Figure S1.
Alignment of genes annotated in *P. fluorescens* Pf0-1 opposite which are found "*nov*" genes. Alignments were produced in ClustalW2 (http://www.ebi.ac.uk/Tools/clustalw2/index.html). Where predicted orthologs existed in other *Pseudomonas* genomes, these were used for alignments. Regions shaded in grey for Pf0-1 lines indicate the portion of the protein specified by DNA which overlaps the *nov* gene.

Colors in alignments:
RED = AVFPMILW (small+ hydrophobic (incl.aromatic -Y))
BLUE = DE (Acidic)
MAGENTA = RK (Basic)
GREEN = STYHCNGQ (Hydroxyl + Amine + Basic - Q)

Consensus symbols in the alignments:
* = residues or nucleotides in that column are identical in all sequences in the alignment.
: = conserved substitutions.
. = semi-conserved substitutions.

Pfl01_ = Pf0-1
PA = P. aeruginosa PA01
PA14_ = P. aeruginosa PA14
PFL = P.fluorescens Pf-5
PputW619_ = P. putida W619
PSPPH_ = P. syringae phaseolicola 1448A
PFLU = P. fluorescens SBW25
SELSPUOL_ = Selenomonas sputigena ATCC 35185
BACCELL_ = Bacteroides cellulosilyticus DSM 14838

Pfl01_0636 (3′ end is opposite 3′ end of *nov1*)

```
Pfl01_0636          MS-RHSQCGGPARQRGAIGLMAALTLGMALVFILVVVDSGRLYLERRHLQQIADVAALEA 59
PA4297              ------MNGWPARQRGAIGILAATTLLLALICLLLVVDTGRLYLEQRNLQRVADVAALES 54
PA14_55820          ------MNGWPARQRGAIGILAATTLLLALICLLLVVDTGRLYLEQRNLQRVADVAALES 54
PFL_0686            MSPLKRFYG-PARQRGAIGLMAAVTFGLALLLMLLVVDSGRLYMEQRKLQRVADNAALEA 59
PputW619_0838       MVPSS-----AARQRGAIGLMAVTTLALALLFMLVVVDSGRLYLEQRKLQRIADMAALEA 55
PSPPH_4415          MSPLDGYTAMPARQRGAIGMMAALTLGLALLCTLIVVDSGRLYLEKRSLQRVADIAALEA 60
                              .********::*. *: :**:  *:***:****:*:* **::** ****:

Pfl01_0636          ATRGGNCGA--GATANAYAQASVVRNNFPIPSAGRTLAVACGTLNLDASNLRVFAVNA-- 115
PA4297              ASQGALCGDQSSAQATSFAKASAMLNGFDADAAGSSLSAEVGGVLS-AGGLRSFIASASN 113
PA14_55820          ASQGALCGDQSSAQATSFAKASAMLNGFDADAAGSSLSAEVGGVLS-AGGLRSFIASASN 113
PFL_0686            VSRGGTCQA--GLTAAAYAGQNATRNGFTVAT-GSSLSTSCGSLTTGANGLRTFTANP-- 114
PputW619_0838       AGQSAVCTGN-GPQATAIASVAAARNGHTP---GSPLVASCGYLQTGANSLRTFTSDN-- 109
PSPPH_4415          AGRRGTCSG--AATAPGFATQSATRNGFTPNTGGRTLTTLCGTLTVGLQSQRVFVADS-- 116
                    . : . *    .  * . *   .  *..     * .* .  * :     . * *  .

Pfl01_0636          --ASTEAIRVVVSHTVPQSFAGAIGGLFGGAGRNATINLSATAVAAVPPP-LASLTIRST 172
PA4297              AAVANEAVHVEVTKSVPGSLVANLGGLFGGG--NANVDLRAEAVARRLPN--ATISAGTG 169
PA14_55820          AAAANEAVHVEVTKSVPGSLVANLGGLFGGG--NANVDLRAEAVARRLPN--ATISAGTG 169
PFL_0686            --AQAVAIRVIATHTVPISVASGVAALFTPGPINLTTQLSATAVAAAPTPTVAQLSIRST 172
PputW619_0838       --ARNEAIRVDVSNTVTTSFAAGIYILTQGGEVPLTSTLQAHAVASKPLPPQAMLSIRTT 167
PSPPH_4415          --TQALAIQVFAAHPVPRSIAAGIVALFEKTPSPANITISATAVAASAAP-LAALTIRSA 173
                      .   *::* .::.*. *... :  *        .  : * ***       * ::  :
```

```
Pfl01_0636         ALSVDTGRSAVLNALFGGLLGGNLSLSAASWNGLVNTNINLLGYLDRLKVDIG---LSAG 229
PA4297             LASVNSGQSALLNPILSGLLGTHIDLSAAAYNGIADAKLSVLDILGADGMGLIGVDTSLG 229
PA14_55820         LASVNSGQSALLNPILSGLLGTHIDLSAAAYNGIADAKLSVLDILGADGMGLIGVDTSLG 229
PFL_0686           LGTVSTAQSSILNPLVGGMLGGSLSLSAVGWNGLLNTNINLLSYLNQLAINLG---VAAG 229
PputW619_0838      LATVDSRQSALLDGLLG-ALGGNVQLGLAGWKGIAATDLNVLNYLDQLAVDLQ---LTVG 223
PSPPH_4415         AVTMDSTRAAILNPLIGSLLGGTLNLSVANWQGLASTDLSLLSYLNRLKTDLN---LTAV 230
                     ::.: ::::*: :..  **  :.*. . ::*:  :.:.:*. *.    .:     :

Pfl01_0636         GYSEVLGNTIAVSQLVQTAINVLDPNGTLSATATILGLQAIKAAAGATQVVLGNLLKVQA 289
PA4297             TIEQLLNTNVGLQQVLAASVNVLAKNGVASVEALRAQLVGVKSAT----LKLGDLLGLSA 285
PA14_55820         TIEQLLNTNVGLQQVLAASVNVLAKNGVASVEALRTQLVGVKSAT----LKLGDLLGLSA 285
PFL_0686           NYTQLLNTTTSVTQLIQAAITVVQANGATADILTALGNLQVAAIN-AAPLKLGDILQMQT 288
PputW619_0838      DYEQLLNADATATQLLEAAVKVLEQSGAAADIVTNLGKVALGAGN-STLLQLGDILDIQN 282
PSPPH_4415         GYSEVLNTSVSVSKLIQSAINVLDPGATLNGTATIAGLQALKLAAGATTVLLGDVLSIQG 290
                      ::*.      ::: :::.*:  ...            :        : **::* :.


Pfl01_0636         GTQ--ATALAVDVRAFDLIQGFVQLANKQNGLVANQTINLG-VAQITASVQVLEPPQLSA 346
PA4297             GEVNSMSQLDTAINALDLIMAVAQVANKNSAVAVNLGIPGLANARLTVVEPKRIVSGPPG 345
PA14_55820         GEVNSMSQLDTAINALDLIMAVAQVANKNSAVAVNLGIPGLANARLTVVEPKRIVSGPPG 345
PFL_0686           GLP--STALDANLQLFQLLQAVIQLSNSNSAVAATLPINVLGLANITVQAKVIEPPQLSA 346
PputW619_0838      GTA--QAGLDASIQLLQLVQGVIQLAASESAATADLPISVLGLINGRVRLKVIEPQQVSA 340
PSPPH_4415         SSD--LAALNTNLRLLDLVQGLAQLANDKTGISTAAQINVGTLAQVNTRFQVVEPPQLSA 348
                   .     : * . :. ::*: .. *:: .:..  .   *      .  .          ..

Pfl01_0636         IGNP-RLAAANP-LGPNRIYVKTAQVRTLLSVNLPLLDTILSLVNAVADLAGPLTNTLNA 404
PA4297             QDES----------GAWRTEVRQSQVRLTADIDSGFLSILATTK---------------- 379
PA14_55820         QDES----------GAWRTEVRQSQVRLTADIDSGFLSILATTK---------------- 379
PFL_0686           IGNPALAKADPM--GANRIYVRTAQVRTLVRVNLSLP-LVSGLSTAVGNLVAPLTPVLNS 403
PputW619_0838      VGDP----------RTDELRVHTAQVRAMISLDLPLLNTVFGLVNAVLDLVSPLTNVLNN 390
PSPPH_4415         IGDPSKIDPLNPKTGANRIYVRTAQMRALVSINLPVLGTITSLANTAGSVVGSLTPILNS 408
                    .:.           . .  *: :*:*    ::  .   :

Pfl01_0636         LLSLNLVGVIDSLTCALGAP-CQTPSIEVLPG------PIRLDVALDVAAANSYVTAFSC 457
PA4297             -----------------------------------------LQLAIEGASGAVWLKSMAC 398
PA14_55820         -----------------------------------------LQLAIEGASGAVWLKSMAC 398
PFL_0686           LLSLNLVATLGSALCLLGAG-CEQLYPAIASS-------SEIDLSLDAGGAIAYVTDYSC 455
PputW619_0838      LLSLNLASTLESVLCLLGVP-CTVTDIVLVPDK------LQLDIGLEVAEATARLDPQSP 443
PSPPH_4415         ALSLNIAGLVTSATCAVGLNSCMVTDFKFLTSDSSASAGPRIDLSLSLASADTYVTGYTC 468
                                                            :::.:. . .   :   :

Pfl01_0636         LTPTN--KTLTTNTTTSVANLKIGRMDPAAVFGSNVTPPAVVVQPLKVIDIGVKTCRRFL 515
PA4297             TRPDT---ALDFGWRSSGATIKIGSPANIDQVGS------------------------IL 431
PA14_55820         TRPDT---ALDFGWRSSGATIKIGSPANIDQVGS------------------------IL 431
PFL_0686           PVNNSGTKSLTAHAISSIADLKVGQIDPANAFSSAAEP---VVKPLPLVDLGIRTCYQFL 512
PputW619_0838      DTFRCSPKRLTVQAQSAAAKLAVGRFDSTNAFFTTGTT---AVKALPLIDIGTKRCTKLL 500
PSPPH_4415         TSNTS--KTLSVKTDAGLLSAKVGWIDSTAAFPASTDPSAITALPLPVLDIGTKTCQKIA 526
                            *     :.     :*       . :                        :

Pfl01_0636         VLPVSCDPRVPAVGGGLDISADTTVGQN--ANIPHVYSAP-PAAS-LPEINQPPFYYSYS 571
PA4297             VLGGLVR---------LDLKLDTSIAGS---------------------SGDTRFNVKAD 461
PA14_55820         VLGGLVR---------LDLKLDTSIAGS---------------------SGDTRFNVKAD 461
PFL_0686           VLPGRCDPVVHYAGGGIAVMVNTSVAQN---TQDLVFSSSASPFPIPPNVNQTPTYQTAA 569
PputW619_0838      IL-GTCESRIPYAGGGLGLRVDSKLLGSGPVEHPLVFQG---PVSEPPNIGQPAAYLNMR 556
PSPPH_4415         GLLGNCTARTPFGGGGIGLTFDTVSQSP--LGSSTVVSTT-FSSPNLPEINSAPYFLTSV 583
                    *              : :  ::                           ...    .

Pfl01_0636         TG--NVVSSLSD-TLNNLNLNMHGPT-----GSLVSGLGAILSSVKTLLVTTINTVLSPL 623
PA4297             GSDLVQSRRLPESGFLASTLKTSINVNPVVLGLCLPLLCGSTALTDLIVNSVVAPLVDGL 521
PA14_55820         GSDLVQSRRLPESGFLASTLKTSINVNPVVLGLCLPLLCGSTALTDLIVNSVVAPLVDGL 521
PFL_0686           PT-TNIVNSLAG-TLAGINLIVYKPVNNNPLGAIVTGLASAISGVSNLLTPLITGLLSPL 627
PputW619_0838      PVNDNVVGSLSD-TLLGVQLQAFKPTANSGLGDVLVIAGNVLGTVKGIIEPLIRGLLSPL 615
PSPPH_4415         AH--TKPSTLLNGTVSSVKVNVYKPATSNVLGNVITGAAATLNSLTVALDAIVENTLTGL 641
                            *    .    :     .     *  :             : . :   :  *
```

```
Pfl01_0636         LDTLINTLLMALGINLNQVDVGANLSC-QSGRATLVI 659
PA4297             LTPILNLVLPLLGVQLG--YIDAEILKVDVGRAELLI 556
PA14_55820         LTPILNLVLPLLGVQLG--YIDAEILKVDVGRAELLI 556
PFL_0686           LDPLLNNLLSGLGINLMDVEVGANLTCGQTGKAYLVI 664
PputW619_0838      IDPLVNVLLKVLGIDLVNTDVGANLSC-STGRAQLVL 651
PSPPH_4415         LTSVVDPLFESLGLSLGDADVGANLSC-NIGQATLII 677
                   : .::: ::  **:.*    :.*::   . *:* *::
```

```
SeqA Name            Len(aa)  SeqB Name            Len(aa)  Score
=================================================================
1    Pfl01_0636      659      2    PA4297          556      29
1    Pfl01_0636      659      3    PA14_55820      556      30
1    Pfl01_0636      659      4    PFL_0686        664      48
1    Pfl01_0636      659      5    PputW619_0838   651      42
1    Pfl01_0636      659      6    PSPPH_4415      677      45
2    PA4297          556      3    PA14_55820      556      99
2    PA4297          556      4    PFL_0686        664      30
2    PA4297          556      5    PputW619_0838   651      28
2    PA4297          556      6    PSPPH_4415      677      29
3    PA14_55820      556      4    PFL_0686        664      30
3    PA14_55820      556      5    PputW619_0838   651      28
3    PA14_55820      556      6    PSPPH_4415      677      28
4    PFL_0686        664      5    PputW619_0838   651      46
4    PFL_0686        664      6    PSPPH_4415      677      41
5    PputW619_0838   651      6    PSPPH_4415      677      37
=================================================================
```

