Supplementary Materials

Figure S1. Multiple sequence alignment with predicted local (secondary) structures.

Human_PREPL Human_POP OPB_TB Consensus ss:	1 1 1	MQQKTKLFLQALKYSIPHLGKCMQKQHLNHYNFADHCYNRIKLKKYHLT- MLSFQYPDVYRDETAVQDYHG- MQTERGPIAAHRPHEVVFGKV eeeee	49 21 21
Human_PREPL Human_POP OPB_TB Consensus_ss:	50 22 22	KCLQNKPKISELARNIPSRSFSCKDLQPVKQENEKPL 	86 51 66
Human_PREPL Human_POP OPB_TB Consensus ss:	87 52 67	PENMDAFEKVRTKLETQPQEEYEIINVEVKHGGFVYYQEGCCLVPFLEQC-PIRGLYKERMTELYDYPKYSCHFKKGKRYFYFYNTGLQNQRKRAVDIKDLAETIYQEHISHIEETDMSAPYVYDRFLYYTRDVKGLSYKhhhhhhhhhhhhhhhheeeeeeeeeeee	130 98 114
Human_PREPL Human_POP OPB_TB Consensus ss:	131 99 115	RSKDEEADNDNYEVLFNLEELKLDQPFIDCIRVAPDEKYVAA VLYVQDSLEGEARVFLDPNILSDDGTVALRGYAFSEDGEYFAY LHCRVPAGKTPGEGEDEEIVLDENKLAEGKSFCVVGCVAPAPPEHALVAY eeeee ehh eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee	172 141 164
Human_PREPL Human_POP OPB_TB Consensus ss:	173 142 165	KIRTEDSEASTCVIIKLSDQPVMEASFPNVSSFEWVKDEEDEDVLFYTFQ GLSASGSDWVTIKFMKVDGAKELPDVLERVKFSCMAWTHDGKGMFYNSYP SVDYCGDEVYSIRFVRDVVADKVEGTNGSVVWGPNAECFFYITKD ee eeeeeee eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee	222 191 209
Human_PREPL Human_POP OPB_TB Consensus ss:	223 192 210	RNLRCHDVYRATFGDNKR-NERFYTEKD-PSYFVFLYLT QQDGKSDGTETSTNLHQKLYYHVLGTDQSEDILCAEFPDEPKWMGGAELS ASKRDNKVWRHIIGQPQSEDVCLYTDDD-PLFSVGVGKS eeeeee eeee eeee	259 241 247
Human_PREPL Human_POP OPB_TB Consensus_ss:	260 242 248	KDSRFLTINIMNKTTSEVWLIDGLSPWDPPVLIQKRIHGV-LY DDGRYVLLSIREGCDPVNRLWYCDLQQESSGIAGILKWVKLIDNFEGEYD GDGKTLIICSMSSETSESLLLDLRKGVKHNTLEMVRPREKGVRYT eeeeee eeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee	301 291 292
Human_PREPL Human_POP OPB_TB Consensus_ss:	302 292 293	YVEHRDDELYILTNVGEPTEFKLMRTAADTPAIMNWDLFFTMKRNTKVIDYVTNEGAVFTFKTNRQ-SPNYRVINIDFRDPEESKWKVLVPEHEKDVLEWVEMHGTDTLIVLTNKDKCVNGKVVLTKRSAPT-DWGTVLIPHDDKVTIDDeeeeeeeeeeeeeeeeeeeee	351 340 341
Human_PREPL Human_POP OPB_TB Consensus_ss:	352 341 342	LDMFK-DHCVLFLKHSNLLYVNVIGLADDSVRSLKLPPWA IACVRSNFLVLCYLHDVKNILQLHDLTTGALLKTFPLDVG VAVFA-KFAVLSGRRDGLTRVWTVRLGPDSLFSSATLKELHFDEPVFTAH eeee eeeeee eeeee eeeee eeeee	390 380 390
Human_PREPL Human_POP OPB_TB Consensus_ss:	391 381 391	CGFIMDTNSDPKNCPFQLCSPIRPPKYYTYKFAEGKLFEETGHEDP SIVGYSGQKKDTEIFYQFTSFLSPGIIYHCDLTKEELEPRVFREVTVKGI VVCSQMKTYDASLLRLRYSSMTTPTVWYDEDVLSGERKVVKARKVG-GGF eeeee eeeee eeeee eeeee	436 430 439
Human_PREPL Human_POP OPB_TB Consensus ss:	437 431 440	ITKTSRVLRLEAKSKDGKLVPMTVFHKTDSEDLQKKPLLVHVYGAYGMDL DASDYQTVQIFYPSKDGTKIPMFIVHKKSIKLDGSHPAFLYGYGGFNISI QSKNYVCRRELATAPDGTKVPISLVYDTSIDLKKPNPTMLYGYGSYGICI eeeeee eeeee	486 480 489
Human_PREPL Human_POP OPB_TB Consensus_ss:	487 481 490	KMNFRPERRVLV-DDGWILAYCHVRGGGELGLQWHAD-GRLTKKLNGLAD TPNYSVSRLIFVRHMGGILAVANIRGGGEYGETWHKG-GILANKQNCFDD EPEFNSRFLPYV-DRGMIYAIAHVRGGGEMGRTWYEVGGKYLTKRNTFMD hhhhhhh h eeeee hhhhhhh hhhhh	534 529 538
Human_PREPL Human_POP OPB_TB	535 530 539	LEACIKTLHGQGFSQPSLTTLTAF S AGGVLAGALCNSNPELVRAVTLEAP FQCAAEYLIKEGYTSPKRLTINGG S NGGLLVAACANQRPDLFGCVIAQVG FIACAEHLISSGLTTPAQLSCEGR S AGGLLVGAVLNMRPDLFHVALAGVP	584 579 588

