```
                 1 |------------ SEC -----------||------------------------------------------------ TPS --------------------------------------------------------
CdiA2_rD_V         MDIRSPLNQCIALSLAGILFLNPIVAAAAGLALDKAAGGNTGLGQAGNGVPIVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNPNLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANP
CdiA2_rB_V         MDIRSPLNQCIALSLAGILFLNPIVAAAAGLALDKAAGGNTGLGQAGNGVPIVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNPNLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANP
CdiA2_rE_V         MDIRSPLNQCIALSLAGILFLNPIVAAAAGLALDKAAGGNTGLGQAGNGVPIVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNPNLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANP
CdiA2_rC_V         MDIRSPLNQCIALSLAGILFLNPIVAAAAGLALDKAAGGNTGLSQAGNGVPVVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNPNLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANP
CdiA1_rA_V         MDIRSPLNQCIALSLAGILFLNPIVATAAGLALDKAAGGNTGLGQAGNGVPIVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNPNLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANP
CdiA1_rA_II        MDIRSPLNQCIALSLAGILFLNPIVATAAGLALDKAAGGNTGLGQAGNGVPIVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNPNLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANP
clustal            **************************:***************.*******:*****************************************************************************************

               141 --------------------------|
CdiA2_rD_V         HGITCQGCGFINTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITRSAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALGGMYAGAIRLVGTEQGVGVKLAGDMAASGGD
CdiA2_rB_V         HGITCQGCGFINTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITRSAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALGGMYAGAIRLVGTEQGVGVKLAGDMAASGGD
CdiA2_rE_V         HGITCQGCGFINTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITRSAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALGGMYAGAIRLVGTEQGVGVKLAGDMAASGGD
CdiA2_rC_V         HGITCQGCGFINTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITRSAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALGGMYAGAIRLVGTEQGVGVKLAGDMAASGGD
CdiA1_rA_V         HGITCQGCGFINTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITRSAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALGGMYAGAIRLVGTEQGVGVRLAGDMAASGGD
CdiA1_rA_II        HGITCQGCGFINTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITRSAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALGGMYAGAIRLVGTEQGVGVKLAGDMAASGGD
clustal            ********************************************************************************************************************************:***********

               281              |------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         IRIDASGKLSLAQASSQGDLKIAAQAVELNGKTYAGGSAEIRSVEELVNRQSLAARERIALEAAHIDNAGVIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGGSLKGATVRVDGGHLDNRGGK
CdiA2_rB_V         IRIDASGKLSLAQASSQGDLKIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIALEAAHIDNAGVIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGGSLKGATVRVDGGHLDNRGGK
CdiA2_rE_V         IRIDASGKLSLAQASSQGDLKIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIALEAAHIDNAGVIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGGSLKGATVRVDGGHLDNRGGK
CdiA2_rC_V         IRIDASGKLSLAQASSQGDLKIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIALEAAHIDNAGVIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGGSLKGATVRVDGGHLDNRGGK
CdiA1_rA_V         IRIDASGKLSLAQASSQGDLKIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIALDAARLDNAGVIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGGSLKGATVRVDGGHLDNRGGK
CdiA1_rA_II        IRIDASGKLSLAQASSQGDLKIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIALDAARLDNAGVIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGGSLKGATVRVDGGHLDNRGGK
clustal            *******************************************.*****************:**::**************************************************************************

               421 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         LLAEGELRVEASSLDNREDGLLQSWDRAVVKTRGDLDNRGGQVVGLNELQVQAAALDNRSAGLLSSKGDMDIEVARLDNSAGGKLVSERRTLLKADRLDNRSGRIVAGQDLDLSSRLIDNRAGDISSTSRVVASAREQLD
CdiA2_rB_V         LLAEGELRVEASSLDNRQDGLLQSRDRAVVKTRGDLDNRGGQVVGLNELQVQAAALDNRSAGLLSSKGDMDIEFARLDNSAGGKLVSERRTLLKADRLDNRSGRIVAGQDLDLSSRLIDNRAGDISSTSRVVASAREQLD
CdiA2_rE_V         LLAEGELRVEASSLDNRQDGLLQSRDRAVVKTRGDLDNRGGQVVGLNELQVQAAALDNRSAGLLSSKGDMDIEVARLDNSAGGKLVSERRTLLKADRLDNRSGRIVAGQDLDLSSRLIDNRAGDISSTSRVVASAREQLD
CdiA2_rC_V         LLAEGELRVEASSLDNRQDGLLQSRDRAVVKTRGDLDNRGGQVVGLNELQVQAAALDNRSAGLLSSKGDMDIEFARLDNSAGGKLVSERRTLLKADRLDNRSGRIVAGQDLDLSSRLIDNRAGDISSTSRVVASAREQLD
CdiA1_rA_V         LLAEGELRVEASSLDNRQDGLLQSRDRAVVKTRGDLDNRGGQVIGLNDLEVGAATLDNGQQGLLGSQ-------------------------------------------------------------------------
CdiA1_rA_II        LLAEGELRVEASSLDNRQDGLLQSRDRAVVKTRGDLDNRGGQVIGLNDLEVGAATLDNGQQGLLGSQ-------------------------------------------------------------------------
clustal            *****************:****** ******************:***:*:* **:*** . ***.*:

               561 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         NRGGKIVGDSGLDITTPRMLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSARLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIR
CdiA2_rB_V         NRGGKIVGDSGLDITTPRMLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIR
CdiA2_rE_V         NRGGKIVGDSGLDITTPRMLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIR
CdiA2_rC_V         NRGGKIVGDSGLDITTPRMLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIR
CdiA1_rA_V         --------------------------------------------------------------------------------------------------------------------------------------------
CdiA1_rA_II        --------------------------------------------------------------------------------------------------------------------------------------------
clustal

               701 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         TGNLNNSRKASIGSDAGLTLVAARVDNSQAGRIAAKGAIDADLQGLDQHDRGNLVSDTGITLDLNTGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLAGIV
CdiA2_rB_V         TGNLNNSRKASIGSDAGLTLVAARVDNSQAGRIAAKGVIDADLQGLDQHDRGNLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIV
CdiA2_rE_V         TGNLNNSRKASIGSDAGLTLVAARVDNSQAGRIAAKGAIDADLQGLDQHDRGNLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGPLTLRIAQALDNSLEGIV
CdiA2_rC_V         TGNLNNSRKASIGSDAGLTLVAARVDNSQAGRIAAKGVIDADLQGLDQHDRGNLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIV
CdiA1_rA_V         ----------------------------QSTRVSAQ-------------------------------ALVNRGDG-----------------------------------------------------------------
CdiA1_rA_II        ----------------------------QSTRVSAQ-------------------------------ALVNRGDG-----------------------------------------------------------------
clustal                                        *: *::*:                               :****.:*

               841 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         SGAGGLDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANSSKGRIAANGSLHAKVGTLSQKGGELTSQDSLTLDLGILNNNAGRIAGNQGVDITARQVDNSVGEIASQGVVALNLTEQLDNRGGK
CdiA2_rB_V         SGAGGLDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANSSKGRIAANGSLHAKVGTLSQKGGELTSQDSLTLDLGILNNNAGRIAGNQGVDITARQVDNSVGEIASQGVVALNLTEQLDNRGGK
CdiA2_rE_V         SGAGGLDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANSSKGRIAANGSLHAKVGTLSQKGGELTSQDSLTLDLGILNNNAARIAGNQGVDITARQVDNSVGEIASQGVVALNLTEQLDNRGGK
CdiA2_rC_V         SGAGGLDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANSSKGRIAANGSLHAKVGTLSQKGGELTSQDSLTLDLGILNNNAGRIAGNQGVDITARQVDNSVGEIASQGVVALNLTEQLDNRGGK
CdiA1_rA_V         ----------------------------------------------------------------------------------------------------------EVSGKRVEARVG--------------SLDNRGGK
CdiA1_rA_II        ----------------------------------------------------------------------------------------------------------EVSGKRVEARVG--------------SLDNRGGK
clustal                                                                                                                      :::.::*:  **              .*******

               981 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         IVGDSGLGITAPHVLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSARLDNQGGTLSSAGALAVTSQGALNNQGGRLVSDAGLSLSSASLDNSQAGAISGKGAVEIRTGNLN
CdiA2_rB_V         IVGDSGLGITAPHVLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIRTGNLN
CdiA2_rE_V         IVGDSGLGITAPHVLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIRTGNLN
CdiA2_rC_V         IVGDSGLGITAPHVLNQDKGVLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIRTGNLN
CdiA1_rA_V         LIGDD------------------------------------------------------------------------------------LLVVASGAIDNRLGLFSAANRLDLRARSLDNSGKGTLSSRGG---------
CdiA1_rA_II        LIGDD------------------------------------------------------------------------------------LLVVASGAIDNRLGLFSAANRLDLRARSLDNSGKGTLSSRGG---------
clustal            ::**.                                                                                    * *.:.**::*: * : :   *.* : *****  *::*.:*.

              1121 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         NSRKASIGSDAGLTLVAARVDNSQAGRIAAKGAIDADLQGLDQHDRGNLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIVSGAGG
CdiA2_rB_V         NSRKASIGSDAGLTLVAARVDNSQAGRIAAKGAIDAALQGLDQHDRGSLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIVSGAGG
CdiA2_rE_V         NSRKASIGSDAGLTLVAARVDNSQAGRIAAKGAIDAALQGLDQHDRGSLVSDTGITLDLNKGSLVNRAQGLIATPGILLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIVSGAGG
CdiA2_rC_V         NSRKASIGSDAGLTLVAARVDNSQAGRIAAKGAIDAALQGLDQHDRGNLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIVSGAGG
CdiA1_rA_V         --------------------------------------------------------------------------------------------------------------------------------------------
CdiA1_rA_II        --------------------------------------------------------------------------------------------------------------------------------------------
clustal

              1261 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         LDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANNSKGRIVAKDDLRAKLGALVQNGGELTTQGALALDADKVDNGAGRIAGNRGVVIDARQVDNRAGEIASQGVATLNLTEQLDNRGGKVVADS
CdiA2_rB_V         LDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLAADEANNSKGRIVAKDELRAKLGALVQNGGELTTQGALALDADKVDNGAGRIAGNRGVVIDARQVDNRAGEIASQGVATLNLTEQLDNRGGKVVADS
CdiA2_rE_V         LDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLAADEANNSKGRIVAKDDLRAKLGALVQNGGELTTQGALALDADKVDNGAGRIAGNRGVVIDARQVDNRAGEIASQGVATLNLTEQLDNRGGKVVADS
CdiA2_rC_V         LDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANNSKGRIVAKDDLRAKLGALVQNGGELTTQGALALDADKVDNGAGRIAGNRGVVIDARQVDNRAGEIASQGVATLNLTEQLDNRGGKVVADS
CdiA1_rA_V         --------------------------------------------------------------------------------------------------------------------------------------------
CdiA1_rA_II        --------------------------------------------------------------------------------------------------------------------------------------------
clustal

              1401 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         GLGITAPRVLNQDKGVIASRDGLRLSGTELFNGNAGLLSSQRHIEITLDGVLDNQGKGALLSDGTLTVSAGRIHNQDATLSSAGALRLSSQEAVDNRGGKLVTDSSLRLTSASLDNSRSGIISANAAAEIHTGVLNNSQK
CdiA2_rB_V         GLGITAPRVLNQDKGVIASRDGLRLSGTELFNGNAGLLSSQRHIEVTLDGVLDNQGKGALLSDGTLTVSAGRIHNQDATLSSAGALRLSSQEAVDNRGGKLVTDSSLRLTSASLDNSRSGIISANAAAEIHTGVLNNSQK
CdiA2_rE_V         GLGITASRVLNQDKGVIASRDGLRLSGTELFNGNAGLLSSQRHIEVTLDGVLDNQGKGALLSDGTLTVSAGRIHNQDATLSSAGALRLSSQEAVDNRGGKLVTDSSLRLTSASLDNSRSGIISANAAAEIHTGVLNNSQK
CdiA2_rC_V         GLGITAPRVLNQDKGVIASRDGLRLSGTELFNGNAGLLSSQRHIEVTLDGVLDNQGKGALLSDGTLTVSAGRIHNQDATLSSAGALRLSSQEAVDNRGGKLVTDSSLRLTSASLDNSRSGIISANAAAEIHTGVLNNSQK
CdiA1_rA_V         -------------------------------------------LEVSLGGLLDNRDEGNLLSQGAQRVMVGQ--------------------------------------------------------------------
CdiA1_rA_II        -------------------------------------------LEVSLGGLLDNRDEGNLLSQGAQRVTVGQ--------------------------------------------------------------------
clustal                                                       :*::*.*:***:.:* ***:*:  * .*:

              1541 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V         GNLGSNDGLGLIATEVDNSQEGRITAKGMIDANIKGLDQQGKGRLVSNAGIILDLNEGTLANGAQGLIATPGTLLLRQLGMVDNSGGEISSDRAFTLTTSALTNQGGRLRSGGVLTLRIAQALDNSLEGVLSGTGGLDIR
CdiA2_rB_V         GNLGSNDGLGLIATEVDNSQEGRITAKGMIDANIKGLDQQGKGRLVSNAGIILDLNEGTLANGAQGLIATPGTLLLRQLGMVDNSGGEISSDRAFTLTTSALTNQGGRLRSGGVLTLRIAQALDNSLEGVLSGTGGLDIR
CdiA2_rE_V         GNLGSNDGLGLIATEVDNSQEGRITAKGMIDANIKGLDQQGKGRLVSNAGIILDLNEGTLANGAQGLIATPGTLLLRQLGMVDNSGGEISSDRAFTLTTSALTNQGGRLRSGGVLTLRIAQALDNSLEGVLSGTGGLDIR
CdiA2_rC_V         GNLGSNDGLGLIATEVDNSQEGRITAKGMIDANIKGLDQQGKGRLVSNAGIILDLNEGTLANGAQGLIATPGTLLLRQLGMVDNSGGEISSDRAFTLTTSALTNQGGRLRSGGVLTLRIAQALDNSLEGVLSGTGGLDIR
CdiA1_rA_V         --------------------------------------------------------------------------------------------------------------------------------------------
CdiA1_rA_II        --------------------------------------------------------------------------------------------------------------------------------------------
clustal
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            1681 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       ALALDNRSGSIGSKGAVDIDVSRLENDDGDLLSEGRLKLTAERANSVRGRIAARGDLHASVTAFNQAGGELSSEGALMLEADSLDNRSGGLVSADGNLTVSARRIDNRAGEIASPGQVTLDVAEQLDNRGGKAIGDSGLR
CdiA2_rB_V       ALALDNRSGSIGSKGAVDIDVSRLENDDGDLLSEGRLKLTAERANSVRGRIAARGDLHASVTAFNQAGGELSSEGALMLEADSLDNRSGGLVSADGNLTVSARRIDNRAGEIASPGQVTLDVAEQLDNRGGKAIGDSGLR
CdiA2_rE_V       ALALDNRSGSIGSKGAVDIDVSRLENDDGDLLSEGRLKLTAERANSVRGRIAARGDLHASVTAFNQAGGELSSEGALMLEADSLDNRSGGLVSADGNLTVSARRIDNRAGEIASPGQVTLDVAEQLDNRGGKAIGDSGLR
CdiA2_rC_V       ALALDNRSGSIGSKGAVDIDVSRLENDDGDLLSEGRLKLTAERANSVRGRIAARGDLHASVTAFNQAGGELSSEGALMLEADSLDNRSGGLVSADGNLTVSARRIDNRAGEIASPGQVTLDVAEQLDNRGGKAIGDSGLR
CdiA1_rA_V       -----------------------------------------------------------------------------------LDNRAGGL-------------------------------------------------
CdiA1_rA_II      -----------------------------------------------------------------------------------LDNRAGGL-------------------------------------------------
clustal                                                                                             ****:***

            1821 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       LAAPRVLNQDGGVLASRDGLRLNGAELFNGNGGLLSSQQSIDVNLDGVLGNQAGSLSSQGRLSVKSGRLDNQGGAVSSAGTLSLSSQGALNNQGGRVVTDAGAVLRSASLDNSQGGIVSAKGAAEIRTGSLNNSQKGGIG
CdiA2_rB_V       LAAPRVLNQDGGVLASRDGLRLNGAELFNGNGGLLSSQQSIDVILDGVLGNQAGSLSSQGRLSVKSGRLDNQGGAVSSAGTLSLSSQGALNNQGGRVVTDAGAVLRSASLDNSQGGIVSAKGAAEIRTGSLNNSQKGGIG
CdiA2_rE_V       LAAPRVLNQDGGVLASRDGLRLNGAELFNGNGGLLSSQQSIDVILDGVLGNQAGSLSSQGRLSVKSGRLDNQGGAVSSAGTLSLSSQGALNNQGGRVVTDAGAVLRSASLDNSQGGIVSAKGAAEIRTGSLNNSQKGGIG
CdiA2_rC_V       LAAPRVLNQDGGVLASRDGLRLNGAELFNGNGGLLSSQQSIDVILDGVLGNQAGSLSSQGRLSVKSGRLDNQGGAVSSAGTLSLSSQGALNNQGGRVVTDAGAVLRSASLDNSQGGIVSAKGAAEIRTGSLNNSQKGGIG
CdiA1_rA_V       -------------LSSRSELNVHGA---------------------------------------------------------------SLDNRGGVLVADAG--------------------------------------
CdiA1_rA_II      -------------LSSRSELNVHGA---------------------------------------------------------------SLDNRGGVLVADAG--------------------------------------
clustal                       *:**. *.::**                                                               :*:*:** :*:***

            1961 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       SGAGLALVADLVDNSQNGRITAKGAIDANLKGLDQQGSGRLVSDTAIALDLRGGELVNRAQGLIATPGALLLRQLGVVDNSGGGEISSDRSFTLAATALSNRGGRVISGDSLTLRIAQALDNSLQGVLSASGGLDVAALV
CdiA2_rB_V       SGAGLALVADLVDNSQNGRITAKGAIDANLKGLDQQGSGRLVSDTAIALDLRGGELVNRAQGLIATPGALLLRQLGVVDNSGGGEISSDRSFTLAATALSNRGGRVISGDSLTLRIAQALDNSLQGVLSASGGLDVAALV
CdiA2_rE_V       SGAGLALVADLVDNSQNGRITAKGAIDANLKGLDQQGSGRLVSDTAIALDLRGGELVNRAQGLIATPGALLLRQLGVVDNSGGGEISSDRSFTLAATALSNRGGRVISGDSLTLRIAQALDNSLQGVLSASGGLDVAALV
CdiA2_rC_V       SGAGLALVADLVDNSQNGRITAKGAIDANLKGLDQQGSGRLVSDTAIALDLRGGELVNRAQGLIATPGALLLRQLGVVDNSGGGEISSDRSFTLAATALSNRGGRVISGDSLTLRIAQALDNSLQGVLSASGGLDVAALV
CdiA1_rA_V       -------------------------------------------------------------------------------------------------------------------------------LSATGG-------
CdiA1_rA_II      -------------------------------------------------------------------------------------------------------------------------------LSATGG-------
clustal                                                                                                                                                 ***:**

            2101 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       FDNHSGIVGSKGDTHIGVNRLENEAGRVVSEGALDLTAKQVSSAKGRIAAKGDLQVTVGTLEQQGGELASQGTLTLDADSLDNRNGGLVSADGGVAAEARQIDNRGGEISSVAKVALAVREQLDNRGGKVIGDSELSLTV
CdiA2_rB_V       FDNHSGIVASKGDTHIGVNRLENEAGRVVSEGALDLTAKQVSSAKGRIAAKGDLQVTVGTLEQQGGELASQGTLTLDADSLDNRNGGLVSADGGVTAEARQIDNRGGEISSVAKVALAVREQLDNRGGKVIGDSELSLTV
CdiA2_rE_V       FDNHSGIVGSKGDTHIGVNRLENEAGRVVSEGALDLTAKQVSSAKGRIAAKGDLQVTVGTLEQQGGELASQGTLTLDADSLDNRNGGLVSADGGVTAEARQIDNRGGEISSVAKVALAVREQLDNRGGKVIGDSELSLTV
CdiA2_rC_V       FDNHSGIVASKGDTHIGVNRLENEAGRVVSEGALDLTAKQVSSAKGRIAAKGDLQVTVGTLEQQGGELASQGTLTLDADSLDNRNGGLVSADGGVTAEARQIDNRGGEISSVAKVALAVREQLDNRGGKVIGDSELSLTV
CdiA1_rA_V       -------------------------------------------------------------------------------AFDNRDGGSASGKAGV---------------------------------------------
CdiA1_rA_II      -------------------------------------------------------------------------------AFDNRDGGSASGKAGV---------------------------------------------
clustal                                                                                         ::***:** .*...**

            2241 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       QRLLNQAKGVLASRDGLHLDGAELLNGDGGLLSSQRLVDVTLSGALDNQGSGALVSEGSLTVKADQVNNQAGTFSSAGSLLVTSRGELNNQGGRLVTDAGATLNSTGFDNSRAGLVSAKGAVAIRTGALNNSQKGSIGGN
CdiA2_rB_V       QRLLNQAKGVLASRDGLHLDGAELLNGDGGLLSSQRLVDVTLSGALDNQGSGALVSEESLTVKADQVNNQAGTFSSAGSLLVTSRGELNNQGGRLVTDAGATLNSTGFDNSRAGLVSAKGAVAIRTGALNNSQKGSIGGN
CdiA2_rE_V       QRLLNQAKGVLASRDGLHLDGAELLNGDGGLLSSQRLVDVTLSGALDNQGSGALVSEGSLTVKADQVNNQAGTFSSAGSLLVTSRGELNNQGGRLVTDAGATLNSTGFDNSRAGLVSAKGAVAIRTGALNNSQKGSIGGN
CdiA2_rC_V       QRLLNQAKGVLASRDGLHLDGAELLNGDGGLLSSQRQVDVTLSGALDNQGSGALVSEGSLTVKADQVNNQAGTFSSAGSLLVTSRGELNNQGGRLVTDAGATLNSTGFDNSRAGLVSAKGAVAIRTGALNNSQKGSIGGN
CdiA1_rA_V       --------------------------------------------------------------------------------------------------------------------------------------------
CdiA1_rA_II      --------------------------------------------------------------------------------------------------------------------------------------------
clustal

            2381 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       TGVTLVAGLVDNGREGRISTKGTLDANLKGLLQQGGGSLVGERGVTLDLNGGTLDNHDLGLVSTPGALLLRQLGMVDNSVGGEISSDRAFTLAANTLNNQGGRLISSEALTLRIAKTLDNSLKGQVLATDGLAIESQVLD
CdiA2_rB_V       TGVTLVAGLVDNGREGRISTKGTLDANLKGLLQQGGGSLVGERGVTLDLNGGTLDNHDLGLVSTPGALLLRQLGMVDNSVGGEISSDRAFTLAANTLNNQGGRLISSEALTLRIAKTLDNSLKGQVLATDGLAIESQVLD
CdiA2_rE_V       AGVTLVAGLVDNGREGRISTKGTLDANLKGLLQQGGGSLVGERGVTLDLNGGTLDNHDLGLVSTPGALLLRQLGMVDNSVGGEISSDRAFTLAANTLNNQGGRLISSEALTLRIAKTLDNSLKGQVLATDGLAIESQVLD
CdiA2_rC_V       TGVTLVAGLVDNGREGRISTKGTLDANLKGLLQQGGGSLVGERGVTLDLNGGTLDNHDLGLVSTPGALLLRQLGMVDNSVGGEISSDRAFTLAANTLNNQGGRLISSEALTLRIAKTLDNSLKGQVLATDRLAIESQVLD
CdiA1_rA_V       --------------------------------------------------------------------------------------------------------------------------------------------
CdiA1_rA_II      --------------------------------------------------------------------------------------------------------------------------------------------
clustal

            2521 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       NRAGIIGSKGDARISVTSLDNAEQGSLVSEGRLELVADQVSNGNQGRIAARGVLEAAVGTLLQQGGELVSQGSLDLRADTLDNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVIGDSGLRLTV
CdiA2_rB_V       NRAGTIGSKGDARISVTSLDNAEQGSLVSEGRLELVADQVSNGNQGRIAARGVLEAAVGTLLQQGGELVSQGSLDLRADTLDNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVIGDSGLRLTV
CdiA2_rE_V       NRAGTIGSKGDARISVTSLDNAEQGSLVSEGRLELVADQVSNGNQGRIAARGVLEAAVGTLLQQGGELVSQGSLDLRADTLDNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVIGDSGLRLTV
CdiA2_rC_V       NRAGTIGSKGDARISVTSLDNAEQGSLVSEGRLELVADQVSNGNQGRIAARGVLEAAVGTLLQQGGELVSQGSLDLRADVLDNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVIGDSGLRLTV
CdiA1_rA_V       ------------RVEVASLRNDQGGKLLSDGRLDLAANAVGNAG-GRIAAKGDLQATLGSLAQQGGELVSEKTLKVAADTLDNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVIGDSGLRLTV
CdiA1_rA_II      ------------RVEVASLRNDQGGKLLSDGRLDLAANAVGNAG-GRIAAKGDLQATLGSLAQQGGELVSEKTLKVAADTLDNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVIGDSGLRLTV
clustal                      *:.*:** * : *.*:*:***:*.*: *.*.. *****:* *:*::*:* ********: :*.: **.************************************************************

            2661 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       QRLLNQAKGVLAGRDGLSLDGGELFNGDGGRLDSQNSLSVSLGGVLDNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAALDNQGGRLLSDAGVTLQGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNA
CdiA2_rB_V       QRLLNQAKGVLAGRDGLSLDGGELFNGDGGRLDSQNSLSVSLGGVLDNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAVLDNQGGRLLSDAGVTLKGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNA
CdiA2_rE_V       QRLLNQAKGVLAGRDGLSLDGGELFNGDGGRLDSQNSLSVSLGGVLDNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAALDNQGGRLLSDAGVTLKGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNA
CdiA2_rC_V       QRLLNQAKGVLAGRDGLSLDGGELFNGGGGRLDSQNSLSVSLGGVLDNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAALDNQGGRLLSDAGVTLKGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNA
CdiA1_rA_V       QRLLNQAKGVLAGRDGLSLDGGELFNGDGGRLDSQNSLSVSLGGVLDNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAALDNQGGRLLSDAGVTLKGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNA
CdiA1_rA_II      QRLLNQAKGVLAGRDGLSLDGGELFNGDGGRLDSQNGLSVSLGGVLHNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAALDNQGGRLLSDAGVTLKGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNA
clustal          ***************************.********.*********.**************************************.****************:*************************************

            2801 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       GITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGAVDNGAGGEISSDRAFTLAAASLDNRGGRLIGADSLTLRIAQALDNSLGGVISGAAGLDIAAARLDN
CdiA2_rB_V       GITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGAVDNGAGGEISSDRAFTLAAASLDNRGGRLIGADSLTLRIAQALDNSLAGVISGAAGLDIAAARLDN
CdiA2_rE_V       GITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGAVDNGAGGEISSDRAFTLAAASLDNRGGRLIGAASLTLRIAQALDNSLAGVISGAAGLDIAAARLDN
CdiA2_rC_V       GITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGVVDNGAGGEISSDRAFTLAAASLDNRGGRLIGAASLTLRIAQALDNSLAGVISGAAGLDIAAARLDN
CdiA1_rA_V       GITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGAVDNGAGGEISSDRAFTLAAASLDNRGGRLIGAASLTLRIAQALDNSLAGVISGAAGLDIAAARLDN
CdiA1_rA_II      GITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGAVDNGAGGEISSDRAFTLAAASLDNRGGRLIGAASLTLRIAQALDNSLGGVISGAAGLDIAAARLDN
clustal          *************************************************************************.******************************** **************.******************

            2941 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       SAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVATGALDNAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRLTV
CdiA2_rB_V       SAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVATGALDNAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRLTV
CdiA2_rE_V       SAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVATGALDNAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRLTV
CdiA2_rC_V       SAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVATGALDNAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRLTV
CdiA1_rA_V       SAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVVTGALDNAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRLTV
CdiA1_rA_II      SAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVATGALDNAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRLTV
clustal          ********************************************************.***********************************************************************************

            3081 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       ERLVQRQGRLIGERGVSLDLRGGDLDNQGGLISARGPLSIERLNVLDNRQGGEISSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGAL
CdiA2_rB_V       ERLVQRQGRLIGERGVSLDLRGGDLDNQGGLISARGPLSIERLNVLDNRQGGEIYSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGAL
CdiA2_rE_V       ERLVQRQGRLIGERGVSLDLRGGDLDNQGGLISARGPLSIERLNVLDNRQGGEISSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGAL
CdiA2_rC_V       ERLVQRQGRLIGERGVSLDLRGGDLDNQGGLISARGPLSIERLNVLDNRQGGEISSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGAL
CdiA1_rA_V       ERLVQRQGRLIGERGVSLDLRGGDLDNQGGLISARGPLSIERLNVLDNRQGGEISSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGAL
CdiA1_rA_II      ERLVQRQGRLIGERGVSLDLRGGDLDNQGGLISARGPLSIERLNVLDNRQGGEISSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGAL
clustal          ****************************************************** *************************************************************************************

            3221 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
CdiA2_rD_V       VSKGAQRIDAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNTGAARLASGGALLLRSASVDNRGGKLVSQGLLEISAGSLDN
CdiA2_rB_V       VSKGAQRIDAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNAGAARLASGGDLLLRSASVDNRGGKLVSQGLLEISAGSLDN
CdiA2_rE_V       VSKGAQRIDAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNTGAARLASGGDLLLRSASVDNRGGKLVSQGLLEISAGSLDN
CdiA2_rC_V       VSKGAQRIDAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNAGAARLASGGDLLLRSASVDNRGGKLVSQGLLEISAGSLDN
CdiA1_rA_V       VSKGAQRIDAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNAGAARLASGGDLLLRSASVDNRGGKLVSQGLLEISAGSLDN
CdiA1_rA_II      VSKGAQRIDAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNAGAARLASGGDLLLRSASVDNRGGKLVSQGLLEITTGSLDN
clustal          ***************************************************************************************************:********* ***********************::*****

            3361 -------------------------------------------------------------- FHA1 ------------------------------------------------------------------------
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CdiA2_rD_V      SASGTLASQAGMSLRLGGGALRNQQDGLIFSQAGALEVQAGSLDNRQGTLQAQGDNRLRIGGALDNQGGRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLKLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALGGD
CdiA2_rB_V      SASGTLASQADMSLRLGGGALRNQQDGLIFSQAGALEVQAGSLDNRQGTLQAQGDNRLRIGGALDNQAGRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLKLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALGGD
CdiA2_rE_V      SASGTLASQADMSLRLGGGALRNQQDGLIFSQAGALEVQAGSLDNRQGTLQAQGDNRLRIGGALDNQGGRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLKLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALSGD
CdiA2_rC_V      SASGTLASQAGMSLRLGGGALRNQQDGLIFSQAGALEVQAGSLDNRQGTLQAQGDNQLRIGGALDNQGGRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLKLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALGGD
CdiA1_rA_V      SASGTLASQAGMSLRLGGGALRNQQDGLIFSQAGALEVQAGSLDNRQGTLQAQGDNRLRIGGALDNQGGRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLKLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALGGD
CdiA1_rA_II     SASGTLASQADMSLRLGGGALRNQQDGLIFSQAGALEVQAGSLDNRQGTLQAQGDNRLRIGGALDNQGGRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLTLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALGGD
clustal         **********.*********************************************:**********.********************************.************************************.**

           3501 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V      NRIVTADFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGGLNNAYGVLESANQDLDLQLGSLANAGGRILHTGNGTFGLDSGQV
CdiA2_rB_V      NRIVTADFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGDLNNAYGVLESANQDLDLQLGSLANAGGRILHTGNGTFGLDSGQV
CdiA2_rE_V      NRIVTADFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGGLNNAYGVLESANQDLDLQLGSLANAGGRILHIGNGTFGLDSAQV
CdiA2_rC_V      NRIVTVDFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGGLNNAYGVLESANQDLDLQLGSLANAGGRILHTGNGTFGLDSGQV
CdiA1_rA_V      NRIVTADFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGGLNNAYGVLESANQDLDLQLGSLANAGGRILHTGNGTFGLDSGQV
CdiA1_rA_II     NRIVTADFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGGLNNAYGVLESANQDLDLQLGSLANAGGRILHTGNGTFGLDSAQV
clustal         *****.*****************************************************************************************.******************************* *********.**

           3641 --------------------------------------------------------------- FHA1 -----------------------------------------------------------------------
CdiA2_rD_V      IRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDGLLASDGSLRLELSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAASLN
CdiA2_rB_V      IRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDGLLASNGSLRLELSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAASLN
CdiA2_rE_V      IRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDGLLASDGSLRLDLSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAASLN
CdiA2_rC_V      IRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDGLLASDGSLRLDLSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAASLN
CdiA1_rA_V      IRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDGLLASDGSLRLELSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAASLN
CdiA1_rA_II     IRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDGLLASDGSFRLDLSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAASLN
clustal         *******************************************************************:**:**:******************************************************************

           3781 ----------------------- FHA1 ---------------------------||----------------------------------- RBD ------------------------------------------
CdiA2_rD_V      NYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDSSGKASSFKNISASVESSNDLRLLAEVVENKKEIFDVSSEFLSGAIGVRCFDC-SAVGGKEDKFASHLVL-LEN-YKTQLLKD
CdiA2_rB_V      NYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDAGGWANRLENISGNLESTGDMRFSVSSLLNRRETLEIEGDLQNSAIGVRCTGCQLSERWGKTRSSSELVW-IRE-YKSTLGDS
CdiA2_rE_V      NYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDAGNRAASLENISANIESSGDTRISASNIVNKKEFFEVSSELVSSAIGMRRT----------SPGNGHMVL-LEN-YESSLKAD
CdiA2_rC_V      NYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDAGGWASSVNNRSSTIEAVGNATVRAEIFENKVDAYSSSETLEYGDITFDQL----------DGGRTNVFY-VDEFYKSNFELA
CdiA1_rA_V      NYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDAGNRAASLRNLSGVIESGKDFSLRASLIENRRAVLESKSGLYTAK--MEQTACIEGVNAGDCSGKRNAIWTITQRDKTEVTAS
CdiA1_rA_II     NYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDAGNRAASLRNLSGVIESGKDFSLRASLIENRRAVLESKSGLYTAK--MEQTACIEGVNAGDCSGKRNAIWTITQRDKTEVTAS
clustal         *********************************************************:.. *  ..* *. :*:  :  . .. . *:    . .  :  .   .                  . .  : :  :: .

