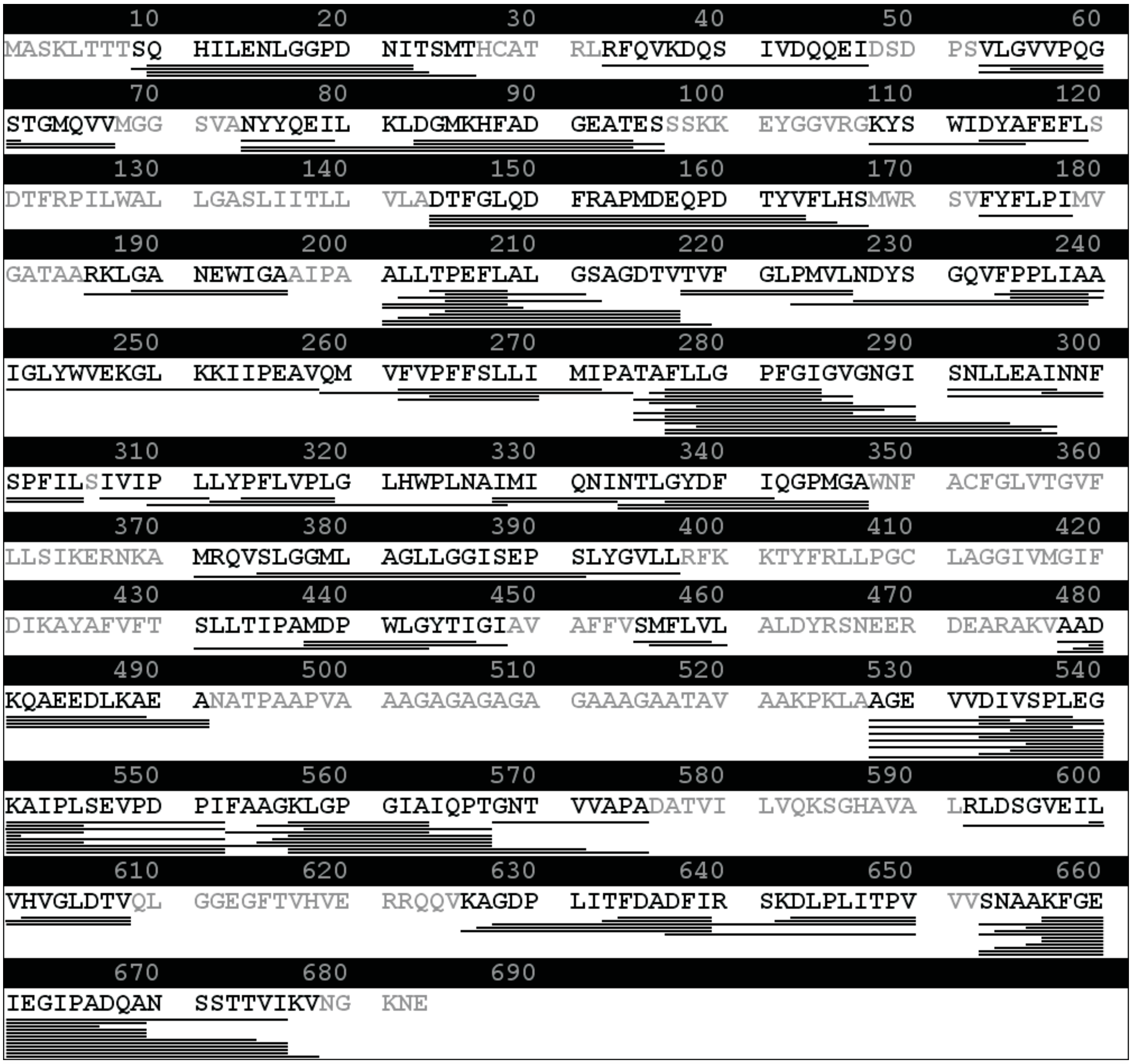
this file contains sequence coverage, predicted TM helix data and the number of tryptic cleavage sites of all membrane proteins among the top 50 CB nLC-ESI/MALDI proteins and BR

	pages
nLC-ESI CB membrane proteins among top 50	**2-27**
nLC-MALDI CB membrane proteins among top 50	**28-42**
BR nLC-ESI and nLC-MALDI	**43-44**

Cg1537 GLUCOSE-SPECIFIC ENZYME II BC COMPONENT OF PTS

ESI 10TMH 72.5 kDa 18 Arg 29 Lys



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        10         20         30         40         50         60
MASKLTTTSQ HILENLGGPD NITSMTHCAT RLRFQVKDQS IVDQQEIDSD PSVLGVVPQG
        70         80         90        100        110        120
STGMQVVMGG SVANYYQEIL KLDGMKHFAD GEATESSSKK EYGGVRGKYS WIDYAFEFLS
       130        140        150        160        170        180
DTFRPILWAL LGASLIITLL VLADTFGLQD FRAPMDEQPD TYVFLHSMWR SVFYFLPIMV
       190        200        210        220        230        240
GATAARKLGA NEWIGAAIPA ALLTPEFLAL GSAGDTVTVF GLPMVLNDYS GQVFPPLIAA
       250        260        270        280        290        300
IGLYWVEKGL KKIIPEAVQM VFVPFFSLLI MIPATAFLLG PFGIGVGNGI SNLLEAINNF
       310        320        330        340        350        360
SPFILSIVIP LLYPFLVPLG LHWPLNAIMI QNINTLGYDF IQGPMGAWNF ACFGLVTGVF
       370        380        390        400        410        420
LLSIKERNKA MRQVSLGGML AGLLGGISEP SLYGVLLRFK KTYFRLLPGC LAGGIVMGIF
       430        440        450        460        470        480
DIKAYAFVFT SLLTIPAMDP WLGYTIGIAV AFFVSMFLVL ALDYRSNEER DEARAKVAAD
       490        500        510        520        530        540
KQAEEDLKAE ANATPAAPVA AAGAGAGAGA GAAAGAATAV AAKPKLAAGE VVDIVSPLEG
       550        560        570        580        590        600
KAIPLSEVPD PIFAAGKLGP GIAIQPTGNT VVAPADATVI LVQKSGHAVA LRLDSGVEIL
       610        620        630        640        650        660
VHVGLDTVQL GGEGFTVHVE RRQQVKAGDP LITFDADFIR SKDLPLITPV VVSNAAKFGE
       670        680        690
IEGIPADQAN SSTTVIKVNG KNE
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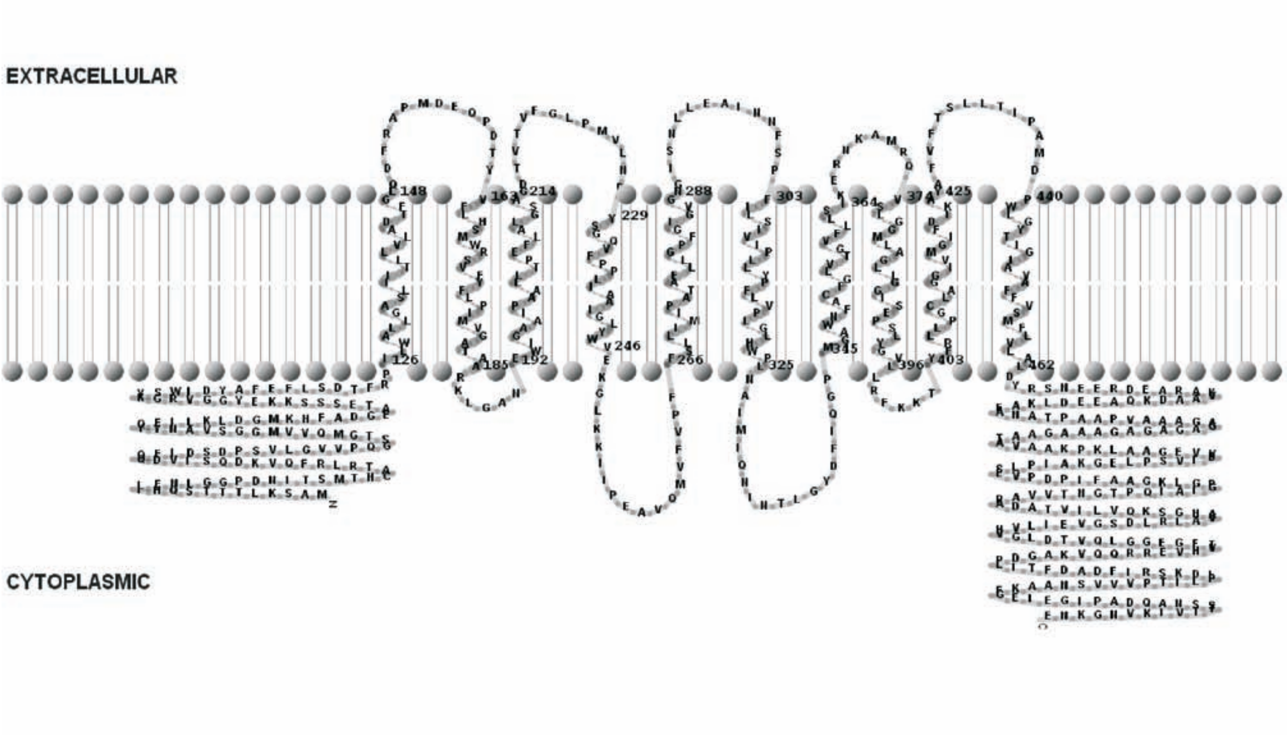
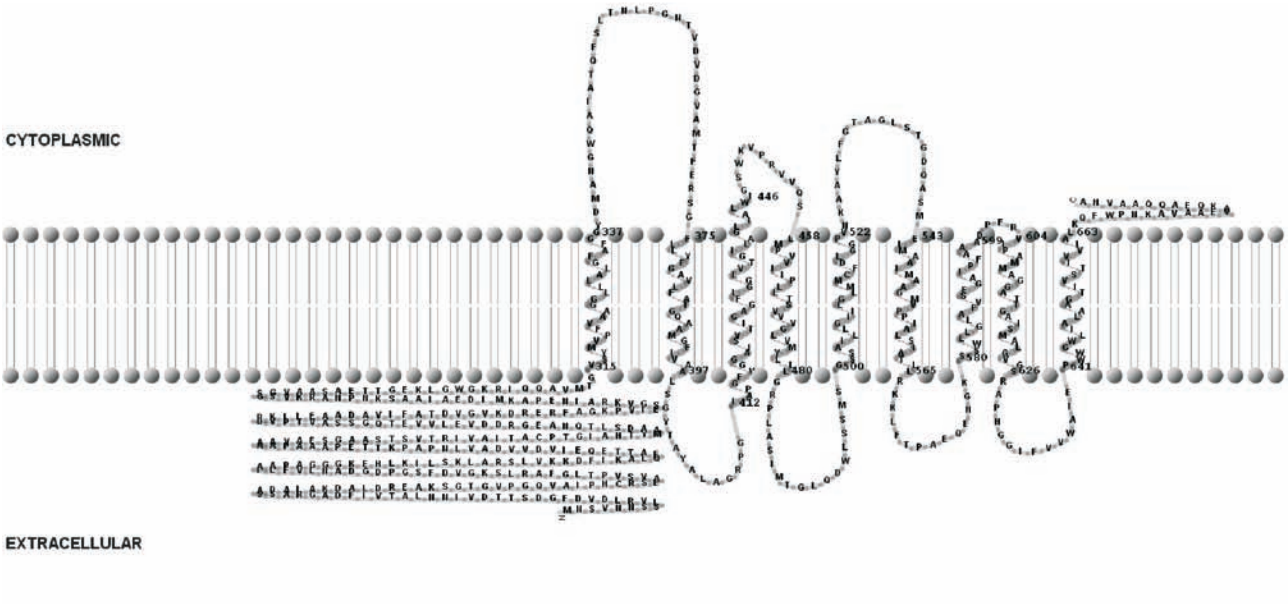


Cg2120 SUGAR SPECIFIC PTS SYSTEM, FRUCTOSE/MANNITOL-SPECIFIC TRANSPORT PROTEIN

ESI 9TMH 70.4 kDa 20 Arg 27 Lys

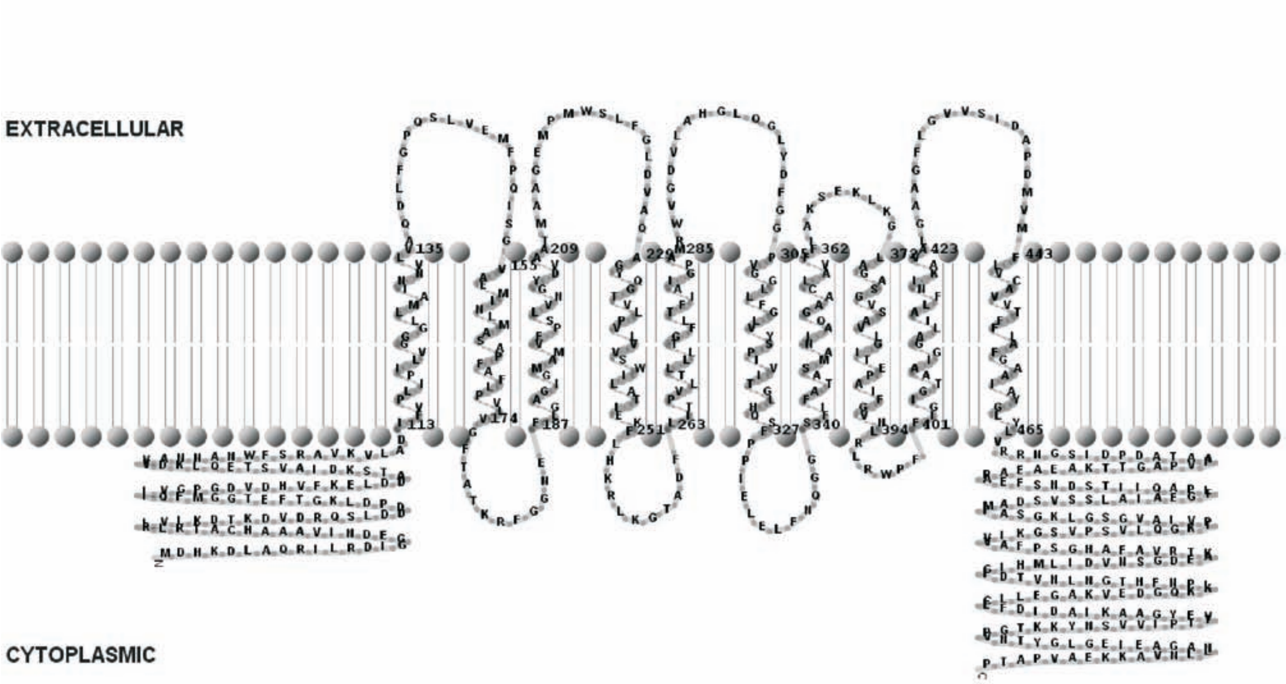
10	20	30	40	50	60
MNSVNNSSLV	**RLDVDFGDST**	**TDVINNLATV**	**IFDAGRASSA**	**DALAKDALDR**	**EAKSGTGVPG**
70	80	90	100	110	120
QVAIPHCRSE	AVSVPTLGFA	**RLSKGVDFSG**	**PDGDANLV**FL	IAAPAGGGKE	HLKILSKLAR
130	140	150	160	170	180
SLVKKDFIKA	**LQEATTEQEI**	**VDVVDAVLNP**	**APKTTEPA**AA	PAAAAVAESG	AASTSVTRIV
190	200	210	220	230	240
AITACPTGIA	HTYMAA**DSLT**	**QNAEGRDDVE**	**LV**VET**QGSSA**	**VTPVDPKIIE**	**AADAV**IFATD
250	260	270	280	290	300
VGVKDRERFA	GKPVIESGVK	RA**INEPAKMI**	**DEAIAA**SKNP	NARKVSGSGV	AASAETTGEK
310	320	330	340	350	360
LGWGKRIQQA	VMTGV**SYMVP**	**FVA**AGGLLLA	LGFAFGGYDM	ANGWQAIATQ	FSLT**NLPGNT**
370	380	390	400	410	420
VDVDGVAMTF	ERSGFLLYFG	AVLFATGQAA	MGFIVAALSG	YTAYA**LAGRP**	**GIAPG**FVGGA
430	440	450	460	470	480
ISVTIGAGFI	GGLVTGILAG	LIALWIGSWK	VPRVVQSLMP	V**VIIPLLT**SV	VVGLV**MYLLL**
490	500	510	520	530	540
GRPLA**SIMTG**	**LQDWLSSMS**G	SSA**ILLGII**L	GLMMC**FDLGG**	**PV**NKA**AYLFG**	**TAGL**STGDQA
550	560	570	580	590	600
SMEIMAAIMA	A**GMVPPIAL**S	IATLLRKKLF	TPAEQENGKS	**SWLLGLAFVS**	**EGAIPFAAAD**
610	620	630	640	650	660
PFRVIPAMMA	GGATTGAISM	ALGVGSRAPH	GGIFVVWAIE	PWWGWLIALA	AGTIVSTIVV
670	680	690			
IALKQFWPNK	AVAAEVAKQE	AQQAAVNA			



Cg2925 ENZYME II SUCROSE PROTEIN

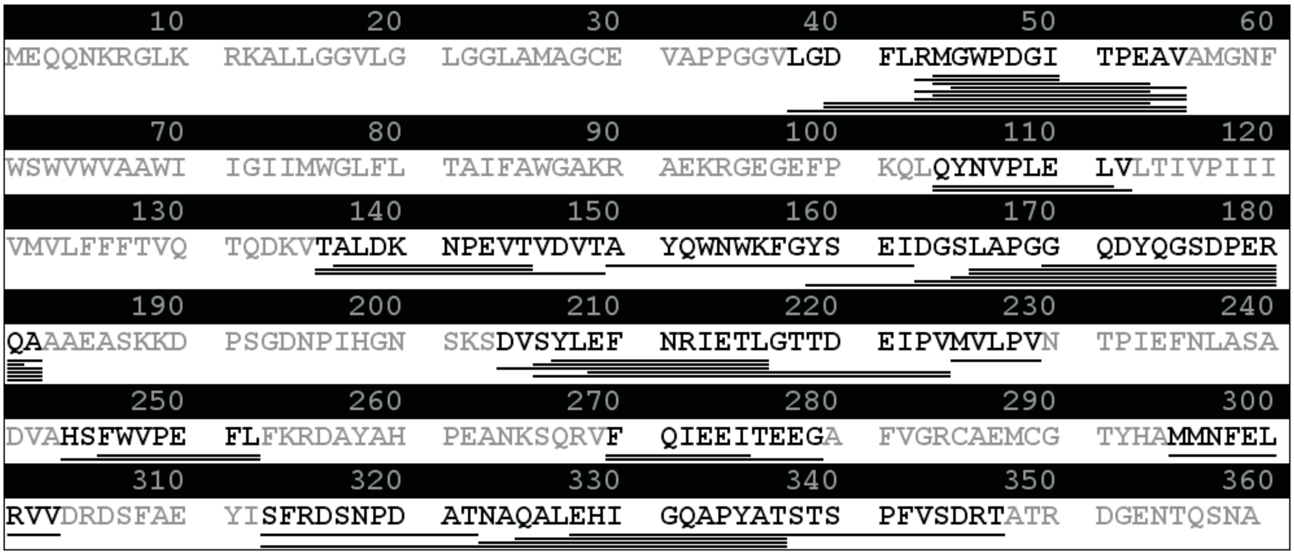
ESI 10TMH 69.1 kDa 14 Arg 29 Lys

10	20	30	40	50	60
MDHKDLAQRI	**LRDIGGEDNI**	**VA**AAHCATRL	RLVLKDTKDV	DRQ**SLDDDPD**	**LKGTFETGGM**
70	80	90	100	110	120
FQIIVGPGDV	**DHVFKELDDA**	**TSKDIAVSTE**	**QLKDVVANNA**	NWFSRAVKV**L**	**ADIFVPLIPI**
130	140	150	160	170	180
LVGGGLLMAI	**NNVLVAQDLF**	**GPQSLVEMFP**	**QIS**GVAEMI**N**	**LMASAPFAFL**	**PVLV**GFTATK
190	200	210	220	230	240
RFGGNEFLGA	GIGMAMVFPS	LVNGYDVAAT	**MAAGEMPMWS**	**LFGLDVA**QAG	YQGTVLPVLV
250	260	270	280	290	300
VSWILATIEK	FLHKRLKGTA	**DFLITPV**LTL	LLTGFLTFIA	IGPAMRWVGD	VL**AHGLQGLY**
310	320	330	340	350	360
DFGGPVGGLL	FGLVYSPIVI	**TGLHQSFPPI**	**ELELFNQGGS**	**FI**FATASMAN	IAQGAACLAV
370	380	390	400	410	420
FFLAKSEKLK	GLAGASGVSA	VLGITEPAIF	GVNLRLRWPF	FIGIGTAAIG	GALIALFNIK
430	440	450	460	470	480
AVALGAAGFL	GVVSIDAPDM	VMFLVCAVVT	FFIAFGAAIA	YGLYLVRRNG	SIDPDATAAP
490	500	510	520	530	540
VPAGTTKAEA	EAPAEFSNDS	TIIQAPLTGE	AIALSSVSDA	MFASGKLGSG	VAIVPT**KGQL**
550	560	570	580	590	600
VSPVSGKIVV	AFPS**GHAFAV**	RT**KAEDGSNV**	**DILMHIGFDT**	**V**NLNGTHFNP	LKKQGDEVKA
610	620	630	640	650	660
GELLCEFDID	AIKAA**GYEVT**	**TPIVV**SNYKK	TGPV**NTYGLG**	**EIEAGANLLN**	**VA**KKEAVPAT
670					
P					

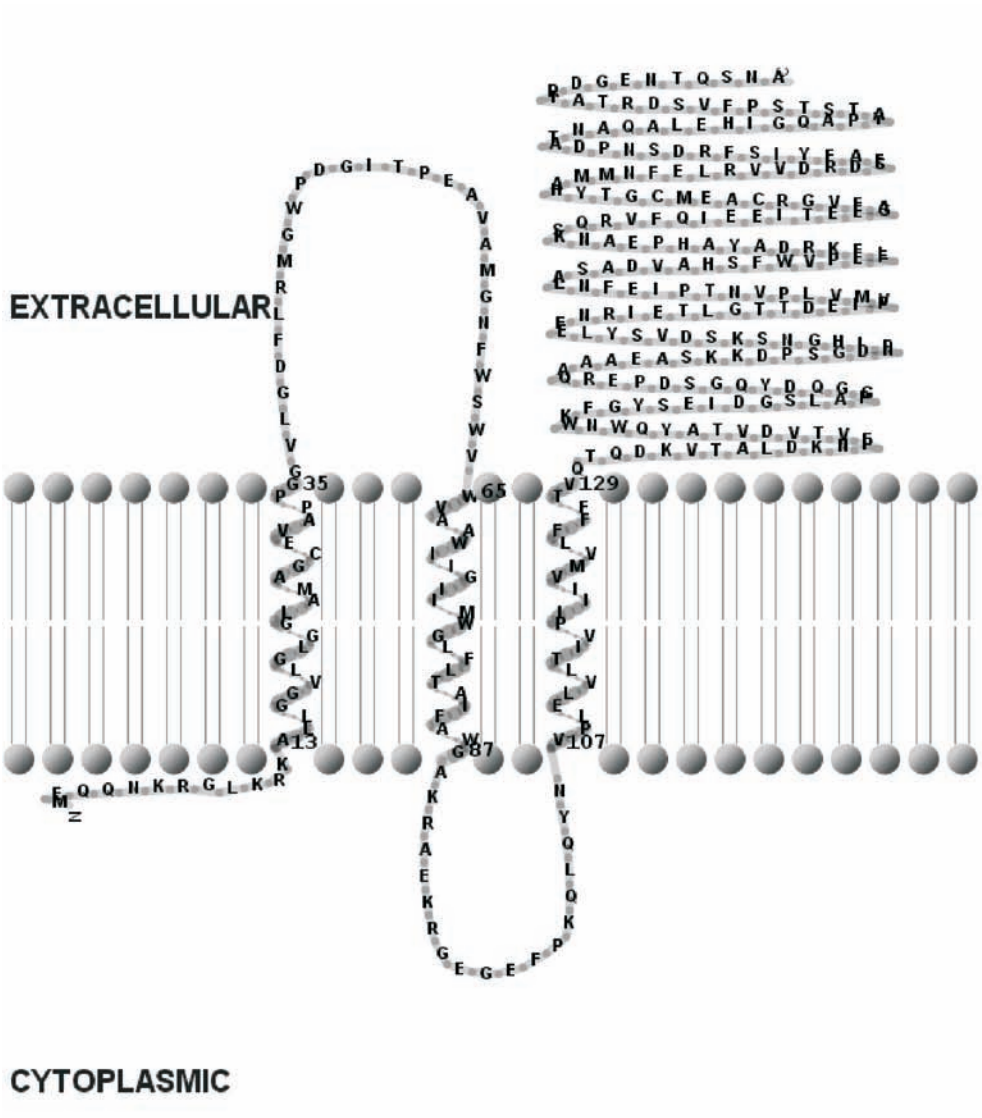


Cg2409 CYTOCHROME C OXIDASE CHAIN II

ESI 3TMH 39.6 kDa 15 Arg 14 Lys



10	20	30	40	50	60
MEQQNKRGLK	RKALLGGVLG	LGGLAMAGCE	VAPPGGV**LGD**	**FLRMGWPDGI**	**TPEAV**AMGNF
70	**80**	**90**	**100**	**110**	**120**
WSWVWVAAWI	IGIIMWGLFL	TAIFAWGAKR	AEKRGEGEFP	KQL**QYNVPLE**	**LV**LTIVPIII
130	**140**	**150**	**160**	**170**	**180**
VMVLFFFTVQ	TQDKV**TALDK**	**NPEVTVDVTA**	**YQWNWKFGYS**	**EIDGSLAPGG**	**QDYQGSDPER**
190	**200**	**210**	**220**	**230**	**240**
QAAAEASKKD	PSGDNPIHGN	SKS**DVSYLEF**	**NRIETLGTTD**	**EIPVMVLPV**N	TPIEFNLASA
250	**260**	**270**	**280**	**290**	**300**
DVA**HSFWVPE**	**FL**FKRDAYAH	PEANKSQRV**F**	**QIEEITEEG**A	FVGRCAEMCG	TYHA**MMNFEL**
310	**320**	**330**	**340**	**350**	**360**
RVVDRDSFAE	YI**SFRDSNPD**	**ATNAQALEHI**	**GQAPYATSTS**	**PFVSDRT**ATR	DGENTQSNA



