRDEISKFKKGDGVAQA
1106 TKVFDDVFTPASNAFIADVQKLLDRQRESIDASASRIHDTNASSRNLI LALGLLAVVVGGFVAVVITRGVT
1107 GPIASAVSAAQRVAAGDLGQSIDSTARDETGVLLRALKDMQGR LQTVLRDVRD NAEGVATASAEIASGNSD
1108 LSARTEQQASALQETAATMEQLGITVRNNAENANHANQLAREANTLATQGGEVVGVVVRTMSDINAGSRKI
1109 GDIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRS LAQRSAAAKEIKTLINSSVEQVEQGT
1110 ALVDQAGARMGEIVGAIQRVSDIVAEISSASAEQRSVGVGQIQAVDQMDQATQQNAALVEEGAAAAESLKH
1111 QAARLLQTVGVFKLAAA
1112 >Massilia_psychrophila_1 |WP_099916041.1 HAMP domain-containing protein
1113 [Massilia psychrophila]
1114 MKNIKIGPRLGIGFALILAMTVFIAIVGVWRLNDVAASTHAMMVQPLTKERLFTDWYQGNFGAIRRTQAI I
1115 KSADPELSAYFKEDGAATAKRVVELTKQAEPMIQGA AEKSLEYEKIMAQRKLYSAARD DALKAKAAGDNEAA
1116 VKLLDQVYTPQAKAYQDMLQDMVTLQRGEIDATAHAIDATASLSTKLIMILTACAVAVGVGFSWLLTIGIT
1117 RPIRQAVELAETVAGGDLTRTIVATSND ETGALLRALANMNSLVGIVTEVRTGTDSITTASNEISAGNHD
1118 LSARTEQQASSLEETAASMEELTSTVKQNADNARQANQLSQTASDVAIQGGAVVGVIVVTMGSINESSRKI
1119 VDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRTL AQRSASAAAKEIKTLIGNSVDQVDAGA
1120 KLVDQAGATMEQVVASIRRVTDIMGEITIASAEQTDGIEQVNQAI AEMDQVTQQNAALVEESAAAAESMQQ
1121 QAGRLAQVSVFKLAQA AKAEPRLRPVPASAVRAAPRTRAI AAPQPKRTARGAGSDEWEEF
1122 >Herbaspirillum_sp._meg3_2 |WP_094563173.1 HAMP domain-containing
1123 protein [Herbaspirillum sp. meg3]

1124 MNIIGNMKIGKRLTLGFALILAFSIVITGIGIWRLQAVSDATRDMSQPLLKERLIGDWYANLASGIRRTI
1125 AIAKSSDPALGPYFAAEAAAASSKSSGEYQKKVEALLETDEEKKLFQQIGEQRKIYLVSRDDINKAKAAGNI
1126 EEAERVLEKVFVPASTAYQDTMRKLVLELQRKDIDETALHIDVIANESRVLLLVLLEGLILALGVLCAWYLTV
1127 GITRPINTAVVLSRRVAEGDLTANVNVNSKDETGQLLQALQDMSNSLRGIVTNVRSRGTDTIATASSEIAAG
1128 NLDLSSRTEQQASALEETASSMEELISTVKQNADNARQANQLAVSASEIATQGGGVVGVVDTMGAINSS
1129 RKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSQAQRSAAAAAKEIKVLINDSVEKVG
1130 NGSKLVEQAGATMQEVVDSVKRVTDIVGEISSASQEQTMGIEQINHAITQMDQVTQQNAALVEEAAAAAAS
1131 MQTQADSLAQLVSVFTISAINGNPALPQARRTIDITPKEPRLS
1132 >Brenneria_sp._EniD312_1 |WP_009112183.1 methyl-accepting chemotaxis
1133 protein [Brenneria sp. EniD312]
1134 MKNYKIGIRLGVGFGVLIVFSLVMLACGIYQLHQIDQRTROMMQEPLOKERLVTDWYGVISASVQRTTAIA
1135 RSSDDALSELFAAENAVASTGSSERQAEFAGRIAGPQEKALFDKLNQVRSYIKVRDLIITVKSSGQLEQA
1136 LTLFEQDFRPAARNYLDLTLQALRDFQRASIDQLGSDISRGASNGYLFLGIIGLLIAVAGSLLAWVLTRSIV
1137 RPLEHAVRITNAVADGDLTQEVPRPEGRDETAALLHALRNMTVRLRTIVGEVVRQGAASIAGASSQISAGNLD
1138 LSSRTEEQSSALQETAATAIEQLASTVQRNADNAKQANQMAQSTAGQAQSGGQLVSEVVQTMGAIDTSSKKI
1139 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSQAQRSASAAAKEIKELIDHSVQTVESGN
1140 RLVEQAGSSILEIVGGVRKVSVDLVEISAASQEQSLGIDQVNVAVTQMEQTTLQNAALVNEAAAATQSLQQ
1141 QAEQLERGVSVFRLTGEQQISGGSSAAGKPASAATAPSVALEHKPATVGGKSAASGEGNWTTF
1142 >Collimonas_sp._OK607_1 |WP_092438538.1 HAMP domain-containing protein
1143 [Collimonas sp. OK607]
1144 MKIANLKVGTMRGIGFAIVLALSVMSTVIGISNLRQVAMATEQMMEKPLVKERLVSDWGVLTTSIAIVRTSF
1145 IVKSTDGSLATTFEAEDIDASVKKGSELQKTLPLLTSDAEKELYKSIKVLREKYQQSKVLAMKAKQDNGE
1146 ESSRIYNDVFLPDSKNYKQQLDELLESLQRKSIDQGTREVAQLYDRSFNLMVLLGVLMIALGAVCAFLISRS
1147 ITRPLGEAIKVAQTVASGDLSSHIEVKTDDTETGQLMQALKDMNDSLLTVVGDVVRTGTDTIATASSQIASGN
1148 QDLSARTEQQASSLEETAASMEQLTSTVKQNADNARQANQLAVSASGVAIKGGGVVSQVVTMGSINTSAK
1149 KIVDIIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSQAQRSAAAAAKEIKTLIGDSVEKVDV
1150 GVKLVQAGTTMGEIVDSVKRVTDIMSEIAAASEEQTAGIEQVNRQAQMMDQVTQQNAALVEEAAAAAASL
1151 QDQANLVNVVSVFNTGEMSMGSAPLKTISSSPAATAASRIAIAPRNIRQSAATNVKPLKRVTKVAAVA
1152 TAADGEWATF
1153 >Acidovorax_sp._62_1 |WP_099742278.1 HAMP domain-containing protein
1154 [Acidovorax sp. 62]
1155 MHIHLSIGSRLALAFSAVIFLTAAILGIGIWQLQAIASETDMAMERPLTKERLVSDWYRTIHTSVRRTTA
1156 VAKSSDPSLATFFAPENAEASRNSTEQKQIEALLETPEEKALFATLSQARQRYIAERDAVNKAKADGQAE
1157 EAEKRFNSDFRPAAGAYLDSLQALLDQQRSTSINTAAANVQSGYTRGRVLMIGLALALLTATALAYIITRS
1158 ITRPLHRAVVVAQTVASGDLSTQAGAAASARDETGQLLRALDAMSEQLRSTVGVQVRQGAETIALASSEIAR
1159 GNLDLSSRTEEQASALQETAASMEQMTATVQRNADNARQANQLAQDASSLAQRGGTVVGNVSTMGGIHTA
1160 SRKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRTLAQRSAAAAAKEIKGLIDDSVQVQV
1161 DAGNRLVEEAGTVIRDVSVGVQVRVTHIVGEISAASQEQTGGLQVNRRAIAQMDQVTQQNAALVEEAAAATG
1162 SLESQATQLVQAVAVFSLGNADTGRQLRHPGAALSIAA
1163 >Oryzisolibacter_propanilivorax_1 |WP_091566973.1 HAMP domain-
1164 containing protein [Oryzisolibacter propanilivorax]
1165 MKNLSIGTRLAAGFALVLLLMACISGFGVWRLQTVASAQMTQQPLAMERMISDWFYVSAARRTSAIV
1166 KSSDPSLVEFFKADTAMTTSKAAELQKRIEALLDSPEEKALWSDIQQARTQYLNARDQAVQAKAEGRTDEA
1167 ERLLQTVQPATAYIDQIQRLLDLQRARIDATAQGIQATYEEESRWLLALGLLALAAGALCAWRLTRGIT
1168 RPLAQAVQVARAVAANDLTTQVQVHGSDETGQLLQALHDMNASLTRVVAQVVRTGAEGIATASSQIDAGNQD
1169 LSARTEEQASSLQOTAASMEQLTGTVQRNADNARQANQLAASAAQTAAQGGQVVAGVVQTMGAIHDSRRM
1170 ADIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSQAQRSAAAAAKDIKTLIDDSVAQVQVQV
1171 QVQVDEAGRTMQTIVSNVQVRVSDLVAEITAASQEQSSGIDQVHQAVTQMDQVTQQNAALVEEAAAATGALKA
1172 QAGQLAAAVSVFRIEGGQAPAAAAAMAATMPAAPRRQPATAPRPAPAPKAPVASAARPLLSPTSAPAAAASA
1173 RRNDDWESF
1174 >Paraburkholderia_nodosa_1 |WP_081772006.1 HAMP domain-containing
1175 protein [Paraburkholderia nodosa]
1176 MDVPSPCVCIFQKKREYVVTFRNLSIGHRLGLGFALVLLALTVSTGVGIYRLQTVADATHTLMSVPLAKER
1177 MISDWQRYLYGGIRRTTAAIAKSSDASLAGFFAADADSSTKKSLLVVKKIEELADSEEEKALLENINHIRTV
1178 FTDARDQVSAAKKAGDQDTAKRSLEEDYLPAAQAYEDAVQKLLDHQRHAIDMAAQHVDEIASTSRALILL
1179 AILAIGLVVCAWLLTKSITLVPVGRAVAAARRIADGDLSDGGALVRNGERTRDEAAILLDALRLMNNENLAH
1180 IVSQVRGGTDAIASASTEIAAGNHDLSTARTEQAASLEETAASMESELTATIRQNLNENARQADQIGTHAVGT

1181 VEKGSTAVEHLVATVVKISDSSARIADIITLIEGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRS
1182 QRSSAAAKEIKELIEASVESVREGVQRADEVGQNMVAVKRAIRRVADLVAEITAASEEQTRGVEQVDAAVS
1183 QMDQVTQQNAALVEQAAAAAQSMDDQAGQLKASVAVFKLADVCAYPVS
1184 >Herbaspirillum_sp._YR522_2 |WP_008115731.1 methyl-accepting chemotaxis
1185 protein [Herbaspirillum sp. YR522]
1186 MNFIGNMKIGKRLTLGFAVILAFSVVIAGIGVWRLLENVSTATREMMSAPLMTERLLSDWYTNLATGIRRTI
1187 AIAKSTDPALGPYFAEAAAASSKSSGDYQKKVEALMSSPEELALFAKIGDLRKYVLSRDEINKAKAAGNN
1188 EEVERLLDKVFPAAATAYQDAMRALVELQRTEIDATARQIDATAANSRLLIIVLEGLILLGLVLSARYLTL
1189 GITRPLDITAVGISQ RVAQGDLSGEVAVRSRDETGQLLHSLNAMNSNLRGIVSNVRSRGTDTITTASAEIAAG
1190 NLDLSSRTEQQASSLEETASAMEELISTVQRNADNARQASQLAVSASEVAEQGGVVSQVVQTMGSINDSS
1191 KKIVDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRS LAQRSASAAKEIKQLINDSVSKVD
1192 DGSRLVEQAGATMHEVVTSVRRVTDIVAEISAASAEQTSGIEQINHAITQMDQVTQQNAALVEQAAAAAS
1193 MQNQADGLARLVSVSFDGSAPVALTRAPVDVTPRVRLPGA
1194 >Pusillimonas_sp._JR1/69-3-13_1 |WP_102074282.1 hypothetical protein
1195 [Pusillimonas sp. JR1/69-3-13]
1196 MNMFTNMRI GNRLGLGFAVIVVLTIVITSIGVWRLYTISQTTTRYLMTVPLAKERMISDWYRHLTNGINRSM
1197 AIAKSTDPALGPYFAEAAEQTKAATQASTELQNKIVPLLVADDEKELFKLIMEHRQVYLSTRDAMTKRKVAGDT
1198 EEATRIFITQQFIPGATTYQASVEKLVLEQRVFMQKGAETAEANASSRRTLIALAVIVALFSVIFYAWKLTT
1199 GITRPLRRAVDAARNVAGGDLGKINHVSTDETGQLLQSLKDMTANLLTLVGNVNRNGTHSIATASSEIASG
1200 NLDLSSRTEEQASSLTETATAMEELTNTVKQTADNAQQANQLAQATSTIAIKGGS AVSEVVSTMG SINESA
1201 RKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGGGFVAVATEVRS LAQRSATAAKEIKLLINDAVEKID
1202 TGGRLVQEAGSTIDEVVVSVKRVTDIVGEISMASNEQSIGIEQVNQITILQMDQVTQQNAALVEQAAAATGS
1203 MQEQADQLTRAVSVFNLGNHTERAPASRQIASTTQETVKGKALSRLKALGTA
1204 >Achromobacter_piechaudii_1 |WP_006217855.1 methyl-accepting chemotaxis
1205 protein [Achromobacter piechaudii]
1206 MKNMKGTRLAGGFSVLLAMIIVMCIVGLVSLANINESVETVTQSRSLIKERLISDWGRNIQTGVTRTTAIA
1207 KSADASLAGFFTEEAASSTRNSSALQQQIEPLIETDEEKQLWEGIRKSRGDYLRTRDAIFKAKQDGNVDAA
1208 NRVFTQEFLPATRFIDQINKLSNLQRADIDARAADIQSAYGAANLWMIVIGSIALITGLVLAVLLTRSIT
1209 RPLADAVRVARTVAANDLTSTITVQSRDEIGQLMQALESMNTNLAATIASIRTGVDSMASASGEIAAGNTD
1210 LSSRTEQQAASLEETAASMEELSSTVKQNADNARQANQLAAAASDTASRGGATVSEVVSTMSAISSSVKI
1211 ADIVSVIDGIAFQTNILALNAAVEAARAGEQGGGFVAVAAEVRTLAQRSQAQAAKEIKTLIEDTVQKISQGS
1212 ISAERAGTTMQEIVSSVQRVSVSTSLCFGLISRSSATSSSAASACCSRSISACVRARFAACARSTSVHVS
1213 ARAAMIAFQKQSKSRNRMTGGLSGPRAAFWCAWTA AAAESERLRFVTFIMRNIWT
1214 >Variovorax_sp._YR216_1 |WP_093165211.1 HAMP domain-containing protein
1215 [Variovorax sp. YR216]
1216 MKNWKIGARLVGFGFLV LAMVLTALGIWRLETTAAAEETHQPLAKERIISDWYRLVEIGVRRTTAIA
1217 KSSDPSLGPYFAEESANSTKAAQAMQKQLEPLLTSEDEKALWKDFQEVTRYLEARDVVVKTKAEGKQEEA
1218 NAALEKQFIPVANTYLG NVQRLLDMQRRADIGTVVQLGASYRTSRDLLLALGA AVLCLGGFFAWRLSTGIT
1219 RPLRRAVTAAQAVASGDL SIKIEADSRDETGQLLLALNDMNASLIQIVGEVRTGTDTIATASGQIATGNQD
1220 LSSRTEQQASSLEQTAASMEELTGTVKQNADNARQANQLALSASQVAIRGGSVVG EVVGTMD SINSSRKV
1221 VDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAAKEIKTLIGDSVERVEEGT
1222 RQVAEAGRTMEEIVESVKRVTDIMGEIAAASQEQTSGIEQINQAITQMDQVTQQNAALVEQASAAAGSLQD
1223 QASQLSRAVGVFKLQR
1224 >Janthinobacterium_agaricidamnosum_1 |WP_038491312.1 methyl-accepting
1225 chemotaxis protein [Janthinobacterium agaricidamnosum]
1226 MSFLRNISIGLRLGVGFAVILALSMLITGISVWRLHDVAAATHAMMEQPLAKERHISDWLTKIESGVRRTT
1227 VIVRSDTALAAIFADDARQSSVISGELQKKIEALISGPEEMEMFRLIGLQRQVYLDARALVSKLKSEGRK
1228 EEADHAFSTVFEPGA AKFQRVIQDLLDRQRKSIDNTAHDIDSVAVTSRNL LGLAVLVLGFGVSWGLLTV
1229 GIVRPLRTAVDVARRVAAGDLTADIDASAKDETGQLLLALKDMNASLLNIVSEVRSGTENIATSSSQIAAG
1230 NQDLSRTEQQAGSLEETASSMEQLTTTVKHNADHARQANQLAASAAQVALKGGTVVAQVVGTMMDTINSSS
1231 NKIVEIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAAKEIKTLIGDSVEQVK
1232 QGSQVLSQAGATMHDIVASVQRVSDIITEITAAGHEQSAGIDEIYQAIGQMDKVTQQNAALVEQSA AAAEA
1233 MQQQAQSLAQVVSFVFLNQHAGTGLSALPAPRRVLR IAHG
1234 >Hylemonella_gracilis_1 |WP_035608590.1 methyl-accepting chemotaxis
1235 protein [Hylemonella gracilis]
1236 MNNLRIGTRLAAGFGLLIVFSLIMLVSGIYQLRHSADATRQMMQEPLQKERLVSDWYTGISASVQRATAVA
1237 RSSDNALTELF AAANAASSKEISERQAQFAKLISTPQEQAMFDKLTEHRQAYIKARDAI IAAKAGGQLEEA

1238 KRLFEQTFLLPASRDYLGSLQGLRDHQRASIDRMGMDIDRSAARGYMLLGAIGLTIAAAGALIAWTLTRSIV
1239 QPLTKSVEAAQAVASGDLTREPRAEGRDEAAQLLRALQDMTQRLRGIVGDVQLQGSQAIASSATQIAAGNLD
1240 LSSRTEEQANSLQETAASMEEITSTVRHNADNARQANQLAQETANQATRSQVADQVVATMGGIHEASRI
1241 VDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSQAQSAEAAKEIKGLIGDVTNKKVDAGT
1242 QLVEQAGASIRDVVTSVQRVRDIVAEISAATQEQTAGLELVNQAMTQMDLVTQQNAALVEESTAATQSLET
1243 QASQLARTIGVFRVNAAPFSTPSPYARKETAIAPPTQPRAKVPTTAAAKSAQITPPRGRAQASRAAAPRL
1244 TQRLHTPAATPAALTGQQGSTPTSGDDWETF
1245 >Rhodoferax_antarcticus_1 |WP_075586367.1 HAMP domain-containing
1246 protein [Rhodoferax antarcticus]
1247 MKHLTSLSIGQRLAAGFALILLLAMVITGIGLWRLQETARETEAMMGAPLTKERLASDWATYVNAAVRRTSA
1248 IAKSTDSSLVDFFAADMTATGKGASEAQKAI GELLEETSEEKAQFEELATIRKKYQSRDSITELKKVSKLD
1249 EANEVLNKEYMPQATAYLSGLDAFKQLQRQAI DTRAAEIKSLNQTSSKLLLVLSVVMLLMGTTIAWLITRA
1250 ITTPLRDAMTAARRVASGDL SHIMTVHTRDETGVLLQCLQEMQSQLGSVVANVRGNAESLATACAEIAQGN
1251 QDLSSRTEQASALEETAAMEELSSTVKQNADNARQANQLAQNASAVAVKGGEVVAQVVNTMKGINESSR
1252 KISDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAGRSAAEAAKEIKTLISTSVERVEQ
1253 GTTLVDQAGTTMTEVVGSI RRVNDIMGEISSASTEQSQGVGQIGEAIQQMDQVTQQNAALVEEMAAAASSL
1254 RSQAQELVSTVAVFKLAPGQELDF SAPAARASAVVSAPKAFAPAQKVMKAATK PANLLHDSTVKAGNDDW
1255 ESF
1256 >Delftia_acidovorans_1 |WP_034393844.1 methyl-accepting chemotaxis
1257 protein [Delftia acidovorans]
1258 MKNLRIGLRLGGGFTILLIIMLLISVTSIVSMGHMARSTTEITEVALAKERMISDWFRNIHSGSRRTTAIA
1259 KSSDPSLATFFAEDAAESSRQSSKLDRIEPLLQTQEEKDIWVEIKKARAGYLAGRDVVTKAKAEGRAEDA
1260 ERLFTQEYQPATQRYIEIVQRLLDMQRAAIDSSAAEVQVRFASRATIIAVVSLAVVLGALA AWWITRGIT
1261 VPLAEALRVARTVANNDLTSRITVDSRDETGQLLQALRQMNDNLAQVVGQVRS GADSIATASGEIDAGNQD
1262 LSSRTEQQASSLEQTAAMEELTSTVKQNAENARQANQLAASASQTAVQGGKVVAGVVDTMGGI SESSRKI
1263 ADIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRLAQRSASAAKDIKDLIADSVSKVDAGT
1264 RQVAEAGRTMDGIVQSVQVSDLVAEITAASQEQSSGINQVHQAI SQMDTVTQQNAALVEEAAAATGSLKS
1265 QVNQLAAAVSVFRIDGLAPARAGTGAASSSVPAARAPSAAAPMRPAARPLAASAPAAGTAPAAAGTAPAAAA
1266 RSASAAPAPAACLPAARQTVAAKGNDDGDWTSF
1267 >Burkholderia_sp._AU16741_1 |WP_089471075.1 HAMP domain-containing
1268 protein [Burkholderia sp. AU16741]
1269 MLTVISKLNIGKRLGLGFAMVLAAMSLIGIVIGLARLSSVAQATRDMVARPLQTERLVNDWSRQISVAVTRT
1270 TAIKASADPGLANYFNDEAIAASKVSAAKQTAIEALMTSDAEKRLF AAI GEQRKRFLAIRDQIYALKKEGQ
1271 AEQADQLLEQQFIPTARQLVEKVDALVKYQREEIDGLAAEIDANYRFGRTLMI AFGMVGMLLSVVCGWLIT
1272 RSITRPLMRATDV AHRVARGDLSVRVDVHGTDELGQLLGLSLRDMQAALLRVVSNVRRGSDNLAASAEIAQ
1273 GNDDLSSRTEQASALEQTAASMEELSSTVARNADNAHEANQLAMNASTVTAQCGEVINQVETMKGINDS
1274 SRQISDITGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAGRSADAAREIKKLIGSSVGRV
1275 AQGSTEVERAWVAMTEVVNSIRRV TETMSEISAASTEQSLGVAQIGEA VGMERTTQQNAALVEQTAAAAI
1276 NLRQQSRELVEVSVFQLGRAEAL
1277 >Delftia_sp._HK171_1 |WP_071955969.1 HAMP domain-containing protein
1278 [Delftia sp. HK171]
1279 MKNLRIGLRLGGGFTILLIIMLLISVTSIVSMGHMARSTTEITEVALAKERMISDWFRNIHSGSRRTTAIA
1280 KSSDPSLATFFAEDAAESSRQSGKLDRIEPLLQTQEEKDIWVEIKKARAGYLAGRDVVTKAKAEGRAEDA
1281 ERLFTQEYQPATQRYIEIVQRLLDMQRAAIDSSAGEVQVRFASRATIIAVVSLAVVLGALA AWWITRGIT
1282 GPLAEALRVARTVANNDLTSRITVDSRDETGQLLQALRQMNDNLAQVVGQVRS GADSIATASGEIDAGNQD
1283 LSSRTEQQASSLEQTAAMEELTSTVKQNAENARQANQLAASASQTAVQGGKVVAGVVDTMGGI SESSRKI
1284 ADIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRLAQRSASAAKDIKDLIADSVSKVDAGT
1285 RQVAEAGRTMDGIVQSVQVSDLVAEITAASQEQSSGINQVHQAI SQMDTVTQQNAALVEEAAAATGSLKS
1286 QVNQLAAAVSVFRIDGVAPARAGAASSSVPAARAPSAAAPMRPAARPLAASAPAAGTAPAAA PRSASAAPA
1287 PAAKLPAARQTVAAKGNDDGDWTSF
1288 >Paraburkholderia_aspalathi_1 |WP_093637546.1 HAMP domain-containing
1289 protein [Paraburkholderia aspalathi]
1290 MPTFISNLP IAKRLGAGFVLV LIMSISIVIGLARLSSVAQATRNLVANPIQTERLVNDWSRNI STAVTRT
1291 TAIKASADPGLASYFVEEAVASSKVS GALQKSIEALMTSDEEKSLFAAI GEQRKAFIATRDQIYALKKSGK
1292 AEEANQLLEQQFIPASRLFVAKVDALVKQQRDEIDRVATQIEANYEYSRTLMI ALGVVSLLLSVVCAWLIS
1293 GSITRPLVKATGVARQVAEGDLTARIDNHSTDEVGQLLTSLRDMQTS LVRVSNVRRGSGESVATASAEIAQ
1294 GNDDL SARTESQASALEETAASMEELSSTVQRNADNARQANQLAMNTSEVAIQCGEVNQVETMKGINDS