           3921 --------------------------------------------------------------- RBD ------------------------------------------------------------------------
CdiA2_rD_V      SPSSNITSGGNIFILGGRFKNQGSTIAAAGDISISAQDFANEGYVLGEYSVRKALDFNYSYEARVEV--WRKIMEYNSINDLAY---DNGKIEYSNFGG---AIHFWNKNWDESIVD-SVYFRTGGRDGY----------
CdiA2_rB_V      SAAASITAGRDLLVVGASLQNIASNISAVRDATLSLSNFENKGYALGEYAVRGVYSPPSKFGEELLM----RILAYNAVNDPSY------GEGYASTGGRLPNIHYFDKNFNEKVSPLEVIHGNGKNGGP---------G
CdiA2_rE_V      APSASISAGGSLYVLGSDFLNSASYVTASKDIDVRVDRFTNQGATLGKYSVRRSFEHPWLREDKSILSFWRSVMEYNASNDSQYLPSRRGGAPNTVSGG---SIHYWDENWNE-----SIAYTGWKMGGTANRETHVLIG
CdiA2_rC_V      SPVSSFSVGGALKGWFKEFNNFGSTVSAGGDVELSAENFSNLSIASGDYTRNRVFK------------------------------------------G---PTDRWSEDKLI-----ELLNDGGGIETYQRRNSKLI--
CdiA1_rA_V      SAMGQLLAGGDFAIDGGTLNNLSSLIGSGGNLTANLEVLDNQGLETGELETIRVLR--------------------------------------TARGGDIGGIDQKSRNFTNLYWYQSANFDPARAGEIPAALNAILSD
CdiA1_rA_II     SAMGQLLAGGDFAIDGGTLNNLSSLIGSGGNLTANLEVLDNQGLETGELETIRVLR--------------------------------------TARGGDIGGIDQKSRNFTNLYWYQSANFDPARAGEIPAALNAILSD
clustal         :. ..:  *  :      : * .* : :  :     . : * .   *.                                                  *     .  ..:        .

           4061 --------------------------------------------------------------- RBD ----------------------------------------------------------||------------
CdiA2_rD_V      WHAGFGTIVID----DIARDKFDYISVAPAYDPSRGALP----PDFLRNAKVFDELTISKSD----VAPVANAVVQAGGKVSINAERSLQNSIVREGQPISRGVEKNLLTGLSGNTSNV-VVLSQALPPDLARKQVNPLT
CdiA2_rB_V      WHLYFGTLDVEYPDTDRWNKAIGRIP-APNYSSK-KTDAI---PDLLKGLAPLDELTINKGA-----NSTVGAVVQAGGRVTVNAAESFNNSVLQGFQAVQETQLPHQDIAVSSTTSAV-VTLKSQLPADLARQQINPLT
CdiA2_rE_V      WQDYWTFITPS--------NFYGIFP-EAKYTEGVRV-PL---PDAIRNVNYFDVLTVSDGA----QKGVADAVVQAAGKVSITASQEINNSVVREGLPVSSELGIALNTQVSANTSSTIVNLNSQLPPDLARQQINPLT
CdiA2_rC_V      -HDYYSVNCME--------GSCQTVPYERKYQGGGKVNPLYGKGNAVDIPKEFNSYTLISDAKVFREGGYLPSVIESGRTVSLVASGNLYNGDIKQWQDYTASRKDLGSTTVGKSSSVVDIVLHSQLPPDLARQQINPLT
CdiA1_rA_V      WSFEYEF-------------------------PSKGPTP------------------ISSGD------QSYAAVIQAAGDVTVNASTRIDNGVTRPGYTFVGSGRQVGDSAVGGSGVSVVVPLTSQLPPDLARRQVNPVT
CdiA1_rA_II     WSFEYEF-------------------------PSKGPTP------------------ISSGD------QSYAAVIQAAGDVTVNASTRIDNGVTRPGYTFVGSGRQVGDSAVGGSGVSVVVPLTSQLPPDLARRQVNPVT
clustal             :                                 .                  : ..           :*:::.  *:: *   : *.  :                :. .   . : * . **.****:*:**:*

           4201 --------------------------------------------------------------- YP -------------------------------------------------------------------------
CdiA2_rD_V      LPGFSLPQGQNGLFRLASQGALVNQASGALKSASDLTQSGHGVSVSAQTGSGASG-WSTQARRVGDDRVTSLAGSAYQGRVAEAIDALRASAPISGDGGNTGRFQAGEHQATTGLGGLVEGNASGHSGNGVILADLRGGP
CdiA2_rB_V      LPGFSLPQGQNGLFRLASQGAQVNQASGALKSASDLTQSGHGVSVSAQTGSGASG-WSTQARRVGDDRVTSLAGSAYQGRVAEAIDALRASAPISGDGGNTGRFQAGEHQATTGLGGLVEGNASGHSGNGVILADLRGGL
CdiA2_rE_V      LPGFSLPQGQNGLFRLASQGAQVNQASGALKSASDLTQSGHGVSVSAQAGSDASG-WSTQARRVGDDRVTSLTGSAYQGRVAEAIDALRASAPISGDGGNTGRFQAGEHQATTGLGGLVEGNASGHSGNGVILADLRGGL
CdiA2_rC_V      LPGFSLPQGQNGLFRLASQGAQVNQASGALKSASDLTQSGHGVSVSAQAGSDASG-WSTQARRVGDDRVTSLAGSAYQGRVAEAIDALRASAPISGDGGNTGRFQAGEHQATTGLGGLVEGNASGHSGNGVILADLRGGL
CdiA1_rA_V      LPGFSLPQGDNGLFRLSSRFAEDGNGSAALGAGADRTQGGSGVSVGQQGAGNVAGTWQGQGVRV---------------------DGLAGAANVQGQGGST-------------LGG-----------------------
CdiA1_rA_II     LPGFSLPQGDNGLFRLSSRFAEDGNGSAALGAGADRTQGGSGVSVGQQGAGNAAGTWQGQGVRV---------------------DGLAGAANVQGQGGST-------------LGG-----------------------
clustal         *********:******:*: *  .:.*.** :.:* **.* ****. * ....:* *. *. **                     *.* .:* :.*:**.*             ***

           4341
CdiA2_rD_V      PSFSSLPAADRVQGTVPGHDGNGTILANWQGAQATVQASPSTVRVEGVVSSPGGNGSILADLPAEQSSVQALPSAVRAQGSLPRLEERSAVLAEPPVGQPALQTLPSVARVEGVPSNATPSNSHKYLIETNPALTELKQF
CdiA2_rB_V      PSFSSLPASDHVQGTVPGHDGNGTILANWQGAQATVQASPSTVRVEGVVSSPGGNGSILADLPAEQSSVQALPSAVRAQGSLPRLEERSALLAEPPVGQPALQTLPSVARVEGVPSNATPSNSHKYLIETNPALTELKQF
CdiA2_rE_V      PSFSSLPAADRIQGTAPGHDGNGTILANWQGAQATVQASPSTVRVEGVVSSPGGNGSILADLPAEQSSVQALPSAVRAQGSLPRLEERSAVLAEPPVGQPALQTLPSVARVEGVPSNATPSNSHKYLIETNPALTELKQF
CdiA2_rC_V      PSFSSLPAADRIQSTVPGHDGNGTILANWQGAQATVQASPSTVRVEGVVSSPGGNGSILADLPAEQSSVQALPSAVRAQGSLPRLEERSALLAEPPVGQPALQTLPSVARVEGVPSNATPSNSHKYLIETNPALTELKQF
CdiA1_rA_V      -------------------------------------------------------------------------------------------------------SLPGVARVQGVPGNATPSASHKYLIETNPALTELKQF
CdiA1_rA_II     -------------------------------------------------------------------------------------------------------SLPGVARVQGVPGNATPSASHKYLIETNPALTELKQF
clustal                                                                                                                :**.****:***.***** ******************

           4481 --------------------------------------------------------------- YP ----------------------------------------------------------------------||-
CdiA2_rD_V      LNSDYLLGGLGINPDDSKKRLGDGLYEQRLVREAIVQRTGQRFIAGLNSDEAMFRYLMDNAIASKDVLGLTPGVTLSAAQVAALTHDIVWLEEVEVNGEKVLAPVVYLAQAEGRLGPNGALIQGRDVNLITGGDLRNAGT
CdiA2_rB_V      LNSDYLLGGLGINPDDSKKRLGDGLYEQRLVREAIVQRTGQRFIAGLNSDEAMFRYLMDNAIASKDVLGLTPGVTLSAAQVAALTHDIVWLEEVEVNGEKVLAPVVYLAQAEGRLGPNGALIQGRDVNLITGGDLRNAGT
CdiA2_rE_V      LNSDYLLGGLGINPDDSKKRLGDGLYEQRLIREAIVQRTGQRFIAGLNSDEAMFRYLMDNAIASKDVLGLTPGVTLSAAQVAALTHDIVWLEEVEVNGEKVLAPVVYLAQAEGRLGPNGALIQGRDVNLITGGDLRNAGT
CdiA2_rC_V      LNSDYLLGGLGINPDDSKKRLGDGLYEQRLVREAIVQRTGQRFIAGLNSDEAMFRYLMDNAIASKDVLGLTPGVTLSAAQVAALTHDIVWLEEVEVNGEKVLAPVVYLAQAEGRLGPNGALIQGRDVNLITGGDLRNAGT
CdiA1_rA_V      LNSDYLLSGLGMNPDASKKRLGDGLYEQRLIRDAVVARTGQRYIDGLSSDEALFRYLMDNAIAYKDQLHLQLGVGLSAEQMAALTHDIVWLEEVEVNGEKVLAPVVYLAQAEGRLAPNGALIQGRDVKLVSGGDLHNVGT
CdiA1_rA_II     LNSDYLLSGLGMNPDDSKKRLGDGLYEQRLIRDAVVARTGQRYIDGLSSDEALFRYLMDNAIAYKDQLHLQLGVGLSAEQMAALTHDIVWLEEVEVNGEKVLAPVVYLAQAEGRLAPNGALIQGRDVKLVSGGDLHNVGT
clustal         *******.***:*** **************:*:*:* *****:* **.****:********** ** * *  ** *** *:**********************************.***********:*::****:*.**

           4621 --------------------------------------------------------------- FHA1 -------------------------------------------------|               |-----
CdiA2_rD_V      LRAQNDLSATAGNIDNSGLIEAGNRLDLLASGSIRNDQGGIIAGREVSLSALTGDVINERTVTQHQSSYRGTGTTEAFADSTARIEAAQKLTVSAGRDVANIGGVIDSKGDLALQGGRDVLVSAAVAERGWTAGSQAYQT
CdiA2_rB_V      LRAQNDLSATAGNIDNSGLIEAGNRLDLLASGSIRNDQGGIIAGREVSLSALTGDVINERTVTQHQSSYRGTGTTEAFADSAARIEAAQKLTVSAGRDVANIGGVIDSKGDLALQGGRDVLVSAAVAERGWTAGSQAYQT
CdiA2_rE_V      LRAQNDLSATAGNIDNSGLIEAGNRLDLLASGSIRNDQGGIIAGREVSLSALTGDVINERTVTQHQSSYRGTGTTEAFADSAARIEAAQKLTVSAGRDVANIGGVIDSKGDLALQGGRDVLVSAAVAERGWTAGSQAYQT
CdiA2_rC_V      LRAQNDLSATAGNIDNSGLIEAGNRLDLLASGSIRNDQGGIIAGREVSLSALTGDVINERTVTQHQSSYRGTGTTEAFADSAARIEAAQKLTVSAGRDVANIGGVIDSKGDLALQGGRDVLVSAAVAERGWTAGSQAYQT
CdiA1_rA_V      LRARNDLSATADNLDNSGLIEAGKRLDLLAGDSIRNRQGGVIAGRDVSLTALTGDVINERSVTRYDSALDGRTWERSFADSAARVEAANSLNVQAGRDIANLGGVLQSRGDLSLDAGRDVTVAAVEDRQGQTRWSTSRLQ
CdiA1_rA_II     LRARNDLSATADNLDNSGLIEAGKRLDLLAGDSIRNRQGGVIAGRDVSLTALTGDVINERSVTRYDSALDGRTWERSFADSAARVEAANSLNVQAGRDIANLGGVLQSRGDLSLDAGRDVTVAAVEDRQGQTRWSTSRLQ
clustal         ***:*******.*:*********:******..**** ***:****:***:**********:**:::*:  *    .:****:**:***:.*.*.****:**:***::*:***:*:.**** *:*.  .:* *  * :

           4761 -------------------------------------------------------------- FHA2 ------------------------------------------------------------------------
CdiA2_rD_V      QTTQMGAEVVAGRDISVSAGRDISVAGSRIDARRDVTFEAGRDVGLVAAANEEHAYGKTKKVTFQDDKITQQATRVDAGGDLAINAGQDLRLVASQASAGDEAYLVAGDKLELLAANDSSYYLYDKKSKGSFGSKKTRRD
CdiA2_rB_V      QTTQMGAEVVAGRDISVSAGRDISVVGSRIDARRDVTFEAGRDVGLVAAANEEHAYGKTKKVTFQDDKITQQATRVDAGGDLAINAGQDLRLVASQASAGDEAYLVAGDKLELLAANDSSYYLYDKKSKGSFGSKKTRRD
CdiA2_rE_V      QTTQMGAEVVAGRDISVSAGRDISVVGSRIDARRDVTFEAGRDVGLVAAANEEHAYGKTKKVTFQDDKITQQATRVDAGGDLAINAGQDLRLIASQASAGDEAYLVAGDKLELLAANDSSYYLYDKKSKGSFGSKKTRRD
CdiA2_rC_V      QTTQMGAEVVAGRDISVSAGRDISVVGSRIDARRDVTFEAGRDVGLVAAANEEHAYGKTKKVTFQDDKITQQATRVDAGGDLAINAGQDLRLVASQASAGDEAYLVAGDKLELLAANDSSYYLYDKKSKGSFGSKKTRRD
CdiA1_rA_V      SVTQLGAEVSAGRDLNVSAGRDLSAVASALEARRDIALSAGRDVTLAAAANEEHAYSKTRKVTYQEDKVAQQGTRVDAGGDLAINAGQDLRLIASQASAGDEAYLVAGDKLELLAANDSNYYLYDKKKKGDFGRKETRRD
CdiA1_rA_II     SVTQLGAEVSAGRDLNVSAGRDLTAVASTLEARRDIALSAGRDVTLAAAANEEHSFATGKKVTAKNDRVEHQSTVVSAGGDLSVQGGNDVTFVASQAKASNEAYLYAGNDLNLLAAHDESYSYYSKKKKGSFGRSSSRMS
clustal         ..**:**** ****:.******::...* ::****:::.***** *.*******::.. :*** ::*:: :*.* *.*****:::.*:*: ::****.*.:**** **:.*:****:*..*  *.**.**.** ..:* .

           4901 ------------------------------- FHA2 -------------------------------|
CdiA2_rD_V      EITDVTAVGSQISSGGVLTLLSGGDQTYQGAKLESGN-DLAIVSGGAVTFDAVKDLHQESHEKSK-GDL-------------AWQSSKGKGQTDET----------VRQSQLVAQGNLAIKAVEGLKID-LKHIDQKTVS
CdiA2_rB_V      EITDVTAVGSQISSGGDLTLLSGGDQTYQGAKLESGN-DLAIVSGGAVTFEAVKDLHQESHEKSK-GDL-------------AWQSSKGKGQTDET----------VRQSQIVAQGNLAIKAVEGLKID-LKHIDQKTVS
CdiA2_rE_V      EITDVTAVGSQISSGGDLTLLSGGDQTYQGAKLESGN-DLAIVSGGAVTFEAVKDLHQESHEKSK-GDL-------------AWQSSKGKGQTDET----------VRQSQLVAQGNLAIKAVEGLKID-LKHIDQKTVS
CdiA2_rC_V      EITDVTAVGSQISSGGDLTLLSGGDQTYQGAKLESGN-DLAIVSGGAVTFEAVKDLHQESHEKSK-GDL-------------AWQSSKGKGQTDET----------VRQSQIVAQGNLAIKAVEGLKID-LKHIDQKTVS
CdiA1_rA_V      EVTDVKAVGSQISSGGDLTLLSGGDQTYQGAKLESGN-DLAIVSGGAVTFEAVKDLHQESHEKSK-GDL-------------AWNSAKGKGQTDET----------LRQTQIVAQGNLAIKAADGLKID-VKHIDQKTVS

                -------------------------------------------------------------- FHA2 ------------------------------------------------------------------------
CdiA1_rA_II     ESEASTVVSSSIQAGQGAELVAKRDVNVEASSASSTKGELAVVAGRDVNLTAAENSYSSVSAKSKSGGLGLSSTSKANAQSSSYTSVQGATLSGDTTVVQAGRDISVAASNVVSTGKTALRAGNDIIIDSVAETSESHRS
clustal         *    ..*.*.*.:*    *::  * . :.:. .* : :**:*:*  *.: *.:: :..   *** *.*             :: * :*   :.:*          :  :::*: *: *::* :.: ** : . .:.  *

           5041
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CdiA2_rD_V       QT-------------IDAMVQADPQLAWLKQMEQR--------GDVDWRRVQEL-------------------------------HDSWKYSNSG--LGVGAQLAIAIVVTYFTAGAASAALGSMAGVGAGSGSMMAAAG
CdiA2_rB_V       QT-------------IDAMVQADPQLAWLKQMEQR--------GDVDWRRVQEL-------------------------------HDSWKYSNSG--LGVGAQLAIAIVVAYFTAGAASAALGSMAGVGAGSGSMMAAAG
CdiA2_rE_V       QT-------------IDAMVQADPQLAWLKQMEQR--------GDVDWRRVQEL-------------------------------HDSWKYSNSG--LGVGAQLAIAIVVAYFTAGAASAALGSMAGVGAGSGSMMAAAG
CdiA2_rC_V       QT-------------IDAMVQADPQLAWLKQMEQR--------GDVDWRRVQEL-------------------------------HDSWKYSNSG--LGVGAQLAIAIVVTYFTAGAASGAIAT-----AGAGTSM--AG
CdiA1_rA_V       ET-------------IDVMVKADPSLAWLREAEKQ--------GDVDWRKVREV-------------------------------HDSFKYSHSG--LGAGAALAIAIVVTYLTW---------------GAGSSM--AG

                 -------------------------------------------------------------- FHA2 ------------------------------------------------------------------------
CdiA1_rA_II      ESKKKSGLMSSGGIGITLGTAKNASTQDTRTVVNQGSTIGSVLGDVDMRAGKNLSITASDVVAGKDINLVGQNVSILAADNQNVSEQTRKTSKSGLTLALSGTVGSAIDAIYQNAKQARNEDDSRLSALQGIKAGL--SG
clustal          ::             *   .  :..    :   ::        **** *  :::                               .:: * *:**  *. .. :. ** . * .                *  : :  :*

            5181                       |-------------------------------------- DUF637 ----------------------------------------------------------------------
CdiA2_rD_V       STAMVQAGTAVGTAAAGWANAAGTAVAMGMASNGAI----------STINNRGNL-------------GD----------------------VVKDVTSSDALRGY-VVAGTTAGLTAGVYDKWTSTQTGTST-ALPNTG
CdiA2_rB_V       STAMVQAGTAVGTAAAGWANAAGTAVAMGMASNGAI----------STINNRGNL-------------GD----------------------VVKDVTSSDALRGY-VVAGTTAGLTAGVYDKWTSTQTGTST-ALPNTG
CdiA2_rE_V       STAMVQAGTAVGTAAAGWANAAGTAVAMGMASNGAI----------STINNRGNL-------------GD----------------------VVKDVTSSDALRGY-VVAGTTAGLTAGVYDKWTSTQTGTST-ALPNTG
CdiA2_rC_V       ATA-----AATATTSAGWLNAAGTAALSGVASNGAI----------STINNRGNL-------------GD----------------------VVKDVTSSDALRGY-VVAGTTAGLTAGVYDKWTSTQTGTST-ALPNTG
CdiA1_rA_V       V----AAKSATGVAANSVASA--------VATNAAI----------STVNNRGNL-------------GA----------------------VAKDVTSSDSLKGY-AVAGISGGF--------MPSSLGA---QLAVRS

                 -------------------------------------------------------------- FHA2 ------------------------------------------------------------------------
CdiA1_rA_II      VQAWQAAQQNGGMTGENSAQFVGISASLGSQKSSSRQRQEQQISQGSTLTAGGNLNIIATGSGAVGEDGDLRVQGSKLQAGKDLQLIANRDVVLEAAANTQKLDGKNKSSGGAVGVSVGV----GSGEAGISIFANANKG
clustal                     . :. .  .           ...:           **:.  ***             *                       * : .:.:: * *    :* : *.         . . *      .  .

