

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	.
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	MMMWPFLLLTSSLFYIVHSGAPIYGFMDLFRPDFEQQQGALWSENPSFLGFEVGPAGALVA
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	.
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	LDELGKKNARGDLELLTAWDIERTEWDKAQTRKNLSTIIIECGDEWKTERCLENLRSTGRQ
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	KECVSKTQGLFLSSAKTQNAQKANLYYLQQTCLILIRSTLTLKQASFRIANLMRVLCEA
Pb_SGC2	.
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	PTLIIGSHKDLASQTSSLHSFINSGLFVYCSADISNSAVVSGPTKDSKGLLNTVRMDNSV
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	VQDPTKVEANVRAQAAERQKKHLKSNAERQLTKEQKTEKKIAKLTEDTTDGVHVTVFID
Pb_SGC2	.
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	FSGNVQAFLKHGYGWTQHLFIISGVFQADYRGAVWDDTLNLVDTSSQKRVRFYPFSFM
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	NLSSPOHKYKVETNAQQFLLTGIMLMHKDHNLIVVEGGPKALRKFKRLMLLRIRWNEDVR
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	EIKDGNTDPFREDARKERTELYEIFKGTAIKHHHSRIVLLFGSQRMVRDMMLEAYDAGMM
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	NRKRCKTLRMHGQQYTNFTFLAGYKKDTLLFKVDIKINCRRDFCRKGLSRQIQLSKSILGL
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	EKNEYVFIPIPTNYFPLYNWTSDLNVYYDLSQKERDEDARKAFQSAFIVTAEVDTKLF
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	QSNEYGFIIIPPTNYFPLYTWEGKDDLYYNKSQKYRDEDARKAFQSAFIITADIDTSRFA
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	GHVREHFRRTVNQRDMDQSERGERETIINVVEDIKKTVRSFECIQLTMIHFLVVVLVKL
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	NFTEKVKERAKDAP.FEYEFSEGREGVPLYAANYHDAVLLWSYAVEHHYNATDSTIDVPKL
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	EFEENVVKERAKQPPFDYDFDKAKRQVPLYAANYHDAVLLWAYALRNHYNSAEKSINVSAL
Bea_Nit1	.....FNYTFPPNRKLPLYAANYHDAVLLWAYAIKHHDPEKKGLQVEEL
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	YKPKRKKGAVRPLSPDGNGSVGGGSVNSWDKIQEDFNDIVDSTGKFTLLIPPLPPPPIPCL
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	YNRTYTKEDFHGIEPVGNIKLNEFGDRVNSFVFWHLDQNSQ.WEQVGRFANGEYTVLKA
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	YNRKFNASNFGGIEPITGDIELDEYGDRINRFKFWHLDADGQKWVEVGKYDGGEYKEIIP
Bea_Nit1	YDKTFTKEHFNGIEPITGNIKLDANGDRENSFLFWHLDHNNGE.WEKVGQYVNDKYEVILVN
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	VRSSFPDKKSLNKATFSIQSKHAFSHRMTKGMTEVEGLNAEMLWTMNYIYGNLDYPVVVTL
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	KLKDLDKITGECFPFSSLARGQVPNESSEAAAGSSSESCKATVPIQCQD1PEKNNIQESLPQRKT
Hs_SGCY2	PPGPPLPSPAAAAAAAAPAPTAAASAAAAAATAGARRVQRRRRVNLDLSLGESISRLTAPS
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	ENEIAWPNGGKSAPPYEPVCGFRNEKCPDRTSLVIGVSVGVSAALLVLVAGLFVMTHMYRK
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	TDKIAWPNGGTAKAPPAEPECGFDGKGC.KSKSQTIAISVGVGAAVILVAGFIVMAYMYRK
Bea_Nit1	EADIAWPNAAKSAPQAEPECGFTGEKC.DN.TLTIAIGATTGAVAILVSGLAVMIYMYRK
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

### STYKc protein kinase domain

	1	10	20	30	40	50	
Hs_SGCY1	.	MYGFVNHALELLVIRNYGEVWEDIKKEAQ	LDDEEGQFLVRIIYDDSKTYDLVAAASKVL	.			
Ml_SGC3	.	.	.	.	.	.	.
Oc_SGC3	.	.	.	.	.	.	.
Ml_SGC1	.	.	.	.	.	.	.
Ca_SGC1	.	.	.	.	.	.	.
Pf_SGC2	.	FAYKSKQPNVNQESFSSYIAFPQLSISSWPRTLETNYATKTQFFRDLENLRSQIDAQQLR	.	.	.	.	.
Pb_SGC2	.	.	.	.	.	.	.
Oc_SGC2	.	.	.	.	.	.	.
Ml_SGC2	.	.	.	.	.	.	.
Vs_SGC2	.	.	.	.	.	.	.
Hc_SGC1	.	.	.	.	.	.	.
Dg_SGC1	.	.	.	.	.	.	.
Bea_SGC1	.	.	.	.	.	.	.
Hc_SGC2	.	.	.	.	.	.	.
Oc_SGC1	.	.	.	.	.	.	.
Ml_SGC4	.	.	.	.	.	.	.
Oc_SGC4	.	.	.	.	.	.	.
Hc_SGC4	.	.	.	.	.	.	.
Pp_SGC2	.	.	.	.	.	.	.
Pb_SGC4	.	.	.	.	.	.	.
Hs_SGCY3	SRSRVLYHTLAESICKLIFPEFERLNVALQRYLAKHKIKESRKSLEREDFEKTIAEQAVA	.	.	.	.	.	.
Hs_SGCY2	PQTIQQTALKRTLQYYEHQVIGYRDAEKNFHNI	SNRCSYADHSNKEIEDVSGILQCTANI	.	.	.	.	.
Ed_SGC4	.	.	.	.	.	.	.
Pb_Nit1	.	.	.	.	.	.	.
Ed_Nit1	.	.	.	.	.	.	.
Hc_Nit1	ARFEAALSAMSWKIPTSEM	RDRPLGSSVFGSRKSSLGTRSSLNSNPS.NLKKPTCQF	.	.	.	.	.
Pf_Nit12	.	.	.	.	.	.	.
Pf_Nit1	.	.	.	.	.	.	.
Ps_Nit1	.	.	.	.	.	.	.
Ca_Nit1	ARYEAFLHAMNWKIQMTEIRNINNSKLGSSIFGT.RSRLTMDSQNSNP	SAKVNGRHTQY	.	.	.	.	.
Bea_Nit1	VTVYEALALAAMSWRIPINNV	RDVARDPLGSSVFGSRRSMLATPDSSLSSQSTNLKGKTQQF	.	.	.	.	.
Bi_SGC1	.	.	.	.	.	.	.
Bi_Nit1	.	.	.	.	.	.	.
Dg_Nit1	.	.	.	.	.	.	.
Lt_Nit1	.	.	.	.	.	.	.
Ml_NIT-like	.	.	.	.	.	.	.
Vs_Nit1	.	.	.	.	.	.	.
Oc_Nit1	.	.	.	.	.	.	.
Ocg_Nit1	.	.	.	.	.	.	.
Ocg_Nit12	.	.	.	.	.	.	.

