

Supplementary materials:

S1

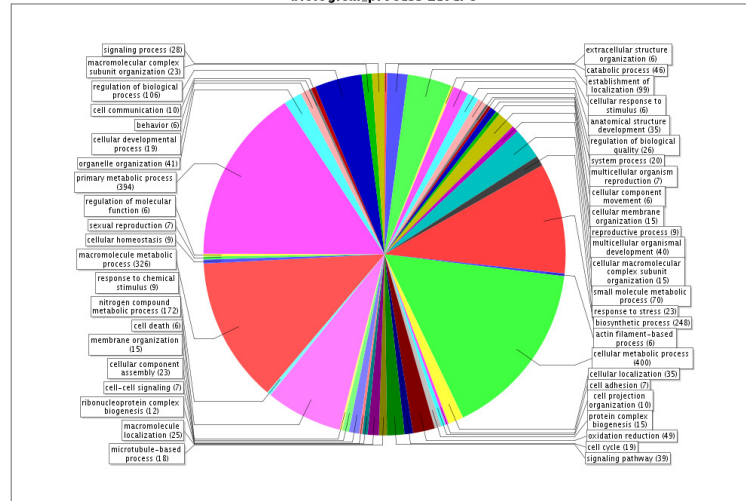
Comparison of male and female gene expression using GO categorization for biological processes (upper) and molecular function (lower), both level 3. Total number of gene objects presented in brackets. The total number of categories for biological processes and molecular function are similar in antennae of both sexes.

S2

Fasta amino acid sequences of annotated *S. littoralis* OBPs, CSPs, ORs and GRs.

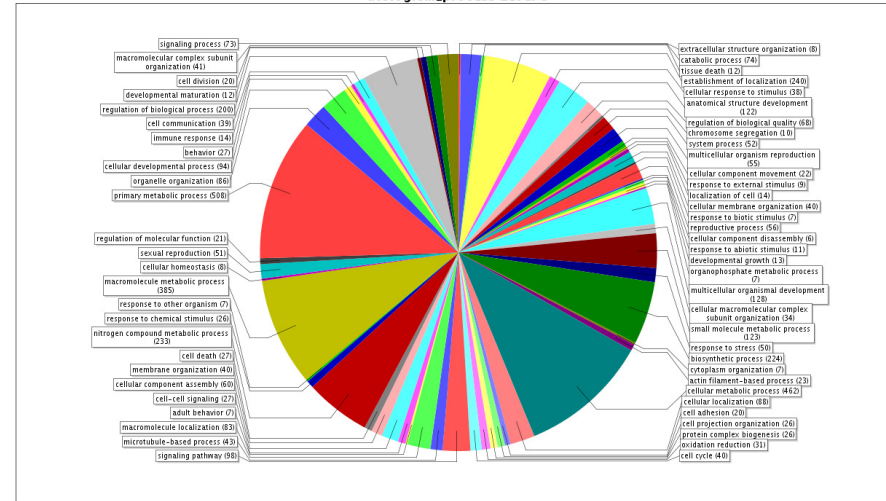
Female

biological_process Level 3

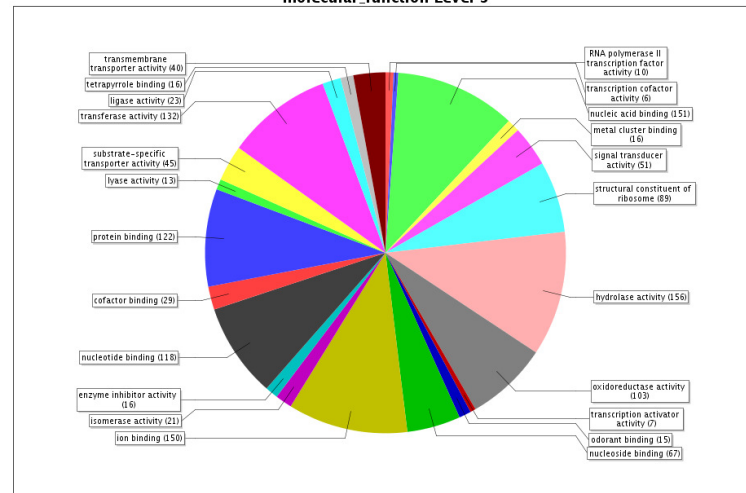


Male

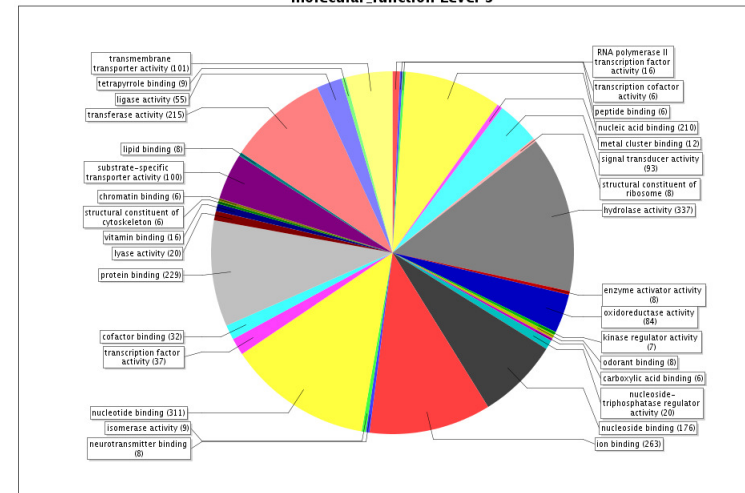
biological_process Level 3



molecular_function Level 3



molecular_function Level 3



>SlitPBP1

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DMYNYWREDYQLINRDMGCMMLLCAKMKLDLMDDDQTMHHGKTEDEFAKSHGADDD
VAKKLVSVIHECEQQHTGIADDCMRVLEVAKCFRTKIHCLKWAPSMEVIMEEVMTA
V

>SlitPBP2

MSLRVALVVAASLLVVVQASQDVMKNLAINFAKPLDDCKKEMDLPDSVTTDFYNF
WKEGYELTNRQTGCAILCLSSKLEILDQELNLHHGRAQEFAMKHGADEAMAKQIVD
MIHTCAQSTPDVAADPCMKTNLVAKCFKLKVHELNWAPSVELIVGEVLAEV

>SlitPBP3

MGSRNVFVALVVLTVMAMRETEPSKDPMKYIASGFVKVLEECKHELMNMDHLIADLF
HYWKLEYTLLNRDTGCAIICMGKKLDLLDANGRMHHGNAQEFAKKHGAGDEVASQ
IVQIIHECEKKHERDDDECLRVLEVAKCFRTGIHELNWQPNVEVIVSEVLTEI

>SlitGOBP1

MLLLLALPLLA AVLPLRADVNVMKDVTLGFGQALDKCRQESQLTEEKMEEFFHFWR
DDFKFEHRELGCAIQCMSRHFNLLTDSSRMHHENTEQFIQSFPNGEVLARQMVELIHA
CEKQHDHEDDHCWRILHVAECFKQACVQQRGIAPSMEMMITEFIMEAEAR

>SlitGOBP2

MATVTSSVMGTAEVM SHVTAHFGKALEECREESGLSAEVLEEFQHFWRDDFEVVHR
ELGCAIICMSNKFSLQDDSRMHVNMHDYVKSFPNGHVLSEKLVGLIHNCEKQFDS
MTDDCERVVKVAACFKVDAKAAGIAPEVAMIEAVMEKY

>SlitOBP1

MFKLCVFLALGFVACHGASNSNP GTPNANPGTYCGVTPDNIYRCLNNPRVVTPEVST
KCGSQFTECEKMT CIFRELKWSKRG AIDKAKV RAYFDQYETEHPEWAQAVQHVKAF
CLASELRAQGVFLNCPAYDIMQCVLASFIKHASPSVWSTATDCAYPKAYAADCPCVCP
SDCYSPQIPYGCNACYTQPRTV*

>SlitOBP2

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LDVIKEEHTMPAQRRRD KREVPFTHDEKRIAGCLLCVYRKVKA VDGYGFP TLEGL
VGLYSDGVNERGYFMAVLEASRECLMKNHDKFSRTVPMDNGRNC DISFDIFECISDR
IGEYCGTSGL