            5321 --------------------------------------------------------------- DUF637 -----------------------------|        |----- Class V C-terminus -----
CdiA2_rD_V       AVAPAAGLGTWQGVGQFTSNQLLQNGTSVLL----DRALGGKGSLGDALQNSLANAFAAYGFKLIGDTTHGVLDDGSLGKIGLHALMGGLAAEAVGGDFRTGALAAGVNEALVDSLAKQYASLPIDDKKGLLT-MSSQLI
CdiA2_rB_V       AVAPAAGLGTWQGVGQFTSNQLLQNGTSVLL----DRALGGKGSLGDALQNSLANAFAAYGFKLIGDTTHGVLDDGSLGKIGLHALMGGLAAEAVGGDFRTGALAAGVNEALVDSLAKQYASLPIDDKKGLLI-MSSQLI
CdiA2_rE_V       AVAPAAGLGTWQGVGQFTSNQLLQNGTSVLL----DRALGGKGSLGDALQNSLANAFAAYGFKLIGDTTHGVLDDGSLGKIGLHALMGGLAAEAVGGDFRTGALAAGVNEALVDSLAKQYASLPIDDKKGLLI-MSSQLI
CdiA2_rC_V       AVAPAAGLGTWQGVGQFTSNQLLQNGTSVLL----DRALGGKGSLGDALQNSLANAFAAYGFKLIGDTTHGVLDDGSLGKIGLHALMGGLAAEAVGGDFRTGALAAGVNEALVNSLAKQYASLPIDDKKGLLI-MSSQLI
CdiA1_rA_V       ALNTVVNGGKFR-------DNVAQAAISMAA---------------DALSGAI--------FDKVGDALVG---SGLPKKVAVHAIVGGLIGEAAGGDFRTAALAAGANEALVSLVGEK--IFPGEAHERVLA-MTSQLI

                 -------------------------------------------------------------- FHA2 --------|
CdiA1_rA_II      AGKEIGNGTTWT-------ETTLDAGQKASLVSGRDTTLKGAQVNGESILAKVGRDLT---LQSLQDRDYYDSKQKNVGGGASLAIVG----QGGGANL---SLSQSKLHSKYDSVQEQTGLFAGKGGFQVEVGKHTQLD
clustal          *     .  .:        :   : . .                  :::   :        :. : *       .      .  *::*    :. *.::   :*: .  .:  . : ::   :. .    :      :**

            5461 -------------------------------------------------------------- Class V C-terminus ----------------------------------------------------------
CdiA2_rD_V       GVLAASTQGDADAKSLQTGA-----------W-----------------------VAGNATQYNF----------------------------------------------LNHAENEERWKSQKACQGGDEAA----CG
CdiA2_rB_V       GVLAASTQGDADAKSLQTGA-----------W-----------------------VAGNATQHNY----------------------------------------------LSHWQEEKKRQEVDGCKDKQLCK----TG
CdiA2_rE_V       GVLAASTQGDADAKSLQTGA-----------W-----------------------VAGNATQHNY----------------------------------------------LSHWQEEKKRQEVDGCKDKQLCK----TG
CdiA2_rC_V       GVLAASTQGDADAKSLQTGA-----------W-----------------------VAGNATQHNY----------------------------------------------LSHWQEEKKRQEVDGCKDKQLCK----TG
CdiA1_rA_V       GMTVAAAAG-GDTKAQEKAA-----------W-----------------------VAQQATVYNN----------------------------------------------LNHAAAESLLKEIKDCRAAGGCGEEKLQG


CdiA1_rA_II      GSVIAST-AEAEKNRLSTGSLGWSEIRNKAEYKSQLQSVSVSSANDGAGAFVSNMPSGMLIAYNHGDSASGTTGSAISEGTLEVRDPARQQQDVATLSRDPSRANDSVSPIFDKEKEQKRLQQVQLIGEIGTQA----MD
clustal          *   *:: . .: :  ...:           :                        :     :*                                               :.:   :.  :. .              .

            5601 -------------------------------------------------------------- Class V C-terminus ----------------------------------------------------------
CdiA2_rD_V       RADAWDKLDRDRDLAL----------------------------------MTA--------------------------CSTG---GQASTCSALRQ--EAWKAA-QSLKQA--------------------SWSPEARE
CdiA2_rB_V       IEAKWAIISAQQDVGI----------------------------------VVG--------------------------VGGGIGLSTAETAVGVYELVKNWRETYAALEQL--------------------ATSPEFRQ
CdiA2_rE_V       IEAKWAIISAQQDVGI----------------------------------VVG--------------------------VGGGIGLSTAETAVGVYELVKNWRETYAALEQL--------------------ATSPEFRQ
CdiA2_rC_V       IEAKWAIISAQQDVGI----------------------------------VVG--------------------------VGGGIGLSTAETAVGVYELVKNWRETYAALEQL--------------------ATSPEFRQ
CdiA1_rA_V       ILGKYEKLSAERSNAI---------------------------GQCASRQCVDDIVDSSIRMDDPVSKELLSLLRQTTYDTPGLLQGNPDAIVSQTPNPSGWGDLFALDKQL--------------------AFAKNLKE


CdiA1_rA_II      ILRTQGQLDADKAARAELEARGISAPDAGASERQVEDYRKALLGTNAYQDIMGKYGTGGDYQKAAQAVTAALQGLAGGDIGSALAGASSPYVAGVIKQVAGDNDTARIMAHAVLGAVVAQAQGNSAAAGGAGAAGSELAA
clustal                 :. ::                                                                      .   . .    .                :                     : . :

            5741 -------------------------------------------------------------- Class V C-terminus ----------------------------------------------------------
CdiA2_rD_V       QYAQA-MQNPELRAYTI--------------------------ESELRS--I-------------------NQVNNPITAGDSKR--LAKALASFGS-------------------------DFVPVYGDTKAFSEA---
CdiA2_rB_V       QFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGV----EGGRFAAELVG--VLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGS--MSSQLGAVG--------------------------DLGRLGGGGKGYVDI--L
CdiA2_rE_V       QFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGV----EGGRFAAELVG--VLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGS--MSSQLGAVG--------------------------DLGRLGGGAKGTATAGKV
CdiA2_rC_V       QFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGV----EGGRFAAELVG--VLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGS--MSSQLGAVG--------------------------DLGRLGGGTKATASAG--
CdiA1_rA_V       GWLTP------EETADLDRWNASTSWLDRTAGRQLDPKEKAYLLSELGGAAAMALLGGRGSVGSNATFGQIKTVLDTAQAPYKGSTVIGHALSKHAG-------------------------RHPEIWGKVKGS------

                              |----------------------- PT-VENN -----------------------|------------------------- Class II C-terminus ------------------------
CdiA1_rA_II      QVISERLYGTRDSSTLNEAQKQTITALASLAGGL----AGSVVDGSSGG--AIAGAAGGKNATENNFLGGGTPPGLISYGQAASS--LTEYMRKNGATTEEITQAQRDLAQGQGFDGVQPANEFIKAWGEAMVAEAAGLG
clustal                       :                              ..  .                      .       .       :   :   .                                *

            5881 -------------------------------------------------------------- Class V C-terminus ----------------------------------------------------------
CdiA2_rD_V       --------------------------------------------------QDPFDYAMAGV-GLVP------------GAGDAAQKVLS-----------KAKKLFQ--EGKVAE-------------------------
CdiA2_rB_V       SHEAKQHILYGDKPGSGGHLWPGQAGKTVFPQNWSADKIVHEVGDIATSPSTKW-YAQTGT-GGVY----------------TSKGDPAKWVAYEVRDGVRMRVVYQPATGKVIT-AFPDNAPIP---------------
CdiA2_rE_V       ADEFI-PPGMERPFRPVNPEFPPNKAVVDAMESPRIKGMTACDGTDCSEIASKLLAAAGGK-GKVI------------EVRPTQRSNLNLYENGNEVPGQAYHQVYT--DGRYVYDPRLSSQPIPKGDWEQHIKGMNPDG
CdiA2_rC_V       -------------------------------------------GQTASTLPKNFGESVLGH-NTQI------------GVRNSKAGTIS---------------------GAHNNDAFLESV------------------
CdiA1_rA_V       --------------------------------------------------MSGWNEQAMKHFKEIV--------RAPGEFRPTMNEKGITFLEKRLIDGRGVRLNLDGTFKGFID-------------------------

                 -------------------------------------------------------------- Class II C-terminus ---------------------------------------------------------
CdiA1_rA_II      IVAGLGRFGLWVGKGAGETAIAVPGRVQSRINIANGRTATTPLRDTGRPVSAGFDHVLQGHFGVEVSNSRSVFTITPSELKDVLQSSPVVKSPVMALPDGQFVRTVD--VGKVIGTTNLKDGGVPTSVLKIFTD--RAGN
clustal

            6021 ----------|
CdiA2_rD_V       -----------
CdiA2_rB_V       -----PYKPIK
CdiA2_rE_V       VTISDKLQGLR
CdiA2_rC_V       -----------
CdiA1_rA_V       -----------

                 ----------|
CdiA1_rA_II      LITTFPIKAVD
```

Figure S1. Alignment of the major *P. aeruginosa* CdiA groups reveals conservation of the amino-terminal half. Representative sequences were chosen to highlight the major Class II and Class V CdiA groups as well as different RBDs. The different domains illustrated in Fig. 1C are emphasized above the sequence alignment. “*” indicate identical residues, “:” are highly similar residues and “.” are weakly similar residues in the Gonnet PAM 250 matrix.

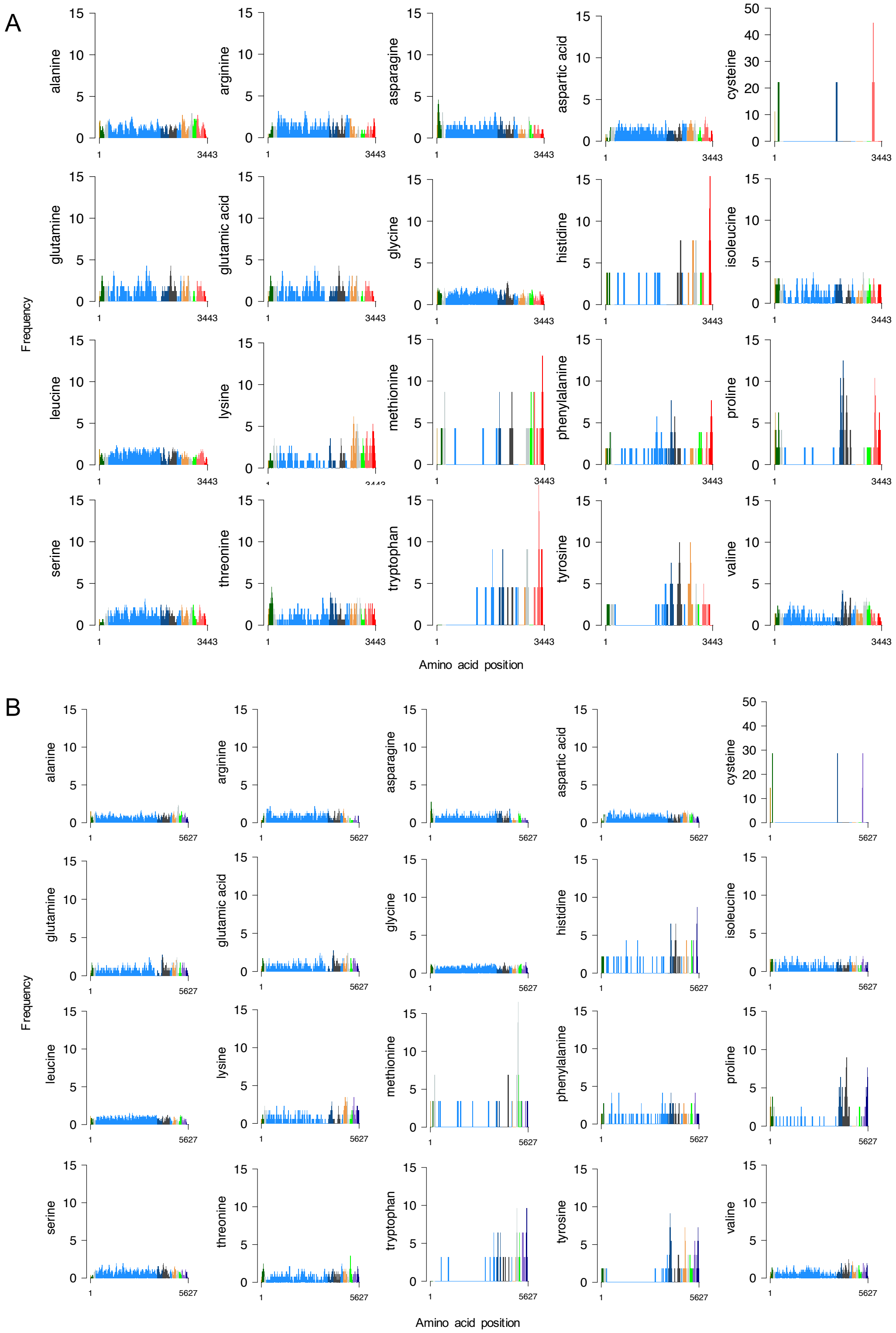
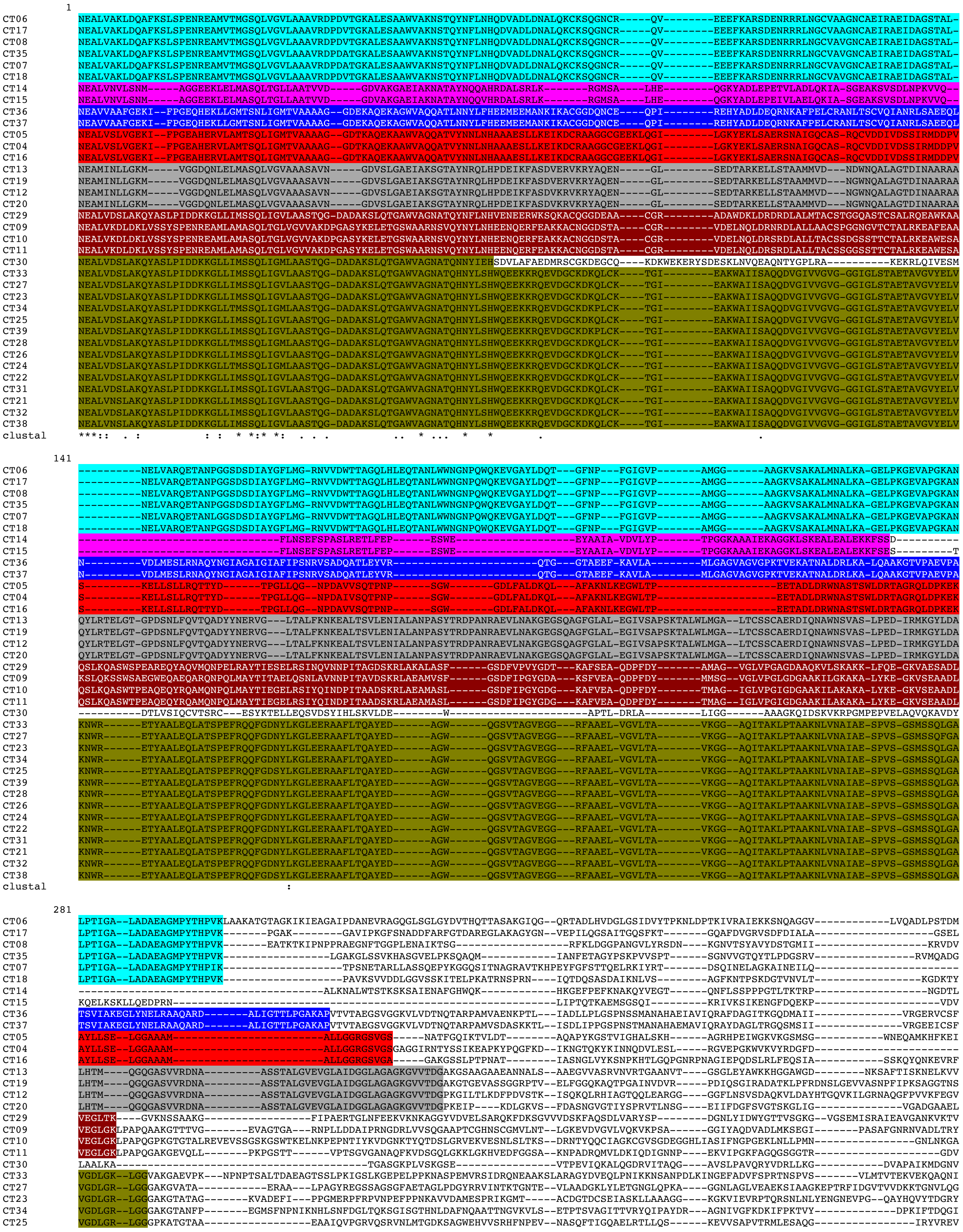


Figure S2. CdiA2 amino acid residue frequency. Amino acid frequency plots of (A) CdiA1^{PAO1} and (B) CdiA2^{PAO1} were determined using a sliding window of 40 residues. Frequency reflects the residue count within the sliding window divided by the total number of occurrences of that residue in CdiA. Colors correspond with protein domains shown in Figure 1C.

A



```
          1
CT06      NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCR-----QV--------EEEFKARSDENRRRLNGCVAAGNCAEIRAEIDAGSTAL-
CT17      NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCR-----QV--------EEEFKARSDENRRRLNGCVAAGNCAEIRAEIDAGSTAL-
CT08      NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCR-----QV--------EEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTAL-
CT35      NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDATGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCR-----QV--------EEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTAL-
CT07      NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDATGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCR-----QV--------EEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTAL-
CT18      NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCR-----QV--------EEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTAL-
CT14      NEALVNVLSNM-----AGGEEKLELMASQLTGLLAATVVD-----GDVAKGAEIAKNATAYNQQAHRDALSRLK-------RGMSA----LHE--------QGKYADLEPETVLADLQKIA-SGEAKSVSDLNPKVVQ--
CT15      NEALVNVLSNM-----AGGEEKLELMASQLTGLLAATVVD-----GDVAKGAEIAKNATAYNQQVHRDALSRLK-------RGMSA----LHE--------QGKYADLEPEIVLAELQKIA-SGEAKSVSDLNPKVVQ--
CT36      NEAVVAAFGEKI--FPGEQHEKLLGMTSNLIGMTVAAAAG--GDEKAQEKAGWVAQQATLNNYLFHEEMEEMANKIKACGGDQNCE----QPI--------REHYADLDEQRNKAFPELCRANLTSCVQIANRLSAEEQL
CT37      NEAVVAAFGEKI--FPGEQHEKLLGMTSNLIGMTVAAAAG--GDEKAQEKAGWVAQQATLNNYLFHEEMEEMANKIKACGGDQNCE----QPI--------REHYADLDEQRNKAFPELCRANLTSCVQIANRLSAEEQL
CT05      NEALVSLVGEKI--FPGEAHERVLAMTSQLIGMTVAAAAG--GDTKAQEKAAWVAQQATVYNNLNHAAAESLLKEIKDCRAAGGCGEEKLQGI--------LGKYEKLSAERSNAIGQCAS-RQCVDDIVDSSIRMDDPV
CT04      NEALVSLVGEKI--FPGEAHERVLAMTSQLIGMTVAAAAG--GDTKAQEKAAWVAQQATVYNNLNHAAAESLLKEIKDCRAAGGCGEEKLQGI--------LGKYEKLSAERSNAIGQCAS-RQCVDDIVDSSIRMDDPV
CT16      NEALVSLVGEKI--FPGEAHERVLAMTSQLIGMTVAAAAG--GDTKAQEKAAWVAQQATVYNNLNHAAAESLLKEIKDCRAAGGCGEEKLQGI--------LGKYEKLSAERSNAIGQCAS-RQCVDDIVDSSIRMDDPV
CT13      NEAMINLLGKM-----VGGDQNLELMASQLVGVAAASAVN-----GDVSLGAEIAKSGTAYNRQLHPDEIKFASDVERVKRYAQEN-----GL--------SEDTARKELLSTAAMMVD---NDWNQALAGTDINAARAA
CT19      NEAMINLLGKM-----VGGDQNLELMASQLVGVAAASAVN-----GDVSLGAEIAKSGTAYNRQLHPDEIKFASDVERVKRYAQEN-----GL--------SEDTARKELLSTAAMMVD---NGWNQALAGTDINAARAA
CT12      NEAMINLLGKM-----VGGDQNLELMASQLVGVAAASAVN-----GDVSLGAEIAKSGTAYNRQLHPDEIKFASDVKRVKRYAQEN-----GL--------SEDTARKELLSTAAMMVD---NGWNQALAGTDINAARAA
CT20      NEAMINLLGKM-----VGGDQNLELMASQLVGVAAASAVN-----GDVSLGAEIAKSGTAYNRQLHPDEIKFASDVKRVKRYAQEN-----GL--------SEDTARKELLSTAAMMVD---NGWNQALAGTDINAARAA
CT29      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQYNFLNHVENEERWKSQKACQGGDEAA----CGR--------ADAWDKLDRDRDLALMTACSTGGQASTCSALRQEAWKAA
CT09      NEALVKDLDKLVSSYSPENREAMLAMASQLTGLVGVVAKDPGASYKELETGSWAARNSVQYNYLNHEENQERFEAKKACNGGDSTA----CGR--------VDELNQLDRNRDLALLAACSPGGNGVTCTALRKEAFEAA
CT10      NEALVKDLDKLVSSYSPENREAMLAMASQLTGLVGVVAKDPGASYKELETGSWAARNSVQYNYLNHEENQERFEAKKACNGGDSTA----CGR--------VDELNQLDRSRDLALLTACSSDGSSTTCTALRKEAWESA
CT11      NEALVKDLDKLVSSYSPENREAMLAMASQLTGLVGVVAKDPGASYKELETGSWAARNSVQYNYLNHEENQERFEAKKACNGGDSTA----CGR--------VDELNQLDRSRDLALLTACSSGGSSTTCTALRKEAWESA
CT30      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGMLAASTQG-DADAKSLQTGAWVAGNATQNNYIEHSDVLAFAEDMRSCGKDEGCQ----KDKWEKERYSDESKLNVQEAQNTYGPLRA----------KEKRLQIVESM
CT33      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT27      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT23      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT34      NEALVDSLAKQYASLPIDDKKGLLTMSSQLIGMLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKPLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT25      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT39      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKPLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT28      NEALVDSLAKQYASLPIDDKKGLLTMSSQLIGMLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT26      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT24      NEALVDSLAKQYASLPIDDKKGLLTMSSQLIGMLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT22      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT31      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT21      NEALVNSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT32      NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
CT38      NEALVNSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQG-DADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCK----TGI--------EAKWAIISAQQDVGIVVGVG-GGIGLSTAETAVGVYELV
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CT06      ----------NELVARQETANPGGSDSDIAYGFLMG-RNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQT---GFNP---FGIGVP-------AMGG------AAGKVSAKALMNALKA-GELPKGEVAPGKAN
CT17      ----------NELVARQETANPGGSDSDIAYGFLMG-RNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQT---GFNP---FGIGVP-------AMGG------AAGKVSAKALMNALKA-GELPKGEVAPGKAN
CT08      ----------NELVARQETANPGGSDSDIAYGFLMG-RNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQT---GFNP---FGIGVP-------AMGG------AAGKVSAKALMNALKA-GELPKGEVAPGKAN
CT35      ----------NELVARQETANPGGSDSDIAYGFLMG-RNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQT---GFNP---FGIGVP-------AMGG------AAGKVSAKALMNALKA-GELPKGEVAPGKAN
CT07      ----------NELVARQETANLGGSDSDIAYGFLMG-RNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQT---GFNP---FGIGVP-------AMGG------AAGKVSAKALMNALKA-GELPKGEVAPGKAN
CT18      ----------NELVARQETANPGGSDSDIAYGFLMG-RNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQT---GFNP---FGIGVP-------AMGG------AAGKVSAKALMNALKA-GELPKGEVAPGKAN
CT14      --------------------------------FLNSEFSPASLRETLFEP------ESWE-------------------EYAAIA-VDVLYP-------TPGGKAAAIEKAGGKLSKEALEALEKKFSSD----------
CT15      --------------------------------FLNSEFSPASLRETLFEP------ESWE-------------------EYAAIA-VDVLYP-------TPGGKAAAIEKAGGKLSKEALEALEKKFSES---------T
CT36      N---------VDLMESLRNAQYNGIAGAIGIAFIPSNRVSADQATLEYVR-----------------------QTG---GTAEEF-KAVLA--------MLGAGVAGVGPKTVEKATNALDRLKA-LQAAKGTVPAEVPA
CT37      N---------VDLMESLRNAQYNGIAGAIGIAFIPSNRVSADQATLEYVR-----------------------QTG---GTAEEF-KAVLA--------MLGAGVAGVGPKTVEKATNALDRLKA-LQAAKGTVPAEVPA
CT05      S---------KELLSLLRQTTYD------TPGLLQG--NPDAVVSQTPNP------SGW-------GDLFALDKQL---AFAKNLKEGWLTP-------------------EETADLDRWNASTSWLDRTAGRQLDPKEK
CT04      S---------KELLSLLRQTTYD------TPGLLQG--NPDAIVSQTPNP------SGW-------GDLFALDKQL---AFAKNLKEGWLTP-------------------EETADLDRWNASTSWLDRTAGRQLDPKEK
CT16      S---------KELLSLLRQTTYD------TPGLLQG--NPDAVVSQTPNP------SGW-------GDLFALDKQL---AFAKNLKEGWLTP-------------------EETADLDRWNASTSWLDRTAGRQLDPKEK
CT13      QYLRTELGT-GPDSNLFQVTQADYYNERVG---LTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLAL-EGIVSAPSKTALWLMGA--LTCSSCAERDIQNAWNSVAS-LPED-IRMKGYLDA
CT19      QYLRTELGT-GPDSNLFQVTQADYYNERVG---LTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLAL-EGIVSAPSKTALWLMGA--LTCSSCAERDIQNAWNSVAS-LPED-IRMKGYLDA
CT12      QYLRTELGT-GPDSNLFQVTQADYYNERVG---LTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLAL-EGIVSAPSKTALWLMGA--LTCSSCAERDIQNAWNSVAS-LPED-IRMKGYLDA
CT20      QYLRTELGT-GPDSNLFQVTQADYYNERVG---LTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLAL-EGIVSAPSKTALWLMGA--LTCSSCAERDIQNAWNSVAS-LPED-IRMKGYLDA
CT29      QSLKQASWSPEAREQYAQVMQNPELRAYTIESELRSINQVNNPITAGDSKRLAKALASF------GSDFVPVYGDT---KAFSEA-QDPFDY-------AMAG--VGLVPGAGDAAQKVLSKAKK-LFQE-GKVAESADL
CT09      KSLQKSSWSAEGWEQAEQARQNPQLMAYTITAELQSNLAVNNPITAVDSKRLAEAMVSF------GSDFIPGYGDA---KSFVEA-QDPFDY-------MMSG--VGLVPGLGDGAAKILGKAKA-LYKE-GKVSEAADL
CT10      QSLKQASWTPEAQEQYRQAMQNPQLMAYTIEGELRSIYQINDPITAADSKRLAEAMASL------GSDFIPGYGDG---KAFVEA-QDPFDY-------TMAG--IGLVPGIGDGAAKILAKAKA-LYKE-GKVSEAADL
CT11      QSLKQASWTPEAQEQYRQAMQNPQLMAYTIEGELRSIYQINDPITAADSKRLAEAMASL------GSDFIPGYGDG---KAFVEA-QDPFDY-------TMAG--IGLVPGIGDGAAKILAKAKA-LYKE-GKVSEAADL
CT30      ----------DTLVSIQCVTSRC---ESYKTELLEQSVDSYIHLSKVLDE--------W----------------------APTL-DRLA---------LIGG------AAAGKQIDSKVKRPGMPEPVELAQVQKAVDY
CT33      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT27      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQFGA
CT23      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT34      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT25      KNWR------ETYAALEQLATSPEFRQQFGDSYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT39      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT28      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT26      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT24      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT22      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT31      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT21      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT32      KNWR------ETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
CT38      KNWR------ETYAALEQLATSPEFRQQFGDSYLKGLEERAAFLTQAYED------AGW------QGSVTAGVEGG---RFAAEL-VGVLTA-------VKGG--AQITAKLPTAAKNLVNAIAE-SPVS-GSMSSQLGA
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CT06      LPTIGA--LADAEAGMPYTHPVKLAAKATGTAGKIKIEAGAIPDANEVRAGQGLSGLGYDVTHQTTASAKGIQG--QRTADLHVDGLGSIDVYTPKNLDPTKIVRAIEKKSNQAGGV------------LVQADLPSTDM
CT17      LPTIGA--LADAEAGMPYTHPVK-------PGAK--------GAVIPKGFSNADDFARFGTDAREGLAKAGYGN--VEPILQGSAITGQSFKT-------GQAFDVGRVSDFIALA--------------------GSEL
CT08      LPTIGA--LADAEAGMPYTHPVK-------EATKTKIPNPPRAEGNFTGGPLENAIKTSG------------------RFKLDGGPANGVLYRSDN----KGNVTSYAVYDSTGMII------------------KRVDV
CT35      LPTIGA--LADAEAGMPYTHPVK-----------------LGAKGLSSVKHASGVELPKSQAQM------------IANFETAGYPSKPVVSPT------SGNVVGTQYTLPDGSRV----------------RVMQADG
CT07      LPTIGA--LADAEAGMPYTHPIK-------------------TPSNETARLLASSQEPYKGGQSITNAGRAVTKHPEYFGFSTTQELRKIYRT-------DSQINELAGKAINEILQ-----------------------
CT18      LPTIGA--LADAEAGMPYTHPVK-------------------PAVKSVVDDLGGVSSKITELPKATRNSPRN----IQTDQSASDAIKNLVS--------AGFKNTPSKDGTVNVLT-----------------KGDKTY
CT14      ---------------------------------------ALKNALWTSTKSKSAIENAFGHWQK------------HKGEFPEFKNAKQYVEGT------QNFLSSPPPGTLTKTRP------------------NGDTL
CT15      KQELKSKLLQEDPRN-------------------------------------------------------------LIPTQTKAEMSGSQI---------KRIVKSIKENGFDQEKP--------------------VDV
CT36      TSVIAKEGLYNELRAAQARD-------ALIGTTLPGAKAPVTVTAEGSVGGKVLVDTNQTARPAMVAENKPTL---IADLLPLGSPNSSMANAHAEIAVIQRAFDAGITKGQDMAII--------------VRGERVCSF
CT37      TSVIAKEGLYNELRAAQARD-------ALIGTTLPGAKAPVTVTAEGSVGGKVLVDTNQTARPAMVSDASKKTL--ISDLIPPGSPNSTMANAHAEMAVIQRAYDAGLTRGQSMSII--------------VRGEEICSF
CT05      AYLLSE--LGGAAAM------------------------ALLGGRGSVGS-----NATFGQIKTVLDT--------AQAPYKGSTVIGHALSKH------AGRHPEIWGKVKGSMSG-----------WNEQAMKHFKEI
CT04      AYLLSE--LGGAAAM------------------------ALLGGRGSVGSGAGGIRNTYSSIKEAPKYPQGFKD--IKNGTQKYKINNQDVLESL-----RGVEPGKWVKVYRDGFD-----------------------
CT16      AYLLSE--LGGAAAM------------------------ALLGGRGSVGA-----GAKGSSLPTPNAT--------IASNGLVYKSNPKHTLGQPGNRPNAGIEPQDSLRLFEQSIA-----------SSKQYQNKEVRF
CT13      LHTM----QGQGASVVRDNA---------ASSTALGVEVGLAIDGGLAGAGKGVVTDGAKGSAAGAAEANNALS--AAEGVVASRVNVRTGAANVT----GSGLEYAWKKHGGAWGD--------NKSAFTISKNELKVV
CT19      LHTM----QGQGASVVRDNA---------ASSTALGVEVGLAIDGGLAGAGKGVVTDGAKGTGEVASSGGRPTV--ELFGGQKAQTPGAINVDVR-----PDIQSGIRADATKLPFRDNSLGEVVASNPFIPKSAGGTNS
CT12      LHTM----QGQGASVVRDNA---------ASSTALGVEVGLAIDGGLAGAGKGVVTDGPKGILTLKDFPDVSTK--ISQKQLRHIAGTQQLEARGG----GGFLNSVSDAQKVLDAYHTGQVKILGRNAQGFPVVKFEGV
CT20      LHTM----QGQGASVVRDNA---------ASSTALGVEVGLAIDGGLAGAGKGVVTDGPKEIP----KDLGKVS--FDASNGVGTIYSPRVTLNSG----EIIFDGFSVGTSKGLIG--------------VGADGAAEL
CT29      VEGLTK----GVKNSSAAKG-----------------FIPAERTGLNFEEKVKNKAGGYVDVELSARQKFDKSGVVVDSKFAQSDLVARYSP--------DGNLYIDWYGTTVSGKG--VGSEMISRAIEAVGANKVKTV
CT09      VEGLGKLPAPQAAKGTTTVG-------EVAGTGA---RNPLLDDAIPRNGDRLVVSQGAAPTCGHNSCGMVLNT--LGKEVDVGVLVQKVKPSA------GGIYAQDVADLMKSEGI-------PASAFGNRNVADLTRY
CT10      VEGLGKLPAPQGPKGTGTALREVEVSSGSKGSWTKELNKPEPNTIYKVDGNKTYQTDSLGRVEKVESNLSLTKS--DRNTYQQCIAGKCGVSGDEGGHLIASIFNGPGEKLNLLPMN----------------GNLNKGA
CT11      VEGLGKLPAPQGAKGEVQLL-------PKPGSTT------VPTSGVGANAQFKVDSGQLGKKLGKHVEDFGGSA--KNPADRQMVLDKIQDIGNNP----EKVIPGKFAGQGSGGTR--------------------GDV
CT30      LAALKA----------------------------------------TGASGKPLVSKGSE----------------VTPEVIQKALQGDRVITAQG----AVSLPAVQRYVDRLLKG-----------DVAPAIKMDGNV
CT33      VGDLGK--LGGVAKGAEVPK---NPNPTSALTDAEAGTSSLPKIGSLKGEPELPPKNASPEMVRSIDRQNEAAKSLARAGYDVEQLPNIKKNSANPDLKINGEFADVFSPRTNSPVS-------VLMTVTEKVEKQAQNI
CT27      VGDLGR--LGGGAKGVATA-----------ERAA---LPAGYREGSSAGSGFAETAGLPDGYRRVINTKTGNTE--VLAADGKLYLETGNGLQPKA----GGNLAGLVEAEKSIAAGKEPTRFIDGVTVVDKKTGNVLQG
CT23      VGDLGR--LGGGAKGTATAG-------KVADEFI---PPGMERPFRPVNPEFPPNKAVVDAMESPRIKGMT-----ACDGTDCSEIASKLLAAAGG----KGKVIEVRPTQRSNLNLYENGNEVPG--QAYHQVYTDGRY
CT34      VGDLGR--LGGGAKGTANFP-------EGMSFNPNIKNHLSNFDGLTQKSGISGTHNLDAFNQAATTNGVKVLS--ETPTSVAGITTVRYQIPAYDR---AGNIVGFKDKIFPKTVY-------------DPKIFTDQGI
CT25      VGDLGR--LGGGPKATGTAA-----------------EAAIQVPGRVQSRVNLMTGDKSAGWEHVVSRHFNPEV--NASQFTIGQAELRTLLQS------KEVVSAPVTRMLESAQG----------------IRYVREV
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CT39        VGDLGR--LGGGAKGTTPTV----------------TAEGRIGNSVFTDVNQTARPAAQANPNQPTLIADRVDA--KIAANGKPHPNGNMADAHAE----IGVIQQAYNAGKTTGAD------------MALKVEGKAVC
CT28        VGDLGR--LGGGAKGATPKT-----------------ETYFRVEGGGSGAATSQNRITVNTDGSIKINPGCSGQ--LCVSVGSADHASYFLTNKRP----DGSVVVFEVDAGLHKQI-------------MDSAIPQRPV
CT26        VGDLGR--LGGGAKATATVI-----DTAPMAQRVMDVRAGLPSNLRRSGNVAIAEIDIPGIPRQMAAHSQVSDAGKGLIGSGSGNFVAQSVPNKAGDMVYRGIDTEYKILDNIADQL-----------GSNTSARGTVNI