Cg2404 RIESKE IRON-SULFUR PROTEIN

ESI 3TMH 45.1 kDa 22 Arg 15 Lys

```
        10         20         30         40         50         60
MSNNNDKQYT TQELNAMSNE DLARLGTELD DVTIAYRKER FPIANDPAEK RAARAVTFWL
        70         80         90        100        110        120
VLGIIGGLGF LATYIFWPWE YKAHGDEGLL AYTLYTPMLG ITSGLCILSL GFAVVLYVKK
       130        140        150        160        170        180
FIPEEIAVQR RHDGPSEEVD RRTIVALLND SWQTSTLGRR KLIMGLAGGG AVLAGLTIIA
       190        200        210        220        230        240
PMGGMIKNPW NPKEGPMDVQ GDGTLWTSGW TLVENDVKVY LGRDTAAIAE SHTDATGEHW
       250        260        270        280        290        300
STTGVSRLVR MRPEDLAAAS METVFPLPAE MVNDGAEYDP AKDVYEHQMH SVHGPRNAVM
       310        320        330        340        350        360
LIRLRTADAE KVIEREGQES FHYGDYYAYS KICTHIGCPT SLYEAQTNRI LCPCHQSQFD
       370        380        390        400        410
ALHYGKPVFG PAARALPQLP ITVDEEGYLI AAGNFIEPLG PAFWERKS
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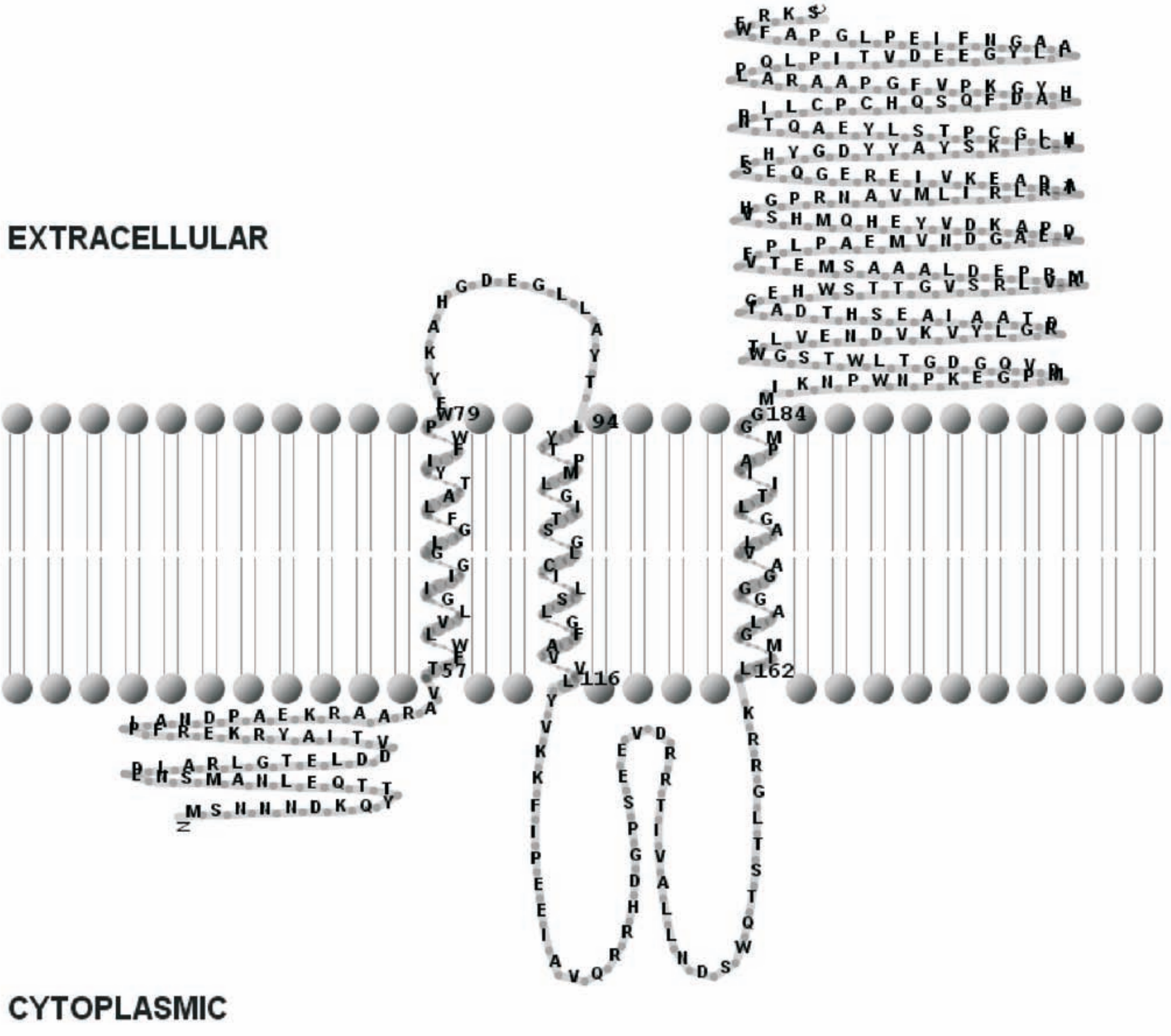
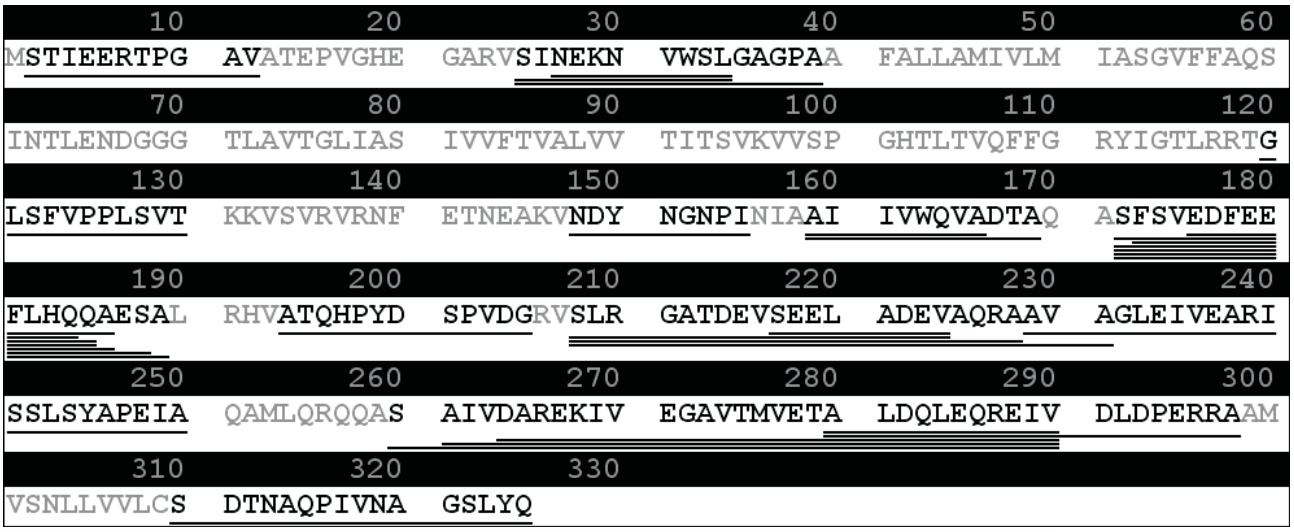


Cg3138 MEMBRANE PROTEASE SUBUNIT, STOMATIN/PROHIBITIN HOMOLOG

ESI 2TMH 34.7 kDa 17 Arg 6 Lys



```
        10         20         30         40         50         60
MSTIEERTPG AVATEPVGHE GARVSINEKN VWSLGAGPAA FALLAMIVLM IASGVFFAQS
        70         80         90        100        110        120
INTLENDGGG TLAVTGLIAS IVVFTVALVV TITSVKVVSP GHTLTVQFFG RYIGTLRRTG
       130        140        150        160        170        180
LSFVPPLSVT KKVSVRVRNF ETNEAKVNDY NGNPINIAAI IVWQVADTAQ ASFSVEDFEE
       190        200        210        220        230        240
FLHQQAESAL RHVATQHPYD SPVDGRVSLR GATDEVSEEL ADEVAQRAAV AGLEIVEARI
       250        260        270        280        290        300
SSLSYAPEIA QAMLQRQQAS AIVDAREKIV EGAVTMVETA LDQLEQREIV DLDPERRAAM
       310        320        330
VSNLLVVLCS DTNAQPIVNA GSLYQ
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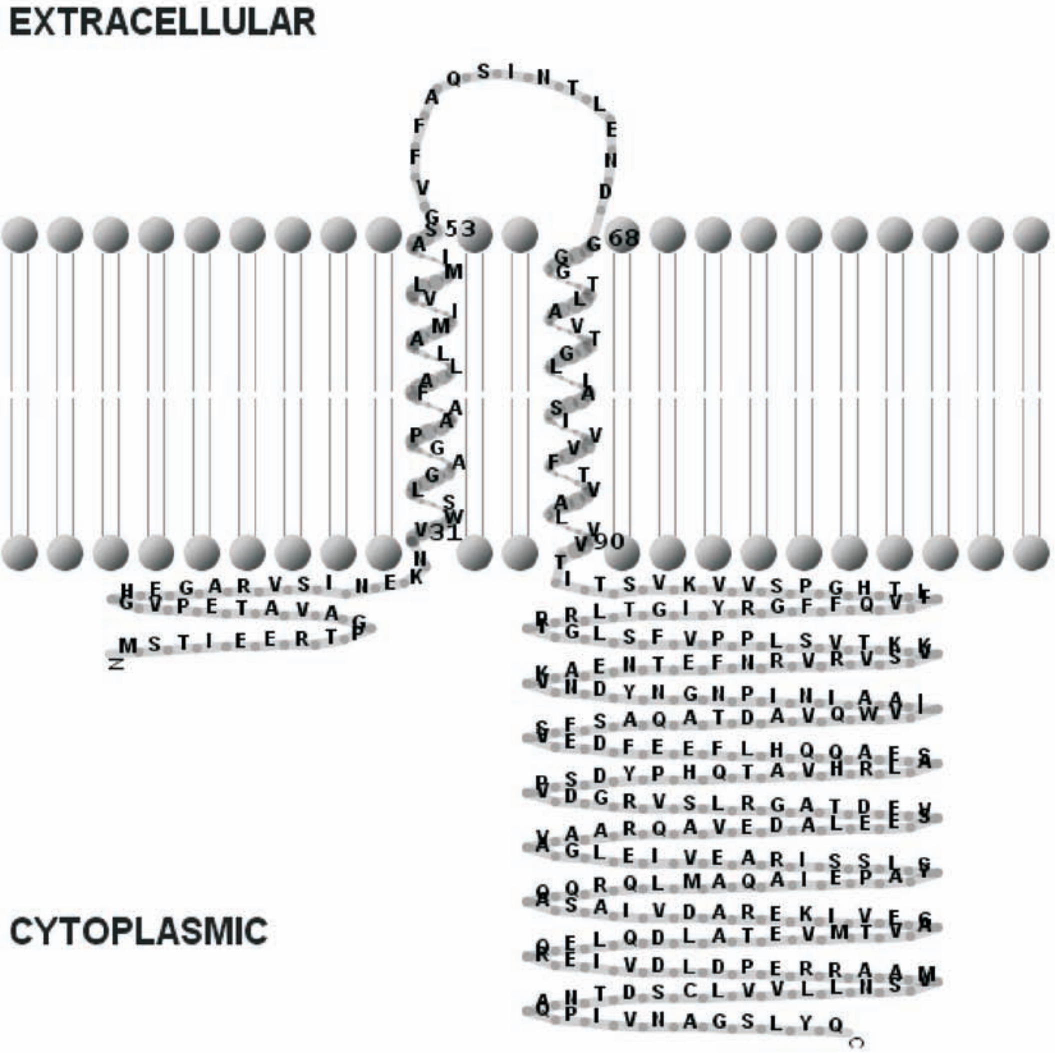
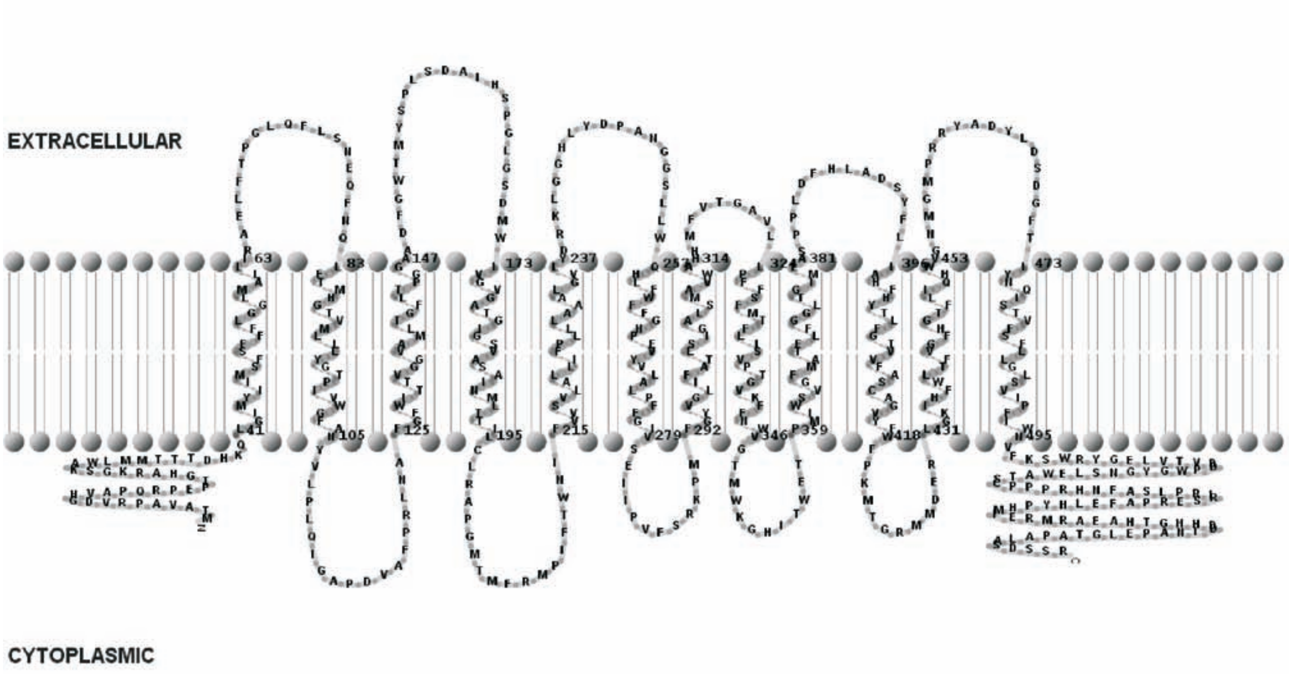


Cg2780 PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE SUBUNIT

ESI 12TMH 65.0 kDa 21 Arg 10 Lys

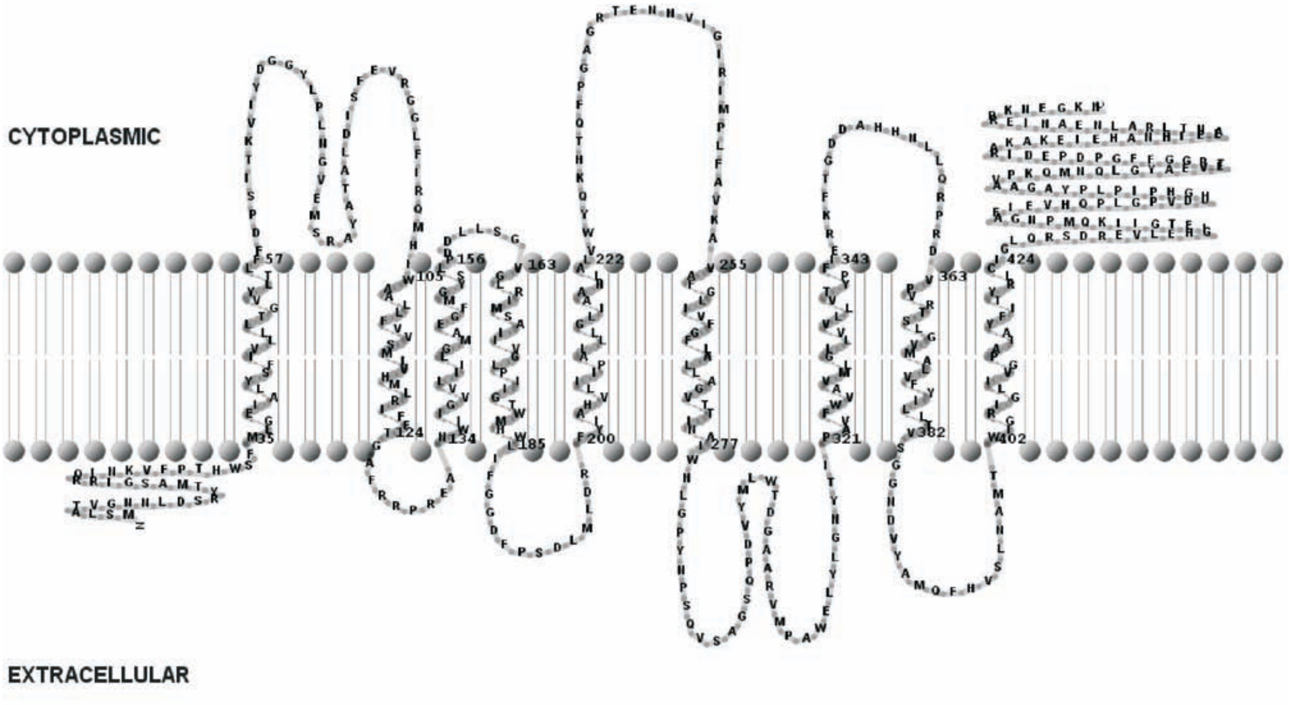
10	20	30	40	50	60
MTAVAPR**VDG**	**HVAPQRPEPT**	GHARKGSKAW	LMMTTTDHKQ	LGIMYIIMSF	SFFFLGGLMA
70	80	90	100	110	120
LLIRAELFTP	GLQFLSNEQF	NQLFTMHGTV	MLLLYGTPIV	WGFA**NYVLPL**	**QI**GAPDVAFP
130	140	150	160	170	180
RLNAFGFWIT	TVGGVAMLT**G**	**FLTPGGAADF**	**GWTMYSPLSD**	**AI**HSPGLGSD	MWIVGVGATG
190	200	210	220	230	240
IGSVASAI**NM**	**LTTILCL**RAP	GMTMFRMPIF	TWNIFVVSVL	A**LLIFPLLLA**	**A**ALGVLYDRK
250	260	270	280	290	300
LGGHLYDPAN	GGSLLWQHLF	WFFGHPEVYV	L**ALPFFGIVS**	**EIIPV**FSRKP	MFGYVGLIFA
310	320	330	340	350	360
TLSIGALSMA	VWAHHMFVTG	AVLLPFFSFM	TFLISVPTGV	KFFNWVGTMW	KGHITWETPM
370	380	390	400	410	420
IWSVGFMAT**F**	**LFGGLTGI**ML	A**SPPLDFHLA**	DSYFLIAHFH	YTLFGTVVFA	SCAGVYFWFP
430	440	450	460	470	480
KMTGRMMDER	LGKIHFWLTF	VGFHGTFLIQ	HWVGNMGMPR	RYA**DYLDSDG**	**FTI**YNQISTV
490	500	510	520	530	540
FSFLLGLSVI	PFIWNVFKS**W**	**RYGELVTVDD**	**PWGYGNSLEW**	**ATSCPPPRHN**	**FA**SLPRIRSE
550	560	570	580	590	
RPA**FELHYPH**	**MIERM**RAEAH	TGHHDDINAP	ELGTAPALAS	DSSR	



Cg2403 CYTOCHROME B, MEMBRANE PROTEIN

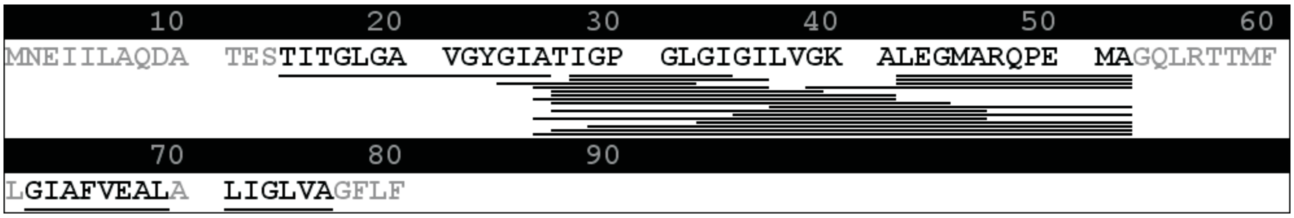
ESI 9TMH 59.7 kDa 27 Arg 11 Lys

10	20	30	40	50	60
MSLA**TVGNNL**	**DSRYT**MASGI	RRQI**NKVFPT**	HWSFMLGEIA	LYSFIVLLLT	GVYLT**LFFDP**
70	80	90	100	110	120
SITKVIYDGG	**YLPLNGVEMS**	RAYATALDIS	FEVRGGLFIR	QMHHWAALLF	VVSMLVHMLR
130	140	150	160	170	180
IFFTGAFRRP	REANWIIGVV	LIILGMAEGF	MGYSLPDDLL	SGVGLRIMSA	IIVGLPIIGT
190	200	210	220	230	240
WMHWLIFGGD	FPSDLMLDRF	YIAHV**LIIPA**	**ILLGLI**AAHL	ALVWYQKHTQ	FPGAGRTENN
250	260	270	280	290	300
VIGIRIMPLF	AVKAVAFGLI	VFGFLALLAG	VTTI**NAIWNL**	**GPYNPSQVSA**	**GSQPDVYMLW**
310	320	330	340	350	360
TDGAARVMPA	**WELYLG**NYTI	PAVFWVAVML	GILVVLLVTY	PFIERKFTGD	DAHHNLLQRP
370	380	390	400	410	420
RDVPVRTSLG	VMALV**FYILL**	TVSGGNDVYA	MQFHVSLNAM	TWIGRIGLIV	GPAIAYFITY
430	440	450	460	470	480
RLCIGLQRSD	REVLEHGIET	**GIIKQMPNGA**	**FIEVHQPLGP**	**VDDHGHPIPL**	**PYAGA**AVPKQ
490	500	510	520	530	540
M**NQLGYAEVE**	**TRGGFFGPDP**	**EDI**RAKAKEI	EHANHIEEAN	TLRALNEANI	ERDKNEGKN



