Structure of the *Dietzia* Mrp complex reveals molecular mechanism of this giant bacterial sodium-proton pump (Supplementary Material)

Bin Li, Kaiduan Zhang, Yong Nie, Xianping Wang, Yan Zhao, Xuejun C. Zhang, and Xiaolei Wu

Discussions

Why does a Na⁺/H⁺ exchanger need multiple subunits?

The Mrp complex is the most complexed Na⁺/H⁺ exchanger known to date (1-3). In this PMF-driven secondary active transporter, protons constitute the driving substance, with sodium ions representing the substrate. Therefore, the energy released by proton transport must be large enough to compensate the free-energy gain by Na⁺. The more protons are transported, the faster the transporter may work. This antiport activity enables the host cell to tolerate high salt concentration in its environment (4). In certain alkaliphilic bacteria, the Mrp complex is also responsible for proton uptake (5, 6), and thus the electrostatic component of PMF is the most probable energy source for such transporters (Fig. S9). In this case, a significant portion of the electrostatic energy from the proton transport is used to overcome the steep ΔpH gradient, with the Na⁺ efflux presumably playing an auxiliary role in the functional cycle of the transporter. A previous study showed that in these alkaliphilic bacteria (e.g. B. pseudofirmus OF4), the membrane potential ($\Delta \Psi$) is as strong as negative 180 mV (compared to -135 mV in neutralophilic bacteria such as E. *coli*), which is established mainly by ATP-driven Na⁺ pumps (4). Thus, we

estimate that the stoichiometry ratio of H⁺: Na⁺ must be higher than 4:1 to maintain the transport process in the desired direction (see below). Such a high ratio would be difficult (if not impossible) to achieve with simpler, canonical Na⁺/H⁺ exchangers (*e.g.* NhaA of a 2:1 stoichiometry ratio). Thus, the multi-subunit Mrp represents a thermodynamic solution to such challenge.

How many protons are needed to drive Mrp?

If it is assumed that n protons are required to exchange for one Na⁺ ion, then for alkaliphilic bacteria *B. pseudofirmus* OF4, the environmental pH can reach 10.5 and the cytosol pH is maintained at 8.3, giving a Δ pH of 2.2 (4). To be imported, each proton needs to overcome the energy uphill of 2.3RT Δ pH. In the same process, each proton is driven by electrostatic energy of the membrane potential ($\Delta\Psi$), *i.e.* FV_m (where V_m =| $\Delta\Psi$ |). Similarly, one Na⁺ ion will be exported against a 10-fold concentration gradient (Δ pNa =1) (7) as well as the membrane potential $\Delta\Psi$.

For the Mrp function cycle to proceed in the right direction, the driving energy from the PMF must be larger than the resistance of sodium ions.

 $n (FV_m - 2.3RT \Delta pH) > (FV_m + 2.3RT \Delta pNa)$

Thus,

 $V_m > (2.3RT/F) (2.2n+1)/(n-1)$

where 2.3RT/F \approx 59 mV. For *B. pseudofirmus* OF4, the membrane potential is approx. –180 mV (4). Therefore, the number of protons being imported in order to exchange for a Na⁺ ion must be larger than 4.

In case of alkaliphilic bacteria, the transporter in its C_{out} state must be able to attract protons from the peripheral space with high affinity (*i.e.* high pK_a). In contrast, the transporter must be able to release the protons to the cytosol, which is of relative low pH (higher proton concentration), with low affinity (*i.e.* low pK_a). Therefore, the (final) pK_a value in the C_{in} state is likely to be lower than that in the C_{out} state. The differential binding energy $\Delta G_D(H^+)$ (= $-2.3n RT \Delta pK_a > 0$) must be compensated by the electrostatic energy during the C_{out}-to-C_{in} transition. $\Delta G_D(H^+)$ is a characteristic parameter of the transporter which does not change with the environmental pH (8).

Comparison of DqMrp with AfMrp

During the revision of our manuscript, Steiner and Sazanov reported the structure of Group-I Mrp complex from *Anoxybacillus flavithermus* (AfMrp) (9). The overall structure of AfMrp is similar to our DqMrp complex (Fig. S13), and many of the structural descriptions are the same for both Mrp complexes. A few differences are, however, worth of discussions. First, in contrast to the six subunits in DqMrp, the AfMrp complex contains seven subunits. In particular, the MrpA subunit of DqMrp is separated into MrpA and MrpB in AfMrp. Nevertheless, this difference in primary structures does not cause major reorganization in the 3D structures of the complexes. Therefore, the structures of AfMrp and DqMrp are representatives of Group-I and -II of the Mrp family, respectively.

Secondly, the AfMrp structure was determined in an elongated dimer form, with the MrpE subunit serving as the dimerization interface. Since MrpE of DqMrp lacks of the two N-terminal transmembrane helices (Fig. S13) which are required for the dimerization of AfMrp by using domain-swapping, our DqMrp complex is unable to adapt the same dimer conformation. Therefore, the dimerization is unlikely to be a general requirement for the function of Mrp complexes.

Thirdly, in the AfMrp complex, a highly negatively charged cavity is reported to be located between the MrpA and MrpF subunits, and this cavity is further suggested to be part of the Na⁺-transport path. However, there is no significant cavity observed in corresponding position in our DqMrp complex; in particular, this region lacks of a cluster of acidic residues. Furthermore, results of our NaCl-resistance assay on the mutations at D36^{F2} in DqMrpF (corresponding to D35 in AfMrpF) suggest that the precise location of the only acidic residue in this region, D36^{F2}, is not critical for the transport function (Fig. 4). Therefore, our DqMrp complex seems to use a Na⁺-transport path distinct from the one proposed for AfMrp.

Supplemental Figures

Figure S1. Sequence alignments of individual Mrp subunits from different species and their counterparts in the MBH

Sequence alignments of homologous MrpA proteins: (A) MrpA; (B) MrpD; (C) MrpC; (D) MrpE; (E) MrpG; (F) MrpE. Conserved residues are highlighted in colors, blue for absolute identity and green for those of conserved properties. Secondary structures observed in the *Dietzia* sp. DQ12-45-1b Mrp complex are marked on the top; missing parts are shown as dash lines. The positions of our mutations are marked with circles: red circles represent loss-of-function mutants, and green circles represent wild-type-like mutants. The mutations summarized in Table S2 are marked with triangles: red triangles represent loss-of-function mutants, and green triangles represent wild-type-like mutants. Protein sequence sources are Dq, *Dietzia* sp. DQ12-45-1b; Rm, *Rhizobium* meliloti (strain 1021); Xc, Xanthomonas campestris pv. campestris (strain B100); At, Agrobacterium tumefaciens; Ba, Brucella abortus biovar 1 (strain 9-941); Pa, Pseudomonas aeruginosa (strain ymp); Bs, Bacillus subtilis (strain 168); Bp, Bacillus pseudofirmus OF4; Sa, Staphylococcus aureus; Dh, Desulfitobacterium hafniense (strain Y51); Hz, Halomonas zhaodongensis; Li, listeria innocua atcc 33091; Pf, Pyrococcus furiosus. The sequences were alignment using the Clustal Omega program (10). (G). Mapping of conservation property of the sequence alignment on to the 3D structure of the Mrp complex.

