**Supplementary Material 1**

**(CRYSTAL STRUCTURE: RCSB entry: 2W69)**

**Query**

MEDFVRQCNPIM逃离AM-keyGDPKIEKNFAAICTHELEVCMYSDHFHIDERGES  60
MEDFVRQCNPIM逃离AM-keyGDPKIEKNFAAICTHELEVCMYSDHFHIDERGES +E+GES

**Sbjct**

MEDFVRQCNPIM逃离AM-keyGDPKIEKNFAAICTHELEVCMYSDHFHINQGES  67

**Query**

IIVESGDPNALLKRFHEIEIEGDRDRTMAWTVN5ICNTT8GEKPKFPDLYDYKENRFIEI  120
I+VE DPNALLKRFHEIEIEGDRDRTMAWTVNSICNTTG EKPKFPDLYDYKENRFIEI

**Sbjct**

IVELDPPNL逃离AM-keyGDRDRTMAWTVNSICNTTGAEKPKFPDLYDYKENRFIEI  127

**Query**

GVTREHVIYLEKANIKEKSEKTHIIFSTGEGMATKADYTLDEESRARIKTRLPTIRQ  180
GVTREHVIYLEKANIKEKSEKTHIIFSTGEGMATKADYTLDEESRARIKTRLPTIRQ

**Sbjct**

GVTREHVIYLEKANIKEKSEKTHIIFSTGEGMATKADYTLDEESRARIKTRLPTIRQ  187

**Query**

EMANGLWDSPRQSERGETTEIERFEITG  209
EMANGLWDSPRQSERGETTEIERFEITG

**Sbjct**

EMANGLWDSPRQSERGETTEIERFEITG  216

... (CRYSTAL STRUCTURE: RCSB entry: 2ZNL)

**Query**

NGCIEGKLSQMSKEVANIEFPFLKTTPPRPLRLEGGAPCSQRKFLMDALKNLISEPSHE  298
NG IEKLSQMSKEVANIEFPFLKTTPPRPLRLEGGAPCSQRKFLMDALKNLISEPSHE

**Sbjct**

NGIEGKLSQMSKEVANIEFPFLKTTPPRPLRLEGGAPCSQRKFLMDALKNLISEPSHE  60

**Query**

GEGIPLYDAIKCMKRTTFSWEPKVGPKINNYLWALKVLAELQDIENNEEKIPGTK  358
GEGIPLYDAIKCMKRTTFSWEPKVGPKINNYLWALKVLAELQDIENNEEKIPGTK

**Sbjct**

GEGIPLYDAIKCMKRTTFSWEPKVGPKINNYLWALKVLAELQDIENNEEKIPGTK  120

**Query**

NMKKTSQLKHALGENMAPEKDVFEDCKVDSLEQRYSDEPEQRSLSAWIWQSEFQKACELT  418
NMKKTSQLKHALGENMAPEKDVFEDCKVDSLEQRYSDEPEQRSLSAWIWQSEFQKACELT

**Sbjct**

NMKKTSQLKHALGENMAPEKDVFEDCKVDSLEQRYSDEPEQRSLSAWIWQSEFQKACELT  180

**Query**

DSSWIELDEIGEDVAPIEHIASMMRNFTAEVSHCRAZYIMKGVYINTALLNASCAAMD  478
DSSWIELDEIGEDVAPIEHIASMMRNFTAEVSHCRAZYIMKGVYINTALLNASCAAMD

**Sbjct**

DSSWIELDEIGEDVAPIEHIASMMRNFTAEVSHCRAZYIMKGVYINTALLNASCAAMD  240

**Query**

DFQILPMISKCRKTEGRKRNLYFIKGRSHLRNDTDVNVFEMFSLTDLRPHELKWE  538
DFQILPMISKCRKTEGRKRNLYFIKGRSHLRNDTDVNVFEMFSLTDLRPHELKWE

**Sbjct**

DFQILPMISKCRKTEGRKRNLYFIKGRSHLRNDTDVNVFEMFSLTDLRPHELKWE  300

**Query**

KYCVLEIGDMILRTAIGQSVRPFLVYRNTGSKIKMKWGMEMRCCQLQQIESMIEA  598
KYCVLEIGDMIL+R+AIGQSVRPFLVYRNTGSKIKMKWGMEMRCCQLQQIESMIEA

**Sbjct**

KYCVLEIGDMILRISAIGQSVRPFLVYRNTGSKIKMKWGMEMRCCQLQQIESMIEA  360

**Query**

ESSVEKEKDTMEFFENKSETWIPIGESPKGVEEGSIGKCRTLAKSFVSNLYASPQLEGF  658
ESSVEKEKDTMEFFENKSETWIPIGESPKGVEEGSIGKCRTLAKSFVSNLYASPQLEGF

**Sbjct**

ESSVEKEKDTMEFFENKSETWIPIGESPKGVEEGSIGKCRTLAKSFVSNLYASPQLEGF  420

**Query**

SAESRKLLLIVQALNRDNLPEGTFDLGGLYEAIEECLINDPWLVLNASFNSFLTHAL  715
SAESRKLLLIVQALNRDNLPEGTFDLGGLYEAIEECLINDPWLVLNASFNSFLTHAL

**Sbjct**

SAESRKLLLIVQALNRDNLPEGTFDLGGLYEAIEECLINDPWLVLNASFNSFLTHAL  477
Supplementary Material 2
PB1 Full Alignment

(CRYSTAL STRUCTURE: RCSB entry: 2ZNL)
Query  MDVNPTLLFLKVPQNAISTFFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGWTTNSE  60
        MDVNPTLLFLKVPQNAISTFFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEK+WTN+E
Sbjct  MDVNPTLLFLKVPQNAISTFFPYTGDPPYSHGTGTGYTMDTVNRTHQYSEKGRWTNTNE  60
Query  TGAPQLNPIDGPLPEDNEPSG  81
        TGAPQLNPIDGPLPEDNEPSG
Sbjct  TGAPQLNPIDGPLPEDNEPSG  81
...