>SlitOBP3

MKSFFVICIVFVVGVCATEKGNKIAS ECIKESGVKSDVLAEAKKGNLGDDPAFKEFT
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KCYQHGT KSHIMFAS

>SlitOBP4

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PHQTAWNYVKCYHEKDPKHAIFL*

>SlitOBP5

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PTYLQALNESGSFIDETDKTPKCFIRC VFENVGIVSEDGKQFNPARAAVIFAGERNGKP
MEDIADMTALCATDRQETCPCDRSYKFLRCLMSMEIERYEKS*

>SlitOBP6

ESKFGEIVKRTVIATAHTCMDHVNATAKDLEHLRDEPPYPETSACIVKCLLEKVKYM
RKQTN

>SlitOBP7

MFTEALPLFVILVAVTHGGKNKPVFSDEIKEIIQTVHDECVAKTGVAEEDITNCENGIF
KEDAKLKCYMFCLLEEASLVDDDDTVDYDMLVSLIPDEYYERTTKMIFACKHLDTP
DKDRCQRAFEVHKCSYEKDPDLYFLF

>SlitOBP8

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EVDLSGPRVSVRSDYYGEGQFNALKIVAYGQVNTTMTDLVYTWKLAGVPEKNGTET
YIRIKDFYMRPDVGSLVTHFRNDNPESRELTDLGTRFANENWRMLYKEFLPYAQAN
WNRIGVRVANKLFLKVPYDQLFPTSS

>SlitOBP9

MCLVKYHVLVLCVILVGSYALNCRSSGGPKEAELKNIYKKCLKMQEGKNSS
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EDFPQS
DEYGGDMGQYNNNNYYSTTQSSRRYKRERRPSNSGQRSQYNPNNHKISGYEDNFRSD
ERN
TDNNSSKETDNKSCALHCFLENLEMTGEDGMPDRYLVTHAITKDVKNEDLRDFLQE
SIEE
CFQILDNENTEDKCEFSKKLIDLSVRE

>SlitOBP10

MKEGNRYSHERRITNDSGDQLMVINATDDDDYSGYSGNMGEKLLTSVPRPATPSNNI
NKNINRRTKRNEPLLNRPSDQCLSQCVFANLQVVDSKGIPREAEWLNKVQSSVTSQ
QSRSAHDQIQACFQELQSEAEDNGCSYSNKLRLCLMLRFSRDKVDGKGNAKKSSTE
QTG

>SlitOBP11

MSKFTCLVLCVAVSLNGVHATAEEKAAFIEAVKPYVQECSKEHGVTPEDIKSAKAA
GNADGINSCLSCVYKKADEVINEKGEYDVKALEKLKKFVSNEDDYAKFANIGKKC
ASVNEKSVSDGEAGCERAALLTSCFLEHKSEISA

>SlitOBP12

MSVVRCSFLVALFCFVSVNAMSGDEEAGIKEALRPFVQECADDFGITEEQFEEAKKK
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KINDEDVSDGDKGCDRAKLLFECIAETKKKME

>SlitOBP13

MITSSLLVLTAVVQVLFAQQPVFESGPPEPWGPPQRPARRQFLPRIPKRCWVPPQRI
NVYNCCPIPTLYPDEDMQSCGFECTSGNTDQPKPVFRPEGTCKEGYCVMGKFDLLF
ANNSVDFVKFREYLDNWAESYPEFANAIRIAKQECAQDGGPEVPPICEPDKLFLCLTS
TIFWNCKLRDGDGCAALQEHMNECKQYYTRQMEPTMKDIEVR*

>SlitOBP14

MDQKRICLFVIAMFLASGSDAMSRQQLKNSGKMLKKNCMNKIGVTDDQVGSIDKKG
FIEDRKVMCIYACIYELTNVIKNNKLNIEASIKQIDLMYPPDVKESAKAAVEKCKDV
QKKYKDICEASFYAAKCMYEEKPEDFIFA

>SlitOBP15

MFNNCFVYSMTREQIKNSGKLIKKTCSAKNDLTEDEVKDVDKGKFIEKKDFMCYIAC
VYKMGQTVKGSTINHDMMLRQVDMMPNDMKAPVKAAIEHCRPVAKNYKDLCEA
SYWTAACIYDFDPANFMFP*

>SlitOBP16

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DLLDEIKTNCINGDLNNYGPPEFCDFIKIKHCVTLHMMNHCSEWSDDGNCKVVKELV
GKCAKVI*

>SlitOBP17

MRTFRLLCCILSIFIFDQSYGMTRQQLKNSGKLMKKSCMPKNDVTEDEVGDIEKGF
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TTKKYKDLCESSYWTAKCMYDYDAQNFVFP*

>SlitOBP18

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AITACRKVADAHKDICDASFHVTKCIYNHN

PSIFYFP*

>SlitOBP19

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YDMKGQLFVPIEGNGGLYSKVPKIQINAEVDLNTKQGKDGDHWIVKSWRHTFELK
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EDLSL

>SlitOBP20

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QRGADHCDTAFRTQQCWQNANKADYFLI

>SlitOBP21

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LIPDEYYERTTKMIFACKHLDTPDKDRCQRAFEVHKCSYEKDPDLYFLILRREQLASR
DDCVAISGIN*

>SlitCSP1

MKFVLVLCLMAAAVLAEDEKYTSKYDNIDLDEILTNKRLLTAYINCIMERGKCSPEGK
ELKEHLVDAIETGCSKCTEAQEKGAYKVIEHLIQNELDTWHELTDKYDSSGKWRKTYE
DRAKANGIIPE

>SlitCSP2

MKVALLTLCFALGVLAQDMYENANDNFDISEVLGNERLLNSYAKCLLNKGPCPTPEVK
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AWKDFLQE

>SlitCSP3

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KNLPDAIKNDCKKCTD

>SlitCSP4

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YRAKYLASKEAKDEKASNVTNSSEDTNVVSKE

>SlitCSP5

MKSFIVLCLFGLAAVALAKPNGSTYTDTRYDNVNLDLGNRRLLMPIYKCIIEEGKCT
ADGKELKSHIREALEQNCAKCTDTQRSCTRRLVGHIIINNEQESWNRLKAKYDPESKY
TVKYELELRKLKQ

>SlitCSP6

MNFLVLSIVVTMAAFVAAETYTDTRYDHINIDEIENRKLVPYIKCTLDQGRCTPEGREL
KAHIKDAMQTSCSKCTEKQKKGARKVVRHIRAKEQEYWKQILAKYDPEDQYKENYET
FLAAED

>SlitCSP7

MQIKYALVLCVAAVSVAQTQRPPVSDTALDDALQDKRFIQRQLKCALGEGPCDPIG
KRLKTLAPLVLRGACPQCSPQETKQIQRTPYVQRNYPQQWAKIVRQYAG*

>SlitCSP8

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TAKYEKELKKIKA

>SlitCSP9

MKVVFLVCVLAADVYAHPHESHYTDKWDNIDLDEILNNKKILASYVKCCLDQGKCT
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YRKMYEDEYKSVKH*

>SlitCSP10

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TGDFTRYFEEFLAKEHYNTIPGSGSALPTSSPLAPPRVPQSPPATNPTPGPTEPTPPRPIVL
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>SlitCSP11

MKVLVALSVFVVLAAAAPLTKDELATLEAFDYDSLFADEEKRKVVFDCLLDKGDCGP
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>SlitCSP12

MKCIYVLSILLVFVAVQADEKYSSENDDLIDAVVADVDALKGFVGCFMDAVTCHA
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HTLEANVANS*

>SlitCSP13

MKADCVLIMTLMAVVAADFYNISKYDSFDVQPLENDRILLSYTKCFLDQGPCTPDAK
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FLAEQE

>SlitCSP14

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GKALKETLPDALEHECSKCTEKQKKSSDKVIRHLVNKRPLWQELSGKYDPENIYQER
YKTQLDAVKRH

>SlitOR1

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NLYELLNYLDKNFKYRSARGLTNMTMEQSCMTARRFGRIYTACTMFSVTMYATLPV
IVHLWTKEPIQSWIYMDVTQPPFFEFVFMLSCLAQMYVGLAMGQFGVFFASNSILICE
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KRMTHIYVDA

