Cotranslational membrane insertion of the voltage-sensitive K^+ channel KvAP

Justin M. Westerfield[1**], Petra Kozojedová[1], Cara Juli[1], Ane Metola[1], Gunnar von Heijne[1,2*]

[1]Department of Biochemistry and Biophysics
Stockholm University, SE-106 91 Stockholm, Sweden
[2]Science for Life Laboratory Stockholm University, Box 1031, SE-171 21 Solna, Sweden
[*, **]Corresponding authors.

Email: justin.westerfield@dbb.su.se, gunnar.von.heijne@dbb.su.se

Abstract

Voltage-sensor domains (VSDs), found in many voltage-sensitive ion channels and enzymes, are composed of four transmembrane helices (TMHs), including the atypical, highly positively charged S4 helix. VSDs are cotranslationally inserted into the membrane, raising the question of how the highly charged S4 helix is integrated into the lipid bilayer as it exits the ribosome. Here, we have used Force Profile Analysis to follow the cotranslational insertion of the six-TMH KvAP voltage-sensitive ion channel into the *E. coli* inner membrane. We find that the insertion process proceeds through three semi-independent steps: (*i*) insertion of the S1-S2 helix hairpin, (*ii*) insertion of the S3-S5 helices, and (*iii*) insertion of the Pore and S6 helices. Our analysis highlights the importance of the concerted insertion of helical hairpins, the dramatic influence of the positively charged residues in S4, and the unexpectedly strong forces and effects on downstream TMHs elicited by amphipathic and re-entrant helices.

Introduction

The great majority of α-helical integral membrane proteins are cotranslationally inserted into their target membrane with the aid of a translocon. In the bacterium *Escherichia coli*, the translocon function is carried out by the SecYEG and YidC translocons located in the inner membrane (1), while in eukaryotic cells this function is carried out by the Sec61 and EMC complexes and accessory proteins in the rough endoplasmic reticulum (ER) (2). During the cotranslational insertion process, transmembrane α-helices (TMHs) partition into the membrane due to their overall hydrophobic character (3), while their in-out orientation relative to the membrane is largely dictated by flanking positively charged residues according to the "positive-inside" rule (4, 5).

While these basic features of membrane protein biogenesis have long been relatively well understood, it is only recently that methods have become available to follow the cotranslational membrane insertion process on a residue-by-residue level. Chief among those methods is Force Profile Analysis (FPA). FPA was first introduced as a method to follow the cotranslational insertion of model TMHs into the inner membrane of *E. coli* and, analogously, into ER-derived rough microsomes (RMs) (6). Subsequently, it has been applied to study the cotranslational folding of globular proteins (7, 8), cotranslational membrane translocation of proteins into the periplasmic space (9, 10), and cotranslational insertion of multispanning membrane proteins (11-13).

From the perspective of cotranslational membrane insertion, the so-called voltage-sensor domains (VSDs), first identified in voltage-sensitive ion channels (14), are of particular interest. VSDs are membrane-embedded domains composed of four TMHs, named S1-S4, and sense changes in the membrane potential via S4. Unique among known TMHs, S4 TMHs contain four to six conserved, positively charged residues that translate changes in the membrane potential into up-down movements of the S3-S4 "paddle" in the membrane (15). In voltage-sensitive ion channels, the movement of the paddle controls the opening and closing of an attached pore domain comprised of S5, a re-entrant helix named the Pore helix, and S6 (16). Cotranslational membrane insertion of VSDs poses a distinct problem due to the high charge density of S4, which has to eventually become embedded in the hydrophobic membrane environment (17).

In order to gain a deeper understanding of the cotranslational membrane insertion of VSDs, we have applied FPA to the archaeal voltage-sensitive K^+ (Kv) channel KvAP from

Aeropyrum pernix. KvAP was chosen because it is a prototypic tetrameric Kv channel of known structure (18) and the overall membrane insertion propensities of the S1-S6 TMHs have been measured (19). Our results unveil a complex insertion process, strongly influenced by the positively charged residues in S4.

Results

Force-profile analysis of cotranslational membrane insertion

Briefly, FPA measures forces on the nascent chain (NC) generated by the cotranslational membrane insertion and folding of TMHs, using so-called translational arrest peptides (APs) engineered into the NC as force-sensors (6, 20-25). The most commonly used AP for this application is from the *E. coli* SecM protein (Uniprot ID P62395, residues 150 to 166; hereafter called the SecM(*Ec*) AP). Immediately upon synthesis, the AP binds in the upper reaches of the ribosome exit tunnel and induces an altered active-site geometry in the peptidyl transferase center (PTC), preventing chain elongation (26). By application of an external force on the AP, however, it can be detached from its binding site, restoring the correct active-site geometry and allowing elongation to continue (6, 8, 26), Fig. 1a. *In vivo* expression, [^{35}S]-Met pulse-labeling, immunoprecipitation, and separation by SDS-PAGE of constructs containing the SecM(*Ec*) AP thus result in two radioactive bands, corresponding to the arrested (A) and the full-length protein (FL), Fig. 1b. The higher the external pulling force applied on the NC at the point when the ribosome reaches the last codon of the AP, the larger will be the fraction of full-length protein, calculated as $f_{FL} = I_{FL}/(I_A + I_{FL})$, where I_A and I_{FL} are the integrated intensities of the arrested and full-length bands, respectively (6, 8).

By analyzing a series of constructs where the SecM(*Ec*) AP is fused to progressively longer truncations of the protein of interest, a force profile (FP) can be generated by plotting f_{FL} against the number of residues, N, measured from the construct's N-terminus to the end of the AP, Fig. 1c. The FP thus represents the variation in the instantaneous force exerted on the AP during translation. High pulling forces are generated during the cotranslational partitioning of TMHs into the membrane, and the FP thereby provides a

detailed picture of how different parts of the protein interact cotranslationally with the translocon/membrane system as they emerge from the ribosome (13).

The KvAP force profile

We determined the full FP for KvAP at four-residue resolution (except for the region N = 150-166, which was mapped at one-to-two-residue resolution), Fig. 2a, using a series of constructs schematically represented in Fig. 1c (see Supplemental Table S1 for sequences of all constructs). Note that the 30-residue HA/AP part has the same sequence in all constructs and fills up most of the exit tunnel, as judged from both biochemical data (27), FPA data on cotranslational folding of water-soluble proteins (28), and the structure of a SecM-stalled ribosome-nascent chain complex (29) (Supplemental Fig. S1). Thus, because the sequence present inside the exit tunnel is the same in all constructs, the variation in pulling force recorded in the FP mainly reflects interactions between the NC and the translocon/membrane environment. In order to be able to visualize the shortest constructs ($N \leq 122$ residues) on the SDS-PAGE gels, a 177-residue part of the *E. coli* inner membrane protein LepB was fused to their N-terminus, as indicated in Fig. 1c (see Materials and Methods); as shown in Supplemental Fig. S2, the FP obtained with the LepB fusion tends to give slightly higher f_{FL} values (the average difference is 0.06) but does not differ significantly in shape over the tested region N = 110-166 residues. Similar control experiments in an earlier study of the GlpG and BtuC inner membrane proteins (13) also showed not significant differences ±LepB, and the replacement of the H2 transmembrane helix in LepB with a 19-residue segment composed of 8 Leu and 11 Ala residues likewise was found to have no effect on f_{FL} for a model membrane protein construct (6).

We previously found that a model 19-residue TMH generates a peak in the FP that reaches half-maximal amplitude at an N value (N_{start}) where its N-terminal end is ~45 (±3) residues away from the PTC, and drops to half-maximal amplitude at an N value (N_{end}) where its C-terminal end is ~45 residues from the PTC (6); similar N_{start} and N_{end} values have been found for TMHs in other inner membrane proteins, both by FPA (10, 13) and a real-time FRET assay (30). Furthermore, if we overlay the KvAP FP and the predicted ΔG of insertion (ΔG_{pred}, water-to-bilayer) free energy profile (3) calculated for the 19-residue sequence window centered 45 residues from the PTC, Fig. 2a, the peak positions correlate, with some exceptions. This indicates that, during cotranslational membrane insertion, the distance between the PTC in the ribosome and the membrane insertion site

in the translocon can be bridged by a ~45 residue-long, mostly extended polypeptide. The FP thus reflects membrane insertion events taking place ~45 residues from the PTC, with a small uncertainty stemming from the fact that the conformation of the ~15 residues between the constant HA/AP part and the insertion site may not be the same for all constructs (e.g., short helical segments could potentially form, depending on the sequence). However, this variation in the physical length of the NC should be small, for two reasons: (i) as soon as a sizeable pulling force is generated on the NC, the variable segment should adopt a more or less extended conformation regardless of sequence, (ii) segments corresponding to loops between TMHs generally have low helix propensities, and TMH segments need to be somewhere between 10-20 residues long to form helices in the exit tunnel even in the absence of a pulling force (24). Because the variable segment between the HA/AP and the insertion site is only ~15 residues long, it is unlikely to have a sufficiently strong helix potential to markedly affect the ~45 residues length needed to bridge the PTC and the insertion site.

Hence, by shifting the sequence by 45 residues relative to the FP, we can visualize the FP on the sequence and on the structure, Fig. 2b. Since the f_{FL} values in the FP vary between 0.15 and 0.87, *i.e.*, the half-maximal amplitude is f_{FL} = 0.51 (dashed line in Fig. 2a), we have colored all residues with $f_{FL} \geq 0.51$ yellow and those with $f_{FL} < 0.51$ blue in Fig. 2b. The f_{FL} = 0.51 cutoff is also used to calculate the N_{start} and N_{end} values below.

In the KvAP FP, Fig. 2a, the first peak has N_{start} = 71±2 residues and N_{end} = 82±2 residues. A^{35} (residue numbering as in PDB file 6UWM) is ~45 residues away from the PTC at N_{start} and Y^{46} is ~45 residues away from the PTC at N_{end}, roughly matching the C-terminal half of the membrane-embedded part of S1 predicted by the hydrophobicity-based ΔG_{pred} and structure-based OPM (Orientation of Proteins in Membranes) algorithms (3, 31), Fig. 2b. The second peak has N_{start} = 83±2 residues and N_{end} = 105±2 residues, with T^{47} in the S1-S2 loop and L^{69} at the end of the hydrophobic core of S2 placed ~45 residues away from the PTC, respectively. The peak has a shoulder that extends to N = 120±2 residues, apparently corresponding to the membrane insertion of the mildly apolar C-terminal end of S2 (W^{70}-A^{77}) and the S2-S3 loop (Y^{78}-A^{84}).

