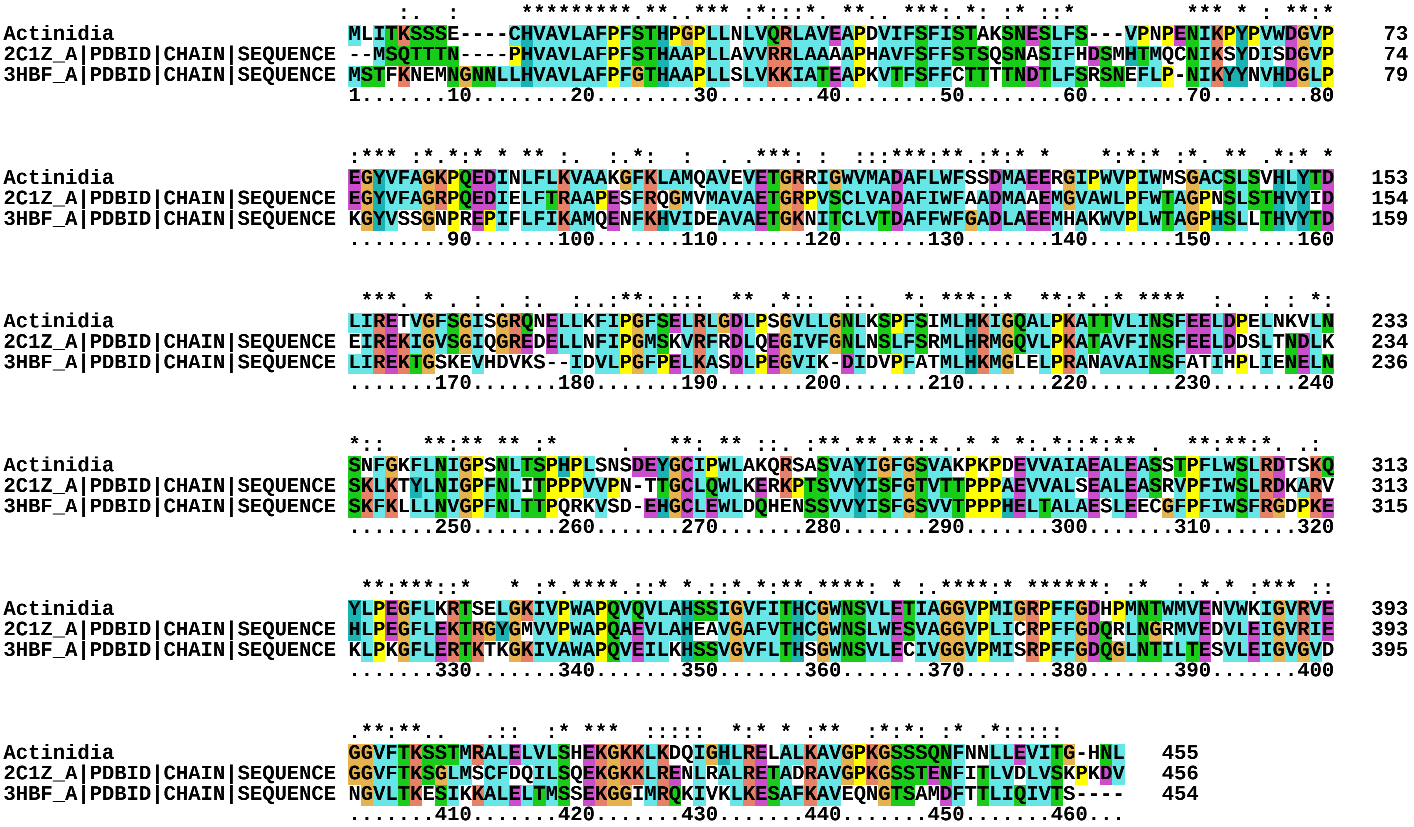
Figure S2 Multiple sequence alignment between query (30F3GTs) and template (PDB ID: 2C1Z, 3HBF and 3WC4) generated by ClustalX



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                                ":.  :     *********.**..*** :*:::*. **.. ***:.*: :* ::*         *** * : **:*
Actinidia                   MLITKSSSE----CHVAVLAFPFSTHPGPLLNLVQRLAVEAPDVIFSFISTAKSNESLFS---VPNPENIKPYPVWDGVP    73
2C1Z_A|PDBID|CHAIN|SEQUENCE --MSQTTTN----PHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

                            :*** :*.*:* * ** :.  :.*:  :  . .***: :  :::***:**.:*:* *    *:*:* :*. ** .*:* *
Actinidia                   EGYVFAGKPQEDINLFLKVAAKGFKLAMQAVEVETGRRIGWVMADAFLWFSSDMAEERGIPWVPIWMSGACSLSVHLYTD   153
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             ***. * . : . :.  :..:**:.:::  ** .*::  ::.  *: ***::*  **:*.:* ****  :.  : : *:
Actinidia                   LIRETVGFSGISGRQNELLKFIPGFSELRLGDLPSGVLLGNLKSPFSIMLHKIGQALPKATTVLINSFEELDPELNKVLN   233
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            *::   **:** ** :*     .   **: ** ::. :**.**.**:*..* * *:.*::*:** .  **:**:*. .:
Actinidia                   SNFGKFLNIGPSNLTSPHPLSNSDEYGCIPWLAKQRSASVAYIGFGSVAKPKPDEVVAIAEALEASSTPFLWSLRDTSKQ   313
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPPVVPN-TTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARV   313
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQRKVSD-EHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKE   315
                            .......250.......260.......270.......280.......290.......300.......310.......320

                             **:***::*   * :*.****.::* *.::*.*:**.****: * :.****:* ******: :*  :.*.* :*** ::
Actinidia                   YLPEGFLKRTSELGKIVPWAPQVQVLAHSSIGVFITHCGWNSVLETIAGGVPMIGRPFFGDHPMNTWMVENVWKIGVRVE   393
2C1Z_A|PDBID|CHAIN|SEQUENCE HLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIE   393
3HBF_A|PDBID|CHAIN|SEQUENCE KLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVD   395
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            .**:**..   .::  :* ***  :::::  *:* * :**  :*:*: :* .*:::::
Actinidia                   GGVFTKSSTMRALELVLSHEKGKKLKDQIGHLRELALKAVGPKGSSSQNFNNLLEVITG-HNL   455
2C1Z_A|PDBID|CHAIN|SEQUENCE GGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE NGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460...
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                                .:   .    *********.*******::.:::*: :* ..**** *: :* ::*  .       **: *:: **:
Arabid7                     MTKPSDPTRDS---HVAVLAFPFGTHAAPLLTVTRRLASASPSTVFSFFNTAQSNSSLFSSGDEADRPANIRVYDIADGV     77
2C1Z_A|PDBID|CHAIN|SEQUENCE ---MSQTTTNP---HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSYDISDGV     73
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRS--NEFLPNIKYYNVHDGL     78
                            1.......10........20........30........40........50........60........70........80

                            *:*** :*.*:* * ** :*  *.*:: :  * :*.*  :.**::***:**.**:* *: . *:.:****.:** :*:*
Arabid7                     PEGYVFSGRPQEAIELFLQAAPENFRREIAKAETEVGTEVKCLMTDAFFWFAADMATEINASWIAFWTAGANSLSAHLYT    157
2C1Z_A|PDBID|CHAIN|SEQUENCE PEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYI    153
3HBF_A|PDBID|CHAIN|SEQUENCE PKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYT    158
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            * ***. * . :    .  :..:.*: :::  *  **::  :::  *: ***:**  **:*.** ****  :.  : *:*
Arabid7                     DLIRETIGVKEVGERMEETIGVISGMEKIRVKDTPEGVVFGNLDSVFSKMLHQMGLALPRATAVFINSFEDLDPTLTNNL    237
2C1Z_A|PDBID|CHAIN|SEQUENCE DEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDL    233
3HBF_A|PDBID|CHAIN|SEQUENCE DLIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENEL    235
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            .*::*  **:**:.* :.     * :  *** *:.::.  **.*****:* **** *:.*::*.** . .**:**:: ..
Arabid7                     RSRFKRYLNIGPLGLLSSTLQQLVQDPHGCLAWMEKRSSGSVAYISFGTVMTPPPGELAAIAEGLESSKVPFVWSLKEKS    317
2C1Z_A|PDBID|CHAIN|SEQUENCE KSKLKTYLNIGPFNLITP--PPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKA    311
3HBF_A|PDBID|CHAIN|SEQUENCE NSKFKLLLNVGPFNLTTP--QRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDP    313
                            .......250.......260.......270.......280.......290.......300.......310.......320

                              :**:***::*:  * :*.****.*:* *.:.*.*:**.****: *.: ****:*.******* **   .* * ***:
Arabid7                     LVQLPKGFLDRTREQGIVVPWAPQVELLKHEATGVFVTHCGWNSVLESVSGGVPMICRPFFGDQRLNGRAVEVVWEIGMT    397
2C1Z_A|PDBID|CHAIN|SEQUENCE RVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVR    391
3HBF_A|PDBID|CHAIN|SEQUENCE KEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVG    393
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            : .**:**..: ..::  : .:.*  :: :   *:* * .**  :* *: :*  *:: * .
Arabid7                     IINGVFTKDGFEKCLDKVLVQDDGKKMKCNAKKLKELAYEAVSSKGRSSENFRGLLDAVVNII--   460
2C1Z_A|PDBID|CHAIN|SEQUENCE IEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE VDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.....
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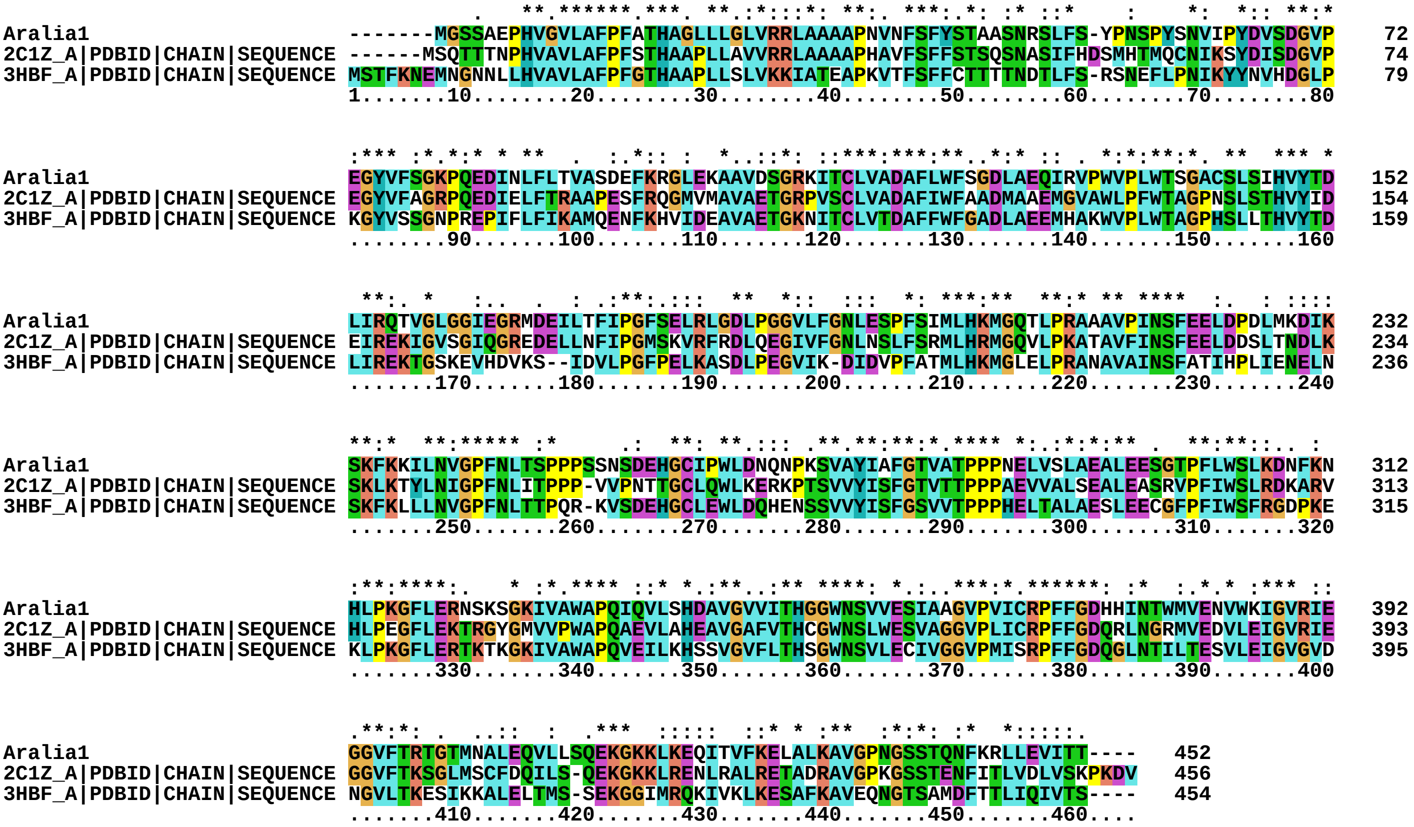

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                                      .   **.******.***. **.:*:::*: **:. ***:.*: :* ::*    :    *:  *:: **:*
Aralia1                     -------MGSSAEPHVGVLAFPFATHAGLLLGLVRRLAAAAPNVNFSFYSTAASNRSLFS-YPNSPYSNVIPYDVSDGVP    72
2C1Z_A|PDBID|CHAIN|SEQUENCE ------MSQTTTNPHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFS-RSNEFLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

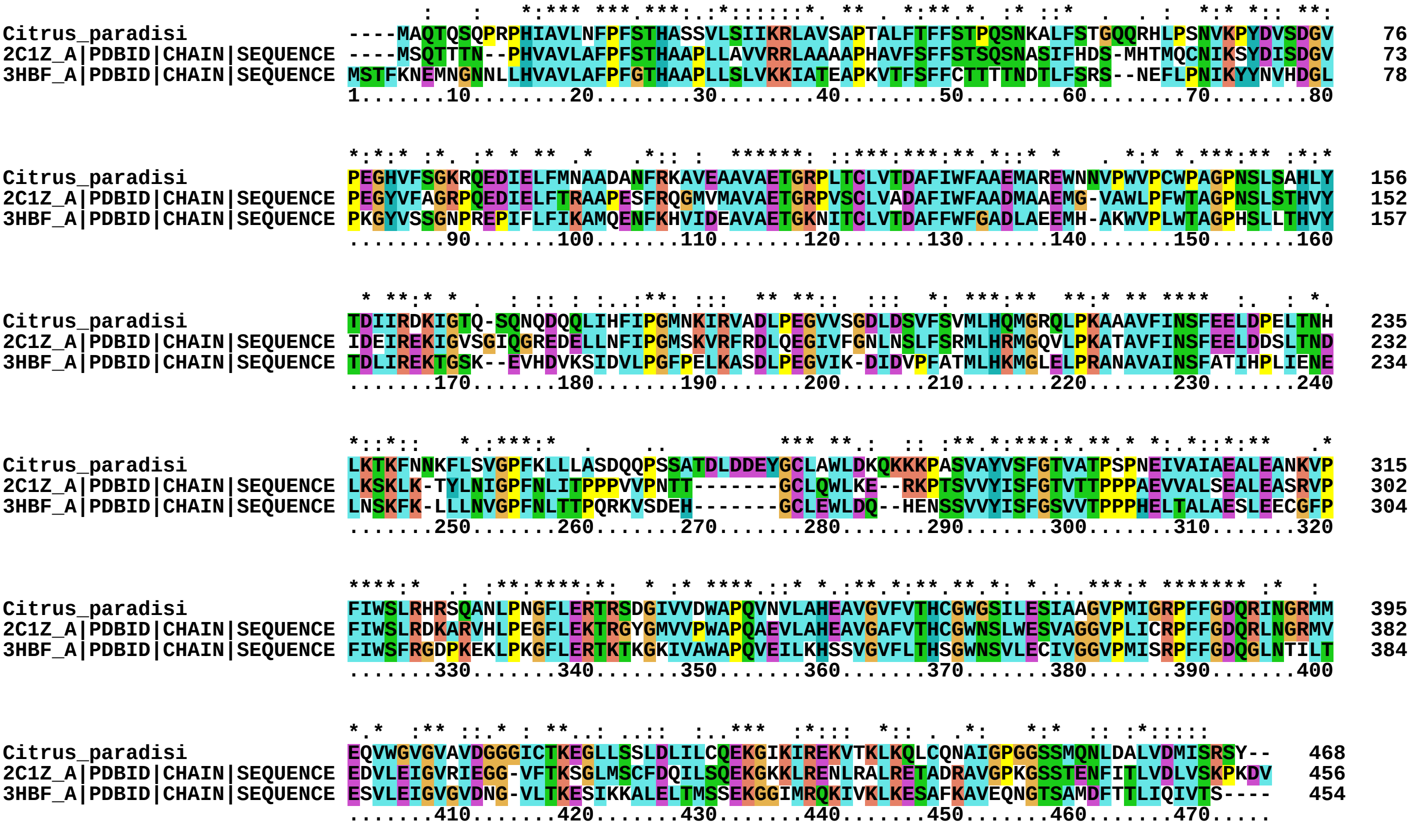
                            :*** :*.*:* * **  .  :.*:: :  *..::*: ::***:***:**..*:* :: . *:*:**:*. **  *** *
Aralia1                     EGYVFSGKPQEDINLFLTVASDEFKRGLEKAAVDSGRKITCLVADAFLWFSGDLAEQIRVPWVPLWTSGACSLSIHVYTD   152
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             **:. *   :..  .  : .:**:.:::  **  *::  :::  *: ***:**  **:* ** ****  :.  : ::::
Aralia1                     LIRQTVGLGGIEGRMDEILTFIPGFSELRLGDLPGGVLFGNLESPFSIMLHKMGQTLPRAAAVPINSFEELDPDLMKDIK   232
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            **:*  **:***** :*     .:  **: **.::: .**.**:**:*.**** *..:*:*:** .  **:**::.. :
Aralia1                     SKFKKILNVGPFNLTSPPPSSNSDEHGCIPWLDNQNPKSVAYIAFGTVATPPPNELVSLAEALEESGTPFLWSLKDNFKN   312
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPP-VVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARV   313
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQR-KVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKE   315
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            :**:****:.   * :*.**** ::* *.:**..:** ****: *.:. ***:*.******: :*  :.*.* :*** ::
Aralia1                     HLPKGFLERNSKSGKIVAWAPQIQVLSHDAVGVVITHGGWNSVVESIAAGVPVICRPFFGDHHINTWMVENVWKIGVRIE   392
2C1Z_A|PDBID|CHAIN|SEQUENCE HLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIE   393
3HBF_A|PDBID|CHAIN|SEQUENCE KLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVD   395
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            .**:*: .  ..::  :  .***  :::::  ::* * :**  :*:*: :*  *:::::.