>SlitOR2

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EVAPRLPLKAWYPFNAMSGTTYIAFAFQVYWLLFSMAIANLMDVMFCSWLIFACEQ
LQHLKAIMKPLMELSASLDTYRPNTAELFRASSTEKSEKIPDTVMDIRGIYSTQQDF
GMTLRGAGGRLQTFGQQNNNPNGLTPKQEMLARSIAKYWVERHKHVRLVASIGD
TYGTALLFHMLVSTITLTLLAYQATKINGINVYAFSTIGYLSYTLGQVFHFCIFGNRLIE
ESSSVMEAAAYSCQWYDGGSEEAKTFVQIVCQQCQKAMSISGAKFFTVSLLDFASVLGA
VVTYFMVLVQLK

>SlitOR3

AFLAFHRVLSFAGISIFAKQNWNNSHRWLAHQTFNFIIGVLCFIFTTGFFVVTNVSDFLLCI
QGACIWTGTGVIMTITLGVCLIFRKEFRNFLEEMVFRDHMLEMPLIDHILLVSPRGEKIQ
ELRNLTGSGEKLKFKYTTLLLSYVANVFLCATLYLCSPVYGMLVREDKSLRLLAFD

MWFPWSLEDYTVYIISFIFHAYAGYLCCIAYPGLQSTIILLGQLIRQTRILTFILLHMN
ELALEVTGVQDERWQDICTLILSQCDHYVKIKR

>SlitOR4

MVNTFRGRLLNIRDRLKQNSCVNLVWLINFLPNLAGFPLLSQKFKFFFWIVHTVLLFY
VYLLGTAMYQTYFAEDFVDSINSFFNISVFILIGNDSWWLISKRNDLNDLLKMVKK
DDLIESGRFQDVHQKLMKSIKIIVMCYMFHFVNDVMIFIPSRRTIGMDDFSTVSCVGM
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SKSHETYYVVKDRLKNIVFRHVLALHTVRKLEDIYSVAIGIGFGLDAISMCLFFVLPLD
VCLNFAPLIYHSLFIFFLYCFQGQRLTTASEKFEMAVYCCGWENLRVKERRQVLLML
KQAQKPVIVYAARVIPRIHTFASTMQSIYKFVTIFKV

>SlitOR5

MTNQKDLDFENIFKITTTALHISGSHPSVPKDLKWALKFTILHGTALGFVTVIYSIIYH
DLKEQNFBVQICKDCVVFVLFVTSVLSQYCVLLIHQDNLVLLIKNINSYEQMQNLSK
EKQLMDKYMNLGAKVCRHWFVLVLVTCLIFLIKSVGFMCYYYLINDIKYIPYYDIKY
PEFIEERKNENFSVFLITYCLMFYFALYSVLIYVAYVPLGPVFMHASGLLEVKNRID
DLFSDSNPEKIREKLKDVVMKLQYIYSIVDDMKTIKFRFGYEVSLKGTAVLLPVTFYAV
LEAAKNGEISMEFISFIAGGIVISAVPCYYSDLLMEKGEAVRLSLYMCGWEQHYDRRT
RTTLQLMLLRALRPIAIQTLFRTLCLDALTDLFQQSYGIFNLMNAMWS

>SlitOR6

MGLKKFLFEDES VQGITA PTDYLYVKLLRMTLR IATWPQTELGEKEPVYLN VFLKYF
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EFFTKMHLFYFKDISEHAMETHKRVLHLSHLFTLWLLFQMLFGVPLFNLVPMYYNYA
AGRYKPGGTQNSTFEHSMYYQYPFDTLTEIKGYIVANIINWILSSLCVIWFCMCDLILL
LMVFNIWGHRLMLTLPLNNFPRPGVETTIQ

>SlitOR7

MPKPLLFDGSLDKLGVLFRYSGMNLEKDIITPMDTIKHRWLYTLNYFSVLSAEIAGIY
YIITGIIQGKS FIEVTSVAPCLTF SLLALIKCSYHHIYEKNIKELINLLRHLEKENDRTEC
ADKQEIIDE EAGFLNKVINVLV LNCCMIVVFDMT PMVLI AVKYYKTKQFEMLLPYL
DVFSFIPYELVYWPFA YVHQIWSKCMVLLSMAAADYLFF

>SlitOR8

MIVSYLSSTLLILSPLISHLILGVELLLPICRYAFISDEYRLMFIYPIYLYQIVSIHFHVLY
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QCIIHFIKVC RFCELIEDAFSATL FVQYSAASCIICVCLCRFTMPAEMGYIVFLASYMSL
MVSQMMAPCWL GTRLMDKSQLLAFSVYNCDWTSRSRQFKSNMRFFVDRANKPLSI
TGGKMFNLSLGTFTSIMNSAYSF

>SlitOR10

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VWGEIDEVSEASYLLFTQASLCYKSTTFMINKKS LLELLDIMDS DIFKPKSAEHEKILA
AQALKIKRLCLF FLTSATTTCTLWAMIPLFDDASKRSFPFRICKQETLTLLFRMPVTPL
KSPDYELGYLYQMISIYISAFPLHISGQRRRVYDHV

>SlitOR11

MFNLDTYAGDAVVGISGPM DYKYMKVLR FVLRIISGWPGKALGEKTLKIEGMGHAY
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AKIFIQKVHLFYFKDKSDYAMSIHVTVHRISYFAAIYVSIMLSIAACLFNLIPMYNNYA
AGNFASF DN LQNKTYEQAISCLYPWNFETNFKGYLVATLSGWYGT VLCGS

>SlitOR12

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WFISGIANKKSFTELTYVSPCITLSFLANFKCFFLNEDTVDKLLETLELEMNERSRP

RHKDKDAIMVHEHKFLTNLISFLNVFFCGLIVAFaipvTLTIFIYVTTNEVDLQLPFLII
YPFDAFQLKNLALGVSSPNLVRSSSYQWSRCSRLSLLHILLKHK

>SlitOR13

MDIKLSSVKIFSDGSDLEGIEKVEDILYLRILKKIMWVIDGWPKEAHKSQFFRYYYICIL
DMVSLIPGTLYLKINTGKIPSFELGHTYITVFMNAIAALRTVLVLTRNYNEIIFYFLKEV
HLFNFRKSKYAYETHILVHKISHFFTMYVFMLMCCGILLFNLTPIYNSYAAGMFRDE
PPPNATFDHAVYFALPFDTSTSFKGYAIVSLYNWYICITCSTYFCIIDLTIFIMVFHLWG
HMRVLSYNLENFPKPASVLAANDTHAYTPCENKYNEEELVEVFNRLRDCIQIHSPVI
TSPS

>SlitOR14

MTETRPKHYFGFHYRILRFLGLGWVHHPEEGNTSNFPGWYLYYSIATQLVWVAGFV
GLETIDPFVGEKEMDRFMFSLSFVITHNLTLIKLYIFFFKNADIQEIVHTLEIGIYDYYQ
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TLPQPIYIPWDYQKDASYIPTFVLETVGLLWTGHIVMTIDTFIASVILHMGSQFEILHEX
NNNCV

>SlitOR15

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GFRLGWRSYLVLSNIAAYSSQVIVPIFLDILRETKSELPICKYYFLSDEDRESHFLFWFIY
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KRFHKLLRHYEVILRYCDTVQDTLNVTLFFQFGVASIICVVMCGLLLPSSTETKVFLV
MYLFTMTLQIFVPGFLGTQLTYGSEGLVTAAYNSEWIPRSESEKSSLKLFREARAPV
VISGLKMFPLSLITFTSIMKTAYSFFTILIRNVQEA

>SlitOR16

MYIKIVRFMLVIVGSWPRREIGEPEPRYQTIMLKLFFFSVVNAALYGSISYVYMHTSEL
SFLEIGHMYIVILMTANDMPRVFTLTLSQKYRDLAKEFLTkiHlFYFKDHSPYAMLTH
KKVHLVCHLVSLCLLSQMLTGLSLFLNIPMYTNYSSGRYASGGTQNSTFEHSMYFSY
PFNTST