A MrpA

•											
			1	TM 10	1 20	30	TM2	- 0	50		60
<mark>DqMrpA</mark> RmPhaA	MTRPASVLAGPKS	SRPPIHSQGDKT		LALAVAFGI <mark>A</mark> A SVFILVPFA G S	I <mark>SP</mark> L L A R L I AIFFPS.I	TM <mark>G</mark> RDA <mark>GW</mark> P DQ R GAIS WF	LAA <mark>MLGG</mark> L AGA IALV C	<mark>Al</mark> yiwfa Fl vtagl	IPVD YPY V ASC	TVAS GVLHYR	VEWMPALG IDWVPELG
XcPhaA AtPhaA							<mark></mark> . Aga <mark>valf</mark> g	 L V ASMFL		Q GALKYD	HA <mark>WLP</mark> QIG VEWLPQLG
BaMnhA PaMrpA			4TMDGR <mark>I</mark> L ML	FLLVLLPFL <mark>G</mark> S YLLSLIALA A V	AITGLFRR.A SAPALTR.I	AD <mark>R</mark> SGS <mark>AWF</mark> LLGART GW L	TAA <mark>IALV</mark> A LMLA PLV A	FVATASI FIWFVQQ	YPIVSGC IPLVAGC	KILHGT ETVLQS	LEWLPAYG LSWIPALG
BsMrpA BpMrpA SaMnhA		••••	MQLLH MTVLH MSLLH	WATISPFLFAF WATISPFLLAI	LIPFLAK.YA LIPFLYK.YA TIPTLYR FI	AKRVHTGWF AR <mark>R</mark> IHT <mark>GWF</mark> FK R THL GWF	VLILPVLL VLVLPLV VLS VPIV I	FIYFIQY FIYMLTL		ETLRSV GVVEHT NTVMKT	LEWIPSLG IP <mark>WVP</mark> SLG LNWMPHFG
DhMrpA HzMrpA			MVW L Y	LILGIPFLF <mark>A</mark> F LAVLMGFVL A A	LVPVLHKRF SSPLLNRV	TP R IHT GWF WFGHRASFV	VVW <mark>IPL</mark> I LALF P ALI	FGILLST AAWLVSO	VPTISS APSVFSD	GIIDLS	LPWIPAYD WOWVPSLG
LiMrpA		•••••	<mark>.</mark> .	M <mark>A</mark> L	L IP LFY R. W	TK <mark>Q</mark> VHT <mark>GWL</mark>	VLP <mark>IPVI</mark> L	FIYFLTF	IPK <mark>T</mark> MD <mark>C</mark>	ATIVS.	MPWIPQLG
		тМ3 80	90	100	TM4	120		TM5	140	1!	• TM6
<mark>DqMrpA</mark> RmPhaA	VELRLSLDPLARV LNFTLRMDGFAWI	FTMIVLGIGAVV	/MAYSSRY /ALYARYY	LGR.G <mark>S</mark> G <mark>H</mark> G <mark>GY</mark> MAE.E D PVP RF	YGLMTLFAA: FalflafmG:	SMLGLVLAD SMLGVVLSG	DVVVLFVA NLILAVF	WEFTTLC	SFF <mark>LI</mark> TI SFLLIGY	AGP <mark>K</mark> WHHNAH2	GTQPAVRT ARDGARMA
XcPhaA AtPhaA	LLFSLRMDGLAWN LNFTLRLDGFAWI	IFALLVLAI <mark>G</mark> ALV Failitgigluv	/VM <mark>Y</mark> AHYY /VLY <mark>A</mark> RYY	LSA.RDSASRF MSA.EDPIPRF	FAYLLL <mark>F</mark> MGI FAFLLA <mark>F</mark> MG:	AMLGMVLSG S <mark>MLGVVL</mark> SG	NLLL NVILLSIF	WELTSLS WEMTSIF	SFL <mark>LI</mark> GF SFL <mark>LI</mark> GY	WSH <mark>R</mark> KD2 WHQNAG2	ARE <mark>GAR</mark> MA ARD <mark>GAR</mark> MA
BaMnhA PaMrpA	LNVTLRMDGFAWI INLSLRLDGLSLI	FAMLITGIGLLV FALLISGIGSLI	VVIYARYY IVLYAGSY	MSP.EDPVPRF LSS.HVHLGRF	FSFLLG <mark>FMG</mark> HAYLLV <mark>F</mark> ML	SMLGIVLSG AMLGLVLAD	NIVLLAVF DLVAMFVF	WELTSVF WELTSIA	SFLLIGY	WYHNAS/ QHDKAV	ARDGARMV SRRAALQA
BSMrpA BpMrpA SaMnhA	INFTVFVDGLGLI INFTVFVDGLSLI MNFDLYLDGLGLI	FALLITGIGSL	/ILYSIFY /VLYSIGY	LSKKTESLNNF LSK.SEOLGNF	YVYLLMFMG YCYLLLFMG	AMLGVVLSD AMLGVVLSD	NVNVLIMF NLIVLYVF NVITLYLF	WELTSLS WELTSLA WELTSFS	SFLLIGI SSLLISY SFLLISF	WFHREK	STYGAQKS
DhMrpA HzMrpA	INITLF IDGLSLI ISLTFMLDGLSLI	FGLLIS GVG FLV FGLLITVI <mark>G</mark> ACV	/ILYSIYY /LIYAGGY	LSQHKEÂLHNF LKG.HVDIARF	YIYLLLFMG HLALVAFMV	AMLGVVLSD SMLGLVLAD	NIFALYVF GLITLFVF	WEMTSIS WELTSIT	SFLLIAY SYLLIGF	WFEREK	SRS <mark>GAR</mark> KS ARKS <mark>A</mark> RQG
LiMrpA	INFTVVVDGLSLI	FALLITGIG S <mark>LV</mark>	/TF YS I <mark>YY</mark>	LGKKK <mark>E</mark> RLS NF	YT <mark>FLFIF</mark> MT2	AMLGVVLSD	NLI <mark>VLYF</mark>	WELTSIS	SFL <mark>LI</mark> GY	WYH <mark>R</mark> ER <mark>:</mark>	SRY <mark>GAR</mark> KS
	TM	6 180	1	90 20	o TM7a	10		7b — 230		TM8	
<mark>DqMrpA</mark> RmPha A	LLVTVA <mark>GGLCLL</mark> I LTITGTGGLAMFN	AAALMVVR TGT GLIIIGKIVGS	TVLSEILV CELDAVLA	DPVWSADPAFA SG D AIRNHPLY	AVIA VLIAM GTV LVLVLL	AAFTKSAQF GALTKSAQF	PFQAWLPD PFHFWLPH	AMVAATP AMAA <mark>P</mark> TP	VSAYLHA VSAYLH <mark>S</mark>	AAMVKA ATMVKA	SIYLLLRF SVFLLVRF
XcPhaA AtPhaA	LVL <mark>T</mark> AG <mark>GGLALL</mark> C LTVTGIGGFSLLA	GVL LIG RIVGSI GLLI LG HMAGS	QLDAVLA DLDK II E	.SG D L <mark>I</mark> RASP LY AGAD I RA H S LY	PY ALVLVLL O L PALILIL GO	GIFTKSAQF GALTKSAQF	PF <mark>H</mark> FWLPH PF <mark>H</mark> FWLPN	AMA <mark>AP</mark> TP AMA <mark>AP</mark> TP	VSAYLH <mark>S</mark> VSAYLH <mark>S</mark>	ATMVKA ATMVKA	SVFLLARL SVFLLARF
BaMnhA PaMrpA BaMrpA	LTVTGIGGFCLLA LLITGG <mark>GGLALL</mark> A	AGVLLLGHVVGS AGL <mark>ILLG</mark> GATGNV AGETILVITEDS	CDLDRVLA VQFSSLSA	AGDLVRAHPLY EQIEG. HALL OVOLTACHELE	TVILVLIALA PAIMLLVLL(TRAMILIVLL)	AAFTKSAQF GCFTKSAQV CAFTKSAQV	PFHFWLPN PFHLWLPN DFYTWLPD	AMAAPTP AMNAPTP	VSAYLHS VSAYLHS	ATMVKA ATMVKA ATMVKA	GVFLLARL GIYLLARL
BpMrpA SaMnhA	MLITVFGGFAMLC LIITVFGGLSLLC	GFSLLYVMTGTH GIILLAIPTOSH	SIRG II E SIQYM I O	NVDLVTSSELF HASEIONSPFF	LPAMILVLLO IFAMILIMIO	GAFTKSAQF GAFTKSAQF	PFHIWLPD PFYIWLPD	AMEAPTP AMEAPTP	VSAYLHS VSAYLHS	ATMVKA ATMVKA	GIYLVARL GLYLIARM
DhMrpA HzMrpA	LLITVFGGLAMLA LFVTVAGGLALMA	AGF ILL TMM TG TH AGL VLLG VASGNU	I S IRE <mark>MI</mark> H V SL YE <mark>I</mark> GQ	SL D G <mark>I</mark> HS HALF MESDLRE HALY	L <mark>PAMVLILL</mark> T P MLICLLL	GAF <mark>TKSAQ</mark> F GAF <mark>TKSAQ</mark> F	PFSIWLPD PFHFWLPN	AMEAPTP AMAAPTP	VSAYLH <mark>S</mark> VSAYLH <mark>S</mark>	ATMVKA ATMVKA	SIYLVARL SIYLLARL
LIMTPA	MWIIN LGCTWWT	GFILLHIMSDS	SIRELIS	NADVISNNS	TRAWITATE	GAFTKSAOV	PRHIWIPD	AMEAPTP	VSAYLH	A MVKA(
								_	-		STITVANT
	260	TM9	280	- <u> </u>	M10 300	31	<u>•</u>		320	TM11	
DqMrpA RmPhaA	260 SEALHDVPVWNLI W PVMAG TEAWFWI	TM9 270 LITCGMTTAVL VGLAGLTTLLL	280 AVFAMQR AYFAIFQ	DDLKELLAYST QDLKGLLAYST	M10 300 ISQLGFLVA ISHLGLITV	31 TIGV LLSL	9 GTP GSP	AA LA	320 M <mark>VAAI</mark> IH A <mark>VAAVF</mark> H	TM11	FKSSLFMF FKASLFMA
DqMrpA RmPhaA XcPhaA AtPhaA BaMnbA	260 SEALHDVPVWNL WPVMAGTEAWFW HPALAGTDLFLY WPVLAGTEEWFWI WPVLAGTEEWFW	TM9 270 SIICCMITAVL VGLAGLITILL VISICAITVLL VGVACVITILL GGLGLISLLI	280 SAVFAMQR SAYFAIFQ SAWHAIFQ SAYFAMFQ SSFEAVFO	DDIKELLAYST QDIKGLLAYST RDIKGVLAYST QDIKGLLAYST ODIKGLLAYST	M10 300 ISQLCFLVA ISHLCLITV ISHLCLITM ISHLCLITT ISNLCLITT	31 TICV LLSL LFGL LLSL	9 GTP GSP STP GSP	AA LA LA LA	320 MVAAIIH AVAAVFH VVAGVFH AVAAIFH AVAAIFH	TM11	FKSSLFMF FKSSLFMF FKASLFMA FKASLFMA FKASLFMA
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA PaMrpA BsMrpA	260 SEALHDVPVWNI WPVMAGTEAWFWI HPALAGTDLFLY WPVLAGTEEWFWI NPVLGGSIGWGTI SPIFAFSAQWFWI	TM9 270 IITCGMTTAVL VGLACLTILL VGLACLTILL UGGACLISLIL IGGACLISLIL IFFGAATAVL VSLVCLFTMVW	280 SAVFAMQR SAYFAIFQ SAWHAIFQ SAYFAMFQ SFFAVFQ SFFAVFQ SFFAVKQ	T DDLKELLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST TDLKSLLAYTT TDLKSLLAYTT TDLKSLLAYST	M10 ³⁰ 0 ISQLGFLVA ISHLGLITM ISHLGLITM ISHLGLITV VTVLGQLIV VSQLGMIIS	31 TIGSL LFSL LLSL LLSL LLGT MLGVSAAAL	9 GTP STP GSP GSP MTS HYG	AA LA MA LA LA YG TEYYTVA	320 MVAAIIH AVAAVFH VVAGVFH AVAAIFH LQAFVLY AMAAIFH	TM11 ITIAHALI IIVNHATI IILNHAVI IMVNHATI IMVNHAII ILVAHSLY ILINHATI	FKS SLFMF FKASLFMA FKASLFMA FKASLFMA FKASLFMA FKGSLFMA
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA PaMrpA BsMrpA BpMrpA SaMnhA	260 SEALHDVPVWNLI WPVMAGTEAWFWI HPALAGTDLFLY WPVLAGTPEWFWI NPVLGGSIGWGTI SPIFAFSAQWFWI TPVFAGSAEWFWI TPIFAASQGWWI	TM9 270 VGLACITTLL VGLACITTLL UGSACITTLL GGACISLI LITFCAATAVL VSLVCLFTMVW UTLVGLITLFW	280 SAVFAMQR SAVFAIFQ SAWHAIFQ SAFFAVFQ SAFFAVFQ SAFFAVRQ SSTSAVRQ ASLNATKQ	DDLKELLAYST QDLKGLLAYST HDLKGVLAYST QDLKGLLAYST QDLKGLLAYST TDLKELLAYTT TDLKELLAYTT TDLKSILAFST KDLKGILAFST QDLKGILAFST	M10 soc_ isqlcflva ishlclitv ishlclitv ishlclitv ishlclitv vvclchtv vsclcmiss vsclcmima	31 TIGSL LLSL LLSL LLSL LIGT MLGVSAAAL LLGLGAISY	GTP GSP STP GSP GSP HYG HYG HYQGD		320 MVAAIIH AVAAVFB VVAGVFB AVAAIFB AVAAIFB LQAFVLY AMAAIFB F TAAIFB	TM11 IIIAHALI IIVNHATI IILNHAVI INVNHATI IVNHATI ILINHATI ILINHATI ILINHATI	FKS SLEMF FKA SLEMA FKA SLEMA FKA SLEMA FKA SLEMA FKA SLEMA FKG SLEMA FKG SLEMA FKG SLEMA
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA PaMrpA BsMrpA BsMrpA SaMnhA DhMrpA HzMrpA	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTEAWFW WPVLAGTEEWFW NPVLGGSIGWGT SPIFAFSAQWFW TPVFAGSAEWFWI TPIFAGGGVWWW TPIFAGSQGWWW DPLGGGQVWWW	TM9 270 UITCGMTTAVL VGLACLTILL VGLACLTILL UGACLIILL LGGACLIILL USUVCLTILW VILCCLITLW VTLVCLIILW VTCCLUTLSV USUVCATTLI	280 SAVFAMOR SAVFAIFO SAWHAIFO SAVFAMFO SFFAVFO SFF	DDLKGLLAYST QDLKGLLAYST HDLKGVLAYST QDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST KDLKGLLAFST QDLKGLLAFST QDLKGLLAFST TDLKALLAYST NDLKALLAYST	M10 300 ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITT ISNLGLITV VYQLGNIN VSQLGNINS VSQLGLIMS ISQLGLIMS IMALGTLTMS	31 TIG9 LL5L LL5L LL5L LLG5L LLGLGSAAL LLGLGSAGL LLGLGSAGL LLGLGSAGL LLGLGSAGL LLGUGAAST	GTP. GSP. STP. GSP. GSP. HYG. HYG. HYGGES. HYQGD. HAPEAGNAQ GTD. IFPDT	AA MA YG TEYYTVA PAFYSFA AAAYALA AAAYALA YA	320 MVAAIIH AVAAVFH AVAAIFH AVAAIFH IMAAIFH IFTAIFH TTAIFH MTAFVTF	TM11 IIIAHALI IIINHATI IIINHATI IIVNHAII ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI	FKS SLEMF FKA SLEMA FKA SLEMA FKA SLEMA FKA SLEMA FKG SLEMA FKG SLEMA FKG LEMA FKG LEMA FKG LEMA FKG LEMA
DqMrpA RmPhaA XcPhaA BaMnhA PaMrpA BsMrpA BsMrpA SaMnhA DhMrpA LiMrpA	260 SEALHDVPVWNLI WPVMACTEAWFWI HPALAGTDLFLWFWI WPVLAGTEEWFWI SDIFAFSAQWFWI TPVFAGSAEWFWI TPIFAASQGWWWI OPELGDTALWVCI TPIFASSGVWFWI TPIFASSGVWFWI	TM9 270 WGLACLTILL VGLACLTILL UGGACLIILL GGACLISLI UGGACLISLI UTGCVTLLW VGLYCLFTWW VTGCVTLLW VTGCLVTLW VTGCLVTLW VTGCLVTLW VTGCLVTLW	280 CAVFAMOR SAVFATFQ SAVFATFQ SAYFAMFQ SAFFAVFQ SSFHAVFQ SSFHAVFQ SSFNATRQ SSFNATRQ SSFNATRQ SSFNATRQ SSFNATRQ SSFNATRQ	T DDLKELLAYST DDLKGLLAYST DDLKGLLAYST DDLKGLLAYST TDLKRLLAYST TDLKRLLAYTT TDLKGLLAYST TDLKGLLAFST TDLKGLLAFST TDLKALLAYST TDLKALLAYST NNIKAILAYST	M10 300 ISQLCFLVA ISHLCLITV ISHLCLITV ISHLCLITV ISHLCLITV VYUCQLTM VSQLCMIMS VSQLCLIMS IMALCTLTM ISQLCLIMS	31 IIGSL LLSL LLSL LLSL LIGT MLGVSAAAL LIGLGSAAI MLGIGSAGI LLGLGSAGI LLGLGSAGI LLGLGSAGI LLGUGAASL	9 GSP GSP GSP MTS HYG HYG HYG HYG HYG HYG HYG HYG HYG HYQD HYQA HYQA HFDT		320 MVAAIIH VVAGVFH AVAAIFH LQAFVLY AMAAIFH IMAAIFH IFTALFH IVAAVFH	TM11 ITIAHALI IIVHATI IILNHAVI IILNHAVI ILVHAII ILVHAI ILINHATI ILVHSTI ILAHSMI ILFNHATI	TKSSLFMF TKASLFMA TKASLFMA TKASLFMA TKSLFMA TKGSLFMA TKGSLFMI TKGALFMI TKGALFMU TKGALFMU
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA PaMrpA SaMnhA DhMrpA HzMrpA LiMrpA	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTDLFLY WPVLAGTEEWFW NPVLGSIGWGT SPIFAFSAQWFW TPVFAGSAEWFWI OPELGDTALWVG TPLFGGGVWFW OPELGDTALWVG TPLFASSGVWFW MULT	TM9 270 UTC CMTTAVL VGLACLTTLL VGLACLTTLL UGGACLTTLL LGGACLISLI LTF CAATAVL VSLVCLTTLW VTLVCLITLW VTLVCLITLW VTCCLVTLSV LSVVCATTMIT VSLVCITTLW	280 SAVFAMOR SAYFATFO SAWHAIFO SAWFAWFO SFFAVFO SFFAVFO SSFAVKO SSFNAVKO SSFNATKO SAFLATKK SSFNATRO SAFLATKK TM12	TDLKGLLAYST QDLKGLLAYST HDLKGVLAYST QDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST KDLKGILAFST KDLKGILAFST TDLKALLAYST NNLKAILAYST NDLKAILAYST 20 370 3	M10 300 ISQLGFLVA ISPLGLITV ISPLGLITV ISPLGLITV VSQLGLITV VSQLGLIMIS VSQLGLIMS IMALGTLTM ISQLGLIMS TM12	31 TIG9 LL5L LL5L LL5L LLG5L LLGLGSAAL LLGLGSAGL LLGLGSAGL LUG GAASL VG1 LLGUGAASL VG1 LLGUGAASL VG1 LLGUGAASL	0 GTP STP GSP GSP NTS HYGES.VD HYQGD.D HYQGD.D HFDT.LS 400 C	A A A A A A A A A A A A A A A A A A A	320 MVAAIIH AVAAVFH VAGVFH AVAAIFH LQAFVLY AMAAIFH IMAAIFH ITALFH MTAFVTF IVAAVFH TM 410	TM11 TIAHALI IIVNHATI IIVNHATI IIVNHATI IIVNHATI IIINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILAHSMI ILFNHATI 13	KISSLEM KASLEMA KASLEMA KASLEMA KASLEMA KGSLEMA KGSLEMT KGSLEMV KGSLEMV KGSLEMV KGSLEMV KGSLEMV
Domrpa RmPhaA XcPhaA AtPhaA BaMnpA BaMrpA BaMrpA BaMrpA LiMrpA LiMrpA DomrpA RmPhaA XcPhaA	260 SEALHDVPVWNII HPALAGTEAWFWI HPALAGTDLFLYT WPVLAGTEEWFWI NPVLGGISWGTI SDFAFSAQWFWI TPIFAASQGWVWI OPELGOTALWCG TPLFASSGVWFWI OPELGOTALWCG TPLFASSGVWFWI CVVDHQTGTRAM AGIIDHESGTRDI	TM9 270 IIIC CMTTAVL VGLACLITLUL VGLACLITLUL VGVACVITLLU VSLVCLISLI IIICGATAVL VSLVCLFTMVW VTLVCLTLW VTLVCLTLW VSLVCLTLW VSLVCATTMUT VSLVCATTMUT SS0 360 ISGLPRLMRIMP RREGGLHMRMP	280 SAVFAMOR SAVFAIFO SAVFAMFO SAFLAFRO SSFHAVKO SSFHAVKO SSFHAVKO SSFHAVKO SSFNAIRO SSFNAIRO SAFLAIH TM12 STAIGVGL TTALLAT	T DDLKELLAYST ODLKGLLAYST HDLKGVLAYST ODLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAFST TDLKALLAYST NIKKLLAYST NIKKLLAYST NIKAILAYST AAASMAGLPPL ASLAMAGLPLL ASLAMAGLPLL	M10 ³⁰ 9 ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV ISNLGLITV ISQLGLIT VSQLGMIA ISQLGLIMS IMALGTLMS IMALGLIMS IMALGLIMS IMALGLIMS IMALGLIMS IMALGLIMS IMALGLIMS IMALSE IMALSE	JIGM LLSL LFSL LLSL LLSL LLGT MLGVSAAAL LLGUSAAAL LLGUSAAAL LLGUSAASL VGI LLGVGAASL COMPANIENTE PAVALEAEG	0 GTP GSP GSP MTS HYG HYG HYG HYG HYG GTD HFDT GAWAG VNPLD		320 MVAAIIH VAQVFH AVAAIFH LQAFVLY AMAAIFH IMAAIFH ITALFH IVAAVFH LVAAVFH LAVFAAT VAIJAGT	TM11 ITIAHALI IIVNHATI IIVNHATI ILVNHATI ILVNHATI ILINHATI ILINHATI ILFNHATI ILAHSMI IFTFAYSA IFTFAYSA IFAVYYSI	TKSSLFMF TKASLFMA TKASLFMA TKASLFMA TKGSLFMT TKGSLFMT TKGSLFMT TKGALFMU TKGALFMU TKGALFMU TKGALFMU TKGSLFMU TKGSLFMU
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA PaMrpA SaMnhA DhMrpA HzMrpA LiMrpA LiMrpA RmPhaA XcPhaA AtPhaA	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTDLFLY WPVLAGTEWFWN NPVLGSIGWGT TPVFAGSAEWFWN TPIFAGSQWFWT OPELGDTALWVGT TPLFASSGVWFWT OPELGDTALWVGT TPLFASSGVWFWT CHLFASSGVWFWT TPLFASSGVWFWT	TM9 270 WGLAGLTTLLL VGLAGLTTLLL VGLAGLTTLLL UGACLTILL LGGACLISLI LTFCAATAVL VSLVGLTTLLW VSLVGLTTLFW VTLVCLITLFW VTCGCLVTLSV TSVGATTMIT VSLVGATTMIT VSLVGATTMIT SSVGATTMIT VSLVGATTMIT RLGGEHEMP IRKLGNLRRLMP IRKLSGLYTMP	280 SAVFAMOR SAYFATFO SAWFAMFO SAFAVFO SFRAVKO SFRAVKO SFRAVKO SFRAVKO SFRAVKO SFRATKO SFRATKO SFRATKO SFRATKO SFRATCA SFRA	DDLKELLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST TDLKRLLAYST TDLKRLLAYST TDLKGILAFST KDLKGILAFST KDLKGILAFST TDLKALLAYST NDLKAILAYST 23 370 3 AAASMAGLPPL ASAAMAGVPLF ASAAMAGVPLF	M10 300 ISQLGFLVA ISALGLITV ISALGLITV ISALGLITV VSQLGHITV VSQLGHIMIS VSQLGLIMS ISQLGLIMS IMALGTLTM ISQLGLIMS CFLSKEMFI NGFLSKEMFI NGFLSKEMFI	31 TIGSL LFSL LLSL LLSL LLG.CSAAL LLGLGSAAL LLGLGSAGL LLGLGSAGL LGGLSAGL LGGLSAGL CGASA CGAS	0 GTP STP GSP GSP GSP HYGES.VD HYQGD.D HYQGD.D HYQGD.D GTD GTD GTD GTD GTD GTD GTD GTD GTD GTD GTD GTD GTD GTD USD COMPACTION COM		320 MVAAIIH AVAAVFH VAAVFH AVAAIFH AVAAIFH IMAAIFH ITAAIFH ITALFH MTAFVTF IVAAVFH LAVFAAT VATIACM AALMAGI VATLSGA VATLSGA	TM11 TIAHALI IIVNHATI IIVNHATI IIVNHATI IIVNHATI ILINHATI	KS SLFM KASLFMA KASLFMA KASLFMA KGSLFMA KGSLFMT KGSLFMT KGSLFMV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGSLFV KGV KGSLFV KGV KGV KGV KGV KGV KGV KGV KGV KGV KKV KK
Domrpa RmPhaa XcPhaa AtPhaa BaMrpa BoMrpa BoMrpa LiMrpa LiMrpa LiMrpa Domrpa RmPhaa XcPhaa BaMnha BaMnha BaMnha BaMnha	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTPEWFWI WPVLAGTEWFWI SPIFAFSAQWFWI TPIFASAQWFWI TPIFASQGWVWI QPELGDTALWVGI TPLFASSGWFWI QPELGDTALWVGI TPLFASSGVFFWI CVDHQTGTRAN AGIIDHETGTRDN AGIIDHETGTRDN AGIIDHETGTRDN GCIDHETGTRDN	TM9 270 ITCGMTTAVL VGLACLTTLLL VGLACLTTLLL USSGATVLC VSVGITTLL IGGACLISLI ITGGATAVL VSLVGLTTLW VILVGLTTLW VILVGLTTLW VSLVGATTLF SS0 350 360 BGLPRLMRIMP RRLGCLHRMP RRLSGLKRMP RRLSGLKRMP RRLSGLKRMP RRLSGLKRMP RRLSGLKRMP RRLSGLKRMP	280 SAVFAMOR SAYFAIFO SAYFAMFQ SSFFAVFQ SSFFAVFQ SSFFAVFQ SSFAVKQ SSFNAIRQ SSFNAIRQ SSFNAIRQ SSFNAIRQ SSFNAIRQ SSFNAIRQ SAFLAIHH MILLAIGUGL TTAIGVGL TTAIGVGL TTAIGVGL TTAILAMA (TATLAMA (TATLAMA (TATLAMA (TATLAMA (TATLAMA	T DDLKELLAYST QDLKGLLAYST HDLKGVLAYST QDLKGLLAYST TDLKRLLAYTT TDLKSLLAFST TDLKGLLAYST TDLKGLLAFST QDLKGLAFST QDLKGLAFST QDLKGLAFST AAASMAGLAFT ASAAMAGVPLL ASAAMAGVPLLASAAMAGVPLL ASAAMAGVPLST AAASMAGLPPT GTFSMAGLPPT GTFSMAGLPPT	M10 ³⁰ 9 ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV ISHLGLITV VSQLGMIIS VSQLGMIS VSQLGLIMS ISQLGLIMS ISQLGLIMS IGFVSKEWMI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI	31 LL SL LF SL LL SL SL SL SL SL SL SL SL SL SL SL SL	9 GTP GSP GSP GSP MTS NTS NTS APEAGNAQ GTD HFDT GAWAG VNPLD PQLLR DSLLD VSWLD FDLFNVQT		320 MVAAIIH AVAAVFH VAAVFH AVAAIFH IMAAIFH ITAAIFH IFTAIFH MTAFVTFH IVAVFH LAVFAAT VATIAGM AALMAGI AALMAGI VATLAGM AALMAGI VATLAGM	TM11 ITIAHALI IIVNHATI IILNHAVI IILNHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI ILINHATI IFTFAYSI IFAVAYSI IFAVAYSI IFAVAYSI IFTYAYSU	PKSSLFMF RASLFMA KASLFMA KASLFMA KKGLFMA KGSLFMT FKGSLFMT FKGSLFMT FKGSLFMY KGALFMV KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA BaMnpA BaMnpA SaMnhA DhMrpA LiMrpA LiMrpA AtPhaA XcPhaA AtPhaA BaMnhA PaMrpA SaMnhA	260 SEALHDVPVWNI WPVMAGTEAWFW HPALAGTDLFLY WPVLAGTEWFWN NPVLGSIGWGT TPVFAGSAEWFWI TPIFAGSQWFWT OPELGDTALWVGT TPLFASSGVWFWT CUDHESGTRDD AGIDHETGTRDD AGIDHETGTRDD AGIDHETGTRDT AGIDHETGT AGIDHETGT AGIDHETGT AGIDHETGT AGIDHETGT AGIDHETGT	TM9 270 WGLAGLTTLLL WGLAGLTTLLL UGACLTTLLL LGGACLISLLI LIFEGAATAVL VSLVGLFTMVW VTLVCLITLW VTLVCLITLW VTLVCLITLW VTSVGATTMIT VSLVGATTMIT SUVGATTMIT SUVGATTMIT RLGGLFHMP IRRLSGLVTVP IRRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLKMP RRLSGLMATMP RRLSGLMATMP RRLSGLMATMP RRLSGLMATMP	280 SAVFAMQR SAYFATFQ SAYFAMFQ ASFFAVFQ SSFFAVKQ SSFNAVKQ SSFNAVKQ SSFNATKQ SSFNATKQ SAFLAFK TM12 SSFNATRQ SAFLATKK TM12 STAIGVGL TATLAMV TTALAMV TTALAMV TTALAMV TTFTISLI VTFTVSLI USFTITVLA	DDLKELLAYST QDLKGLLAYST QDLKGLLAYST PDLKGLLAYST DDLKGLLAYST TDLKCLLAYST TDLKCLLAYST TDLKCLLAYST TDLKGLLAFST KDLKGLLAFST TDLKALLAYST TNIKKLLAYST NDLKAILAYST 370 3 AAASMAGLPPL ASAAMAGVPLL ASAAMAGVPLF ASAAMAGVPLF GLASMAGLPPF GLASMAGLPPF GLASMAGLPPF	M10 300 ISQLGFLVA ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV VSQLGMINS VSQLGLIMT VSQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM FISKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI	31 TIGSL LLSL LLSL LLSL LLGSL LLGSL LLGSL LLGSL LLGSL LLGSL LLGLGSAGL LLGLGSAGL LVGT LLGVGAASL PG FKSMLDAPG FASALEFTHL SACATETHL SACATETHL YALBARG YSTALLARTE LETTTTAS FTAVLNAGE	0 GTP GSP GSP GSP NTS YFGES.VD HYQGD.D HYQGD.D HYQGD.D GTD GTD GTD GAWAG VNPLLR DSLLD SLLD SLLD IG FDLFN.VET MNAFNMET ANLFSVDT		320 MVAAIIH AVAAVFH AVAAVFH AVAAIFH IVAAIFH IMAAIFH ITAAIFH ITALFH MTAFVTF IVAAVFH UATIACH AALMAGI VATIACH AALMAGI VATIACH AALMAGI VATIACH AALMAGI VATIACH AALMAGI VATIACH VATIACH VATIACH VATIACH VATIACH VATIACH VATIACH VATIACH VATIACH VATIACH	TM11 TIAHALI IIVNHATI IIVNHATI IIVNHATI ILVNHATI ILINHATI ILINHATI ILINHATI ILINHATI ILAHSM ILFNHATI IS FTFAYSJ FAVYSJ IGVAYSJ FTVAYSY ILFAAS FTVAYSY ILFFAYSJ FTFLYSJ	KSSLFMF KASLFMA KASLFMA KASLFMA KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KFI KFIHTVF KFIHTVF KFIHTVF KFIHTVF KFIHTVF KFIHTVF