The S3–S5 region generates a more complex series of peaks, between $N \approx$ 128-194 residues. At N_{start} = 128±2 residues, Y^{92} in the middle of S3a (the first half of S3) is ~45 residues away from the PTC; notably, the preceding part of S3a (blue in Fig. 2b) is polar

and not expected to generate pulling force. There is a sharp drop in f_{FL} at N = 155±1 residues, coinciding with the first two Arg residues in S4 (R^{117}, R^{120}) arriving at ~45 residues from the PTC. The next peak has N_{start} = 161±1 residues, with L^{125} located ~45 residues from the PTC. L^{125} is at the beginning of a hydrophobic stretch in the middle of S4 (F^{124}LRILLIIS^{132}) that presumably is responsible for the increase in f_{FL}. The peak ends at N_{end} = 171±2 residues, corresponding to a short polar stretch near the end of S4 (R^{133}GSK^{136}) being ~45 residues from the PTC; at this point, all the 5 Arg residues in S4 should have reached the translocon/membrane insertion site. Finally, there is an unexpected peak between N_{start} = 174±2 residues (with L^{138} ~45 residues from the PTC) and N_{end} = 194±2 residues. The segment from approximately G^{134} to D^{146} forms the amphipathic C-terminal part of S4 that is thought to "kink-and-slide" along the membrane surface during channel closing (32, 33), suggesting that the peak reflects the integration of the apolar face of this part of S4 into the cytoplasmic leaflet of the membrane.

Surprisingly, there is no peak in the FP corresponding to the relatively hydrophobic C-terminal two-thirds of the S5 TMH, but a major peak that extends from N_{start} = 216±2 to N_{end} = 236±2 residues that coincides with the amphipathic and mildly apolar Pore segment (encompassing the Pore helix and the selectivity filter residues) reaching ~45 residues from the PTC. The final peak, with N_{start} = 253±2 and N_{end} = 280±2 residues, starts when M^{217}, located near the middle of the apolar part of S6, is ~45 residues from the PTC, and ends when E^{244} at the C-terminal end of S6 is ~45 residues from the PTC; notably, the last part of S6 (G^{229}TVSNMFQKILV^{240}) is amphipathic and sticks out of the membrane, and partakes in the formation of the tetramer interface in the cryo-EM structure (PDB 6UWM). Similar to the C-terminal part of S4, the last part of the S6 peak likely reflects the integration of the amphipathic helix into the membrane interface region.

Upstream TMHs affect the membrane insertion of neighboring TMHs in KvAP

In previous studies, it was shown that certain KvAP TMHs that are not sufficiently hydrophobic to insert on their own (*e.g.*, S3) can nevertheless insert as helix pairs, or "hairpins" (19). To probe such insertion events in more detail, we recorded partial FPs for constructs where one or more N-terminal TMHs had been deleted and replaced by an N-terminal fragment of the LepB protein (see Materials and Methods), an inner membrane protein with a periplasmic N terminus, two N-terminal TMHs, and a large C-terminal periplasmic domain (34). For KvAP constructs lacking an odd number of TMHs we used

a 232-residue LepB fragment that includes both TMH1 and TMH2 to ensure correct topology of the remaining KvAP TMHs in the membrane; likewise, for KvAP constructs lacking an even number of TMHs we used a 177-residue LepB fragment that includes only TMH1, Fig. 3 (FPs for the different deletions are plotted separately in Supplemental Fig. S3).

We first deleted residues 10-18, that include most of the short amphipathic N-terminal S0 helix (R^{14}-M^{22}) seen in the NMR structure of the KvAP VSD (35). The Δ[S0] FP (dark blue) is similar to the wildtype KvAP FP, except that the S1 peak has N_{start} = 62±2 residues (rather than 71±2 residues in the wildtype FP) and the S2 peak has a higher amplitude. Thus, in the Δ[S0] FP, the S1 peak starts when L^{26} at the very N terminus of S1 reaches ~45 residues from the PTC, *i.e.*, in the wildtype protein, the presence of the S0 amphipathic helix delays the interaction between S1 and the insertion site by ~10 residues.

The Δ[S0-S1] series of constructs yielded the FP shown in blue in Fig. 3. The dip at N = 94-102 residues corresponds to a situation where R^{57} and D^{62}, two polar residues that interrupt the hydrophobic N-terminal half of S2, are located ~45 residues from the PTC. This dip is not seen in the original FP (Fig. 2a), which suggests that S1 helps to accommodate the S2 polar residues in the membrane. In contrast, the C-terminal half of S2 generates a stronger pulling force in the Δ[S0-S1] FP than in the original FP, and S3 generates a more variable pulling force with a peak at N = 134 (with the kink between S3a and S3b ~45 residues from the PTC) and dips at N = 142 (with the polar residues $E^{107}GH^{109}$ at the C-terminal end of S3b ~45 residues from the PTC) and N = 150 (with $G^{112}LG^{114}$ that eventually form the loop between S3b and S4 located ~45 residues from the PTC).

The Δ[S0-S2] FP (light blue) has a low-amplitude peak at N = 130-134, where P^{95} and P^{99}, which form the kink between S3a and S3b, are ~45 residues away from the PTC. The Δ[S0-S2] FP has low f_{FL} values in the hydrophobic S3b region, suggesting that S3 does not insert into the membrane in the absence of S1 and S2. A major peak with N_{start} = 152±2 residues (where F^{116} at the N-terminus of S4 is ~45 residues from the PTC) corresponds

to the membrane insertion of S4; interestingly, however, there is no sharp drop at $N \approx 155$ residues, unlike in the original FP.

For the Δ[S0-S3] FP (green), there is a low-amplitude peak at $N = 154 \pm 2$ residues but the high-amplitude peak in the original FP at $N_{start} = 161 \pm 1$ residues (corresponding to the membrane insertion of the central apolar part of S4) is missing. Instead, f_{FL} increases gradually from $N \approx 170$ residues (where G^{134}, which is located just before the C-terminal amphipathic part of S4, is ~45 residues from the PTC) to a maximum at $N = 194 \pm 2$ residues; at this point M^{158} in the early part of S5 is ~45 residues from the PTC. Thus, the passage of the main part of S4 into the translocon does not generate pulling force in the absence of S3, consistent with the relatively low insertion efficiency into rough microsomes seen for the isolated KvAP S4 helix (17, 19). Assuming that the isolated S4 helix is mostly translocated across the membrane, the "ramp" between $N \approx 170$-194 residues corresponds to the entry into the translocon of the amphipathic C-terminal end of S4, the S4-S5 linker, and the apolar N-terminal third of S5.

The Δ[S0-S4] FP (yellow) has a mid-amplitude peak between $N_{start} = 192 \pm 2$ residues and $N_{end} = 204 \pm 2$ residues that corresponds to the N- and C-terminal ends of S5 reaching ~45 residues from the PTC. Interestingly, unlike in the original FP, this peak agrees better with both the ΔG_{pred}- and OPM-predicted transmembrane region for S5. The following high-amplitude peak at $N_{start} = 222 \pm 2$ residues matches the original FP and corresponds to the membrane insertion of the Pore segment.

In the Δ[S0-S5] FP (pink), only the Pore segment and S6 remain of KvAP. Nevertheless, the peaks in the FP corresponding to the insertion of the Pore segment and S6 are similar to those in the full-length FP, except that N_{end} for the Pore peak and N_{start} and N_{end} for the S6 peak are all increased by 4-5 residues.

Finally, in the Δ[S0-Pore] FP (purple), the peak has $N_{start} = 248 \pm 2$ residues (with I^{212} at the N-terminal end of S6 ~45 residues from the PTC), and has approximately the same N_{end} value as seen in the full-length FP.

Thus, upstream TMHs affect the pulling forces generated by downstream TMHs for the whole S1-S5 region, but do not much affect those generated by the Pore segment and S6. These results are broadly in agreement with, and add considerable detail to, previous studies that have shown that KvAP S1 and S2 can insert independently into the membrane

of ER-derived RMs, but that S3 cannot insert in the absence of S4, and S4 inserts inefficiently by itself (17, 19).

Detailed analysis of the VSD FP

Given the complexity of the FP in the S4 region, we carried out two additional sets of experiments: first, recording a FP in the presence of 2 mM indole in the growth medium, a treatment known to reduce the proton-motive force (pmf) across the inner membrane (9, 36), and, second, recording FPs for mutated constructs in which either the positively charged Arg residues in S4 are mutated to positively charged Lys, negatively charged Asp, or polar but uncharged Gln, or the charged residues E^{45}, D^{62}, D^{72}, R^{76}, E^{93}, and E^{107} in S2 and S3 that could potentially interact with S4 during membrane insertion are mutated to Ala, Fig. 4 and Supplemental Fig. S4.

Strikingly, the dip at $N \approx 174$ residues disappears with indole in the medium while mutation $D^{62}A$ in the middle of S2 significantly deepens the dip at $N = 170$ residues, Fig. 4a; in both cases, the dip at $N \approx 157$ residues is unaffected. The $D^{72}A$ mutation appears to reduce the dip at $N \approx 174$ residues, but the only point that is significantly different from the wildtype FP is $N = 182$ residues. In contrast, mutations $R^{76}A$ at the C-terminal end of S2 and $E^{107}A$ in S3b completely eliminates ($R^{76}A$) or strongly reduces ($E^{107}A$) the dip at $N \approx 157$ residues, but do not affect the dip at $N \approx 174$ residues. Fig. 4b. Notably, R^{76} is not present in the Δ[S0-S2] series of constructs, for which the FP also does not have a dip at $N \approx 157$ residues (Fig. 3). Mutations $E^{45}A$ and $E^{93}A$ have no significant effects on the FP, Supplemental Fig. S4.

With the five Arg residues in S4 simultaneously mutated to either Lys, Asp, or Gln, the dip at $N \approx 157$ residues disappears in the corresponding FPs, Fig. 4c. In addition, the 5R→5D and 5R→5Q (but not 5R→5K) mutants significantly reduce the amplitude of the central peak between N_{start} = 160±1 residues and N_{end} = 172±2 residues, suggesting poor membrane interaction of these mutated S4 sequences, possibly because they cannot interact favorably with negatively charged residues in S2 (19). Single R→Q mutations in

S4 reduce the dip at $N \approx 157$ residues to somewhat varying degrees but have no effect on the central peak, Fig. 4d.

Thus, the sharp dip at $N \approx 157$ residues is seen only when R^{76} at the cytoplasmic end of S2, E^{107} in S3b, and all five Arg residues in S4 are present, while the dip at $N \approx 174$ residues requires an intact pmf across the inner membrane.

Discussion

As it is clear from Fig. 2, the simple ΔG_{pred} hydrophobicity plot provides at best a very rough guide to understand the cotranslational membrane insertion of KvAP. FPA goes further, both in terms of identifying regions in the protein for which the insertion process does not reflect the hydrophobicity profile, and because of its high resolution which allows the effects of individual residues on the insertion process to be discerned.