Cg1363 ATP SYNTHASE C CHAIN

ESI 2TMH 8.1 kDa 2 Arg 1 Lys

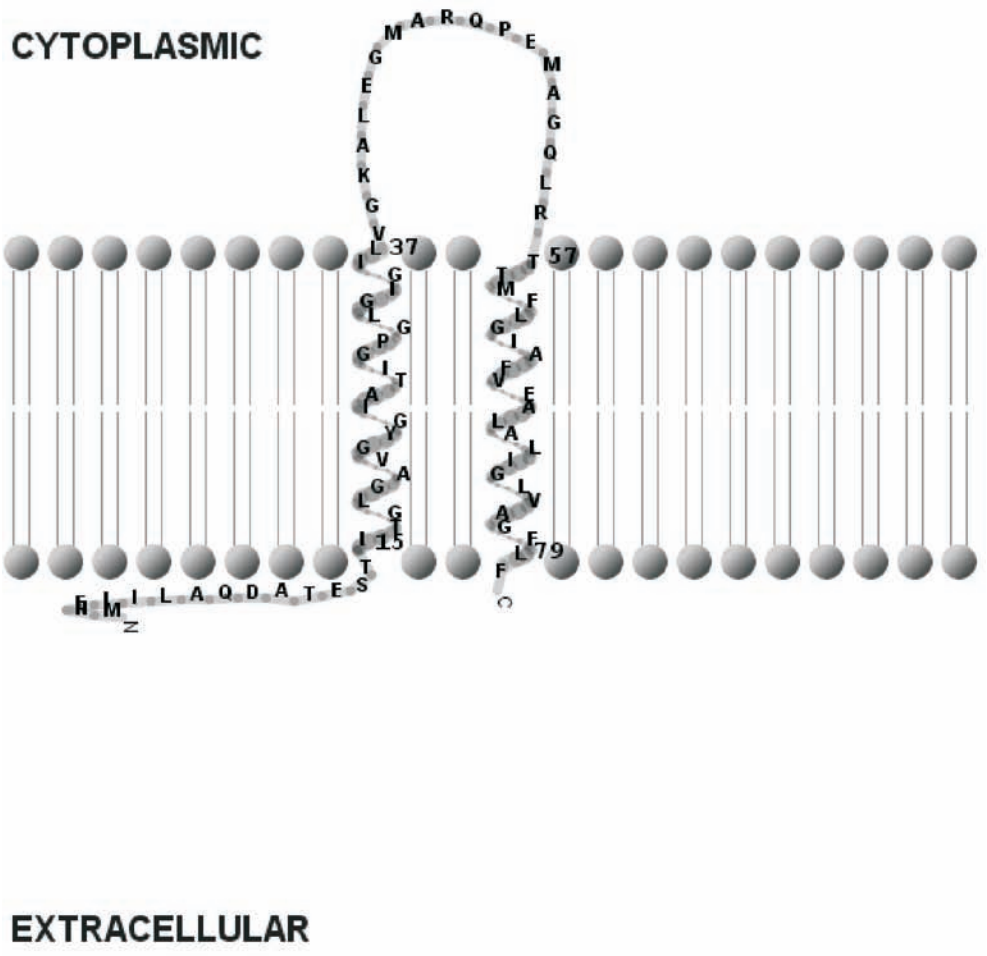


10 20 30 40 50 60

MNEIILAQDA TESTITGLGA VGYGIATIGP GLGIGILVGK ALEGMARQPE MAGQLRTTMF

70 80 90

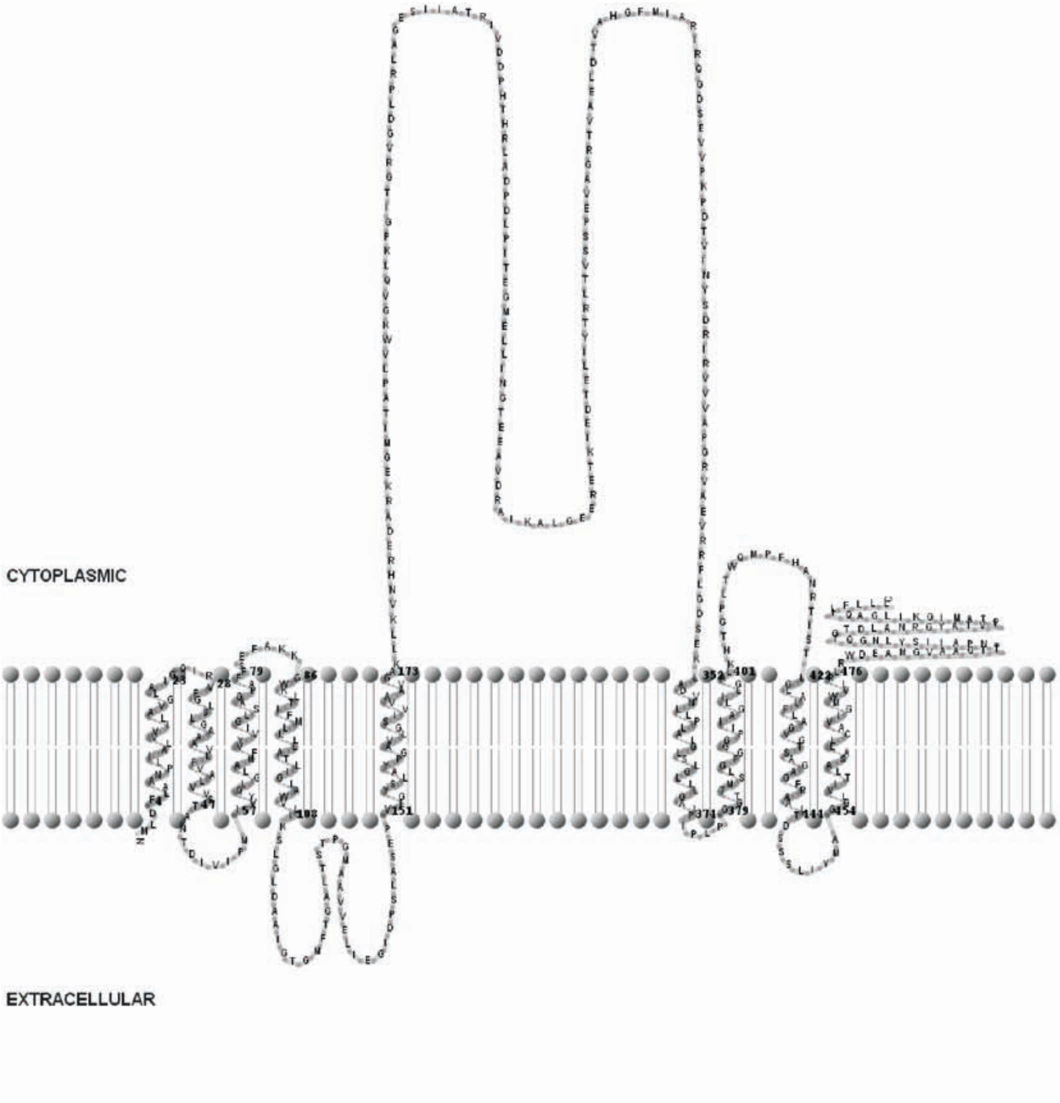
LGIAFVEALA LIGLVAGFLF



Cg0683 PERMEASE

ESI 9TMH 55.6 kDa 23 Arg 15 Lys

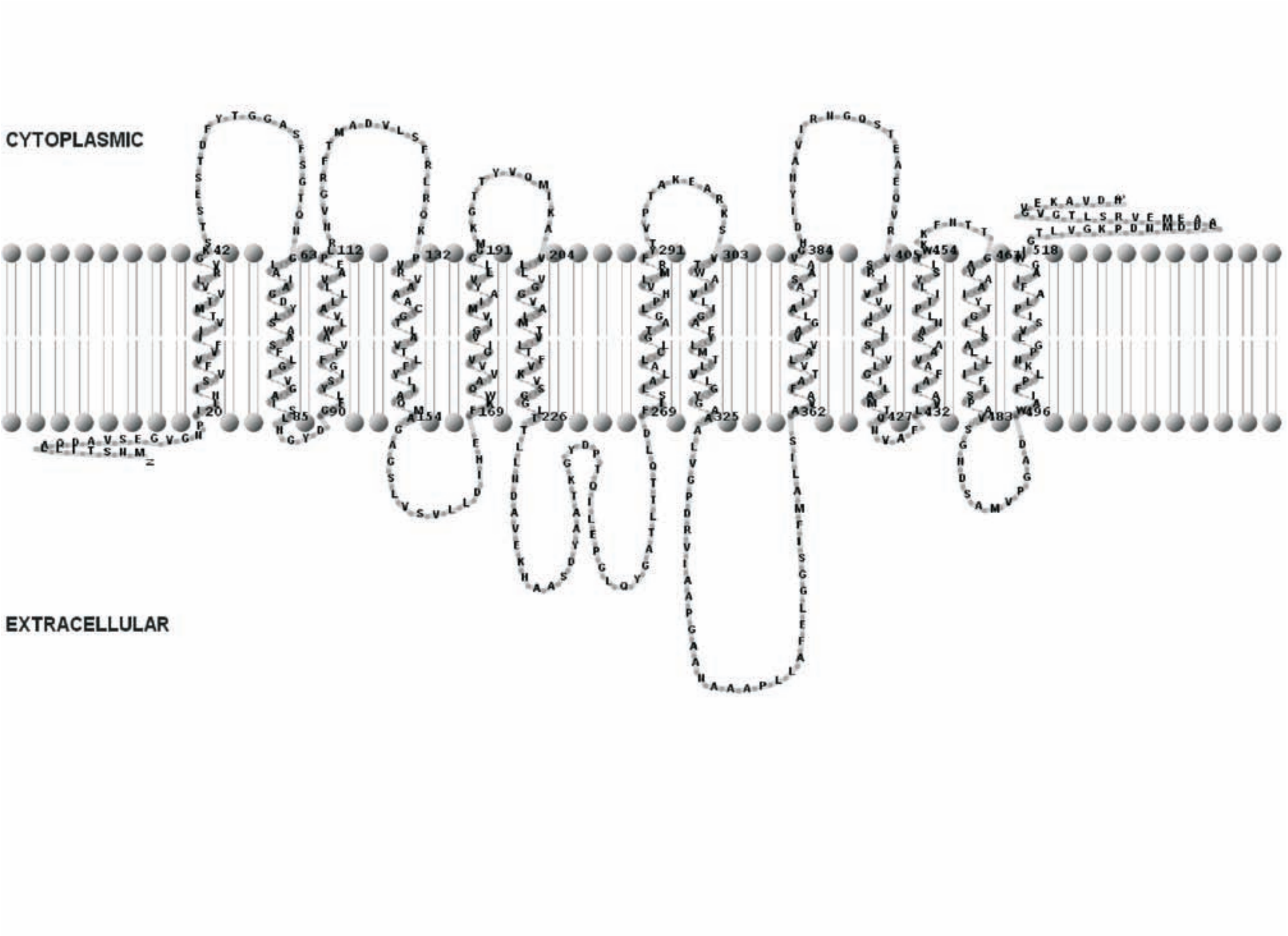
10	20	30	40	50	60
MLDFLAA**NPL**	**IA**LVVILAVG	LAIGQIRVFG	LSLGAAAVLF	VALVVSTANT	DIVIPMIVYQ
70	**80**	**90**	**100**	**110**	**120**
LGLAMFVYVI	GLSAGPAFFS	EFAKKGWKLT	I**FMLLL**LATL	IGLAWVLIKS	LGLDAAIGTG
130	**140**	**150**	**160**	**170**	**180**
MFTGALTSTP	GMAAVV**ELIE**	**GIDPSLA**SEP	VIGYSLAYPG	AVLGSIVVAA	VGAKLLKVNH
190	**200**	**210**	**220**	**230**	**240**
REDARKEGMI	TAPLVWKGVQ	LKPGITGRVG	DLPRLAGESI	IATRIVDDPH	THRL**ADPDLP**
250	**260**	**270**	**280**	**290**	**300**
ITEGMELLIN	**GTEEAVDRAI**	**KA**LGEERETK	IEDTELIYTR	LTVSSPEVAG	RTVAELDTVA
310	**320**	**330**	**340**	**350**	**360**
HGFMIARIRQ	GDSEVVPKPD	TVINYSDRIR	VVVAPGRVAE	VRRFLGDSEK	S**LADVNLLPL**
370	**380**	**390**	**400**	**410**	**420**
AIGLSLGLLL	**GAIPIPLPGG**	**TTM**SLGFGGG	PIIA**GLILGA**	**LKHTGPL**TWQ	MPFHANRTIS
430	**440**	**450**	**460**	**470**	**480**
TLGLALFLAG	VGTSAGAGFR	AALTDSSSLI	YMAGGLVITL	ASALLCAVIG	MWVLRLRWDE
490	**500**	**510**	**520**	**530**	**540**
AMGVAAGTTT	NPAII**SYLNG**	**QTGTDLA**NRG	YATVYPTAMI	GKILGAQILF	LLL



Cg0953 Na+/PROLINE, Na+/PANTOTHENATE SYMPORTER

ESI 13TMH 57.2 kDa 13 Arg 15 Lys

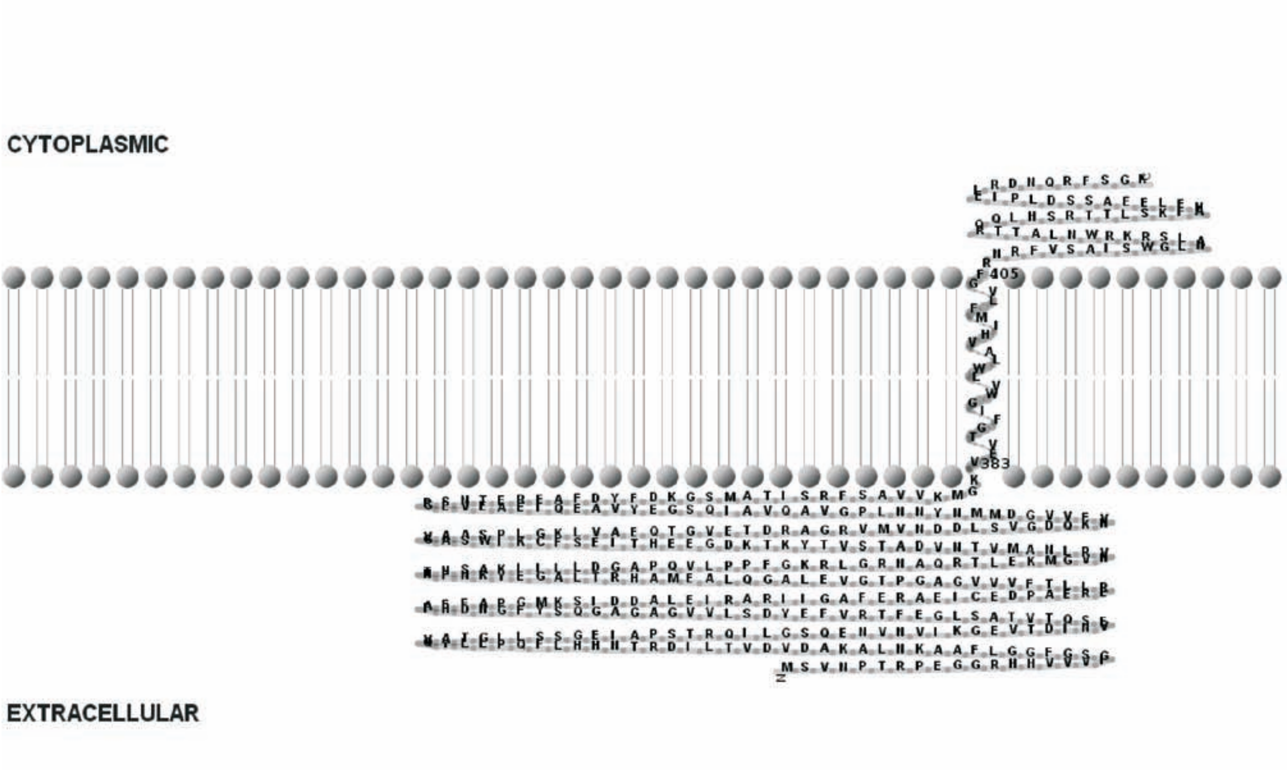
10	20	30	40	50	60
MNSTILLAQD	AVSEGVGNPI	LNISVFVVFI	IVTMTVVLRV	GKSTSESTDF	YTGGASFSGT
70	80	90	100	110	120
QNGLAIAGDY	LSAASFLGIV	GAISLNG**YDG**	**FL**YSIGFFVA	WLVALLLVAE	PLRNVGRFTM
130	140	150	160	170	180
ADVLSFRLRQ	KPVRVAAACG	TLAVTLFYLI	AQMAGAGSLV	SVLLDIHEFK	WQAVVVGIVG
190	200	210	220	230	240
IVMIAYVLLG	GMKGTTYVQM	IKAVLLVGGV	AIMTVLTFVK	VSGGLTTLLN	DAVEKHAASD
250	260	270	280	290	300
YAATKG**YDPT**	**QILEPGLQYG**	**ATLTTQLDFI**	SLALALCLGT	AGLPHVLMRF	YTVPTAKEAR
310	320	330	340	350	360
KSVTWAIVLI	GAFYLMTLVL	GYGAAA**LVGP**	**DRV**IAAPGAA	NAAAPLLAFE	LGGSIFMALI
370	380	390	400	410	420
SAVAFATVLA	VVAGLAITA**S**	**AAVGHDIYNA**	**VIRNGQSTEA**	**EQV**RVSRITV	VVIGLISIVL
430	440	450	460	470	480
GILAMTQNVA	FLVALAFAVA	A**SANLPTIL**Y	SLYWKKFNTT	GAVAAIYTGL	ISALLLIFLS
490	500	510	520	530	540
PA**VSGNDSAM**	**VPGADWAIFP**	**LKNPGLVSIP**	**LAFIAGWIGT**	**LVGKPDNMDD**	**LAAEMEV**RSL
550	560				
TGVGVEKAVD	H				



Cg1656 NADH DEHYDROGENASE

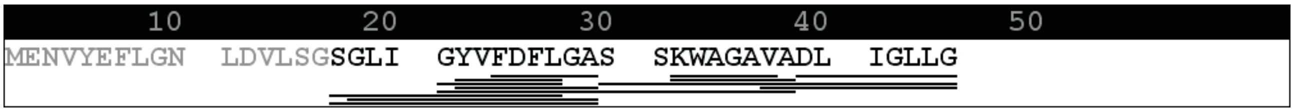
ESI 1TMH 50.9 kDa 28 Arg 19 Lys

10	20	30	40	50	60
MSVNPTRPEG	GRHHVVVIGS	GFGGLFAAKN	LAKADVDVTL	IDRTNHHLFQ	PLLYQVATGI
70	80	90	100	110	120
LSSGEIAPS**T**	**RQILGSQENV**	**NVI**KGEVTDI	NVESQTVTAS	LGEFTRV**FEY**	**DSLVV**GAGAG
130	140	150	160	170	180
QS**YFGNDHFA**	**EFAPG**MKSID	DALEIRARII	GAFERAEICE	DPAERERLLT	FVVVGAGPTG
190	200	210	220	230	240
V**ELAGQLAEM**	**A**HRT**LAGEYK**	**NFNTNSA**KII	LLDGAPQVLP	PFGKRLGRNA	QRTLEKMGVN
250	260	270	280	290	300
VRLNAMVTNV	DATSVTYKTK	DGEEHTIESF	CKIWSAGVAA	**SPLGKLVAEQ**	**TGVETDRA**GR
310	320	330	340	350	360
V**MVNDDLSVG**	**DQKNVFVVGD**	**MMNYNNLPGV**	**A**QV**AIQSGEY**	**VAEQI**EAEVE	GRSNTEREA**F**
370	380	390	400	410	420
DYFDKGSMAT	ISRFSAVVKM	GKVEVTGFIG	WVLWLAVHIM	FLVGFRNRFV	SAI**SWGLNAL**
430	440	450	460	470	
SRKRWNLATT	RQQLHSRTTL	SKFAHELEEA	SSDLPIELRD	NQRFSGK	

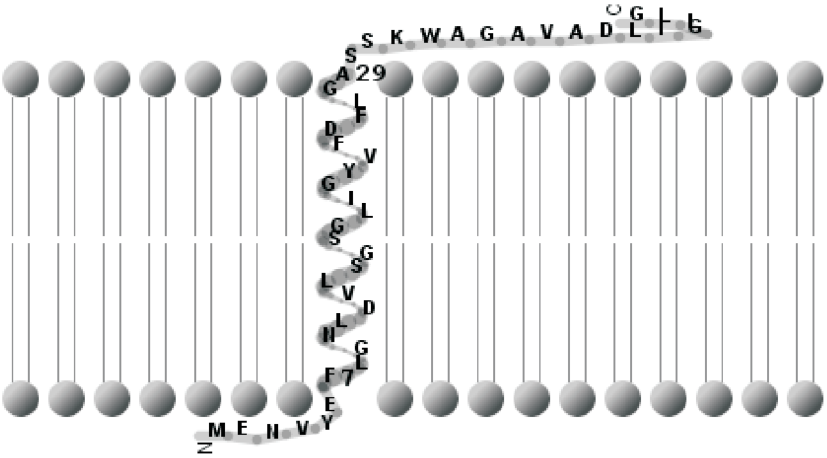


Cg3008 PORIN

ESI 1TMH 4.6 kDa 0 Arg 1 Lys



EXTRACELLULAR

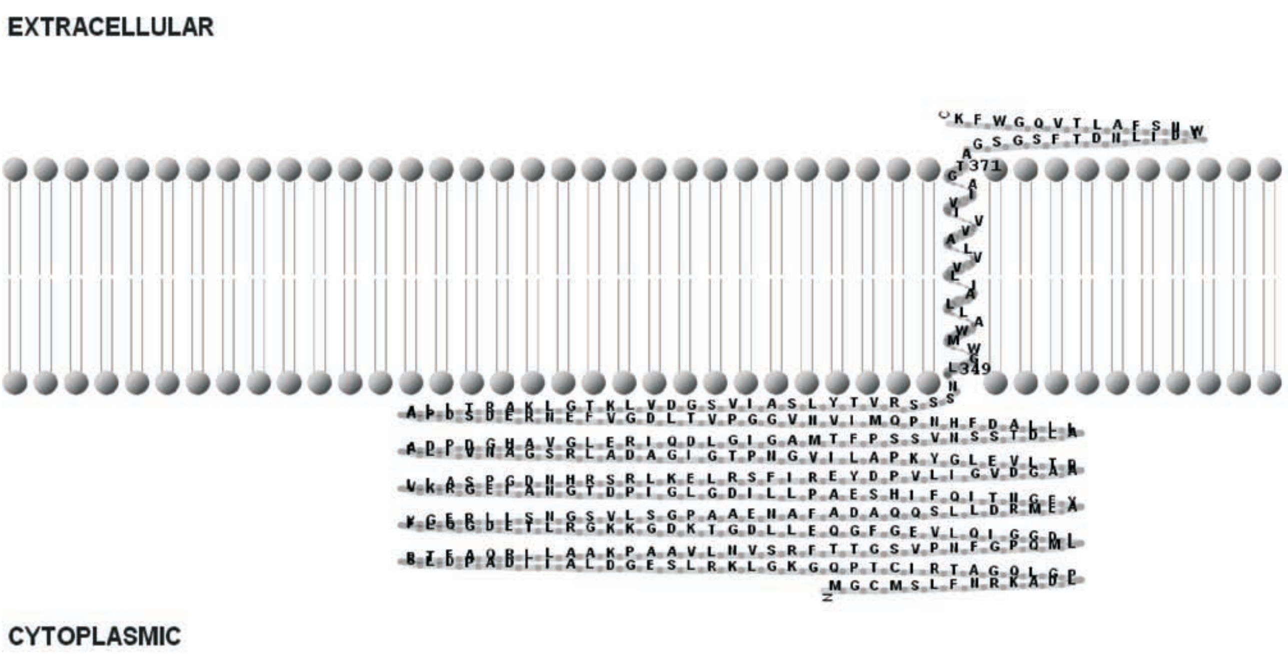


CYTOPLASMIC

Cg1603 CONSERVED MEMBRANE PROTEIN

ESI 1TMH 41.8 kDa 19 Arg 13 Lys

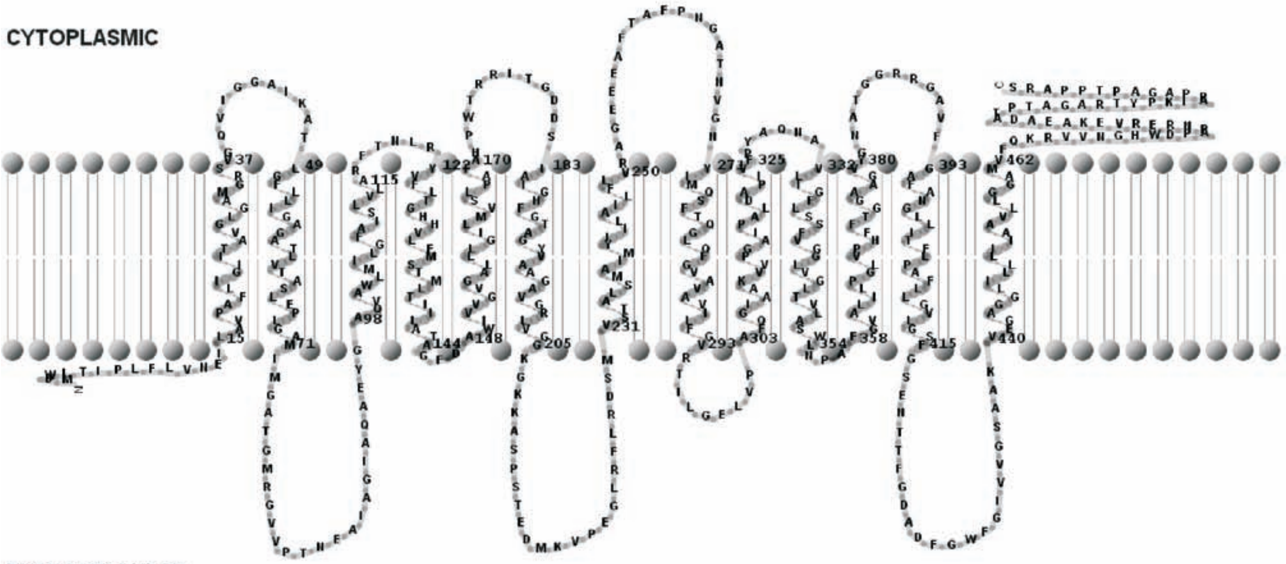
10	20	30	40	50	60
MGCMSLFNRK	ADLPGLQGAT	RICTPQGKGL	KRLSEGDLAI	IDAPDLSRTF	AQRLLAAKPA
70	80	90	100	110	120
AVLNVS**RFTT**	**GSVPNFGPQM**	**LIDGGIQLV**E	GFGQELLDGT	KDGKKGRLTE	DGQLFYGERL
130	140	150	160	170	180
ISNGSVLSGP	AAENA**FADAQ**	**QSLLDRMEAY**	**FGNTIQFIHS**	**EAPLLIDGLG**	**IPDTGNAIEG**
190	200	210	220	230	240
RKVLIASPGD	NHRSRLKELR	SFIREYDPVL	I**GVDGAADTL**	**VEL**GYKPALI	VGNPTGIGAD
250	260	270	280	290	300
ALRS**GANVIL**	**PADPDGHAVG**	**LERIQDLGIG**	**A**MTFPSSVNS	STDLALLLA**D**	**FHNPQMIVNV**
310	320	330	340	350	360
GGPVTLDGVF	**ENREDSDPA**A	LLTRAKLGTK	LVDGSVIASL	YTVRSSSNLG	WMWALLAILV
370	380	390	400		
VLAVVIVIAG	TAGSG**SFTDN**	**LIDTWNSFAL**	**TVQGWFK**		



Cg3365 PUTATIVE RIBITOL TRANSPORT MEMBRANE PROTEIN

ESI 13TMH 52.7 kDa 18 Arg 10 Lys

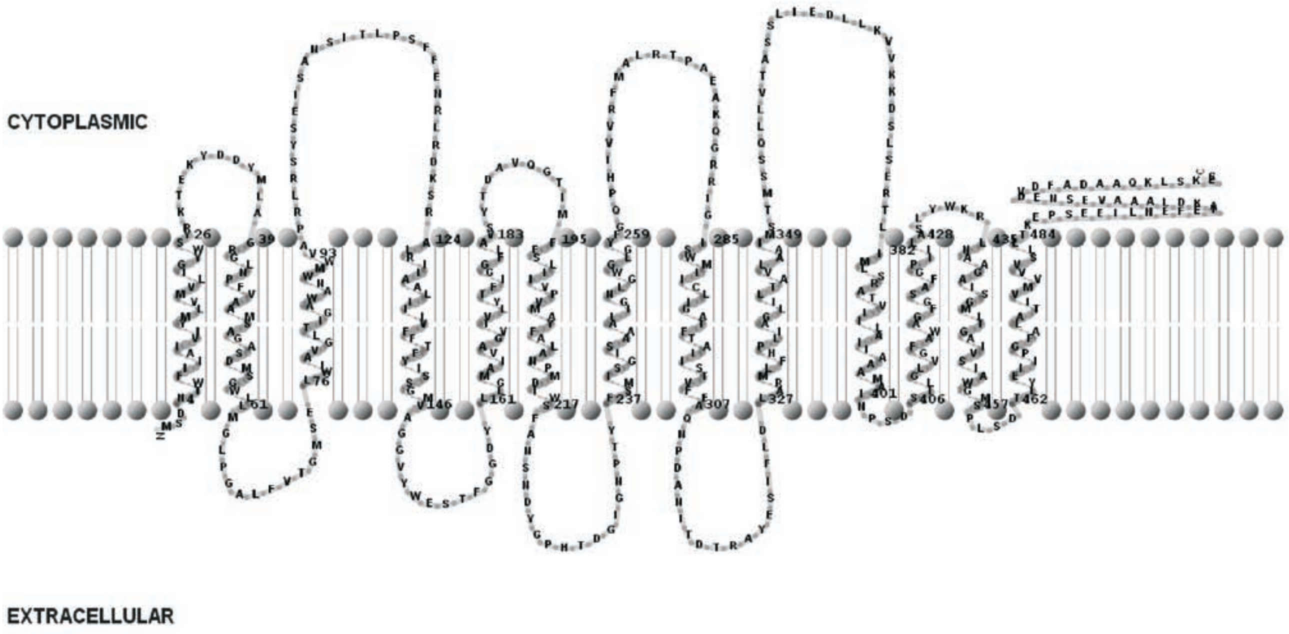
10	20	30	40	50	60
MDWLTI**PLFL**	**VNEI**LAVPA**F**	**LIGIIT**AVGL	GAMGRSVGQV	IGGAIKATLG	FLLIGAGATL
70	80	90	100	110	120
VTA**SLEPLGA**	**MIMGATGM**RG	VVPTNEAIAG	IAQAEYGAQV	AWLMILGFAI	SLVLARFTNL
130	140	150	160	170	180
RYVFLTGHHV	LFMSTMLTII	LATAGFDAWI	**VVGVGALLLG**	**I**LMVSLPAFA	HPWTRRITGD
190	200	210	220	230	240
DSIAIGHFGT	AGYVAAGAVG	RLVGGKGKKA	SPSTEDMKVP	EGLRFLRDSM	VSTALSMAI**M**
250	260	270	280	290	300
YIILAILFLV	RAGEEEAFTA	FPNGATNVGN	YIMQSFTQGL	QFGVAVAVIL	FGVRTILGEL
310	320	330	340	350	360
VPAFQGIAAK	VVPGAIPA**LD**	**APIVFPYAQN**	**AVLI**GFLS**SF**	**VGGLVGLT**VL	ASWLNPAFGV
370	380	390	400	410	420
ALILPGLVPH	**FFTGGAAGV**Y	GNATGGRRGA	VFGAFANGLL	ITFLPAFLLG	VLGSFGSENT
430	440	450	460	470	480
TFGDADFGWF	GIVVGSAAKV	EGAGGL**ILLL**	**I**IAAVLLGGA	MVFQKRVVNG	**HWDPAPN**RER
490	500	510	520		
VEKAEADATP	TAGARTYPKI	APPAGAPTPP	ARS		