	60	70	80	90	100	110
Hs_SGCY1	NLNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQLNLDALHDHLATIYPGMRAPS					
Ml_SGC3	.	.	.	.	.	.
Oc_SGC3	.	.	.	.	.	.
Ml_SGC1	.	.	.	.	.	.
Ca_SGC1	.	.	.	.	.	.
Pf_SGC2	AEEAFKAYHIMIKIIYEGVIQSLQGGSFSLVWNTLVTYETIIFSRYQLFLIESVGVMYFM					
Pb_SGC2	.	.	.	.	.	.
Oc_SGC2	.	.	.	.	.	.
Ml_SGC2	.	.	.	.	.	.
Vs_SGC2	.	.	.	.	.	.
Hc_SGC1	.	.	.	.	.	.
Dg_SGC1	.	.	.	.	.	.
Bea_SGC1	.	.	.	.	.	.
Hc_SGC2	.	.	.	.	.	.
Oc_SGC1	.	.	.	.	.	.
Ml_SGC4	.	.	.	.	.	MTTTTRFY
Oc_SGC4	.	.	.	.	.	.
Hc_SGC4	.	.	.	.	.	.
Pp_SGC2	.	.	.	.	.	.
Pb_SGC4	.	.	.	.	.	.
Hs_SGCY3	AGVPVVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHQCAGKRGR					
Hs_SGCY2	LGLKFEEIQKRFGEFFNCFHENERVLRAVGGTLQDFFNGFDALLEHIRTSGKQATLE					
Ed_SGC4	.	.	.	.	.	.
Pb_Nit1	.	.	.	.	.	.
Ed_Nit1	.	.	.	.	.	.
Hc_Nit1	FSKRAQYQNKKVVALKTILPQYFTVNRELMIEKTLKELRN..ENVLTVYGAIIDHDVCYL					
Pf_Nit12	.	.	.	.	.	.
Pf_Nit1	.	.	.	.	.	.
Ps_Nit1	.	.	.	.	.	.
Ca_Nit1	FSKRAYYQNKKVAMKKVLPQYMTINRSLMVEMKALKELRN..DNLLTVHGAISD.NLCYL					
Bea_Nit1	FSRRGQQENKIVALKTVLPQYMNITRELMVQMKTLKDLRN..ENLLTVYGAIIERDISYL					
Bi_SGC1	.	.	.	.	.	.
Bi_Nit1	.	.	.	.	.	.
Dg_Nit1	.	.	.	.	.	.
Lt_Nit1	.	.	.	.	.	.
Ml_NIT-like	.	.	.	.	.	.
Vs_Nit1	.	.	.	.	.	.
Oc_Nit1	.	.	.	.	.	.
Ocg_Nit1	.	.	.	.	.	.
Ocg_Nit12	.	.	.	.	.	.

### STYKc protein kinase domain

	120	130	140	150	160	170
Hs_SGCY1	FRCT....DAEKKGKGLILHYYSEREGLQDIVIGIICKTVAQQIHGTBEIDMKVIQQRNECD					
Ml_SGC3	.	.	.	.	MYGFVFDAIRLGCFKDFNKKTW	.
Oc_SGC3	.	.	.	.	.	.
Ml_SGC1	.	.	.	.	.	.
Ca_SGC1	.	.	.	.	.	.
Pf_SGC2	.	.	.	.	.	.
Pb_SGC2	NGTISLDIHNLFIGALKLHDYSLQFSQIYGGDTIRSKYQSLIKYSGDLRTLLKQIRGNA					
Oc_SGC2	..MG....TSDFDFVKLYKPKNKILGKVGKSKGKRKGKNNGLRPGBTPESSSSDVGSV					
Ml_SGC2	.	.	.	.	MGTSYFAGSV	.
Vs_SGC2	.	.	.	.	.	.
Hc_SGC1	.	.	.	.	.	.
Dg_SGC1	.	.	.	.	.	.
Bea_SGC1	.	.	.	.	.	.
Hc_SGC2	.	.	.	.	.	.
Oc_SGC1	.	.	.	.	.	.
Ml_SGC4	QQTG....ILDTKLPIRLRKFLDRGSNSASLRNLCKVKAEEKITWSENEVNCKMFGFMFA					
Oc_SGC4	.	.	.	.	.	.
Hc_SGC4	.	.	.	.	.	.
Pp_SGC2	.	.	.	.	.	.
Pb_SGC4	.	.	.	.	.	.
Hs_SGCY3	LEDASIICLDKEDDFLHVYFFFKRTTSSLILPGIICKAAAHVLYETEVEVSLMPPCFHNDC					
Hs_SGCY2	SPSF....LCKELPEGTLMLHYFPHHIVGFMGLGMIAAGKKIYRLDVEVEQVANEKLC					
Ed_SGC4	.	.	.	.	.	.
Pb_Nit1	.	.	.	.	.	.
Ed_Nit1	.	.	.	.	.	.
Hc_Nit1	VTEY....CNKGSLQDLLNDVKKLDDMLKYSILNDLAKGMRFLHSSVIESHGYLKSSNC					
Pf_Nit12	.	.	.	.	MRFLHSSVIESHGYLKSSNC	.
Pf_Nit1	.	.	.	.	MRFLHSSVIESHGYLKSSNC	.
Ps_Nit1	.	.	.	.	.	.
Ca_Nit1	VTEY....CNKGSLQDLLNEEIKLDDTFKFSLINDLVKGMAVLHSTDIGSHGYLKSSNC					
Bea_Nit1	VTEY....CSKGSLQDLLNEEIKLDDTFKFSLINDLAQGLKYIHESEVIDSHGYLKSSNC					
Bi_SGC1	.	.	.	.	.	.
Bi_Nit1	.	.	.	.	.	.
Dg_Nit1	.	.	.	.	.	.
Lt_Nit1	.	.	.	.	.	.
Ml_NIT-like	.	.	.	.	.	.
Vs_Nit1	.	.	.	.	.	.
Oc_Nit1	.	.	.	.	.	.
Ocg_Nit1	.	.	.	.	.	.
Ocg_Nit12	.	.	.	.	.	.

## STYKc protein kinase domain

	180	190	200	210	220	
<b>Hs_SGCY1</b>	H.TQFL.	IIEEKESKEEDFYEDLDREFEENGTOESRISPYTFCKAFTPFIIFDRD				
<b>M1_SGC3</b>	Q.DISKDGS CGS GEF DYS VDY DS DIFY RL ADD ATT KM KY TRSAV LQM FGRW YIA FI WDKWN					
<b>Oc_SGC3</b>	.	.	.	.	.	
<b>M1_SGC1</b>	.	.	.	.	.	
<b>Ca_SGC1</b>	.	.	.	.	.	
<b>Pf_SGC2</b>	.	.	.	.	.	
<b>Pb_SGC2</b>	HVEQS HKIALFWINIGMSYDEH IKS IQDS V A T VNEK MASMI KQ AILY QYATEVV LII LC					
<b>Oc_SGC2</b>	N.SWDR.	T QED FND IV D STG KDD KG EY KR KS RN IS VC II I P ILA VI SY SC YH				
<b>M1_SGC2</b>	N.SWDR.	T QED FND IV D STG KDD KG EY KR KS RN IS VC II I P ILA VI SY SC YH				
<b>Vs_SGC2</b>	.	.	.	.	.	
<b>Hc_SGC1</b>	.	.	.	.	.	
<b>Dg_SGC1</b>	.	.	.	.	.	
<b>Bea_SGC1</b>	.	.	.	.	.	
<b>Hc_SGC2</b>	.	.	.	.	.	
<b>Oc_SGC1</b>	.	.	.	.	.	
<b>M1_SGC4</b>	I.KLGF.	YSDF EKR SWY I CTA ASV P E DY D D Y I D Y E D Q L F L E A V G L M E S Y T				
<b>Oc_SGC4</b>	.	MEL DD VL PL TS LS ILS L S L F P F I Y F D R Y N E I H S V G S T L D Q I				
<b>Hc_SGC4</b>	.	.	.	.	.	
<b>Pp_SGC2</b>	.	.	.	.	.	
<b>Pb_SGC4</b>	.	.	.	.	.	
<b>Hs_SGCY3</b>	S.EFVN.	QPVLLY SVHM KSTKP SISPSK P QSSLVI PTS L FCK TFP FH FM FD K D				
<b>Hs_SGCY2</b>	S.DVSN PGNC SCLT F LIKE C EN T NIMK NL PQGT SQV PA DRIS INTFC RA FP FH LM FD PS					
<b>Ed_SGC4</b>	.	.	.	.	.	
<b>Pb_Nit1</b>	.	.	.	.	.	
<b>Ed_Nit1</b>	.	.	.	.	.	
<b>Hc_Nit1</b>	V.INNH.	FSLKLAD F SRT IFMS DMDRLS RATE E ARN DRL VY R . APELL RM QM				
<b>Pf_Nit12</b>	V.INNH.	FSLKIAD F SRT IFMS DMDRLS KATE E ARN E R L VY R . APELL RM QC				
<b>Pf_Nit1</b>	V.INNH.	FSLKIAD F SRT IFMS DMDRLS KATE E ARN E R L VY R . APELL RM QC				
<b>Ps_Nit1</b>	.	.	.	.	.	
<b>Ca_Nit1</b>	I.IINL.	FSLK I SDF SRT IFMS DMDM ER VSRM SA E ARN E R L VY R . APELL RM TT				
<b>Bea_Nit1</b>	I.IINQ.	FALK I SDF SKT IFMS DMDM RL SRATE E AMN E R L VY R . APELL RM SC				
<b>Bi_SGC1</b>	.	.	.	.	.	
<b>Bi_Nit1</b>	.	.	.	.	.	
<b>Dg_Nit1</b>	.	.	.	.	.	
<b>Lt_Nit1</b>	.	.	.	.	.	
<b>M1_NIT-like</b>	.	.	.	.	.	
<b>Vs_Nit1</b>	.	.	.	.	.	
<b>Oc_Nit1</b>	.	.	.	.	.	
<b>Ocg_Nit1</b>	.	.	.	.	.	
<b>Ocg_Nit12</b>	.	.	.	.	.	

