

Supplementary Materials: Phylogenetic-Derived Insights into the Evolution of Sialylation in EUKaryotes: Comprehensive Analysis of Vertebrate β -Galactoside α 2,3/6-Sialyltransferases (ST3Gal and ST6Gal)

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Data S1. 124 ST3Gal sequences used in Figure 3A: N-terminal part were manually removed and multiple sequence alignment obtained with clustal Omega at the <http://www.ebi.ac.uk/Tools/msa/clustalo/web> site with 228 informative positions. Output format is clustal50 ST6Gal sequences used in figure 3B: N-terminal part were manually removed and multiple sequence alignment obtained with clustal omega at the <http://www.ebi.ac.uk/Tools/msa/clustalo/> web site with 256 informative positions. Output format is clustal.

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124
Oscare12 PRRDSTICPNIGTLLAN--PNLPRILKSKF-HPDVKV-MLTQDTKTLDEPI--NSWWK-K
Spur1/2 -GGQRCCRLLWK-----KGTSWFDEKY-NDSLIP-VWMKENKKMSEEI--GKWWL-S
Bf1o1/2 -TPPVVVQPTC---KRIWQKGGRSSWFDSRF-DDNIRP-VWSRANIELPADA--RKWWM-S
Csav1/2 FPNKKCGRDLD-----ASEKRWFKGFR-NPEIQP-VWTESTLEIDYLV--YDWWL-S
Cint1/2 EIQQNNKCGHQ-----LDAQTRWFARF-NPEIEP-VWTQSALEIDYLV--YDWWL-S
Sacc12 -----KGEYKFFDDRY--SNIST-IWSSKHKEMTPEA--LQWWL-R
Dreri8 -RGHSCSCTSC---IAY--IGVSEWLQDRY-DQKQKP-YLTGRDDVDPLS--LKWWL-S
Ambmex1 -PIRPCSDAC---ISE--SKLSPWFDERF-NDTIPT-LLTKENNEIPEDV--YQWWL-E
Siltrol --RRCQCCDTC---VAEPEASTWFDERF-NLSVLP-LLSKQNNVIPDTV--YKWWL-T
Xlaev1 --RRCQCCDTC---VAEPEASTWFDERF-NLSVLP-LLSKQNNVIPDTV--YKWWL-T
Mondom1 -PQRPCSCSQC---ISE--TGFPAPWFDERF-NHTMQP-LLNRQNAFLENDT--YTWWM-K
Loxafr1 -PPRSCCTSCH---VNE--LRVSHWFDERF-NETMQP-LLTLHNSLIMEET--YSWWL-K
HSa1 IKHRPCTCTHC---IGO--RQLSAWFDERF-NQTMQP-LLTAQNALLEDDT--YRWWL-R
Btaurus1 -SNRPTCTRC---IGQ--RRVSSWFDERF-NRSMQP-LLTAKNALLEDT--YNWWL-R
Ggallus1 -PRRPCSCSTC---ISE--LGHSLWFQDFR-NSTMQP-FLTSQNALIPEDS--YRWWL-K
Taegut1 -PRRPCSCRTC---ISE--LGHSLWFQDFR-NSTMQP-FLTSQNALIPEDS--YRWWL-K
Pytmol1 -SRRPCSCNTC---ILE--QTSAWFDERF-NITMQP-FLTTQNAFIPQES--YRWWL-
Chropic1 YPERPCSCNSC---VPE--LGLSFWFDERF-NQTIQP-FLTTRNTFIPES--YKWWL-K
Acaroll -SRRPCSCSTC---ISE--QGVSLWFQDFR-NQTMQP-FLTTRNAFVPEES--YKWWK-
Latcha8 -DKKLCSCCEK---VSE--KEESAWFDERF-DPNFQP-ILMTEVQDIPSHA--LQWWL-V
Acarol8 LEQRICNCNR-----IDHNPQWFCDHY-DASVNC-LLTRESQRPPEV--LFWWL-K
Pytmol8 MKEEMCHHNRC-----IGLSSWDWFCDHF-DASVNC-LLTPENSIDIPEV--LQWWL-V
Chropic8 SEAKPGCCASC-----IVELSSSAWFNERY-DSAISP-LLTVHTSKTAPDV--LLWWL-K
Galgal8 -SLPTVRCTAS-----ANASAWFSARY-DAAAGP-LLTGAPELSPDV--VHWWL-T
Melund8 LDAPAYACTTS-----TNGSMWFNARY-NRTMGP-LLTGRAHELPSDV--VQWWL-T
Latcha2A SRKKLCSCKLC---TSE--SCLSLWFDERY-NRTVPR-LLTKSNAFISKDI--YEWWLVS
Latcha2B SSVKRCGCRAC-----ISEPGVSPWFDERY-NRTVPR-LLMKSNAFISEDT--YVWWL-S
Dreri2 -QOKTCACSR---VGD--PGVSDWFDENY-DPDISP-VWIRDNIQLPSDV--YYWWV-M
Takrub2 -QQRTECECPRC---VGD--PGVSDWFDENY-DPDVSP-VWTRDNGQLPPDV--YYWWV-M
Pmar_12 -----LSLQ-----S
Latcha2C -LLKMCTCARC-----LGDLGVSDWFDENY-NMDVLP-VWTKENINLPPDV--YYWWL-M
Strop2 RLPKTCSCRQC---LRQ--PGFSAWFDSHY-DASVSP-VWTLENRELSPDV--LHWWM-M
Ambmex2 ALPKHACSKC-----VWEAGVSEWFDTMPNQISP-IWTLENMDLAPDV--QRWWM-M
Acarol2 LFKVSCSCHRC---QVGAEDAEWFRSRY-DARIISP-VWTRENMELPLDV--QRWWMER
Pytmol2 -VVKRACHRC---AIE--SIDTWSFDNRY-DSNISP-VWTKENVDLPLDV--QRWW--M
Ggallus2 -PRGCACRRC---PEDAAAAAAAWFDSRY-DGGVSP-VWTKENMELPLPDV--QRWWM-M
Taegut2 -PRGCSRRC---PAEPEGAADWFQDRY-DGTVSP-VWTKENMDLPPDV--QRWWM-M
Chropic2 --GEGCACRRC---TED--AGALAWFTSHY-DSNISP-VWTKENMDLPPDV--QRWWM-M
Ornana2 --AKSACACRRC---MGD--TGASDWFDSHY-DSNISP-VWTRENMALPPDV--QRWWM-M
Loxafr2 --GKSCACRRC---MGD--TGASSWFDSHF-DSNISP-VWTRENMDLPPDV--QRWWM-M
Mondom2 --SKSACACRRC---MGD--AGASDWFDSHY-DGNISP-VWTKENMDLPLDV--QRWWM-M
Hasa2 --SGKSCACRRC---MGD--AGASDWFDSHF-DGNISP-VWTRENMDLPPDV--QRWWM-M
Btaurus2 LAGKSCACRRC---MGDTGASEWFDSHF-NSNISP-VWTRENMDLPPDV--QRWWM-M
Strop8 -DNQGCCVCGRC---RQEKRKTTEFEKRF-NETVEP-LLLGEQEEMPDPHV--KKWWL-R
Xlaev8a -NSQGCIICGLC---RQEENRKTRTEFFETRF-NGTIEP-LLLGDQDMPDHV--KKWWL-R
Xlaev8b INSQGCMCGHC---RQEKRKTTEFFESRF-NGTIEP-LLLGKYQYMPDHV--KKWWL-R
Ambmex8 -RHKPCSCKQC---ISE--VGVSDWFDRHF-NSSVNP-LLTAKNPETPLSV--QRWWL-K
Protopt2 -----DPGVNP-LLTIRNAFLYNAV--KKWWL-N
Dreriol1C PSERCACCKDC---VREKSHSTWFNLF-DPSIQL-LLTRGNYYVLNKDV--YKYWK-G
Orylat1 FSKDICACDSC---MAD--LGEDAWIADHF-NLSIIP-LMTRDSSALSEDT--YRWWQ-W
Tetnig1 FSRGPCACGQC---MTE--PEDDPWFFTERF-NQSIQP-LMSRENSALSDDET--FKWWQ-W
Takrub1 FARGPCACGQC---MTEMDDDPWFTERF-NQSIHP-LMSRENSALSDDET--FKWWQ-V
Dreriol1D HIFGVACAGQC---VADIFYDAWFRMHY-DPNIEL-LLTKKNSILSDAL--YRWWQ-K
Dreriol1A STGGLCACCNKC---VMDLNDEDWFFIRF-NPTVPT-LLNRRNSAMRSDV--FEWWQ-G
Dreriol1B -KRAACCGNTC---VAS--RENGTWFSERY-NRTIIP-LLNSTNSELNEDI--LKWWK-G
Sacc2/6_1 ----PCTKGYT-----HRAIKRLVPTF--DPDLP-LFLNRDFRKWKF--DRLKET
Sac11 ----PCTKGYT-----HRAIKRLVPTF--DPDLP-LFLNRDFRKWKF--DRLKET
bflo210 -----
Bfl_12648 -EGDTCVPGYA-----RSKVTEMNPKF--NTNLP-LFVKKGFRREWKG--MDDGHDK
Bfl_13015 -QFGIHVKVSRWKDLRKPLYSSLVAGMKILTVPHEIP-PSIPAQAQFWKNY--CNSAL-D

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Dre7 -LSQ SCHSGWS-----VERMRTMLSTPAGLLKIP-VFLENGTGDWA-----
 Tru7 -LSDPCPRWC---LNR-LKR-LPCSEG--LLDIP-VFVQODVPSS-----WD--
 Orylat7 -LSHPCOPHWC---LNH-LKPLSFSKRL---LDIP-VFVQQGRPAE-----WA--
 Cmi5 VLGEKCRSLFA----HQMMAILFFPHKY-DLNLSL-FLKRNSGLTGNVF-----K
 Strop5 -LQAQCRRPAFA---RTQMDRLFSSKY-TKNLS-SFIKKDKSLSNEL---YK--
 Ambmex5 VLEGQCRPAFV---KREMDRLFQERY-SMSLA-SFMRKSPHLNESS-----FK
 Mondom5 VLQGECRPFDA---KKEMLHRLFAQQY-DVNASP-FINENMELLEDL-----YR
 Ornana5 VLQGECRPSFV---KKGMDRLFKEKY-SLGLSP-FVKQNSEANEEA---YQ
 Hsa5 VLQKECRPKFA---KTSMALLFEHRY-SV DLLP-FVQKAPKIDSEAES-----K
 Mmu5 VLQKECRPRYU---KTAMALLFEDRY-SINLEP-FVQKVPTASEAEL-----K
 Anocar5 VLQACPRPSFV---KKEMSRLFGEKY-NINTS-SFIRKDINAHEDI-----FK
 Taegut5 ALQECCRPSYU---KKEMRKLAFAEKY-NMDISP-FVRKNMNEDEAL-----FK
 Galgal5 VLQECCRPSYU---KKAMGKLFAEKY-SMDIP-PFVGKNNIDDEAL-----FK
 Dre5 ILDKECRPSFA---RORMVTEHHGSTPTID-PFLNKNMKLDEQI-----FQ
 Tru5 VLGAQCHLSRT---RKSLLPLLPSSSHMTQ-PFLWKDVPLSDL-----FL
 Melgal9 -----DRP-FKQBLEEVVLWLHK-----
 Ornana4 -----TPC-----THLTP-LCSSPSVFLAAEV-----
 Cmi6 -----
 Hsa6 NKIOPCLSKPA---F-ASLLRF--HQFHP-FLCAADFRKIASL--YGSDK--
 Mmu6 -MTRRNVNVCN---FKKPAFANLLRFPQLYF-FLCRADFIVKAAM---SGINN
 Anocar6 -KEAPRILDQC---LPAVMGWRA---NKLYP-FLCPHNFQQVSEL--HGSFS--
 Taegut6 -VERRNALDTC---LLKPAFESLLGVDKIYF-FLCANDFIRVAEF-QGSNK--
 Gga6 -VERRNALNTC---ILKPAFESLLDVEKIYF-FLCASDFIRVAEF-HGSDK--
 Melgal6 -VERRNALDTC---LLKPAFESLLDVDKIYF-FLCANDFIRVAEF-HGSDK--
 Ambmex6 -RKDDHFADSC---FNQNFKSLLQMPNVRP-FICPEYAKQATEEGSKK--
 Str6 PTDaveKEFKSC---YNEKFLILNTSEIIP-FLCQDFRKQSBNL---GSNK
 Spu2/6_3 -SNVTCRKGYA---RTRLQONLYGDRF--DPDIP-LFVDSFLDRPNA---V-N
 Spu2/6_6 -----
 Spur6b -----
 Bf18275 -EEEVCRPHHA---SSTIVNTHPKF-RKDIP-LFVTNDYKSYSSV---M-N
 Bf18276 -AEEQCRPHHA---SSTIVNTHPKF-RKDIP-LFVTNDYKSYSSV-MN--
 Sacc3_10 -----
 Latcha3 -TEGACKPHYA---ATQMTAIFPRRF-MKPAP-MFLDISFKRWARI---K-D
 Oryla3_r -SEGACKPGYA---AAKMTS1YPKF-MKLAP-MFLDPNFKRLGKV---S-G
 Dre3A -SEGACKPGYA---AAKMTA1YPKF-SKPAS-MFLDRNFKRLAKV---I-N
 Takrub3 -SDGVCKPGYA---AAKMTA1YPKF-IKPAP-MFLDRNFKRLAKV---NS
 Cmi3 -TEGGCRKGYA---SAQMTAIFPKSL-----
 Silt3 -SEGVCKPGYA---SALMNA1YPKF-SKPAP-MFLDDSFRRWAKI---R-E
 Xenlae3 -SEGVCKPGYA---SALMNA1YPKF-SKPAP-MFLDDSFRRWAKI---RE
 Hsa3 -SEGACKPGYA---SAMMTAIFPRF-SKPAP-MFLDDSFRRWAKI---RE
 Mmu3 -SEGACKPGYA---SAMMTAIFPRF-SKPAP-MFLDDSFRRWAKI---RE
 Pytmol3 -SEGVCKPGYA---SALMTA1FPKF-SKPAP-MFLDDSFRRWAKI---R-D
 Acarol3 -SEGVCKPGYA---SALMTS1FPKF-SKSAP-MFLDDSFKKWARI---R-D
 Anocar3 -SEGVCKPGYA---SALMTS1FPKF-SKSAP-MFLDDSFKKWARI---R-D
 Galgal3 -SEGACKPGYA---SAVMTAIFPRF-SKPAP-MFLDDSFRRWAKI---R-D
 Taegut3 -SEGMCKPGYA---SALMTV1FPKF-SKPAP-MFLDDSFRRWAKI---R-D
 Melgal3 FSEGVCKPGYA---SALMTV1FPKF-SKPAP-MFLDDSFRRWAKI---RD--
 Gasac3_r -SEGACKPGFA---AAKMTA1YPKF-IKLPAP-MFLDPNYKRSKI---G-G
 Dre3B -SKGECKQGFA---QAKMTL1YPKF-SKPAP-MFLDPNYKRLSKI---SS
 Pmar4 -----
 Ambmex4 DTRIACSPGSV---ETMAAAIFIENY-TRGHQ-AFLQPSNYFWVKS---NS-T
 Str4 NVHEMCIPGDV---ASKAEILISNY-SRDHP-VFLQLSDYFWVKN---QS-K
 Ornana9 -----
 Hsa4 -KKEPLCLQGEA---ESKASKLFGNY-SRDQP-IFLRLEDYFWVKT---PS-A
 Mmu4 -KKEPCFQGEA---ERQASKIFGNRS-RDQP-IFLQLKDYFWVKT---PST
 Gga4 -NKTVCPIGEV---ERKAAQILIGNY-TRDRP-LFLQLKDYFWVRT---PS-L
 Melgal4 -NKTVCPSGEV---ERKAAQILIGNY-TRDRP-LFLQLKDYFWVRT---PSL--
 Anocar4 -DERMTCPGEV---EKAAQILIANY-TRDHP-LFLQLKDYFWVRT---PS-P
 Pytmol4 -DERMTCPGEV---EKAAQILIANY-TRDHP-LFLQLKDYFWVRT---PSP
 Latcha4 -----
 Cmi4 -----
 Orylat9 -----RI--NKTTK-LFLKLLEDFFWRKY---VSQ
 Dre4 PHPTLALCPNY---RLQKKWENLNLSKMSRKPELFLKLEDDFWKDH---LSA
 Tru4 -----S---V-----SRRTO-LFLKLNDYFWQER---LS-T

LQPF---DNKRDFT-E LAEDLFTV-IPGE-NPFPSPG---VCRRCAVVGTAGRLKGARQ
 LQR---RENSDYIG-ALDKAFEV-IPNP-QRFLTRNVs---RCLRCAVVGNSGNLRNSGY
 LQSH---KDEDPAP-LLNNAFLDMGAPDV-DPWASRNL-T-GCLRCAVVGNSGNLRNOSNY
 LQSS---RGENLDK-VFENLYKIGVPRNNPFBARNHDEAICRCAVVGNSGNLINSKY
 LQSS---EAENLDK-TFEALYKEGVPRKDPMARLTHDREAGCRSCAVVGNSGNILNSNY
 IQQSKDTSTSFLRN-LVGKLL EI-IPDV-MPYATVNSN---RCLQCAVVGNSGNLRDSRY
 LQA---SDGTLKD-VIQKMFKI-ISPP-HEDETPRQN-QCRKCAVVGNSGNLNSKY
 -----MVKKLFET-ISGE-EDFLEASPY---RCRCAVVGNSGNLNSGY
 LQGE---TKPKDIYE-VMEELFEV-IPGD-LDLMQGPY---RCRTCAVVGNSGNLKSSNY
 LQGE---TKPKDIYE-VMEELFEV-IPGD-LDLMQGPY---RCRTCAVVGNSGNLKSSNY
 LQRE---RTPKRLNE-TFMDLFSI-IPGDVDPPLLQKGPL-ICRRCAVVGNSGNLKE SHY
 LQRE---KNPKNLND-TIKELFRV-VPGDVDPMLNESV-GCRRCAVVGNSGNLKQSQY
 LQRE---KKPNLND-TIKELFRV-VPGNVDPMLEKRSV-GCRRCAVVGNSGNLRESSY
 LQRE---KQPNLND-TIKELFRV-VPGDVDPMLLEKGSV-GCRRCAVVGNSGNLRESWY
 LQGE---KSPKNNLND-TIKELFGI-IPGDVDPQLERGTF---SCRRCAVVGNSGNLQSQY
 LQGE---KAPRSLNA-TLAELFGV-IPGDGDPQLERGSD---SCRRCAVVGNSGNLQSQY
 LQPO---FKSHNLNE-VLSKLPQI-VPGE-NPYSSRESQ---SCRRCAVVGNSGNLRGSSY
 LQGE---SNPKNIND-TMKELFEI-IPGDGEQLLERDAS-RCRRCAVVGNSGNLQSQY
 LQGE---RNPKGVNE-TIQEMPEI-IPGNGDQLLERSSS-QCRRCAVVGNSGNLQSQY
 QAG---NKNYNLSE-SIAKLFV-TVPR-T-NHSGIRDPA-HCRKCAVVGNSGNLKGSNH
 LQRS---QDGKQVQK-IKHLFEI-LPS-STAKVQDIT-QCGTCAVVGNSGRLGSKY
 LQRS---QDGQS1QK-IKKLFDL-LQSPATARVQGVA---QCGTCAVVGNSGRLGSKY
 LQGS---KSRAQLQG-IIQQMFDI-LPSL-MVDAWDPS-RCRTCAVVGNSGRLGSHY
 LQGT---PSIVPLRA-ILQKLFV-VPAP-NGSVWDPS-HCRTCAVVGNSGRLGSRH
 LQGP---SRGVQLQA-ILWQLFTV-LPAP-TGSLWDPN-HCRTCAVVGNSRWLKDGH
 LQKE---GNPKNITT-VIQLDFET-IPGA-DLYTHEEPD-RCRKCAVVGNSGNLKGSGY

LQKE---GNPKNITT-VIQLDFET-IPGA-DLYTHEEPD--RCRKCAVVGNSGNLKGSGY
 LQPQ---FKPHNIQQ-VLQRLFQV-IPGR-SPYGSWDPB--RCLRCAVVGNSGNLRGAGY
 LQPQ---FKPHSIQQ-VLLKLFQV-VPGR-SPYGSWDPG--RCLRCAVVGNSGNLRGAGY
 LQSQ---YKAQDLRT-VLNHLFEI-IPGQ-NPYQDHGWA--RCRRCAVVGNSGNLLGAGG
 LQPQ---FKPYNLKN-VLGKLFEI-IPGM-NPYNSWDPQ--SCRRCAVVGNSGNLHGSGY
 LQPQ---FRSHNTPE-ILSQLFQI-IPGQ-NPYQQDPL--TCRRCAVVGNSGNLRGSSY
 LQPQ---FKSQNTNE-VLEKLFQI-VPGT-----
 GERS----FMGVNLNEVLSKLFLI-IPGE-NPYRSRPSP--QCLRCAVVGNSGNLRGSGY
 LQPQ---FKSHNLNE-VLSKLFQI-VPGE-NPYSSRESQ--SCRRCAVVGNSGNLRGSSY
 LQPQ---FKSHNTQE-VLSKLFQI-VPGE-NPYRWRDPR--HCRRCAVVGNSGNLRGSGY
 LQPQ---FKSHNTHE-VLSKLFQI-VPGE-DPYRSRDP--RCRRCAVVGNSGNLRGSGY
 LQPQ---FKSHNTNE-VLGKLFEI-VPGE-NPYGSRDP--KCRRCAVVGNSGNLRGSGY
 LHPQ---FKSHNTNE-VLAJKLFQI-VPGE-NPYGSRDPH--KCQRCAVVGNSGNLRGSGY
 LQPQ---FKSHNTNE-VLEKLFQI-VPGE-NPYRFRDPH--QCRRCAVVGNSGNLRGSGY
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 LQPQ---FKSHNTNE-VLEKLFQI-VPGE-NPYRFRDPH--QCRRCAVVGNSGNLRGSGY
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 LQGR---NNGSDIQK-VLEQMFKV-VSTE-NLYLEQDNR--PCRRCAVVGNSGNLKGSRY
 LQGR---NNASDIQK-VLEQTFKV-VSTE-NLYLEQDNR--PCRRCAVVGNSGNLKGSRY
 LQGS---SNPEQVQE-ALDKLFDV-FPAE-DIYSVRDET--MCRTCIVVGNSGNLKGSKY
 LQGV---HKNSNVDA-IMTKLFEV-IPNT-DPYQSKNET--QCRRAIVGNSGNLKDSYY
 LQKN---KCKSDYRA-UVEKMFSL-FPDK-TRYTNASP--RCRTCAI1GNNSGNLKGSRY
 LQRE---ENPANYTQ-VVEELFRI-IPPE-GVFMDAGPQ--RCRTCSVVGNSGNLKGSNY
 LQSE---RQPANFSW-VVEELFQL-IPDG-ALYMDAGPE--RCRTCAVVGNSGNLKGSY
 LQSE---RQPANFSG-VVEELFQV-IPDE-VLYMDASPE--RCRTCAVVGNSGNLKGSY
 LQ---YKSRVNHYKAVSEMLFGI-FPNE-EDYSDAGPG--RCRTCAVVGNSGNLNGSHY
 LQSD---SQKANFSD-VVDILFSL-FPDE-EHYVVTDPN--RCRICAVVGNSGNILGSHY
 LQGA---ADVINYTY-VVDILFSL-FPDE-DHFSADGP--RCRTCAVVGNSGNLLRSNY
 TEP---YGFKYHVS-FVEKLMQA-LPGN-TPNIMGNDM--KCRRCVIASSGGSIGKHL
 TEP---YGFKYHVS-FVEKLMQA-LPGN-TPNIMGNDM--KCRRCVIASSGGSIGKHL

