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GTCTGGCCCCGCCCTCTCATCAACTAATCCCGTCTTGAAAGAAATTCCTAGAAAAGAAGTTAGGAAAAAG 140

TGGAGCATAGCAGAAAAGGGGTAGAGTTTGAGATGGAGAATGGAAATCATGAAATCCCTGAGGATGCCAA 210
                                 M  E  N  G  N  H  E  I  P  E  D  A  N

TGAGCATTGTCCAGGGCCTCAATCCGAGTCCGCGGGGAAGTCCGATTCTTGCGAAGGTTGTCCTAATCAG 280
  E  H  C  P  G  P  Q  S  E  S  A  G  K  S  D  S  C  E  G  C  P  N  Q

CAAATATGTGCTACTGCTCCGAAGGGCCCTGATCCTGATTTGATTGGAATAGCTGAGAGAATGGCCACTA 350
 Q  I  C  A  T  A  P  K  G  P  D  P  D  L  I  G  I  A  E  R  M  A  T

TCAAGCACAAAATATTGGTTTTATCTGGCAAGGGTGGTGTTGGAAAGAGCACATTCTCAGCCCAACTGTC 420
I  K  H  K  I  L  V  L  S  G  K  G  G  V  G  K  S  T  F  S  A  Q  L  S

ATTTGCTCTTGCAAGCAAGGACTACCAGGTTGGCCTACTTGACATCGACATCTGCGGCCCTAGCATCCCC 490
  F  A  L  A  S  K  D  Y  Q  V  G  L  L  D  I  D  I  C  G  P  S  I  P

AAGATGCTTGGCCTGGAGAGGGAGGACATCCATCAGAGCAACCTGGGCTGGTCCCCCGTCTACGTTGATT 560
 K  M  L  G  L  E  R  E  D  I  H  Q  S  N  L  G  W  S  P  V  Y  V  D

CCAATCTTGGTGTGATGTCCATAGGCTTCATGCTTCCCAATCCTGATGAGGCTGTCATATGGAGGGGACC 630
S  N  L  G  V  M  S  I  G  F  M  L  P  N  P  D  E  A  V  I  W  R  G  P

TCGCAAGAATGGTCTCATCAAGCAGTTCCTGAAGAACGTGAATTGGGGCGAGATTGACTATCTAGTGGTG 700
  R  K  N  G  L  I  K  Q  F  L  K  N  V  N  W  G  E  I  D  Y  L  V  V

GATGCCCCACCTGGGACTTCGGATGAACACATATCGATCGTCCAGTTTCTTCAGGCCTCTGGGATTGATG 770
 D  A  P  P  G  T  S  D  E  H  I  S  I  V  Q  F  L  Q  A  S  G  I  D

GCGCAGTCATAGTTACCACTCCACAGCAGGTGTCTCTAATTGATGTCCGTAAGGAAATAAGCTTCTGCAA 840
G  A  V  I  V  T  T  P  Q  Q  V  S  L  I  D  V  R  K  E  I  S  F  C  K

GAAAGTTGGGATCCAAGTCCTTGGAGTTGTGGAGAACATGAGCGGGCTGAAGCAGCCTGTGCTTGATCTC 910
  K  V  G  I  Q  V  L  G  V  V  E  N  M  S  G  L  K  Q  P  V  L  D  L

AAATTTGAAAGACTGGTTGCAGGTGACAAGGTAGGTGCAGTTGAGGATGTCACTGAGTGGGCTCAGAGGT 980
 K  F  E  R  L  V  A  G  D  K  V  G  A  V  E  D  V  T  E  W  A  Q  R

ATATAAGGCAGAATGCGCCAGAGCTATTGTCTCTCTTTGCTTGCAGTGAGGTGTTCGATATTAGTGGCGG 1050
Y  I  R  Q  N  A  P  E  L  L  S  L  F  A  C  S  E  V  F  D  I  S  G  G