Pfl01_0637 (3′ end is opposite 5′ end of *nov1*)

```
Pfl01_0637         MSSGDKLFDRLLNRQTSTPP----AVMDDPVVPGVGLQLHLDGEGQVIHLTGPLRHVLAQ 56
PA14_55780         --MFEFSRSSSAEAERPEPFSQEGPALWSASLRSWDLCFEMDEQDRVIRVGGRQAYRLQC 58
PA4293             --MFEFSRSSSAEAERPEPFSQEGPALWSASLRSWDLCFEMDEQDRVIRVGGRQAYRLQC 58
PFL_0687           ----------------------------------MGLQLVLDQQGRILSSHGPLRHSLIQ 26
PputW619_0839      ---MSGLFDRWLGSHAAEPA--------AQMPHAVGLQVWLDDQGHVLRLAGPLRTLLAV 49
PSPPH_4416         MPLEKNRLSRWLGRGEAPPVSQAVPVSSEPGPVGVDLYVLLDDEGRIQSISPQLLARLGI 60
                                                      .* . :* :.::          *

Pfl01_0637         QLSAARTPHLLDYLLPHSALAVEGVPADWQGQLLDLDFFSLAGPPLHLRGWVQP--QGDG 114
PA14_55780         AHGLGEQPRPFAEYLERRAPGAPTLAGLRRGERLDLTLRSDAAAPLTCRFQPMQPLDGLG 118
PA4293             AHGLGEQPRPFAEYLERRAPGAPTLAGLRRGERLDLTLRSDAAAPLTCRFQPMQPLDGLG 118
PFL_0687           LPPSREPPHLLAYVLPGSVLALEGGPADWSGQVLDLDLRGAGGQPLHLRGWVQR--CGQE 84
PputW619_0839      P--SHAQARVHDYLYQHSWLALEGVPADWQGQALDLDFQTVHGQALQTRGWLQH--QAIG 105
PSPPH_4416         AAPLSAAQRLMNLLLPNSALVIEGVPHDWLGHMLDLDFKSADAHTLHARGWVQA--HGKG 118
                           :                .    *. *** :    . .*  *        .

Pfl01_0637         WVLQL-LDIGDLLSERRQAHSREQCQWLAAHIRDHLRLCGLARLPQVLGEQLQCLSQRFQ 173
PA14_55780         RSLLLGMDISDLNWQSDSQQHQLQSLSLGKLILSRLRHVSHGHLAEAVQEILESLSGAFQ 178
PA4293             RSLLLGMDISDLNWQSDSQQHQLQSLSLGKLILSRLRHVSHGHLAEAVQEILESLSGAFQ 178
PFL_0687           WHLQL-LDIGDLVQQRQQALGREQCRVFAAQASEQLRLCNLTRLPDVLHDQLTDLARYWH 143
PputW619_0839      WMLQL-FDISDLLRQGAQQEQWLTLRQLAADVGQAVRDCSEDWLTQTTAEQLMRLAEHWH 164
PSPPH_4416         WLLQL-LDISDLMEEASAARSRQQCLRFAGQMAERVRVCNVDRLTAVVTEQLEELAQLWR 177
                     * * :**.**  :            :.    . :*  .   *. .  : *  *:  ::

Pfl01_0637         VPCLAVALLDEETEGWQIHQHYSAPDAPRLWDMAQRLGTGLDSLNGAAPQRVLP----AE 229
PA14_55780         MQAIALLLGDGKGFCTVFASHVRPGSDSLLRPTLQLADDDLREGAGARLLRRGE-----G 233
PA4293             MQAIALLLGDGKGFCTVFASHVRPGSDSLLRPPLQLADDDLREGAGARLLRRGE-----G 233
PFL_0687           IPCLGLALLDEQEQGWVIHSCYSAHDAPRLWQEGQALGAGLDSLSGNTPQHLNQIQGLNE 203
PputW619_0839      AGSVRLMLADQS--GWRAHTCS---ESDWPWPDDQRLQPWLQALPAHFQQVAP------D 213
PSPPH_4416         VPCLALVLPEVSGSGWRVYCQYSAHTAPELWQVGQRLGNALDRFDANITHQLRFGGGVDQ 237
                     .: : * : .                      *     *    .

Pfl01_0637         HPRLSSVFGPAEGFAVPYRDAHGVAAWLLFGCFSAQPHTAELSDHDWLQLAAAVAAPLLE 289
PA14_55780         ASTLLRQIGEDALYLVPAAMRGGRLGALLVRPMSLEQLAQGPAPQDWQYLAELLANQVAD 293
PA4293             ASTLLRQIGEDALYLVPATMRGGRLGALLVRPMSLEQLAQGPAPQDWQYLAELLANQVAD 293
PFL_0687           HPRLQGIFGHREGFLVPYRDDHGVAAWLLCGCYAVQQHAPYLLDRDWLMLAAALAGPLLS 263
PputW619_0839      LPQWRATCAGLPLFLVPYSHGHEVQAWLLCAGAPSVP-----SPEAAMALLQALLEPLLA 268
PSPPH_4416         GP-LQSAFGNADGFLIPHSRDNVAKAWLMFGFYNPQQQAPDLGEREWLNLCSALAGPVLF 296
                    .      .    : :*        . *:               .    *   :   :

Pfl01_0637         RLREHRHHLQLERLEILQSLLGTGWWEVFSDSAEVLLADALAVSLGLSAG--RLPIQAWF 347
PA14_55780         RCELHEQHDSSRKLGLLQEMIGGGWWRYWAEQELFELAPALHDSLGLTGEYRRVPLEHLQ 353
PA4293             RCELHEQHDSSRKLGLLQEMIGGGWWRYWAEQELFELAPALHDSLGLTGEYRRVPLEHLQ 353
PFL_0687           RLREHRHHLHLERLEALQGLLGAGWWELCPDTAEILLASRLAASLHLPEDGARLNVQAWL 323
PputW619_0839      RLRQHQLQQRSRHLDELQQQLGAGWWQ-WPVQGPLHFDPALAASLDLPSA---VSIEQWL 324
PSPPH_4416         RLSEQHNRHHVERLAVLQDLLGTGWWELMPARDEILLAPQLARSLRLGDRVESLSRQDWL 356
                   *   :. :   .:*  **  :* ***.  .    . :   *  ** *      :  :

Pfl01_0637         ARVHPADREELRSRLQALQDEGQALELCVRLQPVDQAQPQ-WFRLQGQSLGIGAERRLVG 406
PA14_55780         GLLQPADADELGLRLRASLRSGQALAQDLCLRQPDSCGERRWLRIEGRPLGRGSALGLSG 413
PA4293             GLLQPADADELGLRLRASLRSGQALAQDLCLRQPDSRGERRWLRIEGRPLGRGSALGLSG 413
PFL_0687           ELIHPADRGELSSRLQELK-LGKPLLLNVRLHEPDPSAPQRWYRLQGQALGRGESQRLVG 382
PputW619_0839      ARLHPADREAAQMALEQLR-NGVALSLNVRLLEADRGAEPRWLHWVGQLHG-GQAH---G 379
PSPPH_4416         ALIHPADRQELSSRLAQLRDKGTPLLLCVRLAQSDPAQETLWYRIQGQALISGQVQRVLG 416
                     ::***       *      * .*   : *   *      * :  *:    *      *

Pfl01_0637         FMLDISDIKNQQQQAAAAHARLDNLIASAPAVIYVQRYVEGALQPTFFSASLQPLLGWSL 466
PA14_55780         VLLDISEGRRQEERAQAAHARLRSLIDSAPVVIYVQRVEQGHLVPEFYSESASNLLGLDL 473
PA4293             VLLDISEGRRQEERAQAAHARLRSLIDSAPVVIYVQRVEQGHLVPEFYSESASNLLGLDL 473
PFL_0687           FMLDISDIKNQQQQAAAAHARLDNLIASSPAVIYVQRYQEGALQPSFFSASLQPLLGWSL 442
PputW619_0839      FVLDISALKAQELQASAARARLENLIASSPAVIYIQRCCEGALHGEFFSASLTPMLGWPK 439
PSPPH_4416         FMLDVSDIKNQETEAAAAHARLDNLIASSPAVIYVQRYDHGNLEPTFFSDSLTPLLGWTL 476
                   .:**:*  : *: .* **:*** .** *:*.***:**  .* *   *:* *   :**
```

```
Pfl01_0637         ADCADGALVNHVHPDDRAAYFERTRQLLREGSVSTRYRMLDTQGNTHWLLDEAKLLRDDL 526
PA14_55780         QGQSWQALAERVHPDDLEAFFARGRELLREGRVKTRYRLADGQGNWHWLYDEAKLLRDAQ 533
PA4293             QGQSWQALAERVHPDDLEAFFARGRELLREGRVKTRYRLADGQGNWHWLYDEAKLLRDAQ 533
PFL_0687           ADCTAQPLAEWVHPDDRDLYFQRCRQLLREGSVHTRYRLRDRHGVYHWVLDEAKLLRDDL 502
PputW619_0839      DSELARQPGQAVHPHDRALWLERTRTLLRDGQVRSRYRLRDHLGGYHWVLDEARLLRDDL 499
PSPPH_4416         ADCVDGQLAEYIHPEDRDIWFERNRQLLRGGVVSRRYRLRNKNGHYHWLLDEARLLRDDL 536
                    .       : :**.*   :: * * *** * *  ***: :  *  **: ***:****

Pfl01_0637         GLPVEAVGLWLDVTDATLAAERIKTSEERYRILVEDSPAMICRYRPDLTLTFGNRPLAMY 586
PA14_55780         GLPSEAVGLWLDVTEQHLAAQRIAESEERYRVLVEDSPALICRYTADLVLTYVNRTFADS 593
PA4293             GLPSEAVGLWLDVTEQHLAAQRIAESEERYRVLVEDSPALICRYTADLVLTYVNRTFADS 593
PFL_0687           GLPVEAVGLWLDVTEATLAAEQVRQSEERYRILVEDSPAMICRYRPDLTLTFGNRPLAAY 562
PputW619_0839      GQPVEVVGLWLDVSEATEAAERVRQSEERYRVLVEDSPAMICRYTPDLQLLFGNRPLAEQ 559
PSPPH_4416         GMPVEAVGLWLDVTEATLAAEHVRQSEERYRILVEDSPAMICRYSPDLVLSFGNRPLANY 596
                   * * *.*******::   **:::  ******:*******:**** .** * : **.:*

Pfl01_0637         LECAPEQLPGVNLGSWMSDEQREAFVQRLAQLTPDAPVSSAEINLRLPGREHAWWIWSDR 646
PA14_55780         LATSPERLVGRRLDEWLAAEDASALRARLLGSPREGASEVPELRFNLPGQRFLWLVWAER 653
PA4293             LATSPERLVGRRLDEWLAAEDASALRARLLGSPREGASEVPELRFNLPGQRFLWLVWAER 653
PFL_0687           LECAPEELPGSNLGQWLSAEQREGFERRLKLLSPEYPVSTAEINLQLPGREHAWWVWSDR 622
PputW619_0839      LECTPEQLSEMNLGQWMSDGQRLSFIQRLAALTPEQPLGSAEICLQLPGHRHAWWVWAER 619
PSPPH_4416         MECTPEQLTGINLGDWLSDEQREAFIRRIGQLTPQAPVSTEEICIELPGREYAWWVWADR 656
                   :  :**.*   .*..*::  :  .:  *:   . : .    *: :.***:.. * :*::*

Pfl01_0637         GVFDEQGRLLEVQAVGRDNTEVRRSQQQLTQSAKMATLGEMATGLAHEINQPLNVMRMAI 706
PA14_55780         PLFDARGELCEVQAVGRDNTPVRRAQQQLAQGAKMASLGEMVSGLAHEVKQPLHVLRMTL 713
PA4293             PLFDARGELCEVQAVGRDNTPVRRAQQQLAQGAKMASLGEMVSGLAHEVKQPLHVLRMTL 713
PFL_0687           GVFDEQGQLLEIQAVGRDNTEVRRAQQQLTQSAKMATLGEMATGLAHEINQPLNVMRMAI 682
PputW619_0839      GLFNEQGQLLEVQAVGRDNTQVRQSQQQLMQGAKMATLGELATGLVHEINQPLNVMRLAI 679
PSPPH_4416         GIFDEHGTLVEVQAVGRDNTDVRRSRMQLNQSAKMATLGEMSTGLAHEINQPLNVMRMAV 716
                    :*: :* * *:******** **::: ** *.****:***: :**.**::***:*:*:::

Pfl01_0637         VNVLKRLGNGDVQIDYLTDKLNRIDTQVQRAARVVDHMRVFGRRSEIEQHPFNPLDAIEG 766
PA14_55780         FNMRQRMNSVGLDGDYLGEKLERMDAQVLRVDRLVSHLGVFSRKSALEALPFDPYAAFEG 773
PA4293             FNMRQRMNSVGLDGDYLGEKLERMDAQVLRVDRLVSHLGVFSRKSALEALPFDPYAAFEG 773
PFL_0687           VNVLKRLGNGDVQIDYLTDKLKRIDAQVQRAARVVDHMRVFGRRSEVEQQPFNPAHAIEG 742
PputW619_0839      ANTLKRVESGVVEVEYLTGKLQRIDAQVGRVARLVEHMRTYGRRSALEHQVFAAWTAVDG 739
PSPPH_4416         VNVLKRLGRGDVDIEYLTEKLNRIDTQVQRAARVVDHMRVFGRRSEVEEHLFDPAQAVEV 776
                    *  :*:    :: :**  **:*:*:** *. *:*.*: .:.*:* :*   * .  *.:

Pfl01_0637         TLSLLSEGLRGKGVELRIGEANFQLQVRGYVDQLEQVLINLMVNARDALLSKRESNRDFQ 826
PA14_55780         ALGLLGEGLRQHAIEVECPAPTQRMVVRGQADQLEQVIINLLANARDALLGNPGLASR-R 832
PA4293             ALGLLGEGLRQHAIEVECPAPTQRMVVRGQADQLEQVIINLLANARDALLGNPGLASR-R 832
PFL_0687           TLSLLAEGMRGKGLELRISELGFEVQVLGFVDQLEQVLINLLVNARDALLGKQEKQHDFK 802
PputW619_0839      AVALLAEGLRGKGVALQVEEPDFCPEVQGHEDQLEQVLINLMVNARDALLERQVAS---- 795
PSPPH_4416         TLSMLAEGMKGKGVQLRVGTMIEDVQVRGHVDQLEQVLINLMVNARDALLSRREKDRDFE 836
                   ::.:*.**:: :.: :.         * *  ******:***:.******* .

Pfl01_0637         PWIAVHAEHDEHVVRLWVEDNGGGIDPRLLERIFEPFFTTKPVGVGTGLGLSVSYGIVEN 886
PA14_55780         VRLEQVACREPGWVELHVHDNGGGIEPLLLERIFEPFFTTKAEGKGTGLGLSVSHDLVRN 892
PA4293             VRLEQVACREPGWVELHVHDNGGGIEPLLLERIFEPFFTTKAEGKGTGLGLSVSHDLVRN 892
PFL_0687           PWIAVYGQRDEQWVRLWVEDNGGGIDPRLLERIFEPFFTTKPVGIGTGLGLSVSYGIVQN 862
PputW619_0839      PRIGICQRIEQGQLCLQVEDNAGGIDPCLIERIFEPFFTTKPAGVGTGLGLSVSFGIVEA 855
PSPPH_4416         PWISVEAERDENIIRLAVQDNGGGIDPRLLERIFEPFFTTKPVGVGTGLGLSVSYGIVDQ 896
                     :      :   : * *.**.***:* *:***********. * *********..:*

Pfl01_0637         MGGRLSVRNGDDGARFCIELPIALDDQITSVARPD 921
PA14_55780         MGGSLTAANQGEGALFVVRLPLAAPAEAGG----- 922
PA4293             MGGSLTAANQGEGALFVVRLPLAAPAEAGG----- 922
PFL_0687           MGGRLSVSNSQDGARFCIELPIAEADQITR----- 892
PputW619_0839      MGGRLEALNGVDGACFRVLLPIYNTN--------- 881
PSPPH_4416         MGGQLSVGNVGEGARFQIELPIFNAG--------- 922
                   *** * . *  :** * : **:
```

```
SeqA Name            Len(aa)  SeqB Name            Len(aa)  Score
=================================================================
1    Pfl01_0637      921      2    PA14_55780      922      40
1    Pfl01_0637      921      3    PA4293          922      40
1    Pfl01_0637      921      4    PFL_0687        892      72
1    Pfl01_0637      921      5    PputW619_0839   881      52
1    Pfl01_0637      921      6    PSPPH_4416      922      60
2    PA14_55780      922      3    PA4293          922      99
2    PA14_55780      922      4    PFL_0687        892      41
2    PA14_55780      922      5    PputW619_0839   881      35
2    PA14_55780      922      6    PSPPH_4416      922      38
3    PA4293          922      4    PFL_0687        892      41
3    PA4293          922      5    PputW619_0839   881      36
3    PA4293          922      6    PSPPH_4416      922      38
4    PFL_0687        892      5    PputW619_0839   881      52
4    PFL_0687        892      6    PSPPH_4416      922      63
5    PputW619_0839   881      6    PSPPH_4416      922      50
=================================================================
```