 LP---FYLSDQDCKKIDQQLLD-LPNS-EPALLTGGG--KCRRCIVVGSSGLVSGENL
 KSPNDYVIAVEEVAGKKIDQQLLD-LPNS-EPALLTGGG--KCRRCIVVGSSGLVSGENL
 LPPP---LGLQGSEE-MAEQALKA-LPFT-AVPTGPET---CRRCVVVGSGRILHSKNL
 LPPP---LGLRGSSEE-HLALALAS-LPQL-GLPPSLRGE--GGCRCCVVVGNGGVLHGSHL
 LGPP---LGLHGSEE-HLALTLAS-MPEP-GLPPSLKTK-DSCRCCVVVGNGGVLQGSHL
 YHPP---FGFHKHN-FTSELIGL-LPKV-SLSEELERK--PCKRCIVLGSGGIL-----
 YEPP---FGFRHRYVD-ELSDLLEM-MPED-GLPKELHSK--HCKRCIVIGSGGILHGEL
 YGPP---FGFHDYMY-HLQELLRL-MPAQ-DLPQALKAK--QCKRCIVLGSGSILHGQI
 YDPP---FGFRKFSY-KLQSLLLK-LPEH-GLPENLAKAK--PCKHCVVMGNNGVLNGLGL
 YDPP---FGFRKFSR-KLQNLLK-LPEH-DLPEHLKTK--SCKRCIVIGSGGILHGGL
 YDPP---FGFRKFSS-KVQTLLEL-LPEH-DLPEHLKAK--TCRRCVVIGSGGILHGEL
 YDPP---FGFRKFSS-KVQSLLDM-LPEH-DFPEHLRAK--ACKRCVVVGNGGILHGEL
 YEPP---FGFHKFSE-KLKDLLEL-LPEY-DLPEGLQSK--HCKHCVVGNGGVLHGEL
 YEPP---FGFHKFSD-KLKDLLEL-LPEH-DLPEDLKSK--HCKRCVVVGNGGILHGSEL
 YGPP---FGFHKFFD-KLKDLLEL-LPEH-DLPEDLKSK--HCKRCVVIGSGGILYGSEL
 YPPP---FGFLDMKK-KLEEILNL-LPVS--SEQRLGER--DCRRCVVVGNGGILKGGL
 YPPP---FGFQGLRS-KVAELLKS-LPLP-GSAQELKNRSDKCRRCVVVGNGGILRGLEL
 --LP---FGLHSSGC-PMEVIARLRVMVSAATGSSLCL--WCQRCIVVGNGYSVHGHI
 -----LL--LPQQ-GLPKSIKRL--PCRKCIVVGNSFSLRGQGL
 -----LSKLQFT-VPGD-NPYEPWDRS--RCRRCAVVGNSGNLHGQSY
 FDLP---YGMRTSAE-YFRLALSK-LQSC-DLFDEFDNI--PCKKCVVGNGGVLKNTL
 FPLP---YGIKTFFET-YFSSALSK-LQSC-DLFDEFDRV--PCKRCVVVGNGGVLKNTL
 FDLP---YGIIRRAER-FFQLALSK-SNNC-GLFAEDDSP--SCKKCVVGNGGVLRNKL
 FELP---YGIKRAEQ-FFRLALSR-LQNC-GLSSEEDSI--PCRRCVVVGNGGVLRNKL
 FELP---YGIKRAEQ-FFRLALSK-LQNC-GLSNKDDSV--ACRRCVVVGNGGVLRNKL
 FELP---YGIKRAEQ-FFRLALSK-LQNC-GLSNEDDSV--ACRRCVVVGNGGVLRNKL
 LDLP---YGIRNGER-FRLRVFSK-LKNC-NLPSEINVP--CRKCVVGNGGVLRNKL
 LDLP---YGIRNGER-FFDLALKN-LPQC-TLPPEIKNI--SCKKCVVGNGGVLRNSTL
 LPMP---FGFRDAER-TVNLILKH-MPET-EIPEDIQD--SCLRCVVQVGNGGIASRTL
 -----RTASD-VVGG---LPDT-DIPADIKKL--PCRRCIVIGNGGILKGSKL
 -----LP-----CRRCIVIGNGGILKGSKL
 YSPP---FGLRGTDK-DLMNVLK1-LPQASTMPENIERI--PCKRCIVVGSGGILLGKKL
 YSPP---FGLRGTDK-DLMNVLK1-LPQASTMPENIERI--PCKRCIVVGSGGILLGKKL
 -----D-----GCRRCIIVGSGGILKNKGH
 FPPP---FGIKGQDN-1IQRILET-TKEY-NLTPELMSR--SCKRCIVVGNGGVLANKSL
 YMPP---FGFKTQEK-LISSILSE-TKYY-GLGEHLDLS--SCKRCIIVGNGGILSNKSL
 YLPP---FGFRTQER-IIDVILSA-ARNY-GLGPELDLS--ICKRCIIVGNGGILSNKSL
 YLPP---FGFKTQER-IIIDSILTT-TKNY-GLGEQLDSR--SCKRCIIVGNGGILSNKSL
 -----TCKRCIIIGNGGIVANKSL
 YVPP---FGIKGQDN-LIKAILSA-TKEY-RLKPALDSL--NCRRCIIVGNGGVLANTS
 YVPP---FGIKGQDN-LIKAILAA-TKEY-RLKPALDSL--NCRRCIIVGNGGVLANTS
 FVPP---FGIKGQDN-LIKAILSV-TKEY-RLTPALDSL--CRRCIIVGNGGVLANKSL
 FVPP---FGIKGQDN-LIKAILSV-TKEY-RLTPALDSL--SCKRCIIVGNGGVLANKSL
 FVPP---FGIKGQDN-LIKAILSA-TKDY-RLTPALDSL--SCKRCIIVGNGGVLANKSL
 FVPP---FGIKGQDN-LIKAILSA-TKDY-RLTPALDSL--SCRRCCIIVVGNGGILANKSL
 FVPP---FGIKGQDN-LIKAILSA-TKDY-RLTPALDSL--SCRRCCIIVVGNGGILANKSL
 FVPP---FGIKGQDN-LIKAILSA-TKDY-RLTPALDSL--SCRRCCIIVVGNGGILANKSL
 YSPP---FGVKSQER-IIDILLSA-TKSY-GVGEELDSM--NCKTCIVVGNGGILANRSL
 YPPP---FGVRTQER-IDNILAA-TRSY-FLGPELDIS--PCKKCIIIGNGGILFNKSL

 YTLP---FGTKGIED-LILKILSI-TTSF-NLPPAMKSL--QCKTCVVVGNGNRQNSL
 YRLP---YGTYGSEE-LLIKFLAL-TNRY-HVPEDIKRL--RCRRCAVVGNGHQLKNSSL

 YELP---YGTKGSED-LLRLVLA-TSS--SIPKNIQSL--RCRRCAVVGNGHRLRNSSL
 YELP---FGTKGSED-LLRLVLA-ITSY-SIPESIKSL--ECRRCAVVGNGHRLRNSSL
 YELP---YGIKGSED-VLLRLLS--VTSY-SLPESIQLS--KCRRCAVVGNGHRLRNSSL

YELP---YGTKGSED-VLLRLLSV--TSY-SLPESIQLS--KCRRCVVVGNGHRLRNSSM
 YELP---YGTGAEE-ILLRLLA-VTSY-SLPESVQLS--KCRKCAVVGNGHRLRNSSM
 YELP---YGTGAEE-ILLRLLAI-----TSYSLPESI--QCRKCAVVGNGHRLRNSSM
 -----SL--PCKTCVVVGNGYIILKNSSL
 -----LP-----CKTCVVVGNGYIILKNSSL
 QPLP---YGIKGSEL-LLLKVLSA-TKSY-DMPAHIESL--ECRTCVVGNGFAIKNTSL
 EALP---YGIKGSEL-LLLKVLA-ISSF-TMPANIELD---CRTCAVIGNGFALKNSSL
 RALP---YGMKGSEL-MLLKVLA-IPNY-EPAKIESL--ECRTCVVGNGFAIKNSL
 GKLIDSHDFIVI-RMNRSPVKGYEVGVGSKTSYHLVYPEAVGYRAES--SGKLVLFPK
 GTAIDKHDVVV-RINQAKVKGFEKDVQKETHRLMYPESFMDIAP---ETNFVLLSFK
 GEKIDGYDLIF-RMNDATKGWEKDVGHRTHHFMPYPESATDLPD---DVSFVLLNFK
 GKNIDSHDFVI-RLNKGPTEGFENDVGRKTTHRHMYPATASSLAQ---GVSLVLLPFQ
 GNVIDGHDFVI-RMNKGPTYNYENDVGSKTTTHRFMYPPTASSLPQGKLFSGVSLVLPFQ
 QGLIDSHDYIM-RMNTAKTVGFEKDVGSRTTTHHFMPYPESFVEVIG---ETKFVLLIPFK
 GALIDSHSTVI-RMNKAVTGVGFEDEDVGYRTTTHHFMPYPESAIHLRP---GVHLVLLPFK
 GMWIDNHDIF--RMNYAPTVGYPEADVGCRRTTHQFIYPESAAKLQE---NATLIVIPFK
 GPEIDEHDVFV--RMNHAPTARFEKDVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GPEIDEHDVFV--RMNHAPTARFEKDVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GKIDSHDFV--RMNRAPTAGFEVDPGRKTTHHFVYPEVSRDLQA---NVSMILIPFK
 GSQIDEHDVFV--RMNKAPTMGFEADVGSKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GPEIDSHDFV--RMNKAPTAGFEADVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GPQIDSHDFV--RMNKAPTAGFEADVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 QDQIDSHDFV--RMNRAPTAGFEADVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GPDIDSHDFV--RMNRAPTAGYESDVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GQEINGHDFIM--RMNQAPTVGFEPDVGSKTTTHHFVYPEVSRDLQA---EVSMILIPFK
 QDIDSHDFV--RMNRAPTAGFEADVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GQEIDNHDVFV--RMNKAPTAGFEADVGKTTTHHFVYPEVSRDLQA---NVSMILIPFK
 GKEIDAHFFVI--RMNRAARTAGFEPDVGIKTTTHHFVYPEVSRDLQA---GVHLVLLPFK
 GENIDSHHFV--RINTAPTAGFEEDVGAKTTHHFVYPEVSRDLQA---GVHLVLLPFK
 GQKIDSQHOFV--RMNTAQIAQFQEDVGRTRTTTHHFVYPEVSRDLQA---GIVHLVLPFK
 GREIDSHHWV--RMNRAQTAGFEADVGKTTTHHFVYPEVSRDLQA---GVHLVLPFK
 GLQIDAHHWV--RMNRAKTAGFEMDVGARTTHHFVYPEVSRDLQA---GVHLVLPFK
 GLRIDAHDWV--RMNRAKIAGFELDVGMRRTTHHFVYPEVSRDLQA---GVHLVLPFK
 GNQIDHNHFV--RMNRAPTTGFEVDVGSKTTTHHFVYPEVSRDLQA---NISLVLIPFK
 GNQIDHDFVM--RMNHPATGFEVDVGSKTTTHHFVYPEVSRDLQA---NISLVLIPFK
 GPVIDGHDFIM--RMNLAPTVGFEEDAGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GATIDGHNYIM--RINLAPTVGFEEDAGSHTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GKEIDQHDFV--RINLAPTVGFEADVGKTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GKAIDMHDFV--RINLAPTVGFEADVGKTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GKIDGHEFIM--RMNQAPTVGFEMDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
 -----VPM--RMNQAPTAGFETDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GREINGHDFVM--RMNQAPTVGFEADVGKTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GQEINGHDFIM--RMNQAPTVGFEADVGKTTTHHFVYPEVSRDLQA---NVSFVLPFK
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 GPEIDGHDFVM--RMNQAPTVGFEGDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
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 QDQDVGHNFM--RMNQAPTVGFQDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
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 GKKIDSHGLIF--RMNGARTYGFQDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GKKIDSHRFIF--RMNGARTYGFQDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GKNIDSHQIVI--RMNGARTYGFQDVGSRTTTHHFVYPEVSRDLQA---NVSFVLPFK
 GAKIDSHDFV--GMNRAKTSGFEKDVGNKSTHYFMPYPESAHLLPP---GVHFVLIPFK
 GRLIDAHNFVI--RINMGPTKGYEDDVGSKTTTIRFLIYPEVSRDLQA---STYLVLPFK
 GALIDTSDFVI--RMNKAPTKGFQDVGSRTTTHHFVYPEVSRDLQA---TTSLVLPFK
 GRLIDSSDFII--RMNQAPTLGFQDVGSRTTTHHFVYPEVSRDLQA---GTSVLIPFK
 GRLIDSSDFII--RMNQAPTSGFQDVGSRTTTHHFVYPEVSRDLQA---GTSVLIPFK
 GVLIDAHDLVI--RINKGPTEGFERDVGLKTTTHRFMYPESAVMDN---STYLVLPFK
 GOLIDSHDFVI--RINKGPTEKGYETDVGSKTTTHRFMYPESAMLDN---STHVLVLLPFK
 GRLIDLHDFV--RINKGPTEKDVGSKTTTHRFMYPESAVDLSN---STHVLVLPFK
 GSLIDRYDVVI--RMNDAPVRNEYERDVGSITAFRMLYPESATAKRDIS--DAYIVFLPYK
 GSLIDRYDVVI--RMNDAPVRNEYERDVGSITAFRMLYPESATAKRDIS--DAYIVFLPYK
 -----RMNDAPVKGYESDVGSRTDFRRFFYPESTLNQADLDS-GTYVVVVMYK
 GSTIDKYDIVM--RMNEAPVHGKEYDKIGSKTTFRFLYPEPESATSKEVDP---DADYIIVPYK
 GSTIDKYDIVM--RMNDAPVHGKEYDKIGSKTTFRFLYPEPESATSKEVDP---DADYIIVPYK
 GAHIDHANIII--RVNNAPVFGFEDAGSRTTIRLILYPEPEGAPSHIQEYER-TEVVALVVFK
 GAHIDQYDVII--RMNNAAPVSGFERDAGSRTTIRLILYPEPEGAPHSQEYRE-TTVALVVFK
 GPHIDQYDVII--RMNNAAPVVGFERDVGSRRTTIRLILYPEPEGAPHSANEYRK-TSMIALVVFK
 -----RLNSAPIHGFQDVGNKTTIRMSYPEGTPKSLLHDYDP-HMLFVAVMYK
 GQMVDQFDIVI--RLNNAPVHGQAQDVGNKTTIRMTYPEPEGAPVSEQEYQH-SSLFVTVLFK
 GOAVDQFDIVI--RLNNAPVKGFEKDVGNKTTIRMTYPEPEGAPVSEHEYHH-NGLFVAVLFK
 GHILNQFDVVI--RLNSAPVQGYTDHVGKTTIRMTYPEPEGAPLSDEYYYS-NDLFVTVLFK
 GPALNQFDIVI--RLNNAPVQGYADHVGKTTIRMTYPEPEGAPLSDEYYYS-NGLFVAVLFK
 GHTLNQFDVVI--RLNSAPVVEGYSEHVGKTTIRMTYPEPEGAPLSDEYYYS-NDLFVAVLFK
 GHALNQFDVVI--RLNSAPVVEGYSEHVGKTTIRMTYPEPEGAPLSDEYYYS-NDLFVAVLFK
 GYVLNQFDIVI--RLNSAPVQGYTDHVGKTTIRMTYPEPEGAPLSQHEYPP-DSLFBVAVLFK
 GHLLNQFDIVI--RLNDAPVQGYTDHVGKTTIRMTYPEPEGAPLSDEHEYPP-ASLFVAVLFK
 GHLLNQYDIVI--RLNDAPVQGYTDHVGKTTIRMTYPEPEGAPLSDEHEYPP-ASLFVAVLFK
 GHLLNRFDIII--RLNSGPLQDFSADVGNRRTTIRMSYPESCPKWEDTDP-DLKYVAVIFK
 GSLINRFDVVI--RLNSGPLGLEYTADVGNRRTTIRMSYPEGTPLHWVSDP-DITFVAVVYK
 GKMIDSHHVII--RLNDAPVKEYKKDVGERTSIRLFFFPEPALPDPLENSDNNTLMFVVPFK
 GQKIDSPDIII--RLNDAPVKGQEDVGEKTTIRLFFFPEPALPNPLDNNEEDTLMVLPFK
 GNQIDSHDFIM--RLNSGPVIGYENDVGKTTIRLCPESIISDPSQYDA-NTILVFPVFK
 GEKIDSYDVII--RMNNGPVLGHEEEVGRRTTIRLCPESVFSDFPIHNDP-NTTVILTAFK
 GATIDSYDVII--RMNNGPVLGHEEEVGRRTTIRLCPESVFSDFSSHYDP-NTTAVLUVVFK
 GETIDSPDVVI--RMNNGPVPVGYEEDVGRTTIRLCPESVFSDFPIHYDP-NTTAVLUVVFK
 GEKIDSYDVII--RMNNGPVPVGYEEDVGRTTIRLCPESIIFSDPDIHYDP-NTTVLUVVFK

GGKIDSYD VII-RMNNGPVIGYEEDVGRRTTFLRSYSESIFSDPIHYDP-NTTVVIIVFK
GGKIDSYD VII-RMNNGPVIGYEEDVGRRTTFLRSYSESIFSDPIHYDP-NTTVVIIVFK
GSKIDSYD VII-RMNDAPVVGYEEDVGRKTTFRFCYPSESIFSDPQHYDE-NTTIVLLAFK
GKKIDSYD III-RMNDGPVLGYEDDVGRKTTFRLCYPESIFSNSLHYDP-NSTVLLMFK
GEVIDNDVVF-RLNSAPТИNHENDVGRKTTFRMAYPESAFRRPEQYDP-GWTFVLMMFK
GSHIDQYDAVF-RLNVAPIKGYESDVGTKTTIRAVYEPSSNIGSKAYTQ-NWTLVVVPK
GSHIDQYDAVF-RLNIAPIKGYESDVGTKTTIRAVYEPSSNIGSKAYTQ-NWTLVVVPK
GPIQIDDPDIVI-RMNNGPVKGYEEDVGHKTTIRMSYPEGALQDPGGYHQ-DSLFLMVBFK
GPQIDDPDIVI-RMNNGPVKGYEEDVGHKTTIRMSYPEGALQDPGGYHQ-DSLFLMVBFK
GRVIDEYD VVI-RMNNPSVKGYEKDVGTKTTIRITYPSEGAPRKNLYDVB-DALLGIVVVK
GSKIDEYD VII-RLNGAPVKGYESDVGTKTTIRITYPSEGAIQKAEGYEK-DSLFLVFAGFK
GSRIDQYDV VI-RLNEAPVKGYSKDVGSKTTMRITYPSEGAIQKPENYED-NSLFVFSAFK
GSRIDEYDV VI-RLNEAPVSGYKVGDVGTKTTMRITYPSEGAIQKPERYEK-DSLFLVFSAFK
GSRIDEYDV VI-RLNEAPVKGFEKDVGSKTTLRITYPSEGAIQKPERYEK-DSLFLVLAGFK
GSKIDDYDV VI-RLNEAPVKGFKEVDVGSKTTLRITYPSEGAIQKPERYEK-DSLFLVAGFK
GSKIDEYEV VI-RLNSAPVKGFEKDVGSKTTLRITYPSEGAIQKLEQYEK-DSIFVLAGFK
GSKIDEYEV VI-RLNSAPVKGFEKDVGSKTTLRITYPSEGAIQKLEQYEK-DSIFVLAGFK
GSRIDDDIV VI-RLNSAPVKGFEKDVGSKTTLRITYPSEGAMQRPEQYER-DSLFLVLAGFK
GSRIDDDIV VI-RLNSAPVKGFEDVGSKTTMRITYPSEGAMQRPEQYER-DSLFLVLAGFK
GLKIDDYDV VI-RLNSAPVKGFEDVGGKTTMRITYPSEGAIQKPEQYEK-DSLFLVLAGFK
GVKIDDYDV VI-RLNSAPVKGFEDVGGKTTMRITYPSEGAIQKPEQYEK-DSLFLVLAGFK
GVKIDDYDV VI-RLNSAPVKGFEDVGGKTTMRITYPSEGAIQKPEQYEK-DSLFLVLAGFK
GLKIDDYDV VI-RLNSAPVKGFEDVGGKTTLRITYPSEGAIQKMEQYEK-DSLFLVLAGFK
GLKIDDYDV VI-RLNSAPVKGFEDVGGKTTLRITYPSEGAIQKMEQYEK-DSLFLVLAGFK
GORIDDDIV VI-RLNEAPVRGFERDVGSKTTMRITYPSEGAIQKTERYEA-QSLFVLSAFK
GTKIDQYDV VI-RLNEAPVAGFEKDVGSKTTMRITYPSEGAIQRAERYEK-SSLFVLSAFK
-----MNDAPLRGHVGDVGSRMMRLCYPESAHVRREDFP-SALLAFVFPK
GHQINKYDIVI-RLNNAPVHQYQSDVGNKTTMRLFYPESADFDTPQLDNPDTLLVLPFK
GETINKYDV VI-RINNAPVHKYEKDVGSKTTMRLFYPESADFDTPQLDNPDTLLVLPFK
-----K
GDAINKYDV VI-RLNNAPVAGYEGDVGSKTTMRLFYPESAHFDPKVENNPDTLLVLPFK
GGVINKYDV VI-RLNNAPVAGYEGDVGSKTTIRLFYPESAHFDPKIENNPDPLLVLVLPFK
GDTINTYDV VI-RLNNAPVHGYEQDVGSKTTMRLFYPESAHFDPQAENNPTLLVLPFK
GDTINTYDV VI-RLNNAPVHGYEQDVGSKTTMRLFYPESAHFDPQAENNPTLLVLPFK
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GDVINKYDV VI-RLNNAPVHGYEHDVGSKTTMRLFYPESAHFNPKTENNPTLLVLPFK
GNEIDKYDV VI-RLNSGPVGRYEKDVGTKTTMRLFYPESAILDTYKHDTSDTLEVFPVYK
GAKINTYDV VI-RINNGPIRGFEKDVGNKTTLRLFYPESAIANPSREDNPDTLHVFPVYK
GRIINNYDV VI-RLNDAPVRGEEDVGNTKTTMRFFYEPESASHNPDLIHDNPDTLMVLVLPFK
GRNINKYDV VI-RLNEGPVDRYEDDVGNKTTMRFFYEPESASHNPDLIHDNPDTLMVLVLPFK
VLDIEWLKSIFFTTHPI-----SKGWTHLPTNGLKPT--DAMVHPEFIYYVAKTW-L
VIDLOWARSAITRTGEI-----TKTYTNVRKIRVTPS-KLFYNPALMYHIREW-I
PLDLKWMKTSLTDGSI-----TRTWTRVKGRKANKT--KILVYNPAFFKYVNDKW-T
PQDVKWLSSALTGEL-----TNTYQPVISRVTCDKS-KIVIISPTFIRVHDRW-T
PLDIKWLSSALTGEI-----TRYQPPLVRVTCDKS-KITIIISPTFIRVHDRW-T
PLDVSWLSSALTGTI-----VRTYMPVRKQINVSKX-MIEVYNPAFMYYVHKTW-N
LKDMQWLLSSALTGEI-----KMTYMRVKNRIDADKD-KVMVVPNAFFKYTHDRW-T
VLDIEWLKVSSALTGTI-----SHTYAMVPSRIKTSRD-KILVYNPAFFKYVNEYW-L
TLDLQLWLASALTHTGI-----NRTYVQVPRKIRVSKD-KVLVYSPLEMKYVYDKW-L
TLDLQLWLASALTHTGI-----NRTYVQVPRKIRVSKD-KVLVYSPLEMKYVYDKW-L
TMDDLQLWLISALTKGTI-----NFTYVPVPRKIHVNRE-KILIYHPAFIKYVFDW-L
ITDLQWVVSATTKGTI-----SHTYVPVPMKIKVKE-KILIYHPAFIKYVFDW-L
TIDLEWVVSATTGTI-----SHTYIPVPAKIRVKQD-KILIYHPAFIKYVFDW-L
TVDLEWVVSATTGTI-----SHTYVPVPAKIKVKN-KILIYHPAFIKYVFDW-L
TLDLWRIVTALTGTI-----NFTYVPVPRKIKVKE-KVLVYNPSPIFIKYVNEYW-L
TLDLWRIVVTTALTGTI-----NFTYVPVPRKIKVKE-KILVYNTFMKYIYEW-L
ILDLRWVVISALTNGTI-----NSTYIPVPRKIKKANKD-KIMVYHPTFMKYVYDNW-L
TLDLWRIVSALTGTI-----NSTYVPPVPRKIKVKRD-QILVYHPPFIKYVYDW-L
TLDLWRIVSALTGTI-----NSTYVPPVPRKIKKANKN-KILVYHPVFIKYVYDNW-L
IMDFEWIRSALTGEI-----TRTYFRVQOFIKADKD-KVLIINPTFFKYVCDHW-T
PLDLKWLASAFSSGEI-----PSTYRRVKQFVEADKS-QVRIINPAFLKYIQDKW-T
PLDLKWLASALTGD-----RHTYKRVKQFIKADKS-KVRLYPGFLKYIQDKW-T
PLDLKWITSASFSTGEL-----RYTYTRVKQFIEADRS-QVLILNPNAFLKYIHDWK-T
PLDLKWITSASFSTGEL-----THTYTRVKQFIKADRN-KVLILNPNAFLKYIHENW-T
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TLDLQWVVISALTGSI-----KHTYIPVPAKIRVKQD-KILIYNPAAFFKYIHDWK-T
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TLDLWVVISALTSGI-----RFTYAPVKQFLRVDKD-KVQIFNPNAFFKYIHDWK-T
TLDLWVVISALTSGQI-----RLTYAPVQFLRVDKD-KVQIFNPNAFFKYVHDWK-T
VLDLWWVITSALSTGEI-----TRYGQKPLDVNIKTDSRQLVLIYNPAFFKYIHDWK-T
TLDLWWVITSALSTGEI-----RFTYAPVKQFLRVDKD-KVQIYNPAFFKYIHDWK-T
ALDLLWVITSALSTGQI-----RFTYAPVKFLRVDKE-KVQIYNPAFFKYIHDWK-T
ALDLLWVITSALSTGQI-----RFTYAPVKFLRVDKE-KVQIYNPAFFKYIHDWK-T
ALDLLWVITSALSTGQI-----VFTYAPVKFLRVDKE-KVQIYNPAFFKYIHDWK-T
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TLDLWWVITSALSTGQI-----RFTYAPVKFLRVDKE-KVQIYNPAFFKYIHDWK-T
TLDLWWVITSALSTGQI-----RFTYAPVKFLRVDKE-KVQIYNPAFFKYIHDWK-T
TLDLWWVITSALSTGQI-----RFTYAPVKFLRVDKE-KVQIYNPAFFKYIHDWK-T
ALDLLWVITSALSTGQI-----RFTYAPVKSFLRVDKE-KVQIYNPAFFKYIHDWK-T
LQDLKWITSALTGEV-----TYTYTRMKKFIKADKD-KVLIFNPSFFFKYVNDNW-T
LQDLKWITSALTGEV-----TYTYTRVKKFIQADKD-KVLIFNPSFFFKYVHDNW-T
LQDLKWITSALTGEV-----TYTYTRVKKFIQADKD-KVLIFNPSFFFKYVHDNW-T
PQDLKWVVASAFSTGEL-----KFTYMRVQKFQFIKADRD-KVLIFNPSFLKYIHDWK-T
PLDMEWIWSALTTGNI-----KFTYRVVSVSKIHLQDQD-KVLIFNPAFLKYIHDWK-T