Cg1317 PROLINE TRANSPORT SYSTEM

ESI 13TMH 56.6 kDa 17 Arg 12 Lys

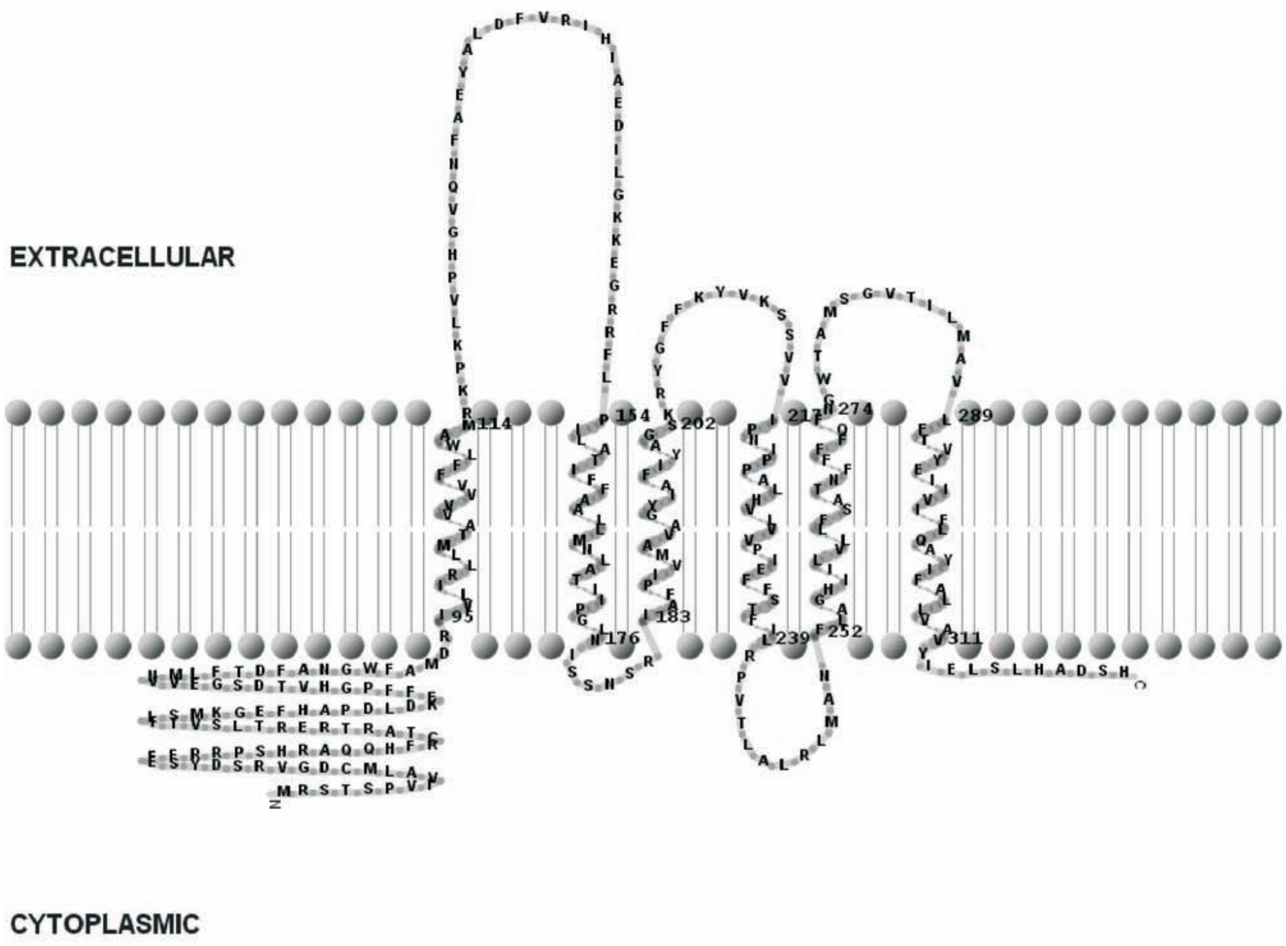
10	20	30	40	50	60
MSDNTWFIIA	IVIYMLVMVL	IGYWSYRKT**E**	**KYDDYMLA**GR	GLNPFVAAMS	AGASDMSGWL
70	80	90	100	110	120
LMGLPGALFV	TGMSELWIAV	GLTIGAWANW	MWVAPRLRSY	SEISANSITL	PSFFENRLRD
130	140	150	160	170	180
KSRALRIIAA	LIIIVFFTFY	ISSGMVAGGV	YWESTFGGDY	LLGMAIVAGV	TVLYTFIGGF
190	200	210	220	230	240
LAVSYTDAVQ	GTIMFFSLII	VPVMAYFA**LA**	**NPMDIWSFAN**	**SNDYGPHTDG**	**IGNPT**YFSMI
250	260	270	280	290	300
SGISAAAIIG	**NLGWGLG**YFG	QPHIVVRFMA	LRTPAEAKQG	RRIGISWMII	CLIGATFTAI
310	320	330	340	350	360
ISTVFFAQNP	DANIT**DTRAY**	**ESIFLDLA**RM	LFHPLIAGLI	LTAVLAAIMS	TMSSQLLVTA
370	380	390	400	410	420
SSLIEDLLKV	**V**KKDSLSERT	LIMLSRATVI	ILAIIAAA**MA**	**INPSDSILGL**	**V**GFAWAGFGS
430	440	450	460	470	480
AFGPIILASL	YWKRLNAAGA	ISGMITGAIV	SIAWGMSPLS	DTLYE**IIPGF**	**ALA**TIVMVVV
490	500	510	520	530	
SLLTKEPSEE	**ILNEFETA**KD	LA**AAVESNED**	**VDFA**DAAQKL	SKES	



Cg1362 ATP SYNTHASE F0 SUBUNIT 6

ESI 6TMH 36.3 kDa 19 Arg 9 Lys

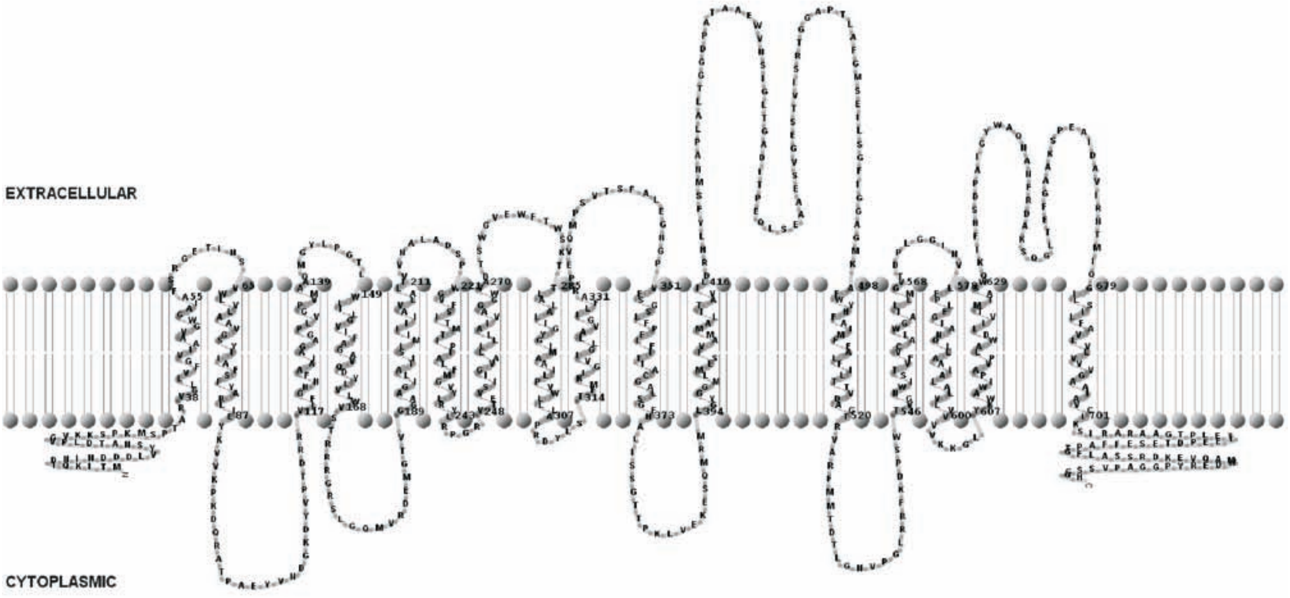
10	20	30	40	50	60
MRSTSPVIVA	LMCDGVRSDY	SEFFRRPSHR	AQQHFRCTAR	TRERTLSVTT	LS**MKGEFHAP**
70	80	90	100	110	120
DLDKEFFPGH	**VTDSGEVVNM**	**LFTDFA**NGWF	AMDRIVLIRL	LMTAVVVVFF	LWAMRKPKLV
130	140	150	160	170	180
PH**GVQNFAEY**	**ALDFV**RIHIA	EDILGKKEGR	RFLPILATIF	FAALLMNLAT	IIPGLNISSN
190	200	210	220	230	240
SRIAFPIVMA	VAGYIAFIYA	GSKRYGFFKY	VKS**SVVIPNI**	**PPALHVLVVP**	**IEFFSTFILR**
250	260	270	280	290	300
PVTLALRLMA	NFLAGHIILV	LLFSATNFFF	FQFNGWTAMS	GVTILMAVLF	TVYEIIVIFL
310	320	330			
QAYIFALLVA	VYIELSLHAD	SH			



Cg0756 PUTATIVE CARBON STARVATION PROTEIN A

ESI 16TMH 81.0 kDa 29 Arg 22 Lys

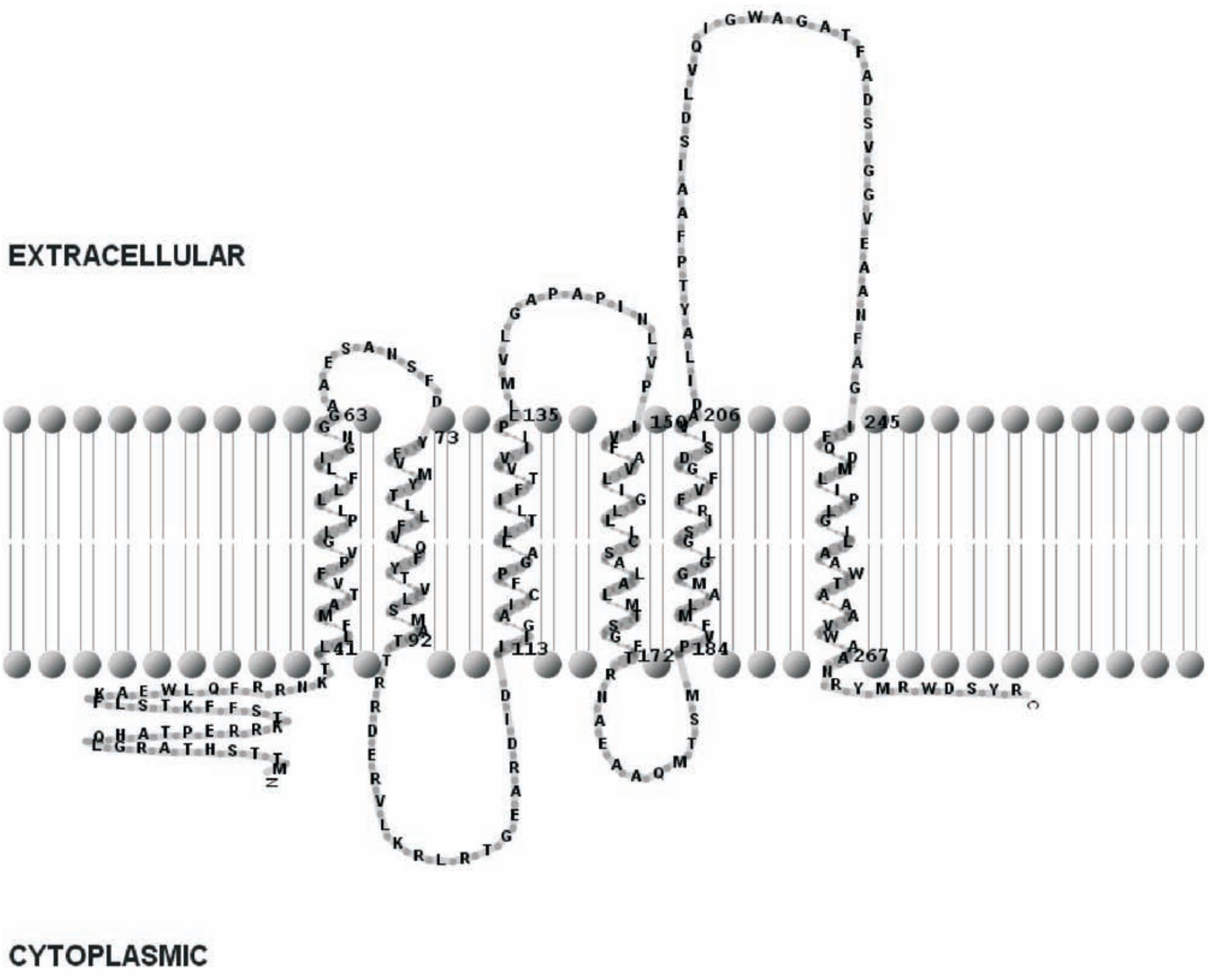
10	20	30	40	50	60
MTIKQTDNIN	DDDLVYSNAT	DLPVGVKKSP	KMSPTARVGL	LVFGVIAAVG	WGAIAFSRGE
70	80	90	100	110	120
TINSVWLVLA	AVGSYIIAFS	FYARLIEYKV	VKPKDQRATP	AEYVNDGKDY	VPTDRRVLFG
130	140	150	160	170	180
HHFAAIAGAG	PLVGPVMAAQ	MGYLPGTLWI	ILGVIFAGAV	QDYLVLWVST	RRRGRSLGQM
190	200	210	220	230	240
VRDEMGTVGG	AAGILATIS**I**	**MIII**IAVLAL	IVVNALADSP	WGVFSITMTI	PIALFMGVYL
250	260	270	280	290	300
RYLRPGRVTE	VSIIGVALLL	LAIVAGGWVA	DTSWGVEWFT	WSKTTLALAL	IGYGIMAAIL
310	320	330	340	350	360
PVWLLLAPRD	YLSTFMKIGV	IGLLAVGI**LF**	**ARPEVQMPS**V	TSFALEGNGP	VFSGSLF**PFL**
370	380	390	400	410	420
FITIACGALS	GFHALISSGT	TPKLVEKESQ	MRMLGYGGML	MESFVAMMAL	ITAVILDRHL
430	440	450	460	470	480
YFSMNAPLAL	TGGDPATAAE	WVNSIGLTGA	DITPEQLSEA	AESVGESTVI	SRTGGAPTLA
490	500	510	520	530	540
FGMSEILSGF	**IGGAGMKA**FW	YHFAIMFEAL	FILTTVDAGT	RVARFMMTDT	LGNVPGLRRF
550	560	570	580	590	600
KDPSWTVGNW	ISTVFVCALW	GAILLMGVTD	PL**GGINVLFP**	**LFGI**ANQLLA	AIALALVLVV
610	620	630	640	650	660
VVKKGLYKWA	WIPAVPL**AWD**	**LIVT**MTASWQ	KI**FHSDPAIG**	**YWAQNA**NFRD	AKSQGLTEFG
670	680	690	700	710	720
AAKSPEA**IDA**	**VIRNT**MIQGI	LSILFAVLVL	VVVGAAIAVC	IKSIRARAAG	TPLET**TEEPD**
730	740	750	760		
TESEFFAPTG	**FLA**SSRDKEV	QA**MWDERYPG**	**GAPV**SSGGH		



Cg1082 PUTATIVE MEMBRANE PROTEIN

ESI 6TMH 30.1 kDa 16 Arg 5 Lys

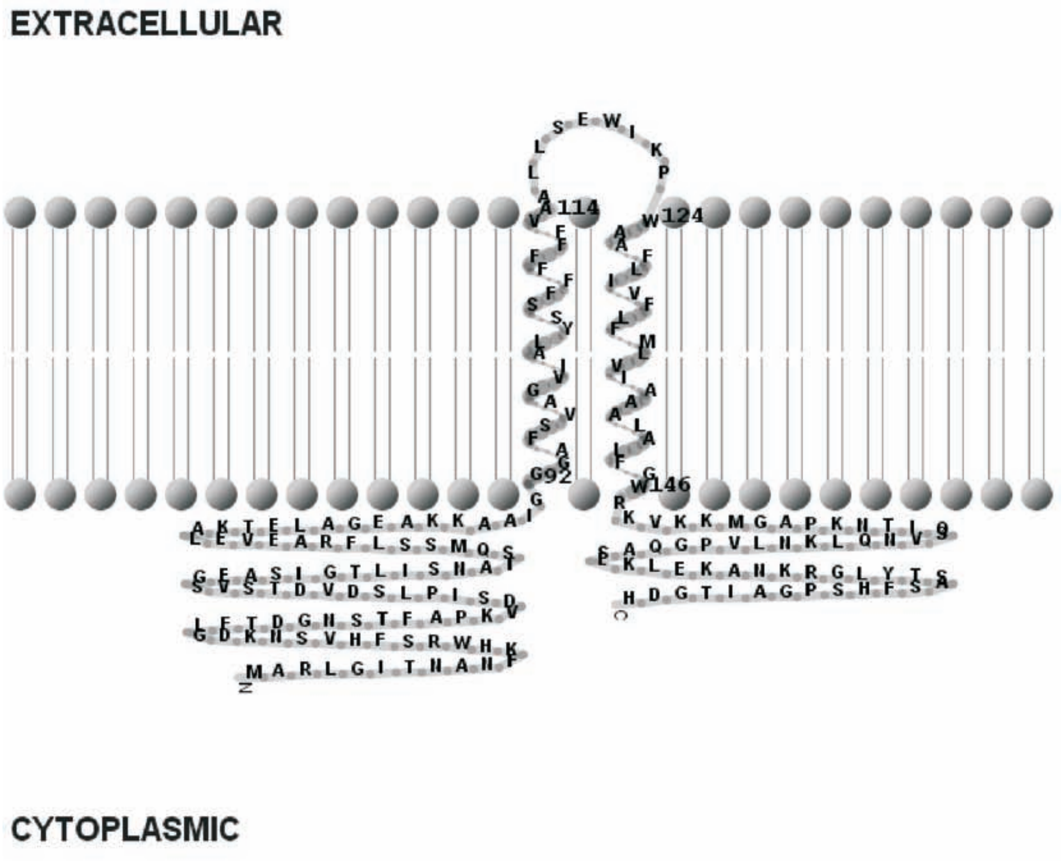
10	20	30	40	50	60
MTTSHTARGL	QHATPERRKT	SFFKTSLFKA	EWLQFRRNKT	LLFMA**TVFPV**	**GIPLLLFLIG**
70	80	90	100	110	120
NGGAAESANS	FDYFVMYTLL	FVQFYTVLSM	ATTRRDERVL	KRLRTGEARD	IDIIGAICFP
130	140	150	160	170	180
GALLTLIF**TV**	**VIIPLLMVL**G	APAPINLVPI	VFAV**LIGLLL**	CSALALMTSG	FTRNAEAAQM
190	200	210	220	230	240
TSMPVFMLAM	GGLGSIRFVF	GDSIVA**DILA**	**YTPFAAISDL**	**VQI**GWAGATF	ADSVGGVEAA
250	260	270	280		
NFAGIFQDML	**IPLGILAA**WT	AAAVWAANRY	MRWDSYR		



Cg0359 PUTATIVE MEMBRANE PROTEIN

ESI 2TMH 21.5 kDa 5 Arg 15 Lys

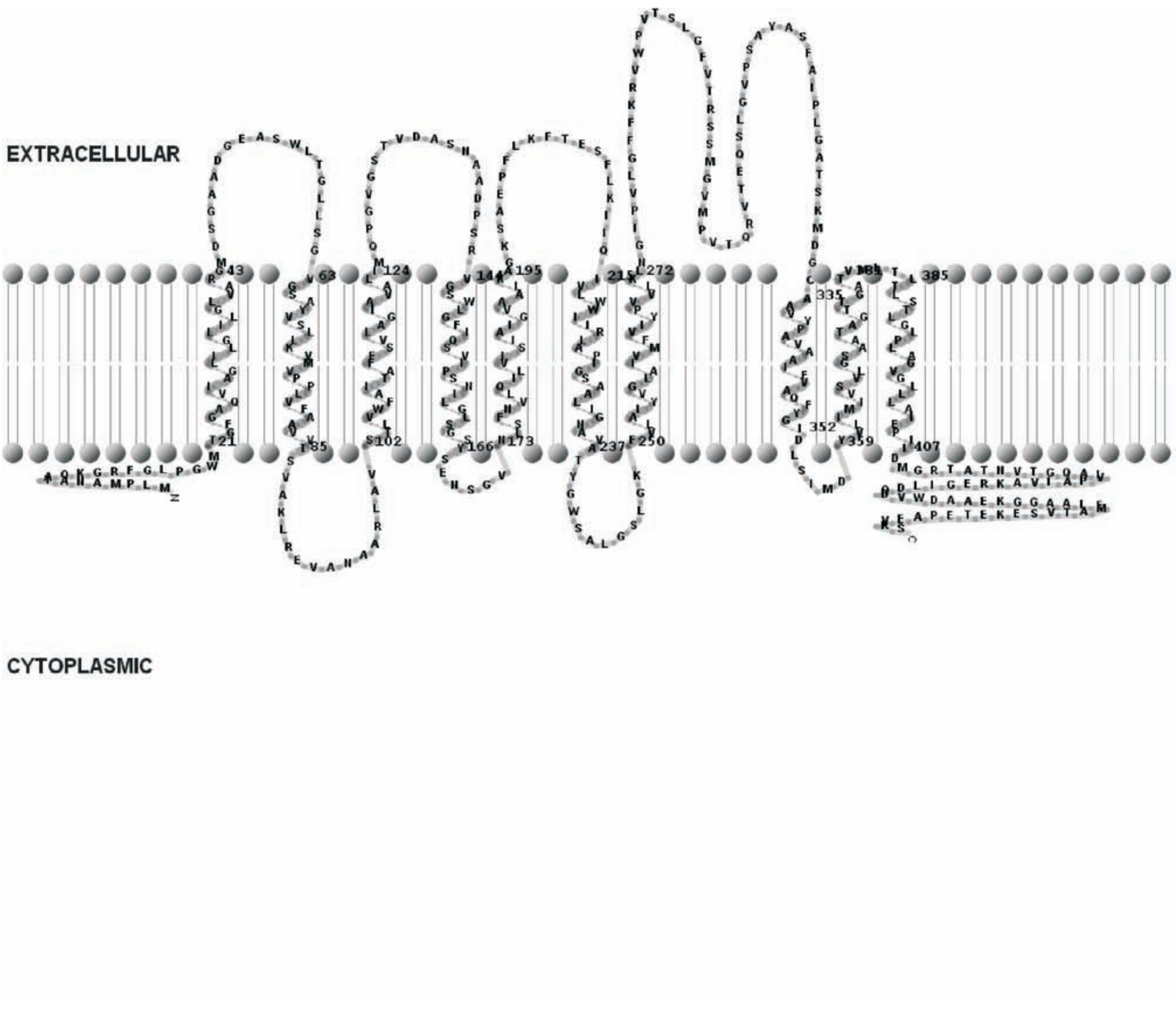
10	20	30	40	50	60
MARLGITNAN	FKHWRSFHV**S**	**NKDGLFTDGN**	**STFAPKVDSI**	**PLSDVDTSVS**	**GEA**SIGTLIS
70	80	90	100	110	120
NATSQMS**SLF**	**RAEVELA**KTE	LAGEAKKAAI	GGGAFSVAGV	IALYSSFFFF	FFVAALLSEW
130	140	150	160	170	180
IKPWAAFLIV	FL**FMLVIA**AA	LALFGWRKVK	KM**GAPKNTIQ**	**SVNQLKNLVP**	**G**QASEKLEKA
190	200	210			
NKRGLYTSA**S**	**FHSPGAITGD**	**H**			



Cg2810 Na+/H+-DICARBOXYLATE SYMPORTER

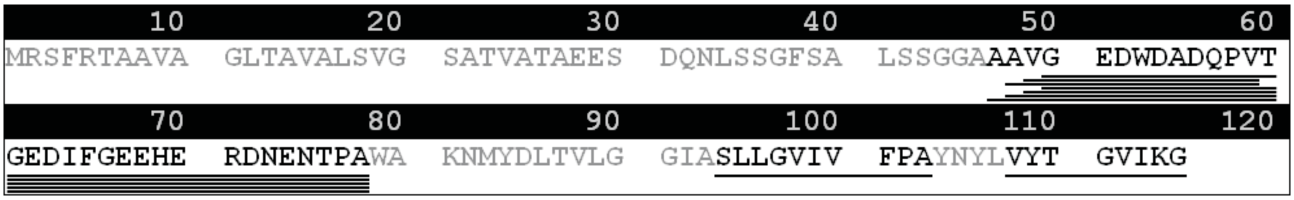
ESI 10TMH 47.9 kDa 12 Arg 14 Lys

10	20	30	40	50	60
MLPMANATAQ	KGRFGLPGWM	TGFGAQVIAG	L**ILGLILGLV**	**A**RGMDSGAA**D**	**GEASWLTGLL**
70	80	90	100	110	120
SGVGSAYVSL	LKVMVPPLVF	AAVVTSVAKL	REVANAARLA	VSTLVWFAIT	AFFSVLAGIA
130	140	150	160	170	180
VALIMQPGVG	STVDAS**NAAD**	**PSRVGSWLGF**	**IQSVIPS**NIL	GLSGSYSENS	GVNLSFNVLQ
190	200	210	220	230	240
ILVISIAIGV	AALKAGKSAE	PFLKFTESFL	KIIQIVLWWI	IRLAPIGSAA	LIGNAVATYG
250	260	270	280	290	300
WSALGSLGKF	VLAIYVGLAI	VMFVIYPVVL	KLNGIPVLGF	FKRVWPVTSL	GFVTRSSMGV
310	320	330	340	350	360
MPVTQRVTEQ	SLGVPSAYAS	FAIPLGATSK	MDGCAAVYPA	VAAIFVAQFY	GIDLSIMDYV
370	380	390	400	410	420
LIMIVSVLGS	AATAGTTGAT	VMLTLTLSTL	GLPLAGVGLL	LAIEPIIDMG	RTATNVTGQA
430	440	450	460	470	
LVPAIV**AKRE**	**GILDQDVWDA**	AEKGGAAIEM	A**TVSEKETEP**	**AEV**RS	



