

hPat1a (1) -----MNCLEG-----PG--KTCGPLASEEELVSAQCLEKEEENEG-----EEEEEEDEEDLDPLDPLDLEE-----EENDLGDPAILGAVHNT  
hPat1b (1) ---MFRYESLEDCPLDEDEDAFOGLGEEDEEIDQFNDDTFGSGAVDDDDQEAHERLAELEEKLPVAVNEQTGNGERDEMDDLGDHEENLAER-----LSKMWIENELEDPAIMRAVQTR  
mPat1a (1) -----MKCLEGL-----HLQQRPS--KFSVSLAPEEGLVCAFOLEEEKENE-----DECVCSDQAEVKE-----EGCGLGDPAILSAFQNT  
mPat1b (1) ---MFRYESLEDCPLDEDEDAFOGLGEEDEEIDQFNDDTFGSGAVDDDDQEAHERLAELEEKLPVAADEQTGNGERDEMDDLGDHEENLAER-----LSKMWIENELEDPAIMRAVQTR  
xPat1a (1) MNLGSEQILPEDFYLAEEGALLFEMAEEDEEIDLNEWTFCLEQESDEEPVKLEDDHTKPIQMPAPKEEPEALQPVKEAKGSEKAPLHEVKIVVEPHEDHVDLSIDSGGHTMNSTMDDSELGDPVAMKAFHGK  
xPat1b (1) -----MESLVDGDGFDDL EEEDEEIDQFNDDTFGAGAVDDDWKEEHERLAELEEKLPATHILARVTS SPINDLLGDQEEBLEQS-----LNQLVRENE--EPALPQGSLTQ  
Consensus (1) ED L ED DALEGLGEEDEEIDQFNDDTFGSGAVDDDW EAHERLAELEEKLP A E GE DE DLLGD EEL E L MVEENELGDPAIMRAVQTR

hPat1a (74) QR-----ALLSSPGVKAPGMLGMSLASLHFLWQTLDYLSPIPFW-P---TFPSTSSPAQ-HFGFRLP-----SP-----  
hPat1b (112) PVLQPQPGSLNSSIWDGSEVLRRIRGPLLAQEMPTVSVL-EYALPQRPPQG-PEDDDRDLSERALPRRSTSPIIGSPPVRAVPVIGTPPKQ-MAVPSFT-QQILCPKPVHVRPPMPPRYPAPYGERMSNQ LCSVPN  
mPat1a (71) QVPQ-----QRGLHSSHRVKVSGALGMSASLHFMWQ-----S-----VFPRASSPAH-HFGFQQP-----SP-----  
mPat1b (112) PVLQPQPGSLNSSIWDGSEVLRRIRGPLLAQEMPTVSVL-EYALPQRPLQG-PEDDDRDLSERALPRRSTSPIIGSPPVRAVPVIGTPPKQ-MAVPSFN-QQILCPKPVHVRPPMPPRYPAPYGERISNQ LCSVPN  
xPat1a (136) PTLLESLDSAVVDSGIGSTWSELDTDYDQSGMDSGLWEASPKVSTYATQOILEDKAILRIMERAPYLPPTNLEFLG---SPLQRFMPQSQRLOQFEMGAMSPKPYRPRFMR-----QQSP-----LV  
xPat1b (99) FSAG----MNSSIWDTSRTIRPIRGPLLMEDMTPLSLILHEYGLATVAPPGRDDTERDASERALPRRSTSPIIGSPPVRAVPVIGTPPKH-GASENFHSHTQVLCFNPIHIRASS-----AFSGPHNNP-----  
Consensus (136) PVLQ SLNSSIWD S LR IRGPLLA DM VSL EYAL G LG EADRDLSERALPRRSTSPIIGSPPVRAVPVIGTPPKQ MAGP F QILCPKPVHVR A G SP