Aralia1                     GGVFTRTGTMNALEQVLLSQEKGKKLKEQITVFKELALKAVGPNGSSTQNFKRLLEVITT----   452
2C1Z_A|PDBID|CHAIN|SEQUENCE GGVFTKSGLMSCFDQILS-QEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE NGVLTKESIKKALELTMS-SEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460....
```



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                                  :   :   *:*** ***.***:.:*:::::*.  ** . *:**.*. :*  ::* .  . :  *:* *:: **:
Citrus_paradisi             ----MAQTQSQPRPHIAVLNFPFSTHASSVLSIIKRLAVSAPTALFTFFSTPQSNKALFSTGQQRHLPSNVKPYDVSDGV    76
2C1Z_A|PDBID|CHAIN|SEQUENCE ----MSQTTTN--PHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSYDISDGV    73
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRS--NEFLPNIKYYNVHDGL    78
                            1.......10........20........30........40........50........60........70........80

                            *:*:* :*. :* * ** .*   .*:: :  ******: ::***:***:**.*::* *   . *:* *.***:** :*:*
Citrus_paradisi             PEGHVFSGKRQEDIELFMNAADANFRKAVEAAVAETGRPLTCLVTDAFIWFAAEMAREWNNVPWVPCWPAGPNSLSAHLY   156
2C1Z_A|PDBID|CHAIN|SEQUENCE PEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMG-VAWLPFWTAGPNSLSTHVY   152
3HBF_A|PDBID|CHAIN|SEQUENCE PKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMH-AKWVPLWTAGPHSLLTHVY   157
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             * **:* * .  : :: : :..:**: :::  ** **::  :::  *: ***:**  **:* ** ****  :.  : *.
Citrus_paradisi             TDIIRDKIGTQ-SQNQDQQLIHFIPGMNKIRVADLPEGVVSGDLDSVFSVMLHQMGRQLPKAAAVFINSFEELDPELTNH   235
2C1Z_A|PDBID|CHAIN|SEQUENCE IDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTND   232
3HBF_A|PDBID|CHAIN|SEQUENCE TDLIREKTGSK--EVHDVKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENE   234
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            *::*::   *.:***:*  .    ..         *** **.:  :: :**.*:***:*.**.* *:.*::*:**   .*
Citrus_paradisi             LKTKFNNKFLSVGPFKLLLASDQQPSSATDLDDEYGCLAWLDKQKKKPASVAYVSFGTVATPSPNEIVAIAEALEANKVP   315
2C1Z_A|PDBID|CHAIN|SEQUENCE LKSKLK-TYLNIGPFNLITPPPVVPNTT-------GCLQWLKE--RKPTSVVYISFGTVTTPPPAEVVALSEALEASRVP   302
3HBF_A|PDBID|CHAIN|SEQUENCE LNSKFK-LLLNVGPFNLTTPQRKVSDEH-------GCLEWLDQ--HENSSVVYISFGSVVTPPPHELTALAESLEECGFP   304
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            ****:*  .: :**:****:*:  * :* ****.::* *.:**.*:**.**.*: *.:..***:* ******* :*  :
Citrus_paradisi             FIWSLRHRSQANLPNGFLERTRSDGIVVDWAPQVNVLAHEAVGVFVTHCGWGSILESIAAGVPMIGRPFFGDQRINGRMM   395
2C1Z_A|PDBID|CHAIN|SEQUENCE FIWSLRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMV   382
3HBF_A|PDBID|CHAIN|SEQUENCE FIWSFRGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILT   384
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            *.*  :** ::.* : **..: ..::  :..***  :*:::  *:: . .*:   *:*  :: :*:::::
Citrus_paradisi             EQVWGVGVAVDGGGICTKEGLLSSLDLILCQEKGIKIREKVTKLKQLCQNAIGPGGSSMQNLDALVDMISRSY--   468
2C1Z_A|PDBID|CHAIN|SEQUENCE EDVLEIGVRIEGG-VFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE ESVLEIGVGVDNG-VLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......470.....
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                            **  .      .  ****:.***.***:**: :.:::*:  *...****  . :* .:     .    .*: *:: **:*
Dianthus_1                  MSANSNYMN-KSRLHVAVFPFPFGTHATPLFNITQKLASFMPDVVFSFFNIPQSNAKISSDFKN---DTINMYDVWDGVP    76
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTT------TNPHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNE-FLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

                            :***  *.*:* * **  *   .: . :  * .***  ::*:: ***:**  ::* :  . *:. : :  :** :*:  *
Dianthus_1                  EGYVFKGKPQEDIELFMLAAPPTLTEALAKAEVETGTKVSCILGDAFLWFLEELAQQKQVPWITTYMSEEHSLLAHICTD   156
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             **:. *     .  :.  ::.:**:.:::  ** **::  :::  *: ***:**  **:*.** *.*   :.    *:*
Dianthus_1                  LIRQTIGIHEKAEERKDEELDFIPGLSKIRVQDLPEGIVMGNLDSYFARMLHQMGRALPRASAVCISSCQELDPVATNEL   236
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSG-IQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDL   233
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKE-VHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENEL   235
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            : *::  :*:**:.* *    :..    .* **.:::  .**.*:***:*. * . *:.**:::** . .  ****:*..
Dianthus_1                  NRKLNKLINVGPLSLITQSNSLPSGTNKSLGWLDKQESENSVAYVSFGSVARPDATEITALAQALEASQVKFIWSIRDNL   316
2C1Z_A|PDBID|CHAIN|SEQUENCE KSKLKTYLNIGPFNLITPPPVVPN-TTGCLQWLKERKP-TSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKA   311
3HBF_A|PDBID|CHAIN|SEQUENCE NSKFKLLLNVGPFNLTTPQRKVSD-EHGCLEWLDQHEN-SSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDP   313
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            : :** **:*.*:  *  :*.*.**. :*  *.:**.*:** * **: *.:.. **:* ***:*:* **  :.*    **:
Dianthus_1                  KVHLPGGFIENTKDKGMVVSWVPQTAVLAHKAVGVFITHFGHNSIMESIASEVPMIGRPFIGEQKLNGRIVEAKWCIGLV   396
2C1Z_A|PDBID|CHAIN|SEQUENCE RVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVR   391
3HBF_A|PDBID|CHAIN|SEQUENCE KEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVG   393
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            ::.**:**..:  .::  :.. :*  :*.::  *:  . :*:  .*:.  ::  *:::: .
Dianthus_1                  VEGGVFTKDGVLRSLNKILGSTQGEEMRRNIRDLRLMVDKALSPDGSCNTNLKHLVDMIVTSN--   459
2C1Z_A|PDBID|CHAIN|SEQUENCE IEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE VDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.....
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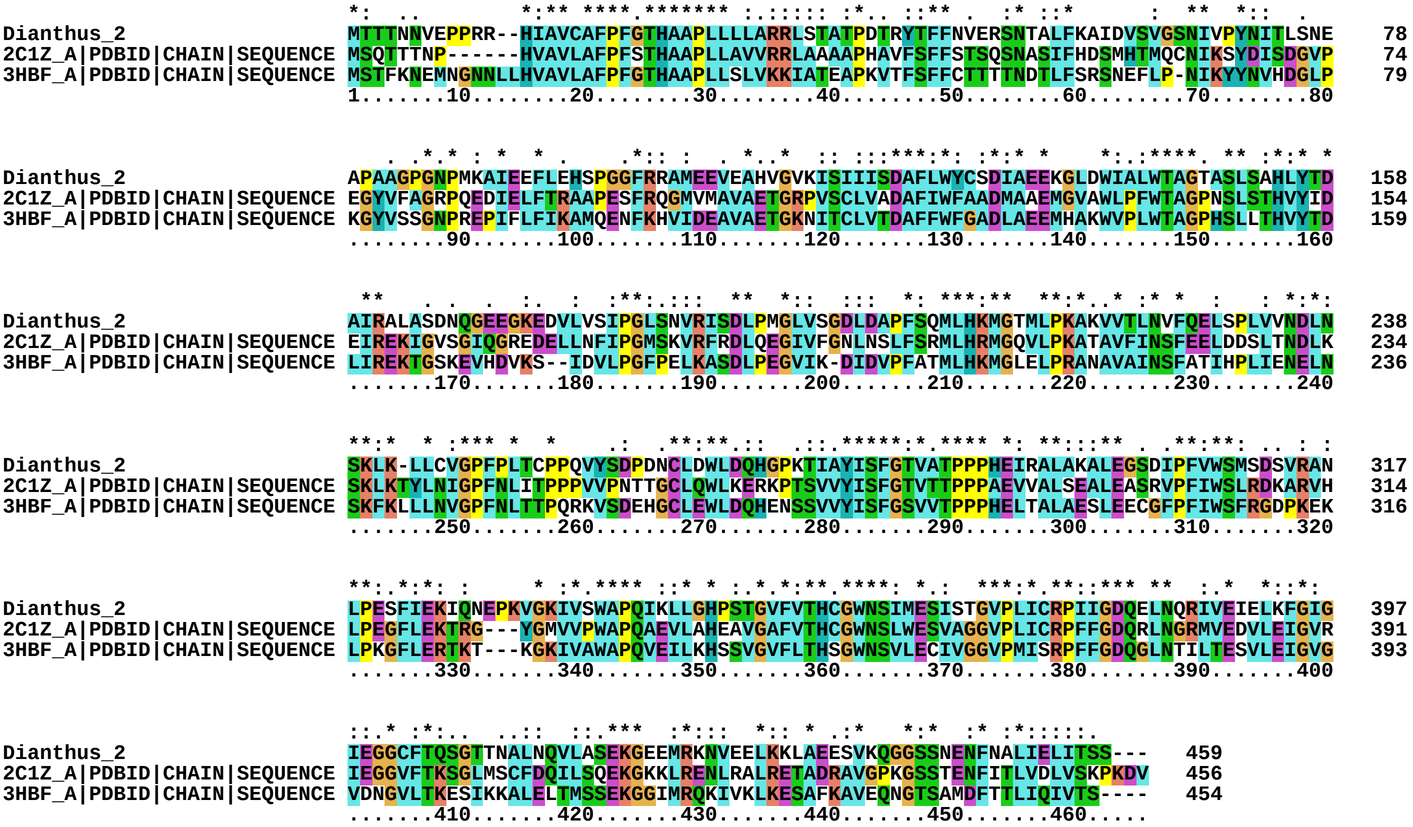

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                            *:  ..        *:** ****.******* :.::::: :*.. ::** .  :* ::*      :  **  *::  .
Dianthus_2                  MTTTNNVEPPRR--HIAVCAFPFGTHAAPLLLLARRLSTATPDTRYTFFNVERSNTALFKAIDVSVGSNIVPYNITLSNE   78
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTTTNP------HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP   74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGLP   79
                            1.......10........20........30........40........50........60........70........80

                               . .*.* : *  * .    .*:: :  . *..*  :: :::***:*: :*:* *    *:.:****. ** :*:* *
Dianthus_2                  APAAGPGNPMKAIEEFLEHSPGGFRRAMEEVEAHVGVKISIIISDAFLWYCSDIAEEKGLDWIALWTAGTASLSAHLYTD   158
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             **   . .  .  :.  :  :**:.:::  **  *::  :::  *: ***:**  **:*..* :* *  :   : *:*:
Dianthus_2                  AIRALASDNQGEEGKEDVLVSIPGLSNVRISDLPMGLVSGDLDAPFSQMLHKMGTMLPKAKVVTLNVFQELSPLVVNDLN   238
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            **:*  * :*** *  *    .:  .**:**.::  .::.*****:*.**** *: **:::** . .**:**: .. : :
Dianthus_2                  SKLK-LLCVGPFPLTCPPQVYSDPDNCLDWLDQHGPKTIAYISFGTVATPPPHEIRALAKALEGSDIPFVWSMSDSVRAN   317
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARVH   314
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKEK   316
                            .......250.......260.......270.......280.......290.......300.......310.......320

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Dianthus_2                  LPESFIEKIQNEPKVGKIVSWAPQIKLLGHPSTGVFVTHCGWNSIMESISTGVPLICRPIIGDQELNQRIVEIELKFGIG   397
2C1Z_A|PDBID|CHAIN|SEQUENCE LPEGFLEKTRG---YGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVR   391
3HBF_A|PDBID|CHAIN|SEQUENCE LPKGFLERTKT---KGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVG   393
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Dianthus_2                  IEGGCFTQSGTTNALNQVLASEKGEEMRKNVEELKKLAEESVKQGGSSNENFNALIELITSS---   459
2C1Z_A|PDBID|CHAIN|SEQUENCE IEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE VDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.....
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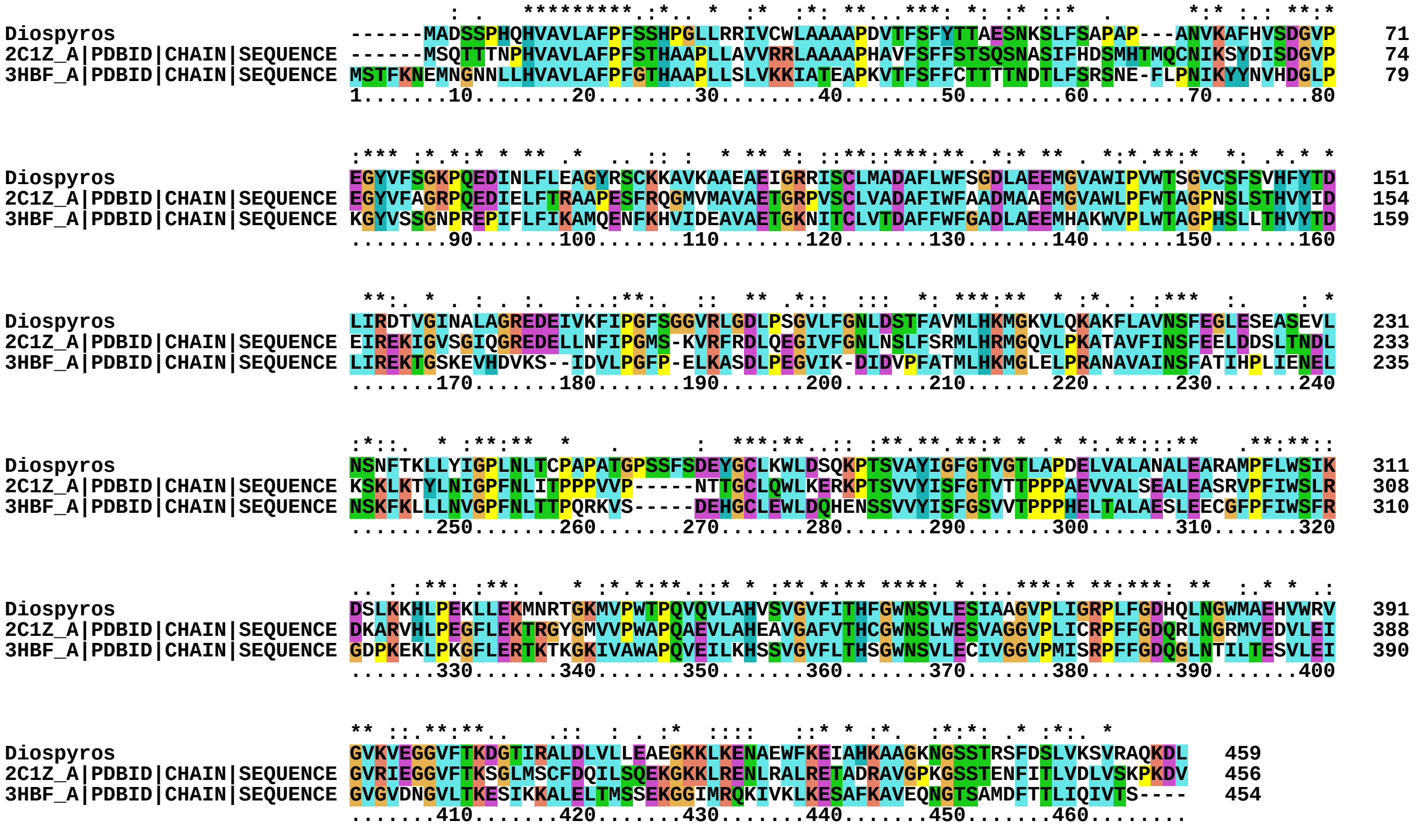

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                                    : .   *********.:*.. *  :*  :*: **...***: *: :* ::*  .      *:* :.: **:*
Diospyros                   ------MADSSPHQHVAVLAFPFSSHPGLLRRIVCWLAAAAPDVTFSFYTTAESNKSLFSAPAP---ANVKAFHVSDGVP    71
2C1Z_A|PDBID|CHAIN|SEQUENCE ------MSQTTTNPHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNE-FLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

                            :*** :*.*:* * ** .*  .. :: :  * ** *: ::**::***:**..*:* ** . *:*.**:*  *: .*.* *
Diospyros                   EGYVFSGKPQEDINLFLEAGYRSCKKAVKAAEAEIGRRISCLMADAFLWFSGDLAEEMGVAWIPVWTSGVCSFSVHFYTD   151
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             **:. * . : . :.  :..:**:.  ::  ** .*::  :::  *: ***:**  * :*. : :***  :.    : *
Diospyros                   LIRDTVGINALAGREDEIVKFIPGFSGGVRLGDLPSGVLFGNLDSTFAVMLHKMGKVLQKAKFLAVNSFEGLESEASEVL   231
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMS-KVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDL   233
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFP-ELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENEL   235
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :*::.  * :**:**  *   .      :  ***:**..:: :**.**.**:* * .* *:.**:::**   .**:**::
Diospyros                   NSNFTKLLYIGPLNLTCPAPATGPSSFSDEYGCLKWLDSQKPTSVAYIGFGTVGTLAPDELVALANALEARAMPFLWSIK   311
2C1Z_A|PDBID|CHAIN|SEQUENCE KSKLKTYLNIGPFNLITPPPVVP-----NTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLR   308
3HBF_A|PDBID|CHAIN|SEQUENCE NSKFKLLLNVGPFNLTTPQRKVS-----DEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFR   310
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            .. : :**: :**: .  * :*.*:** .:* * :**.*:** ****: *.:..***:* **:***: **  :.* * .:
Diospyros                   DSLKKHLPEKLLEKMNRTGKMVPWTPQVQVLAHVSVGVFITHFGWNSVLESIAAGVPLIGRPLFGDHQLNGWMAEHVWRV   391
2C1Z_A|PDBID|CHAIN|SEQUENCE DKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEI   388
3HBF_A|PDBID|CHAIN|SEQUENCE GDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEI   390
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            ** ::.**:**..   .::  : . :*  ::::   ::* * :*.  :*:*: .*  :*:. *
Diospyros                   GVKVEGGVFTKDGTIRALDLVLLEAEGKKLKENAEWFKEIAHKAAGKNGSSTRSFDSLVKSVRAQKDL   459
2C1Z_A|PDBID|CHAIN|SEQUENCE GVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE GVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460........
