

CONSENSUS_VER	MP.LGpEE..RrllrLiAfL?rtNPYPp?vE..GTARQRRRRRRRrqrQ?Q?raLaERiw??rqE?QlvqaiDqL?ld?QHLai...QqL.....PDPpss?	80
VER_TYO	--.-----FV---WL-YS-----SG-.-----Q-D-I-V-V--L.....-Y-V-R-ADEA-----H-A	84
VER_155	---S---Y-S---S---.-----KN-K-IY-----GT--D-----V--T---VT.....QA	89
VER_3	---S---NKN-----A-E-L-----HS-V-E-----V-Q-----S	89
VER_963	---KVFS---Y-N-----E-R-L-F-----NETK-R--E-TL--A--V-----H-----N-S.	89
GRI_677	MS.LGKEE..KQALKIIKTLYGSNPYPQ.FS..GTARQRRRARQRWRKQQQQIDKIAGRVLNTPFEDQQLVAQLQELQLENKDLVL...QHL.....PDPpPHIh	89
CONSENSUS_SAB	MS.LG?Ee?LRRF.RIIKyLYTTNPYPp.GQ..GTARQRRRARQRWakRQQRQiiHLAERiL....qTpVSQID?LAQEfDQLVLDnLQQP.....Pplppghpses???SS?.	91
SAB_SAB1C	---Q--L-----F-----V-----E-----H-----S-----T-NQTAN--S.	99
SAB_D30	---K--E-----L-----N-----L-----A-----KNLE--A.	99
SAB_D42	---P-DI-----H-----C-----S-----S-----EDQAVQ-S-.	92
TAN_TAN1	MS.LGSEDL.RRIIQIIRILYHSNQYPP.GE..GTARQRRRRRQRFRQQQRQVAALSERIFIAQRRRDPNPGGE.SLAAAFDQLVLDN.QQLVIETLPDPPQEPHDSSTA.	103
SYK_SYK	MPDQGSEQL.AVFLRMIAHLQE..PYPG.PE..GPRQTRRRRRRQRWRQRRTQRLYLQQRIFEAIFGSRRTAALEDSL.....QQLQISD	77
LHOEST_LHOEST	MS.TGNDELPRYLRLSRIL.EP.....RTARQRRRRRSRYRDYHLQLRAVQERIFQATVERGLERAFTRLA.....VSD.SPEVAQGRGNTPPITSVAEPQLAVAFVDPFLPKWATPLADQQQMD	113
SUN_SUN	MS.TGDDSI.NQYLRIKRLYEG..LAP.GNLPQTHRQRRRRDRERKNLHQLRAVQERIFATTLDSRLGRAFERLS.....VSD.SSQAESLGNPSTKHLPPAKFLVAPTYDFLPSWATPLADPQRLA	120
LHOEST_LHOEST	GGKRSEDELAQGEMQKEQRTVIEH\$	138
SUN_SUN	GFAPYSGYEQDQERVQNQQGESIIVSEGKK\$	150