Domrpa RmPhaa XcPhaa AtPhaa BaMnpa BaMnpa SaMnha DhMnpa LiMnpa LiMnpa RmPhaa XcPhaa BaMnpa BaMnpa BaMnpa BaMnpa BaMnpa BaMnpa LiMnpa	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTPEWFWI WPVLAGTPEWFWI SPIFAFSAQWFWI TPIFASQGWVWI CELGDTALWVGI TPLFASSGWFWI DELGDTALWVGI TPLFASSGVWFWI CELGDTALWVGI CUDHOTGTRAN AGIIDHESGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD	TM9 270 TGLCCTTLUL UGLACLTTLUL UGLACLTTLUL UGLACLTTLUL UGVACVITLLL UGCACLISLI LIFCAATAVL VSLVGLTTNWI VTLVGLTTLWI VTLVGLTTLWI VTLVGLTTLWI VTGGCLVTLSY LSVVGATTNLT USLVGATTNLT	280 SAVFAMOR SAYFAMFQ SAYFAMFQ SAFLAFRQ SSFHAVKQ SSFHAVKQ SSFNAIRQ S	DDLKELLAYST QDLKGLLAYST HDLKGVLAYST QDLKGLLAYST DDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAFST QDLKGLLAFST QDLKGLLAFST DDLKALLAYST TDLKALLAYST NDLKALLAYST NDLKALLAYST NDLKALLAYST AAASMAGUPPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL GTFAMAGUPPF GLASMAGUPPF GLASMAGUPPF GLASMAGUPPF GTFSMAGUPPF GTFSMAGUPPF GTFSMAGUPPF GTFAMAGUPPF GTFAMAGUPPF	M10 ³⁰ 9 ³⁰ 9 ISPLGLITA ISPLGLITA ISPLGLITA ISPLGLITA ISPLGLITA ISPLGLITA ISPLGLIMS IMALGT	31 LL	Q GTP GSP GSP GSP GSP MTS NTS NTS MAPEAGNAQ GTD HFDTLS 400 GAWAG VNPLD PQLR DSLLD VSWLD FDLFNVQT MNAFFNMET IS FR QLFDAST		320 MVAAIIH AVAAVFH VAAVAVFH VAAVAIFH AVAAIFH IMTAAIFH IFTALFH MTAFVTFH VATLSCA VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM VATLACM	TM11 IIINHATI	PKS S LFMF FKA S LFMA FKG S LFMT FKG S LFMY FK S LFMY FK FK TF FK THY S TF FK L LFX TF L I M FK TF I I A LFY F I I F FK TF
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA BaMnpA SaMnpA HzMrpA LiMrpA LiMrpA AtPhaA XcPhaA AtPhaA XcPhaA AtPhaA AtPhaA AtPhaA AtPhaA AtPhaA AtPhaA AtPhaA AtPhaA AtPhaA AtPhaA	260 SEALHDVPVWNI WPVAGTEAWFWI HPALAGTDLFLWFWI WPVLAGTPEWFWI SPIFAFSAQWFWI TPIFAGGGVWFWI OPELGOTALWVGI TPLFASQGWVWT TPIFAGGGVWFWI OPELGDTALWVGI TDLFASSGWFWI CIDHETGTRDJ AGIIDHETGTRDJ AGIIDHETGTRDJ CAIDHATGTRDJ CAIDHATGTRDJ CAIDHATGTRDJ CAIDHATGTRDJ CAIDHATGTRDJ AGIIDHETGTRDJ AGIIDHETGTRDJ AGIIDHETGTRDJ AGIIDHETGTRDJ AGIIDHETGTRDJ AGIIDHETGTRDJ	TM9 270 WGLAGLTTLLU VTSICAITILLU VTSICAITILLU UGGACLISLU LGGACLISLU LIGGACLISLU ITFCAATAVLO VSIVCLTTLW VTLVCLITLW VTLVCLITLW VTLVCLITLW VTGICLVTLSV ISVVGATTMIT VSIVGATTMIT VSLVGATTMIT WSLVGITTLW RRLGCLRHMP RRLGCLRHMP RRLGCLRAMP RRLGCLRAMP RRLGCLRAMP RRLGCLRAMP RRLGCLRAMP RKLGCLMAIMP TAMGGLRGMP TRLGGLRMMP	280 SAVFAMQR SAYFATFQ SAYFAFQ SAFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFATFQ SFFATFQ SFFATFQ SFFATFQ SFFATFQ SFTATGVGL SFTATGVGL SFTITVI SFTITVI SFTITVI SFTITVI SFTITVI SFTITVI SFTITATIAFY CTATIAFI	DDLKELLAYST QDLKGLLAYST QDLKGLLAYST HDLKGVLAYST QDLKGLLAYST TDLKRLLAYST TDLKCLLAYST TDLKCLLAYST TDLKCLLAYST TDLKGLLAFST TDLKALLAYST TNIKKLLAYST NDLKAILAYST 370 3 AAASMAGLPPL ASAAMAGVPLL ASAAMAGVPLF ASAAMAGVPLF GLSMAGLPPF GLSMAGLPPF GLSMAGLPPF GLSMAGLPPF ALSLAGVPPL GTFAMAGLPPF	M10 300 ISQLGFLVA ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV VSQLGMINS VSQLGLIMS ISQLGLIMS IMALGTLTM IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM I	31 TIGSL LLSL LLSL LLSL LLGT LLGLGSAAL LLGLGSAAL LLGLGSAGL LLGLGSAGL LLGLGSAGL LGGT LGGVGAASL PAEALETHL P	0 GTP GSP GSP GSP GSP GSP GSP GSP GSP GSP GSP GSP GSP GSP GGNAG GTD GGNAG GTD GGNAG GTD GGNAG GTD SLLD		320 MVAAIIH AVAAVFH VAGVFH AVAAIFH INAAIFH ITAAIFH ITAIFH MTAFVTF IVAAVFH VATIACH	TM11 TIAHALI IIVHATI IIVHATI IIVHATI IIVHATI ILVHATI ILINHA	KSSLFMF KASLFMA KASLFMA KASLFMA KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KGLFMU KFIHTVF RFIHTVF RFIHTVF KFIHTVF LRFIHTVF LRFIHTVF LRFIHTVF LRFIHTVF
Domrpa RmPhaa XcPhaa AtPhaa BaMnpa BaMnpa BaMnpa LiMnpa LiMnpa LiMnpa RmPhaa XcPhaa AtPhaa BaMnpa BaMnpa BaMnpa LiMnpa LiMnpa LiMnpa	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTPEWFWI NPVLAGTEWFWI SPIFAFSAQWFWI TPVFAGSAEWFWI TPIFASQGWVWI QELGDTALWVGI TPLFASSGVWFWI CELGDTALWVGI TPLFASSGVWFWI CELGDTALWVGI CUDHETGTRDD AGIIDHETGTRD AGIIDHETGTRD AGIIDHETGTRD AGIIDHETGTRDD AGIIDHETGTRD AGIIDHETGTR	TM9 270 1 TC GMTTAVL VGLACLTTLLL VGLACLTTLLL VGLACLTTLLL USLVGITTLL 1 GGCLISLLI 1 TFCAATAVL VSLVGLFTMWN VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW SSQ 1 GCD RLVRLMP RRLGGLTHPMP RRLGGLTHPMP RRLGGLTHPMP RRLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP RKLGGLTHPMP	280 SAVFAMOR SAYFAMFQ SAYFAMFQ SSFFAVFQ SSFFAVFQ SSFNAIRQ S	DDLKELLAYST DDLKELLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST TDLKSLLAYST TDLKSLLAYST TDLKSLLAFST QDLKGLLAFST QDLKGLLAFST QDLKGLLAFST QDLKGLLAFST ALX AAASMAGLPF AAASMAGLPFI ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL GTFAMAGLPPF GLSMAGLPPF GLSMAGLPPF GTFAMAGLPPF GTFAMAGLPPF ALSLAGVPFL GTFAMAGLPPF MALSAAVEGLVLG	M10 300 300 ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV VSQLGMIS VSQLGLIMT ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM IGFUSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI NGFLSKEMFI	31 TIG	Q GTP GSP GSP GSP GSP HYG.SH YYGES.VD HAPEAGNAQ GTD HFDTLS GAWAG VNPLD PQLR SULD VSWLD IFD.FNVQT ANLFSVDT SR FR QLFDAST 90 GEGYEA		320 MVAAIIH AVAAVFH VAQVFH AVAAIFH LQAFVLY IMAAIFH ITAAIFH ITAAIFH ITAAFVTF IVAAVFH VATLAFVTF VATLAFVTF VATLAGN VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI VATLAGI FAPELFH	TM11 TIAHLI TIAHLI TINHATI ILINHATI ILVHATI ILVHATI ILINHAT	KSSLFMA KASLFMA KASLFMA KASLFMA KGSLFMT KGSLFMT KGSLFMT KGSLFMT KGSLFMT KGSLFMV KGALFMV KGSLFMV KGALFMV KGALFMV KGSLFMV KGALFV KGALFV K KGALFV K KGALFV K K K K K K K K K K K K K K K K K K K
Domrpa RmPhaa XcPhaa AtPhaa BaMnpa BaMnpa BaMnpa LiMnpa LiMnpa LiMnpa LiMnpa LiMnpa AtPhaa SaMnha BaMnha SaMnha LiMnpa SaMnha LiMnpa SaMnha SAMnha SAMNHA SA	260 SEALHDVPVWNI WPVAGTEAWFWI HPALAGTDLFLWFWI NPVLAGTPEWFWI NPVLAGTEWFWI TPFAGSIGWGTI SIFAFSAQWFWI TPIFASQGWWWI OPELGDTALWCG VGVVDHQTGTRAN AGIIDHETGTRON AGIIDHETGTRON AGIIDHETGTRON CAI	TM9 270 TITCCMTTAVL VGLAGLTTLLL VGLAGLTTLLL VGLAGLTTLLL USSUGUTTLLU SSUGUTTLLU SSUGUTTLL	280 SAVFAMOR SAVFAMOR SAYFAMFQ SAYFAMFQ SSFHAVKQ SSFHAVKQ SSFHAVKQ SSFHAVKQ SSFHAVKQ SSFHAVKQ SSFNAIRQ SAFLAIHH SSINAIKQ TATIGVGL TATIANY TTAIANY TTAIANY TTAIANY TTAIANY TTAIANY TTAIANY TTAIANY TATIANY SFTIVI SFTIVI SFTIALI SFTIALI SFTIALI SFTIACI SFTVIC CVUVICCY	DDLKCLLAYST QDLKGLLAYST QDLKGLLAYST HDLKGVLAYST DDLKGLLAYST TDLKSLLAYST TDLKSLLAYST TDLKSLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST NLKGLLAYST NLKGLLAYST NLKGLLAYST NLKGLLAYST ASAMAGLPPL ASAMAGLPLL ASAAMAGVPLL ASAAMAGVPLF ASAAMAGVPLF ASAAMAGVPLF GLASMAGLPPF GLASMAGLPPF GLASMAGLPPF GLASMAGLPPF GLASMAGLPPF GLASMAGLPPF ALSAGVPFI GTFAMAGLPFF ALSAGVPFI GTFAMAGLPFF ALSAGVPFI GTFAMAGLPFF ALSAGVPFI GTFAMAGLPFF	M10 300 300 300 SCLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV ISHLGLITV ISHLGLITV ISHLGLITV ISLGLIT SQLGLIM SQLG SQLM SQL	TIGV ILGSI LLSI LLSI LLSI LLGSI LLGSI LLGSI LLG.LGSAAI LLGLGSAAI LLGLGSAGI LGGLGSAGI LGGLGASAGI VGAAARASI FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL FAEAIETHL SISSAIL CONSTRUCTION CONSTR	0 GTP GSP STP GSP NTS YFGES.VD HYQGD YFGES.VD HYQGD GTD GTD GTD GTD GAWAG VNPLLD PQLLR SLLD SLLD SLLD TG FR LQLFDAST 90 GEG.YEA P DYEN STR		320 AVAAIIH AVAAIFH AVAAIFH I AVAIIFH I TAAIFH I TAAIFH I TAIFH MTAFVTF I VAAVFAIFH AVAIIAIFH TAFVTF I VAAVFH VATIACH AALFACH AALFACH VATIACH AALMAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH AALTAGI VATIACH VATIAC	TM11 TIAHALI IIVNHATI IIVNHATI ILVNHATI ILVNHATI ILINHATI I	KSSLFMF KASLFMA KASLFMA KASLFMA KGSLFMA KGSLFMT KGSLFMT KGSLFMV KGSLFMV KGSLFMV KGSLFMV KGSLFMV KGSLFMV KGSLFMV KGSLFMV KGLFMV KGSLFMV KGLFMV KGSLFMV KS KS KS KS KS K
Domesia Randowski Domesia Bastripa Bastripa Bastripa Bastripa Bastripa Bastripa Bastripa LiMripa LiMripa Randria Bastrip	260 SEALHDVPVWNI HPALAGTDLFLY WPVLAGTPEWFWI NPVLAGTEWFWI NPVLGTEWFWI TPVFAGSIGWGTU TPFFASAQWFWI TPFFGGGVWFWI OPLGDTALWVG TPLFASSGVWFWI OPLGDTALWVG TPLFASSGVWFWI CPLGDTALWVG TPLFASSGVWFWI CPLGDTALWVG TPLFASSGVWFWI CPLGDTALWVG TPLFASSGVWFWI CPLGDTALWVG CVVDHOTGTRAN AGIIDHETGTRDI AGIIDHETGTRDI AGIIDHETGTRDI CAUDHSTGTRDI AGIIDHETGTRDI CAUDHSTGTRDI COUCHSTGT	TM9 270 1 TC GMTTAVL VGLACLTTLLL VGLACLTTLLL VGLACLTTLLL USLVGLTTLL 1 GG GLISLLI 1 TF GAATAVL VSLVGLTTLW VTLVGLTTLW VTLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW VSLVGLTTLW 1 GGLVTLSY 1 SVGLTTLW 1 GGLVTLSY 1 SVGLTTLP 1 SSO 1 GGLPFLVR 1 RLSGLVTLSY 1 SVGLTTL 1 RLSGLT 1 RLSGLUT 1 RLSG 1 RLS 1 SP 1 SP	280 SAVFAMOR SAYFAMFQ SAYFAMFQ SSFFAVFQ SSFFAVFQ SSFAVFQ SSFNAIRQ SS	DDLKELLAYST DDLKELLAYST QDLKGLLAYST QDLKGLLAYST QDLKGLLAYST TDLKSLLAYST TDLKSLLAYST TDLKSLLAYST KDLKGLLAYST TDLKGLLAYST TDLKALLAYST NDLKALLAYST NDLKALLAYST NDLKALLAYST NDLKALLAYST NDLKALLAYST NDLKALLAYST NDLKALLAYST AAASMAGIPPL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL GTFAMAGIPPF GLSMAGLPPF GLSMAGLPPF GTFAMAGIPPF GTFAMAGIPPF MALSAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAMAGIPFT NLSMAGVPFL GTFAVV GVF GVF GVF GVF GVF GVF GVF G	M10 300 300 150LGFLVA ISHLGLITV ISHLGLITV ISHLGLITV VSQLGMIS VSQLGLIMT VSQLGLIMT ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM IGFUSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF NGFLSKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFISKEMF IGFFLSKEMF IGFFLSKEMF IGFFLSKEMF IGFFLSKEMF IGFFLSKEMF IGFFLSKEMF IGFFLSKEMF IGFFLSKEMF IGFFLHSAV	31 TIG9 LL5L LL5L LL5L LL5L LL5L LLG.LGSAAL LLGLGSAAL LLGLGSAAL LLGLGSAAL LLGUGAAS LLGVGAAS PACAVETHA FACAVETHA FACAVETHA FACAVETHA FACAVETHA FACAVETHA FACAVETHA FACAVETHA FACAVETHA FACAVETHA SALENT TAULRATE LEAVLAAEG FAVLNAGE ESNUNYTQ C Q Q Q Q Q Q Q Q Q Q Q Q Q	0 GTP GSP STP GSP GSP MTS HYG.S YFGES.VD HAUGD HYG.S GAWAG VNPLD PQLLR VSWLD IFD.LF.V.T IS FR IQLFDAST 90 GEGYEA P P P		320 MVAAIIH AVAAVFH VVAGVFH AVAAIFH IVAAIFH ITAAIFH ITAAIFH IFTALFH MTAFVTF IVATIAGI VATIAGI VATIAGI VATIAGI VATIAGI VATIAGI VATIAGI VATIAGI FAPELFN VAWVASV FAFVSAI S FAPELFN WNIPLIN IN VPLIN FNLPLIN FNLPLIN	TM11 TIAHLI TIAHLI TINHATI ILVNHATI ILVNHATI ILVNHATI ILVNHATI ILINH	KSSLFMA KASLFMA KASLFMA KASLFMA KSLFMA KGLFMY KGSLFMT KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGSLFMY KGLFWY KGSLFMY KGLFWY KGSLFMY KGLFKTF LFFHTY KFIHGVF LFFKTF LFFKTF LKFIHGVF LFFKTF LKFIHGVF KFIFKTF SCOLGUY KGSLFMY KGSLFY KGSLFY KGSLFMY KGSLFY K KGSLFY K K K K K K K K K K K K K K K K K K K
Domrpa RmPhaa XcPhaa AtPhaa BaMrpa BaMrpa BaMrpa LiMrpa LiMrpa LiMrpa Domrpa RmPhaa XcPhaa AtPhaa BaMnha DaMrpa LiMrpa LiMrpa LiMrpa BaMrpa LiMrpa LiMrpa Bampa LiMrpa	260 SEALHDVPVWNII HPALAGTDLFLYT WPVLAGTPEWFWI NPVLAGTEWFWI TPFAGSIGWGTI SIFAFSAQGWVWI TPIFAASQGWVWI OFLGGGGVWFWI OFLGDTALWCG VGVVDHQTGTRAN AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD AGIIDHETGTRDD YGIVDHETGTRDD YGIVDHETGTRDD YGIVDHETGTRDD YGIVDHETGTRDD YGIVDHETGTRDD CAPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPPADLPR.KI FGQPAPLEKCY	TM9 270 ITCCMTTAVL VGLACLTTLUL VGLACLTTLUL VGLACLTTLUL VSCVACVTTLL IGCACLISLI ITCCATAVL VSLVCLTTLW VTLVCLTTLW VTLVCLTTLW VTLVCLTTLW VSLVCATTMIT VSLVCATTMIT VSLVCATTMIT SS0 350 360 IRRLSCLTLW VSLVCATTMIT SS0 360 IRRLSCLTLW VSLVCATTMIT VSLVCA	280 SAVFAMOR SAYFAIFQ SAYFAFQ SFFAVFQ SFFAVFQ SFFAVFQ SFFAVFQ SFFAVFQ SFFAVFQ SFFAVFQ SFTAIFQ SFTAIFQ TTTLAM TTTTLAM TT	DDIKELLAYST ODIKELLAYST ODIKELLAYST ODIKELLAYST ODIKELLAYST TDIKELLAFST ODIKELAFST TDIKELLAFST TDIKELLAFST TDIKELLAYST TDIKELLAYST TDIKELLAYST TDIKELLAYST NIKELLAYST NIKELLAYST NIKELLAYST NIKELLAYST NIKELLAYST AAASMACIPFL ASAAMACVPLF ASAAMACVPLF ASAAMACVPLF ASAAMACVPLF ASAAMACVPLF GIFSMAGIPPF GIFSMAGIPPF GIFSMAGIPPF GIFSMAGIPPF GIFAMACIPFF O ALFAVGUVGLV O ALFAVGUVGLS. FIGAWNAWP. SLFFPNIL.	M10 309 309 159LGELVA ISHLGLITV ISHLGLITV ISHLGLITV ISHLGLITV VSQLGMIS VSQLGMIS VSQLGLIM ISQLGLIMS ISQLGLIMS ISQLGLIMS IGFVSKEMFI NGFLS	31 TIG	9 GTP GSP GAWAG HFDT QCD GAWAG VNPLD QLIR DSLLD VSWLD VSWLD FDLFNVQT MNAFNMET IS FR QLLFDAST 90. GEG PP QLFDAST DGEG VP DGHEKFHW		320 MVAAIIH AVAAVFH VVAGVFH AVAAIFH IMAAIFH IFTALIFH MTAFVTF IVAVAUFH VATLAGV	TM11 ITIAHALI ITIAHALI ITIAHALI ITIAHALI ITIAHALI ITIAHALI ITIAHATI ITIAHATI ITIAHATI ITIAHATI ITIAHATI ITIAHATI ITIAHATI ITIAHATI ITIAHALI ITII ITIIAHALI ITII ITII ITIII ITIII ITIII ITIIII ITIIII ITIIII ITIIII ITIIII ITIIII ITIIIII ITIIIII ITIIIII ITIIIIII	PKS SLFMF KASLFMA KASLFMA KASLFMA KASLFMA KASLFMA KGSLFMT KFIHST KFIHST <
DqMrpA RmPhaA XcPhaA AtPhaA BaMnpA BsMrpA SaMnhA JaMrpA LiMrpA LiMrpA LiMrpA AtPhaA XcPhaA AtPhaA XcPhaA AtPhaA SaMnhA BsMrpA SaMnhA LiMrpA LiMrpA BsMrpA SaMnhA BaMnhA BaMrpA SaMnhA BaMnpA SaMnhA	260 SEALHDVPVWNI WPVAGTEAWFWI HPALAGTDLFLWFWI WPVLAGTPEWFWI SPIFAFSAQWFWI TPIFASQGWVWT TPIFAGGGVWFWI OPELGDTALWVCI TPLFASSGWFWI TPLFASSGWFWI TPLFASSGWFWI OPELGDTALWVCI TPLFASSGWFWI CPLFASSGWFWI AGLIDHETGTRDI AGLIDHETGTRDI AGLIDHETGTRDI CAVDHSTGTRDI CAVDHSTGTRDI CAVDHSTGTRDI CAUDHETGTRDI CAUGUNANT CONSTRUCTION CONSTR	TM9 270 270 270 270 270 270 270 270	280 SAVFAMOR SAYFANFQ SAYFAFQ SAYFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFAVKQ SFFAFQ SFFAVKQ SFFAV	DDLKELLAYST DDLKELLAYST QDLKGLLAYST QDLKGLLAYST DDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST TDLKGLLAYST NDLKGLLAYST NDLKGLLAYST NDLKGLLAYST NDLKGLLAYST NDLKGLLAYST NDLKGLAYST AAASMAGLPPI ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL ASAAMAGVPLL GTFSMAGLPPF GLSMAGLPPF GLSMAGLPPF QCLSMAGLPPF QCLSMAGLPPF AALSIAGVPFL GTFAMAGVPFL GTFAMAGVPFL GTFAMAGVPFL GTFAMAGVPFL GTFSMAGLPFF NLSI VVGIVPAWT. UVGVPAWT. UVGVPAWT. UVGVPAWT. UVGSLS. SLFFPNIL. VFGLFPNIL. VFGLFPGIL. LLFFPNVL.	M10 300 300 1SQLGFLVA ISQLGFLVA ISHLGLITV ISHLGLITV ISHLGLITV VSQLGHITS VSQLGLIMT ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGTLTM ISQLGLIMS IMALGT	31 TIC	0 GTP GSP STP GSP GSP HYG.S HYG.S HYG.S HYG.S GTD HFDT GAWAG VNPLD PQLR SWLD IG FR IG.LFNVF MAFNMET ANLFSVDT FR IG.LFDAST 90. GEG VP YP DGEG YP YP YP		320 MVAAIIH AVAAVFH VVAGVFH AVAAIFH IMAAIFH ITTAIFH TTAIFH TTAIFH MTAFVTF IVAVFAIF VATIAGN VATIAGN VATIAGN VATIAGN VATIAGN VATIAGN VATIAGN VATIAGN VATIAGN VATIAGN STOP VATIAGN VATIAGN VATIAGN VATIAGN STOP STOP STOP STOP STOP STOP STOP STOP	TM11 TIAHAI TIAHAI TINHAVI MVNHATI LVASL MVNHATI LVASL MVNHATI LUASL MVNHATI LUNHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI LINHATI SALASSA FTFAYSS FTFAYSS FTFAYSS FTFYSS LIFVYS	KSLFMA KASLFMA KASLFMA KASLFMA KASLFMA KGLFMI KGLFMI KGLFMV KGLFV KFI KFI KFI KFI KFI KFI KFI KFI KFI KFI