Cg2195 PUTATIVE SECRETED OR MEMBRANE PROTEIN

ESI 2TMH 11.8 kDa 3 Arg 2 Lys



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        10         20         30         40         50         60
MRSFRTAAVA GLTAVALSVG SATVATAEES DQNLSSGFSA LSSGGAAAVG EDWDADQPVT
        70         80         90        100        110        120
GEDIFGEEHE RDNENTPAWA KNMYDLTVLG GIASLLGVIV FPAYNYLVYT GVIKG
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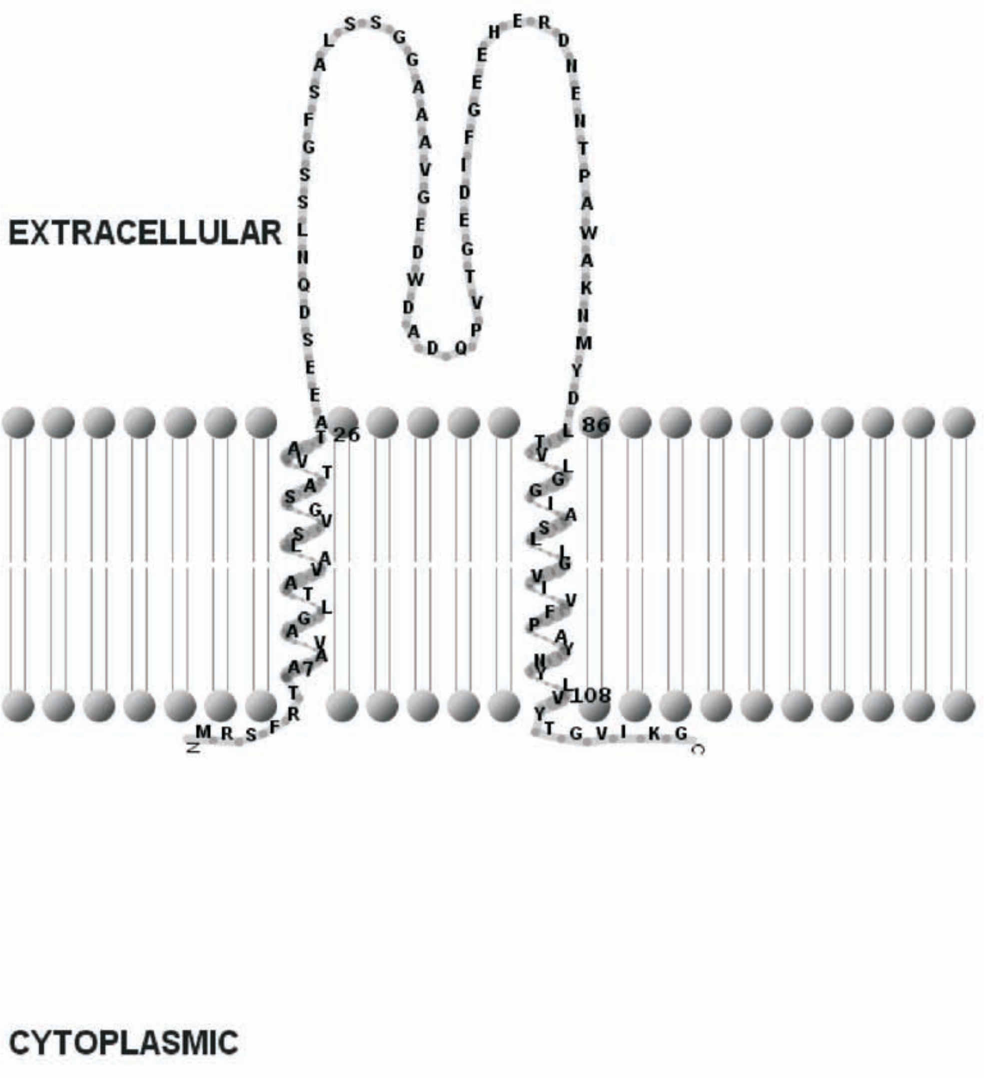
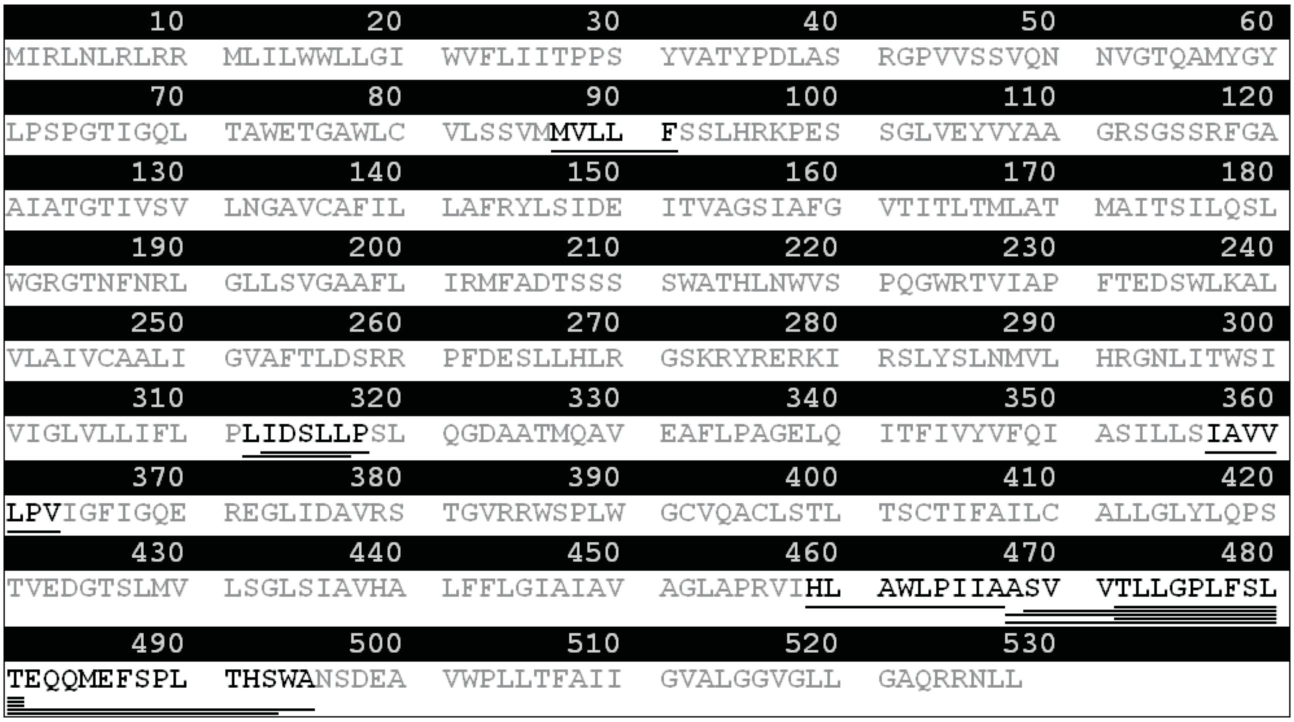
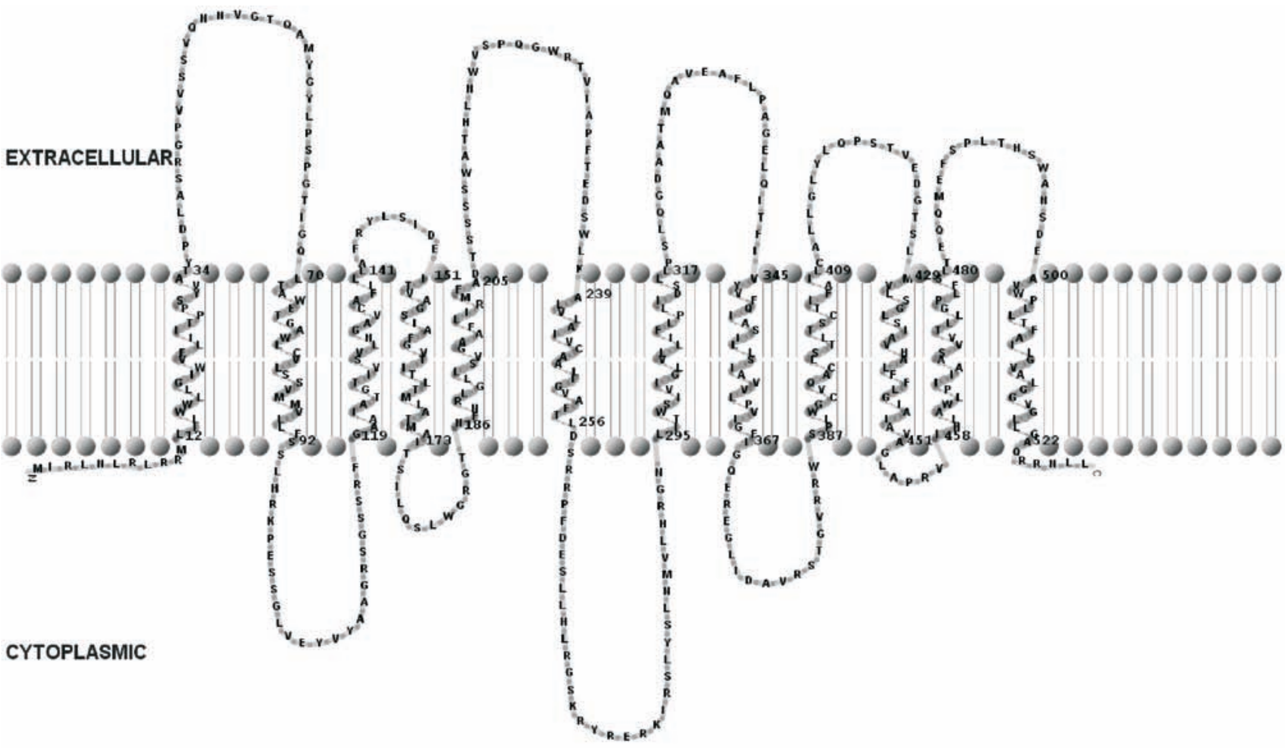


Cg3368 ABC-TRANSPORTER PERMEASE PROTEIN

ESI 12TMH 57.1 kDa 28 Arg 4 Lys



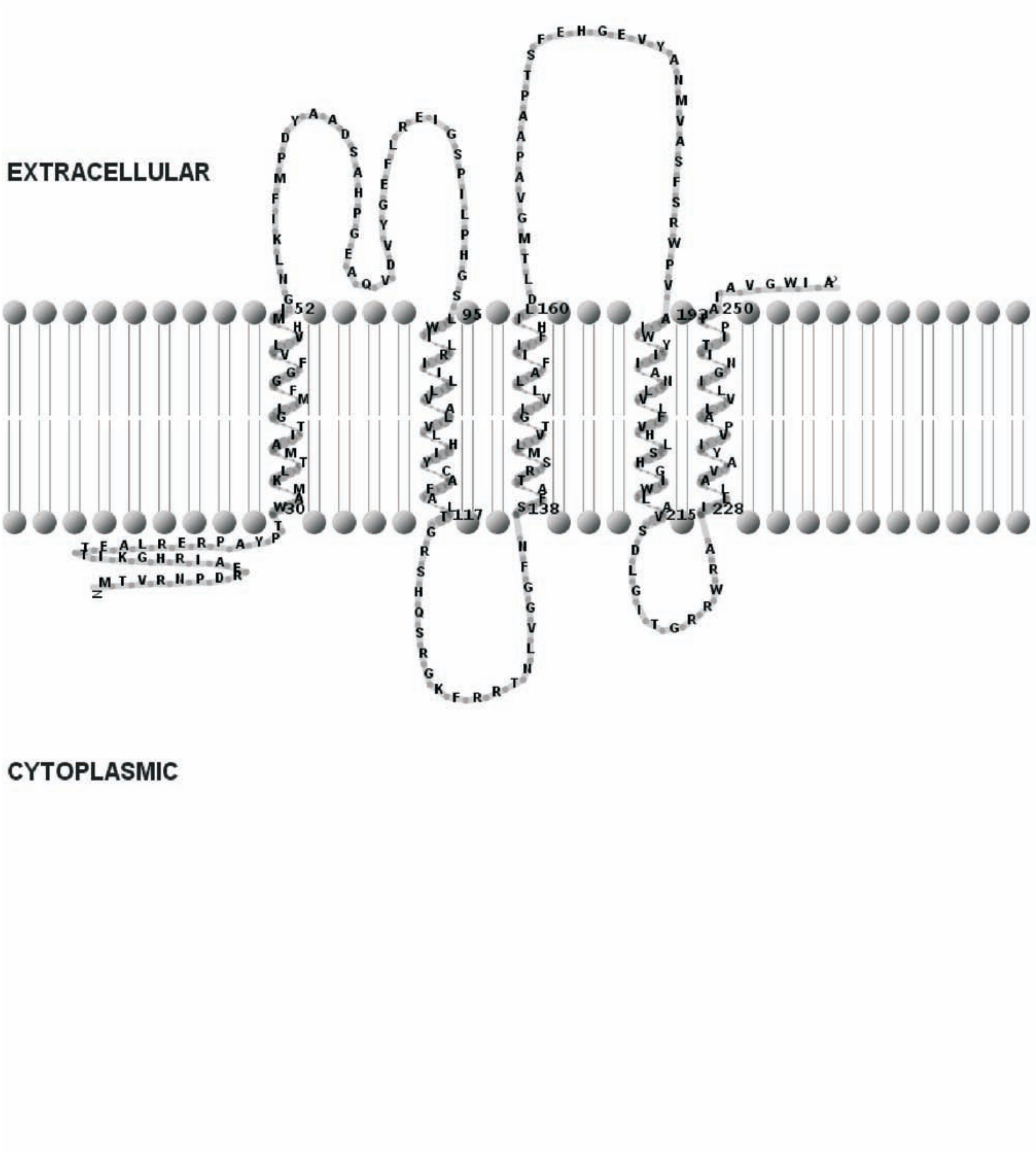
10	20	30	40	50	60
MIRLNLRLRR	MLILWWLLGI	WVFLIITPPS	YVATYPDLAS	RGPVVSSVQN	NVGTQAMYGY
70	80	90	100	110	120
LPSPGTIGQL	TAWETGAWLC	VLSSVM**MVLL**	**F**SSLHRKPES	SGLVEYVYAA	GRSGSSRFGA
130	140	150	160	170	180
AIATGTIVSV	LNGAVCAFIL	LAFRYLSIDE	ITVAGSIAFG	VTITLTMLAT	MAITSILQSL
190	200	210	220	230	240
WGRGTNFNRL	GLLSVGAAFL	IRMFADTSSS	SWATHLNWVS	PQGWRTVIAP	FTEDSWLKAL
250	260	270	280	290	300
VLAIVCAALI	GVAFTLDSRR	PFDESLLHLR	GSKRYRERKI	RSLYSLNMVL	HRGNLITWSI
310	320	330	340	350	360
VIGLVLLIFL	P**LIDSLLP**SL	QGDAATMQAV	EAFLPAGELQ	ITFIVYVFQI	ASILLS**IAVV**
370	380	390	400	410	420
LPVIGFIGQE	REGLIDAVRS	TGVRRWSPLW	GCVQACLSTL	TSCTIFAILC	ALLGLYLQPS
430	440	450	460	470	480
TVEDGTSLMV	LSGLSIAVHA	LFFLGIAIAV	AGLAPRVI**HL**	**AWLPIIAASV**	**VTLLGPLFSL**
490	500	510	520	530	
TEQQMEFSPL	**THSWA**NSDEA	VWPLLTFAII	GVALGGVGLL	GAQRRNLL	



Cg0445 SUCCINATE DEHYDROGENASE CD

ESI 5TMH 28.3 kDa 16 Arg 4 Lys

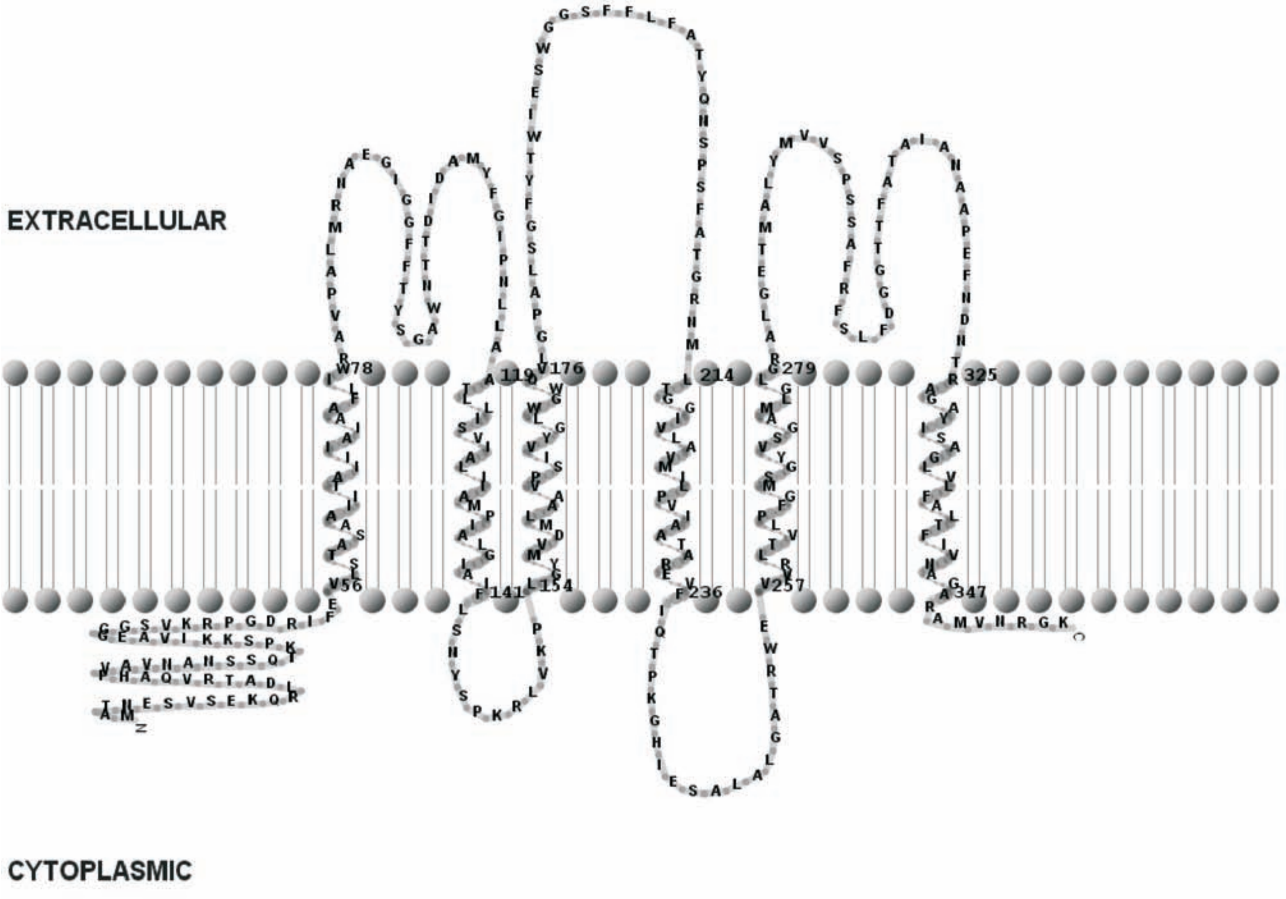
10	20	30	40	50	60
MTVRNPDREA	IRHGKITTEA	LRERPAYPTW	AMKLTMAITG	LMFGGFVLVH	MIGNLKIFMP
70	80	90	100	110	120
DYAADSAHPG	EA**QVDVYGEF**	**LREI**GSPILP	HGSVLWILRI	ILLVALVLHI	YCAFALTGRS
130	140	150	160	170	180
HQSRGKFRRT	NLVGGFNSFA	TRSMLVTGIV	LLAFIIFHIL	DLTMGVAPA**A**	**PTSFEHGEVY**
190	200	210	220	230	240
ANMVASFSRW	PVAI**WYIIA**N	LVLFVHLSHG	IWLAVSDLGI	TGRRWRAILL	AVAYIVPA**LV**
250	260				
LIGNITIPFA	**I**AVGWIA				



Cg2845 ABC-TYPE PHOSPHATE TRANSPORT SYSTEM, PERMEASE COMPONENT

ESI   6TMH   37.5 kDa   16 Arg   9 Lys

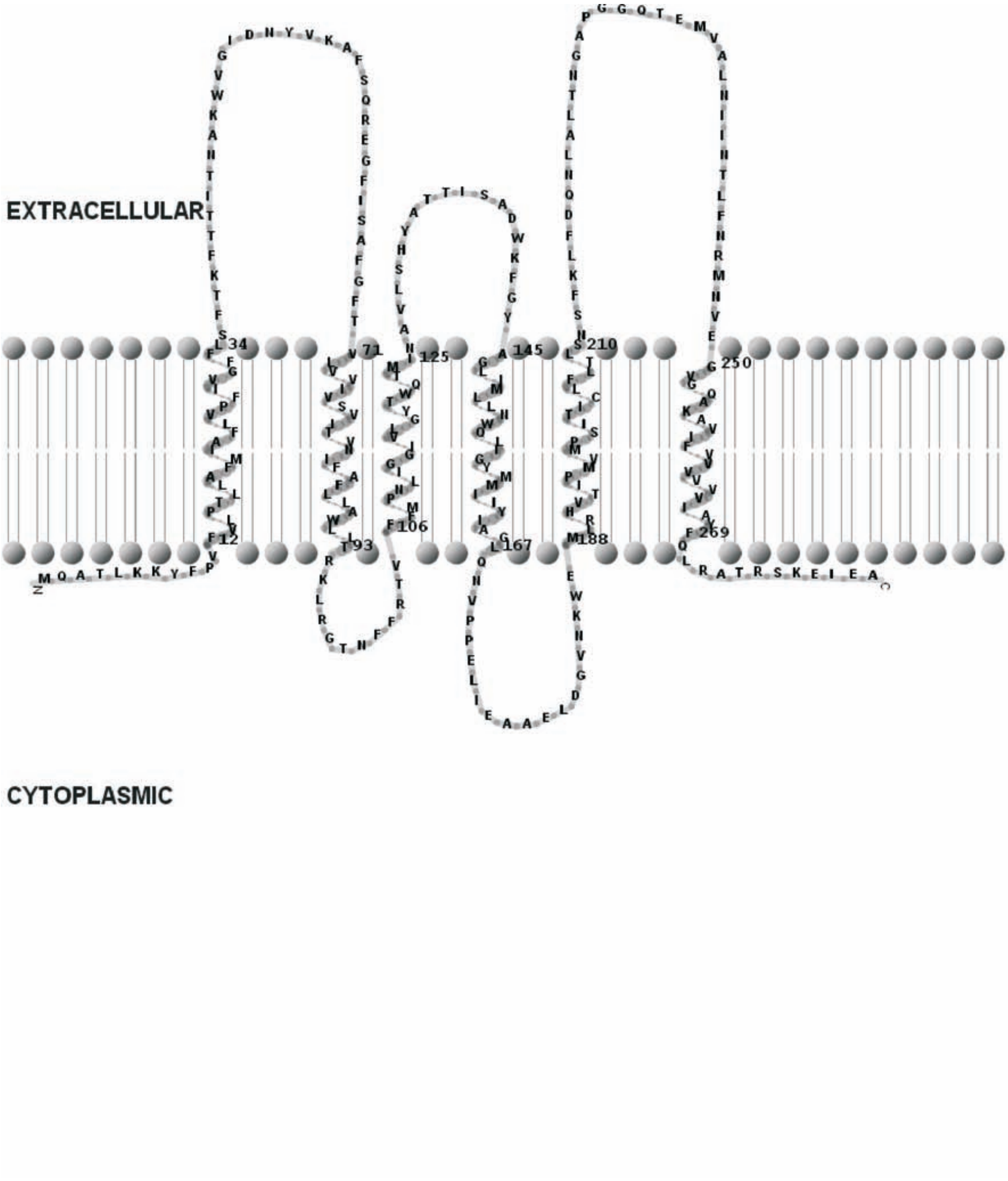
10	20	30	40	50	60
M**ATNESVSEK**	**QRLDAT**RVQA	HPVAVNANSS	QTKPSKKIVA	EGGGSVKRPG	DRIFEVLSTA
70	80	90	100	110	120
SAAIITAIII	AIAAFLIWRA	VPALMRNAEG	IGGFFTYSGA	WNTTDI**DAMY**	**FGIPNLLAA**T
130	140	150	160	170	180
LLISVIALII	AMPIALGIAI	FLSNYSPKRL	VKPL**GYMVDM**	**LAAVPSIV**YG	LWGWQVLGPA
190	200	210	220	230	240
LSGFYTWIES	WGGSFFLFAT	YQNSPSFATG	RNMLTGGIVL	A**VMILPVIAA**	TAREVFIQTP
250	260	270	280	290	300
KGHIESALAL	GATRWEVVRL	TVLPFGMSGY	VSGA**MLGLGR**	**ALGETMA**LYM	VVSPSSAFRF
310	320	330	340	350	360
SLFDGGTTFA	TAIANAAPEF	NDNTRAGAYI	SAGLVLFALT	FIVNAGARAM	VNRGK



Cg2704 ABC-TYPE SUGAR TRANSPORT SYSTEM, PERMEASE COMPONENT

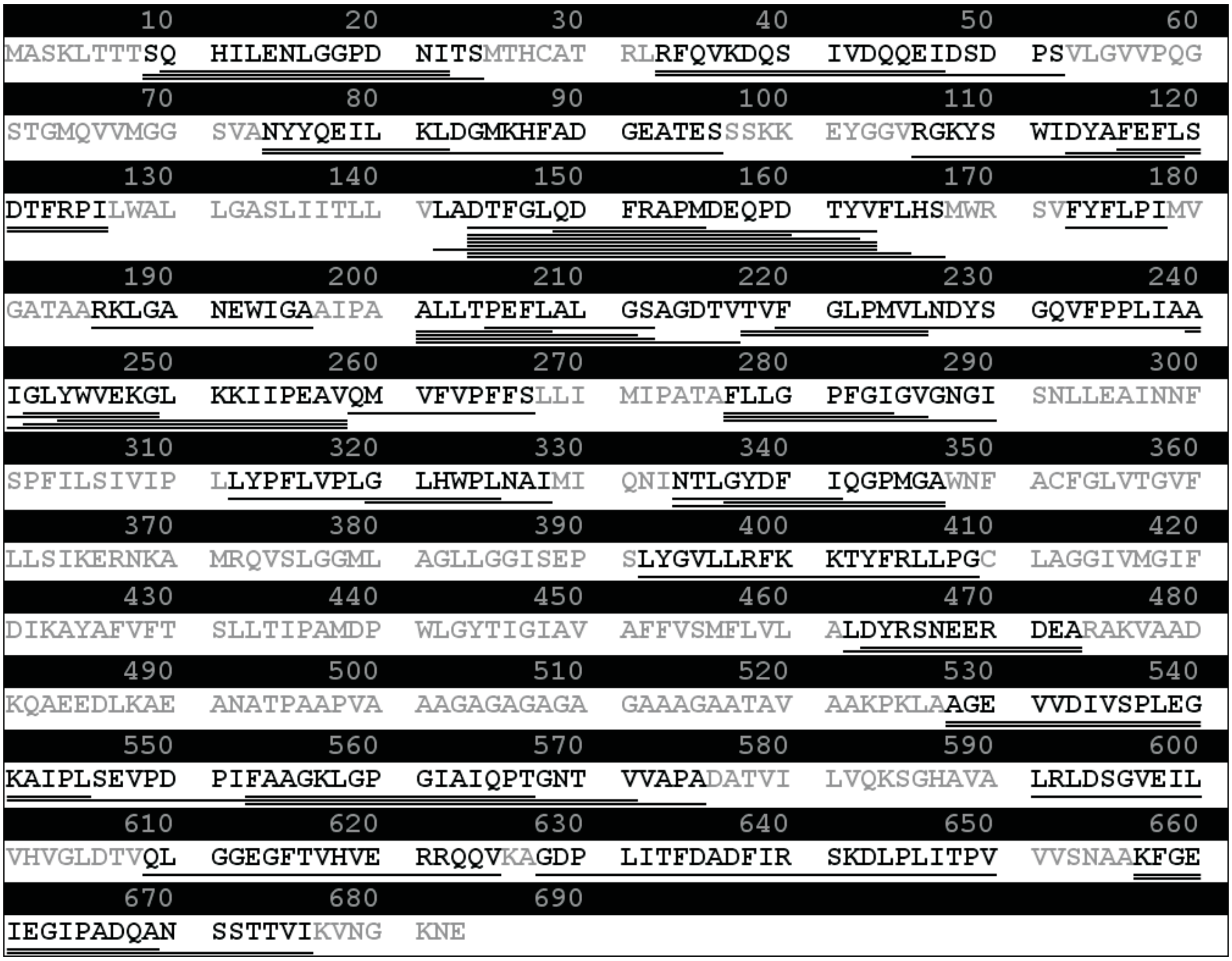
ESI 6TMH 31.5 kDa 8 Arg 11 Lys

10	20	30	40	50	60
MQA**TLKKYFP**	**V**FVLPTLLAF	MIAFLVPFIV	GFFLSFTKFT	TITNA**KWVGI**	**DNYV**KAFSQR
70	**80**	**90**	**100**	**110**	**120**
EGFISAFGFT	VLVVIVSVIT	VNIFAFLLAW	LLTRKLRGTN	FFRTV**FFMPN**	**LIGGIVL**GYT
130	**140**	**150**	**160**	**170**	**180**
WQTMINAVLS	HYATTISADW	KFGYAGLIML	LNWQLIGYMM	IIYIAGLQNV	PPELIEAAEL
190	**200**	**210**	**220**	**230**	**240**
DGVNKWEMLR	HVTIPMVMPS	ITICLFLTLS	**NSFKLFDQNL**	**A**LT**NGAPGGQ**	**TEMVALNIIN**
250	**260**	**270**	**280**	**290**	
TLFNRMNVEG	**VGQA**KAVIFV	VVVVVIAYFQ	LRATRSKEIE	A	