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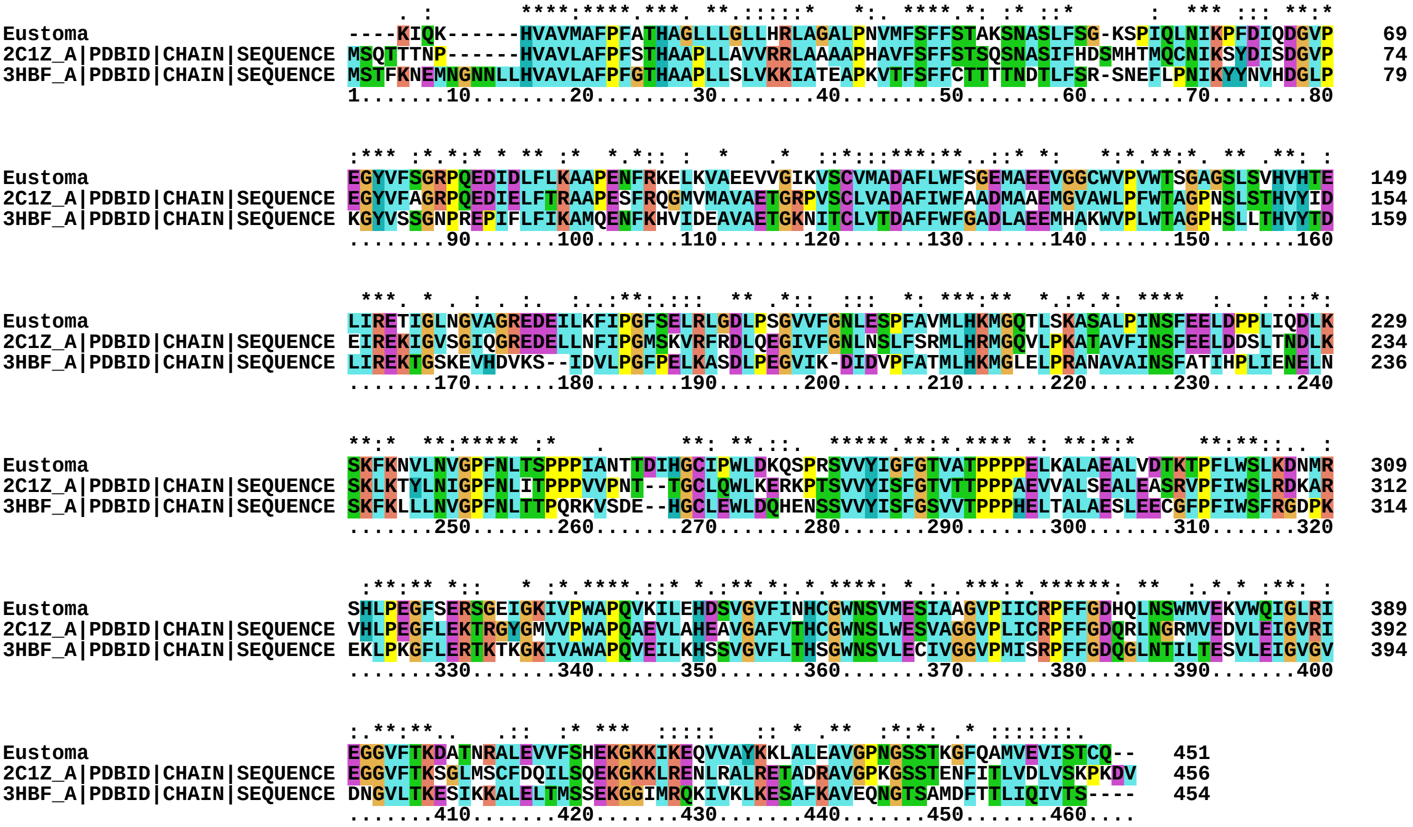

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Eustoma                     ----KIQK------HVAVMAFPFATHAGLLLGLLHRLAGALPNVMFSFFSTAKSNASLFSG-KSPIQLNIKPFDIQDGVP     69
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTTTNP------HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP     74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSR-SNEFLPNIKYYNVHDGLP     79
                            1.......10........20........30........40........50........60........70........80

                            :*** :*.*:* * ** :*  *.*:: :  *   .*  ::*:::***:**..::* *:   *:*.**:*. ** .**: :
Eustoma                     EGYVFSGRPQEDIDLFLKAAPENFRKELKVAEEVVGIKVSCVMADAFLWFSGEMAEEVGGCWVPVWTSGAGSLSVHVHTE    149
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID    154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD    159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             ***. * . : . :.  :..:**:.:::  ** .*::  :::  *: ***:**  *.:*.*: ****  :.  : ::*:
Eustoma                     LIRETIGLNGVAGREDEILKFIPGFSELRLGDLPSGVVFGNLESPFAVMLHKMGQTLSKASALPINSFEELDPPLIQDLK    229
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK    234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN    236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            **:*  **:***** :*   .      **: **.::.  *****.**:*.**** *: **:*:*     **:**::.. :
Eustoma                     SKFKNVLNVGPFNLTSPPPIANTTDIHGCIPWLDKQSPRSVVYIGFGTVATPPPPELKALAEALVDTKTPFLWSLKDNMR    309
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPPVVPNT--TGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKAR    312
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQRKVSDE--HGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPK    314
                            .......250.......260.......270.......280.......290.......300.......310.......320

                             :**:** *::   * :*.****.::* *.:**.*:.*.****: *.:..***:*.******: **  :.*.* :**: :
Eustoma                     SHLPEGFSERSGEIGKIVPWAPQVKILEHDSVGVFINHCGWNSVMESIAAGVPIICRPFFGDHQLNSWMVEKVWQIGLRI    389
2C1Z_A|PDBID|CHAIN|SEQUENCE VHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRI    392
3HBF_A|PDBID|CHAIN|SEQUENCE EKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGV    394
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            :.**:**..   .::  :* ***  :::::   :: * .**  :*:*: .* :::::::.
Eustoma                     EGGVFTKDATNRALEVVFSHEKGKKIKEQVVAYKKLALEAVGPNGSSTKGFQAMVEVISTCQ--    451
2C1Z_A|PDBID|CHAIN|SEQUENCE EGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV    456
3HBF_A|PDBID|CHAIN|SEQUENCE DNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----    454
                            .......410.......420.......430.......440.......450.......460....
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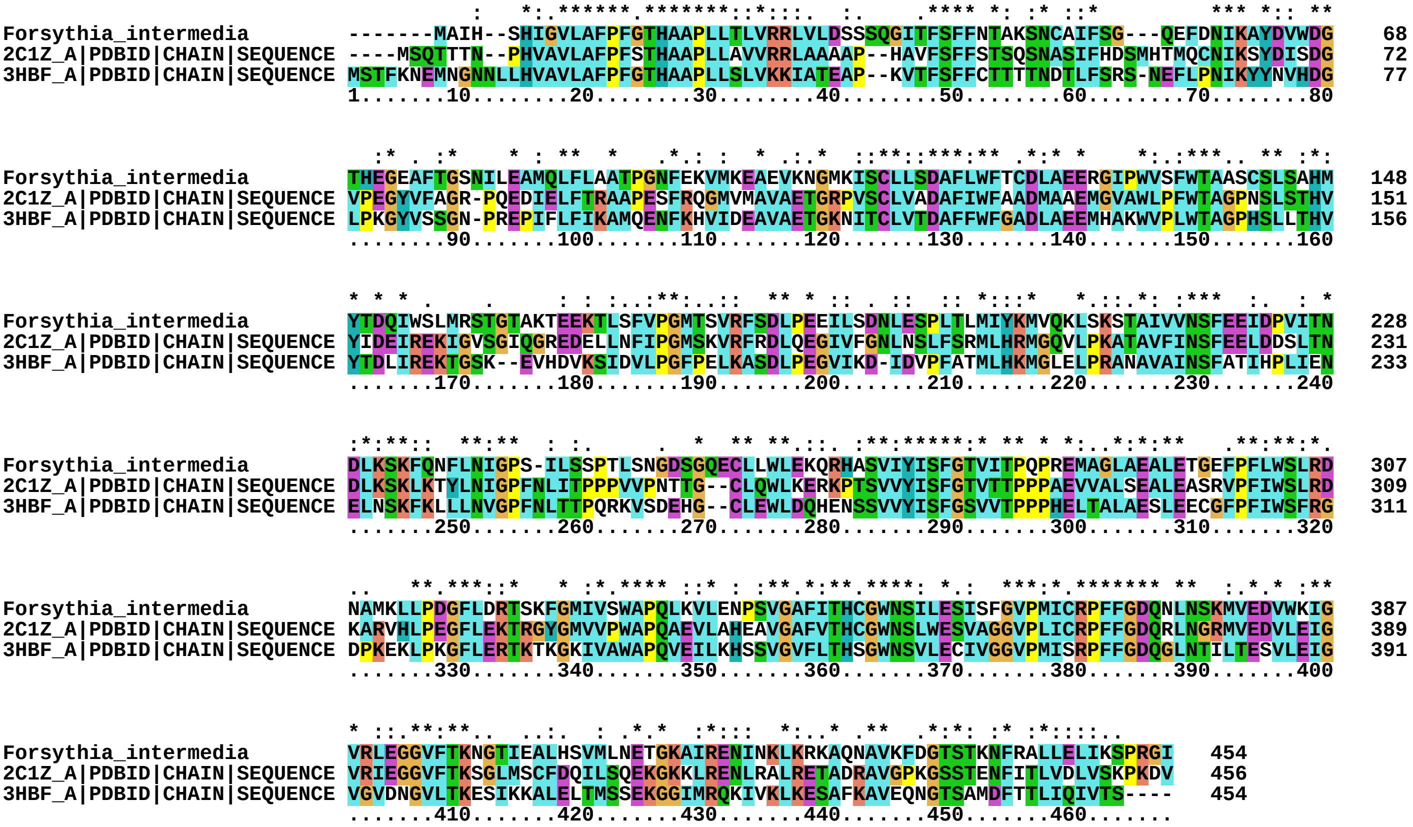

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                                      :   *:.******.*******::*:::.  :.    .**** *: :* ::*         *** *:: **
Forsythia_intermedia        -------MAIH--SHIGVLAFPFGTHAAPLLTLVRRLVLDSSSQGITFSFFNTAKSNCAIFSG---QEFDNIKAYDVWDG    68
2C1Z_A|PDBID|CHAIN|SEQUENCE ----MSQTTTN--PHVAVLAFPFSTHAAPLLAVVRRLAAAAP--HAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDG    72
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAP--KVTFSFFCTTTTNDTLFSRS-NEFLPNIKYYNVHDG    77
                            1.......10........20........30........40........50........60........70........80

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Forsythia_intermedia        THEGEAFTGSNILEAMQLFLAATPGNFEKVMKEAEVKNGMKISCLLSDAFLWFTCDLAEERGIPWVSFWTAASCSLSAHM   148
2C1Z_A|PDBID|CHAIN|SEQUENCE VPEGYVFAGR-PQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHV   151
3HBF_A|PDBID|CHAIN|SEQUENCE LPKGYVSSGN-PREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHV   156
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            * * * .    .     : : :..:**:..::  ** * :: . ::  :: *:::*   *.::.*: :***  :.  : *
Forsythia_intermedia        YTDQIWSLMRSTGTAKTEEKTLSFVPGMTSVRFSDLPEEILSDNLESPLTLMIYKMVQKLSKSTAIVVNSFEEIDPVITN   228
2C1Z_A|PDBID|CHAIN|SEQUENCE YIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTN   231
3HBF_A|PDBID|CHAIN|SEQUENCE YTDLIREKTGSK--EVHDVKSIDVLPGFPELKASDLPEGVIKD-IDVPFATMLHKMGLELPRANAVAINSFATIHPLIEN   233
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :*:**::  **:**  : :.     .  *  ** **.::. :**:*****:* ** * *:..*:*:**   .**:**:*.
Forsythia_intermedia        DLKSKFQNFLNIGPS-ILSSPTLSNGDSGQECLLWLEKQRHASVIYISFGTVITPQPREMAGLAEALETGEFPFLWSLRD   307
2C1Z_A|PDBID|CHAIN|SEQUENCE DLKSKLKTYLNIGPFNLITPPPVVPNTTG--CLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRD   309
3HBF_A|PDBID|CHAIN|SEQUENCE ELNSKFKLLLNVGPFNLTTPQRKVSDEHG--CLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRG   311
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            ..   **.***::*   * :*.**** ::* : **.*:**.****: *.:  ***:*.******* **  :.*.* :**
Forsythia_intermedia        NAMKLLPDGFLDRTSKFGMIVSWAPQLKVLENPSVGAFITHCGWNSILESISFGVPMICRPFFGDQNLNSKMVEDVWKIG   387
2C1Z_A|PDBID|CHAIN|SEQUENCE KARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIG   389
3HBF_A|PDBID|CHAIN|SEQUENCE DPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIG   391
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            * ::.**:**..  ..:.  : .*.*  :*:::  *:..* .**  .*:*: :* :*:::. .
Forsythia_intermedia        VRLEGGVFTKNGTIEALHSVMLNETGKAIRENINKLKRKAQNAVKFDGTSTKNFRALLELIKSPRGI   454
2C1Z_A|PDBID|CHAIN|SEQUENCE VRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE VGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......
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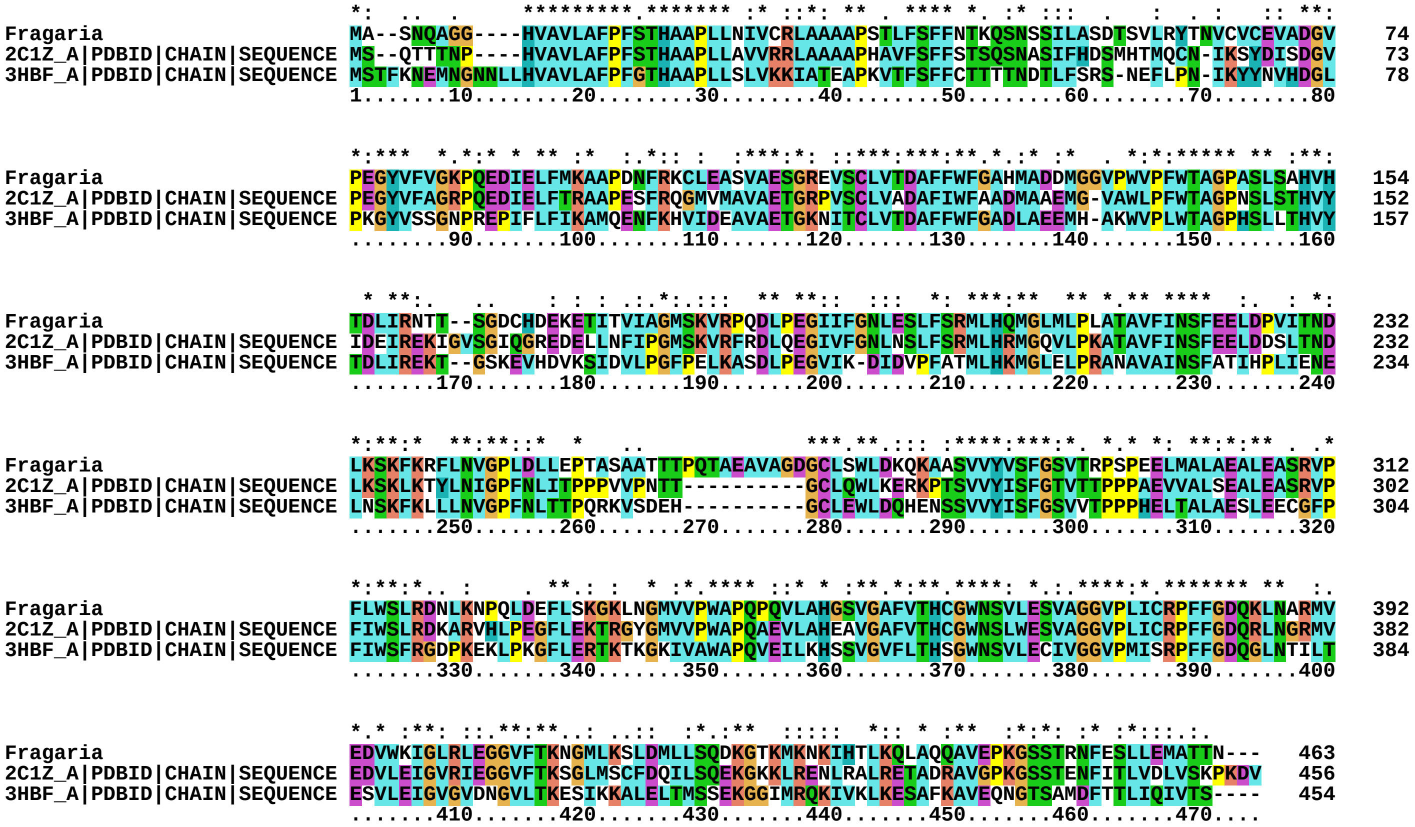

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                            *:  ..  .     *********.******* :* ::*: ** . **** *. :* :::  .   :  . :   :: **:
Fragaria                    MA--SNQAGG----HVAVLAFPFSTHAAPLLNIVCRLAAAAPSTLFSFFNTKQSNSSILASDTSVLRYTNVCVCEVADGV    74
2C1Z_A|PDBID|CHAIN|SEQUENCE MS--QTTTNP----HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCN-IKSYDISDGV    73
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRS-NEFLPN-IKYYNVHDGL    78
                            1.......10........20........30........40........50........60........70........80

                            *:***  *.*:* * ** :*  :.*:: : :***:*: ::***:***:**.*.:* :*  . *:*:***** ** :**:
Fragaria                    PEGYVFVGKPQEDIELFMKAAPDNFRKCLEASVAESGREVSCLVTDAFFWFGAHMADDMGGVPWVPFWTAGPASLSAHVH   154
2C1Z_A|PDBID|CHAIN|SEQUENCE PEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMG-VAWLPFWTAGPNSLSTHVY   152
3HBF_A|PDBID|CHAIN|SEQUENCE PKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMH-AKWVPLWTAGPHSLLTHVY   157
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             * **:.   ..    : : : .:.*:.:::  ** **::  :::  *: ***:**  ** *.** ****  :.  : *:
Fragaria                    TDLIRNTT--SGDCHDEKETITVIAGMSKVRPQDLPEGIIFGNLESLFSRMLHQMGLMLPLATAVFINSFEELDPVITND   232
2C1Z_A|PDBID|CHAIN|SEQUENCE IDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTND   232
3HBF_A|PDBID|CHAIN|SEQUENCE TDLIREKT--GSKEVHDVKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENE   234
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            *:**:*  **:**::*  *   ..             ***.**.::: :****:***:*. *.* *: **:*:** . .*
Fragaria                    LKSKFKRFLNVGPLDLLEPTASAATTTPQTAEAVAGDGCLSWLDKQKAASVVYVSFGSVTRPSPEELMALAEALEASRVP   312
2C1Z_A|PDBID|CHAIN|SEQUENCE LKSKLKTYLNIGPFNLITPPPVVPNTT----------GCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVP   302
3HBF_A|PDBID|CHAIN|SEQUENCE LNSKFKLLLNVGPFNLTTPQRKVSDEH----------GCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFP   304
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            *:**:*.. :    . **.: :  * :*.**** ::* * :**.*:**.****: *.:.****:*.******* **  :.