>SlitOR17

MSVCAGSVAPHVRCLRRVGFCRWGAAAPANPLLATAARFYHVFALAATSTYVLQQ
LIYAYQERSDMDKLSQVMFVLLCHVTCVAKQVAFHVDADRIDELIARLDEPLLNC
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DHNVVFGAVLLYSFYTTNLVAIGNTTMDAFMATILDQCKTQLRILRLNFETLPERAR
ALQQSGGGVYEASLQRLFVDCLLHYNITETCTVLHDVFVAVPLLIQFGVGGWILCMA
AYKIVSLNVFSIEFASTTLFIICILIELFIFCYYGNEVTVESSRVSESLYSMEWARAGLSF
RRSLVLVMERAKRPLRPAAGRVIPLSLDTYVTILKSSYSFYAVLRQTK

>SlitOR18

MEMKSDILTQKKYKTFNDTFKLCAFSLAFAFLYPNRNTALKRCITITLIVTFCGGQLF
WFITYTFKCLYTLDLYNFARNMTLAVVLILFFIKTYYAIYATQKFATLLDKISEDLL
EANNLGERQQKLYDEHITIAKFGEISWLLVPVLMSALFPIYAGTLMSESITDDYQRRM
VHDMELLYVEDIQSETPFFQCMFAYNCVQCQVVLVPNYCAFDGSCFIATTHIQLKLKL
MVLKVHDAFKYSKNKYELRMKMNEAIRDQQEALDFYFPPKMCLGPWLFAVLMPDF
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>SlitOR19

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ATMGDFPPDEKRDSVSFAVSHTIAMIKIFSVIANKSLIKKLNHKMVTVCERYEENTLM
AEKYKIMKINVLAIFYVTYASAFFVFEGLRKMLTGSHFVTVVTYYPKFEDDSIGATS
ARVLATVILYILMITMIMSVDSFTMIYLYMYKYKFITLKQYY

>SlitOR20

AEELIFYFTNVGALSKALAFIFLRDKVKKMLYMLESEMFQTDNPeeVKLIEKAKEKSL
FYWKITFGLSVSANTVNVFLPFVLHLIFSikleFPVCrySFIPEQYEAIFLYPAYLYQSIG
ITSHMLYNVNIDTFLLGVMFLAMAQLDILDRKLRKVTDVcVNVdAPrgSIDKMIDDQ
NAVLEINKCIKHYDAVCEYCKLIQEAfSEILFVLFSSGSKICMCLFRFPMPAETQYFV
FLTLYIVVMTLQVMVPCWFGSRLMEKSSQITFAVYDCDWTPRCRRFKSNLRLLLVERA
NRPIIIKGGKMFLLSLATFTAIMNSSYSFFALLRNVQTR

>SlitOR21

MYKLGIAlKA VHNDCEAEQKMITRSKFFSWALIFNCVMSVIMYTIEGVLRVIRAGDT
FNTVITAWPDVHDRSVLSNIGRTVIYITWWIYLTRIFSVYSLVICLTIAVSHQFKNLKS
FYSLSKIFENDNLPQTEKEQEYEKAfKVGISMHSETLKCTDEIQTICREVFSGQIIFNLT
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>SlitOR22

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VVKMNEEFiYVCSLGPryRKPFLEGQLLIWQLCYAWFGFVSFVGGLYVVFPLVGLIY
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>SlitOR23

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QITSKVDIWIWSISDLLVDIHPAGSEESVYFSYLIKARMRDILLHHQSMYSLMEDYAV
VYKKMLMFEQKCCGSVVCLTAYCIAEAFDAGEFQAIIllLCIGTTVLHFVPCYFCTFL
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NAYSLENMLRQANI

>SlitOR24

MRVLShVWRRISQSKALELAGPLETAFFASVYRLSFVVGLSTSDDYLLYTMYSsFIRII
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GYNMFTWYLMCRWCeeITIKSQRIGQSAyFSGWESGISLAPGARATIVLVIARANKPL
VFVAGGMYTSLSSYTTLVKASYNALNILLTMRHE

>SlitOR25

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KTSYSALTvLLRFRHD

>SlitOR26

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SKMFILVLAysSYVTTLVGIANttMDAFMATVLNqCKTQLRILRMNFECLPLQAVEV
LKTSPGQSYDAVLMKLFKECLLHYEKITKTAKMLQDIFGTAILHFGIGGWILCRAAY
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>SlitOR27

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>SlitOR28

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>SlitOR29

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VITDKQCEEVVRQLHGIHVMLIKYSRLFNSLLSPVMFFYMVMCMLCASAYQLTSA
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>SlitOR30

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VVQYAKRGVTVCKFWLVFGFGTSTIFPIKALVLTGYNWYWKGEFVYVHVFDLIYPQPI
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ANI

>SlitOR31

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FSLALAYMTVLITFQAYGNVTMDCTIVAFYAQAKIQLQMLRYNLEQLVEFRNIKKFN
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>SlitOR32

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>SlitOR33

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>SlitOR34

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>SlitOR35

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>SlitOR36

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GRNLPENYFLIYGLEPMLETPNYQIAYFMMIASVFFVCYVPASVTAFLIVITGYAEAQ
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>SlitOR37

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QNH SKIMEFLYILSETYKWPSIIPILGILL

>SlitGR1

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RR

>SlitGR2

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YERIMILRSIRRFDDYIYAILFVIFLVP HFWIPFVGWGV AHQVAIYKTNWGKFQVRYC
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ALRYINCQRIKI

>SlitGR3

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LVSYVLYLSLHKVQILRTAEGKFEEAVIEYLFTVYLFP MIAVPILWYETRKIADVLNG
WVEFEVVYKQLSGRTL PVKLYKKALAI AIIIPILSTTTVIVTHITMVHFKPMQLVPYVF
LEILTYMLGGYRYLLCQTL SICAHILAE EFQSALHP

>SlitGR4

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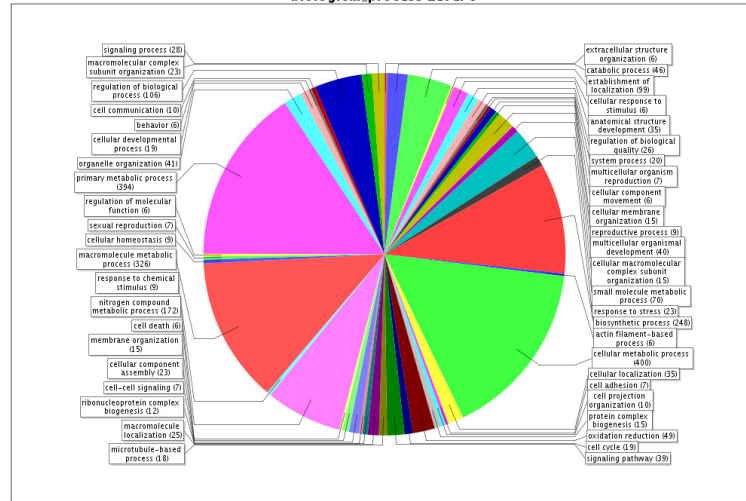
>SlitGR5

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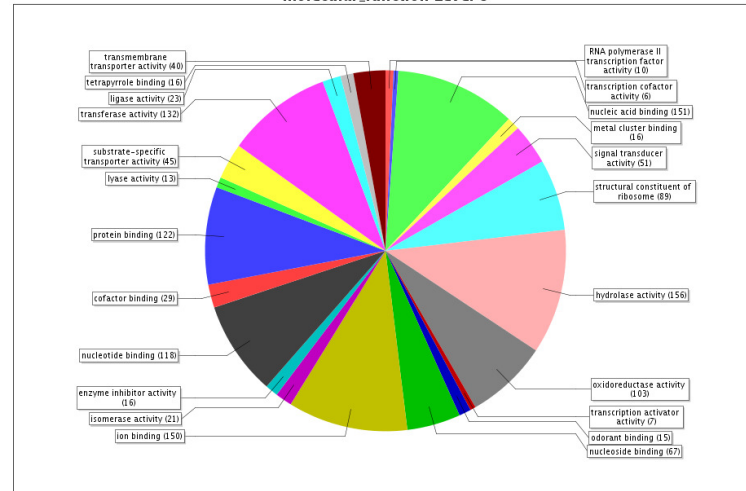
S1