M	rı	0	д
	•	~,	

MrpA													
	TM15 -	HL helix			HL helix	·	_	,	TM16				ГМ17
DqMrpA RmPhaA XcPhaA BaMnhA PaMrpA BsMrpA SaMnhA DhMrpA HzMrpA LiMrpA MbhDEF	520 IVLVVVR IGLYFLM VILYMAL VFFYLLR IGLHWLL IIGYLSL IILFIMM ILLFIMM GLLYKTL FLLFKHW	530 HPVDRFLDR RSYLATAVE(RSYLATAVE(GGYFSRCDDO DRVRQVLDR NKWK.GIYK KNWA.KAAF SYWV.KLLQ KKWV.KLLYR DRVRSHLAT KYWKPWITT	54 ELAPITC. AIENRSPG SPPVFRHLQG SPPVFRHLQG ANAAWNVSG LFPSKLTL YMKERDPL . RQPGKLTF LAPVMRYGP . RVPKALRI	Q QATVDALR QRIFERVL QRIFERIL QRIFERIL DLLWDRLL NKLYDKLL NWYYNRSA NHUYERAL EAGYEGLM GKTYDNG	SSO RWAIAGG VTLSWKW RALFAAS VTVSWKW VTLSWNW KRVFFFA SGVITGS NVIPNYS ELMESIS NYIVRFS YYLEQG	560 ARVGDVT ARWLEQR ARATDAI ARWLEST GLLAARF YRVTKQY QFVTRIQ QFVTRIQ EKMTNSY LSLTKRY YRMTMFI MHIS	RTDRIS LGTRRL TNG.NL LGTRRL QHGSLR MTGLLR MTGLLR MTGLLR MTGSLR MTGSY R MTGYMR MKKKGVR	570 RHVWAVI QPOMRLI QPOLRII RPCLRIV QHLVLLA DYLLYIF DYFAYMI NLVII NLVII NLVII TLVMI TYLNYMI	580 UVLVAL VFLALA UVALU UAFAVV LAVGGL AGFIIL VFMILL SFIVVA LVLIAL SAFIVA	5 AAVGVVAV AGASPLLI AGFSPLFI AAAWPILE LAVGLLPA IGGAFAIK LGYTMFRY T.FVTIFS VGGALVLA IGNSILLF MASVMIFI	90 RPEPEVGSE GNFELPPLV GGALRPWPT SEFSLSLPF AGIPTGMLG LPQLLQGSY GGFSFKTEG DAFAIDTN VPFNINFKI QGIAFDSF HSPQLALTI NALDFNFSS	600 VRAE JIRGIDPA VTTFDPI SVQPVDPI SVQFVDPI VSPISLI VSPIRIF DAAFSIY DAAFSIY MTKVTVV G	DWIVVV FALWA GWALWL FAIWL GAAGCL EIILTL IWVITI EVCIVI ELALLA EVVVVG DFVLAA
	TM	17	т	N/10		▶ MbhD	TN (1)	\ \	_			Т	420
	610 61	620	630	WI I O		650	- TMTS	eo			6	580 [.]	690
DqMrpA RmPhaA XcPhaA BaMnhA PaMrpA BsMrpA SaMnhA DhMrpA HzMrpA LiMrpA MbhDEF	LLVVGTA IGIACAI IGMIAAM LGGACAV VALAGGV VMISATV VFIVATL LLLSAAF GMVVCAT TMVMGAI VILVTLV .IILSSV	AMVI SRS GSA¥QAKFH GSLFLYR.Q GAA¥QAKFH AAAFLPG1 ATVFARS SIPFINK1 LILFAKS AVLLAGT GIVFSKS1 LMI¥TRD	LGAVANVGI LASLVLG LLASLVLG LLASLVLG LLASLVLG LLASL LLASL LIASL LIASL	VGFAMALW AGLVTCIT SGLVTCLT AGLITCIT VGYTLALF IGFLLALL VGYAVSVL MGFLVVFF MGFSIALI MGYTISIF	FTLGAV FVWLSAP FVWLSAP FVWLSAP FVWLSAP FVVFRAP FVIFRAP FVFRAP FUFFKAP FULFRAP FILFSAP FULSAP FVISRAP	DVALTQL DLALTQL DLALTQL DLALTQL DLATQL DLATQL DLALTQL DLALTQL DLALTQL DLALTQL DLALTQL DLALTQL DLALTQL DLALTQL	LVEV.L LVEI.V LVEI.V LVEI.V LVEI.V VLET.I VIET.I VVES.I VVES.I LVET.I LVET.L LVET.I LVET.I	TVVVIVI TTVLILI TTVLILI SLIFLAL SVALFLI TVLLLI TVLLLMI STALFLI TVLFLI TVLLVI SVVLYLI VTALVMY	VLQR LP GLRW LP GLRW LP GLRW LP CFYH LP CFYH LP CFYH LP VLFR LP VLFR LP VLFR LP AISK TE	RA KRIEEPVA ETSF KRFEKVDS KRWEDPDA TVP ELR NLN KLR RF QFS RWER	FHTVS AED.ISIRV PE RA SD ELPA AAS.VNFGE P.SGARA LKTKT KEFKE RYNEKF KESTPI NIEEKE NIEEKE NIEEKE NIEEKE	RSRTLVS (RLRRLRD) APLRKVRD AQLRRARD PWKRRLH RTFRMTN SFQLTN. SFQLTN. PSKVVN. KWFSMK. GFLSLLV	AAVAIV LLLAIG ACIAVV FLLAAA LALAVV AGVAIL FIISIG ALIAG GLLSIA GLLSIA GLLSIA TILSIG IFASLL
	TM2	20					_	1	TM21				
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA BaMrpA BsMrpA SaMnhA DhMrpA HzMrpA LiMrpA MbhDEF	VGLASGAMLL AGGGMAL SGIGMSV SGAGVAV FGLSVTG VGVIVTL VGFFITA VGLSVITL VGLVMTL VGLVMTL VGLVMTL VGVIITL VGVIITL	AVWAMTG. AVTVMT. LAYTLMT. LAYAVMT. LAYAMMT. LALAVS. LGIASS. LGIASS. LGIASS. LALSSLALGI IALSSLALGI IALSSLALGI IALSSLALGI SLSAY. IMTAWS. SLSAY. IKFGVGGEI	RELISDYGR RELISDYGR .RPLPETIAS .QPSP.TIAG .LPVPNAIAT .RPSPSSIGD .LPLPGEVAQ SQRTKDSIAS .VEAGIEPISQ SNRHFESISK SNPLPESIAG .IDQFEPISV .TTFYDSISK DWLKYRYTDN	YFLDNAEQ YFLDERAYR YFLDERAYR YFLDERAYS YFLDENAYS YFFURAYS FFVKHSHD FFIENSKE YYEN AYD YMIDENSAP YYUDNAYV YYIDHGIE	DTGGINV EGCGTNV EGCGTNV EGCGTNV EGCGTNV EGCGTNV LGGGMNV LAGGYNM LAGKNI LAGAKNI LAGAKNI LAGAKNI EAAGRNI EVGGTI	0 VNTVLVD VNVILVD VNVILVD VNVILVD VNVILVD VNVILVD VNVILVD VNVILVD VNVILVD VNVILVD	YRALDT FRGFDT FRGFDT FRAFDT FRAFDT FRGLDT FRGLDT FRGLDT FRGFDT YRALDT FRGFDT YRGYDT	LCELTVI FCELTVI FCELAVI FCELAVI FCELAVI FCELVV MFELVV MFELVV LFESSVI MLELVI LCEMFVI LCEATVI	GVAGLA CIVALT AIAGLV AIVALT ALSALA TIAALG GIAALG SMACLA SMACLA SIAAIG FTAIA G	VILAIHAR VFALILRF VFALIRRF VFALIRRF VFALIRRF VFALIRRF AASLIGSG VIALIKLF VYTMIKLF VYTMIKLF VIAMIKLF AVALIRFW	RALPRRDV RPQSDSLE RMAPERIM RPAHESIG QRIG VKEEGKSG MTGRED KKRQTQGN MAG.GKEN HDGTVNEG LTKRGEND RREE	LAVHADS PEQQKVQ GPAIKLP PEQQMQ EHGGEDA MNEQKIN MKNLKSN VKNHEMN RSMKDPN KNNTKEP NEMMKIN EMNEDMG ►MbhF	PLLS NAFDDD NAFDAE DAYDEA FT RQQN YDGM
		790	TN	[22 8	10	A 8 2 0 A	Т	M23	840	8.5	0	TM24	
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA PaMrpA BsMrpA BpMrpA SaMnhA SaMnhA JhMrpA LiMrpA MbhDEF	HPDRAAG RPDRSKG MPGRKAG	AQDNGVEJ DSVAEYLFI DTVRDYLYV ETLADYLAV 	RTFARILG AULAQIMF ADLAQIMF SIVMQWMF SVIMHWLF RQGIRFLAW QTATKLVSF HTLTRVVT QFAAVITF RMVTKVVVV NTAARFLMP RNVTKVVAF RTNARALIP	LIVLLSLY VIGMLAAF UTLTVSLF VIITFSIF VIIVLAVH IILFSFY MVMVFGFS IILFFSVF MVMVFGFS IILFFSVF IIFLFSLH FIGIFGAY	FIVRGHN LFLRGHN LFLRGHD LFLRGHD LLFLRGHD LLFLSGHN LFLSGHN LFFAGHY LFVSGHH LLLRGHY LFFAGHY IVTHGHL	APGGGFN LPGCGFA APGCGFI MPGCGFI LPGCGFI APGCGFI TPGCGFV HPGCGFI EPGCGFV TPGCGFV TPGCGFV	S A L I G G A G I AM S A G I V L A A G I T M A A G I T L A G G L V A G G L L F A G G L L F A A G L V A A G L T T A G G A T I A	AGIAIYY IGFILQY IAFLLQY IAFLLQY IAFLLQY SSIVLLI SSIVLLI SSLVIII GAFTLYI GAITLTI GAGVLFI	LRAP SD MSGGTR LAGGAR LAGGAR LAYDLK LGFDMR LAYDLK LGFDMR LYGIE FAFGVS LAYDTK LAFGVK	KAARIRVE WVEERLRI SVESRFGE WVEDRLRI QIRRVLPI SIKKAIPF TMRKIFPI KVRQNFPV TVASMLNI AKEKINK	YVAVIAA H.PLRWMSI L.PLRWMGF L.PLRWMGF D.FTYWIGI N.FIYVAGA D.FTYKMIAF D.FKLIGJ D.FKALAGY VDPRDLIGV N.TIMLIGY N.TIMLIGY	CVIIGVU CLLCALL CLLATA CLLFAAA CLCCAAG CLLAVG CLLAVG CLLAVG CVIIGVISVL CLLGMI CLLGMI CLVFALG CGLVFLG	TG LAGF TG VGSW SGAGSL TG IGSW TG MGAW AG ILGL TG VGSF TG FGGL TF IASW TG ARGM SV VPAW TG MIGI AMLGL
8.	7.0	880		0	TM25	91	0	920	9		940	- — — — - 950	
DqMrpA RmPhaA XcPhaA AtPhaA BaMnhA BaMrpA BsMrpA BsMrpA SaMnhA DhMrpA LiMrpA LiMrpA MbhDEF	UDCSFLL FFGYPFL FFGYPFL FFGYPFL LAGSAFL VFGAPFL LVGDPYL FLGKNFF FVGEPFL FMGOPFL SVAFFYN	PLHAYLG TSHAQYASLI TSGHAEIPT TSFFRYAEI TGLWIFP THTFGYFQL TQAFGYYQLI TQAFGYVHLI TQAFGYVHLI TAQWWTIPVLI TAQWWTIPVLI THVTFGHVDLI TLWHEGFIF	DVHLTT VVCKFPLAS WLCELELAS YICKMPTAS ILCKTELAT ILCETELT ILCETELT LCETELT LCETELAT ILCETELT ILSPVHMTT SCPCTLSA	ALIFDU ALL.FDU ALM.FDU ALM.FDU PLL.FDV ATI.FDU AVF.FDU AVF.FDV PLI.FDV QFLPIMNU	CVYLAVL CVYLVVF CVFSLVV GVFLVVF GVFLVV GVFLVV GVFLVVV GVLVVV CVALAVI CVALAVI CVYLVVV GVLLVVV GVCLKVF	GVIMAA GATVLIL GAAMLML GSTVLIL GATVLVL GATVLVL GIALTIII GIALTIII GTSLTII GTVMITII GVVLITIII GVVLITIII GLVSAL	DKLGGD IAL SMMGTI IAL IAL UKLTO VLTIA ISIG MSIG MALMEV QTIG FALSVF	DRSDEPA AHQSVR KPSRTRD AHQSIR AHQSIR RH DKDEP RRWKS.	AVPPPPP APRAHA SHRGEI RNYRVRT RKHRVEK	TGPGAEAT KAARSDKE DPTQRSTF PEAAKAEL LAAAKEEN ENE ENE ENE ENE ENE ENE	APAATEDAL AVR TAEQH V M	PRVIDVTD	NREVQA