Fragaria                    FLWSLRDNLKNPQLDEFLSKGKLNGMVVPWAPQPQVLAHGSVGAFVTHCGWNSVLESVAGGVPLICRPFFGDQKLNARMV   392
2C1Z_A|PDBID|CHAIN|SEQUENCE FIWSLRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMV   382
3HBF_A|PDBID|CHAIN|SEQUENCE FIWSFRGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILT   384
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            *.* :**: ::.**:**..: ..::  :*.:**  :::::  *:: * :**  :*:*: :* :*:::.:.
Fragaria                    EDVWKIGLRLEGGVFTKNGMLKSLDMLLSQDKGTKMKNKIHTLKQLAQQAVEPKGSSTRNFESLLEMATTN---   463
2C1Z_A|PDBID|CHAIN|SEQUENCE EDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE ESVLEIGVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......470....
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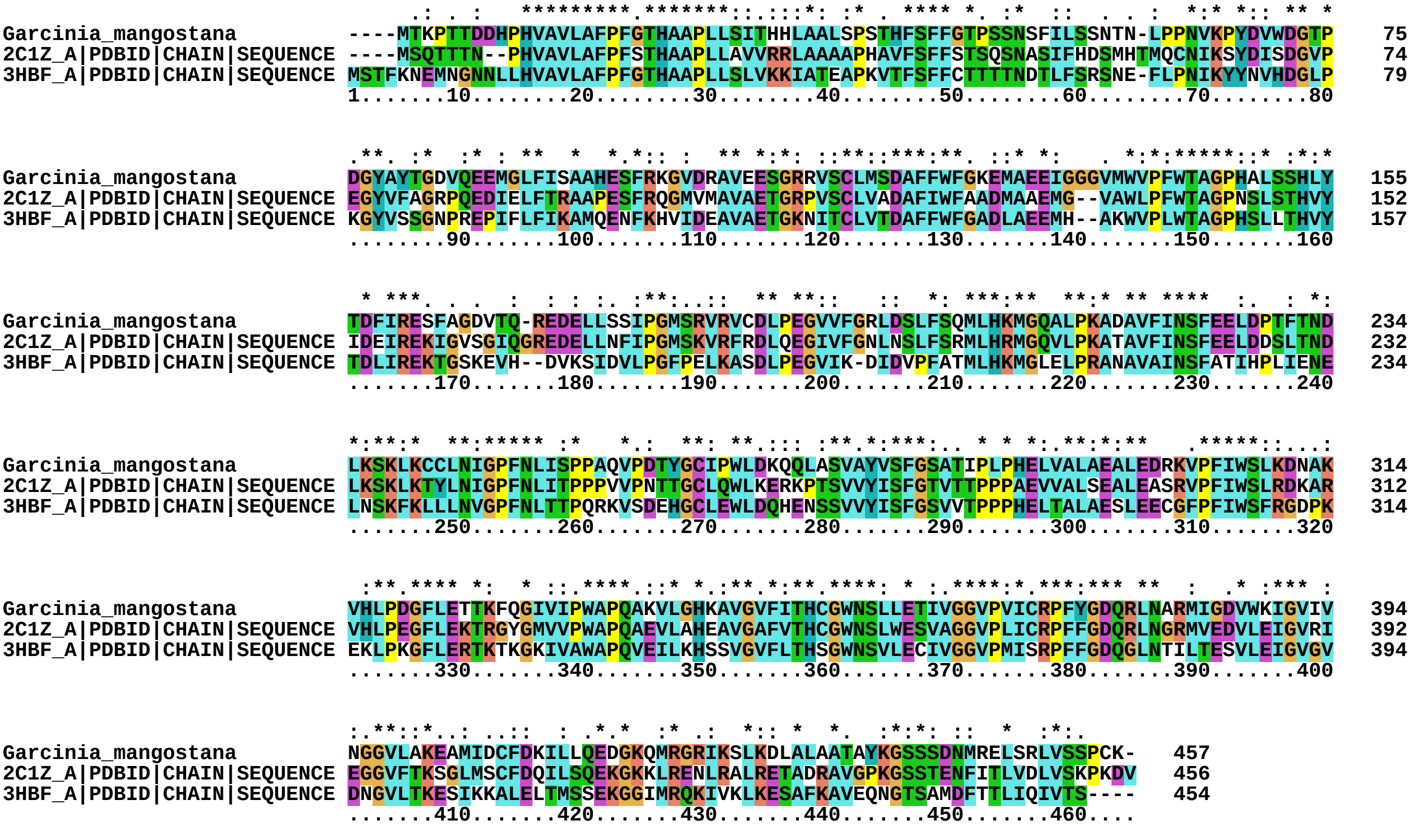

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Garcinia_mangostana         ----MTKPTTDDHPHVAVLAFPFGTHAAPLLSITHHLAALSPSTHFSFFGTPSSNSFILSSNTN-LPPNVKPYDVWDGTP    75
2C1Z_A|PDBID|CHAIN|SEQUENCE ----MSQTTTN--PHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNE-FLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

                            .**. :*  :* : **  *  *.*:: :  ** *:*: ::**::***:**. ::* *:   . *:*:*****::* :*:*
Garcinia_mangostana         DGYAYTGDVQEEMGLFISAAHESFRKGVDRAVEESGRRVSCLMSDAFFWFGKEMAEEIGGGVMWVPFWTAGPHALSSHLY   155
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMG--VAWLPFWTAGPNSLSTHVY   152
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMH--AKWVPLWTAGPHSLLTHVY   157
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             * ***. . .  :  : : :. :**:..::  ** **::   ::  *: ***:**  **:* ** ****  :.  : *:
Garcinia_mangostana         TDFIRESFAGDVTQ-REDELLSSIPGMSRVRVCDLPEGVVFGRLDSLFSQMLHKMGQALPKADAVFINSFEELDPTFTND   234
2C1Z_A|PDBID|CHAIN|SEQUENCE IDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTND   232
3HBF_A|PDBID|CHAIN|SEQUENCE TDLIREKTGSKEVH--DVKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENE   234
                            .......170.......180.......190.......200.......210.......220.......230.......240

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Garcinia_mangostana         LKSKLKCCLNIGPFNLISPPAQVPDTYGCIPWLDKQQLASVAYVSFGSATIPLPHELVALAEALEDRKVPFIWSLKDNAK   314
2C1Z_A|PDBID|CHAIN|SEQUENCE LKSKLKTYLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKAR   312
3HBF_A|PDBID|CHAIN|SEQUENCE LNSKFKLLLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPK   314
                            .......250.......260.......270.......280.......290.......300.......310.......320

                             :**.**** *:  * ::.****.::* *.:**.*:**.****: * :.****:*.***:*** **  :  .* :*** :
Garcinia_mangostana         VHLPDGFLETTKFQGIVIPWAPQAKVLGHKAVGVFITHCGWNSLLETIVGGVPVICRPFYGDQRLNARMIGDVWKIGVIV   394
2C1Z_A|PDBID|CHAIN|SEQUENCE VHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRI   392
3HBF_A|PDBID|CHAIN|SEQUENCE EKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGV   394
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Garcinia_mangostana         NGGVLAKEAMIDCFDKILLQEDGKQMRGRIKSLKDLALAATAYKGSSSDNMRELSRLVSSPCK-   457
2C1Z_A|PDBID|CHAIN|SEQUENCE EGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE DNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460....
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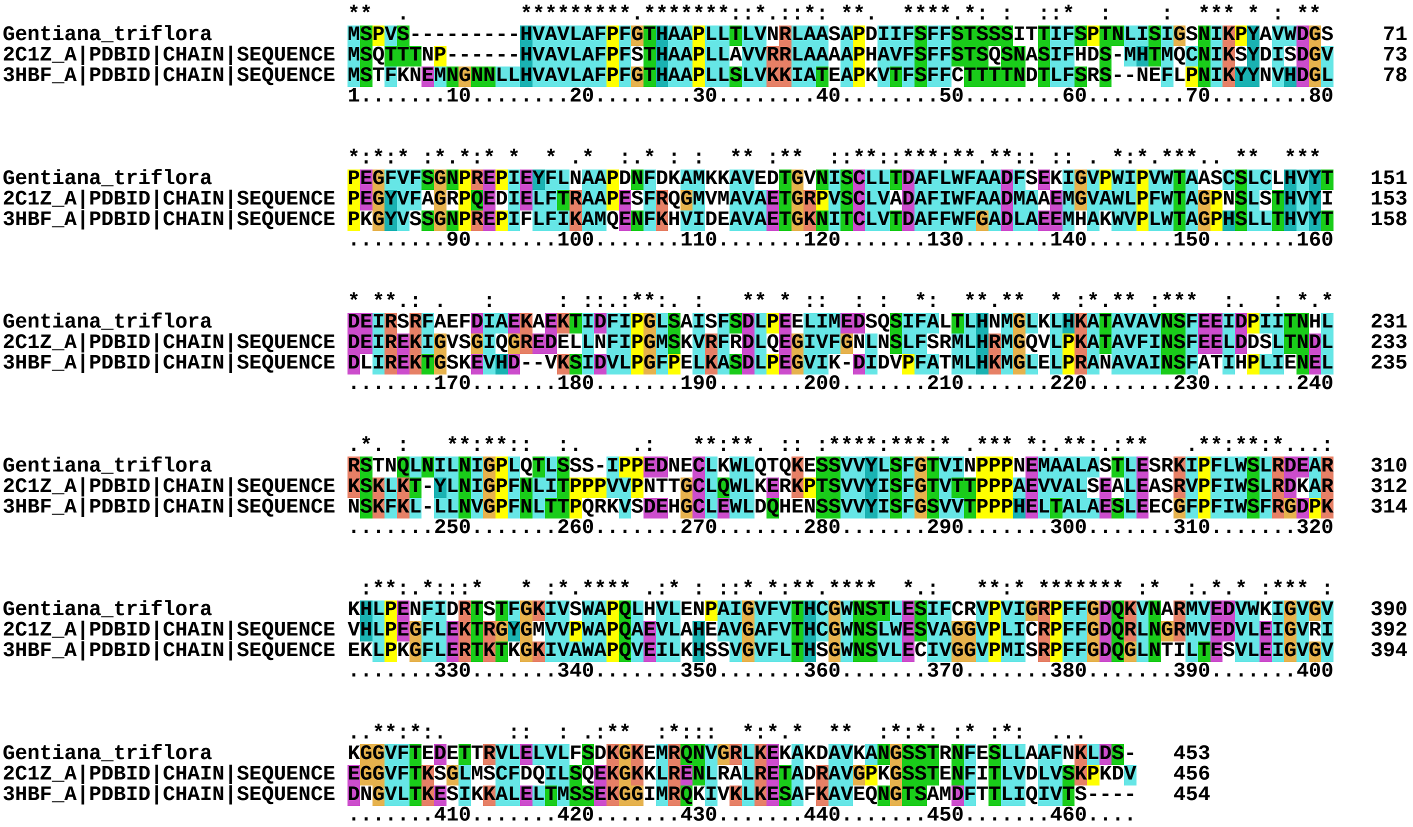

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                            **  .         *********.*******::*.::*: **.  ****.*: :  ::*  :    :  *** * : **
Gentiana_triflora           MSPVS---------HVAVLAFPFGTHAAPLLTLVNRLAASAPDIIFSFFSTSSSITTIFSPTNLISIGSNIKPYAVWDGS     71
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTTTNP------HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSYDISDGV     73
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRS--NEFLPNIKYYNVHDGL     78
                            1.......10........20........30........40........50........60........70........80

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Gentiana_triflora           PEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAADFSEKIGVPWIPVWTAASCSLCLHVYT    151
2C1Z_A|PDBID|CHAIN|SEQUENCE PEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYI    153
3HBF_A|PDBID|CHAIN|SEQUENCE PKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYT    158
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            * **.: .   :     : ::.:**:. :   ** * ::  : :  *:  **.**  * :*.** :***  :.  : *.*
Gentiana_triflora           DEIRSRFAEFDIAEKAEKTIDFIPGLSAISFSDLPEELIMEDSQSIFALTLHNMGLKLHKATAVAVNSFEEIDPIITNHL    231
2C1Z_A|PDBID|CHAIN|SEQUENCE DEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDL    233
3HBF_A|PDBID|CHAIN|SEQUENCE DLIREKTGSKEVHD--VKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENEL    235
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            .*. :   **:**::  :.    .:   **:**. :: :****:***:* .*** *:.**:.:**   .**:**:*...:
Gentiana_triflora           RSTNQLNILNIGPLQTLSSS-IPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWSLRDEAR    310
2C1Z_A|PDBID|CHAIN|SEQUENCE KSKLKT-YLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKAR    312
3HBF_A|PDBID|CHAIN|SEQUENCE NSKFKL-LLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPK    314
                            .......250.......260.......270.......280.......290.......300.......310.......320

                             :**:.*:::*   * :*.**** .:* : ::*.*:**.****  *.:   **:* ******* :*  :.*.* :*** :
Gentiana_triflora           KHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDVWKIGVGV    390
2C1Z_A|PDBID|CHAIN|SEQUENCE VHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRI    392
3HBF_A|PDBID|CHAIN|SEQUENCE EKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGV    394
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            ..**:*:.     ::  : .:**  :*:::  *:*.*  **  :*:*: :* :*:  ...
Gentiana_triflora           KGGVFTEDETTRVLELVLFSDKGKEMRQNVGRLKEKAKDAVKANGSSTRNFESLLAAFNKLDS-    453
2C1Z_A|PDBID|CHAIN|SEQUENCE EGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV    456
3HBF_A|PDBID|CHAIN|SEQUENCE DNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----    454
                            .......410.......420.......430.......440.......450.......460....
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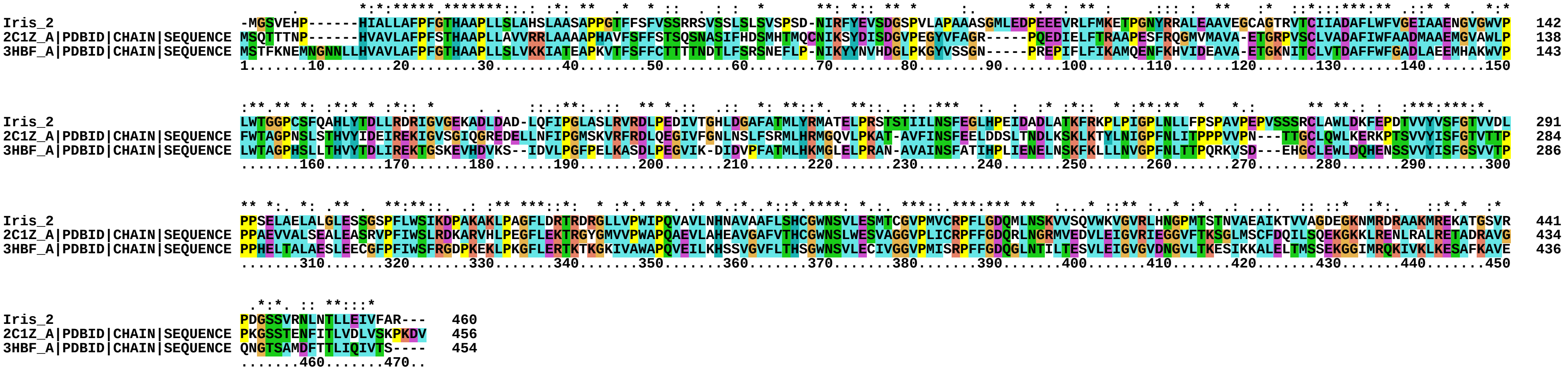

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                                         .       *:*:*****.*******:.:.: :*: **   .*  * ::   . : :  *       **: *:: ** *      :.       *.* : ** :     .::: :  **    :*  ::*:::***:** .::* *   . *:*
Iris_2                            -MGSVEHP------HIALLAFPFGTHAAPLLSLAHSLAASAPPGTFFSFVSSRRSVSSLSLSVSPSD-NIRFYEVSDGSPVLAPAAASGMLEDPEEEVRLFMKETPGNYRRALEAAVEGCAGTRVTCIIADAFLWFVGEIAAENGVGWVP   142
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTTTNP------HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVPEGYVFAGR-----PQEDIELFTRAAPESFRQGMVMAVA-ETGRPVSCLVADAFIWFAADMAAEMGVAWLP   138
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGLPKGYVSSGN-----PREPIFLFIKAMQENFKHVIDEAVA-ETGKNITCLVTDAFFWFGADLAEEMHAKWVP   143
                            1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                            :**.** *: :*:* * :*:: *      . .    ::.:**:..::  ** *.::   .::   *: **::*.  **::. :: :***  :.  :   :* :*::  * :**:**  *   *.:        ** **.: :  :***:***:*.