  

	230	240	250	260	270	
<b>Hs_SGCY1</b>	L VVT QCGN . A I Y R V L P Q L Q P G N C S L L S V F S L V R P H I D I S F H G I L S H I . . .					
<b>M1_SGC3</b>	MGMIG RTPGE FFRNWS DFF EY K S Q E Y P L F I H D R F K I I R N L H I F Y V L G . . .					
<b>Oc_SGC3</b>	.	.	.	.	.	
<b>M1_SGC1</b>	.	.	.	.	.	
<b>Ca_SGC1</b>	.	.	.	.	.	
<b>Pf_SGC2</b>	.	.	.	.	.	
<b>Pb_SGC2</b>	L I L S V F A V I D I R K I K Q I Y L Y L K V S T G H L L P C I Y L V D T I P S S R D S F V W L V E T G G T M K V L K					
<b>Oc_SGC2</b>	I Y Q G H I S H R Q S R A N H N L V G S S Q Q F S K A V E G L N A E M L W T M M Y I Y G N L D . . .					
<b>M1_SGC2</b>	I Y Q G H I S H R Q S R A N H N L V G S S Q Q F S K A V E G L N A E M L W T M M Y I Y G T L D . . .					
<b>Vs_SGC2</b>	.	.	.	.	.	
<b>Hc_SGC1</b>	.	.	.	.	.	
<b>Dg_SGC1</b>	.	.	.	.	.	
<b>Bea_SGC1</b>	.	.	.	.	.	
<b>Bi_SGC2</b>	.	.	.	.	.	
<b>Oc_SGC1</b>	.	.	.	.	.	
<b>M1_SGC4</b>	VSK ED E Q G F D L . . . . . A M R C W A P N M A Y F G L G . . .					
<b>Oc_SGC4</b>	M P N L V R T K L N K N F F L R K P Y G T L T W N Y I R S N T H M I F E L C T K A S E G I T . . .					
<b>Hc_SGC4</b>	.	.	.	.	.	
<b>Pp_SGC2</b>	.	.	.	.	.	
<b>Pb_SGC4</b>	.	.	.	.	.	
<b>Hs_SGCY3</b>	M T I L Q F G N G I R R L M N R R D F Q G K P N F E E Y F E I I T P K I N Q T F S G I M T M L . . .					
<b>Hs_SGCY2</b>	M S V L Q I G E G L R K Q L . R C D T H K V L K F E D C F E I V S P K V N A T F E R V L L R L . . .					
<b>Ed_SGC4</b>	L I H Q P S T . . D V Y S F . A I I L V E I G D R T E I S P P E E T I F D P L W R P E L P E L . . .					
<b>Pb_Nit1</b>	.	.	.	.	.	
<b>Ed_Nit1</b>	.	.	.	.	.	
<b>Hc_Nit1</b>	V P C K G T K E G D M Y S F . A I I V H E I I V R Y G P F G L S N M D C D L T A T E V I N M V . . .					
<b>Pf_Nit12</b>	I P C K G T R E G D M Y S F . A I I V H E I I V R Y G P F G L S N M D A D L T A T E V I N M V . . .					
<b>Pf_Nit1</b>	I P C K G T R E G D M Y S F . A I I V H E I I V R Y G P F G L S N M D A D L T A T E V I N M V . . .					
<b>Ps_Nit1</b>	I P C K G T R E G D M Y S F . A I I V H E I I V R Y G P F G L S N M D A D L T A T E V I N M V . . .					
<b>Ca_Nit1</b>	V P C Q G T K E A D V Y S F . G I I L H E V L L R E G P F G L S S M E C D L T S T E V I H L V . . .					
<b>Bea_Nit1</b>	V P C Q G T R E G D I Y S F . G I I V H E I L V R E G P F G L S S M Q S D L T A T E V I C M I . . .					
<b>Bi_SGC1</b>	.	.	.	.	.	
<b>Bi_Nit1</b>	.	.	.	.	.	
<b>Dg_Nit1</b>	I P C Q G T K E G D V Y S F . G I I V H E I L V R E G P F G L S S M E C D L T A A E V M S M I . . .					
<b>Lt_Nit1</b>	.	.	.	.	.	
<b>M1_NIT-like</b>	.	.	.	.	.	
<b>Vs_Nit1</b>	.	.	.	.	.	
<b>Oc_Nit1</b>	.	.	.	.	.	
<b>Ocg_Nit1</b>	I P C K G T K E G D M Y S F . G I I V H E I L V R E G P F G L S N M R C D L T A T E V I N L V . . .					
<b>Ocg_Nit12</b>	I P C K G T K E G D M Y S F . G I I V H E I L V R E G P F G L S N M R C D L T A T E V I N L V . . .					

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_sGC1	.
Ca_SGC1	.
Pf_SGC2	IQKDKSEALLFRMLPYSVVRELRKCRESDNLVGSYQSATVLFADLADFQRLAARDMSPF
Pb_SGC2	.
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	.
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

### STYKc protein kinase domain

	280	290	300
Hs_SGCY1	NTVFVL	RSKEGLLDVEKLECEDELTGT	EISCLRLKGQ
Ml_SGC3	MSKTSTA		ELEYDTPLVLQGQ
Oc_SGC3			
Ml_sGC1	YPVVVV		SDLRIKSNESLDL
Ca_SGC1			
Pf_SGC2	AYVRFLFYTIAEVLESHTVNEIETAAGECLTLFCIQIKAAQREPRMFQFLHRPISAE		
Pb_SGC2	YPV	... VVV	SDLRIKSNESLAE
Oc_SGC2	YPV	... VVV	SDLRIKSNESLAE
Ml_SGC2			
Vs_SGC2			
Hc_SGC1			
Dg_SGC1			
Bea_SGC1			
Hc_SGC2			
Oc_SGC1			
Ml_SGC4	IIKFVL		KNLFRHLHEEGMSV
Oc_SGC4	KLMKNE		ETEIDLHFRLQGQ
Hc_SGC4			
Pp_SGC2			
Pb_SGC4			
Hs_SGCY3	NMQFVV		RVRRWDNSVKSSRVMIDLKGQ
Hs_SGCY2	STPFVVI		RTKPEASGESENKDVKMEVKQ
Ed_SGC4	N		EQDNDQDNKC
Pb_Nit1			
Ed_Nit1			
Hc_Nit1	T		KTDRTPFPRPEFP
Pf_Nit12	I		KTDRVTPFPRPEFP
Pf_Nit1	I		KTDRVTPFPRPEFP
Ps_Nit1	I		KTDRVTPFPRPEFP
Ca_Nit1	T		KTDTAQPYRPTFP
Bea_Nit1	R		KGTTTPYRPEFP
Bi_SGC1			
Bi_Nit1			
Dg_Nit1	S		RSDELETPYRPEFP
Lt_Nit1			
Ml_NIT-like			
Vs_Nit1			
Oc_Nit1	T		KLHSQVVPYRPEFP
Ocg_Nit1	T		KLHSQVVPYRPEFP
Ocg_Nit12			

