```
PviR      ------------------------------MGSS-----------TAFLL----------      9
PLR6      ------------------------------MGKAIQTSN----KEVSLFV----------      16
PLR5      ------------------------------MGNGKENSL--------TIL----------      12
PLR3      -------------------------------------MGN--------QFL----------      6
PLR7      ----------------------------------------M--------KIL----------      4
LuxR      ---------------------------------------MNIKNINANEKIIDKIKTCN      20
PLR2      ------------------------------MGKPTEQDSYNPFKDGESIRRIIDLFDSIH      30
CviR      MVTSKPINARPLPAGLTASQQWTLLEWIHMAGHIETEGE------LKAFLDN--------      46
PLR1      ------------------------------MGFLGCTKE------LSSVLKAIELLKTSI      24

PviR      -------------LDKEPINTIGINV--LQPLLKTQGLDVVTGTDISEVPE--D-----      46
PLR6      -------------LTHNKTDTQDFEFIRFVKILEATSNQIKIDTRLPDTPLRAQ-----      57
PLR5      IADD--HHLVRQGL---------------RSLIERSQTQYNI-SDVATGEQAWQFISQY-      53
PLR3      IADD--HPLFREAL---------------KGALQNQFEGLEVIES-ENFEQTLERLSQYD      48
PLR7      VVED--QALVRNAI---------------SALLSLE-ANLEVVGQAEDGQQALEY-LANH      45
LuxR      NNKDINQC-LSEIAKIIHCE--YYLFAIIYP-HSIIKPDVSI---IDNYPEKWRK--YYD      71
PLR2      HADDLKEA-LTTIARDVGYD--CLAFVDYSP-LPNHIQPVQV---YGHYQEELSV--LFE      81
CviR      ------------ILSQAPSDRIILVLGRLNNQNQIQRMEKVL---NVSYPSDWLN--QY-      88
PLR1      IERSLDGIVFQEAMSFAESDELYLALIDKS---SL-EVKTEC---LRSFPQDFKE--DLL      75

PviR      -----TRLLFIETAVNDA-WGKLKEQ-LVNLKVSCDIVLFNLDENPELANRALLSGIR-G      98
PLR6      -----HHLYLVDISHREC-QDLLSAE-VSALAAQQNVLLFNAQPSLVNEQTALLARIK-G      109
PLR5      Q----PDLAILDIAMGDL-SGLKVCEHVKQRKLKTRIIFLSMHDDIKVIHRAFEVGAD-A      107
PLR3      D----LDLLLLDLHMPGN-GDLYGLIRIREDHPSLPIVVVSGSEDLNVISKVMGYGAM-G      102
PLR7      E----PDIVLSDIEMPNV-TGLELAQIIQEKYPRVKVVIMTTFSRAGYIRRAMAADVK-G      99
LuxR      DA----GLLEYDPVVDYSKSHHSPIN-WN-----VFEKKTIKKESPNVIKEAQESGLITG      121
PLR2      S----------DKVLAHSKSGIRLCS-LA-----KLTGALNIAESLHV-----------      113
CviR      ---SQENFAQHDPIMRIH-LGQGPVI-WE-----ERFSRAKGSEEKRFIAEASSNGMGSG      138
PLR1      TVAKVKKFTNINILKSLC-KDR------------------------------NPLSDI      102
                    :

PviR      VFYTTDNAD-------------VLMKGIRLLMEDQLWYRREIMCNALNRMLQFNKDA--L      143
PLR6      VIYQNTSAE-------------NIFKGIQRVLNGELWFCRTSISQAFNELIQQIPNIPRP      156
PLR5      Y-------------LSKSEAFDTLNQALQTVAAGHSFI-SPSIESELARYKAAS------      147
PLR3      F-------------IPKASSSQDIVSALQQVLDGENWL-PADIKEKINDLDGED------      142
PLR7      F-------------ILKEAPSDYLVNALKKISVGQKVI-DPELAM--NALDDS-------      136
LuxR      FSFPIHTASNGFGMLSFAHSDKDIYTDS--LFLHASTNVPLMLPSLVDNYQKIN------      173
PLR2      --LPLRGIKGIIGALVFNVPC-DLAHKV--TVEQVDWYWTILSPALLN----AA------      158
CviR      ITFSAASDRNNVGSILSIGGKEPGRNAA--LVAMLNCLTPHLHQAAVRIA-NL-------      188
PLR1      TIYDLDNPNSNFLTLVAFNNKRSNRTAP--ASYLIELVLPYLHKAQISRYQND-------      153

PviR      HKLTEGDIEPVKLTKREKAIISLMSKGAKNKEIAEDLNISPHTVKTHLYSAFRKTKCRNR      203
PLR6      QSLDIQDSELELLTAREKSVIKLLASGAKNDDIADSLNISSHTVKTHIYSAFKKTNSRNR      216
PLR5      ---T-----QFLLTAREKQIVSYITQGKSNRQIADTLCISIKTVDNHRTKAMRKLGVNKA      199
PLR3      ---RELAQQIASLTPQQYKVLQYLHEGLLNKQIAYELNISEATVKAHITAIFRKLGVYNR      199
PLR7      ----------DPLSDKERKALRLASEGMKTRQIAESLFLSEGTVRNYLSDAIAKLNATNR      186
LuxR      ---TTRKKSDSILTKREKECLAWASEGKSTWDISKILGCSERTVTFHLTNTQMKLNTTNR      230
PLR2      ---LRCRKDHFNITKRERDCVLWASEGKTSWEISQILGITERTVNFHLTNCIEKTQSANR      215
CviR      ---PPASPSNMPLSQREYDIFHWMSRGKTNWEIATILNISERTVKFHVANVIRKLNANNR      245
PLR1      ---KTSRSPIQSLTNREKEVLDWISSGKTNGEIGMILGISQYTVKNHVAKILEKLNAPNR      210
                    :: ::   .     *  . :*.  *  :  **  :      *    :

PviR      IELLSWAQQNIPDEIR*-------    219
PLR6      IELANWAQKHIPLNSAPVSIQRH*    239
PLR5      AELVKYGLEEGLVV*---------    213
PLR3      TQAVLIASKLQLEPIEAAK---*-    218
PLR7      VDAARIARQKGWL*----------    199
LuxR      CQSISKAILTGAINCPYLK---N*    250
PLR2      QQAIVKCLINNLI*----------    228
CviR      THAIVLGMHLAMTPRELVN---G*    265
PLR1      SAAMALTKELSFS*----------    223
```