TGGTGCAGCAAAGATGTGCACTGAGATGGGTGTACCGTTCCTCGGCAAGGTGCCTTTAGATCCTCAGCTC 1120
  G  A  A  K  M  C  T  E  M  G  V  P  F  L  G  K  V  P  L  D  P  Q  L

TGCAAAGCAGCAGAGGATGGGCGGTCGTGCTTCGAAGAAGACCAGAAATGCAGATTAAGTGCCCCGTCTC 1190
 C  K  A  A  E  D  G  R  S  C  F  E  E  D  Q  K  C  R  L  S  A  P  S

TCCTGGGAATTGTTGAACAACTCATTGCTTCTCACGAGTAGTTCATGTCACAGGGAAAAAATACAGATTT 1260
L  L  G  I  V  E  Q  L  I  A  S  H  E  .

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AGAAATCGAAAAAAAAAAAA 1350
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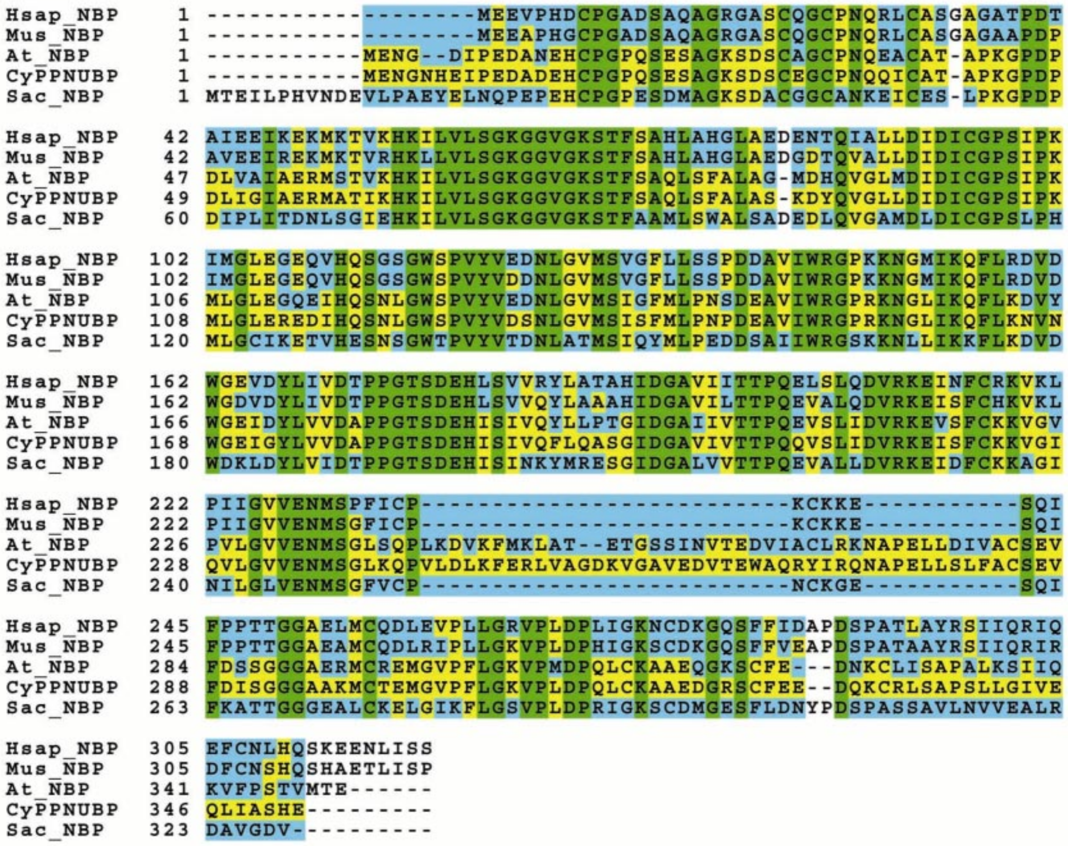
Figure 3-3