1295 SRKIADIIGVIDGIAFQTNILALNAAVESARAGEQGRGFVAVNEVRSLAARSADAAKEIKKLISASVERV
1296 AOGSAQVEQAGVAMTEVVRSIRRVTDTMGEISAASNEQSLGVAQVGEAVTQMDETTQNAALVEQMTAAAN
1297 SLRNQSHLVQVVSIFKLDGGASLMSLG
1298 >Rhizobacter_1 |WP_056802308.1 MULTISPECIES: methyl-accepting
1299 chemotaxis protein [Rhizobacter]
1300 MKLNDVRVGARLGGGFAVTLALLCLIMVVGWVRLGSLAQATQQMMAEPLAKERLAAEWARNVVSIGVTRGKA
1301 IAKSPDATLEGLFSDDAKASTARANEITQALKAFPTSPDEQVLLDRIAETRKYTLVARDGMATAAKRAGNTE
1302 EATRIYDSSFQVVPVYVAVVMQAYVDYQKKAIDEMAKRIDADALRGRLIGVGTGLALVFGAVFALLTRS
1303 ITVPVAEAARLADAVAGGDLRRVTAKGRDEIAGLMRSLGKMNASLHDMVTQVRQSADSIQVASGEVATGN
1304 QDLSARTEQTASNLOQTASSMGLTGTVKQTADSARTANQLASSAQGAAGKGGEVVSVVSTMNDIHASSK
1305 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAQRSAQAAKEIKSLIDASVDKVDL
1306 GSRLVADAGQSMTEIVNSVRRVTDIIGEITSAASEQSDGIGQVNTAVTQLDQMTQNAALVEQSAAAAESL
1307 KEQALRLSGVSVFRLTA
1308 >Bordetella_genomosp._5_1 |WP_094857089.1 HAMP domain-containing
1309 protein [Bordetella genomosp. 5]
1310 MKNLKLGTRLAAGFAVLLAMMIVMCVGLYSLADINRAVDNVTHQSLTKDRMVNDWSRFIHTGVTRTTAIA
1311 KSSDPSLAGFFTQDAAASTAQASKLQQQIEPLIQGDAEKQVWAGIGKARTEYLSSRDRIFKAKQEGNVELA
1312 ERIFTQEYLSASRRFIDLITQLSDMQRADIDAQAVSIESSYNVANLWMIVLGAIIVLSGLALSILLTRSIT
1313 RPLADAVRVARTVADNDLTSRITATSKDEIGELMHAE SMNNNLALT VTRIRAGVENIASASGQIAAGNTD
1314 LSSRTEQQAASLEETAASMEELSSTVKQNAESARQANQLAAAASDTASRGGSTVSEVVSTMSAIISSSVKI
1315 ADIVSVIDGIAFQTNILALNAAVEAARAGEQGGGFVAVAAEVRTLAQRSAQAAKEIKTLIEDTVQKIQGGS
1316 DSAARAGATMQEIVSSVQRVTDIMGEIAAASAEQADGIEQVNRVAQMDEVTQNAALVEEAAAAAGSMQD
1317 QAADLRGAVSAFKLQAGQQAQDARAAAPRLSGAPLQLAAY
1318 >Herbaspirillum_sp._RV1423_4 |WP_034294266.1 methyl-accepting
1319 chemotaxis protein [Herbaspirillum sp. RV1423]
1320 MNFFANLNISKRLNLGFAILFSAIGVIALSIWRLHIVAETTQDMMQKPLAKERLVSDWYRTIHTSVRRTT
1321 AIAKSADPSSLAFFADDAATATKLSNEQQKALEGLSSDKEKTLFSQLTVVRKSYIAARDAISKAKADGQV
1322 EEANRILEKDFPAAAKGYLDLLQQLLDLQRSSIDEIAASIHDLTYQSRNLLVAFVGLLFFVAGWLFARLAL
1323 SITRPLNQAVDIAETVAAGDLTSRIDTRRKDETGKLLLALKTMNDNLLRIVGQVRSGTDTIATASAEIATG
1324 NLDLSSRTEQQAGSLEETASAMEELTSTVRQADNARQANQLAVSASEVAIQGGAVVQVVDTMGAINASS
1325 KKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAQRSASAAKEIKGLIDDSVEKVG
1326 SGSKLVQEAGQTMTEVVASVKRVTDIVGEISSASQEQSEGIEQVNQAIQMDETTQNAALVEQAAAAAQS
1327 LQDQAATLTEVVGIFKLDHAATGTSVARVAPKAASAPRPLVAVAMPASPAPTVPKPVAPSPAPSRMPRI PA
1328 STSDDDWEQF
1329 >Acidovorax_valerianellae_1 |WP_092745165.1 HAMP domain-containing
1330 protein [Acidovorax valerianellae]
1331 MNLQNISIGKRLGLAFGLVILFIVTMLGVGTWKLQSVAEETASMMALPLTKERLISDWYRTIFSNVRRHSV
1332 VARSTDSTLAQQFAADNAAASKMSSEQSQSLKLISSPQEQALFDKTGEERKRFVTARDAIYKAKAEGRSE
1333 DAERILNADFTPAGEQYLQALQALLDFQRAQINESSEAVQANYQSGRLQLIVLGALATVIALTLVAITRS
1334 ITHPLHDAVTMAKT VATGDLTITSGSTAQDETGQLLRTLNAMGEQLRATVGVQRHGAEGIAVASSEIARGN
1335 LDLSSRTEEQASALQQTAAASMEQMTATVRQADNARTANQLAQATSDKAVRGGEVSVNVSTMGEIHAASR
1336 KIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRMLAQRSAEAAKEIKGLIDDSVQRVDS
1337 GNKLVEQAGEAMREVVDGVRVTDIVGEISVASQEQTTGLEQVNQAIQMDTQNAALVEEAAAATGSL
1338 ESQTAQLVRAVAVFRVGNAAQAGGAPALAAARHMPAIAAG
1339 >Rhodoferax_saidenbachensis_2 |WP_076069470.1 HAMP domain-containing
1340 protein [Rhodoferax saidenbachensis]
1341 MAFFFNNSVSGKRLGAFAFVLLALSIVVILVLSRLSVAADASREMIASPIKTERIIGDWYRNIYAGIRRT
1342 SAIARSSDPSLAFFAEDQAASTKSSTEYQKMLEELMETDKEKALYAAVGEQRKAYIQVRDAVVNLKKEGK
1343 AEESLKLMEEFVYPAGKVYQAKMEELLTMQRQEIDEIGKSIDEIYKSSRTLMIALGVVSVLLGLTVAWLLS
1344 NSITRPLNQASAVARQVAEGDLTTHIDNQRTEVGVQLSSQLQMDQTSLVKVVSNVRSSESATASAEIAQ
1345 GNNDLSARTEQQAASALEETAASMEELGSTVKQNAESARQANQLAMNASTVAIKGGEVVGVVETMKGINES
1346 SRKISDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAGRSAAEAAKEIKSLIGASVERV
1347 EQGTALVDQAGTTMTEVVSSI KRVTDIMGEISAASNEQASGVAQVGEAVTQMDQATQNAALVEEMAAAAS
1348 SLKSQANELVQVAVFKLGAADQTVTRSPSPVHVKAAPVKVAARSAPAAAGAKASVKAMPKVPKAAATK
1349 VASLSAPKASAKVTPAGGDDDWETF
1350 >Achromobacter_sp._Root83_1 |WP_057287277.1 methyl-accepting chemotaxis
1351 protein [Achromobacter sp. Root83]

1352 MKNMKLGTRLAGGFVLLAMIMVMCIVGLVSLANIHESVETVTQSRSLTKERLINDWARNIQTGVTRTTAIA
1353 KSADAGLAGFFSEEAATSSRNSSALQOKIEPLIQTDEEKQLWDGVGKSRAAYLSTRDRIFKAKTDGDVETA
1354 NKVFSQEFLPATRQFIDQITRLSSLQRADIDARAAEIEDAYRSANFWMIAIGSIAVVSGLLLAVLLTRGIT
1355 RPLSEAVRVARTVAANDLSSTIVATSRDEIGQLMRALESNMNANLAGTVARIRTGVDSIASASGEIAAGNTD
1356 LSSRTEQQAASLEETAASMEQLSSTVKQNADSAKQANQLAAAASDTASRGGATVSEVSTMSAIAASSVKI
1357 SDIVSVIDGIAFQTNILALNAAVEAARAGEQGGKGFVVAEVRTLAQRSAAAKEIKILIEDTVQKISQGS
1358 GSAERAGSTMQEILSSVQVRVTDIMGEIAAASAEQADGIEQVNRVAVSQMDEVTTQNAALVEEAAAAAGSMQD
1359 QAAELTRAVSAFKLPGGGQGAIPAAAPRSSAALRLAAY
1360 >Massilia_alkalitolerans_2 |WP_084416306.1 HAMP domain-containing
1361 protein [Massilia alkalitolerans]
1362 MRTFNNLGIGIRLTVGFTLTLVMAVLIAGSGMWRLEQVSSAARDTLAAPTAKERLIAEWYTOIFAARRTA
1363 AIVKSSDPSLTAYFKEDAATAKTSADLVKQIEPLIAGEQESALFKRITEQRKLYGAARDNAVKAKEGNQ
1364 ELADQILEQSFTPAAKAYQESINELVAMQRDHITATAAGIDATATRGQMI IAGLTAGAVLLGALFSWMLTR
1365 GITRPIRAAVQAAETVAGGDLSSRIDADTNDDETGALLRALGHMNDSLVKIVSEVRSGTDTIATASGEISAG
1366 SLDLLSSRTEQQAASLEETAASMEELTGTVRQNADNARQANQLAITASKVALDAGSVVDQVITTMGSINDSS
1367 KKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRTLAQRSAAAAKEIKTLIGASVEKVE
1368 AGTRLVDQGTMEQVVTSIRRVTDIMAEIASASQEQIHGIEQVNOAIGLMDESTQNAALVEESAAAAGA
1369 LQDQAARLAGMVNVFRLEAQASTPATPAPRSLAGGAGIGKLLIS
1370 >Delftia_tsuruhatensis_3 |WP_047328078.1 methyl-accepting chemotaxis
1371 protein [Delftia tsuruhatensis]
1372 MKNLRIGLRLGGGFTILLIIMLLISVTSIVSMGHMARSTTEITEVALAKERMISDWFRNIHSGSRRTTAIA
1373 KSSDPSLATFFAEDAAESSRQSSKLQDRIEPLLQTQEEKDIWVEIKKARAGYLAGRDVVTAKAEGRAEDA
1374 ERLFTQQYQPATQRYIDMVQRLLDMQRAAIDSSAADVLVRFASRAAIIITVVS LAFVLGALAAWWITRGIT
1375 RPLAEALRVARTVANNDLTSRITVDSRDETGQLLQALRQMNDNLAQVVGQVRSAGDSIATASGEIDAGNQD
1376 LSSRTEQQAASSLEQTAAMEELTSTVKQNAENARQANQLAASASQTAVQGGKVVAGVVDTMGGISESSRKI
1377 ADIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRALAQRSASAADIKDLIADSVSKVEAGT
1378 RQVAEAGRTMDGIVQSVQVSDLVAEITAASQEQSSGINQVHQAI SQMDTVTQNAALVEEAAAATGSLKS
1379 QVHQLAAAVSVFRIEGVASARPAVPAPAPAGRAQPAQAQMRAPARPLAAPAAAASPGAPAAKPAKPLPAS
1380 RQSVPATGKDDGDWTSF
1381 >Curvibacter_gracilis_1 |WP_027477789.1 methyl-accepting chemotaxis
1382 protein [Curvibacter gracilis]
1383 MSIFQHLSVAKRLAVGFVVLILLSIAVIGLSIYRLSALADADEMVKIPIKAERLVS DWSRNLHVGITRRTA
1384 AVARSSDPALATFFAEDAKASSTRSGELQKAVEAMLVRDSDKAI FREIGELRSLYLKNRDGVVALKKEGKT
1385 DEANVLEKQFLPDAKRYAGKMDLELLLTQREQVDLLSQAIEANRQSSRQFLIVLGVLSLALGTVVCWLLAQ
1386 SVTVPLKQASQLARRVADGDLAAEVPAGHTDELGELMDALALMQGNLAKVVQNVRESSDQVSSASEEIAQG
1387 NHDLSARTEHQASSLEQTAASMEELSSTVRLNADNARQANQMAMAASEIASKGGEVVGQVVDTMKGIQDAS
1388 RKISEIISVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLASRSADAAKEIKTLINASVERVE
1389 QGTVQVDQAGETMNEVVSSIRRVTDIMGEISAASQEQTAGVAQVGEAVTSIDEATQNAALVEEMAAAASS
1390 LRNQAHDLVQAVSVFRLSAHEQSGGARVSREAAGVRQPAVRKPVARAHSAGSLQAKAQSSPLPKAASLKIA
1391 SAPATSTNKAERDDNWESF
1392 >Rhodoferrax_sp._DCY110_1 |WP_076197176.1 HAMP domain-containing protein
1393 [Rhodoferrax sp. DCY110]
1394 MPSFSLNLSVAKRLGLGFALLLALSMAVILVGISRLNDVAARAQEMVASPIKTERLVSDWYRNIYTGVRRT
1395 GAIKSNPDSLQVFFAEDQAASKASSEYQKAVEPMMETEKEKALFAQIGEERKNYILVRDAVVATRAQ GK
1396 AEEANQMLDQKFPVASKTYMGKMEELLNFRQREIDDSARRIEASYAASRNLMILLGIVSLLLSAVIAWLLS
1397 GSITRPLAEASAMAKRVAAGDLTGRIENNRTDELGQLLTSLODMQASLVGVVSNVRSSESVATASQISQ
1398 GNNDLSARTESQASALQQTAAASMEELSSTVQRNADNARQANQLAMSASTVAIQGGEVVGQVVTMKGINDS
1399 SKKISDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAGRSADAAKEIKNLINASVERV
1400 GQGTALVDRAGTTMTEVVNSIRRVTDIMGEISAASTEQSQGVAQVGEAVTQMDQATQNAALVEEMAAAAS
1401 SLRTQAQDLVQVAVFKLGQGEGRGLSLSSSGVLAIR
1402 >Cupriavidus_sp._USMAHM13_1 |WP_071018009.1 HAMP domain-containing
1403 protein [Cupriavidus sp. USMAHM13]
1404 MKIRDMKIGTRLAFGFVILALLVNLNTAFSVYRMRELSQQTRAMMSEPLAKERLVADWTSLVAVGIVRTSA
1405 IARSSDPALAGFFAEQTKASSARGAALMKQIEAQADETDKPVLRQAAEVRQAYIARDEIMKIKGSASEAE
1406 IERLMQERYLPSAKGYEEALRSLLDLQRSINATAQRIDALAEERTRTVLIVTAALVAFAIGFAWWLTVGI
1407 TQPMRHAVQAAQVAQGDLSGQAGAQQGPYARDESGQLLQALAEMRGLNGIVHEVHRGTQTIGGASRQIA
1408 AGNLDLSSRTEQQAASSLEQTAASMEELTSTVQRNADNARQANQLAVSASAVANHGGEVVARVVQTMESIHT

1409 SSKHIVEIIGVIEGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRLAQRSASAAKEIKSLIDASVAQ
1410 VEGESALVGQAGSTMAEIVESVKRVTDIMGEITAATQEQTGIEQVNQAITQIDETTQONAALVEQASAAT
1411 QALEDQARLLLLQAVGTFRLDAGAGIEAAPPASAQPVQAARAGKPEAGAGATQGTAPRSPRQPAPARLPAQ
1412 RLEPAMAQPQRQAAAAARAAAASSDDWEQF
1413 >Pectobacterium_carotovorum_1 |WP_015841603.1 methyl-accepting
1414 chemotaxis protein [Pectobacterium carotovorum]
1415 MKNYKIGTRLAGGFGLLIALSLAMLTSGIYQLNQVSSSTKQMMQEPLRKERLASDWHATLVAGVQRSMAVA
1416 RSNDDSLVELFAAENTRASKEGKRQEQFASLISTPEEKALFDKVGGEYRQSYIKKRDAIIAEKGAGNFDRA
1417 RSLFDNEFVPASNGYLASVEALRDHQRASIDQMGQDINTGASRGDLILAVTGALSATIGVLIWVLRTRIV
1418 QPLARAVRATQAVAAGDLTHNVQPEGRDEAAQLLHALQDMTVRLRTIVGEVRQGSSEIAGASSQLAAGNID
1419 LSSRTEEQASALQETAASIEQLSSTVRQADNARQANLAQSTTQQAQSGGQLVTEVVETMGAIDSSSKKI
1420 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRLAQRSASAAKEIKELIDRSVQTVQV
1421 RLVVQAGASIQDIVNGVRKVSIDLVEISSASNEQTMGIEQVNVAVNQMEVTTQONASLVNEASAATQSLQQ
1422 QAAQLAETVSQFRLGNSHQIARTPAAAPSLALQPALAAPGKNVATAGEGDWTSF
1423 >Herbaspirillum_huttiense_2 |WP_039788802.1 methyl-accepting chemotaxis
1424 protein [Herbaspirillum huttiense]
1425 MIKNIIRIGSRLGAGFAVVLVFSMVVAAVGIWRLKTVAAQQTQOMMDVPLKTERLVSQWNTLLLIATQRTTTV
1426 VKSRDPELEAFLAKEAAAASSKESAQTLKDVEQLLTSEEEKLFAAINAARKQFLAIRDQIYAAKKEGDAAK
1427 VDQLYQQQYVGIANNTOGAMRSLDFERARIDEISADIQKDAASSQWQIFALEAVILACGIAFALLLRSI
1428 TRPVHAALAIISQVAAGDLTSRAQPMGQDELGQLVASLQGMSERLHGVVSTVRLGADSI AVASGEIANGNL
1429 DLSARTEEQAGALEETAASIEQLTSSVRTNSENANQANDLVKSAASIAGQGGQVMQELIDTMGNINSSSRK
1430 IVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRLAQRSASAAKEIKQLIDDSVSKVDAG
1431 SELVERAGKTMQEVVGSVQGAHALVGDISTASREQAEGIHQVNQAVSQMDGVTQONAALVEQAAAAAKSLE
1432 DQAAQLKRAVAFFSLQAA
1433 >Achromobacter_xylosoxidans_1 |WP_063954850.1 methyl-accepting
1434 chemotaxis protein [Achromobacter xylosoxidans]
1435 MKNMKLGLTRLAGGFALLLAMIMVMCVVGLVSLANINDSVDTLTQRSLTKERLINDWARNIQTGVTRTTAIA
1436 KSADASLAGFFTEEAASSTRNSSALQQKIEPLIETDEEKALWQIGKARADYLRTRDGIKAKQEGNVEEA
1437 NKIFTQEFLPATRQFIDNINRLSALQRADIDARAAEIEASYGNANLWMIVIGSIAVVCGLLMSVLLTRSI
1438 RPLSDAVRVARTVAANDLTSTITVRSRDEIGQLMMALESNMNANLAATVARIRTGVDSIASASGEIAGNTD
1439 LSSRTEEQAASLEETAASMEQLSSTVKQADNARSQANQLAAAASETASRGGATVSEVSTMNAISSSVKI
1440 SDIVSVIDGIAFQTNILALNAAVEAARAGEQKGFVAVVAAEVRTLAQRSAQAAKEIKVLIEDTVQKIGQGS
1441 GSAERAGATMQEIVSSVQRVTDIMGEIAAASAEQADGIEQVNRAVSQMDEVTTQONAALVEEAAAAAGSMQD
1442 QSADLTRAUSAFAFRPLGGGERVLAVEAVSSVHAAGTPASRRLAAY
1443 >Orrella_dioscoreae_1 |WP_098020966.1 HAMP domain-containing protein
1444 [Orrella dioscoreae]
1445 MNQYKIGVRLAAGFGLLILFSLVMLASSLLQLQHVAAEETRNMMASPLHKERLISDWYRTVHTGVRRATAIA
1446 HSTDTSLAALFAEDNAEGTRQSTAAQKLETLTLLATPEEKTFLDQLGRNRIAYVKARDAISAEKSAGRVEEA
1447 NRIFQNDYLPASKLYLGLSLQSLLEDEQRATIDRSAAEIDASATRQYVVLVSGIGIAIVFIGVLLGWRFRTRIV
1448 HPIGHSVLAQAQRVAAGDLTHDVRVTGRDEAAQLLQALSMDTARLRSIVGELRSGSETIAGASSQIAAGNAD
1449 LSSRTEEQASALQQAASIEELTSTVRQADNARQANQLARATASQAQEGGQLVSEVVQTMGAIDASSKKI
1450 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRLAQRSASAAKEIKALIDNSVGTVEEEN
1451 RLVERTGGAIKDIVQGVQVSDLVGEISAASEEQTHGIEQVNAVAQMEQTTQONAALVEEASAATMALQD
1452 QAGQLAGVAGVFRVTRGAVPVALPGAQARRHEDEDFQDPRGPRLLPA
1453 >Achromobacter_marplatensis_1 |WP_088587806.1 HAMP domain-containing
1454 protein [Achromobacter marplatensis]
1455 MKNMKLGLTRLAGGFVLLAMIIMSIVGLVSLANINDSVETVTQRSLIKERLISDWARNIQTGVTRTTAIA
1456 KSADASLAGFFTEEAASVTKNSSALQQQIEPLIETDEEKKLWEGIRKSRGDYLRTRDAIFKAKQDGDVDA
1457 NRVFTQEFLPATRQFIDQITKLTNLQRADIDASAADIQSAYGIANFWMIAIGSIALISGLLLAILLRSIT
1458 RPLSDAVRVARTVAANDLTSTITVRSRDEIGQLMQALESMNANLAGTVASIRTGVDSMASASGEIAGNTD
1459 LSSRTEEQAASLEETAASMEQLSSTVKQADNARSQANQLAAAASDTASRGGATVSEVSTMSAIISSSVKI
1460 ADIVSVIDGIAFQTNILALNAAVEAARAGEQKGFVAVVAAEVRTLAQRSAQAAKEIKTLIEDTVQKISQGS
1461 ISAERAGATMQEIVSSVQRVTDIMGEIAAASAEQADGIEQVNRAVSQMDEVTTQONAALVEEAAAAAGSMQD
1462 QAAELTRAUSAFAFKLPGAGQAGGGEAQAVRLAAPVRQIAAY
1463 >Janthinobacterium_sp._HH01_3 |WP_008444154.1 methyl-accepting
1464 chemotaxis protein [Janthinobacterium sp. HH01]

1465 MKITDLSIGRRLSLGFAVILAILILNTGLGVYRLQGVADSTRAMMELPLAKERLIADWYRVVFAGIRRTTA
1466 VAKSADPVLATFFFAEEAKNSTAYAQGLIKKIEELATDDDKALMADLVNTRKVVYVASRDGVMKAKAAGDADG
1467 ATKLLDEAYI PAAKTYEAMLQKMLDHQRKEIDAAAARIDQVAKDSRNLVAMAALVVAFAVFWLLTAGI
1468 TRPINEAVALAECVAGGDLVDHGNRAAAGYSQDEPGKLLQALHRMSGGLVRIVSDVRNGTDAIATASQAIA
1469 AGNLDLSSRTEQQASSLEETASSMEELTSTVKQNAENARQANQLAASASDVAQRGGAVVSDVVQTMASIDE
1470 SSKKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKALIGDSVGK
1471 VAAGTRLVGQAGSTMEEVVASIRRVTDIMAEISSASSEQTNGIEQINNSITQMDHVTTQNAALVEQAAAAA
1472 DAMQEQAACLADAVSIFKLGDAAPRRPAMQGRGGARPMLARGG
1473 >Curvibacter_delicatus_1 |WP_066710381.1 HAMP domain-containing protein
1474 [Curvibacter delicatus]
1475 MNQLSRLSVAKRGLGFALVLLLSIVVIGVSI SQLNAVANATEEMVQNP I KTERLVSDWYRNLRGTGIRTTI
1476 AVSRSGDPTLADFFAEDAKASSKSSGELQKAVEGLMFLSEKKLYQEIGELRLLYLKNRDAIVALKKEGRV
1477 EEANTLLEKQFIPDANKYAAAMEALLKNQRDQVDTLAQDISARRQSSRQLLVVLGLLSVAFGALCAWLLAS
1478 SITRPLAQASDVAQRVASGDLTAVI PAHGTDEVGQLLTSLQHMQNLI SVVSNVRSSESSTASAEIAQG
1479 NQDLSRSTESQASALEETAASMEELSSTVKQNADNARQANQLAQSASTVAVQGGVEVAQVVDTMKGINEAS
1480 RKINDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSAAEAAKEIKTLITDSVTRVE
1481 QGSALVDQAGSTMSEVVASIRRVTDIMGEISASSEQSAGVGQVSEAVTSMDQATQNAALVEEMAAAAAS
1482 LRGQAQELVQTVAVFKLSAKDSAVSYAPATAENATPVVPRPAPAVPAKPKVKSAAKLSAPASAPTPKPAK
1483 AADGDDWETF
1484 >Massilia_sp._BSC265_1 |WP_081897558.1 HAMP domain-containing protein
1485 [Massilia sp. BSC265]
1486 MNWIVNMNIGRRLGVGFALILAMATACAGFSLWRLSMVAASTEAMALPLKKERMIVEWVKQVFGAIRRTTA
1487 I IKSSDDSLKTFKDDAATTSGRSTELINMIKPLLDTPAEQSLYQKIVDQRKVYKDATTAAEMAKAEGQHE
1488 AALKLINDVYLPAAKTYQDQLLVVMQHRNMDAQGA IQEIQVQTRNLVILFAGVIVIVGFVMAWLLTRS
1489 IVAPIRQAVTVAETVASGDLTHRFDARTKDETGALLRALRHMNDSLTRIVGEVRRGTSIIHLAAAEIAAGN
1490 LDLSARTEQQAASLEETAASMAHLTDTVRQNANNARQANELSIAASGVASQGGQVVAQVVTMGSIDASSR
1491 KIVDIIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLAQRSAAAAKEIKSLIDDSVSKVEA
1492 GTRLVDQAGTTMEQVVS IQRVTDIMAEIASASQEQTSGIEQVNGAIGQMDAVTQNAALVEEAAAAAESL
1493 QSQAVKLTAEVDLFLKLDRAALQVAARPLLGQNEVRVVA
1494 >Xylophilus_sp._Leaf220_1 |WP_055841875.1 methyl-accepting chemotaxis
1495 protein [Xylophilus sp. Leaf220]
1496 MRLQNLNIGARLGLGFGILILLTAAI LAVGVWRLQAVAAESAEMMALPLTKERLVSDWYSVIQASVKRTTA
1497 VAKSADPSLATFFFAEESAQSSRNSTEQQRLEELLASPKEKTLFAALVQDRKAYIAVRDAVAKAKQEGRAD
1498 EADRLFTAEFQ PAVRYLKSLQALLDEQRAAIDAAAASVRQGYERGLAQMLVLGAAALLVAAVLAYLITRS
1499 ITRPLDRALAVAQTVAAGDLTDDVGATSLDETGRLLQALDAMGQRLRETQVVRHGADGIATASSEIASGN
1500 LDLSTRTEEQASALQQTAAASMEQMTATVRQNADNARQANQLAQSTSDLAARGGVVGVNVVSTMAEIH TASR
1501 KIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAAEVRTLAQRSATAAKEIKGLIDDSVMRVDA
1502 GNRLVDEAGGVIREVVQGVRRVTDIVGEITSASQEQTTGLEQVNTAITQMDQVTQNAALVEEAAAATGSL
1503 ESQAAQLVAAVAVFRLQHEGAPRLAA
1504 >Methylibium_sp._YR605_1 |WP_052204918.1 methyl-accepting chemotaxis
1505 protein [Methylibium sp. YR605]
1506 MKLNDVRVGARLGGGFVAVTLALLCLIMVVGIVWRLGAVGQATQTMMEVPLAKERLASEWLRNVHIGVMRGRA
1507 IAKSSDPSLEALFADEVKASTVRGNEIVQALKALPTGAEQQLLVDKINDTRKPYLAARDTMMAAKRAGNAD
1508 EAMRIYESGFMVASPIYVAAMTAYVDFQKKSIDDMARQIEADGARGRWLIGVTGCLALVFGAVFALLTRS
1509 ITVPVAEAAASLADAVAAGDL SRRVTVDGSD E IAGLMRSLGKMNASLHDMVTQVRQSADSIQVASSEVATGN
1510 QDLSRTEQTASNLOQTASSMGLTGTVKQTADSARTANQLASSAQGAAGKGGVEVVSQVVTMNDIHASSK
1511 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRS LAQRSAAKEIKSLIDASVDKVD S
1512 GSRLVADAGQSMTEIVTSVRRVSDIIGEITSAASEQSDGIGQVNTAVTQLDQMTQNAALVEQSAAAAESL
1513 KEQAVKLSGVVSVFRLSA
1514 >Massilia_timonae_1 |WP_071361774.1 HAMP domain-containing protein
1515 [Massilia timonae]
1516 MGNFIKLNIGTRLAAGFALTLMTVIIATVGVWRLNQVAHETEAILAEPLAKERMIAEWYTIQIFA AVRRTA
1517 AIVKSSDPSLTEFFKEDSAATGKLSADLVKQIEPLISGDDETALFKSVMEHRAAYS KARDGAVKAKAEGNV
1518 ELAEQILTQQFNPTAKAYQERVKELVDLQHKRIAASAGLIASTAARGNVVIGSLAAGALLLGGVFAWLLTR
1519 SITRPLRQAVHAAEQVAAGDLTVEIDTRATDETGALLRALGHMNTSLSKIVDEVRSQTITISGASSEIAAG
1520 SFDLSSRTEQQAALAEETAASMEELTGTVRQNADNARQANQLAIAASSVATQAGQAVDQVVTMGSINDSS
1521 RKIVDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLAQRSAAAAKEIKQLIGDSVEKVD

1522 TGTRLVDHTGATMREVVDSIQRVTDIMGEISSASQEQITGIDQVNOAMGQMDNATQQNAALVEEATAATAA
1523 LQDQAQRLAQVVDVFKLDARYVTPAAPVAVKRPAPALAKPVARAAAKPAPVAKPAAAKATGKPAAPAK
1524 VNEAEWEEF
1525 >Acidovorax_3 |WP_056411403.1 MULTISPECIES: methyl-accepting chemotaxis
1526 protein [Acidovorax]
1527 MSRLSDLSVAKRLALGFSVLVLLLLIGAIALSISRLNAVADATLEMVQNPIKTERLVSDWSRNLRTGITRRTA
1528 AVARSSDPALADFFAEDSKASSKSSGELQKAVEALMFLDSEKKLFAEIGTLRTIYLKNRDDIFALKKEGKV
1529 DEANAMLVKQFMPEAANYAAKMDPELLNNQREQVDALGRAVEENRQTSRQLLIALGVLSVAVAALFSWVLSR
1530 SVTVPLGQASDLARRVAAGDLTATVPQHGKDEVGALMESLALMQANLASVNNVRHGAESVSNASSEIAQG
1531 NTDLSSRTEHQASALQQTAAASMEQLNSAVRNNADNARQANQLAMTASSVAAQGGAVVGDVVTMKGINDAS
1532 RKISDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSRSLAGRSAAEAAKEIKNLIHASVERVE
1533 HGTALVDKAGETMSEVVSIRRVTDIMGEISSASGEQSAGVAQVGEAVTSMDQATQQNAALVEEMAAAASS
1534 LRNQAHDLVQVVAVFKLSGDQSRPAMAPAKAPAPQARPARPAVAQAPAKPLAKAAIARAPSPAARPA
1535 APALAQPAAPRPDPRSAPKGGDDWESF
1536 >Achromobacter_sp._DH1f_1 |WP_025136919.1 methyl-accepting chemotaxis
1537 protein [Achromobacter sp. DH1f]
1538 MNNLKLGTRLAGGFVALLAMILTMCIVGLVSLANINASVETVTQSRSLIKERLINDWARNIQTGVRTTTAIA
1539 KSADASLAGFFAEAAATSTRNSSALQKIEPMIESAEERQLWEGIGKSRAEYLRTRDGFIFKAKQEGNVEAA
1540 NKIFTQEFLPATRFIDQITKLSNLQRADIDAQGAIESAYGVANFWMIAIGSIAVVSGLLLAVLLTRGIT
1541 RPLSQAVRVARTVAANDLTSAISVTSRDEIGQLMLALQSMNATLVGTVARIRTGVDSIASASGEIAAGNTD
1542 LSSRTEQQAASLEETAASMEELSSTVKQNADSAKQANQLAAAASDTASRGGATVSEVVSTMSAISASSVKI
1543 ADIVSVIDGIAFQTNILALNAAVEAARAGEQGGKGFVVAEVRTLAQRSAAAKEIKVLIEDTVSKIRQGS
1544 GSAERAGATMQEIVSSVQRVTDIMGEIAAASAEQADGIEQVNRAVSQMDEVTTQQNAALVEEAAAAAGSMQD
1545 QAAELTRAVSAFKLPGGSQVAGR PALASTGSTDHPSGPALRIIAY
1546 >Diaphorobacter_polyhydroxybutyrativorans_2 |WP_088886815.1 HAMP
1547 domain-containing protein [Diaphorobacter polyhydroxybutyrativorans]
1548 MENFRIGTRLTAGFGLLILFAVLMLTVGVWQLQEVAGSTRQILSVPLQKERLVTDWYGVIRASIQRATAVA
1549 RSSDDSLTELFAAENAASSKETNERQAQFVKLISGSEEQALFDTLSGHRQAYIQARDAAIAAKKGGQAEQV
1550 TTLPERAQFVFPASRQLESALALRDFQRASIDRNGQDIDSSATASSWLMGGIGLVVLVAGIGVAWILTHSIT
1551 APLARAVQATQVVAAGDLTHAVHSSGRDEGAQLLQALQAMTDRLRRTIVSEVRQGADSIAGASAEIAAGNLD
1552 LSRTEQQAASLEETAASLEELTSTVRQNADNAHQANQLARTAAEQAGGQVMDDVMQTMRAIDASSRKI
1553 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSRSLAGRSSEAAKEIKDLIGRSVNTVEAGN
1554 QLVAKAGTSIQDIIRSVDQVSALVGEISSASREQSSGIEQVNI AVAHMDQATQQNAALVEEATAATQSLQG
1555 QAAQVAQAVGVFRVDSSAVALPAPQA
1556 >Massilia_sp._KIM_1 |WP_078034342.1 HAMP domain-containing protein
1557 [Massilia sp. KIM]
1558 MITFNKLNIGTRLAAGFALTLLMTVLI AAAGVWRLNQVAAETRE IMAEPIAKERMIAEWYTQIFA AVRRTA
1559 AIVKSSDPSLTTYFKEDSAATSKLSTELVKRIEPMIKGEDETALFKAVIEHRKTYSTARDNAVKAKAEGNV
1560 ELADQILEQSFTPAAKAYQEQVRKLELQHQRIAASAATIDANARSGETMIIALAAAALALGAVFSWLLTR
1561 SITGPLREAVKAAETVAAGDLTVSLDTSRQDETGALLRALRHMNDSLARIVSEVRTGTEQISTASGEIASG
1562 SFDLSARTEQQAASLEETAASMEELTGTVRQNADNARQANQLAIAASTVATDAGSAAEQLIATMGSINESS
1563 RKIVDIIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSASAAKEIKQLIGDSVEKVD
1564 AGAKLVDRTGATMQEVVTSIRRVTDIMGEISSASQEQIQGIDQVNRAMSEMDQATQQNAALVEEATAATSA
1565 LQEAVRLAKVVDVFKLDPSQRAAAPAATRPAATLPALRASAPLKRPAPLKAAKAAKATATVDGDWEQF
1566 >Massilia_yuzhufengensis_1 |WP_091876734.1 HAMP domain-containing
1567 protein [Massilia yuzhufengensis]
1568 MRTFNLP IGVRLAAGFALT LIMAVLIAGTGMWRLQVATAAQVTLAAPLAKERLIAEWYTQIFA AVRRTA
1569 AIVKSSDPSLTAYFKEDAAATGKLAADLVKQIEPLIAGDKIEALFKRVQEQRKLYGAARDNAVKAKSEGNO
1570 ELADKILDESFTPVSKAYQESVRELVALQRDAIAATAQDIDATAERGGMIIAGLTAAAVILGALFSWMLTR
1571 GITRPIRAAVQAAERVAAGDLTHRIDADSKDETGALLRALGHMNDLSVKIVSEVRSGTETIGTASGEISAG
1572 SLDLSARTEQQAASLEETAASMEELTGTVRQNADNARQANQLAITASSVATQAGSVVEQVITTMGSINESS
1573 RKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLAQRSAAAKEIKGLIGASVEKVE
1574 AGTRLVDQTGETMEQVVTSIRRVTDIMGEISSASQEQIHGIDQVNOAMGLMDEATQQNAALVEESAAAAGS
1575 LQDQASRLAQMVNVFRLDARAAAPAGKPPRALAVTAKPAASY
1576 >Bordetella_genomosp._1_1 |WP_094830849.1 HAMP domain-containing
1577 protein [Bordetella genomosp. 1]

