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.

E-mail: justin.westerfield@dbb.su.se, gunnar.von.heijne@dbb.su.se (lead contact)

SUMMARY

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.

Keywords: Membrane protein biogenesis; voltage-sensor domain; ion channel; KvAP; Force Profile Analysis

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]. 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 [21]. 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 [6,8,21], 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 fractions, 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 generated 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 I 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, hence 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).

It was previously demonstrated that the distance between the PTC and the mouth of the ribosomal exit tunnel can be bridged by an approximately 33 residues long, extended polypeptide [22], which fits well with FPA data on cotranslational folding of water-soluble proteins [23]. Similarly, we previously found that a model 19-residue TMH generates a peak in the FP that reaches half-maximal amplitude (N_{start}) at an N value where its N-terminal end is ~45 residues away from the PTC, and drops to half-maximal amplitude (N_{end}) at an N value 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 [24]. 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, corresponding to a PTC–insertion site distance of 135-155 Å (assuming a length of 3.0 to 3.4 Å for a residue in an extended conformation , Fig. 1a). The FP thus reflects membrane insertion events taking place ~45 residues from the PTC. 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 $N_{start} = 71\pm2$ residues and $N_{\mathrm{end}} = 82\pm2$ 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 ΔG_{pred} and OPM algorithms [3,25], Fig. 2b. The second peak has $N_{start} = 83\pm2$ residues and $N_{end} = 105\pm2$ 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 $N = 120\pm2$ 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}), with a subtle separation between the two at $N = 114\pm2$ residues (corresponding to the positively charged segment $R^{76}AYK^{79}$ at the end of S2).

The S3–S5 region generates a more complex series of peaks, between $N \approx 128$-194 residues. At $N_{start} = 128\pm2$ 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 $N = 155\pm1$ 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 $N_{start} = 161\pm1$ 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 $N_{end} = 171\pm2$ 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 $N_{start} = 174\pm2$ 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 [26,27], 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 [28]. 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.

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 [29]. 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±2 residues but the high-amplitude peak in the original FP at N_{start} = 161±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±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±2 residues and N_{end} = 204±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±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±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 [9,30], and, second, recording FPs for mutated constructs in which either the positively charged residues in S4 are mutated to Lys, Asp, or 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 are mutated to Ala, Fig. 4 and Supplementary Fig. S1.

Strikingly, the dip at $N \approx 174$ residues disappears with indole in the medium while the dip at $N \approx 157$ residues is unaffected, Fig. 4a. In contrast, none of the mutations in S2 and S3 have much effect on the dip at $N \approx 174$ residues, but two – $E^{107}A$ in S3b and $R^{76}A$ at the C-terminal end of S2 – strongly reduce ($E^{107}A$) or completely eliminate ($R^{76}A$) the dip at $N \approx 157$ residues, Fig. 4b and Supplementary Fig. S1. 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).

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 $N_{start} = 160 \pm 1$ residues and $N_{end} = 172 \pm 2$ residues, suggesting poor membrane interaction of these mutated S4 sequences. 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 [31], 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 [32,33]. 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 translocon-mediated membrane translocation of NCs, possibly due to the high pKa of the Arg side chain [34].

We also tested several Ala substitutions of charged residues in S2 and S3 (Fig. 4b, Supplementary Fig. S1). 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 [29]. 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, to a lesser extent, in 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.

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 [26].

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 [31]. 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.

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 [35] or mycolactones [36] 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 unexpected disagreements between the hydrophobicity profile and the FP suggest longer-range intra- or inter-molecular folding events [12].

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. 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 [13,37].

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AUTHOR CONTRIBUTIONS

Conceptualization, J.W., A.M., and G.v.H.; investigation, J.W., P.K., C.J., and A.M.; validation, J.W.; formal analysis, J.W. and G.v.H.; visualization, J.W. and G.v.H.; supervision, G.v.H.; funding acquisition, G.v.H.; writing – original draft, J.W. and G.v.H.; writing – review & editing, J.W., A.M., and G.v.H.

DECLARATION OF INTERESTS

The authors declare no competing interests.

FIGURE TITLES AND LEGENDS

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. (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. Cytoplasmic and periplasmic loops are indicated by red and blue lines, respectively.

Figure 2. The KvAP force profile. (a) KvAP FP (black), 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 [25] and ΔG_{pred} algorithms (using a 19-residue window). (b) FP mapped onto the structure [18] and amino acid sequence of KvAP (PDB 6UWM). 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 the PDB structure, 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 KvAP [29].