Pfl01_1000 (overlaps *nov3*)

```
Pfl01_1000          MYKLAFFVPDSHVEVVKEAVFAAGGGRIGDYDHCAWQVLGSGQFRPLDGSQPFIGQAGQV 60
PA14_15770          MYKLCFYVPESHLDVVKQAVFAAGGGRIGAYDSCCWQSLGQGQFRPLDGSQPYLGQVGQV 60
PA3762              MYKLCFYVPESHLDVVKQAVFAAGGGRIGAYDSCCWQSLGQGQFRPLDGSQPYLGQVGQV 60
PFL_1077            MYKLSFFVPPSHVESVKSAVFAAGGGRIGAYDQCAWQVLGQGQFRPLDGSQPFLGQTGQV 60
PputW619_4188       MYKLAFFVPASHVDVVKAAVFAAGGGRIGGYDHCAWQTLGHGQFRPLDGSQPFLGQTGQV 60
PSPPH_1342          MYKLAFFVPPSHVDEVKSAVFAAGAGRIGAYDHCSWQVLGQGQFRPLNGSQPFVGQSGVV 60
                    ****.*:** **:: ** ******.**** ** *.** ** ******:****::** * *

Pfl01_1000          ERVEEWKVELVVGDELIRSVVAALKLSHPYETPAYEVWRLEDF-- 103
PA14_15770          EHVAEWKVELVVADELIHASVKALKAAHPYETPAYEVWRLTDMVF 105
PA3762              EHVAEWKVELVVADELIHASVKALKAAHPYETPAYEVWRLTDMVF 105
PFL_1077            ERVEEWKVELVVADELIRDLVLALKQSHPYETPAYEVWRLEAF-- 103
PputW619_4188       EVVEEWKVELVVADDLIAQVVAALRQSHPYETPAYEVWRLADF-- 103
PSPPH_1342          ESVEEWKVELVVADDLIQQAVLALKQSHPYETPAYEVWRLEEF—103

                    * * ********.*:**   * **: :*************  :
SeqA Name             Len(aa)   SeqB Name             Len(aa)   Score
=================================================================
1     Pfl01_1000      103       2     PA14_15770      105       75
1     Pfl01_1000      103       3     PA3762          105       75
1     Pfl01_1000      103       4     PFL_1077        103       85
1     Pfl01_1000      103       5     PputW619_4188   103       84
1     Pfl01_1000      103       6     PSPPH_1342      103       79
2     PA14_15770      105       3     PA3762          105       100
2     PA14_15770      105       4     PFL_1077        103       77
2     PA14_15770      105       5     PputW619_4188   103       76
2     PA14_15770      105       6     PSPPH_1342      103       73
3     PA3762          105       4     PFL_1077        103       77
3     PA3762          105       5     PputW619_4188   103       76
3     PA3762          105       6     PSPPH_1342      103       73
4     PFL_1077        103       5     PputW619_4188   103       82
4     PFL_1077        103       6     PSPPH_1342      103       84
5     PputW619_4188   103       6     PSPPH_1342      103       81
=================================================================
```

Pfl01_2430 (overlaps *nov4*)

No predicted orthologs in *Pseudomonas* genomes; no matches in GenBank.

