

**Table S1. Amino acid sequence comparison and percentage identity using ClustalW, Emboss Needle alignment for Yeast, XM, XP.** Alignment studies and amino acid comparison for Three protein sequences and the Swiss-model sequences.

YEAST vs XM complete protein vs XP complete protein	Percent Identity Matrix - created by Clustal2.1			
	1: YEAST	100.00	40.69	41.33
	2: XM_COMPLETE	40.69	100.00	77.56
	3: XP_COMPLETE	41.33	77.56	100.00
YEAST	-----MSETELRKRQAQFTRELHGDDIGKKTGLSALMSKNNSAQKEAVQKYLRNW			
XM_COMPLETE	MSLFLLGVSIVVIGFVVYLFKFKNQIKGYHL-----TNENVGTGYQDLF---			
XP_COMPLETE	--MFLI-ILTVIVGGFILYLFKFKREQIKGSHL-----TDDKTASYQELF---			
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YEAST	DGRDTKDAEERRLEDYNEATHSYYNVVTDFYEYVGWSSFHFSRFYKGESFAASIRHEHY			
XM_COMPLETE	-AQDTKDTHDKRKNAGWDVAGKYDDMTDFYLYGWGRSFHFAPRHKKESMIESIQRHEYW			
XP_COMPLETE	-ATDNQQTHEKRKKAGWDVAGKYDDMTDFYLYGWGRSFHFATRHSRESLIESILRHEYW			
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YEAST	LAYKAGIQRGDLVLDVGCVGVPAREIARFTGCNVIGLNNNDYQIAKAKYYAKKYNLSQD			
XM_COMPLETE	LAKQMDLKKGMKCLDLGCGVMGPATNISRFTGAHITGVNNHPYQSQAKEYISQMGLSEQ			
XP_COMPLETE	LAKQLDLKPGMKCLDLGCGVMGPVNIARFSGCNVTGVNNHPYQSERAKVFINEMGMDGR			
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YEAST	MDFVKGDFMKM---DFEENTFDKVYAEIATCHAPKLEGVSEIYKVLKPGGTFAVYEWV			
XM_COMPLETE	CQIVRGDFNNLDDNSDLPSESDAAYTIEASCHAKDRPHCYKQIYNLKPGAIFAGYEWV			
XP_COMPLETE	CNIVRGDFNNLDDNKDLPAESYDAAYAIEATCHAKDRPHCYKQIFNKLKPGAVFGGYEWV			
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YEAST	M-TDKYDENNPEHRKIAYEIELGKGIPKMFHVDVARKALKKNCGEVLVSEDLADND--DE			
XM_COMPLETE	MISGKYDSKNEEHNKIKFDIMKGDGLPEILMDKEIDESLRKAGFEVKTEDVGVTQDIHP			
XP_COMPLETE	MITGKYDSKNEEHNKIKFDIMKGDGLPEILMDKEIDDALVKAGFEVIRTEDAVITDKINP			
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YEAST	IPWYYPL-TGEWKYVQNLANLATFFRTSYLGRQFTTAMVTVMKLLGLAPEGSKEVTAALE			
XM_COMPLETE	VPWYQPIDNGGW-----DFTSWFQTSY-GRFIVHKLVGILESVLGVPKSSQAYEFLLM			
XP_COMPLETE	IPWYQPLDNGGW-----ELTNWFQTSY-GRWVVHKLVGILEKIGLVPKTSQQAYEFLLM			
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YEAST	NAAVGLVAGGSKLFTPMMLFVARKPENAEPSQTSQEATQ			
XM_COMPLETE	AGASGLVAGGKTGIFTPCYFFMARKPLTAEE-----			
XP_COMPLETE	AGA-GLVGGGKTGIFTPSYFFLARKPLKN-----			
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Yeast vs XM Swiss-model vs XP Swiss-model