Based on the FPA data and the "sliding" model for membrane protein insertion (37), we propose the following scheme for the insertion process, Fig. 5. S1 starts to insert when approximately half of it has reached the translocon/membrane insertion site, ~45 residues away from the PTC (Fig. 2a, b); in contrast, if the S0 amphipathic helix is deleted, S1 starts to insert as soon as its N-terminal end reaches the insertion site (Fig. 3). The continued partitioning of S1 into the cytoplasmic leaflet of the inner membrane generates high pulling force on the NC until the charged S1-S2 loop enters the insertion site (seen as the small dip in the FP at $N \approx 82$ residues). When the first few apolar residues in S2 arrive at the insertion site ($N \approx 85$ residues), f_{FL} starts to increase again and remains high even though S2 has two charged residues (R^{57}, D^{62}) in its N-terminal half. Presumably, this is because the highly hydrophobic C-terminal part of S1 (V^{39}IVVVV^{44}) moves deeper into the membrane in step with the N-terminal part of S2, Fig. 5a (left), thus offsetting the energetic cost of inserting the charged residues. This interpretation is consistent with the Δ[S0-S1] FP, where the dip expected from R^{57} and D^{62} is visible at $N \approx 94$-102 residues (Fig. 3), as in this case there is no upstream apolar segment that co-inserts with S2, Fig. 5a (right). At $N \approx 122$ residues, the force drops. By this length, the entire S1-S2 region is sufficiently far from the PTC to have access to the membrane interior. This implies that a few residues in the S2-S3 loop must reach the insertion site on the cytoplasmic side of the membrane to allow full membrane insertion of the S1-S2 hairpin.

Membrane insertion of the S3-S5 region is more complex, both because there is interdependency between TMHs (19), and because of the unique composition of S4 with five regularly spaced, positively charged Arg residues. In the cryo-EM structure (PDB 6UWM), S3 has a break at P^{95}-P^{99}, between the more polar S3a and more apolar S3b helices. S3 starts to insert into the cytoplasmic membrane leaflet at $N \approx 128$ residues when the C-terminal end of S3a reaches the insertion site, and S3b keeps generating a high pulling force until $N \approx 155$ residues when the first Arg residues (R^{117}, R^{120}) in S4 appear at the insertion site. As shown by the Δ[S0-S2] FP (Fig. 3), S3 generates a high pulling force only if S2 is present. In the Δ[S0-S2] constructs, S3 is preceded by a long, polar cytoplasmic segment from LepB and S3's modest hydrophobicity (Fig. 2a) might not be sufficient for re-targeting the ribosome to the SecYEG translocon for efficient membrane insertion (38, 39). In agreement with these results, previous studies on KvAP (19) have also shown that, in the absence of S1 and S2, S3 does not insert by itself but only when part of the S3-S4 hairpin.

The sharp drop in f_{FL} at $N \approx 155$-160 residues appears to be almost entirely dependent on the S4 Arg residues. Mutating any or all of the five Arg residues to Gln results in increased f_{FL} at $N = 158$ residues (Fig. 4c, d). An effect is even seen for $R^{133}Q$, which is only ~35 residues away from the PTC at this point and therefore presumably has not reached the insertion site. Mutating all of the Arg residues to Lys or Asp also results in increased f_{FL} (Fig. 4c), while dissipation of the pmf with indole has no effect (Fig. 4a). Notably, Arg – but not Lys – residues have been observed to be rate-limiting for (apparently pmf-independent) translocon-mediated membrane translocation of proteins into *E.coli*-derived proteoliposomes or inverted inner-membrane vesicles (40), possibly due to the much higher pKa of the Arg side chain that prevents its de-protonation even in non-polar environments (41, 42).

We also tested several Ala substitutions of charged residues in S2 and S3 (Fig. 4b, Supplemental Fig. S4). Remarkably, mutations $R^{76}A$ (at the cytoplasmic end of S2) and $E^{107}A$ (near the C-terminal end of S3b) cause a significant increase in f_{FL} at $N = 158$ residues; the same effect is seen in the Δ[S0-S2] FP, which lacks R^{76}, and, albeit less pronounced, in the Δ[S0-S1] FP (Fig. 3). The $E^{107}A$ mutation increases the hydrophobicity of S3b, which may help the S3-S4 hairpin insert into the membrane, Fig. 5b (left). The effect of the $R^{76}A$ mutation is more difficult to understand. One possibility is that the

increase in f_{FL} at N = 158 residues caused by this mutation might be due to disruption of the native contacts between the C-terminal end of S2 (D^{72}-K^{79}) and the amphipathic N-terminal S0 helix (35). This scenario suggests a previously unobserved long-range interaction between S0, S2, and the tip of the S3-S4 hairpin during the early stages of membrane insertion of the latter, Fig. 5b (left).

Once the apolar segment in the middle of S4 (F^{124}LRILLIIS^{132}) arrives at the insertion site at N = 162 residues, there is a rapid increase in f_{FL}. This peak is absent or diminished in the Δ[S0-S3], 5R→5Q, and 5R→5D mutants, but not in 5R→5K, nor in any of the single R→Q mutants (Fig. 3, Fig. 4c, d). Thus, this peak seems to minimally require S3 and one positive charge flanking the hydrophobic stretch (R^{126}ILLIISR^{133}). The 5R→5Q mutation increases f_{FL} at N = 158 residues and decreases it at N = 162-166 residues, further demonstrating the intricate effects caused by the S4 Arg residues during membrane insertion, and the difficulty of predicting f_{FL} from simple hydrophobicity plots.

A second dip in the S4 region of the FP at $N \approx 172$ residues coincides with the arrival at the insertion site of two positively charged residues (R^{133}, K^{136}) at the end of the membrane-embedded part of S4, Fig. 5b (middle). This dip is not seen when constructs are expressed in the presence of indole (Fig. 4a), suggesting that it is caused by an electrostatic interaction between positively charged residues in S4 and the membrane potential. As discussed in Allen et al. (40), the role played by the pmf during membrane translocation is still not fully understood, and our finding that indole has no effect on the Arg-dependent dip at $N \approx 157$ residues but does affect the dip at $N \approx 172$ residues underscores this point. In contrast to indole, the D^{62}A mutation deepens the dip at N = 170 residues, suggesting that D^{62} in the middle of S2 facilitates the insertion of the second half of S4; in agreement with this, a similar mutation (D^{62}V) has been shown to reduce the overall membrane insertion efficiency of the S3-S4 hairpin (19).

The following peak ($N \approx$ 178-194 residues) is displaced by ~10 residues compared to what would be expected for a peak generated by S5. Its position is unchanged in the Δ[S0-S2] FP but is shifted towards S5 in the Δ[S0-S3] FP and overlaps fully with the predicted membrane-embedded region of S5 in the Δ[S0-S4] FP (albeit with a low amplitude). The similarity between the original FP and the Δ[S0-S2] FP in this region rules out the possibility that the peak originates from a folding transition of the whole VSD after the final insertion of S4. Instead, the data suggest that the amphipathic C-terminal end of S4 and

the early part of S5 are responsible: our working hypothesis is that S4 kinks near G^{134} such that the amphipathic part does not enter the translocon but rather partitions into the cytoplasmic leaflet of the membrane, Fig 5b (right), as proposed for the closed conformation of the KvAP channel (32).

The amphipathic Pore segment generates a strong pulling force, despite its rather low overall hydrophobicity. A similarly strong pulling force was previously recorded for an amphipathic re-entrant helix in BtuC (13). This suggests that NC tension has a similar effect on the ribosome whether it is induced by polypeptide segments destined to become TMHs or those destined to become re-entrant helices, meaning that a similar insertion mechanism is likely responsible for both cases. Since the re-entrant helix of BtuC and the Pore helix of KvAP are amphipathic, we propose that amphipathic helices “slide” across the membrane via the lateral gate region in the SecYEG translocon (or the cleft in the YidC translocon), with their polar side facing the translocon channel and their apolar side facing the surrounding lipid (37). In this way their apolar face can generate a strong pulling force while the polar face prevents partitioning into the lipid bilayer and formation of a TMH. Once the Pore helix has translocated across the membrane, its amphipathic character is also required for the proper folding of the KvAP monomer (43).

The Pore segment delays the insertion of S6 by 8-10 residues compared to the insertion of S6 by itself (the Δ[S0-Pore] FP, Fig. 3), and, likewise, the amphipathic S0 helix delays the insertion of S1 by a similar number of residues (the Δ[S0] FP, Fig. 3). As noted above, the amphipathic C-terminal end of S4 also seems to have an attenuating effect on the insertion of S5. Interestingly, a similar delay in the insertion of an immediate downstream TMH was seen for the amphipathic re-entrant helix in BtuC (13) and was traced to a stretch of hydrophobic residues in the re-entrant helix (11). Further studies will be required to understand the precise mechanism behind this effect; a speculative hypothesis is that amphipathic helices may bind transiently in the Sec61 channel and delay or block entry of a downstream TMH in a similar way that Sec61 inhibitors such as cotransin-related compounds (44) or mycolactones (45) block the entry of signal peptides.

On a more general level, for the serial TMH deletion mutants (Fig. 3) we find that the FP is most affected in the region immediately following the deletion. For example, in the Δ[S0-S1] deletion mutant the S2 region is most disturbed, the S3 region less so, and the S4 region less still. Hence, cotranslational insertion forces are primarily locally determined

and correlate with the local segmental hydrophobicity, while major disagreements between the hydrophobicity profile and the FP suggest longer-range intra- or inter-molecular folding events (12). Notably, despite the fact that the purified monomeric S0-S4 paddle domain can fold by itself (16, 35) – and hence presumably also folds cotranslationally during membrane insertion – the only strong evidence for long-range interactions in our data are the effects of the $D^{62}A$, $R^{76}A$ and Δ[S0-S1] mutations on the insertion of the early part of S4 (the dip at N ≈ 158 residues, Fig. 3).

In summary, the cotranslational membrane insertion of KvAP proceeds through three semi-independent steps: (*i*) insertion of the S1-S2 hairpin, (*ii*) insertion of the S3-S5 region, and (*iii*) insertion of the Pore-S6 region. Each stage presents a more complex FP than excepted from a simple hydrophobicity plot, highlighting the importance of concerted insertion of helical hairpins, the – sometimes dramatic – influence of positively charged residues, and the unexpectedly strong forces, and effects on downstream TMHs, elicited by amphipathic helical segments, *e.g.*, S0, the C-terminal ends of S4 and S6, and the re-entrant Pore helix. Overall, the peculiar insertion characteristics of the S1-S4 domain are presumably shared between KvAP and VSDs in other voltage-sensitive ion channels, while the strong pulling forces generated by amphipathic helical segments may be a common phenomenon among multi-spanning helix-bundle membrane proteins. Thus, at the level of detail afforded by FPA, translocon-mediated membrane-protein insertion reveals itself as a much richer process than implied by the simple picture apparent from hydrophobicity plots or coarse-grained molecular dynamics simulations (13, 46).

Materials and Methods

Enzymes and chemicals. Cloning enzymes, reagents, and buffers were acquired from New England BioLabs (Ipswich, Massachusetts, U.S.) and ThermoFisher Scientific (Waltham, Massachusetts, U.S.). [^{35}S] L-Methionine was ordered from PerkinElmer (Shelton, Connecticut, U.S.). All other chemicals were acquired from Sigma-Aldrich (subsidiary of Merck Life Science, Darmstadt, Germany) unless otherwise stated.