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.

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 (light green). (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), $R^{120}Q$ (light blue), $R^{123}Q$ (green), $R^{126}Q$ (light green), and $R^{133}Q$ (red) mutants. See also Supplementary Figure S1.

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 Δ[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.

EXPERIMENTAL PROCEDURES

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 KvAP 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 [38]. Further mutagenesis was either similarly ordered, or performed in-house by a combination of Q5 PCR and Gibson assembly [39] with a homemade reaction mixture.

In vivo pulse-labeling analysis. For expression, constructs were transformed into BL21 (DE3) cells [40]. 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. Phosphoimaging plates (BAS-IP, Fujifilm, Tokyo, Japan) were exposed to gels for 2-3 days before imaging on a FLA-9000 imager (Fujifilm, Tokyo, Japan).

Analysis. 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 $I_{Full\text{-}length}$ 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.

SUPPLEMENTAL INFORMATION TITLES AND LEGENDS

Supplemental Table I: Force Profile constructs

Supplemental Figure S1: Same as in Figure 4, but for mutations $E^{45}A$ and $D^{62}A$ (panel a), and mutations $D^{72}A$ and $E^{93}A$ (panel b)

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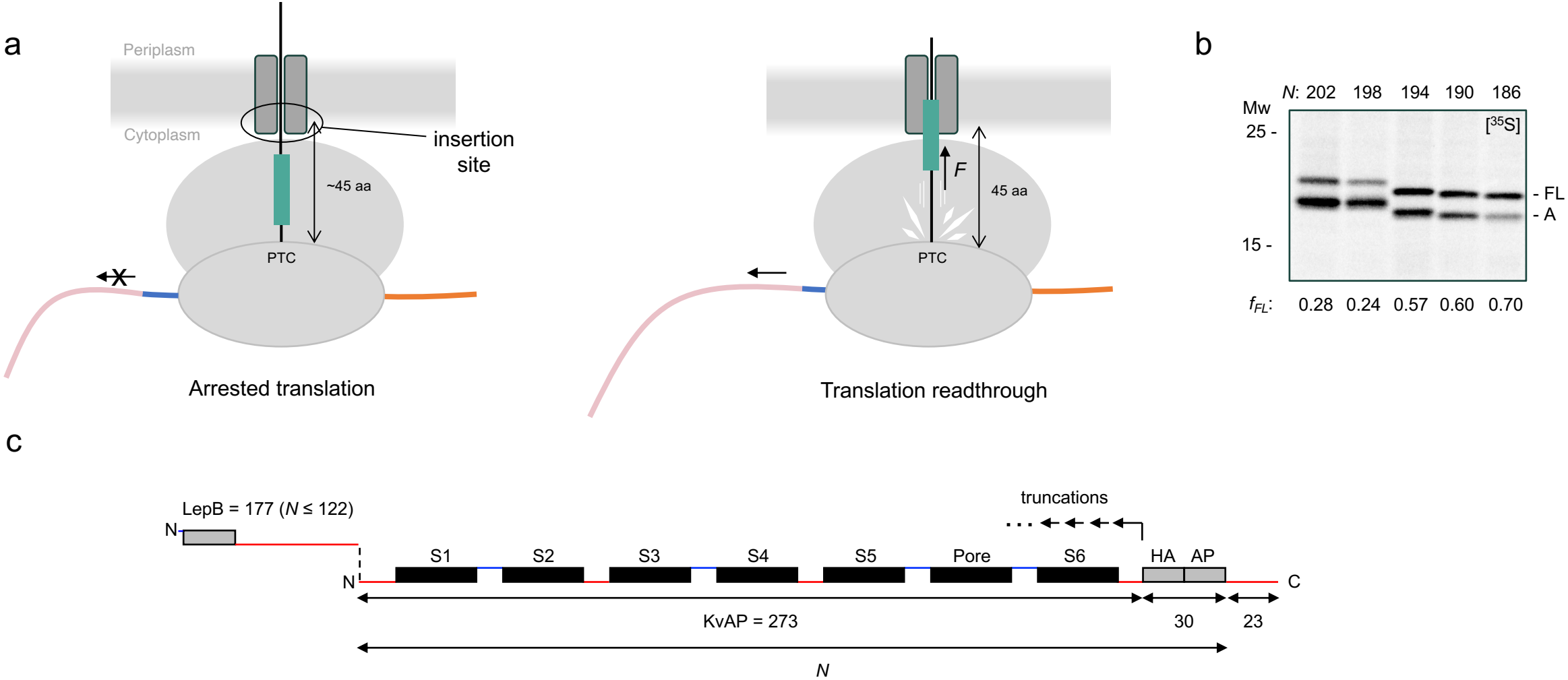
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Cytoplasm
insertion site
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PTC
Arrested translation
F
45 aa
PTC
Translation readthrough
b
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Mw
25 -
15 -
[35S]
- FL
- A
fFL: 0.28 0.24 0.57 0.60 0.70
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