Female

biological_process Level 3

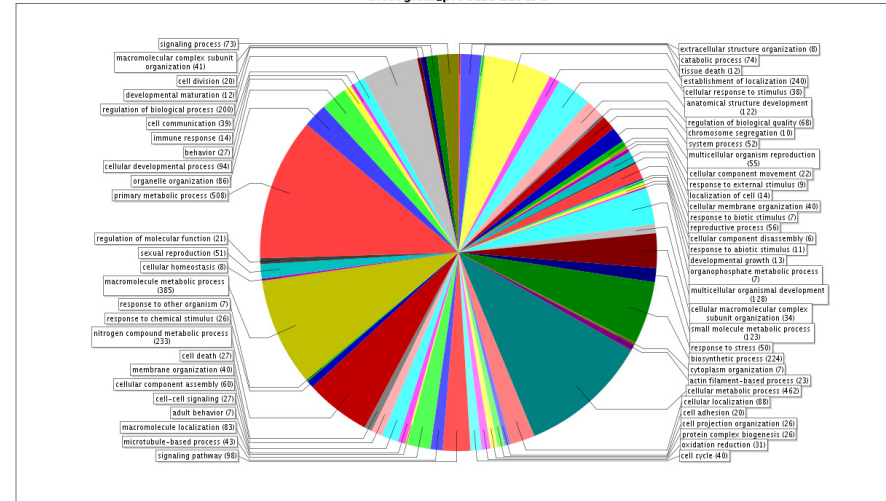


molecular_function Level 3

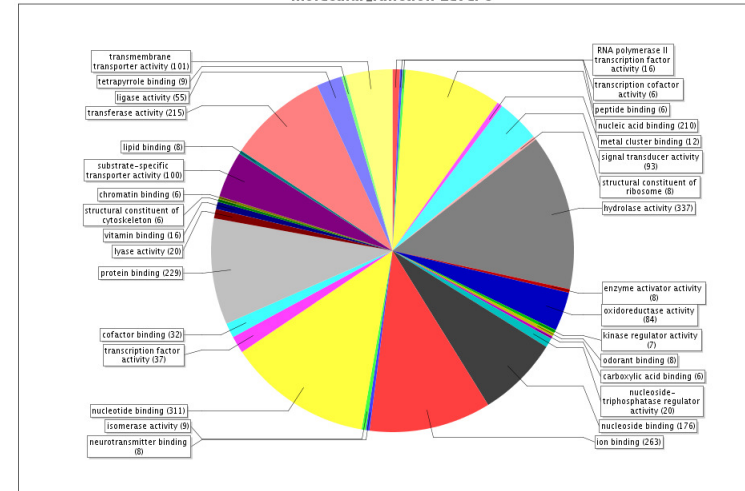


Male

biological_process Level 3



molecular_function Level 3



S2

>SlitPBP1

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VAKKLVSVIHECEQQHTGIADDCMRVLEVAKCFRTKIHCLKWAPSMEVIMEEVMTA
V

>SlitPBP2

MSLRVALVVAASLLVVVQASQDVMKNLAINFAKPLDDCKKEMDLPDSVTTDFYNF
WKEGYELTNRQTGCAILCLSSKLEILDQELNLHHGRAQEFAMKHGADEAMAKQIVD
MIHTCAQSTPDVAADPCMKTNLVAKCFKLKVHELNWAPSVELIVGEVLAEV

>SlitPBP3

MGSRNVFVALVVLTVAMRETEPSKDPMKYIASGFVKVLEECKHELMNMNDHLIADLF
HYWKLEYTLLNRDTGCAIICMGKKLDLLDANGRMHHGNAQEFAKKHGAGDEVASQ
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>SlitGOBP1

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>SlitGOBP2

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>SlitOBP1

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>SlitOBP2

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IGEYCGTSGL

>SlitOBP3

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>SlitOBP4

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PHQTAWNYVKCYHEKDPKHAIFL*

>SlitOBP5

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MEDIADMTALCATDRQETCPCDRSYKFLRCLMSMEIERYEKS*

>SlitOBP6

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RKQTN

>SlitOBP7

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DKDRCQRAFEVHKCSYEKDPDLYFLF

>SlitOBP8

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>SlitOBP9

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EDFPQS
DEYGGDMGQYNNNNYYSTTQSSRRYKRERRPSNSGQRSQYNPNNHKISGYEDNFRSD
ERN

TDNNSSKETDNKSCALHCFLNLEMTGEDGMPDRYLVTTHAITKDVKNEDLRDFLQE
SIEE

CFQILDNENTEDKCEFSKKLIDLSVRE

>SlitOBP10

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QTG

>SlitOBP11

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>SlitOBP12

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>SlitOBP13

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ANNSVDFVKFREYLDNWAESYPEFANAIRIAKQECAQDGGPEVPPICEPDKLFLCLTS
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>SlitOBP14

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QKKYKDICEASFYAAKCMYEEKPEDFIFA

>SlitOBP15

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SYWTAACIYDFDPANFMFP*

>SlitOBP16

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GKCAKVI*

>SlitOBP17

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>SlitOBP18

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PSIFYFP*

>SlitOBP19

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>SlitOBP20

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>SlitOBP21

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>SlitCSP1

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DRAKANGIIPE

>SlitCSP2

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AWKDFLQE

>SlitCSP3

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>SlitCSP4

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>SlitCSP5

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TVKYELELRKLKQ

>SlitCSP6

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>SlitCSP7

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>SlitCSP8

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>SlitCSP9

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>SlitCSP10

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>SlitCSP11

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>SlitCSP12

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>SlitCSP13

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FLAEQE

>SlitCSP14

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>SlitOR1

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NLYELLNYLDKNFKYRSARGLTNMTMEQSCMTARRFGRIYTACTMFSVTMYATLPV
IVHLWTKEPIQSWIYMDVTQPPFFEFVFMLSCLAQMYVGLAMGQFGVFFASNSILICE
QLDLLCCSLRNARYTALLQRGVKHAALVASHSDIQRDEDHNYIYNFSEIKDSMYHYD
KRMTHIYVDA

>SlitOR2

MMTKVKAQGLVSDLMPNKLMAAGHFLFNYHAENGGMSGLLRKIYASTHAILITIH
FACMGINMAQYSDEVNELTANTITVLFFTHTIKLGFFALNSKSFYRTLAVWNQSNH
PLFTESDARYHQIALTKMRLLYFICGMTVLSVSVSWVTLTFFGESVRLITSKETNETLT
EVAPRLPLKAWYPFNAMSGTTYIAFAFQVYWLLFSMAIANLMDVMFCSWLIFACEQ
LQHLKAIMKPLMELASLDTYRPNTAELFRASSTEKSEKIPDVTMDIRGIYSTQQDF
GMTLRGAGGRLQTFGQQNNPNGLTPKQEMLARSIAIKYWVERHKKHVRLVASIGD
TYGTALLFHMLVSTITLTLLAYQATKINGINVYAFSTIGYLSYTLGQVFHFCIFGNRLIE
ESSSVMEAAAYSCQWYDGSSEAKTFVQIVCQQCQKAMSISGAKFFTVSLLDFASVLGA
VVTYFMVLVQLK

>SlitOR3

AFLAFHRVLSFAGISIFAKQNWNSHRWLAHQTFNFIIGVLCFIFTTGFFVVTNVSDFLLCI
QGACIWTTGVMITITLGVCLIFRKEFRNFLEEMVFRDHMLEMPLIDHILLVSPRGEKIQ
ELRNLVTGSQEKLFKYTTLLLSYSVANVFLCATLYLCSPVYGMLVREDKSLRLLAFD
MWFPWSLEDYTVYIISFIFHAYAGYLCCIAYPGLQSTIILLGQLIRQTRILTFILLHMN
ELALEVTGVQDERWQDICTLILSQCVDHVYVKIKR

>SlitOR4

MVNTFRGRLLNIRDRLKQNSCVNLVWLINFLPNLAGFPLLSQKFKFFFWIVHTVLLFY
VYLLGTAMYQTYFAEDFVDSINSFFNISVFILIGNDSWWLISKRNDLNDLLKMVKKN
DDLIESGRFQDVHQKLMKSIKIIIVIMCYMFHFVNDVMIFIPSRITIGMDDFSTVSCVGM
EPLTSSPNRQACMVVLAALQELTAIVAVCSYDVALLFLFSHTTAVFQILYQDMTEFANI
SKSHETYYVVKDRLKNIVFRHVLALHTVRKLEDIYSVAIGIGFGLDAISMCLFFVLPLD
VCLNFAPLIYHSLFIFFLYCFQGGQRLTTASEKFEMAVYCCGWENLRVKERRQVLLML
KQAQKPVIVYAARVPIRIHTFASTMQSIYKFVTIFKV