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Mus_NBP     1 -------------------MEEAPHGCPGADSAQAGRGASCQGCPNQRLCASGAGAAPDP
At_NBP      1 -----------MENG--DIPEDANEHCPGPQSESAGKSDSCAGCPNQEACAT-APKGPDP
CyPPNUBP    1 -----------MENGNHEIPEDADEHCPGPQSESAGKSDSCEGCPNQQICAT-APKGPDP
Sac_NBP     1 MTEILPHVNDEVLPAEYELNQPEPEHCPGPESDMAGKSDACGGCANKEICES-LPKGPDP

Hsap_NBP   42 AIEEIKEKMKTVKHKILVLSGKGGVGKSTFSAHLAHGLAEDENTQIALLDIDICGPSIPK
Mus_NBP    42 AVEEIREKMKTVRHKLLVLSGKGGVGKSTFSAHLAHGLAEDGDTQVALLDIDICGPSIPK
At_NBP     47 DLVAIAERMSTVKHKILVLSGKGGVGKSTFSAQLSFALAG-MDHQVGLMDIDICGPSIPK
CyPPNUBP   49 DLIGIAERMATIKHKILVLSGKGGVGKSTFSAQLSFALAS-KDYQVGLLDIDICGPSIPK
Sac_NBP    60 DIPLITDNLSGIEHKILVLSGKGGVGKSTFAAMLSWALSADEDLQVGAMDLDICGPSLPH

Hsap_NBP  102 IMGLEGEQVHQSGSGWSPVYVEDNLGVMSVGFLLSSPDDAVIWRGPKKNGMIKQFLRDVD
Mus_NBP   102 IMGLEGEQVHQSGSGWSPVYVDDNLGVMSVGFLLSSPDDAVIWRGPKKNGMIKQFLRDVD
At_NBP    106 MLGLEGQEIHQSNLGWSPVYVEDNLGVMSIGFMLPNSDEAVIWRGPRKNGLIKQFLKDVY
CyPPNUBP  108 MLGLEREDIHQSNLGWSPVYVDSNLGVMSISFMLPNPDEAVIWRGPRKNGLIKQFLKNVN
Sac_NBP   120 MLGCIKETVHESNSGWTPVYVTDNLATMSIQYMLPEDDSAIIWRGSKKNLLIKKFLKDVD

Hsap_NBP  162 WGEVDYLIVDTPPGTSDEHLSVVRYLATAHIDGAVIITTPQELSLQDVRKEINFCRKVKL
Mus_NBP   162 WGDVDYLIVDTPPGTSDEHLSVVQYLAAAHIDGAVILTTPQEVALQDVRKEISFCHKVKL
At_NBP    166 WGEIDYLVVDAPPGTSDEHISIVQYLLPTGIDGAIIVTTPQEVSLIDVRKEVSFCKKVGV
CyPPNUBP  168 WGEIGYLVVDAPPGTSDEHISIVQFLQASGIDGAVIVTTPQQVSLIDVRKEISFCKKVGI
Sac_NBP   180 WDKLDYLVIDTPPGTSDEHISINKYMRESGIDGALVVTTPQEVALLDVRKEIDFCKKAGI

Hsap_NBP  222 PIIGVVENMSPFICP--------------------------KCKKE-----------SQI
Mus_NBP   222 PIIGVVENMSGFICP--------------------------KCKKE-----------SQI
At_NBP    226 PVLGVVENMSGLSQPLKDVKFMKLAT--ETGSSINVTEDVIACLRKNAPELLDIVACSEV
CyPPNUBP  228 QVLGVVENMSGLKQPVLDLKFERLVAGDKVGAVEDVTEWAQRYIRQNAPELLSLFACSEV
Sac_NBP   240 NILGLVENMSGFVCP--------------------------NCKGE-----------SQI