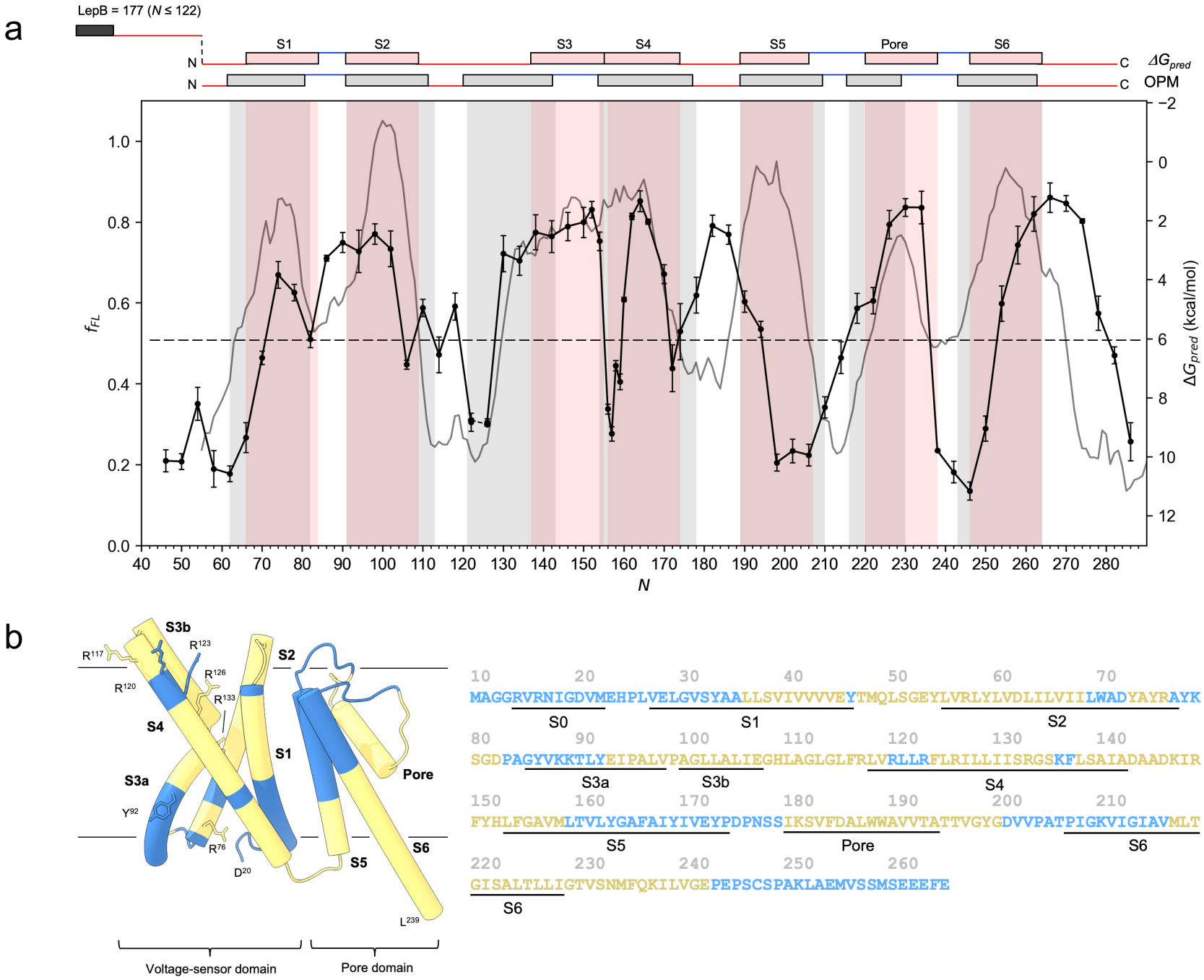
a
LepB = 177 (N ≤ 122)
S1
S2
S3
S4
S5
Pore
S6
N
C
ΔG_pred
OPM
f_FL
ΔG_pred (kcal/mol)
N
b
S3b
S2
S4
S1
S3a
Pore
S6
S5
R117
R120
R123
R126
R133
Y92
R76
D20
L239
Voltage-sensor domain
Pore domain
10 20 30 40 50 60 70
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYK
S0
S1
S2
80 90 100 110 120 130 140
SGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIR
S3a
S3b
S4
150 160 170 180 190 200 210
FYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLT
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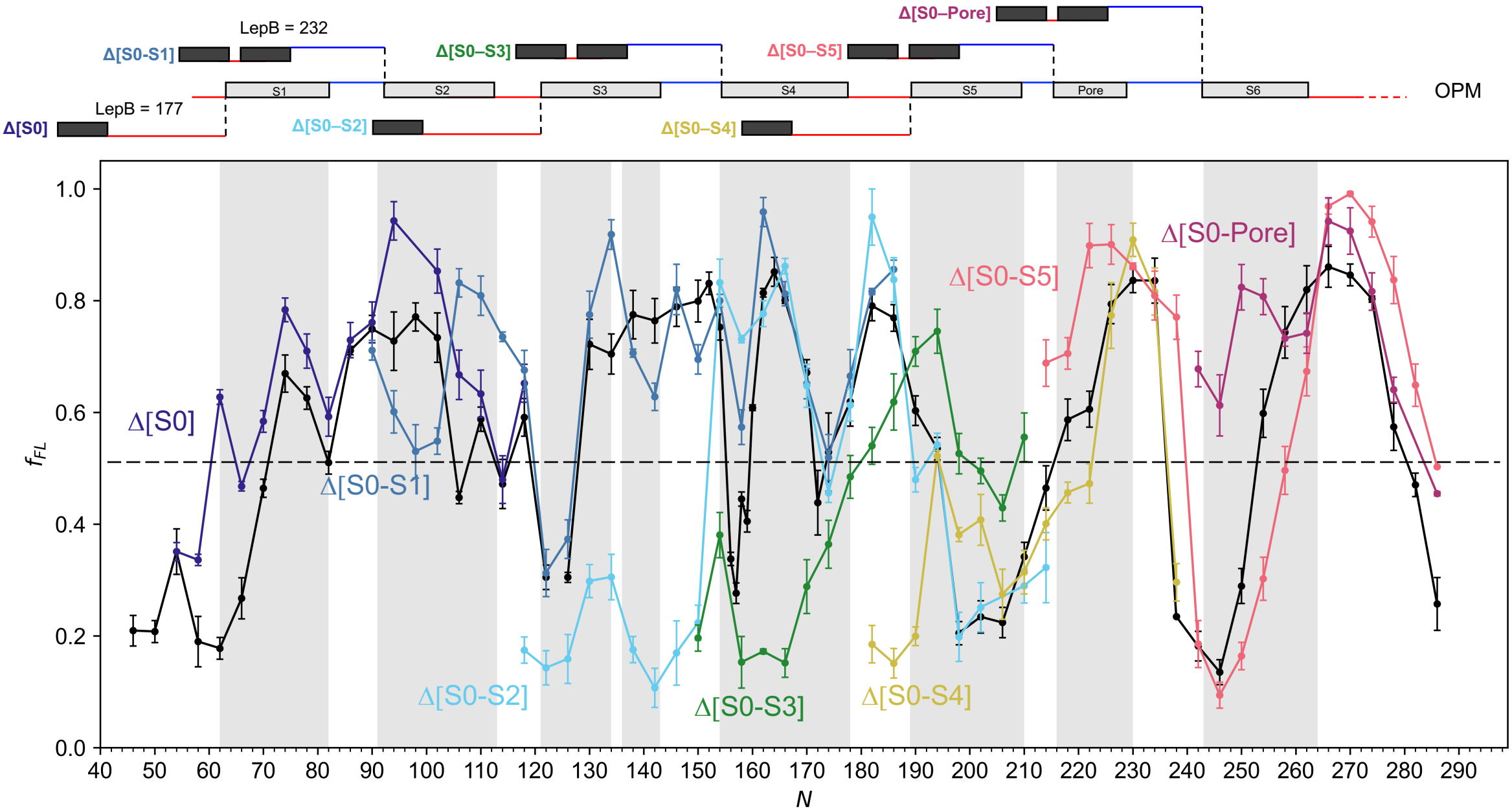