		TM1 —	TM2			
DqMrpD RmPhaD XcPhaD AtPhaD BaMnhD PaMrpD BpMrpD BpMrpD SaMnhD DhMrpD HzMrpD LiMrpD PfMbhH	MILESALTLFVAVPI MTDWLDHLLILPILIPI MNHLLILPILIPI MMSFPFHIVIAPILVPI MNQALLVAPILIPI MNVALLVAPILIPI MNNFVILPILIP MNNLVILPILIPI MRNNLVILPILIPI MRPEVALPVLLPI MRNNLILPILIPI	LTAGVIVAVASTI AVAAVIIPINERDI IIGASASIFVEHRRQI VTAAVILIFDERQI CSILLATVIRRHI IISATILIFMEKAH IVGSFIIIFAKHH ITAILVFIGKRP MACMIMVILRNHI ISGALSLIFWRSR IGAFSMPIVSLIK	30. 40. A. TIK GANGERSTUNGT R. TIK GANGFASTLUNGT YGPRVQ RAVAWTSMALLAV R. VAKAAISLASTIILLAV R. VAKAAISLASTIILLA R. AVRAISLAGTGILLA M. LMRIPSTAASAIGT S. LQRVISGFAVVGMLI IIKRYVALGTLILLA PMQRFIAVAGNIALLI PVQRVFALIFSGILVV GKAKINASMISFATLI	AAVATVPWVSDGSV LISMILMRLAAAGTG VAVVALFARAAHGV VAILFREVNSTVN LAITLVGMASEKAP AGLALVWQAAHGVV VSIYLAVDVYQNGI VSIYLAVDVYQNGI VSIVLAVDVYQNGI VSLWLFVAVWSDGYI VGLQVFREVWSKGI	60 VHQVALWA VYLLGDWP VYLLGDWP VYLLGDWP VYLLGDWP 	PGVSIPFVLDMFSALM APFGIVLVLDRLSALM APFGIVLVADRLSALM APFGIVLVADRLSGLM APFGIVLVADRLSGLM APFGISLVIDRLSAVM APYGIVLVADLFALM APYGIVLVADLFATMM APFGIFVLMATAILL APFGITFVADMTAILL APFGITLIADMLSAVM APFGITLIADMLSAVM APFGITLIADMLSAVM
	•• TM3	110	TM4 -	TM5	150 160	TM6
DqMrpD RmPhaD XcPhaD AtPhaD BaMnhD PaMrpD BsMrpD SaMnhD DhMrpD HzMrpD LiMrpD PfMbhH	LTVTSILTLTCAAFAV LCLTSGLALAAQAYSM MTTLVGGAACLHAC VLLTALLAIPSLIYSM LVLASLIGLAALSFSE VLTAIIQLLVGLYSF VILTAIIGLLVGLYSF VILTAIITALVVCLFFAR VLVTAIVTFCCVSYAF ILMTGIIGLAMGIYSL TATTSIILFCVILYSY VL1	AGEMYKRFYP RWHIAGHHFHA G.WDRAPHFHA K.WHMAGAHFHS S.WHKASPHFHI SVGEKRERSFYY SIGSCRERSFYY SIGSCRERYFYP TIGIERERYYYY TIGRGHEKFGYYP TIGRGHEKFGYYP TIGRCHEKFLYF	LVILVTAGVNGALLTGDI LFQLLVAGLAGAFLTGDI LFQFLLVAGLAGAFLTGDI FQMMLMGVNGAFLTGDI FQLLLMGLNGAFLTGDI FVQGLLTGICAFITADI FVQGLLTGICAFITADI FVFFLLAGVNGAFLTGDI FYFFLLAGVNGAFLTGDI LSQFLIAGVNGSFLTGDI LSQFLIAGVNGSFLTGDI AILFMIVGVNGSFLTGDI FILMILLAGVAGAFLTGDI LILIELGMLGIAITGDI	FNFFVFVEVNLLPSYG FNLFVFFEVMLASYG FNLFVFFEVMLASYG FNLFVFFEVMLASYG FNLFVFFEVMLASYG FNLFVFFELLLISSY FNLFVFFEVFLASYT FNLFVFFEVFLASYF FNLFVCFEVFULSSYF FNLFVCFEVMLVASFA FNMFVFFEVMLVASFA FNMFVFFEVMLMASYA	IMMITRSGRASVVGVAA LLLHGSGPLRVKA LLLSGGRGLQMRI LLLHGSGQQRVKA LALHGSGPARVKA LALHGGSSRLAG LIVLGGTKIQLRE LVLGGTKIQLQE LIVLGGTKIQLQE LIVLGGTKIQLQE LLVIGGTKIQLKE LLVIGGTXIQLKE LLVIGGTXQUEKA LVAFRNDTWEGLEA	$\begin{array}{c} \mathbf{SRL} \underline{\mathbf{YI}} \mathbf{SVNL} \mathbf{LAS} \mathbf{TILI} \\ \mathbf{GLH} \underline{\mathbf{YV}} \mathbf{VNL} \mathbf{LAS} \mathbf{ALFL} \\ \mathbf{GLH} \underline{\mathbf{YV}} \mathbf{FNVC} \mathbf{AS} \mathbf{LFL} \\ \mathbf{GLH} \underline{\mathbf{YV}} \mathbf{VFNVC} \mathbf{AS} \mathbf{LFL} \\ \mathbf{GLH} \underline{\mathbf{YV}} \mathbf{VINL} \mathbf{AALFFL} \\ \mathbf{GLH} \underline{\mathbf{YI}} \mathbf{AINL} \mathbf{VALFFL} \\ \mathbf{SLK} \underline{\mathbf{YI}} \mathbf{VFNIVSS} \mathbf{SLFV} \\ \mathbf{SLK} \underline{\mathbf{YV}} \mathbf{VINVFAS} \mathbf{ILFL} \\ \mathbf{SLK} \underline{\mathbf{YV}} \mathbf{VINVFAS} \mathbf{SLFV} \\ \mathbf{SLK} \underline{\mathbf{YV}} \mathbf{VINVFAS} \mathbf{SFFV} \\ \mathbf{SLK} \underline{\mathbf{YV}} \mathbf{VINVFSS} \mathbf{SFFV} \\ \mathbf{SIFP} \underline{\mathbf{YI}} \mathbf{LINM} \mathbf{ISSFLFL} \\ \mathbf{AIK} \underline{\mathbf{YV}} \mathbf{LNL} \mathbf{AS} \mathbf{VIFN} \\ \mathbf{GL} \mathbf{K} \underline{\mathbf{YM}} \mathbf{FAGS} \mathbf{LAS} \mathbf{SFVL} \\ \end{array}$
1	TM6 190	200	TM7a	TM7b	TM8	260
DqMrpD RmPhaD XcPhaD AtPhaD BaMnhD PaMrpD BsMrpD SaMnhD DhMrpD HzMrpD LiMrpD PfMohH	IGVALIYGVTGTVNIAG IGVSLIYGAAGTLNMAH IGVSLIYGVTGTLNMAH IGVSLIYGVTGTLNMAH IGVSLIYGVTGTLNMAH IGVSLIYGVTGTLNMAH VGVAYIYSITGTLNMAH NGVAILYSVVGTLNLAH IAAFLYRLTGTLNMAH VAIALLYSMIGTLNMAH LGIALLYGQYGTLTMAH	2LHGAASEDTA SLATKLAALEPRSR LSORLATLPAADV DLAHRIEGINPDOR JLAORISHVAAODR JLAMIMR.SGEAP DLSVKIS.ESGOT DLAVKVG.ELEOT JISNKLANLSAHDS JISNKLANLSAHDS JISNKLANLSAHDS JIALRLD.EAEHS JIACKTDLNGANT LSOKITDLNGANT	VAVAT. AUVIFALATKAA TLVEMGSALLGVAFLVKAG PLAKATLGLLLVFCSKAA MLUETGAAVLGIAFLVKAG GVIPALLMLSFAIKAA GUITVIGVLLLVFGMKGG GVINVIAVIFLVFAKKG GLWNVFIFFIVFATKAG GLWNVAVFFLVFATKAG GMISVVAVMFFFVFGIKAG	AVVPVHGWLARAYPK SMWPLSFWLPTAYAA SMWPLNFWLPSAYGSA SMWPLNFWLPSAYGSA SMWPLNFWLPSAYTAA SIFPLYFWLPGSYYAP SVFPMFVWLPSAYYAP SLFPLFFWLPGSYSA SLFPLFFWLPGSYFAP SAAPVHMWLADAHPAA	SPAVTAMFSGLHTKIA. TPPVAGVFA.VLTKVG. PASVAALFA.IMSKVG. AAPVGGLFA.IMSKVG. ITAVSAMFACLLTKVG. PAAISALFGGLLTKVG. PAAIALFGGLLTKVG. PAAIALFAGLLTKVG. PVAVSALFAGLLTKVG. PVAVSALFAGLLTKVG. PIPVLALFGGLLTKVG. PISVLALFGGLLTKVG. PSSISAMLSGLVIKIGG	IYAIYRIYAVIFDG IYVIRLHLUVFGTAA IYAVIRVSIWFGAGA IYVIARLSFLLFGQTA IYVIARLSFLLFFGQTA IYVILRLSPLMFGISA VYAIIRUVTLIVP IYAIMRTFTLIFNH VYAIARTLSLFFSD IYSIMRLFSLVFYH VYSIFRVFTLMFDQ VYAIIRTYTLFFSS IYAI
		ГМ9 —	TM10		TM11	
	070 000	0.0.0	200 210	200	220	240 250
DqMrpD RmPhaD XcPhaD AtPhaD BaMnbD BaMrpD BpMrpD SaMnbD DhMrpD HzMrpD LiMrpD LiMrpD	270 280 DSRYLWVGVVVF37 GASSCFGQEWLVTGGMI GASHCFGRHALLWGII GESACFGHDALLVGGI EYGLPHQLLWVGCI DYGFHTLILLAG VSFSHYVILFLAI FNSFSHYVILFLAI TMGYLQDIMLWGAVI LTDFVVPLGILAI TINLGTIGWIIIIFAC	290 TMI I CVLGAVGEA TAFCGI CVLASQ TLFGAI GVLASQ TLFGAI GVLASQ TLFGLI CVVASQ TLFGVL CAAQT TVIFGVL CAAQT TVIFGVL CAAQT TMFFGVL CAAQA TMLLGAMGAVAFG TMU TGVL CAAQY TILGVI GAISYY TLIVGNA MAVVQE	300 310 APRSILAFHWVSQIGYII AMGRLAGYSVIVSGTILA RLRVMVSVLVVFSAATLFI ALGRLAGFSVIVSGTILA AMGRLASFSVIVSGTILA AVGRLASFSIVSGTILA EVRRILSFHIVSQVGYMI NVMKIVINNITAVGVIL DFKRILSVHIISQVGYIV DIKSILLYNVVGGFILA EFRRILSFHUSOIGYMI DMKTIVIYNIMIAIGVIL DLKRLLSFSVGQIGYII	320 LGVAL	330 IGLTAGIFYLLHHMIVK GMLAGALFYLVSSTLTI RALGAGLYYLPHSCFVA TVAAGALYYLVSSTLTI LALGAVFYLSSTLAI LALGAVFYLLHDMLIK LATAGAIYYIAHHIIVK SGMIGAIYYIAHDMIVK LATAGGVFAIVHNIVVK ESMTGAVFYLHDMIK IALAGAIYHTVNHALMK	$\begin{array}{c} 340, \qquad 350, \\ \hline \textbf{AALFL} & \textbf{IGATEVRYGP} \\ \hline \textbf{GAFFL} & \textbf{IEVERGRDA} \\ \hline \textbf{AALFMVSDLIRRRGR} \\ \hline \textbf{AAFFL} & \textbf{IEVERGODA} \\ \hline \textbf{AAFFL} & \textbf{IEVEVEGODA} \\ \hline \textbf{AAFFL} & \textbf{IEVEVEGODA} \\ \hline \textbf{AAFFL} $
DcMrpD RmPhaD XcPhaD AtPhaD BaMnhD BsMrpD BsMrpD BsMrpD SaMnhD DhMrpD HzMrpD LiMrpD PfMbhH	270 280 DSRYLWVGVVVFS/ GASSCFGQEWLVTGMI GESACFGRHALLVGGI/ GESAGFGHDALLVGGI/ SSYGFGNDWLYFGGI/ .EYGLPHQLLLWVAC/ .DTAFTHQLMIWLAAI .DVGFTHTLLILAGI .NVSFSHYVILFIAII .EYEVTHLLIGVLAAI .TMCYLQDIMLWGAV .LTDFVVPLLGILAIV TINLGTIGWIIIIFACI	290 THI I GVLGAVGEA TLAFGGI GVLASQ TLVMAAFGVNAAS TIFGAI GVLASQ TLAFGLI GVVASQ TMI VGVLGAAQT TVIFGVI GSLAYS TMFFGVLGAVSQF TIIFGCVLGAVAYA TMILGAMGAVAFG TMI CVLGAAQVAFQ TIICVLGAAQVAFQ TIICVLGAAQVAFQ TMILGVLGAAQVAFQ TIICVLGAAQVAFQ TMILGAVGAVAFQ TMILGANGAVAFQ TMICVLGAAQVAFQ TIICVLGAAQVAFQ TAICVLGAAQVAFQ TIICVLGAAQVAFQ TAICVLGAAQVAFQ	300 310 APRESILAFHUVSOIGYII AMGRLAGYSVIVSSCILIA ALGRLAGYSVIVSSCILIA ALGRLAGYSVIVSSCILIA EVRRILSFHUSSVVVSCTLIA EVRRILSFHUSOVCYMI DFKRILSFHUSOVCYMI DFKRILSFHUSOUGYMI DKILIYNVVVCVGVFILA EFRRILSFHUSOIGYMI DKIIVINNIAICVII DLKRLAYSVQ0IGYII 370 380	320 AAVGL	330 IGLTAGIFYLLHHMIVK GMLAGALFYLVSSTLTI RALGAGLYYLPHSCFVA TVAAGALYYLVSSTLAI LALAGAVFYLIHHIIVK ASTOGAIYYIAHHIIVK LAIAGAIYYIAHHIIVK SGMIGAIYYIAHDMLVK TGLRGSIYYLAHDMIVK LAIAGUFAIVHNIVK ESMTGAVFYLIHDMIK IALAGAIYHTVNHALMK	340 350 AALFIAIGATEVRYGP GAFFLIELVERGRDA AALFMVSDLIRRRGR SAFFMLIELVERGQDA AAFFLIELVERGQDA ANLFFIGGLAARICGS GALFMLAGTLIALTGT ALLFLLIGIMIKITGT ALLFLISGITHRLQGT AALFLIVGIVMAITGY ALLFLVAGAVIHEIGT FM13 420
DqMrpD RmPhaD XcPhaD BaMnhD PaMrpD BsMrpD SaMnhD LiMrpD LiMrpD PfMbhH DqMrpD XcPhaD XcPhaD XcPhaD XcPhaD BaMnhD BaMnhD BpMrpD SaMnhD DhMrpD HzMrpD HzMrpD HzMrpD	270 280 DSRYLWVGVVVFS/ GASSCFGQEWLVTGVI GSSSCFGPHALLWGI GSSGFGHDALLVGI GSSGFGHDALLVGGI .EYGLPHQLLUVVG/ .DTAFTHQLMIWLAAI .DPCFHTLILILAG .NVSFSHYVILFLALI .PCFHTLILILAGI .TMCYUPLLGILAI TINLGTIGWI IIFACI GADVLAVTMEAYGDEPDE AS	290 TMIIGVLGAVGEA TIAFGGIGVLASQ TLVMAAFGVMAAS TLVMAAFGVMAAS TLFGAIGVLASQ TMIFGVLGAAQT TVIFGVLGAAQT TVIFGVLGAAQT TVIFGVLGAAQT TVIFGVLGAAQY TIGVLGAAQY T	300 310 APRESILAFHUVSQTGYTI AMGRLAGYSVIVSGTLIA ALGRLAGFSVIVSGTLIA ALGRLAGFSVIVSGTLIA ALGRLAGFSVIVSGTLIA ALGRLAGFSVIVSGTLIA ALGRLAGFSVIVSGTLIA EVRILSFHIVSQVGYMI NVMKIVINNITTAVGVIL DFKRILSFHIVSOTGYMI DFKRILSFHIVSOTGYMI DKKILSFHIVSOTGYMI DKKILSFHIVSOTGYMI DKKILSFHIVSOTGYMI DKKILSFHIVSOTGYMI DKKILSFHISOTGYMI AKTIVINNIMIATGVIA GAR EPLVAVAFFASAMSIAG TLAILGTCFCCALLAG TLAILGTCFCCALLAG TLAILGTCFCCALLAG TLAILGTCFCCALLAG THQUAMFFISAISLAG YPVLGWFFISAISLAG RWLAVAFFISAFSLAG RWLAVAFFISAFSLAG KFSLGWFFISAFSLAG KFSLGWFFISAFSLAG KFSLGWFFIATLGSCG	320 LGVALFGP AAVGLGHD AAVGLGHT LGFSLDDA AMGTGNT LGLALATP FGVAVHTP FGVAWHTP CVAMMTE LGLALYTQ ZVAMMTE CLGLALYTQ FSVSIMTR DFLSGFIAKFALISG PPLSGFIAKFALISG PPLSGFIAKFALISG PPLSGFIAKFALISG IPPLSGFIAKFALISG IPPLSGFVGKFKIAEG IPPLSGFVGKFALILYA PPLSGFVGKFALILYA PPLSGFVGKFFIAEG IPPLSGFIGKIFVTEG IPPLSGFIGKILYTES IPPLSGFIGKILYES	330 IGLTAGIFYLUBHMIVK GMLAGALFYLVSSTLTI RALGAGLYYLPBSCFVA TVAAGALYYLVSSTLTI LALAGAVFYUSSTLAI LALAGAVFYLHHIIVK SGMIGAIYYILHDMLIK LATAGAIYYIAHMIVK LATAGAIYYIAH INFORMA SILAAAWW.AAATAA SLDAAAWW.AAGIALL AFINENYI.IAAVALA TFERGFYL.SGVIVLLA AFSAQIYV.ATGIALA AFSAQIYV.ATGIALA AFSAQIV.GGIIILL	340 350 AALFIA IGAIEVRYGP GAFFLIEVERGRDA AALFMVSDLIRRRRGR AAFFILIELVERGQDA AAFFILIELVERGQDA AAFFILIELVERGQDA AAFFILIELVERGQDA AAFFILIELVERGDA ALFIGGLAARICGS GALFMLAGTLIALTGT TALFILIGIMIKITGT ALLFILIGIMIKITGT ALLFILIGTIMIKITGT ALLFILIGTIMIKITGT ALLFILSGITHRLGT TNLFLISGITHRCGT ALLFILIGTIMIKITGT ALLFILIGTT