Pfl01_2664 (overlaps *nov6*)

No predicted orthologs in *Pseudomonas* genomes; there are matches in GenBank.

```
Pfl01_2664         MEQFKQFNASKTEVIKSLDNLQKLVGALEALGLDVSQDIEKIRKAIGDVQSDALRIALLG 60
Shewana3_2033      MEQLKQFEVEKQSAISTLQQLKEVLTELGAIGMDVSVDIQKLEAALNTIKDDVLRIALLG 60
E. coli LeoA       MEQFKQFSIEKQAAINSLLQLRGMLEMLGEMGINISDDLQKVTSAINAIESDVLRIALLG 60
SELSPUOL_01925     MEKLERLSDWEACAKRRYLAVQEKMEELHDLNVDCAEDLQKIEDKLGSMGQEKISLALVG 60
BACCELL_05373      METSKNSGNEKQ---HRLIALKSLVEKGITLGLDLTDVLEKIENVIKSSKDNIIRMVLLG 57
                   **  :.    :         ::  :     :.:: :  ::*:   :    .: : :.*:*

Pfl01_2664         AFSDGKTSVVAGWLGQVMKDMKIDTNESSDALAIYRPDNLQDRCEIVDTPGLFGDKEKAA 120
Shewana3_2033      AFSDGKTSVIAAWLGKIMADMKIDMDESSDRLAIYRPEGLPDKCEIVDTPGLFGDKQKED 120
E. coli LeoA       AFSDGKTSVIAAWLGKVMDDMNISMDESSDRLSIYKPEGLPDQCEIVDTPGLFGDKEREV 120
SELSPUOL_01925     AFSDGKTSVIAGLFGEELEGMQISVDESTDEIQIYEPNNPKISCRIVDTPGLFGTKEKQR 120
BACCELL_05373      TFSDGKTSVVAGLLGKLEDSMKIDQDESSDELKVYRPNGLKEGFEIVDTPGLFGTKEKEV 117
                   :********:*. :*:   .*:*. :**:* : :*.*:.     .********* *::

Pfl01_2664         ENGALVQYGDITKNYISEAHLIFYVVDATNPLKESHQDIVRWVLRDLNKLSSTIFVINKM 180
Shewana3_2033      EN-LQIMYEDITRNYISEAHLILYVVDATNPLKESHHQIVRWVLRDLNKLSSTVFIINKM 179
E. coli LeoA       DG-RLVMYEDLTRRYISEAHLIFYVVDATNPLKESHSDIVKWVLRDLNKLSSTIFVINKM 179
SELSPUOL_01925     SD-GVVQLGEIAKRYLAEAHMLLYVVESKNPIKDSHKDTLRWIMKDLQKTDRMIFVINKM 179
BACCELL_05373      DG-KNIRYSELTQKYISEAHVVIYVCDAVTPLKESHKDIIKLVMRDFNKLESTIFVINKM 176
                   ..   :   ::::.*::***:::** ::  .*:*:** : ::  :::*::* .  :*:****

Pfl01_2664         DEV-ADLRDAEEFEQQSTIKKNNLLDKLQRFVDLSAAERDAINVVCVASNPNSRGLEFWL 239
Shewana3_2033      DEV-TDLSDPTLFSEQAAIKTETLKEKLQRAASLTDEEVKALRIVCIASNPNGRGLPFWF 238
E. coli LeoA       DEV-TSLTDQALFDEQAAIKKANLKGKLQRAADLTAQECEQLNIVCVASNPNGRGLTYWF 238
SELSPUOL_01925     DDV-ADLSDEEEFLSQAAIKKEAVREKLRELVGVRADDAAKVRIVCIAADPDRRGMDFWK 238
BACCELL_05373      DEAGTDMLDEEDYNEMSSIKKDNLLKRLRDTIGLTAEEESKMRIACVAADPKGKGLKHWF 236
                   *:. :.: *   : . ::**.  :  :*:   .:   :   :.:.*:*::*. :*: .*

Pfl01_2664         EQKDLYDQRSRISELKVVTQQVLDGSGRETLIKKTGIDVVRDVLGKKIALAQDELIKFRL 299
Shewana3_2033      EKLDVYRNRSRIDELKKTTTSILDSSVRSTIIAKTGIDVVAGVVSQRVLAAQNSLDELEV 298
E. coli LeoA       TKPEHYESRSRINDLKNAATEILKTNVPEVLLVKTGMDVVKDIVIQRVTLASRHLDELNT 298
SELSPUOL_01925     EHTDVYEKRSHIVDLEDAIEGVLQKHSAEEFFANAALGVCKAVLGRYIEEVPTFVKAQEK 298
BACCELL_05373      TDMDGYLKRSHIEVLREYISSITDTLDTDAAKNNAKTAVIKDVLLSMSKRVDAVFGPLSL 296
                    . : * .**:*  *.     : .    .    ::   *   ::      .   .

Pfl01_2664         LADNQRRDSARIQEDIAEGKRKVLATVGNLYEELNNLETDLLNSIRTLPRDQVRAFLESQ 359
Shewana3_2033      FAKQREQECERIREDLNNGKREVKRLAGQLFNELEGLEKQLMGKLRPLDFEDIRPFMEDE 358
E. coli LeoA       FVEKNDEDMHRFSNDIKQSRIEVKRLAGELFEELNLMEKQLMSQLRPLDLDDIRPFMDDE 358
SELSPUOL_01925     MREKLAESVSRQEADFQETRKHLLLAGEECWEELAAYRQRLLDGIHALSLESAEKFIDLE 358
BACCELL_05373      ALRRYDDELKDMNNDLNILKGELNQSKAIMTERLNDLKKSIKMDINNATQNSFGTVIDDD 356
                      .   .      *:   : .:        :.*   .  :   :.    :.   .:: :

Pfl01_2664         IGFSNNDIG-EKLRFRIDHLFSTAFNQSSSIMSGISAKIEHQLDSSSDFADSITASALSA 418
Shewana3_2033      IGYTQDNIG-YKLSIKIKTIVDSYYDQTSLITSRLNQEINSQLDSSTSFLDSLGSDALKF 417
E. coli LeoA       LGYTEDGVG-FKLHLRIKQSVDRFFEQSTAVSQRLSDDITRQLSSSESFLSGLGEGAFRS 417
SELSPUOL_01925     FGRSGDTIG-KHFEQQLTHIMEKHLGRMREDIETFKKKFEQETDVQSNIFLGLGRQAQSW 417
BACCELL_05373      LGMEDKKVTGYILLRKVNQILSECAEKNNATLSMKEIDFNLRFDKQDSMLKDVLKQGGSY 416
                   :*   . :    :  ::   ..    :     .  . .:  . . . .:  .:   .

Pfl01_2664         SSRALTAVSKIPVESIKSGVFLARETLKNLTGYVYKFKPWEATKLAANISRWAGPIGAGI 478
Shewana3_2033      VGSGLSNVSKISPDAIKATIFVARDLLAKTTGVVYKFKPWQASKLAAGISKWAGPAGMVF 477
E. coli LeoA       LGGAFKGVSKISPATLKTTILAARDTIGKLTGYVYKFKPWEATKLAGSIAKWAGPVGAAF 477
SELSPUOL_01925     IKYIP---PTKMVDFARKGIFIGRDLLKRIG-IIIKFKPWQVVKFAKAVPILT----VLL 469
BACCELL_05373      LG---------KVNISGEMVKAARDIFAKS----YKFKPWGAVNLGKSMTKLAKVGGAAL 463
                                      :  .*: : .      ***** . ::.  :.  :      :
```

```
Pfl01_2664         QVLTDVISVAQQQRAETELKQLQGDLAEVVKSYFAEPMKLLMDHEKVMDIFAPQIKAFEK 538
Shewana3_2033      SLTADFYNAYKASELEAELKETKNEISTMIKEAFKDLYDIVSDDQKLFDFFAPQLKIFDQ 537
E. coli LeoA       TIGSDLWDAYKAHEREQELKEVKASLAKIIKEPFEDIYDVLSSDEKMFAFFAPQIQQMEQ 537
SELSPUOL_01925     ELLMLVVDALVQSKRDARLKELKETLLQGVEETFQEIQSTLQG-DALFENYVPDFLSVQS 528
BACCELL_05373      ALAIEVVSFISAARNEKKLKDLKADIVGEVDKIFKSIFEMFDKDDKYYENFASSYIEMTK 523
                    :   . .     . : .**: :  :   :.. * .  . .   :     :...   . .

Pfl01_2664         ILVEQEASLDDLRNRQTQLAELETHLSQAFDSQNVIEGEYGVV 581
Shewana3_2033      LITDTESQVKDIRVSQNSLRGISEKLKSLPSY----------- 569
E. coli LeoA       VVTELAEKSQAIRDNRQKLSLIQTQLAQLMVPATENHTAR--- 577
SELSPUOL_01925     DLEAAQKELQDLKENMRLLAVWTEAAKELQLGLENLR------ 565
BACCELL_05373      RLHARMQEISVMRHKVANLEDYGRSLKDWFKEDAEDADFEEI- 565
                    :     . . ::     *        .

SeqA Name            Len(aa)  SeqB Name            Len(aa)  Score
=================================================================
1    Pfl01_2664      581      2    Shewana3_2033   569      48
1    Pfl01_2664      581      3    E.              577      45
1    Pfl01_2664      581      4    Selenomonas     565      30
1    Pfl01_2664      581      5    Bacteroides     565      30
2    Shewana3_2033   569      3    E.              577      57
2    Shewana3_2033   569      4    Selenomonas     565      29
2    Shewana3_2033   569      5    Bacteroides     565      31
3    E.              577      4    Selenomonas     565      28
3    E.              577      5    Bacteroides     565      32
4    Selenomonas     565      5    Bacteroides     565      27
=================================================================
```