VLDIIEWLISSFTTKNI-----TRTYKKVVRASINANRH--KVMILHPAFIKYVHEIW-L
 TLDLQWIIISALTTGTI-----SRTYMRVKERIQADKD--KVVVINPRFIKYVYESW-L
 TLDLQWIIISALTTGTI-----KHKYVPVMSRIKANKD--KVVIYSPTFFKVVYESW-L
 TLDLQWIIISALTTGAI-----KHTYVPVMSRIKANKD--KVVIYSPTFFKVVYESW-L
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 VKDMQWLISVFTTKHI-----TSTYLKVRPTINADRE--KVMIIHPAFIKYVYESW-L
 ILDMQWLISVFTTKHI-----TRTYMSVPSTINADRD--KVMILHPBEFIKYVNDKW-A
 LSDYQWLYDVVIKGKNP--LKRIGAHFWSVPMFDKNVN--KIRILNPYIHEEAKVYH-L
 LSDYQWLYDVVIKGKNP--LKRIGAHFWSVPMFDKNVN--KIRILNPYIHEEAKVYH-L
 SNDLNWLQALILTGVK-----TGQFWKGVAQKLIDPA--QFLILNPQVLHVAARDV-
 TDDLAWLAVVQKEKP-----EGSFWKEIGETLNVDS--HHILNLPQIARSTSYEH-
 TDDLAWLAVVQKEKP-----EGSFWKEIGETLNVDS--HHILNLPQIARSTSYEH-
 SLDDLAWMTSVVTKEPL--VWWSLWFWFKWDVIDSIPQPE--NVRILNPPEIMYRTGQL-Q
 SLDDLWLSIVSVTRRPL--GFWSKLWFWRREVVEDIPLTRE--SFRILHPEIIRRGTGQL-Q
 SLDDLWLSVITKPL--SFWSKMWFWRREVVDIPLSPE--SFKILHPEIIHKTGQL-Q
 GVDFSWLKAMVKEEVVSIFIHKLWFWQSUVESIPLKVE--NFRIFLNDIIRETALNFB-L
 HADFRWLLEAVLNQNKL--SAWNRRFFWKRTVDKIPLNSS--QFRVLNPLIIKETAIDI-L
 SADFRWLQAMLKNESL--SIWSRMFFWKQVVEENIPVQSK--QFRILNPPLIVKETAIDI-L
 SVDFNWLQAMLKNETM--PLWVQLFFFWKVAEKIPLQSK--QFRILNPVIIKNTAIDM-L
 SVDFNWLQAMVKNESV--PLWVRLFFFWKVAEKIPLQSK--QFRILNPVIIKETALDI-L
 SVDFNWLQAMVKKETL--PFWVRLFFFWKVAEKIPLQPK--HFRILNPVIIKETAFDI-L
 SVDFKWLQAMVKNESL--PFWVRLFFFWKVAEKVPLQPK--HFRILNPVIIKETAFDI-L
 SVDFGWQIAVAVVKNETL--PLWMRLLFFFWKVAEKIPVMPK--QFRILNPAAIKETALDI-L
 GVDFNWLQAMVKNETL--HLWVRLFFFWKVAEKIPFTPK--QFRILNPVIIKETALDI-L
 SVDFNWLQAMVKNETL--SLWIRLFFFWKVAEKIPFTSK--QFRILNPVIVKETALDI-L
 SVDFHWRLLRAMISRTPV--SLWDRLLFWQNVPMSVPVKT--QFHLLNPQIIREMALDL-L
 GVDVSWTTAMINRISV--PLWDWLFFFWKVDPHDIPLDOSH--RFRLLNPGVIRETALDL-L
 PLDFWLRLREVLLKTKN--KTKEGFWRQOPQEWNWNIS--QIRILNPYVTYBAYTKL-L
 AEDFIWVKEILRKTPS--KTSKGFWKPPPQVWNGKAS--HLRVLPNPFVTYETTYII-L
 PLDLRWLVDVIVPKNKV--VRGFWKPPASIIYRNN--QIRILNPSIVKRAAFDL-L
 PHDLRWLELLMGDKI--NTNGFWKKPALNLIYKPY--QIRILDPEIIRTAAYEL-L
 PQDLRWLVEILLGKKI--NTQGFWKTPALKIYKQY--QIRILDPEIISEAAFQML-L
 PYDLKWLWDLLSGQRI--KTSAFWKKPALQLIYNAQ--QIRILDPAITRRTAHDM-L
 PRDLKWLWEILGGQKI--SAKGFWKPKPALNMIFYKSS--QIRILDPSITRKTAYEW-L
 PRDLKWLWEILGGQKI--SAKGFWKPKPALNMIFYKSN--QIRILDPSITRKTAYDW-L
 PRDLKWLSELLLHKRA--STFGFWRKPAKMMYDLE--QIRILNPTLVRKVAHGL-L
 PHDVKWLSELLMHKR--STYGFWRKPAKMNLIYKPH--QLRVLNPFILRQASQNL-L
 PLDLWVLETIIRGRKM--NSRDGFWKPKPLSVPKPTK--DFRIFNPPEILQDTASM-M
 TNDLKWFDTVIEGRDL--GFWSTTVDVFVPKPRK--DLRLYNPEITSELFSNL-I
 ANDLKWLDTIIEGRDL--VSKKLKGFWSTTVDVFVPKPRK--DLRLYNPEITSELFSNL-I
 SLDFLWLQRIIGKQSV--GDTASRFWKSIAHAIPKNAD--KFRIVNPALLQETSFDL-I
 SLDFLWLQKIIIGKQSV--GDIASRFWKSIAHAIPKNAD--KFRIVNPALLQETSFDL-I
 LADLNWLDSVLHRKTP--STKGFWKSIAMSVPKNPR--QTRIINPLIIREASFDBL-L
 PQDFKWLKCIVYKEKV--SPSDGFQWVQEATRIPINPS--QFRILNPPLIVKETALDM-L
 PLDFKWLQMVYKEKV--RGMEGFWSVQAQVVPRAFA--DMRILNPYFIEAAQFQF-I
 PLDFKWLQMVYKEKL--VRLEGFWKSVARVYVPREPS--EIRILNPYFIEAAQFQF-I
 PLDFKWLQMVFKEKL--KGTEGFWKSVAHVVPREPT--EIRILNPYFIEAAQFQF-I
 PQDFKWLKYIVYKEKV--SPSDGFQWKSVATAVPKEPK--DIRILNPYFIREAAFMF-I
 WQDFKWLKYIVYKEKV--SADGFQWKSVATRVPREPH--EIRILNPYFIEAAQFSF-I
 WQDFKWLKYIVYKEKV--SASDGFWKSVATRVKEPP--EIRILNPYFIEAAQFTL-I
 WQDFKWLKYIVYKEKV--SASDGFWKSVATRVKEPP--EIRILNPYFIEAAQFTL-I
 WQDFKWLKYIVYKEKV--SASDGFWKSVATHVPREPH--EIRILNPYFIEAAQFSF-I
 WQDFKWLKYIVYKEKV--SASDGFWKSVATHVPREPH--EIRILNPYFIEAAQFSF-I
 WQDFKWLKYIVYKEKV--SASDGFWKSVATHVPREPH--EIRILNPYFIEAAQFSF-I
 WQDFKWLKYIVYKEKV--SASDGFWKSVATHVPREPH--EIRILNPYFIEAAQFSF-I
 ALDFKWLRLHMVNQRL--HSTDGFWKSVARHVPRDGL--DMRILNPYFIRASFBL-I
 SNDFKWLRLHMVYKDRL--WRMDGFWKSVARVVPRAPO--DMRILNPYFIEAESFRL-I
 TRDLQWLGLVNLNHHR--GPRGFWKVKVPTELQFPAS--RIRILNPFAVREAATEP-L
 VLDLQWLKSILNNEKR--PAKGFWKPKPPIIWLGVKAS--NLRILNPYFMEVTASKL-L
 PLDIQWNMKIIILNNEKR--VRKGFWKMPPIIWEVEPE--NIRILNPYFMSVTATQI-L
 NQSIHYEKVMLKAMR--VYRGFWKRPPIIWKSNSPE--YVRILNPFFMRRMTATRL-L
 AMDFHWTIILSDKKR--VRKGFWKQPPLIWDVNPK--QIRILNPFFMEEAADKL-L
 AMDFHWTIILSDKKR--VRKGFWKQPPLIWDVNPK--QIRILNPFFMEEAADKL-L
 PVDQWNEMAILSDKR--VRKGFWKQPPLIWDANPE--QVRILNPYFMEVTAAKL-L
 PMDFQWNEMAILNDKKR--VRKGFWKQPPLIWDANPE--QVRILNPYFMEVTAAKL-L
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 PMDFLWNETILHDKKR--IRKGFWKQPPLIWDANPE--QVRILNPYFMEVTAAKL-L
 ENDLRWLKSILNNEQR--QV1VQGLWKSAPIVWNVSPT--KIRILNPYFMEVTAAKL-L
 VGDIQWLKLTILYHEPA--VQGFQWKLPPSVVRTNSS--NFRILNPYFMEVTAAKL-L
 PDDLRWLKEILYDEKR--VRKGFWKQPPLIWLQGSS--KVRVLDPYFMCQTANKL-L
 QDQLRWLKEILYDEKR--VSKGFWKPPPKIWLGRAS--QIRVLDPYFLLITARKF-L
 QDQLRWLKEILYNEKR--VRRGFWRPPPQVWLGDVS--KIRVLDPHFLQTAEML-L
 -----EGKGGRWASAGALSVVWALHICNEVDVFGFA---NKYGNWDHYE
 -----DRKGGRYPSSGTIALVFFALQFCDEVSVYGMGA---NSKGFWDHYWE
 -----EHHGRYSSSTGSILVLFAVHVCDDEVVYGYGA--DAQGNWHHYWE
 -----QHHGRYPSTGLIAIYALHECDQVLDLYGFGA--DSAGNWWHHYWE
 -----QHHGRYPSTGLALALIYALHECDEVVYGYGA--NRAGNWWHHYWE
 -----ELHGRYPSTGMIVLLFAMHICDQVNFGFGA--TSKGHNWDHYQ
 -----ERHGRYPSTGIVAIIFALHLCDEVSVPGYGA--DAQGNWHHYWE
 -----NRHGKYPSTGIMCIVFALHVCDQVLDLYGFGA--DANGNWWHHYFE
 -----LNHGRYPSTGLLAVIFALHVCDKVDLYGFGA--DSKGHWWHHYWE
 -----LNHGRYPSTGLLAVIFALHVCDKVDLYGFGA--DSKGHWWHHYWE
 -----QAHGRYPSTGILSVILSILHICDKVDLYGFGA--DSKGHNWHHYWE
 -----QGHGRYPSTGILSVIFSLHICDEVLDLYGFGA--DSKGHNWHHYWE
 -----QGHGRYPSTGILSVIFSMHVCDDEVLDLYGFGA--DSKGHNWHHYWE
 -----QGHGRYPSTGILSVIFSLHVCDDEVLDLYGFGA--DSKGHNWHHYWE

----- QNHGRYPSTGLLSVIFALHVCDEVNVYGFQA --- DSKGHWHHYWE
----- EHHGRYPSTGLLSLMFALHVCDEVNVYGFQA --- DSKGHWHHYWE
----- QRHGRYPSTGFLSII FALHLCDEVLDLYGFQA --- DSKGNWHHYWE
----- QNHGRYPSTGILSVIFALHLCDEVDVYGFQA --- DSNGNWHHYWE
----- QHHGRYPSTGFLSVIFALHLCDEVDLYGFQA --- DSKGNWHHYWE
----- EHHGRYPSTGMLTALVFALHICDEVSVPGYGA --- DSNGNWHHYWE
----- KHHGRYPSTGFLTAIFAHTCQVSAGFGA --- DNNGNWHHYWE
----- KYHGRYPSTGLTALIFAHTCTQVSAGFGA --- NSNGNWHHYWE
----- QHHGRYPSTGLTALLFALHICDQSVSRVCGA --- DSRGNWHHYWE
----- ERHGRYPSTGTALLFALHACQQSVPGFQA --- DSKGNWHHYWE
----- QHHGRYPSTGTALLFALHACQQSVPGFQA --- DTKGNWHHYWE
----- EHHGRYPSTGMVLFFALHVCDEVDVYGFQA --- DSRGNWHHYWE
----- KKGRYPSTGMTLIFALHICDEVNLYGFQA --- DSRGNWHHYWE
----- RHHGRYPSTGMVLFFALHVCDEVNVYGFQA --- DSRGNWHHYWE
----- RHHGRYPSTGMVLFFALHVCDEVNVYGFQA --- DGRGNWHHYWE
----- EHHGRYPSTGMVALFFALHVCDEVDVYGFQA --- DSRGNWHHYWE
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----- EHHGRYPSTGMVLFFALHVCDEVNVYGFQA --- DSRGNWHHYWE
----- NHHGKYPTGMIALVFAHLHICDEISVFGFQA --- DQHGNWHHYWE
----- NHHGKYPTGMIALVFAHLHICDEISVFGFQA --- DQHGNWHHYWE
----- NHHGKYPTGMIALVFAHLHICDEISVFGFQA --- DQHGNWHHYWE
----- VHKGKYPTGMIALFFAIHICDESVFVFGYGA --- DSNGDWHHYWE
----- NHHGKYPTGMIALVFAHLHICDEISVFGFQA --- DRKGSWHHYWE
----- VKHKGKYPTGFLAIIFALHICDQVSTFGFQA --- DQYGNWHHYFE
----- EGRGHYPSTGFLTMALFALHICDEEVSVFGFQA --- DQHGNWHHYWE
----- EGHGRYPSTGFLSLLAVHICDKVSFVFGFQA --- DQYGNWHHYWE
----- DCHGRYPSTGFLSLLAHIICDQVSFVFGFQA --- DHYGNWHHYWE
----- QKHGRYPSTGFTLIFALHICDQVSFVFGFQA --- DKDGNWHHYE
----- RKHSYPTGFTLIFALHICDQVSFVFGFQA --- KLDGNWHHYFD
----- EGHGHPSTGFLTLMALFALHICDEEVNFVFGFQA --- TSEGQWHHYFD
KNNVSTS ----- MTKHQKPSCGIVGVIMALHYCDEVDFVFGFQA --- NKYGNWDHYYE
KNNVSTS ----- MKTHQKPSCGIVGVIMALHICNEVDVFGFQA --- NKYGNWDHYYE
----- RLQGKWPITGLIATTFAHLHVCDVVDLAGFY --- GSSIFSHYYE
----- VGMINIPTIGTISIITAFHFCDMVDIVGFGL --- RHDKLYHYE
----- VGMINIPTIGTISIITAFHFCDMVDIVGFGL --- RHDKLYHYE
TYAEQ ----- QRKVMVPTLGITAVVVALQVCDEVSIAFGFY - DLQHPGAPLHYYG
RYTL ----- TRGKMPVTLgasavvmalqvcdqvsLAGFY - DMQHPQSOLHYE
KYTL ----- KQGNMNPTLgasalvmaqlcdqvsLAGFY - NMQHPEARLHYE
SYPDPHSSQW ----- KWMVNIPTLGVSAVVLATHLCDEVSLAGFY - NLGEPDPTLHYE
GFPKPQKRWL ----- GWDKNVPPTGMAVIALATHLCDEVNLAGFY - DLSQPDASLHYD
QYPEPQNKWW ----- GWEKNVPPTLGVAVVLATHLCDEVSLAGFY - DLRQPRAPLHYD
HYSEPQPRIW ----- GWSKNVPPTMGVVAVVLATHLCDEVSLAGFY - DLSRPKPLHYFD
QYSEPPRSKIW ----- GWDKNVPPTGIVTAVVLATHLCDEVSLVGFY - DLSQPNTPLHYD
----- QKGRYPSTGFTLIFALHICDQVSFVFGFQA --- DQYGNWHHYE
----- RKHSYPTGFTLIFALHICDQVSFVFGFQA --- KLDGNWHHYFD
----- EGHGHPSTGFLTLMALFALHICDEEVNFVFGFQA --- TSEGQWHHYFD
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EYEPPRPKFW ----- GWDKNVPPTGIVTAVVLATHLCDEVSLAGFY - DLSQPNTPLHYD
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QLNASMP ----- HKGKRYATTGIIALNLALHLCQEVNIAGFGYPGNHDTTTPHYYN
KLR ----- KSSQKWSTTGFIALNLALHICHEVSIVGFYGDINDNVTVPHYKK
KLPMDP ----- LQPPQYPTGIIIAISMALTCNEVHAGFY - DFINMNSTLHYYS
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GYPTNGL ----- KMKNVPTSGTISIMLALRCLDEVDVVVGFY - NTKEPEALIHYE
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 KSKKMT-----PKMI PKPTTGLLAITFALHFCDMVHIAFGFGYPALTNKQPIHYYE
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 QPFLAPKK-----GQNHFHPTTGLLAIFVALNYCDMVHIAFGFGYPKSDKRQPIHYYG
 Q-----IPVQVHPTTGLLAIFVALNYCDVHVAGFGGPASRNQNQPIHYYG
 HMRQQIKG-----RPNLVHPTTGLLAIVALVANLYCDEVHIAFGFGYPNSKRESQPIHYFG
 KFSSK-----EKDPFRR-----TGVHDANIEE-----
 VNDSG-----RNSAFLK-----THVHDSVHEFEVIKLLADEKIIT--MFQGVR-----
 THYSG-----AAHRS-----TGVHDSBFERVLLKELKQSEGIK--IHRGNAANK-----
 DLPPH-----IAGAFRQ-----TGVHDSKESSMINQLIHHLRLL--LHVPKGDL-----
 DLPPH-----VAGAFRK-----TGVHDSAQENEIIDQLHIIHGLR--VHRSEQSS-----
 PPVEPSLEKSAFKL-----TGVHNAEFETDINVQLEEIGKIT--VYRGSRV-----
 YNRYA-----GAFRK-----TGVHNADEFETEIQRSAEGKIK--LYR-----
 NTTKP-----SGFRK-----SGVHDADFQANITENLSSINKIN--FFTGR-----
 NNASA-----GAFRL-----TGVHDCDFEASILANLTSINKVL--MFRGR-----
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 ENHYA-----GAFRK-----TGVHDANFELGLIERLILAEGKVL--FYK-----
 DNRYG-----GAFRK-----TGVHNATFELQLIERLILAEGKLS--FYK-----
 ANRYP-----GAFRK-----TGVHNAGFELTLIKKLAEGKIS--FYN-----
 ENRWS-----GAFRR-----TRVHDADVEFSLIQRLAAEGRIL--FYQ-----
 KNRWS-----GAFRR-----TGVHDADTEFSLIERLAAEGRIL--FHR-----
 NNRYA-----GEFRK-----TGVHDADFEAIIDSLVQIGKIR--VYRGK-----
 NNQHA-----GAFRA-----TMVHDCDFEANITRALASIKKVN--IFKG-----
 QNORYS-----GEFRK-----TGVHDADFEAQIIDKLAKAGKIS--VFPGK-----
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 RNRFA-----GAFR-----TRVHNNAEFELDLIRQLAYEGKVT--YH-----
 NNKHA-----GAFQK-----TGVHDAKMEMIIRKLVVEEGKIT--FYNETKVKY-----
 KTSSR-----VR-----TGAHSGSFEDTMMQMLYLELESKIR--VFRGR-----
 HNOLA-----GAFRH-----TGVHDCDYEVNTLLTLADKHKIQ--MFRGR-----
 ENSLA-----GAFRH-----TGVHDCDYEVNTLLTLADKHKIQ--MFRGR-----
 ENSLA-----GAFRH-----TGVHDCDYEVNTLLTLADKHKIQ--MFRGR-----
 HKKHP-----RN-----AGNHGGSYERYLIALKLHEKQGIR--LYKGW-----
 ESLAH-----FNR-----GRHGGDYENRTHKLLLMNKA--LHKGL-----
 DSMTS-----F-----SNLHGGDFENQTIHFHLHQQNKIS--LHKGWT-----
 KFSSK-----EKDPFRR-----TGVHDANIEETVRMELHKEKIIIR--FHPGNPA-----
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 RDKTG-----GLPAG-----GTQHNVTVEKEYLIRLDEGVISHDLTGVYKNSSKTRSS-----
 NKTIE-----GEFEG-LFSYFTLICHDAKEKEYIKDLVRNAVNN-DLTHGYED-----
 NKTIQ-----GEFEG-LFSYFTVIHDAKEKEYIKDLVRNAVNN-DLTHGYED-----
 SLRMD-----AMKT-----QVHVDSAETVFLKELVKAGAVR-DLTGAL-----
 AVPM-----AMKA-----QVHVDIAGAEKLFLRDILVAAGATT-DLTGAL-----
 AIRMD-----AMKA-----QVHVDSAELKFLRDILVAAGAVT-DLTGAL-----
 NVRME-----AMKA-----QTMHNVETERKFLAGIVEKGVV-TDLGGI-----
 NRCMN-----SMND-----QPMHDVTKEKKMLRTLVKEGVVR-DLGGIHCACFCDTQH-----
 DLCMS-----EMKA-----QKMHDVTKEKLLQKLIKEGVVK-DITGGI-----
 NLCMA-----AMNI-----QTMHNLTETRFLQKLVKEGIVK-DLGGIHCCEF-----
 TLCMA-----AMNG-----QTMHNVTRETLFLQKLVQEEVVK-DLGGIHCDFCKKES-----
 SQCMCA-----AMNF-----QTMHNVTETKFLKLVKEGVVK-DLGGIDREF-----
 SQCMG-----AMHW-----QVMHNVTETKFLKLKKEGVVE-DLGGIHC-----