CT24        VGDLGK--LGGGPKGSATAL--------------------QNFGGRTANDLVAAATEPIN----------------KEGLTKAARALTKHASGQRA----TGTFPKLTGGIENQNSV---------------AQKIVDEI
CT22        VGDLGR--LGGGTKATASAG----------GQTASTLPKNFGESVLGHNTQIGVRNSKAG-------TISGAHN--NDAFLESVEITGAKVSNKIT----DARFPGIVEYSYQLPRTNTKGEFIGGYKSVSTKTTYDPKI
CT31        VGDLGR--LGGGTKATASAG----------GQTASTLPKNFGESVLGHNTQIGVRNSKAG-------TISGAHN--NDAFLESVEITGAKVSNKIT----DARFPGIVEYSYQLPRTNTKGEFIGGYKSVSTKTTYDPKI
CT21        VGDLGR--LGGGAKGVQK-------------------LPELGGVDTFLSSQAANLNKKLGAKIGEGRLPYEASR--AGVEQAKLAVKETLENATAV----SDIIPKSAVRGNYDLVH----------------------V
CT32        VGDLGR--LGGGGKGYVDIL-------------------------SHEAKQHILYGDKPGSGGH------------LWPGQAGKTVFPQNWSADKIVHEVGDIATSPSTKWYAQTGT-----------------GGVYTS
CT38        VGDLGR--LGGGAKATPSAD-------------------SLINLASNQRSQHILLGDATGG--------------------------GHLWPGAPG----KTAFPASWNGDKVMHNV--------------------SDL
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CT06        SSIAARMWGKTNAQSIKTIFFQK------------PDGSLVRFDRP-------AGGG--------------------------------------------
CT17        LQRAQSLGIGLRSGGTRTGPLSG------------RDLQALGLKDLARKLSAQAGREVNFMIYDS-AATAASRAPSLVLPK--------------------
CT08        SGASHANIPTPHVIEYGRNILPD------------GSVRVQSPSTK-------LAPRPANSDEIP------------------------------------
CT35        RSPQRASFENANGGPIDPTTGKPP-----------QPPKGLSKAER-------KQWIRERTHIEQVD----------------------------------
CT07        SGVKSNGAGGRYPGGWITYTL--------------PDGRAASWGG--------DGKFIGFRGVQK------------------------------------
CT18        TFYSRSKTTGLPSAELKIGGNSKK-----------NIAVKIRFENP-------------------------------------------------------
CT14        LFDPKTNTFGVKDANGAPRTMFR------------PQDGINYWNRQ-------------------------------------------------------
CT15        WRNPKTGRLEIQDGHHRTEAAKKA-----------GLDKIPVSIWE-------------------------------------------------------
CT36        CRSSNNILAAADRSGLNSLKLVEA-----------ESGKIFTWTRGI------EGWK--------------------------------------------
CT37        CQSSTNILAAAERSGLNSLKLVEA-----------KTGRTFTWTRGI------DGWR--------------------------------------------
CT05        VRAPGEFRPTMNEKGITFLEKRL------------IDGRGVRLNL--------DGTFKGFID---------------------------------------
CT04        -SAGNKISVHYFQS---------------------QSGKVFDVKVK-------SGWSN-------------------------------------------
CT16        AVDSRGDIHRFEGANGEFHWNGSSGD---------LRNPLVGSQIP-------NDIQKQLGVRVK------------------------------------
CT13        LQSPQVVKTPAYQSPTSGNFIRTV-----------DMGRPIGIDAK-------AGGQPTNFMTVI----------------TDSKGNLVNTFPGKTF----
CT19        MMDFLPEATRVIEPGGKIFINANAAN---------PYGKIPSASEL-------ESLGLRIIQNGPLDSRFSGQTFLRTDGSVITNLDSMKTIVLEKIK---
CT12        TGTNVNLGVGITDQATNVFIIKGT-----------KSPSIVPTN---------PNWSPK------------------------------------------
CT20        VGPLRKMLSYSQSQGAQTITLKGHYAS--------EQGSMLGTGSV-------NNVNQKFSFSFP------------------ATTDGLKAFLKELGK---
CT29        SAQLGKDNLDAFKAGSSRGLSKEQAVW--------NTPLGKTMNSLGFTEVEVHGASVKFLHLE-------------------------------------
CT09        TSNGTPVVVRIADKTGDSDFS--------------HFVVVDGVTTR-------NGVSVVAIRDPH---------GTQYFSPVATFEKSFTGEVVVPRSALK
CT10        WKSMENTWSSALKQGQMVSVKIEPVYSGSSV----RPDRFTVRYSI-------DGGRPVIVDFKNSPGGI-------------------------------
CT11        FFRIKGDDVVVTKPDGTFVTIMKD-----------GINNTSVKNAL-------KGNPQ-------------------------------------------
CT30        IVDGNHRYIAAKILGRNLDVTPGSL----------SPNKVHQTKPV-------SELKIDQVDWGNK-----------------------------------
CT33        VVNLADSPLTFKQIENALSVK--------------PVDGLKNLYLL-------KDGQFKVIEVGR------------------------------------
CT27        TVDLGPTLDRIKSGGSYPHKNDGSIFQNRAGDLPVKPAGYYTEYVHPTPGVTGPGAQRIVVGKGG---------------EMYYTADHYKTF-IPINN---
CT23        VYDPRLSSQPIPKGDWEQHIKGM------------NPDGVTISDKL-------QGLR--------------------------------------------
CT34        LDLGQQAAAGGYKDALSKGVS--------------QYDSVAGGITFRVYLDKFTGTVTNFHPK--------------------------------------
CT25        NLSGPIGIDKFSGQPTSTMTVLTD-----------RFGNLITTT---------PGVVK-------------------------------------------
CT39        SYCRGDIAAAAEKAGLNSLQINEV-----------TTGKTLYWK---------PGMRSLRELE--------------------------------------
CT28        PGVPRDPSAPKIVDPSQPGVALE------------LPKMWESLLEK-------HSSNARLYSHDE--------------------------FLKEFGR---
CT26        LTEKAACASCLNVAEQFKAK---------------YPNITVNILDN-------QGVMLRPPRKTP------------------------------------
CT24        VTDPKAVYTNLSRGGLEIRV---------------PDGRGIRYNS--------DGSFSTFLDPKL------------------------------------
CT22        LPDSKVADMSSRAAVQAESVFKA------------NPALRETSIKV-------DGYYFQVTRNSK-------------------TGEITNSFITMPPRIK-
CT31        LPDSKVADMSSRAAVQAESVFKA------------NPALRETSIKV-------DGYYFQVTRRGC-------AEFCVTGVRVTAAAGGLRS----------
CT21        YSSKTNSTVSLRVLPGGKYEF--------------DTLISEKSSKF-------------------------------------------------------
CT32        KGDPAKWVAYEVRDGVRMRVVYQP-----------ATGKVITAFP--------DNAPIPPYKPIK------------------------------------
CT38        ATDPKASWTQLTGKPGAQFTTKG------------KPVRWAVEGVR-------DGVNIRVIVEPHGEGIITAYPK--------------------------
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CT01        TENNYLGTGVNLFGHQLGSNQVDAFHKELKASCSGSGGTQACLNTYSKWKETSYKQGGLESKNEQAGWEDFVRAAYAENIVPLCKGNSVCLDNVNAKMASDMVVYAGDAVGLKDSVGATARGVNIANGNWVRTGLQVVED
CT03        TENNFLGGGT-------------------PPGLISYGQAASSLTEYMR------KNGATAEEITQAQRD-------------LAQGQG--FDGVQP--ANEFIKAWGEAM--------------------------VAEA
CT02        TENNFLGGGT-------------------PPGLISYGQAASSLTEYMR------KNGATAEEITQAQRD-------------LAQGQG--FDGVQP--ANEFIKAWGEAM--------------------------VAEA
clustal     ****:** *.                    ..  . * : :.*. * :      *:*.  .:  **  :             *.:*:.  :*.*:.  *.:::   *:*:                          *.*

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CT01        AGLLAAIGGVFGVGSSTAAKATVNAEGAALPAGYREGSSAGSAFLETAGLPEGYRRVINTKTGNTEVLAADGKLYFETGNGLQPKAGGNLSGLVEAEKSIALRQQASKITAPIDFDGHIIRAEVKPNGNVVGGHSTVTGD
CT03        AGL----GIVAGLGRF----------------GLWGAKGA-TPVVTAEGRI--------GNSVFTDVNQTARPAAQANPN--QPTLI------------------ADRVDAKIAAKG-----TPHPNGNMADAHAEIGVI
CT02        AGL----GIVAGLGRF----------------GLWVGKGAGETAIAVPGRVQSRINIANGRTATTPLRDTGRPVSAGFDHVLQGHFG------------------VEVSNSRSVFTI-----TPSELKDVLQSSPVVKSP
clustal     ***    * * *:*                  *   ...*  . : . *           .:  * :  :         :  *                      ..   :                 ::  . . :

         281
CT01        VRVIPGTESVPNAQGVYSAKIEVADPANPGSYLPKTNNGGVSTMFPKSWTADRIKVEVDAAFQNRTVTGNKWNGTTP------------SGVRVEGYLSPKTTVYPKL
CT03        QKAFN--------EGKTVGSDMTMNVV--GKDVCGYCRGDIAAAASKS------------GLKSLTIQAKDDITGLPKTYYWEVGMKSIREKKIYWEVGMKSIREKKI
CT02        VMALP--------DGQFVRTVDVGKVI--G--TTNLKDGGVPTSV----------------LKIFTDRAGNLITTFP----------------------IKAVD----
clustal       .:         :*    .  . .    *        *.:.:                  ::  *  . .     *                       *:
```

Figure S3. CdiA C-terminal alignments highlight C-tip diversity. Amino acid alignment of Class V (A) and Class II (B) CdiA C-termini was performed using sequence immediately after the DUF637 or PT-VENN domains respectively. Predicted TD are highlighted in different colors: TD1, TD2, TD3, TD4, TD5, TD6, TD7, TD8, TD9. "*" indicate identical residues, ":" are highly similar residues and "." are weakly similar residues in the Gonnet PAM 250 matrix.

```
            1 |------------------------------------------------------------ CdiA1 --------------------------------------------------------------
PABL012       ATGGACATCCGCAGCCCGCTGAACCAGTGCATCGCCCTGTCCCTGGCCGGCATCCTGTTCCTCAACCCGATCGTCGCCGCGGCGGCGGGGCTGGCGCTGGACAAGGCCGCCGGCGGCAACACCGGCCTGG
PABL001       ATGGACATCCGCAGCCCGCTGAACCAGTGCATCGCCCTGTCCCTGGCCGGCATCCTGTTCCTCAACCCGATCGTCGCCGCGGCGGCGGGGCTGGCGCTGGACAAGGCCGCCGGCGGCAACACCGGCCTGG
clustal       **********************************************************************************************************************************

          131 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GCCAGGCGGGCAACGGGGTGCCCATCGTCAATATCGCCACGCCCAACGGCGCCGGGCTGTCGAACAACCATTTCCGCGACTACAACGTCGGCGCCAACGGGCTGATCCTCAACAACGCTACCGGCAAGAC
PABL001       GCCAGGCGGGCAACGGGGTGCCCATCGTCAATATCGCCACGCCCAACGGCGCCGGGCTGTCGAACAACCATTTCCGCGACTACAACGTCGGCGCCAACGGGCTGATCCTCAACAACGCTACCGGCAAGAC
clustal       **********************************************************************************************************************************

          261 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CCAGGGTACCCAGCTCGGCGGGATCATCCTCGGCAACCCCAACCTCAAGGGCCAGGCGGCGCAGGTGATCCTCAACCAGGTCACCGGCGGCAACCGCAGCACCCTGGCCGGCTACACCGAGGTGGCCGGG
PABL001       CCAGGGTACCCAGCTCGGCGGGATCATCCTCGGCAACCCCAACCTCAAGGGCCAGGCGGCGCAGGTGATCCTCAACCAGGTCACCGGCGGCAACCGCAGCACCCTGGCCGGCTACACCGAGGTGGCCGGG
clustal       **********************************************************************************************************************************

          391 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CAGTCGGCGCGGGTGATCGTCGCCAACCCGCACGGCATCACCTGCCAGGGCTGCGGCTTCATCAACACGCCGCGCGCGACCCTCACCACCGGCAAGCCGATCATGGACGGCCAGCGCCTGGAGCGCTTCC
PABL001       CAGTCGGCGCGGGTGATCGTCGCCAACCCGCACGGCATCACCTGCCAGGGCTGCGGCTTCATCAACACGCCGCGCGCGACCCTCACCACCGGCAAGCCGATCATGGACGGCCAGCGCCTGGAGCGCTTCC
clustal       **********************************************************************************************************************************

          521 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       AGGTGGATGGCGGCGACATCGTCGTCGAAGGCGCCGAACTGAACGTCGGCAACCTCGAACAGTTCGACCTGATCACCCGCAGCGCCAAGCTCAACGCCAAGCTCTACGCGAAGAACCTCAACATCGTCAC
PABL001       AGGTGGATGGCGGCGACATCGTCGTCGAAGGCGCCGAACTGAACGTCGGCAACCTCGAACAGTTCGACCTGATCACCCGCAGCGCCAAGCTCAACGCCAAGCTCTACGCGAAGAACCTCAACATCGTCAC
clustal       **********************************************************************************************************************************

          651 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CGGCCGCAACGACGTCCAGGCCGACAGCCTGCAGGCCACGCCGCGCGCCGCCGATGGCAGCGAGAAGCCGCAGCTGGCGATTGACAGCTCGGCCCTGGGCGGGATGTACGCCGGGGCGATCCGCCTGGTC
PABL001       CGGCCGCAACGACGTCCAGGCCGACAGCCTGCAGGCCACGCCGCGCGCCGCCGATGGCAGCGAGAAGCCGCAGCTGGCGATTGACAGCTCGGCCCTGGGCGGGATGTACGCCGGGGCGATCCGCCTGGTC
clustal       **********************************************************************************************************************************

          781 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GGCACCGAGCAGGGCGTGGGGGTGAAGCTGGCCGGCGACATGGCCGCCAGCGGCGGCGACATCCGCATCGACGCCAGCGGCAAGCTGAGTCTGGCCCAGGCCTCCAGCCAGGGCGACCTGAAGATCGCGG
PABL001       GGCACCGAGCAGGGCGTGGGGGTGAAGCTGGCCGGCGACATGGCCGCCAGCGGCGGCGACATCCGCATCGACGCCAGCGGCAAGCTGAGTCTGGCCCAGGCCTCCAGCCAGGGCGACCTGAAGATCGCGG
clustal       **********************************************************************************************************************************

          911 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CCCAGGCCGTGGAGCTGAATGGCAAGACCTACGCCGGCGGCAGCGCCCAGATTCGCAGCGCGGAGGAACTGGTCAACCGGCAGAGCCTGGCGGCGCGCGAACGCATCGCGCTGGAGGCGGCGCATATCGA
PABL001       CCCAGGCCGTGGAGCTGAATGGCAAGACCTACGCCGGCGGCAGCGCCCAGATTCGCAGCGCGGAGGAACTGGTCAACCGGCAGAGCCTGGCGGCGCGCGAACGCATCGCGCTGGAGGCGGCGCATATCGA
clustal       **********************************************************************************************************************************

         1041 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CAACGCCGGGGTGATCGAAGCCGGCGTCGAGCCAGACGAGCGGCGCAACGCGCGCGGCGACCTCGAGCTGCGCAGCGGCACCCTGCGCAACGCCGGCAGCCTGGTGGCCAGCCGCGCGCTGGAAGCGAAG
PABL001       CAACGCCGGGGTGATCGAAGCCGGCGTCGAGCCAGACGAGCGGCGCAACGCGCGCGGCGACCTCGAGCTGCGCAGCGGCACCCTGCGCAACGCCGGCAGCCTGGTGGCCAGCCGCGCGCTGGAAGCGAAG
clustal       **********************************************************************************************************************************

         1171 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GCGAGCCAGGCGCTGGACAACCAGGGCGGCAGCCTGAAGGGGGCGACCGTCCGGGTCGACGGCGGACACCTGGACAACCGTGGCGGCAAGCTGCTCGCCGAGGGCGAACTGCGGGTCGAGGCGAGCAGCC
PABL001       GCGAGCCAGGCGCTGGACAACCAGGGCGGCAGCCTGAAGGGGGCGACCGTCCGGGTCGACGGCGGACACCTGGACAACCGTGGCGGCAAGCTGCTCGCCGAGGGCGAACTGCGGGTCGAGGCGAGCAGCC
clustal       **********************************************************************************************************************************

         1301 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       TGGACAACCGCCAGGACGGCCTGTTGCAGAGCCGGGACCGCGCCGTGGTCAAGACCCGTGGCGATCTCGACAACCGTGGCGGCCAGGTGATCGGCCTGAACGATCTGGAGGTCGGCGCGGCGACGCTCGA
PABL001       TGGACAACCGCCAGGACGGCCTGTTGCAGAGCCGGGACCGCGCCGTGGTCAAGACCCGTGGCGATCTCGACAACCGTGGCGGCCAGGTGATCGGCCTGAACGATCTGGAGGTCGGCGCGGCGACGCTCGA
clustal       **********************************************************************************************************************************

         1431 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CAACGGCCAGCAAGGCCTGCTCGGCAGCCAGCAGTCCACCCGCGTCAGCGCCCAGGCGCTGGTCAACCGGGGGGACGGCGAAGTCTCCGGCAAGCGCGTCGAGGCCCGCGTCGGTAGCCTCGACAATCGC
PABL001       CAACGGCCAGCAAGGCCTGCTCGGCAGCCAGCAGTCCACCCGCGTCAGCGCCCAGGCGCTGGTCAACCGGGGGGACGGCGAAGTCTCCGGCAAGCGCGTCGAGGCCCGCGTCGGTAGCCTCGACAATCGC
clustal       **********************************************************************************************************************************

         1561 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GGCGGCAAGCTGATCGGCGACGACCTGCTGGTGGTCGCCAGCGGTGCCATCGACAACCGCCTCGGCTTGTTCTCCGCAGCCAACCGCCTCGACCTGCGGGCGCGCAGCCTGGACAACAGCGGCAAGGGCA
PABL001       GGCGGCAAGCTGATCGGCGACGACCTGCTGGTGGTCGCCAGCGGTGCCATCGACAACCGCCTCGGCTTGTTCTCCGCAGCCAACCGCCTCGACCTGCGGGCGCGCAGCCTGGACAACAGCGGCAAGGGCA
clustal       **********************************************************************************************************************************

         1691 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CGCTGAGCAGCCGGGGCGGCCTGGAGGTCAGCCTCGGCGGCCTGCTGGACAACCGCGATGAAGGCAACCTGCTCAGCCAGGGCGCGCAGCGCGTGACGGTGGGGCAACTGGACAACCGCGCCGGCGGCCT
PABL001       CGCTGAGCAGCCGGGGCGGCCTGGAGGTCAGCCTCGGCGGCCTGCTGGACAACCGCGATGAAGGCAACCTGCTCAGCCAGGGCGCGCAGCGCGTGACGGTGGGGCAACTGGACAACCGCGCCGGCGGCCT
clustal       **********************************************************************************************************************************

         1821 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GCTGTCGAGCCGCAGCGAGTTGAACGTCCACGGCGCCAGCCTGGACAACCGTGGCGGCGTGCTGGTGGCCGACGCCGGCCTGAGCGCCACGGGAGGCGCCTTCGACAACCGCGACGGCGGCAGCGCCAGC
PABL001       GCTGTCGAGCCGCAGCGAGTTGAACGTCCACGGCGCCAGCCTGGACAACCGTGGCGGCGTGCTGGTGGCCGACGCCGGCCTGAGCGCCACGGGAGGCGCCTTCGACAACCGCGACGGCGGCAGCGCCAGC
clustal       **********************************************************************************************************************************

         1951 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GGCAAGGCTGGCGTGCGCGTGGAGGTCGCCAGCCTGCGCAACGACCAGGGTGGCAAGCTGCTCAGCGATGGCCGCCTGGACCTCGCAGCGAACGCCGTCGGCAACGCCGGAGGGCGTATCGCCGCCAAGG
PABL001       GGCAAGGCTGGCGTGCGCGTGGAGGTCGCCAGCCTGCGCAACGACCAGGGTGGCAAGCTGCTCAGCGATGGCCGCCTGGACCTCGCAGCGAACGCCGTCGGCAACGCCGGAGGGCGTATCGCCGCCAAGG
clustal       **********************************************************************************************************************************

         2081 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GCGACCTGCAGGCGACGCTTGGCAGCCTGGCCCAGCAAGGTGGCGAACTGGTCAGCGAAAAGACCCTGAAGGTCGCGGCCGACACGCTCGACAACAGCCAGTCCGGGCTGATCGCCGCGAATGGCGGCAT
PABL001       GCGACCTGCAGGCGACGCTTGGCAGCCTGGCCCAGCAAGGTGGCGAACTGGTCAGCGAAAAGACCCTGAAGGTCGCGGCCGACACGCTCGACAACAGCCAGTCCGGGCTGATCGCCGCGAATGGCGGCAT
clustal       **********************************************************************************************************************************

         2211 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CGCTATCGAGGCGCGGCAGGTCGACAACCGCGCCGGCGAGATTTCCAGCACCTCGAGGGTCGCCGTGAACGCCCGCGAGCAACTGGACAACCGCGGCGGCAAGGTCATCGGCGACAGCGGCCTGCGCCTC
PABL001       CGCTATCGAGGCGCGGCAGGTCGACAACCGCGCCGGCGAGATTTCCAGCACCTCGAGGGTCGCCGTGAACGCCCGCGAGCAACTGGACAACCGCGGCGGCAAGGTCATCGGCGACAGCGGCCTGCGCCTC
clustal       **********************************************************************************************************************************

         2341 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       ACCGTGCAGCGCCTGCTGAACCAGGCCAAGGGGGTGCTGGCCGGGCGCGACGGCCTGAGCCTGGACGGCGGCGAACTGTTCAACGGCGACGGCGGTCGGCTCGACAGCCAGAACAGCCTGAGCGTGAGCC
PABL001       ACCGTGCAGCGCCTGCTGAACCAGGCCAAGGGGGTGCTGGCCGGGCGCGACGGCCTGAGCCTGGACGGCGGCGAACTGTTCAACGGCGACGGCGGTCGGCTCGACAGCCAGAACAGCCTGAGCGTGAGCC
clustal       **********************************************************************************************************************************

         2471 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       TCGGCGGCGTGCTGGACAACCAGGGCGGCGCGCTGGTCAGCGAAGGCAGCCTGACGGCGCGCGCCGCGCGCCTGGACAACCGTGGCGGGACCTTCTCCAGCGCCGGTGCGCTGGCGCTGACCAGCCAGGC
PABL001       TCGGCGGCGTGCTGGACAACCAGGGCGGCGCGCTGGTCAGCGAAGGCAGCCTGACGGCGCGCGCCGCGCGCCTGGACAACCGTGGCGGGACCTTCTCCAGCGCCGGTGCGCTGGCGCTGACCAGCCAGGC
clustal       **********************************************************************************************************************************

         2601 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       CGTGCTGGACAACCAGGGCGGCAGGCTGCTCAGCGATGCCGGCGTGACGCTGCAGGGCGCCAGCCTCGACAACAGCCGTTCCGGCGTGATCAGCGCCAAGGGCGCGGTGGATATCCGCACCGGCGTACTG
PABL001       CGTGCTGGACAACCAGGGCGGCAGGCTGCTCAGCGATGCCGGCGTGACGCTGCAGGGCGCCAGCCTCGACAACAGCCGTTCCGGCGTGATCAGCGCCAAGGGCGCGGTGGATATCCGCACCGGCGTACTG
clustal       **********************************************************************************************************************************


         2731 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012       GACAACAGCCGCAACGGCGGCATCGGCAGCAACGCCGGCATCACCCTGGTGGCCGCCCGGCTGGACAACGGCCAGCAGGGCCGGGTCAGCGCCAAGGGCCTGCTCGACGCCAACCTGAAAGGCCTCGACC
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PABL001         GACAACAGCCGCAACGGCGGCATCGGCAGCAACGCCGGCATCACCCTGGTGGCCGCCCGGCTGGACAACGGCCAGCAGGGCCGGGTCAGCGCCAAGGGCCTGCTCGACGCCAACCTGAAAGGCCTCGACC
clustal         **********************************************************************************************************************************

           2861 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         AGCGCGGAGGCGGCGTCCTGGTCAGCGAAACCGGCGTCACCCTCGACCTCAATGGCGGCACGCTGGTCAACCGCGACGGCGGCCTGATCGCCACGCCCGGCGCGCTGCTGCTGCGCCAGCTCGGCGCGGT
PABL001         AGCGCGGAGGCGGCGTCCTGGTCAGCGAAACCGGCGTCACCCTCGACCTCAATGGCGGCACGCTGGTCAACCGCGACGGCGGCCTGATCGCCACGCCCGGCGCGCTGCTGCTGCGCCAGCTCGGCGCGGT
clustal         **********************************************************************************************************************************

           2991 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GGACAACGGCGCCGGCGGGGAAATCTCCAGCGACCGCGCCTTCACCCTCGCCGCCGCCAGCCTGGACAACCGCGGCGGGCGCCTGATCGGCGCCGCCAGCCTGACCCTGCGCATCGCCCAGGCCCTGGAC
PABL001         GGACAACGGCGCCGGCGGGGAAATCTCCAGCGACCGCGCCTTCACCCTCGCCGCCGCCAGCCTGGACAACCGCGGCGGGCGCCTGATCGGCGCCGCCAGCCTGACCCTGCGCATCGCCCAGGCCCTGGAC
clustal         **********************************************************************************************************************************

           3121 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         AACAGCCTGGGCGGGGTGATCTCCGGCGCCGCCGGCCTGGACATCGCGGCCGCTCGCCTGGACAACAGCGCCAAGGGCACCCTGGCCAGCCGCGCCGGCATCGACCTGCGCGTCGATGGCGCGTTGGACA
PABL001         AACAGCCTGGGCGGGGTGATCTCCGGCGCCGCCGGCCTGGACATCGCGGCCGCTCGCCTGGACAACAGCGCCAAGGGCACCCTGGCCAGCCGCGCCGGCATCGACCTGCGCGTCGATGGCGCGTTGGACA
clustal         **********************************************************************************************************************************

           3251 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         ACCACGCCGAAGGCACCGTTTCCGGCGCTCGCCTGACGCTCGCCAGCGCCTCGCTGGACAACAGCGGCAAGGGCCTGCTCTCCGGCAACGCCGGCCTGAGCGTCGTCACTGGTGCGCTGGACAACGCCGA
PABL001         ACCACGCCGAAGGCACCGTTTCCGGCGCTCGCCTGACGCTCGCCAGCGCCTCGCTGGACAACAGCGGCAAGGGCCTGCTCTCCGGCAACGCCGGCCTGAGCGTCGTCACTGGTGCGCTGGACAACGCCGA
clustal         **********************************************************************************************************************************

           3381 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GGGTGGCCAACTGATCAGCCAGGGCGTGCTGGACGTCAGCAGCGCCGACCTCGACAACCGTGGCGGCGCCCTCAGTGGCAAGCAGTCGCTGCGCCTGAGCGCCGCCAACCTGGACAACCGTGGCGGCCTG
PABL001         GGGTGGCCAACTGATCAGCCAGGGCGTGCTGGACGTCAGCAGCGCCGACCTCGACAACCGTGGCGGCGCCCTCAGTGGCAAGCAGTCGCTGCGCCTGAGCGCCGCCAACCTGGACAACCGTGGCGGCCTG
clustal         **********************************************************************************************************************************

           3511 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CTCACCAGCGACGGCGAACTGGAACTGACGGCAGGGCGCGTCGATTCCGCCGACGGCGGCGAAATCTCCGCCCGGGGCGACCTGCGCCTGACGGTCGAGCGCCTGGTGCAACGCCAGGGCCGGCTGATCG
PABL001         CTCACCAGCGACGGCGAACTGGAACTGACGGCAGGGCGCGTCGATTCCGCCGACGGCGGCGAAATCTCCGCCCGGGGCGACCTGCGCCTGACGGTCGAGCGCCTGGTGCAACGCCAGGGCCGGCTGATCG
clustal         **********************************************************************************************************************************

           3641 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GCGAGCGCGGCGTCAGTCTCGACCTGCGGGGCGGCGACCTGGACAACCAGGGCGGCCTGATCAGTGCCCGCGGCCCGCTGAGCATCGAGCGGCTGAACGTCCTCGACAACCGCCAGGGCGGCGAGATTTC
