Supplementary Data

Α		
UNIPROT CLUSTAL O(1.2.4) multi SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	<pre>ple sequence alignment MWNLLHETDSAVATARRPRWLCAGALVLA-GGFFLLGFLFGWFIKSSNEATNITPKH-NM MWNALQDRDSAEVLGHRQRWLRVGTLVLALTGTFLIGFLFGWFIKPSNEATGNVSHSGMK MWNAQQDSDSAEALGRRQRWFCAGTLVLAFTGTFIIGFLFGWFIKPSNDSTSSVSYPGMK MWNLLHETDSAVATARRPRWLCAGALVLA-GGFFLLGFLFGWFIKSSSEATNITPKH-NM MWNLLHETDSAVATARRPRWLCAGALVLA-GGFFLLGFLFGWFIKSSSEATNITPKH-NM *** :: ***:* **: .*:**** * *::********</pre>	60 60 58
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	KAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVILS KEFLHELKAENIKKFLYNFTRTPHLAGTQNNFELAKQIHDQWKEFGLDLVELSHYDVLLS KAFLQELKAENIKKFLYNFTRTPHLAGTQHNFELAKQIHAQWKEFGLDSVELSDYDVLLS KAFLDELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELTHYDVLLS KAFLDELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELTHYDVLLS * **.*********************************	120 120 118
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	YPNKTHPNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVN YPNKTHPNYISIINEDGNEIFKTSLSEQPPPGYENISDVVPPYSAFSPQGTPEGDLVYVN YPNKTHPNYISIINEDGNEIFKTSLAELSPPGYENISDVVPPYSAFSPQGTPEGDLVYVN YPNKTHPNYISIINEDGNEIFNTSLFEPPPAGYENVSDIVPPFSAFSPQGMPEGDLVYVN YPNKTHPNYISIINEDGNEIFNTSLFEPPPAGYENVSDIVPPFSAFSPQGMPEGDLVYVN *******************************	180 180 178
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	YARTEDFFKLERDMKINCSGKIVIARYGKVFRG N KVKNAQLAGAKGVILYSDPADYFAPG YARTEDFFKLEREMKISCSGKIVIARYGKVFRGN <u>M</u> VKNAQLAGAKGMILYSDPADYFVPA YARTEDFFKLERVMKINCSGKIVIARYG <mark>Q</mark> VFRGNKVKNAQLAGAKGIILYSDPADYFVPG YARTEDFFKLERDMKINCSGKIVIARYGKVFRGNKVKNAQLAGATGVILYSDPADYFAPG YARTEDFFKLERDMKINCSGKIVIARYGKVFRGNKVKNAQLAGATGVILYSDPADYFAPG ************************************	240 240 238
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	VKSYPDGWNLPGGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIG VKSYPDGWNLPGGGVQRGNVLNLNGAGDPLTPGYPANEHAYRHELTNAVGLPSIPVHPIG VKSYPDGWNLPGGGVQRGNVLNLNGAGDPLTPGYPANEYAYRHEFTEAVGLPSIPVHPIG VKSYPDGWNLPGGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGMAEAVGLPSIPVHPIG VKSYPDGWNLPGGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIG ***********************	300 300 298
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	YYDAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTNE <mark>VTRIYNV</mark> YDDAQKLLEHMGGPAPPDSSWKGGLKVPYNVGPGFAGNFSTQKVKMHIHSYTKVTRIYNV YDDAQKLLEHMGGSAPPDSSWKGGLKVPYNVGPGFAGNFS K QKVKLHIHSYNKVTRIYNV YYDAQKLLEKMGGSASPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTSEVTRIYNV YYDAQKLLEKMGGSASPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTSEVTRIYNV * *******	360 360 358
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	IGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILF IGTLKGALEPDRYVILGGHRDAWVFGGIDPQSGAAVVHEIVRSFGTLKKKGRRPRRTILF IGTLKGAVEPDRYVILGGHRDAWVFGGIDPQSGAAVVHEIVRSFGTLKKKGWRPRRTILF IGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILF IGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILF ****:**	420 420 418
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	ASWDAEEFGLLGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLT ASWDAEEFGLLGSTEWAEEHSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLT ASWDAEEFGLLGSTEWAEEHSRLLQERGVAYINADSSIEGNYTLRVDCTPLMHSLVYNLT ASWDAEEFGLLGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLT ASWDAEEFGLLGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLT ************************************	480 480 478
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	KELKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFORLGIASGRARYT KELQSPDEGFEGKSLYDSWKEKSPSPEFIGMPRISKLGSGNDFEVFFORLGIASGRARYT KELPSPDEGFEGKSLYDSWKEKSPSTEFIGMPRISKLGSGNDFEVFFORLGIASGRARYT KELESPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFORLGIASGRARYT KELESPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFORLGIASGRARYT	540 540 538
SP Q04609 FOLH1_HUMAN	KNWETNKFSGYPL YH SVY E TYELVEKFYDPMFKYHLTVAQVRGGMVFELANSI <mark>VLPFDCR</mark>	598