NLCMA-----AMNE-----QTMHNVTETKFLQQLIKEGVVK-DLSGGIFCTYCKSS
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 NLCMA-----AMNR-----QTMHNVTGETKLLQKLKEVVK-DLTGGIH-----
 SVPMT-----TILK-----EAMHNVKETVFLKRIVASGSIT-DLTGGIHCSFC-----
 KLPMR-----VMQQ-----QTSHNVKEBETAFLQQLIQDGAVT-DLTGGIHCSFCPR-----
 TGLSR-----KNE-----LFQHNLTAEERNWLLKMIIEWGVIA-DLTSH-----
 NDYVS-----SL-R-----LMPHDIPTEQMWLKLVEKGTLIS-DLSLT-----
 NDTMS-----SMGK-----
 NATMS-----LMNK-----NAYHNVTAEQLFLKDIIBKNLVI-NLTQD-----
 NATMS-----LMKQ-----NAYHNLTAEQLFLNDI1KKKMVI-NLTQN-----
 NDTMS-----QMMK-----NAYHDIAVEQRFLKELIDLKILI-NLT-----
 NETMS-----QMMQ-----NEYHNITAEQKFLKKLDKNFVV-NLT-----
 NETMS-----QMMQ-----NEYHDISAEQKFLKKLDKNFVV-NLT-----
 NETMS-----QMMQ-----NEYHDISAEQKFLKKLDKNFVV-NLT-----
 NDTMF-----SMTK-----TEYHNITAE-QMLLFIEKNNTIV-----
 NETMS-----VMAQ-----NEYHNISAEQMFIIRDIEHKTIK-NLT-----
 SLPMR-----EIWK-----SWTHDIDHERGLRLLKQQGIIT-DLSGGI-----
 SQKTK-----AILS-----SFTHDIDHETKFLHKLVEQGVIN-DITGGRTKL-----
 SQKTK-----AILS-----SFTHDIDHETKFLHKLVEQGVIN-----
 DAKMS-----SIAK-----SWTHDINKEKEFLKTLVRNGVIT-DLTGGIIGHV-----
 DAKMS-----SIAK-----SWTHDINKEKEFLKTLVRNGVIT-DLTGGIIGHV-----
 KVJKM-----IITS-----LFTHDINHETAFLKKLVEF-----
 SIKML-----AIKE-----SWTHNIGREKEFLRKLVKGQVIS-DLTNGI-----
 TVRMS-----TIKE-----SWTHNIPKEKEFLRKLVKANVIT-DLTNGI-----
 SVKMS-----AIKE-----SWTHNISKEKEFLRKLVKANIIT-DLTNGI-----
 TFKMS-----AIKE-----SWTHNIAKEKEFLRKLVVRANVIT-DLTNGI-----
 TIKMS-----AIKE-----
 TIKMA-----AIKE-----SWTHNIQKEKEFLKKLVKARVIN-DLTNGI-----
 TIKMA-----AIKE-----SWTHNIQKEKEFLKKLVKARVIN-DLTNGI-----
 TVRMA-----AIKE-----SWTHNIQREKEFLRKLVKARVIT-DLSGGI-----
 TVRMA-----AIKE-----SWTHSIQREKEFLRKLVKARVIT-DLSGGI-----
 NIKMS-----AIKE-----SWTHNIQREKEFLRKLVKARVIT-DLTSGI-----
 TIKMS-----AIKE-----SWTHNIQREKEFLRKLVKARVIT-DLTSGI-----
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 KIRMA-----AIKE-----SWTHNILREKEFLRKLVKAGVIQ-DLTNGI-----
 KLRMS-----AIKE-----SWTHNISREKEFLRKLVKAGVIE-DLTGHI-----
 QDTMS-----SIIK-----STYHNITIERTFLKKLKEGEAIV-DLTQLAGT-----
 KATLK-----SM-A-----VSDHN-----
 KVTLK-----SMF-----ASEHNITVEAQAIKNLFQQNIIH-NLTYP-----
 KVMLK-----TMRP-----SG-HNISQEALAIKRLLDIAIK-NLTYP-----
 QITLK-----SMAG-----SG-HNVSQEALAIKRMLEMGAIK-NLTSP-----
 QITLK-----SMAG-----SG-HNVSQEALAIKRMLEMGAVK-NLTYP-----
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 QITVK-----SMAV-----SG-HNVSHEAFAIKKMLEGLV-----
 SSTML-----VM-----
 QRNMK-----TMSVS-----
 YHTMK-----SM-K-----NSPHDVSGREGRALKRLEDGAVM-YLH-----
 QQTMK-----SMFQ-----NSYHDLNQEQAQILHRLEEQGVIL-YLHPHS-----
 RDTMK-----SM-Q-----NSYHDLGHEAEALKRQLDSGAIL-KLH-----

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Skow_ST6GAL_02430 VCTLR-TA-A---LKILDRTQSPFNKLG-LSRYLPN----GSAFLEM----KTYKWC
 Skow_ST6GAL_02428 VCKFKLSA-N---ASVLDKSTRPYQDGLG-LSKYFPK----KNIFNAH----EKRYNTC
 Skow_ST6GAL_02427 LCDLKRR-A---YDVLKRDTPFKBEG-ISKYFPB----ISLYEKF----KGFBSC
 Skow_ST6GAL_02429 -----MMGYDTTPFKEMG-ISKYFPG----RNIFYKY----N-YSRC
 Dsim_ST6GAL_02400 TCLVMEA-G---VRVLRKDAPFNKLP-FGRLFPR----QKLFRN----VKDIKTC
 Dsec_ST6GAL_02401 TCLVMEA-G---VRVLRKDAPFNKLP-FGRLFPR----QKLFRN----VKDIKTC
 Aaeg_ST6GAL_02407 LCRLKRA-D---VRTLSWRDPFWNNE-IGSYFPL----NPLFKE----R-NASC
 Cqui_ST6GAL_02409 LCRLTR-A---VRTVTWRDSPFDWNE-IGRYIPP----GPLFRE----R-NATC
 Bflo_ST6GAL_02425 LCELKNRV-W---FKTLPSTECPFKALN-YSLEPK----NTLYQLH----HDGFKTC
 Bflo_ST6GAL_02426 LCSLQSA-AR---FRTLPADESPWKQLG-YGDIEAR---PGLLQLY----AGGFRTC
 Phumcor_ST6GAL_02412 KCRLKSEL----RLTCKKDLFSFTLN-NLNRNDKN--EKEEEFLE----GMQYKTC
 Apis_ST6GAL_02408 TCDMASSVEK----FRTLEKND--IDHM-LTKNIPD----VPLFDD----NEVFGTC
 Tcas_ST6GAL_02413 MCELEKI-Q---VKTLLKRGDVAGGPBNH-LGDFLPK----RGLFE----NRNFNSC
 Bmor_ST6GAL_02414 MCALKRI-K---VNTVTKRDEPFAR--YDFQIPE----GPLQD----GTFYNTC
 Dpul_ST6GAL_02410 TPSMLLENL----QNSLEKSHFTITS-LTTVFPKEKQLLKNSQAF----QKRYKSC
 Isca_ST6GAL_02411 VCSLSRLFP----TPRDLTEPFKRMG-YSRVFPT----TNLY----ESCYNSC
 Lpol_ST6GAL_02415 VCSAKHDHPV-----SMLSADDTFFKEIG-LAPLFPN----KNFNQV----LGLYNSC
 Pmar_ST6GAL_02423 LCLVAERV-TALRSTLTLGGSEPPFSAMGAWSREALDA----GGLERA-VSGGSRSLERC
 Cmil_ST6Gal12 LCELKRV-R---LRTLDGNETPFSLLG-WKYYVPK----IPLSKIKLKL-RVFRKC
 Stro_ST6Gal12 LCVLKDRA-Q---VKTLDGKDAPFSSLG-WEKYFPK----IALNKL-YP-HGFSTC
 Oana_ST6Gal12 LCQLRDRV-H---VRTLDGKEAPFSAWG-WDKHVP-----TPLAKL-YP-RGFSC
 Mdom_ST6Gal12 LCELDRV-S---VRTLDGKEAPFSDLG-WEKHVPQ----EPLSKL-YP-QGLGSC
 Acar_ST6Gal12 FCELKARV-N---IRTIDGKEAPFSILG-WEKHVPQ----ISLNKL-YP-NGFGSC
 Cpicbel_ST6GAL2 ICELKDRV-H---VKTIDGKEDPFSALG-WEKHVPQ----IPLGKL-YP-HGFSC
 Ggal_ST6Gal12 FCELKERV-D---VKTIDGKEAPFSTLG-WEKHVPQ----IPLGKL-YT-HGFSC
 Tgut_ST6Gal12 FCELKERV-N---VKTIDGKEAPFSTLG-WEKHVPQ----IPLVKL-YT-HGFSC
 Btau_ST6Gal12 LCALRGRV-Q---VRTLDGTEPPFSALG-WRALVPP----VPLSRL-LP-RRLRTC
 Hsap_ST6Gal12 LCQLRSRA-R---VRTLDGTEAPFSALG-WRRLVPA----VPLSQL-HP-RGLRSC
 Ocun_ST6Gal12 LCELRRRA-Q---VRTLNGTEAPFAALG-WRRLVPA----VPLSQL-HP-RGLRTC
 Drer_ST6Gal12-r LCQMKQEA-Q---IRTLNQTEQPFADLG-FQQLVSP-----PLQQKYRTC
 Drer_ST6Gal12 LCELKKRE-K---IRTLDGAEMPFSSLG-WQKIVPA----LPLSQIHR-PGLKTC
 Olat_ST6Gal12 LCQMKNQO-Q---LRTVDGSEQPFSLLG-WADFVPP----VPLQRWNKQRGRGSFR
 Alim_ST6Gal12 LCQMKQA-Q---LRTLDGSEEFSSLG-WDFVPP----LPLERLSRRQEKSSLKTC
 Trub_ST6Gal12 LCEMKQA-Q---LQMDVGTQOPFSSLG-WASLVP-----LPLEQLHKRPDQGSFKSC
 Tnig_ST6Gal12 LCELQQA-R---LQTVGDTEPPFSSLG-WARLVP-----LPLDQLHQQPARGSFN

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 Pbiv_ST6GAL1
 Stro_ST6Gall1
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 Svul_ST6Gall1
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 Dpul_ST6GAL_02410

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 KY-RFGSSLKYKNITLVAVWDPAPYNIDL-HKFLH--PDYDLFTPTYITHRKAPEQPFYI
 MH-RFNSSLKYKNITLVAVWDPAPYTTLNL-HQWYSN--PDYNLFPTPYMEYRMRFPSPQPFYI
 KH-EFKTSSSIYKNITLVAVWDPAPYTTLNL-DEWFAS--PDYDLFGPYVEHRKRKHAEQLPYI
 TY-QFNNTSSIYKNITLVAVWDPTPYSVNL-HKWTTS--PDYDLFGPYVDRHKVHPDQPFYI
 NH-RFNNTSSIYKDVLVAVWDPAPYTTLNL-HKWTAS--PDYNLFGPYMEHRRRAHPDQPFYI
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 YFED-FEDDSCTFGVWHPPLSAEK1L1NEM-NDS-VVFNTGFI1KGYKDL-KC-
 YYHE-KVDTVCTFGVWHPPLSAEK1L1NEM-TMD-QDQ-TVFHGFLS1PGYKSP-ICTS
 YYDP-EDNPACTFGVWHPPLAAEKL1YVLMNTA-DDR-TVFGYV1R1LGFKNF-KC-
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Lpol_ST6GAL_02415	YYDV-HENLGCTLGDWHPLASEKLLSLAMNAA--SDL-QVFVNKGKISIKGDVKC-----
Pmar_ST6GAL_02423	YHED-YTDRACTEGAYHPLLYEKNFKVRLSTS--SDH-DLFWAGRATLPGLRAMESCPP
Cmil_ST6Gal2	YHER-YYDSACTLGAHPLLYEKLLVQRMNKG--TEA-DLYSKGRVSLPGFHSI--KCAG
Stro_ST6Gal2	YHEQ-YYDAACTLGAHPLLYEKMLIQRINQG--TED-NLLRGKVILPGFSSI--HCPI
Oana_ST6Gal2	YHEL-YYDAACTLGAHPLLYEKLLVQRMNKG--ERD-DLYRKGVILPGFRAL--RCPA
Mdom_ST6Gal2	YHEL-YYDAACTLGAHPLLYEKLLVQRMNKG--IRD-DLYRKGVILPGFRAL--RCPA
Acar_ST6Gal2	YHEL-YYDAACTLGAHPLLYEKLLVQRMNKG--FQD-DLYRKGVILPGFRSV--KCPG
Cpicbel_ST6GAL2	YHEL-YYDAACTLGAHPLLYEKLLVQRMNKG--LQD-DLYRKGVILPGFRSV--KCPG
Ggal_ST6Gal2	YHEL-YYDAACTLGAHPLLYEKLLVQRMNKG--LQD-DLYRKGVILPGFKSV--KCPE
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Btau_ST6Gal2	YHEP-YYDAACTLGAHPLLYEKLLVQRLNVG--THG-DLHRKGKVVLPGLQAV--RCPP
Hsap_ST6Gal2	YHEL-YYDAACTLGAHPLLYEKLLVQRLNMG--TQG-DLHRKGKVVLPGFQAV--HCPA
Ocun_ST6Gal2	YHEL-YYDAACTLGAHPLLYEKLLVQRLNMG--TQG-DLHRKGKVVLPGFQAV--QCPC
Drer_ST6Gal2-r	YHEL-QYDMACTFGAYHPLLYEKLLVQRMSTA--SEE-DLRKKGVTLPGFSKI--KCLL
Drer_ST6Gal2	YHER-YYDAACTLGAHPLLYEKMLIQRMNIG--SED-ELKRKGKVTLPGFNKV--HCEP
Olat_ST6Gal2	YHEN-YYDAACTLGAHPLLYEKLNIRRNLG--SEK-DLLKKGRVTLPGFSTL--TCGA
Alim_ST6Gal2	YHER-YYDAACTLGAHPLLYEKSLIQRINTG--PEN-DLRRKGRTLPGFSTV--DCDI
Trub_ST6Gal2	YHER-YYDAACTLGAHPLLYEKSLIQRINTG--PGS-DLRRKGRTLPGFSTV--DCDI
Tnig_ST6Gal2	YHER-YYDAACTLGAHPLLYEKSLIQRINTG--PES-DLRKKGVTLPGFSAV--NCDI
Locu_ST6GAL1	YYQR-FFDAACTLGAHPLLYMEKLNVKRMNKG--TDK-EIYQYGRVTLPGLATL--NCTA
Pbiv_ST6GAL1	YYQD-FSDDACTLGAHPLLYFEKNLVVRMNKG--TQA-DLAQGRVTLPGFQVL--NCTQ
Stro_ST6Gal1	YER-YDRACTLGAHPLLYFEKNLVKLNIG--DDN-SIFHFGRTLPGLRGL--QC--
Acar_ST6Gal1	YYQK-IFDQACTMGMAYHPPLLFEKNIHKLNIG--KDE-DIYNYGKATLPGLRNV--QC--
Gfor_ST6GAL1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYTLGKVTLPGFRKV--Q--
Tgut_ST6Gal1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYTHGKVTLPGFRKV--HC--
Svul_ST6GAL1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYTHGKVTLPGFRKV--HC--
Falb_ST6GAL1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYTHGKVTLPGFRQV--QC--
Ggal_ST6Gal1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYTHGKVTLPGFRNV--HC--
Fche_ST6GAL1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYTHGKVTLPGFRKV--HC--
Cliv_ST6GAL1	YYQK-FHDHACTMGMAYHPPLLFEKNLVKHMNQG--TDE-DIYMHGKVTLPGFRNV--HC--
Mdom_ST6Gal1	YYQQ-FFDSACTMGMAYHPPLLFEKNMVKHLMQG--TDE-DIYLKGKVTPGLQGV--RC--
Btau_ST6Gal1	YYQR-YFDSACTMGMAYHPPLLFEKNMVKYLNIG--TDE-DIYLLGKATLPGFRTI--RCGA
Hsap_ST6Gal1	YYQK-FFDSACTMGMAYHPPLLFEKNLVKHLNQG--TDE-DIYLLGKATLPGFRTI--HC--
Cfam_ST6Gal1	YYQK-FFDSACTMGMAYHPPLLFEKNLVKHLNQG--TDE-DIYLLGKATLPGFRTI--RC-

Data S2. 27 vertebrate ST6Gal sequences used in Figure 5: poorly aligned regions in the N-terminal part of ST6Gal sequences were manually removed and multiple sequence alignment obtained with clustal Omega at the <http://www.ebi.ac.uk/Tools/msa/clustalo/> web site. Output format is Phylip/interleaved. 91 vertebrate ST3Gal sequences used in Figure 5: N-terminal part were manually removed and multiple sequence alignment obtained with clustal omega at the <http://www.ebi.ac.uk/Tools/msa/clustalo/> web site. Output format is Phylip/interleaved.