Cloning and mutagenesis. We refer to the amino acid numbering presented in (18). Therefore, the first residue of K_VAP in our constructs is numbered as residue 10. Constructs were designed to include various lengths of KvAP truncated from the C-terminus, an SGMG linker (both to flexibly isolate KvAP and to add an extra Met residue

for more labeling), an HA-tag for immunoprecipitation, the SecM(*Ec*) AP, and a C-terminal fragment of LepB (residues 306-324) to allow separation of the arrested and full-length fragments by SDS-PAGE (Fig. 1c). In constructs in which KvAP is heavily truncated ($N \leq 122$) we added an N-terminal fragment of LepB (residues 1-226, but excluding TM2 (residues 58-114) to ensure proper membrane orientation of the KvAP part). Not only does the added mass improve visualization by SDS-PAGE but the LepB fragments also promotes efficient cotranslational insertion of fusion proteins into the inner membrane (13). The added LepB residues are ignored in the calculation of the *N* values; see the Supplementary Materials for full sequences of all constructs. An initial set of 60 constructs was ordered from Invitrogen GeneArt Gene Synthesis Services (ThermoFisher Scientific, Waltham, Massachusetts, U.S.) in a pBAD/*Myc*-His A background (47). Further mutagenesis was either similarly ordered, or performed in-house by a combination of Q5 PCR and Gibson assembly (48) with a homemade reaction mixture.

In vivo pulse-labeling analysis. For expression, constructs were transformed into BL21 (DE3) cells (49). Cultures (1-4 mL) were seeded to an OD_{600} of 0.1 in minimal media (1x M9 salts [M6030, Sigma-Aldrich, subsidiary of Merck, Darmstadt, Germany], 1 g/L complete supplement mixture without methionine (CSM-Met, 4510712, MP Biomedicals, California, U.S.), 0.1 mg/mL thiamine, 0.4% (w/v) fructose, 100 µg/mL ampicillin, 2 mM $MgSO_4$, and 0.1 mM $CaCl_2$). After reaching OD_{600} of 0.5, expression was induced with 0.2% arabinose for 5 minutes, then the cultures were radiolabeled by supplementation with 10-20 µCi [^{35}S]-Met (NEG009T001MC, Perkin-Elmer, Shelton, Connecticut, U.S.) for an additional 2 minutes before stopping expression by precipitation with ice-cold trichloroacetic acid (10% final). For experiments using indole (Fig. 4a), 2 µL of a 1.5 M stock solution was added (final concentration 3 mM), one minute before adding [^{35}S]-Met. The precipitate was washed with 1 mL of ice-cold acetone before resuspension.

Proteins were resuspended in 10 mM Tris, 2% SDS, pH 7.5. The suspension was centrifuged to remove insoluble material, then mixed with 10 µL of protein G-agarose beads (PROTGA-RO, Roche, Basel, Switzerland) and incubated for 15 minutes on ice to capture proteins that non-specifically bind to the beads. Then, the supernatant was transferred to a tube containing 10 µL of fresh beads and 1 µL of α-HA antibody (901515, BioLegend, San Diego, California, U.S.) and incubated under gentle agitation overnight at 4º C. Beads were washed first with 10 mM Tris, 150 mM NaCl, 2 mM EDTA, 0.2% (w/v)

Triton X-100, then again with only 10 mM Tris. After removing as much buffer as possible, proteins were recovered from the beads by denaturation with sample buffer. Peptidyl-tRNA was then digested with RNAse A (400 µg/µL). Samples were run on NuPAGE 12% Bis-Tris pre-cast gels, fixed in 30% ethanol and 10% acetic acid, and then soaked in Gel-Dry Drying Solution (Invitrogen, ThermoFisher, Waltham Massachusetts, U.S.) before drying on a Hoefer GD 2000 gel dryer (Hoefer Inc., U.S.) for 1 hour at 65º C. Phosphorimaging plates (BAS-IP, Fujifilm, Tokyo, Japan) were exposed to gels for 2-3 days before imaging on a FLA-9000 imager (Fujifilm, Tokyo, Japan).

Quantification. Full-length and arrested band intensity profiles were extracted with ImageJ. The profiles were then fit to one or more gaussian curves using an in-house python script to determine the integrated band intensities. f_{FL} was calculated as $f_{FL} = \frac{I_{Full-length}}{I_{Full-length} + I_{Arrested}}$ where $I_{Full-length}$ and $I_{Arrested}$ are the integrated intensities of the full-length and arrested bands, respectively. For certain constructs where band assignment was ambiguous, control constructs were cloned and expressed. Full-length controls were made by mutating the terminal proline of SecM(*Ec*) to alanine, which prevents SecM(*Ec*)-induced stalling. Arrested controls were made by mutating the terminal proline of SecM(*Ec*) to a stop codon.

Statistical analysis. The significance of observed differences between the wildtype KvAP FP and FPs for the mutants reported in Fig. 4 was estimated by the multiple comparisons Dunnett's test ($p < 0.05$) (50), using the Python (version 3.12) library SciPy (51). For the data in Supplemental Fig. S1, a Bonferroni-corrected t-test (52) was used to estimate the significance of observed differences between the FPs obtained with and without the N-terminal LepB fusion, and to correct for the average difference in f_{FL} values (0.06) between the ±LepB FPs, 0.06 was added to the measured f_{FL} values for the -LepB FP before performing the t-test.

Acknowledgments

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Figures and Tables

Figure 1. *Force profile analysis.* (a) When translating a construct harboring a target protein (pink), an arrest peptide (AP) (blue) and a C-terminal extension (orange), the ribosome will stall with the C-terminal residue of the AP in the PTC (left). When a sufficiently hydrophobic segment (green) reaches the insertion site ~45 residues from the PTC, the stall is released by the force *F* generated by the segment partitioning into the membrane (right). (b) SDS-PAGE analysis of immunoprecipitated, [^{35}S]-Met labeled constructs (identified by their *N* values, *c.f.* panel *c* and Fig. 2a). Stalling efficiency is quantified as the fraction of full-length protein (f_{FL}), calculated from the integrated intensities of the full-length (FL) and arrested (A) bands. A 2' labeling time was used throughout this work to optimize the dynamic range of the full FP (c.f., Fig. 2a). (c) The basic construct design, comprising full-length KvAP, an HA tag, the SecM(*Ec*) AP, and a 23-residue C-terminal extension. A series of constructs were generated by truncating four residues at a time from the C-terminal end of the KvAP segment; each construct corresponds to one data point on the FP (see Supplementary Materials for sequences; note that the C-terminal 53-residues are common to all constructs). For constructs with $N \leq 122$, a 177-residue segment derived from the N-terminal part of the *E. coli* LepB protein (including its N-terminal TMH, in gray) was fused to the N-terminus of KvAP in order to ensure sufficient mass for separation in SDS-PAGE and proper membrane topology, c.f., Supplemental Fig. S1. Cytoplasmic and periplasmic loops are indicated by red and blue lines, respectively.

Figure 2. *The KvAP force profile.* (a) KvAP FP (black; error bars show SEM values), plotted alongside the predicted free energy of membrane insertion (ΔG_{pred}; gray). ΔG_{pred}

was calculated as in (3) for 19-residue wide sequence segments whose centers are 45 residues upstream from the PTC at the corresponding value of *N*. Vertical shadings show predicted transmembrane domains (also shifted by 45 residues relative to the PTC) from the OPM (31) and ΔG_{pred} algorithms (using a 19-residue window). (b) FP mapped onto the structure (18) and amino acid sequence of KvAP (PDB 6UWM). The S0 helix from the NMR structure PDB 2KYH (35) was manually added to the structure. A cutoff of f_{FL} = 0.51 (midway between the highest and lowest f_{FL} value in the FP; horizontal dashed line in panel *a*) was selected to define N_{start} and N_{end} values; regions with f_{FL} values higher than the cutoff are in yellow, while those below the cutoff are in blue. Approximate membrane boundary locations are indicated as black lines according to the OPM database (cytoplasm down). The sequence used in this study is the same as in PDB 6UWM, where the initiator Met residue is counted as residue number 10; for ease of reference, we use the PDB numbering when referring to individual residues in the text and therefore subtract 45 - 9 = 36 residues from a given *N* value when referring to the residue 45 residues away from the PTC. The N-terminal sequence differs from the corresponding UniProt entry Q9YDF8, which matches the sequence used here from residue G^{12} onwards (numbered G^{25} in UniProt). OPM-predicted transmembrane domains are underlined. S0 is also underlined as defined in the NMR structure of the KvAP VSD (35).

Figure 3. *FPs for serial TMH deletion mutants.* FPs are plotted alongside the KvAP FP from Fig. 2 (black). OPM-predicted transmembrane regions are shaded. The schematic above outlines the various construct designs used to maintain proper topology: a LepB-TMH1-THM2 fragment (232 residues) was fused to the N terminus of constructs lacking an odd number of TMHs and a LepB-TMH1 fragment (177 residues) was fused to constructs lacking an even number of TMHs. Separate plots of the individual deletion FPs are included in Supplemental Fig. S3.

Figure 4. *Mutational analysis of the S4 region of the FP*. Each panel shows the S4 region of the KvAP FP in black alongside the FPs discussed in the main text. (a) FP expressed in the presence of 2 mM indole (yellow). FPs for the $D^{62}A$ and $E^{72}A$ mutants are shown in green and red, respectively. (b) FPs for the $R^{76}A$ (light blue) and $E^{107}A$ (green) mutants. (c) FPs for the [$R^{117}K$, $R^{120}K$, $R^{123}K$, $R^{126}K$, $R^{133}K$] (blue), [$R^{117}D$, $R^{120}D$, $R^{123}D$, $R^{126}D$, $R^{133}D$] (red), and [$R^{117}Q$, $R^{120}Q$, $R^{123}Q$, $R^{126}Q$, $R^{133}Q$] mutants (purple). (d) FPs for the

individual $R^{117}Q$ (blue), $R^{120}Q$ (cyan), $R^{123}Q$ (green), $R^{126}Q$ (yellow), and $R^{133}Q$ (red) mutants. Sequence contexts of the mutations are shown along the bottom of the panels. Significant differences (Dunnett's test, $p < 0.05$) between mutant and wildtype f_{FL} values are indicated by *.

Figure 5. *Model for the membrane insertion of KvAP.* (a) The S1-S2 hairpin of KvAP generates high f_{FL} when the N-terminus of S2 reaches the insertion site ($N \approx 95$; left). In contrast, the ∆[S0-S1] mutant does not generate high f_{FL} until more of S2 is exposed, possibly due to R^{57} and D^{62} (right). (b) The S3-S4 region in KvAP generates low f_{FL} at $N \approx 157$ (left) and $N \approx 172$ (middle), when the positively charged stretches in S4 traverse the insertion site. In contrast, high f_{FL} is generated at $N \approx 182$ (right) when the 'kinked' end of S4 and the start of the S4–S5 linker reaches the insertion site. The SecM(*Ec*) AP is indicated in black. As the relative importance of the YidC and SecYEG translocons in the membrane insertion of KvAP is not known, only a "generic" translocon is depicted in the Figure.