1578 MKNLKLGTRLAGGFVLLAMTTVMCLVGLYALSNI SGAVEDMTQQRSLIKERMISDWSRYIHTGVTRTTAIA
1579 KSSDPSLVQFFSQAADSTKRASQLQQQIEPLIQSDEEKRIWADLGTARTAYLSSRDRSYKAKQDGDIAAA
1580 TRIFEQEYQLQASRRFIDVITQLQELQRNAIDAQAASIDSAYRSANLWMVVLGVVAVVSGLLLAVLLTRGIT
1581 RPLAQAVRVARTVASNDLTSRITATSRDEIGELMGALQTMNANLAGTVTRIRSGVENIASASSQIAAGNAD
1582 LSSRTEQQAASLEETAASMEQLSSTVKQNAESARQANQLAAAASDTASRGGATVTEVVGTMSSAISASSVKI
1583 ADIVSVIDGIAFQTNILALNAAVEAARAGEQGGKGFVVAEVRSLAQRSAQAAKEIKTLIEDTVHKIGQGS
1584 DSAERAGATMQDILSAVQRVTDIMGEIAAASAEQADGIEQVNRVAQMDQEVTTQQAALVEEAAAAAGSMQD
1585 QAADLRGAVSAFKLQGGTPTQADAQTTPRPGAAPLALAAAY
1586 >Paucibacter_sp._KCTC_42545_1 |WP_058719952.1 methyl-accepting
1587 chemotaxis protein [Paucibacter sp. KCTC 42545]
1588 MSVTLISGHSIGRRLNIAFIVLLIALAGSAMGYWSLQKVANETATMYEETLLAERLAGDWQRNIVSGVNR
1589 STAIASVSKDNSLAEIFSTAAAESTRQSSELQKQLEVLTTSPERKLFQELSQRKPYLASRDALTKAKKAG
1590 DAEGAEIIFKQFLPAAAQFQDSIKLIVQEERNQLDAAAKRVANTNSQARIALLVFVSVCALLVGATLALRL
1591 TRSIARPLSQAAASADAIAHFDSLRRIVVDSNDETQGLQQAQKTMQESLIRLIGEVRSSTDSISTASAEIA
1592 TGNHDLARSARTEQTAASLQEAASMAQLTGTVRQTAESAVTANQLANSAAEVARRGGTVVAQVVSTMEDISA
1593 SSRITDIIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSAAEAAKEIKTLIGASAER
1594 VESGTQLVQAGATMSDIVASVQRVSDIIAEISTASREQSDGINQVNSAVGQLDQMTQQAALVEESAAAA
1595 ESLRDQSGRLASAISVFRLL
1596 >Caballeronia_sordidicola_2 |WP_051888411.1 methyl-accepting chemotaxis
1597 protein [Caballeronia sordidicola]
1598 MNMLRDMKIGKRLAVGFALIFLVSLASSLVSIWRLHDVATTTHEMMHTPLAKERMISDWYRATYGSIRRTM
1599 AIAKSNDSLDSFFAKDAADALQLATDMQNKIAPLLETDQEKALYTALIDARGKYAKSRDALKKAKEDGKN
1600 ELASKMLDETFVPAAKEYELRLRDLDAQRTSIDHVSDEIDAAEFRTRNALIMMAVLSMLAGGLVALLLTL
1601 SITRPLASALRMARFVADGDLTASIRNSAKDEPGQLLDALDQMSVTLRGIVAQVRSQSDMIEVASSEVAAG
1602 NIDLSARTEEQAASLEQTSATMGSLTQTVRNSSNAREVDQLARVASEVALRGSMEVAEVAATMAVISSSA
1603 KQIVNIIGVIDSIAFQTNILALNAAVEAARAGEQGGKGFVAVASEVRGLAHRSAASAAREIKALIGDSVQKVD
1604 TGTYLVERAGKTILEMVENIKHVQHLVGEISSASQTSISIEEVNQAILQIDTQQAALVEEAAAAASS
1605 LKEHSAKLTQIVSVFKIGTIG
1606 >Janthinobacterium_sp._CG3_1 |WP_017874946.1 methyl-accepting
1607 chemotaxis protein [Janthinobacterium sp. CG3]
1608 MMKITDFNIGTRFLFGGFASILVVAIAASAVGIWQLRTVAIETRTMAEQPLAKERFVSDWYRNTASNILRRT
1609 SIVRSADDTLASFPAADIAATSASITDIQKAIIEPLLASAAEKTAYEHVGEARKLYIKARDGAIAAKRGDA
1610 DASARLMEQQFLPAAKQYNEALSALLAMQRESINANAQNIIEKQYQTGLTLMLLLIALLAAFGIACATLITR
1611 SIVKPLQTAVAARKVASGDLSDGDIVAQGTGDETQGLLLALRDMNNSLRGIVGTVRGGADAIATASSEVATG
1612 NLDLSARTEEQAASLQETASSMEEITSTVKHNADNTRQASALVASTSDVARQGGALVARVVATMGGINASS
1613 KQIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRNLAQRSAAAAKEIKTLIGDSVTQVE
1614 QGSTLVGQAGAIMQIVASVQRVTLVMGEIATASGEQEHGIEQINQAI SQMDTQQAALVEEAAAAAES
1615 LQDQSAKLARAVSVFKLVRHEHA
1616 >Acidovorax_sp._Leaf78_1 |WP_056166736.1 methyl-accepting chemotaxis
1617 protein [Acidovorax sp. Leaf78]
1618 MSRLSDLSVAKRLALGFSLVLLLLIGAIALSISRLNAVADATLEMVQNPIKTERLVSDWSRNLRTGITRRTA
1619 AVARSSDPALADFFAEDSKASSKSSGELQKAVEALMILVSEKKTFAEIGALRTIYLKNRDDIFALKKEGKV
1620 DEANAMLVKQFMPEAANYAAKMDPELLRNQREQVDALGRSVEQNRQTSRQLLLALGALSVAVAVLFSWILAR
1621 SITVPLSQASDLAKQVAAGNLTATVPQHGKDEVGELMSSLALMQTNLASVVNNVRHGAESVSNASSEIAQG
1622 NTDLSSRTEHQASALQQTAAASMEQLNSAVRNNADNARQANQLAMTASSVAAQGGAVVGDVVETMKGINDAS
1623 RKISDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSAAEAAKEIKNLIQASVDRVE
1624 HGTALVDKAGETMSEVVSSIRRVTDIMGEISAASGEQSAQAQVGEAVTSMDQATQQAALVEEAAAAASS
1625 LRNQAHLVQVVAVFKLSGDQARPAATPARAPAPIPQSRPAPARPVTLAKPSAKPANPTKPAIARAPSPTP
1626 AARKPAAPALPSSPAPRPDPSAQKGGDDWESF
1627 >Diaphorobacter_sp._J5-51_2 |WP_084002049.1 HAMP domain-containing
1628 protein [Diaphorobacter sp. J5-51]
1629 MGTRLTAGFGLLILFAVLMLTVGVWQLQGVAGSTRQILSVPLQKERLVTDWYGVIRASIQRATAVARSSDD
1630 SLTELFAAENAASSKEINERQAQFVKLISGSEEQALFDTLSGHRQAYIQARDAIIAAKKGQAEQVTTLFE
1631 RQFVPASRGYLESALALRDFQRASIDRAGQDIDSSATASSWLMGGMGLVVLVAGIGVAVILTHSITAPLAR
1632 AVQATQVVAAGDLTHAVHSSGRDEGAQLLQALQAMTDRLRTIVGEVRQGADSIAGASAEIAAGNLDLSRRT
1633 EQQASSLEETAASLEELTSTVRQNADNAHQANQLARTAAEQAGQGGQVMDVMQTMRAIDASSRKIVDIIIG
1634 VIDSIQFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAGRSSEAAKEIKDLIGRSVDTVEAGNQLVAK

1635 AGTSIQDIIRSVDQVSALVGEISAASREQSSGIEQVNI AVAHMDQATQQNAALVEEATAATQSLQGQAAQV
1636 AQAVGVFRVDSSAVALPAPQA
1637 >Dickeya_zeae_1 |WP_016943041.1 HAMP domain-containing protein [Dickeya
1638 zeae]
1639 MKNYKIGTRLSIGFGILIAFSLIMLASGIYQLNQITRNAEQIMLVPLRKERLVADWAATLSAGIQRTTATA
1640 RSSDPSLAQVFAADNANATKENNERVAKFTELVSSKEEQGLLDQLNADRQAYIKARDEIFSAKSSGNAEQA
1641 KQVFEQRLLPVSVQYQKSMTTLRDYQRTNIDRMREEISARAQSSYLFLGVLGLLITVVGSLLAWMLTRSIV
1642 RPLQTSVQVNTSVARGDLTAEISPOGRDELAQLQHALQDMTGQLRTVVGEVREGAEIAGASSQLAAGNQD
1643 LSNRTDEQSSALQETAASIEQLTSTVRQNADNARQANQLAQDTASQAQAGGQLVSEVVQTMGAIDSSSKKI
1644 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSASAAREIKELIGHSVETVDAGN
1645 RLVEKAGVSIQGIQVGVKSELVGEISVASQEQSLGIEQVNQAINKMEQTTLQNASLVREGYNATQSLQQ
1646 QAEQLKQVVSIFHLEEARGGSYNLAGNRPMISPSAPA AKTLALKKPAAKTSASADDWQSF
1647 >Achromobacter_arsenitoxydans_1 |WP_043517407.1 methyl-accepting
1648 chemotaxis protein [Achromobacter arsenitoxydans]
1649 MKNMKLGTLAGGYAILLAMIMVMCIVGLVSLADINVSVDTLTHRS LTKERLINDWARNIQAGVTRTTAIA
1650 KSADASLASFFAEAAATSSRNSSALQOKIEPLIESDEEKT LWQGIGKARGEYLRTRDGIFKAKQEGNVEAA
1651 NKIFTQEFLPATRFIDHITRLSDLQRADIDARATDIESAYGAANFWMIVIGSVAVVAGLLAVRLTRSIT
1652 RPLSEAVRVARTVAANDLTSTIVVTSRDEIGQLLRALETMNANLAGTVARIRTGVDSIASASGEIAAGNTD
1653 LSSRTEQQAASLEETAASMEQLSSTVKQNADSAKQANQLAAAASDTASRGGATVSEVVSTMNAISASSVKI
1654 SDIVSVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAEVRTLQRSQAQAKEIKVLIEDTVQKISQGS
1655 GSAERAGTTMQEIVSSVQRVTDIMGEIAAASAEQADGIEQVNRAVSQMDEVTTQQNAALVEEAAAAGSMQD
1656 QSAELTRAVSAFRLPGGQGGVAVAAIEVVES SAALRIAAY
1657 >Comamonas_terrae_1 |WP_066475921.1 HAMP domain-containing protein
1658 [Comamonas terrae]
1659 MQLKDLTIGKRLGIGFALVLLALIASTAVISVLR LHALETATRQMMDVPLSKERMLADWSRYVYGGIRRTIA
1660 IAKTGDAALAEMFAK DSETSTKNSQDLAKQIEALPSSDEEKAIQOKFAQVRKDYLS TRNAIGKEQEAGNKA
1661 EAARLLEQHFLPTAKLYENTLDELVKLQRRTIDELADQVSDMARQSRQQLILLALLTAFCIWWAWWLTQG
1662 ITRPIHRAMAAASRVAQGD LASDLRSDESLIRKDETGQLLRSLRDMNEGLVRIVGNVRAGAESIAGASRQI
1663 AAGNLDLSSRTEQQASSLEQTAASMEELTATVKQNADNAQANQLAATASSVAGRGGTVVSVQVVTMEAIN
1664 ASSRKIVDII SVIEGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRALAGRSAAEAAKEIKALIGDSVT
1665 QISQGSELVHLAGNTMKEIVDSVRRVTDIMGEITAATSEQSAGIEQVNQAVVHIDQATQQNAALVEEQASAA
1666 AQSMQEQANQLTQTVSVFKLGHVG
1667 >Comamonas_kerstersi_1 |WP_054065345.1 methyl-accepting chemotaxis
1668 protein [Comamonas kerstersi]
1669 MPLQHISIGKRLGLAFVLTFLFIATMLAVGIWR LQAVAQSTADMMARPLSKERVISDWYRTVYSNVNRHAL
1670 VARSSDAELARQFVADNVEASKASSRQQAQLKLISTPEEQALFDQVSVLRTRFVQARDTIYQAKAEGRAD
1671 EAERLLRSDFQPAADAYLQTLQALLDHQRQRI SEAAAGVQAEFERGRMQLAGLGGLAVLIAVALAVAITRS
1672 ITSPLARAVHAVETVAAGDLTHRVHSDAQDETGQLLRALDGMGDQLRNVVGVQVRQADGVASASSQIASGN
1673 LDLSSRTEEQASALQQTAA SMEQMTSTVRQNADNARTANQLAVSASELASRGGQVVDQVVGTMGDIHEASR
1674 KIVDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRTLQRSADA AKQIKDLITASVERVDA
1675 GHTLVEEAGVVMRDVVAGVRRVTDIVGEISAASQEQTQGLEQVQHAI TQMDAVTQQNAALVEEAAAATRAL
1676 EAQSVQLVQAMAHFQVGQERAVTATPALLTRA
1677 >Acidovorax_wautersi_1 |WP_092940912.1 HAMP domain-containing protein
1678 [Acidovorax wautersi]
1679 MNLHHFSIGKRLGLAFGLMTLFIIGMVVSATGR LHSVANDTAVMMNPLTKERLISDWYRTIYSNVS RSHSL
1680 VARSTDATLATQFTQENAEASRASTAQQOQLAKLISGP EEQALFDRVGVLRQQFIKARDAIYKAKAEGRAE
1681 DAQRILDAEFLPSGKGYLEGLQALLDFQRQQINAAAQSVQNNYEGGRNALIGLGVLATVAAIALAWAITRS
1682 VTGPLHRAVSVAESVAAGDLSVRAESTARDEAGQLLRALDAMGRQLSDTVGVKVR LGADNIAMASSEIANGN
1683 LDLSSRTEEQASALQQTAA SMEEMTATVRRNADSAALADQLARSASELAVRGGDVVGNVSTMGGIHSSSR
1684 KIVDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRTLQRSATAAKEIKALIDDSVTQVDA
1685 GNRLVEEAGQVISDVVAGVRRVTDIVGEISAASQEQTRGLEQVNQAVTQMDQVTQQNAALVEEAAAATASL
1686 EAQSAQLAQAVAVFRLTA
1687 >Dickeya_dianthicola_1 |WP_024104304.1 methyl-accepting chemotaxis
1688 protein [Dickeya dianthicola]
1689 MKNYKIGIRLSVGFVGLIAFSLVMMASGIYQLRQISQNAEKIMQIPLQKERLVADWGATLAAGIQRATATA
1690 RSSDASLAQVFAADNANATKENNERAAKFTALVSLNEEKALLDKLNIDRQAYIKARDDIFA AKAAGNAEQA
1691 KQLFEQQLQPI SVAYQKSMNLLRDYQRTSIDQMRTDIAERANNSYLFLGGLGV LITAIIGSLLAWMLTHSIV

1692 QPLQKAVQVTHAVARGELTDDDISPQGRDELAQLQHALQEMTAQLRTVVGEVREGAEAIADASSQLSAGNQD
1693 LSNRTDEQSGALQETAASIEQLTSTVVRQNADNARQASQLAQDTASQAQSGGQLVSEVVQTMGAIDSSSKKI
1694 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSQAQRSASAAREIKELIGHSVQTVVDAGN
1695 RLVEKAGVSIQGGIVDGVKRVSELVGEISVASQEQLGIEQVNMAINKMEQTTLQNASLVREGTTATQALQQ
1696 QAEQLKQVVGIFHLEKARPDAYRVSGSRPMLAASPATKTLALKPAASSRKASASEDDWQAF
1697 >Roseateles_terrae_1 |WP_088451840.1 HAMP domain-containing protein
1698 [Roseateles_terrae]
1699 MRLASRLAMGFGVVLVLLAAIVLIGGMSLGRTAESTRQMMDIPLOKERLVAEWYTLTLVGVKRYTAIAKSS
1700 DASLADYFTNDVKIISTARGNEI IKALDGLPKSDEEKVVVDKLEARKVYTGTRDRIGAAKKSNADEAIRI
1701 LEQEFRPQADVFLGNMVDYLKFFQKTLDEMAKEVDASTTSAQWRIGLIGALALVVGAVFAWVLRVSVTVPL
1702 QRARQMVAVAGGDLTRSAAKAEQDEIAQMMTQLDAMRLSLQTAISTVRDSSSENIQNACQEVSAQNSQDL
1703 RTEQTAGNVQQAASAMEQLNGTVGQTAQSSREAAQLATNAVQVATRGGEVVAQVVARMQGIHGSSRKIADI
1704 IGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVTEVRNLAGRSAAAAKEIKSLIEASVEQVEAGTDLV
1705 NRAGDTMNEVVGAIQRVTVGIVGEISVASAEQAEGVSQVSGAVTQMDAATQQNAAMVEEIAAAAASSLRGQAQ
1706 SLVDVAVRVFRL
1707 >Acidovorax_caeni_1 |WP_054257022.1 methyl-accepting chemotaxis protein
1708 [Acidovorax_caeni]
1709 MHKLSIGTRLAVGFGLLFFALLNSALS IWQLQASSQGAQAIIEKPLAKERLISDWYRFIHTAVRRTTAIA
1710 KSSDPSLATYFAAEQKESAESTTAIHKQVETLMVTDEEKRLFGDITLALRANYVAARDEVIRLKREGRAEES
1711 ARLLEATFVPAKVYVERVNDLLKLQRHALDQAAEPIREANNRTSLGILALGLLTLALGVVASLAIARGIV
1712 RPLGRSLGVARQVAAGDLSPVVFDAAQEQETREDESSALLQALGSMQQSLTRVILTIREAAESMATASAEIATG
1713 NLDLSQRTEQTASHLQTTAASMEELTGTVEHTAQAAARTASALAGSAATVAGRGGALVEQVVHTMESIDGSA
1714 RRIADITGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSQAQRSAAAAREIKDLIADSTRRVG
1715 EGSRLVREAGDTMREIVSAVQRVTVDEVAGIAAAAGQSSAGIAQVNASVSQLDQMTQQNAALVEESAAAQSS
1716 LREQSERLSHVAFAFVLPTEAAVRGRALALPA
1717 >Pseudoduganella_violaceinigra_2 |WP_083941309.1 HAMP domain-containing
1718 protein [Pseudoduganella_violaceinigra]
1719 MQVLSQLRIGPRLAAGFGIVLILLSAIGTSYALYHSNDTANATRAMMDRPLAKERLVS DWYVLIYSAIARTQ
1720 LIARSSDAELSKTFATVIADSTKRGGELLKQVEALLEPEERKIYDDAMVLRKYQEAQNNIMKANQAGNA
1721 TEGERLYRDVFDPAKGYQEKVKELLAQRKAIDATAAGINAAHERSTRMLVTLILLSFGAWAAWVISR
1722 SITVPLNSALGIANTVAEGDLTTRFDDKTARDEIGDLMIALRGMNDALRRLVSQVQTGTTAIATASSEIAE
1723 GNLDLSSRTEQQASSLEETASSMEELTSTVVRQNADNANQANQLAHAASDVAARGGEIVGQVETMGSIDAS
1724 SRKIVDIIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAAAREIKELIDNSVSQV
1725 NAGTSLVQQAGTTMGEVVTSVRRVTDIMGEITSASREQSVGIDEVNOAIGQMDQVTQQNAALVEEAAAAA
1726 SMQEQAAQLAQVAASFGLGTDVARWSAQPRPATQRTDNRDAVAPALNSAPPKRLSTTEARSAPRATPRP
1727 AANTSDDSDRSAERRTKAERRSPAAANDEWEEF
1728 >Roseateles_sp._YR242_1 |WP_092949773.1 HAMP domain-containing protein
1729 [Roseateles_sp._YR242]
1730 MRVKVMAGDGAMARNGRHRIHSTATRARQPISSQVFLSRDGLHTWRLGPATGMTTLPSRI PAICRESTNCT
1731 VNAGLLPLCPPGGARYSDASVCRCARRKYRVKLNMMRLSSRLAMGFGVVLVLLAAIVF IGGMSLGRTAQST
1732 REMMDVPLEKERLVSEWYTLTLVGVKRYTAIAKSTDASLADYFVNDVKVSTARGNEI IKALDELPKSDEEK
1733 KVVEQLIEARKTYVATRDRIAAAKKSNAEDATRILEQEFRPQADTYLEKMMGYLKFQKTLDEMSAGVNT
1734 ATTDQWRIGLIGALALIVGGVFAWVLRVSVTVPLARAQSLVDAVASGDLTQSVQPDGRDEIAQMMTQLDA
1735 MRLSLQRAISTVRDSSSENIQNACQEVSAQNSQDLQRTEQTAGNVQQAASAMEQLNGTVGQTAQSSREANQL
1736 ATNAAEVAQRGGQVAVDVSVMQGIHGSSRKIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAV
1737 TEVRNLAGRSAAAAKEIKSLIEASVEQVEAGTNLVNRAGETMTEVVS AIHRVTGIVSEISVASAEQAEGVS
1738 QVSGAVTQMDAATQQNAAMVEEIAAAAASSLRGQAQSLVDVAVRVFRL
1739 >Dickeya_1 |WP_038917615.1 MULTISPECIES: methyl-accepting chemotaxis
1740 protein [Dickeya]
1741 MKNYNIGIRLSIGFGILIAFSLTMLASGIYQLRQISQNAEQIMQIPLRKERLVADWGAALAAGIQRATATA
1742 RSSDASLTQVFAADNANATKENNERAAQFTALVSSSEEKALLDNLNTNRQAYIKARDDIFAAKSAGNSEQA
1743 KQFFEQLRQPIAIEYQKSMNILRDYQRTSIDRMRMDIAERASNSYFFLGGLGVLITVIGSLLAWMLTRSIV
1744 RPLQKAVLITHAVAKGDLTAEISPQGRDELAQLQFALKAMIAQLRTVVGEVREGAEAIAGASSQLSAGNLD
1745 LSSRTEEQSGALQETASSIEQLTSTVVRHNADNARQASQLAQDTAIQAQSGGQLVSEVVQTMGAIDSSSKKI
1746 VDIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSQAQRSASAAREIKELIGHSVQTVVDAGN
1747 QLVEKAGASIQGGIVDGVKRVSELVGEISVASQEQLGIEQVNMAINKMEQTTLQNASLVREGNTATQALQQ
1748 QAEQLKQVVSIFHQEETSHRAYSAPGNKPRLSAPPAKTLALKPAASSGKASGSEDDWHAF