>SlitOR5

MTNQKDLDFENIFKITTTALHISGSHPSVPKDLKWALKFTILHGTALGFVTVIYSIIYH
DLKEQNFVQICKDCVVFLFCVTSLQYCVLLIHQDNLVLLIKNINSYEQMQNLSKD
EKQLMDKYMNLGAKVCRHWFVLVLVTCLIFLIKSVGFMCYYYLINDIKYIPYYDIKY
PEFIEERKNENFSVFLITYCLMFYFALYSVLIYVAYVPLGPVFMHASGLLEVVKNRID
DLFSDSNPEKIREKLKDVVMKLQYIYSIVDDMKITFRFGYEVSLKGTAVLLPVTIFYAV
LEAAKNGEISMEFISFIAGGIVISAVPCYYSDDLMEKGEAVRLSLYMCGWEQHYDRRT
RTTLQLMLLRALRPIAIQTLFRTLCLDALTDLFQQSYGIFNLMNAMWS

>SlitOR6

MGLKKFLFEDESQQGITAPTDYLYVKLLRMTLRITATWPQTELGEKEPVYLNVLKYF
YLVATIGCQIGSYCYLRTYSDELTMMEAGHNYIMIMMTFIDISRTSLTFSTEYRKLC
EFFTKMHLFYFKDISEHAMETHKRVHLISHLFTLWLLFQMLFGVPLFNLVPMYYNYA
AGRYKPGGTQNSTFEHSMYYQYPFDTLTEIKGYIVANIINWILSSLCVIWFCMCDLILL
LMVFNIWGHRLMLTLPLNNFPRPGVETIQ

>SlitOR7

MPKPLLFDGSLDKLGVLFVRYSGMNLEKDIITPMDTIKHRWLYTLNYFSVLSAEIAGIY
YIITGIIQGKSFIEVTSVAPCLTFSLLALIKCSYHHIYEKNIKELINLLRHLERKENDRTEC
ADKQEIIDEEAGFLNKVINVLYVLNCCMIVVFDMPMVLIYVYKTKQFEMLLPYL
DVFSFIPYELVYWPFAVYVHQIWSKCMVLLSMAAADYLF

>SlitOR8

MIVSYLSSTLLILSPLISHLILGVELLLPICRYAFISDEYRLMFIYPIYLYQIVSIHFHVLY
NVNVDIFFFGLMVLAIQDLDRKLRKVTEGNKVEDTDSEASRSPIDKNKEDVMKIN
QCIIHFIKVCRCFELIEDAFSATLFVQYSAASCIICVCLCRFTMPAEMGYIVFLASYMSL
MVSQMMAPCWLGTRLMDKSQLLAFSVYNCDWTSRSRQFKSNMRFFVDRANKPLSI
TGGKMFNLSLGTFTSIMNSAYSF

>SlitOR10

MEAEKNTTLFLGRPCKILTAHGVWPHPNNYIILRKLYMLFVMWTQYSFLLFEIIVN
VWGEIDEVSEASYLLFTQASLCYKSTTFMINKKSLELLDIMDSDFKPKSAEHEKILA
AQALKIKRLCLFFLTSAATTTCTLWAMIPLFDDASKRSFPFRICKQETLTLLFRMPVTPL
KSPDYELGYLYQMISIIYISAFPLHISGQRRRVYDHV

>SlitOR11

MFNLDTYAGDAVVGISGPM DYKYMKVLRFLRIISGWPGKALGEKTLKIEGMGHAY
YNTILSLIYLALGIAYLKKNNAHRFGFLELGQLYIVLLMNMLSTSRAFTLCLSEKYRTV
AKIFIQKVHLFYFKDKSDYAMSIHVTVHRISYFAAIYVSIMLSIAACLFNLIPMYNNYA
AGNFASFDNLQNKTYEQAISCLYPWNFETNFKGYLVATLSGWYGTVLCGS

>SlitOR12

MEEEP LLINKTIKKIEIWLPTTGTNVKSTSKTRMDTIKSRAIYIINFFWLNMDLGGAVV
WFISGIANKKSFTELTYVSPCITLSFLANFKCFFLFLNEDTVDKLLETRELEMNERSRP
RHKDKDAIMVHEHKFLTNLISFLNVFFCGLIVAFAGPVTLTIFIYVTTNEVDLQLPFLII
YPFDAFQLKNLALGVSSPNLVRSSSYQWSRCSRLSLLHILLKHK

>SlitOR13

MDIKLSSVKIFSDGSDLEGIEKVEDILYLRILKKIMWVIDGWPKEAHKSQFFRYIICIL
DMVSLIPGTLYLKINTGKIPSFELGHTYITVFMNAIAALRTVLVLTRNYNEIIFYFLKEV
HLFNFRRKSKYAYETHILVHKISHFFTMYVFMLMCCGILLFNLTPIYNSYAAGMFRDE
PPPNATFDHAVYFALPFDTSSTFKGYAIVSLYNWYICITCSTYFCIIDLTIFIMVFHLWG
HMRVLSYNLENFPKPASVLAAANDTHAYTPCENKYNEEELVEVFNRRLRDCIQIHSPVI
TSPS

>SlitOR14

MTETRPKHYFGFHYRILRFLGLGWWHHPEEGNTSNFPGWYLYYSIATQLVWVAGFV
GLETIDPFVGEKEMDRFMFSLSFVITHNLTLIKLYIFFFKNADIQEIVHTLEIGIYDYYQ
NDDKNRKTVRVSKIITAAFIFFGWVTIGNGNVYGTIQDLKWKSLVATLNDSDVRPVR
TLPQPIYIPWDYQKDASYIPTFVLETVGLLWTGHIVMTIDTFIASVILHMGSQFEILHEX
NNNCV

>SlitOR15

MPSDQSKMFDNSFRIAKIFGIWPGLKPSRYYKFYSFIYLFATFVCYNLLLTLNLLYTPR
KIELLLREVIFYFTEITVATKILTILFMRDKIIQALNFIDCDEFVGDYENKKGILYKTNM
GFRLGWRSYLVLSNIAAYSSQVIVPIFLDILRETKSELPICKYYFLSDEDRESHFLFWFIY
QSFGMYGHMMYNVNIDSIIAGLLLIAIAQLKLLGNNLTNLKLSDEESKLPKDSQDKIQI
KRFHKLLRHYEVILRYCDTVQDTLNVTLFFQFGVASIIICVVMCGLLLPSTETKVFLV
MYLFTMTLQIFVPGFLGTQLTYGSEGLVTAAYNSEWIPRSESFKSSLKLFREARAARPV
VISGLKMFPLSLITFTSIMKTAYSFFTILIRNVQEA

>SlitOR16

MYIKIVRFMLVIVGSWPRREIGEPEPRYQTIMLKLFFFSVVNAALYGSISYVYMHTSEL
SFLEIGHMYIVILMTANDMPRVFTLTLSQKYRDLAKEFLTKIHLFYFKDHSPYAMLTH
KKVHLVCHLVSLCLLSQMLTGLSLFNLPMTNYSSGRYASGGTQNSTFEHSMYFSY
PFNTST

>SlitOR17

MSVCAGSVAPHVRCLRRVGFCRWGAAAPANPLLATAARFYHVFALAAATSTYVLQQ
LIYAYQERSDMDKLSQVMFVLLCHVTCVAKQVAFHVDADRIDELIARLDEPLLNC
AGPRGALLHGTARRAARLLRVYSGCAVATCVLWIVFPVLYRIRGISFEFPFWAGVSY
DHNVVFGAVLLYSFYTTNLVAIGNTTMDAFMATILDQCKTQLRILRLNFETLPERAR
ALQQSGGGVYEASLQRLFVDCLLHYNITETCTVLHDVFVAVPLLIQFGVGGWILCMA
AYKIVSLNVFSIEFASTTLFIICILIELFICYGNEVTVESSRVSESLYSMEWARAGLSF
RRSLVLVMERAKRPLRPAAGRVIPLSLDTYVTILKSSYSFYAVLRQTK