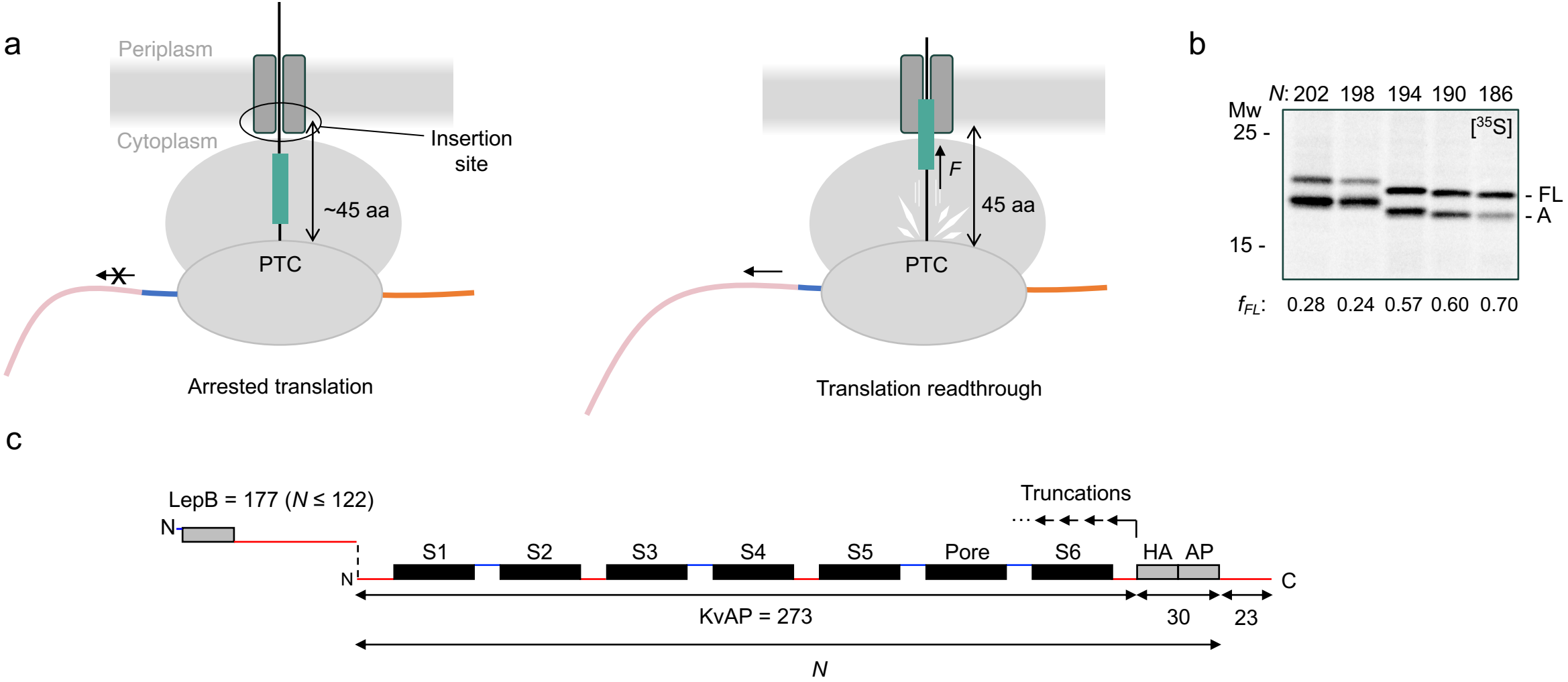

a
Periplasm
Cytoplasm
Insertion site
~45 aa
PTC
Arrested translation
F
45 aa
PTC
Translation readthrough
b
N: 202 198 194 190 186
Mw
25 -
15 -
[35S]
- FL
- A
fFL: 0.28 0.24 0.57 0.60 0.70
c
LepB = 177 (N ≤ 122)
N
Truncations
S1
S2
S3
S4
S5
Pore
S6
HA
AP
N
C
KvAP = 273
30
23
N

Figure 1

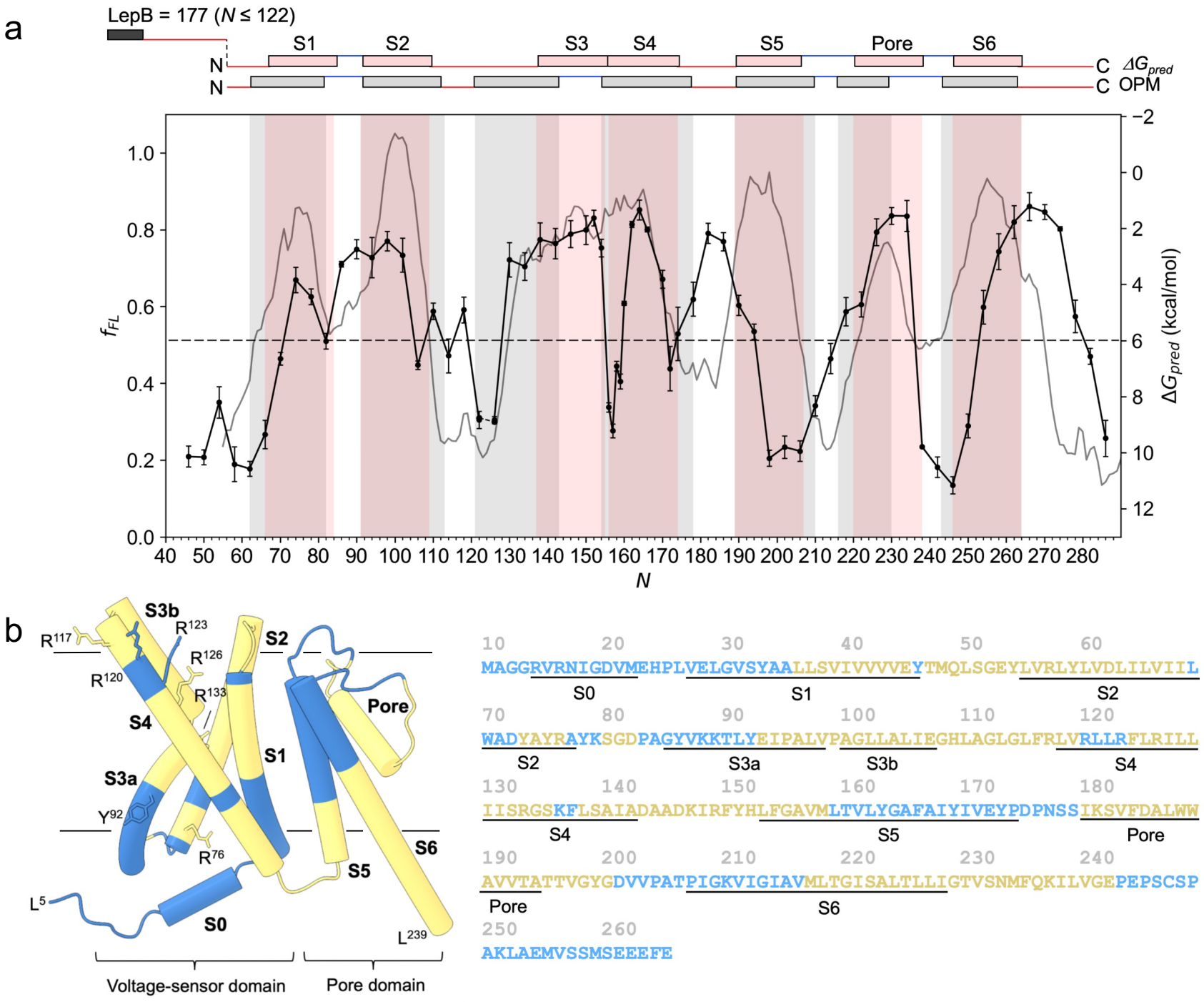

a
LepB = 177 (N ≤ 122)
S1
S2
S3
S4
S5
Pore
S6
N
C
ΔGpred
OPM
fFL
ΔGpred (kcal/mol)
N
b
S3b
R117
R123
R126
R120
R133
S2
Pore
S4
S1
S3a
Y92
R76
S6
S5
L5
S0
L239
Voltage-sensor domain
Pore domain
10 20 30 40 50 60
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIIL
S0 S1 S2
70 80 90 100 110 120
WADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILL
S2 S3a S3b S4
130 140 150 160 170 180
IISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWW
S4 S5 Pore
190 200 210 220 230 240
AVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSCSP
Pore S6
250 260
AKLAEMVSSMSEEEFE

