Supplementary Material 1

PA Full Alignment

(CRYSTAL STRUCTURE: RCSB entry: 2W69)

```
Query      MEDFVRQCFNPMIVELAEKAMKEYGEDPKIETNKFAAICTHLEVCFMYSDFHFIDERGES  60
             MEDFVRQCFNPMIVELAEKAMKEYGEDKIETNKFAAICTHLEVCFMYSDFHFI+E+GES
Sbjct      MEDFVRQCFNPMIVELAEKAMKEYGEDLKIETNKFAAICTHLEVCFMYSDFHFINEQGES  67

Query      IIVESGDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGVEKPKFLPDLYDYKENRFIEI  120
            I+VE  DPNALLKHRFEIIEGRDRTMAWTVVNSICNTTG EKPKFLPDLYDYKENRFIEI
Sbjct      IVVELDDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDYKENRFIEI  127

Query      GVTRREVHIYYLEKANKIKSEKTHIHIFSFTGEEMATKADYTLDEESRARIKTRLFTIRQ  180
            GVTRREVHIYYLEKANKIKSE THIHIFSFTGEEMATKADYTLDEESRARIKTRLFTIRQ
Sbjct      GVTRREVHIYYLEKANKIKSENTHIHIFSFTGEEMATKADYTLDEESRARIKTRLFTIRQ  187

       Query      EMANRGLWDSFRQSERGEETIEERFEITG  209
                   EMANRGLWDSFRQSERGEETIEERFEITG
       Sbjct      EMANRGLWDSFRQSERGEETIEERFEITG  216
```

…

(CRYSTAL STRUCTURE: RCSB entry: 2ZNL)

```
Query      NGCIEGKLSQMSKEVNARIEPFLKTTPRPLRLPEGPPCSQRSKFLLMDALKLSIEDPSHE  298
            NG IEGKLSQMSKEVNARIEPFLKTTPRPLRLP GPPCSQRSKFLLMDALKLSIEDPSHE
Sbjct      NGYIEGKLSQMSKEVNARIEPFLKTTPRPLRLPNGPPCSQRSKFLLMDALKLSIEDPSHE  60

Query      GEGIPLYDAIKCMKTFFGWKEPNIVKPHEKGINPNYLLAWKQVLAELQDIENEEKIPKTK  358
            GEGIPLYDAIKCM+TFFGWKEPN+VKPHEKGINPNYLL+WKQVLAELQDIENEEKIPKTK
Sbjct      GEGIPLYDAIKCMRTFFGWKEPNVVKPHEKGINPNYLLSWKQVLAELQDIENEEKIPKTK  120

Query      NMKKTSQLKWALGENMAPEKVDFEDCKDVSDLRQYDSDEPEQRSLASWIQSEFNKACELT  418
            NMKKTSQLKWALGENMAPEKVDF+DCKDV DL+QYDSDEPE RSLASWIQ+EFNKACELT
Sbjct      NMKKTSQLKWALGENMAPEKVDFDDCKDVGDLKQYDSDEPELRSLASWIQNEFNKACELT  180

Query      DSSWIELDEIGEDVAPIEHIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNASCAAMD  478
            DSSWIELDEIGEDVAPIEHIASMRRNYFT+EVSHCRATEYIMKGVYINTALLNASCAAMD
Sbjct      DSSWIELDEIGEDVAPIEHIASMRRNYFTSEVSHCRATEYIMKGVYINTALLNASCAAMD  240

Query      DFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWE  538
            DFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWE
Sbjct      DFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWE  300

Query      KYCVLEIGDMLLRTAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEA  598
            KYCVLEIGDML+R+AIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEA
Sbjct      KYCVLEIGDMLIRSAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEA  360

Query      ESSVKEKDMTREFFENKSETWPIGESPKGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGF  658
            ESSVKEKDMT+EFFENKSETWPIGESPKGVEE SIGKVCRTLLAKSVFNSLYASPQLEGF
Sbjct      ESSVKEKDMTKEFFENKSETWPIGESPKGVEESSIGKVCRTLLAKSVFNSLYASPQLEGF  420

Query      SAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHAL  715
            SAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHAL
Sbjct      SAESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHAL  477
```

Supplementary Material 2

PB1 Full Alignment

(CRYSTAL STRUCTURE: RCSB entry: 2ZNL)

```
Query  MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGKWTTNSE  60
       MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKG+WTTN+E
Sbjct  MDVNPTLLFLKVPAQNAISTTFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGRWTTNTE  60

Query  TGAPQLNPIDGPLPEDNEPSG  81
       TGAPQLNPIDGPLPEDNEPSG
Sbjct  TGAPQLNPIDGPLPEDNEPSG  81
```