31 237	
ST6Gal2_Daniorerio	CAVTSAGAM LHSGLGEID SHDAVLRFNT APTVGYERDV GNKTTIRIIIN SQILANPMHR FNRSILYKNV TLVAWDPAPY
ST6Gal2_Olatipes	CAVSSAGAI LHSGLGEID SHDAVLRFNA APTEGYEQDV GTKTTIRIIIN SQILANPKHE FKTSSIIYKNI TLVAWDPAPY
ST6Gal2_Alligmissi	CAVTSAGAM LRSRLGEID SHDAVLRFNS APTDGYERDV GNTKTTIRIIIN SQILANPYQ FNTTSSIIYKNV TLVAWDPTPY
ST6Gal2_Takirubri	CAVTSAGAI LRSRLGEID AHDAVLRFNA APTEGYERDV GNKTTIRIIIN SQILANPNHR FNTSSLYKDV VLVAWDPAPY
ST6Gal2_Calamili	CAVVASAGAI LNSSLGDEID SHDAVMRFNA APTKLYEQDV GSCKTTIRILN SQILANSKHN FINNALYKNI ILVVWDPAPY
ST6Gal2_Silutropi	CAVSSAGAI LNSSLGAEID SHDAVLRFNS APTRNYEKD VGNKTTLRIIN SQILTNPNNH FTDSSLYKDV TLIAWDPSPY
ST6Gal2_Monodomes	CAVMSAGAI LNSSLGEIDEID SHDAVLRFNS APTGHGYERDV GNKTTMRNIIN SQILTNPNNH FIDSSLYKDV ILVAWDPAPY
ST6Gal2_Anolcarol	CAVMSAGAI LNSSLGEIDEID SHEAVLRFNS APTGRGYEKDV GNKTTMRNIIN SQILTNPNNH FIENSLYKDV ILVAWDPAPY
ST6Gal2_Chryspicta	CAVMSAGAI LNSSLGDEID SHDAVLRFNS APTGRGYEKDV GNKTTMRNIIN SQILTNPNNH FIDSSLYKDV ILVAWDPAPY
ST6Gal2_Taenopsgut	CAVMSAGAI LNSSLGEIDEID SHDAVLRFNS APTGRGYEKDV GNKTTMRNIIN SQILTNPNNH FVDSSLYKDV ILVAWDPAPY
ST6Gal2_Gallusgal	CAVMSAGAI LNSSLGDEID SHDAVLRFNS APTGRGYEKDV GNKTTMRNIIN SQILTNPNNH FVDSSLYKDV ILVAWDPAPY
ST6Gal2_Struthcam	CAVMSAGAI LNSSLGEIDEID SHDAVLRFNS APTGRGYEKDV GNKTTMRNIIN SQILTNPNSH FVDSSLYKDV ILVAWDPAPY
ST6Gal2_Bostaurus	CAVTSAGAI LNSSLGEIDEID SHDAVLRFNS APTGRGYEKDV GNKTTTVRIIN SQILTNPNSYH FMDSALYKDV ILVAWDPAPY
ST6Gal2_Homosap	CAVMSAGAI LNSSLGEIDEID SHDAVLRFNS APTGRGYEKDV GNKTTIRIIIN SQILTNPNSH FIDSSLYKDV ILVAWDPAPY
ST6Gal2_Musmus	CAVMSAGAI LNSSLGEIDEID SHDAVLRFNS APTGRGYEKDV GNKTTTVRIIN SQILANPSHH FIDSALYKDV ILVAWDPAPY
ST6Gal1_Oryzlatip	CAVVSAGSL RNSGLGEID SHDAVMRFNA APTSGFEKD VGSKTTMRLIN SQVMASEEYR FLSSSLYSSG VLVAWDPAPF
ST6Gal1_Gasterost	CAVVSAGSL RNSGLGEID SHDAVLRFNA APTTYGYEKDV GSCKTTIRILN SQVMASDDH FLSSSLYSSG VLVAWDPAPF
ST6Gal1_Takirubri	CAVTSAGSM RSSGLGEID SHDAVLRFNA APTSGYENDV GSCKTTIRLVN SQVMASEAHR FLSSSLYSSG TLVAWDPAPF
ST6Gal1_Amblymexi	CAVVSAGSL RNSGLGEID SHDAVVRFN APTAGFEKD VGSKTTVRILN SQVMASEDDH FLSSSLYSSG TLVAWDPAPY
ST6Gal1_Daniorerio	CAVVSAGSL KNSGLGEID SHDAVIRFN APTAGFEKD VGSKTTVRILN SQVMASEDDH FLSSSLYSSG ILVSWDPSPY
ST6Gal1_Silutropi	CAVVSAGSI KHSRLGQEI THDAVLRFNA APVLYQADV GTKTTFRLN SQLVSRLPELK FLEDPLYKEG SLIMWDPAPY
ST6Gal1_Alligmissi	CAVVSAGSL KSSHGLGEID GHDAVLRFNG APTKGFQDV GEKTTTIRLVN SQLVTVEEEK FLADPQYNGF TLILWDPAPY
ST6Gal1_Taenopsgut	CAVVSAGSL KSSHGLGEID SHDAVLRFNG APVPRGFQDV GKTTTIRLVN SQLVTVEEEQ FLREPLYNTG ILIWWDPAPY
ST6Gal1_Gallusgal	CAVVSAGSL KSSHGLGEID SHDAVLRFNG APVKGQFQDV GKTTTIRLVN SQLVTVEEEQ FLKDALYNTG ILIWWDPAPY
ST6Gal1_Struthcam	CAVVSAGSL KSSHGLGEID SHDAVLRFNG APTGRGYEKDV GEKTTTIRLVN SQLVTVEEEQ FLTDALYNTG ILIWWDPAPY
ST6Gal1_Anolcarol	CAVVSAGSM KSSHGLGEDID SHDAVLRFNG APIKGFQADV GEKTTTIRLVN SQLITVEEKK FLADPQYNGF TLILWDPAPY
ST6Gal1_Pythonmor	CAVVSAGSM KQSHGLGEID SHDAVLRFNG APTRKGFQDV GEKTTTIRLVN SQLITVEEKK FITDVQYNGF TIIIVWDPSPY
ST6Gal1_Monodomes	CAVSSAGSL KASYLGQEID NHDAVLRFNG APTKTYEEHV GKTTTIRLVN SQLVTTD-KR FFDDSLYKNG ILIMWDPSPY
ST6Gal1_Musmuscul	CAVSSAGSL KNSQLGREID NHDAVLRFNG APTDNFQDV GTKTTTIRLVN SQLVTTE-KR FLKDSLTYEG ILILWDPSVY
ST6Gal1_Homosap	CAVSSAGSL KSSQLGREID DHDAVLRFNG APTANFQDV GTKTTTIRLMN SQLVTTE-KR FLKDSLTYNEG ILIVWDPSVY
ST6Gal1_Ovisaries	CAVSSAGSL KSSRLGREID DHDAVLRFNG APTRVLFQDV GTKTTTIRLVN SQLVTTE-AG FLKDSLTYNEG ILIVWDPSVY
TLNLHQWSN	PDYNLFTPYM EYRMRFPSPQ FYILHPKYIW QLWDVIQANN LENIQPNPPS SGFIGILLMM SLCEEVHVE
TLNLDEWFAS	PDYDLFGPYV EHRKNHAEQL FYILHPSPYL QLWDLIQSNT QEIQPNPPS SGFIGILLMM ALCDKLHVYE
SVNLHKWYT5	PDYDLFGPYV DHRKVHPDQP FYILHPSPYV KLWDLIQSNT QEIQPNPPS SGFIGILLMM ALCEQVHVE
TLDLHKWYAS	PDYNLFGPYM EHRRRAHPDQF FYILHPRYVW RLWDVIQGNT QEIQPNPPS SGFIGILLMM TLCEQVHVE
SINLIKWYKK	PDYNLFTPYL RYRRRNPAQP FYILHPRFILW QLWDIIQENT QEIQPNPPS SGFIGIVIMM ALCDSINIYE
YADLHWYHK	PDYNLFTPYE KHRKRNPQDQ FYILHPKFVW ELWKIIQENS NEKIQPNNPPS SGFIGILIMM SMCRVHVE
SANLHWYKK	PDYNLFTPYI QHRRKNPNQDQ FYILHPKFVW QLWDIIQENT KEKIQPNNPPS SGFIGILIMM SMCNEVHVE
SANLNWVFKK	PDYNLFTPYV QHRRKNPNQDQ FYILHPKFVW QLWDIIQENT KEEIQPNPPS SGFIGILIMM SMCNEVHVE
SANLNWVYKK	PDYNLFTPYV QHRRRNPNQDQ FYILHPKFVW QLWDIIQENT KEKIQPNNPPS SGFIGILIMM SMCNEVHVE
SANLSQWYKK	PDYNLFTPYV QHRRKNPQTQ FYILHPKFVW QLWDIIQENT KEKIQPNNPPS SGFIGSLIMM SMCNEVHVE

SANLN-WYKK PDYNLFTPYY QHRKKNPQF FYILHPKF1W QLWDIIQENT KEKIQPNPPS SGFIGILIMM SMCNEVHVYE
 SANLNWYKK PDYNLFTPYY QHRRKNPQF FYILHPKF1W QLWDIIQENT KEKIQPNPPS SGFIGILIMM SMCSEVHVYE
 SANLNRYKK PDYNLFTPYY QHQRQNPQF FYILHPKF1W QLWDIIQENT KEKIQPNPPS SGFIGILLMM NLCGEVHVYE
 SANLNLYKK PDYNLFTPYY QHRRQNPQF FYILHPKF1W QLWDIIQENT KEKIQPNPPS SGFIGILIMM SMCREVHVYE
 SANLNWYKK PDYNLFTPYY QHRRKYPQF FYILHPKF1W QLWDIIQENT REKIQPNPPS SGFIGILIMM SMCKEVHVYE
 SSDLTQWLNR TDYPIFAQYQ RYRKLHMPQP FYILHPRFEW QVWQVQENM AESIQKNPPS SGFLGTVLMM SLCEVVHVYE
 SADLTQWFNR TDYPIFTQYQ RYRMLHMPQP FYILHPRFEW QVWQRIQDNM AEPIQKNPPS SGLLGTVLMM SLCEVVHVYE
 SSDLNEWYNK TDYPIFKQYQ RYRRLHPPQP FYILHPSVWQ QLWKRIQDNM AEPIQKNPPS SGLLGTVLMM SLCDVVHVYE
 SSDLWEWNK TDYPIFKQYQ RYRRLHPPQP FYIVHPRMEW QLWQRIQDNM GEAIQKNPPS SGLLGTVLMM SLCEVVHVYE
 NANVEEWHKN PDYKFFERYS EYRRRNPEQM FYVLNPHAAQ QLWDIIQQNA PEDINPGPPS SGLLGILLMM NLCDQVNYYE
 HAEIHEWYRK LDYNFLETYK KYRSQHPEQL FYILNPKMEW ELWDILQENS LEDIQPNPPS SGMLGIIIMM TICDEVNVYE
 HAEIHEWYRK PDYNFFESYK AYRRAHPEQP FYILNPKMOW QLWDILQENS LEHIQPNPPS SGMPGIVLMM TLCQDVYDYE
 HAEIHEWYRK PDYKFFEAYK SYRIRHPEQP FYILNPKMOW QLWDILQENS LEHIQPNPPS SGMLGIVIMM TLCDEVDVYE
 HADIHEWYRK PDYKFFENYK LYRIKHPPEQF FYILNPKMOW QLWDILQENS LEHIQPNPPS SGMLGIVIMM TLCDEVHVYE
 HSSIKEWYKK PDYNFYGSFK HYRKKYPKQP FYILNPHMQW QLWDILQENS PEDIQPNPPS SGMLGKLIIMM NFCDEVDVYE
 HANIDEWFRK PDYFFFESYK HYRKRPKQP FYILNPFMQW QLWDILQENS PEDIQPNPPS SGMLGIVLMM NFCDEVDVYE
 HSEIPEWYKK PDYNFFHNYK LYRKLNPQF FYILNPKMPW ELWDILQENS PEDIQPNPPS SGMIGIVIMM NFCDTVDIYE
 HADIPQWYQK PDYNNFFETYK SYRRLHPSQP FYILKPQMPW ELWDIIQFEIS PDLIQPNPPS SGMLGIIIMM TLCQDVDIYE
 HSDIPKWYQN PDYNNFFNYK TYRKLHNPQF FYILKPQMPW ELWDILQENS PEIOPNPPS SGMLGIIIMM TLCQDVDIYE
 HSDIPKWYRN PDYSFFNNFK SYRKLPDQP FYILKPQMPW ELWDIIQFEIS SELIQPNPPS SGMLGIAIMM SLCDQDVDIYE
 YIPSLRQTDL CHYHERYYDA ACTLGAYHPL LYEKMLIQRN NIGSEDELKR KGKVTLPGFN KVHCEP-----
 YIPSMRQTDL CHYHERYYDA ACTLGAYHPL IYEKNLIRI NLGSEKDLLR KGRVTLPGFS TLTCGA-----
 YIPSMRQSDL CHYHERYYDA ACTLGAYHPL LYEKSLIQRN NTGPENDLRR KGRVTLPGFS TVDCDI-----
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 YIPSVRQTDL CHYHELYYYDA ACTLGAYHPL LYEKLLVQRM NKGQLDQLYR KGKVILPGFK SVKCPERNNF PHL-----
 YIPSVRQTDL CHYHEPYHDA ACTLGAYHPL LYEKLLVQRL NVGTHGDLHR KGKVLPGLQ AVRCPGA-----
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 YIPSVRQTEL CHYHELYYYDA ACTLGAYHPL LYEKLLVQRL NTGTAQDLHH KGKVLPGLQ TLRCPVTSN NTHS-----
 FLPSKRKTTEL CHYYQHFYDA ACTLGAYHPL LYEKNLVCRM NQGADRDITY HGRVTLPGFN AINCTRAAQE PEGM-----
 FLPSSRKTTEL CHYYQRFHDH ACTLGAYHPL LYEKNLVCRM NRGPDREDITY HGRVTLPGFG KMNCTEAAGG STSR-----
 FLPSSRKTTEL CHYYQRFDA ACTLGAYHPL LYEKNLVCRM NQGPERDITY HGRVTLPGFN TLNCTGDAGG ALVDMRH-----
 FLPSSRKTTEL CHYYQRFSDA ACTLGAYHPL LYEKNLVCRM NQGSDRDITY HGRVTLPGFS TYNCTASILS KP-----
 FLPSSRKTTEL CHYYQRFSDA ACTLGAYHPL LYEKNLVCRM NQGSDRDITY LGRVTLPGFA TFNCTSSTHS KT-----
 FLPSSRQSDL CHYYERYQDA ACTLGAYHPL LYEKNLVCRM NLGDDNSIFH FGRITLPGLR GLQC-----
 FIPSKRQTDI CHYYQKFHDH ACTMGAYHPL MFEKNLVKYL NQGTDYNIYA HGKVLPGLR NLRC-----
 FIPSKRQTDI CHYYQKFHDH ACTMGAYHPL LFEKNLVKHM NQGTDDEDIYT HGVTLPGFR KVHC-----
 FIPSKRQTDI CHYYQKFHDH ACTMGAYHPL LFEKNLVKHL NQGTDDEDIYT HGVTLPGFR NVHC-----
 FIPSKRQTDI CHYYQKFHDH ACTMGAYHPL LFEKNLVKHL NQGTDDEDIYT HGVTLPGFR NVHC-----
 FIPSKRQTDI CHYYQKFHDH ACTMGAYHPL LFEKNLVKHL NQGTDDEDIYT HGVTLPGFR NVQC-----
 FIPSKRQTDI CHYYQKFHDH ACTMGAYHPL LFEKNLVKHL NQGTDDEDIYT HGVTLPGFR KAQC-----
 FIPSKRQTDI CHYYQQFFDS ACTMGAYHPL LFEKNMVKHL NQGTDDEDIYL KGKVTPVGLQ GVRC-----
 FIPSKRQTDI CHYYQQFFDS ACTMGAYHPL LFEKNMVKHL NQGTDDEDIYL LGKATLPGFR TIHC-----
 FIPSKRQTDI CHYYQQFFDS ACTMGAYHPL LFEKNMVKHL NQGTDDEDIYL LGKATLPGFR TIRCGA-----

91 276

Oscararm CRRCAVGTA GRLKGARQGE LIDSFDIVI- RMNRSVPVKY EVDVGSKTS----- YHLV YPESAVGYRG AE---SSGKLV
 Cionint12 CRSCAVVGNS GNILNSNYGN VIDGHDFVI- RMNKGPTYYN ENDVGSKTT----- HRFM YPTTASSLPQ GKLFSGVSLV
 BfloridA CLRCAVVGNS GNLRQSNYGE EIDGYDLIF- RMNDAPTKW EKDVGHRRT----- HRFM YPESATDLP----- DDVSFV
 BfloridB CLRCAVVGNS GNLRQANYGE EIDGYDLIF- RMNDAPTKW EKDVGHRRT----- HRFM YPESATDLP----- DDVSFV
 Saccogl12 CLQCAVGNS GNLRQDSRYQQ LIDSHDYIM- RMNTAKTVGF EKDVGSRRT----- HRFM YPESFVEVI----- GETKVF
 Tgutta3g1 CRRCAVGNS GNLRQSQYGP DIDSHDFVL- RMNRAPTAGY ESDVGGKTT----- HHFV YPESYRELA----- ANVSMI
 Ggallus3g1 CRRCAVGNS GNLRQSQYGP DIDSHDFVL- RMNRAPTAGY ESDVGSKTT----- HHFV YPESYKELA----- ENVSMI
 Strcamelg1 CRRCAVGNS GNLRQSQYGH DIDSHDFVL- RMNRAPTAGF ESDVGSKTT----- HHFV YPESYKELA----- ENVSMI
 Chryseml CRRCAVGNS GNLRQSQYGH DIDAHDFVL- RMNRAPTAGF ESDVGSKTT----- HHLV YPESFRDLA----- ENVSMI
 Acarolgal1 CRRCAVGNS GNLKQSQYQG EIDNHDVFV- RMNKAPTVGF ESDVGSKTT----- HHFV YPESYKELG----- ENVSMV
 Pythongal1 CRRCAVGNS GNLRRSQYQG EI----- RMNKAPTVGF EPDVGSKTT----- HHFV YPESYRELG----- EEVSMI
 Hsapiensg1 CRRCAVGNS GNLRRESSYGP EIDSHDFVL- RMNKAPTAGF EADVGKTT----- HHLV YPESFRELG----- DNVSMI
 Oanatigall CRRCAVGNS GNLKESRYGS DIDSHDFVL- RMNRAPTVGF EADVGSKTT----- HRFM YPESFTELA----- ENVSMI
 Trubrigall CHTCAVGNS GRLRQSGNGK IIDSHDSVI- RMNKAVTRGF AKDVGVRRT----- HHFV YPESAVDVD----- HGVSLV
 Olatrigall CRRCAVGNS GNLRESGHGE RIDSHSFVI- RMNKALTRGF EKDVGVRRT----- HHFL YPESAVDVD----- GGVSLV
 Xenlaegall CRTCAVGNS GNLKSSNYGP EIDEHDFVL- RMNHAPTARF EKDVGKTT----- HHFV YPESVRDLQ----- ANVSMI
 Acarolgal8 CGTCAVVGNS GRLKGSKYGE NIDSHHFVL- RINTAPTAGF EEDVGAKTT----- HHFV YPESAMNLH----- AGVHLM
 Pythongal8 CGTCAVVGNS GRLRGSKYQG KIDSQHVFV- RMNTAQIAGF QEDVGTRT----- HHFV YPESAVNLH----- PGIHLV
 Stropgal2A CRRCAVGNS GNLKGSRHGK NIDSHGLIF- RMNGARTYGF EKDVGSKTT----- HHFV YPESAVHVQ----- PGVHLV
 Chrysgal8 CRTCAVGNS GRLRGSHYGR EIDSHHWVL- RMNRAQTAGF EEDVGTRTT----- HRFM YPESAVDLQ----- PGVHLV
 Drerigal2A CRKCAVGNS GNLKLSKYGA LIDSHSTVI- RMNKAVTVGF DEDVGYRTT----- HHFL YPESAIHLR----- PGVHLV
 Pmargal2 CRRCAVGNS GNLLLGAGGGK EIDQHDFV- RINQAPTLGF ETDVGARTT----- HHFV YPESAKNLP----- ANVSMV
 Olatigal2B CLRCAVVGNS GNLRGSGYGYK IIDEHNFM- RINLAPTVGF EEDVGSRTT----- HOFM YPESAKNLA----- PNISFV
 Drerigal2B CLRCAVVGNS GNLRGAGGYGP VIDGHDFIM- RMNLAPTVGY EEDAGSRTT----- HHFV YPESAKNLA----- ANVSMV
 Acarogal2B CLRCAVVGNS GNLRGSGYGR EINGHDFVM- RMNQAPTVGF EADVGSRTT----- HHFV YPESAKNLP----- ANVSMV
 Stropgal2B CRRCAVGNS GNLRGSSYGYK DIDGHEFV- RMNQAPTVGF EMDVGSRTT----- HHFV YPESAKNLP----- ANVSMV
 Pythongal2 CRRCAVGNS GNLRGSSYQG EINGHDFIM- RMNQAPTVGF EADVGSRTT----- HHFV YPESAKNLP----- ANVSMV
 Oanatgal2 CQRCAVVGNS GNLRGSGYGR DIDGHNFIM- RMNQAPTLGF EQDVGSRRT----- HHFV YPESAKNLP----- ANVSMV
 Chrysegal2 CRRCAVGNS GNLRGSGYGR EIDGHNFIM- RMNQAPTVGF EADVGGRTT----- HHFV YPESAKNLP----- ANVSMV
 Ggallusga2 CRRCAVGNS GNLRGSGYGR EIDGHDFIM- RMNQAPTVGF EGDVGSRRT----- HHFV YPESAKNLP----- ANVSMV
 Hsapiegala2 CRRCAVGNS GNLRGSGYQG DVGHNFIM- RMNQAPTVGF EQDVGSRRT----- HHFV YPESAKNLP----- ANVSMV
 Tgutta gal2 CRRCAVGNS GNLRGSGYGP EIDGHDFV- RMNQAPTVGF EGDVGSRRT----- HHFV YPESAKNLP----- ANVSMV
 Strcamgal2 ----- MCLTLR- RMNQAPTVGF EGDVGSRRT----- HHFV YPESAKNLP----- ANVSMV
 Olatigal1A CRTCIVVGNS GNLKGSNYGA LIDTSDFVI- RMNKAPTKGF EKDVGAKTT----- HHVM YPESAVDLS----- NTTSLV
 Thigral1A CRTCIVVGNS GNLKGSQYGR LIDTSDFII- RMNQAPTLGF EDDVGTRT----- HHVM YPESAKDLD----- NGTSLV
 Trubrgal1A CRTCIVVGNS GNLKGSQYGR LIDSSDFII- RMNQAPTSGF EDDVGTRT----- HHIM YPESAKDLD----- NGTSLV
 Drerigal1C CRTCAIIGNS GNLKGSRYGR LIDAHFVI- RINMGPTKG EDDVGSKTT----- HRFI YPESAVDFD----- NSTYLV