Cg1537 GLUCOSE-SPECIFIC ENZYME II BC COMPONENT OF PTS

MALDI 10TMH 72.5 kDa 18 Arg 29 Lys



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        10         20         30         40         50         60
MASKLTTTSQ HILENLGGPD NITSMTHCAT RLRFQVKDQS IVDQQEIDSD PSVLGVVPQG
        70         80         90        100        110        120
STGMQVVMGG SVANYYQEIL KLDGMKHFAD GEATESSSKK EYGGVRGKYS WIDYAFEFLS
       130        140        150        160        170        180
DTFRPILWAL LGASLIITLL VLADTFGLQD FRAPMDEQPD TYVFLHSMWR SVFYFLPIMV
       190        200        210        220        230        240
GATAARKLGA NEWIGAAIPA ALLTPEFLAL GSAGDTVTVF GLPMVLNDYS GQVFPPLIAA
       250        260        270        280        290        300
IGLYWVEKGL KKIIPEAVQM VFVPFFSLLI MIPATAFLLG PFGIGVGNGI SNLLEAINNF
       310        320        330        340        350        360
SPFILSIVIP LLYPFLVPLG LHWPLNAIMI QNINTLGYDF IQGPMGAWNF ACFGLVTGVF
       370        380        390        400        410        420
LLSIKERNKA MRQVSLGGML AGLLGGISEP SLYGVLLRFK KTYFRLLPGC LAGGIVMGIF
       430        440        450        460        470        480
DIKAYAFVFT SLLTIPAMDP WLGYTIGIAV AFFVSMFLVL ALDYRSNEER DEARAKVAAD
       490        500        510        520        530        540
KQAEEDLKAE ANATPAAPVA AAGAGAGAGA GAAAGAATAV AAKPKLAAGE VVDIVSPLEG
       550        560        570        580        590        600
KAIPLSEVPD PIFAAGKLGP GIAIQPTGNT VVAPADATVI LVQKSGHAVA LRLDSGVEIL
       610        620        630        640        650        660
VHVGLDTVQL GGEGFTVHVE RRQQVKAGDP LITFDADFIR SKDLPLITPV VVSNAAKFGE
       670        680        690
IEGIPADQAN SSTTVIKVNG KNE
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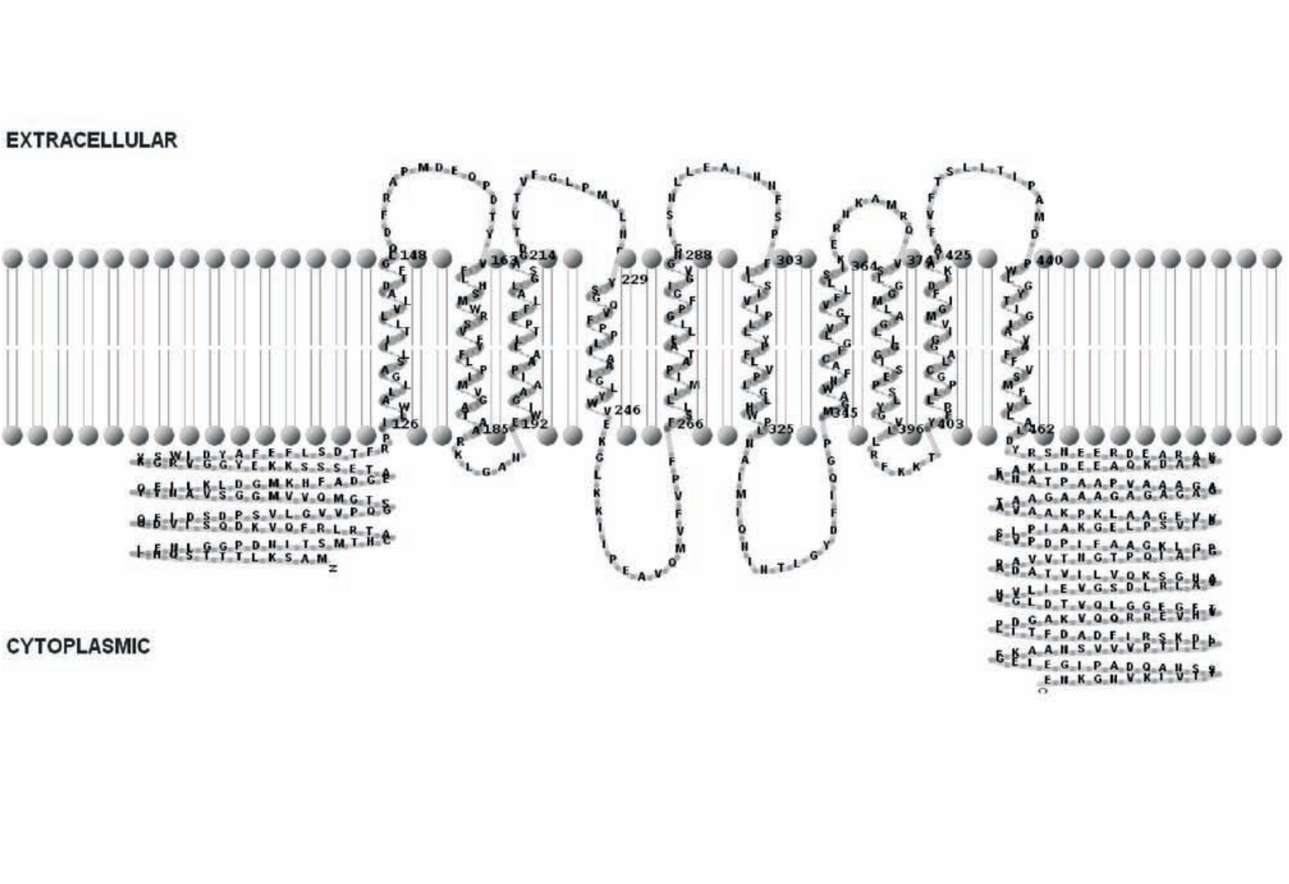
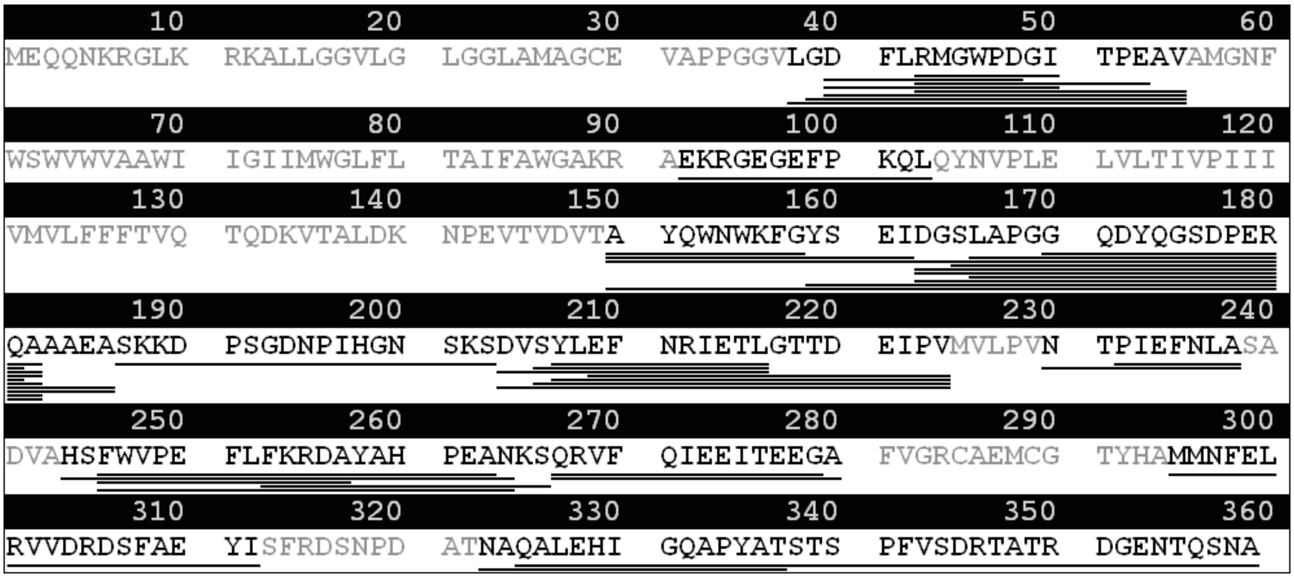