(CRYSTAL STRUCTURE: RCSB entry: 4F7P)
Query  FYRYGFVANF  505
        FYRYGFVANF
Sbjct  FYRYGFVANF  10
...

(HOMOLOGY MODEL #1 ALIGNMENT. TEMPLATE: 2YKG)
Query  DTQIQTRRSFLKFWQTRSKAGLLVSDGGPNLNYRINR-------------LHIPEVCLK  612
        +++I  + ++  +L  T S A  + D  NL  I+N  +  +  C+
Sbjct  ESRISDKFYIQAQLMRDTESLAKCRIKDL-ENLSQIQNREFGTQKYEQWFIVTVQKACMV  293
Query  WEIMDQDVGRLCNPLNPFSHKEIESVNNAVMPAHGP--SMEY  657
        +++ D+D  + R+C  L  + SH  + N+A  +++  H  K  +++Y
Sbjct  FQMPDKDEESRICKALFYTSH--LKYNDALIISEHARMKDALDY  337
...

(CRYSTAL STRUCTURE: RCSB entry: 3A1G)
Query  SQRGILEDEQYQQKCCNLFEKFPPPSSYSRYRPGGISSVEAMVSRARIDARIDFESGRK  737
        SQR+LEDEQ YQ+CCNLFEKFPPPSSYRRPGGISS VEA VSRARIDARIDFESGRK
Sbjct  SQRGVLEDEQXYQCCNLFEKFPPPSSYRRPGGISSXVEAXVSRARIDARIDFESGRK  60
Query  EEFAEIMKICSTIELRRQK  757
        EEF EI KICSTIELRRQK
Sbjct  EEFEIXXKICSTIELRRQK  80
**Supplementary Material 3**

**PB2 Full Alignment**

**(CRYSTAL STRUCTURE: RCSB entry: 2ZTT)**

| Query | ERIKELRDLMSQRSRTREILTKTTVDHMAIIKKYTSG | 37 |
|-------|----------------------------------------|----|
| Sbjct | ERIKELRNLXSQRSRTREILTKTTVDHXAIKKYTSG | 40 |

...

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

| Query | PGHADLSAKEAQDVIMEVFPFNEVGARILTSESQRSTKEKEELQDCKIAPILVAYMLE | 208 |
|-------|--------------------------------------------------------------|----|
| Sbjct | PGATNITNEELLELEVVLAPAAEEVITKKNADNIKIAEVANGPVTEADEILFE       | 332 |

| Query | RELVRKTRFLPVAGGTSSVYIEVLHITQGTCW | 240 |
|-------|---------------------------------|----|
| Sbjct | KGILQIPDFLCNAGGVTSFWQVNITGYYW  | 364 |

...

**(CRYSTAL STRUCTURE: RCSB entry: 4ENF)**

| Query | LRISSSFSGGFTTFRKRTSSGSSVKEREEVLNLQTLKIRVHEGTYEFTMVGRRTAILRK | 376 |
|-------|-------------------------------------------------------------|----|
| Sbjct | MIRISSSFSGGFTTFRKRTSSGSSVKEreeVLNLQTLKIRVHEGTYEFTMVGRRTAILRK | 63 |

| Query | ATRRLIQIVSQRDEQSIAMVAMVFSQEDCMIAVRGDLNFWVNRANQRLNPMEQLLR | 436 |
|-------|-----------------------------------------------------------|----|
| Sbjct | ATRRLIQIVSQRDEQSIAMVAMVFSQEDCMIAVRGDLNFWVNRANQRLNPMEQLLR | 123 |

| Query | HFQKDAKVLFQWNGIEMIDNVMGIMLDPDFTSTEMLGRIVSKM | 483 |
|-------|----------------------------------------------|----|
| Sbjct | HFQKDAKVLFQWNGIEMIDNVMGIMLDPDFTSTEMLGRIVSKM | 170 |

...

**(CRYSTAL STRUCTURE: RCSB entry: 3L56)**

| Query | EINGPESVLYQWIIRNWETVKIQWQDSQDFTMLYNKMEFEPPQSSLVPAARGQYSVFVR | 597 |
|-------|------------------------------------------------------------|----|
| Sbjct | EINGPESVLYQWIIRNWETVKIQWQDSQDFTMLYNKMEFEPPQSSLVPAARGQYSVFVR | 60 |

| Query | TLFQQMRDVLGTDFTVQIIKLLPFAAAPEPQRSMQFSSLTVNVRGSRMLVGRGNSVFN | 657 |
|-------|-------------------------------------------------------------|----|
| Sbjct | TLFQQMRDVLGTDFTVQIIKLLPFAAAPEPQRSMQFSSLTVNVRGSRMLVGRGNSVFN | 120 |

| Query | YTKTKLRTEVLGKDAGALTEDPEDTAGVESAVLGFLGKGEDKRYGPALSINELNSLA | 717 |
|-------|------------------------------------------------------------|----|
| Sbjct | YNKATKRLVTLKGDAGALTEDPEDTAGVESAVLGFLGKGEDKRYGPALSINELNSLA | 180 |

| Query | KGKEANVLIGGQGDVVLVMKRRDSILTSQATKIRMAIN | 759 |
|-------|------------------------------------------|----|
| Sbjct | KGKEANVLIGGQGDVVLVMKRRDSILTSQATKIRMAIN | 222 |