Figure 2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Δ[S0–S3]
Δ[S0–S5]
S1
S2
S3
S4
S5
Pore
S6
OPM
LepB = 177
Δ[S0]
Δ[S0–S2]
Δ[S0–S4]
Δ[S0]
Δ[S0-S1]
Δ[S0-S2]
Δ[S0-S3]
Δ[S0-S4]
Δ[S0-S5]
Δ[S0-Pore]
f_{FL}
N
0.0
0.2
0.4
0.6
0.8
1.0
40
50
60
70
80
90
100
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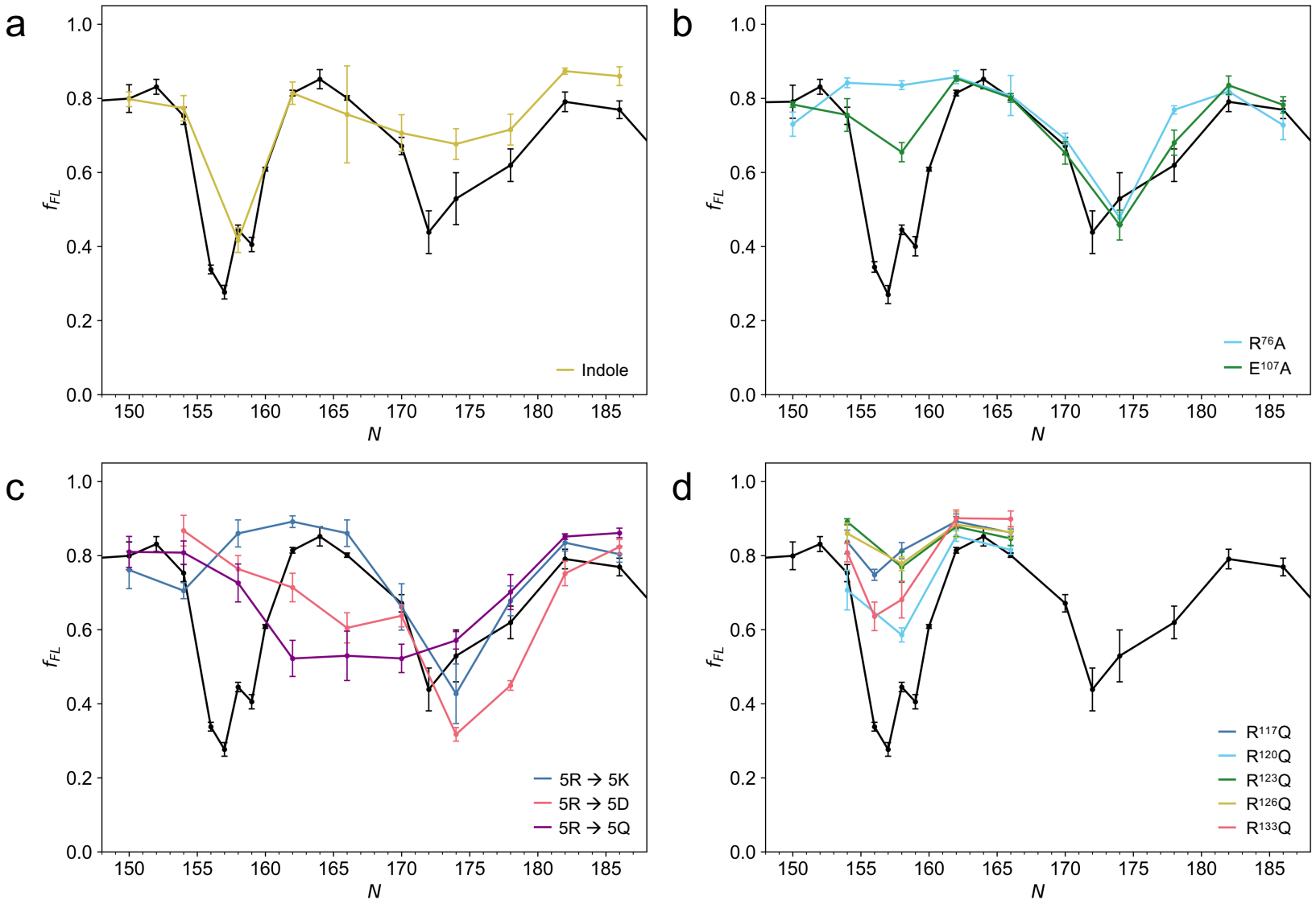