Consensus ss:		<mark>hhhhhhhhhh</mark>	hhheeeeee hhh	hhhhhhh	eeeeee	
Human_PREPL Human_POP OPB_TB Consensus ss:	585 580 589	S FLDVLNTMMDTTLPI VMDMLKFHKYTI FVDVMTTMCDPSIPI hhhh	31 LEELEEWGNPSS IGHAWTTDYGCS-D JTTGEWEEWGNP-N hhhhhhh *	DEKHKNYIKRY SKQHFEWLVKY EYKFFDYMNSY hhhhhhhh	CPYQNIKPQ SPLHNVKLPEA SPIDNVRAQ hhhhhh	632 625 635
Human_PREPL Human_POP OPB_TB Consensus_ss:	633 626 636	HYPSIHITAYEN DDIQYPSMLLLTADH DYPHLMIQAGLH eeeeee *	IDERVPLKGIVSYT IDDRVVPLHSLKFI IDPRVAYWEPAKWA hhhhhhhh	EKLKEAIAEHA ATLQYIVGRSR .SKLRELKT hhhhh	KDTGEGYQTPN KQSNP -DSNE e	679 669 672
Human_PREPL Human_POP OPB_TB Consensus_ss:	680 670 673	IILDIQPGGN H V LLIHVDTKAG H GAGH VLLKMDLESG H FSAS eeeeee	IEDSHKKITAQI (PTAKVIEEVSDMF 3DRYKYLRENAIQQ hhhhhhhhhhhh	KFLYEELGLDS AFIARCLNVDW AFVLKHLNVRQ hhhhhh	T <mark>SVFEDLKKYL</mark> IP LLRK	725 710 715
Human_PREPL Human_POP OPB_TB Consensus_ss:	726	KF 727 				