>SlitOR18

MEMKSDILTQKKYKTFNDTFKLCAFSLAFAFLYPNRNTALKRCITITLIVTFCGGQLF
WFITYTFKCLYTLDLYNFARNMTLAVVLILFFIKTYYAIYATQKFATLLDKISEDLEA
NNLGERQQKLYDEHITIAKFGEISWLLVPVLMSALFPIYAGTLMSIESIQTDDYQRRM
VHDMELLYVEDIQSETPFFQCMFAYNVCVQCVLVPNYCAFDGSFCIATTHIQLKLKL
MVLKVHDAFKYSKNKYELRMKMNEAIRDQQEALDFYFPPKMCLGPWLFAVLMPDF
FLISFHLDPPKKFAANKSPKHLHLGWSGFFPIYPCPVKSEAP

>SlitOR19

MKNHYILKTYCKRIFLIGSGNFWYKESEIGNDQSLLYRTYNAVLYFIYGFMTILEIMA
ATMGDFPPDEKRDSVSFAVSHTIAMIKIFSVIANKSLIKKLNHKMVTVCERYEENTLM
AEKYKIMKINVLAIFYVTYASAFFVFEGLRKMLTGSHFVTVVITYPKFEDDSIGATS
ARVLATVILYILMITMIMSVDSFTMIYLYMYKYKFITLKQYY

>SlitOR20

AEELIFYFTNVGALSKALAFIFLRDKVKKMLYMLESEMFQTDNP EEVKLIEKAKEKSL
FYWKITFGLSVSANTVNVFLPFVLHLIFS IKLEFPVCRY SFIPEQYEAIFLYPAYLYQSIG
ITSHMLYNVNIDTFLLGVMFLAMAQLDILDRKLRKVTDVCVNV DAPRGSIDKMIDDQ
NAVLEINKCIKHYDAVCEYCKLIQEAFSEILFVLFSSG SCKICMCLFRFPM PAETQYFV
FLTLYIVVMTLQVMVPCWFGSRLMEKSSQITFAVYDCDWT PRCRRFKSNLRL LVERA
NRPIIKGGKMFLLSLATFTA IMNSSYSFFALLRNVQTR

>SlitOR21

MYKLGIALKAVHNDCEAEQKMITRSKFFSWALIFNCVMSVIMYTIEGVLRVIRAGDT
FNTVITAWPDVHDRSVLSNIGRTVIYITWWIYLTRIFS VYSLVICLTIAVSHQFKNLKS Y
FYSLSKIFENDNLPQTEKEQEYEKAFKVGISMHSETLKCTDEIQTICREVFSGQIIFNL T
LLIVLMYQMMNSPRTFSNVLT LGLTALTILFSTGFFMW

>SlitOR22

LCLRCKMRLQIIKDFLMKASFDFDRPDINLYNFHPQLRIFLAVKGVFFTNRGS RFRLIW
PSICIQLSIIGMTFEEMFIWRGVSLKDYSFATECFCYWLL LGCIPTVYVSILVHTNKIYDI
VVKMNEEFIYVCSLGPYRKPFLEGQLLIWQLCYAWFGFVSFVGGLYVVFPLVGLIY
QSLFATLNENTTRPLQFPMWLP HDDPYRTPNYELFLFIQSTLCFCFVQTFCVYIYTLFH
ILLHYYMIMDMIIINFSVIFDGLEKSVALLPRHDIPRNGNPTNN

>SlitOR23

MWQKLKEFYNKTHTD FSKGYIDPYEFHKTFYQIMVNFKVADLSNENPPSYFNQNAII
FMTGFVAKLLCIS SFYHGLMTFNLRLATEAGTYIIVMAYALLISSCTRRNVPQYHNFL
RAMKEDFQFICTSGEKYRVPYFSNQLLTWKICIFACIFTASIAVGMVSFAFLSLFYFLA
TYKEEIGGSRPLLFPFWLPNVDFGETPVYEIAFMFSNICALLYA YNYIFMIQTQIVWIR
QITSKVDIVISISDLLVDIHPAGSEESVYFSYLIKARMRDILLHHQSMYSLMEDYAV
VYKKMLMF EQKCCGSVVCLTAYCIAEAFDAGEFQAILLLL CIGTTVLHFVPCYFCTFL
AVKVSSVCDACWNIPFWKAGPLIRPYMVLIMQRSRLRHLPLQAAGFEDISIETF SKKMT
NAYSLFNMLRQANI

>SlitOR24

MRVLSHVWRRISQSKALELAGPLETAF FASVYRLSFVVGLSTSDDYLLYTMYS SFIRII
SALVVWF EIWSVLGNTDVSLDQISSVNVI FHLVTFWKLVTVTIAENLGKFVMSLLYL
GYNMFTWYLMCRWCEEITIKSQRIGQSAYFSGWESGISLAPGARATIVLV IARANKPL
V FVAGGMYTSLSLSSYTTLVKASYNALNILLTMRHE

>SlitOR25

PLLGQLAASGVLIYFIGYQATATIGQS VVACMTSFLFLAYNL FDFYMICRWCQEITNQ
SANVGEAIYCSGWECGVSKLP GVRSTIMFVIARANKPLVLTAGGMYDLSLTSY TSLV
KTSYSALTVLLRFRHD

>SlitOR26

MSLSSGSVATHLRILRRCGYCRLAGGARVARLGSLHALYRGFTLALT TLYLLQECIY
AYQVRQDMDKLARVMFLLLCHITSIAKQLVFHLKADRIDEMLGGLNEPLYNQSA AV
HQRLLRVTAARAARFVRAYAGCAVVTCTLWITFPVMYHLQGQLVEFPFWINVDYNQ
SKMFILVLAYSYVTTLVGIANTTMDAFMATVNLNQCKTQLRILRMNFECLPLQAVEV
LKTSPGQSYDAVLMKLFKECLLHYEKITKTAKMLQDIFGTAILIHF GIGGWILCRAAY
KIVTLNVMSVEFASMTL FISCITELFLYCYYGNEVTDESSRVSESLSMEWARAGLS
FRRSLVLVMERAKRPLRPAAGRVIPLSLDTFVKIIKSSYTFYAVLRQTK

>SlitOR27

MIILNENMKTKLAFLSPVVPYGVFESWEDLNPQLYHAVHIYWLK FYGMWFNDFSPQ
SIKFWVQMMYTLIVLWLVCF FPGIGEVVYLLRRRENIGDVAEGLYLFLSEMYTYFKV
VFWLNRNKVIDLLKYLHCEEFKPKEPEHRDIIKS IKSARFVMTYYSTMCVGAVSVG
IIMPLTENFDILPTNVEY PFFNVYQTPAYEAVYIHHIYK PATCIIDGVM DTLAAFVAS
AIGQIEILXFNLRFELLAERQRKR DVAENKYIEEYKPPYYVRSVLKDCIVHHNCIIRY

VSMIESAFSLASALQFMLSVMVLCLIGIQFLSIENPTSHPMQIAWMGIYLTCLMLIEVFIL
CWFGDELIWKSMDLAKAAFEQPMWNSDRKSNMFIIIFLERCKRPMRLTAGKIFTLSL
DTYTVLINWSYKAFVVMRNMKK

>SlitOR28

MTSLYRKFLFKKKLKQRIDERVYNKRDYDASYAPTKKVLGWVAIRMTHNISEKTTM
LWDMFYWFEMMNLFLVGPSELVSMLTTAYEAKTFRDSIKVFRTMPCFGCVVLSMFK
SIKMVVHRPVYENLANELRDMWPEGEVSEEEHQIISAALKQLNFIVKGYWYWCNNALL
ISFLSPPYFITLARYFGYDSPMGLHFLYWLFPDPYQSVYYEITLVLQTWHALVVIWFN
VAWDMFLFCLFLCHITTQFDLLARRVQRLFYVQVDNQLVRSYPMASVSREFIQTEGER
VNSYGAQYWEARHQKEITEIVLRHHSRLRLTGDVENMFSLLALLINFMNSSIIICFCGFC
CVLIEKWNEVAYKSFLVTALSQTWLLCWYGGQKLIDSSQRLADALYGCGWYNSSKRA
RSAVLIMLHRAQKGIYVTTTHGFSVISLASYSTIIKTAWSYFTLLLNNFFKEKSVN