Figure 3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b
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d
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Indole
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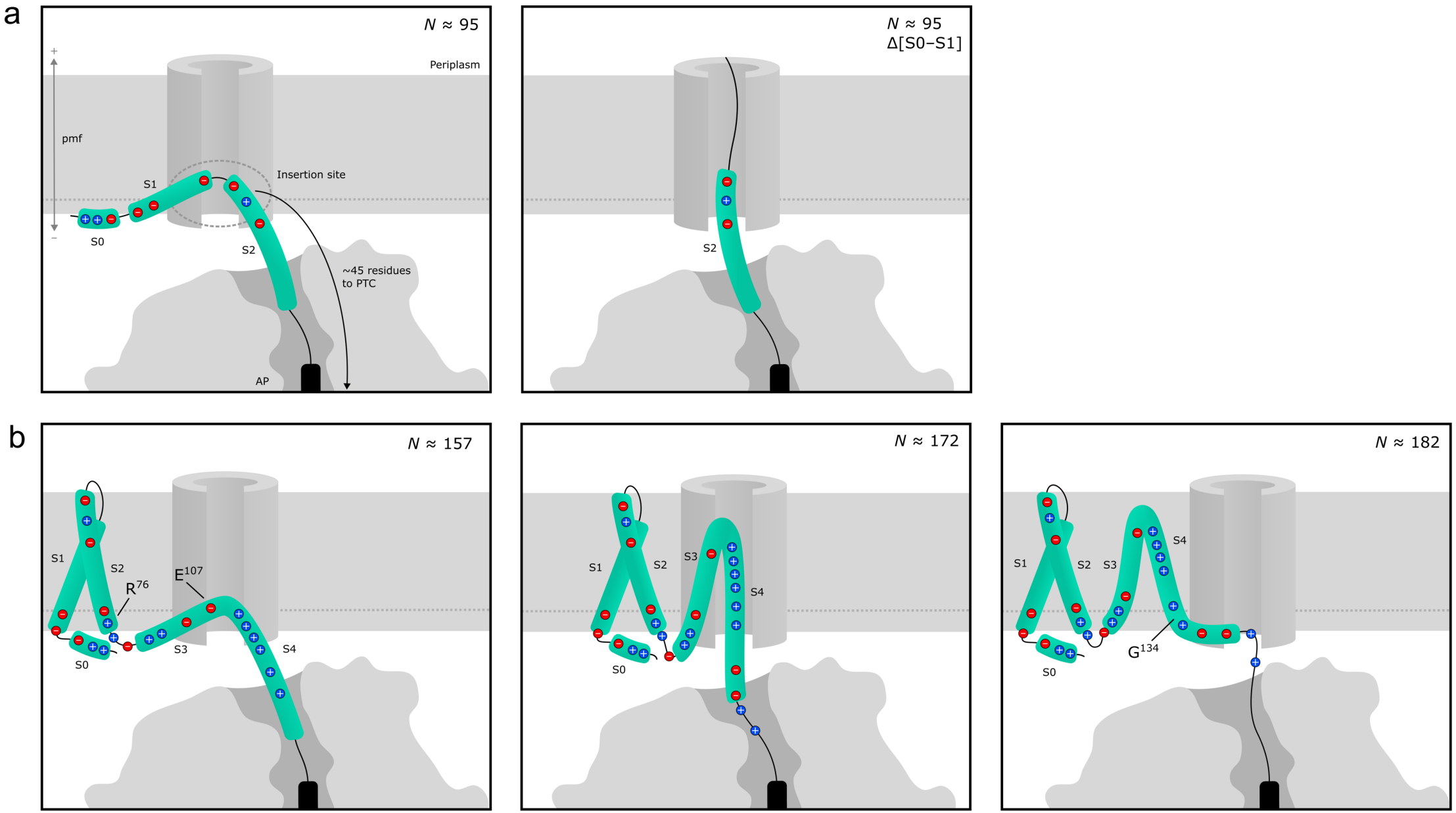
R120Q
R123Q
R126Q
R133Q