## STYKc protein kinase domain

HNOB

	310	320	330	340	350	360	
<b>Hs_SGCY1</b>	MIYLPEADSILFLCSPSVMNLDLTRRGGLYSDIPLHDATRDLVLLGEQFRE	EYKLTQEL					
<b>M1_SGC3</b>	MVTGMVDKSALFLCYPAVGCFLSR.RNAFYVGDLPPGPLKHTVIALICLKNSLVEHSDL						
<b>Oc_SGC3</b>	ISTWPPTLETNYASKLEFIADLEKLRLGLIDAQLRAEEAFKAYHIMIKI	IYEGVIQSLQG					
<b>M1_SGC1</b>	ISSWPRTLETNYATKTQFFRDLENLRSQIDAQQLRAEEAFKAYHIMIKI	IYEGVIQSLQG					
<b>Ca_SGC1</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Pf_SGC2</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Pb_SGC2</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Oc_SGC2</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>M1_SGC2</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Vs_SGC2</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Hc_SGC1</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Dg_SGC1</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Bea_SGC1</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Hc_SGC2</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>Oc_SGC1</b>	ISSWPRTLETNYATKTQFIHDLERLRGQIDAKQLRAEEAFKAYHVMIKI	IYEGVIQSLQG					
<b>M1_SGC4</b>	VVEPQQVDGYIFQNNFRQLQFDNTPFFRNSDEEDFSNDNEDEIMPLTSLSILSLFPFFYF						
<b>Oc_SGC4</b>	IYVFEDTGDAIFLCSPRLESMSAC..KSTFFGDLEAHDTTKNQLVSSTLRLHLIRRLLDE						
<b>Hc_SGC4</b>							
<b>Pp_SGC2</b>	MASFKSVYLSDMMAHDPIKSQVLAPSLRMHLTRRMIDE						MIDE
<b>Pb_SGC4</b>	MIYIVESSAILFLGSPCVDRLEDFTGRGLYSDIPIHNALRDVVLIGEQARAQDGLKKR						
<b>Hs_SGCY3</b>	MIHVPESENSILFLGSPCVDKLDELMGRLGLHSIDIPIHDA	RDVILVGEQAKAQDGLKKRM					
<b>Hs_SGCY2</b>	PEASKYVDLIVSCWQD.RPSARPTFEGVKTLHIINP..YKENPVDM	MMKLMEXYS					
<b>Ed_SGC4</b>							
<b>Pb_Nit1</b>	FTTDVKQARVAAMCRDCWSE.DPLVRPTFPSLRSTLRSIGVE.SSGGIVGNLLSRMEKYA						
<b>Ed_Nit1</b>	FSTDSDKQARLAAVAREAWHE.DPGMRPTFQSIRASFRSIGIE.SSGGIVGNLLSRMEKYA						
<b>Hc_Nit1</b>	FSTDSDKQARLAAVAREAWHE.DPGMRPTFQSIRASFRSIGIE.SSGGIVGNLLSRMEKYA						
<b>Pf_Nit1</b>	FSTDSDKQARLAAVAREAWHE.DPGMRPTFQSIRASFRSIGIE.SSGGIVGNLLSRMEKYA						
<b>Ps_Nit1</b>	FSTDSDKQARLAAVAREAWHE.DPGMRPTFQSIRASFRSIGIE.SSGGIVGNLLSRMEKYA						
<b>Ca_Nit1</b>	FTNDSKLKRAIQMANECWNE.SAHQRPTFASLRGSMKYLKE						
<b>Bea_Nit1</b>	FSTDSDKLKATVSLSRDCWKE.DPYQRPTIQSIRSSLRSIRTEGSSGGIVENLLSRMEKYA						
<b>Bi_SGC1</b>							
<b>Bi_Nit1</b>							
<b>Dg_Nit1</b>	FSTDNKFSTIISMARSSWDE.DPLQRPTFSNIRTTLRAIRVD.TSGGIVENLLGRMEKYA						
<b>Lt_Nit1</b>							MGGQRRVREVDSSGGIVENLLGRMEKYA
<b>M1_NIT-like</b>							
<b>Vs_Nit1</b>							
<b>Oc_Nit1</b>							
<b>Ocg_Nit1</b>	FSNDPKVSRIINMAREAWSE.EAQWRPNFQSIRSTLRSIRVD.ASGGIVENLLGRMEKYA						
<b>Ocg_Nit12</b>	FSNDPKVSRIINMAREAWSE.EAQWRPNFQSIRSTLRSIRVD.ASGGIVENLLGRMEKYA						

## domain

	370						
<b>Hs_SGCY1</b>	EILTDRDQL						
<b>M1_SGC3</b>	EKENMRYRE						
<b>Oc_SGC3</b>							
<b>M1_SGC1</b>	GSFSLVWNT						
<b>Ca_SGC1</b>							
<b>Pf_SGC2</b>							
<b>Pb_SGC2</b>	GSFSLVWNTLVTYETIIIFSRYQLFLIESVGVMYFMNGTISLDIHNLFIGALKLHDYSI	QF					
<b>Oc_SGC2</b>	GSFSLVWNTLVTYETIIIFSRYQLFLIESVGVMYFMNGTISLDIHSLFIGALKLHDYSI	QF					
<b>M1_SGC2</b>	GSFSLVWNT						
<b>Vs_SGC2</b>							
<b>Hc_SGC1</b>							
<b>Dg_SGC1</b>							
<b>Bea_SGC1</b>							
<b>Hc_SGC2</b>							
<b>Oc_SGC1</b>							
<b>M1_SGC4</b>	DRFNIEHSV						
<b>Oc_SGC4</b>	EREQSMLQN						
<b>Hc_SGC4</b>							
<b>Pp_SGC2</b>	ETMQGDIQA						
<b>Pb_SGC4</b>	ETMQGDIQA						
<b>Hs_SGCY3</b>	GKLKATLQE						
<b>Hs_SGCY2</b>	DKLKATLER						
<b>Ed_SGC4</b>	KHLEMVVCE						
<b>Pb_Nit1</b>							
<b>Ed_Nit1</b>							
<b>Hc_Nit1</b>	SNLEEVVVE						
<b>Pf_Nit12</b>	TNLEEVVVE						
<b>Pf_Nit1</b>	TNLEEVVVE						
<b>Ps_Nit1</b>	TNLEEVVVE						
<b>Ca_Nit1</b>							
<b>Bea_Nit1</b>	TNLEDVVVE						
<b>Bi_SGC1</b>							
<b>Bi_Nit1</b>							
<b>Dg_Nit1</b>	TNLEEVVVE						
<b>Lt_Nit1</b>	SNLEELVVE						
<b>M1_NIT-like</b>							
<b>Vs_Nit1</b>							
<b>Oc_Nit1</b>							
<b>Ocg_Nit1</b>	TNLEELVVE						
<b>Ocg_Nit12</b>	TNLEELVVE						

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_sGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	SQIYGGDTIRSKIYQSLIKYSGDLRTLLKQIRGNAHVEQSHKIALFWINIGMSYDEHIKS
Oc_SGC2	SQIYGGDTIRSKIYQSLIKYSGDLRTLLKQIRANAHVEQSHKIALFWINIGMSYDEHIKS
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	.
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_sGC1	.
Ca_SGC1	.
Pf_SGC2	.
Pb_SGC2	IQDSVAATVNEKMASMIKQAILYQYATEVVLLCLILSVFAVIDIRKIKQIYLYLKSQS
Oc_SGC2	IQDSVAASVNEKMASMIKKAILYQYATEVVLLCLILSVFAVIDIRKIKQIYLYLKSQS
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	.
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	.
Pb_Nit1	.
Ed_Nit1	.
Hc_Nit1	.
Pf_Nit12	.
Pf_Nit1	.
Ps_Nit1	.
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	.
Dg_Nit1	.
Lt_Nit1	.
Ml_NIT-like	.
Vs_Nit1	.
Oc_Nit1	.
Ocg_Nit1	.
Ocg_Nit12	.