Iris_2                            LWTGGPCSFQAHLYTDLLRDRIGVGEKADLDAD-LQFIPGLASLRVRDLPEDIVTGHLDGAFATMLYRMATELPRSTSTIILNSFEGLHPEIDADLATKFRKPLPIGPLNLLFPSPAVPEPVSSSRCLAWLDKFEPDTVVYVSFGTVVDL   291
2C1Z_A|PDBID|CHAIN|SEQUENCE FWTAGPNSLSTHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKAT-AVFINSFEELDDSLTNDLKSKLKTYLNIGPFNLITPPPVVPN---TTGCLQWLKERKPTSVVYISFGTVTTP   284
3HBF_A|PDBID|CHAIN|SEQUENCE LWTAGPHSLLTHVYTDLIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRAN-AVAINSFATIHPLIENELNSKFKLLLNVGPFNLTTPQRKVSD---EHGCLEWLDQHENSSVVYISFGSVVTP   286
                            .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                            ** *:. *: .** .   **:**::. .: :** ***::*:  * :*.* **. :* *.:*..*::*.****: *.:. ***::.***:*** **  :...* ::** :..* :*. .: ..:.  :: ::*  :*:.   ::*.*  :*
Iris_2                            PPSELAELALGLESSGSPFLWSIKDPAKAKLPAGFLDRTRDRGLLVPWIPQVAVLNHNAVAAFLSHCGWNSVLESMTCGVPMVCRPFLGDQMLNSKVVSQVWKVGVRLHNGPMTSTNVAEAIKTVVAGDEGKNMRDRAAKMREKATGSVR   441
2C1Z_A|PDBID|CHAIN|SEQUENCE PPAEVVALSEALEASRVPFIWSLRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVG   434
3HBF_A|PDBID|CHAIN|SEQUENCE PPHELTALAESLEECGFPFIWSFRGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVE   436
                            .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                             .*:*. :: **:::*
Iris_2                            PDGSSVRNLNTLLEIVFAR---   460
2C1Z_A|PDBID|CHAIN|SEQUENCE PKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE QNGTSAMDFTTLIQIVTS----   454
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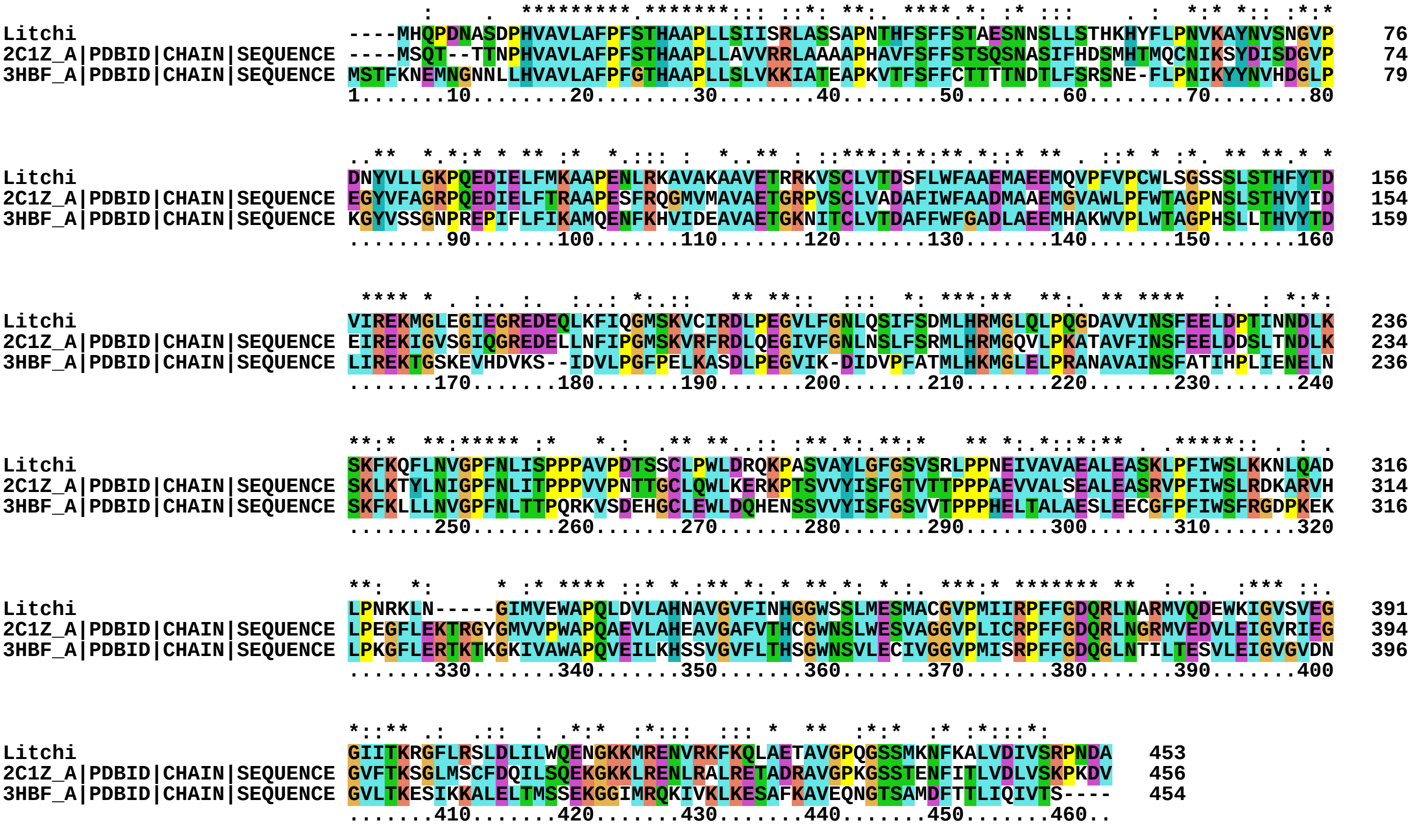

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Litchi                       ----MHQPDNASDPHVAVLAFPFSTHAAPLLSIISRLASSAPNTHFSFFSTAESNNSLLSTHKHYFLPNVKAYNVSNGVP    76
2C1Z_A|PDBID|CHAIN|SEQUENCE  ----MSQT--TTNPHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE  MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNE-FLPNIKYYNVHDGLP    79
                             1.......10........20........30........40........50........60........70........80

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Litchi                       DNYVLLGKPQEDIELFMKAAPENLRKAVAKAAVETRRKVSCLVTDSFLWFAAEMAEEMQVPFVPCWLSGSSSLSTHFYTD   156
2C1Z_A|PDBID|CHAIN|SEQUENCE  EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE  KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                             ........90.......100.......110.......120.......130.......140.......150.......160

                              **** * . :.. :.  :..: *:.::   ** **::  :::  *: ***:** **:. ** ****  :.  : *:*:
Litchi                       VIREKMGLEGIEGREDEQLKFIQGMSKVCIRDLPEGVLFGNLQSIFSDMLHRMGLQLPQGDAVVINSFEELDPTINNDLK   236
2C1Z_A|PDBID|CHAIN|SEQUENCE  EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE  LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                             .......170.......180.......190.......200.......210.......220.......230.......240

                             **:*  **:***** :*   *.:  .** **..:: :**.*:.**:*   ** *:.*::*:** . .*****:: . : .
Litchi                       SKFKQFLNVGPFNLISPPPAVPDTSSCLPWLDRQKPASVAYLGFGSVSRLPPNEIVAVAEALEASKLPFIWSLKKNLQAD   316
2C1Z_A|PDBID|CHAIN|SEQUENCE  SKLKTYLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARVH   314
3HBF_A|PDBID|CHAIN|SEQUENCE  SKFKLLLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKEK   316
                             .......250.......260.......270.......280.......290.......300.......310.......320

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Litchi                       LPNRKLN-----GIMVEWAPQLDVLAHNAVGVFINHGGWSSLMESMACGVPMIIRPFFGDQRLNARMVQDEWKIGVSVEG   391
2C1Z_A|PDBID|CHAIN|SEQUENCE  LPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIEG   394
3HBF_A|PDBID|CHAIN|SEQUENCE  LPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVDN   396
                             .......330.......340.......350.......360.......370.......380.......390.......400

                             *::** .:  .::  : .*:*  :*:::  ::: *  **  :*:*  :* :*:::*:
Litchi                       GIITKRGFLRSLDLILWQENGKKMRENVRKFKQLAETAVGPQGSSMKNFKALVDIVSRPNDA   453
2C1Z_A|PDBID|CHAIN|SEQUENCE  GVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE  GVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                             .......410.......420.......430.......440.......450.......460..
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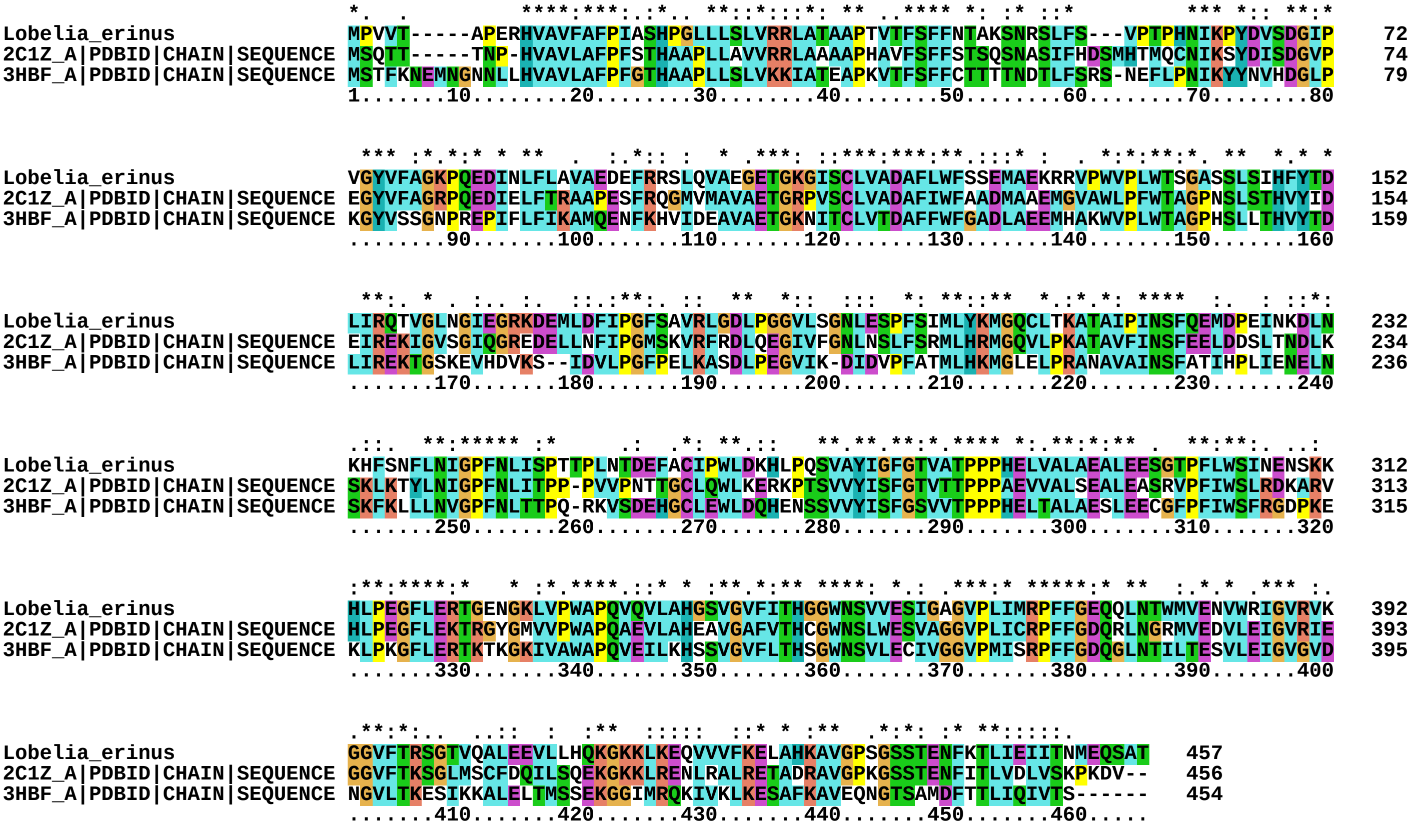

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Lobelia_erinus              MPVVT-----APERHVAVFAFPIASHPGLLLSLVRRLATAAPTVTFSFFNTAKSNRSLFS---VPTPHNIKPYDVSDGIP    72
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTT-----TNP-HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRS-NEFLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

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Lobelia_erinus              VGYVFAGKPQEDINLFLAVAEDEFRRSLQVAEGETGKGISCLVADAFLWFSSEMAEKRRVPWVPLWTSGASSLSIHFYTD   152
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

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Lobelia_erinus              LIRQTVGLNGIEGRKDEMLDFIPGFSAVRLGDLPGGVLSGNLESPFSIMLYKMGQCLTKATAIPINSFQEMDPEINKDLN   232
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            .::.  **:***** :*     .:  .*: **.::   **.**.**:*.**** *:.**:*:** .  **:**:. ..:
Lobelia_erinus              KHFSNFLNIGPFNLISPTTPLNTDEFACIPWLDKHLPQSVAYIGFGTVATPPPHELVALAEALEESGTPFLWSINENSKK   312
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPP-PVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARV   313
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQ-RKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKE   315
                            .......250.......260.......270.......280.......290.......300.......310.......320

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Lobelia_erinus              HLPEGFLERTGENGKLVPWAPQVQVLAHGSVGVFITHGGWNSVVESIGAGVPLIMRPFFGEQQLNTWMVENVWRIGVRVK   392
2C1Z_A|PDBID|CHAIN|SEQUENCE HLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIE   393
3HBF_A|PDBID|CHAIN|SEQUENCE KLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVD   395
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Lobelia_erinus              GGVFTRSGTVQALEEVLLHQKGKKLKEQVVVFKELAHKAVGPSGSSTENFKTLIEIITNMEQSAT   457
2C1Z_A|PDBID|CHAIN|SEQUENCE GGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV--   456
3HBF_A|PDBID|CHAIN|SEQUENCE NGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS------   454
                            .......410.......420.......430.......440.......450.......460.....
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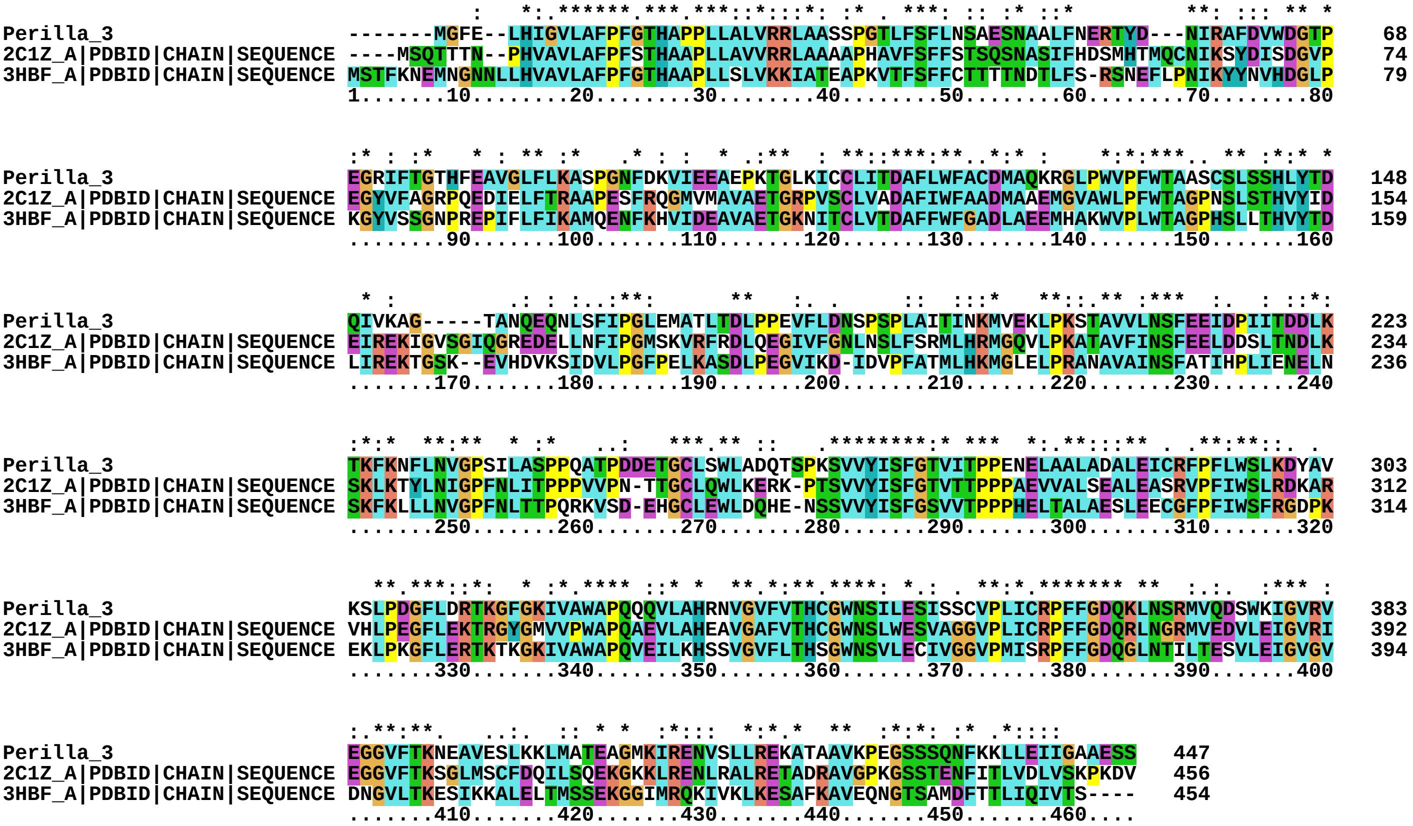

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Perilla_3                   -------MGFE--LHIGVLAFPFGTHAPPLLALVRRLAASSPGTLFSFLNSAESNAALFNERTYD---NIRAFDVWDGTP    68
2C1Z_A|PDBID|CHAIN|SEQUENCE ----MSQTTTN--PHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFS-RSNEFLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

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Perilla_3                   EGRIFTGTHFEAVGLFLKASPGNFDKVIEEAEPKTGLKICCLITDAFLWFACDMAQKRGLPWVPFWTAASCSLSSHLYTD   148
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             * :         .: : :..:**:      **   :. .     ::  :::*   **::.** :***  :.  : ::*:
Perilla_3                   QIVKAG-----TANQEQNLSFIPGLEMATLTDLPPEVFLDNSPSPLAITINKMVEKLPKSTAVVLNSFEEIDPIITDDLK   223
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSK--EVHDVKSIDVLPGFPELKASDLPEGVIKD-IDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :*:*  **:**  * :*   ..:   ***.** ::   .********:* ***  *:.**:::** . .**:**::. .