**HELIX X**

hPat1a (133) -----DPTLFCSLLTSWPPRF-----SHLTQ LHPHQHRILOQQQ-----HS  
hPat1b (243) SSLLGHPFPSPVPPVLSPLQRAQLLGGAAQLQPG-RMSPSQFARVPGFVGSPLAAMNPKLLQGRVGMQLPPAPG-FRAFFSAPPSATPPPQHPGPGPHLQNLRSQAP-MFRPDTHLHPQHRRLHQRQQNRS  
mPat1a (123) -----DFFLFYSPLTPWP PKLSL-----SHLTQ LHPHQHRILOQQQ-----RW  
mPat1b (243) SSLLGHPFPSPVPPVLSPLQRAQLLGGAAQLQPG-RMSPSQFARVPGFVGSPLAAMNPKLLQGRVGMQLPPAPS-FRAFFSAPPPATPPPQHPGPGPHLQNLRPQAP-MFRADTHLHPQHRRLHQRQLQRN  
xPat1a (249) PRSMRPSYPFTTP-----RRGPSVFAPNQSPG-FVSTQTPFRMSPNVSTPTREMTPKMVRMHFGPMSPS-----PSFSPFFSPMGNALQRFKVPGHVTQLHPQHRRLSQRQ---RP  
xPat1b (215) ASILRHFPFS---ALSPQLQRAQLLGGAAQTVAQMSPSQFSR-PGLHGPTLASVAPKLLQGHVGMVAVVGGGFRPFVGP-----SAPGAHIKNMSLRSSQQQFRPDTHLHPQHRRLYQRQ-QNRN  
Consensus (271) SSL HPFP P LSPLQRAQLLGGAA PG MSPSQFARVPGLVGSPLAAM PKLLQGVGMQLPP FR FF P P GPG HL NL A FRSHTTQLHPQHRRLHQRQ Q R

hPat1a (169) QTP-----SPPAKKPWSQQ---PDYANLMTREKDWIKVQMVQLQSAKPRLLDDYYQYQYQKLEKKQADEELGRRNRVSLKLVTPIYIPKA EAYESVVRIEGSLGQVAVSTCFSPRRADAVPHGTQEODI  
hPat1b (375) QHRNLNGAGDRGSHRSSHQDHLRKDPYANLMLQREKDWVSKIOMMQLQSTDPYLLDDFYQNYFEKLEKLSAAEEIQDGGPKKERTKLTTPQVAKLEHAYKPVQFEGSLGKLTVSSVNNPRKMDAVVTSRSEDE  
mPat1a (162) RRRRSPTARSVPAQKPWSREPAASDAYANLMTREKDWIRVQMVQLQSENPRLLDDYYQYQYQKLEKQADKELGQKTRAESLKLVTPIYIQPEVYESVVRIEGSLGQVAVSTCFSPRRADAVSHGTQEODT  
mPat1b (375) QHRNLNGTDRGGHQSSHQDHLRKDPYANLMLQREKDWVSKIOMMQLQSTDPYLLDDFYQNYFEKLEKLSAAEEIQDGGPKKERTKLTTPQVAKLEHAYKPVQFEGSLGKLTVSSVNNPRKMDAVVTSRSEDE  
xPat1a (352) QSS-----SRRQWESR-----PDYASLMSQKEKEWVIKLOMIQLQSENPHLLDDYYQYQYENLEKRLSEEEFLGERKKREPTKLVTPIYIQKAEYVESVVRIEGSLGQVAVSTCYSPRRADAVSYAMPDEAI  
xPat1b (333) QHRGVNGSGGERTCPAQMELNRRDPYAGLMLQREKEWVCRIQLQLQSTDPYHDDYYQNYFEKLDKLSVSQDRSREGPKKERTKLTTPQVAKLEHTYKPVQFEGSLGKLTVSSVNNPRKMDAVATSRSEDE  
Consensus (406) QHR L NGAG A KPS QD R KDPYANLMLQKEKDWIKIQMMQLQSTDPYLLDDYYQNYFEKLEKLSADEEILGDGPKKERTKLTPIYIAKLEHYYSVVQIEGSLGQLTVSSVNSPRKMDAVTSRSEDE