## Percent Identity Matrix - created by Clustal2.1

1: YEAST	100.00	44.03	45.78
2: XM_SWISS	44.03	100.00	80.88
3: XP_SWISS	45.78	80.88	100.00

YEAST	MSETELRKRQAQFTRELHGDDIGKKTGLSALMSKNNSAQKEAVQKYLNRWDGRTDKDAEE
XM_SWISS	-----
XP_SWISS	-----

YEAST	RRLEDYNEATHSYYNVVTDFEYEGWGSSFHFSRFYKGESFAASIRHEHYLAYKAGIQRG
XM_SWISS	-----DLKKG
XP_SWISS	-----KQLDLKPG

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YEAST	DLVLDVGCVGVPAREIARFTGCNVLNNNDYQIAKAKYYAKKYNLSDQMDVFKGDFMK
XM_SWISS	MKCLDLGCGVMGPATNISRFTGAHITGVNNHPYQSQAKEYISQMGLEQCQIVRGDFNN
XP_SWISS	MKCLDLGCGVMGPAVNIARFSGCNVTGVNNHPYQSERAKVFINEMGMDGRCNIVRGDFNN

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YEAST	M----DFEENTFDKVYAIEATCHAPKLEGVYSEIYKVLKPGGTFAVYEWVM-TDKYDENN
XM_SWISS	LDDNSDLPSESYDAAYTIEASCHAKDRPHCYKQIYNKLPKGAIFAGYEWVMISGKYDSKN
XP_SWISS	LDDNKDLPAESYDAAYAIEATCHAKDRPHCYKQIFNKLKPGAVFGGYEWVMITGKYDSKN

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YEAST	PEHRKIAYEIELGDGIPKMFHVDVARKALKNCGFVLSVSEDLADND--DEIPWYYPL-TG
XM_SWISS	EEHNKIKFDIMKGDGLPEILMDKEIDSLRKAGFEVIKTEDVGVTQIHPVPWYQPIDNG
XP_SWISS	EEHNKIKFDIMKGDGLPEILMDKEIDDALVKAGFEVIRTEDVAITDKINPIPWYQPLDNG

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YEAST	EWKYVQNLANLATFFRTSYLGRQFTTAMVTVMKLGLAPEGSKEVTAALENAAVGLVAGG
XM_SWISS	GW-----DFTSWFQTSY-GRFIVHKLVGILESVGLVPKSSQAYEFLMAGASGLVAGG
XP_SWISS	GW-----ELTNWFQTSY-GRWVVHKLVGILEKIGLVPKTSQAYEFLMAGAEGLVGGG

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YEAST	KSKLFTPMMLFVARKPENAEPTPSQTSQEATQ
XM_SWISS	KTGIFTPCYFFMAR-----
XP_SWISS	KTGIFTPSYFFLARKPL-----

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**Table S2. Yeast Top ligand Binding pockets and their descriptions.**

Pocket	Volume [Å <sup>3</sup> ]	Drug Score	Hydrogen bond donors	Hydrogen bond acceptors	Hydrophobic interactions	Negative amino acids	Positive Amino acids
Orange	1869.89	0.81	31	126	19	8	7
Purple	425.73	0.6	15	38	21	5	4
Green	250.82	0.46	8	16	16	2	2