Figure 2

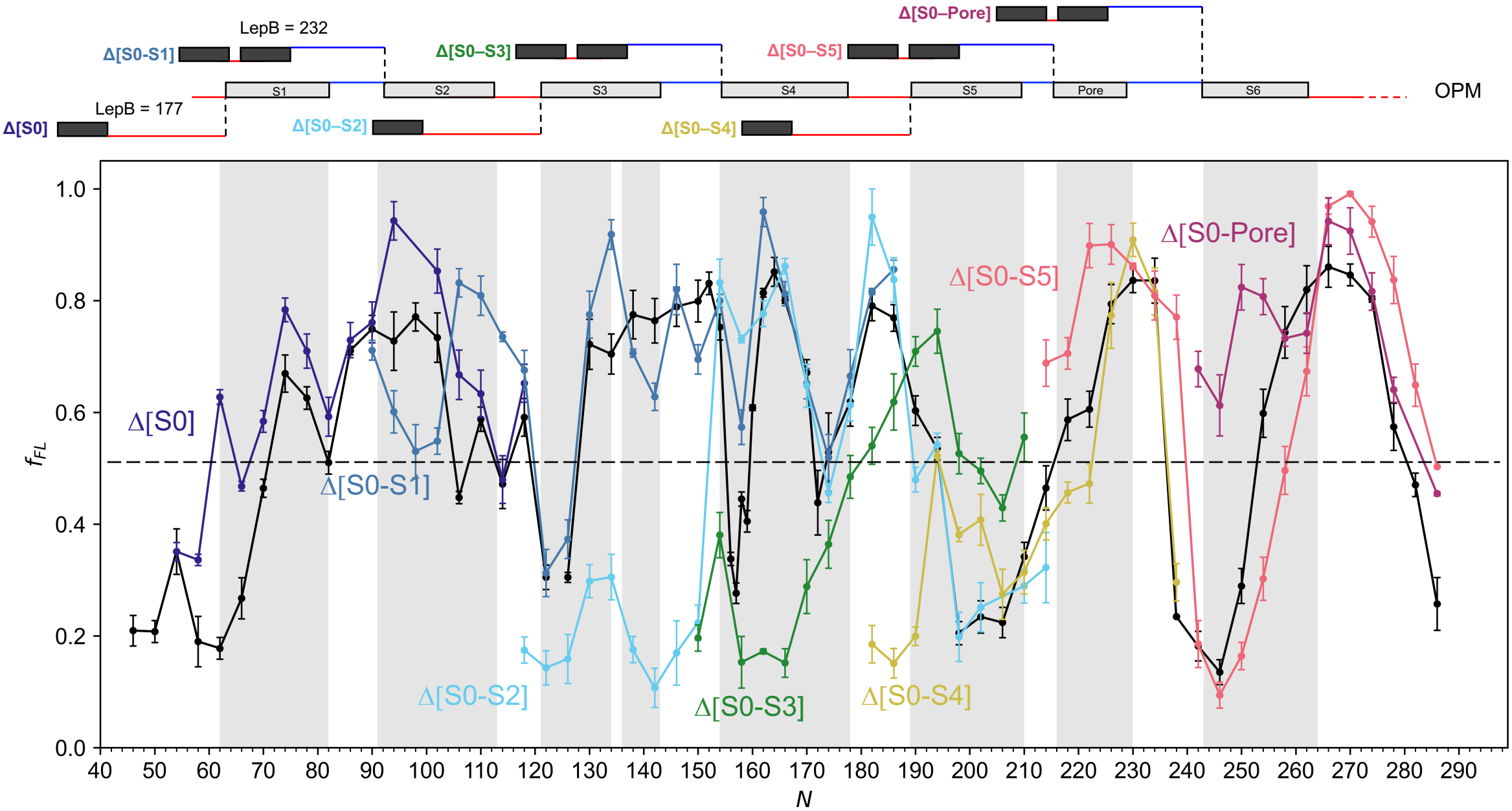

Δ[S0–Pore]
LepB = 232
Δ[S0-S1]
Δ[S0–S3]
Δ[S0–S5]
S1
S2
S3
S4
S5
Pore
S6
OPM
LepB = 177
Δ[S0]
Δ[S0–S2]
Δ[S0–S4]
Δ[S0]
Δ[S0-S1]
Δ[S0-S2]
Δ[S0-S3]
Δ[S0-S4]
Δ[S0-S5]
Δ[S0-Pore]
f_{FL}
N
0.0
0.2
0.4
0.6
0.8
1.0
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
280
290

Figure 3

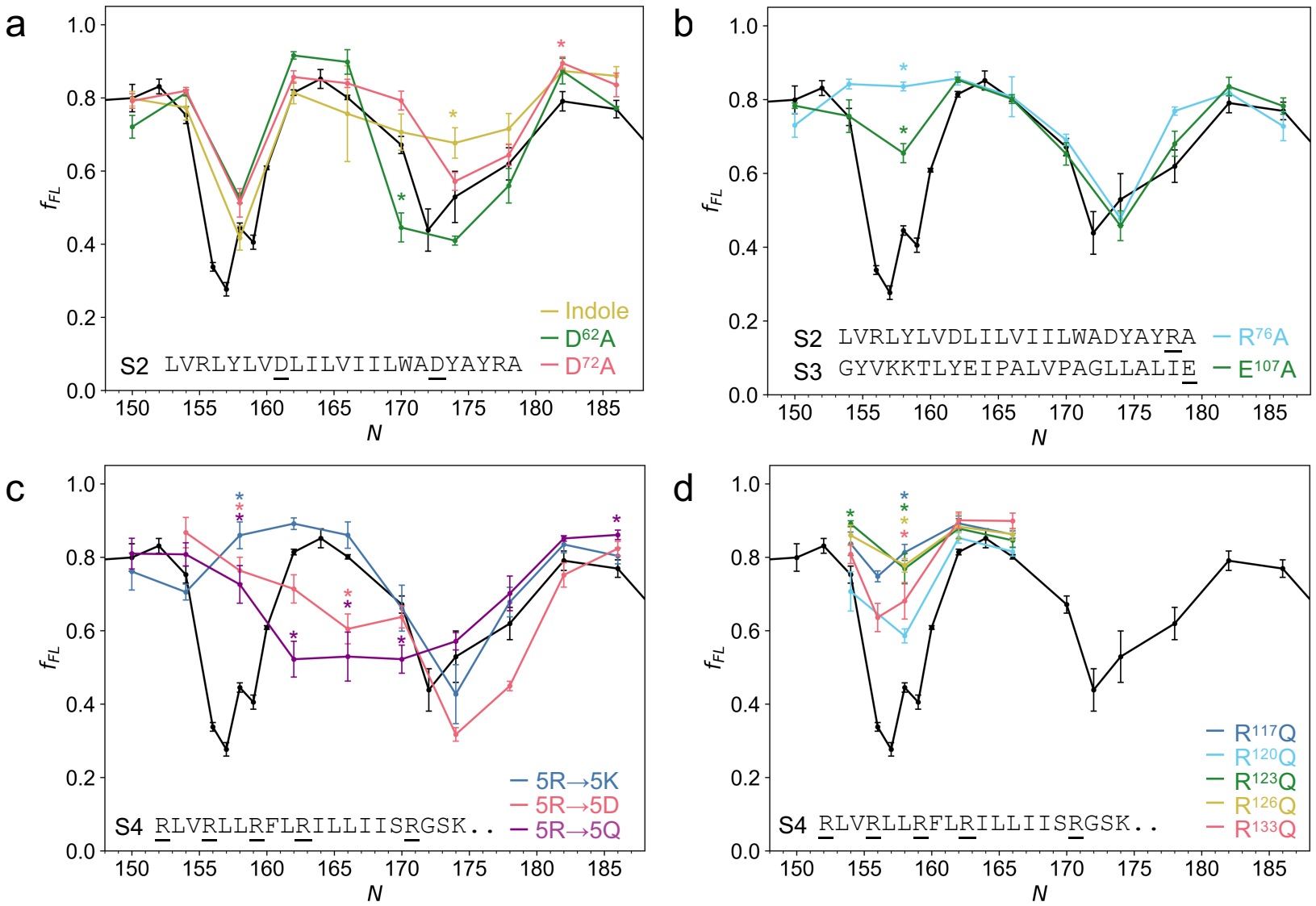

a
b
c
d
f_{FL}
N
S2 LVRLYLVDLILVIILWADYAYRA
Indole
D62A
D72A
S2 LVRLYLVDLILVIILWADYAYRA
S3 GYVKKTLYEIPALVPAGLLALIE
R76A
E107A
S4 RLVRLLRFLRILLIISRGSK..
5R→5K
5R→5D
5R→5Q
S4 RLVRLLRFLRILLIISRGSK..
R117Q
R120Q
R123Q
R126Q
R133Q

Figure 4

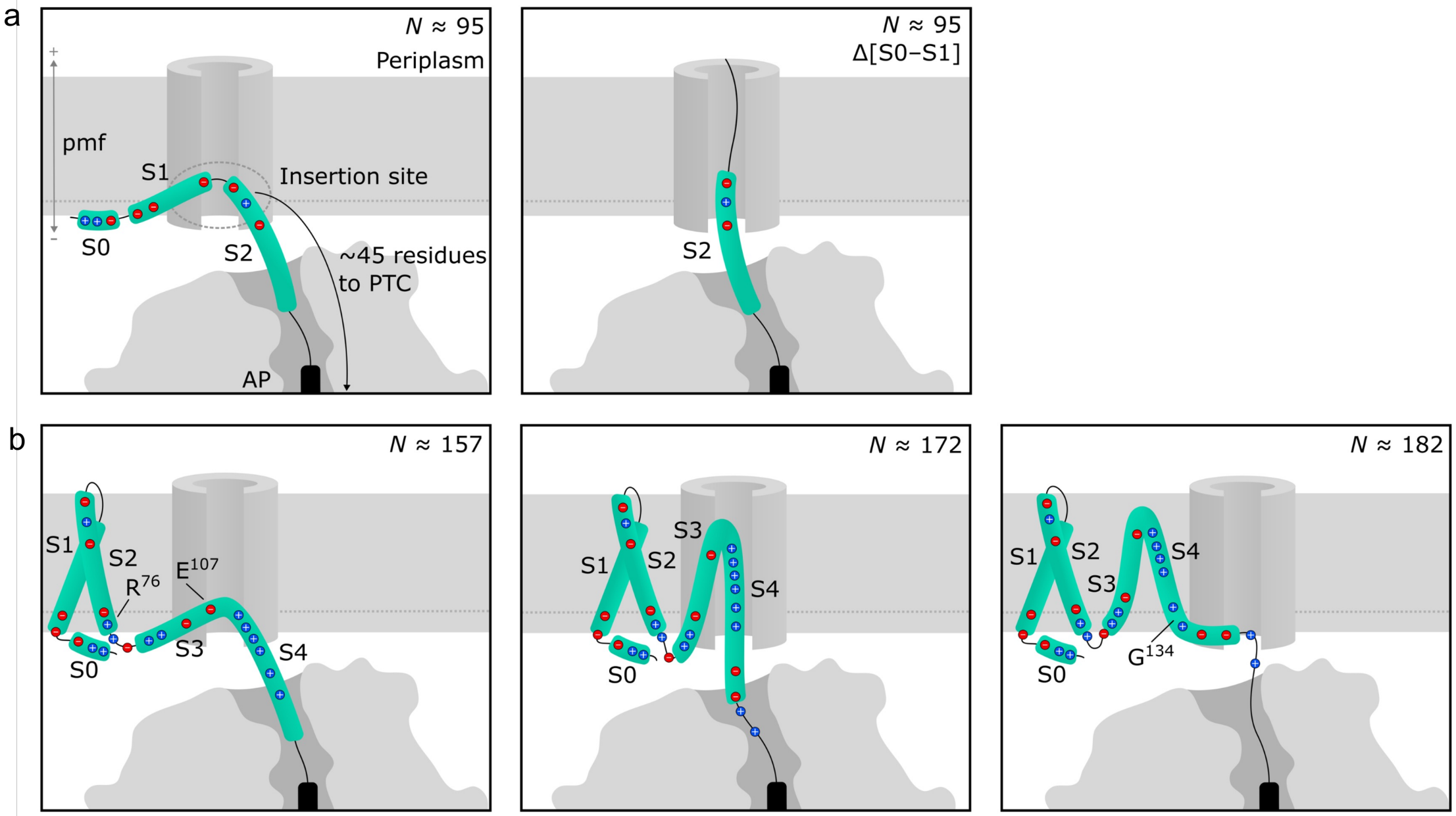

a
N ≈ 95
Periplasm
pmf
S1
Insertion site
S0
S2
~45 residues
to PTC
AP
N ≈ 95
Δ[S0–S1]
S2
b
N ≈ 157
S1
S2
R76
E107
S0
S3
S4
N ≈ 172
S3
S1
S2
S4
S0
N ≈ 182
S1
S2
S4
S3
G134
S0