MrpD

		TM14			
	530	540	550	560 5	7 <u>0</u>
DqMrpD	GLA <mark>L</mark> AA <mark>PAL</mark>	ALSVVTLA <mark>LG</mark> LG	GQLLLE.LS	GTA A AN L Y DP TT Y	IQAVLG
RmPhaD	VVI <mark>E</mark> IT PVV	VL LGAC <mark>I</mark> F <mark>LS</mark> LQ	AGPAMR.YM	I <mark>Q</mark> AT <mark>A</mark> DD <mark>L</mark> LA P LTH	SER <mark>VL</mark> SAPRAGSQ
XcPhaD	R P V <mark>E</mark> T A <mark>A T I</mark>	ILLSGL <mark>V</mark> AMTIG	AGPLMH.YT	D AA <mark>G</mark> AQ L R DP GA Y	LEQ <mark>VR</mark> GTTPQRRQP
AtPhaD	LVI <mark>E</mark> IA <mark>PI</mark> M	L L LGLT <mark>LA</mark> MTVQ	agp vmr. y m	I <mark>Q</mark> ET A RI L DL P AS Y	IQ <mark>GVI</mark> SAPRAGSNPEAQP
BaMnhD	LVR <mark>E</mark> VV PIA	<mark>g L</mark> L G V C <mark>L A <mark>L T</mark> I A</mark>	AGP TMR . <mark>Y</mark> M	I <mark>D</mark> ET A RS L H NP DD Y	INSVLRAPRTGAETAGAQ
PaMrpD	MRA <mark>A</mark> WL <mark>GMA</mark>	G L A L L T <mark>V</mark> L <mark>I G</mark> L G	AGPLID.YA	. V AA <mark>A</mark> AQ <mark>L</mark> A DP QA <mark>Y</mark>	LQPFAAVGGN
BsMrpD	G <mark>L</mark> LY <mark>PAA</mark>	IFLLLS <mark>L</mark> LF G LG	TEWVSP.YV	D QA A ET L L NP EK Y	IEAVLKE
BpMrpD	K <mark>l</mark> ll piv	P L VALT <mark>I</mark> I LG FA	AEPIFQ.YS	LQVADQILDPTIY	IES <mark>VL</mark> KE
SaMnhD	Y <mark>L</mark> TT IAI	V AVVIT V L YG LS	ADYLYP.MV	KAG A ETFY NP ST Y	VK <mark>AVL</mark> GGK
DhMrpD	G <mark>L</mark> LL <mark>PIA</mark>	L L TACT I A LG LG	AEGLHG. <mark>V</mark> V	DLA <mark>A</mark> AG <mark>L</mark> L DP QT Y	IEAVLQERHP
HzMrpD	LWM <mark>M</mark> YL PVV	VL AAMS <mark>L</mark> L IG VF	AEPIMQ. <mark>V</mark> M	ILI <mark>G</mark> DQ L M NP SG Y	IE A <mark>VM</mark> GTSASAEAALLEPFEGQAEPISEDAEGNP
LiMrpD	K <mark>M</mark> LV PVV	il lais <mark>i</mark> g <mark>yg</mark> vf	SNAIYP. F I	EQAVDPLVDPSVY	IDAVIKE
PfMbhH	.IA <mark>M</mark> ML <mark>PMI</mark>	ILVVTI IVMG FF	<u>P W Q</u> I S D R <mark>I</mark> M	I <mark>V</mark> PT A RA L W DV ID Y	<mark>IS</mark> S <mark>LM</mark> GGG

MrpC

		TI	M 1					TM2			-]	CM3		
	1	. 10		20	•		30			40		5	o.	60		7 9		8 O		
DqMrpC	. N	IT LAI S <mark>VGVI</mark>	MAGF	VFLV <mark>L</mark> (QRG.	MVRVI	LGF	E LLS H	I A AH	LTLM.	A A <mark>C</mark>	.GASR	REAPL\	SDPDPALT	SDG.	LPQAF	VLTAIV	IAFA	I TIY L I	JV L
RmPhaC	. ME I	JI <mark>L</mark> SA <mark>GIGTI</mark>	TASG	VYLL	RPR.	ΤΥΩΥΙ	IGL S	G <mark>LLS</mark> F	AVN	LFIF	G M <mark>G</mark>	. RLRV	NAPPII	DPGGVGDLAR	Y T D P	V P Q A L	VLT <mark>A</mark> IV	IG <mark>FA</mark> I	M TA LF I	JVV
XcPhaC	M ME I	JA <mark>LA</mark> SA <mark>IGVI</mark>	TALA	IYLL	RAR.	SFDVI	[LGL]	Г <mark>F L S</mark> Ү	ATN	LLIF.	A G <mark>G</mark>	. RLRS	GQPPVI	RDGISADLSQ	H T D P	LPQAL	VLTAIV	IAFA	M TAV SI	JVL
AtPhaC	. ME I	JI <mark>LAI</mark> G <mark>IGIN</mark>	T G S G	VWLI <mark>L</mark> I	RPR.	ΤΥΩΥΙ	[VGL	5 <mark>L L S</mark> Y	AVN	LFIF	GVG	. GIKT	NAPPVI	VNGVDSST	LADP	V P Q A L	VLTAIV	IGFA	TALFI	JVV
BaMnhC	. ME	JV <mark>LA</mark> LA <mark>IGVI</mark>	MASG	VWLI <mark>L</mark> I	RPR.	T F Q V A	IGL	б <mark> L V S</mark> Ү	AVN	LFIF	SIG	. RLRT	DAPPVI	ESGLDVQAAQ	Y T D P	V <mark>P Q A</mark> L	VLTAIV	IG <mark>FA</mark> I	M TA LF I	JVV
PaMrpC	. ME	IL <mark>AAI</mark> T TG GI	AGLG	LWML <mark>L</mark> I	DRN.	LKRV	/LGV	/ <mark>VL</mark> GN	AIN	LGVL	T A <mark>G</mark>	. RFFG	ER P AFN	DAGNG.AS	TANA	LPQAL	VLTAIV	IGFS	LFVFAI	AL
BsMrpC	. <u>ME</u>]	L <mark>MAV</mark> L <mark>AGI</mark>	FMAA	. TYLLS	sĸs.	LLRVI	IGTA	A lls H	IG V H	L <mark>M</mark> LL	ΓMG	. <mark>GL</mark> KK	GAAPII	SEHAKS	FVDP	LPQAL	ILTAIV	'IS <mark>FG</mark> '	V TSF I I	JVM
BpMrpC	. <mark>ME</mark> 1	L <mark>MSI</mark> T <mark>AGVI</mark>	FMVG	TYLI <mark>L</mark> :	ΓKS.	LLRV	/VGL	E lls H	IGAH	LLL	ΓMΑ	. GL QR	GAPPLI	HLEATT	YSDP	LPQAL	ILTAIV	'IS <mark>FG</mark>	V TSF L I	JVL
SaMnhC	. <mark>ME</mark> 1	I <mark>MIF</mark> VS GII	TAIS	VYLV <mark>L</mark> :	SKS.	LIRIV	/MGT]	T LL TH	I <mark>a</mark> a n	LFLI	ΓMG	. GLKH	GTVPIY	EANVKS	YVDP	IPQAL	ILTAIV	IAFA	T TAF F I	VL
DhMrpC	. <mark>ME</mark>]	L MAI V IGII	FTIG	TYLI <mark>L</mark> :	SKT.	LLRI	LGTS	S <mark>IIG</mark> H	I G V N	LLIL	ΓMG	. <mark>Gl</mark> kk	GGPPLI	GLKESL	FTDP	LPQAL	LLTAIV	INFA	TALFI	JVL
HzMrpC	. ME	PL <mark>MA</mark> LA <mark>IGLI</mark>	YATA	IFMML	RRS.	IVKL	/IGL	LLSN	I G A N	LLIF	ΤA	. <mark>GM</mark> TR	GAPPLI	PEGMLQPLGD	VADP	LPQAV	VLTAIV	IAFG	VLAFAV	/VL
LiMrpC	. ME	L <mark>MSI</mark> L <mark>IGL</mark> I	FAAA	VYLI <mark>L</mark> :	SKS.	LLRII	IGTA	AVLS H	I G V N	LLVL	ΓMG	. <mark>Gl</mark> kk	GRVPII	GTPGSG.T	YNDP	LPQAL	ILTAIV	ISFG	V TAF FI	JVL
PfMbhG	. <u>M I</u> Z	AFQYLT <mark>ATIN</mark>	ILLG	IYAL <mark>L</mark>	YKRN	L I K L V	/LAL	1 <mark>LID</mark> S	GIH	LLLI	SEG	Y <mark>R M</mark> E N	GIPPT/	PIYTGYEGGA	MVAP	IPQAL	VLTSIV	'IG <mark>VC</mark>	V <mark>LSL</mark> AI	AL

	90	100	110	120	130	
DqMrpC	AVIG	DDDDTDIGDL) P L D L L P E T P <mark>G</mark>	GAH <mark>PE</mark> DPEPDE	PSTHDAEGVHR	
RmPhaC	LLAS	GFT	<mark>G</mark>	TDHVDGREQRG	GD . <mark>.</mark>	
XcPhaC	AIRS	SDN	<mark>G</mark>	S D H <mark>VD</mark> AHEDAI	TG <mark>E</mark> DTREARR	
AtPhaC	LLAAI	GLT	<mark>G</mark>	TDH <mark>VD</mark> GRESK.	· · · <mark>·</mark> · · · · · · · · · · · ·	
BaMnhC	LLAS	GLT	<mark>R</mark>	TDH <mark>VD</mark> GKEN	• • • • • • • • • • • • • • • • • • •	
PaMrpC	LK R T	ELHG	DK <mark>T</mark>	TD S <mark>V S</mark> S I T E Q F	PAP D WHAGEHESDGN(GAEARR
BsMrpC	AF RA	ZQEL	<mark>K</mark>	S D DMDQMRGNE)QH <mark>E</mark>	
BpMrpC	AY <mark>R</mark> T	К ЕН	<mark>K</mark>	TDDLDQLRG.S	SAD <mark>E</mark>	
SaMnhC	AF R T	KEL	<mark>G</mark>	TDN <mark>VE</mark> SMKGVF	ed <mark>d</mark>	
DhMrpC	SY <mark>R</mark> T	K VL	<mark>G</mark>	TDNLEELRG.C	CDD <mark>E</mark>	
HzMrpC	IR <mark>R</mark> A	ZEIV	<mark>K</mark>	A D D <mark>LD</mark> KMKDTE) T . <mark>.</mark>	
LiMrpC	AY <mark>R</mark> A	ZQEL	<mark>D</mark>	S E S <mark>VS</mark> KTRGHE	AD <mark>D</mark> E	
PfMbhG	TVNA	7 RHY	<mark>G</mark>	T L D <mark>V T</mark> K L R R L F	RG . <mark>.</mark>	