Pfl01_2848 (overlaps *nov7*)

```
Pfl01_2848      MKITVFGSGYVGLVQAAVLAEVGHDVVCMDIDEKKIELLRQGHVSIFEPGLASLVREGLD 60
PA14_18300      MKISVFGSGYVGLVQAAVLAEVGHDVLCMDIDRNKVERLAQGLASIYEPGLDALLREGLD 60
PA3559          MKISVFGSGYVGLVQAAVLAEVGHDVLCMDIDRNKVERLAQGLASIYEPGLDALLREGLD 60
PFL_3050        MKISVFGSGYVGLVQAAVLAEVGHDVICMDIDEQKVKQLQQGHVSIFEPGLASLVKENLE 60
PSPPH_2809      MRISVFGSGYVGLVQATVLAEVGHDVVCMDIDQAKIDQLRQGQVHIYEPGLANLVRDNLD 60
                *:*:************:*********:*****. *:. * ** . *:****  *:::.*:

Pfl01_2848      AGRLQFTCDEILAVQHGKVAFIAVGTPSNEDGSADLRYVLSVGDAVARHREKPLILVEKS 120
PA14_18300      SGRLRFSSDARLAVEHGRVQFIAVGTPPGEDGAADLGAVFAVADAIAEHRRKPVIVVEKS 120
PA3559          SGRLRFSSDARLAVEHGRVQFIAVGTPPGEDGAADLGAVFVVADAIAEHRRKPVIVVEKS 120
PFL_3050        AKRLHFTHDEKLAVQHGQVLFIAVGTPSSEDGSADLRYVLSVGDAVARHREQPVILVEKS 120
PSPPH_2809      HERLHFTTDERLAVEHAEVLFIAVGTPSRADGSADLGGFFAVGEAIARHRCEPLIIVEKS 120
                  **:*: *  ***:*..* *******.  **:***  .: *.:*:*.** :*:*:****

Pfl01_2848      TVPVGTGDTLRAHLDKALVKAGRLLQFDIVSNPEFLKEGSAVADCRRPDRIVIGCEREEV 180
PA14_18300      TVPVGTGDRLRAHIERRLEADGRELEFEIVSNPEFLKEGSAVADCRRPDRIVVGCDNEEV 180
PA3559          TVPVGTGDRLRAHIERRLEADGRELEFEIVSNPEFLKEGSAVADCRRPDRIVVGCDNEEV 180
PFL_3050        TVPVGTGDTLKAHIEKVLD--GRALQFDIVSNPEFLKEGSAVTDCRRPDRIIIGCEREEV 178
PSPPH_2809      TVPVGSGDALRGHIDKVLRQAGRLLQFDIVSNPEFLKEGSAVNDCRRPDRIVIGCENEAV 180
                *****:** *:.*::: *    ** *:*:************** ********::**:.* *

Pfl01_2848      RDVMRDLYSPFNRNHDRIMFMDLRSAELTKYAANCMLATKISFINQIAELAEHLGADIES 240
PA14_18300      RQVMRELYEPFNRNHDRMLFMGLRSAELTKYAANGMLATKISFINQIAELAEHLGADIEA 240
PA3559          RQVMRELYEPFNRNHDRMLFMGLRSAELTKYAANGMLATKISFINQIAELAEHLGADIEA 240
PFL_3050        RDVMRDLYAPFNRNHDRIMFMDLRSAELTKYAANCMLATKISFINQIAELAEHLGADIEA 238
PSPPH_2809      RKVMRELYAPFNRNHDRIMFMDLRSAELTKYAANCMLATKISFINQIAELAEHLGADVES 240
                *.***:** ********::**.************ **********************:*:

Pfl01_2848      VRQGIGADSRIGYHFIYPGCGYGGSCFPKDMRALIHSAEEAHCSSDLLQAVEAINQRQKH 300
PA14_18300      VRQGIGADPRIGYHFIYPGCGYGGSCFPKDMRALIHSAEQAHCSSDLLQAVEAINRRQKH 300
PA3559          VRQGIGADPRIGYHFIYPGCGYGGSCFPKDMRALIHSAEQAHCSSDLLQAVEAINRRQKH 300
PFL_3050        VRLGIGADTRIGYHFIYPGCGYGGSCFPKDMRALIHSAQQAHCSSDLLQAVEAINERQKH 298
PSPPH_2809      VRLGIGADSRIGYDFIYPGCGYGGSCFGKDIRALIHSAREAHCSNDLLSVVEAINERQKN 300
                ** *****.****.************* **:*******.:****.***..*****.***:

Pfl01_2848      KLFERINAFYKGELRGKTFAVWGLAFKPNTDDMRDAPSRVLLESLWAAGANVRAFDPEAM 360
PA14_18300      KLFERIRVFYDGDLRGKTFALWGLAFKPNTDDMRDAPSRELMEALWRHGAQVRAYDPEAM 360
PA3559          KLFERIRVFYDGDLRGKTFALWGLAFKPNTDDMRDAPSRELMEALWRHGAQVRAYDPEAM 360
PFL_3050        KLFERIKAFYKGDLKGKTFALWGLAFKPNTDDMRDAPSRVLLDALFAAGAQVRAFDPEAM 358
PSPPH_2809      KLFERVNAFYQGDLRGKTFALWGLAFKPNTDDMRDAPSRMLMEALWEAGASVRAFDPEAM 360
                *****:..**.*:*:*****:****************** *:::*:  **.***:*****

Pfl01_2848      QETQNLYPDESKLMLMGTPESVLAGSDALIICTEWQQFKAPDFDLIQQRLKAPVIFDGRN 420
PA14_18300      QETQRLYGHDERLSLMGTPEATLGGADALVICTEWQQFKAPDFELLKERLKAPVIFDGRN 420
PA3559          QETQRLYGHDERLSLMGTPEATLGGADALVICTEWQQFKAPDFELLKERLKAPVIFDGRN 420
PFL_3050        QETQRLYPDESRLMLMGTPESVLVGADALVICTEWQQFKAPDFDLIQQRLKAPVIFDGRN 418
PSPPH_2809      QETQRIYGHRKDLILMGTPESVLNDADALIICTEWQQFKAPDFELIQQRLNAPIIFDGRN 420
                ****.:* . . * ******:.* .:***:*************:*:::**:**:******

Pfl01_2848      LYDAERLARNGFHYFPMGRGESRTLPIPLQQWPHASDVA----- 459
PA14_18300      LYDPERMARHGFHYYPMGRGQSCSLPINEASLAQEDGVRLLRQA 464
PA3559          LYDPERMARHGFHYYPMGRGQSCSLPINEASLAQEDGMRLLRQA 464
PFL_3050        LYDAERLARNGFTYFPIGRGESRNLPIPHQQWSAEA-------- 454
PSPPH_2809      LYDTERLATRGFHYFPIGRGESCDLPIPQKRWTPYDQLTSSQAI 464
                ***.**:* .** *:*:***:*  ***     .
```

```
SeqA Name         Len(aa)  SeqB Name         Len(aa)  Score
===========================================================
1    Pfl01_2848   459      2    PA14_18300   464      76
1    Pfl01_2848   459      3    PA3559       464      76
1    Pfl01_2848   459      4    PFL_3050     454      87
1    Pfl01_2848   459      5    PSPPH_2809   464      78
2    PA14_18300   464      3    PA3559       464      99
2    PA14_18300   464      4    PFL_3050     454      77
2    PA14_18300   464      5    PSPPH_2809   464      73
3    PA3559       464      4    PFL_3050     454      77
3    PA3559       464      5    PSPPH_2809   464      73
4    PFL_3050     454      5    PSPPH_2809   464      78
===========================================================
```

Pfl01_3080 (overlaps *nov8*)

```
Pfl01_3080         MSDILWQPDAKRIARSRMDGFRRFINQRHHLKLDDYPALHQWSIDQREAFWQAIVDFFGI 60
PA14_38690         MPAPLWSPSAERIAASRMEAFRRFVNQRHALGLADYPALHAWSVQRREAFWQAIVDFFEV 60
PA1997             MPAPLWSPSAERIAASRMEAFRRFVNQRHALGLVDYPALHAWSVQRREAFWQAIVDFFEV 60
PFL_3577           MSDLLWQPSAERIGKTRMDAFRRFVNQRHGLNLHDYPALHQWSIDQRESFWQAIVDFFEV 60
PputW619_2720      MNDVLWCPAAAQIEASRMDAFRRWINLRYNLQLNDYAALHGWSVEQRAAFWQSIADYFQV 60
                   *   ** * * :*  :**:.***::* *: * * **.*** **:::* :***:*.*:* :

Pfl01_3080         SFHTQPDAVLRGGLKMPGAEWFPGATLNFAEHLLSRRDDAIAVIAIGENGQRELLTWAEL 120
PA14_38690         RFQQPPRAVLEEGTQMPSARWFPGATLNFAEHLLRRRDDAPALIAVSEDGRREVLSHAEL 120
PA1997             RFQQPPRAVLEEGAQMPSARWFPGATLNFAEHLLRRRDDAPALIAVSEDGRREVLSHAEL 120
PFL_3577           SFHQPAECVLREGPQMPSAQWFPGATLNFAEHLLKRRDDSVAVVAINENGQREQLTHAEL 120
PputW619_2720      LWHTPPSQVLSEGAQMPDARWFAKATLNFAEHLLRRRDDHPAVTAMREDGQRRSLSHAQL 120
                    ::  .  **  * :**.*.**. ********** ****  *: *: *:*:*. *: *:*

Pfl01_3080         AQQVAGFQASLQAAGVLVGDRIAACMPNTWQTLVAMLATTSLGAIWSCSSPDFGTHGVID 180
PA14_38690         ARHVAGLQKRLAALGIGPGDRVAALMPNTWQTVVGMLATASLGATWSSCSPDFGTQGVID 180
PA1997             ARHVAGLQKRLAALGIGPGDRVAALMPNTWQTVVGMLATASLGATWSSCSPDFGTQGVID 180
PFL_3577           AAQVAGLQRSLRAAGVGLGDRVAACMPNTWQTLVGMLASTSLGAVWSSCSPDFGTQGVVD 180
PputW619_2720      AAEVAGLQKAFKNAGIEPGDRIGAVMPNTWETLVAMLACTSLGAVWSTSSPEFGLHGIID 180
                   * .***:*  :   *:  ***:.* *****:*:*.*** :**** ** .**:** :*::*

Pfl01_3080         RFGQIEPKVLITCAGYRYAGKEIDQTVKVNEILEQLPSLQQLIIVPYARPQAHATDYRTP 240
PA14_38690         RFGQIEPRVLIACAGYRYAGKSLDLTAKLNEVLAGLPGLEQLLVVPYDRPQAQPQDYRCQ 240
PA1997             RFGQIEPRVLIACAGYRYAGKSLDLTAKLNEVLAGLPGLEQLLVVPYDRPQAQPQDYRCQ 240
PFL_3577           RFGQIEPKVLITCAGYRYAGKDIDQTAKVNQILERLPSLEQLLIVPYARSQARAEDYRTP 240
PputW619_2720      RFGQIEPKLLIVCAGYQYAGKQIDQVDKINQVCTQLPGLQQLIVVPYTRPHTQADEFSTQ 240
                   *******::**.****:****.:* . *:*::   **.*:**::*** *.:::. ::

Pfl01_3080         ANVTLWDDFYEPGDEPQFVPVPFDHPLYVLYSSGTTGVPKCIVHSTGGVLLQHVKEHGLH 300
PA14_38690         ARVALWDGFYQAEGEPVFTPVPFEQPLYILYSSGTTGVPKCIVHATGGVLLQHLKEHGLH 300
PA1997             AQVALWDGFYQAEGEPVFTPVPFEQPLYILYSSGTTGVPKCIVHATGGVLLQHLKEHGLH 300
PFL_3577           ASVSLWDDFYRPGGEPEFTPVPFAHPLYILYSSGTTGVPKCIVHGTGGVLLQHLKEHGLH 300
PputW619_2720      AKVSLWGDFYQAGGEPTFTPLPFDHPLYILYSSGTTGVPKCIVHSAGGVLLQHLKEHGLH 300
                   * *:**..**.. .** *.*:** :***:***************.:*******:******

Pfl01_3080         VDLGPGDRLFYYTTCGWMMWNWLVSALAVGSAVVLYDGSPFYPDNERLLELLDDEQVSVF 360
PA14_38690         TDLGDGDRLFYYTTCGWMMWNWLASGLAVGASLVLYDGSPFHPGPERLLDLVDAEDIAVF 360
PA1997             TDLGDGDRLFYYTTCGWMMWNWLASGLAVGASLVLYDGSPFHPGPERLLDLIDAEDIAVF 360
PFL_3577           ADLGPGERLFYYTTCGWMMWNWLVSALATGASLVLYDGSPFHPDNEHLMDLIDREAISVF 360
PputW619_2720      NDLKADDVLFYYTTCGWMMWNWLASGLAVGATLVLYDGSPFHPGPERLLDLIDAEGIQAF 360
                    **  .: ***************.*.**.*:::********:*. *:*::*:* * : .*

Pfl01_3080         GTSPKFLATLESSGIKPRESYDLSHLRTLLCTGSALSPQSYDFVYRDFKPDVCLSSMSGG 420
PA14_38690         GASAKYLAALEKAGVRPRHSHRLDSLRTLLSTGSPLAHESFDYVYRELKSDLCLSSISGG 420
PA1997             GASAKYLAALEKAGMRPRHSHRLDSLRTLLSTGSPLAHESFDYVYRELKSDLCLSSISGG 420
PFL_3577           GTSPKYLAALEKAGSRPRQSHRLESLKTLLCTGSPLSPQSYDYVYREIKSELCLASMSGG 420
PputW619_2720      GTSAKYLAALEQEGLEPARSHRLDSLRLILSTGSPLSPHSYDYVYAKIKADLCLASMSGG 420
                   *:*.*:**:**. * .* .*: *. *: :*.***.*: .*:*:** .:*.::**:*:***

Pfl01_3080         TDIVSCFVNGNPMSAVRRGEIMGKSLAMAVEVWNDAGQPVVGEKGELVCTRSFPAVPIGL 480
PA14_38690         TDIVSCFAIGNPVLPVWRGELQCKALGMAVEIWDDDGRRLASGKGELVCTRHFPSIPLGF 480
PA1997             TDIVSCFAIGNPVLPVWRGELQCKALGMAVEIWDDDGRRLASGKGELVCTRHFPSIPLGF 480
PFL_3577           TDIVACFVAGNPIQPVRRGEMQGKGLGMAIEVWNDQGQPVIGEKGELVCTRHFPSIPVGL 480
PputW619_2720      TDIVSCFVLGNPTLPVRRGEIACKGLGMAVQVWNEHGQPVTGEKGELVCTRHFPSMPLGF 480
                   ****:**. ***  .* ***:  *.*.**:::*:: *: : . ******** **::*:*:

Pfl01_3080         WNDPDGEKLRKSYFSQFPGVWAQGDYAEQLPHGGMLIHGRSDAVLNPGGVRIGTAEIYRQ 540
PA14_38690         WNDPDGTRFHDAYFASFPGVWAHGDYAEETAHGGLVIHGRSDAVLNPGGVRIGTAEIYRQ 540
PA1997             WNDPDGTRFHDAYFASFPGVWAHGDYAEETVHGGLVIHGRSDAVLNPGGVRIGTAEIYRQ 540
PFL_3577           WHDPDQSKLKASYFSLFPGVWAQGDYAEQLAEGGWLIHGRSDAVLNPGGVRIGTAEIYRQ 540
PputW619_2720      WNDNDGSRYREAYFSQFPGVWAQGDYAEQLATGGMVIHGRSDAVLNPGGVRIGTAEIYRQ 540
                   *:* *  : : :**: ******:*****:   ** :************************
```

```
Pfl01_3080         VEKVPQVLDSVAIGQQWQDDVRVVLFVHLKDGVTLDDTLQQQIRQVIRANTTPRHVPAKI 600
PA14_38690         VEKVEEVLESIAIGQDWQGDVRVLLFVRLRDGVRLDEPLRERIRQTIRANATPRHVPAKI 600
PA1997             VEKVEEVLESIAIGQDWQGDVRVLLFVRLRDGVRLDEPLRERIRQTIRANATPRHVPAKI 600
PFL_3577           VEKLEQVLESLAIGQSWEQDVRVVLFVRLQDGVELDEALQEHIRQVIRSNTTPRHVPAKI 600
PputW619_2720      VEKVEQVLESVAIGQQWKGDVRVVLFVRLRDGLVLDEPLQQRIRQVIRQYTTPRHVPAVI 600
                   ***: :**:*:****.*: ****:***:*:**: **:.*:::***.**  :******* *

Pfl01_3080         VAVTDIPRTISGKVVELAVRNVVHGEPVKNTDALANPQALEQFRDRPELNS-- 651
PA14_38690         IQVADIPRTLSGKIVELAVRNVIHGRPVKNTDALANPQALELYRDLAELRD-- 651
PA1997             IQVADIPRTLSGKIVELAVRNVIHGRPVKNTDALANPQALELYRDLAELRD-- 651
PFL_3577           LAVTDIPRTISGKIVELAVRNVVHGLPVKNTDALANPEALEQFRDREELRH-- 651
PputW619_2720      LQVSDIPRTISGKLVELAVRNVVHGLPVKNTDALANPEALEFFRDRTELHVQA 653
                   : *:*****:***:********:** ***********:*** :**  **.

SeqA Name            Len(aa)  SeqB Name            Len(aa)  Score
=================================================================
1    Pfl01_3080      651      2    PA14_38690      651      68
1    Pfl01_3080      651      3    PA1997          651      68
1    Pfl01_3080      651      4    PFL_3577        651      77
1    Pfl01_3080      651      5    PputW619_2720   653      69
2    PA14_38690      651      3    PA1997          651      99
2    PA14_38690      651      4    PFL_3577        651      73
2    PA14_38690      651      5    PputW619_2720   653      70
3    PA1997          651      4    PFL_3577        651      73
3    PA1997          651      5    PputW619_2720   653      70
4    PFL_3577        651      5    PputW619_2720   653      71
=================================================================
```