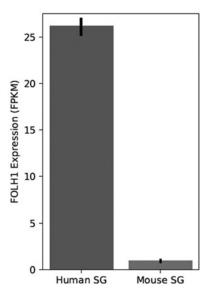
SUPPLEMENTARY FIG. S1. (A) PSMA conservation across available orthologs. These data were extrapolated from published literature on structure of PSMA (FOLH1)¹ Protease domain (residues 56–116 and 352–591in *pink*), an apical domain (residues 117–351 in *gray*), and a helical domain (residues 592–750 in *green*) are highlighted in the sequence analysis. Overall, PSMA (FOLH1) exhibits 81.1% identity across available sequences of the studied orthologues. *Bold* amino acids are predicted to be adjacent to the amino acids involved with the protease domain/active site; 100% of the predicted active site amino acids are conserved across the orthologues. Underlined amino acids are not conserved and are adjacent to conserved active site amino acids. Alternately, regions where there is identity between human and mouse but not rat are marked in *bold red*. (B) Table describing protein sequence conservation across species.

SP 035409 F0LH1_MOUSE SP P70627 F0LH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	KNWKTNKVSSYPLYHSVYETYELVVKFYDPTFKYHLTVAQVRGAMVFELANSIVLPFDCQ KNWKNNKVSSYPLYHSVYETYELVEKFYDPTFKYHLTVAQVRGAMVFELANSIVLPFDCQ KNWETNKFSSYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSVVLPFDCR KNWETNKFSSYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSVVLPFDCR ***:.**.*	600 598
SP Q04609 FOLH1_HUMAN	${\tt DYAVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERLQDFDKSNP$	658
SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT	SYAVALKKYADTIYNISMKHPQEMKAYMISFDSLFSAVNNFTDVASKFNQRLQELDKSNP SYAVALKKHAETIYNISMNHPOEMKAYMISFDSLFSAVNNFTDVASKFNORLODLDKSNP	660 660
TR F7FA05 F7FA05 MACMU	DYAVVLRKYADKIYNISMKHPOEMKTYSVSFDSLFSAVNNFIDVASKFNQRLQDLDKSNP	658
TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	
SP Q04609 FOLH1 HUMAN	IVLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK	718
SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE	IVLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK	
SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT		720
SP 035409 F0LH1_M0USE SP P70627 F0LH1_RAT TR F7FA05 F7FA05_MACMU	ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK ILLRILNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINNK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK	720 720 718
SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT	ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK ILLRILNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINNK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK	720 720 718
SP 035409 F0LH1_M0USE SP P70627 F0LH1_RAT TR F7FA05 F7FA05_MACMU	ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK ILLRILNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINNK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK	720 720 718
SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE	ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK ILLRILNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINNK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK :ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK ::*:::****: VDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA 750 VNASKAWNEVKRQISIATFTVQAAAETLREVA 752	720 720 718
SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_HOUSE SP P70627 FOLH1_RAT	ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK ILLRILNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINSK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK *:**::*****:*************************	720 720 718
SP 035409 FOLH1_MOUSE SP P70627 FOLH1_RAT TR F7FA05 F7FA05_MACMU TR A0A2K5VNZ0 A0A2K5VNZ0_MACFA SP Q04609 FOLH1_HUMAN SP 035409 FOLH1_MOUSE	ILLRIMNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSK ILLRILNDQLMYLERAFIDPLGLPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDINSK ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK :ILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK *:**::*****:*************************	720 720 718

B Protein sequence conservation across tested species.

Species	Protein Sequence Identity
mouse	83.4%
rat	87.4%
rhesus macaque	93.0%
crab-eating macaque	97.5%
Conserved identity across orthologs	81.1%

SUPPLEMENTARY FIG. S1. (Continued).



SUPPLEMENTARY FIG. S2. Expression in FPKM of PSMA (*FOLH1*) in salivary gland (SG) for both human and mouse was plotted. *FOLH1* is expressed at low levels in the mouse salivary gland, compared with moderate expression of FOHL1 in the human salivary gland (Error bars represent mean \pm SD; n = 2 for human and n = 3 for mice).