Hsap_NBP  245 FPPTTGGAELMCQDLEVPLLGRVPLDPLIGKNCDKGQSFFIDAPDSPATLAYRSIIQRIQ
Mus_NBP   245 FPPTTGGAEAMCQDLRIPLLGKVPLDPHIGKSCDKGQSFFVEAPDSPATAAYRSIIQRIR
At_NBP    284 FDSSGGGAERMCREMGVPFLGKVPMDPQLCKAAEQGKSCFE---DNKCLISAPALKSIIQ
CyPPNUBP  288 FDISGGGAAKMCTEMGVPFLGKVPLDPQLCKAAEDGRSCFEE--DQKCRLSAPSLLGIVE
Sac_NBP   263 FKATTGGGEALCKELGIKFLGSVPLDPRIGKSCDMGESFLDNYPDSPASSAVLNVVEALR

Hsap_NBP  305 EFCNLHQSKEENLISS
Mus_NBP   305 DFCNSHQSHAETLISP
At_NBP    341 KVFPSTVMTE------
CyPPNUBP  346 QLIASHE---------
Sac_NBP   323 DAVGDV----------
```

Figure 3-4.

```
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 L  S  F  H  Y  M  L  P  L  S  V  P  P  W  R  H  E  L  K  R  S  L  W

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E  S  Y  V  L  A  N  K  I  F  S  Q  K  V  I  E  V  I  N  P  E  E  D  Y

CGTCTGGATTCATGATTACCATCTCATGGCTCTCCCCACCTTCCTCCGCCGCCGCTTCAATCGCCTTCGG 210
  V  W  I  H  D  Y  H  L  M  A  L  P  T  F  L  R  R  R  F  N  R  L  R

ATGGGATTCTTTCTCCACAGCCCCTTTCCATCGTCTGAGATCTACCGCACTCTCCCTGTGCGCGAGGAGA 280
 M  G  F  F  L  H  S  P  F  P  S  S  E  I  Y  R  T  L  P  V  R  E  E

TCCTGAAAGCTCTTCTCAACTGCGACCTCATTGGCTTCCATACCTTCGACTATGCCCGCCACTTCCTCTC 350
I  L  K  A  L  L  N  C  D  L  I  G  F  H  T  F  D  Y  A  R  H  F  L  S

CTGCTGCAGTCGGATGCTTGGAATGGAGTATCAGTCCAAGCGTGGCTATATTGGCCTCGACTACTTTGGC 420
  C  C  S  R  M  L  G  M  E  Y  Q  S  K  R  G  Y  I  G  L  D  Y  F  G

CGCACCGTCGGCATCAAGATCATGCCGGTGGGCATTCAAATGGCGCAGCTTCAATTGACACTTTCCCTCC 490
 R  T  V  G  I  K  I  M  P  V  G  I  Q  M  A  Q  L  Q  L  T  L  S  L

CGGACAAGGCCTGGCGTGTCTCTGAGCTCCAGCAGCAGTTTTTTGGTAAAACTGTTTTGCTTGGTGTTGA 560
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TGACATGGACATTTTCAAAGGCATCAATCTCAAGCTCCTTGCATTTGAGCAGATGCTCAAGATACATTCC 630
  D  M  D  I  F  K  G  I  N  L  K  L  L  A  F  E  Q  M  L  K  I  H  S

AAGTGGCAGGGGAATGCGGTTCTTGTGCAGATTGCTAATCCTGCTCGGGGCAAGGGAAGGGACCTTGAGG 700
 K  W  Q  G  N  A  V  L  V  Q  I  A  N  P  A  R  G  K  G  R  D  L  E

AGATTCAAGCAGAGATTCGGCAAAGCTGCAAAAGGATTAATGAGCAGTTTGGTAATGCTAATTACAACCC 770
E  I  Q  A  E  I  R  Q  S  C  K  R  I  N  E  Q  F  G  N  A  N  Y  N  P