Perilla_3                   TKFKNFLNVGPSILASPPQATPDDETGCLSWLADQTSPKSVVYISFGTVITPPENELAALADALEICRFPFLWSLKDYAV   303
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPPVVPN-TTGCLQWLKERK-PTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKAR   312
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQRKVSD-EHGCLEWLDQHE-NSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPK   314
                            .......250.......260.......270.......280.......290.......300.......310.......320

                              **.***::*:  * :*.**** ::* *  **.*:**.****: *.: . **:*.******* **  :.:.  :*** :
Perilla_3                   KSLPDGFLDRTKGFGKIVAWAPQQQVLAHRNVGVFVTHCGWNSILESISSCVPLICRPFFGDQKLNSRMVQDSWKIGVRV   383
2C1Z_A|PDBID|CHAIN|SEQUENCE VHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRI   392
3HBF_A|PDBID|CHAIN|SEQUENCE EKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGV   394
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            :.**:**.   ..:.  :: * *  :*:::  *:*.*  **  :*:*: :* .*::::
Perilla_3                   EGGVFTKNEAVESLKKLMATEAGMKIRENVSLLREKATAAVKPEGSSSQNFKKLLEIIGAAESS   447
2C1Z_A|PDBID|CHAIN|SEQUENCE EGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE DNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460....
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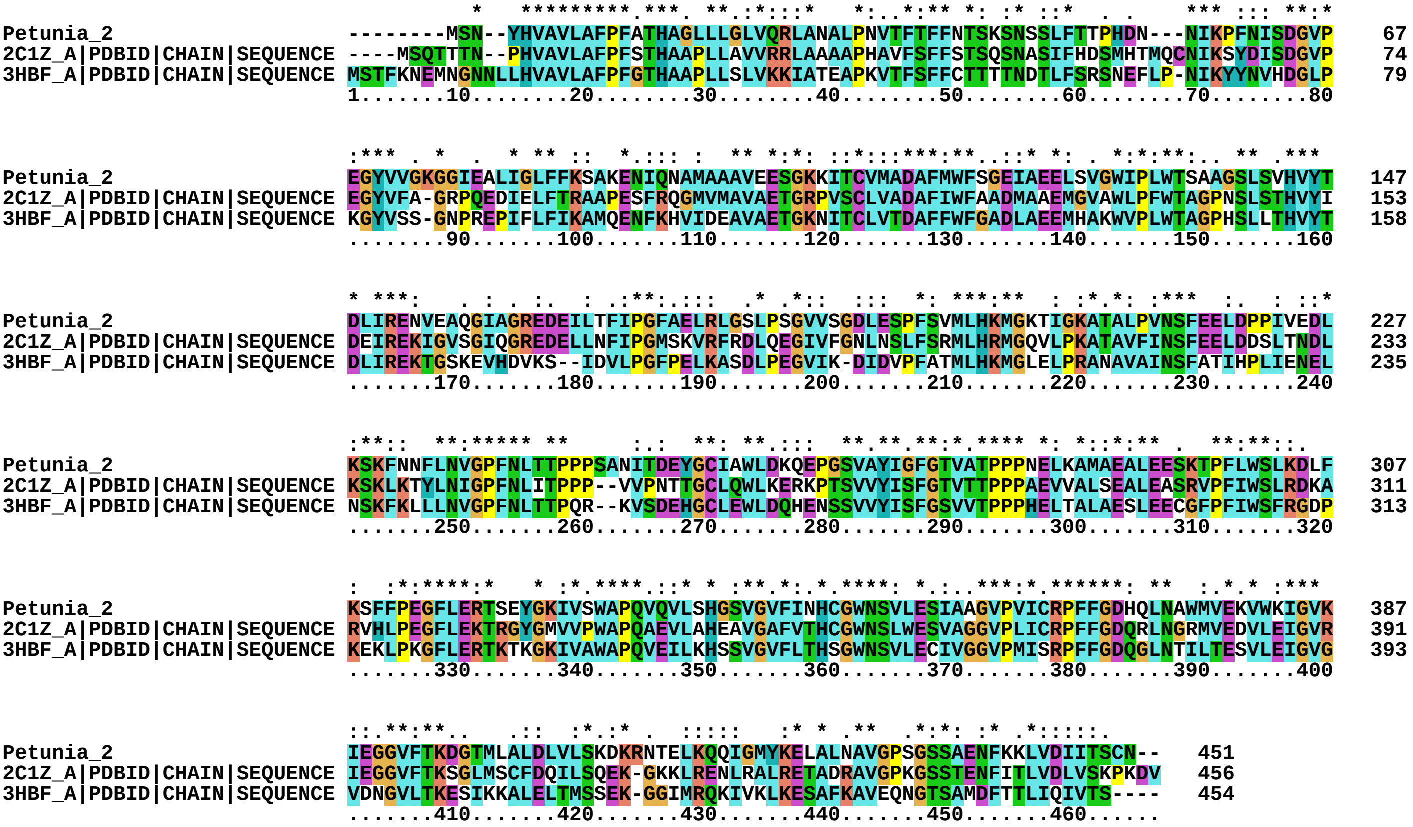

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                                      *   *********.***. **.:*:::*   *:..*:** *: :* ::*. .      *** ::: **:*
Petunia_2                   --------MSN--YHVAVLAFPFATHAGLLLGLVQRLANALPNVTFTFFNTSKSNSSLFTTPHDN---NIKPFNISDGVP    67
2C1Z_A|PDBID|CHAIN|SEQUENCE ----MSQTTTN--PHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

                            :*** . *  .  * ** ::  *.::: :  ** *:*: ::*:::***:**..::* *: . *:*:**:.. ** .***
Petunia_2                   EGYVVGKGGIEALIGLFFKSAKENIQNAMAAAVEESGKKITCVMADAFMWFSGEIAEELSVGWIPLWTSAAGSLSVHVYT   147
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFA-GRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYI   153
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSS-GNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYT   158
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            * ***:   . : . :.  : .:**:.:::  .* .*::  :::  *: ***:**  : :*.*: :***  :.  : ::*
Petunia_2                   DLIRENVEAQGIAGREDEILTFIPGFAELRLGSLPSGVVSGDLESPFSVMLHKMGKTIGKATALPVNSFEELDPPIVEDL   227
2C1Z_A|PDBID|CHAIN|SEQUENCE DEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDL   233
3HBF_A|PDBID|CHAIN|SEQUENCE DLIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENEL   235
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :**::  **:***** **     :.:  **: **.:::  **.**.**:*.**** *: *::*:** .  **:**::.
Petunia_2                   KSKFNNFLNVGPFNLTTPPPSANITDEYGCIAWLDKQEPGSVAYIGFGTVATPPPNELKAMAEALEESKTPFLWSLKDLF   307
2C1Z_A|PDBID|CHAIN|SEQUENCE KSKLKTYLNIGPFNLITPPP--VVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKA   311
3HBF_A|PDBID|CHAIN|SEQUENCE NSKFKLLLNVGPFNLTTPQR--KVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDP   313
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            :  :*:****:*   * :*.****.::* * :**.*:.*.****: *.:..***:*.******: **  :.*.* :***
Petunia_2                   KSFFPEGFLERTSEYGKIVSWAPQVQVLSHGSVGVFINHCGWNSVLESIAAGVPVICRPFFGDHQLNAWMVEKVWKIGVK   387
2C1Z_A|PDBID|CHAIN|SEQUENCE RVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVR   391
3HBF_A|PDBID|CHAIN|SEQUENCE KEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVG   393
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Petunia_2                   IEGGVFTKDGTMLALDLVLSKDKRNTELKQQIGMYKELALNAVGPSGSSAENFKKLVDIITSCN--   451
2C1Z_A|PDBID|CHAIN|SEQUENCE IEGGVFTKSGLMSCFDQILSQEK-GKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE VDNGVLTKESIKKALELTMSSEK-GGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460......
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                                    .     ****:****.*******::::::*: :*:. ****.*  :* ::*       : :  *** *:: *
Populus2                    -------MSD----HVAVFAFPFGTHAAPLLAIIHRLATASPNTHFSFFSTQQSNSSIFSIYKKKMNIMQPNIKAYEVWD     69
2C1Z_A|PDBID|CHAIN|SEQUENCE --MSQTTTNP----HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIF---HDSMHTMQCNIKSYDISD     71
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFS----RSNEFLPNIKYYNVHD     76
                            1.......10........20........30........40........50........60........70........80

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Populus2                    GAPEGYVFSGNPQEHIELFMKSARESLKKAMEVAVSETGRKVSCLVSDAFFWFACEMAEEIGVGWLPFWTAGPNSLSAHV    149
2C1Z_A|PDBID|CHAIN|SEQUENCE GVPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHV    151
3HBF_A|PDBID|CHAIN|SEQUENCE GLPKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHV    156
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            * * ***. *   :   : : :..: *:.:::  ** **::  : :  *: ***:**  **:* ** ****  :.    :
Populus2                    YTDLIRETFGDGGMVGREDKTISLIQGMSKIRICDLPEGVLFGNTESFFSNMLHKMGKALPQAAAVFINSFEELDPGTIK    229
2C1Z_A|PDBID|CHAIN|SEQUENCE YIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTN    231
3HBF_A|PDBID|CHAIN|SEQUENCE YTDLIREKTGSKEVH--DVKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIEN    233
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :*:*::*  **:** :*  .   : :  **: **.::: :**.*:***:*.**** *:.**:*:** .  *****:....
Populus2                    DLKSRFKKFLNIGPSHLILSPPPMEDTYGCMTWLDKQKLASVAYVSFGSVTTPPPHELVALAEALETSETPFIWSLKDNS    309
2C1Z_A|PDBID|CHAIN|SEQUENCE DLKSKLKTYLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKA    311
3HBF_A|PDBID|CHAIN|SEQUENCE ELNSKFKLLLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDP    313
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            : :**.***::*   * :*.*:** *:* * :**.*:**.****: *.:.****:*.******* **  : *.* ***:
Populus2                    KVHLPHGFLDRTTSQGLVVPWSPQLEVLAHRAVGVFVTHCGWNSLLESIAGGVPMICRPFFGDQRLNGRMIEDVWEIGLK    389
2C1Z_A|PDBID|CHAIN|SEQUENCE RVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVR    391
3HBF_A|PDBID|CHAIN|SEQUENCE KEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVG    393
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Populus2                    VEDGVFTKLEVLNSLNKILSHEGGQKMRENIRALKQLAKKAIGPNGSSINNFIALSNLVFNTKI-   453
2C1Z_A|PDBID|CHAIN|SEQUENCE IEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE VDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.....
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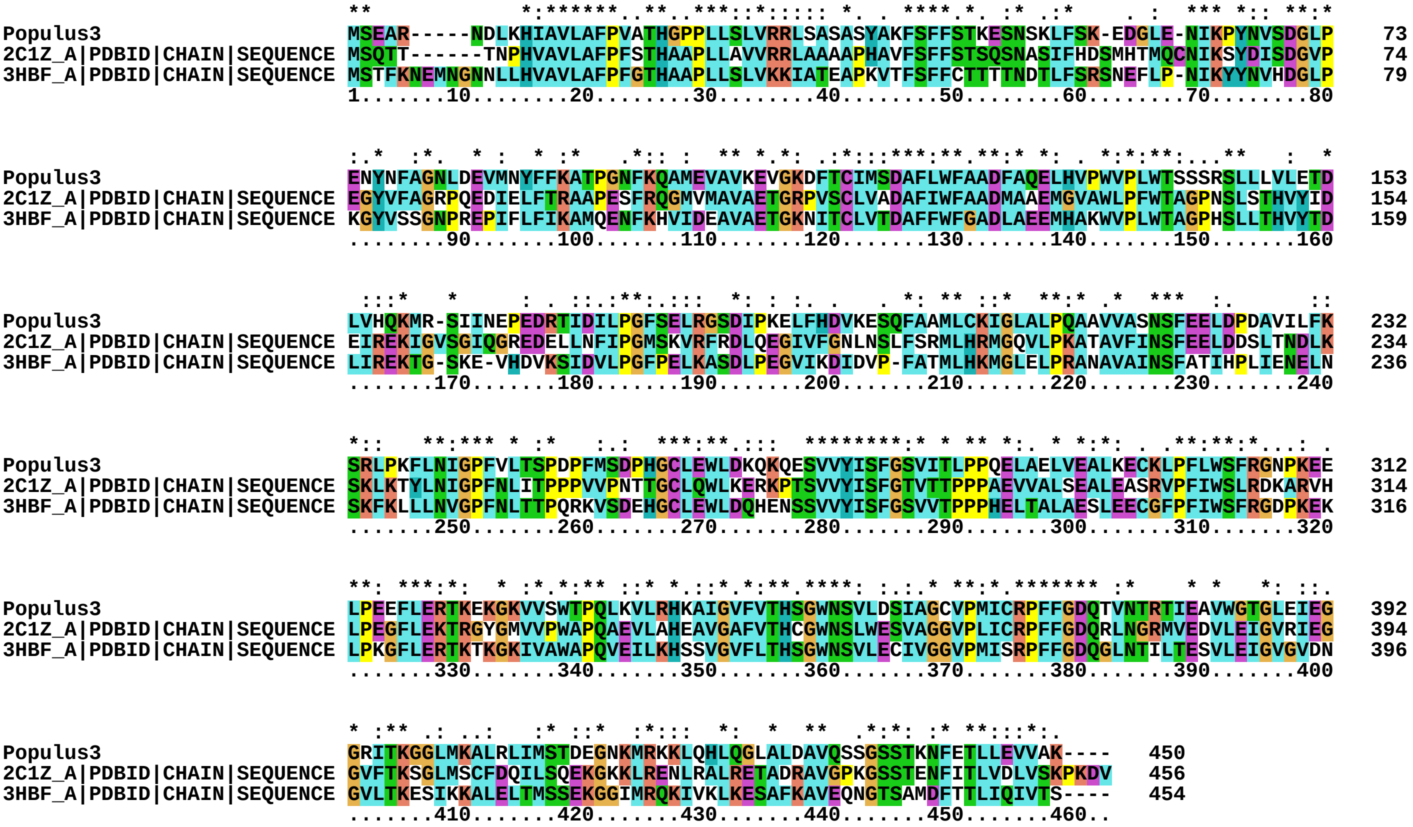

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                            **            *:******..**..***::*::::: *. .  ****.*. :* .:*    . :  *** *:: **:*
Populus3                    MSEAR-----NDLKHIAVLAFPVATHGPPLLSLVRRLSASASYAKFSFFSTKESNSKLFSK-EDGLE-NIKPYNVSDGLP    73
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTT------TNPHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

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Populus3                    ENYNFAGNLDEVMNYFFKATPGNFKQAMEVAVKEVGKDFTCIMSDAFLWFAADFAQELHVPWVPLWTSSSRSLLLVLETD   153
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID   154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD   159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             :::*   *     : . ::.:**:.:::  *: : :. .   . *: ** ::*  **:* .*  ***  :.      ::
Populus3                    LVHQKMR-SIINEPEDRTIDILPGFSELRGSDIPKELFHDVKESQFAAMLCKIGLALPQAAVVASNSFEELDPDAVILFK   232
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK   234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTG-SKE-VHDVKSIDVLPGFPELKASDLPEGVIKDIDVP-FATMLHKMGLELPRANAVAINSFATIHPLIENELN   236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            *::   **:*** * :*   :.:  ***:**.:::  ********:* * ** *:. * *:*: . .**:**:*...: .
Populus3                    SRLPKFLNIGPFVLTSPDPFMSDPHGCLEWLDKQKQESVVYISFGSVITLPPQELAELVEALKECKLPFLWSFRGNPKEE   312
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARVH   314
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKEK   316
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            **: ***:*:  * :*.*:** ::* *.::*.*:**.****: :.:.* **:*.******* :*    * *   *: ::.
Populus3                    LPEEFLERTKEKGKVVSWTPQLKVLRHKAIGVFVTHSGWNSVLDSIAGCVPMICRPFFGDQTVNTRTIEAVWGTGLEIEG   392
2C1Z_A|PDBID|CHAIN|SEQUENCE LPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIEG   394
3HBF_A|PDBID|CHAIN|SEQUENCE LPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVDN   396
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            * :** .: ..:   :* ::*  :*:::  *:  *  **  .*:*: :* **:::*:.
Populus3                    GRITKGGLMKALRLIMSTDEGNKMRKKLQHLQGLALDAVQSSGSSTKNFETLLEVVAK----    450
2C1Z_A|PDBID|CHAIN|SEQUENCE GVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV    456
3HBF_A|PDBID|CHAIN|SEQUENCE GVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----    454
                            .......410.......420.......430.......440.......450.......460..
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                            *.      .  .  *********.:******::::::*: :*:. ****.*  :* ::*  *      *** *:: **:*
Populus_1                   MP-----QTAAGPDHVAVLAFPFSSHAAPLLAIIHRLATSSPNTHFSFFSTQQSNNSIF--SIYKQNRNIKAYDVWDGVP     73
2C1Z_A|PDBID|CHAIN|SEQUENCE MS-----QTTTNP-HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP     74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGLP     79
                            1.......10........20........30........40........50........60........70........80

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Populus_1                   EGYVFAGKPQEHIELFMKSAPNSFKKAMEVAVSETGRKVSCLVSDAFFWFAGEMAEEIGVVWLPFWTAGPTSLSAHVYTD    153
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYID    154
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYTD    159
                            ........90.......100.......110.......120.......130.......140.......150.......160

                             **:. *   : . :.  :..:**:.:::  ** **::  :::  *. ***:**  **:* ** ****  :.  : .:*:
Populus_1                   LIRDTFGVGGVAGHEDELLSLIPGMSKIRIRDLPEGVLFGNLEAVFPNMLHKMGRALPKAAAVFINSFEELDPRITRDLK    233
2C1Z_A|PDBID|CHAIN|SEQUENCE EIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLK    234
3HBF_A|PDBID|CHAIN|SEQUENCE LIREKTGSKEVHDVKS--IDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENELN    236
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            *::*  **:****: :*   ..:  **: **..:: :**.*:***::.**** *:.**:*:** . .*****::...: :
Populus_1                   SRFKEFLNIGPFNMISPAPPAADTYGCITWLDRQKLASVAYLSFGSITTPPPHELVALAEALETSGVPFIWSLKDNSKVH    313
2C1Z_A|PDBID|CHAIN|SEQUENCE SKLKTYLNIGPFNLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARVH    314
3HBF_A|PDBID|CHAIN|SEQUENCE SKFKLLLNVGPFNLTTPQRKVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGDPKEK    316
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            **:***::*   *  :*.*:** *:* *.:**.*:**.****: *.:.****:*.******* **  :.*.. :**: ::.