>SlitOR29

MKISMLSVCIVKVNTFVLWQKHWREVLDYITEADNFERQNEPDKSQIVEAYTKY
CRRLTYFYWALVSTTFLTTTCSPLMRYLSSTFRENMRNGTEPFPHFSSWMPFDKYH
SPGCWITVLWHTVLCAYGAAIMAAAYDTCIVVTMVFFGGKLDLLRERCKHMFSGYGT
VITDKQCEEVVRQLHGIHVMLIKYSRLFNSLLSPVMFFYMMVMCSMLLCASAYQLTSA
QNAAQKLLMAEYLIFGIAQLFVFCWHSNDVLIKNENMTSGPFESNWTANYRQKKD
VLLSGQLRIKNIFTAGPFANLTLPTFINILKGAYSYYTLLRK

>SlitOR30

MDATCLNFEELFKIRTVFMRLNRSYPSIARDRPWKFQFSIIMMIIFSHFFFLSYSVFYHD
IRSGNFAVACLNASVAIICITITLKYIILLYHQESIKQLKIAMERDYAAAQEFNEDKEI
VVQYAKRGVTVCKFWLVFGFGTSTIFPIKALVLTGYNWYWKGEFVYVHVFDLIYPQPI
EDYKNVTICFWLLFIFNNSFGLLASSMFVGFDPMPVIFMLHTCGQLDLLSRHISTLFVD
ANI

>SlitOR31

MEDNVAYSTFEGFRPHFDALARVGYFKIVLKPISLKPFFHNRYRIISWSLILTYNLQH
VIRVVKVRHSFHLIVDTLFTLLTNTLGKQTAFNLRSRIDDIISIINGPTFAASKPYHV
EVLKQNALVMSRLTLTYHGAIFTCGTLWTVFPVNRALGKEVQFTGYFPFETTSTLA
FSLALAYMTVLITFQAYGNVTMDCTIVAFYAQAKIQLQMLRYNLEQLVEFRNIKKFN
SIKTQYRDEGEEKTELQERLKKCVRHYDQIVRYAKEVESIFGEAMVVQFFVMAWVIC
MTVYKIVGLSICSAEFVSMAYVLGCMLAQLFIYCYFGTQLKVESELVNQSIYCCDWL
CLSPQFRRQLLVMQCCGRPLAPRTAYVIPMSLDTYIHVLRSSYTLFTFLNR

>SlitOR32

MVSSDELFLNRAKFVMKYLGVWVLADNASYFLKAYRGFMITLQYLFLIFQTIYIIQV
WGDLDVAVSQASYLLFTQACLCLKVTVFQINMPMLKDLLRLMDSKIFRPENDVHEKL
LELQAARIKRLLLAFMVSSQITCGMWALKPLFDDADRKFPPDMWMPVSPEDAVQYY
IGYAFQLGTICISAYMYFGVDSVTFSSVIFGCPQIN

>SlitOR33

MSNQIKMYTPNEMTKLLGKLVNCFIFGLKNIWVEDVKLTNRFISTRSCNRLLLF AEIF
YIIFASTILGSLFTQKNLSEKQKTDQMMFSITLPGNIMFHYILLYRRHEIRNLLYHLAV
LKEHYNDEDLEREMIKKIKVFSISLCGLVGMVVVSYGLSAFYRVVTAGETFTVITSA
WPDIHDRSTAAGLVRVVFVFWWYPFAARIMVTFLLVLTMLVSICYQFKNLQSYFYSL
DEIFSDGTQSQEKEKK

>SlitOR34

MNFFRNPEVPTQLYKETDTTRMIDKYNKFWFLCCCPDFWVKKVDYPDPFTRVYRPS
MLVNHIVMVIFCSCFLSLWTQHDLSSQSQKSDRLAYAASTPIITVLYHFVILYYTEDV
KQVLYKLAVVLRVDHNDKNAEDEMKKQ

>SlitOR35

MWNKIRKFGLEYCDLPTMIWNVAVFLKVLTLNVYGKKKTGIPFIFYIVVVVAALSYL
YVYLICMVWFVFRSRETEDLGAAMVILSLGISSEIGTLKLLYMFLYIKDIRNLTD AFL
DFDSHMVPGTRMYTNLLRYLRDVKKRAIFYWAVIMGNGTLYVTMPMLRPGRHLTE
DMLVIYGLEPMFESP NYEIAWFMMAASVATICYISANVTAYFIVIIIGYAESQMRALSD
EVTHVWKDAEKHFEDLNYGTDLQDFDRKKMIINEHVFKNLKYIIKRHATIKTLINQV
EDVCSGPTAVGLTFLLLGLISELLGGLNTFLQMPFVFMQVGTDCFIGQRIMDAGEVF
EWAVYDCQWENFDHKNMKMILLMLQISQKTSSISAGGMTKMSFRCLMGAMRV TYS
AYTAFRSIM

>SlitOR36

MLTFHEIIHEIRKFGLEYCDLPTMLENVSILLRVLTVNIDSKYKKGITILSYIVTAVTAA
CFYYVFLFSMTWFWFWRARITGELVGAMVVL SLGISSEIGPFKLFYMCYYMDKTHKI
ADGFLECDANTIKGTRFHSNLMKCLRN VKKRAMLYWVVVAGNGVLYVMKPVAMR
GRNLPENYFLIYGLEPMLETPNYQIA YFMMIASVFFVCYVPASVTAFLIVITGYAEAQ
MLALSEEMLXXYGQML

>SlitOR37

EVDKLVLPFLIQDILGHNVFNPKWTWTTRIPQQFFIVFLLVYVILGTQDYLKDATDIN
DIGEAYYTLIIILFFPIKYLLFIQNRFTLQQLYVMAKTTLLDMIKSDSNEKLEELFAKIKL
AVKILFGTIFWSISVYFMVAMWNYAQGTRVTL SKTTTILMPMTSPYYELGLAIHTVFL
FEMAFTYCVIDLWFVVL MFSFCTAIDSTINRLKIEGKRPDETDEQYMDRLNDALRIFY
QNHSKIMEFLYILSETYKWPSIIPILGILL

>SlitGR1

MYKSLIILCVVYCVVIEARPKWQVLPPMPGYVPVYIRPGDTPLEEINLDLAEAFHELPS
GRSVGKQVEASPEAPEQADQPQPDEVPAPADEIVDHRPYEKKILEKKKKKTDSEIPKPIE
RR

>SlitGR2

MTIPDHLFDEGINNTLFHNDMRHIQQNKTVYEKTQRDYEQEQRDLLSSQDGDTC EIH
DQFYRDHKLLLVLFRALAVMPITRSRPGTITFSWKS RATMYAVCFYIAATAVVLIVG
YERIMILRSIRRFDDYIYAILFVIFL VPHFWIPFVGWGV AHQVAIYKTNWGKFQVRYC
RVTGENLQFPNLKTTIVIISVGCLLLAVCFLLSLCILMDGFLLRHTSAYYHIITMINMNC
ALRYINCQRIKI

>SlitGR3

MRNNLVEPHISNDIIYENIKPVFTVLRIMGVLPITRPASCINQFQIASASMLYSVLVFC S
LVSYVLYLSLHKVQILRTAEGKFEEAVIEYLFTVYLFPMIAVPILWYETRKIADVLNG
WVEFEVVYKQLSGRTL PVKLYKKALAI AIIIPILSTTTVIVTHITMVHFKPMQLVPYVF
LEILTYMLGGYRYLLCQTLSICAHILAE EFQSALHP

>SlitGR4

MLLCLLLHLVITPYHVITNIFNKSRSRSDRSSPTLQLNWVVLHFINLLLIVEPCHRTHEEM
KRTRHLISQMLRHTTTDNNGLLSELQIFYQHLSLNEVSYAPLKMFP LDRTLIVTILGSIT
TYLVVIAQL

>SlitGR5

MENVFRCSCFIGVLGAKKWICYVWSAFILFVLLVMESQAIWKVIKALGGWAIDTAGQ
RSVTARLAGTIFYTIAIISLILASKLFRSWGELSALWVRVERVMAVKVPSDGTKRRM
YFIIGFMTVCSLLEHLLSIVSAIGLDCPSYLI IKRYILISHGF MILRHEYSDWYAIPLAFM
STIATMLWNFQDQLIVLISMGIDFKIPQT