TGTTGTCTTCATTGATCTCCCAATCTCCCTAGAAGAGAGGGTTGCGTTCTACACCATTGCGGAATGTGTG 840
  V  V  F  I  D  L  P  I  S  L  E  E  R  V  A  F  Y  T  I  A  E  C  V

GTTGTCACAGCAGTCAGAGATGGGATGAACTTGACACCATATGAGTACATTGTATGTAGACAGGGGATTA 910
 V  V  T  A  V  R  D  G  M  N  L  T  P  Y  E  Y  I  V  C  R  Q  G  I

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TAAGAGGAGGTGCTGGGGGATTGGTTTGGGATTTGGGTTTAGGGTGGTTGCATTGGATCCCAATTTTAGG 1260
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AAGCTTAACATTGATGCAATTGTTTCAGCACATGAGAGGGCTAAAAGCAGGGCTATTTTGTTGGATTATG 1330
  K  L  N  I  D  A  I  V  S  A  H  E  R  A  K  S  R  A  I  L  L  D  Y

ATGGCACGATGATGCCACAAATGCCTATTAACAAGACTCCAAGTGCAGAAATTATCTCTATTATCAATAC 1400
 D  G  T  M  M  P  Q  M  P  I  N  K  T  P  S  A  E  I  I  S  I  I  N  T

ACTTTGTGGTGATAAAAAGAATGTGGTCTTTATTGTAGTGGTAGAGGAATGGTGTAACTTGGAGAAGTGG 1470
  L  C  G  D  K  K  N  V  V  F  I  V  V  V  E  E  W  C  N  L  E  K  W

TTCTCCCCTTGCAGGAAACTGGGGCTTGCAGCAGAGCATGGATACTTCACGAGGTGGAGTCGCGATGAAA 1540
 F  S  P  C  R  K  L  G  L  A  A  E  H  G  Y  F  T  R  W  S  R  D  E

GTTGGGAAATATGCAGTCAAAGCTCTGATTTTGAATGGATGCAGATAGCTGAGCCTGTGATGAAATTGTA 1610
S  W  E  I  C  S  Q  S  S  D  F  E  W  M  Q  I  A  E  P  V  M  K  L  Y

TACAGAATCGACTGATGGATCCTATATTGATAAGAAAGAGAGTGCATTGGTGTGGCACCATCATGATGCT 1680
  T  E  S  T  D  G  S  Y  I  D  K  K  E  S  A  L  V  W  H  H  H  D  A

GATCCTGATTTTGGATCAGCTCAGGCCAAGGAGATGCTGGACCACCTTGAGAGTGTACTTGCAAATGAGC 1750
 D  P  D  F  G  S  A  Q  A  K  E  M  L  D  H  L  E  S  V  L  A  N  E

CTGTTTCAGTGAAGAGCGGCCAGTTCATCGTTGAAGTCAAGCCTCAGGGAGTGACCAAAGGTATTGTCGT 1820
P  V  S  V  K  S  G  Q  F  I  V  E  V  K  P  Q  G  V  T  K  G  I  V  V

GGAGAAGATCTTATCCTCTATGGTCAACTACAATAAACAAGCAGACTTCTTGCTTTGTATTGGTGATGAT 1890
   E  K  I  L  S  S  M  V  N  Y  N  K  Q  A  D  F  L  L  C  I  G  D  D

AGATCACATGAAGACATGTTTGAATGCATCAGTGCTATCCTCTCCAAGGATCTTGTTGCGCCAAACACAA 1960
  R  S  H  E  D  M  F  E  C  I  S  A  I  L  S  K  D  L  V  A  P  N  T

CAAGTGTTTGCTTCCACAAGTGGGACAGAAACCGAGCAAAAGCAAGATACTATCTTGACGACACGGTCGA 2030
T  S  V  C  F  H  K  W  D  R  N  R  A  K  A  R  Y  Y  L  D  D  T  V  E

GGTGACTAACATGCTTGGAGCACTTGCAGATAGCTCCCAGCCATCTTCACCTATTTCTGATGTTAAACTG 2100
  V  T  N  M  L  G  A  L  A  D  S  S  Q  P  S  S  P  I  S  D  V  K  L

GAATCTTTATCTTTCTCTGAGATGGCTGCCAAGCCTAACATGTCCACCTAAAAACTGATGGTGATTGTTA 2170
 E  S  L  S  F  S  E  M  A  A  K  P  N  M  S  T  .