1749 >Acidovorax_sp._56_3 |WP_099657573.1 HAMP domain-containing protein
1750 [Acidovorax sp. 56]
1751 MNQIAIGKRLSLGFGLLLALSLLGTLGLVWQLQTASTSTQAVIEQPLAKERLISDWYRLIHTAVRRTTAVA
1752 KSSDASLATYFADEQKLSANTTTDIQTKEVGLMQTDAERALFKDISNLRRSYTEARDAVIELRRSGQHEQA
1753 DAQLETRFVPAAKQYMARVEALMELQKALDESAAPIKAANDQARYWLIALGAITCGLGMALAVTITRSIT
1754 LPLSDSVAVADTIARGDLTSSIMSTRKDETGHLRLALGDMQHSLSMIGQIRDAGNQIASASDQIAGGTQD
1755 LSSRTEHTAANLQQTASSMEQFTATVQQSAEAARTASGLASSAAEVASQGGSIIVAVVDTMEDIHTSSRRI
1756 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSQAQSAEAAKEIKGLISTSVDKVGEGT
1757 QLVHNAGAAMQNIVSSVQKVTEVIAHIASSAREQSDGIALVNDIAIQLDQATQQNAALVEESAAAAQSLRE
1758 QAYRLAQAASTFKVADSAAPLRPGRQQPQLTAA
1759 >Rubrivivax_gelatinosus_1 |WP_043783764.1 methyl-accepting chemotaxis
1760 protein [Rubrivivax gelatinosus]
1761 MLKTLGSAKISIGRRLSTVLALVLLISFVSGSGFYWALSRTAAANQDMLLEDVSLVSERLASDWYRNISGGVNR
1762 TTAIAVSSDANLKGKFFADVSAESTKQSTELQKKLEPMMKTEAEKALYEKLAATRKIYLGSRDEVYAARQAG
1763 EAEKAHDIFQNKFPAAAQFQDAIRALVQMQRDELDAEAVKAADANRAARIALVVFQTCALVVGAAALALWL
1764 TRSITVPLNEAVEVADTIASFDLRSPITPRGEDETGRLLRSLQSMQSSLRRLIGEVRASDTSIGTASSEIA
1765 SGNMDLSARTEQTASNLQAAAASMTQLASTVVRQTADAAGTASGLANTAASVAQRGGEVVSQVVSTMEIST
1766 SSHRISDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSQAQSAEAAKEIKGLIGSAVDS
1767 VETGSRMVQEAGSTMTTELVASVQRVNQLIGEIGNATREQSDGISQLNAGVSQLDQMTQQNAALVEEAASAA
1768 GSLKDQSTRLASAVSVFRL
1769 >Mitsuaria_chitosanitabida_1 |WP_084452165.1 HAMP domain-containing
1770 protein [Mitsuaria chitosanitabida]
1771 MNDMRLAARLSMGFGVLLLVAAIMTVGWLGLNRTEQATRMTMAVPLQKERLVSEWYMLTIVGVKRYTAIA
1772 KSSDPSLADYFTADVKVSTARGNEIVKSLDALPKSDDEKRVVAELTEARKTYIATRDKIAALKKAGDAEAT
1773 ERLLTEQFRPQADAYLEKMTGYLRFQKTLDDMAAEVDEATNAAQARILVIGLLALAAGALFAWALTRSVT
1774 RPLARAMDLVESVAQGDLTRVATAEGRDEIATMVGAIERMNASLQTAITQVRSSSESIQNACHEVSAGNQD
1775 LSQRTEQTASNVRRAASTMEQLSGTVGHTAQSSGEANKLANSAAEVATRGGEVVSQVVARMQGIHGSSRRI
1776 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLASRSAAEAAKEIKTLIAASVDEVEAGT
1777 ALVNRAGETMNEVVDAIRHVHRIVGEISVASAEQAQGVSVQVSGAVSEMDAATQQNAAMVEEIASAASSLRG
1778 QALSIVDAVSVFRIHRA
1779 >Massilia_niastensis_1 |WP_020652850.1 HAMP domain-containing protein
1780 [Massilia niastensis]
1781 MMVTFNKLNIQTRLTAGFALTLLMTVLIAGAGAWRLNDVAQETRDILAQPLAKERYIAEWYTIQIFAVRRT
1782 AAIVKSSDPSLGAFFKEDAATTSALSTEMVKKIEPLLEGEDEHAIFKASQELRKAYSNARDTAIKARAEGN
1783 VELAEQILVQTYTPTARAYQLKVVRELLDLQRKRIDDAATIQTATAERSNMLIASLAAAALLGAVFSWLLT
1784 RSITHPLRDAVRAAETVASGDLTSRIESSAKDETGALLRALRHMNDSLAQIVSEVRTGTQTMGASSELAA
1785 GSFDLSSRTEQQAASLEETAASMEELTGTVRQONADNARQANQLAITASSVAAQAGTAVEQVIATMGSINES
1786 SRKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLAQRSAAAKEIKQLIGDSVEKV
1787 DAGARLVDPHTGVTMDEVVTSIQRVTDIMAEITSASQEQIQGIDQVNVQAMVQMDGATQQNAALVEEATAATA
1788 ALQDQAARLAQVVDVFKLDDRHAAPQAIAAAARPAARPAARTPALTAAPATRPAARAPAAASSRTRTRPAA
1789 TPTTESDWEEF
1790 >Rhizobacter_sp._Root1221_1 |WP_056657280.1 methyl-accepting chemotaxis
1791 protein [Rhizobacter sp. Root1221]
1792 MRVFSFASRSIQRLAGVLGLVLLISFTGSSSLGYWALAAARETRAMYTDLSLATERLASDWYRNISAGVFR
1793 TTAIAASSDSSLADFFAASAAEASKQSSELQKALDERMQSPAERAAFDKLTVEVRKDYIAARDAISAARKAG
1794 DADQAKQILETRFKPLAVSYQDNIKNIVQAQRDELDAQAQRVEAANSAARTGLIVFALCALGVGGVLSAWL
1795 SRSITRPLREAGEVADAIARFDLTRPITVRQDET SRLMQSLQTMQAALLKLIQEVGRVSTESISTASTEIA
1796 VGNQDLSSRTEQTAANLQAAAASMTQLTGTVRQTAAAASTANQLASSATEVAQRGGRVSEVVATMEEISH
1797 SSKKINDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSQAQSAEAAKEIKALIGASVER
1798 VESGTQLVQNAGATMTEIVTSVQRVTDIAEISAASHEQSDGIGQINAVTQLDDMTQQNAALVEESAAAA
1799 ESLRGQSGRLQEAIAVFRHLHDGAKAPAPAAWVPAPAVKPRGVSPAAAVKPKALKSPLKAGVKAAPAVKVA
1800 AAPVKGKVPSPSPAASGSTDWESF
1801 >Collimonas_fungivorans_1 |WP_061540704.1 methyl-accepting chemotaxis
1802 protein [Collimonas fungivorans]
1803 MKIVNLKVGTRMGIGFAIVLSLSVISIAIGIWNLRQVATETQRMESPLAKERIVSDWSVLTNAAIARTSF
1804 IVKSTDETLATTFEAEDIDASAKKGTIEIQNSLEPLLTSSLEKEKYALIKTLREKYQQSKVAAMKAKQGGKAE
1805 EASKIYNSEFMPTAKSYQGELFAFLSLQRKNIDQTGQQIAQLYSRFSNLMVLLGLVIVLGVAVCAFLISRS

1806 ITRPLGEAIKVAQTVASGDLSSRIEVKTSDETGQLMQALKDMNDSLLKVVSEVRSRGTDTIATASNQIASGN
1807 LDLSSRTEQQASSLEETAASMEQLTSTVKQNADNARQANQLAVSASGVAVRGGGVVSQVVTMDLINTSAK
1808 KIVDIIISVIDNIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAVAKEIKHLIDDSVEKVDV
1809 GVKLVGQAGATMGEIVDSVKRVTDIMSEITAASQEQTAGIEQVNQAIMQMDQVTQQNAALVEQAAAAAASL
1810 QDQAGNLVQVVSVMTEGTQAHAGASLKAASRAAPVAAPVYVAARNARLPSANVKTFRKRVANASAAAGSE
1811 WDQF
1812 >Achromobacter_spanius_1 |WP_050447183.1 methyl-accepting chemotaxis
1813 protein [Achromobacter spanius]
1814 MNNLKLGTRLAGGFGILLAMITVMCLVGLISLANINESVETVTQRSLIKERLISDWARNIQAGVTRTTAIA
1815 KSTDASLAAFFTTDEAAASSRNSSALQQQIEPLIQTPPEEKQLWQGVGKSRGDYLRTRDAIFKAKQSGDVDTA
1816 NRVFTQEFLPATRFIDQITKLSALQRAEIDARAADIQSAYRTANFWMIVIGSVALISGLLLAVLLTRGIT
1817 RPLSAAVRVARTVAANDLTSTVIVKSRDEIGQLMQALASMNANLADTVARIRTGVDSMASASGEIAAGNAD
1818 LSSRTEQQAASLEETAASMEQLSSTVKLNADSRQANQLAATASDTASRGGATVSEVSTMSAISSSSVKI
1819 ADIVSVIDGIAFQTNILALNAAVEAARAGEQGGKGFVVAEVRTLAQRSAAAKEIKTLIEDTVHKISQGS
1820 ISAERAGATMGEIVSSVQRVTDIMGEIAAASAEQADGIEQVNRAVSQMDEVTTQQNAALVEEAAAAAGSMQD
1821 QAADLTRAUSAFKLPGSVAVERVAGGRALAMTGAVALRA
1822 >Oxalobacteraceae_bacterium_AB_14_2 |WP_026334184.1 HAMP domain-
1823 containing protein [Oxalobacteraceae bacterium AB_14]
1824 MNLLTQLRIGTRLALGFAIVLLLLAICATSVALYNARANAEEATRHMMEQPLAKERLASDWYVLIYSAVARTA
1825 LIARSSDDSLSTTFADVIGASVKGGLMGLKQLLATDQEKAVFEASVGLRNTYQKAKTDIMNAKKAGNA
1826 AEAERLYKDFMFAAEAYQNKVKDLLSVQRKAIDDTAHAIDAANERSNMLLMVLAVLMVAIGTLAAWVISR
1827 SITVPLKSALEIASTVANGDLTTRFDAQTSQCEIGDLMTALKGMNDALRNVVSQVQSGTTTTIATASNQIAA
1828 GNMDLSQRTEEQASSLEETASSMEELTSTVRQNAENAKQANQLAQAASDVAERGGAIIVGQVVDTMGSIDAS
1829 SRKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAAAKEIKELIGNSVQQV
1830 DLGAKLVQQAGATMGDVVASVRRVTDIMGEITSASSEQSIGIDQVNTAITQMDQVTQQNAALVEQAAAAA
1831 SMQEQAAARLADVAASFGLGDEAARPPAPAARPAAPAARPALRQAAPARPAAKLGASKPATVGGEQDWEEF
1832 >Janthinobacterium_sp._64_3 |WP_100874105.1 hypothetical protein
1833 [Janthinobacterium sp. 64]
1834 MHALSHLRIGTRLAAGFALVLLLLSVISTSYALYSARVNAEATRQMMKPLAKERLVSVDWYVLIYSAIARTS
1835 MIAKSTDETLSSVFADTIADSTKQGGSELLKKIEALLDSDEEKAIKSSIAERVKYQDAKTLVMNARKAGNA
1836 AQAESTYRDSFAPAAAKYQNNVKALLAQORQAIDATAHAIEAANGRSFTLLLTLCALVVALGSVCWLITR
1837 SITAPLQAAVKVAETVAAGDLRTHFGTAASDEIGDLMRALHGMNEALRKKVSEVQGTGNAIATASGEIAAG
1838 NQDLSARTEQQASSLEETASSMEELTSTVKQNADNARQANQMAVAASSVAERGGSIVSQVVDTMGAIDTAS
1839 TKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVATEVRSLAQRSAAAAREIKTLIGDSVEQVN
1840 NGTRLVQQAGSTMSEVVDSVRRVTDIMAEITAASAEQSMGIDQVNQAIQMDQVTQQNAALVEEAAAAAES
1841 MQDQAARLAQVAAGFQLEHVTVQAVPVRAARPAAPTQLAKPAARSATARQPSIAARSAPAARKPQVQVAGEQ
1842 DWEEF
1843 >Acidovorax_oryzae_1 |WP_026434023.1 methyl-accepting chemotaxis
1844 protein [Acidovorax oryzae]
1845 MKFQDLSIGKRLALAFGLLTFIVGMLAVGTWRLQSVQDQTAAMMNLPLAKERLISDWYRTIYTNVSRHAL
1846 VARSSDTALAGRFTQENAAASRQSTEQQQQLAQLISGPEEQALFDRAGVLRKQFVTARDAIYQAKVDGRSD
1847 DAQRILDTEFTPSGKGYLDALQALLDFQRKQINEAAASVHRNYESGRNALVLLGLLATVAVALALGITRS
1848 VTRPLHRAVSVAEAVAGGDLTARSASTARDEMGQLLRALDAMATQLRDTVGQVRRGADGIALASSEIATGN
1849 LDLSSRTEEQASALQQTAAASMEQMTATVRQNADNAAQADQLARSASDMAVRGGEVVGNVVTMGGIHSASR
1850 KIVDIIIGVIDSIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRLAQRSATAAKEIKALIDDSVTQVDA
1851 GNRLVEEAGTVIRDVVTGVRVTDIVAEISAASQEQTSGLEQVNRAVAQMDQVTQQNAALVEEAAAATGSL
1852 EAQASHLVQAVAVFRLAESGTAVPRLAA
1853 >Janthinobacterium_sp._HH107_2 |WP_070312024.1 HAMP domain-containing
1854 protein [Janthinobacterium sp. HH107]
1855 MHALSHLRIGTRLAAGFALVLLLLSVISTSYALYSASVNAEATRQMMKPLAKERLVSVDWYVLIYSAIARTS
1856 MIARSTDETLSSNVFADTIADSTKQGGELLKQIETLLVSDEEKAIKASIAERVKYQDAKTLVMNARKGGNA
1857 AQAESVYRDSFAPAAAKYQNNVKALLSQORQAIDATAHAIEAANGRSFTLLLTLCALVVALGSVCWLITR
1858 SITQPLKAAVKVAETVADGDLRTHFGTPASDEIGDLMRALHGMNEALRKKVSEVQGTGNAIATASGEIAAG
1859 NQDLSARTEQQASSLEETASSMEELTSTVKQNADNARQANQMAVAASGVAERGGGIVSQQVVDTMGAIDTAS
1860 TKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVATEVRSLAQRSAAAAREIKTLIGDSVEQVN
1861 NGTRLVQQAGSTMGEVVDSVRRVTDIMAEITAASAEQSMGIDQVNQAIQMDQVTQQNAALVEEAAAAAES

1862 MQDQAARLAQVAAGFQLEHVATAAPVRAARPAKAAIATTQKLABRPPQARAGKPAAPKAASAAARKTPSHI
1863 AGEQDWEEF
1864 >Roseateles_depolymerans_1 |WP_058933831.1 methyl-accepting chemotaxis
1865 protein [Roseateles depolymerans]
1866 MKLNNMRLASRLAMGFGVVLVLLAAIVLIAGMSLGRTAESTRNMMAVPLQKERLVSEWYMLTLVGVKRYTA
1867 IAKSTDASLADYFANDVKISTARGNEIIKALDGLPKSDEEKVVDRLIEARKVYTGTDRDRIGAAKKNAGNAD
1868 EAIRILEQEFRPQADTFLGNMVDYLKFKQKTLDEMAKEVDAATTSAQWRIGLIGALALVVGAVFAWVLTTRS
1869 VTVPLIRAQQMVQAVASGDLTRSVKAEGRDEIAQMMTQLDAMRVSLQTAISTVRDSSENIQACQEVSAAGN
1870 QDLSQRTEQTAGNVQQAASAMEQLNGTVGQTAQSSREANQLATNAVEVATRGGQVVAEVVSRMQGIHGSSR
1871 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVATEVRNLAGRSAAAAKEIKSLIEASVEQVEA
1872 GTTLVNRAGDTMNEVVTAIQRVGTGIVGEISVASAEQADGVSQVSGAVTQMDAATQQNAAMVEEIAAAASSL
1873 RGQAQSLVDVAVRVFRL
1874 >Janthinobacterium_svalbardensis_4 |WP_096237432.1 HAMP domain-
1875 containing protein [Janthinobacterium svalbardensis]
1876 MHALSHLRIGTRLAAGFALVLLLSVSTSYALYSARVNTAATRQMMKPLAKERLVSDWYVLIYSAIARTS
1877 MIAKSTDETLSSVFADTIADSTKQGSSELLKIEALLDSDEEKNIKFASIAERVKYQDAKTLVMNARKAGNA
1878 AQAESAYRDSFAPAAAKYQNNVKALLSQQRQAIDATAQAI EAANRRSFTLLLTLCALVVALGSVCWLITR
1879 SITQPLKAAVKVAETVADGDLRTHFGTPASDEIGDLMRALHGMNEALRKVVSEVQTGTNAIATASGEIAAG
1880 NQDLSARTEQQASSLEETASSMEELTSTVKQNADNARQANQMAVAASSVAERGGNIVSQVVDTMGAIDTAS
1881 TKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVATEVRSLAQRSAAAAREIKTLIGDSVEQVN
1882 NGTRLVQQAGSTMSEVVDSVRHVTDIMAEITAASAEQSMGIDQVNQAI AQMDQVTQQNAALVEEAAAAAES
1883 MQDQAARLAQVAAGFQLEHVTPAVAPVRAARPARTAPAATPRLATQRQSQATASKPAAPRAAGAAARKTPS
1884 HVAGEQDWEEF
1885 >Curvibacter_lanceolatus_2 |WP_031255881.1 methyl-accepting chemotaxis
1886 protein [Curvibacter lanceolatus]
1887 MSVFQRLRIGARLALAFALILMMVVMLIVGVWRLQDIASQTHQMMERPLAKERLVSDWYRTIHTSVRRTT
1888 AVVKSADPALATFFAEENQAASKVSSQQQKLDLEGLLETADEQAVFKQLLVHRIAYVKARDAITASKTAGQD
1889 EEVERLFRQDFQPAGANYLGLSLQTLDDQORRAIDQTAFLIEDNNRSGRNQMLVLGALAVVLGALAVLITR
1890 SITQPLSQAVEVAHLVAAGDLRRQISSDRNDEVGQLLNALGTMNERLRDIVNQVRQGTTHAMLHASSEIAQG
1891 NLDLSGRTESQASALEQTAASMEEITSTVRQNADNARQAKQLVQATSERATAGGQAVGVQVQTMGQIHAAS
1892 GRIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRVLAQRSQAQAAKEIKGLISASVENVD
1893 QGHQLVEGAGSTMAQVESGVRQVADIVAHIASASQEQTGLGIEQINQAI AQMDSVTTQNAALVEQAAAATEA
1894 LQRQAHLADLVAVFRLEGAGPALGYSRG
1895 >Variovorax_sp._CF079_1 |WP_093109719.1 HAMP domain-containing protein
1896 [Variovorax sp. CF079]
1897 MFLSTISIAKRLAIVLGVILALFLASSVIAALKLRQLGVEITGMVQDNVTRERAGADWLRHTTSGVQRAAA
1898 IAKSSDASLIAYFAPATAASIKETNELQKFI EGQMVKPEERELFQKVGELRKDYLAAREEVSKLKLGLDLE
1899 GAGRVFSARFEPTSVSYLAGVKQMVLDQRAGLDAQAQRAEGLRAQTTMLLIVCSTLSLIFGTLLAWFLARS
1900 ITHPLRRAETMAQSIADMDLTGAPQASYANDETGRLLRAIDLRTALQKSLQVQGVVVNVSTASSQIASG
1901 NQDLSRSTEEQASSLEQTAASMEELTSTVKQNADNARQANQLALSASEVAVKGGDVVSQVVTMTASINASS
1902 KKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAAEVRNLAQRSAAAAKEIKGLIDDSVGKVD
1903 AGSQLVGEAGKTMEEIVGSVKRVTDIIGEITAASHEQTQGIEQINQAITQMDQVTQQNAALVEEAAAAAQS
1904 LQEQAAGLSQAVSVFKLDGQQQVIRPVVPLARKAAAQPARARQAIAPQRKQLAAAGTATGGGDWETF
1905 >Roseateles_aquatilis_1 |WP_088386753.1 HAMP domain-containing protein
1906 [Roseateles aquatilis]
1907 MSSALTSHRSIGRLGLVQAVVLFIALIGSALGYWGLSRVAAQTAAMYEDSIVTERVAADWYRNVFNATR
1908 TTAIAASADAGLAIYFAQQAESTKASTELQQRMEKLLTSPEERANFEKVVQLRKNYIAARDIISDAKKQG
1909 DMARAKQVFEEQQFQAAAKDYLDGLRVVVQQQRDQLDAALAALRETNQRARWALVAFGLVALVGGALATWL
1910 SRSITRPLGQAVDVADAIARFDLTHRIETGGNDETGQLLRSLDVMQRALLKLI GEVRGSTDISTASAQIA
1911 SGNMDLSARTEQTASNLQEAASLTELGTVRQTADAATTANQLVSSASSTAQRGGAVMGQVVTMTMGDISD
1912 SSRRIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSAAEAAKQIKTLIATSVER
1913 VESGSRLVSDAGSTMNDIVTSVQRVTDIIAEISAASQEQSDGINQVNAAVGHLDQMTQQNAALVEEAAASAA
1914 ESLKDQSQRLSGAI VFRLA
1915 >Variovorax_sp._EL159_1 |WP_093240577.1 HAMP domain-containing protein
1916 [Variovorax sp. EL159]
1917 MFLSNVSIKRLAIVLGAIALFLATSVAAVLKLQQLSLEIDAMIQDNVKTERRAGSDWLRHTTSGVQRAAA
1918 IAKSGDTSLEIYFAPATAKSIKETNELQKFIETKLVPAERELFEKVGNLKRAYLASREEVSKLKLQIGDLA

