(a)

```
At HPAT2    MGFRGKYFFPILMTLSL-FLIIRYNYIVSDDP-PLRQELPGRRSA----SSGDDITYT--
At HPAT1    MGCGGTLFYPLLITLSV-AL-ITYNIIISANA-PLKQGFPGRSSS----SDIS-IDPVIE
At HPAT3    ---MGKASGLLLFLLGFGFFVVTYNLLTLIV--HNRSGV-------SNSDGSPLLDPVVQ
Pp HPATa    ---MARITFPVLVFLALAAMVVTYNTITMINSYHNRSDLIDSRAGEEDDDNQFAFDPLIR
Pp HPATb    ---MTRIKFPVLVFLALAAMVATYNTITMINSYHNRSGHVGPAG--EDDNKFSFESLIK
                      :*. *..  :   ** :        :.            .    :

At HPAT2    ------VKTPSKKTKRLFHTAVTATDSVYSTWQCRVMYYWYNRFR--DEPGSDMGGYTRI
At HPAT1    LPRGGGSRNNDGKRIRLFHTAVTASDSVYNTWQCRVMYYWFKKIQASAGPGSEMGGFTRI
At HPAT3    MPLNI---RKAKSSPAPFHVALTATDAPYNKWQCRIMYYWYKQKK--ALPGSDMGGFTRI
Pp HPATa    MPKDM---K-RNGPKRLFHVAVTANDSPYNRWQCRIMYYWYKKFK--DAPGSEMGGFTRI
Pp HPATb    PSEET---K-RSSPTRLFHVAVTANDFPYNRWQCQIMYYWYKKFK--DAPGSEMGGFTRV
                             **.*:**.*  *. ***::****::: :    ***:***:**:

At HPAT2    LHSGRPDGLMDEIPTFVADPLPSGVDKGYVVLNRPWAFVQWLQQAHIEEDYILMAEPDHI
At HPAT1    LHSGKPDQYMDEIPTFVAQPLPSGMDQGYVVLNRPWAFVQWLQQTDIKEDYILMSEPDHI
At HPAT3    LHSGNSDNLMDEIPTFVVDPLPPGLDRGYVVLNRPWAFVQWLERATIKEDYVLMAEPDHV
Pp HPATa    LHSGKADNFMDEIPTVVVDPLPDGEDRGYIVLNRPWAFVQWLRKADIPEDYILMAEPDHI
Pp HPATb    LHSGKPDNFMEEIPTVVVDPLPDGEDRGYIVLNRPWAFVQWLRKTDIPEDYILMAEPDHI
            ****. *  *:****.*.:*** * *:**:************.:: * ***:**:****:

At HPAT2    IVKPIPNLARGNLAAAFPFFYIEPKKYESVLRKFFPKENGPISRIDPIGNSPVIVTKNAL
At HPAT1    IVKPIPNLAKDGLGAAFPFFYIEPKKYEKVLRKYYPEVRGPVTNIDPIGNSPVIVGKDAL
At HPAT3    FVNPLPNLAVGGFPAAFPFFYITPEKYENIVRKYYPAEMGPVTNIDPIGNSPVIISKESL
Pp HPATa    FIRPLPNLATEEMPAAFKFFYIVPTENEKVLRKFFPNEKGPIANIDPIGNSPVIIKKSQL
Pp HPATb    FIRPLPNLATEDIPAAFKFFYIVPTKNEKVLRKFFPKEKGPISNIDPIGNSPVIIKKSQL
            ::.*:****   : *** **** * : *.::**::*   **::.**********: *. *

At HPAT2    MKIAPTWMNVSLAMKNDPQTDKAFGWVLEMYAYAVSSALHGVSNILHKDFMIQPPWDTET
At HPAT1    KKIAPTWMNVSLAMKKDPEADKAFGWVLEMYAYAVSSALHGVSNILHKDFMIQPPWDIEV
At HPAT3    EKIAPTWMNVSLTMKNDPETDKAFGWVLEMYGYAIASAIHGVRHILRKDFMLQPPWDLST
Pp HPATa    EKIAPTWSDVSIKMKDDPETDKAFGWVLEMYGYATASALHGIRHMLVKDFMLQPPWDTDL
Pp HPATb    EKVAPTWSDVSIKMKDDPETDKAFGWVLEMYGYATAAALHGIRHTLVKDFMLQPPWDTDR
             *:**** :**: **.**::***********.** ::*:**: . * ****:***** .

At HPAT2    KKTFIIHYTYGCDFDMKGKMMVGKIGEWRFDKRSYGDKPPPRNLTLPPRGVPESVVTLVT
At HPAT1    GDKYIIHYTYGCDYDMKGKLTYGKIGEWRFDKRSYDSKPPPRNLTMPPPGVSQSVVTLVK
At HPAT3    KGKFIIHYTYGCDYNMKGELTYGKIGEWRFDKRSHLRGPPPRNMSLPPPGVPESVVTLVK
Pp HPATa    GNKYIIHYTYGCDYNMQGKLTYGKIGEWRFDKRSFTTGAPPKNLTLPPPGVPETVVTLVK
Pp HPATb    GNNYIIHYTYGCDYSMKGQLTYGTIGEWRFDKRSYSTGAPPKNLTLPPPGVPETVVTLVK
              .:*********:.*:*::  *.**********.    **:*:::** ** ::*****.

At HPAT2    MINEATANIPNWES--
At HPAT1    MINEATANIPNWGS--
At HPAT3    MVNEATATIPNWDTL-
Pp HPATa    MVNEATASIPGWKGGE
Pp HPATb    MVNEATANIPGWKEGE
            *:*****.** *
```

(b)

Comparison	**% identity**	**% similarity**	**% gaps**
At HPAT3 vs. Pp HPATa	65.3	77.2	3.0
At HPAT1 vs. Pp HPATa	61.0	76.7	5.0
At HPAT2 vs. Pp HPATa	60.1	74.7	4.0
At HPAT3 vs. Pp HPATb	63.2	74.7	2.5
At HPAT1 vs. Pp HPATb	60.3	76.0	4.5
At HPAT2 vs. Pp HPATb	59.8	74.7	4.6