Figure 5

Supporting Information for

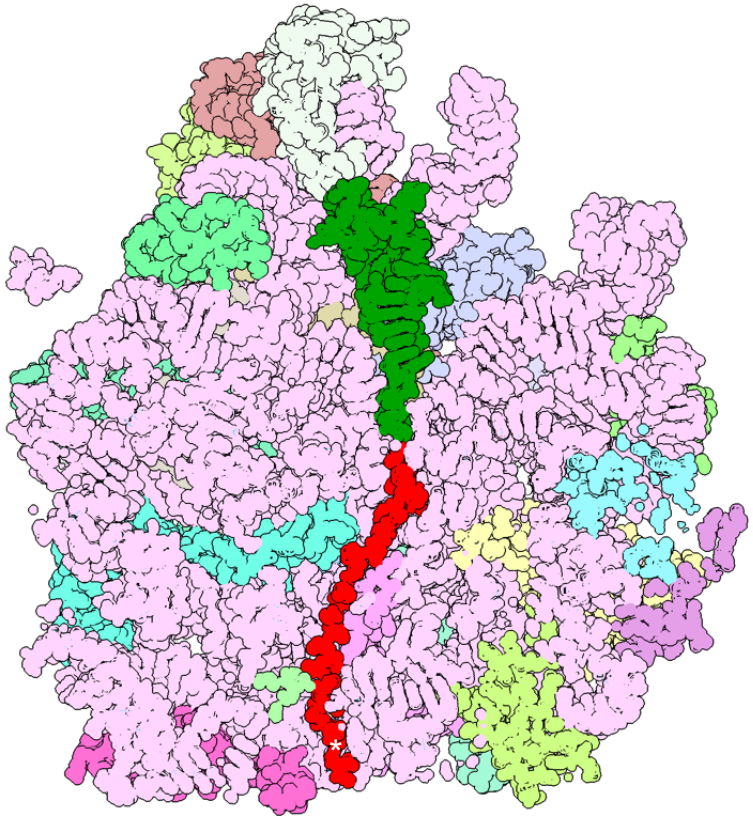
Cotranslational membrane insertion of the voltage-sensitive K^+ channel KvAP

Justin M. Westerfield, Petra Kozojedová, Cara Juli, Ane Metola, Gunnar von Heijne

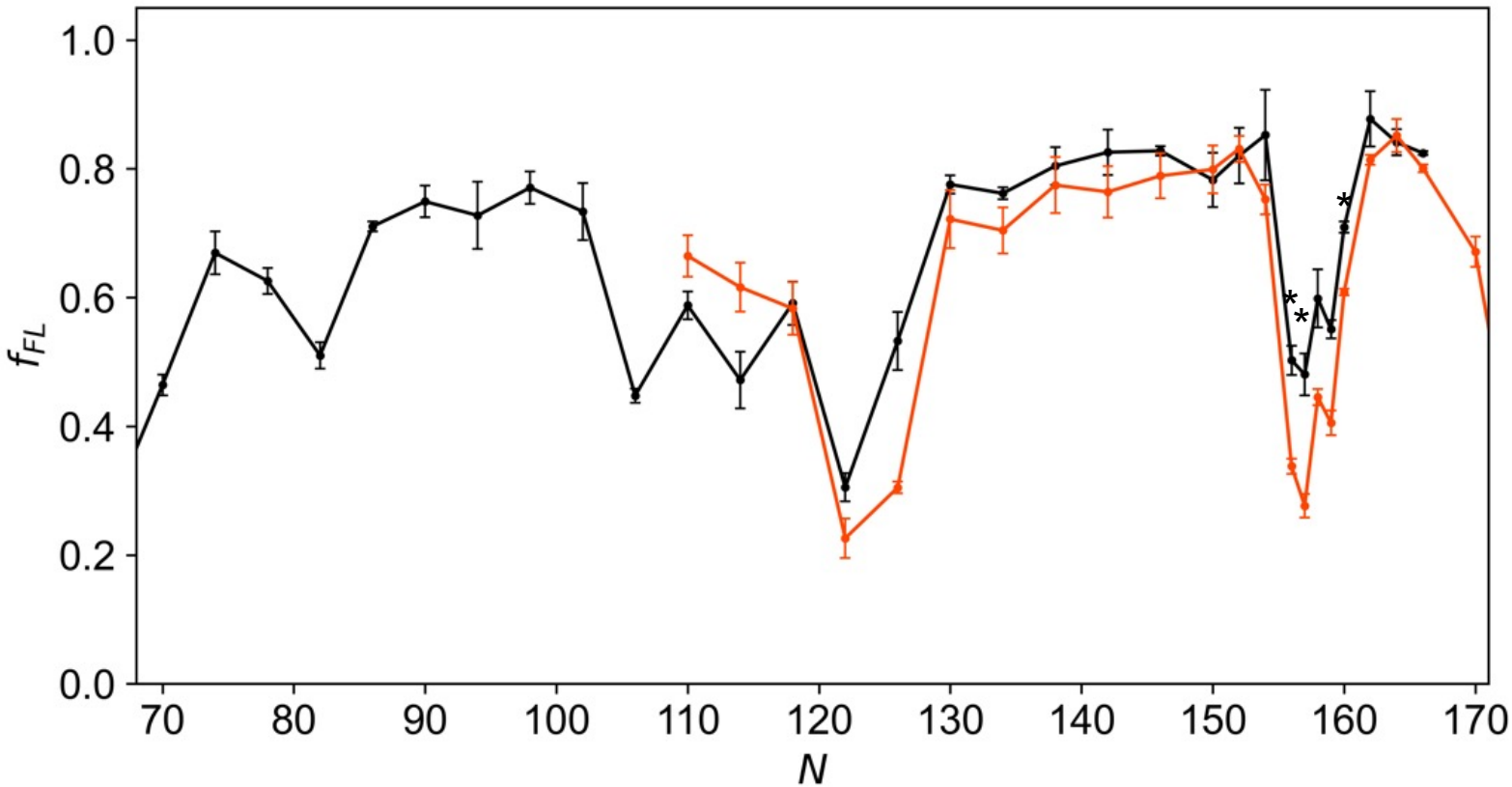
Corresponding authors: Justin M. Westerfield, Gunnar von Heijne
Email: justin.westerfield@dbb.su.se, gunnar.von.heijne@dbb.su.se

This PDF file includes:

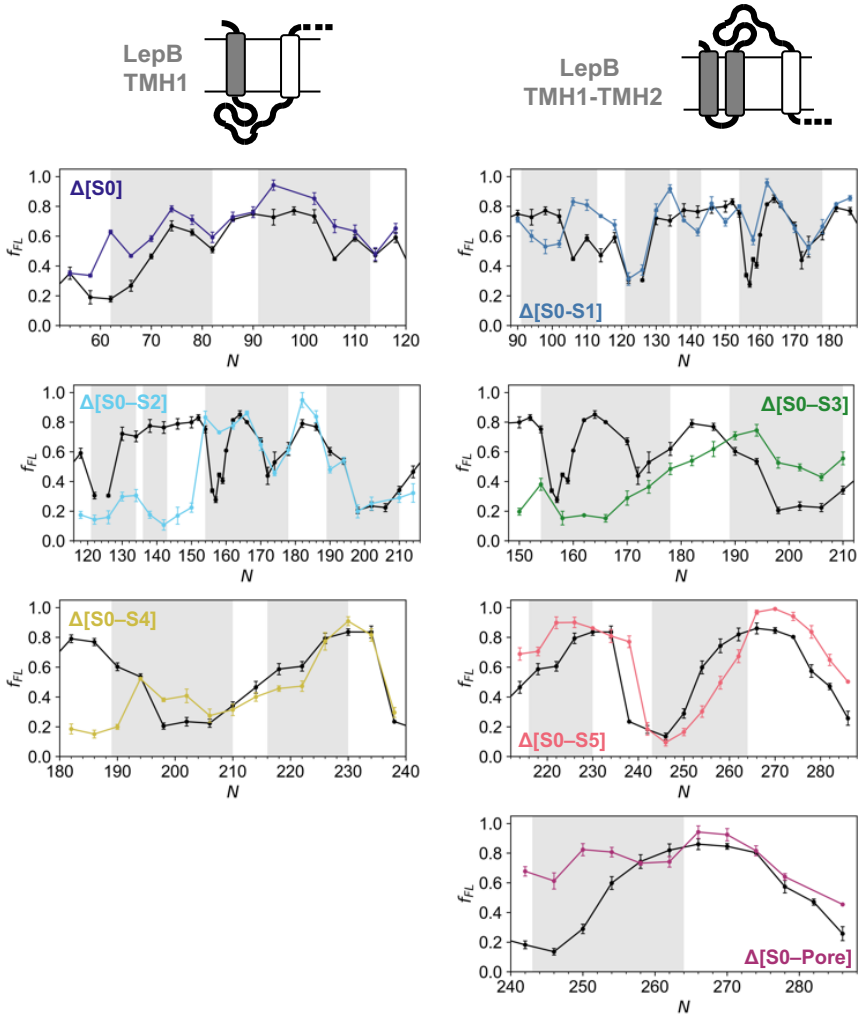
Supplemental Figures S1-S4
Table S1



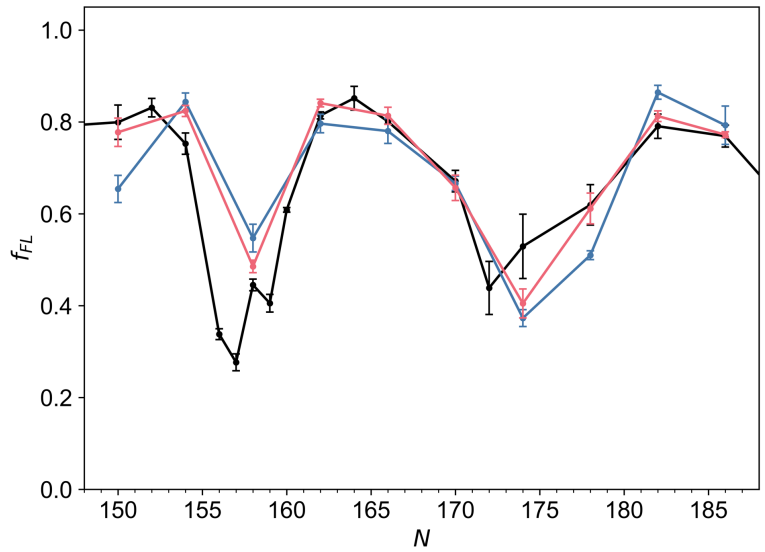
Supplemental Figure S1. Structure of a SecM-stalled ribosome-nascent chain complex (Ahn M*, et al.* (2022) *Nat Commun* 13:4243. doi: 10.1038/s41467-022-31906-z; PDB 7ZP8). The visible part of the NC (in red) is 33 residues long and has an extend conformation; the NC also includes a folded N-terminal FLN5 domain (not visible in the structure) that generates a substantial pulling force on the NC. The N-terminal residue of the 30-residue HA/AP constant part in the KvAP constructs (*c.f.*, Fig.1 in the main text) would correspond to residue E^{137} (marked by *). The SecM AP used is a mutant version of the wildtype *E. coli* SecM AP that causes stronger translational arrest (necessary to withstand the pulling force generated by the folding of the FLN5 domain). The P-site tRNA is in dark green, RNA is in pale pink, and other colors indicate ribosomal proteins. Image prepared in ChimeraX (Goddard TD*, et al.* (2018) *Protein Sci* 27:14-25).