PABL001         GCGAGCGCGGCGTCAGTCTCGACCTGCGGGGCGGCGACCTGGACAACCAGGGCGGCCTGATCAGTGCCCGCGGCCCGCTGAGCATCGAGCGGCTGAACGTCCTCGACAACCGCCAGGGCGGCGAGATTTC
clustal         **********************************************************************************************************************************

           3771 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CAGCCAGCAGGGCTTCGAGCTGCTGGCCAGGCGCATCGACAACGGCCAGCAGGGGCGCATCATCAGCGCCGGGAAACTGCGCCTGGACGCCGACGCGCTGGGCAACGCCGGCGCCGGCCTGCTCTCCGGA
PABL001         CAGCCAGCAGGGCTTCGAGCTGCTGGCCAGGCGCATCGACAACGGCCAGCAGGGGCGCATCATCAGCGCCGGGAAACTGCGCCTGGACGCCGACGCGCTGGGCAACGCCGGCGCCGGCCTGCTCTCCGGA
clustal         **********************************************************************************************************************************

           3901 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         TGGCAGGGCCTGACGGTGACAGGCGGGAGCCTGGACAACAGCGCCGGCGGCACCCTTTCGAGCAAGGACGGCGAGCTGGCCATCAGCCTCGGCGGCGCGCTGGACAACCACGGCCAGGGCGCGCTGGTCA
PABL001         TGGCAGGGCCTGACGGTGACAGGCGGGAGCCTGGACAACAGCGCCGGCGGCACCCTTTCGAGCAAGGACGGCGAGCTGGCCATCAGCCTCGGCGGCGCGCTGGACAACCACGGCCAGGGCGCGCTGGTCA
clustal         **********************************************************************************************************************************

           4031 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GCAAGGGCGCGCAACGGATCGACGCCGCCAGCCTGGATAACGCCCAGGGCATTGTCTCCGGCGAAAGCGACGTGACCCTGAGCATCGCCGGGAAGCTGGACAACGGCCAGGGCGGCCTGGTCTCGGCGCA
PABL001         GCAAGGGCGCGCAACGGATCGACGCCGCCAGCCTGGATAACGCCCAGGGCATTGTCTCCGGCGAAAGCGACGTGACCCTGAGCATCGCCGGGAAGCTGGACAACGGCCAGGGCGGCCTGGTCTCGGCGCA
clustal         **********************************************************************************************************************************

           4161 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GCGCGCGCTGAGCTTCGAGCGCGACGATACGCTGCTGAACAACGCCGGCGGCCGGATCAACGGCGGCAGCCTGCTGCTCAAGGGCGCCAGCCTGGATAACAGCGACGGCCAGTTGATCAGTCAGGGCCGG
PABL001         GCGCGCGCTGAGCTTCGAGCGCGACGATACGCTGCTGAACAACGCCGGCGGCCGGATCAACGGCGGCAGCCTGCTGCTCAAGGGCGCCAGCCTGGATAACAGCGACGGCCAGTTGATCAGTCAGGGCCGG
clustal         **********************************************************************************************************************************

           4291 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CTCGACGCCATCCTCGGCGGCGCCCTGGTCAACGCCGGCGCGGCGCGCCTGGCCAGCGGCGGCGACCTGCTGCTGCGCAGCGCCAGCGTCGACAACCGCGGCGGCAAGCTGGTCAGCCAGGGGCTGCTGG
PABL001         CTCGACGCCATCCTCGGCGGCGCCCTGGTCAACGCCGGCGCGGCGCGCCTGGCCAGCGGCGGCGACCTGCTGCTGCGCAGCGCCAGCGTCGACAACCGCGGCGGCAAGCTGGTCAGCCAGGGGCTGCTGG
clustal         **********************************************************************************************************************************

           4421 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         AGATCAGCGCCGGCAGCCTCGACAACAGCGCCTCCGGCACCCTCGCCAGCCAGGCCGACATGAGCCTGCGCCTGGTCGGCGGCGCCCTGCGCAACCAGCAGGACGGCCTGATCTTCAGCCAGGCCGGCGC
PABL001         AGATCAGCGCCGGCAGCCTCGACAACAGCGCCTCCGGCACCCTCGCCAGCCAGGCCGACATGAGCCTGCGCCTGGTCGGCGGCGCCCTGCGCAACCAGCAGGACGGCCTGATCTTCAGCCAGGCCGGCGC
clustal         **********************************************************************************************************************************

           4551 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CCTCGAGGTGCAGGCCGGCAGCCTGGACAACCGCCAGGGCACGCTCCAGGCCCAGGGTGACAACCGGCTGCGTATCGGCGGCGCGCTGGACAACCAGGGCGGCCGCCTGGACAGCCGGGCCGGCAACCTC
PABL001         CCTCGAGGTGCAGGCCGGCAGCCTGGACAACCGCCAGGGCACGCTCCAGGCCCAGGGTGACAACCGGCTGCGTATCGGCGGCGCGCTGGACAACCAGGGCGGCCGCCTGGACAGCCGGGCCGGCAACCTC
clustal         **********************************************************************************************************************************

           4681 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GACCTGCAGAGCGGCAGCCTCGACAACGGCGCCGGCGGCGTGCTCAACAGCGCCAAGGGTTGGCTGAAGCTGGTCACCGGGCTGTTCGACAACAGCGCCGGCGTCACCCAGGCGCAGTCGCTGGAGATTC
PABL001         GACCTGCAGAGCGGCAGCCTCGACAACGGCGCCGGCGGCGTGCTCAACAGCGCCAAGGGTTGGCTGAAGCTGGTCACCGGGCTGTTCGACAACAGCGCCGGCGTCACCCAGGCGCAGTCGCTGGAGATTC
clustal         **********************************************************************************************************************************

           4811 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         GCGCCGGGCAAGGCGTGCGCAACCAGCAGGGCCATCTCTCGGCGCTGGGCGGCGACAACCGCATCGTCACCGCCGACTTCGACAACCAGGGCGGCGGCCTCTACGCCAGCGGCCTGCTCAGCCTCGACGG
PABL001         GCGCCGGGCAAGGCGTGCGCAACCAGCAGGGCCATCTCTCGGCGCTGGGCGGCGACAACCGCATCGTCACCGCCGACTTCGACAACCAGGGCGGCGGCCTCTACGCCAGCGGCCTGCTCAGCCTCGACGG
clustal         **********************************************************************************************************************************

           4941 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CCAGCGCTTCCTCAACCAGGGCGCGGCGGCGGGCCAGGGCGGCAAGGTCGGCGCCGGGCGCATCGACTTCAGCCTGGCCGGCGCGCTGGCCAACCGCTTCGGCCAGTTGGAAAGCGAAAGCGAGCTGCAC
PABL001         CCAGCGCTTCCTCAACCAGGGCGCGGCGGCGGGCCAGGGCGGCAAGGTCGGCGCCGGGCGCATCGACTTCAGCCTGGCCGGCGCGCTGGCCAACCGCTTCGGCCAGTTGGAAAGCGAAAGCGAGCTGCAC
clustal         **********************************************************************************************************************************

           5071 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CTGCGCGCCGCCGCGATCGACAACAGCGGCGGCAGCCTGCGCGCCCTTGGCCGCAGCGGCAGCACGCGGCTGGTCGCTGGCGGCCTGAACAACGCCTACGGCGTGCTGGAAAGCGCCAACCAGGACCTCG
PABL001         CTGCGCGCCGCCGCGATCGACAACAGCGGCGGCAGCCTGCGCGCCCTTGGCCGCAGCGGCAGCACGCGGCTGGTCGCTGGCGGCCTGAACAACGCCTACGGCGTGCTGGAAAGCGCCAACCAGGACCTCG
clustal         **********************************************************************************************************************************

           5201 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         ACCTGCAACTGGGCAGCCTGGCCAACGCCGGTGGGCGCATCCTCCACACCGGCAACGGCACCTTCGGCCTGGATTCCGGGCAGGTGATCCGCGCCGGCGGCGAACTGACCACCAATGGCTTGCTGGACAT
PABL001         ACCTGCAACTGGGCAGCCTGGCCAACGCCGGTGGGCGCATCCTCCACACCGGCAACGGCACCTTCGGCCTGGATTCCGGGCAGGTGATCCGCGCCGGCGGCGAACTGACCACCAATGGCTTGCTGGACAT
clustal         **********************************************************************************************************************************

           5331 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         CCGCGCCAGCGAATGGACCAACAGCAGCGTGCTGCAAGCCGGACGCCTGAACCTGGACATCGGCACCTTCCGCCAGACGGCCGAGGGCAAGCTGCTGGCGGTGCAGTCCTTCACTGGCCGCGGCGGCGAC
PABL001         CCGCGCCAGCGAATGGACCAACAGCAGCGTGCTGCAAGCCGGACGCCTGAACCTGGACATCGGCACCTTCCGCCAGACGGCCGAGGGCAAGCTGCTGGCGGTGCAGTCCTTCACTGGCCGCGGCGGCGAC
clustal         **********************************************************************************************************************************

           5461 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         TGGAGCAACGACGGCCTGCTGGCCAGCGACGGCAGCTTGCGACTCGAGCTGAGCGGCGGCTACCGTGGCAACGGCCGCGCCACCAGCCTCGGCGACTTCGCCCTGAACGCCGCCAGCCTCGACCTCGGCA
PABL001         TGGAGCAACGACGGCCTGCTGGCCAGCGACGGCAGCTTGCGACTCGAGCTGAGCGGCGGCTACCGTGGCAACGGCCGCGCCACCAGCCTCGGCGACTTCGCCCTGAACGCCGCCAGCCTCGACCTCGGCA
clustal         **********************************************************************************************************************************

           5591 ------------------------------------------------------------ CdiA1 ---------------------------------------------------------------
PABL012         ATGCCGCCAGCCTCGCCGGCGGTGCCAATGTCACGCTCGGCGCCGGCAACCTGCTGGTCAACCGTGGGCGGATCACCGCCGCCGGCGACCTCGTGGCCAGCGCCGCGAGCCTGAACAACTACGGCACCCT
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PABL001        ATGCCGCCAGCCTCGCCGGCGGTGCCAATGTCACGCTCGGCGCCGGCAACCTGCTGGTCAACCGTGGGCGGATCACCGCCGCCGGCGACCTCGTGGCCAGCGCCGCGAGCCTGAACAACTACGGCACCCT
clustal        **********************************************************************************************************************************

          5721 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        GGGCGGCGGCGGCAACCTGCGATTGAACGCGCCCGCCCTGCTCAACGAGCGCGGGTTGCTGTTCAGTGGCGCCGACATGACCCTGCGCGCCGGCGACATCACCAACCTCTACGGGGATGTGTACAGCCTC
PABL001        GGGCGGCGGCGGCAACCTGCGATTGAACGCGCCCGCCCTGCTCAACGAGCGCGGGTTGCTGTTCAGTGGCGCCGACATGACCCTGCGCGCCGGCGACATCACCAACCTCTACGGGGATGTGTACAGCCTC
clustal        **********************************************************************************************************************************

          5851 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        GGCAGGCTGGATATCGCCCGCGACGATGCCGGCAACCGTGCCGCCAGCCTGCGCAACCTTTCCGGGGTGATCGAGAGCGGCAAGGACTTCAGCCTGCGTGCCAGCCTGATCGAGAACCGTCGCGCCGTGC
PABL001        GGCAGGCTGGATATCGCCCGCGACGATGCCGGCAACCGTGCCGCCAGCCTGCGCAACCTTTCCGGGGTGATCGAGAGCGGCAAGGACTTCAGCCTGCGTGCCAGCCTGATCGAGAACCGTCGCGCCGTGC
clustal        **********************************************************************************************************************************

          5981 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        TGGAAAGCAAGTCGGGCCTGTACACCGCGAAGATGGAGCAGACCGCCTGCATCGAAGGCGTCAACGCGGGCGACTGCAGCGGCAAGCGCAACGCCATCTGGACCATCACCCAGCGCGACAAGACCGAGGT
PABL001        TGGAAAGCAAGTCGGGCCTGTACACCGCGAAGATGGAGCAGACCGCCTGCATCGAAGGCGTCAACGCGGGCGACTGCAGCGGCAAGCGCAACGCCATCTGGACCATCACCCAGCGCGACAAGACCGAGGT
clustal        **********************************************************************************************************************************

          6111 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        CACCGCCAGCAGCGCCATGGGGCAACTGCTGGCCGGAGGCGACTTCGCCATCGACGGCGGCACCCTGAACAACCTTTCCAGTCTGATCGGCAGCGGCGGCAACCTCACCGCCAACCTCGAAGTCCTCGAC
PABL001        CACCGCCAGCAGCGCCATGGGGCAACTGCTGGCCGGAGGCGACTTCGCCATCGACGGCGGCACCCTGAACAACCTTTCCAGTCTGATCGGCAGCGGCGGCAACCTCACCGCCAACCTCGAAGTCCTCGAC
clustal        **********************************************************************************************************************************

          6241 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        AACCAGGGCCTGGAAACCGGCGAGCTGGAAACCATCCGCGTGCTGCGTACCGCTCGCGGCGGCGATATCGGCGGCATCGACCAGAAGTCGCGCAACTTCACCAACCTCTACTGGTACCAGAGCGCCAATT
PABL001        AACCAGGGCCTGGAAACCGGCGAGCTGGAAACCATCCGCGTGCTGCGTACCGCTCGCGGCGGCGATATCGGCGGCATCGACCAGAAGTCGCGCAACTTCACCAACCTCTACTGGTACCAGAGCGCCAATT
clustal        **********************************************************************************************************************************

          6371 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        TCGACCCGGCGCGCGCGGGCGAGATCCCCGCCGCGCTCAACGCGATCCTCAGCGACTGGTCCTTCGAGTACGAATTCCCGAGCAAGGGGCCGACCCCGATCAGCAGTGGCGACCAGTCCTACGCAGCGGT
PABL001        TCGACCCGGCGCGCGCGGGCGAGATCCCCGCCGCGCTCAACGCGATCCTCAGCGACTGGTCCTTCGAGTACGAATTCCCGAGCAAGGGGCCGACCCCGATCAGCAGTGGCGACCAGTCCTACGCAGCGGT
clustal        **********************************************************************************************************************************

          6501 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        GATCCAGGCCGCCGGCGACGTCACGGTCAATGCCAGCACGCGCATCGACAACGGCGTCACCCGCCCCGGCTACACCTTCGTCGGCAGCGGCCGCCAGGTGGGCGACAGCGCGGTGGGCGGCAGCGGGGTT
PABL001        GATCCAGGCCGCCGGCGACGTCACGGTCAATGCCAGCACGCGCATCGACAACGGCGTCACCCGCCCCGGCTACACCTTCGTCGGCAGCGGCCGCCAGGTGGGCGACAGCGCGGTGGGCGGCAGCGGGGTT
clustal        **********************************************************************************************************************************

          6631 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        TCGGTGGTCGTGCCGCTGACCTCGCAACTGCCGCCCGACTTGGCGCGGCGCCAGGTCAACCCGGTTACCCTGCCCGGCTTCAGCCTGCCCCAGGGTGACAACGGCCTGTTCCGTCTCAGCTCGCGCTTCG
PABL001        TCGGTGGTCGTGCCGCTGACCTCGCAACTGCCGCCCGACTTGGCGCGGCGCCAGGTCAACCCGGTTACCCTGCCCGGCTTCAGCCTGCCCCAGGGTGACAACGGCCTGTTCCGTCTCAGCTCGCGCTTCG
clustal        **********************************************************************************************************************************

          6761 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        CCGAGGACGGCAATGGCAGCGCCGCGCTCGGTGCCGGCGCCGACCGCACCCAGGGCGGTAGCGGCGTCTCGGTCGGCCAGCAAGGCGCCGGCAACGCCGCCGGTACCTGGCAGGGCCAGGGCGTGCGAGT
PABL001        CCGAGGACGGCAATGGCAGCGCCGCGCTCGGTGCCGGCGCCGACCGCACCCAGGGCGGTAGCGGCGTCTCGGTCGGCCAGCAAGGCGCCGGCAACGCCGCCGGTACCTGGCAGGGCCAGGGCGTGCGAGT
clustal        **********************************************************************************************************************************

          6891 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        CGACGGCCTGGCTGGCGCGGCCAACGTCCAGGGTCAGGGCGGCAGCACGCTCAGCGGTAGCCTGCCGGGCGTCGCCCGGGTCCAGGGCGTGCCCGGCAACGCCACGCCGAGCGCCAGCCACAAGTACCTG
PABL001        CGACGGCCTGGCTGGCGCGGCCAACGTCCAGGGTCAGGGCGGCAGCACGCTCAGCGGTAGCCTGCCGGGCGTCGCCCGGGTCCAGGGCGTGCCCGGCAACGCCACGCCGAGCGCCAGCCACAAGTACCTG
clustal        **********************************************************************************************************************************

          7021 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        ATCGAGACCAACCCGGCGCTCACCGAACTGAAGCAGTTCCTCAACTCGGACTACCTGCTCAGCGGCCTGGGCATGAACCCGGACGATAGCAAGAAGCGTCTCGGCGACGGTCTCTACGAGCAGCGGCTGA
PABL001        ATCGAGACCAACCCGGCGCTCACCGAACTGAAGCAGTTCCTCAACTCGGACTACCTGCTCAGCGGCCTGGGCATGAACCCGGACGATAGCAAGAAGCGTCTCGGCGACGGTCTCTACGAGCAGCGGCTGA
clustal        **********************************************************************************************************************************

          7151 ------------------------------------------------------------- CdiA1 --------------------------------------------------------------
PABL012        TCCGCGACGCGGTGGTGGCGCGCACCGGCCAGCGCTACATCGACGGGCTGAGCAGCGACGAGGCGCTGTTCCGCTACCTGATGGACAACGCCATCGCTTACAAGGACCAACTGCACCTGCAACTGGGTGT
PABL001        TCCGCGACGCGGTGGTGGCGCGCACCGGCCAGCGCTACATCGACGGGCTGAGCAGCGACGAGGCGCTGTTCCGCTACCTGATGGACAACGCCATCGCT--------------------------------
clustal        **************************************************************************************************

          7281 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        GGGCCTGAGCGCGGAGCAGATGGCGGCGCTGACCCACGACATCGTCTGGCTGGAAGAGGTCGAGGTGAACGGCGAGAAGGTCCTCGCGCCGGTGGTCTACCTGGCCCAGGCGGAGGGTCGGCTGGCACCC
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          7411 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        AACGGTGCGCTGATCCAGGGCCGCGACGTGAAGCTGGTGAGCGGCGGCGACCTGCATAACGTCGGCACCCTGCGCGCGCGGAACGACCTCTCGGCGACGGCCGACAACCTCGACAACAGCGGCCTGATCG
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          7541 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        AGGCCGGCAAGCGCCTCGACCTGCTCGCCGGCGACTCGATCCGCAACCGCCAGGGCGGGGTCATCGCCGGGCGTGACGTGAGCCTCACCGCGCTGACCGGCGACGTGATCAACGAACGCAGCGTGACCCG
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          7671 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        CTACGACAGCGCGCTCGACGGCCGCACCTGGGAACGCAGCTTCGCCGACAGCGCCGCGCGGGTGGAGGCGGCGAACAGCCTGAACGTCCAGGCCGGACGCGACATCGCCAACCTCGGCGGGGTGCTGCAG
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          7801 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        AGCCGCGGCGACCTCAGCCTCGACGCCGGACGCGACGTCACCGTCGCCGCCGTCGAGGACCGCCAGGGCCAGACCCGCTGGAGCACGTCGCGGCTCCAGAGCGTGACCCAGCTCGGCGCCGAAGTCAGCG
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          7931 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        CCGGGCGGGACCTGAACGTCAGCGCCGGCCGCGACTTGACGGCGGTGGCCAGCACCCTCGAAGCGCGCCGCGACATCGCCCTCTCCGCCGGGCGCGACGTGACCCTGGCGGCGGCGGCGAACGAGGAGCA
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          8061 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        CAGCTTCGCCACCGGCAAGAAGGTGACGGCGAAGAACGATCGGGTGGAACACCAATCGACCGTGGTCAGCGCCGGCGGCGATCTCAGCGTGCAAGGCGGCAATGACGTGACCTTCGTTGCCAGTCAGGCG
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          8191 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        AAGGCCAGCAACGAGGCCTATCTGTACGCCGGCAACGACCTCAATCTGCTGGCGGCTCACGACGAAAGCTATTCCTACTACTCGAAGAAGAAAAAAGGCTCGTTCGGGCGCAGCAGTAGCCGGATGAGCG
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

          8321 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012        AGAGCGAAGCCAGTACCGTGGTGTCGTCGTCGATCCAGGCGGGACAAGGGGCGGAACTGGTCGCCAAGCGTGACGTCAACGTCGAGGCCTCTTCCGCCTCCAGCACGAAGGGCGAGCTGGCGGTCGTGGC
PABL001        ----------------------------------------------------------------------------------------------------------------------------------
clustal

         8451 ------------------------------------------------------------- CdiA1 class II ----------------------------------------------------
PABL012        GGGGCGCGATGTGAACCTCACGGCAGCTGAGAACAGCTACTCCAGCGTGTCCGCGAAATCCAAGTCCGGAGGCTTGGGGCTGTCATCCACCAGCAAGGCCAACGCCCAGTCCTCTTCCTACACCAGCGTT
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PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         8581 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CAGGGCGCCACGTTGAGTGGCGATACCACCGTGGTGCAGGCGGGAAGGGACATCTCGGTGGCCGCCAGCAATGTGGTTTCTACCGGGAAGACTGCGCTGCGTGCCGGCAACGACATCATCATCGACAGCG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         8711 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       TGGCGGAGACGTCGGAGTCGCATCGCAGCGAGTCGAAGAAGAAGTCCGGCCTGATGAGTTCCGGAGGGATCGGCATCACGCTCGGCACGGCGAAGAATGCCTCGACACAGGACACCCGTACCGTCGTCAA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         8841 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CCAGGGCAGCACCATCGGCAGTGTGCTCGGCGATGTCGACATGCGGGCGGGCAAGAACCTGTCTATCACGGCTTCGGATGTGGTGGCCGGCAAGGACATCAACCTCGTCGGGCAGAACGTGAGCATTCTC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         8971 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GCTGCCGACAACCAGAACGTCAGCGAGCAGACCCGCAAGACCAGCAAGAGCGGCTTGACGCTGGCCTTGTCGGGAACGGTCGGTAGCGCAATCGACGCCACCTACCAGAATGCCAAGCAGGCCAGGAACG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9101 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       AAGACGACAGTCGCCTTTCCGCGTTGCAGGGGATCAAGGCCGGCTTGAGCGGCGTCCAGGCCTGGCAGGCAGCTCAGCAGAGCGGCGGCATGACGGGCGAGAACAGCGCGCAGTTCGTCGGCATCAGCGC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9231 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       TTCGCTGGGCTCGCAGAAGTCCAGCTCTCGGCAGCGCCAGGAGCAGCAGATCAGCCAGGGAAGCACGCTCACCGCCGGTGGCAACCTGAACATTATCGCCACGGGTTCCGGGGCTGTCGGCGAAGACGGC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9361 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GACTTGCGCGTGCAAGGCAGCAAGCTGCAGGCTGGCAAGGACCTCCAACTGATCGCCAACCGCGACGTCGTGCTGGAAGCCGCGGCCAATACGCAGAAGCTCGATGGCAAGAACAAGAGCAGCGGCGGCG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9491 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CTGTCGGGGTAAGCGTCGGCGTTGGTTCGGGCGAGGCTGGCATCAGCATTTTCGCCAACGCCAACAAGGGCGCCGGCAAGGAAATCGGCAACGGCACCACCTGGACCGAAACCACCCTGGACGCGGGCCA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9621 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GAAGGCCAGCTTGGTCAGCGGGCGCGACACCACGCTGAAAGGGGCGCAGGTCAATGGTGAAAGCATCCTGGCGAAAGTGGGTCGTGACCTTACCCTGCAAAGCCTGCAGGATCGCGATTACTACGATTCC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9751 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       AAGCAGAAGAACGTCGGTGGTGGGGCGAGTTTGGCTATCGTTGGCCAGGGTGGCGGCGCCAACTTGAGTCTCAGCCAGAGCAAGCTGCATTCGAAGTACGACAGCGTGCAGGAGCAGACCGGGCTGTTCG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

         9881 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CCGGCAAGGGCGGCTTCCAGGTGGAGGTGGGCAAGCACACGCAGCTGGATGGCAGCGTGATCGCCAGCACCGCCGAAGCCGAGAAGAATCGCCTGAGCACAGGCTCCTTGGGCTGGAGCGAGATCCGTAA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10011 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CAAGGCCGAGTACAAGAGCCAACTTCAGAGTGTCAGTGTCAGCAGCGCCAACGATGGCGCCGGTGCGTTCGTCAGCAACATGCCTAGCGGCATGCTCATTGCCTACAACCACGGCGATAGTGCCAGCGGT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10141 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       ACCACGGGTTCGGCGATATCCGAAGGCACCCTGGAGGTTCGCGATCCGGCGCGCCAGCAACAGGATGTGGCGACGCTCAGCCGTGACCCGAGCCGCGCCAACGATAGCGTCAGTCCGATCTTCGACAAGG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10271 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       AGAAAGAGCAGAAGCGTCTGCAGCAGGTCCAACTGATCGGCGAGATCGGCACCCAGGCCATGGATATCCTGCGGACGCAGGGCCAACTCGACGCCGACAAGGCGGCGCGGGCCGAACTGGAAGCGCGGGG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10401 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       TATCTCCGCGCCGGACGCCGGCGCCAGCAAGCGGCAAGTCGAGGACTACCGCAAAGCGCTTCTGGGCACGAATGCCTACCAGGACATCATGGGCAAGTACGGCACCGGAGGCGACTACCAGAAGGCCGCC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10531 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CAGGCGGTGACCGCAGCCTTGCAAGGGCTGGCCGGCGGCGACATTGGCTCGGCGTTGGCGGGAGCTTCCTCGCCCTATGTGGCGGGCGTGATCAAGCAGGTGGCAGGCGACAATGACACGGCGCGGATCA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10661 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       TGGCCCATGCGGTTCTTGGCGCGGTGGTTGCGCAGGCCCAGGGCAATTCGGCTGCTGCGGGGGGCGCAGGAGCGGCGGGGAGCGAACTGGCGGCGCAGGTGATCAGCGAGCGACTGTACGGAACCCGGGA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10791 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       CAGCTCGACGCTGAACGAAGCGCAGAAGCAGACTATCACCGCGCTGGCCAGCCTGGCCGGCGGATTGGCCGGCTCCGTTGTCGATGGGAGCAGCGGAGGAGCCATTGCCGGGGCCGCAGGCGGGAAGAAC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        10921 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GCAACGGAAAACAACTTCCTTGGCGGCGGAACCCCGCCGGGCTTGATCAGCTATGGTCAGGCAGCGAGCTCCTTGACCGAGTACATGCGCAAGAACGGGGCGACAGCCGAGGAGATCACCCAGGCGCAAC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        11051 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GTGATCTGGCCCAGGGACAGGGCTTCGATGGCGTACAGCCAGCGAATGAGTTCATCAAGGCCTGGGGCGAGGCCATGGTTGCGGAAGCTGCCGGCCTTGGGATTGTTGCGGGGTTGGGTAGATTTGGGTT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        11181 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GTGGGGTGCAAAGGGAGCGACTCCTGTTGTAACTGCTGAGGGGCGAATCGGTAACTCAGTATTTACGGATGTTAACCAGACGGCTAGACCAGCAGCCCAGGCGAATCCCAACCAACCGACCTTGATTGCC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        11311 ------------------------------------------------------------- CdiA1 class II -----------------------------------------------------