Figure S1. Multiple sequence alignment with predicted local (secondary) structures. Sequences of human PREPL (longer isoform), human POP and oligopeptidase B from *T. brucei* (OPB_TB) were aligned at the PROMALS3D multiple sequence and structure alignmentserver (*PROMALS3D: a tool for multiple sequence and structure alignment. Jimin Pei, Bong-Hyun Kim and Nick V. Grishin. Nucleic Acids Res. 2008 36(7):2295-2300*). The α -helix sections are shown in red letters and the β -strands in blue letters. For PREPL these secondary structural elements were predicted by the PROMALS3D whereas for POP they were based on the PDB 3EQ7 and for OPB_TB on the PDB 4BP8. Asterisks are placed to show the residues of the conserved catalytic triad, which are also highlighted in gray. The region in which there are residues important to the substrate binding S₁ sub-site of POP and OPB_TB and consequently thought to form also the S₁ sub-site of PREPL is boxed.

Comments on Figure S1. It is noteworthy that using only regular default sequence alignments (such as ClustalW), the histidine residue of the catalytic triad was incorrectly aligned: The PREPL His696 was incorrectly aligned with the His680 of POP and His683 of OPB_TB, while, the correct residue of the catalytic triad of PREPL is the His690, as already experimentally verified by site-directed mutagenesis (*Jaeken, J.; Martens, K.; François, I.; Eyskens, F.; Lecointre, C.; Derua, R.; Meulemans, S.; Slootstra, J.W.; Waelkens, E.; De Zegher, F.; et al. Deletion of PREPL, a gene encoding a putative serine oligopeptidase, in patients with hypotonia-cystinuria syndrome. Am. J. Hum. Genet. 2006, 78, 38–51.*). However, by making the alignment by PROMALS, considering the secondary structures, as showed above, the PREPL His690 is correctly aligned.



Figure S2. Comparison of the CD spectra obtained for PREPL and POP.

Comments on Figure S2. The spectrum obtained for human PREPL is more intense than the spectrum obtained for human POP. This most probably arise from the experimental errors intrinsic of the protein concentration measurements. However, in Figure 1S, it can be observed two helix sections predicted to exist in the PREPL structure that is not present in the structure of POP (one near the PREPL N-terminus, from residue number 3 to 16 or even to residue number 22, and another near the C-terminus, from residue number 715 to residue 725). These two extra helix sections may indicate that PREPL has a higher α-helix content than POP. Therefore, in order to check such difference a parallel CD measurement with the porcine POP (which we have already prepared at our lab) was done. The CD spectra obtained for human PREPL and porcine POP superimposed perfectly. Confirming that the difference in the intensities of the CD spectra observed between the human PREPL and human POP probably is due to the errors intrinsic to our practical methodologies. An additional indication that this difference relies on practical manipulations reasons is that: we were able to use a 0.2 mm cuvette for the measurements with human PREPL and porcine POP what permitted the collection of reliable spectra (HT < 600V) at wavelengths as low as ~192 nm. However, we had to work with a 1 mm cuvette for samples of human POP to decrease the signal to noise ratio, but this larger pathlength increased the total absorbance of light and then we could just get a reliable CD signal until 199 nm.

Figure S2. Comparison of the CD spectra obtained for human PREPL, human and porcine POP.



Figure S3. Adjusted sensorgrams obtained in the SPR assays with PREPL or POP immobilized and α -Syn as the analyte injected at increasing concentrations.

Figure S3. Adjusted sensorgrams obtained in the SPR assays with PREPL (upper panel) or POP (lower panel) immobilized and α -Syn as the analyte injected at increasing concentrations.

Time (0 - baseline)

700

900

1100

500

300

Comments on Figure S3. Although we could not observe the saturation of the doseresponse curve of the titrations with α -Syn of the POP immobilized on the sensor chip, by the association constants obtained in the SPR analysis (ka values shown in the Figure S3), it can be affirmed that the affinity of the α -Syn for POP is higher than its affinity by PREPL, mainly because of a higher association constant.