…

(CRYSTAL STRUCTURE: RCSB entry: 4F7P)

```
Query  FYRYGFVANF  505
       FYRYGFVANF
Sbjct  FYRYGFVANF  10
```

…

(HOMOLOGY MODEL #1 ALINGMENT. TEMPLATE:2YKG)

```
Query  DTQIQTRRSFELKKLWEQTRSKAGLLVSDGGPNLYNIRN------------LHIPEVCLK  612
       +++I  +  + + +L   T S A  +  D   NL  I+N            + + + C+
Sbjct  ESRISDKFKYIIAQLMRDTESLAKRICKDL-ENLSQIQNREFGTQKYEQWIVTVQKACMV  293

Query  WELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAK-SMEY  657
       +++ D+D + R+C  L  + SH  +   N+A+++  H   K +++Y
Sbjct  FQMPDKDEESRICKALFLYTSH--LRKYNDALIISEHARMKDALDY  337
```

…

(CRYSTAL STRUCTURE: RCSB entry: 3A1G)

```
Query  SQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVSRARIDARIDFESGRIKK  737
       SQRG+LEDEQ YQ+CCNLFEKFFPSSSYRRPVGISS VEA VSRARIDARIDFESGRIKK
Sbjct  SQRGVLEDEQXYQRCCNLFEKFFPSSSYRRPVGISSXVEAXVSRARIDARIDFESGRIKK  60

Query  EEFAEIMKICSTIEELRRQK  757
       EEF EI KICSTIEELRRQK
Sbjct  EEFTEIXKICSTIEELRRQK  80
```

Supplementary Material 3

PB2 Full Alignment

(CRYSTAL STRUCTURE: RCSB entry: 2ZTT)

```
Query  2   ERIKELRDLMSQSRTREILTKTTVDHMAIIKKYTSG  37
             ERIKELR+L SQSRTREILTKTTVDH AIIKKYTSG
Sbjct  5   ERIKELRNLXSQSRTREILTKTTVDHXAIIKKYTSG  40
```

…

(HOMOLOGY MODEL #2 ALINGMENT. TEMPLATE:1GTM)

```
Query       PGHADLSAKEAQDVIMEVVFPNEVGARILTSESQLTITKEKKEELQDCKIAPLMVAYMLE  208
              PG  +++ +E  ++ ++V+ P  +   ++T ++   I  +   E+ +  + P     + E
Sbjct       PGATNITNEELLELEVDVLAPAAI-EEVITKKNADNIKAKIVAEVANGPVTPEADEILFE  332

   Query       RELVRKTRFLPVAGGTSSVYIEVLHLTQGTCW  240
                 + +++   FL  AGG +  Y E +    G  W
   Sbjct       KGILQIPDFLCNAGGVTVSYFEWVQNITGYYW  364
```

…

(CRYSTAL STRUCTURE: RCSB entry: 4ENF)

```
Query       LRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRK  376
              +RISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRK
 Sbjct       MRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQTLKIRVHEGYEEFTMVGRRATAILRK  63

Query       ATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLR  436
              ATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLR
Sbjct       ATRRLIQLIVSGRDEQSIAEAIIVAMVFSQEDCMIKAVRGDLNFVNRANQRLNPMHQLLR  123

      Query       HFQKDAKVLFQNWGIEPIDNVMGMIGILPDMTPSTEMSLRGIRVSKM  483
                    HFQKDAKVLFQNWG+EPIDNVMGMIGILPDMTPS EMS+RG+R+SKM
      Sbjct       HFQKDAKVLFQNWGVEPIDNVMGMIGILPDMTPSIEMSMRGVRISKM  170
```

…

(CRYSTAL STRUCTURE: RCSB entry: 3L56)

```
Query       EINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVR  597
              EINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVR
 Sbjct       EINGPESVLVNTYQWIIRNWETVKIQWSQDPTMLYNKMEFEPFQSLVPKAARGQYSGFVR  60

Query       TLFQQMRDVLGTFDTVQIIKLLPFAAAPPEQSRMQFSSLTVNVRGSGMRILVRGNSPVFN  657
              TLFQQMRDVLGTFDTVQIIKLLPFAAAPP+QSRMQFSSLTVNVRGSGMRILVRGNSPVFN
Sbjct       TLFQQMRDVLGTFDTVQIIKLLPFAAAPPKQSRMQFSSLTVNVRGSGMRILVRGNSPVFN  120

Query       YTKTTKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLA  717
              Y K TKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLA
Sbjct       YNKATKRLTVLGKDAGALTEDPDEGTAGVESAVLRGFLILGKEDKRYGPALSINELSNLA  180

        Query       KGEKANVLIGQGDVVLVMKRKRDSSILTDSQTATKRIRMAIN  759
                      KGEKANVLIGQGDVVLVMKRKRDSSILTDSQTATKRIRMAIN
        Sbjct       KGEKANVLIGQGDVVLVMKRKRDSSILTDSQTATKRIRMAIN  222
```