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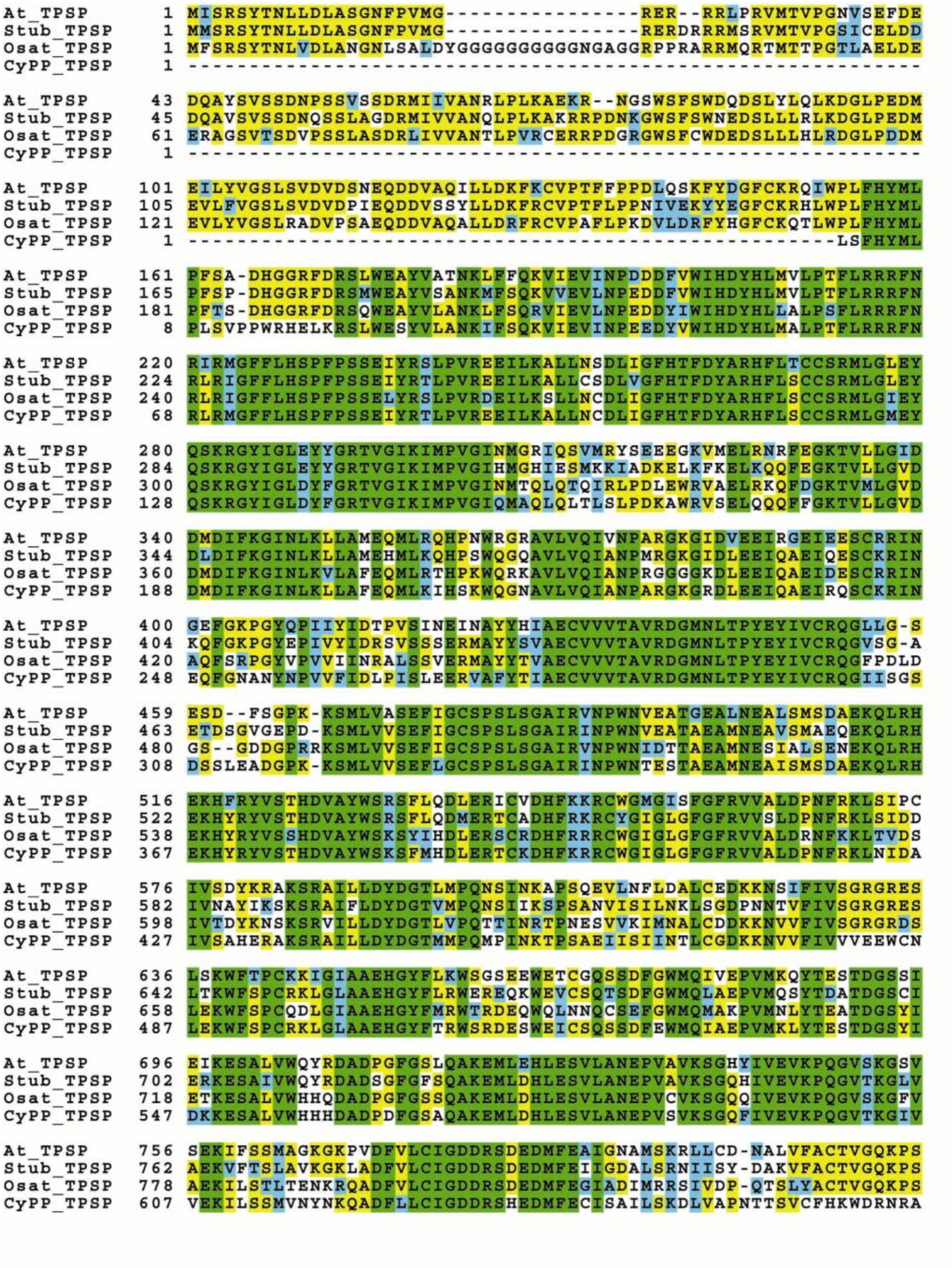
Figure 3-5.