PABL012       GATCGAGTGGACGCAAAGATAGCGGCTAAGGGGACGCCTCACCCGAATGGGAATATGGCGGATGCTCATGCAGAGATTGGCGTTATTCAGAAGGCATTTAATGAAGGTAAAACGGTAGGCTCCGATATGA
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PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal
        11441 ------------------------------------------------------------ CdiA1 class II ------------------------------------------------------
PABL012       CCATGAACGTAGTAGGTAAGGATGTTTGTGGATACTGCAGAGGTGATATTGCTGCGGCAGCTAGCAAGTCTGGTTTGAAATCTTTAACTATTCAAGCCAAGGATGATATTACAGGTTTGCCGAAGACGTA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

                                                                |------------------ CdiI ---------------------------------------------------------------
        11571 ---------------------------------------------|
PABL012       TTACTGGGAGGTAGGAATGAAGTCAATTAGAGAGAAAAAAATATGATTGTTCTTGGTGGGTATTTGATTGCTCCTGAGGCTAAAAGAACTCAATTTCCGGTGATGTTTGATCCTGACGAAGAAGAAGTTC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        11701 ------------------------------------------------------------- CdiI ---------------------------------------------------------------
PABL012       TGGAAGCGCTTTCTAAACTTCGCCACAGTTCGGGGGTGTTGGTTCTAAGAGTTAAGCCGGAACCTGAGATTGGCGCTTATGAAGTGGCGCTTCATGCAGAGAATGGACGATTTATAGTTATGCTTAGCCA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        11831 ------------------------------------------------------------- CdiI ---------------------------------------------------------------
PABL012       GCATGCTGAAGATGGTGAGCATGAGGTTTTCACGTTAAGAGGGGCTGGTGAAGGTAATGGATTTACTTATATTTTAGGCGAGGCATATCCTATGGCGGCAGTGACAGAAAATTTTGGGTTGATATGTAAT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        11961 -----------------------------------------------------|
PABL012       TGTTTCAAAAAATTTTTGCTAGAGAGGAAAGTGTCTTCTGATGTGTGGGTTTAATGTTTCAACGTAAATGAAATAATAAAGGGAATAAAGGGAATAAAGGGAATAAAGGGAATAAAGGGAGTTGGTTTAT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12091
PABL012       TTTCCCTACTCTAATTTTCTAAGCAGGGAGGCTCCAGCGCAGACGCCGTAAGGAGGCTCCGCGATGCCTAGGTAAGGGCGCATGGTTTAGCGAATTATTTGCTTTGAGCGTTTCAGAGTGGGCGCAGTCG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12221
PABL012       CCGAAACTAGAGTGGTAAAAATAAATCTGTCCATTTTCCTGTCCCTTTTTCTACATTTAGTCCGAGGTAGATCAGATTATGGACGAAAGGCAGAAAGTATTATGTGCACAGTTTGTTAAAATGGGATCTG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12351
PABL012       AGCAGGCTGCCGAATGGTTAGTAAACAGATATCCGGTAGACTCCATAGATTATGGTGAGGCTCTGTTGTTGATCCTGCATCGATCTTGGAGGCGATCCGACCAGAAGCGACTGGCTCAGCATTATTTTAG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12481
PABL012       AAAACTGCCTTTCTCTGGTGCGGGAGGGTATGAGGCGTTTGCTTCATTCATGTCTGTAAAGACTTTTCTGGAATGTGCTAGGGAACGCTTGCCAATGAGCGCTTCTGATGCAAGCTTGCTGCTGTATTAC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12611
PABL012       TTGACCCCTGTCCTTAACAAGTTTGCAAAAAACGAATCTGATCGACAGCTTATTATGAATTTTTTAAATGAAATACGGCCCTCATGATCATACTGATTTGCTACAATCCGCTGCTCTGCTGGGCCTGCTG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12741
PABL012       TTGTAGAAGTAAAAAATAAAGAAAGAATAAAGTGGGCAGATTTATTTTTCCTACTCTAATTTTCTAAGCAAGGAGGCTCCAGCGCAGACGCCGTAAGGAGGCTCCGCGATGCCTAGGCAAGGGCGAGTGG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        12871
PABL012       TTTTACCGAATTATCCGCTTCACATGGTCCAGCGGGGACACAGTCGCCAAGTGGTATTCGCCGAGGACGAGGACTACCAGCGTTACCTCTCCGATCGACGGAACCTCGAGGATGCCTTTGATAACAAGCT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13001
PABL012       CCATGCATTTTGCCGAGCATAAAGGGGATAGATTTATTTTCCCTACTCTAATTCTCTGAGCAGAGAGGCTCCAGTGCAGACACCGTGAGGAGGCTCCGCGATGCCCTAGGTAAGGGCGATTGGTTTAGCG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13131
PABL012       AGTTATTCGCTTTGAGTGGTTTGGCGTGGGCGGTTGCTGAGATTATAGTAGTAAAAATAAATCTGTCCCCTTTTTCCTGGATGGGCAATTCGTGAGGACCGTTGATGTAGGTAAAGTAATTGGCACTACC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13261
PABL012       AATTTAAAGGATGGAGGAGTGCCCACCTCGGTATTAAAAATATTTACTGACAGAGCTGGTAATTTGATCACAACCTTCCCAATCAAGGCGGTGGATTAATTGAGCTATCTTCCAATACGTGTATGGACTG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13391
PABL012       ACTTTCAATCAGCTGTAAGACTGCTGAGCGCTGAGGCTTCTCCAAAAGAAGTTCTTGATTTAATTCTAAATTGGATAAAAAGGAATAGAAAATTTTTCCTGTCTGGCTCATTTGCTGTTTATGGGTTTGA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13521
PABL012       GGAGTTCCTGGGTCTAAGTGGAGAGGAGATGCCTGTTAACTTTTCAAATTTTTCATCATCCGAGTTAGAGAATTTTAAGAAATTTACTTTCAAATATCAGGCTAAGGATGTGGACTATATTGCGCAATTT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13651
PABL012       TTAAGAGATGTTATTGAGACTTTGATAACTGTAGAGGTTGATAAAAAAATGTCCTAATTGTAATTCTGAAGGGATGCATGTCTTTATAGGGAAGTATAATAACCTAGTGGCTTATCAATGCAATGTGTGTG
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13781
PABL012       GGCACTCGCAATACTCGGACGGCTCAAAAGTAGAAGTCGGCGGTTTGGAGTTTATAACGGAGAGAAAGCTTCGAGATCTAAAGTTAATTTAAAATTTCATAAAGATGAATGATTTATTTTTCCTGCTCTA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        13911
PABL012       ACTTCTGAGTATGGAGACATCCGCGATTCCTAGGCAAGGGCGAGGGCGCTGATGTCGAGTGAATCAGTTCTCTCAAAAAGTCGGAATTAAGTGTCGGGGTAATATGTCTAGTCATTATTAGTCACCGGCA
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        14041
PABL012       CCTGCTGCATCGAAAGTGGGTTTGTCACAAGAAAATTTTTCTCCGCATGATGACTAATGGAAGCCATGATTGACGATTCGATTTTTGAAAAAATTGATAATCTGATTGGCAGGTTGTCAGTCAGTAGGTC
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal

        14171
PABL012       TACGGTAGATGAAAATGAGCTTTGCCGTGTTGCGAGGGTTTTGCCTGGCGATAGGGAGTTAGATGTTATAGAGAGGCTGAAAAACAAAGGGGACGTATTTATTTTTGCTGCTCTAAAGATAAAACGCAGG
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PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal       

       14301  
PABL012       TAGGTTTTCCCTGTTCAGTAATTTCTTGCTCTTTAAAAAATTTACCTTTTCGATTTAGAAGAAGAGCACCGTGCAAGACCTCCCTGTCGCCACATCCGCAGAGTCCTGAACCCCCGGCCCTGTCATCCCT
PABL001       ----------------------------------------------------------------------------------------------------------------------------------
clustal       

       14431                                                     ---------- CdiA1 class V ------------------------------------------------------
PABL012       GACGGGTCGCTCGCCGGGGCAACGCATGCCTTGCCTGTTTCCGGCTCGCCCTACAAGGACCAACTGCACCTGCAACTGGGTGTGGGTCTGAGCGCGGAGCAGATGGCGGCGCTGACCCACGACATCGTCT
PABL001       ---------------------------------------------------TACAAGGACCAACTGCACCTGCAACTGGGTGTGGGTCTGAGCGCGGAGCAGATGGCGGCGCTGACCCACGACATCGTCT
clustal                                                          *******************************************************************************

       14561  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GGCTGGAAGAGGTCGAGGTGAACGGCGAGAAGGTCCTCGCGCCGGTGGTCTACCTGGCCCAGGCGGAGGGTCGGCTGGCACCCAACGGTGCGCTGATCCAGGGCCGCGACGTGAAGCTGGTGAGCGGCGG
PABL001       GGCTGGAAGAGGTCGAGGTGAACGGCGAGAAGGTCCTCGCGCCGGTGGTCTACCTGGCCCAGGCGGAGGGTCGGCTGGCACCCAACGGTGCGCTGATCCAGGGCCGCGACGTGAAGCTGGTGAGCGGCGG
clustal       **********************************************************************************************************************************

       14691  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CGACCTGCATAACGTCGGCACCCTGCGCGCGCGGAACGACCTCTCGGCGACGGCCGACAACCTCGACAACAGCGGCCTGATCGAGGCCGGCAAGCGCCTCGACCTGCTCGCCGGCGACTCGATCCGCAAC
PABL001       CGACCTGCATAACGTCGGCACCCTGCGCGCGCGGAACGACCTCTCGGCGACGGCCGACAACCTCGACAACAGCGGCCTGATCGAGGCCGGCAAGCGCCTCGACCTGCTCGCCGGCGACTCGATCCGCAAC
clustal       **********************************************************************************************************************************

       14821  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CGCCAGGGCGGGGTCATCGCCGGGCGTGACGTGAGCCTCACCGCGCTGACCGGCGACGTGATCAACGAACGCAGCGTGACCCGCTACGACAGCGCGCTCGACGGCCGCACCTGGGAACGCAGCTTCGCCG
PABL001       CGCCAGGGCGGGGTCATCGCCGGGCGTGACGTGAGCCTCACCGCGCTGACCGGCGACGTGATCAACGAACGCAGCGTGACCCGCTACGACAGCGCGCTCGACGGCCGCACCTGGGAACGCAGCTTCGCCG
clustal       **********************************************************************************************************************************

       14951  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       ACAGCGCCGCGCGGGTGGAGGCGGCGAACAGCCTGAACGTCCAGGCCGGACGCGACATCGCCAACCTCGGCGGGGTGCTGCAGAGCCGCGGCGACCTCAGCCTCGACGCCGGACGCGACGTCACCGTCGC
PABL001       ACAGCGCCGCGCGGGTGGAGGCGGCGAACAGCCTGAACGTCCAGGCCGGACGCGACATCGCCAACCTCGGCGGGGTGCTGCAGAGCCGCGGCGACCTCAGCCTCGACGCCGGACGCGACGTCACCGTCGC
clustal       **********************************************************************************************************************************

       15081  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CGCCGTCGAGGACCGCCAGGGCCAGACCCGCTGGAGCACGTCGCGGCTCCAGAGCATGACCCAGCTCGGCGCCGAAGTCAGCGCCGGGCGGGACCTGAACGTCAGCGCCGGCCGCGACTTGACGGCGGTG
PABL001       CGCCGTCGAGGACCGCCAGGGCCAGACCCGCTGGAGCACGTCGCGGCTCCAGAGCATGACCCAGCTCGGCGCCGAAGTCAGCGCCGGGCGGGACCTGAACGTCAGCGCCGGCCGCGACTTGACGGCGGTG
clustal       **********************************************************************************************************************************

       15211  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GCCAGCACCCTCGAAGCGCGCCGCGACATCGCCCTCTCCGCCGGGCGCGACGTGACCCTGGCGGCGGCGGCGAACGAGGAGCATGCCTACAGCAAGACCAGGAAGGTCACCTACCAGGAAGACAAGGTCG
PABL001       GCCAGCACCCTCGAAGCGCGCCGCGACATCGCCCTCTCCGCCGGGCGCGACGTGACCCTGGCGGCGGCGGCGAACGAGGAGCATGCCTACAGCAAGACCAGGAAGGTCACCTACCAGGAAGACAAGGTCG
clustal       **********************************************************************************************************************************

       15341  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CCCAGCAAGGCACCCGCGTGGACGCCGGCGGCGACCTGGCGATCAATGCCGGACAGGACCTGCGCCTGATCGCGAGCCAGGCCAGCGCCGGCGACGAGGCCTACCTGGTGGCCGGCGACAAGCTGGAACT
PABL001       CCCAGCAAGGCACCCGCGTGGACGCCGGCGGCGACCTGGCGATCAATGCCGGACAGGACCTGCGCCTGATCGCGAGCCAGGCCAGCGCCGGCGACGAGGCCTACCTGGTGGCCGGCGACAAGCTGGAACT
clustal       **********************************************************************************************************************************

       15471  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GCTGGCCGCCAACGACAGCAACTACTACCTGTACGACAAGAAGAAGAAAGGCGACTTCGGCCGCAAGGAAACCCGGCGCGACGAAGTCACCGACGTCAAGGCGGTGGGCAGCCAGATCAGCAGCGGCGGC
PABL001       GCTGGCCGCCAACGACAGCAACTACTACCTGTACGACAAGAAGAAGAAAGGCGACTTCGGCCGCAAGGAAACCCGGCGCGACGAAGTCACCGACGTCAAGGCGGTGGGCAGCCAGATCAGCAGCGGCGGC
clustal       **********************************************************************************************************************************

       15601  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GACCTCACCCTGCTCAGCGGCGGCGACCAGACCTACCAGGGCGCGAAGCTGGAATCGGGCAACGACCTGGCCATCGTCAGCGGCGGCGCGGTGACCTTCGAGGCGGTGAAGGACCTGCACCAGGAAAGCC
PABL001       GACCTCACCCTGCTCAGCGGCGGCGACCAGACCTACCAGGGCGCGAAGCTGGAATCGGGCAACGACCTGGCCATCGTCAGCGGCGGCGCGGTGACCTTCGAGGCGGTGAAGGACCTGCACCAGGAAAGCC
clustal       **********************************************************************************************************************************

       15731  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       ACGAGAAGAGCAAGGGCGACCTGGCGTGGAACAGCGCCAAGGGGAAAGGGCAGACCGATGAAACGCTTCGGCAGACCCAGATCGTGGCCCAGGGGAATCTGGCGATCAAGGCCGTGGAAGGGCTGAAGAT
PABL001       ACGAGAAGAGCAAGGGCGACCTGGCGTGGAACAGCGCCAAGGGGAAAGGGCAGACCGATGAAACGCTTCGGCAGACCCAGATCGTGGCCCAGGGGAATCTGGCGATCAAGGCCGTGGAAGGGCTGAAGAT
clustal       **********************************************************************************************************************************

       15861  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CGACCTCAAGCATATCGACCAGAAGACCGTAAGCCAGACCATCGACGCGATGGTGCAGGCGGATCCGCAACTGGCGTGGCTGAAGGAGGCCGAGCAGCGCGGGGATGTGGACTGGCGCATGGTGCAGGAG
PABL001       CGACCTCAAGCATATCGACCAGAAGACCGTAAGCCAGACCATCGACGCGATGGTGCAGGCGGATCCGCAACTGGCGTGGCTGAAGGAGGCCGAGCAGCGCGGGGATGTGGACTGGCGCATGGTGCAGGAG
clustal       **********************************************************************************************************************************

       15991  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GTGCACGATAGCTGGAAGTACAGCAACTCGGGCATGGGGCCGGCGACGCAGATCGCTGTCGCCATCGCGGCGGCAGCCATCGGTGGCATGGCGGCAGCGGGAGCGCTCAGTGGTGCAGGAGTGGGTGCCA
PABL001       GTGCACGATAGCTGGAAGTACAGCAACTCGGGCATGGGGCCGGCGACGCAGATCGCTGTCGCCATCGCGGCGGCAGCCATCGGTGGCATGGCGGCAGCGGGAGCGCTCAGTGGTGCAGGAGTGGGTGCCA
clustal       **********************************************************************************************************************************

       16121  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GTAGCTTCGCCATGGGCGCAGGAGTTGGTGCGGCAGGAAGCCTGTCGGGCACGGCAGCGGTCAGCCTGATCAACAACAAGGGCGATCTCGGGAAGGTGCTGAAAGACAGCTTCAGTAGTGACAGTCTGAA
PABL001       GTAGCTTCGCCATGGGCGCAGGAGTTGGTGCGGCAGGAAGCCTGTCGGGCACGGCAGCGGTCAGCCTGATCAACAACAAGGGCGATCTCGGGAAGGTGCTGAAAGACAGCTTCAGTAGTGACAGTCTGAA
clustal       **********************************************************************************************************************************

       16251  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GCAGATTGCTATTGCGAGCCTGACCGGGGGGCTGACGGCTGAGTACTTCGACGGGATTCTTCAGACCAAGACTGATCCGCTTACTGGAAAGGTCACGGTAGACCTCAGCAGCCTATCTGGTGTTGGTCGC
PABL001       GCAGATTGCTATTGCGAGCCTGACCGGGGGGCTGACGGCTGAGTACTTCGACGGGATTCTTCAGACCAAGACTGATCCGCTTACTGGAAAGGTCACGGTAGACCTCAGCAGCCTATCTGGTGTTGGTCGC
clustal       **********************************************************************************************************************************

       16381  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       TTCGCTGCCAATCAGGCGATGCAGAACGCTACATCCACTGTACTGAGCCAGGCCTTGGGCCAGGGCGGGAGCCTGAACGAGGCGCTGAAGAGCGCGCTCTACAACAGTTTCGCGGCGGCAGGTTTCAACT
PABL001       TTCGCTGCCAATCAGGCGATGCAGAACGCTACATCCACTGTACTGAGCCAGGCCTTGGGCCAGGGCGGGAGCCTGAACGAGGCGCTGAAGAGCGCGCTCTACAACAGTTTCGCGGCGGCAGGTTTCAACT
clustal       **********************************************************************************************************************************

       16511  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       TCGTCGGCGATATCGGCCAGGAATACAGCCTGAAGCCAGGCGATCCTTCGATGGTGACCATGCACGCCCTGATGGGTGGCCTGGCGGCGCAGGTCAGCGGTGGCGATTTCGCCACGGGCGCCGCGGCGGC
PABL001       TCGTCGGCGATATCGGCCAGGAATACAGCCTGAAGCCAGGCGATCCTTCGATGGTGACCATGCACGCCCTGATGGGTGGCCTGGCGGCGCAGGTCAGCGGTGGCGATTTCGCCACGGGCGCCGCGGCGGC
clustal       **********************************************************************************************************************************

       16641  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       TGGCGCCAATGAAGCGCTGGTGGCCAAGCTAGACCAGGCCTTCAAGAGCTTGAGCCCTGAGAACCGTGAAGCCATGGTCACTATGGGGTCGCAATTGGTTGGTGTTCTGGCTGCGGCGGTACGCGATCCT
PABL001       TGGCGCCAATGAAGCGCTGGTGGCCAAGCTAGACCAGGCCTTCAAGAGCTTGAGCCCTGAGAACCGTGAAGCCATGGTCACTATGGGGTCGCAATTGGTTGGTGTTCTGGCTGCGGCGGTACGCGATCCT
clustal       **********************************************************************************************************************************

       16771  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GATGTGACAGGCAAAGCTCTGGAAAGCGCTGCTTGGGTAGCGAAGAACTCGACGCAATACAACTTCCTCAACCATCAGGATGTGGCCGATCTGGATAATGCCTTGCAGAAATGCAAGTCCCAGGGAAATT
PABL001       GATGTGACAGGCAAAGCTCTGGAAAGCGCTGCTTGGGTAGCGAAGAACTCGACGCAATACAACTTCCTCAACCATCAGGATGTGGCCGATCTGGATAATGCCTTGCAGAAATGCAAGTCCCAGGGAAATT
clustal       **********************************************************************************************************************************

       16901  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GCCGTCAGGTAGAGGAAGAGTTCAAGGCGCGTAGCGACGAGAACCGGCGGAGGTTGAATGGCTGCGTGGCTGTGGGTAATTGCGCGGAGATTCGTGCGGAGATCGATGCGGGGTCTACGGCTCTCAACGA
PABL001       GCCGTCAGGTAGAGGAAGAGTTCAAGGCGCGTAGCGACGAGAACCGGCGGAGGTTGAATGGCTGCGTGGCTGTGGGTAATTGCGCGGAGATTCGTGCGGAGATCGATGCGGGGTCTACGGCTCTCAACGA
clustal       **********************************************************************************************************************************

       17031  ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GCTGGTGGCCCGGCAGGAAACAGCTAATCCGGGAGGAAGTGACAGCGATATAGCCTACGGTTTCCTGATGGGCCGAAATGTTGTCGACTGGACGACGGCTGGTCAGTTGCACCTGGAGCAGACCGCCAAC
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PABL001       GCTGGTGGCCCGGCAGGAAACAGCTAATCCGGGAGGAAGTGACAGCGATATAGCCTACGGTTTCCTGATGGGCCGAAATGTTGTCGACTGGACGACGGCTGGTCAGTTGCACCTGGAGCAGACCGCCAAC
clustal       **********************************************************************************************************************************

        17161 ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CTCTGGTGGAACGGTAATCCACAGTGGCAGAAGGAAGTCGGTGCATACCTGGACCAGACGGGGTTCAATCCGTTCGGAATCGGCGTTCCGGCAATGGGCGGTGCCGCTGGCAAGGTAACGGCCAAGGCGC
PABL001       CTCTGGTGGAACGGTAATCCACAGTGGCAGAAGGAAGTCGGTGCATACCTGGACCAGACGGGGTTCAATCCGTTCGGAATCGGCGTTCCGGCAATGGGCGGTGCCGCTGGCAAGGTAACGGCCAAGGCGC
clustal       **********************************************************************************************************************************

        17291 ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       TCATGAATGCGCTGAAGGCGGGAGAGTTGCCCAAAGGAGAGGTGGCCCCAGGAAAGGCTAATCTGCCTACCATTGGGGCGTTGGCGGATGCTGAGGCGGGAATGCCTTATACCCATCCAGTTAAGCTCGC
PABL001       TCATGAATGCGCTGAAGGCGGGAGAGTTGCCCAAAGGAGAGGTGGCCCCAGGAAAGGCTAATCTGCCTACCATTGGGGCGTTGGCGGATGCTGAGGCGGGAATGCCTTATACCCATCCAGTTAAGCTCGC
clustal       **********************************************************************************************************************************

        17421 ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CGCAAAAGCGACTGGGACAGCAGGGAAGATTAAGATTGAAGCCGGCGCAATACCTGACGCAAATGAAGTACGTGCAGGACAAGGGTTATCTGGTCTTGGGTACGATGTTACGCACCAAACCACTGCGTCA
PABL001       CGCAAAAGCGACTGGGACAGCAGGGAAGATTAAGATTGAAGCCGGCGCAATACCTGACGCAAATGAAGTACGTGCAGGACAAGGGTTATCTGGTCTTGGGTACGATGTTACGCACCAAACCACTGCGTCA
clustal       **********************************************************************************************************************************

        17551 ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       GCTAAAGGTATTCAAGGGCAGCGAACTGCGGACTTGCATGTTGATGGACTCGGTTCCATTGATGTGTATACGCCGAAGAGTCTTGATCCGACAAAGATAGTTCGAGCGATAGAGAAGAAGTCGAATCAAG
PABL001       GCTAAAGGTATTCAAGGGCAGCGAACTGCGGACTTGCATGTTGATGGACTCGGTTCCATTGATGTGTATACGCCGAAGAGTCTTGATCCGACAAAGATAGTTCGAGCGATAGAGAAGAAGTCGAATCAAG
clustal       **********************************************************************************************************************************

        17681 ------------------------------------------------------------- CdiA1 class V ------------------------------------------------------
PABL012       CCGGCGGAGTCTTGGTGCAGGCGGACTTGCCAAGCACTGACATGTCGTCCATTGCTGCTCGTATGTGGGGGAAGACTAACGCGCAGAGTATAAAAACTATATTTTTCCAGAAACCAGACGGATCATTGGT
PABL001       CCGGCGGAGTCTTGGTGCAGGCGGACTTGCCAAGCACTGACATGTCGTCCATTGCTGCTCGTATGTGGGGGAAGACTAACGCGCAGAGTATAAAAACTATATTTTTCCAGAAACCAGACGGATCATTGGT
clustal       **********************************************************************************************************************************

        17811 ------------------------------|  |--------------------------- CdiI ---------------------------------------------------------------
PABL012       CCGATTTGATCGACCTGCTGGAGGAGGCTGATTATGCCGAAGTACACGTGTACCTGTGGCTACGTTATGAACCTTTCGCAAGGATGGTCAGACTATGAGTTGACTCTAATTCCTGAGTCAGCAATAGAGA
PABL001       CCGATTTGATCGACCTGCTGGAGGAGGCTGATTATGCCGAAGTACACGTGTACCTGTGGCTACGTTATGAACCTTTCGCAAGGATGGTCAGACTATGAGTTGACTCTAATTCCTGAGTCAGCAATAGAGA
clustal       **********************************************************************************************************************************

        17941 ------------------------------------------------------------- CdiI ---------------------------------------------------------------
PABL012       GCTTGGGGGATAGGCTAGATAGCGAGGATAAGCTGTCTTCTGATCAGTTATATGAAGCTCTTGATGAAAAGGCCATTACGGTGTACCGATGCCCGAAGTGTAGAAGGTTGCACTTGGAGGAAGAGCCAAA
PABL001       GCTTGGGGGATAGGCTAGATAGCGAGGATAAGCTGTCTTCTGATCAGTTATATGAAGCTCTTGATGAAAAGGCCATTACGGTGTACCGATGCCCGAAGTGTAGAAGGTTGCACTTGGAGGAAGAGCCAAA
clustal       **********************************************************************************************************************************

        18071 ---------------------------|
PABL012       TAGATTCACCACTTATATAGTTGAGTAA
PABL001       TAGATTCACCACTTATATAGTTGAGTAA
clustal       ****************************
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Figure S4. Alignment between class II and class V *cdiA1* homologs. Nucleic acid sequence for the Class II *cdiA1* gene and downstream intergenic region from PABL012 and the Class V *cdiA1* gene alone from PABL001 were aligned to highlight the integration of a Class II C-terminus. The conserved sequence between the Class II and Class V *cdiA* genes is labeled above the alignment as “CdiA1”. The respective C-termini are then labeled as “CdiA1 class II” or “CdiA1 class V” as well as the downstream *cdiI* immunity genes. “*” indicate identical residues, “:” are highly similar residues and “.” are weakly similar residues in the Gonnet PAM 250 matrix.