## HNOB domain

### CYCc

	380	390	400	410	420	
Hs_SGCY1	....TLRALEDEKKKTDTLLYS	VLPPTS	VANE	LHKR.	....PVPAAKR	
M1_SGC3	....SCLEAAAKEAELSDNLLNQ	LMPPHI	HKA	RVGRPY.	YDNV <b>T</b> IL <b>F</b> SGIV	
Oc_SGC3	....	.....	.....	.....	YNNATVLLS <b>D</b> MV	
M1_SGC1	HDYSLQFSQIYGGDSIRSKIYQS	LFKYRL	LNKN	ANESSHTRSPTGSERT	NEDNNES <b>F</b> EADAE	
Ca_SGC1	.....	MLPYSV	VRE	LRKCKD.	GESCEL	
Pf_SGC2	.....	MLPYSV	VRE	....TPYVGSS	YQSAT <b>T</b> VL <b>F</b> ADLA	
Pb_SGC2	DRTKVTMKVLKIQKDKSEALLFRM	MLPYSV	VRE	LRKCRESD.	NLYVGSS <b>Y</b> QSAT <b>T</b> VL <b>F</b> ADLA	
Oc_SGC2	ERTKVTMKVLKIQKDRSEALLFRM	MLPYSV	VRE	LRKCRETN.	.TVVVGSS <b>Y</b> QSAT <b>T</b> VL <b>F</b> ADLA	
M1_SGC2	ERTKVTMKVLKIQKDRSEALLFRM	MLPYSV	VRE	LRKCRQTS.	.TLYVGSS <b>Y</b> QSAT <b>T</b> VL <b>F</b> ADLA	
Vs_SGC2	.....	MLPYSV	VRE	LRKCRQTS.	.TLYVGSS <b>Y</b> QSAT <b>T</b> VL <b>F</b> ADLA	
Hc_SGC1	.....	.....	.....	.....	.....	
Dg_SGC1	.....	.....	.....	.....	.....	
Bea_SGC1	.....	.....	.....	.....	.....	
Hc_SGC2	.....	.....	.....	.....	.....	
Oc_SGC1	.....	.....	.....	.....	.....	
M1_SGC4	.....GSTLDQ	IMPNL	VRSK	LNKNF.	....SLRKPKARSRC <span style="color:red">SKTR</span> ETL	
Oc_SGC4	....QYLSVLNTEMRITEGLI	IQ	IMPRDV	IADQ	....VNTCEE <span style="color:red">SEA</span> <b>T</b> VL <b>F</b> SDLV	
Hc_SGC4	....MTECLVRQ	IMPRE	IADQ	MRDGEF	....VNTCQE <span style="color:red">FKEV</span> <b>S</b> V <span style="color:red">F</span> DMV	
Pp_SGC2	....DYLISILSTEMK	ITC	ELVRQ	ILPKELAQ	....IRDGTPF <span style="color:red">FSEV</span> <b>T</b> VV <span style="color:red">F</span> SDMV	
Pb_SGC4	....EYLPSILSTE	MK	ITC	ELVRQ	ILPKELAQ	....IRDGTPF <span style="color:red">FSEV</span> <b>T</b> VV <span style="color:red">F</span> SDMV
Hs_SGCY3	....AHQALEEEKKKTV	DLCS	IFPC	EV	AQQLWQGQ.	
Hs_SGCY2	....THQALEEEKKKTV	DLCS	IFPGD	V	AQQLWQGQ.	
Ed_SGC4	....RTFDLIEEKKKTV	DLCS	MLPAS	VADQ	KQGK.	
Pb_Nit1	....MQIIKIRTS	CSLK	IICSKV	NKL	LIG.	
Ed_Nit1	....RTAQLQCEKKRT	DDLLIES	MLPKS	VADQ	LKTGN.	
Hc_Nit1	....RTAQLRCEKKRT	DDLLIES	MLPKS	VADQ	RSGS.	
Pf_Nit1	....RTAQLRCEKKRT	DDLLIES	MLPKS	VADQ	RSGS.	
Ps_Nit1	....RTAQLRCEKKRT	DDLLIES	MLPKS	VADQ	RSGS.	
Ca_Nit1	....RTAQLRCEKKRT	DDLLIES	MLPKS	VADQ	RSGS.	
Bea_Nit1	....RTAQLQVEKKRT	DDLLIES	MLPKS	VADQ	RSGS.	
Bi_SGC1	....	.....	MLPRA	VAEK	MKQGQ.	
Bi_Nit1	....RTSQLQAEKKRT	DDLLIES	MLPKS	VADQ	KAGT.	
Dg_Nit1	....RTSQLQAEKKRT	DDLLIES	MLPKS	VADQ	KAGT.	
Lt_Nit1	....RTAQLQSEKKK	TDDLLIES	MLPKS	VADQ	KGSH.	
M1_NIT-like	....	.....	.....	.....	....MVLPEK <span style="color:red">FECV</span> <b>T</b> IY <span style="color:red">F</span> SDIV	
Vs_Nit1	....RTAQLQVEKKK	TDDLLIES	MLPKS	VADQ	LKSGN.	
Oc_Nit1	....RTAQLQVEKKK	TDDLLIES	MLPKS	VADQ	LKSGN.	
Ocg_Nit1	....RTAQLQVEKKK	TDDLLIES	MLPKS	VADQ	LKSGN.	
Ocg_Nit12	....RTAQLQVEKKK	TDDLLIES	MLPKS	VADQ	LKSGN.	

	430	440	450	460	470	480
Hs_SGCY1	G <b>F</b> NAFCSKHASGEGAMKIV	VNL	NDLY	YTRFDT	TD	SRKNP <span style="color:red">F</span> VYK.
M1_SGC3	G <b>F</b> TSICSQ.IS	PM	MDV	ARML	NAMY	MTFDSD <span style="color:red">I</span> SNRKS.
Oc_SGC3	.....	.....	.....	.....	.....	.VYKRNVQ <span style="color:red">VETI</span> <b>G</b> DGY <span style="color:red">MV</span> VG
M1_SGC1	RHVRSTVSDD.	.....	.....	.....	.....	.....
Ca_SGC1	D <b>F</b> QRLAARDMS.	PF	FAV	RFL	ETFY	TRIAEV <span style="color:red">LE</span> SH.N.
Pf_SGC2	PF	QRLAARDMS.	PF	FAV	RFL	ETFY
Pb_SGC2	D <b>F</b> QRLAARDMS.	PF	FAV	RFL	ETFY	PRIAEV <span style="color:red">LE</span> SH.T.
Oc_SGC2	D <b>F</b> QRLAARDMS.	PF	FAV	RFL	ETFY	TRIAEV <span style="color:red">LE</span> SH.S.
M1_SGC2	D <b>F</b> QRLAARDMS.	PF	FAV	RFL	ETFY	YARIAEV <span style="color:red">LE</span> SH.S.
Vs_SGC2	D <b>F</b> QRLAARDMS.	PF	FAV	RFL	ETFY	YARIAEV <span style="color:red">LE</span> SH.S.
Hc_SGC1	.....	.....	.....	.....	.....	.....
Dg_SGC1	.....	.....	.....	.....	.....	.....
Bea_SGC1	.....	.....	MS.	PF	FAV	RFL
Hc_SGC2	.....	.....	MS.	PF	FAV	RFL
Oc_SGC1	.....	.....	MS.	PF	FAV	RFL
M1_SGC4	S <b>F</b> SVPHGWSL	.....	.....	.....	.....	.....
Oc_SGC4	G <b>F</b> TEICCS	LS.	.....	.....	.....	.....
Hc_SGC4	GF	STICKT.	LT.	PMQ	TA	CLLN
Pp_SGC2	G <b>F</b> NELCSS.	LT.	PMQV	ALL	NSM	YMTFDK <span style="color:red">L</span> QSHPK.
Pb_SGC4	G <b>F</b> NELCSS.	LT.	PMQV	ALL	NSM	YMTFDK <span style="color:red">L</span> QSHPK.
HS_SGCY3	G <b>F</b> TAICSQ.CS.	PLQV	IT	TM	NALY	TRFDQCGEL.D.
Ed_SGC4	G <b>F</b> TAICAO.CT.	PMQV	ISML	NELY	TRFDHQC <span style="color:red">G</span> FL.D.	
Pb_Nit1	AIGRFLCLR.	QKV	DEM	NDLY	TLFDT	IEKY.D..CYK.
Ed_Nit1	G <b>F</b> THLCSK.SA.	PIEV	U	NDLY	TLFDT	IEKY.D..CYK.
Hc_Nit1	G <b>F</b> TAISSL.ST.	POQV	LEM	NDLY	TLFDT	IEKY.D..CYK.
Pf_Nit12	G <b>F</b> TAISSL.SS.	PHQV	LEM	NDLY	TLFDT	IEKY.D..CYK.
Pf_Nit1	G <b>F</b> TAISSL.SS.	PHQV	LEM	NDLY	TLFDT	IEKY.D..CYK.
Ps_Nit1	G <b>F</b> TAISSL.SS.	PHQV	LEM	NDLY	TLFDT	IEKY.D..CYK.
Ca_Nit1	G <b>F</b> TSLSGD.ST.	AMQV	LDL	NDLY	TVFDEC	IEKY.D..CYK.
Bea_Nit1	G <b>F</b> TAISSG.SK.	PIEV	UDM	NDLY	TLLDT	IEKY.D..CYK.
Bi_SGC1	S <b>F</b> TNLCSQ.ST.	PMEV	VAF	DDM	YTMFD <span style="color:red">S</span>	IESY.D..VYK.
Bi_SGC1	.....	.....	.....	.....	.....	....VETI <span style="color:red">GDAY<span style="color:red">ML</span>.</span>
Dg_Nit1	G <b>F</b> TAISSK.SK.	PMEV	LDML	NDLY	TVFDT	IEKY.D..CYK.
Lt_Nit1	G <b>F</b> TAISSL.SK.	PMEV	LDML	NDLY	TVFDT	IEKY.D..CYK.
M1_NIT-like	G <b>F</b> TAISSL.SK.	PMEV	LDML	NDLY	TVFDT	IEKY.D..CYK.
Vs_Nit1	.....	.....	.....	.....	.....	.....
Oc_Nit1	G <b>F</b> TAISSL.SK.	PMEV	LDML	NDLY	TVFDT	IEKY.D..CYK.
Ocg_Nit1	G <b>F</b> TAISSL.SK.	PMEV	LDML	NDLY	TVFDT	IEKY.D..CYK.
Ocg_Nit12	G <b>F</b> TAISSL.SK.	PMEV	LDML	NDLY	TVFDT	IEKY.D..CYK.