Figure 4


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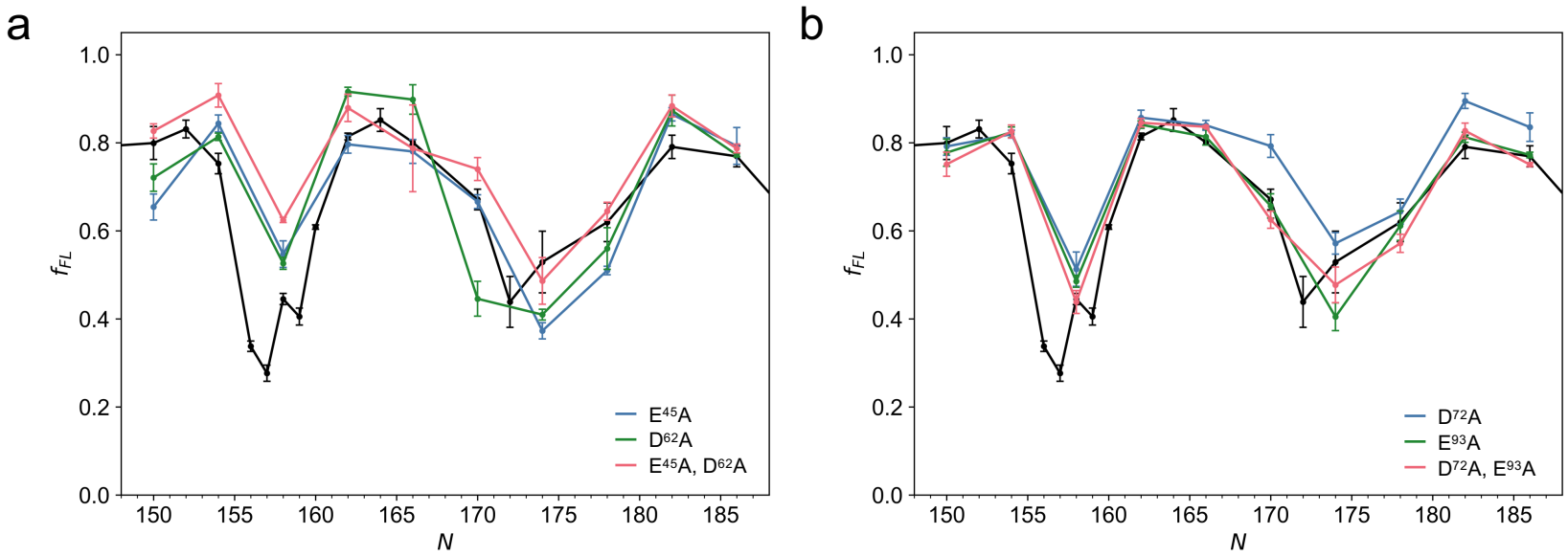
S1
S2
S3
S4
G134
S0

Figure 5



Supplemental Figure S1. Same as in Figure 4, but for mutations $E^{45}A$ and $D^{62}A$ (panel a), and mutations $D^{72}A$ and $E^{93}A$ (panel b)

Supplemental Table I

Force profile constructs (Fig. 2a) **2**

N-terminal truncation mutants (Fig. 3) **4**
Δ[S0] *4*
Δ[S0-S1] *4*
Δ[S0-S2] *5*
Δ[S0-S3] *7*
Δ[S0-S4] *7*
Δ[S0-S5] *8*
Δ[S0-Pore] *9*

Point mutations (Figs. 4, S1) **9**
$E^{45}A$ *9*
$D^{62}A$ *9*
$D^{72}A$ *10*
$E^{93}A$ *10*
$R^{76}A$ *10*
$E^{107}A$ *10*

Double mutations (Fig. S1) **10**
$E^{45}A$, $D^{62}A$ *10*
$D^{72}A$, $E^{93}A$ *11*

S4 arginine mutations (Fig. 4) **11**
5R→5Q *11*
5R→5K *11*
5R→5D *11*
$R^{117}Q$ *11*
$R^{120}Q$ *11*
$R^{123}Q$ *11*
$R^{126}Q$ *12*
$R^{133}Q$ *12*

Force profile constructs (Fig. 2a)

N286:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSEEEFESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N282:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N278:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N274:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGEPEPSSSPAKLASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N270:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGEPEPSSSPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N266:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGEPEPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N262:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKILVGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N258:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNMFQKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N254:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGTVSNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N250:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTLLIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N246:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
ALTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N242:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGIS
GMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N238:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMSGMGY
PYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N234:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGSGMGYPYDV
PDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N230:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGSGMGYPYDVPDYA
FSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N226:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDVVPASGMGYPYDVPDYAFSTP
VWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N222:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVGYGDSGMGYPYDVPDYAFSTPVWIS
QAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N218:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTATTVSGMGYPYDVPDYAFSTPVWISQAQG
IRAGPGSSDKQEGEWPTGLRLSRIGGIH
N214:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTSGMGYPYDVPDYAFSTPVWISQAQGIRAG
PGSSDKQEGEWPTGLRLSRIGGIH
N210:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSS
DKQEGEWPTGLRLSRIGGIH
N206:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQE
GEWPTGLRLSRIGGIH
N202:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWP
TGLRLSRIGGIH
N198:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLR
LSRIGGIH
N194:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRI
GGIH
N190:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N172: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N164: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N160: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N159: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N157: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N156: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N152: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N146: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N142: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N138: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N134: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N130: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N126: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N122: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N118: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N114: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N110: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N106:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N102:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N98:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVDLILVIILWADYAYRASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N94:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVDLILVIILWADYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N90:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVDLILVIILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N86:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVDLILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N82:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRLYLVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N78:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGEYLVRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N74:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQLSGESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N70:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEY
TMQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N66:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVES
GMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N62:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSVIVSGMGY
PYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N58:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYAALLSGMGYPYDV
PDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N54:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELGVSYSGMGYPYDVPDYA
FSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N50:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPLVELSGMGYPYDVPDYAFSTP
VWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N46:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAGGRVRNIGDVMEHPSGMGYPYDVPDYAFSTPVWIS
QAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N-terminal truncation mutants (Fig. 3)