Pfl01_3654 (overlaps *nov11*)

```
Pfl01_3654          MSLPSQVRLIEVGPRDGLQNEAQPISVADKVQLVDALSAAGLGYIEVGSFVSPKWVPQMA 60
PA14_38490          MNLPKKVRLVEVGPRDGLQNEKQPIEVADKIRLVDDLSAAGLDYIEVGSFVSPKWVPQMA 60
PA2011              MNLPKKVRLVEVGPRDGLQNEKQPIEVADKIRLVDDLSAAGLDYIEVGSFVSPKWVPQMA 60
PFL_3934            MSLPSHVRLIEVGPRDGLQNEAQPISVEDKVQLVDALAAAGLGYIEVGSFVSPKWVPQMA 60
PputW619_1943       MPLPEKVRLVEVGPRDGLQNEAQPISVADKVRLVDDLTDAGLAYIEVGSFVSPKWVPQMA 60
PSPPH_2629          MSLPQKVNIVEVGPRDGLQNEAQPISIDDKVRLVDDLTAAGLSHIEVGSFVSAKWVPQMA 60
                    * **.:*.::*********** ***.: **::*** *: *** :********.*******

Pfl01_3654          GSAEVFAQIQRKPGVTYGALAPNLRGFEDALAAGVKEVAVFAAASEAFSQRNINCSISES 120
PA14_38490          GSAEVFAGIRQRPGVTYAALAPNLKGFEAALESGVKEVAVFAAASEAFSQRNINCSIKDS 120
PA2011              GSAEVFAGIRQRPGVTYAALAPNLKGFEAALESGVKEVAVFAAASEAFSQRNINCSIKDS 120
PFL_3934            GSAEVFARIQRKPGVVYGALAPNLRGFEDALAAGVKEVAVFAAASQAFSQRNINCSISES 120
PputW619_1943       GSADVFAAIEQRAGVTYAALAPNLRGFEDALAAGVKEVAVFAAASEAFSQRNINCSISES 120
PSPPH_2629          GSAQVFENIQRREGVIYSALAPNLRGFEDALAAGVREVAVFAAATEGFSRRNLNCSISES 120
                    ***:**  *.:: ** *.******:*** ** :**:********::.**:**:****.:*

Pfl01_3654          LARFAPIMESAKQHGVTVRGYVSCVLGCPYEGEVAPEQVAMVARELYAMGCYEVSLGDTI 180
PA14_38490          LERFVPVLEAARQHQVRVRGYISCVLGCPYDGDVDPRQVAWVARELQQMGCYEVSLGDTI 180
PA2011              LERFVPVLEAARQHQVRVRGYISCVLGCPYDGDVDPRQVAWVARELQQMGCYEVSLGDTI 180
PFL_3934            LERFVPIMDAAKQHGISVRGYVSCVLGCPYEGEVAPEQVAMVARELHDMGCYEVSLGDTI 180
PputW619_1943       LNRFEPIMQAARSHGVRVRGYVSCVLGCPYEGRVSAEQVAPVAKALHEMGCYEVSLGDTI 180
PSPPH_2629          LERFAPIMAAARMHGVQVRGYVSCVLGCPYEGSVSPQQVAAVANELYAMGCYEVSLGDTI 180
                    * ** *:: :*: * : ****:********:* * ..*** **. *  ************

Pfl01_3654          GTGTAGATRRLFEVVSKQVPREKLAGHFHDTYGQAMANIYASLLEGIAVFDSSIAGLGGC 240
PA14_38490          GVGTAGATRRLIEAVASEVPRERLAGHFHDTYGQALANIYASLLEGIAVFDSSVAGLGGC 240
PA2011              GVGTAGATRRLIEAVASEVPRERLAGHFHDTYGQALANIYASLLEGIAVFDSSVAGLGGC 240
PFL_3934            GTGTAGATRRMFEVVGAQVPREKLAGHFHDTYGQALANVYASLLEGIAVFDSSIAGLGGC 240
PputW619_1943       GTGTAGDTRRLFEVVSAHVPREQLAGHFHDTYGQALANVYASLLEGISVFDSSVAGLGGC 240
PSPPH_2629          GTGTPGATRALFNAVSAQIPRGKLAGHFHDTYGQALVNIYASLEEGIQVFDSSVAGLGGC 240
                    *.**.* ** :::.*. .:** :************:.*:**** *** *****:******

Pfl01_3654          PYAKGASGNVATEDVVYLLNGLGIETGIDLDALIAAGQQISSVLGRPTGSRVAKARSAQ- 299
PA14_38490          PYAKGATGNVASEDVLYLLNGLEIHTGVDMHALVDAGQRICAVLGKSNGSRAAKALLAKA 300
PA2011              PYAKGATGNVASEDVLYLLNGLEIHTGVDMHALVDAGQRICAVLGKSNGSRAAKALLAKA 300
PFL_3934            PYAKGASGNVATEDVLYLLNGLGIHTGIDMDRLIDAGRQICNVLGRPSGSRVAKARNAS- 299
PputW619_1943       PYAKGATGNIATEDVVYLLQGLGIETGIDLDRLIAAGQRISKVLGRANGSRVARARSAQ- 299
PSPPH_2629          PYAKGASGNVATEDVQYMLQGMGIETGVDLDQVIAAGQRICGVLRRSNGSRVARARLSA- 299
                    ******:**:*:*** *:*:*: *.**:*:. :: **::*. ** :..***.*:*  :

SeqA Name           Len(aa)  SeqB Name           Len(aa)  Score
=============================================================
1    Pfl01_3654     299      2    PA14_38490     300      77
1    Pfl01_3654     299      3    PA2011         300      77
1    Pfl01_3654     299      4    PFL_3934       299      89
1    Pfl01_3654     299      5    PputW619_1943  299      83
1    Pfl01_3654     299      6    PSPPH_2629     299      78
2    PA14_38490     300      3    PA2011         300      100
2    PA14_38490     300      4    PFL_3934       299      77
2    PA14_38490     300      5    PputW619_1943  299      77
2    PA14_38490     300      6    PSPPH_2629     299      71
3    PA2011         300      4    PFL_3934       299      77
3    PA2011         300      5    PputW619_1943  299      77
3    PA2011         300      6    PSPPH_2629     299      71
4    PFL_3934       299      5    PputW619_1943  299      81
4    PFL_3934       299      6    PSPPH_2629     299      75
5    PputW619_1943  299      6    PSPPH_2629     299      78
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Pfl01_3948 (overlaps *nov13*)

```
Pfl01_3948      MIFTPEHEALRRTVRQFVEHEINPHVDEWEKAGRFPIHEIFRKAGDLGLLGISKPEKFGG 60
PA14_26700      MIFTQEHEELRRTVRSFVEREINPNVDQWEKDGRFPIHEIFRKAGELGLLGISKPEKFGG 60
PA2889          MIFTQEHEELRRTVRSFVEREINPNVDQWEKDGRFPIHEIFRKAGELGLLGISKPEKFGG 60
PFL_4197        MIFTQEHEELRRTVRQFVDREINPHVEEWEKAGRFPIHEIFRKAGELGLLGISKPEKFGG 60
Pmen_2692       MIFTQEHEELRRTVRNFVDKEINPHVDAWEKEGRFPIHEIFKKAGELGLLGISKPEKFGG 60
                **** *** ******.**::****:*: *** *********:***:**************

Pfl01_3948      MGLDYSYSIVAAEEFGTIHCGGIPMSIGVQTDMCTPALARFGSDELREEFLRPAITGEQV 120
PA14_26700      MGLDYSYSIVAAEEFGSITCGGIPMAIGVQTDMCTPALARFGSDELREEFLRPAIAGEMV 120
PA2889          MGLDYSYSIVAAEEFGSITCGGIPMAIGVQTDMCTPALARFGSDELREEFLRPAIAGEMV 120
PFL_4197        MGLDYSYSIVAAEEFGTIHCGGIPMSIGVQTDMCTPALARFGSDELRDEFLRPAITGEQV 120
Pmen_2692       MGLDYSYSIVAAEEFGTIHCGGIPMSIGVQTDMCTPALARFGSDELREEFLRPAISGEMV 120
                ****************:* ******:*********************:*******:** *

Pfl01_3948      GCIGVSEVGAGSDVAGLKTTARKDGDDYVINGSKMWITNSPSADFICLLANTSDDKPHIN 180
PA14_26700      GCIGVSEVGAGSDVAGLKTTARKDGDDYVINGSKMWITNSPSADFMCLLANTSDDKPHVN 180
PA2889          GCIGVSEVGAGSDVAGLKTTARKDGDDYVINGSKMWITNSPSADFMCLLANTSDDKPHVN 180
PFL_4197        GCIGVSEVGAGSDVAGLKTHARKDGDDYVINGSKMWITNSPSADFICLLANTSDDKPHVN 180
Pmen_2692       GCIGVSEVGAGSDVAGLKTTARKDGDDYVINGSKMWITNSPSADFICLLANTSDDKPHVN 180
                ******************* *************************:************:*