Populus_1                   LPNGFLDRTTSQGLLVPWTPQMEVLAHKAVGVFITHCGWNSLLESIAGGVPMICRPFFGDQRLNGRMVEDAWKIGLQVED    393
2C1Z_A|PDBID|CHAIN|SEQUENCE LPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIEG    394
3HBF_A|PDBID|CHAIN|SEQUENCE LPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGVGVDN    396
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Populus_1                   GVFRKHGVLNSLDKVLSQDSGEEMRENIRALQQLAKKAIGPNGSSINNFVSLSDLV------   449
2C1Z_A|PDBID|CHAIN|SEQUENCE GVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE GVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460..
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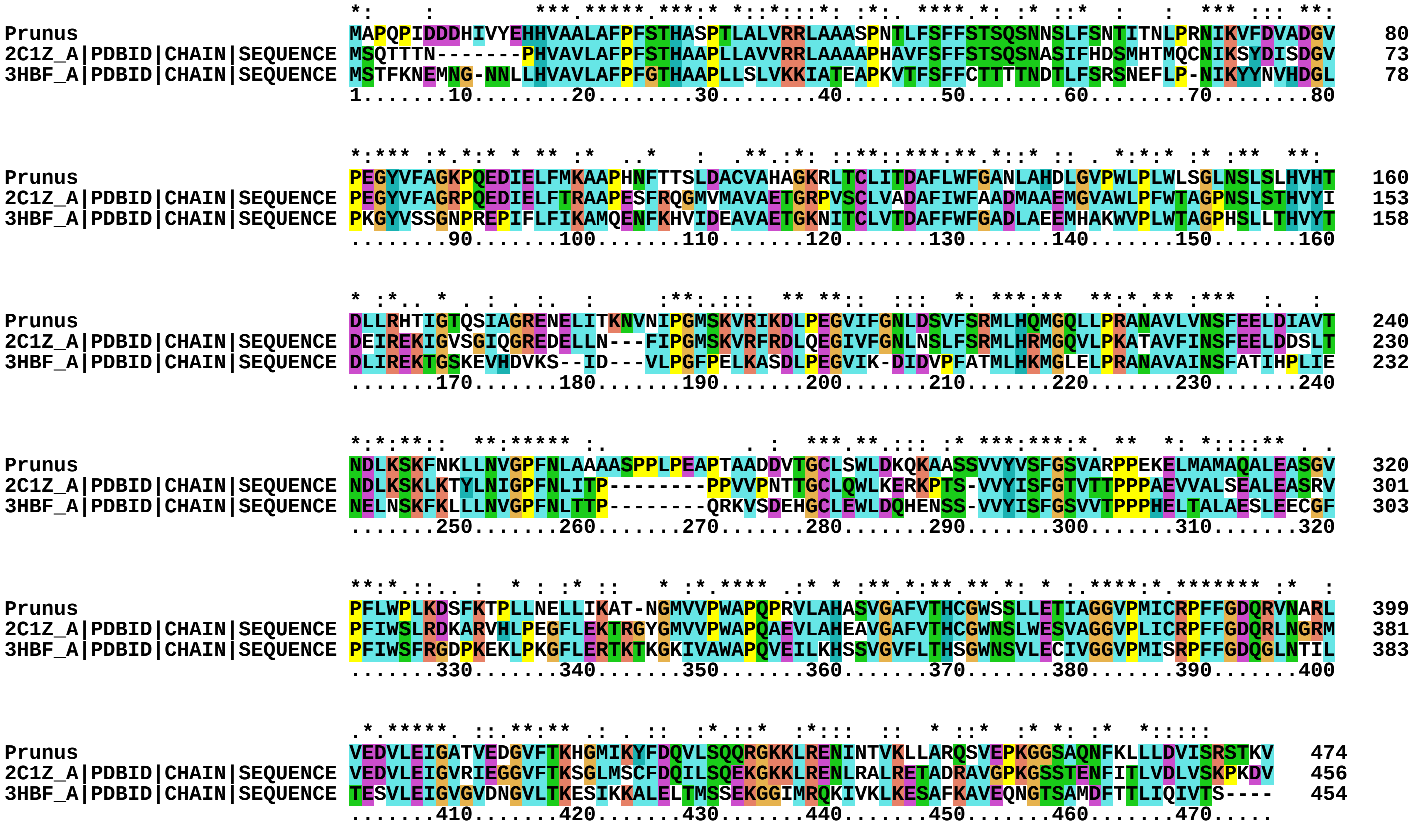

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                            *:    :        ***.*****.***:* *::*:::*: :*:. ****.*: :* ::*  :   :  *** ::: **:
Prunus                      MAPQPIDDDHIVYEHHVAALAFPFSTHASPTLALVRRLAAASPNTLFSFFSTSQSNNSLFSNTITNLPRNIKVFDVADGV    80
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTTTN-------PHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGV    73
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNG-NNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSNEFLP-NIKYYNVHDGL    78
                            1.......10........20........30........40........50........60........70........80

                            *:*** :*.*:* * ** :*  ..*   :  .**.:*: ::**::***:**.*::* :: . *:*:* :* :**  **:
Prunus                      PEGYVFAGKPQEDIELFMKAAPHNFTTSLDACVAHAGKRLTCLITDAFLWFGANLAHDLGVPWLPLWLSGLNSLSLHVHT   160
2C1Z_A|PDBID|CHAIN|SEQUENCE PEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYI   153
3HBF_A|PDBID|CHAIN|SEQUENCE PKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYT   158
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            * :*.. * . : . :.  :     :**:.:::  ** **::  :::  *: ***:**  **:*.** :***  :.  :
Prunus                      DLLRHTIGTQSIAGRENELITKNVNIPGMSKVRIKDLPEGVIFGNLDSVFSRMLHQMGQLLPRANAVLVNSFEELDIAVT   240
2C1Z_A|PDBID|CHAIN|SEQUENCE DEIREKIGVSGIQGREDELLN---FIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLT   230
3HBF_A|PDBID|CHAIN|SEQUENCE DLIREKTGSKEVHDVKS--ID---VLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIE   232
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            *:*:**::  **:***** :.           . :  ***.**.::: :* ***:***:*. **  *: *::::** . .
Prunus                      NDLKSKFNKLLNVGPFNLAAAASPPLPEAPTAADDVTGCLSWLDKQKAASSVVYVSFGSVARPPEKELMAMAQALEASGV   320
2C1Z_A|PDBID|CHAIN|SEQUENCE NDLKSKLKTYLNIGPFNLITP--------PPVVPNTTGCLQWLKERKPTS-VVYISFGTVTTPPPAEVVALSEALEASRV   301
3HBF_A|PDBID|CHAIN|SEQUENCE NELNSKFKLLLNVGPFNLTTP--------QRKVSDEHGCLEWLDQHENSS-VVYISFGSVVTPPPHELTALAESLEECGF   303
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            **:*.::.. :  * : :* ::   * :*.**** .:* * :**.*:**.**.*: * :.****:*.******* :*  :
Prunus                      PFLWPLKDSFKTPLLNELLIKAT-NGMVVPWAPQPRVLAHASVGAFVTHCGWSSLLETIAGGVPMICRPFFGDQRVNARL   399
2C1Z_A|PDBID|CHAIN|SEQUENCE PFIWSLRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRM   381
3HBF_A|PDBID|CHAIN|SEQUENCE PFIWSFRGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTIL   383
                            .......330.......340.......350.......360.......370.......380.......390.......400

                            .*.*****. ::.**:** .: . ::  :*.::*  :*:::  ::  * ::*  :* *: :*  *:::::
Prunus                      VEDVLEIGATVEDGVFTKHGMIKYFDQVLSQQRGKKLRENINTVKLLARQSVEPKGGSAQNFKLLLDVISRSTKV   474
2C1Z_A|PDBID|CHAIN|SEQUENCE VEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE TESVLEIGVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......470.....
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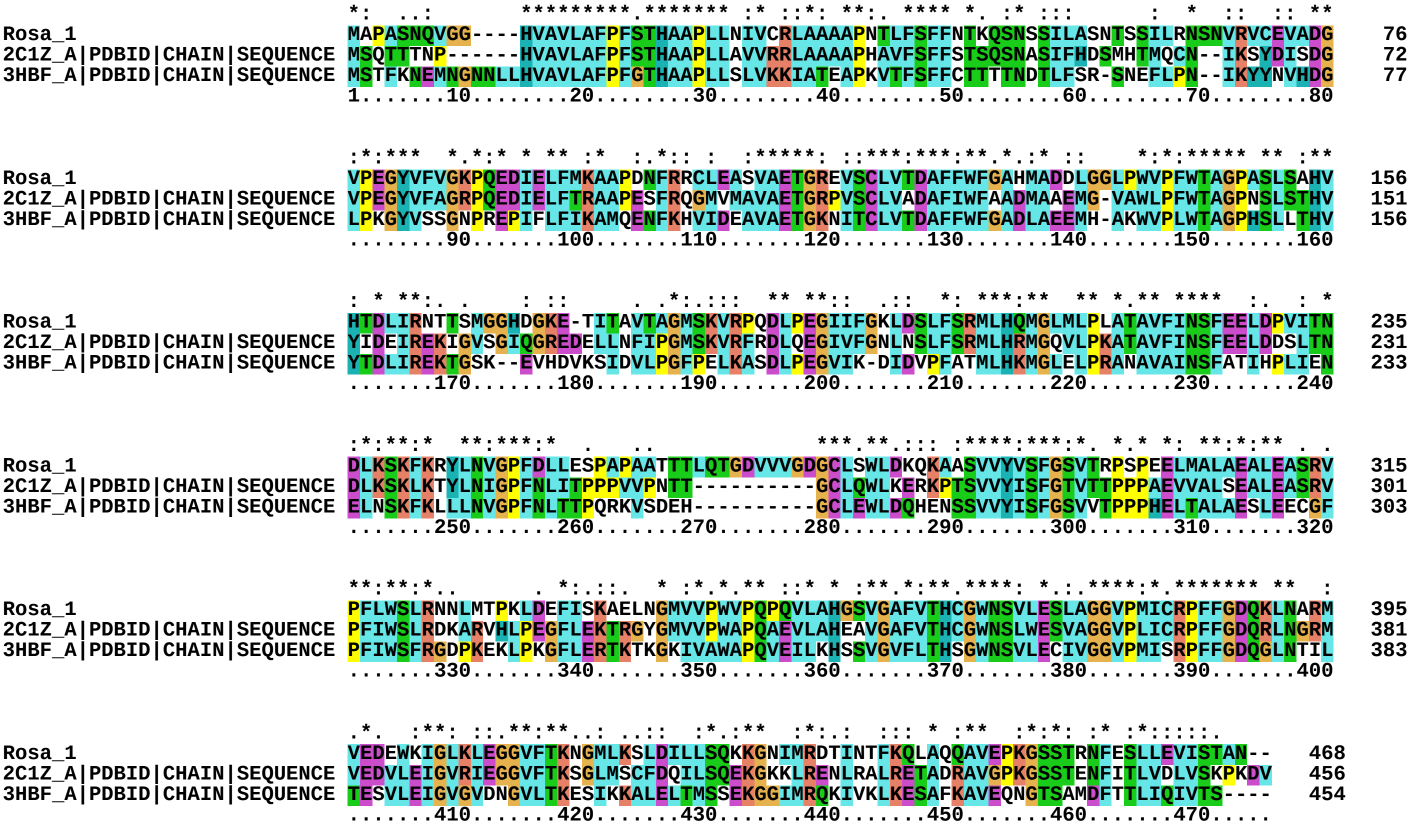

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                            *:  ..:       *********.******* :* ::*: **:. **** *. :* :::      :  *  ::  :: **
Rosa_1                      MAPASNQVGG----HVAVLAFPFSTHAAPLLNIVCRLAAAAPNTLFSFFNTKQSNSSILASNTSSILRNSNVRVCEVADG    76
2C1Z_A|PDBID|CHAIN|SEQUENCE MSQTTTNP------HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCN--IKSYDISDG    72
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSR-SNEFLPN--IKYYNVHDG    77
                            1.......10........20........30........40........50........60........70........80

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Rosa_1                      VPEGYVFVGKPQEDIELFMKAAPDNFRRCLEASVAETGREVSCLVTDAFFWFGAHMADDLGGLPWVPFWTAGPASLSAHV   156
2C1Z_A|PDBID|CHAIN|SEQUENCE VPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMG-VAWLPFWTAGPNSLSTHV   151
3HBF_A|PDBID|CHAIN|SEQUENCE LPKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMH-AKWVPLWTAGPHSLLTHV   156
                            ........90.......100.......110.......120.......130.......140.......150.......160

                            : * **:. .    : ::     . .*:.:::  ** **::  .::  *: ***:**  ** *.** ****  :.  : *
Rosa_1                      HTDLIRNTTSMGGHDGKE-TITAVTAGMSKVRPQDLPEGIIFGKLDSLFSRMLHQMGLMLPLATAVFINSFEELDPVITN   235
2C1Z_A|PDBID|CHAIN|SEQUENCE YIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTN   231
3HBF_A|PDBID|CHAIN|SEQUENCE YTDLIREKTGSK--EVHDVKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIEN   233
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :*:**:*  **:***:*  .   ..             ***.**.::: :****:***:*. *.* *: **:*:** . .
Rosa_1                      DLKSKFKRYLNVGPFDLLESPAPAATTTLQTGDVVVGDGCLSWLDKQKAASVVYVSFGSVTRPSPEELMALAEALEASRV   315
2C1Z_A|PDBID|CHAIN|SEQUENCE DLKSKLKTYLNIGPFNLITPPPVVPNTT----------GCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRV   301
3HBF_A|PDBID|CHAIN|SEQUENCE ELNSKFKLLLNVGPFNLTTPQRKVSDEH----------GCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGF   303
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            **:**:*..      . *:.::.  * :*.*.** ::* * :**.*:**.****: *.:.****:*.******* **  :
Rosa_1                      PFLWSLRNNLMTPKLDEFISKAELNGMVVPWVPQPQVLAHGSVGAFVTHCGWNSVLESLAGGVPMICRPFFGDQKLNARM   395
2C1Z_A|PDBID|CHAIN|SEQUENCE PFIWSLRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRM   381
3HBF_A|PDBID|CHAIN|SEQUENCE PFIWSFRGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTIL   383
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Rosa_1                      VEDEWKIGLKLEGGVFTKNGMLKSLDILLSQKKGNIMRDTINTFKQLAQQAVEPKGSSTRNFESLLEVISTAN--   468
2C1Z_A|PDBID|CHAIN|SEQUENCE VEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE TESVLEIGVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......470.....
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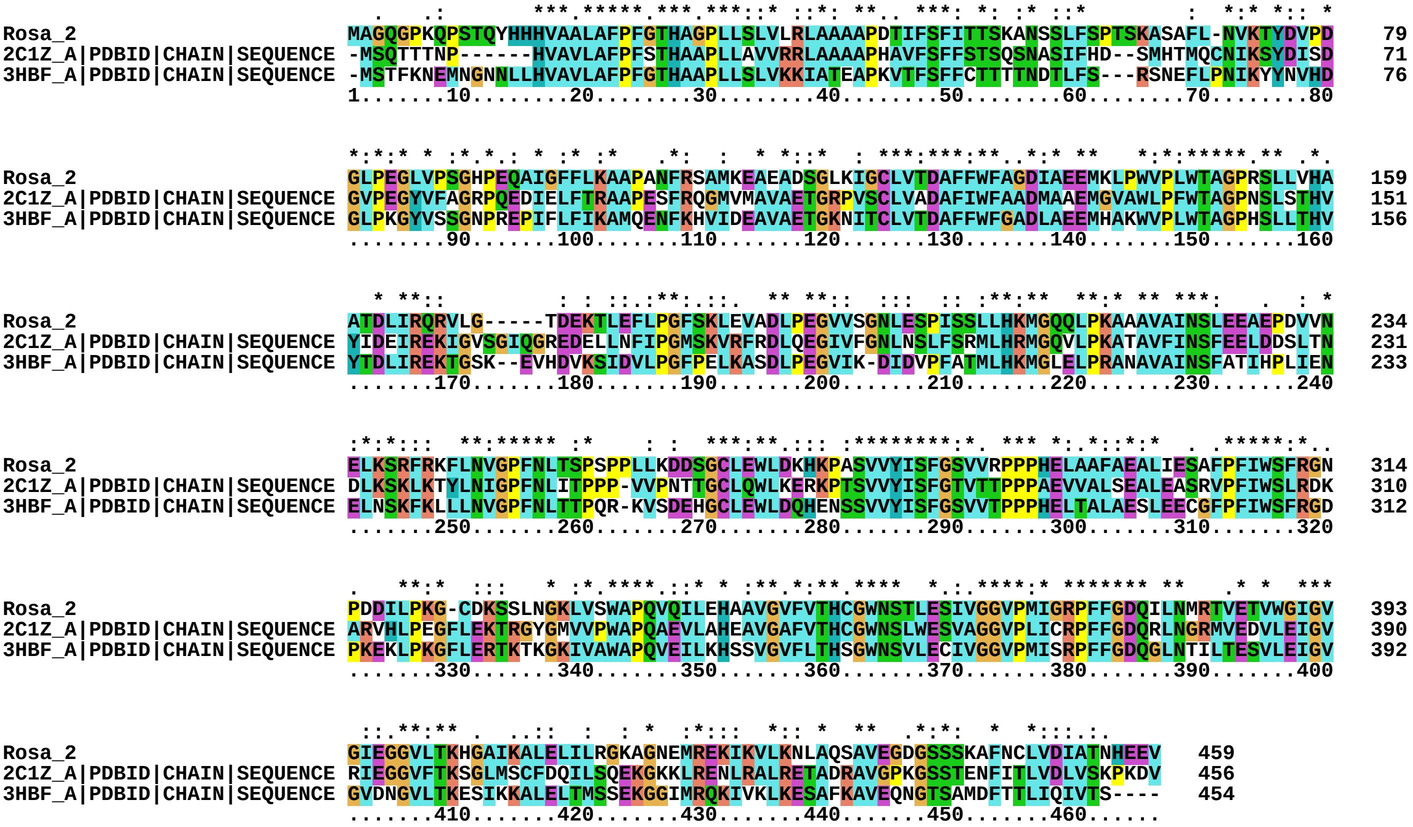

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                              .   .:       ***.*****.***.***::* ::*: **.. ***: *: :* ::*        :  *:* *:: *
Rosa_2                      MAGQGPKQPSTQYHHHVAALAFPFGTHAGPLLSLVLRLAAAAPDTIFSFITTSKANSSLFSPTSKASAFL-NVKTYDVPD     79
2C1Z_A|PDBID|CHAIN|SEQUENCE -MSQTTTNP------HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHD--SMHTMQCNIKSYDISD     71
3HBF_A|PDBID|CHAIN|SEQUENCE -MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFS---RSNEFLPNIKYYNVHD     76
                            1.......10........20........30........40........50........60........70........80

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Rosa_2                      GLPEGLVPSGHPEQAIGFFLKAAPANFRSAMKEAEADSGLKIGCLVTDAFFWFAGDIAEEMKLPWVPLWTAGPRSLLVHA    159
2C1Z_A|PDBID|CHAIN|SEQUENCE GVPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHV    151
3HBF_A|PDBID|CHAIN|SEQUENCE GLPKGYVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHV    156
                            ........90.......100.......110.......120.......130.......140.......150.......160

                              * **::         : : ::.:**:.::.  ** **::  :::  :: :**:**  **:* ** ***:   .  : *
Rosa_2                      ATDLIRQRVLG-----TDEKTLEFLPGFSKLEVADLPEGVVSGNLESPISSLLHKMGQQLPKAAAVAINSLEEAEPDVVN    234
2C1Z_A|PDBID|CHAIN|SEQUENCE YIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTN    231
3HBF_A|PDBID|CHAIN|SEQUENCE YTDLIREKTGSK--EVHDVKSIDVLPGFPELKASDLPEGVIK-DIDVPFATMLHKMGLELPRANAVAINSFATIHPLIEN    233
                            .......170.......180.......190.......200.......210.......220.......230.......240

                            :*:*:::  **:***** :*    : :  ***:**.::: :********:*. *** *:.*::*:*  . .*****:*..