MrpE

					- – - S1			SI	
					1 <u>,</u> 10)		20	30
DqMrpE	(.	. <mark></mark> . <mark>.</mark>		,MTSTLTWP L F	₹ <mark>.</mark> .	IA V	7 F L L W F F W Q C	T TT <mark>SA</mark> K <mark>V</mark> VRD
RmPhaE	MRTWFPYPL	LS <mark>I</mark> ALLLN	4 <mark>WL</mark> L <mark>L</mark> SQ	<mark>sv</mark> tpgsi <mark>v</mark> l <mark>g</mark> l	V VSTVLAWV <mark>T</mark> I	L.NL.QPARS <mark>R</mark> L	HRWSR <mark>IA</mark> G	G <mark>F</mark> ILR <mark>V</mark> VG D V	IRS<mark>NI</mark>AV TLI
XcPhaE	MSAQVSWQRRLFPSRP	l s <mark>v</mark> mvfle	FWLLLSD	SFGPQQW <mark>V</mark> L <mark>G</mark> L	LL G WVVPIFAA	A.RL.DREFA <mark>R</mark> I	GSLRS <mark>VP</mark> F	RMLLVAAVDI	V RS NI K V ALQ
AtPhaE	MMSRVLPYPL	L T <mark>V</mark> S L I F H	TIN	SF SPGHL LLG T	CVALIASWAMA	A.SL.RPAKP <mark>R</mark> I	RNWHKL V F	(LIAIVLYDI	IRSNISVMRI
BaMnhE	MKKILPYPL	LFVSLVLE	WLLN	SFTRAQFILGL	VIAFGACRVMM	1.AL.EPQKNHI	RSPRMMIV	LYAASID	LRSNIAVVRL
PamrpE	MPFLVH		AWSLGSA	HLGGGGLLAFAT	LYLLARLLGLA TICMICIEERE	AV.ARLERYA	NKLICTI	SECLWEIAQV	FLATIHVATL
BoMrpE	MARQIL MAROTI		WMFLSN	SP SAAGE 11G1	TLGMLSLFFFF VVCTETIEVIC	N DE IDEDE V M	I. WALIS ii	TTGIFIKEI	TIANTDVIKI
SaMnhE	MAVOLV	INFTTAVE	WI.FVTN	SYTTNNEVLCE	TFCLVLVVLLH	I RV LPCRF V V	TTLVR TT		TKANEDVIKI
DhMrpE	MOVI	INLEIGVI	WMFLOD	DWSILTFASCY	LFGTLVLFTL	R. RF. LDSKF <mark>Y</mark> L	FTLOAVV	TFFLFIYEI	FTSSTMVTRE
HzMrpE		WNLLLGLA	WVLLŜG	DFSGLNLLVGM	IFGYIALVLIE	EPOV.ESLKG <mark>Y</mark> P	ARVPRII	FVGFFIKEI	MOANLRVAFD
LiMrpE	MAFQLI	LNIILACI	WMFLES	sf sfatf i i g f	I I G IFLLLF M F	R.RF.LGSRF <mark>Y</mark> L	FRLFA lV Å	(LVFR F LH DI	I VS TV HVSRI
PfMbhA	MSFIT	AF I WAYFI	L <mark>WL</mark> V L TAGSKGM	LWSTQEL <mark>I</mark> A <mark>G</mark> L	I FASIVGYS T F	RNIIGEKASR <mark>F</mark> L	NPVKWIL FV A	A Y A P V <mark>L</mark> F W <mark>G M</mark>	IV KA <mark>NL</mark> D <mark>V</mark> AYR
			S2				- \$3	-	
	40	5 <u>0</u>	S2		80 <u>.</u>	<u>9</u> 0	- S3	- 110	120
DqMrpE	40. AFLPH.ASITPGFVRF	50 PTRCRSEI	S2 60 LEVTMLSSLITL	70. TPGTLTLGAHH	80 PGEG E DWEIVV	9 1 H G M Y F P D P	- S3 100 DDLTASLHDI	- 110 .ENHMLRAIF	120 REGLTR
<mark>DqMrpE</mark> RmPhaE	40 AFLPH.ASIT PGFV RF ILRAGRRPVNAGFMTV	50 TRCRSEI SL <mark>DL</mark> DDEN	S2 60 L EVTMLS S LITL NALALLACVVTA	7 9 TPGTLTLGAHH TPGTAWLEYDR	80 PGEGEDWEIVV RQKILLE	2 9. 7 H G MY FP D P H V LD IE N E	- S3 100 DDLTASLHDI DLWRKT I T.F	- 110 ENHMLRAIF YAADLK EI F	120 RREGLTR
<mark>DqMrpE</mark> RmPhaE XcPhaE	40 AFLPH.ASITPGFVRF ILRAGRRPVNAGFMTV VLGPE.SRIHPGFIWV	50 PTRCRSEI SLDLDDEN PLDIENI	S2 60 EVTMLSSLITL NALALLACVVTA GIAALTSMITL	79 TPGTLTLGAHH TPGTAWLEYDR TPGTVSAALSD	80 PGEGEDWEIVV RQKILLF DRKYLLV	20. HGMYFPDP HVLDIENE HVLDIENE	- S3 100 DDLTASLHDI DLWRKTIT.F DALIAEIKSF	- 110 ENHMLRAIF YAADLKEIF YETPLMEIF	120 RREGLTR 'E
<mark>DqMrpE</mark> RmPhaE XcPhaE AtPhaE	40 AFLPH.ASITPGFVRF ILRAGRRPVNAGFMTV VLGPE.SRIHPGFIWV ILFQRERDRKSGFLAV	50 PTRCRSE1 SLDLDDE1 PLDIENIE PLEIRDPN	S2 60 LEVTMLSSLITL NALALACVVTA 1GIAALTSMITL 4GLAVLATILTS	TPGTLTLGAHH TPGTLYDR TPGTVSAALSD TPGTVSAALSD TPGSAWLEYNS	80 PGEGEDWEIVV RQKILLE DRKYLLV SQGTLLI	90 HGMYFPDP HVLDIENE HVLHLDPP HVLHLDP	- S3 100 DDLTASLHDI DLWRKTIT.F DALIAEIKSF AAWISLIKNF	- 110 ENHMLRAI YAADLKEI YETPLMEI YEKLLMEI	120 REEGLTR 'E
DqMrpE RmPhaE XcPhaE AtPhaE BaMnhE	40 AF LPH.ASITPGFVRF ILRAGRRPVNAGFMIV VLGPE.SRIHPGFIWV ILFORERDRKSGFLAV ILSPG.RQRHPGFVVI	50 PTRCRSEI SLDLDDE PLDIENI PLEIRDPN PLELQNR	S2 60 EVTMLSSLITI VALALLACVVTA IGLALLSMITL GLAVLACMITA	7 0 TPGTLTLGAHH TPGTAWLEYDR TPGTVSAALSD TPGSAWLEYNS SPGTAWVDYNA	80 PGEGEDWEIVV RQKILLF SQGTLLI SQGTLLI	20 HGMYFPDP HVLDIENE HVLHLDDP HVLDDVDE HVLDA	DLLTASLHDI DLWRKTIT.F DALIAEIKNF AAWISLIKNF ETWRHLIKEF	HMLRAI VAADLKEI VETPLMEI VERPLIEI VERPLIEI	120 REGLTR P CAVDIVEGEK
DqMrpE RmPhaE XcPhaE AtPhaE BaMnhE PaMrpE	40 AFLPH.ASITPGFVRF ILRAGRRPVNAGFMTV VLGPE.SRIHPGFIWV ILFORERDRKSGFLAV ILSPG.RORHPGFVVI VLARR.VEVEPAVLAV	50 SLDLDDEN PLDIENI PLDIENI PLEIRDPN PLELQNR PVTRREVI	S2 60 LEVTMISSLITI NALALLACVVTA IGIAALTSMITI GLAVLATILTS NALAVLACMITA SVUTLIGTLLTI	7 9 TPGTLTLGAH TPGTAWLEYDR TPGSAWLEYDR SPGTAWVDYNA SPGTLALEYDE	80 PGEGEDWEIVV RQKILLF DRKYLLV SQGTLLI RGILTI ERGILYI	20 HGMYFPDP HVLDIENE HVLHLDDP HVLDDVDE HVLDLEDA HALDARR	DLUTASLHDI DLWRKTIT.F DAUIAEIKSF AAWISLIKNF ETWRHLIKEF SEOVTHILTE	LIO ENHMLRAI YAADLKEI YETPLMEI YERLIEI YERLIEI	120 REGLTR P GAVDIVEGEK
DqMrpE RmPhaE XcPhaE AtPhaE BaMnhE PaMrpE BsMrpE BsMrpE	40 AFLPH.ASITPGFVRF ILRAGRRPVNAGFMTV VLGPE.SRIHPGFIWV ILFORERDRKSGFLAV ILSPG.RORHPGFVVI VLARR.VEVEPAVLAY VLSPK.LNIRPGIFAF	50 PTRCRSEI SLDLDENIH PLDIENIH PLEIRDPN PLEIRDPN PLEIRDPN FLEIRDPN FLEIRDPN	S2 60 EVTMLSSLITL NALALLACVVTA GLAVLATISMITL GLAVLATILTS NALAVLACMITA ETIMLSLITL ETIMLSLITL	70 TPGTLTLGAHH TPGTAWLEYDR TPGSAULS SPGTAWVDYNA TPGTLWVDYNA TPGTLVMDISD	80 PGEGEDWEIVV RQKILLF DRKYLLV SQGILTI ARGILTI DRTILYI DRTILYI	20 HGMYFPDP HVLDIENE HVLLDP HVLDDP HVLDAPA HALDARR HALDARR	BOLTAS HDI DUWRKTIT.F DALIAEIKSF AAWISLIKNF ETWRHLIKEF SEDVTHILTE EKAIFDIRES	110 ENHMLRAIR YAADLKEIF YEKLLMEIF YERPLIEI LERRLLAWI FERAIQEVS	120 REGLTR P GAVDIVEGEK DAGKREGVSP
DqMrpE RmPhaE XcPhaE AtPhaE BaMnhE PaMrpE BsMrpE BpMrpE SaMnbF	40 AF LPH.ASITPGFVRF ILRAGRRPVNACFMTV VIGPE.SRIHPGFIWV ILFORERDRKSGFLAV ILSPG.RORHPGFVU VLARR.VEVEPAVLAY VLSPK.LNIRPGIFAF VLSPK.NNIQPGIVAV	50 PTRCRSEI SLDLDDEN PLDIENIP PLEIRDPN PVTRRVI KTELTKDU PTKLKKDU	S2 60 LEVTMLSSLITL NALALLACVVTA GIAVLATILLS CALAVLACMITA KVTLLGTLLTL VEITMLSLLITL VEISLLASLISL VEISLLASLISL	70 TPGTLTLGAHH TPGTAWLEYDR TPGSAWLEYNS SPGTAWLDYNS SPGTLALEYDE TPGTLWDISD TPGTLSMDFSD TPGTLSMDFSD	80 P G E G E D M E I VV RQKILLK RQGTLLI ARGILTI ARGILTI ARGILTI D NK YI YI DNK YI YI	20 HGMYFPDP HVLDIENE HVLDDP HVLDDVDE HVLDLEDA HALDARR HAMDIEDA HAMDIEDA	DULTASTHDI DIWKKTIT.F DALIAEIKSF AAWISLIKNF ETWRHLIKEF EKAIFDIRES EKAIFDIRES	110 ENHMLRAIF YETPLMEIF YEKLLMEIF LERRLAWI FEKAIQEV SFRAILEVI	120 RREGLTR 'P 'GAVDIVEGEK DAGKREGVSP 'R
DqMrpE RmPhaE XcPhaE AtPhaE BaMnhE BsMrpE BsMrpE SaMnhE SaMnhE DhMrpE	40 AF LPH. ASITPGFVRF ILRAGRRPVNAGFMIV VLGPE.SRIHPGFIWV ILFORERDRKSGFLAV ILSPG.RORHPGFVVI VLARR.VEVEPAVLAY VLSPK.LNIRPGIFAF VLSPK.MNIOPGIVAV IIKPS.IKNEPGFFVY IKPS.IDTKPGFVSF	50 PTRCRSEI PLDIDDE PLDIENTH PLEIRDEN PLELQNR PVTREVI KTELTKDI PTKLKTDI HTDLKKDI	S2 60 LEVTMLSSLITL NALALLACVVTA GLAALTSMITL GLAVLATILTS NUTLIGTLLTI VEITMLSLITL VELSLLASLISL VQIVLLSNLITL FUTLIALLITL	79 TPGTLTLGAHH TPGTAWLEYDB TPGTAWLEYDB SPGTAWLEYDB SPGTAWUDYNA TPGTLAEYDE TPGTLWDISD TPGTLSMDFSD TPGTVVLGVSD TPGTVVLGVSD	80 PGEGEDMEIVV , RQMILLE , RQMILLE , RGILTI , RGILTI , RGILTI , RGILYI , DRILYI , DRILYI , DRIKIYI , DRIKIYI	20 HGMYFPDP HVLDIENE HVLDDVDE HVLDLEDA HALDARR HAMDIEDA HAIDFDA HAIDFSTK HAIDFSTK	DILTAS HDI DIWRKTIT.F DALIAEIKSF AAWISLIKNF ETWRHLIKEF SEDVTHILT EKAIFDIRES EKMIRDIHDT EQEVESIKTS	110 ENHMLRAI YEADLKEI YETPLMEI YERLIEI FERALEV FERALEV LERALEV LEKIVREV	120 RREGLTR P GAVDIVEGEK DAGKREGVSP R K P.
DqMrpE RmPhaE XcPhaE AtPhaE BaMnhE BsMrpE BsMrpE SaMnhE DhMrpE HzMrp5	40 AFLPH.ASITPGFVRF ILRAGRRPVNAGFMTV VLGPE.SRIHPGFIWV ILFORERDRKSGFLAV ULSPG.RQHPGFVVI VLSPK.LNIRPGIFAF VLSPK.NIQPGIVAV IKPS.IKNEPGFFVY IKPQ.IDIKPGISF VLTPP.WHMOPGVAV	50 PIRCRSEI SLDLDDE PLDIENLE PLELRDE PLELUNR PUTRREVI KTELTKDI HTDLKKDI ATSLESDI ISARTEN	S2 60 EVTMLSSLITL GLALLACVVTA GLAVLATILTS ALAVLATILTS KVTLLGTLLTL VELSLASLISL VQIVLLSNLITL EVTLLALLTL EVTLLALLTI	70 TPGTLTLGAHH TPGTYAALSD TPGSAWLEYNS SPGTAWUDYNA TPGTLAEYDD TPGTLWDISD TPGTLWDSD TPGTVULGVSD TPGTVULGVSD TPGSVVMEITP TPGTDV	80 PGEGEDMELVV RQMILL PRVLLV SQGILI PRGLYI PRGLYI DRTILYI DRTILYI DRKYYI DKKFYI DKKVYY	20 HGMYFPDP HVLDIEDP HVLDDP HVLDDDP HALDARR HALDARR HALDARR HAIDYPK HAIDFSTK HAMDIPEL HAMDIPL	DULTAS HDI DUMKTIT.F DALIASIKSF AAWISLIKNF ETWHLIKF EKMIFDIRES EKMIFDIRES SDAVIRSKEF SDAVIRSKEF	LIO ENHMLRAIR YADLKEIF YETPLMEIF YERPLIEI LERRLLAWI FEKAIQEVS FERAILEV LEKIVREV FEAIKKVI	120 REGLTR P GAVDIVEGEK DAGKREGVSP R K EI RP
DqMrpE RmPhaE XcPhaE BaMnhE PaMrpE BpMrpE SaMnhE DhMrpE HzMrpE LiMrpE	40 AFLPH.ASITPGFVRF ILRAGRRPVNAGFMTV VLGPE.SRIHPGFIWV ILFORERDRKSGFLAV ILSPG.RQRHPGFVV VLSPK.LNIRPGIFAF VLSPK.MNIQPGIVAV ILKPG.IKNEPGISF VLTPP.WHMQPGVIAM VLKPQ.WNIRPGIFRY	50 PIRCRSEI SLDLDDE PLDIENLE PLEIRDPN PLELQNR2 PVTRREVI KTELTKDE PTKLKTE HTDLKKE ATSLESDI PLSARTEN DTTLETDE	S2 60 EVTMLSSLIT NALALLACVVTA GIAALTSMIT GIAAUATILTS NALAVLACMITA VEITMLSLLIT VEITMLSLLIT UQUVLISNLIT EVTLLALLET 4EITMVANLISL	TPGTLTLGAHH TPGTAWLEYDR SPGTAWLEYDR SPGTAWUDYNA TPGTLALEYDE TPGTLLEYDE TPGTLSMDFSD TPGTLSMDFSD TPGTLSUDYSD TPGTLSDVSD	80 PGEGEDMELVV RQKILLF DRKYLLV SQGTLLI RGLLVI DRKILVI DRKILVI DRKVLYI DRKVLYI DRKVLYI DRKVLYI	20 H GMYFPDP H VLD IENE H VLD VDE H VLD LEDA H ALDARR H ALDARR H AID VPNK H AID VPNK H AMFLDD H AMFLDD	DULTASIHDI DIWRKTIT.H DALIAELKSF AAWISLIKNF ETWRHLIKSF EEVTHLITE EKAIFDIRES EKMIRDIHDI SDAVIRSKEF EEELRRNIKE EEELRRNIKE	110 ENHMLRAIR VADLKEIR VEKLLMEIR VEKLLMEI FEKAIQEV FERAILEV FERAILEV GEEAIKKVI MEHRALELR	120 REGLTR P. GAVDIVEGEK DAGKREGVSP R R. R. R. R. R. R. R. R. R. R. R.

Е



G



Figure S2. Purification and cryo-EM of Dietzia sp. DQ12-45-1b Mrp complex

- (A). A representative size-exclusion chromatography trace of the purified Mrp complex solubilized with DDM.
- (B). SDS-PAGE shows the presence of all six Mrp subunits as labeled on the right. Protein markers (PM in kDa) are labeled as shown on the left.
- (C). Representative cryo-EM micrograph of Mrp particles.





Figure S3. Cryo-EM Analysis of Dietzia sp. DQ12-45-1b Mrp complex

- (A). The workflow of cryo-EM data processing. A total of 293,049 particles were selected using the Gautomatch software from 1,835 motion corrected micrographs. After removing detergent micelles and other false positives in several rounds of 2D classification, 137,082 particles were selected to generate the initial model.
- (B). Angular distribution of all particles used in the final 3D reconstruction.
- (C). The Fourier shell correlation (FSC) curve between partial 3D maps is shown in red. The FSC curve between the atomic model and the experimental map is shown in black. 3D maps are colored according to their local resolution, as determined by ResMap.
- (D). Local resolution of the Mrp, The range of resolution is color-coded from the higher resolution blue (2.5 Å) to the lower resolution red (4.5 Å).
- (E). Representation of the refined composite coordinate model, colored according to the B factors of the model atoms.

А



Figure S4. A gallery of EM density maps of representative transmembrane helixes of Mrp complex

- (A). Maps are superimposed with their corresponding atomic models in cartoon (main chains) and stick (side chains) presentations.
- (B). Representative densities of lipid molecules are shown in their stick models.





Figure S5. Structural twist and constraint of Mrp complex

- (A). Structural twist within the Mrp complex viewed from different directions.
- (B). The arrangement of TM helixes from different subunits along the central curve of the Mrp complex. Subunits are colored identical to (A).
- (C). HL-helix and β H-belt (green) of the Mrp complex.



Figure S6. Sequence alignments of individual Mrp subunits and their counterparts in the Complex I from different species

- (A). Sequence alignments of MrpA A domain and its counterparts in the Complex I. Conserved residues in the central polar axis are marked with stars.
- (B). Structural alignment of MrpA A domain (green) and Nqo12 (grey, PDBID: 4HEA). The conserved charged residues are shown as stick models.
- (C). Structural alignment of MrpD (green) and Nqo14 (grey, PDB ID: 4HEA).The conserved charged residues are shown as stick models.
- (D). Sequence alignments of MrpD and the counterparts in the Complex I and MBH. Conserved residues in the central polar axis are marked with stars.