Cg2409 CYTOCHROME C OXIDASE CHAIN II

MALDI   3TMH   39.6 kDa   15 Arg   14 Lys



```
        10         20         30         40         50         60
MEQQNKRGLK RKALLGGVLG LGGLAMAGCE VAPPGGVLGD FLRMGWPDGI TPEAVAMGNF
        70         80         90        100        110        120
WSWVWVAAWI IGIIMWGLFL TAIFAWGAKR AEKRGEGEFP KQLQYNVPLE LVLTIVPIII
       130        140        150        160        170        180
VMVLFFFTVQ TQDKVTALDK NPEVTVDVTA YQWNWKFGYS EIDGSLAPGG QDYQGSDPER
       190        200        210        220        230        240
QAAAEASKKD PSGDNPIHGN SKSDVSYLEF NRIETLGTTD EIPVMVLPVN TPIEFNLASA
       250        260        270        280        290        300
DVAHSFWVPE FLFKRDAYAH PEANKSQRVF QIEEITEEGA FVGRCAEMCG TYHAMMNFEL
       310        320        330        340        350        360
RVVDRDSFAE YISFRDSNPD ATNAQALEHI GQAPYATSTS PFVSDRTATR DGENTQSNA
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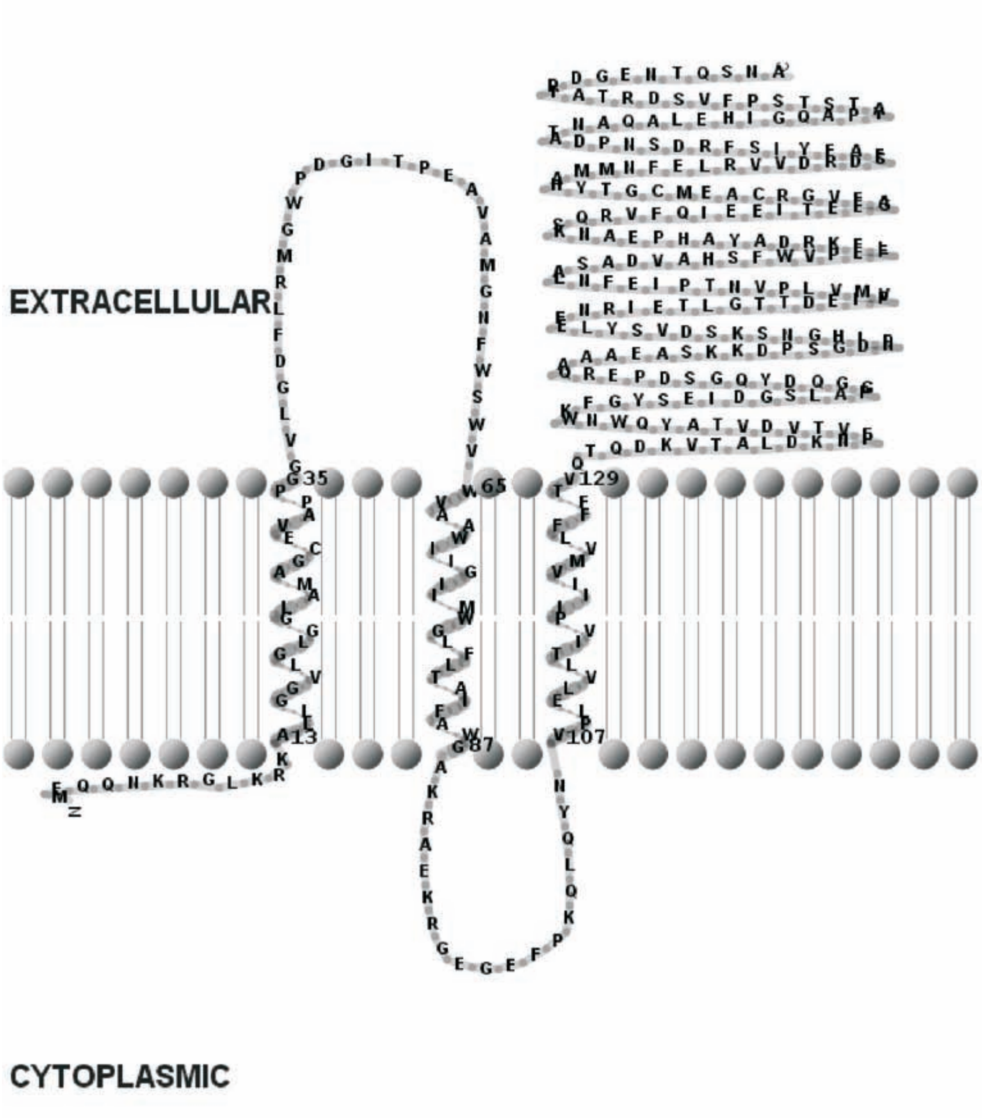
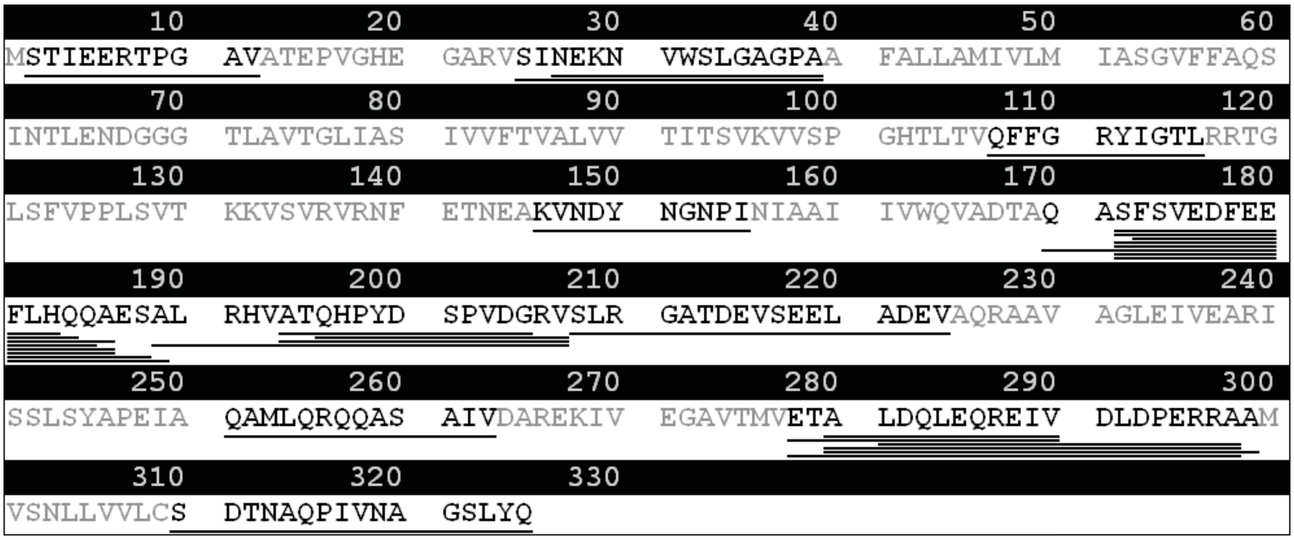
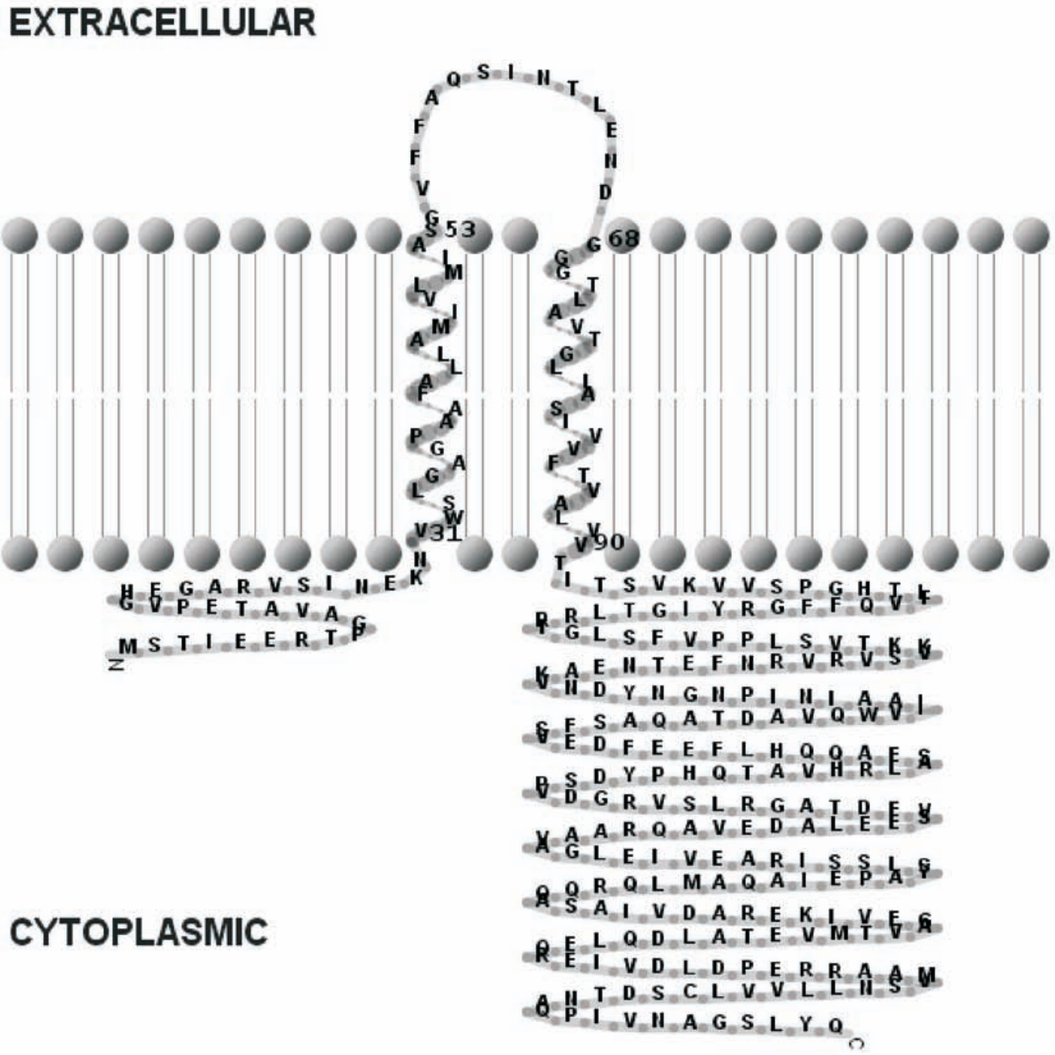


Cg3138 MEMBRANE PROTEASE SUBUNIT, STOMATIN/PROHIBITIN HOMOLOG

MALDI 2TMH 34.7 kDa 17 Arg 6 Lys



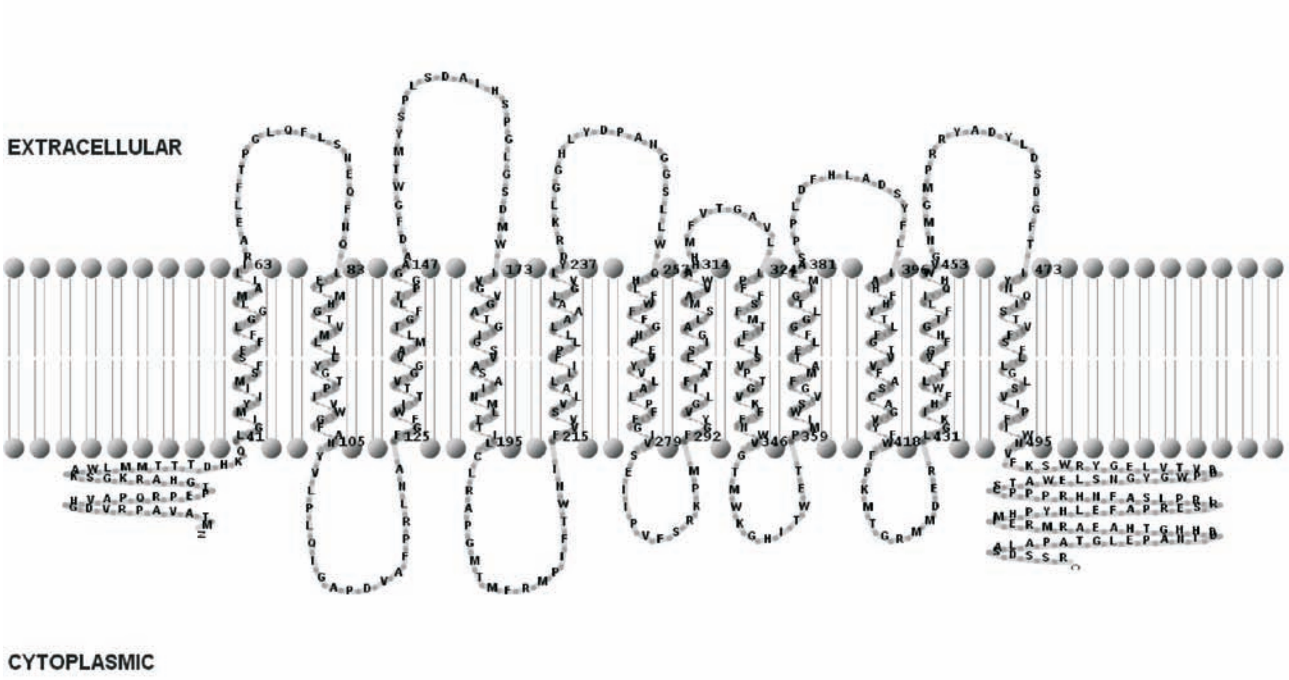
10	20	30	40	50	60
M**STIEERTPG**	**AV**ATEPVGHE	GARV**SINEKN**	**VWSLGAGPA**A	FALLAMIVLM	IASGVFFAQS
70	**80**	**90**	**100**	**110**	**120**
INTLENDGGG	TLAVTGLIAS	IVVFTVALVV	TITSVKVVSP	GHTLTV**QFFG**	**RYIGTL**RRTG
130	**140**	**150**	**160**	**170**	**180**
LSFVPPLSVT	KKVSVRVRNF	ETNEA**KVNDY**	**NGNPI**NIAAI	IVWQVADTA**Q**	**ASFSVEDFEE**
190	**200**	**210**	**220**	**230**	**240**
FLHQQAESAL	**RHVATQHPYD**	**SPVDGRVSLR**	**GATDEVSEEL**	**ADEV**AQRAAV	AGLEIVEARI
250	**260**	**270**	**280**	**290**	**300**
SSLSYAPEIA	**QAMLQRQQAS**	**AIV**DAREKIV	EGAVTMV**ETA**	**LDQLEQREIV**	**DLDPERRAA**M
310	**320**	**330**			
VSNLLVVLC**S**	**DTNAQPIVNA**	**GSLYQ**			



Cg2780 PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE SUBUNIT

MALDI 12TMH 65.0 kDa 21 Arg 10 Lys

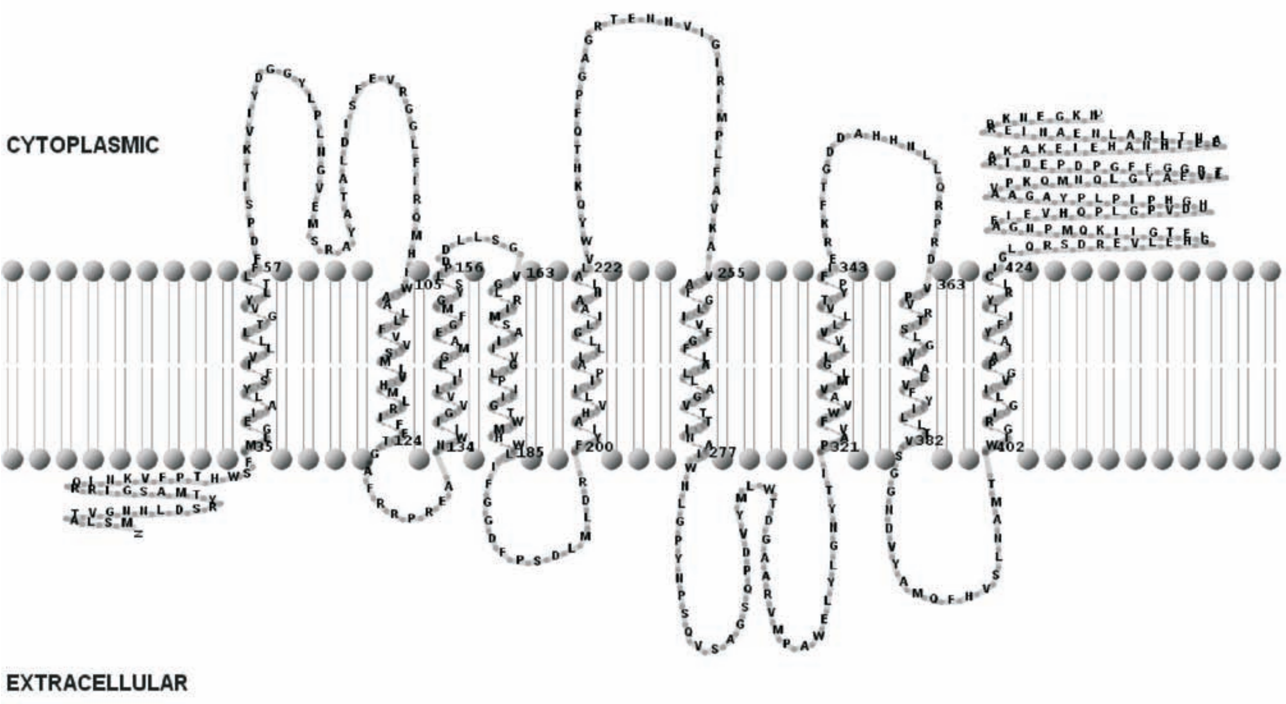
10	20	30	40	50	60
MTA**VAPRVDG**	**HVAPQRPEPT**	GHARKGSKAW	LMMTTTDHKQ	LGIMYIIMSF	SFFFLGGLMA
70	80	90	100	110	120
LLI**RAELFTP**	**GLQFLSNEQF**	**NQLFTMHGTV**	MLL**LYGTPIV**	**WGFA**NYVLPL	QIGAPDVA**FP**
130	140	150	160	170	180
RLNAFGFWIT	TVGGVAMLT**G**	**FLTPGGAADF**	**GWT**MYSPLSD	AI**HSPGLGSD**	**MWIVGV**GATG
190	200	210	220	230	240
IGSVASAINM	LTTILCLRAP	GMTMFRMPIF	TWNIFVVSVL	ALLIFPLLLA	AALGV**LYDRK**
250	260	270	280	290	300
LGGHLYDPAN	**GGSLLWQHL**F	WFFGHPEVYV	LAL**PFFGIVS**	EIIPVFSRKP	MFGYVGLIFA
310	320	330	340	350	360
TLSIGALSMA	VWAHHMFVTG	AVLLPFFSFM	TFLISVPTGV	**KFFNWVGT**MW	KGHITWETPM
370	380	390	400	410	420
IWSVGFMATF	LFGGLTGIML	A**SPPLDFHLA**	DSYFLIAHFH	YTLFGTVVFA	SCA**GVYFWFP**
430	440	450	460	470	480
KMTGRMMDER	LGKIHFWLTF	V**GFHGTFLI**Q	HWVGNMGMPR	RYADYLDSDG	FTIYNQISTV
490	500	510	520	530	540
FSFLLGLSVI	PFIWNVFKS**W**	**RYGELV**TVDD	PWGYGNSLEW	ATSCPPPRHN	FASLPRIRSE
550	560	570	580	590	
RPA**FELHYPH**	**MI**ERMRAEAH	TGHHDDINAP	ELGTAPALAS	DSSR	



Cg2403 CYTOCHROME B, MEMBRANE PROTEIN

MALDI 9TMH 59.7 kDa 27 Arg 11 Lys

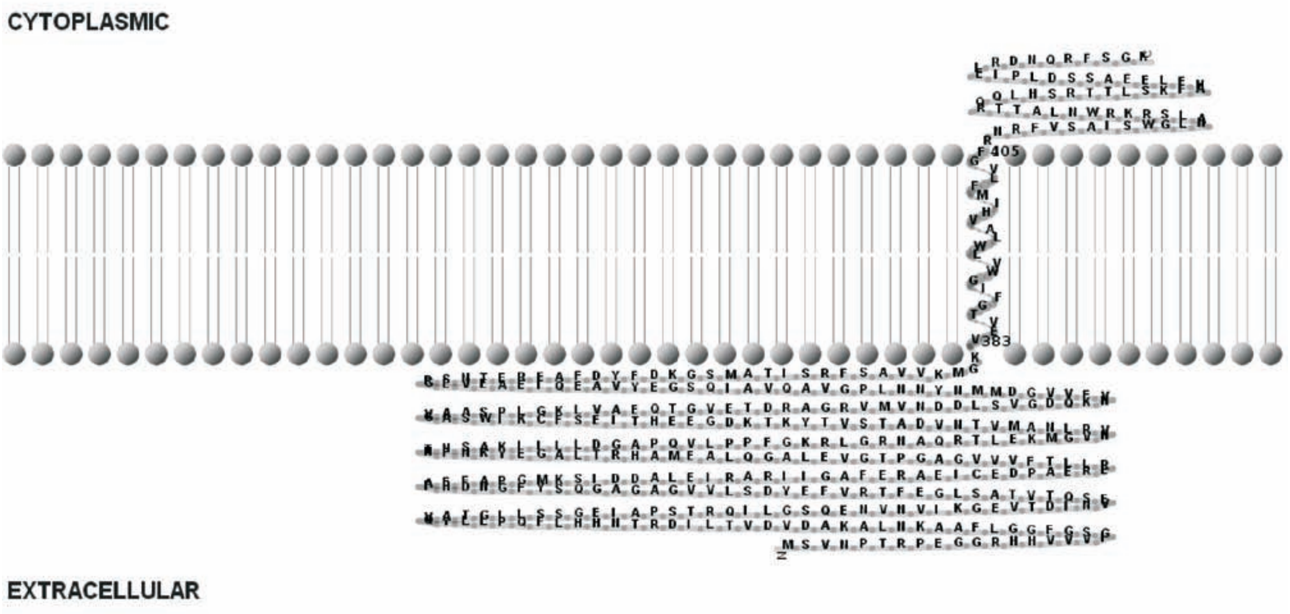
10	20	30	40	50	60
MSLA**TVGNNL**	**DSRYT**MASGI	RRQI**NKVFPT**	HWSFMLGEIA	LYSFIVLLLT	GVYLT**LFFDP**
70	80	90	100	110	120
SITKVIYDGG	**YLPLNGVEMS**	RAYATALDIS	FEVRGGLFIR	QMHHWAALLF	VVSMLVHMLR
130	140	150	160	170	180
IFFTGAFRRP	REANWIIGVV	LIILGMAEGF	MGYSLPDDLL	SGVGLRIMSA	IIVGLPIIGT
190	200	210	220	230	240
WMHWLIFGGD	FPSDLMLDRF	YIAHV**LIIPA**	**ILLGLI**AAHL	ALVWYQKHTQ	FPGAGRTENN
250	260	270	280	290	300
VIGIRIMPLF	AVKAVAFGLI	VFGFLALLAG	VTTI**NAIWNL**	**GPYNPSQVSA**	**GSQPDVYMLW**
310	320	330	340	350	360
TDGAARVMPA	**WELYLG**NYTI	PAVFWVAVML	GILVVLLVTY	PFIERKFTGD	DAHHNLLQRP
370	380	390	400	410	420
RDVPVRTSLG	VMALV**FYILL**	TVSGGNDVYA	MQFHVSLNAM	TWIGRIGLIV	GPAIAYFITY
430	440	450	460	470	480
RLCIGLQRSD	REVLEHGIET	**GIIKQMPNGA**	**FIEVHQPLGP**	**VDDHGHPIPL**	**PYAGA**AVPKQ
490	500	510	520	530	540
M**NQLGYAEVE**	**TRGGFFGPDP**	**EDI**RAKAKEI	EHANHIEEAN	TLRALNEANI	ERDKNEGKN



Cg1656 NADH DEHYDROGENASE

MALDI 1TMH 50.9 kDa 28 Arg 19 Lys

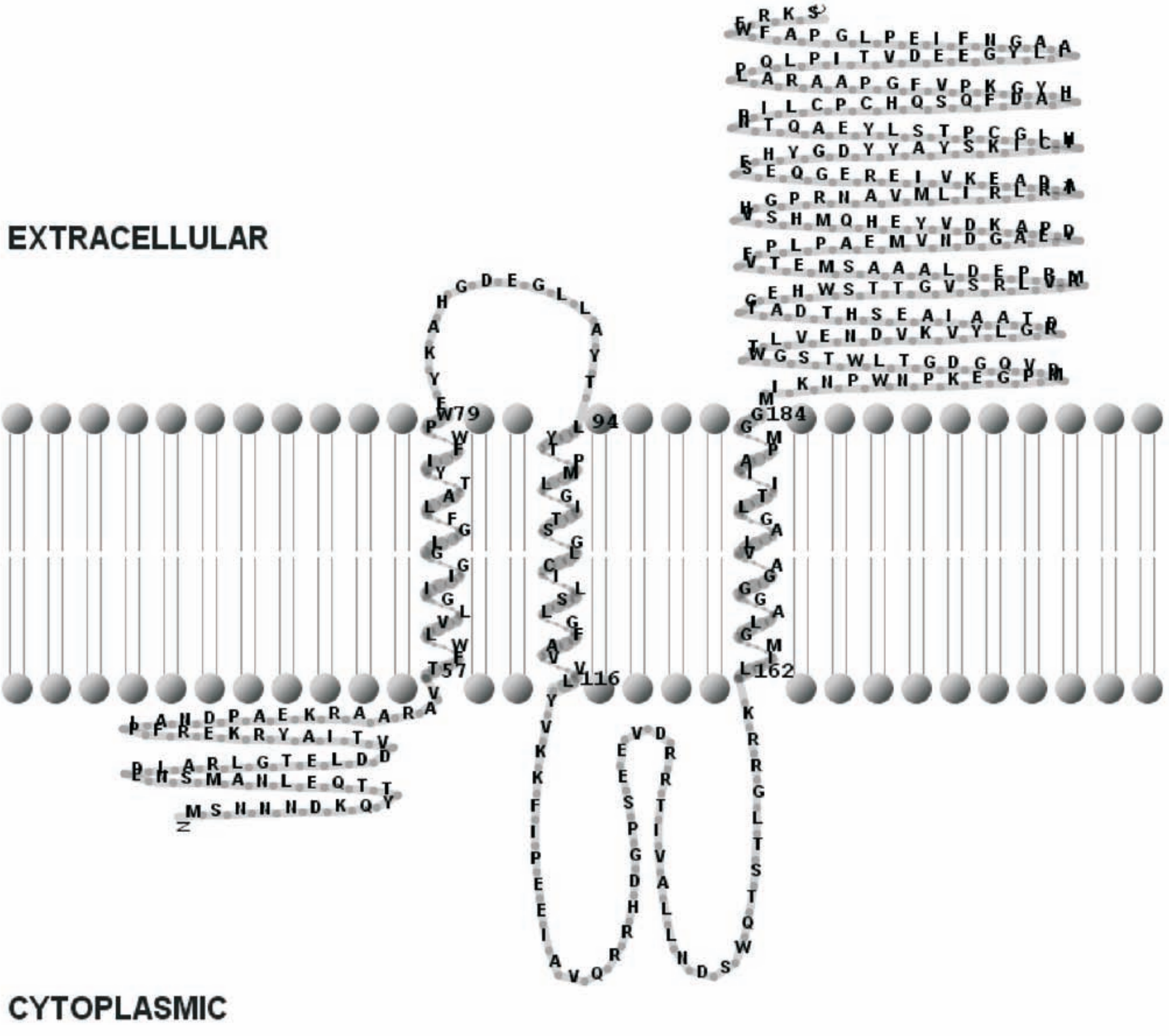
10	20	30	40	50	60
MSVNPTRPEG	GRHHVVVIGS	GFGGLFAAKN	LAKADVDVTL	IDRTNHHLFQ	PLLYQVATGI
70	80	90	100	110	120
LSSGEIAPST	RQILGSQENV	NVIKGEVTDI	NVESQTVTA**S**	**LGEFTRVFEY**	**DSLVV**GAGAG
130	140	150	160	170	180
QS**YFGNDHFA**	**EFAPGMKSID**	**DALEI**RARII	GAFERAEICE	DPAERERLLT	FVVVGAGPTG
190	200	210	220	230	240
VELAGQLAEM	A**HRTLAGEYK**	**NFNTNSA**KI**I**	**LLDGAPQVLP**	**PFGKRLGRNA**	QRTLEKMGVN
250	260	270	280	290	300
VRLNAMVTNV	DATSVTYKTK	DGEEHTIESF	CKIWSAGVAA	SPLGKLVAEQ	TGVETDRAGR
310	320	330	340	350	360
VMVNDDLSVG	DQKNVFVVGD	MMNYNNLPGV	AQVAIQSGEY	VAEQI**EAEVE**	**GRSNTEREAF**
370	380	390	400	410	420
DYFDKGSMAT	ISRFSAVVKM	GKVEVTGFIG	WVLWLAVHIM	FLVGFRNRFV	SAISWGLNAL
430	440	450	460	470	
SRKRWNLATT	RQQLHSRTTL	SKFAHELEEA	**SSDLPIELRD**	**NQRFSGK**	



Cg2404 RIESKE IRON-SULFUR PROTEIN

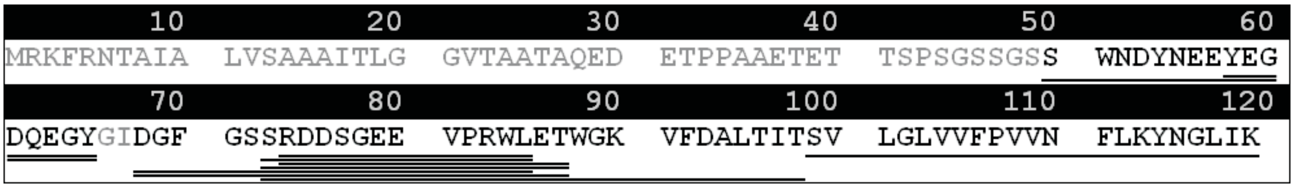
MALDI 3TMH 45.1 kDa 22 Arg 15 Lys

10	20	30	40	50	60
MSNNNDKQYT	TQELNAMSNE	DLARLGTELD	DVTI**AYRKER**	**FPI**ANDPAEK	RAARAVTFWL
70	**80**	**90**	**100**	**110**	**120**
VLGIIGGLGF	LA**TYIFWPWE**	**YKA**HGDEGLL	AYTLYTPMLG	ITSGLCILSL	GFAVV**LYVKK**
130	**140**	**150**	**160**	**170**	**180**
FIPEEIAVQR	RHDGPSEEVD	RRTIVALLND	SWQTSTLGRR	KLIMGLAGGG	AVLAGLTIIA
190	**200**	**210**	**220**	**230**	**240**
PM**GGMIKNPW**	**NPKEGPMDV**Q	GDGTLWTS**GW**	**TLVENDVKVY**	**LGRDTA**AIAE	SHTDATGEHW
250	**260**	**270**	**280**	**290**	**300**
STTGVSRLVR	MRPEDLAAAS	METVFPLPAE	MVNDGAEYDP	A**KDVYEHQMH**	**SVHGPRNA**VM
310	**320**	**330**	**340**	**350**	**360**
LIRLRTADAE	KVIEREGQES	**FHYGDYYAYS**	KICTHIGCPT	SLYEAQTNRI	LCPCHQSQFD
370	**380**	**390**	**400**	**410**	
ALHYGKPV**FG**	**PAARALPQLP**	**ITVDEEGYLI**	**AAGNFIEPLG**	**PA**FWERKS	

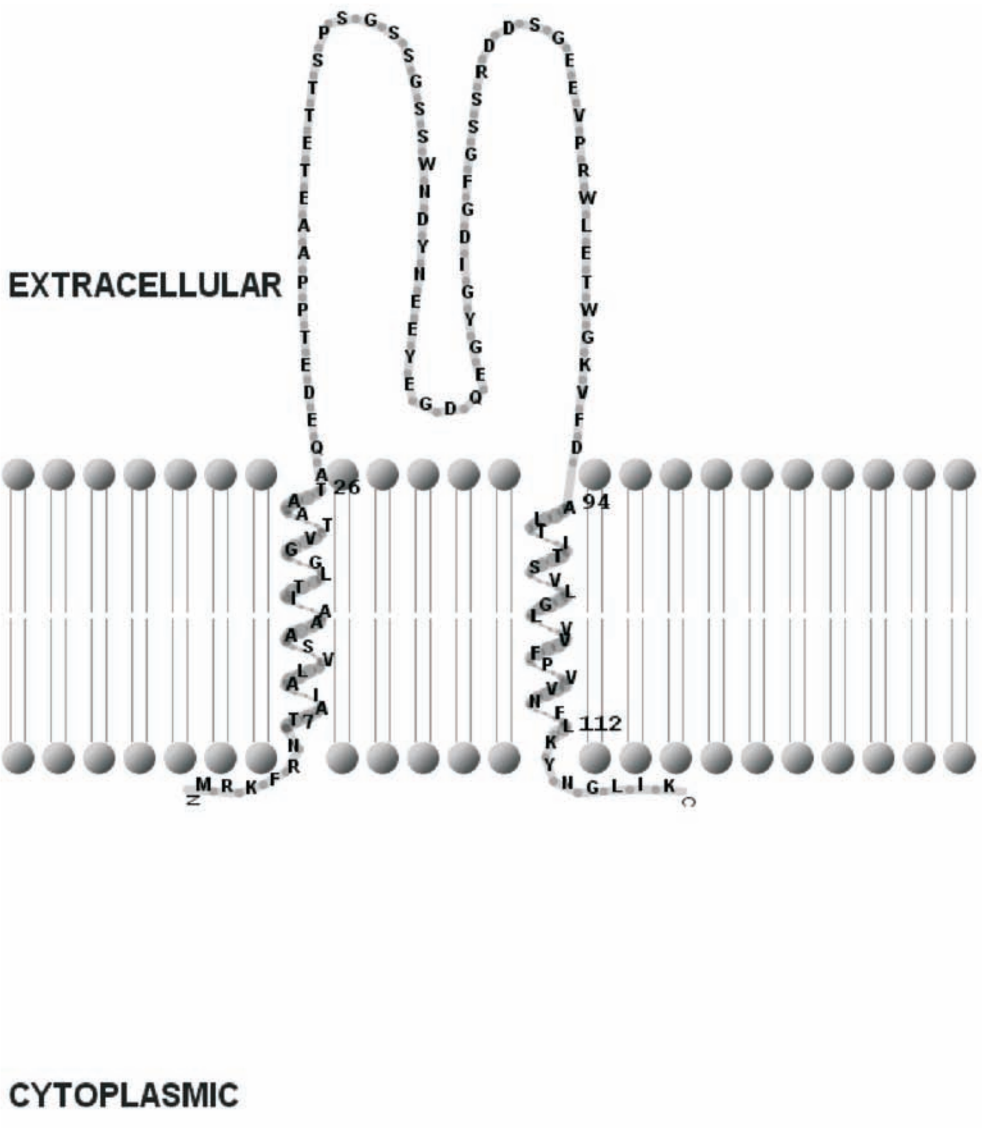


Cg2196 PUTATIVE SECRETED OR MEMBRANE PROTEIN

MALDI 2TMH 12.7 kDa 4 Arg 4 Lys



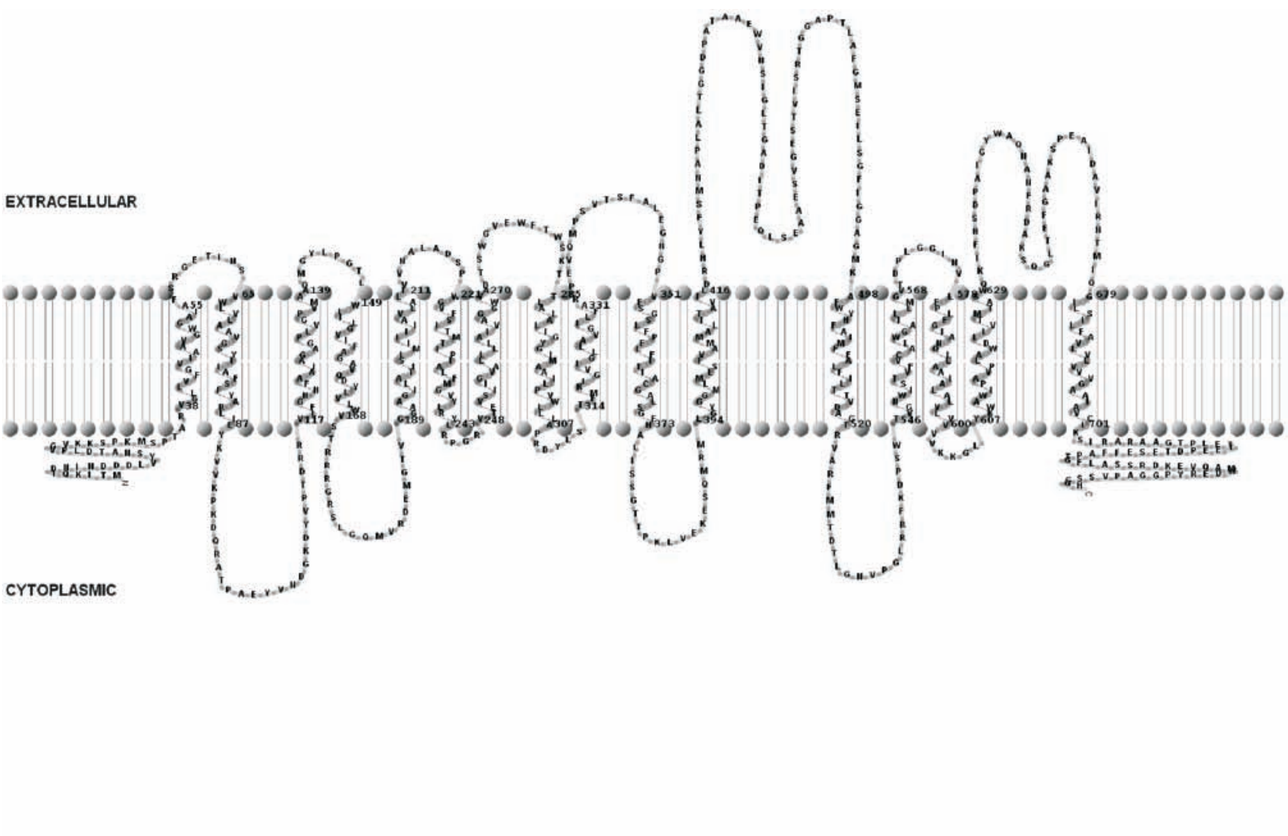
```
        10         20         30         40         50         60
MRKFRNTAIA LVSAAAITLG GVTAATAQED ETPPAAETET TSPSGSSGSS WNDYNEEYEG
        70         80         90        100        110        120
DQEGYGIDGF GSSRDDSGEE VPRWLETWGK VFDALTITSV LGLVVFPVVN FLKYNGLIK
```



Cg0756 PUTATIVE CARBON STARVATION PROTEIN A

MALDI 16TMH 81.0 kDa 29 Arg 22 Lys

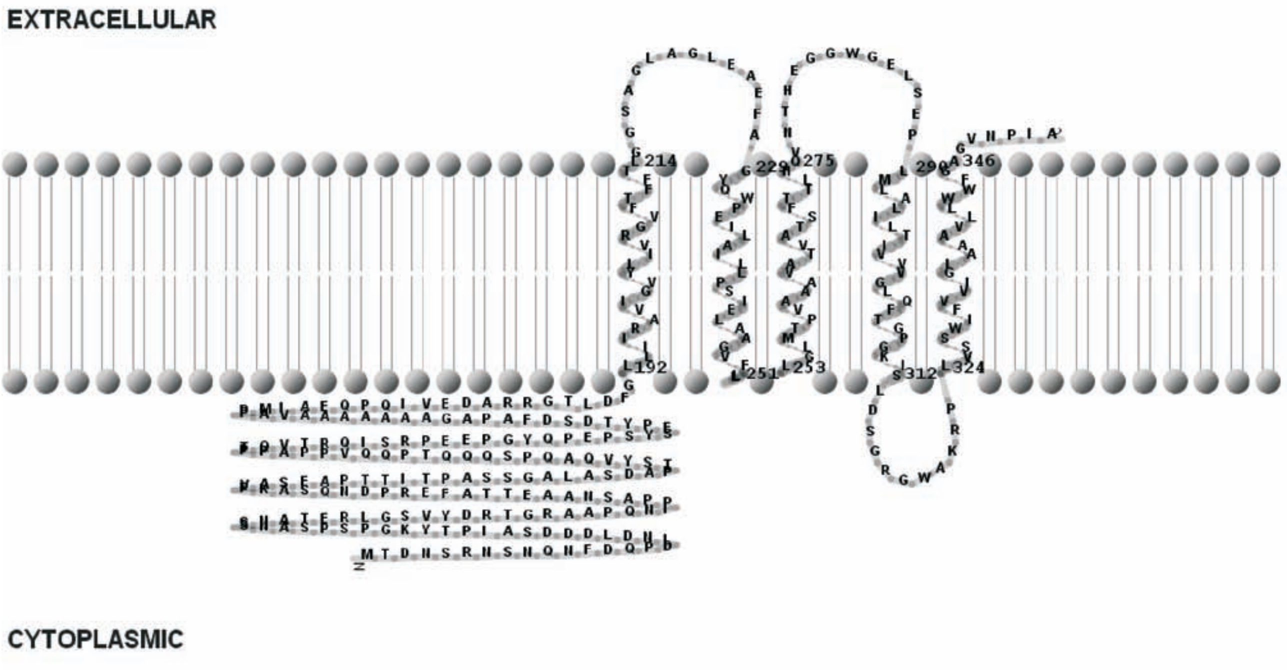
10	20	30	40	50	60
MTIKQTDNIN	DDDLVYSNAT	DLPVGVKKSP	KMSPTARVGL	LVFGVIAAVG	WGAIAFSRGE
70	80	90	100	110	120
TINSVWLVLA	AVGSYIIAFS	FYARLIEYKV	VKPKDQRATP	AEYVNDGKDY	VPTDRRVLFG
130	140	150	160	170	180
HHFAAIAGAG	PLVGPVMAAQ	MGYLPGTLWI	ILGVIFAGAV	QDYLVLWVST	RRRGRSLGQM
190	200	210	220	230	240
VRDEMGTVGG	AAGILATISI	MIIIIAVLAL	IVVNALADSP	WGVFSITMTI	PIALFMGVYL
250	260	270	280	290	300
RYLRPGRVTE	VSIIGVALLL	LAIVAGGWVA	DTSWGVEWFT	WSKTTLALAL	IGYGIMAAIL
310	320	330	340	350	360
PV**WLLLAPRD**	**YLST**FMKIGV	IGLLAVGI**LF**	**ARPEVQMPSV**	**T**SFALEGNGP	VFS**GSLFPFL**
370	380	390	400	410	420
FITIACGALS	GFHALISSGT	TPKLVEKESQ	MRMLGYGGML	MESFVAMMAL	IT**AVILDRHL**
430	440	450	460	470	480
YFSMNAPLAL	TGGDPATAAE	WVNSIGLTGA	DITPEQLSEA	AESVGESTVI	SRTGGAPTLA
490	500	510	520	530	540
FGMSEILSGF	IGGAGMKA**FW**	**YHFAI**MFEAL	FILTTVDAGT	RVARFMMTDT	LGNVPGLRRF
550	560	570	580	590	600
KDPSWTVGNW	ISTVFVCALW	GAILLMGVTD	PLGGINVLFP	LFGIANQLLA	AIALALVLVV
610	620	630	640	650	660
VVKKGLYKWA	WIPAVPLAWD	LIVTMTASWQ	KIFHSDPAIG	YWAQNANFRD	AKSQGLTEFG
670	680	690	700	710	720
AAKSPEAIDA	VIRNTMIQGI	LSILFAVLVL	VVVGAAIAVC	IKSIRARAAG	TPLETTEEPD
730	740	750	760		
TESEFFAPTG	FLASSRDKEV	QA**MWDERYPG**	**GAPV**SSGGH		



Cg1429 PUTATIVE MEMBRANE PROTEIN

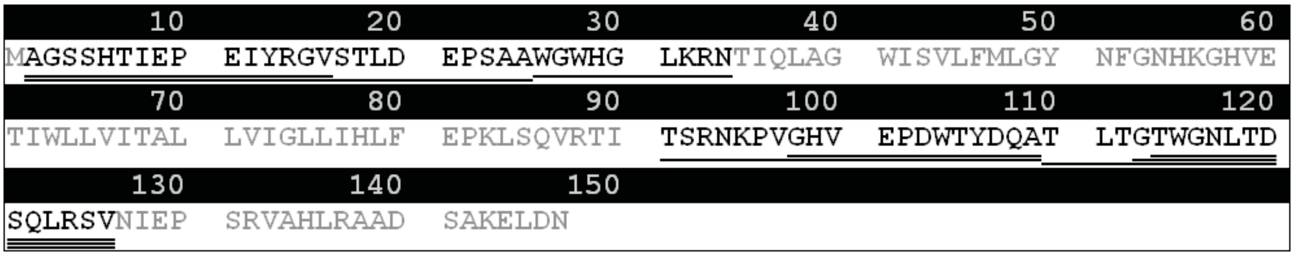
MALDI 5TMH 36.8 kDa 13 Arg 4 Lys

10	20	30	40	50	60
MTDNS**RNSNQ**	**NFDQPDLNDL**	**DDDSAIPT**YK	GPSPSANSSN	ATERLGSVYD	RTGRAAPQNI
70	80	90	100	110	120
PPASNAAETT	**AFERPDNQSA**	**KPV**ASEAPTT	ITPASSGALA	SDAPTSYVQA	QPSQQQTPQQ
130	140	150	160	170	180
V**PPAPPTQVT**	**RQISRPEEPG**	**YQPEPSYSEP**	**YTDSDFAPA**G	AAAAAAAVAP	PMIAEQPQIV
190	200	210	220	230	240
EDARRGTLDF	GLLIIRAVIG	VYLIVRGVFT	FFTLGGSAGL	AGLEAEFAGY	QWPEILAILL
250	260	270	280	290	300
PSIELAAGVF	LLLGLMTPVA	AAVATVATSF	TTLHQV**NTHE**	**GGWGELSEPL**	MLALILTIVV
310	320	330	340	350	360
VGLQFTGPGK	ISLDSGRGWA	KRPLVSSWIF	VVIGIAAAVL	LWWFGAGVNP	IA



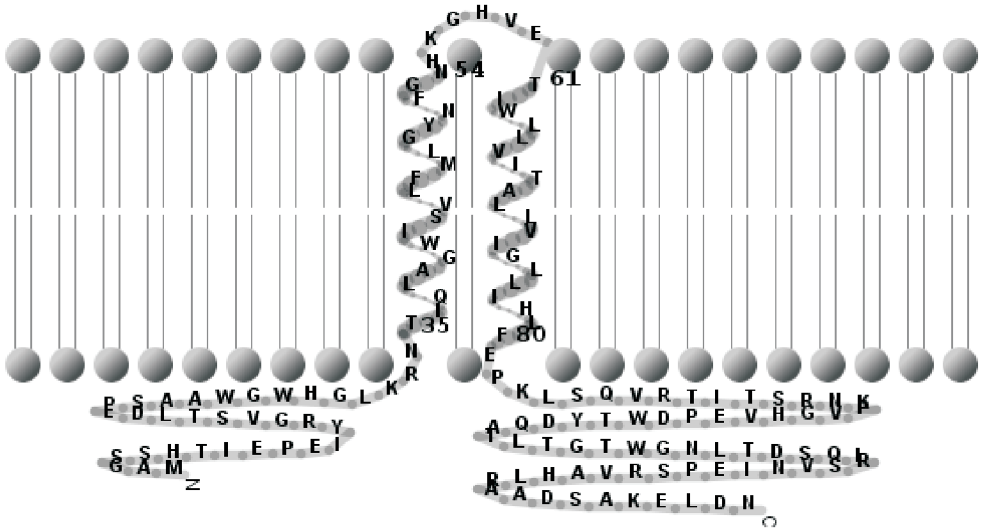
Cg2211 PUTATIVE MEMBRANE PROTEIN

MALDI   2TMH   16.5 kDa   7 Arg   5 Lys



```
        10         20         30         40         50         60
MAGSSHTIEP EIYRGVSTLD EPSAAWGWHG LKRNTIQLAG WISVLFMLGY NFGNHKGHVE
        70         80         90        100        110        120
TIWLLVITAL LVIGLLIHLF EPKLSQVRTI TSRNKPVGHV EPDWTYDQAT LTGTWGNLTD
       130        140        150
SQLRSVNIEP SRVAHLRAAD SAKELDN
```

CYTOPLASMIC



EXTRACELLULAR

Cg1685 SEC-INDEPENDENT PROTEIN SECRETION PATHWAY COMPONENT

MALDI 1TMH 12.0 kDa 5 Arg 5 Lys