Drerigal1D CRTCAVVGNS GNLNQSHYGV LIDAHLVI- RINKGPTEGF ERDVGKLT- -----HRMI YPESAVMD- ---NSTYLV
 Drerigal1A CRICAVVGNS GNILQSHYQG LIIDSHDFV- RINKGPTKGY ETDVGSKTT- -----HRIM YPESAMLD- ---NSTHLV
 Drerigal1B CRTCAVVGNS GNLLRSNYGR LIDLHDFVL- RINKGPTKGF EKDVGSKTT- -----HRIM YPESAVDLD- ---NSTHLV
 Sarcopgal3 CRRCIIIGNG GVLANKSLGA RIDDYDIVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAMQR-P EEEYKDSLFB
 Hsapiegala3 CRRCIIIVGNG GVLANKSLGS RIDDYDIVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAMQR-P EGYERDSLFB
 Oanatgal3 CRRCIIIVGNG GVLANKSLGA KIDDYDVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-P EGYERDSLFB
 Btaurugal3 CRRCIIIVGNG GVLANKSLGS RIDDYDIVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAMQR-P EGYERDSLFB
 Xlaevigal3 CRRCIIIVGNG GVLANKSLGS KIDEYEVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-L EGYEKDSIFV
 Stropigal3 CRRCIIIVGNG GVLANKSLGS KIDEYEVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-L EGYEKDSIFV
 Pythongal3 CRRCVIVGNG GILANKSLGL KIDDYDIVI- RLNSAPVKGF EKDVGSKTT- -----MRIT YPEGAIQK-P EGYEKDSLFB
 Acarolgal3 CRRCVIVGNG GILANKSLGV KIDDYDIVI- RLNSAPVKGF EKDVGSKTT- -----MRIT YPEGAIQK-P EGYEKDSLFB
 Chrysegala3 CRRCVIVGNG GVLANKSLGL KIDDYDVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-L EGYEKDSLFFF
 Ggallugal3 CRRCVIVGNG GVLANKSLGL KIDDYDVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-M EGYEKDSLFB
 Strcangal3 CRRCVIVGNG GVLANKSLGS KIDDYDVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-M EGYEKDSLFB
 Tguttagal3 CRRCVIVGNG GVLANKSLGL KIDDYDVVV- RLNSAPVKGF EKDVGSKTT- -----LRIT YPEGAIQK-M EGYEKDSLFB
 Drerigal3a CKKCIIGNG GILFNKSLGT KIDQYDVVV- RLNEAPVAGF EKDVGSKTT- -----MRIT YPEGAIQR-A ERYEKSLSFV
 Oryzlagal3 CRRCVIVGNG GILSNKSLGS RIDQYDVVI- RLNEAPVKGY SKDVGSKTT- -----MRIT YPEGAIQK-P ENYEDNSLFV
 Trigrogal3 CRRCVIVGNG GILSNKSLGS RIDQEYDVVV- RLNEAPVFGY DKDVGSKTT- -----LRIT YPEGAIQK-P DVYERDSLFB
 Dreriogal3 CRRCVIVGNG GILSNKSLGS RIDEYDVVV- RLNEAPVSGY TRDVGSKTT- -----MRIT YPEGAIQK-P ERYEKSLSFV
 Dreriogal7 CRRCVVVGSR GILHSKNLGA HIDHANIII- RVNNAPVFGY ESDAGSRTT- -----IRLI YPEGAPSH-I QEYERTEVVA
 Trigrogal5 CRRCVVVGSG GVLHGSQLGT HIDQYDVII- RMNNAPVAGF ERDAGSHTT- -----VRLM YPEGAPRS-T NEYQDTTMVA
 Oryzlagal5 CRRCVVVGNG GVLQGSHLG HIDQYDVII- RMNNAPVVF ERDVGSRRTT- -----IRLM YPEGAPHS-A NEYRKTSMIA
 Trubrigal5 CRRCVVVGNG GILRGLLELG LINRQFDVVI- RLNSGPLGEY TADVNRTT- -----IRMS YPEGTPLH-W VDSDPDITFV
 Dreriogal5 CRRCVVVGNG GILKGLGLGH LLNRNFDII- RLNSQPLQDF SADVGNRTT- -----IRMS YPESCPKV-W EDTDQDLKYV
 Pmaringal5 CRRCVVVGSG GNLRGTGLGP LDNDNFVVIR RLNNAPIIKF ENDVGSKTT- -----VRIT YPEGAPKS-M EEEYKPDLSIFA
 Stropigal5 CRRCVIVGSG GILHGELGLG MVDQFDIVI- RLNNAPVHG AQDVGSKTT- -----IRMT YPEGAPVS-E QEQYQHSSLFV
 Hsapiegal5 CRRCVIVGSG GILHGELGLH TLNQYDVVI- RLNSAPVEGY SEHVGSKTT- -----IRMT YPEGAPLS-D LEYYSNDLFV
 Oanatgal5 CRRCVIVGSG GILHGELGLH ALNQFDIVI- RLNNAPVQGY ADHVGSKTT- -----IRMT YPEGAPLS-E HEYYSNGLFV
 Acarolgal5 CKHCVVGNG GVLHGELGLY VLNQFDIVI- RLNSAPVQGY TDDVGSKTT- -----IRMT YPEGAPLS-Q HEYYPDLSFV
 Chrysegal5 CRKCVVGNG GILHGELGLH VLNFEDIVI- RLNDAPVQGY TDHVGSKTT- -----IRMT YPEGAPLS-E NEYNPOSLSFV
 Ggallugal5 CRKCVVGNG GILYGGELGH LLNQYDIVI- RLNDAPVQGY TDHVGSKTT- -----IRMT YPEGAPLS-E HEYPPASLSFV
 Strcangal5 CRKCVVGNG GILHGSELGH LLNQFDIVI- RLNDAPVQGY TDHVGSKTT- -----IRMT YPEGAPLS-E REYHPPASLSFV
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 Stropigal6 CKKCVVGNG GVLRNSTLGLK KIDSYDIII- RMNDGPVILY EDDVGKRTT- -----FRLC YPESIFS-S LHYDPNSTV
 Sarcopal6 CKKCVVGNG GVLKNKTLGE KIDSYDVII- RINDGPVRGH EEDVGKRTT- -----FRFLC YPESVFTN-P EDSDPESVA
 Hsapiegala6 CKKCVVGNG GVLKNKTLGE KIDSYDVII- RMNNGPVILY EEEVGRTT- -----FRLC YPESVFTN-P IHNDPNNTV
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 Chrysegal6 CRRCVVVGNG GVLRNKTLGE KIDSYDVII- RMNNGPVRY EEDVGKRTT- -----FRLC YPESVFTD-P IHYDPNTTAV
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 Strcangal6 CRRCVVVGNG GVLRNKTLGE KIDSYDVII- RMNNGPVIGY EEDVGKRTT- -----FRLS YPESIFS-P VHYDPNTTAV
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 Pmaringal6 CRKCVVGNG RVLKGSSGLG RIDSYDVVI- -MNDAPLRGH VGDVGSRRTT- -----MLRC YPESAHVR-R EDFDPSALLA
 Dreriogal4 CRTCAVIGN GALKNSSLGE IINKYDVVI- RLNDAPVRF EEDVGKRTT- -----LRLF YPESASYNPNG IHNDPTLLV
 Oryzlagal4 CRTCVVVGNG FAIKNSSLGE IIINYYDVVI- RLNDAPVRY EEDVGKRTT- -----LRLF YPESASSNPN LHNEEDTLMV
 Oranatgal4 CRRCVVVGNG YRLRNSSLGD VIDMYDVII- RYPLAELAE WALPGCGSWV VPHATDDWQY WANGGL-----
 Stropigal4 CRRCVVVGNG HQLRNSSLGE TINKYDVVI- RIINNAPVHKY EKDVGSKTT- -----MLRF YPESADFDPQ LDNNPDTLLV
 Xlaevigal4 CRRCVVVGNG HHLRNSSLGE TINKYDVVI- RLNNAPVHKY EKDVGSKTT- -----MLRF YPESADFDPQ LDNNPDTLLV
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 Mondongal4 CLRCVVVGNG HRLKNSSLGN TIDKYDVVI- RLNNAPVVGY EGDVGSKTT- -----MLRF YPESAHFSK VNQNPDTLLV
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 Btaurugal4 CRRCVVVGNG HRLRNSSLGE AINKYDVVI- RLNSAPVAGY EQDVGSKTT- -----MLRF YPESAHFNPK VEDNPDTLLV
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 MIPFKTLDDL WIVTALETTGT INF----TY VPVPRKIK- VKEKILVYN PAFIKVYYEN WLQNH-----
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 LIPFKTLDDL WIISALTTGT INS----TY IPVPRKIK- ANKTKILVYN PVFIKVVYDN WLQHH-----
 LIPFKILDLL WIISALTTNGT INQ----TY IPVPRKIK- ANKDKIMVYH PTFMKVYDN WLQRH-----
 LIPFKTIDLE WVSAITTGT ISH----TY IPVPAKIR- VKQDKILYH PAFIKVYFDN WLQGH-----
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 -----NI PTLGTVAITM ALHNC---DE VAVAGFGYDM NTP-HAPLHY YEKL----- MSAI-KESWT HNISREKEFL
 -----NI PTLGTVAITM ALHNC---DE VAVAGFGYDM NMP-YAPLHY YETVR----- MSTI-KESWT HNIPIKEKEFL
 -----NI PTLGTVAITM ALHNC---DE VAVAGFGYDM NTP-HAPLHY YETVK----- MSAI-KEQWT HNIAREKEFL
 -----NI PTLGTVAITM ALHNC---DE VAVAGFGYDM NTP-HAPLHY YESVK----- MSAI-KESWT HNISKEKEFL
 -----VMV PTLGITAIVV ALQVC---DQ VSIAFGFYDQ QHP-GAPLHY YGSLR----- MDAM-KTQVV HDVSAETVFL
 -----NMV PTLGASAVVM ALQVC---DQ VSLAGFGYDM RHP-ESRLHY YETIP----- MGAM-KAQVV HDISAEKLFL
 -----NMN PTLGASALVM AMQLC---DQ VSLAGFGYNN QHP-EARLHY YEAIR----- MDAM-KAQVV HDVSAEKFL
 -----QQNV PTIGMSALNL ASLLC---DE VSLAGFGYNF SVN-SARLHY YDKLP----- MRVM-QQTS HNVKEETAFL
 -----DQNI PTLGLTALNL ATYIC---DE VSLAGFGYNF SQK-EAPLHY YDSVP----- MTI-LKBAM HNVQKETVFL
 -----WQNI PTLGVSAAVF ATHLC---DE VSLAGFGYDL SRP-DAPLHY YENVR----- MDAM-KAQPM HNDGKEKLFL
 -----DKNV PTIGMTAVIL ATHLC---DE VNLAGFGYDL SQP-DASHLY YDNRC----- MNSM-NDQPM HDVTKEKKML
 -----DKNV PTIGVIAVVL ATHLC---DE VSLAGFGYDL NQP-RTPLHY FDSQC----- MAAM-NFQTM HNVTTETKFL
 -----DKNV PTIGVTAIVL ATHLC---DE VSLAGFGYDL SQP-NTPLHY FDTC----- MAAM-NGOTM HNVTRETLFL
 -----DKNV PTIGVTAIVL ATHLC---DE VSLAGFGYDL SQP-NTPLHY YDNLC----- MAAM-NEQTM HNVTTETKFL
 -----DKNV PTIGVTAIVL ATHLC---DE VSLAGFGYDL RQP-NTPLHY YDNLC----- MAAM-EGOTM HNVTTETKFL
 -----DKNV PTIGVMAVVL ATHLC---DE VSIAFGFYDL NQP-STPLHY YNNLC----- MAAM-NRQTM HNVGETKLL
 -----DKNV PTIGVTAIVL ATHLC---DE VSLAGFGYDL DQP-STPLHY YNNLC----- MAAM-NGOTM HNVTTETKFL
 -----DKNV PTIGVTAIVL ATHLC---DE VSLAGFGYDL DQP-STPLHY YNNLC----- MAAM-KEQTM HNVTTETKFL
 -----PKH PTGIIIAITL AFHIC---NE VHIAGFKYNN TS-LNSSLHY YGNET----- MSVMAQN-EY HNISAEQMF
 -----PKH PTGIIIAITL AFYIC---HE VHLAGFKYNF TD-KDGPLHY YGNTT----- MSFMS-KY HNITAEQIFL
 -----PKH PTGIIIAITL AFYIC---HE VHLAGFKYNF SD-LKSPHY YGNTT----- MSLMNKN-AY HNVTAEQFL
 -----PRH PTGIIIAITL ALQIC---SE VHLAGFKYNN ND-RNSSLHY YGNDT----- MSQMMKN-AY HDIAVEQRFL
 -----PKH PTGIIIAITL AFHIC---NE VHAGFKYNF AD-RNSSLHY YGNET----- MSEMEN-GY HNIIAEQKFL
 -----PKH PTGIIIAITL AFHIC---HE VHLAGFKYDF TD-RNSSLHY YGNET----- MSQMMQN-EY HDISAEQKFL
 -----PKH PTGIIIAITL AFHIC---HE VHLAGFKYDF TD-RNSSLHY YGNET----- MSQMMQN-EY HNINAEQKFL
 -----QKN PTGIIIAITL ALHLC---DE VHLAGFGYEV NSP-GSPVHY YGQDT----- MSSIIKKSTY HNITIERTFL
 -----QVH PTTGLLAIVF ALNYC---DV VHAGFGYPA SRNQNQPIHY YGQQT----- MKSMFQN-SY HDLNQEAQIL
 -----HFH PTTGLLAIVF ALNYC---DM VHIAGFGYPP KSDKRQPH YGYHT----- MKSM-KN-SP HDVSREGRAL
 -----KQK PTTGLLAITL ALHLC---DL VHIAGFGYPS SSNKKQTHY YEQVT----- LKSM-AA-SE HNVSHALAI
 -----IPK PTTGLLAITL ALHFC---DM VHIAGFGYPA LTNKKQPH YEKVT----- LKSM-FA-SE HNITVEAQAI
 -----TPK PTTGMLAITF ALHFC---DT VHIAGFGYPA LTNKKQPH YEKVT----- LKSM-AV-SG HNITLEAQAI
 -----KQK PTTGLLAITL ALHFC---DV VHIAGFGYPS SDNKKQSIHY YEQIT----- VKSM-AV-SG HNVSHAFAI
 -----KQK PTTGLLAITL ALHLC---DL VHIAGFGYPD SSNKKQTHY YEQIT----- LKSM-SV-SE HNVSHALAI
 -----KQK PTTGLLAITL ALHLC---DL VHIAGFGYPD AYNKKQTHY YEQIT----- LKSM-AG-SG HNVSQEALAI
 -----KQK PTTGLLAITL ALHLC---DL VHIAGFGYPD AHQKKQSIHY YEQIT----- LKSM-MW-SG HNVSQEALAI
 -----KQV RVKDPAPPB GRRVHRPRS LRLGPVGAPV SPPVFPQ--F -----
 -----KQK PTTGLLAITL ALHFC---DL VHIAGFGYPD SANKKQTHY YEQIT----- LKSM-AA-SE HNISHEALAI
 -----KQK PTTGLLAITL ALHFC---DL VHIAGFGYPD SANKKQTHY YEQIT----- LKSM-AA-SE HNISHEAVAI

 DQLHINHGLLR VRHSEQSS-----
 EKLQSEGIIK IHRGNAANK-----
 EKLQSEGIIK IHRGNAANK-----
 KQLEEEIGKIT VYRGSRV-----
 LT LASIEKIK FFKGR-----
 LT LASIEKIK FFKGR-----
 LT LASIEBKIN FFKGR-----
 LT LASIDKIR FFKGR-----
 LT LASIDKIR FFKGR-----
 HT LASVAKVR LFKGR-----
 ATLASINKIR LFKGR-----
 ASLASEDKIR IFKGR-----
 HNLAKEKGIR LYL-----
 QOLAIIEGKIT LHR-----
 ANLTSINKVL MFRGR-----
 ERLADEGKV FVK-----
 ERLAIEGKLS FYK-----
 AKLAEEGRLK LYK-----
 KKLAAEKGIS FYN-----
 QRLSAEGKIK LYR-----
 KQLTEAGKIS VRHGR-----
 QDLAKAGKIT VFPGK-----
 DKLAKAGKIS VFPGK-----
 GVLEKTGKD VYRGN-----
 DNLAKEKGK VYRST-----
 DILEKTNKIS VYRGN-----
 DMLAKASKIE VYRGN-----
 DMLAKTSKIQ VYRGN-----
 DMLAKTSRIE GVPQ-----
 DMLAKSKIE VYRGN-----
 DMLAKTSKIE VYRGN-----
 DMLAKTSKIE VYRGN-----
 LT LADKHKIQ MFRGR-----

```

LLLADKHKIQ MFKG----- -----
LLLADKHKIQ MFKG----- -----
MQLYLESKIR VFRGR----- -----
LKLHEKQGIR LYKGW----- -----
HKLHLMNKIA LHKG----- -----
HPLHQQNKIS LHKGWT----- -----
----- -----
RKLVKARVIT DLSSGI----- -----
----- -----
rklvkarvit dltsgi----- -----
KKLVKARVIN DLTNGI----- -----
KKLVKARVIN DLTNGI----- -----
RKLVKARVIT DLTSGI----- -----
RKLVKAGVIE DLTHGI----- -----
RKLVKANVIT DLTNGI----- -----
RKLVRANVIA DLTNGI----- -----
RKLVKANIIT DLTNGI----- -----
KELVKAGAVR DLTGAL----- -----
RDLVSAGAVT DLTGAL----- -----
RDLVAAGAVT DLTGAL----- -----
OKLIQDGAVT DLTGGIHCSF CPR----- -----
KRLVASGSIT DLTGGIHCSF C----- -----
AGLINAGVIS DLTGGV----- -----
RTLVKEGVVR DLSGGIHCAF CDTQHYTE----- -----
LKLVKEGVVK DLSGGIDREF----- -----
QKLVQEDEVVK DLSGGIHCDF CKKESEQSKR KMPLGI
OKLIKEGVVK DLSGGIFCTY CKKSS----- -----
QKLIKDGIVK DLSGGIQCEF CKKPS----- -----
QKLVKEKVVK DLTGGIHCEF----- -----
QKLIKEKVVK DLTGGIHCEF CIKDS----- -----
QKLIKEKIVK DLTGGIYCEF----- -----
RDIEHHTIK NLT----- -----
KNIEEKNFVI NLTKD----- -----
KDIIEKNLVI NLTDQ----- -----
KELIDLKILI NLT----- -----
KSLIEKQFVV SLT----- -----
KKLIDKNFVV NLT----- -----
KKLIDKNFVV NLT----- -----
KKLIDKNFVV NLT----- -----
KKLKEGEAIV DLTQLAGT----- -----
HRLEEQGVIL YLHPHS----- -----
KRLEDSGAVM YLHRHL----- -----
KRMLDIGAVK NLKDF----- -----
KNLFQQNIIH NLTYF----- -----
KSSLQQRIIS NLTYF----- -----
KKMLELGLVK NLTYF----- -----
KRMLEIGAIK NLTYF----- -----
KRMLEMGAIK NLTSF----- -----
KRMLEIGAVK NLTYF----- -----
----- -----
KRMLELGVLK NLTHF----- -----
KRMLELGVLK NLTYF----- -----

```

Data S3. 101 ST6Gal sequences used in Figures 8 and 9: (48 ST6Gal I and 53 ST6Gal II. The alignment was build using profile-profile mode with clustalX, one profile comprises ST6Gal I and the other ST6Gal II sequences. Output format is FASTA.

```

>Hsap_ST6Gal1
----- MIHTNLKKK----- FSCCVLVFLFAVICVWKE-
----- KKKGSYYDSFKLQ----- TKEFQV-
----- LKSLGKLAMGSDSQSVSSSTQD----- PHRGRQTLGSLR-
----- GLAKAKPEASFQVWNKDSSSKNLIPLRQKIKWKN
YLSMNKYKVSYKPGPGIKFSA-- EALRCHLRDHVNVSVMVEVTDFPFNTSEWE-GYLPK
ESIR---- -TKAGPWGRCAVVSAGSLKSSQLGREIDDHDAVLRFNGAPTANFQQDVGT
KTTFRLMNSQLVITEKR- FLKDSLNEGILIVWDPSVYHSDIPKWKYQNPDYNFFNNYKTY
RKLHPNQPFYILKPQMPWELWDILQEISPEEIQPNNPSSGMILGIIIMMTLCDQVDIYEFL
PSKRKTDVCYYYQKFFDSACTMGAYHPLLFEKNLVKHLNQGTDEDIYLKGKATLPGFRTHC
>Mdmon_ST6Gal1
----- MVHINFFRR----- IMYGLLAFLLLFTICLWNE-
----- SKKG-YSVSFRLD----- SKGFQL-
----- PRTLENLSRRLRTKPVNITAMVG----- PQRESE--APR-
----- PRPKVDK-FSYKVWDKDSSSKNLPARLQKVRKN
YLHMNKYNVSFEGTRQVEKLS--- SGLLCQLANRVKVTMIGQTDFFPNTSEWE-KSLPP
KNIR----- ESFGRLGTCAVVSSAGSLKASYLGLTEIDNHDAVLRFNGAPTKKYEEHVVK
KTTFRLMNSQLVITDDK- FFDDSLYKNGILIMWDPSFYHSEIPEWYKKPDYNFFHNYKLY
RKLNPQPFYILNPKMPWELWDILQENSPEDIQPNPSSGMIGIVIMMFCDTVDIYEFL
PSKRKTDICHYYQQFFDSACTMGAYHPLLFEKNMVKHLNQGTDEDIYLKGKVTVPGLQGV
RC-----
>Cfam_ST6Gal1

```

```

-----MIHTNLKKK-----FSCCVLAFLFAVICVWKE-
-----KKKGSYYDSLKLQ-----TKEFQM-----
-----VRG-----LEKQAATLSSTQN-----PPRASQALGSPR-----
-----GPVKAKSEASFQVWNKDSSSKNLI PRLQKIWRN
YLNMNKVKVSYKGPGPGVKFSA--EALRCHLIRDHVNVSMVEATDFPNTSEWE-GYLPK
ENIR---TKAGPWGRCAVVSAGSLKSQLGREIDDHDAVLRFNGAPTASFQODVGT
KTTIRLMNSQLVITEGR-FLKDSLYNEGILIVWDPSVYHSDIPKWYQSPDYSFFENYKS
RKLHPDQPFYILKPQMPWELWDIIQEVSPEEIQPNNPSSGMLGIIIMMLCDQVDIYEFL
PSKRKTVCYYQKFFDSACTMGAYHPLLFEKNLVKHLNQGTDEDIYLLGKATLPGFRRI
RC-----
>Mmul_ST6Gal1
-----MIHTNLKKK-----FSCCVLVFLLFAVICVWKE-
-----KKKGSYYDSLKLQ-----TKEFQV-----
-----LKSLGKLAMGSDSQSVSSSTQD-----PHRGRQALGSLR-----
-----DIPKAKPEAFFQVWNKDSSSKNLI PRLQKIWKN
YLSMNKVKVSYKGPGIKFSA--EALRCHLIRDHVNVSMVEATDFPNTSEWE-GYLPK
DNIR---TKAGPWGRCAVVSAGSLKSQLGREIDDHDAVLRFNGAPTANFQODVGT
KTTIRLMNSQLVITEKR-FLKDSLYNEGILIVWDPSVYHSDIPKWYQNPDYNFFNNYKS
RKLHPDQPFYILKPQMPWELWDILQEISPEEIQPNNPSSGMLGIIIMMLCDQVDIYEFL
PSKRKTVCYYQKFFDSACTMGAYHPLLFEKNLVKHLNQGTDEDIYLLGKATLPGFRRI
HC-----
>Pabe_ST6Gal1
-----MIHTNLKKK-----FSCCVLVFLLFAVICVWKE-
-----KKKGSYYDSLKLQ-----TKEFQV-----
-----LKSLGKLAIGSDSQSVSSSTQD-----PHRGRQTLGSLR-----
-----GLAKAKPEASFQVWNKDSSSKNLI PRLQKIWKN
YLSMNKVKVSYKGPGIKFSA--EALRCHLWDYVNVSMVEATDFPNTSEWE-GYLPK
ESIR---TKAGPWGRCAVVSAGSLKSQLGREIDDHDAVLRFNGAPTANFQODVGT
KTTIRLMNSQLVITEKR-FLKDSLYNEGILIVWDPSVYHSDIPKWYQNPDYNFFNNYKS
RKLHPDQPFYILKPQMPWELWDILQEISPEEIQPNNPSSGMLGIIIMMLCDQVDIYEFL
PSKRKTVCYYQKFFDSACTMGAYHPLLFEKNLVKHLNQGTDEDIYLLGKATLPGFRRI
HC-----
>Btau_ST6Gal1
-----MTRTSLKKV-----FSCCVLIFLLFAAIICVWKE-
-----KKKGNYYEFLKLQ-----NKEQV-----
-----LQGLEKLAVSSSQPVSSSTH-----PQRNIQALGGP-----
-----KAALKATFQVWDKDSSSKNLAAPRLQTIRKN
YLNMKVKVTYKGPGPGVKFSA--EALLCHLIRDHVNIISMIEASDFPNTSDWE-GYLPK
EDIR---SKAGPWGRCAVVSAGSLKSQLGREIDDHDAVLRFNGAPTVKFQODVGT
KTTIRLVSOLVITEAG-FLKDSLYNEGILIVWDPSVYHSDIPKWYRNPDYSFFNNFKSY
RKLHPDQPFYILKPQMPWELWDIIQEISSELEIQPNNPSSGMLGIAIMMSLCDQVDIYEFL
PSKRKTVCYYQRYFDSACTMGAYHPLLFEKNMVKYLNLTGDEDIYLLGKATLPGFRRI
RCGA-----
>Mmus_ST6Gal1
-----MIHTNLKRK-----FSCFVLVFLLFAAIICVWK-
-----KGSDYEALTLQ-----AKVQPM-----
-----PKSQEKVAVGPAPQAVFSNSKQD-----PEGVQILSYPR-----
-----VTAKVKPQPSLQVWDKDSTYSKLNPRLLKIWRN
YLNMKVKVSYKGPGPGVRSV--EGLRCHLIRDHVNVSMIEATDFPNTTEWE-GYLPK
ETFR---TKAGPCTKCAVVSAGSLKNSQLGREIDNHDAVLRFNGAPTDNFQODVGT
KTTIRLVSOLVITEKR-FLKDSLYTEGILILWDPSPVYHADIPQWYQKPDYNFFETYKS
RRLHPSQPFYILKPQMPWELWDIIQEISPDLIQPNPSSGMLGIIIMMLCDQVDIYEFL
PSKRKTVCYYHQKFFDSACTMGAYHPLLFEKNMVKHLNEGTDEDIYLLFGKATLSGFRNN
RC-----
>Rnor_ST6Gal1
-----MIHTNLKKK-----FSLFILVFLLFAVICVWK-
-----KGSDYEALTLQ-----AKEFQM-----
-----PKSQEKVAMGSASQVVFNSNKQD-----PKEDIPILSYHR-----
-----VTAKVKPQPSFQVWDKDSTYSKLNPRLLKIWRN
YLNMKVKVSYKGPGPGVKFSA--EALRCHLIRDHVNVSMIEATDFPNTTEWE-GYLPK
ENFR---TKAGPWGRCAVVSAGSLKNSQLGREIDNHDAVLRFNGAPTDNFQODVGS
KTTIRLMNSQLVITEKR-FLKDSLYTEGILIVWDPSVYHADIPKWYQKPDYNFFETYKS
RRLNPSQPFYILKPQMPWELWDIIQEISADLIQPNNPSSGMLGIIIMMLCDQVDIYEFL
PSKRKTVCYYHQKFFDSACTMGAYDPLLFEKNMVKHLNEGTDEDIYLLFGKATLSGFRNI
RC-----
>Ttru_ST6Gal1
-----MIPTNLKKK-----FSCCVLVFLLFAAIICVWKE-
-----KKKGSYYESLKLQ-----TKEFQV-----
-----LR-----SGSQSVSSSGTHN-----PQRGSQALSGP-----
-----KAKPEATFQVWNKDSSSKNLI PRLQKIWKN
YLSMNKVKVSYKGPGPGVKFSA--EALLCHLIRDHVNVSMVEATDFPNTSEWE-GYLPK
ENIR---TKAGPWGRCAVVSAGSLKSQLGREIDDHDAVLRFNGAPTANFQODVGT
RTTIRLMNSQLVITEGR-FLKDSLYNEGILIVWDPSVYHSDIPKWYKNPDYSFFDSFKSY
RKLHPDQPFYILKPQMPWELWDVIQEISPEQIQPNNPSSGMLGIIIMMLCDQVDIYEFL
PSKRKTVCYYQKFFDSACTMGAYHPLLFEKNMVKHLNEGTDDEDDIYLLGKATLPGFRSI
RCG-----
>Ptro_ST6Gal1
-----MIHTNLKKK-----FSCCVLVFLLFAVICVWKE-
-----KKKGSYSDSFKLQ-----TKEFQV-----
-----LKSLGKLAMGSDSQSVSSSTQD-----PHRGRQTLGSLR-----
-----GLAKAKPEASFQVWNKDSSSKNLI PRLQKIWKN
YLSMNKVKVSYKGPGPGIKFSA--EALRCHLIRDHVNVSMVEVTDFPNTSEWE-GYLPK