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Osat_TPSP     1 MFSRSYTNLVDLANGNLSALDYGGGGGGGGGGNGAGGRPPRARRMQRTMTTPGTLAELDE
CyPP_TPSP     1 ------------------------------------------------------------

At_TPSP      43 DQAYSVSSDNPSSVSSDRMIIVANRLPLKAEKR--NGSWSFSWDQDSLYLQLKDGLPEDM
Stub_TPSP    45 DQAVSVSSDNQSSLAGDRMIVVANQLPLKAKRRPDNKGWSFSWNEDSLLLRLKDGLPEDM
Osat_TPSP    61 ERAGSVTSDVPSSLASDRLIVVANTLPVRCERRPDGRGWSFCWDEDSLLLHLRDGLPDDM
CyPP_TPSP     1 ------------------------------------------------------------

At_TPSP     101 EILYVGSLSVDVDSNEQDDVAQILLDKFKCVPTFFPPDLQSKFYDGFCKRQIWPLFHYML
Stub_TPSP   105 EVLFVGSLSVDVDPIEQDDVSSYLLDKFRCVPTFLPPNIVEKYYEGFCKRHLWPLFHYML
Osat_TPSP   121 EVLYVGSLRADVPSAEQDDVAQALLDRFRCVPAFLPKDVLDRFYHGFCKQTLWPLFHYML
CyPP_TPSP     1 -----------------------------------------------------LSFHYML

At_TPSP     161 PFSA-DHGGRFDRSLWEAYVATNKLFFQKVIEVINPDDDFVWIHDYHLMVLPTFLRRRFN
Stub_TPSP   165 PFSP-DHGGRFDRSMWEAYVSANKMFSQKVVEVLNPEDDFVWIHDYHLMVLPTFLRRRFN
Osat_TPSP   181 PFTS-DHGGRFDRSQWEAYVLANKLFSQRVIEVLNPEDDYIWIHDYHLLALPSFLRRRFN
CyPP_TPSP     8 PLSVPPWRHELKRSLWESYVLANKIFSQKVIEVINPEEDYVWIHDYHLMALPTFLRRRFN

At_TPSP     220 RIRMGFFLHSPFPSSEIYRSLPVREEILKALLNSDLIGFHTFDYARHFLTCCSRMLGLEY
Stub_TPSP   224 RLRIGFFLHSPFPSSEIYRTLPVREEILKALLCSDLVGFHTFDYARHFLSCCSRMLGLEY
Osat_TPSP   240 RLRIGFFLHSPFPSSELYRSLPVRDEILKSLLNCDLIGFHTFDYARHFLSCCSRMLGIEY
CyPP_TPSP    68 RLRMGFFLHSPFPSSEIYRTLPVREEILKALLNCDLIGFHTFDYARHFLSCCSRMLGMEY

At_TPSP     280 QSKRGYIGLEYYGRTVGIKIMPVGINMGRIQSVMRYSEEEGKVMELRNRFEGKTVLLGID
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Osat_TPSP   300 QSKRGYIGLDYFGRTVGIKIMPVGINMTQLQTQIRLPDLEWRVAELRKQFDGKTVMLGVD
CyPP_TPSP   128 QSKRGYIGLDYFGRTVGIKIMPVGIQMAQLQLTLSLPDKAWRVSELQQQFFGKTVLLGVD