hPat1a (295) EAAS---SQRLRVLYRIEKMFLQLLEIEGWK-----YRPPPPCFSEQSNQVEKLFQTLKTQEQNNLEEAADGFLQVLSVRKGKALVARLLBFLPDQDAVTILLATTHHLLPLVLRDVAQALQMLFKPLGKC  
hPat1b (510) TKEKQVRDKRRKTLVIIIEKTYSLLLDVEDYERRYL LSLLEE-ERPALMDDRKHKICSMYDNLRGKLPQGERPSDDHFVQIMCIRKGKRMVARILBFLSTEQAADILMTARNLPFLIKKDAQDEVLPCLLSPFSL  
mPat1a (297) GAAS---SQRLRVLSQIEKMFLQLLKEIEGQN-----DGLPQLYHTREQSSQVEKLFQALKTQEQNNLEEAADNLLQVLSVRKGKVLVARLLBFLPDQAVSLLLYITYHLLPLIQDMADQGLHMLFKPLGKY  
mPat1b (510) TKEKQVRDKRRKTLVIIIEKTYSLLLDVEDYERRYL LSLLEE-ERPALMDDRKHKICSMYDNLRGKLPQGERPSDDHFVQIMCIRKGKRMVARILBFLSTEQAADILMATARNLPFLIKKDAQDEVLPCLLSPFSL  
xPat1a (475) KALG---YQRLRVLKHAKEVFLMFLEVEBELARKMSHIPPEE-EHVHFQHKQNYKVQRIYDV LKIA PCHNEE--SEFLQLLOVQKGKKLVARLLBFLRSEQAREILLLVQHLTFLIKND SAEESLSVLYGPKLPKI  
xPat1b (468) TREKQVRDKRRKTLVIIIEKMFSLLLDLEDFERRFSLCCEEAEHEVLTBEQKQKLQQLCDTLRGKEVG-ERVAAEQFVQIMCIRKGKRMISRI LPLLLQLAAVLSIMAHNLLFLIKKDIQDQALPCLLAATCSLV  
Consensus (541) TAEKQVRDQRRRVLVIIIEKMFSLLLDVEDYERRY L EE E P LTDEQKHV KLYD LKGKE GNEREADD FLQILCIRKGKRLVARILPFLPTEQAADILL IAHNLPFLIKKDMQDQALPCLFSPLSLL

hPat1a (421) ISHLLTHELLQGLQGLTLLPPGS-----SERPVTVVLQNFQGISLLYALLSHGELVLSLHSSLEEPSNDHTANTDMVLI AWEIAQMP TASLAELP AFPSNLLPLFCHHVDKQLVQQL EARM EFAWIY-----  
hPat1b (644) LYHLPSVSTISLLRQLMNL PQSAATPALSNPHLTAVLNQKFGLSLLILLSRGEDLQSSDPATES--TQNNQWTEVMFMATRELLRIPOAALARPISIPTNLVSLFSRYVDQKLN LLETKLQVQGIR-----  
mPat1a (423) ISHLLTFHQLLHAMQGLMLLSPGS-----SERPVSVVLQNFQGISLLYALLSHGELVSLDPSLRS-SSDCATWTDLVILIAWEIAQLPAASLAELP AFRNLLPCSAITWTSN-----  
mPat1b (644) LYHLPSVTVTSLQLQMLNLPQSAAPASNSHLTAVLNQKFGLSLLILLSRGEDLQSSDPATES--TQNNQWTEVMFMATRELLRIPOAALARPISIPTNLVSLFSRYVDQKLN LLETKLQVQGIR-----  
xPat1a (604) INGLSFTLELIGVTQELTRLPES-----NDLPLTLAFQNFQGISLLYCLLSHGERRLLSSDLPM EPCIGDFEKWTDTVFLVAKELSHVSKSSMVEPLFLPSNLLSLFCRYLDKQTIHKLEDKMECPVIPPYTAVPS  
xPat1b (602) LCQLSLPALTSLLQLNLCGATS-----QQQLSSILQNFQGITLLYQLERGEDLLSSGDPMSQ--SQP-TWTSLLVQAACHLLQVSELSLPRPLCSFELTALAHFSRYLDTQNSSLLQSKLG-----  
Consensus (676) I HLS LTSLLQQLM LPP S SN PLTVVLQNFQGISLLY LLSRGEDLLSSDPALES SQ WTDLVFLAARELLQIP ASLAELPAIPSNLLSLFSRYVDKQ LNLLETKL

Supplementary Figure 2