## CYCc

## Adenylyl- / guanylyl cyclase, catalytic domain

	490	500	510	520	530
Hs_SGCY1	LPEPC	.IHHARS	IChLA	DMMEIA	GQVQVD.
M1_SGC3	IPNTQ	.ERKHAEY	AADM	IDMLAGLKKVELP	LEGK.MAVKL.
Oc_SGC3	IPTYO	.EKHAEY	AAEMA	IDMLIGLRSVELP	LE.DNM.RVKI.
M1_SGC1	LPDRS	PTT	KHCSE	IALTA	GLRSVMCRGLQLC
Ca_SGC1	LPDR	T	S	KHCSE	IATA
Pf_SGC2	...	...	...	GFRSIMCRGLQLC	VHGDFVCFRL
Pb_SGC2	LPDT	T	P	KHCSE	ALTA
Os_SGC2	LPDRI	T	P	KHCSE	ALTA
M1_SGC2	LPDRI	T	P	KHCSE	ALTA
Vs_SGC2	LPDRI	T	P	KHCSE	ALTA
Hc_SGC1	...	...	...	...	...
Dg_SGC1	...	...	...	...	...
Bea_SGC1	LPDRS	STS	KHCSE	IATA	GLRSVMCRGLQLC
Hc_SGC2	LPDRS	PTS	KHCAE	ALTA	GLRSVMCRGLQLC
Oc_SGC1	LPDRS	PTS	KHCSE	ALTA	GLRSVMCRGLQLC
M1_SGC4	LPDRI	...	EHHAKH	ADAVNEMVQAI	QKVVKINEL.
Oc_SGC4	LPDRT	...	EHHAKH	ADIA	EMIQATQNVKIAFL.
Hc_SGC4	LPIED	...	DNHARH	ADIA	DMVQIAEVKVDPL.
Pp_SGC2	LPTKD	...	DNHAKY	ANANIA	EMVQIKQQVKVDFL.
Pb_Nit1	LPTKD	...	DNHAKY	ANANIA	EMVQIKQQVKVDFL.
Hs_SGCY3	LHKES	DTHAVO	IALMA	KMMEL	DDEVMSPH.
Hs_SGCY2	LHRKS	LC	CHAKP	I ALMA	KMMEL
Ed_SGC4	VPNKG	DKHAE	I	AMMA	KIVMFCRGFRVPRADQI
Pb_Nit1	LPIRNE	DRHAAQ	I	ALMS	LDFLDNIRNFKIAH
Ed_Nit1	LPIRNG	LRHAAQ	I	SLMS	LEFLNKVESFVIRH
Hc_Nit1	LPIRNG	DRHAAQ	I	ALMS	LDFLDSIRNFKIAH
Pf_Nit1	LPIRNG	DRHAAQ	I	ALMS	LDFLDSISNFKIAH
Pf_Nit1	LPIRNG	DRHAAQ	I	ALMS	LDFLDSISNFKIAH
Ps_Nit1	LPIRNG	DRHAAQ	I	ALMS	LDFLDSISNFKIAH
Ca_Nit1	LPIRNG	DRHAAQ	I	ALMS	LDFLDNVKNFVIRHKPDAQLM
Bea_Nit1	LPIRNG	ERHAAQ	I	GLMS	LDFLDNVNNFVIGH
Bi_SGC1	...	...	...	...	...
Bi_Nit1	LPVRNG	DRHAAQ	I	ALMS	LNFLSCLKTFVISH
Dg_Nit1	LPIRNG	DRHAAQ	I	ALMS	LDFTLCIKHFVVSHE
Lt_Nit1	LPVRNG	DRHAAQ	I	ALMS	LDFLGCIKTFVISH
M1_NIT-like	LPVRNG	DRHAAQ	I	ALMS	LDFLSCLNTFVISH
Vs_Nit1	LPVRNG	DRHAAQ	VALMS	LDFLSS	KTFVISHLPDKKLNI
Oc_Nit1	LPVRNG	DRHAAQ	VALMS	LDFLSS	LNTFVISHLPDKKLNI
Ocg_Nit1	LPVRNG	DRHAAQ	VALMS	LDFLSS	LNTFVISHLPDKKLNI
Ocg_Nit12	LPVRNG	DRHAAQ	VALMS	LDFLSS	LNTFVISHLPDKKLNI

	540	550	560	570	580
Hs_SGCY1	PRYCI	FGNTVNLT	SRTETTGEKGKIN	SETYTYRC	L MSPENS DPOF
M1_SGC3	PRYGV	FGDTVN	VNLEST.	SES	SKNF
Oc_SGC3	PRYGV	FGDTVN	VNLESTSKPNRIH	...	...
M1_SGC1	...	...	...	...	...
Ca_SGC1	PRFCV	FGNTVN	TAARMKSTCLGMRIQ	TEACKYVL	EEEF
Pf_SGC2	PRFCV	FGDTINTA	ARMKSTAIGMRQI	TDVCCDIL	EEEF
Pb_SGC2	PRFCV	FGDTINTA	ARMKSTAIGMRQI	TDVCCSVEL	EEEF
Oc_SGC2	PRFCV	FGDTVN	TAARMKSTAIGMRQI	TDVCSVEL	EDEF
M1_SGC2	PRFCV	FGDTVN	TAARMKSTAIGMRQI	TDVCCDIL	EDDF
Vs_SGC2	PRFCV	FGDTVN	TAARMKSTAIGMRQI	TDICSVIL	EEGF
Hc_SGC1	PRFCV	FGDTVN	TAARMKSTAIGMRQI	TDICSIIL	EEGF
Dg_SGC1	PRFCV	FGDTVN	TAARMKSSCLGMRIQ	TDICSFIL	EEGF
Bea_SGC1	PRFCV	FGDTVN	TAARMKSTCLGMRIQ	SDSTNEHL	KRYGNY
Hc_SGC2	PRFCV	FGDTVN	TAARMKSTCLGMRIQ	SDSTNEHL	KRYGNY
Oc_SGC1	...	...	...	...	...
M1_SGC4	PRYCI	FGDTVN	SRMESA	SEALRIH	KRYGNY
Oc_SGC4	PRYCI	FGDTVN	SRMESA	SEALRIH	KRYGNY
Hc_SGC4	PRYCI	FGDTVN	SRMESA	SEALRIH	KRYGNY
Pp_SGC2	PRYCI	FGDTVN	SRMETS	SEALRIH	KRYGNY
Pb_SGC4	PRFCV	SLYLCLSV	FGDINTWC	PRQVSMSPMSVCL	WWDGRCRGNY
Hs_SGCY3	PRYCI	FGNNVTLA	NKFECS	CVPRKIN	SPPTYRL
Hs_SGCY2	PRYCI	FGNNVTLA	NKFECS	SHSPRIN	SPPTYQL
Ed_SGC4	PRFCI	FGDTVN	SRMEST	GEALKI	KRED
Pb_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	SSQSHDIL
Ed_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	...
Hc_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	SLQSHDIL
Pf_Nit12	PRYCI	FGDTVN	SRMEST	GEALKI	NIHGGF
Pf_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	SSQSHDIL
Lt_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	KIHGGF
M1_NIT-like	PRYCI	FGDTVN	SRMEST	GEALKI	SSQSHDIL
Vs_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	SEQTYNIL
Oc_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	IKHGGF
Ocg_Nit1	PRYCI	FGDTVN	SRMEST	GEALKI	SEQSYKIL
Ocg_Nit12	PRYCI	FGDTVN	SRMEST	GEALKI	DNHGGF