Rosa_2                      ELKSRFRKFLNVGPFNLTSPSPPLLKDDSGCLEWLDKHKPASVVYISFGSVVRPPPHELAAFAEALIESAFPFIWSFRGN    314
2C1Z_A|PDBID|CHAIN|SEQUENCE DLKSKLKTYLNIGPFNLITPPP-VVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDK    310
3HBF_A|PDBID|CHAIN|SEQUENCE ELNSKFKLLLNVGPFNLTTPQR-KVSDEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSFRGD    312
                            .......250.......260.......270.......280.......290.......300.......310.......320

                            .   **:*  :::   * :*.****.::* * :**.*:**.****  *.:.****:* ******* **   .* *  ***
Rosa_2                      PDDILPKG-CDKSSLNGKLVSWAPQVQILEHAAVGVFVTHCGWNSTLESIVGGVPMIGRPFFGDQILNMRTVETVWGIGV    393
2C1Z_A|PDBID|CHAIN|SEQUENCE ARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGV    390
3HBF_A|PDBID|CHAIN|SEQUENCE PKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLEIGV    392
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Rosa_2                      GIEGGVLTKHGAIKALELILRGKAGNEMREKIKVLKNLAQSAVEGDGSSSKAFNCLVDIATNHEEV    459
2C1Z_A|PDBID|CHAIN|SEQUENCE RIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV    456
3HBF_A|PDBID|CHAIN|SEQUENCE GVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----    454
                            .......410.......420.......430.......440.......450.......460......
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                            **      . *    ***: ***.:*.:.** .:: ::: **.  *:**.*: :* ::*  *      *:* *:: **:*
Rosa_3                      MS--HKLASSNPQAPVAVFNFPFASHPSSLLRFIRTISAVAPDIKFTFFSTSRTNSSLFSGSNNKGLDNVKPYNVWDGLP    78
2C1Z_A|PDBID|CHAIN|SEQUENCE MS----QTTTNP--HVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVP    74
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAPKVTFSFFCTTTTNDTLFSRSN-EFLPNIKYYNVHDGLP    79
                            1.......10........20........30........40........50........60........70........80

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Rosa_3                      EGYVPPSGPPLEQIGLFLDQAPQSFERALKEVEAETGHKFGCLISDAFLWFSGDIAQKMNVPWVTTWS-GPRPLLVHLET   157
2C1Z_A|PDBID|CHAIN|SEQUENCE EGYVF-AGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYI   153
3HBF_A|PDBID|CHAIN|SEQUENCE KGYVS-SGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVYT   158
                            ........90.......100.......110.......120.......130.......140.......150.......160

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Rosa_3                      DMIREKVGAPGQED---KTLDFLPGFSNEFLASDLPKEVVFGNIESPLANMLYKMGQKLPQATAVAVNSFETMDLKVSEE   234
2C1Z_A|PDBID|CHAIN|SEQUENCE DEIREKIGVSGIQGREDELLNFIPGMS-KVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTND   232
3HBF_A|PDBID|CHAIN|SEQUENCE DLIREKTGSKEVHDV--KSIDVLPGFP-ELKASDLP-EGVIKDIDVPFATMLHKMGLELPRANAVAINSFATIHPLIENE   234
                            .......170.......180.......190.......200.......210.......220.......230.......240

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Rosa_3                      LKKRLKKLLLVGPLHLVRPVPSAQSDDDEEEKDACLPWLDNHKPASVAYISFGSVGALPPMEVAALAEALEEGGFPFLWS   314
2C1Z_A|PDBID|CHAIN|SEQUENCE LKSKLKTYLNIGPFNLITPPPVVP------NTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWS   306
3HBF_A|PDBID|CHAIN|SEQUENCE LNSKFKLLLNVGPFNLTTPQRKVS------DEHGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWS   308
                            .......250.......260.......270.......280.......290.......300.......310.......320

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Rosa_3                      FRGN-LEDFPKGFIERTST-GRVVPWVNQVQILNHPSIGVFVTHGGWKSVLESVTCGVPMIGRPHFADQTLNMRSVEVVW   392
2C1Z_A|PDBID|CHAIN|SEQUENCE LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVL   386
3HBF_A|PDBID|CHAIN|SEQUENCE FRGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVL   388
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Rosa_3                      KIGMRIEGGVFTKSGAIKVLEQALSLEQGKEMRQRVGVLKQLAQETVGPNGSSAQDLKVW----------   452
2C1Z_A|PDBID|CHAIN|SEQUENCE EIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE EIGVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQNGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......470
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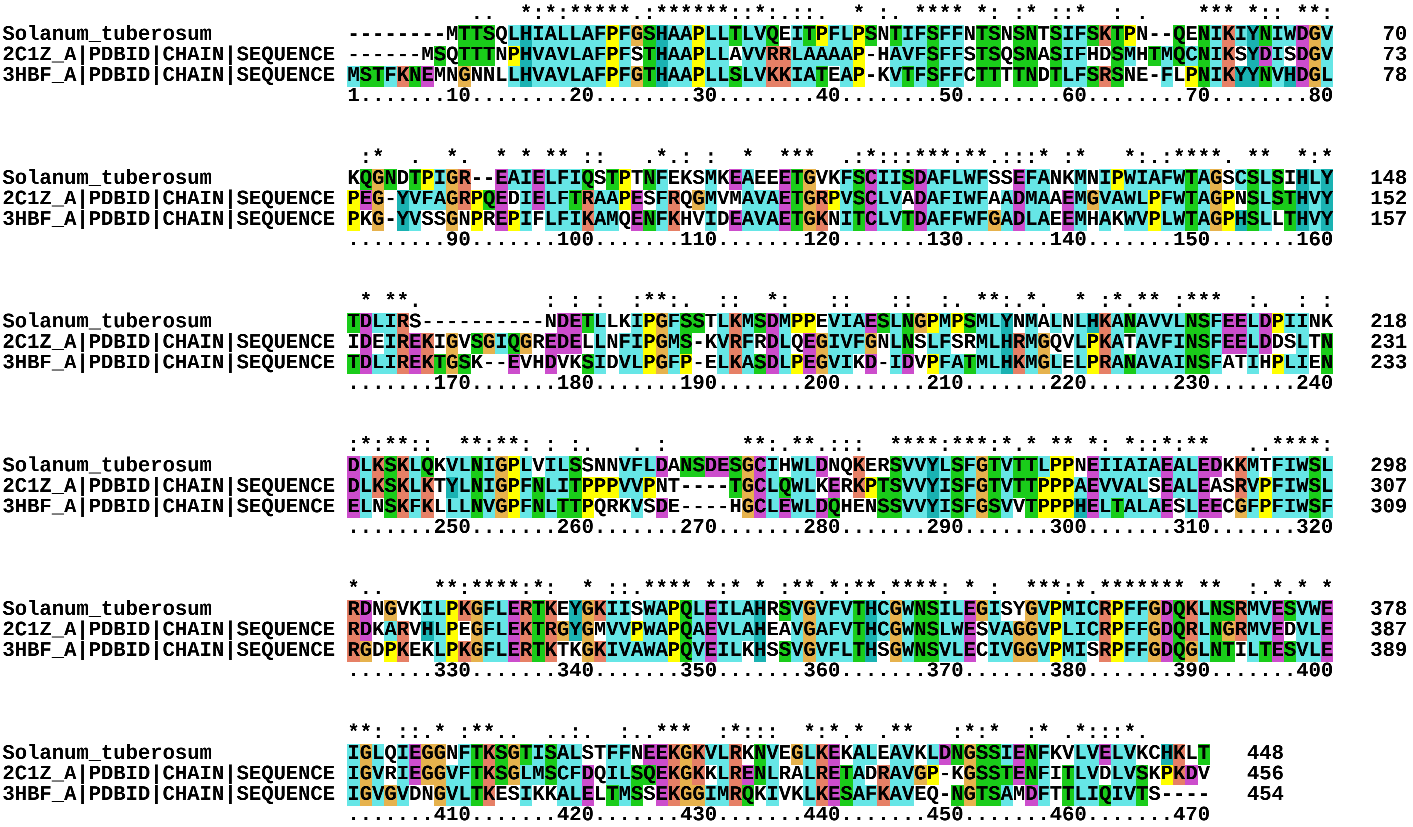

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Solanum_tuberosum           --------MTTSQLHIALLAFPFGSHAAPLLTLVQEITPFLPSNTIFSFFNTSNSNTSIFSKTPN--QENIKIYNIWDGV    70
2C1Z_A|PDBID|CHAIN|SEQUENCE ------MSQTTTNPHVAVLAFPFSTHAAPLLAVVRRLAAAAP-HAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGV    73
3HBF_A|PDBID|CHAIN|SEQUENCE MSTFKNEMNGNNLLHVAVLAFPFGTHAAPLLSLVKKIATEAP-KVTFSFFCTTTTNDTLFSRSNE-FLPNIKYYNVHDGL    78
                            1.......10........20........30........40........50........60........70........80

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Solanum_tuberosum           KQGNDTPIGR--EAIELFIQSTPTNFEKSMKEAEEETGVKFSCIISDAFLWFSSEFANKMNIPWIAFWTAGSCSLSIHLY   148
2C1Z_A|PDBID|CHAIN|SEQUENCE PEG-YVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVY   152
3HBF_A|PDBID|CHAIN|SEQUENCE PKG-YVSSGNPREPIFLFIKAMQENFKHVIDEAVAETGKNITCLVTDAFFWFGADLAEEMHAKWVPLWTAGPHSLLTHVY   157
                            ........90.......100.......110.......120.......130.......140.......150.......160

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Solanum_tuberosum           TDLIRS----------NDETLLKIPGFSSTLKMSDMPPEVIAESLNGPMPSMLYNMALNLHKANAVVLNSFEELDPIINK   218
2C1Z_A|PDBID|CHAIN|SEQUENCE IDEIREKIGVSGIQGREDELLNFIPGMS-KVRFRDLQEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTN   231
3HBF_A|PDBID|CHAIN|SEQUENCE TDLIREKTGSK--EVHDVKSIDVLPGFP-ELKASDLPEGVIKD-IDVPFATMLHKMGLELPRANAVAINSFATIHPLIEN   233
                            .......170.......180.......190.......200.......210.......220.......230.......240

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Solanum_tuberosum           DLKSKLQKVLNIGPLVILSSNNVFLDANSDESGCIHWLDNQKERSVVYLSFGTVTTLPPNEIIAIAEALEDKKMTFIWSL   298
2C1Z_A|PDBID|CHAIN|SEQUENCE DLKSKLKTYLNIGPFNLITPPPVVPNT----TGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSL   307
3HBF_A|PDBID|CHAIN|SEQUENCE ELNSKFKLLLNVGPFNLTTPQRKVSDE----HGCLEWLDQHENSSVVYISFGSVVTPPPHELTALAESLEECGFPFIWSF   309
                            .......250.......260.......270.......280.......290.......300.......310.......320

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Solanum_tuberosum           RDNGVKILPKGFLERTKEYGKIISWAPQLEILAHRSVGVFVTHCGWNSILEGISYGVPMICRPFFGDQKLNSRMVESVWE   378
2C1Z_A|PDBID|CHAIN|SEQUENCE RDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLE   387
3HBF_A|PDBID|CHAIN|SEQUENCE RGDPKEKLPKGFLERTKTKGKIVAWAPQVEILKHSSVGVFLTHSGWNSVLECIVGGVPMISRPFFGDQGLNTILTESVLE   389
                            .......330.......340.......350.......360.......370.......380.......390.......400

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Solanum_tuberosum           IGLQIEGGNFTKSGTISALSTFFNEEKGKVLRKNVEGLKEKALEAVKLDNGSSIENFKVLVELVKCHKLT   448
2C1Z_A|PDBID|CHAIN|SEQUENCE IGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGP-KGSSTENFITLVDLVSKPKDV   456
3HBF_A|PDBID|CHAIN|SEQUENCE IGVGVDNGVLTKESIKKALELTMSSEKGGIMRQKIVKLKESAFKAVEQ-NGTSAMDFTTLIQIVTS----   454
                            .......410.......420.......430.......440.......450.......460.......470
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                                 *  :    : ***::.***.:*  .*** :* :*:   **:   ***:.*   ** :::    . *  :    .*: : ****:***:* .
Vigna_mungo                      MGNSEEKKHVAVFSFPFGSHPTPLLNLVLKLTNAAPNLQFSFIGTEHSNKSLLISKPH-IPDTIKFYSISDGVPEGHVPG    79
3WC4_A|PDBID|CHAIN|SEQUENCE      MKN---KQHVAIFPFPFGSHLPPLLNLVLKLAHIAPNTSFSFIGTHSSN-AFLFTKRH-IPNNIRVFTISDGIPEGHVPA    75
2C1Z_A|PDBID|CHAIN|SEQUENCE      MSQTTTNPHVAVLAFPFSTHAAPLLAVVRRLAAAAPHAVFSFFSTSQSNASIFHDSMHTMQCNIKSYDISDGVPEGYVFA    80
                                 1.......10........20........30........40........50........60........70........80

                                 ..* * ::**  :.*:.:::*: :***.* . *:*:::***:  :  :*  :.*.*:..*.   . *** :.  : **:.
Vigna_mungo                      GHPVERVNLFLQASPQNLQKGIDMAVAHTKERVTCVISDAFVAPSLTVAQRLNVPWVPVWPPLSCSLSAHFYTELIRQTC    159
3WC4_A|PDBID|CHAIN|SEQUENCE      NNPIEKLDLFLSTGPDNLRKGIELAVAETKQSVTCIIADAFVTSSLLVAQTLNVPWIAFWPNVSCSLSLYFNIDLIRDKC    155
2C1Z_A|PDBID|CHAIN|SEQUENCE      GRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAADMAAEMGVAWLPFWTAGPNSLSTHVYIDEIREKI    160
                                 ........90.......100.......110.......120.......130.......140.......150.......160

                                 .         :  *:*:**:**:*..*: :.::   *: ::***: *  :* ***:* **.:* * ***  . :.: ::**:
Vigna_mungo                      NSA----AGDTPLDFVPGLSKMRVEDLPEDVIQGAGEEETLFSKTLASLGSVLPQAEAVVVNFFEELDPPLLVNDMKSKF    235
3WC4_A|PDBID|CHAIN|SEQUENCE      SKD----AKNATLDFLPGLSKLRVEDVPQDMLD-VGEKETLFSRTLNSLGVVLPQAKAVVVNFFAELDPPLFVKYMRSKL    230
2C1Z_A|PDBID|CHAIN|SEQUENCE      GVSGIQGREDELLNFIPGMSKVRFRDLQEGIVF--GNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDS-LTNDLKSKL    237
                                 .......170.......180.......190.......200.......210.......220.......230.......240

                                 :  * :    .*  *    .  : .***.**..:.   **.*:.****.:*** *:**::**** *  .**:*:*::
Vigna_mungo                      KYYLYVGFLTLSLPLPPLPPSDTDETGCLSWLDKQKGGSVVYVSFGTVVTPPPHEIVAVAEALEASGFPFLWSLKEHLKG    315
3WC4_A|PDBID|CHAIN|SEQUENCE      QSLLYV----VPLPCPQLLLPEIDSNGCLSWLDSKSSRSVAYVCFGTVVSPPPQEVVAVAEALEESGFPFVWALKESLLS    306
2C1Z_A|PDBID|CHAIN|SEQUENCE      KTYLNIG--PFNLITPPPVVP--NTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIWSLRDKARV    313
                                 .......250.......260.......270.......280.......290.......300.......310.......320

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Vigna_mungo                      VLPNGFLERTSERGKVVGWAPQTQVLGHGSVGVFVTHCGCNSVFESMSNGVPMICRPFFGDHGLTGRMVEDVWEIGVRVE    395
3WC4_A|PDBID|CHAIN|SEQUENCE      ILPKGFVERTSTRGKVVSWVPQSHVLSHGSVGVFVTHCGANSVMESVSNGVPMICRPFFGDQGIAARVIQDIWEVGVIVE    386
2C1Z_A|PDBID|CHAIN|SEQUENCE      HLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPLICRPFFGDQRLNGRMVEDVLEIGVRIE    393
                                 .......330.......340.......350.......360.......370.......380.......390.......400

                                 * ****.*::..:   ** :*.*: ::.*   ::: .   *.*.:*.::::* ***:::* .
Vigna_mungo                      GGVFTKDGLLKSLRLILVEEEGNLMKKNAVKVKKTVLDAAGAQGKAAQDFNTLVELVSRS---    455
3WC4_A|PDBID|CHAIN|SEQUENCE      GKVFTKNGFVKSLNLILVQEDGKKIRDNALKVKQIVQDAVGPHGQAAEDFNTLVEVISSS---    446
2C1Z_A|PDBID|CHAIN|SEQUENCE      GGVFTKSGLMSCFDQILSQEKGKKLRENLRALRETADRAVGPKGSSTENFITLVDLVSKPKDV    456
                                 .......410.......420.......430.......440.......450.......460...
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