D		TM2	_		TMA	
	8 0	90	100	110	120	130
DqMrpD PfMbhH EcNuoN TtNqo14 YiND2 TeNdhB HsND2 OaND2 BtND2	SIPFVL. DMFSALM PIRIVWEVDKFGALM DVTPLMRVDGFAMLY AFGPYA.VDGVSQVF DMLIYFIMIVISSLY SFFGSFISDHLSLFF	LTVTSLLT <mark>L</mark> TCAAF VLIVTFVSFLAVIY TGLVLLASLATCTF TLLALLGALWTVGL GYNLYNNNLYKTLF RGLIALSALGTILM	AVAAG E SIEYMK.HI AYPWLEGYN VRS EP SIRYVEQTC	AYKRFYPPL TGLEKFYTLI IDNKDEFYLL GRFEFYLL KKELIILF SSSLGEFMTII MNPLAOPVIY MNPIILIII MNPIIFII	(LUTAGUNGAI LILELGMLGI LIAALGGILL LAALGMHLLA LINILGALLI STIFAGTLITA MTVMLGTIIV LTIMLGTIIV	LTGDLFNF FV FVEV ITGDIFNF YV FLEI NANHLASLFLGIEL STRHLLLML V ALEA HSNDFITLFVAIEL GAQELVFIFVALET LSSHWFFTWVGLEM ISTHWLLIWIGFEM
	TM5	_	TM6			TM7a
1	140 150	160	170	180	190	200
DqMrpD PfMbhH EcNuoN TtNqo14 YiND2 TeNdhB HsND2 OaND2 BtND2	MLLPSYGLMMITRSG MSIASYALVAFRNDT ISLPLFGLVGYAFRO LSLPLYALATWRR QSYSIYLITAIYNSS LSIASYLLTGYTKRD NMLAFIPVLT.KKMN NMLAIIPIMM.KKHN NMLAIIPIMM.KNHN	R A S V V G V A A S R L Y I WE G I E A G I K Y M KR SLE A S I K Y M G G L E A S L K Y F Y K A S K A S M L Y F S R S N E A S M L Y L P R S T E A S T K Y F P R A T E A S T K Y F	SVNLL AS TI FAGSL AS SE ILSAA AS E LGALAAAE FMGGILSII LIGAASSAI LTQAT AS MI LTQST AS MI LTQST AS MI	LLIGVALIY VLLGIALLY FLYGAALFY FLYGAALFY FLYGSSLLY LLMAILFNN LMAIIINLM	; VTG.TVNIAQI ; QYG.TLTMGYI ; QYG.TLTMGYI ; ATG.SLVLGA ; SVLN.SYTLHSI ; LSGGHTQLPA 11LSG.QWTMTN 1FSG.QWTVMKI 1FSG.QWTVMKI	HGAASEDTAV AVKIAENPTIVA GKNLGDGMLNEPLL GEGPLY DSLIINTLDL AQALSSESLGL TN FN
	TM7a	— TM7b	— TM	18		·
	210 220	230	240	250	260	270
DqMrpD PfMbhH EcNuoN TtNqo14 YiND2 TeNdhB HsND2 OaND2 BtND2	AVATALVLFALAIKA KVALALFIGGLLFKS LAGFGLMIVGLGFK ALALGLLLVGLGFKA NLILIALSLGLLFKI VVALVFVIAGISFKI QYSSLMIMMAMAMKL PMASMLMTMALAMKL	AVVPVHGWLARAYP GAAPVHMWLADAHP SLVPFHLWTPDVYQ GIAPLHKWLISIYE SAVPFHGWTPDVYQ GMAPFHFWVPEVTQ GMAPFHFWVPEVTQ GMAPFHFWVPEVTQ	KMSPAVTAN AAPSSISAN GAPAPVSI SSPTPVVLE NTPILITIY GAPTPVVAE GTPLTSGLI GIPLSSGLI	MES.GLHTKIA MLSGLVIKIGO LA.TASKIAI MA.TSVKAAY IS.LIPKISI LS.VGSKAAO LL.TWQKLAP LL.TWQKLAP LL.TWQKLAP	AIYAIYRI YAVI Siyalarivesi FGVVMRIVESI FGALLRVAP ILSYLVLSNISI SFALAIRFLTLP MSVLYQILPSI MSVLYQIFPSI	FDGDSRYLW V FSPTINLGTIGW I PVGDSEAIRV. V NSL V FPSVTDQWQL. I NVSLL NLDLI
	TM9	— Т	M10	—	TM	[11
DqMrpD PfMbhH EcNuoN TtNqo14 YiND2 TeNdhB HsND2 OaND2 BtND2	280 290 VVVFSATMLIGVLGA IIFACITLIVGNAMA AIIAFASIIFGNLMA ALLVALSVVVGNLAA SILAILTLLVGSVGG TVLAILSMILGNVVA LTLSILSIMAGSWGG LTLSILSITIGGWGG LTLSVLSILIGGWGG	JOO VGEAAPRSILAFHM VVQEDLKRLLAYSS LSQTNIKRLLGYSS LAQKEAKRLLAYSS LLQIKIKRLLAFSG LAQTSMKRMLAYSS LNQTQLRKILAYSS LNQTQLRKIMAYSS	JIO VSQIGYILI SHLGYLLV ISHLGYLLV ISHLGYLLV ISHLGYMAI LTNAGYMMI IGQAGFVMI ITHMGWMMA IAHMGWMTA IAHMGWMTA	320 GVALFGPIG. GLGIGMVAYG ALIALQTGE. ALYTGN GFVVGTEAG. VLPYNP VLYNP VLYNP	TRVGEIALAG TRVGEIALAGA AQAI EFSY YASM NMT TMT	330, 340, SIFYLLHHMIVKAAL AIYHTVNHALMKALL GVYLAGYLFSSLGA GFYLLTYVLATGLA KLYYITQYSISHLAI ALFYLLVYLFMNLGA CILNLTIYIILTTA CLLNLIIYIIMTSTM CLLNLIIYIIMTSTM
	TM11			TM12a		TM12b
DqMrpD PfMbhH EcNuoN TtNqo14 YiND2 TeNdhB HsND2 OaND2 BtND2	350 FLAIGAIEVRYG FLVAGAVIHEIG FGVVSLMSSPYRGPD FAVLSQISPD FMIIIFSIYYINYIN FTCVILFSLRTG FLLINLNS FTLFMANS FTMFMANS	360 PRRLGQ LSG TRNMNE LSG ADSLFS YRG RVPLEA LRG NQYNPIIYVNQ LKG TDQISE YAG STTTLL LSR TTTTLS LSH	JAKTEPLV LAKTMPKTJ LFWHRPILF LYRKDPLLC LYRKDPLLC TWRKLTWLJ TWNKLTWLJ TWNKLPIMJ	380 VAFFASAMSI FAFLIGAAAI AVMTVMMLSI LAFLVAMLSI LSLSLCLSI PLIPSTLLSI VLILATLLSM	390 AGIPPFSGFVA VGLPPLNGFAS AGIPMTLGFIG IGIPPLAGFWG GGIPPLAGFFG GGLPPLAGFFG IGGLPPLSGFME IGGLPPLSGFME	400 AKLSIIIAALDAGQI KWLIYESSALFN.P KFYVLAVGVQAHLW KYLAFAEAARAGAW KLNILMSILNNGYY KIYLFWAGWQAGAY KWMIIQEMTKNDSI KWMIIQEMTKNNSI

Figure S7. Salt-resistance assay in E. coli KNabc cells

- (A). Colony formation on solid medium lacking NaCl.
- (B). Colony formation on solid medium containing 200 mM NaCl.
- (For completeness, certain results already shown in Fig. 4 are shown here again in their original form.)

(Fig. S7A 1/2)



(Fig. S7A 2/2)

		10:	xdilut	tion	
	1x10 ⁻¹	1x10 ⁻²	1x10 ⁻³	1x10-4	1x10-
WT		۲	٩	*	100
Control(-)	•	٠			39
A-E132A	•				<i>2</i> 5
A-K213A	•	•			ŝŧ
A-K244A	•	•			54%
A-K329A	•	•			2
A-K384A	۲				
A-E385A	ø	0	\$	-	ъ.°
WT	۰	۲	•	*	*
Control(-)	۲	۲	•		1
A-D647A	•	•			3
A-E656A	•	•			4
A-V657A	•	•	۲		
A-D736A	•	•	۲		-5'
A-R738A	•				광
A-D741A	Ô	Ô	0	鬱	博
WT	٠	•	•	癰	20
Control(-)	٠	۲		•	辞
A-E745A	•				
D-E137A	۲		•		26
D-K220A	۲				den.
D-K251A	•		۲		5.er -
D-K392A	۲			di.	1.
D-I396Q/L400N	٢	۲	0	<i>\$</i> *	,ŝ
WT	0	۲	\$	M	e
Control(-)	•	•	٠		-125- 1
F-D36A	•	۲			1.
MrpA(1-522)	•	•			500
MrpD	•	•	•	-	13
$\Delta MrpE$	•	•	0	*	-54

1x10 ⁻¹	1x10 ⁻²	1x10 ⁻³	1x10 ⁻⁴	1x10	-5	1x1
•	0	۲	۲	dia.a		0
0	•	•	•	-		•
	0	•	•	#		•
		•	•	-		•
		•	۲	*		•
۲	۲	0	٥	0		۰
•	•	•	۲	\$		۲
0	۲	•	•	۲		0
Ģ	۲	۹	۲			0
•				\$		•
				<i>4</i> 26		•
				帶		•
				ąŝ.		•
				۰		•
				s₩4		۲
6	٢	۲	-	150		6
0	۲	-	-	je.		۲
0				4 0		•
0				Сr		۲
				4		0
						Ø
				ŵ.		
0				ş.,		0
ø	۲	ø .	0	re _k		0
•	۲	۲	•	34		0
•	0	•	•	۲		۲
	•	0	-	:		•
•	•	•		÷.		0
•	0	•	1	320		•
0	0	*	*	13		•

10xdilution							
	1x10 ⁻¹	1x10 ⁻²	1x10 ⁻³	1x10 ⁻⁴	1x10 ⁻⁵		
	0	۲	0	۲	1		
	•	•	•	•	dige.		
	•		•	٠	\$		
	•	•	٠	6	-		
	•	•		*	R:-		
	•	•	•				
	•	•	•	•	-		
	•	•	•	-	127		
	۲		0	۲	1		
	•	•	•	٠	14		
	•		•	٠	-		
	•	•	۲	•	25.95 100		
	•	•		\$	·*		
	•	•	•				
	•	•	•	•	-		
	•	0	0	-	-		
	۲		۲	۲	Aig's		
	•	•	•	۲	202		
	•				190		
	0		•	*	*		
	ø	•		de-	¢. ⁴ y		
				•	ŝte I		
	0	•		8			
	0	0	0	4	15		
		•	•	0	35		
			•		10		
	•	•	0	6	.79		
			~		3		
	-			-	46-		
	0	0	•		and the second s		
					1 March		



Figure S8. Liquid salt-resistance assay in E. coli KNabc cells

Results from negative controls at 0 M NaCl (A and E) and from assays in the presence of 200 mM NaCl (B and F) are presented. The histograms (C, D, G, H) represent cell concentrations of corresponding growth curve at plateau phase. The experiments were repeated in triplicate, each including three biological repeats. The results shown represent the mean of at least six determinations, with error bars representing std deviations. (For completeness, some data shown in Fig. 4 are repeated here.)



Figure S9. HPLC assay of different mutants and Western Blot of individual subunits.

- (A). HPLC assay of different mutants that lost their resistance to high salt concentrations. The vertical axis represents GFP fluorescence signal. The levels of best and worst expression differed by a factor smaller than 4.
- (B). SDS-PAGE of MrpA (residues 1–522), MrpD, and ΔMrpE, with both Coomassie Brilliant Blue stain and the fluorescence of their fused GFP.
- (C). Western Blot of MrpA (residues 1–522), MrpD and ΔMrpE. The blot was probed for Strep-II tag using anti-Strep-II antibody and horseradish peroxidase-conjugated secondary antibody.



Figure S10. Mapping of point mutations to the Mrp complex structure

Mutations included are those from this study as well as from previous reports (1, 7, 11-13) (also see Table S2). Mutations of wild-type like behavior are depicted as green spheres; loss-of-function mutations are shown as red spheres and labeled in the side view panel; intermediates are shown as yellow spheres.



Figure S11. Hypothetical functional cycle of the Mrp complex

The two Mrp pumps are represented by rectangles, with other stabilizing parts (on the right side) omitted for simplicity. Substrates (Na⁺) and driving substances (protons) are represented by magenta and cyan spheres, respectively. The dynamic connection of the central polar axis is represented by combinations of an ellipse and a (bule/red) sphere. The major point of this mechanistic model is the conformational cooperativity between subunits and competition between Na⁺ and nH⁺.



Figure S12. Simplified energy landscape scheme of the Mrp complex

Gibbs free-energy landscape plot describing the thermodynamic relationship between different states (8). Horizontal lines represent states; dashed lines are for hypothetical states. Ascending and descending thin arrows represent exoergic and endoergic transitions between states, respectively. Green (purple) arrows are associated with the electrostatic energy of protons (Na⁺). Cyan (red) arrows are associated with the chemical potential of protons (Na⁺). Subscripts L and R refer to energy terms associated with loading and releasing steps, respectively. ΔG_C is the change of conformational energy; $\Delta G_D \equiv RTIn(K_{d,1}/K_{d,0})$, where subscripts 0 and 1 represent initial and final states] denotes differential binding energy of a given ligand(s). During one functional cycle, the starting and ending states are identical (e.g. CoutH⁺ is chosen arbitrarily), only being differed by the energy dissipation (*i.e.* Qx) of the Mrp complex which can be considered as the measure of the driving force. Notes: (i) Many energy terms in the plot are variable, depending on the cellular/experimental conditions, *e.g.* the membrane potential $\Delta \Psi$ and ΔpH . However, in any case, the steps shown in this plot must meet the requirements of the *First* and *Second Laws* of thermodynamics. (ii) Steps marked as 'coupled' are likely to occur simultaneously.



Figure S13. Comparison of DqMrp with AfMrp

(A). Overlay of DqMrp (green) with AfMrp (grey, PDB ID: 6Z16) shown in carton presentation (helices and ropes).

(B). The structural difference between DqMrpE and AfMrpE in the circled area of panel (A).

(C). The surface charge distribution of AfMrp. Protein surface is shown in red for negatively charged, white for neutral, and blue for positively charged area.

(D). Cavity between AfMrpA and AfMrpF in the circled area in panel (C). Lipid molecules are shown in yellow sticks.

(E). The surface charge distribution of DqMrp. Colored as in (C).

(F). The region between DqMrpA and DqMrpF as circled in panel (E) and corresponding to the AfMrpF region shown in panel (C).







Е







Supplemental Tables

Data collection			
Microscope	Titan Krios		
camera	Gatan K2 Summit		
Magnification	130,000 x		
Voltage (kV)	300		
Electron dose (e ⁻ / Ų)	~60		
Dose rate (e ⁻ /pixel/s)	10		
Defocus range (µm)	1.8–2.3		
Pixel size	1.04		
Reconstruction			
Micrographs	1,835		
Particles in 3D classification	137,082		
Particles in final refinement	93,505		
<u>Refinement</u>			
Resolution (Å)	3.0		
Number of atoms	14,320		
Protein residues	1872		
Ligands	LMT:28		
Sharpening B-factor (Å ²)	-82.30		
R.m.s deviations			
Bond lengths (Å)	0.004		
Bond angles (°)	0.591		
Ramachandran plot			
Favored (%)	94.28		
Allowed (%)	5.72		
Disallowed (%)	0.00		
Rotamer outliers (%)	0.50		
Map CC	0.83		
MolProbity score	2.14		
Clash score	18.06		

Table S1. Cr	vo-EM data	collection.	refinement	and	validation	statistics

Table S2. Summary of mutation analyses on the Mrp complex

(Excel sheet)

References

- 1. M. Morino, S. Natsui, T. H. Swartz, T. A. Krulwich, M. Ito, Single gene deletions of mrpA to mrpG and mrpE point mutations affect activity of the Mrp Na+/H+ antiporter of alkaliphilic Bacillus and formation of hetero-oligomeric Mrp complexes. *J Bacteriol* **190**, 4162-4172 (2008).
- M. H. Saier, Jr., A functional-phylogenetic classification system for transmembrane solute transporters. *Microbiol Mol Biol Rev* 64, 354-411 (2000).
- 3. T. H. Swartz, S. Ikewada, O. Ishikawa, M. Ito, T. A. Krulwich, The Mrp system: a giant among monovalent cation/proton antiporters? *Extremophiles* **9**, 345-354 (2005).
- 4. T. A. Krulwich, G. Sachs, E. Padan, Molecular aspects of bacterial pH sensing and homeostasis. *Nat Rev Microbiol* **9**, 330-343 (2011).
- T. Hamamoto *et al.*, Characterization of a gene responsible for the Na+/H+ antiporter system of alkalophilic Bacillus species strain C-125. *Mol Microbiol* 14, 939-946 (1994).
- T. A. Krulwich, A. A. Guffanti, M. Ito, pH tolerance in Bacillus: alkaliphiles versus non-alkaliphiles. *Novartis Found Symp* 221, 167-179; discussion 179-182 (1999).
- M. Morino *et al.*, Single site mutations in the hetero-oligomeric Mrp antiporter from alkaliphilic Bacillus pseudofirmus OF4 that affect Na+/H+ antiport activity, sodium exclusion, individual Mrp protein levels, or Mrp complex formation. *J Biol Chem* 285, 30942-30950 (2010).
- 8. X. C. Zhang, Y. Zhao, J. Heng, D. Jiang, Energy coupling mechanisms of MFS transporters. *Protein Sci* **24**, 1560-1579 (2015).
- 9. J. Steiner, L. Sazanov, Structure and mechanism of the Mrp complex, an ancient cation/proton antiporter. *Elife* **9** (2020).
- 10. F. Madeira *et al.*, The EMBL-EBI search and sequence analysis tools APIs in 2019. *Nucleic acids research* **47**, W636-W641 (2019).
- E. Sperling, K. Gorecki, T. Drakenberg, C. Hagerhall, Functional Differentiation of Antiporter-Like Polypeptides in Complex I; a Site-Directed Mutagenesis Study of Residues Conserved in MrpA and NuoL but Not in MrpD, NuoM, and NuoN. *PLoS One* **11**, e0158972 (2016).
- 12. M. Morino, S. Ogoda, T. A. Krulwich, M. Ito, Differences in the

phenotypic effects of mutations in homologous MrpA and MrpD subunits of the multi-subunit Mrp-type Na(+)/H(+) antiporter. *Extremophiles* **21**, 51-64 (2017).

13. Y. Kajiyama, M. Otagiri, J. Sekiguchi, T. Kudo, S. Kosono, The MrpA, MrpB and MrpD subunits of the Mrp antiporter complex in Bacillus subtilis contain membrane-embedded and essential acidic residues. *Microbiology* **155**, 2137-2147 (2009).