1919 GASRAFEDQFQPTSTSYLAGVQVQVDMQREQLDAAAARAKDLQAQTRTLLIVCSAVSLVLGALLAWQLARS
1920 ITRPLRSAETIAQSIADMDLTGMPQPGYAKDETGRLLRALDLMRSALQGSLMQVHGVVMNVSTASTQIAMG
1921 NQDLSRTEAQASSLEQTAASIEELTSTVKQNADNARQANQLATSASEVAVKGGSVVSVQVVDTMGSINASS
1922 KKIVDIIIGVIDGIAFQTNILALNAAVEAARAGDQGRGFVAVASEVRSLAQRSAAAAKEIKTLIGNSVEKVE
1923 EGSRQVADAGRMTDEIVGSVKRVTDIMGEISAASQEQTSGIEQINQAITQMDQATQQNAALVEEASAAAQS
1924 LQEQAAGLSKIVGEFKLEQGGQGGRSATPALGYAG
1925 >Ideonella_sp._B508-1_1 |WP_022980002.1 methyl-accepting chemotaxis
1926 protein [Ideonella sp. B508-1]
1927 MNLNQMRSLSHRLMAGFGLVLVLLGAVMAVGSMSLASTADETRQMMAVPLTKERLVGEWYRSLQVGVKRYTA
1928 IAKSSDPSLADFFAADVKVSTARGNEIIQQLDALPKNDAETAAVAQLAARKDYIAMRDRIAAAKKAGDAQ
1929 EAQRVLEQDFLPRANAYLAKMQEYLLQQLQSSILDGMAARVSSERTSAAQWRMGTLGLLALLAGAGCALWTRTS
1930 VTRPLQQASRLAEAVAAGDLTHRVQIEGQDEIATMMRALDRMGESLHRAVDQVRSSSENIQTACREVSMGN
1931 QDLSHRTEDTASNLRASAMSQNSVVSQTAQAAQEANHLAASAVTVAGRGGEVMGQVVQTMEGIHASSR
1932 KIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRNLASRSAAEAAKEIKSLIGASVEQVES
1933 GTSLVAHAGQTMDEVVGAIRRVTDIVGEISVASAEQARGVAQISTAVSEMDAATQQNAAMVEQMAAAASSL
1934 QGQAQNLVGAQVVFQLADAEPALPV
1935 >Variovorax_sp._JS1663_1 |WP_086920191.1 HAMP domain-containing protein
1936 [Variovorax sp. JS1663]
1937 MFLDNLSIGKRLAFVLGLILALFLASSVVSALKLSQLGDEITLMTEQKVKAERAGADWLRHTTSGVQRAAA
1938 IAKSSDASLIAYFAPFTAASIKETNELQKFIETQMTTPEERQLFDKVGELRKNYLAAREEVSKLKLKAGDLE
1939 GAGRVFDARFEPTSVAYLAGVQQIVDLQRAGLDAAAQRAEALRTQTTTTLVTCALSLSLVAGVLLAWFLARS
1940 ITRPLRLAERTAGAIADMDLSGQPQARYAGDETGRLLQAIIDRMRAALQNALQQVQGVVGNVSTASTQIASG
1941 NQDLSRTEEQASSLQQTAAASMEELTSTVKQNADNARQANQLAMSASEIAVKGGGVVSVQVVDTMGAIHASS
1942 RKVVDDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAAEVRNLAQRSAAAAKEIKGLIDDSVGVKVD
1943 TGSALVSEAGRMTNEVVDSIRRVTDIMGEITAASHEQTQGIEQINQAITQMDQATQQNAALVEEAAAAASS
1944 LQEQAAGLSEVVGVFRLGERPLEAMPARSAVTPAPRPATLPRGKTQARTARPPQLAAAADARDGDWETF
1945 >Variovorax_sp._YR266_2 |WP_093176484.1 HAMP domain-containing protein
1946 [Variovorax sp. YR266]
1947 MFLSNVSIKRLAIVLGTILALFLATSVAAVWKLQQLSQEIDAMIEDNVKTERAGSDWLRHTTSGVQRAAA
1948 IAKSSDASLIDYFAPATAKSIKDTNELQKFIKGLAKPEERELLEKVGNLKAYLASREEVSKFKLKGDLK
1949 GANRIFDSQFQPTSVSYIAGVQVQVDMQREQLDAAAARANNLRAQTSTLLIVCSAVSLVLGTLALLLARS
1950 ITRPLRSAETIAQSIEMDLTGAVQPSYAKDETGHLLRALDQMRTALQGSALTQVHGVVMNVSTASSQIATG
1951 NQDLSRTEEQASSLEQTAASLEELTSTVKQNADNARQANQLATSASEVAVKGGSVVQVVDVETMGSINASS
1952 KKIVDIIISVIDGIAFQTNILALNAAVEAARAGDQGRGFVAVASEVRSLAQRSAAAAKEIKTLIGDSVDKVE
1953 EGSRQVADAGRMTMEEIVGSVKRVTDIMGEISAASQEQTSGIEQINQAVTQMDQATQQNAALVEEASAAAQS
1954 LQEQAAGLSRIVGRFKLERQHTAASATTSVSALGTYPNAPRAYQELIASH
1955 >Herminiimonas_arsenitoxidans_1 |WP_076592488.1 HAMP domain-containing
1956 protein [Herminiimonas arsenitoxidans]
1957 MSFLSNVRIGTRLAIGFILVLALSVAISVALIHAKQNADATRNMMEKPLTKERITSDWYVLIYSAIARTS
1958 MIAKSSDDTLVSVFADVIADSTKRGTVLLKSLETLLTSDEEKMYQASIDLKTYQSSKDAVMAAKKAGDK
1959 AEADRVYSDVFLPSAKAYQDKVLEFLSMQRKTIIDIAASIDAAQQRSWNLMVLLGILMVALGAICAVITR
1960 SITRPLKQAIIEVASSAAAGDLTSEIGPQPKDEIGDLMRALGGMNDGLKQIVNDVKAGTDFINTASAEIASG
1961 NLDLSSRTEQQAASLEETASSMEELTATVKQNAENAQQANQLAVSASTVAAKGGAVVKEMIDTMGAINGSS
1962 RKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVATEVRNLAQRSAAAAKEIKSLIDDSVNNVD
1963 AGSKLVAEAGKTMDDVVGSIRHVTDIMNEIMAASQEQSIEQVNTAIGQMDQVTQQNAALVEEAAAAASQS
1964 LRDQADKLAQIVSVFKLDSKQAAHAGNHTLTHRSHPSLGYDAEPFRN
1965 >Janthinobacterium_sp._CG23_2_1 |WP_063896263.1 methyl-accepting
1966 chemotaxis protein [Janthinobacterium sp. CG23_2]
1967 MSFLSQRIIAYWNYLILNYQENNMPLNLRIGSRLAAGFAIVLALSILSTAYAMLAARANARATQGMMAQPL
1968 AKERMMSDWYVLTYSAVARTALIARSTDDTLATTTFAATIADSVKRSTELIRQIEPLLADDQEKAMLQAILA
1969 QRAAYQAAKEKVVAACKAGDSAATGLAFDASFLPAASAYQNSIQAMLAMQRKSIDETASAIEQANSRTVAL
1970 LLLLGLTAVLTGAACAVLITRSITVPLKAAVALAGTVASGDLSTRFGPAARDEIGDLMRALQAMNDALTRV
1971 VSQVQNGTKAIAIGSTGIAAGNLDLSARTEQQASSLEETAAMEELTSTVRQNADNAHQANQLALAASQVA
1972 RKGGAIVGQVVDVETMGSIEASSRKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRTLAQ
1973 RSAGAAREIKALIGDSVAQVSNTRLVREAGSTIGDVVDSVARVTDIMSEISAAGNEQRAGIGQVNQAIQ
1974 MDQVTQQNAALVEEAAAAAASLEEQAARLAHVAAGFTLTAPGRRPRVAGRMALTLAA

1975 >Aquicola_tertiaricarbonis_1 |WP_046114622.1 methyl-accepting
1976 chemotaxis protein [Aquicola tertiaryarbonis]
1977 MFLSSMSGKRLAVVLGVILSLCFASSLFAVVKLRHIGQHVDMVTDNARTERATADWLRNTTAGVQRAAA
1978 IAKSSDSGLIEYFAPATAASIAETNKLQEQIDKAMRTPEERKLFDEVGAMRKAYLAARAEVSKLQAGDLA
1979 GASKLFDERFEPTAKAYLAGVTQIADLQRSYLDQAAAQSAELTERTASLLVACAVLATGLGVVLAWLLAGS
1980 ITRPLREAIEKRASAIQMDLTGQPQARYASDETQGLLRAIDAMRSALQQALGQVRGVVDSISTASSEIATG
1981 NHDLARSARTEQAASNLQQTASSMEELTATVHQSDMASQVNQLAASAVDAARRGGQVVSQVSTMEIEHSSS
1982 RKVADITGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRLLAQRSAAEAAREIKALIGASVDKVE
1983 HGTRLVQEAGGTMEDVVTSAQRVTDMIGEVTVATAEQRDGIGQVNGAVSQLDQMTQQNAALVEQSTAATTS
1984 LQEQAQRLAGVVAGFRLQGR
1985 >Duganella_phyllosphaerae_1 |WP_070248719.1 HAMP domain-containing
1986 protein [Duganella phyllosphaerae]
1987 MNFLSHTRIGTRLAVAFGIVLALLALVATTVGLLNARSQANATREMMEKPLAKERLVSVDWYVLMYSAIARTE
1988 LIARSKDATLPTIFADVIAASSKRGAEMLGKVKELVASDEERAMFDKIVVLRNTNYQNLKTAVGKARAAGDD
1989 AASEKIFNGEFIPAAKAYSVAVEGLLAHQKAI DATARAIDAANDRANQLLLLLLTVLMVTIGSAAAWVISR
1990 SITVPLKSAVDIAAKVADGDLTTRFDQVQRSEIGELMTALKGMNDALVNVVSQVQTGTRTIASASHEIAA
1991 GNMDLSQRTEEQASSLEETASSMEELTSTVRQADNARQANQLAKTASEVAEKGGAIVSQVNTMGTINDS
1992 SRKIYDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSAGAAKEIKELIGNSVDQV
1993 DIGSKLVQEAGATMDDVVASVRRVTDIMGEITSASSEQSIGIDQVNTAITQMDQVTQQNAALVEEAAAAAA
1994 SMQEQAERLADVASSFRLEAGMAAAPAVAAAPRQVAPATRPVAAARQPAPALKTAVKLTTPATKPKPKPAL
1995 ASAPRKPATVGSDDQDWEFF
1996 >Massilia_sp._B2_1 |WP_099875675.1 HAMP domain-containing protein
1997 [Massilia sp. B2]
1998 MFPNVRIGSRLAIGFAIVLVLSILSTGYAMMAASENARATERMMAQPLTKERMISDWYVMTYSAVTRTSLI
1999 ARSADDTLSTTFVAVAIADSVKRSTELIRQIEPLLSDEEKATMQAAILAQRATYQAAKEKVMMAKKAGDGAS
2000 TDLAFNGTFLPAASAYQNGIQAMLGMQRKTIDDTAVAIEKSNRRTISLLLLLGLTAVLTGAVCAFLITRSI
2001 TGPLKAAVAVAGTVAGGDLTTEFGHAARDEIGDLMRALQAMNDSLTRVVSEVQSGTNAIAIGSTEIAAGNL
2002 DLSARTEQQASSLEETAASMEELTSTVRQADNAHQANQLALAAASQVARKGGAIVSQVETMGSIEASSRK
2003 IVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRTLAQRSAGAAKEIKGLIGDSVAQVSNG
2004 TRLVQEAGTTIGEVVDSVARVTDIMSEITAASNEQVRVIGIDQVNEAIAQMDQVTQQNAALVEEAAAAAGSLE
2005 EQAARLADVAGGFKLAATSKGRPQRVAGMKPLKLA
2006 >Duganella_sp._CF458_2 |WP_090439479.1 HAMP domain-containing protein
2007 [Duganella sp. CF458]
2008 MQFLSQLRIGPRLAAGFGIVLALLSAIGTSYALYHSNETANATRMMDRPLAKERIVSDWYVLIYSAIARTQ
2009 MISRSSDAELSNTFATAIADSAKRGAEMLLKSIEGLLETDEERKIYQDAVTIRGKYQDAKNQVMNAKKAGDA
2010 AGERLYREVFDPAAKAYQEKVKELLAQQRKAIDATAAGINEANARSNRLMLTLGVLLLLAFGAWAAWVISR
2011 SITVPLNSALGIANTVAEGDLTTRFDEHTARDEIGDLMKALRGMNDALRRVVSQVQTGTTAIATASSEIAE
2012 GNLDLSSRTEEQASSLEETASSMEELTSTVRQADNANQANQLAQAASDVAARGGEIVGQVVQTMGSIDAS
2013 SRKIVDIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSAAAAREIKELIDNSVQV
2014 NAGTSLVQQAGTTMGEVVTSVRRVTDIMGEITSASREQSVGIDEVNQAIGQMDQVTQQNAALVEEAAAAAA
2015 SMQEQAAQLAQVAASFKLGTDAVARWSAQPRAAARAVEYGARDEGSAASSEGSSARTKRLTAPDQRASSRAA
2016 ASDASTTADRTSDRRSKTERRTPAAANDEWEEF
2017 >Morganella_morganii_1 |WP_071233384.1 HAMP domain-containing protein
2018 [Morganella morganii]
2019 MLHPGIQERWIVNKYKISTRLTAGFGVLIVCSLLMMVCGIWLQWQTDKNVHRMTAFVPLKERIAADWYAAV
2020 STSTQRVSALAQSTDSSLGETFAAENIKSGKAVSELLSRFSELVNTPEEGHFLTTLIDIRAAYVRRARDEVT
2021 LANRRGEYDVAGQRYSAADFITAADHYLGILNEIRDYQRDTISLMKSDIDKKTDDGYIFLGLLGFIIITVAGS
2022 LMAWRLSLSIITPLNSATGLTKSVTEGDLTAEVCIRGRDETAGLLHSVQEMTVRLRDIAGNVRQGA AVSG
2023 AATLMTEANTELSGRTEEQSAALQESAAAIEQLASTVRRNADNAGHAELLVKTAEQARSGAQLMENVIKT
2024 MRDIESASDKIVDIIAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVAGEVRNLAQKSADSAKEIKMLI
2025 GTSVQTVGAGHILVDKAGEAMTGIASNILQVSDLVTEITDAGREQAQGIDQISVAVSQMEHSTQQNVSLVS
2026 EASSAMLSLQQAEQLEQVVSIFRLPDDSGMAGEKNDG
2027 >Mitsuaria_sp._HZ7_1 |WP_088406013.1 HAMP domain-containing protein
2028 [Mitsuaria sp. HZ7]
2029 MSNTNVRGSIGRRLGLVQALVLVIALIGSAMGYLGLSRVAAQTEAMYQETIVTERVASDWYRNVYNGGTRT
2030 TAIAVSADPALATFFAEQAAESTKSSSTELQTRMDKLLDSPERAADFDRVIELRKAYIKVRDTITEAKKQGD
2031 PARAKQLFDEQFKPAAAAYLESIRVIAQQQRDQLDTALKALSNTNARARTALVVFGFLVALAAGGALAVWLT

2032 RSITRPLAQAAEVADAI SRFDLTRIETTSGDETGQLLRSLSEMQGALVRLIGEVRGSTDSIGTASAEIAT
2033 GNMDLSARTEQTASNQQAAASLTQLTGTVRQTADAATTANQLAGSAAETAQRGGAVMGQVVATMGEISDS
2034 SRRIADIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSAQAAKEIKTLIATSVERV
2035 DSGSRLVSDAGTTMNDIVTSVQRVTDIIAEIRAASQEQSDGINQVNAAVGHLDQMTQQNAALVEEAAASAAE
2036 SLKDKQSNRLSTAI AVFRLN
2037 >Duganella_sp._Root1480D1_2 |WP_082565276.1 HAMP domain-containing
2038 protein [Duganella sp. Root1480D1]
2039 MQFLSQLRIGPRLAAGFGIVLLLLSALGTSYALYHSNDTANATRMMDRPLAKERIVSDWYVLIYSAVARTQ
2040 MIARSSDGELSNTFATAIADSAKRGAE LLKSI EGGLETDEERKIYQDAVAIRAKYQDAKNQVMNAKKAGDA
2041 AEGERLYREVFEPAAKAYQEKVKDLLAQQRKAIDATAASINEANARSNRLMLTLGILLLAFGGWAAWVISR
2042 SITVPLNSALGIANTVAEGDLTTHFDEQATARDEIGDLMKALRGMNDSLRRVVSQVQTGTTAIATASSEIAE
2043 GNLDLSSRTEQQASSLEETASSMEELTSTVRQNADNANQANQLAQAAASDVAARGGEIVGQVVTMGSIDAS
2044 SRKIVDIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSAAAAKEIKELIDNSVQV
2045 NAGTSLVQQAGTTIGEVVNSVRRVTDIMGEITSASREQSVGIDEVNTQAIQMDQVTQQNAALVEEAAAAA
2046 SMQEQAQLAQVAASF LKLGTEAVARWSAQPRRVADGGGAAEVEAARPKRLSAPDQRAMPRAAPRTAGSSAS
2047 SASDHATDRRTKTERRAPATPNDEWEEF
2048 >Polaromonas_jejuensis_1 |WP_068834368.1 HAMP domain-containing protein
2049 [Polaromonas jejuensis]
2050 MNLANLKIGTRLGMGFALVLLLLTVIAGLGVWR LQNVGDATQEMVKEALVKERLAAHVLVATGTNSVRTFA
2051 LVKSTDLEDQKYFQKGITQTS LGITENSKKLV SMLDTP EEEKSLYEESMAKRAAYIDLRTAALKLKADGQHA
2052 QAVQLADAKLVPAL EAYDASIRNMLLHQEANIDQTASAI DALYRSGRFS LIALTLIALAMGGMLAWWLTIG
2053 ITSPLKQAVQVAQTVASGDLTSHIESTARDETGQLMQALKAMNDSL VGIVGQVRQGTDTMATASSQIAAGN
2054 QDLSSRTEEQASSLEETAASMEELTSTVKQNADNARQANQLAVSASSVALKGGSVVAQVVDTMGAINASSR
2055 KIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSAAAAKEIKVLIDDSVKGVEE
2056 GSQQVVSQAGKTMDEIVDSVKRVTDIMAEITAASQEQTAGIEQINQAITQMDQVTQQNAALVEEAAAAA QSL
2057 QEQASGLSRVVSFVKLDHAQQMHVAPAKPAIAAPRRAPAGQLAAA
2058 >Mitsuaria_sp._7_1 |WP_067279719.1 methyl-accepting chemotaxis protein
2059 [Mitsuaria sp. 7]
2060 MMSNTNVRGSI GRRLGLVQALV LVLVIALIGSAMGYLGLSRVAAQTEAMYQETIVTERVASDWYRNVFNGGTR
2061 TTAIAVSADPALATFFAEQA AESTKSSSTELQNRMDKLLNSPEERAAFDRVIELRKAYIKVRDTITEAKKQG
2062 DPAKAKQLFDEQFKPAAASYLESIRVIAQQORDQLDTALKVLAETNARARTALVLFGLVALAAGGALAVWL
2063 TRSITRPLAQAAALVADAIARFDLTGRIETAGGDETGQLLRSLSEMQGALVRLIGEVRGSTDSISTASAEIA
2064 TGNMDLSARTEQTASNQQAAASLTQLTGTVRQTADAATTANQLAGSAAETAQRGGAVMGQVVATMGEISD
2065 SSRRIADIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSAQAAKEIKTLIATSVER
2066 VESGSRLVSDAGTTMTDIVTSVQRVTDIIAEIRAASQEQSDGINQVNAAVGQLDQMTQQNAALVEEAAASAA
2067 ESLKDKQSTR LSTAI AVFRLT
2068 >Herbaspirillum_sp._CF444_10 |WP_007881303.1 methyl-accepting
2069 chemotaxis protein [Herbaspirillum sp. CF444]
2070 MKQLSNMRISSRLIFGFAIVLILAIISTSMGLINAKRNAESTRAMMELPLAKERLVADWFVLTYSIVRTS
2071 MIARSSDVNLADTFKEAIAASVSVSGSIIKQIEPRLSSEDEKALFKEIIAARNTYQAAKELVMNTRKTGDA
2072 AAAEKAYKDVFEPAKAYADKVHGLLAMQRKAIDQMAVDIDRTNTRGMQLMMALGVLLVVISVAVIIISR
2073 SITTPLKRALQVARMVAAGDLTANIEKHGKDEIAELMRALDEMNEALRKIVSEVQTGTESISTAANEIASG
2074 NFDLSSRTEQQAGSLEETAASIEQLTSTVKQNAENARQANQLAQASDVAVKGSGVVSQVVDTMGAINASS
2075 NKIVDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSAAAAKEIKMLIGDSVEKVG
2076 SGSRLVEQAGVTMSEMVESVKRVTLIMSEIATASQEQSQGIEQINQAVTEMDNTTQQNAALVEQASATSEL
2077 LQAQAGKLA EAGRHF KLGHA
2078 >Duganella_sp._Leaf61_3 |WP_056140634.1 methyl-accepting chemotaxis
2079 protein [Duganella sp. Leaf61]
2080 MNFLSHTRIGTRLAAAFGIVLLLLALVATTVGLMNRSAQAIATREMMEKPLAKERLVSDWYVLMYSAIARTE
2081 LIARSKDASLPTVFADVIAASSKRGAE LMGVKELVASDEERV MFDKIVVLR TNYQNLKTAVGNARKAGDD
2082 AAAEKIFTGFEPTPAKAYSVAVEGLLAHQRKAIDDTAHAIDAANDRANQLLLVLTVLMVTIGSLAAWIIISR
2083 SITVPLKSAVDIAAKVADGDLTTRFD TQVQRSEIGALMTALKGMNDSL VNVVSQVQTGTRTIASASHEIAA
2084 GNMDLSQRTEEQASSLEETASSMEELTSTVRQNADNARQANQLARTASEVAEKGGAI VQVVTMGTINDS
2085 SRKIYDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSAGAAKEIKELIGNSVDQV
2086 DIGSKLVKEAGATMDDVVASVRRVTDIVGEITSATSEQSIGIDQVNTAITQMDQVTQQNAALVEEAAAAA
2087 SMQEQAERLADVASSFRLEAGAVSVPVAATATARKLAAVKPVAARRPAPALKPASRPATKPALTSVPRKPA
2088 TVGGDKDWEEF