**Table S3. Pockets for yeast SMT and the amino acids involved.**

Pocket	Amino acids involved
Orange	GLU3, LEU6, ARG7, GLN10, GLY27, LEU28, LEU31, MET32, GLN39, TYR66, ASN67, THR70, HIS71, TYR73, TYR74, VAL77, ASP79, PHE80, TYR83, TRP85, SER87, PHE89, HIS90, PHE91, SER92, PHE94, PHE100, ILE104, GLU 108, ASP125, VAL126, GLY127, CYS128, GLY129, VAL130, GLY131, GLY132, PRO133, LEU148, ASN149, ASN150, ASN151, GLN154, LYS175, GLY176, ASP177, PHE178, TYR192, ALA193, ILE194, GLU195, ALA196, CYS198, HIS199, ALA200, TRP225, GLY248, ASP249, ILE251, TRP286, PRO289, LEU290, ALA304, PHE307, ARG308, THR309, GLY313, ARG314, PHE 316, THR317, MET320, VAL321, MET324, ALA330, PRO331, SER334, VAL 337, THR338, LEU341, GLU342, ALA325, LEU348
Purple	SER92, ARG93, PHE94, VAL226, THR228, ASP229, LYS230, VAL257, ARG261, ASP276, LEU277, ALA278, ASP279, ASN280, ASP281, ASP281, ILE284, PRO285, TRP286, TYR287, GLY351, GLY352, LYS355, LEU356, PHE357, THR358, MET360, MET361
Green	TRP85, GLY86, SER87, SER88, PHE100, ALA101, ILE104, ALA105, GLU108, GLY132, ARG135, GLU136, TYR165, LEU165

**Table S4. XP Top ligand binding pockets and their descriptions**

Pocket	Volume [Å <sup>3</sup> ]	Drug Score	Hydrogen bond donors	Hydrogen bond acceptors	Hydrophobic interactions	Negative amino acids	Positive Amino acids
Orange	576.58	0.86	13	46	38	4	5
Purple	516.35	0.75	9	45	38	2	2
Green	113.98	0.18	4	16	8	2	1

**Table S5. Pockets for XP SMT and the amino acids involved.**

Pocket	Amino acids involved
Orange	ASP116, LEU117, GLY118, CYS 119, GLY120, PRO124, VAL139, ASN140, HIS142, GLN145, GLY149, ASP168, PHE169, ASN170, ASN171, LYS73176, ALA188, ILE189, GLU190, ALA191, THR192, HIS194, ALA195, ASP197, HIS200, CYS201, GLN204, LYS208
Purple	TRP220, VAL221, MET222, ILE223, ASP228, SER229, LYS230, ASN231, GLU233, HIS234, ASN235, ILE241, MET242, ILE250, TYR 285, GLN286, LEU339, GLY341, GLY342, GLY343, THR345, GLY356, PRO350, SER351
Green	ASN235, ASP240, MET242, LYS243, LEU247, PRO248, GLU249, ILE250

**Table S6. XM Top ligand binding pockets and their descriptions.**

Pocket	Volume [Å <sup>3</sup> ]	Drug Score	Hydrogen bond donors	Hydrogen bond acceptors	Hydrophobic interactions	Negative amino acids	Positive Amino acids
Orange	1011.26	0.81	23	59	60	4	4
Purple	577.86	0.78	11	42	42	5	5
Green	212.42	0.41	3	16	13	3	1

**Table S7. Pockets for XM SMT and the amino acids involved.**

Pocket	Amino acids involved
Orange	ASP110, LEU111, CYS117, PRO127, ASN130, ILE131, PHE134, THR135, ALA188, AA189, TRY190, ILE192, GLU193, ILE217, PHE218, ALA219, TRY221, GLU222, TRP223, MET225, GLY228, LYS229, TYR230, HIS237, LYS241, GLY277, VAL278, THR279, ASP280, GLN281, PRO284, VAL285, PRO286, TRP287, SER305, PHE309, ILE310, LYS313, LEU314, ILE317, LEU318, LEU342, GLY349, ILE350, PHE351, THR352, PRO353, CYS354, TYR355, PHE357
Purple	LEU120, GLY121, CYS123, VAL124, PRO127, VAL142, ASN143, ASN144, HIS145, GLY170, ASP171, PHE172, ASN173, LEU175, THR191, ILE192, GLU193, ALA194, SER195, HIS197, ALA198, LYS199, ARG201, HIS203, CYS204, TYR205, GLU222
Green	ASP243, ILE244, MET245, LYS246, GLY247, ASP248, GLY249, PRO251, GLU252, ILE253, LEU254, VAL321