Pfl01_3948      KSLIMVPMNTPGISLSSHLDKLGMRSSETAQVFFDNVRVPQRNRIGHEGAGFMMQMLQFQ 240
PA14_26700      KSLIVVPMKTPGITLSPHLDKLGMRSSETAQVFFDNVRVPQRNRIGAEGAGFMMQMLQFQ 240
PA2889          KSLIVVPMKTPGITLSPHLDKLGMRSSETAQVFFDNVRVPQRNRIGAEGAGFMMQMLQFQ 240
PFL_4197        KSLIMVPMNTPGISLSSHLDKLGMRSSETAQVFFDNVRVPQRNRIGHEGAGFMMQMLQFQ 240
Pmen_2692       KSLIMVPMKTPGISVSPHLDKLGMRSSETAQVFFDNVRVPQRYRIGAEGAGFMMQMLQFQ 240
                ****:***:****::*.************************* *** *************

Pfl01_3948      EERLFGAANMIKGLEYCVDSTIEYCKERKTFGNALIDNQVIHFRLAELQTEIECLRALVY 300
PA14_26700      EERLFGAANMIKGLEHCIDVTIEYCKERRTFGQPLIDNQVIHFRMAEMMTEVEALRALVY 300
PA2889          EERLFGAANMIKGLEHCIDVTIEYCKERRTFGQPLIDNQVIHFRMAEMMTEVEALRALVY 300
PFL_4197        EERLFGAANMIKGLEYCVDSTIEYCKERKTFGSPLIDNQVIHFRLAELSTEIECLRALVY 300
Pmen_2692       EERLFGAANMIKGLEHCVDATIDYCKQRHTFGQPLIDNQVIHFRMAELQTEIECLRALVY 300
                ***************:*:* **:***:*:***..**********:**: **:*.******

Pfl01_3948      QATEQYVKGQDVTRLASMAKLKAGRLGREVSDSCLQYWGGMGFMWDNPVARAYRDVRLVS 360
PA14_26700      QATELYVKGRDVTRLASMAKLKAGRLGREVSDACLQYWGGMGFMWDNPVSRAYRDTRLVS 360
PA2889          QATELYVKGRDVTRLASMAKLKAGRLGREVSDACLQYWGGMGFMWDNPVSRAYRDTRLVS 360
PFL_4197        QATEQYVRGQDVTRLASMAKLKAGRLGREVSDSCLQYWGGMGFMWDNPVARAYRDVRLVS 360
Pmen_2692       QATEQYVKGRDVTKLASMAKLKAGRLGREVSDACLQYWGGMGFMWDNPVSRAYRDVRLVS 360
                **** **:*:***:******************:****************:*****.****

Pfl01_3948      IGGGADEIMLGIICKLMGILPGKKK- 385
PA14_26700      IGGGADEIMLGIICKLMGILPGKKKG 386
PA2889          IGGGADEIMLGIICKLMGILPGKKKG 386
PFL_4197        IGGGADEIMLGIICKLMGILPGKKK- 385
Pmen_2692       IGGGADEIMLGIICKLMGILPGKKKG 386
                *************************

SeqA Name         Len(aa)  SeqB Name         Len(aa)  Score
===========================================================
1    Pfl01_3948   385      2    PA14_26700   386      90
1    Pfl01_3948   385      3    PA2889       386      90
1    Pfl01_3948   385      4    PFL_4197     385      96
1    Pfl01_3948   385      5    Pmen_2692    386      92
2    PA14_26700   386      3    PA2889       386      100
2    PA14_26700   386      4    PFL_4197     385      90
2    PA14_26700   386      5    Pmen_2692    386      92
3    PA2889       386      4    PFL_4197     385      90
3    PA2889       386      5    Pmen_2692    386      92
4    PFL_4197     385      5    Pmen_2692    386      92
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Pfl01_4213 (overlaps *nov14*)

```
Pfl01_4213          MRRVVITGLGIVSCLGNDKETVSANLRASRPGIRFNPEYAEMGLRSQVSGSIDLNLEELI 60
PA14_43690          MRRVVITGLGIVSCLGNDKDTVSANLRAGRPGIRFNPSYAEMGLRSHVSGSVDLNLEELI 60
PA1609              MRRVVITGLGIVSCLGNDKDTVSANLRAGRPGIRFNPSYAEMGLRSHVSGSVDLNLEELI 60
PFL_1736            MRRVVITGLGIVSCLGNDKETVSANLRASRPGIRFNPEYAEMGLRSQVSGSIDLNLEELI 60
PputW619_3498       MRRVVITGLGIVSCLGNDKATVTENLRNSRPGIRYNPEYKEQGLRSQVSGSIDLNLEELI 60
PSPPH_1989          MRRVVITGLGIVSCLGNDKETVTANLRANRPGIRFNPEYAEMGLRSQVSGSIDLNLEELI 60
                    ******************* **: *** .*****:**.* * ****:****:********

Pfl01_4213          DRKIYRFVGHAAAYAYLAMKDAIADSGLTEEQVSNPRTGLIAGSGGASTLNQMEALDILR 120
PA14_43690          DRKVFRFMGDAAAYAYLAMEQAIKDSGLTPEQISNPRTGLIAGSGGASTLNQMEAIDTLR 120
PA1609              DRKVFRFMGDAAAYAYLAMEQAIKDSGLTPEQISNPRTGLIAGSGGASTLNQMEAIDTLR 120
PFL_1736            DRKIYRFVGHAAAYAYLAMKDAIADSGLSEEQVSNPRTGLIAGSGGASTLNQMEALDILR 120
PputW619_3498       DRKVYRFVGHAAAYAYLAMQDAIKDAGLTEEQVSNPRTGLVAGSGGASTLNQMEALDTLR 120
PSPPH_1989          DRKIFRFVGHAAAYAYLAMKDAITDSGLTEEQVSNVRTGLIAGSGGASTLNQMEALDTLR 120
                    ***::**:*.*********::** *:**: **:** ****:**************:* **

Pfl01_4213          EKGVKRVGPYRVTRTMSSTVSACLATPFKIKGLNYSIASACATSAHCIGTAMEQIQMGKQ 180
PA14_43690          EKGVKRIGPYRVTRTMGSTVSACLATPFQIKGVNYSISSACATSAHCIGQAMEQIQLGKQ 180
PA1609              EKGVKRIGPYRVTRTMGSTVSACLATPFQIKGVNYSISSACATSAHCIGQAMEQIQLGKQ 180
PFL_1736            EKGVKRVGPYRVTRTMSSTVSACLATPFKIKGLNYSIASACATSAHCIGTAMEQIQMGKQ 180
PputW619_3498       EKGVKRVGPYRVTRTMGSTVSACLATPFKIKGLNYSISSACATSAHCIGTALEQIQWGKQ 180
PSPPH_1989          EKGVKRVGPYRVTRTMGSTVSACLATPFKIKGVNYSISSACATSAHCIGNAVEQIQLGKQ 180
                    ******:*********.***********:***:****:*********** *:**** ***

Pfl01_4213          DIVFAGGGEEEHWSQSFLFDAMGALSSKRNDTPEQASRAYDADRDGFVIAGGGGMVVVEE 240
PA14_43690          DVVFAGGGEEEHWSQSCLFDAMGALSTQYNETPEKASRAYDAKRDGFVIAGGGGMVVVEE 240
PA1609              DVVFAGGGEEEHWSQSCLFDAMGALSTQYNETPEKASRAYDAKRDGFVIAGGGGMVVVEG 240
PFL_1736            DIVFAGGGEEEHWTQSFLFDAMGALSTQYNETPEKASRAYDAKRDGFVIAGGGGMVVVEE 240
PputW619_3498       DIVFAGGGEEEHWSQSFLFDAMGALSTKRNDTPELASRAYDADRDGFVIAGGGGMVVVEE 240
PSPPH_1989          DIVFAGGGEEEHWSQSFLFDAMGALSTQYNETPEKASRAYDAKRDGFVIAGGGGMVVVEE 240
                    *:***********:** *********:: *:*** *******.****************

Pfl01_4213          LEHALARGAKIYAEIVGYGATSDGYDMVAPSGEGAIRCMQQALSTVDTP-IDYLNTHGTS 299
PA14_43690          LEHALKRGAKIYAEIVGYGATSDGYDMVAPSGEGAIRCMQQALATVDAP-IDYLNTHGTS 299
PA1609              LEHALKRGAKIYAEIVGYGATSDGYDMVAPSGEGAIRCMQQALATVDAP-IDYLNTHGTS 299
PFL_1736            LEHALARGAKIYAEIVGYGATSDGYDMVAPSGEGAIRCMEMAMSTVDTP-IDYLNTHGTS 299
PputW619_3498       LEHALARGAKIYAEIVGYGATSDGYDMVAPSGEGAIRCMQQALATVDTP-IDYLNTHGTS 299
PSPPH_1989          LEHALARGAKIYAEIVGYGATSDGYDMVAPSGEGAIRCMQMALGDINSGDIDYINTHGTS 300
                    ***** *********************************: *:. :::  ***:******

Pfl01_4213          TPVGDVAEMKGVREVFGDKAPAISSTKSLSGHSLGAAGVHEAIYCMLMMEGNFIAGSANI 359
PA14_43690          TPVGDVAEIRGVREVFGDKAPAISSTKSLSGHSLGAAGVHEAIYCLLMMEGGFIAGSANI 359
PA1609              TPVGDVAEIRGVREVFGDKAPAISSTKSLSGHSLGAAGVHEAIYCLLMMEGGFIAGSANI 359
PFL_1736            TPVGDVAEMKGVREVFGDKAPAISSTKSLSGHSLGAAGVHEAIYCMLMMEGNFMAGSANI 359
PputW619_3498       TPVGDVAEIKGVRAVFGDKAPKISSTKSLSGHSLGAAGVHEAIYCLLMMENNFIAGSANI 359
PSPPH_1989          TPVGDAKEMEGVREVFGAKAPAISSTKSLSGHSLGAAGVHEAIYCLLMMENNFIAGSANI 360
                    *****. *:.*** *** *** ***********************:****..*:******

Pfl01_4213          DELDPEVADLPVLTKTRENATINTVMSNSFGFGGTNATLVLKRWEGK 406
PA14_43690          DELDPEVADLPILRETRENAKLDTVMSNSFGFGGTNATLVLKRWQG- 405
PA1609              DELDPEVADLPILRETRENAKLDTVMSNSFGFGGTNATLVLKRWQG- 405
PFL_1736            DELDPEVADMPILTKTREDATINTVMSNSFGFGGTNATLVLKRWQGK 406
PputW619_3498       DELDPEVADLPILRKTEENAKIDTVMSNSFGFGGTNATLVLKRWTGK 406
PSPPH_1989          DELDPVVADMPILLKTREDAKLDLVMSNSFGFGGTNATLVLKRWAGK 407
                    ***** ***:*:* :*.*:*.:: ******************** *
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SeqA Name            Len(aa)  SeqB Name            Len(aa)  Score
=================================================================
1    Pfl01_4213      406      2    PA14_43690      405      88
1    Pfl01_4213      406      3    PA1609          405      88
1    Pfl01_4213      406      4    PFL_1736        406      96
1    Pfl01_4213      406      5    PputW619_3498   406      92
1    Pfl01_4213      406      6    PSPPH_1989      407      89
2    PA14_43690      405      3    PA1609          405      99
2    PA14_43690      405      4    PFL_1736        406      88
2    PA14_43690      405      5    PputW619_3498   406      88
2    PA14_43690      405      6    PSPPH_1989      407      88
3    PA1609          405      4    PFL_1736        406      88
3    PA1609          405      5    PputW619_3498   406      88
3    PA1609          405      6    PSPPH_1989      407      88
4    PFL_1736        406      5    PputW619_3498   406      89
4    PFL_1736        406      6    PSPPH_1989      407      90
5    PputW619_3498   406      6    PSPPH_1989      407      88
=================================================================
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Pfl01_4382 (overlaps *nov15*)

```
Pfl01_4382      MALNGFGEPGTFLPLSQQLIHSRERPMFDSLSIRLKIVLLSGLCLLGVVALIVGINIYQT 60
PA14_29760      -------------------------MFLRRLSIQWKITLLAGLCLLGVVALLVGLSVYRM 35
PA2654          -------------------------MFLRRLSIQWKITLLAGLCLLGVVALLVGLSVYRM 35
PFL_4630        --------------MLSIRPFARSPPMFDSLSIRLKIVLLSGLCLLGVVALIVGMNLYQS 46
PFLU4971        ----------------------MSEPMFNTLSIRLKIVLLSGLCLLGVIALVVSINIYNT 38
                                          ::  ***: **.**:*******:**:*.:.:*.