2089 >Variovorax_sp._HW608_1 |WP_088957862.1 HAMP domain-containing protein
2090 [Variovorax sp. HW608]
2091 MKFLSNVRIGTRLAIGFGIVLALTIVSSVFALVSARSTAEATRQMMESPLAKERLISDWYVLTYSAIARTS
2092 MIAKTTDETLPVTFADVISDSVVKRGTEINSKVEALLVTDDEKSMFKSIMERRAKYQAAKEVVS KAKASGDS
2093 AETERAFKEQFQPAAKAYETGVLDDL SMERKAINDMSQAI DAANARAFTLRVAFFVLT MVFGGGFAVLI SR
2094 SIVKPLGEAVKLAETVAAGDLSRIEVQSKDET GQLMRALKEMNESLARVVGEVRTGTDTIATASTQIASG
2095 NQDLSRTEEQASSLEETAASMEELTSTVKQ NADNARQANQLAVSASEVAVRGGSVVSQVVD TMG SINASS
2096 RKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGGF AVVAAEVRNLAQRSAAAAKEIKGLIDDSV GKVE
2097 EGSRQVAEAGRTMDEIVGSVKRVTDIMGEI TAASQEQTSGIEQV NQAI AQMDQVTQQNAALVEEAAAAA GS
2098 LQDQATSLVQAVSVFRLDAHAQVKAAPA AKRAPPAPKGRARPAPAVRGKAVKTEPRLATSGAASGDWTEF
2099 >Variovorax_sp._KK3_1 |WP_077003508.1 HAMP domain-containing protein
2100 [Variovorax sp. KK3]
2101 MKSFSNLRIGTRLALGFGVLLLLTLLSAAFALVSASRNAEATRVMMSPLVKERLISDWYVLTYSAIARTA
2102 MIARTSDATLPVTFAEVIADSTKKGTE TMGKVEALLFTDEEKTAFKSIVDLRAKYQLAKDAVQKAKAGGSV
2103 QESEAVYKDFVQPAAKAYENEV LALLSIQRKDIRMSGEIDAANAASLKLRLAMTALTLLLAGAACFLIAR
2104 SITRPLGQAVKVAETVAGGDL SRIEVE SRDET GQLMQALKNMNESLARVVTQVRSGTDTIATASGQIASG
2105 NQDLSRTEEQASSLQQTAA S MEELTSTVKQ NADNARQANQLALSASEVAVKGGEVVNQVVD T MGSIHASS
2106 KKIVDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGF AVVAAEVRNLAQRSAAAAKEIKGLIDDSV GKVD
2107 AGSELVAEAGRTMNEVVDSVKRVTDIMGEI TAASHEQTQGIEQV NQAITQMDQVTQQNAALVEEAAAAA AS
2108 MQEQAASLVQAVGVFRLGDDLAVAKVLAQAKATSR SVQPLVKVPVRTAAASAPERRVAVKPAAKPAASTAA
2109 PSGDWTEF
2110 >Variovorax_sp._WDL1_2 |WP_068675583.1 HAMP domain-containing protein,
2111 partial [Variovorax sp. WDL1]
2112 MKNWKIGTRLGIGFALV LALLAIVAGIGVLR LQNVGKAMEEMVQRSLVKERLAATWLQNTSNN SIRT FALL
2113 KSNDAEVQDFLQKNITKTSAL ISETQKKLEGLLDTPEEQAISAEIKKRRSDYLGLRNGILK LKAEGGQDEA
2114 ARLTNEKLI PMLDAYDASIRGMLTHQAARIDLAAGSVDTLYRSGRMNVIVLALVALALGAVLAWLLTR SIT
2115 RPLNEAVQVAQTVAAGDLRSEVVVKTGDE TGLLMQALQGMNASLARVVGQVRNGTDTIAA ASTQIASGNQD
2116 LSTRTEEQASSLQQTAA S MEELTSTVKQ NADNARQANQLALSASEVAVKGGSVVSQVVD T MASIHASSRKI
2117 VDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGF AVVASEVRNLAQRSAAAAKEIKGLIDDSV GKVDAGT
2118 TLVGEAGKTMEEIVGSIRRVTDIVGEI SAASHEQTQGIEQINQAITQMDQVTQQNAALV
2119 >Variovorax_sp._YR750_1 |WP_093202010.1 HAMP domain-containing protein
2120 [Variovorax sp. YR750]
2121 MFLSNVSIGKRLAIVLGIILALFLATSAAAVWKLQQLSREIDAMIEDNVKTERAGSDWLRHTTAGVQRAAA
2122 IAKSSDASLIDYFAPATAASIKNTNELQKFIEEKLVPDERALLEKVG NLRKAYLGAREEVSKLKLAGDLD
2123 GANRVFDSQFQPTSVSYIAGVQVQVDMQREQLDAAAARANNLRAQTSTLLIVCSAVSLALGALLAWLLARS
2124 ITRPLRSAESMAQSIAAMDLTGKAQSSYASDETGHLLRALDQMRDALQGS LAQVHGVVANVSTASTQIAVG
2125 NQDLSRTEEQASSLEQTAASLEELTSTVRQ NADNARQANQLAASASEVATRGGNVVFQV VETMG SINASS
2126 KKIVDIIIGVIDGIAFQTNILALNAAVEAARAGDQGRGF AVVASEVRS LAQRSAAAAKEIKTLIGDSVEKVE
2127 EGSRQVADAGRTMEEIVGSVKRVTDIMGEI SAASQEQTSGIEQINQAVTQMDQTTQQNAALVEEASAAAQS
2128 LQEQAAGSLSQIVGRFRLEHQ RQAEEDTTPGIAFSPMHLIAR
2129 >Variovorax_soli_1 |WP_068642850.1 HAMP domain-containing protein
2130 [Variovorax soli]
2131 MQFLRNMLIGRRALGFGFLV LVLVSLASTAFTLQSMR SSAQTTQQT VLGPLAKERLVS DWYVLTYS AIARTE
2132 LIARSTDAALS KTFAEVIAASSKKGSETMAKVEPLLVTDEERAI FKHIGELRAKYQSAKELVMNTKTAGDA
2133 ALAERQFNEVFMPAAKTYEKRVLDLLSHERQTIDA AVVAAREASAERFMTLMLFAAVSLVAGVAASLLIAR
2134 SIVRPLGQAVDVARTVAGGDLGSRIVVDSRDET GQLLEALREMND SLARVVGEVRS GTDNIATASGQIATG
2135 NQDLSRTEEQASSLEETAASMEELTSTVKQ NADNARQANQLAVSASEVAVKGGTVVGVVD T MASIN ESS
2136 RKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGF AVVAAEVRNLAQRSAAAAKEIKGLIDDSV GKVQ
2137 AGSELVGEAGQTMQEIVGSVKRVTDIMGEI TAASQEQTAGIEQINQAITQMDQVTQQNAALVEEAAAAA AS
2138 LQEQAAGLVQAVSVFRMGGASQAAPAARKPAGTAVARKATAPAGKARASAKAKPSVRETTRAEPAMAPSGA
2139 SSAAGDWTEF
2140 >Variovorax_boronicumulans_1 |WP_095946608.1 HAMP domain-containing
2141 protein [Variovorax boronicumulans]
2142 MTFFSNLRIGTRLTLFAIVLGLTLISSAVGLMSAHKNAEATRIMMSPLAKERLISDWYVLTYSAIARTS
2143 MIARTTDEALPMLFADVISESVKKGSETMAKVEALLVTDDEEKATYKSIVELRAKYQAAKDEVTRAKASGNT
2144 VETVRAYQLSFQPAAKAYENRVLELLAIERRAIDDMSHAIDAANA KSFNLRLLLLTALT VLLGGLFAFFISR
2145 SIVRPLAKAVGVAETVAAGDLSANIRVDSRDET GQLMQALKDMNANLAKVVGEVRTGTETIATASGQIASG

2146 NQDLSRTEEQASSLEQTAASMEELTSTVKQNADNARQANQLAVSASEVAVKGGAVVSQVVDTMGSINASS
2147 KKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSAAAAKEIKTLIGDSVEKVE
2148 EGSKQVAEAGRTMEEIVGSVKRVTDIMGEITAASQEQTSGIEQINQAITQMDQVTQQNAALVEEASAAAQS
2149 LQEQAQALVQAVSVFKLDANAVATTRASFRITPIPKPPKPTPKPRAKALPTRREPTGTPQLAMAGDAKGD
2150 WSEF
2151 >Acidovorax_temperans_1 |WP_044396904.1 HAMP domain-containing protein
2152 [Acidovorax temperans]
2153 MFLNQISIGKRLTLVLGVILALFLASSVVAVVKLRQLGAEIDTVVNDNVKTERAGSDWLRHTTSGVQRAAA
2154 IAKSSDASLIAYFAPATAASIRDTNELQKFIESKMVTPEEKQLFAKVGELRKHLYLAAREEVSKHKQAGDAD
2155 AANKVFTERFEPTSRSYLAGVQQLVDGQRAQLDAAGKRSEDLRAQNTLLLQICTAVSLLLGLLAWLLANS
2156 ITRPLRHAETIAEAIADMDLTGAPQSIYANDEPGRLLRALDLMRSAQLORSLLQVRGVVDSISTASTQIAIG
2157 NQDLSARTEQATASSLQETASSMEELTSTVRQSADSAVQANQLATSAAQVAQRGGDVVSQVVTMDEINASS
2158 KKISDIIGTIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSAAAKEIKTLIGVSVEKVE
2159 SGSALVQNAGTTMDEIVSSVRRVTDIIGEISAAASEQSQGIGQVNVAVTQLDQMTQQNAALVEESTAAAES
2160 LKEQAARLADVGAFFRLGASAGAPRLR
2161 >Collimonas_arenae_1 |WP_082797792.1 HAMP domain-containing protein
2162 [Collimonas arenae]
2163 MALANTRIGVRLAIGFTLILLVVVITGVGIWRLOQTGAAVNAMVVSQFLVRERLAAEWQDAVTINAVRTMA
2164 VVRSNDSKTQQAFQSEMSATSERASELQTKLHGLSSEEGRQALGEIAAARAAYTELRESVLTTRQHGSAET
2165 VNAMIEKELDPARKEYMAKQKFVDVQRKAIDDEALKIDANYRSGRILLIAFGSLAIIILGALLSWRLTAGI
2166 VNPLQAAVAVARRVAAGDLTSTIEVKSDETQGLLQGIKEMNRALQDTSRVRNGTDNIVTASRQIAAGNL
2167 ELSSRTEQQAASLEQTAASMEQLTSTVKQNADNARQANQLAENASSVALGGGRMVSEVVATMSQIKESSHK
2168 INDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAAEVRNLAQRSAVAAKDIKLLIGDSVDKVDAG
2169 NRQVDAAGKTMSEIVDSIRRVVDIMAEIAAASTEQSSGIEQVNQAVVQMDQATQQNAALVEEAAAAHSLQ
2170 EQADELLQAVHIFNLADEEEMHPPGGSGKETVVSPLPTRQESSEVQFNDVNKVPFLAAAN
2171 >Variovorax_sp._R01_1 |WP_101489176.1 hypothetical protein [Variovorax
2172 sp. R01]
2173 MTFFSNLRIGTRLTLAFAIVLGLSIISSAVGLMSAHKNAEATRIMMQSPLAKERLIADWYVLTYSIAIARTS
2174 MIARTTDEALPMLFADVISESVKKGTEMAKVEALLVTDEEKATYKSIVELRAKYQSAKDDVTRAKASGNT
2175 VETVRAYQLSFQPAAKAYENRVLELLAIERRAIDDMSHAIDAANAKSFNLRLLLTALTIVLLGGLFAFFISR
2176 SIVRPLAKAVGVAETVAAGDLSANIRVDSRDETQQLMQALKDMNANLAKVVGEVVRTGTETIATASGQIASG
2177 NQDLSRTEEQASSLEQTAASMEELTSTVKQNADNARQANQLAVSASEVAVKGGAVVSQVVDTMGSINASS
2178 KKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSAAAAKEIKTLIGDSVEKVE
2179 EGSKQVAEAGRTMEEIVGSVKRVTDIMGEITAASQEQTSGIEQINQAITQMDQVTQQNAALVEEASAAAQS
2180 LQEQAQALVQAVSVFKLDANAVATTRASFRITPIPKPPKPTPKPRAKALPTRREPTGTPQLAMAGDAKGD
2181 WSEF
2182 >Variovorax_sp._YR752_3 |WP_097198356.1 HAMP domain-containing protein
2183 [Variovorax sp. YR752]
2184 MKFLSNLRIGNRLAVAFIVLGLTVIISTAIALVSSRNNAEATRVMMQSPPLAKERLISDWYVLTYSIAIARTS
2185 MIARTTDETLPVVFADVISDSVKKGSETIAKVEKLLVTEEEKAVLKSILDLRAKYQTAKDDVGGKAKASGNA
2186 VDTARAFKESFQPAAKAYETRVLDLLSMERQAIIDMSQAIIDAANTRSFNLQLLLLTVLTVVSGGIFAFFISR
2187 SIVRPLAQAVQVAETVAAGDLSMHIEVESRDEAGQLMQALKNMNANLAKVVGEVVRTGTETIATASGQIASG
2188 NQDLSRTEEQASSLEQTAASMEELTSTVKQNADNARQANQLAVSASEVAVKGGSVVSQVVDTMGSINASS
2189 KKIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVASEVRSLAQRSAAAAKEIKTLIGDSVEKVE
2190 EGSKQVEEAGRTMDEIVGSVKRVTDIMGEITAASQEQTSGIEQINQAITQMDQVTQQNAALVEEASAAAQS
2191 LQEQAQALVQAVSIFKLDDEGRQAAPRAQARTQPAKRVGSPLPATPQLAVAGAGAGDWREF
2192 >Mitsuaria_sp._PDC51_2 |WP_091731740.1 HAMP domain-containing protein
2193 [Mitsuaria sp. PDC51]
2194 MSNTNARGSIGRRLGMVQTGVLVIALIGSALGYWGLNRVAEQTAAMYTDIVTERAASDWYRNVFNNGTTRT
2195 TAIAVSADPGLATFFFTQAAAEATKVSTELQQRDLKLLTKPEERATFDKVAELRKYTLTVRDAITAACKQGD
2196 MAQAKQIFDEQFQKASSAYLDGIRAVAQQQRDLQAIQALAAATNERARIALVVFGLVALAAGGALAVWLT
2197 RSITRPLGQAAQVADAIARFDLTGRIETRGSDETAQLLRALDAMQGSLLRLIGEVRGSTDSIGTASAEIAS
2198 GNMDLSARTEQTASNQQAAAASLTQLTGTVRQTADAALTANQLASSAAETAQRGGSVMGQVVTMGEISDS
2199 SRRIADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAGEVRSLAQRSAAAKEIKSLIATSVDV
2200 ESGSRLVTDAGTTMTDIVTSVQRVTDIIAEIRAASQEQSDGINQVNAAVGHLDQMTQQNAALVEQAASAAE
2201 SLKDQSKRLSAAIAVFRLA

2202 >Duganella_sp._Leaf126_1 |WP_056156977.1 methyl-accepting chemotaxis
2203 protein [Duganella sp. Leaf126]
2204 MKFLTHTRIGTRLAAAFGIVLLLLLALVATTVGLLNARQQAAATRDMMEKPLAKERLVSVDWYVLMYSIAIRTE
2205 LIARSSDTALPTVFADVIAASSKRGAEIMGKVKELVASDEERAMFDRIVVLRTNYQNLKTAVGNARKAGDA
2206 AAAEKIFNDEFTPAAKAYTIAVEGLLTYQRKAIDDDTARAIDAANVRANGLLLLLLTVLMVTIGSAAAWIITR
2207 SITAPLKSAVDIAATVARGDLTTRFDASVQRSEIGELMTALKGMNDALRNVVSQVQTGTRTIASASQEIAA
2208 GNLDSLQRTEEQASSLEETASSMEELTSTVRQNADNARQANQLVKTASDVAEKGGAIVSQVVDTMGSINDA
2209 SRKIYDIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAGAAKEIKELIGNSVEQV
2210 DIGARLVQDAGTTMDEVVASVRRVTDIMGEISSASSEQSIGIDQVNSAITQMDQVTQQNAALVEEAAAAAS
2211 SMQEQAERLAEVAASFRLEPGAVVTPAAHRPAPASQLATASATASHRPAHGPAKSPASRLTMKSTITSPI
2212 PPAEPPKATASRKPATVGSDDSDWEEF
2213 >Variovorax_sp._OV329_1 |WP_093384234.1 HAMP domain-containing protein
2214 [Variovorax sp. OV329]
2215 MEFLENMRIGRRLAVGFGLVLIILSLASTAFTLVSLRSSAQTQRTVLGPLAKERLVSVDWYVLTYSIAIRTE
2216 LIARSSDAQLSNTFAEVIAASSKKGSETMAKVAPLLDDEERAIKFKHIGELRVKYQGAKELVMNAKTAGDA
2217 ALAERQFNEVFMPAAKAYEKRVLELLSHERGTIDEAVRVGREATERFQMLMLLAVALIAGVLASLLISR
2218 SITRPLREAVGVAKAVAGGDLGSRIESNSKDETGQLLALREMNTSLVRIVSEVRSGTDTIATASGQIASG
2219 NQDLSRTEEQASSLQETAASMEQLTSTVKQNADNARQANQLAESASEVAVKGGEVVGVVHTMASINASS
2220 KKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAQRSAAAAKEIKGLIDDSVGKVQ
2221 AGSELVGEAGQTMQEVSSVKRVSDIIGEITAASHEQTQGIEQINQAITQMDQVTQQNAALVEEAAAAAQS
2222 MQEQAGSLVHAVSVFRLARA
2223 >Variovorax_paradoxus_10 |WP_019658724.1 methyl-accepting chemotaxis
2224 protein [Variovorax paradoxus]
2225 MKFKDLRISTRGLGFVAMLLLVACMAGIGLWRLAHVSQATERMMTQALTKERLAGEWQSTLRSNSVATIA
2226 MIKAPDTRLEAYFAKLQSTGMERISSVQKEFQSKLSTPEEKALYEQVMVARTKVREIVTNLTMLKDRGQIE
2227 EAQKMDVDTTFSEALAAYGSAVDKVDQHQHDEIDAAARDIAEDYFSGRIMLLSLAAVAVVLGALFAWRLSAG
2228 IVRPLRHAVEAAETVASGDLRVDIRVENRDEVGQLMQALKDMNTSLAKVVGEVRLGTDTIATASSQIASGT
2229 QDLSRTEEQASSLEQTAASMEELTSTVKQNADNARQANQLAVFASEVATKGGMVVSQVVDTMGSINASSR
2230 KIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAQRSAAAAKEIKTLIGDSVEKVEE
2231 GSKQVEEAGRTMDEIVGSVKRVTDIMGEITAASQEQTSQIEQINQAITQMDQVTQQNAALVEEASAAAQSL
2232 QEQAGSLVQTVGIFKLDPAAGAMRRPGFSPIAPIAKPTKPAKAISPRGEKGGNPMHQLVMSGADGNEWTF
2233 >Collimonas_sp._OK412_2 |WP_092398824.1 HAMP domain-containing protein
2234 [Collimonas sp. OK412]
2235 MNFANTRIGVRLSIGFTAILLVVAITGIGIWRLQQTGAAVDAMVSQFLVRERLAAEWQDAVAVNAVRTMA
2236 VVRSDDSKTKQIFQAEMSATSERASALQTKLHGLSDDQGRQALGEIAAARAAYTEMRDVTLTTRQYGSAES
2237 AVAMIEKDLDPARKEYLEKLQKQFVGVQRQAIDEAALDIAANYRAGRNLVTFGAIAIFLGAFAWRLTAGI
2238 VKPLHAAVAVAQRVAKGDLGASIEVKGKDETGQLLLGIREMIFSLRDTVSRVRNGTESIVTASRQIAAGNQ
2239 DLSSRTEEQAASLEQTAASMEQLTSTVRQNADNARQANQLAENAASVALGGGMVSEVVATMALIRDSHQ
2240 ISDIIGVIDSIAFQTNILALNAAVEAARAGDQGRGFVAVAAEVRNLAQRSABAADIKVLIIGASVDKVDAG
2241 GRQVDAAGAAMSEIVASIRRVVDIMAEIAAASEQSSGIEQVNVQAVGQMDQATQQNAALVEQAAAAHSLQ
2242 EQAGELLQAVSIFQLAEDAAYSMPERQDSGPAEAAADMPEEHHAGSRPVLVSIN
2243 >Variovorax_sp._URHB0020_1 |WP_028253133.1 HAMP domain-containing
2244 protein [Variovorax sp. URHB0020]
2245 MKDWKIGTRLGGGFALVLAIVAIAGIGVMRLQSVGEATREMARGSLERLAGSWLLSTSTNSVRTFALL
2246 KSEDAEVQEFQKNISKTSAFISENQKKEEVLSSPEELALSADIKKKRAEYVDLRNVILKCLKSEGNLAEA
2247 KRLSGEKLLSTLESYDASIRAMLSHQQAQIDQSASTIDALYRSGRNLVILAALALAVGSVLAWTLTRSIV
2248 QPIDEALLIAETVASGDLKFEFETQRGGDFGRLLRGMGEMEDTLTDLVSRIKIATDSIVVASKEIAAGNQD
2249 LSSRTEEQASSLEQTAASMEELTSTVKQNADNARQANQLAASASEVAVKGGSVVSQVNTMASINASSKKI
2250 VDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVAAEVRNLAQRSAAAAKEIKGLIDDSVGKVDVGS
2251 ALVGEAGRTMEEIVGSVKRVTDIMGEITAASQEQTSQIEQINQAITQMDQVTQQNAALVEEAAAAAASLQE
2252 QAGGLSQIVSTFKLDDEEAAAPAVVPSRPAVVARSPSRPPAPPSVVTTHRTRQSTAPKLAASHTSNGDWT
2253 EF
2254 >Thiobacillus_denitrificans_1 |WP_011312132.1 methyl-accepting
2255 chemotaxis protein [Thiobacillus denitrificans]
2256 MKIGARLGLGFASVLLLLLVVAVIGVWRLQTVGMMTDSLKVNEMHKARIINWESIINANAVRALAAAKTN
2257 NPETEKFFVDASAAASKGGIALQKQLESLLTDAESRALFAAIADKRSAYLAARDAALKEKAAGNVLGAKKF
2258 VDEDMKPRLDAYLES LHD LARYQKQAI DATAGNIHRQYESGRMLLIGLSIVALMMGIGFAFWITRSITRPM