Supplemental Figure S2. Overlapping KvAP FPs obtained with (black) and without (red) an N-terminal LepB (1-177) fusion (c.f., Fig. 2 in the main text). Significant differences (t-test with Bonferroni correction, $p < 0.05$) between mutant and wildtype f_{FL} values are indicated by *. These differences become non-significant if a correction is made for the average difference of 0.06 in the f_{FL} values for the ±LepB FPs.



Supplemental Figure S3. Same as in Fig. 3 (main text), but with each deletion FP plotted separately. The relevant portions of the full KvAP FP (Fig. 2) are in black.



Supplemental Figure S4. Same as in Fig. 4 (main text), but for mutations $E^{45}A$ and $E^{93}A$.

Table S1. Amino acid sequences for all constructs

Force profile constructs (Fig. 2a)

N-terminal truncation mutants (Figs. 3, S3)
Δ[S0]
Δ[S0-S1]
Δ[S0-S2]
Δ[S0-S3]
Δ[S0-S4]
Δ[S0-S5]
Δ[S0-Pore]

Point mutations (Figs. 4, S4)
$E^{45}A$
$D^{62}A$
$D^{72}A$
$E^{93}A$
$R^{76}A$
$E^{107}A$

S4 arginine mutations (Fig. 4)
5R→5Q
5R→5K
5R→5D
$R^{117}Q$
$R^{120}Q$
$R^{123}Q$
$R^{126}Q$
$R^{133}Q$

Force profile +LepB (Fig. S2)

Force profile constructs (Fig. 2a)

N286:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSEEEFESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGL
RLSRIGGIH

N282:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSR
IGGIH

N278:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N274:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N270:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N266:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N262:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKILVGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N258:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNMFQKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N254:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGTVSNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N250:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
IGIAVMLTGISALTLLIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N246:
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LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
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N242:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
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N238:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
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N234:
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LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKV
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N230:
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LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGSG
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N226:
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N218:
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LRLSRIGGIH

N182:
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N174:
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LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
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N164:
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N162:
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N160:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N159:
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LAGLGLFRLVRLLRFLRILLIISRGSKFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N157:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N156:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N152:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N146:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N142:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N138:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N134:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N130:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
SGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N126:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALSGM
GYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N122:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGSGMGYP
YDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N118:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALSGMGYPYDVP
DYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N114:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAF
STPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N110:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPV
WISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N106:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEW
PTGLRLSRIGGIH
N102:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLR
LSRIGGIH
N98:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRI
GGIH
N94:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N90:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N86:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N82:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N78:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N74:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N70:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N66:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N62:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N58:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N54:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N50:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N46:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPSG
MGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N-terminal truncation mutants (Fig. 3, S3)

Δ[S0]

N118:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEG
EWPTGLRLSRIGGIH

N114:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEW
PTGLRLSRIGGIH

N110:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGL
RLSRIGGIH

N106:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRI
GGIH

N102:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N98:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N94:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD

KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N90:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N86:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVDLILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N82:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRLYLVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N78:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGEYLVRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N74:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQLSGESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N70:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVEYTMQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N66:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVVVVESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N62:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSVIVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N58:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD

KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAAL
LSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N54:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYSG
MGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S1]
N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRL
SRIGGIH
N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIG
GIH
N178:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST

DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N146:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLLRFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N142:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRLVRLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N138:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR

RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LGLFRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N134:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAG
LSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N130:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHSGM
GYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N126:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALSGMGYP
YDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N122:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGSGMGYPYDVP
DYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N118:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPAL*SGMGYPYDVPDYAF*
*STPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

N114:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAFSTP
VWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N110:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPVWIS
QAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N106:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGSGMGYPYDVPDYAFSTPVWISQAQG
IRAGPGSSDKQEGEWPTGLRLSRIGGIH
N102:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGSGMGYPYDVPDYAFSTPVWISQAQGIRAG
PGSSDKQEGEWPTGLRLSRIGGIH
N98:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSS
DKQEGEWPTGLRLSRIGGIH
N94:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQE
GEWPTGLRLSRIGGIH
N90:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWP
TGLRLSRIGGIH
N86:
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DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGL
RLSRIGGIH
N82:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH

Δ[S0-S2]

N214:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTSGMGYP
YDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
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PDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N206:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDSGMGYPYDVPDYAF
STPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N202:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSGMGYPYDVPDYAFSTPV
WISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N198:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
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VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSGMGYPYDVPDYAFSTPVWISQ
AQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N194:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYSGMGYPYDVPDYAFSTPVWISQAQGI
RAGPGSSDKQEGEWPTGLRLSRIGGIH
N190:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
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VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYSGMGYPYDVPDYAFSTPVWISQAQGIRAG
PGSSDKQEGEWPTGLRLSRIGGIH
N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD

KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGS
SDKQEGEWPTGLRLSRIGGIH

N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQ
EGEWPTGLRLSRIGGIH

N178:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEW
PTGLRLSRIGGIH

N174:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGL
RLSRIGGIH

N170:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSR
IGGIH

N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H

N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N158:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N154:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLRILL*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH
N146:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLLRFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N142:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRLVRLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N138:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLGLFRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N134:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHLAGLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N130:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALIEGHSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N126:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGLLALSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N122:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
VPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N118:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPAL
SGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N114:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYE*SGM*
*GYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S3]
N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N206:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N202:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N198:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSGM
GYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N194:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYSGMGYPY
DVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N190:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST

DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYSGMGYPYDVPD
YAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAF
STPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPV
WISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N178:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQ
AQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N174:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGI
RAGPGSSDKQEGEWPTGLRLSRIGGIH

N170:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGP
GSSDKQEGEWPTGLRLSRIGGIH

N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSS
DKQEGEWPTGLRLSRIGGIH

N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR

RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQE
GEWPTGLRLSRIGGIH
N158:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEW
PTGLRLSRIGGIH
N154:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGL
RLSRIGGIH
N150:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGGLFRLVRLLRFLRILL*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLS
RIGGIH

Δ[S0-S4]
N238:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGL
RLSRIGGIH
N234:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRI
GGIH
N230:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
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N226:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD

KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N222:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N218:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N214:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWAVVTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDALWWSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N206:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSVFDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N202:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSSIKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N198:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYPDPNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N194:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYIVEYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N190:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD

KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
AFAIYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYG
ASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTV*SG*
*MGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S5]
N286:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GEPEPSSSPAKLAEMVSSMSEEEFESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N282:
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DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GEPEPSSSPAKLAEMVSSMSESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N278:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GEPEPSSSPAKLAEMVSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N274:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GEPEPSSSPAKLASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N270:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GEPEPSSSPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N266:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GEPEPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N262:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILV
GSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N258:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKSG
MGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N254:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNSGMGYP
YDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N250:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGSGMGYPYDVP
DYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N246:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTSGMGYPYDVPDYA
FSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N242:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISGMGYPYDVPDYAFSTP
VWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N238:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST

DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMSGMGYPYDVPDYAFSTPVWIS
QAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N234:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGSGMGYPYDVPDYAFSTPVWISQAQ
GIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N230:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGSGMGYPYDVPDYAFSTPVWISQAQGIRA
GPGSSDKQEGEWPTGLRLSRIGGIH

N226:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPASGMGYPYDVPDYAFSTPVWISQAQGIRAGPG
SSDKQEGEWPTGLRLSRIGGIH

N222:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDK
QEGEWPTGLRLSRIGGIH

N218:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGE
WPTGLRLSRIGGIH

N214:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPT
GLRLSRIGGIH

N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR

RNGGEATSGFFEVPKQETKENGIRLSETSGGPGDPNSSIKSVFDALWW*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLS
RIGGIH

Δ[S0-Pore]
N286:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSEEEFESGM
GYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N282:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSESGMGYP
YDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N278:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSGMGYPYDVPD
YAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N274:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLASGMGYPYDVPDYAFS
TPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N270:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPSGMGYPYDVPDYAFSTPV
WISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N266:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSGMGYPYDVPDYAFSTPVWISQA
QGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N262:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR

RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGSGMGYPYDVPDYAFSTPVWISQAQGIR
AGPGSSDKQEGEWPTGLRLSRIGGIH

N258:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKSGMGYPYDVPDYAFSTPVWISQAQGIRAGP
GSSDKQEGEWPTGLRLSRIGGIH

N254:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSD
KQEGEWPTGLRLSRIGGIH

N250:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEG
EWPTGLRLSRIGGIH

N246:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWP
TGLRLSRIGGIH

N242:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLR
LSRIGGIH

N238:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNST
DFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSR
RNGGEATSGFFEVPKQETKENGIRLSETSGGPGVPATPIGKVIGIAVM*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRI
GGIH

Point mutations (Figs. 4, S4)

$E^{45}A$

N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$D^{62}A$
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH

LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$D^{72}A$
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH

N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$E^{93}A$
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH

LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$R^{76}A$
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH

N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$E^{107}A$
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH

LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGH
LAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

S4 arginine mutations (Fig. 4)

5R→5Q
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPT
GLRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH

LAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGG
IH
N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLIISQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVQLLQFLQILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

5R→5K
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H

N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLIISKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFKLVKLLKFLKILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

5R→5D
N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTG
LRLSRIGGIH
N182:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLS
RIGGIH
N178:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGI
H

N174:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLIISDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFDLVDLLDFLDILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$R^{117}Q$
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFQLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
$R^{120}Q$

N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVQLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVQLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVQLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVQLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

R^{123}Q
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLQFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLQFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLQFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLQFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
R^{126}Q
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLQILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLQILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLQILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLQILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$R^{133}Q$
N166:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISQGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISQGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISQGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGH
LAGLGLFRLVRLLRFLRILLIISQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

Force profile +LepB (Fig. S2)

N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N164:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKFLSAIADSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N160:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD

KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKFLSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N159:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N158:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N157:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N156:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRGSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N154:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N152:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLII
SGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N150:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE

LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLS
GMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N146:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLSGMG
YPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N142:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLSGMGYPY
DVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N138:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRSGMGYPYDVPD
YAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N134:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLSGMGYPYDVPDYAFS
TPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N130:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHSGMGYPYDVPDYAFSTPV
WISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N126:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALSGMGYPYDVPDYAFSTPVWISQA
QGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N122:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGSGMGYPYDVPDYAFSTPVWISQAQGI
RAGPGSSDKQEGEWPTGLRLSRIGGIH

N118:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALSGMGYPYDVPDYAFSTPVWISQAQGIRAGP
GSSDKQEGEWPTGLRLSRIGGIH
N114:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSS
DKQEGEWPTGLRLSRIGGIH
N110:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGD
KVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVE
LGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQE
GEWPTGLRLSRIGGIH
N46–N106: See section “Force Profile (Fig. 2a)”