```
        10         20         30         40         50         60
MSLGPWEIGI IVLLIIVLFG AKKLPDAARS IGRSMRIFKS EVKEMNKDGD TPEQQQQPQQ
        70         80         90        100        110
QIAPNQIEAP QPNFEQHYQG QQVQQPQNPQ TPDYRQNYED PNRTS
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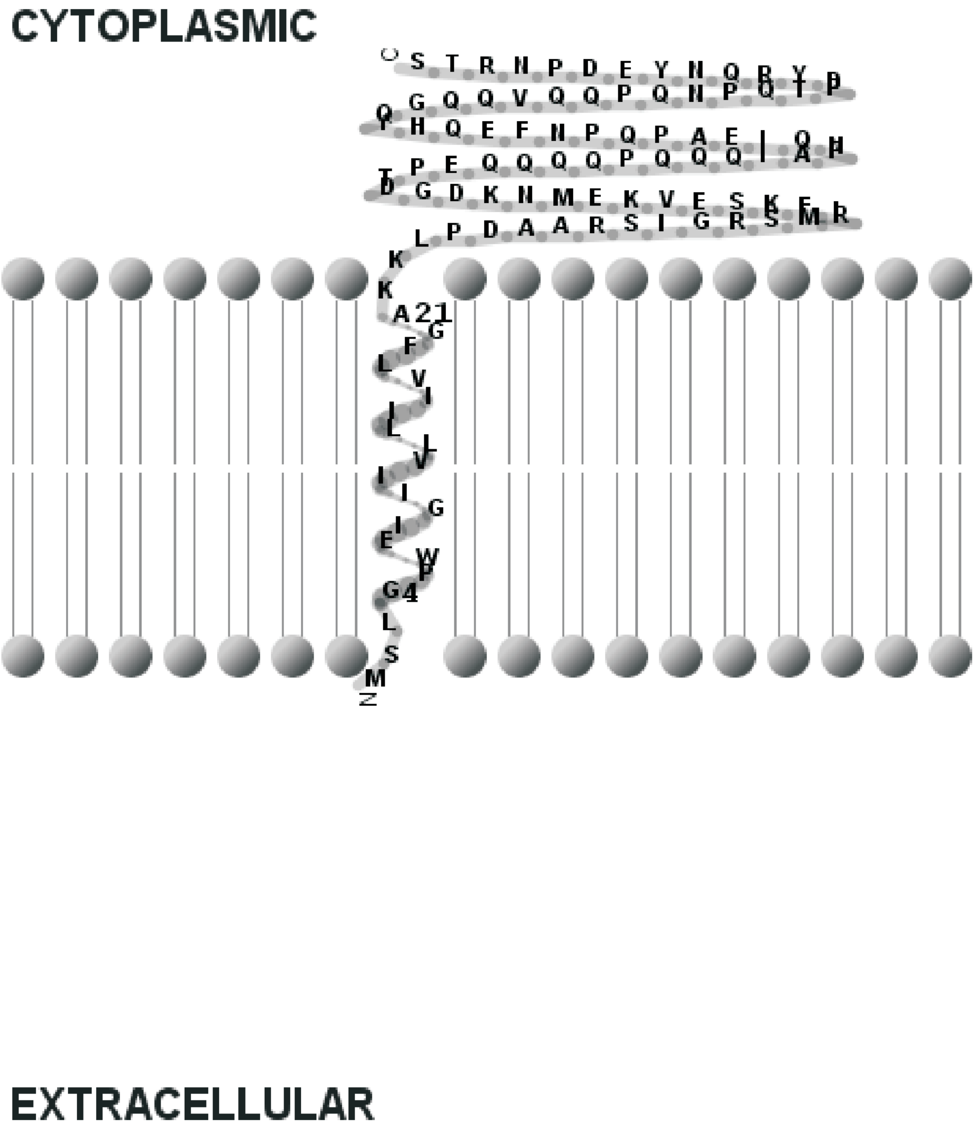
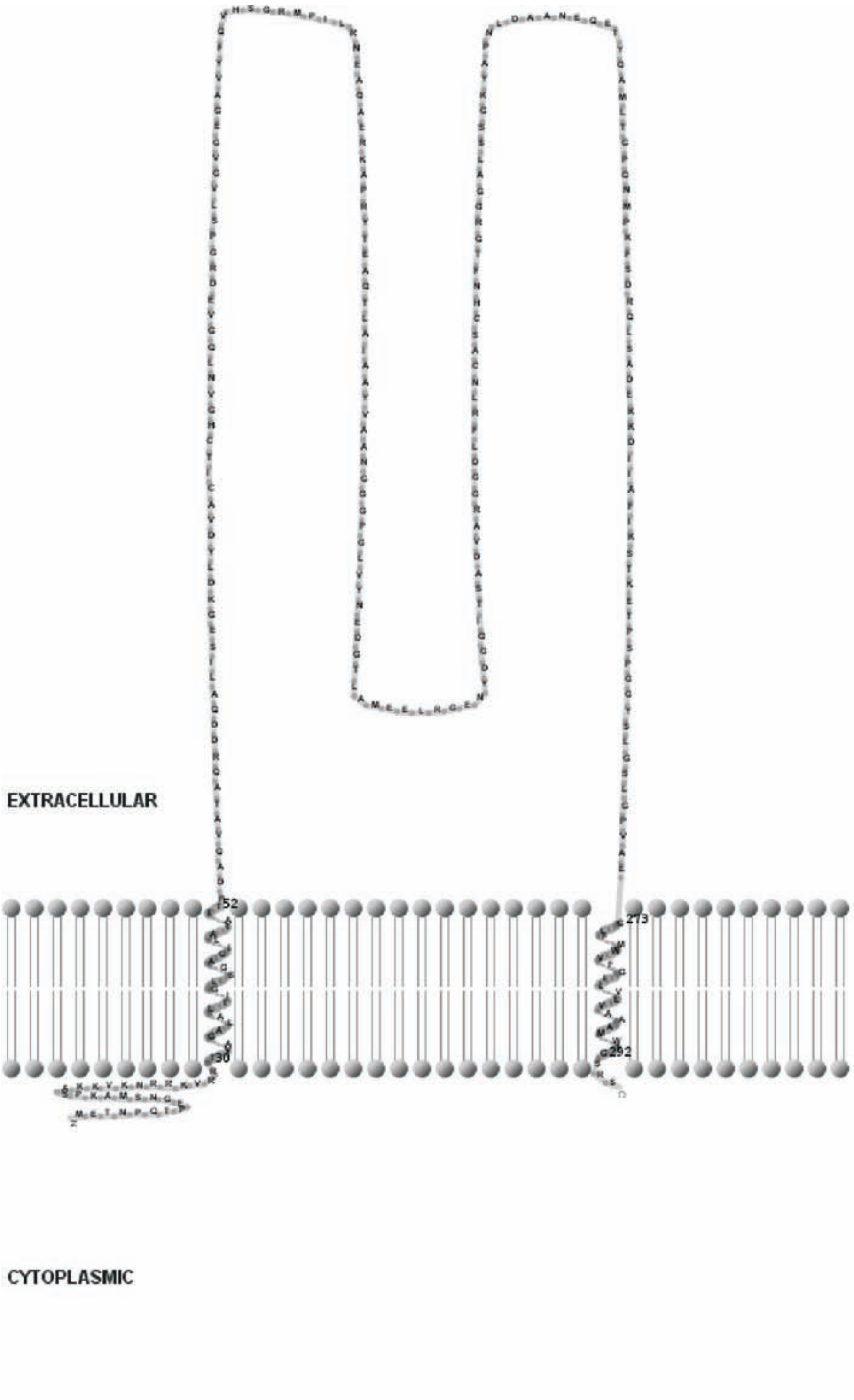


Cg2405 CYTOCHROME C1

MALDI   2TMH   31.1 kDa   16 Arg   13 Lys

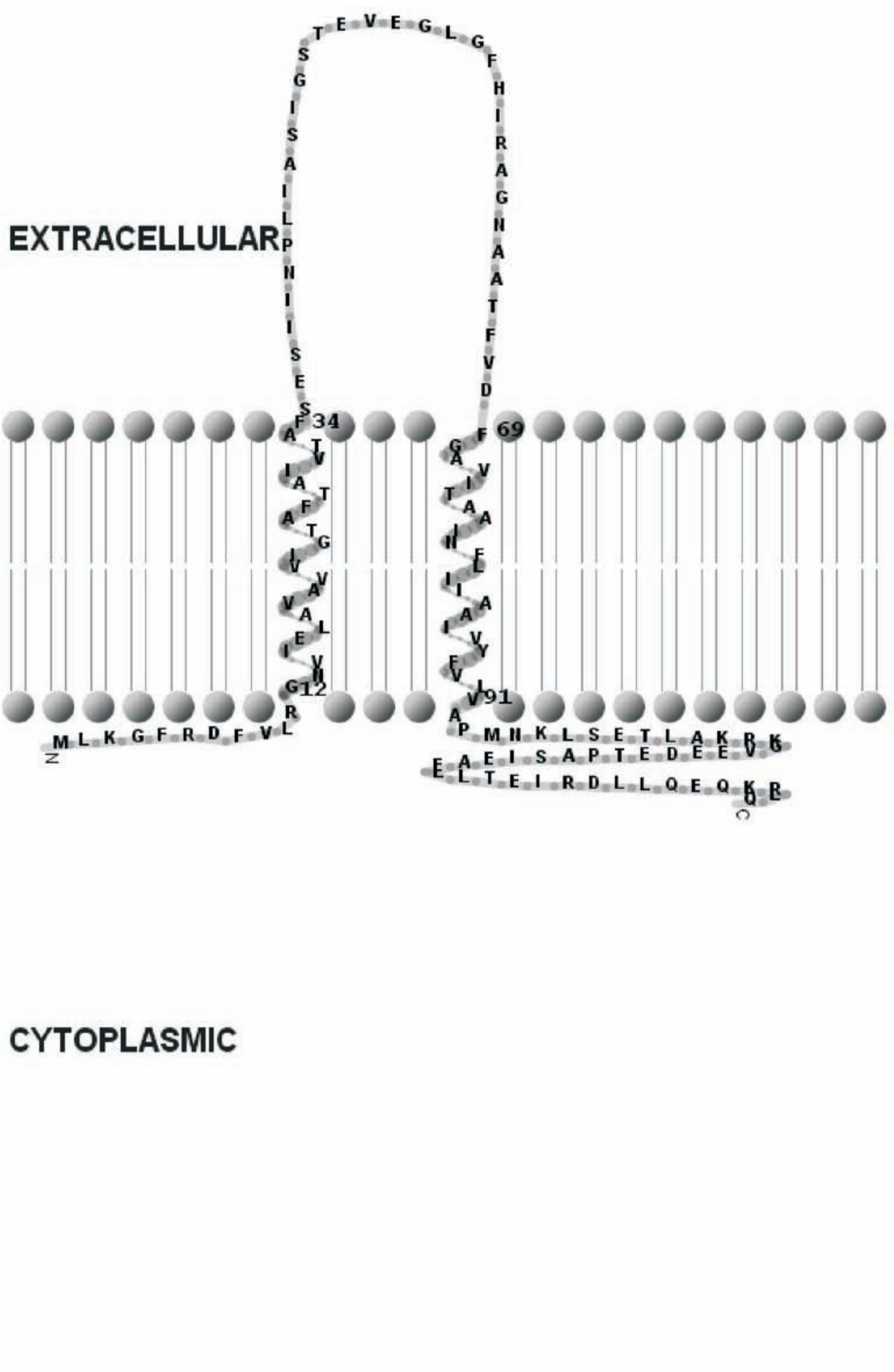
10	20	30	40	50	60
METNPQTPEG	NSMAKPSAKK	VKNRRKVRRT	VAGALALTIG	LSGAGILATA	ITPDAQVATA
70	80	90	100	110	120
QRDDQALISE	GKDLYDVACI	TCHGVNLQGV	EDRGPSLVGV	GEGAVYFQVH	SGRMPILRNE
130	140	150	160	170	180
AQAERKAPRY	TEAQTLAIAA	YVAA**NGGGPG**	**LVYNEDGTLA**	**MEELRGENYD**	**GQIT**SADVAR
190	200	210	220	230	240
GGDLFRLNCA	SCHNFTGRGG	ALS**SGKYAPN**	**LDAANEQEIY**	**QAMLTGPQNM**	**PKFS**DRQLSA
250	260	270	280	290	300
DEKKDIIAFI	KSTKETPSPG	GYSLGSLGPV	AEGLFMWVFG	ILVLVAAAMW	IGSRS



Cg1001 LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL

MALDI 2TMH 14.5 kDa 6 Arg 5 Lys

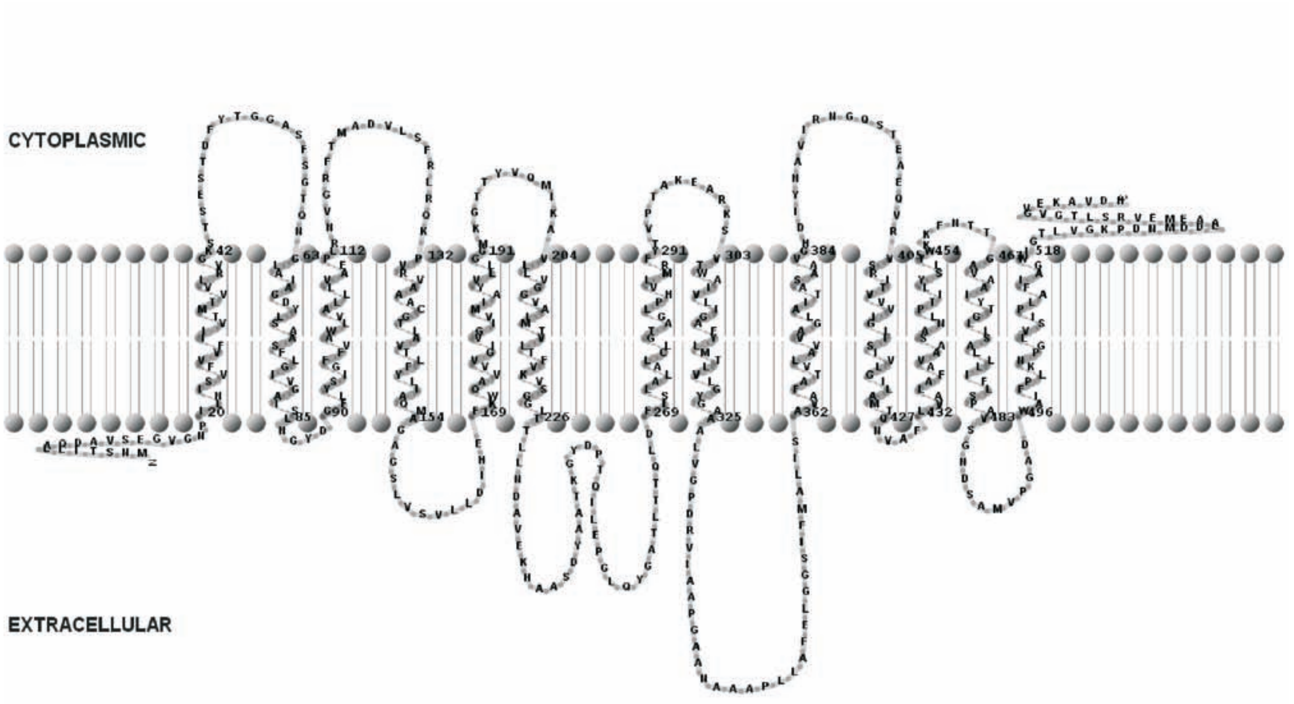
10	20	30	40	50	60
MLKG**FRDFVL**	**RG**NVIELAVA	VVIGTAFTAI	VTAFSESIIN	PLIA**SIGSTE**	**VEGLGFHI**RA
70	80	90	100	110	120
GNAATFVDFG	AVITAAINFL	IIAAIVYFVL	VAPMNKLSET	LAKRKGVEED	ETPA**SIEAEL**
130	140				
LTEIRDLLQE	**QKRLQ**				



Cg0953 Na+/PROLINE, Na+/PANTOTHENATE SYMPORTER

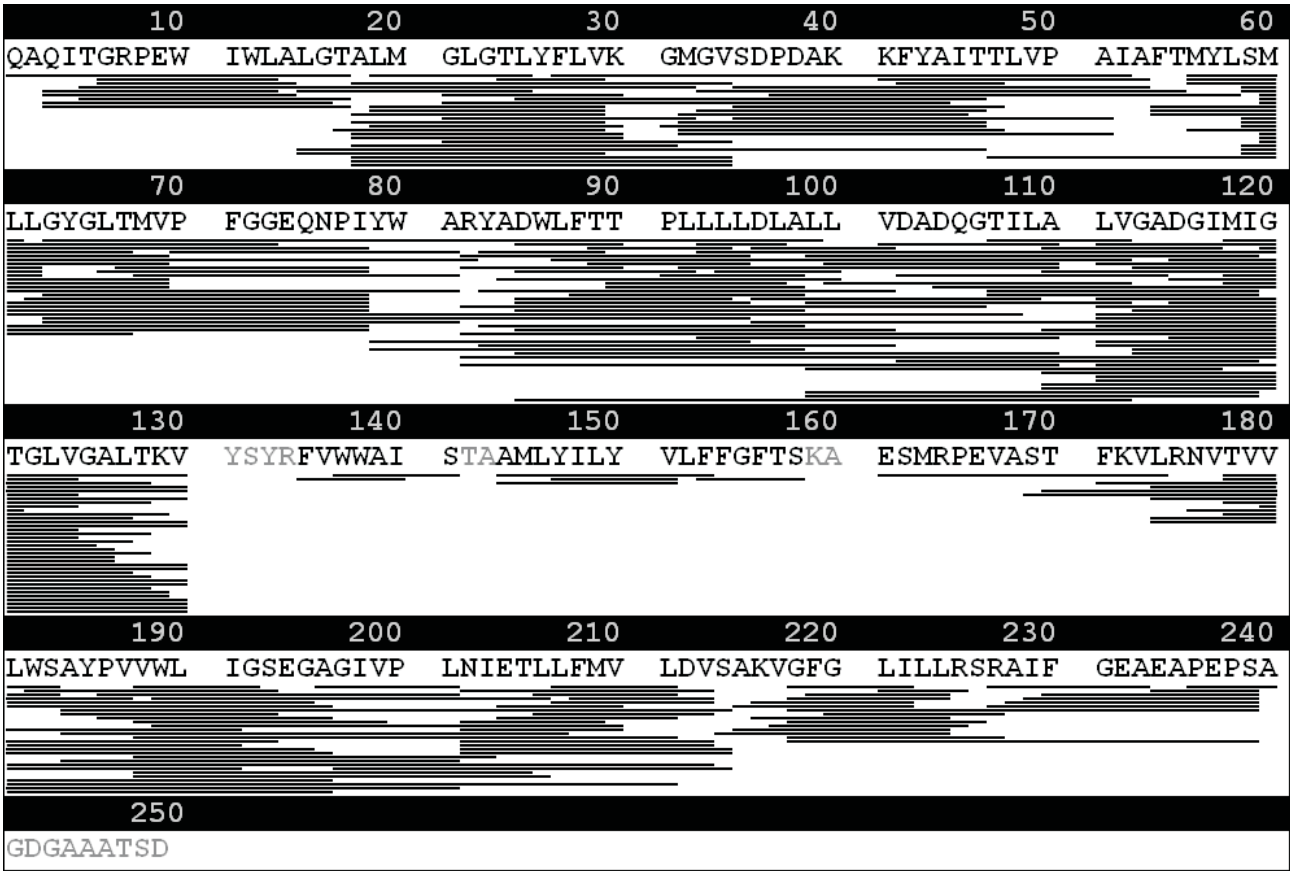
MALDI 13TMH 57.2 kDa 13 Arg 15 Lys

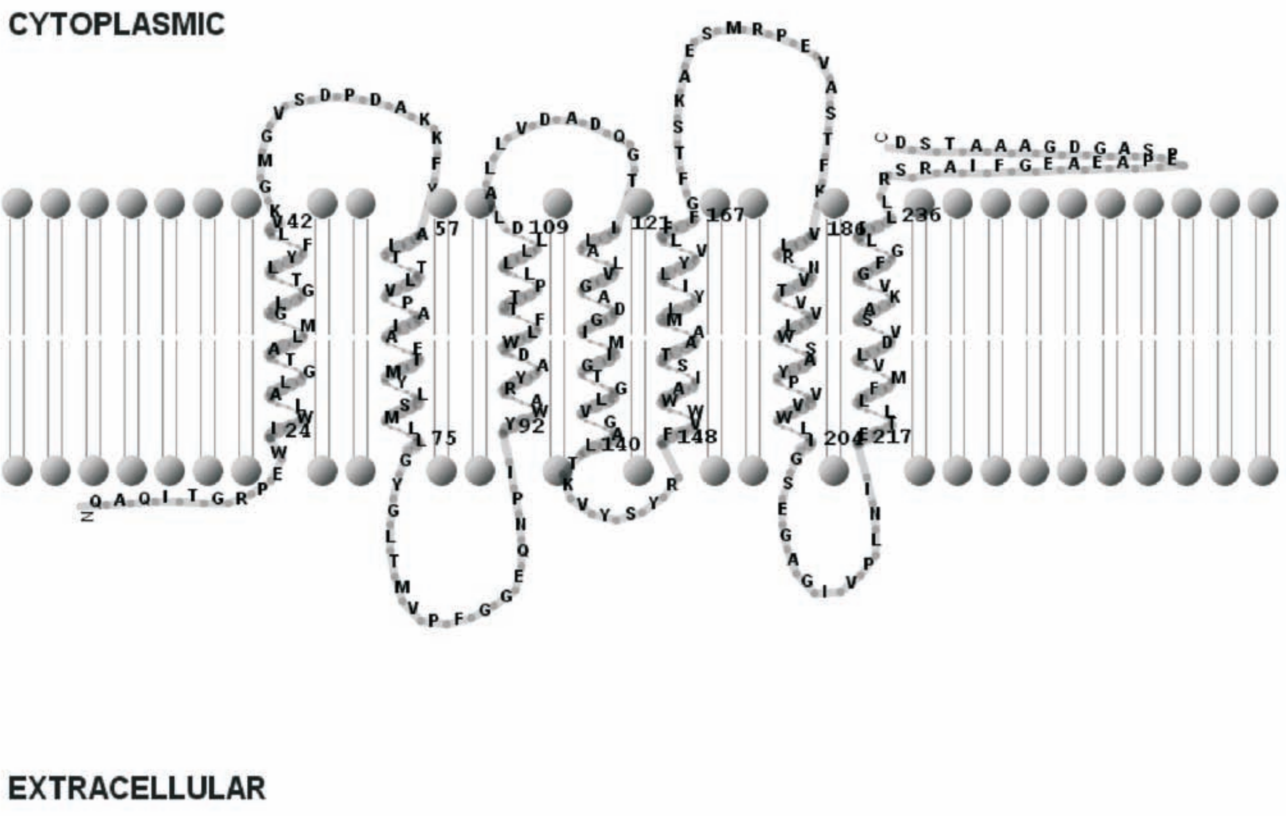
10	20	30	40	50	60
MNSTILLAQD	AVSEGVGNPI	LNISVFVVFI	IVTMTVVLRV	GKSTSESTDF	YTGGASFSGT
70	80	90	100	110	120
QNGLAIAGDY	LSAASFLGIV	GAISLNGYDG	FLYSIGFFVA	WLVALLLVAE	PLRNVGRFTM
130	140	150	160	170	180
A**DVLSFRLRQ**	**KPV**RVAAACG	TLAVTLFYLI	AQMAGAGSLV	SVLLDIHEFK	WQAVVVGIVG
190	200	210	220	230	240
IVMIAYVLLG	GMKGTTYVQM	IKAVLLVGGV	AIMTVLTFVK	VSGGLTTLLN	DAVEKHAASD
250	260	270	280	290	300
YAATKGYDPT	QILEPGLQYG	ATLTTQLDFI	SLALALCLGT	AGLPHVLMRF	YTVPTAKEAR
310	320	330	340	350	360
KSVTWAIVLI	GAFYLMTLVL	GYGAA**ALVGP**	**DRVIAAPG**AA	NAAAPLLAFE	LGGSIFMALI
370	380	390	400	410	420
SAVAFATVLA	VVAGLAITAS	AAVGHDIYNA	VIRNGQSTEA	EQVRVSRITV	VVIGLISIVL
430	440	450	460	470	480
GILAMTQNVA	FLVALAFAVA	A**SANLPTILY**	**SLYWKKFNTT**	GAVAAIYTGL	ISALLLIFLS
490	500	510	520	530	540
PAVSGNDSAM	VPGADWA**IFP**	**LKNPGLV**SIP	LAFIA**GWIGT**	**LVGKPDNMDD**	**LA**AEMEVRSL
550	560				
TGVGVEKAVD	H				



P02945 BACTERIORHODOPSIN

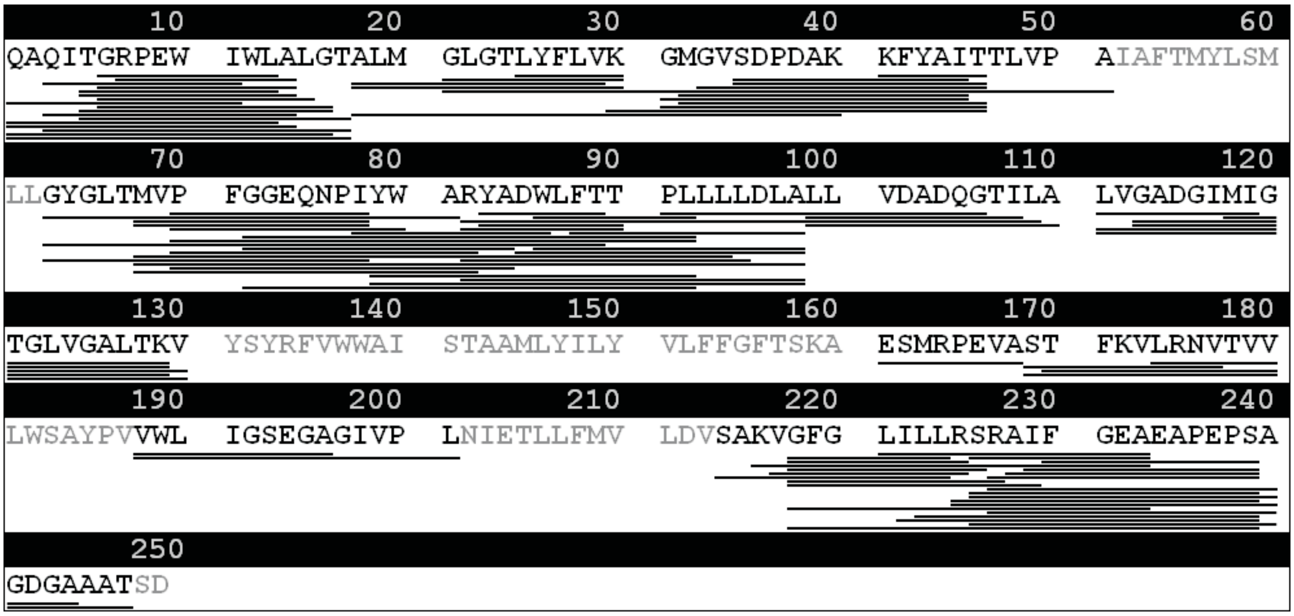
ESI 7TMH 26.8 kDa 7 Arg 7 Lys





P02945 BACTERIORHODOPSIN

MALDI   7TMH   26.8 kDa   7 Arg   7 Lys



```
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QAQITGRPEW IWLALGTALM GLGTLYFLVK GMGVSDPDAK KFYAITTLVP AIAFTMYLSM
        70         80         90        100        110        120
LLGYGLTMVP FGGEQNPIYW ARYADWLFTT PLLLLDLALL VDADQGTILA LVGADGIMIG
       130        140        150        160        170        180
TGLVGALTKV YSYRFVWWAI STAAMLYILY VLFFGFTSKA ESMRPEVAST FKVLRNVTVV
       190        200        210        220        230        240
LWSAYPVVWL IGSEGAGIVP LNIETLLFMV LDVSAKVGFG LILLRSRAIF GEAEAPEPSA
       250
GDGAAATSD
```