2259 NQAVKVAQTVAAGDLTSRIEVEGKDETGRLLQALKDMNDSLKIVGQVRLGTDATASSEIATGNLDLSS
2260 RTEEQASSLEETASSMEQLTSTVKQNADHARQANQMAVSASEVAVKGGAVVAQVVDVTMGSINESSRKIVDI
2261 IAVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSAGAAKEIKTLIGDSVEKADIGSKLV
2262 GQAGATMDEIVASVKRVTDIMGEITAASQEQSAGIEQVNQAIQMDQVTTQNAALVEEAAAAASSMQDQAA
2263 NLAEAVSVFRLAGVNTQRPEQLTSNERIAALPARTHTAAAPVVRTKKLAAIQGSSGGEEF
2264 >Herbaspirillum_aquaticum_4 |WP_088755470.1 HAMP domain-containing
2265 protein [Herbaspirillum aquaticum]
2266 MKNLKGIVRLAIGFIALMLMAMVGLGVWRLGNIGDATDEMTQIALKKERDAVQWHAAIKENGVRTFAVM
2267 KSDDDAFQYFQKQIDAQSAKISQLQKQVEAAITDPEEKRLFAEVGKLRRAAYRDRQKIFDIKTAGDDARA
2268 REMTDTTLVKMMDEYADSVLRYADYQKKVIDQAAAEINGDYRSGRSMLLMLGALEIVLGAALAWLLTRSIT
2269 RPLNQAVSIAETVAAGDLTSRIEANSRDETGQLLAALKSMNGNLQDIVGRVRSRGTDTINVASREIATGNLD
2270 LSARTEQAGSLEETASAMEQLTSTVKQNADNARQANALASASQVASQGGAVVEQVATMGEIHASSQKI
2271 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSASAAKEIKQLIGDSVEKVDGDS
2272 RLVAQAGDTMQEVVHSVARVTEIVREITLASQEQSDGIEQVNLAIITHIDEATQQNAALVEEAAAAARSMQD
2273 QAASLTEAVSVFRLDTSVALPGAQAQRGTSPSTVVR
2274 >Bordetella_genomosp._8_1 |WP_086066325.1 HAMP domain-containing
2275 protein [Bordetella genomosp. 8]
2276 MDFLSNIRIGTRLAIGFMLVLALSIGSTAFALIEARHNAEETRLMMEKPLTKERITADWYVFIYSAIARTA
2277 MIAKSTDGTLSDVFADVIADSVKQGGALLKSLEELISNDEERKLYQASVDGRNAYQKAKNDVMAAKMAGDA
2278 AKADRAYTQSFLPTAKAYQESVQAFRAYQKQINAIASADIAANERSMGLLMLLGAACAVVITR
2279 SITRPLRSIAIVANRAAEGDLTARIATTSKDEIGDLIRAMETMNRGLKEIVRDVKSQTDLINNASAEIASG
2280 NLDLSSRTEQQAASLEETAASMEELTATVKQNAENARQANQLAVSASQVAARGGAVVKNMISTMGAI DGSS
2281 RKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSASAAKEIKSLIDDSVSNVV
2282 AGNKLVAETGGTMDEVVGNIRQLAEMMNEIVAASQEQSTGIEQVNIASIQMDQATQQNAALVEQAAAASS
2283 LRDQADTLGRVVSFRIDAADTGNAANASLGMSGHAHTLLARPDDAYVAAA
2284 >Polaromonas_sp._JS666_1 |WP_074580422.1 HAMP domain-containing protein
2285 [Polaromonas sp. JS666]
2286 MFLGNLSIGKRLAVVVGLLILFLTSSVLAVLKLSQLGEEIKAMVEKNIKTERAGSDWLRHTTAGIQRAAA
2287 IAKSSDVGLVAYFAPASATS IKNTNELQKFLEQQMDTPEKKQLFDKVGELRKVYLAAREDVSKAKQAGDME
2288 GANRIFNERFEPTSRDYLAGVQKMVDTERELLDDAAQRGEALRARISLLLVVCSVSVSLGLGALLLWLLVRS
2289 ITRPLSNVQVARAVAAGDLTSRIEVESQDETQQLMQALKDMNDALVGIVGNVRSRGTDTIATASSEIAAGN
2290 HDLSSRTEQQAASLEETAASMEELTSTVKQNADNARQANQLAVSASSVAVKGGTVVAEVVGTMGAINASSR
2291 KIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSASAAKEIKTLIDDSVSKVEE
2292 GSSQVAEAGKTMDEIVDSVKRVTDIMAEITAASQEQSTGIEQINQAITQMDQVTTQNAALVEQAAAASSL
2293 QEQAGSLSDAVSVFKVEGGHVT PARRPAASRPAATPKQPPQARQAIASRKAVPASGELAVAGGSWETF
2294 >Herbaspirillum_sp._WT00C_4 |WP_075256362.1 HAMP domain-containing
2295 protein [Herbaspirillum sp. WT00C]
2296 MKNLKGIVRLAIGFIALMLMAMVVALGVWRLGSGDATDDMTRIALKKERDAVQWHAAIKENGVRTFAVM
2297 KSDDDAFQYFQKQVDAQSARISQLQKEVEAAITDAEEKRFLFDEVGKLRRAAYRATRQSFIDVKTAGDDARA
2298 REMTDTTLVKMMDDYANSVLRADYFQKQVIDQTAAEINRDYRSGRSMLLALGAIEIVLGAALAWLLTRSIT
2299 RPLNQAVTIAETVAAGDLTSRIDSSRDETGKLLAALKTMNGNLLDIVGRVVMGTETINTASREIATGNLD
2300 LSARTEAQAGSLEETASAMEQLTSTVKQNADNARQANELAASASQVATQGGAVVDQVATMGAIHASSQKI
2301 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRSLAQRSASAAKEIKQLIDDSVEKVDGDS
2302 RLVARAGDTMQEVVQSVARVTEVVREITLASQEQSDGIEQVNLAIITHIDETTQQNAALVEQAAAAARSMQD
2303 QAASLTDVAVSVFRLDQVLAVALVQRGTSPSTVVR
2304 >Bordetella_genomosp._11_1 |WP_094843473.1 HAMP domain-containing
2305 protein [Bordetella genomosp. 11]
2306 MRFLSNIRIGTRLAIGFVLVLVLSIGSTGFALI QARDNATETRLMMEKPLTKERITADWYVFIYSAIARTA
2307 LIAKSTDTTLSDVFADVIADSVKQGGALLKSLEDLISSTDEERKLYQTSVNGRNAYQKAKNEVMAAKMKGDA
2308 AEADRVTQSFLPTAKAYQESVQAFRAYQRTQINAIASASIAANARSIDLMLFVLLVMLGAACAIITR
2309 SITRPLRSIAIVANRAAKGDLTAQIAPASTDEIGDLMRALETMNRGLKAIVRDVKSQTELINNASAEIASG
2310 NLDLSSRTEQQAASLEETAASMEELTATVKQNAENARQANQLAVSASQVAVRGGTVVKDMISTMGAI DGSS
2311 RKIVDIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVVASEVRNLAQRSASAAKEIKSLIDDSVSNVV
2312 AGNKLVAETGGTMDEVVANIRHLAEMMNEIVAASQEQSSGIEQVNIASIQMDQATQQNAALVEQAAAASS
2313 MRDQADTLERVVSFRIDARDAFDDAVALGTSGAAPRSGDAYIAVA
2314 >Variovorax_sp._R01_2 |WP_101489172.1 hypothetical protein [Variovorax
2315 sp. R01]

2316 MTIKNWTGMRGAGFALVLLVAVAGIGVLRRLQGVGEATQDLASRTLKERLATAWQLGTATNSVRTFS
2317 LLKSDDAQVQAYLQKQIAATSATISSETQTALEALLSTPEELALSADIQKRRGDYIALRKQILQLKADGQKD
2318 EAATRTDTQLLPLMDGYDASIRAMVTHQQKHIDRTAAAI DAQYRAGRLYIVALAAAALALGAVLAWLLTRS
2319 IAQPIAEALLIAETVASGDLSQEFETDRGGDFGRLLRGMGEMEDTLTDLVTRIKASTDSIAVASRQIAAGN
2320 QDLSSRTEEQASSLEQTAASMEELTSTVKQNADNARQANQLAVSASEVAVKGGAVVSQVVDTMGSINASSR
2321 KIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAQRSAAAAKEIKTLIGDSVEKVEE
2322 GSKQVAEAGRTMEEIVGSVKRVTDIMGEITAASQEQTSGIEQINQAITQMDQLTQQNAALVEEASAAQSL
2323 QEQASNLVEAVSTFKLDADEAVVA
2324 >Duganella_sp._HH105_5 |WP_070357647.1 HAMP domain-containing protein
2325 [Duganella sp. HH105]
2326 MNNLKIGTRLGFGFSLILLTAMTIIIGILRLSSASSMTHMINVKIRDERLIAEWGKIEVNAARTTGAW
2327 MVADPADQKTLEGMMAESSGRATKIQDQIGADIEDEELKPLFQKVLETRKAYTEIRKSVFAAKNAGDLEKG
2328 KKLYETDMAQSRTLYLDALKKFADRQGALLDQAAVDIQQQYTSGRLLMLLGVAAIILGVTAAWWITRTIT
2329 QPINEAVKVAETVSSGDLTSDIQVGSNDETGQLMTALKNMNTNLVNIQVRSQVSGTDLMAHASTEIAAGNHD
2330 LSSRTEEQASSLQETASSMEQLTSTVRFNAENAREANKLAVNASEIASRGGAVVGEVHTMGSINDSSRKI
2331 VDIIISVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAAADIKGLIDDSVQKVALGS
2332 DLVDKAGQTMSEIVDSIGRVTQIMNQISNASEEQSIGIAQVNDAITQMDQVTQQNAALVEQAAAAESMQE
2333 QSAKLADVSVFKLDAQAQMAVKTALPPARPAAPVAVPKTRPAPTVAAPARKALAAAPKRATVASSES DGWEE
2334 F
2335 >Polaromonas_sp._CG9_12_1 |WP_081932374.1 HAMP domain-containing
2336 protein [Polaromonas sp. CG9_12]
2337 MNIKNLIRIGSRLALGFGVLLLSIIISGLGIWRLQEVGSAADAMAKRALVKERIAAEWLVTSTNSIRTF
2338 LVKSTDAADQQYFQKQIAQTS LGITENSKKLFLLD TAE EKALFEEGVAKRAAYVGLR TSI M K L K A E G Q N A
2339 EVAQLTEEKLVPAALSAYDASIKNMLLHQKTTIDQTVMAINALYRSGQF SVLVLAAMALGLGAF LSWRLTRG
2340 ITLPLSEALLVAKTVAAGDLTSRIEVTSKDETGQLMQALKDMNDSL SRVVGEVRQGTDTIATASSQIAAGN
2341 QDLSSRTEEQASSLEETAASMEELTSTVKQNADNARQANQLAVSASSVAVRGGAVVSQVVDTMSAINASSK
2342 KIVDIIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAAADIKGLIDDSVQKVEE
2343 GSKQVAEAGKTMDEIVGSVRRVTDIMAEIQAAASQEQTQIEQINQAITQMDQVTQQNAALVEEAAAAQSL
2344 QEQAGGLSQVVGVFRLNPAAHREQPATRPHSARRAGAAGPTAFAFKQAPAPRHALAVPKASPSLASNSPAA
2345 PSRRPAVAAAANSGTGEWEEF
2346 >Janthinobacterium_sp._61_5 |WP_101482122.1 hypothetical protein
2347 [Janthinobacterium sp. 61]
2348 MKNLKIGVRLGGFAFAVLLLSLTSLTVVGVQMQSASKETDLVNVKVRNERLIAEWTKVIEVNAARTAAAW
2349 KVSDPEHQKQFEKEMAVSSARATEIQNDIGKSELNTEEALYQEV LSTRKAYTEVRKNVFKAKNAGDLELG
2350 KRLYEGEMVAKRDIYLAALKKLEVL EARLLDEAAAQIRSRYESGRLLLSL GALA ILLGIACAYWITRSIT
2351 RPITRAVQVAEAVSAGDLTSHIVVESHDETGQLMHALKNMNDKLVSIQVQVRAGTESISTASSEIAAGNLD
2352 LSSRTEEQASSLEETASSMEELTSTVKLNADNARSANQLAIDASQIASKGGVVSEVSTMG SINDSSRKI
2353 VDIIISVIDAIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAAADIKGLIDDSVQKVEAGS
2354 QLVDKAGRTMDEIVQSI SHVTQIMNQITDASDEQRAGIEQVNQAIQMDQVTQQNAALVEEAAAAESMQE
2355 QAAKLAEVVGVFKLDATQQYVSTRAASSVKASAPARTAMRPAVQAAVRRAPAQPVAAPAEAMRRAPKAPV
2356 ASGADEWEEF
2357 >Janthinobacterium_sp._BJB426_4 |WP_099378255.1 HAMP domain-containing
2358 protein [Janthinobacterium sp. BJB426]
2359 MKNLKIGVRLGGGFAAVLFLLSLTSLTVVGVQMQSASKETDALVNVKVRNERLIAEWTKVIEVNAARTAAAW
2360 KVSDPEHQKQFEKEMAVSSARATEIQNDIGKSEL SADEALYQEV LSTRKAYTEVRKNVFKAKNAGDLELG
2361 KRLYEGDMAVKRDIYLAASLKKLELLEAKLLDETAQAQIRSRYENGRLLLSLGVVA ILLGIACAYWITRSIT
2362 RPITRAVEVAEAVSAGDLTSHIVVSRDETGQLMHALKNMNDKLVSIQVQVRAGTESISTASSEIAAGNLD
2363 LSSRTEEQASSLEETASSMEELTSTVKLNADNARSANQLAIDASQIASKGGVVSEVSTMG SINDSSRKI
2364 VDIIISVIDAIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSAAAADIKGLIDDSVQKVEAGS
2365 QLVDKAGRTMDEIVQSI SHVTQIMNQITDASDEQRAGIEQVNQAIQMDQVTQQNAALVEEAAAAESMQE
2366 QAARLAEVVGVFKLDATQQYVAASAGPSMTASAPIKAATRVAMQAAARPAIRPAKRQAPASAVTASTSDKA
2367 APVEAMRPRAPKAPVASGADEWEEF
2368 >Janthinobacterium_sp._RA13_4 |WP_035820608.1 methyl-accepting
2369 chemotaxis protein [Janthinobacterium sp. RA13]
2370 MKNLKIGVRLGGGFAAVLFLLSLTSLTVVGVQMQSASKETDALVNVKVRNERLIAEWTKVIEVNAARTAAAW
2371 KVGDPHQKQFEKEMAVSSARATEIQNDIGKSELNAEEQSLYQEV LSTRKAYTEVRKNVFKAKNAGDLELG
2372 KRLYEGDMAVKRDIYLAASLKKLELLEAKLLDETAQAQIRSRYESGRLLLSLGGVA ILLGIACAYWITRSIT

2373 RPITRAVEVAEAVSAGDLTSHIVVESRDETGQLMHALKNMNDKLVSVIGQVRAGTESISTASSEIAAGNLD
 2374 LSSRTEEQASSLEETASSMEELTSTVKLNADNARSANQLAIDASQIASKGGVVVSEVSTMGSIINDSSRKI
 2375 VDIISVIDAIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSSAAAKEIKGLIDDSVQKVEAGS
 2376 QLVDKAGRTMDEIVQSI SHVTQIMNQITDASDEQRAGIEQVNQAIGQMDQVTQQNAALVEEAAAAAESMQE
 2377 QAAKLAEVVGVFKLDATQQYVSASAGPSVTAPAPAAAMRAAMRPAIQPAKRRAPAPAVTAPTPGKAAQADAA
 2378 RARAPKAPVASGADEWEEF
 2379 >Acidovorax_delafieldii_2 |WP_085943602.1 HAMP domain-containing
 2380 protein, partial [Acidovorax delafieldii]
 2381 MNQLRIAHKLWLA VVLIVIMLVLVVGFSGYRS AKVQAQADAVAREMETRVAAAIRWAGLTETNAARTQALI
 2382 VSSDSAVEAEFKDVI PATSAQISEVQKSLEGM SLSEADRAQMAKIAAARKAMTDLRAQARQLKADGQAEQA
 2383 VALIKQSYNPAVAAYLQTLRDFVQMQQTAQASLADMAASRMLTVKIAAVAVAALLLAI IAGAYFLIRSIQ
 2384 QPLALANDLAARIAGGDL SMQGTVTRGDEFGLLRSQYAMSDALGRVVRVHRVQSTDSIALASAEIASGNHD
 2385 LSARTEQTSSNLQQTAAAMEQFTSTIQQSAGSAQQASSLATGATGVARRGGEVVTQVVSTMEEIQHSSKKI
 2386 ADIIGVIDGIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRSLAQRSAEAAAKEIKQLINTSVEKVD TGS
 2387 RLVADAGTTMADIVQSVQRVTD MIGEITAASTEQSAGIAQVNQAVGNLDQMTQQNAALVEESAAAAQSLRE
 2388 QAEQLAQVVS VFKV NAGRQAAQPLVAAAKPAASRPSAAVQ
 2389 >Janthinobacterium_sp._TND4EL3_4 |WP_076567014.1 HAMP domain-containing
 2390 protein [Janthinobacterium sp. TND4EL3]
 2391 MKNLKIGVRLGGGF AAVLLLLLTS LTVVGVIVQM QSASLET DQLVNVKVRNERLIGEWTKVIEVNAARTAAAW
 2392 KVSDPEHQKQFEKEMAVSSARATEIQNDIGKSEL SAEQALYQEV LSTRKAYTDVRKDVFKAKNAGDLELG
 2393 KRLYEGDMAVKRDIYLAALKK LAVREARLLDE TAAQIRARYENGRLLLLISLGMAAMLLGIACAYWITRSIT
 2394 RPITRAVQVAEAVSAGDLTSHIVVESRDETGQLMHALKNMNDKLVSVIGQVRS GTESISTASSEIAAGNLD
 2395 LSSRTEEQASSLEETASSMEELTSTVKLNADNARSANQLAIDASQIASKGGAVVSEVSTMGSIINDSSRKI
 2396 VDIISVIDAIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSSAAAKEIKGLIDDSVQKVEAGS
 2397 QLVDKAGRTMDEIVESIGHVTQIMNQITDASDQQRSGIEQVNQAIGQMDQVTQQNAALVEQAAAAAESMQE
 2398 QAARLAGVVG VFKLDATQQYVASSASPVVAPV PVPKPAIRRAAASAVAAPATGKAAPAEAVRTRTPKAP
 2399 VASSADEWEEF
 2400 >Janthinobacterium_sp._ROICE36_5 |WP_102122362.1 hypothetical protein
 2401 [Janthinobacterium sp. ROICE36]
 2402 MKNLKIGVRFGGFAFAAVLLLLLTS LTVVGVIVQM QSASKETD TLVNVKVRNERLIAEWTKVIEVNAARTAAAW
 2403 KVSDPEHQKQFEKEMAVSSARATEIQNDIGKSEL NAEQALYQEV LSTRKAYTEVRKNVFKAKNAGDLELG
 2404 KRLYEGDMAAKRDIYLAALKK LEVLEARLLDE AAAHIRSRYENGRLLLLISLGAVAILLGIACAYWITRSIT
 2405 RPITRAVEVAVAVSAGDLTSHIVVESRDETGQLMHALKNMNDKLVSVIGQVRAGTESISTASSEIAAGNLD
 2406 LSSRTEEQASSLEETASSMEELTSTVKRNADNALSANQLAIDASQIASKGGVVVSEVSTMGSIINDSSRKI
 2407 VDIISVIDAIAFQTNILALNAAVEAARAGEQGRGFVAVSEVRNLAQRSSAAAKEIKGLIDDSVQKVEAGS
 2408 QLVDKAGRTMDEIVQSI SHVTQIMNQITDASDEQRAGIEQVNQAIGQMDQVTQQNAALVEEAAAAAESMQE
 2409 QAAKLADVVGVFKLDV TQQYVSASVSARPAAGQ PAARRAVNAAARTSASTVVAR SASGPVKAVKPD TAHTS
 2410 KPRTPVASGADEWEEF
 2411

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