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Osat_TPSP   360 DMDIFKGINLKVLAFEQMLRTHPKWQRKAVLVQIANPRGGGGKDLEEIQAEIDESCRRIN
CyPP_TPSP   188 DMDIFKGINLKLLAFEQMLKIHSKWQGNAVLVQIANPARGKGRDLEEIQAEIRQSCKRIN

At_TPSP     400 GEFGKPGYQPIIYIDTPVSINEINAYYHIAECVVVTAVRDGMNLTPYEYIVCRQGLLG-S
Stub_TPSP   404 KQFGKPGYEPIVYIDRSVSSSERMAYYSVAECVVVTAVRDGMNLTPYEYIVCRQGVSG-A
Osat_TPSP   420 AQFSRPGYVPVVIINRALSSVERMAYYTVAECVVVTAVRDGMNLTPYEYIVCRQGFPDLD
CyPP_TPSP   248 EQFGNANYNPVVFIDLPISLEERVAFYTIAECVVVTAVRDGMNLTPYEYIVCRQGIISGS

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Stub_TPSP   463 ETDSGVGEPD-KSMLVVSEFIGCSPSLSGAIRINPWNVEATAEAMNEAVSMAEQEKQLRH
Osat_TPSP   480 GS--GDDGPRRKSMLVVSEFIGCSPSLSGAIRVNPWNIDTTAEAMNESIALSENEKQLRH
CyPP_TPSP   308 DSSLEADGPK-KSMLVVSEFLGCSPSLSGAIRINPWNTESTAEAMNEAISMSDAEKQLRH

At_TPSP     516 EKHFRYVSTHDVAYWSRSFLQDLERICVDHFKKRCWGMGISFGFRVVALDPNFRKLSIPC
Stub_TPSP   522 EKHYRYVSTHDVAYWSRSFLQDMERTCADHFRKRCYGIGLGFGFRVVSLDPNFRKLSIDD
Osat_TPSP   538 EKHYRYVSSHDVAYWSKSYIHDLERSCRDHFRRRCWGIGLGFGFRVVALDRNFKKLTVDS
CyPP_TPSP   367 EKHYRYVSTHDVAYWSKSFMHDLERTCKDHFKRRCWGIGLGFGFRVVALDPNFRKLNIDA

At_TPSP     576 IVSDYKRAKSRAILLDYDGTLMPQNSINKAPSQEVLNFLDALCEDKKNSIFIVSGRGRES
Stub_TPSP   582 IVNAYIKSKSRAIFLDYDGTVMPQNSIIKSPSANVISILNKLSGDPNNTVFIVSGRGRES
Osat_TPSP   598 IVTDYKNSKSRVILLDYDGTLVPQTTINRTPNESVVKIMNALCDDKKNVVFIVSGRGRDS
CyPP_TPSP   427 IVSAHERAKSRAILLDYDGTMMPQMPINKTPSAEIISIINTLCGDKKNVVFIVVVEEWCN

At_TPSP     636 LSKWFTPCKKIGIAAEHGYFLKWSGSEEWETCGQSSDFGWMQIVEPVMKQYTESTDGSSI
Stub_TPSP   642 LTKWFSPCRKLGLAAEHGYFLRWEREQKWEVCSQTSDFGWMQLAEPVMQSYTDATDGSCI
Osat_TPSP   658 LEKWFSPCQDLGIAAEHGYFMRWTRDEQWQLNNQCSEFGWMQMAKPVMNLYTEATDGSYI
CyPP_TPSP   487 LEKWFSPCRKLGLAAEHGYFTRWSRDESWEICSQSSDFEWMQIAEPVMKLYTESTDGSYI

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Stub_TPSP   762 AEKVFTSLAVKGKLADFVLCIGDDRSDEDMFEIIGDALSRNIISY-DAKVFACTVGQKPS
Osat_TPSP   778 AEKILSTLTENKRQADFVLCIGDDRSDEDMFEGIADIMRRSIVDP-QTSLYACTVGQKPS
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Figure 3-6.