

Figure S1. Evaluation of the model quality of FcXTH2. (A) Ramachandran plot by PROCHECK software, (B) Energetic evaluation using ProSA software, (C) and Verify3D graph of the FcXTH2 before (blue line) and after (red line) of Molecular Dynamic simulation.

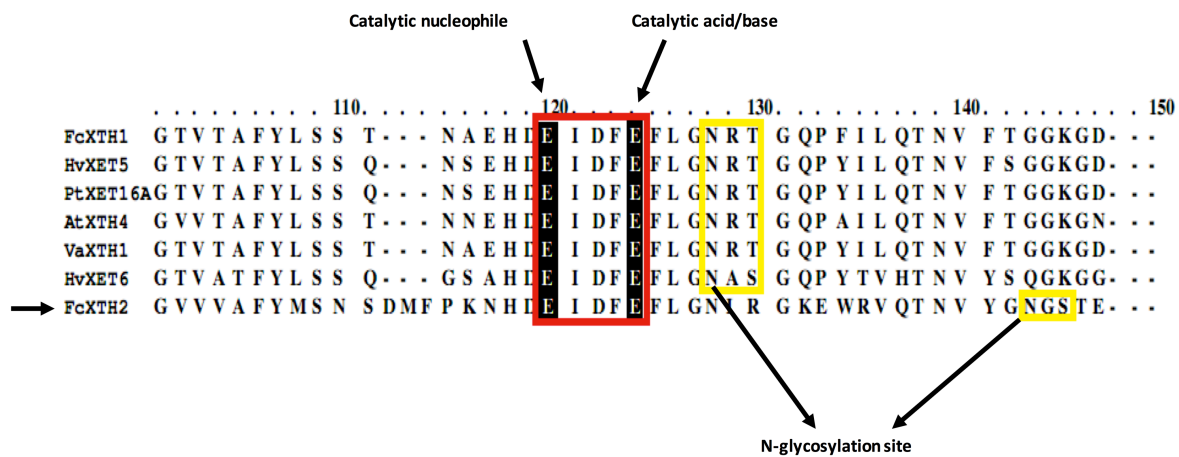


Figure S2. Distance of the N-glycosylation site (in yellow box) of the active site of different XTH including FcXTH2 (red box).

1UMZ	-----XETAFAALRKPVDVAFGRNVPTWAFDHIKYFNGGNEIQLHLDKYTGTFQSKG	55
2UWA	AYVQGPPSPGYYPSSQITSLGFDQGYTNLWGPQHQRV--DQGSLTIWLDSTSGSGFKSIN	58
FcXTH2	-----KTLPIMSFDEGYNKLFGDDNLMILKDGKSVHLTLDERGTSGGFVSQD	46
	:.*...* :. : . : : ** . :*:** * .	
1UMZ	SYLFGHFSMQMKLVPGDSAGTVTAFYLLSQN---SEHDEIDFEFLGNRTGQPYILQTNVF	112
2UWA	RYRSGYFGANIKLQSGYTAGVITSFYLSNNQDYPGKHDEIDIEFLGTIPGKPYTLQTNVF	118
FcXTH2	LYIHGFFSASIKLPTDYTAGVVVAFYMSNSDMFPKNHDEIDFEFLGNIRGKEWRVQTNVY	106
	* *.*. .:*** . :**...:***:*. . : :*****:****. *: : :*****:	
1UMZ	TGGKGD-----REQRIYLWFDPTKEFHYYSVLWNMYMIVFLVDDVPIRVFKNCKDLGVKF	167
2UWA	IEGSGDYNIIIGREMRIHLWFDPTQDYHNYAIYWTPSEIIFVDDVPIRRYPRK--SDATF	176
FcXTH2	--GNGSTE-TGREERYNLWFDPSEDYHQYSILWTDSQIIFYVDNIPIRVVKKSESMGGDY	163
	.: . ** * *****:..* *:: * . *: * **::*** . . :	
	<u>Loop2</u>	
1UMZ	PFNQPMKIYSSLWNADDWATRGGLEKTDWSKAPFIASYSRFHIDGCEASVEAK---FCAT	224
2UWA	PL-RPLWVYGSVWDASSWATENGKYKADYRYPFVKGYEDFKLGSCVVEAASS----CNP	231
FcXTH2	PS-KPMSLYATIWDGSGWATDGGKYRVNYKYAPFRAEFSDLVLHGCAVDPIEQVSKKCDK	222
	* :*: :*:..*...*** .* :.: ** ..: .: : .* .. . *	
1UMZ	QGARWWDQKEFQDLDAFYRRLSWVRQKYTIYNYCTDRSRYPSMPPECKRDRDI-----	278
2UWA	ASVSPYG---Q--LSQQQVAAMEWVQKNYMVYNYCDDPTRDHTLTPEC-----	274
FcXTH2	TQSEYI---PTGVTRLQRMRESFRKRQMTYSYCYDRIRYKVPPECVITPQEAERLRV	279
	: : * :. .:.. *.** * * ***	
1UMZ	-----	278
2UWA	-----	274
FcXTH2	FDPVTFGHGHRQRKHHHRSSSRASVADTSSV	311

Figure S3. Alignment of the deduced full-length amino acid sequence of FcXTH2 with TmNXG1 and PttXET16A. TmNXG1 showed *in vitro* XEH activity but not XET activity. Meanwhile, PttXET16A showed *in vitro* only XET activity.