	590	600	
Hs_SGCY1	HLEH[R]	G[PVSM[KGK[K[EPM[Q[VWFL	SRKNT.
M1_SGC3	ISR.	...[T[YWL[C...	GRRTSDTNPFENEAAEDEALP.
Oc_SGC3	...	...	...
M1_sGC1	...	...	...
Ca_SGC1	LISKR.	GVIYV[KGKG[EME[T[HWL[I...	GVRNN.
Pf_SGC2	LISKR.	G[TIFV[KGKG[EME[T[HWL[I...	GNRNS...NEDINN.
Pb_SGC2	LISKR.	G[TIFV[KGKG[EME[T[HWL[I...	GSRNSNEDMNSYSNNNNNNNGGNKSGGGGR
Oc_SGC2	IVSKR.	G[IIFV[KGKG[EME[T[HWL[I...	SERNS...NEDLS.
M1_SGC2	IVSKR.	GVI[FV[KGKG[EME[T[YWL[I...	GVRNSTEDLTSYNNNSNNNN.
VS_SGC2	IVSKR.	GVI[FV[K...	...
Hc_SGC1	LIAKR.	G[TIFV[KGKG[EME[T[HWL[I...	GNRTS.
Dg_SGC1	LVTKR.	G[TIFV[KGKG[EME[T[HWL[I...	GERN.
Bea_SGC1	VVTKR.	G[TIFV[KGKG[EME[T[HWL[I...	SERNS.
Hc_SGC2	VISR.	G[IIFV[KGKG[ELE[T[HWL[I...	GERNS...NDD.
Oc_SGC1	...	...	...
M1_SGC4	ITRQR.	GWHSH[KGKG[QLP[T[YWL[C...	GQGDNLILPSYTQTELMEEEAK.
Oc_SGC4	ITRQR.	GWHAH[KGKG[QLP[T[YWL[C...	GQGDTILASYTKNELMEEEAK.
Hc_SGC4	...	...	...
Pp_SGC2	ITRQR.	GWHDH[KGKG[QLP[T[YWL[C...	GQGDTILT SYTKEELTEEEAK.
Pb_SGC4	ITRQR.	GWHDH[KGKG[QLP[T[YWL[C...	GQGDT.
Hs_SGCY3	VFTP[R.	...[SREELP[PNEPS	...
Hs_SGCY2	TFIPR.	...[SREELP[DNFPK	...
Ed_SGC4	RFEVR.	GKVEV[KGKG[TQE[T[HWL[L...	GRDN.
Pb_Nit1	VTESR.	GLVEM[KVLEM[LNDLYTLFDTCIEKYDCKVETIGDAYMVVS.	...
Ed_Nit1	...	...	...
Hc_Nit1	VTESR.	GLVEM[KGKG[KVP[T[FWL[K...	GVEND.
Pf_Nit1	VTECR.	GLVEM[KGKG[KVE[T[FWL[K...	GVENN.
Ps_Nit1	VTECR.	GLVEM[KGKG[KVE[T[FWL[K...	GVENN.
Ca_Nit1	VIEYR.	GLVEM[KGKG[KLP[T[YWL[Q...	GLDE.
Bea_Nit1	IIEAR.	GLIEM[KGKG[LVQ[T[YWL[Q...	GVDKA.
Bi_SGC1	...	...	...
Bi_Nit1	IIDPRB.	GLVDM[KGKG[KQQ[T[YWL[Q...	GVEKD.
Dg_Nit1	VIEPR.	GLVEM[KGKG[KIP[T[YWL[Q...	SIEKD.
Lt_Nit1	EIDPRB.	GLIEM[KGKG[LQQ[T[YWL[Q...	GVEKD.
M1_NIT-like	VIOPR[D	GLVDM[KGKG[LQQ[T[YWL[Q...	GVEKD.
VS_Nit1	VIOPR[D	GLVDM[KGKG[KOO[T[YWL[Q...	GVEKD.
Oc_Nit1	VIOPR[D	GLVDM[KGKG[GLOQ[T[YWL[H...	GVEKY.
Ocg_Nit1	IIEPRD	GLVDM[KGKG[GLOQ[T[YWL[Q...	GVEKY.
Ocg_Nit12	IIEPRD	GLVDM[KGKG[GLOQ[T[YWL[Q...	GVEKY.

Hs_SGCY1	...	...	...
M1_SGC3	...	...	...
Oc_SGC3	...	...	...
M1_sGC1	...	...	...
Ca_SGC1	...	...	...
Pf_SGC2	...	...	...
Pb_SGC2	NKKKQS[NWSMESAARGVVRQIALTN PILVITHNLCSNPPFTFVKEAGVTEGLGGASADDG	...	...
Oc_SGC2	...	...	...
M1_SGC2	...	...	...
VS_SGC2	...	...	...
Hc_SGC1	...	...	...
Dg_SGC1	...	...	...
Bea_SGC2	...	...	...
Hc_SGC2	...	...	...
Oc_SGC1	...	...	...
M1_SGC4	...	...	...
Oc_SGC4	...	...	...
Hc_SGC4	...	...	...
Pp_SGC2	...	...	...
Pb_SGC4	...	...	...
Hs_SGCY3	...	...	...
Hs_SGCY2	...	...	...
Ed_SGC4	...	...	...
Pb_Nit1	...	...	...
Ed_Nit1	...	...	...
Hc_Nit1	...	...	...
Pf_Nit12	...	...	...
Pf_Nit1	...	...	...
Ps_Nit1	...	...	...
Ca_Nit1	...	...	...
Bea_Nit1	...	...	...
Bi_SGC1	...	...	...
Bi_Nit1	...	...	...
Dg_Nit1	...	...	...
Lt_Nit1	...	...	...
M1_NIT-like	...	...	...
VS_Nit1	...	...	...
Oc_Nit1	...	...	...
Ocg_Nit1	...	...	...
Ocg_Nit12	...	...	...