Table S1. *P. aeruginosa* NCBI reference genomes

Strain	Accession[a]	Strain	Accession[a]	Strain	Accession[a]
8380	SAMD00027370	M37351	SAMN02894351	Pa84	SAMN05020322
12939	SAMN07831757	MTB-1	SAMN02389526	PAER4-119	SAMN04209275
12_4_4	SAMN04351367	N17-1	SAMN03145716	PAK	SAMN02596970
AR-0095	SAMN04014936	NCGM-1900	SAMD00018700	PAO1	SAMN02603714
AR-0354	SAMN07291497	NCGM-1984	SAMD00019082	PAO1-Orsay	SAMEA3485223
AR-0357	SAMN07291500	NCGM2.S1	SAMD00061003	PASGNDM345	SAMN06689794
AR-0360	SAMN07291503	NCGM257	SAMD00020552	PASGNDM699	SAMN06689795
ATCC-15692	SAMN05715193	NCTC10332	SAMEA2479570	PB350	SAMN08101543
ATCC-27853	SAMN04589231	NHmuc	SAMN03940420	PB353	SAMN08101545
BAMCPA07-48	SAMN04893615	Ocean-1155	SAMN07347483	PB354	SAMN08101544
BL22	SAMN02360735	Ocean-1175	SAMN07347485	PB367	SAMN08101542
C-NN2	SAMEA104083446	PA-150577	SAMN04452273	PB368	SAMN08101546
Carb01-63	SAMN03389320	PA-154197	SAMN04452263	PB369	SAMN08101547
DK1	SAMEA3484633	PA-D1	SAMN04910034	PcyII-10	SAMEA26686918
DK2	SAMN02603895	PA-D16	SAMN04914381	RIVM-EMC2982	SAMN05583819
DN1	SAMN05717682	PA-D2	SAMN04910045	RP73	SAMN02603771
E6130952	SAMN06349407	PA-D21	SAMN04914386	RW109	SAMEA104432335
F22031	SAMN02673269	PA-D22	SAMN04914475	S86968	SAMN02894350
F23197	SAMN02894358	PA-D25	SAMN04914479	SCV20265	SAMN02415141
F30658	SAMN02894357	PA-D5	SAMN04910061	SCVFeb	SAMN03940423
F5677	SAMN02887043	PA-D9	SAMN04910066	SCVJan	SAMN03940421
F63912	SAMN02894356	PA1	SAMN02603191	SJTD-1	SAMN02894349
F9670	SAMN02894359	PA1088	SAMN04455104	T38079	SAMN02894348
F9676	SAMN03852256	PA11803	SAMN04455162	T52373	SAMN02894348
FA-HZ1	SAMN05729608	Pa1207	SAMN05020325	T63266	SAMN02894347
FRD1	SAMN02732380	PA121617	SAMN05006707	UCBPP-PA14	SAMN02603591
H27930	SAMN02894354	PA124	SAMN05020323	USDA-41639	SAMN04158502
H47921	SAMN02894353	Pa1242	SAMN05020326	VA-134	SAMN04284690
ID4365	SAMN02732281	PA127	SAMN05020324	W16407	SAMN02894346
IOMTU133	SAMD00042491	PA14Or	SAMEA4393802	W36662	SAMN02894344
L10	SAMN06234157	PA1RG	SAMN04074798	W45909	SAMN02894345
LES431	SAMN02641592	Pa58	SAMN05020321	W60856	SAMN02894343
LESB58	SAMEA1705916	PA7	SAMN02603435	X78812	SAMN02894342
M1608	SAMN02894352	PA7790	SAMN04455155	YL84	SAMN02641599
M18	SAMN02603849	PA8281	SAMN04455156		

[a] https://www.ncbi.nlm.nih.gov/biosample/

Table S2. *P. aeruginosa* PABL CDI sequences

Strain	CDI	Accession[a]	Strain	CDI	Accession[a]	Strain	CDI	Accession[a]	Strain	CDI	Accession[a]
PABL001	CDI1	MK509178	PABL030	CDI1	MK509223	PABL057	CDI1	MK509267	PABL083	CDI1	MK509312
PABL001	CDI2	MK509179	PABL030	CDI2	MK509224	PABL058	CDI1	MK509268	PABL083	CDI2	MK509313
PABL002	CDI1	MK509180	PABL031	CDI1	MK509225	PABL058	CDI2	MK509269	PABL084	CDI1	MK509314
PABL002	CDI2	MK509181	PABL031	CDI2	MK509226	PABL059	CDI1	MK509270	PABL084	CDI2	MK509315
PABL003	CDI1	MK509182	PABL032	CDI1	MK509227	PABL059	CDI2	MK509271	PABL085	CDI1	MK509316
PABL003	CDI2	MK509183	PABL032	CDI2	MK509228	PABL060	CDI1	MK509272	PABL085	CDI2	MK509317
PABL004	CDI1	MK509184	PABL034	CDI1	MK509229	PABL060	CDI2	MK509273	PABL086	CDI1	MK509318
PABL004	CDI2	MK509185	PABL034	CDI2	MK509230	PABL061	CDI1	MK509274	PABL086	CDI2	MK509319
PABL006	CDI1	MK509186	PABL035	CDI1	MK509231	PABL062	CDI1	MK509275	PABL088	CDI1	MK509320
PABL006	CDI2	MK509187	PABL035	CDI2	MK509232	PABL062	CDI2	MK509276	PABL088	CDI2	MK509321
PABL007	CDI1	MK509188	PABL036	CDI1	MK509233	PABL063	CDI1	MK509277	PABL089	CDI1	MK509322
PABL007	CDI2	MK509189	PABL036	CDI2	MK509234	PABL063	CDI2	MK509278	PABL089	CDI2	MK509323
PABL009	CDI1	MK509190	PABL037	CDI1	MK509235	PABL064	CDI2	MK509279	PABL090	CDI1	MK509324
PABL010	CDI1	MK509191	PABL037	CDI2	MK509236	PABL064	Cdil1	MK509280	PABL091	CDI1	MK509325
PABL010	CDI2	MK509192	PABL038	CDI1	MK509237	PABL065	CDI1	MK509281	PABL091	CDI2	MK509326
PABL011	CDI1	MK509193	PABL038	CDI2	MK509238	PABL065	CDI2	MK509282	PABL092	CDI1	MK509327
PABL012	CDI1	MK509194	PABL040	CDI1	MK509239	PABL066	CDI1	MK509283	PABL092	CDI2	MK509328
PABL012	CDI2	MK509195	PABL040	CDI2	MK509240	PABL066	CDI2	MK509284	PABL093	CDI1	MK509329
PABL013	CDI1	MK509196	PABL041	CDI1	MK509241	PABL067	CDI1	MK509285	PABL093	CDI2	MK509330
PABL014	CDI1	MK509197	PABL041	CDI2	MK509242	PABL067	CDI2	MK509286	PABL094	CDI1	MK509331
PABL015	CDI1	MK509198	PABL042	CDI1	MK509243	PABL068	CDI1	MK509287	PABL094	CDI2	MK509332
PABL016	CDI1	MK509199	PABL042	CDI2	MK509244	PABL068	CDI2	MK509288	PABL095	CDI1	MK509333
PABL016	CDI2	MK509200	PABL044	CDI1	MK509245	PABL069	CDI1	MK509289	PABL095	CDI2	MK509334
PABL017	CDI1	MK509201	PABL044	CDI2	MK509246	PABL069	CDI2	MK509290	PABL096	CDI1	MK509335
PABL018	CDI1	MK509202	PABL045	CDI1	MK509247	PABL070	CDI1	MK509291	PABL097	CDI1	MK509336
PABL018	CDI2	MK509203	PABL045	CDI2	MK509248	PABL070	CDI2	MK509292	PABL097	CDI2	MK509337
PABL019	CDI1	MK509204	PABL046	CDI1	MK509249	PABL071	CDI1	MK509293	PABL098	CDI1	MK509338
PABL019	CDI2	MK509205	PABL047	CDI1	MK509250	PABL071	CDI2	MK509294	PABL100	CDI1	MK509339
PABL020	CDI1	MK509206	PABL047	CDI2	MK509251	PABL072	CDI1	MK509295	PABL100	CDI2	MK509340
PABL020	CDI2	MK509207	PABL048	CDI1	MK509252	PABL072	CDI2	MK509296	PABL101	CDI1	MK509341
PABL021	CDI1	MK509208	PABL048	CDI2	MK509253	PABL073	CDI1	MK509297	PABL101	CDI2	MK509342
PABL021	CDI2	MK509209	PABL049	CDI1	MK509254	PABL074	CDI1	MK509298	PABL102	CDI1	MK509343
PABL022	CDI1	MK509210	PABL049	CDI2	MK509255	PABL074	CDI2	MK509299	PABL103	CDI1	MK509344
PABL022	CDI2	MK509211	PABL051	CDI1	MK509256	PABL075	CDI1	MK509300	PABL103	CDI2	MK509345
PABL023	CDI1	MK509212	PABL052	CDI1	MK509257	PABL075	CDI2	MK509301	PABL104	CDI1	MK509346
PABL023	CDI2	MK509213	PABL052	CDI2	MK509258	PABL076	CDI1	MK509302	PABL104	CDI2	MK509347
PABL024	CDI1	MK509214	PABL053	CDI1	MK509259	PABL076	CDI2	MK509303	PABL105	CDI1	MK509348
PABL024	CDI2	MK509215	PABL053	CDI2	MK509260	PABL077	CDI1	MK509304	PABL106	CDI1	MK509349
PABL026	CDI1	MK509216	PABL054	CDI1	MK509261	PABL078	CDI1	MK509305	PABL106	CDI2	MK509350
PABL027	CDI1	MK509217	PABL054	CDI2	MK509262	PABL079	CDI1	MK509306	PABL107	CDI1	MK509351
PABL027	CDI2	MK509218	PABL055	CDI1	MK509263	PABL079	CDI2	MK509307	PABL107	CDI2	MK509352
PABL028	CDI1	MK509219	PABL055	CDI2	MK509264	PABL080	CDI1	MK509308	PABL108	CDI1	MK509353
PABL028	CDI2	MK509220	PABL056	CDI1	MK509265	PABL081	CDI1	MK509309	PABL108	CDI2	MK509354
PABL029	CDI1	MK509221	PABL056	CDI2	MK509266	PABL082	CDI1	MK509310			
PABL029	CDI2	MK509222	PABL057	CDI1	MK509267	PABL082	CDI2	MK509311			

[a] https://www.ncbi.nlm.nih.gov/genbank/

Table S3. *P. aeruginosa* CdiA C-terminal amino acid sequence diversity.

TD	CT	TD + CT Sequence	Domain Family	Enzymatic Activity	CdiI	Sequence
TD01	CT01	TENNYLGTGVNLFGHQLGSNQVDAFHKELKASCSGSGGTQACLNTYSKWKETSYKQGGLESKNEQAGWEDFVRAAYAENIVPLCKGNSVCLDNVNAKMASDMVVYAGDAVGLKDSVGATARGVNIANGNWVRTGLQVVEDAGLLAAIGGVFGVGSSTAAKATVNAEGAALPAGYREGSSAGSAFLETAGLPEGYRRVINTKTGNTEVLAADGKLYFETGNGLQPKAGGNLSGLVEAEKSIALRQQASKITAPIDFDGHIIRAEVKPNGNVVGGHSTVTGDVRVIPGTESVPNAQGVYSAKIEVADPANPGSYLPKTNNGGVSTMFPKSWTADRIKVEVDAAFQNRTVTGNKWNGTTPSGVRVEGYLSPKTTVYPKL	pfam14436	Nuclease	CdiI01	MKIRYFWTGEGENKEPSCQSDVLSDDGIDLLACLFVDHGGQKYESSIAWLDEGLSRVNQIRRGAIECSDWSRDSWGVELRNGMARIYSLYDEDCSAAIALDDFERALLGWKRFIQAD
TD02	CT02	TENNFLGGGTPPGLISYGQAASSLTEYMRKNGATAEEITQAQRDLAQGQGFDGVQPANEFIKAWGEAMVAEAAGLGIVAGLGRFGLWVGKGAGETAIAVPGRVQSRINIANGRTATTPLRDTGRPVSAGFDHVLQGHFGVEVSNSRSVFTITPSELKDVLQSSPVVKSPVMALPDGQFVRTVDVGKVIGTTNLKDGGVPTSVLKIFTDRAGNLITTFPIKAVD	unknown	unknown	CdiI02	LSYLPIRVWTDFQSAVRLLSAEASPKEVLDLILNWIKRNRKFFLSGSFAVYGFEEFLGLSGEEMPVNFSNFSSSELENFKKFTFKYQAKDVDYIAQFLRDVIETLITVEVDKKCPNCNSEGMHVFIGKYNNLVAYQCNVCGHSQYSDGSKVEVGGLEFITERKLRDLKLI
TD02	CT03	TENNFLGGGTPPGLISYGQAASSLTEYMRKNGATAEEITQAQRDLAQGQGFDGVQPANEFIKAWGEAMVAEAAGLGIVAGLGRFGLWGAKGATPVVTAEGRIGNSVFTDVNQTARPAAQANPNQPTLIADRVDAKIAAKGTPHPNGNMADAHAEIGVIQKAFNEGKTVGSDMTMNVVGKDVCGYCRGDIAAAASKSGLKSLTIQAKDDITGLPKTYYWEVGMKSIREKKIYWEVGMKSIREKKI	pfam14437	Deaminase	CdiI03	MIVLGGYLIAPEAKRTQFPVVSDPDEEEVLAALSKLRHSSGVLVLRVKPEPEIGAYEVALHAESGRFIVMLSQHAEDGEHEVFTLRGAGEGNGFTYILGEAYPMAAVTENFGLICNCFKKFLLEREVSSDVWV
TD04	CT04	NEALVSLVGEKIFPGEAHERVLAMTSQLIGMTVAAAAGGDTKAQEKAAWVAQQATVYNNLNHAAAESLLKEIKDCRAAGGCGEEKLQGILGKYEKLSAERSNAIGQCASRQCVDDIVDSSIRMDDPVSKELLSLLRQTTYDTPGLLQGNPDAIVSQTPNPSGWGDLFALDKQLAFAKNLKEGWLTPEETADLDRWNASTSWLDRTAGRQLDPKEKAYLLSELGGAAAMALLGGRGSVGSGAGGIRNTYSSIKEAPKYPQGFKDIKNGTQKYKINNQDVLESLRGVEPGKWVKVYRDGFDSAGNKISVHYFQSQSGKVFDVKVKSGWSN	unknown	unknown	CdiI04	MRLCYEIEASQAEGFLSIFILGVLWSLKKGVINIEDAEGFIFKPATSKVVRDEFGFEELALLIDAGCELEDVKSLVFDKLDENIDTLIERVSYIVSAKTDGRGLIDKNIFLVNEGEE
TD04	CT05	NEALVSLVGEKIFPGEAHERVLAMTSQLIGMTVAAAAGGDTKAQEKAAWVAQQATVYNNLNHAAAESLLKEIKDCRAAGGCGEEKLQGILGKYEKLSAERSNAIGQCASRQCVDDIVDSSIRMDDPVSKELLSLLRQTTYDTPGLLQGNPDAVVSQTPNPSGWGDLFALDKQLAFAKNLKEGWLTPEETADLDRWNASTSWLDRTAGRQLDPKEKAYLLSELGGAAAMALLGGRGSVGSNATFGQIKTVLDTAQAPYKGSTVIGHALSKHAGRHPEIWGKVKGSMSGWNEQAMKHFKEIVRAPGEFRPTMNEKGITFLEKRLIDGRGVRLNLDGTFKGFID	unknown	unknown	CdiI05	MKELFEVIFEGVNTSRLFFLLKEIESKSDRIFDFNFSEDFFSSNVNVFSELLIDSFLGFNGDLYFGVSMEGFSVKDGLKLPVVLLRVLKYEGGVDVGLCFYMNDFNSAGKVMLEFQKYMNGISADFGFENFYGGLEPASDQETRFFTNNRLGPLL
TD05	CT06	NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAAGNCAEIRAEIDAGSTALNELVARQETANPGGSDSDIAYGFLMGRNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVSAKALMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPVKLAAKATGTAGKIKIEAGAIPDANEVRAGQGLSGLGYDVTHQTTASAKGIQGQRTADLHVDGLGSIDVYTPKNLDPTKIVRAIEKKSNQAGGVLVQADLPSTDMSSIAARMWGKTNAQSIKTIFFQKPDGSLVRFDRPAGGG	cd13442	tRNase	CdiI06	MPKYTCTCGYVMNLSQGWSDYELTLIPESAIESLGDRLDSEDKLSSDQLYEALDEKAITVYRCPKCRRLHLEEEPNRFTTYIVE
TD05	CT07	NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDATGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTALNELVARQETANLGGSDSDIAYGFLMGRNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVSAKALMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPIKTPSNETARLLASSQEPYKGGQSITNAGRAVTKHPEYFGFSTTQELRKIYRTDSQINELAGKAINEILQSGVKSNGAGGRYPGGWITYTLPDGRAASWGGDGKFIGFRGVQK	unknown	unknown	CdiI07	MKVNLIFEKVGDINSDYPYLCVYREGEREPFMEISVSKERKIEFVFYSRTDNFTLSSEEFYEIYGRAEAFLPQALENEDSL
TD05	CT08	NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTALNELVARQETANPGGSDSDIAYGFLMGRNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVSAKALMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPVKEATKTKIPNPPRAEGNFTGGPLENAIKTSGRFKLDGGPANGVLYRSDNKGNVTSYAVYDSTGMIIKRVDVSGASHANIPTPHVIEYGRNILPDGSVRVQSPSTKLAPRPANSDEIP	pfam15529	RNase	CdiI08	MKKIVSFKDLKCLSNYELWRSGWENKNEIDVFSYISYEIRPEDLLILGKLVFPDFILDRGAVILEMNYEEKKFNDWMERLENDIQSVERFINHTHIYDIFSGCNEDVEDEIFEQLAHMLSLSWRLILKEKFPDRDFSVLLSCSDQDYGPTITFFQK
TD06	CT09	NEALVKDLDKLVSSYSPENREAMLAMASQLTGLVGVVAKDPGASYKELETGSWAARNSVQYNYLNHEENQERFEAKKACNGGDSTACGRVDELNQLDRNRDLALLAACSPGGNGVTCTALRKEAFEAAKSLQKSSWSAEGWEQAEQARQNPQLMAYTITAELQSNLAVNNPITAVDSKRLAEAMVSFGSDFIPGYGDAKSFVEAQDPFDYMMSGVGLVPGLGDGAAKILGKAKALYKEGKVSEAADLVEGLGKLPAPQAAKGTTTVGEVAGTGARNPLLDDAIPRNGDRLVVSQGAAPTCGHNSCGMVLNTLGKEVDVGVLVQKVKPSAGGIYAQDVADLMKSEGIPASAFGNRNVADLTRYTSNGTPVVVRIADKTGDSDFSHFVVVDGVTTRNGVSVVAIRDPHGTQYFSPVATFEKSFTGEVVVPRSALK	pfam03412	Peptidase	CdiI09	MKLRIEFPKDIRTGYLLRQERIPCLCKVSKEFEISFSDTIPESSGVVLEWNRKELELRAIAGGGGRYTHYGNGLITLKDVGADTYQIIDLEIFYARFGWCVVLKDGEYAPPGDFWDEE
TD06	CT10	NEALVKDLDKLVSSYSPENREAMLAMASQLTGLVGVVAKDPGASYKELETGSWAARNSVQYNYLNHEENQERFEAKKACNGGDSTACGRVDELNQLDRSRDLALLTACSSDGSSTTCTALRKEAWESAQSLKQASWTPEAQEQYRQAMQNPQLMAYTIEGELRSIYQINDPITAADSKRLAEAMASLGSDFIPGYGDGKAFVEAQDPFDYTMAGIGLVPGIGDGAAKILAKAKALYKEGKVSEAADLVEGLGKLPAPQGPKGTGTALREVEVSSGSKGSWTKELNKPEPNTIYKVDGNKTYQTDSLGRVEKVESNLSLTKSDRNTYQQCIAGKCGVSGDEGGHLIASIFNGPGEKLNLLPMNGNLNKGAWKSMENTWSSALKQGQMVSVKIEPVYSGSSVRPDRFTVRYSIDGGRPVIVDFKNSPGGI	pfam13930	Nuclease	CdiI10	MGDQELYQKIGQLLVDAGPADAREIIVRAELFSEGDGGKYEFDYVDQSGELNWFDPDGRAVGDLTELLVQLRDYFSANNLTAGEGGWSGCVIKLHVDEMKFGIAFNYGK
TD06	CT11	NEALVKDLDKLVSSYSPENREAMLAMASQLTGLVGVVAKDPGASYKELETGSWAARNSVQYNYLNHEENQERFEAKKACNGGDSTACGRVDELNQLDRSRDLALLTACSSGGSSTTCTALRKEAWESAQSLKQASWTPEAQEQYRQAMQNPQLMAYTIEGELRSIYQINDPITAADSKRLAEAMASLGSDFIPGYGDGKAFVEAQDPFDYTMAGIGLVPGIGDGAAKILAKAKALYKEGKVSEAADLVEGLGKLPAPQGAKGEVQLLPKPGSTTVPTSGVGANAQFKVDSGQLGKKLGKHVEDFGGSAKNPADRQMVLDKIQDIGNNPEKVIPGKFAGQGSGGTRGDVFFRIKGDDVVVTKPDGTFVTIMKDGINNTSVKNALKGNPQ	pfam11429	tRNase	CdiI11	MIVVSEAFKSWLIGCIGLRLLLVWGLFHVFESKKNGNPQAVALLFDGKDFGTLKCAPDGSSIAYSSDVVAECDLGEFGAEKIFPLESDEAFSSVVGEALNSVSLILSSVEDSVAGVLLRFGNSECLSFINLGDELFVYKEIPSEIIKCEGLEFLKLS
TD07	CT12	NEAMINLLGKMVGGDQNLELMASQLVGVAAASAVNGDVSLGAEIAKSGTAYNRQLHPDEIKFASDVKRVKRYAQENGLSEDTARKELLSTAAMMVDNGWNQALAGTDINAARAAQYLRTELGTGPDSNLFQVTQADYYNERVGLTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLALEGIVSAPSKTALWLMGALTCSSCAERDIQNAWNSVASLPEDIRMKGYLDALHTMQGQGASVVRDNAASSTALGVEVGLAIDGGLAGAGKGVVTDGPKGILTLKDFPDVSTKISQKQLRHIAGTQQLEARGGGGFLNSVSDAQKVLDAYHTGQVKILGRNAQGFPVVKFEGVTGTNVNLGVGITDQATNVFIIKGTKSPSIVPTNPNWSPK	pfam15542	tRNase	CdiI12	MSSQPTLEEWNFQVLMLIQALVGAISANFRMIALLWDGDEWVLRFYLEESNEEDVEEIEDVVCQYTAYQGSSLRCRSELIVGRERLPGLSEVGRVVYRRRESFDI
TD07	CT13	NEAMINLLGKMVGGDQNLELMASQLVGVAAASAVNGDVSLGAEIAKSGTAYNRQLHPDEIKFASDVERVKRYAQENGLSEDTARKELLSTAAMMVDNDWNQALAGTDINAARAAQYLRTELGTGPDSNLFQVTQADYYNERVGLTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLALEGIVSAPSKTALWLMGALTCSSCAERDIQNAWNSVASLPEDIRMKGYLDALHTMQGQGASVVRDNAASSTALGVEVGLAIDGGLAGAGKGVVTDGAKGSAAGAAEANNALSAAEGVVASRVNVRTGAANVTGSGLEYAWKKHGGAWGDNKSAFTISKNELKVVLQSPQVVKTPAYQSPTSGNFIRTVDMGRPIGIDAKAGGQPTNFMTVITDSKGNLVNTFPGKTF	unknown	unknown	CdiI13	MYYLMIWDRYLASIGRDGCLDKVEIPLDVANFFFRLDVEQYPILSSLSFDDYDMFSGAQIDSLVGELCSVASINPLISETVESMVDIMLKARALGKNILFDPFKVD