```

ESIR-----TKAGPWGRCAVSSAGSLKSSQLGREIDDHDAVLRFNGAPTANFQODVGT
 KTTIRLMNSQLVITEKR -FLKDSLYNEGILIVWDPSVYHSD1PKWYQNPDYNNFKYTY
 RKLHPNQPFYILKPQMPWELWDILQEISPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRKTDVYYYQKFFDSACTMGAYHPLLYEKNLVKHLNQGTDEDIYLLGATLPGFRTI
 HC-----
 >Ggor_ST6Gal1
 -----MIHTNLKKK-----FSCCVLVFLLFAVICVWKE-----
 -----KKKGSYYDSFKLQ-----TKEFQV-----
 -----LKSLGKLAGMSDQSOSVSSSTQD-----PHRGRQTLGSLR-----
 -----GLAKAKPEASFQVWNKDSSS-NLIPRLQKIWKN
 YLSMNKYKVSYKGPGPGIKFSA -- EALRCHLDRDHVNVSVMVEATDFPNTSEWE-GYLPK
 ESIR-----TKAGPWGRCAVSSAGSLKSSQLGREIDDHDAVLRFNGAPTANFQODVGT
 KTTIRLMNSQLVITEKR -FLKDSLYNEGILIVWDPSVYHSD1PKWYQNPDYNNFKYTY
 RKLHPNQPFYILKPQMPWELWDILQEISPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRKTDVYYYQKFFDSACTMGAYHPLLYEKNLVKHLNQGTDEDIYLLGATLPGFRTI
 HC-----
 >Ogar_ST6Gal1
 -----MIHTNLKKK-----FSCCVLAFLLFAVICLWKE-----
 -----KKKGSFYNSFKLP-----AKEFQA-----
 -----LKYLGKPAAGSESQSASLSSTQD-----PHRGSQAPSGVR-----
 -----GPAKAKPEASFQVWNKDSSSKNLIPLQKIWKN
 YLNMNKYKVSYKGPGPGVKFSA -- EALHCQLRDHVNVSMVEATDFPNTSEWE-GYLPK
 ENIR-----IKAGPWGRCAVSSAGSLKSSQLGEIDSHDAVLRFNGAPTANFQODVGT
 KTTIRLMNSQLVITEKR -FLKDSLYNEGILIVWDPSVYHSD1PKWYQNPDYNNFKYTY
 RKLHPNQPFYILKPQMPWELWDILQEISPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRRTDVYYYQKFFDSACTMGAYHPLLFENKNVKYLNQGTDEDIYLLGATLPGFRTV
 RC-----
 >Cpor_ST6Gal1
 -----MIHTSLRKK-----FSYCVLAFVLFAAACVWKE-----
 -----RKKGSYGGSLKLQ-----TNEFQE-----
 -----PKNLEKLTGSGSQHVSSRSTQV-----PHQLSRTL-SPR-----
 -----VPHKTKPQPTFQVWNKDSSSKNLPRLQKIWKN
 YVRMNKYKVSYKGPGPGVKFSV -- DALLCHLDRDHVNVSMDTDFPNTSEWE-GYLPR
 ENIR-----TKAGPWRRCAVSSAGSLKSSQLGEIDSHDAVLRFNGAPTANFQODVGT
 KTTIRLMNSQLVITEKR -FLKDSLYNEGILIVWDPSVYHSD1PKWYQNPDYNNFKYTY
 RKLHPNQPFYILKPQMPWELWDILQEISPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRRTDVYYYQKFFDSACTMGAYHPLLFENKNVKYLNQGTDEDIYLLGATLSGFRNL
 RC-----
 >Tbel_ST6Gal1
 -----MIHTNLKKK-----FSCCVLAFLLFAVICVWKE-----
 -----KKKGSYYDSKLQ-----AKEFQV-----
 -----LKSLEKLAIGSSQTVSSSTQD-----PHR-----SAK-----
 -----DLVKAKPEASFQVWNKDSSSKNLIPLQKIRKN
 YLNMNKYKVSYKGPGPGVKFSA -- EALRCHLDRDHVNVSVMVEATDFPNTSEWE-GFLPT
 ENIR-----TKAGPWGKCAVSSAGSLKSSQLGEIDNHDAVLRFNGAPIANFQODVGT
 KTTIRLMNSQLVITDKR -FLKDSLYSEGILIVWDPSVYHSD1AKWYKTPDYNFNNFKYTY
 RKLHPNQPFYILKPQMPWELWDILQETAPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRKTDVYYYQKFFDSACTMGAYHPLLFENKNVKHLNQGTDEDIYLGKATLLGLKLN
 HC-----
 >Btel_ST6Gal1
 -----MIQVILKKK-----LSYCVLAFFLFAAIICVWKE-----
 -----RKKVGYYESLKLE-----TEGFQV-----
 -----VSNQEKLVLVSGSPQ -SSVGTQD-----LHTGNPALSSTK-----
 -----SSVTKKPPSFQVWNKESSSRNLPRLQSIRKN
 YLNMNKYKVSYKGPGPGVKLTB -- EALRCYLDRDVNVSMVEATDFPNTSEWE-GYLPG
 ENFR-----TKAGPWGRCAVSSAGSLKSSQLGEIDDDHDAVLRFNGAPTANFQODVGT
 KTTIRLMNSQLVITAGR -FLKDSFYNEGIMIMWDPAXXSD1PKWYKHDYPDNFSSNYTY
 RRLHPEQPFYILKPQMPWELWDILQEISPEKIQPNPPSSGMLGIMIMMTLCDQDLYEFL
 PSKRKTDVYYYQKFFDSACTMGAYHPLLFENKNVKHLNQGTDEDIYLGKATLLGLKLN
 HC-----
 >Pvam_ST6Gal1
 -----MIHTNLKKK-----FSCCVLAFLLFAVICMWKE-----
 -----KKKGSYYNTLKLE-----TKVVR-----
 -----LEKLS -IGFGSQPVPSSTQD-----LHRNSQALSSPK-----
 -----ERVKTKLEPFFQVWNKDSSSKNLIPLKKIWKN
 YLSMNKYKVSYKGPGPGVKFSA -- EALLCHLDRDVNVSMVEATDFPNTSEWE-GYLPK
 EKIR-----TKAGPWGRCAVSSAGSLKSSQLGEIDNHDAVLRFNGAPTADFCQDVG
 KTTIRLMNSQLVITTEGR -FLKDSLYNEGILIVWDPSVYHSD1PKWYQNPDYKFFDNYRSY
 RKLHPDQLFYILKPQMPWELWDILQETAPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRKTDMCYYYQKFFDSACTMGAYHPLLFENKNVKHLNQGTDEDIYLGKATLPGFRTI
 HC-----
 >Eeur_ST6Gal1
 -----MIHTSLRKK-----FSYCVLFFLFAVICVWKE-----
 -----KKKGSDYNSKLQ-----SKEFQV-----
 -----LKNLA -MGSRSRAASSSTRA-----PPRASKALSSPR-----
 -----GPAKAKLEPSYPVWNKESSSKNLPRLQKIWKN
 YQNMNKYKVAYKGPGPGVKFSA -- KDLSCLLRNHVNVSMVEATDFPNTSEWE-GYLPR
 ENIR-----TKAGPWGRCAVSSAGSLKSSQLGEIDDDHDAVLRFNGAPTANFQODVGT
 KTTIRLMNSQLVITTEKR -FLKDSLYNEGILIVWDPSVYHSD1PKWYQNPDYGFFDNYKTY
 RKLHPDQLFYILKPQMPWELWDILQQIAPEEIQPNPPSSGMLGIIIMMTLCDQDLYEFL
 PSKRKTDVYYYQKFFDSACTLGAYHPLLYEKNMVKHLNQGTDEDIYLGKATLPGFRTI
 QC-----
 >Dnov_ST6Gal1

-----MIHINLKKK-----LSYCLLAFFLFVGIVICIWKE-----
 -----MKKGYYDSLKLE-----TKDFQV-----
 -----LRSLER-----PHGGSQAVSTLR-----
 -----SSAKAKPEFSFQVWNKDSSSKNLIPLRQKILRN
 YLNMMNKFKVSYKGPGPVKFSA--EALYCHI.RDHVNVSVMVEATDFPFNTSEWE-GYLPS
 ENIR--TKAGPWKKCAVVSAGSLKSSQLQEIDDDHDAVMRFNGAPTANFQQDVGT
 KTTIRLMNSQLVITEKR-FLKDSFYNEGILIVWDPSVYHTDIPKWYQNPDYNNFNNYKSY
 RKMHPDQPFYILKPQMPWELWDILQEVSPEAIQPNPPSSGMLGIIVMMTLCQDVDIYEFL
 PSKRKTDCVYYYQKFFDSACTMGMAYHPLLFEKNLVKHLNQGTDEDIYLHGKTTLPGFRSI
 HC-----
 >Stro_ST6Gal1
 -----MARCISKFGV-----ISIILCTFSFFLLDFYSKSK
 CLESCTTVHGKVEARDVKNNLNKALERENPLEREKD-----LEREKQLER-----
 -----QKELEKEQKLKREREKQLERERELE-----REKQLEKEQKLEREKQLEKQL
 -----EREKELERQKIAEAEHLHKIWLNO-----
 -----RQGAQSRLRFANRYGVWNEMHMSKDILPRLVMVKK
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 YLFAAGQPSH-LQEIEKFISADINNPKGNILQNNW
 SHQRRTRRRST-----
 -----KHRRS-QMFDESDDWDG GLY-STMSKSFLYKLWKG
 DVSSSKMLNPRLQKAMKD
 YLSTNKHGVFR--GKR-NSKL-TGDLQFC EKARVN
 VNK TIDG
 KEAPF STI LGWE-KH VPQ
 I PLV-KLYTH--GFGSCAVVMSAGAI LNSSLGDE
 IDSHDAVLFNSAPTRGYEKDVG
 KTMRIINSQILTNPNHFFDSSLYKDVILVWADPAPYSANL
 SQWYKKPDYNLFTP
 YQH
 RKNPQNPQFYILHPKFIWQLDIIQENTKEEIQPNPPSSGF
 FIGISLIMMSMC
 NEHVYEYI
 PSVRQTDLCHYHELYYYDACTLGAYHPLLYEKL LVQRMNKG
 FQDDLYRKGKVIL
 PGF KAI
 KCPKRNNFPHL---
 >Mdom_ST6Gal2
 -----MKPNLKQWKQVMLFGIFA WGLLFLVIFIYFTDSNTAEP
 -V PSSFS-----FVETKRLPIQGKQR-----SIMGAMHDPSF SATIDGN
 EVLLNGDLFDFNSGPNSLQKWTM KDG LE NE-EFFPSQM--RKKS
 PR IFYQGEDD
 YFTFMQGPMMSH GQQMVK FITLSEEDQKG
 GIRHN-QKRIISR-----
 -----HRRS--OLP-HNWDRLY-STMSKSFLYRLWKG
 NVSSKMLNPRLQKAMKD
 YLTTNKHGVFR--GKR-NSKL-TREQLLC ELD RVS
 VRTLDG
 KEAPF S D L G W E-KH VPQ
 EPLS-KLYPQ--GLGSCAVVMSAGAI LNSSLGEE
 IDSHDAVLFNSAPTHGYERDVGN
 KTMRIINSQILTNPNHFFDSSLYKDVILVWADPAPYSANL
 HMWYKKPDYNLFTP
 YQH
 RKNPQNPQFYILHPKFIWQLDIIQENTKEEIQPNPPSSGF
 FIGISLIMMSMC
 NEHVYEYI
 PSVRQTDLCHYHELYYYDACTLGAYHPLLYEKL LVQRMNKG
 FQDDLYRKGKVIL
 PGF KAI
 SCPAPNHFPNP---
 >Drer_ST6Gal2-r
 -----MVVQDSRLLRVQHAMKQSAQVLLALLVWMLLALLVFTYFADFQLN-
 -----QNPKT VSSF NSESS-----
 --RSTYSQHSGR-----AIKSSS-NARWG VFAERRGP
 Y---QRRQVF LPPHAK-EYFYFRKF DRRGLGVKKS KII
 PPED-----
 -----NDRDD-----Y-FSNPWSVVRGLWKG
 HVHTNKHGVFRYK- GQR-KLNK-SKQELL
 CQMKEQAQI RTLN
 GTEQPFADLGFK-QLVSP
 -PLQQKYR-----TC AVVASAGAI LNSSLG
 HEID SHDAVLFNSAP
 TEGYERDVGS
 KTTIRIMNSQILANPKYRGSSLLYKNITLV
 AWDPAPYNI
 DLHKWF
 LHPDYD
 LFTP
 YITH
 RKAFPEQPFYILHPSFIWKL
 DIVQSITEENI
 QPNPPSSGF
 FIGI
 ILMMNL
 CEKIH
 HVYEYI
 PSMRQTDLCHYHEQYDMACTFGAYHPLLYEKL
 LVKRM
 STASEEDLRKKGKV
 TLPGF SKI
 KCLL-----
 >Ocun_ST6Gal2

- - - - - MKPHLKQWRQRMLFGIFAWGLLFSVVFIYFTDSNPAEP
 - VPSSFS - - - - - FLETQGLLPVQGKQR - - - - - AIMGALHEPSSPGGADAS
 RALPGAQVAGAHPHSGPGDPQQWAQVPARFEDED - - - - - EFFASQV - - GRKSQSAFYPEDYD
 SLFAAARPGWPSHTQGTLGLPSPGAPGQ - - - - - SPHEREKRRHR - - - -
 - - - - - RQRRSR - - APLDEGEDGDRLA - - ASMSRAFLYRLWKGNVSSKMLNPRLQKAMRD
 YLAANKHGVFR - - GPR - AARR - SRAQLLCRLRRAQVRTLNGTEAPFAALGWR - RLVP
 VPLS - - QLHPR - - GLRCAVVMMSAGAILNSLLGEEIDSHDAVLRFNSAPTRGYEKDVG
 RTTMRIINSQILTNPHFVDSSLYKDVLVAVDPAPYSANLNLYWKKPDYNNLFTPYI
 RQRNPQPFYILHPKFIWQLWDIIQENTKEKIQPNPPSSGFIGILIMMSMCREVHVYEYI
 PSIRQTELCHYHELYYYDAACTLGYHPLLVEKLLVQRLNMGQTQDHLRKKGKVVLPGFQAV
 QCPAPNPDAPH - -
 >Oana_ST6Gal2
 - - - - - MKPNLKQWKQMLMFGIFAWGLLFLAIFIYFADSNTAP
 - VPSTF - - - - - YVEPVRLLPVQGKQR - - - - - AIMGAVPEPAPFEGEARS
 - - - ETRCESLLCADLPDSLWPEPEDAGDIEE - - - - - EFFSPQVQRGRSPRAHDPALGD
 SSFTADRPGPGLRARRGASLVSA - - - - - QGLFRSGRVPRKRICKRRS - - - -
 - - - KRGRS - - RPPEADEWERLYS - SAMSRSFLYRLWKGNVSSRMLNPRLQKAMKD
 YLSINKHGVFRQ - - GPR - NGRL - TGEQLLCQLRDRVHVRTLDGKEAPFSALGD - KHVPR
 TPLA - - KLYPR - - GFGCAVVMMSAGAILNSLLGAEIDAHDAVLRFNSAPTRGYEKDVG
 KTSLRINISQILTNPSHHFDIDSLYKDVLVAVDPAPYSANLNLYWKKPDYNNLFTPYI
 RRRYRPSQPFYILHPKFIWQLWDIIQENTREKIQPNPPSSGFIGILIMMSMCREVHVYEYI
 PSVRQTELCHYHELYYYDAACTLGYHPLLVEKLLVQRMNRGERDDLYRKKGKVVLPGFRAL
 RCPAPD - HLPHS - -
 >Cpor_ST6Gal2
 - - - - - MKPHLKQWRQCMLFGIFAWGLLFLAIFIYFADSNTAP
 - APSALS - - - - - FLETTRLLPVQGKQR - - - - - AIMGAHEP - APR - - - -
 - - - VHPGGRAHAVPADPQEAVGSGQGGPRDED - - - - - EFTSQV - - GRKSQSAFYPEDYD
 YFFLGLSEPGRRGRALGVGLGLASPQQLRKTR - - - - - G - - - -
 - - - RSSLS - - - PRGLDGDRLA - - APLGVLLRRLWTGEASARMLSPRLQKAMRD
 YVRANKHGVFRYR - - - - - LSCCARSRLSPRS - - - - - GGR - SLVPA
 TALS - - QLHP - - GLRCAVVMMSAGAILNSLLGAEIDAHDAVLRFNSAPTRGYEKDVG
 KTTIRIINSQILANPGYHFIDSLYKDVLVAVDPAPYSSNLYLWYKKPDYNNLFTPYI
 RQRHPAQPQPFYILHPKFIWQLWDIIQENTKEKIQPNPPSSGFIGIVIMMSMCDEVHVYEYI
 PSVRQTELCHYHELYYYDACTLGYHPLLVEKLLVQRLNMGQADLYRKKGKVVLPGFRAA
 QCPEPGPGDARS - -
 >Mmur_ST6Gal2
 - - - - - MKPHLKQWRQRMLFGIFAWGLLFLAIFIYFADSNTAP
 - APSSFS - - - - - FLETTRLLPVQGKQR - - - - - VIMGAMHEPASPAGSMAD
 PALPAGRPAFPFHVGPGLDQWQAQADDFENE - - - - DFFSSQV - - ERKSQNAFYAEDDA
 YFFAAGQPGWHSHTQGTLGFSSPGEPGQKQRALPAGQVQSVRKDRHR - - - -
 - - - - - RQRRT - - HVLEVDDESR - - - - PFMRSALLYQLWKGNVSSKMLSPRLQKAMKA
 YTANKHGVFR - - GRR - AAA1 - SRAELLCRRLSRLRVRVRLTLDGTEAPFSALGWQ - RLVP
 VPLS - - QLHP - - GLRCAVVMMSAGAILNSLLGEEIDSHDAVLRFNSAPTRGYEKDVG
 KTTMRIINSQILTNPSHHFDIDSLYKDVLVAVDPAPYSANLNLYWKKPDYNNLFTPYI
 RQRNPQPFYILHPKFIWQLWDIIQENTKEKIQPNPPSSGFIGILIMMSMCREVHVYEYI
 PSVRQTELCHYHELYYYDACTLGYHPLLVEKLLVQRLNMGQADLYRKKGKVVLPGFRAA
 RCPAPNSAGPHS - -
 >Pabe_ST6Gal2
 - - - - - MKPHLKQWRQRMLFGIFAWGLLFLIIFIYFADSNTAP
 - VPSSLS - - - - - FLETTRLLPVQGKQR - - - - - AIMGAHEPSPGGDLAR
 QALPRVHPAGSFHAGPGDLQWKAQSQDGFENE - - - - EFTSSQV - - GRKSQSAFYPEDDD
 YFFAAGQPGWHSHTQGTLGFSSPGEPGPREGAPAAVQVRRRLKKRHR - - - -
 - - - - - RQRRS - - HVLEEGDDGDRLY - - SSMRSAFLYRLWKGNVSSKMLSPRLQKAMKD
 YTANKHGVFR - - GKR - EAGL - SRAQLLCQLRSRARVRLTLDGTEAPFSALGW - RLVP
 VPLS - - QLHP - - GLRCAVVMMSAGAILNSLLGEEIDSHDAVLRFNSAPTRGYEKDVG
 KTTVRIINSQILTNPSHHFDIDSLYKDVLVAVDPAPYSANLNLYWKKPDYNNLFTPYI
 RQRNPQPFYILHPKFIWQLWDIIQENTKEKIQPNPPSSGFIGILIMMSMCREVHVYEYI
 PSVRQTELCHYHELYYYDACTLGYHPLLVEKLLVQRLNMGQADLYRKKGKVVLPGFQAV
 HC PAPSPVIPH - -
 >Ggor_ST6Gal2
 - - - - - MKPHLKQWKQMLFGIFAWGLLFLIIFIYFADSNTAP
 - VPSSLS - - - - - FLETTRLLPVQGKQR - - - - - AIMGAHEPSPGGDLAR
 QALPRAXPAGSFHAGPGDLQWKAQSQDGFENH - - - - EFTSSQV - - GRKSQSAFYPEDDD
 YFFAAGQPGWHSHTQGTLGFSSPGEPGPREGAPAAVQVRRRKKRHR - - - -
 - - - - - RQRRS - - HVLEEGDDGDRLY - - SSMRSAFLYRLWKGNVSSKMLSPRLQKAMKD
 YTANKHGVFR - - GKR - EAGL - SRAQLLCQLRSRARVRLTLDGTEAPFSALGW - RLVP
 VPLS - - QLHP - - GLRCAVVMMSAGAILNSLLGEEIDSHDAVLRFNSAPTRGYEKDVG
 KTTVRIINSQILTNPSHHFDIDSLYKDVLVAVDPAPYSANLNLYWKKPDYNNLFTPYI
 RQRNPQPFYILHPKFIWQLWDIIQENTKEKIQPNPPSSGFIGILIMMSMCREVHVYEYI
 PSVRQTELCHYHELYYYDACTLGYHPLLVEKLLVQRLNMGQADLYRKKGKVVLPGFQAV
 HC PAPSPVIPH - -
 >Stro_ST6Gal2
 - - - - - MKPNLKQWKQMLFGIFAWGLLFLVIFYFTDSNSVEP
 - VPSAFS - - - - - YVESKKHFLQGKQR - - - - - AIMGAHQDQLFSYAIDQ
 D - LLKEGILDSDFIVPGMSKMMAGADNYFESEQ - - EFIMSKK - - TQKSTSNNHEDDD
 EYLH - - - - - KNIDSVSKKKAPAYGKRYYHDTQRQHKKIRRNMQ - - - -
 - - - - - RKKQH - - MIEDSYDWNGFS - - SSMSKSFLQKLWKGNVSSKMLTPRLQKARRE
 YLRANKLGVNFN - - GKQNSRKL - - NPQELLCVLKDRAQVKTLGDKDAPFSSLGWE - KYFPK
 IALN - - KLYPH - - GFSTCAVVSAGAIDSHDAVLRFNSAPTRNYEKDVG
 KTTLRIINSQILTNPNHHFTDSSLYKDVTIADWPSPYADLHMWYHCPDYNLFPFYKH
 RKRNPQPFYILHPKFTWELWKIIQENSNEKIQPNPPSSGFIGILIMMSMCREVHVYEYI
 PSVRQTELCHYHEQYYDACTLGYHPLLVEKMLIQRINQGTEDNLLRKKGKVVLPGFSSI
 HCPIKDHIT - - - -
 >Olat_ST6Gal2
 - - - - - MRFMSMRQWRKLVLAAIAWLALLFLGLLSYFLDNRVE - E
 PLTPAGSLVSO - - HSDTRRLTSIQQSSQQQQPVGRLSEQQGLNSIRTSHGNQPEAG - -
 - - VLSSSETPGMVNVHIPPSSSPYQTYGSQEANH - - QNDLDPQS - - LAAWSFGTQNVD
 S - - NFNIA - SQHRER - - ASQSIFSNN - - VEDEELPNEIS - - - -
 - - - PLVERRAD - - ADN - - - - VVQHMWRGTVSSGMLSPLRKRAMND
 YINAKHHVSYQ - - RHR - KVAR - SAKELLCQMKNQSQLRTVDGSEQPFFSLGWA - DFVPL

```

VPLQRWNKQRGGRS - FRTCAVSSAGA1LHSGLGKEIDSHDAVLRFNAAPTEGYEQDVGT
KTIRIINSQILANPKHEFKTSSIYKNITLVAWDPAPYTLNLDEWFASPDYDLCFGPYVEH
RKNHAEQLFYILHPSYLWQLWDLIQSNHQEKIQPNPPSSGFIGILTMMALCDKLHVYEYI
PSMRQTDLCHYHENYYDAACTLGYAHPLIYENLIRRINLGSEKDLLKKGRVTLPGFSTL
TCGA-----
>Gacu_ST6Gal2
-----MKSSMRQWRRLVLLGMLAWVLLFLGLLSYFLDARVN-E
PLTSVGSLSFQS---HPDTRRLASIQAHSQ-QHANLGPRLPELASTLTTTHPGVPEPET--R
PSASSATPQLSLDMSHSPKSAYAVGSHETSRS---PDYLDPQS---LAAWSSFGTENVG
S---HSDPS-VQSRER---TSQYENHISTSRYRGDGEEEEEEDDERD-----NVDEE
LRKRTPAGRRVG----DDSDADLEYYY---FSESGSVVQRLWGRVSAGMLSPLQRAMKD
YSANKHRVSYT---GHR-RAAQ-SANELLCQMKEQARLRTVDGSEQPSSLGWA-RLVPS
RPLERLHKRQDRSS-FKTCAVVTSAGAILRSLGLGKEIDAHDAVLRFNAAPTEGYERDVGS
KTIRIINSQILANPKHFRNTSSIYKNVTLVAWDPAPYTVDLHKWYAGPDYDNLFGPYIEH
RKLHPDQPFYILHPSYVWRLWDVIQGNTQENIQPNPPSSGFIGILLMMALCEQLHVYEYI
PSIRQTDLCHYHERYYDAACTLGYAHPLLVEKSLIQRHTGPKNDLRKGRVTLPGLSTV
NCDI-----