Pfl01_4382      NQNDELVSTSSSKMLTASVQDLLQAKAAEQAVQVQKTFGESLLVITALADQVKDMRVMAA 120
PA14_29760      QHSSVLVKSASTQMLDESARLRLEARGELQALRIQRYFMDAFQYGKGFSRQILFLRDQAQ 95
PA2654          QHSSVLVKSASTQMLDESARLRLEARGELQALRIQRYFMDAFQYGKGFSRQILFLRDQAQ 95
PFL_4630        QQNNQLVNTSSTRMLTAGVEELLQAKAADQAVRVQKTFGESNLVITALADQVRDLRDMAS 106
PFLU4971        TQNDQLVSDSSSRMLTASVEQLLQARAAEQAVQLQKTFGDSLVALTALADQVKDLRNLAA 98
                 :.. **. :*::**  ...  *:*:.  **:::*: * ::    ..:: *:  :*  *

Pfl01_4382      KRSLDAGALREELNQSLKTAFERNSKVLGIWLAFEPNGLDGKDSEFANDAARQSNEAGRF 180
PA14_29760      KRFLDAYDLREDLTRQVRTALAANPEVLGLYVVFEPNALDGKDELFVDQPALGSNDKGRF 155
PA2654          KRFLDAYDLREDLTRQVRTALAANPEVLGLYVVFEPNALDGKDELFVDQPALGSNDKGRF 155
PFL_4630        KRGLEAAALREELNHSLKTAFERNPKVLGIWLAYEPNALDGKDSEFLNDAARASNERGRF 166
PFLU4971        QRGLEPGALREALNQSLKSAFERNNKVLGIWLSFEPNGLDGKDNEFIDDKARVSNEKGRF 158
                :* *:.  *** *.:.:::*:  * :***::: :***.*****. * :: *  **: ***

Pfl01_4382      ASYWSRAA-GPSLNTIMVEDDMNKTTLSVSGTPYNSWYTCPRDNKRTCLLDPYADTVGG- 238
PA14_29760      SLYWAQATPGQLESESMVESELADTSSGPSGAAYNAWYTCPKESAQPCVLDPYFDKVGE- 214
PA2654          SLYWAQATPGQLESESMIESELADTSSGPSGAAYNAWYTCPKESGQPCVLDPYFDKVGE- 214
PFL_4630        ATYWSRSG-GQQLNTVMVEDDLTKTTLNLSGTPYNVWYTCPRDSRRTCLLDPYADTIGED 225
PFLU4971        SSYWSRAG-GQGLNTIMVEDDLTKTSLNLSGTPYNIWYTCPRDSRSICLLDPYEDTVAG- 216
                : **:::  *   .  *:*.::  .*: .  **:.** *****::.   *:**** *.:.

Pfl01_4382      -KEMLMTTISVPLLVDGKAIGVVGIDIALDALQAAAVNSQRELFNSAGHMLIVSGSGVLG 297
PA14_29760      -RQLLMTSIAFPLELDGKVIGVMGLDINLSNLQALSEQGNRELYDGVGQVGILSPAGLFA 273
PA2654          -RQLLMTSIAFPLELDGKVIGVMGLDINLSNLQALSEQGNRELYDGVGQVGILSPAGLFA 273
PFL_4630        KKQVLMTTISQPLLVDGKVIGVIGVDIALDSLQAAAGESQRFLFNGAGHMMIVAGSGLLA 285
PFLU4971        -KPVLMTTISLPLIVDGKVIGVVGVDIALTALQATTDAAQKNLFNGAAHLEILSSSGLIA 275
                 : :***:*: ** :***.***:*:** *  *** :  .:: *::...:: *:: :*::.

Pfl01_4382      AYSTDATKVGKGITETLGAEGKDILQLLSAGTPKILEQGDLIRAVYPVDPIGNSRAWGVV 357
PA14_29760      GNSRDAGLLGKNLAKADPQHADELLQLLAAGKSQLFNENDDLKVLQPLQPIPGAKPWGVL 333
PA2654          GNSRDAGLLGKNLAKADPQHAGELLQLLAAGKSRLFNENDDLKVLQPLQPIPGAKPWGVL 333
PFL_4630        AVGADASQVGKNINETLGAQGKDILALLAGNQNKVLQQGELIRAVYPFSPIADAKPWGVT 345
PFLU4971        AYSGEPAKVGKNLIDTLGTEGKEIVQLLASDNRMIREQDGTIRAVYPVKPIAEAKSWGVV 335
                . . :.  :**.: .:   .. ::: **:..   : ::.  ::.: *..**  ::.***

Pfl01_4382      IDLPKQVLLADSVKLQAVLDDAQQTGMITALAVAVIAGLIGLLLIWLTASGVTRPINSVA 417
PA14_29760      LEVPKSALLGPALALERQLDDMRREGTWVELGLGLGAAVLGLLVLWLSARGVTRPILGVA 393
PA2654          LEVPKSALLGPALALERQLDDMRREGTWVELGLGLGAAVLGLLVLWLSARGVTRPILGVA 393
PFL_4630        IDLPQQVLLADSVKLQGLLDEAQTSGTVKTVLVAVGAGLLGLLLIWLSASGVTRPINSVA 405
PFLU4971        IKLPKAVMLADNVKLQGVLDEAQAAGTLKALLVAAAAGLLGLLLIWLTATGVTRPINSVA 395
                :.:*: .:*.  : *:  **: :  *    : :.  *.::***::**:* ****** .**

Pfl01_4382      EMLKNIASGEGDLTQRLNYTKKDELGELVNWFNRFLDKLQPTIAQIKQSITEARGTADQS 477
PA14_29760      HMLRDIASGEGDLTQRLPHTGRDELGELAGWFNRFLDKLQPIIRDVKVSVRDARSTADQS 453
PA2654          HMLRDIASGEGDLTQRLPHTGRDELGELAGWFNRFLDKLQPIIRDVKVSVRDARSTADQS 453
PFL_4630        QMLKAIASGDGDLTQRLDYSKKDELGELVGWFNRFLDKLQPTIAQIKQSITEARGTADQS 465
PFLU4971        AMLKDIASGEGDLTQRLAYAKKDELGELVNWFNRFLDKLQPTIAQIKQSITEARGTADQS 455
                 **: ****:******* :: :******..*********** * ::* *: :**.*****

Pfl01_4382      SEIARQTSEGMQVQFREIDQVATASNEMSATAHDVANSASNAANAAKGADQSAKDGMSII 537
PA14_29760      AAISSQTSAGMQQQFREIDQVATASHEMTATAQDVARSAAQAADAARGADQATRDGLALI 513
PA2654          AAISSQTSAGMQQQFREIDQVATASHEMTATAQDVARSAAQAADAARGADQATRDGLALI 513
PFL_4630        SEIARQTSEGMQVQFREIDQVATASNEMSATAHDVANSASNAAQAARGADQSAKEGMTII 525
PFLU4971        SAIARQTSEGMQVQFREIDQVATASNEMSATAHDVANSASNAANAARGADQSAREGMQII 515
                : *: *** *** ************:**:***:***.**::**:**:****::::*: :*
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Pfl01_4382      ERSTRDINQLADEVSKAVTEVEELAVNSEQIGSVLEVIRSIAEQTNLLALNAAIEAARAG 597
PA14_29760      DRTTQSIDSLAANLTSAMGQVEQLASSSEEIGSVLEVIRAIAEQTNLLALNAAIEAARAG 573
PA2654          DRTTQSIDSLAANLTSAMGQVEQLASSSEEIGSVLEVIRAIAEQTNLLALNAAIEAARAG 573
PFL_4630        ERSTRDISLLADEVSKAVGEVEALAVSSEQIGSVLEVIRSIAEQTNLLALNAAIEAARAG 585
PFLU4971        EQSTRDITTLAEEVSKAVTEVEALAVNSEQIGSVLEVIRSIAEQTNLLALNAAIEAARAG 575
                :::*:.*  ** :::.*: :** ** .**:*********:********************

Pfl01_4382      ESGRGFAVVADEVRNLAKRTQDSVEEIRVVIERIQTGTRGVVATMHSSQTQAHNNAGQIR 657
PA14_29760      DAGRGFAVVADEVRNLARRTQDSVEQIRGVIEGLQQGTRDVVDAMHGSHRQAQGSVEQVD 633
PA2654          DAGRGFAVVADEVRNLARRTQDSVEQIRGVIEGLQQGTRDVVDAMHGSHRQAQGSVEQVD 633
PFL_4630        ESGRGFAVVADEVRNLAKRTQDSVEEIRVVIERIQSGTRDVVTTMHASQSQAQNNAGQIQ 645
PFLU4971        ESGRGFAVVADEVRNLAKRTQDSVEEIRLVIERIQSGTRGVVATMHSSQSQAQSNAGQIH 635
                ::***************:*******:** *** :* ***.** :**.*: **:... *:

Pfl01_4382      QAVDALGKISDAVTVISDMNLQIASAAEQQSAVAEEVNRNVSAIRTVTETLTEQATESAA 717
PA14_29760      EAVAALQRIGEAVTVINDMNLQIASAAEEQSSVAEEINRNVAAIRDVTESLSSQAEESAQ 693
PA2654          EAVAALQRIGEAVTVINDMNLQIASAAEEQSSVAEEINRNVAAIRDVTESLSSQAEESAQ 693
PFL_4630        QAVQALGKISDAVTVISDMNLQIASAAEQQSAVAEEVNRNVSAIRTVTETLTEQASESAQ 705
PFLU4971        QAVQALGKISDAVTVISDMNLQIASAAEQQSAVAEEVNRNVSAIRTVTETLTGQATESAA 695
                :** ** :*.:*****.***********:**:****:****:*** ***:*: ** ***

Pfl01_4382      ISSQLNALASQQMKLMDQFRV 738
PA14_29760      VSQSLNRLANHQQGLMEQFKA 714
PA2654          VSQSLNRLANHQQGLMEQFKA 714
PFL_4630        VSSQLNALATQQMKLMDQFRV 726
PFLU4971        ISSQLNALASQQMKLMDQFKV 716
                :*..** **.:*  **:**:.

SeqA Name         Len(aa)  SeqB Name         Len(aa)  Score
===========================================================
1    Pfl01_4382   738      2    PA14_29760   714      52
1    Pfl01_4382   738      3    PA2654       714      52
1    Pfl01_4382   738      4    PFL_4630     726      80
1    Pfl01_4382   738      5    PFLU4971     716      80
2    PA14_29760   714      3    PA2654       714      99
2    PA14_29760   714      4    PFL_4630     726      54
2    PA14_29760   714      5    PFLU4971     716      53
3    PA2654       714      4    PFL_4630     726      54
3    PA2654       714      5    PFLU4971     716      53
4    PFL_4630     726      5    PFLU4971     716      78
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