TD08	CT14	NEALVNVLSNMAGGEEKLELMASQLTGLLAATVVDGDVAKGAEIAKNATAYNQQAHRDALSRLKRGMSALHEQGKYADLEPETVLADLQKIASGEAKSVSDLNPKVVQFLNSEFSPASLRETLFEPESWEEYAAIAVDVLYPTPGGKAAAIEKAGGKLSKEALEALEKKFSSDALKNALWTSTKSKSAIENAFGHWQKHKGEFPEFKNAKQYVEGTQNFLSSPPPGTLTKTRPNGDTLLFDPKTNTFGVKDANGAPRTMFRPQDGINYWNRQ	unknown	unknown	CdiI14	MRYPCPCCGYLTFDEEPCGTYEICPVCYWEDDIAQNKDPDYDGGANGISLNNAKENFFKYGAIKREFLKNVRKPLDDESL
TD08	CT15	NEALVNVLSNMAGGEEKLELMASQLTGLLAATVVDGDVAKGAEIAKNATAYNQQVHRDALSRLKRGMSALHEQGKYADLEPEIVLAELQKIASGEAKSVSDLNPKVVQFLNSEFSPASLRETLFEPESWEEYAAIAVDVLYPTPGGKAAAIEKAGGKLSKEALEALEKKFSESTKQELKSKLLQEDPRNLIPTQTKAEMSGSQIKRIVKSIKENGFDQEKPVDVWRNPKTGRLEIQDGHHRTEAAKKAGLDKIPVSIWE	smart00470	ParB-like Nuclease	CdiI15	VARYSVAFALPIGTDVSFSEDGWEFKSPAPLSLNVKSEFISKFNLELVECYSGVEKFSVDGLEFLVFYNDLHAIEYIYFKIYDKSFLVKLREYWSDNLRDYCYLFFPGE

TD04	CT16	NEALVSLVGEKIFPGEAHERVLAMTSQLIGMTVAAAAGGDTKAQEKAAWVAQQATVYNNLNHAAAESLLKEIKDCRAAGGCGEEKLQGILGKYEKLSAERSNAIGQCASRQCVDDIVDSSIRMDDPVSKELLSLLRQTTYDTPGLLQGNPDAVVSQTPNPSGWGDLFALDKQLAFAKNLKEGWLTPEETADLDRWNASTSWLDRTAGRQLDPKEKAYLLSELGGAAAMALLGGRGSVGAGAKGSSLPTPNATIASNGLVYKSNPKHTLGQPGNRPNAGIEPQDSLRLFEQSIASSKQYQNKEVRFAVDSRGDIHRFEGANGEFHWNGSSGDLRNPLVGSQIPNDIQKQLGVRVK	unknown	unknown	CdiI16	MIVGDPFYFALQFDVVDSWNSPGDSWRNGIFYLYVSGEKIFSVVDVLELETIFSFYSKAPIEGLCVNDVQLNSADIYKSASEYFWGDGVEVVKGLFDLTATAMSDNGCFLYFIKTSIGDRLVWSVDGGACVKEVYLEMDVVLNVIKKLRSCSL
TD05	CT17	NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAAGNCAEIRAEIDAGSTALNELVARQETANPGGSDSDIAYGFLMGRNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVSAKALMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPVKPGAKGAVIPKGFSNADDFARFGTDAREGLAKAGYGNVEPILQGSAITGQSFKTGQAFDVGRVSDFDIALAGSELLQRAQSLGIGLRSGGTRTGPLSGRDLQALGLKDLARKLSAQAGREVNFMIYDSAATAASRAPSLVLPK	unknown	unknown	CdiI17	MIAYDLYGTKNLSLFLAREHIEKIFGVSLDERNSSYQGGDYYMLGSNDSENFILKANLDPLDDEPVELNFPDYPILLYINATTRSSAIEGVIKKGACFKLLRHEMF
TD05	CT18	NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTALNELVARQETANPGGSDSDIAYGFLMGRNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVSAKALMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPVKPAVKSVVDDLGGVSSKITELPKATRNSPRNIQTDQSASDAIKNLVSAGFKNTPSKDGTVNVLTKGDKTYTFYSRSKTTGLPSAELKIGGNSKKNIAVKIRFENP	unknown	unknown	CdiI18	MNSSCQHVLCGLVDFSKKLPDNVVKVKKGMTFFVERSALYSLSILKLLFFVSVNSSAKKIFFCFLVAQKNKFEISSVYEVDLLEINFTEIENRLCALYEKHVLVGEVGRIVAFSDMVSWVLYEEVLEELGVLVMLDETKSVYSNFDFGEFVSREFMMEQADLGLYRKEYVDKLISNY
TD07	CT19	NEAMINLLGKMVGGDQNLELMASQLVGVAAASAVNGDVSLGAEIAKSGTAYNRQLHPDEIKFASDVERVKRYAQENGLSEDTARKELLSTAAMMVDNGWNQALAGTDINAARAAQYLRTELGTGPDSNLFQVTQADYYNERVGLTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLALEGIVSAPSKTALWLMGALTCSSCAERDIQNAWNSVASLPEDIRMKGYLDALHTMQGQGASVVRDNAASSTALGVEVGLAIDGGLAGAGKGVVTDGAKGTGEVASSGGRPTVELFGGQKAQTPGAINVDVRPDIQSGIRADATKLPFRDNSLGEVVASNPFIPKSAGGTNSMMDFLPEATRVIEPGGKIFINANAANPYGKIPSASELESLGLRIIQNGPLDSRFSGQTFLRTDGSVITNLDSMKTIVLEKIK	pfam08241	Methyltransferase	CdiI19	MIFVDFDELDTFNCTYGFSEEKSGALRVFVEGGLAFPYGMFLKEENGVRFFKCEKDNSENVGEIFPRHYIYDPSRRVEYVEWELSDDHLLRARTKSGEWVQYTSKADSQYAMHEFVGGCWFVFEGAHFSKRIINEYTDGREKSAGNKVIQEFGSRSCIDALSREYLLEGVLEVQPGPGWMLWYIYAKSFHIEIPDV
TD07	CT20	NEAMINLLGKMVGGDQNLELMASQLVGVAAASAVNGDVSLGAEIAKSGTAYNRQLHPDEIKFASDVKRVKRYAQENGLSEDTARKELLSTAAMMVDNGWNQALAGTDINAARAAQYLRTELGTGPDSNLFQVTQADYYNERVGLTALFKNKEALTSVLENIALANPASYTRDPANRAEVLNAKGEGSQAGFGLALEGIVSAPSKTALWLMGALTCSSCAERDIQNAWNSVASLPEDIRMKGYLDALHTMQGQGASVVRDNAASSTALGVEVGLAIDGGLAGAGKGVVTDGPKEIPKDLGKVSFDASNGVGTIYSPRVTLNSGEIIFDGFSVGTSKGLIGVGADGAAELVGPLRKMLSYSQSQGAQTITLKGHYASEQGSMLGTGSVNNVNQKFSFSFPATTDGLKAFLKELGK	unknown	unknown	CdiI20	VKIRRSIEKRMKDLEGSGRGCFYEREEEGQILFSTHLEEGRLDIYINGFAFGVEGRMRKLLFSEVVRIVSHLSIEMFSSAGDQGDLDFYVPLDVECESLNVTLSVPFLAYSNIMNILLGLREDWIKRDYSDG
TD09	CT21	NEALVNSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKGVQKLPELGGVDTFLSSQAANLNKKLGAKIGEGRLPYEASRAGVEQAKLAVKETLENATAVSDIIPKSAVRGNYDLVHVYSSKTNSTVSLRVLPGGKYEFDTLISEKSSKF	unknown	unknown	CdiI21	MIIGEKIFEFRFRSFFMSGSLVCKMLVLFLRFSRSGWVSLDIGEGVLRILSFGSEPKLLGLDEISDDFAYPIQSSNELDRYFGKDLLAVYKYLISDVEDGCVGVYFDFGDCGFSVLESEDNLSIIDGVVRVSDDVALSKLEI
TD09	CT22	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGTKATASAGGQTASTLPKNFGESVLGHNTQIGVRNSKAGTISGAHNNDAFLESVEITGAKVSNKITDARFPGIVEYSYQLPRTNTKGEFIGGYKSVSTKTTYDPKILPDSKVADMSSRAAVQAESVFKANPALRETSIKVDGYYFQVTRNSKTGEITNSFITMPPRIK	unknown	unknown	CdiI22	MMACLSWLEKLKESFASTGLDYEDLYELIEASITRKRTNFPAFINEASKGVGFSVGEGHFYSLDQDWDDPEEFNEVSFFLGEVETSSIPVLDYVFLMKIAADVYSDFFPEERDSVLSSAKKLEERYSKRFPV
TD09	CT23	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKGTATAGKVADEFIPPGMERPFRPVNPEFPPNKAVVDAMESPRIKGMTACDGTDCSEIASKLLAAAGGKGKVIEVRPTQRSNLNLYENGNEVPGQAYHQVYTDGRYVYDPRLSSQPIPKGDWEQHIKGMNPDGVTISDKLQGLR	unknown	unknown	CdiI23	MNTPEIKRESSSLLELIEALGETEWRKCVNSQFINKERGEWVIKDQSSHPPRVWFRFIQEDPAIISRLRVAIESYQGRVKWVLDEHKRVDLPGTNWGIVPSRLLEVWDLARALDLAPNQYMAKYEPEFGSIAYEDIIDLTEHIRRAFPEVTSKNPSL
TD09	CT24	NEALVDSLAKQYASLPIDDKKGLLTMSSQLIGMLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGKLGGGPKGSATALQNFGGRTANDLVAAATEPINKEGLTKAARALTKHASGQRATGTFPKLTGGIENQNSVAQKIVDEIVTDPKAVYTNLSRGGLEIRVPDGRGIRYNSDGSFSTFLDPKL	unknown	unknown	CdiI24	VIMKLERNPDFEILRSSDVRYEHLTTEVQYKGEPVAQINQDKGKENLELEIFADLKDAVLRVPLDDFLESLRLARNSLLSND
TD09	CT25	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDSYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGPKATGTAAEAAIQVPGRVQSRVNLMTGDKSAGWEHVVSRHFNPEVNASQFTIGQAELRTLLQSKEVVSAPVTRMLESAQGIRYVREVNLSGPIGIDKFSGQPTSTMTVLTDRFGNLITTTPGVVK	unknown	unknown	CdiI25	VKLIGSLAEQSCREELSKSWGGLRESGNQLFSILADRLGLIGSAFVLSWTPEQAEDLYTILVNGSEVVWLEVSRSNGEVVDFQTTSVKEYERSLRSRQSRIKLAVALDLARQH
TD09	CT26	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKATATVIDTAPMAQRVMDVRAGLPSNLRRSGNVAIAEIDIPGIPRQMAAHSQVSDAGKGLIGSGSGNFVAQSVPNKAGDMVYRGIDTEYKILDNIADQLGSNTSARGTVNILTEKAACASCLNVAEQFKAKYPNITVNILDNQGVMLRPPRKTP	pfam14424	Deaminase	CdiI26	MEERVTYGEIRAWFLGSYYNYCRVKLNHQSPWVEGESEVGYAYSELENSFDLPIEKLMLEVLALILSAGRSSDKVKRYHLDIIHGLLKEIKLSSVLDDLPSDEAAELRDDLRVLGLY
TD09	CT27	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQFGAVGDLGRLGGGAKGVATAERAALPAGYREGSSAGSGFAETAGLPDGYRRVINTKTGNTEVLAADGKLYLETGNGLQPKAGGNLAGLVEAEKSIAAGKEPTRFIDGVTVVDKKTGNVLQGTVDLGPTLDRIKSGGSYPHKNDGSIFQNRAGDLPVKPAGYYTEYVHPTPGVTGPGAQRIVVGKGGEMYYTADHYKTFIPINN	cd00607	RNase	CdiI27	LRVTSLSIKYYESMPSYSAAEVFYVRVDPGISVPDELLKALYYLLWFPGYFGFNWDALYDCLNDFEWIPCKKIVIVHERLPNFADEDLKIYLEILRDAVASWSGSEAHEFEVFFRESDQCRVESILAS
TD09	CT28	NEALVDSLAKQYASLPIDDKKGLLTMSSQLIGMLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKGATPKTETYFRVEGGGSGAATSQNRITVNTDGSIKINPGCSGQLCVSVGSADHASYFLTNKRPDGSVVVFEVDAGLHKQIMDSAIPQRPVPGVPRDPSAPKIVDPSQPGVALELPKMWESLLEKHSSNARLYSHDEFLKEFGR	cd16400	Nuclease	CdiI28	MTQWQLLADDLWGGEKNICFFVHSGACFWVVDDKFNFSLDAEKDYRAYLDKGHITQEQYASACMTFRGGVLKLTAENFLKYLRAEERWVLSRQDLKDMFVCGLDLSESLHGRIEDYYLSGVELSASYFHDANTVASRLPMFYVNFDRKIYMHMDCNRAHEELAYSDWLAKCSDFCHLVPDRERYWVLEGMDYWKYRFLQSA

TD9	CT29	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQYNFLNHVENEERWKSQKACQGGDEAACGRADAWDKLDRDRDLALMTACSTGGQASTCSALRQEAWKAAQSLKQASWSPEAREQYAQVMQNPELRAYTIESELRSINQVNNPITAGDSKRLAKALASFGSDFVPVYGDTKAFSEAQDPFDYAMAGVGLVPGAGDAAQKVLSKAKKLFQEGKVAESADLVEGLTKGVKNSSAAKGFIPAERTGLNFEEKVKNKAGGYVDVELSARQKFDKSGVVVDSKFAQSDLVARYSPDGNLYIDWYGTTVSGKGVGSEMISRAIEAVGANKVKTVSAQLGKDNLDAFKAGSSRGLSKEQAVWNTPLGKTMNSLGFTEVEVHGASVKFLHLE	unknown	unknown	CdiI29	MDKVDIIRELIRLGKVKVVLEFVEGDSVYISDASEGVPQHPDLRRIWVMMVHHLRFVSEFGDALETQCKDGKYLSPHYEEFEAWLSAGAPGIADKDLRAYLKENPL
TD9	CT30	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGMLAASTQGDADAKSLQTGAWVAGNATQNNYIEHSDVLAFAEDMRSCGKDEGCQKDKWEKERYSDESKLNVQEAQNTYGPLRAKEKRLQIVESMDTLVSIQCVTSRCESYKTELLEQSVDSYIHLSKVLDEWAPTLDRLALIGGAAAGKQIDSKVKRPGMPEPVELAQVQKAVDYLAALKATGASGKPLVSKGSEVTPEVIQKALQGDRVITAQGAVSLPAVQRYVDRLLKGDVAPAIKMDGNVIVDGNHRYIAAKILGRNLDVTPGSLSPNKVHQTKPVSELKIDQVDWGNK	unknown	unknown	CdiI30	MITIFFETGEKLDLPLASFAKSNLSGLELHRAIFDGLDLSEADFTASNLRNASFNHALLGGAVMNSAALMNASFVDAIMKGVKLVDAMAAYADFSGADLSMASLKNADIGGSNFINSNLRDVNIDVARIDGAVFRGAIYNDRTIWPKGFIPENFGAIKG
TD09	CT31	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGTKATASAGGQTASTLPKNFGESVLGHNTQIGVRNSKAGTISGAHNNDAFLESVEITGAKVSNKITDARFPGIVEYSYQLPRTNTKGEFIGGYKSVSTKTTYDPKILPDSKVADMSSRAAVQAESVFKANPALRETSIKVDGYYFQVTRRGCAEFCVTGVRVTAAAGGLRS	unknown	unknown	CdiI31	MGYTVSSGRDCQALTSSATASVTEEIRLGDTSAPYISCKCAWISRTVMPRAYSERILSSKPVQRVWCFSMICGSKVPCRSRGTSMGSSPNSPLSFFLLKPLRVLPIQLLTG
TD09	CT32	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGGKGYVDILSHEAKQHILYGDKPGSGGHLWPGQAGKTVFPQNWSADKIVHEVGDIATSPSTKWYAQTGTGGVYTSKGDPAKWVAYEVRDGVRMRVVYQPATGKVITAFPDNAPIPPYKPIK	pfam14436	Nuclease	CdiI32	MYADRIVKFGERFQGRLESTLLQGALDYVGYNEESLAFEVLCDHICEYDVSITDEEYREAVQLALDMGFDLEEGPFKHLKGLKS
TD09	CT33	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGKLGGVAKGAEVPKNPNPTSALTDAEAGTSSLPKIGSLKGEPELPPKNASPEMVRSIDRQNEAAKSLARAGYDVEQLPNIKKNSANPDLKINGEFADVFSPRTNSPVSVLMTVTEKVEKQAQNIVVNLADSPLTFKQIENALSVKPVDGLKNLYLLKDGQFKAIEVGR	cd13442	tRNase	CdiI33	MSITMALEIQVGATLESIASTLSSLGESCSLGDTRLDANFESSGCQFSVRSLEQPEGIVAEGCSMSWKVGLRGAFHCRGSNLSESWVDIKLFLQELSLNIEFGFVLSFQYESIYAIRDSDGLSFKRSMID
TD09	CT34	NEALVDSLAKQYASLPIDDKKGLLTMSSQLIGMLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKPLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKGTANFPEGMSFNPNIKNHLSNFDGLTQKSGISGTHNLDAFNQAATTNGVKVLSETPTSVAGITTVRYQIPAYDRAGNIVGFKDKIFPKTVYDPKIFTDQGILDLGQQAAAGGYKDALSKGVSQYDSVAGGITFRVYLDKFTGTVTNFHPK	pfam14436	Nuclease	CdiI34	VLVKELFGQPYSESDPYWVVKGYFDRMYDDGYFIEALGYIVKRWGFSTDGAYCNFPDENSPFDEEHFEGVEFSYGYPPKDEDTIVVSEAVCSKFIRLACEKYLQRHPEDTEKVKELLDKLSF
TD05	CT35	NEALVAKLDQAFKSLSPENREAMVTMGSQLVGVLAAAVRDPDATGKALESAAWVAKNSTQYNFLNHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAVGNCAEIRAEIDAGSTALNELVARQETANPGGSDSDIAYGFLMGRNVVDWTTAGQLHLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVSAKALMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPVKLGAKGLSSVKHASGVELPKSQAQMIANFETAGYPSKPVVSPTSGNVVGTQYTLPDGSRVRVMQADGRSPQRASFENANGGPIDPTTGKPPQPPKGLSKAERKQWIRERTHIEQVD	cd07562	Protease	CdiI35	MFDLLRLVISFLPLCIKTVEWDGDSLVISGDNWSFITSSAWRISQGKELLFACWDDQVDTRTEGLVGLSIVDMSWVTSGQPIDPSFILSDGRRLDVFCSSFSEPWVMNLPDNSVYVGNS
TD03	CT36	NEAVVAAFGEKIFPGEQHEKLLGMTSNLIGMTVAAAAGGDEKAQEKAGWVAQQATLNNYLFHEEMEEMANKIKACGGDQNCEQPIREHYADLDEQRNKAFPELCRANLTSCVQIANRLSAEEQLNVDLMESLRNAQYNGIAGAIGIAFIPSNRVSADQATLEYVRQTGGTAEEFKAVLAMLGAGVAGVGPKTVEKATNALDRLKALQAAKGTVPAEVPATSVIAKEGLYNELRAAQARDALIGTTLPGAKAPVTVTAEGSVGGKVLVDTNQTARPAMVAENKPTLIADLLPLGSPNSSMANAHAEIAVIQRAFDAGITKGQDMAIIVRGERVCSFCRSSNNILAAADRSGLNSLKLVEAESGKIFTWTRGIEGWK	pfam14437	Deaminase	CdiI36	MFDLEDEKPICLELCYLDRSNSPPAVIVENPVWESISEGIRKVYKFGGFVRLSVNEPQSSLVRELSMDSLPGRFKLAVLTSSPNPKEEYLEWWEFGDSPFRGVVRFGDDEFDSRTVCADISIAEAVFKELYETGGLDVGLAQMRSPWNPKP
TD03	CT37	NEAVVAAFGEKIFPGEQHEKLLGMTSNLIGMTVAAAAGGDEKAQEKAGWVAQQATLNNYLFHEEMEEMANKIKACGGDQNCEQPIREHYADLDEQRNKAFPELCRANLTSCVQIANRLSAEEQLNVDLMESLRNAQYNGIAGAIGIAFIPSNRVSADQATLEYVRQTGGTAEEFKAVLAMLGAGVAGVGPKTVEKATNALDRLKALQAAKGTVPAEVPATSVIAKEGLYNELRAAQARDALIGTTLPGAKAPVTVTAEGSVGGKVLVDTNQTARPAMVSDASKKTLISDLIPPGSPNSTMANAHAEMAVIQRAYDAGLTRGQSMSIIVRGEEICSFCQSSTNILAAAERSGLNSLKLVEAKTGRTFTWTRGIDGWR	pfam14437	Deaminase	CdiI37	MILDYEDDLEPVLELCCGDNSASSLAVVVEQPVWESIEKGIVNSFKFGGFVRVEVIRPKKSFVRQLSMKSLPGRFRINILTRSTNPKEEYLEWWELDESPYRGMIKFGDDDFDSRTVCTDISIAEAIFKELYETGDLDVGLSQMRSPWNPKP
TD09	CT38	NEALVNSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDSYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKATPSADSLINLASNQRSQHILLGDATGGGHLWPGAPGKTAFPASWNGDKVMHNVSDLATDPKASWTQLTGKPGAQFTTKGKPVRWAVEGVRDGVNIRVIVEPHGEGIITAYPK	pfam14436	Nuclease	CdiI38	MREPEKIIQAVLEEISGCFGDDTERNVKELLACGEPGVALEVFCSQLVEFDIAIPLEKKEQLTVAAGVMGMEIEELQDLKSL
TD09	CT39	NEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQGDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKPLCKTGIEAKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQLATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAELVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGRLGGGAKGTTPTVTAEGRIGNSVFTDVNQTARPAAQANPNQPTLIADRVDAKIAANGKPHPNGNMADAHAEIGVIQQAYNAGKTTGADMALKVEGKAVCSYCRGDIAAAAEKAGLNSLQINEVTTGKTLYWKPGMRSLRELE	pfam14437	Deaminase	CdiI39	MAAFSLSWVFGVGAQAKGGRNRFPSWDDVLSCLELIREGKGSVTLELISKTAVGPQSLQVQSEGGKYVVSLGEDDGVDYIVRSYRNLKLQGIPFEVLGDVWDGVLICDEFSILKNIFEEFFLTGDVSKELLN

TD = Translocation Domain, CT = C-terminal domain

METHODS

Complete assemblies for all *P. aeruginosa* NCBI reference genomes included in this study were accessed through NCBI (https://www.ncbi.nlm.nih.gov/refseq/) and are listed in Supplementary Table 1. Genome assemblies of the *P. aeruginosa* PABL strains can be accessed through NCBI (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA485889/). The *cdiA1* and *cdiA2* genes of all *P. aeruginosa* strains were identified by BLASTn search using the PAO1 query sequences of PA0041 (*cdiA1*) and PA2462 (*cdiA2*). Sequences of the *cdi* loci from all PABL strains were deposited in NCBI and are listed in Supplementary Table 2. Sequences were aligned using Clustal Omega (1) and annotated protein domains were identified using the CD-search function of the Conserved Domain Database (2). Amino acid frequency plots were determined using a 40-amino-acid sliding window and visualized in R with the ggplot2 package (3). kSNP3 was used to determine phylogenetic relationships between strains and construct maximum likelihood trees (4). Trees were visualized in R using ggtree (5).

Supplemental References

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