Hs_SGCY1	.....VAVAKQPVTKTKTTVP.....
Ml_SGC3	.....
Oc_SGC3	.....
Ml_SGC1	.....
Ca_SGC1	.....MTEEEMS VYAGNKMSST.....
Pf_SGC2	.....YSNNNNSGGNTGHKQSGSR.....
Pb_SGC2	KEGHKS KSKSSKSNAFQFLTTSVNIIFSLHHISLAPQPI SLYITQVSGSCEWTRLRSRSS
Oc_SGC2	.....NYNSGNNSASKNTS.....
Ml_SGC2	.....NNNNNNNNNNNNNGNKTNSR.....
Vs_SGC2	.....
Hc_SGC1	.....NDEMN NYNGSSGDSRQGATD GREPVR.....
Dg_SGC1	.....
Bea_SGC1	.....IQRLTNKSTITNHASAPAAA.....
Hc_SGC2	.....
Oc_SGC1	.....
Ml_SGC4	.....KQVNQVLEQVNNEGAQLSADVLNQLSNP.....
Oc_SGC4	.....KQVNQVLEQVNNEGALSVDVLQQLSNNPALQRQIN.....
Hc_SGC4	.....
Pp_SGC2	.....KQVN D VLEQI PDGST AAAEMI QQMG FNPALQR.....
Pb_SGC4	.....
Hs_SGCY3	.....EIPGICHFLDAYQOG.....
Hs_SGCY2	.....EIPGICYFLEVTRGPKP.....
Ed_SGC4	.....LSISNC LSPASHKRIFKGALP.....
Pb_Nit1	.....GLPRINEDR HAAQIALMSLDFLDNIRNFKIAHLPEEKLRIRIGMHSDNLTSR.....
Ed_Nit1	.....
Hc_Nit1	.....INLN NNPRHFTDQA ALL.....
Pf_Nit12	.....INLTNP RPTFDQAVLA.....
Pf_Nit1	.....INLTNP RPTFDQAVLA.....
Ps_Nit1	.....INLTNP RPTFDQAVLA.....
Ca_Nit1	.....
Bea_Nit1	.....LNLTNP RQFTDQTTQK.....
Bi_SGC1	.....
Bi_Nit1	.....LNIDN PRHFTDRTA LQ.....
Dg_Nit1	.....LHV LNP RQFTDQATA L.....
Lt_Nit1	.....LNVDN PRHFTDHTA LL.....
Ml_NIT-like	.....LNIDN PRHFTDKTALL.....
Vs_Nit1	.....LNIDN PRHFTDKTALL.....
Oc_Nit1	.....LNVDN PRQFTDKATLM.....
Ocg_Nit1	.....LNIGNP RHF TDKTALL.....
Ocg_Nit12	.....LNIGNP RHF TDKTALL.....

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Hs_SGCY1	.....GTEETKQDDD.....
Ml_SGC3	.....TDMGLDVMVDP ESSVISAEGVRSVEERWKIVV EKIRKFEKE.....
Oc_SGC3	.....
Ml_SGC1	.....
Ca_SGC1	.....OKVQDIPNEDQVTSSKSSNKKQKDDKSFKSMNSKSLGPFS.....
Pf_SGC2	.....SOKKQSNWSMEEGLGGAGDEGKG GHKSKAKSSRSNG.....
Pb_SGC2	IDQSEDCVTIPSGRPTTAPDTSQVSFRTRQNSAAGSRDFINLQE QSTKNVSMVN RSTH
Oc_SGC2	.....NRKKASNW SGT DQTNGVGAEDSKSKS KTPGRSNGGVNGR.....
Ml_SGC2	.....KQPVRTTWPGQPTSTHTNEAKSKNPKAGHSNGGLNSR.....
Vs_SGC2	.....
Hc_SGC1	.....KAKKQSSWSIEEGLRGGATDDLKDGHKSKPKSDRSPKG.....
Dg_SGC1	.....
Bea_SGC1	.....NHDYDDI P RHAGNSNQNKS.....
Hc_SGC2	.....RQKGTNNKQEVPLTPMQAGSGAVNSPAATAAVSGPNVSTS.....
Oc_SGC1	.....
Ml_SGC4	.....ALQRQINPLQKV AELSAESRELNN DDEREHK NKRQTFNVRNV.....
Oc_SGC4	.....PLQKV AELGKEEQGVVEEGARKIKEEEENG RKKKGAIK IENV.....
Hc_SGC4	.....
Pp_SGC2	.....QLQPGGSTSSKPNVKT PGGGPLN KIHPKIS PSEVG SVLAAP.....
Pb_SGC4	.....LLSSYTKEELTEEAKKQVNDVLEQVGH.....
Hs_SGCY3	.....TNSKPCFQKKDVEDGNANFLGKASGID.....
Hs_SGCY2	.....
Ed_SGC4	.....PKPLTPTPAMLAETPDTSEPAANSTPTPPAEPTVPI LPPP.....
Pb_Nit1	ILAHRYP SGPVVAGIVGKMP RYCLFGDTVNTASRMESNGEVNNRIFKKLKNQKQIISCF.....
Ed_Nit1	.....
Hc_Nit1	.....KK.G.....SYGDQPG.AGF MNI VNI YNPSEEKTH.D.....
Pf_Nit12	.....KRSG.....VYSDGGAPPN YM NI VNI YNPDYDKTHND.....
Pf_Nit1	.....KRSG.....VYSDGGAPPN YM NI VNI YNPDYDKTHND.....
Ps_Nit1	.....KRSG.....VYSDGGAPPN YM NI VNI YNPDYDKTHND.....
Ca_Nit1	.....
Bea_Nit1	.....RKK.....
Bi_SGC1	.....
Bi_Nit1	.....KRESNAVTTHATNI VYTVDSNSKKNTVKSSSPNDMVNNL.....
Dg_Nit1	.....KKNSFVEDRK SNNKHL YNNLNHE NNKH KHD THYKEFP.....
Lt_Nit1	.....KRD TSSQ.....ILIDSSKEKKQSIKS KSV VPDI INFNNL.....
Ml_NIT-like	.....KRESNSQF.....YTD TDTKQTVLPKTPQS KDMV K LQQS.....
Vs_Nit1	.....KRESNSQF.....YTD TDTKQTVLPKTPQS KDMV N FNNL.....
Oc_Nit1	.....KKESNNQFY L.....
Ocg_Nit1	.....KKEASNQI.....FLVG DSSKEGGKSPQ..PSPEMVNNL.....
Ocg_Nit12	.....KKEASNQI.....FLVG DSSKEGGKSPQ..PSPEMVNNL.....

Hs_SGCY1	
Ml_SGC3	SKIC SIC . . . . .
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	
Pb_SGC2	WKI A SAG GRPEK S CT DSK L DIS KILA Q VEL K N KM R D E A F R P E Y S I M E L E R I K A M N M W L S
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	ASATTA AVQHSPV.
Oc_SGC1	.
Ml_SGC4	STIC TIL . . . . .
Oc_SGC4	SAIC N I L . . . . .
Hc_SGC4	.
Pp_SGC2	PTPI R ASR Q D E L S C S R L C S I M . . . . .
Pb_SGC4	.
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	PYST S P S R E R S S G S T S S R D K L L V . . . . .
Pb_Nit1	KL C E L V N I E K T L S X L Q Y K N . . . . .
Ed_Nit1	.
Hc_Nit1	KHLQ . . . . .
Pf_Nit12	KHLQ . . . . .
Pf_Nit1	KHLQ . . . . .
Ps_Nit1	KHLQ . . . . .
Ca_Nit1	.
Bea_Nit1	.
Bi_SGC1	.
Bi_Nit1	NHV DSK NH KV H L N N K E F Q . . . . .
Dg_Nit1	.
Lt_Nit1	NH S D K K SH KV H L N N K E F R S . . . . .
Ml_NIT-like	.
Vs_Nit1	NHV DSK NH KV H L N N K E F Q . . . . .
Oc_Nit1	.
Ocg_Nit1	NHV DSK D H KV H L N N K E F P . . . . .
Ocg_Nit12	NHV DSK D H KV H L N N K E F P . . . . .

Hs_SGCY1	.
Ml_SGC3	.
Oc_SGC3	.
Ml_SGC1	.
Ca_SGC1	.
Pf_SGC2	
Pb_SGC2	LHL VAM QFLN MYHLL HAI YNVV SFSS NLL I
Oc_SGC2	.
Ml_SGC2	.
Vs_SGC2	.
Hc_SGC1	.
Dg_SGC1	.
Bea_SGC1	.
Hc_SGC2	.
Oc_SGC1	.
Ml_SGC4	.
Oc_SGC4	.
Hc_SGC4	.
Pp_SGC2	
Pb_SGC4	
Hs_SGCY3	.
Hs_SGCY2	.
Ed_SGC4	
Pb_Nit1	
Ed_Nit1	
Hc_Nit1	
Pf_Nit12	
Pf_Nit1	
Ps_Nit1	
Ca_Nit1	
Bea_Nit1	
Bi_SGC1	
Bi_Nit1	
Dg_Nit1	
Lt_Nit1	
Ml_NIT-like	
Vs_Nit1	
Oc_Nit1	
Ocg_Nit1	
Ocg_Nit12	