```

Data S4. SDP prediction results are shown below; MSA used is the one present in supplementary data C obtained with 101 ST6Gal sequences (48 ST6Gal I and 53 ST6Gal II). The header contains information about the parameters used in the server, followed by a table with the SDPs predictions sorted by scores. A detailed explanation of the output format can be found at Help section on the SPEER web server (<http://www.hpppi.iicb.res.in/ss/help.html>).

```

Number of columns in the alignment = 615
Number of sequences in the alignment = 101
Number of supplied subfamilies = 2
Subfamily 1 consists of 48 sequences
Subfamily 2 consists of 53 sequences
Gap percentage for each columns selected = 20%
SPEER-SERVER scoring term weights:-
Relative entropy term weight = 1
PC property distance term weight = 1
Evolutionary rate term weight = 0
SPEER-SERVER predicted scores for columns containing 20% gaps are shown below.
Columns are sorted based on SPEER-SERVER Score
    SPEER-SERVER Result
#####
# Column %ID Score Z-score P-value TYPE #
#####
307 47.7 5.892 3.104 0.001 TypeII
426 48.6 5.395 2.842 0.002 TypeII
539 49.7 5.328 2.807 0.003 TypeII
540 47.6 5.261 2.771 0.003 TypeII
553 49.7 5.120 2.697 0.004 TypeII
586 49.7 4.946 2.605 0.005 TypeII
448 38.9 4.803 2.530 0.006 TypeII
576 47.6 4.692 2.472 0.007 TypeII
387 49.5 4.655 2.452 0.007 TypeII
280 46.8 4.532 2.387 0.008 TypeII
522 48.8 4.453 2.346 0.010 TypeII
358 47.8 4.307 2.269 0.012 TypeII
555 47.9 4.262 2.245 0.012 TypeII
480 48.5 4.190 2.207 0.014 TypeII
41 33.7 3.966 2.089 0.018 TypeI
23 35.9 3.877 2.042 0.021 TypeI
389 39.9 3.850 2.028 0.021 TypeII
297 39.6 3.834 2.020 0.022 TypeII
55 31.6 3.780 1.991 0.023 TypeI
552 49.0 3.758 1.979 0.024 TypeII
24 32.6 3.636 1.915 0.028 TypeI
54 31.4 3.515 1.851 0.032 TypeI
431 38.9 3.514 1.851 0.032 TypeII
283 37.3 3.422 1.803 0.036 TypeI
304 28.3 3.296 1.736 0.041 TypeI
543 19.7 3.168 1.669 0.048 MC
432 36.5 3.123 1.645 0.050 TypeI
388 42.7 3.118 1.643 0.050 TypeII
435 37.0 3.097 1.631 0.051 TypeI
473 39.2 3.087 1.626 0.052 TypeI
573 33.4 3.061 1.612 0.053 TypeI
446 37.1 3.033 1.598 0.055 TypeI
282 27.4 3.030 1.596 0.055 MC
51 34.6 3.027 1.594 0.055 TypeI
300 36.5 2.933 1.545 0.061 TypeI
476 34.5 2.845 1.499 0.067 TypeI
478 18.1 2.841 1.497 0.067 MC
352 35.6 2.743 1.445 0.074 TypeI
383 35.2 2.659 1.401 0.081 TypeI
440 29.4 2.653 1.398 0.081 TypeI
80 28.8 2.590 1.364 0.086 TypeI
339 21.8 2.559 1.348 0.089 MC
29 33.7 2.538 1.337 0.091 TypeI
497 20.2 2.537 1.336 0.091 MC
521 40.7 2.534 1.335 0.091 TypeII
589 34.1 2.519 1.327 0.092 TypeI

```

45	32.1	2.331	1.228	0.110	TypeI
583	30.9	2.289	1.206	0.114	TypeI
52	34.1	2.270	1.196	0.116	TypeI
588	25.5	2.179	1.148	0.125	MC
434	34.4	2.145	1.130	0.129	TypeI
56	17.5	2.048	1.079	0.140	
114	21.6	1.981	1.044	0.148	
285	26.7	1.939	1.021	0.154	MC
85	31.7	1.909	1.006	0.157	TypeI
26	20.4	1.814	0.956	0.170	MC
414	54.3	1.775	0.935	0.175	TypeII
317	31.7	1.738	0.915	0.180	
508	34.2	1.732	0.912	0.181	TypeI
298	31.8	1.676	0.883	0.189	TypeI
57	17.7	1.503	0.792	0.214	
525	37.8	1.465	0.772	0.220	TypeI
342	31.2	1.406	0.741	0.229	
50	25.0	1.380	0.727	0.234	MC
88	20.8	1.327	0.699	0.242	
111	21.8	1.300	0.685	0.247	
420	31.2	1.268	0.668	0.252	TypeI
509	15.2	1.240	0.653	0.257	MC
83	23.8	1.199	0.632	0.264	MC
273	32.9	1.143	0.602	0.274	
361	11.6	1.100	0.579	0.281	
77	18.6	1.085	0.572	0.284	
82	19.2	1.075	0.566	0.286	MC
461	41.2	1.010	0.532	0.297	TypeI
345	34.7	0.996	0.525	0.300	
48	22.6	0.989	0.521	0.301	MC
43	38.7	0.968	0.510	0.305	TypeI
362	28.9	0.931	0.490	0.312	TypeI
545	50.0	0.888	0.468	0.320	TypeI
279	22.0	0.769	0.405	0.343	MC
58	19.0	0.756	0.398	0.345	
496	32.2	0.744	0.392	0.348	MC
172	23.9	0.728	0.383	0.351	
447	19.8	0.667	0.351	0.363	MC
86	26.2	0.642	0.338	0.368	MC
479	16.4	0.590	0.311	0.378	MC
357	20.0	0.557	0.293	0.385	MC
408	31.4	0.544	0.287	0.387	MC
371	10.3	0.542	0.285	0.388	
291	20.4	0.533	0.281	0.389	MC
554	24.9	0.519	0.274	0.392	MC
127	11.7	0.509	0.268	0.394	
580	19.9	0.502	0.265	0.396	MC
322	16.1	0.443	0.233	0.408	
356	12.8	0.442	0.233	0.408	MC
320	11.4	0.410	0.216	0.415	
343	36.6	0.394	0.208	0.418	
168	15.4	0.357	0.188	0.425	
462	59.0	0.344	0.181	0.428	TypeI
511	17.1	0.306	0.161	0.436	MC
126	10.6	0.305	0.161	0.436	
562	57.1	0.298	0.157	0.438	TypeI
171	12.1	0.294	0.155	0.438	
141	12.0	0.283	0.149	0.441	
139	9.7	0.267	0.141	0.444	
336	50.7	0.251	0.132	0.447	TypeI
278	15.7	0.225	0.118	0.453	
146	13.7	0.219	0.115	0.454	
44	26.4	0.208	0.110	0.456	MC
284	23.2	0.204	0.108	0.457	MC
459	30.6	0.201	0.106	0.458	MC
275	22.9	0.197	0.104	0.459	
272	17.5	0.184	0.097	0.461	
587	41.5	0.158	0.083	0.467	TypeI
577	56.6	0.153	0.080	0.468	TypeI
25	30.0	0.150	0.079	0.469	MC
441	18.5	0.144	0.076	0.470	MC
351	48.5	0.136	0.072	0.471	
412	17.0	0.136	0.071	0.472	MC
467	19.7	0.085	0.045	0.482	MC
170	19.7	0.079	0.042	0.483	
415	59.9	0.060	0.032	0.487	TypeI
593	54.1	0.059	0.031	0.488	TypeI
289	53.3	0.033	0.017	0.493	TypeI
316	14.1	0.032	0.017	0.493	
140	13.4	0.013	0.007	0.497	
390	26.5	0.008	0.004	0.498	MC
364	15.0	-0.020	-0.011	0.504	MC
436	13.7	-0.040	-0.021	0.508	MC
178	13.7	-0.059	-0.031	0.512	
176	14.2	-0.074	-0.039	0.515	
271	22.4	-0.080	-0.042	0.517	
128	13.9	-0.080	-0.042	0.517	
442	51.1	-0.088	-0.046	0.519	TypeI
148	12.7	-0.089	-0.047	0.519	
143	10.6	-0.155	-0.082	0.533	

556	43.9	-0.164	-0.086	0.534	TypeI
131	17.0	-0.168	-0.088	0.535	
142	23.1	-0.174	-0.092	0.536	
460	32.6	-0.180	-0.095	0.538	MC
376	27.4	-0.182	-0.096	0.538	
42	18.3	-0.185	-0.098	0.539	MC
49	32.9	-0.207	-0.109	0.543	MC
337	19.8	-0.215	-0.113	0.545	MC
136	10.8	-0.216	-0.114	0.545	
584	17.5	-0.218	-0.115	0.546	MC
84	20.9	-0.250	-0.132	0.552	MC
475	21.6	-0.263	-0.139	0.555	MC
463	17.3	-0.313	-0.165	0.566	MC
169	15.4	-0.320	-0.169	0.567	
392	24.1	-0.327	-0.172	0.568	MC
340	53.3	-0.339	-0.178	0.571	TypeI
575	64.5	-0.342	-0.180	0.572	TypeI
452	53.4	-0.367	-0.193	0.577	TypeI
493	53.8	-0.374	-0.197	0.578	TypeI
147	11.3	-0.378	-0.199	0.579	
451	57.0	-0.380	-0.200	0.579	TypeI
112	17.7	-0.391	-0.206	0.582	
483	25.8	-0.401	-0.211	0.584	MC
79	34.1	-0.408	-0.215	0.585	MC
331	31.7	-0.438	-0.231	0.591	MC
302	36.3	-0.440	-0.232	0.592	MC
506	39.7	-0.449	-0.236	0.593	MC
344	18.2	-0.452	-0.238	0.594	
321	15.0	-0.458	-0.241	0.595	
138	14.7	-0.474	-0.250	0.599	
115	21.3	-0.477	-0.251	0.599	
495	28.2	-0.480	-0.253	0.600	MC
548	53.8	-0.492	-0.259	0.602	TypeI
133	9.4	-0.493	-0.260	0.603	
416	26.9	-0.498	-0.262	0.603	MC
535	56.7	-0.498	-0.262	0.603	TypeI
310	18.7	-0.518	-0.273	0.608	MC
110	11.0	-0.523	-0.275	0.609	
530	55.7	-0.551	-0.290	0.614	TypeI
346	15.4	-0.565	-0.297	0.617	
144	11.8	-0.573	-0.302	0.619	
175	15.3	-0.584	-0.307	0.621	
308	30.8	-0.609	-0.321	0.626	MC
464	24.5	-0.609	-0.321	0.626	
532	29.5	-0.610	-0.321	0.626	MC
87	33.4	-0.613	-0.323	0.627	MC
274	11.4	-0.629	-0.331	0.630	
378	32.3	-0.635	-0.335	0.631	MC
472	49.2	-0.638	-0.336	0.632	TypeI
276	18.3	-0.640	-0.337	0.632	MC
277	28.9	-0.664	-0.350	0.637	MC
132	14.2	-0.684	-0.360	0.641	
27	36.4	-0.692	-0.364	0.642	MC
349	45.4	-0.697	-0.367	0.643	
363	61.1	-0.702	-0.370	0.644	TypeI
28	43.9	-0.710	-0.374	0.646	MC
427	47.3	-0.712	-0.375	0.646	TypeI
113	20.1	-0.724	-0.381	0.648	
504	62.2	-0.726	-0.383	0.649	TypeI
533	28.9	-0.732	-0.386	0.650	MC
437	43.3	-0.751	-0.396	0.654	TypeI
395	21.7	-0.785	-0.413	0.660	MC
326	16.1	-0.786	-0.414	0.661	
312	23.4	-0.791	-0.417	0.662	MC
296	57.7	-0.793	-0.418	0.662	TypeI
129	27.6	-0.811	-0.427	0.665	
334	21.3	-0.818	-0.431	0.667	MC
335	26.3	-0.826	-0.435	0.668	MC
53	24.9	-0.829	-0.437	0.669	MC
78	45.7	-0.839	-0.442	0.671	
529	35.8	-0.844	-0.445	0.672	MC
145	21.3	-0.856	-0.451	0.674	
524	64.8	-0.877	-0.462	0.678	TypeI
503	39.3	-0.884	-0.466	0.679	MC
514	67.5	-0.893	-0.471	0.681	TypeI
130	14.0	-0.908	-0.478	0.684	
499	49.7	-0.930	-0.490	0.688	MC
137	15.9	-0.932	-0.491	0.688	
484	47.0	-0.938	-0.494	0.689	TypeI
469	69.1	-0.955	-0.503	0.692	TypeII
299	44.1	-0.976	-0.514	0.696	MC
46	51.9	-0.983	-0.518	0.698	TypeI
327	26.1	-1.008	-0.531	0.702	
338	53.8	-1.026	-0.540	0.705	TypeI
570	62.4	-1.028	-0.542	0.706	TypeI
550	71.7	-1.073	-0.565	0.714	TypeII
303	23.4	-1.094	-0.576	0.718	MC
332	66.6	-1.113	-0.586	0.721	TypeI
558	49.8	-1.114	-0.587	0.721	TypeI
287	57.7	-1.141	-0.601	0.726	TypeI

456	65.2	-1.146	-0.603	0.727	TypeI
598	26.4	-1.158	-0.610	0.729	MC
288	24.8	-1.159	-0.611	0.729	
502	63.7	-1.189	-0.627	0.735	TypeI
360	13.1	-1.195	-0.629	0.735	MC
468	27.9	-1.196	-0.630	0.736	MC
582	24.3	-1.198	-0.631	0.736	MC
458	71.4	-1.269	-0.668	0.748	TypeII
486	15.4	-1.311	-0.691	0.755	MC
444	69.5	-1.332	-0.702	0.759	TypeI
270	19.8	-1.335	-0.703	0.759	
457	70.8	-1.348	-0.710	0.761	TypeI
599	19.8	-1.406	-0.740	0.770	MC
319	22.3	-1.406	-0.741	0.771	
536	68.8	-1.409	-0.742	0.771	TypeI
399	40.2	-1.411	-0.743	0.771	MC
350	21.1	-1.418	-0.747	0.772	
134	11.3	-1.435	-0.756	0.775	
424	44.6	-1.452	-0.765	0.778	MC
600	32.0	-1.453	-0.766	0.778	MC
47	25.9	-1.461	-0.770	0.779	MC
601	21.4	-1.471	-0.775	0.781	MC
353	96.1	-1.479	-0.779	0.782	TypeII
301	98.0	-1.480	-0.779	0.782	TypeII
293	98.0	-1.485	-0.782	0.783	TypeII
359	98.0	-1.486	-0.783	0.783	TypeII
581	98.0	-1.486	-0.783	0.783	TypeII
347	98.0	-1.525	-0.804	0.789	
507	67.6	-1.527	-0.804	0.789	TypeI
579	96.1	-1.538	-0.810	0.791	TypeII
485	98.0	-1.549	-0.816	0.793	TypeII
292	54.4	-1.564	-0.824	0.795	TypeI
578	34.2	-1.577	-0.831	0.797	MC
413	64.7	-1.580	-0.832	0.797	TypeI
295	60.3	-1.596	-0.841	0.800	TypeI
329	55.2	-1.601	-0.843	0.800	MC
465	98.0	-1.603	-0.844	0.801	TypeII
423	98.0	-1.614	-0.850	0.802	TypeII
135	32.9	-1.628	-0.858	0.804	
449	40.1	-1.628	-0.858	0.804	MC
177	22.9	-1.633	-0.860	0.805	
534	90.4	-1.676	-0.883	0.811	TypeII
328	90.4	-1.744	-0.918	0.821	TypeII
592	59.6	-1.754	-0.924	0.822	TypeI
333	48.2	-1.776	-0.936	0.825	MC
377	29.2	-1.812	-0.954	0.830	
354	25.2	-1.818	-0.958	0.831	MC
315	69.8	-1.824	-0.961	0.832	
482	32.1	-1.863	-0.982	0.837	MC
348	96.1	-1.864	-0.982	0.837	
311	40.3	-1.891	-0.996	0.840	
421	94.1	-1.917	-1.010	0.844	TypeII
89	36.3	-1.939	-1.021	0.846	
411	79.7	-1.966	-1.036	0.850	TypeII
574	83.4	-1.967	-1.036	0.850	TypeII
341	33.3	-1.989	-1.048	0.853	
546	85.3	-2.042	-1.076	0.859	TypeII
500	81.4	-2.060	-1.085	0.861	TypeII
433	47.6	-2.069	-1.090	0.862	MC
443	71.2	-2.108	-1.110	0.867	TypeI
526	44.8	-2.137	-1.126	0.870	MC
591	50.5	-2.139	-1.127	0.870	MC
547	54.0	-2.155	-1.135	0.872	MC
294	88.7	-2.223	-1.171	0.879	TypeII
401	88.7	-2.244	-1.182	0.881	TypeII
404	83.1	-2.273	-1.197	0.884	TypeII
466	76.9	-2.276	-1.199	0.885	TypeII
597	83.6	-2.306	-1.215	0.888	TypeII
585	92.2	-2.307	-1.215	0.888	TypeII
286	92.3	-2.388	-1.258	0.896	TypeII
569	94.1	-2.388	-1.258	0.896	TypeII
488	90.4	-2.416	-1.273	0.898	TypeII
477	92.3	-2.423	-1.276	0.899	TypeII
595	90.4	-2.445	-1.288	0.901	TypeII
491	94.1	-2.530	-1.333	0.909	TypeII
510	96.1	-2.595	-1.367	0.914	TypeII
474	94.1	-2.605	-1.372	0.915	TypeII
418	98.0	-2.641	-1.391	0.918	TypeII
528	98.0	-2.647	-1.395	0.918	TypeII
397	98.0	-2.651	-1.396	0.919	TypeII
393	98.0	-2.652	-1.397	0.919	TypeII
602	98.0	-2.662	-1.402	0.920	
566	98.0	-2.667	-1.405	0.920	TypeII
492	98.0	-2.670	-1.407	0.920	TypeII
417	96.1	-2.671	-1.407	0.920	TypeII
490	96.1	-2.681	-1.412	0.921	TypeII
450	98.0	-2.700	-1.422	0.923	TypeII
594	98.0	-2.705	-1.425	0.923	TypeII
396	98.0	-2.732	-1.439	0.925	TypeII
513	98.0	-2.743	-1.445	0.926	TypeII

512	98.0	-2.744	-1.445	0.926	TypeII
290	98.0	-2.744	-1.446	0.926	TypeII
515	98.0	-2.746	-1.446	0.926	TypeII