Δ[S0]

N118:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N114:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N110:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N106:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYAYRAYKSGDPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N102:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYAYRAYKSGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N98:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYAYRASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N94:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILWADYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N90:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILVIILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N86:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVDLILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N82:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRLYLVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N78:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEY
LVRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N74:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGES
GMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N70:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVEYTMQSGMGY
PYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N66:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVVVVESGMGYPYDV
PDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N62:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSVIVSGMGYPYDVPDYA
FSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N58:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYAALLSGMGYPYDVPDYAFSTP
VWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N54:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGGDVMEHPLVELGVSYSGMGYPYDVPDYAFSTPVWIS
QAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S1]

N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N146:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N142:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N138:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N134:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N130:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N126:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N122:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N118:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPAL*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH
N114:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N110:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N106:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N102:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N98:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYAYRASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N94:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILWADYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N90:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILVIILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N86:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVDLILSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N82:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGTMQLSGEYLVRLYLVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S2]

N214:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWAVVTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N206:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N202:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N198:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N194:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N190:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLRILL*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH
N146:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLLRFLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N142:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRLVRLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N138:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLG
LFRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N134:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLS
GMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N130:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALIEGHSGMGY
PYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N126:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGLLALSGMGYPYDV
PDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N122:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALVPAGSGMGYPYDVPDYA
FSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N118:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYEIPALSGMGYPYDVPDYAFSTP
VWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N114:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGKSGDPAGYVKKTLYE*SGMGYPYDVPDYAFSTPVWIS*
*QAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S3]

N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDALWWSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N206:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSVFDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N202:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N198:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N194:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYIVEYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N190:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGAFAIYSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGGLFRLVRLLRFLRILL*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S4]

N238:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N234:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTATTVGYGDVVPATPIGKVIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N230:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTATTVGYGDVVPATPIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N226:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTATTVGYGDVVPASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N222:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTATTVGYGDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N218:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTATTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N214:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWAVVTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDALWWSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N206:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SVFDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N202:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSSIK
SGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N198:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYPDPNSGMG
YPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N194:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYIVEYSGMGYPYD
VPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N190:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGAFAIYSGMGYPYDVPDY
AFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N186:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFST
PVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGDKIRFYHLFGAVMLTV*SGMGYPYDVPDYAFSTPVWI*
*SQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-S5]

N286:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSEEEFESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N282:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N278:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N274:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N270:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N266:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N262:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N258:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N254:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGTVSNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N250:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTLLIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N246:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISALTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N242:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMLTGISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N238:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGIAVMSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N234:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGKVIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N230:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPATPIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N226:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDVVPASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N222:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVGYGDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

N218:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTATTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N214:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWWAVVTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N210:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGDPNSSIKSVFDALWW*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Δ[S0-Pore]

N286:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSEEEFESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N282:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSMSESGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N278:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLAEMVSSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N274:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPAKLASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N270:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSSSPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N266:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGEPEPSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N262:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKILVGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N258:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNMFQKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N254:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGTVSNSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N250:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTLLIGSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N246:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISALTSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N242:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVMLTGISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N238:
MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVP
KQETKENGIRLSETSGGPGVPATPIGKVIGIAVM*SGMGYPYDVPDYAFSTPVWISQAQGIRAGP*GSSDKQEGEWPTGLRLSRIGGIH

Point mutations (Figs. 4, S1)

$E^{45}A$

N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

$D^{62}A$

N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH

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N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$D^{72}A$

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$E^{93}A$

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$R^{76}A$

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYAAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$E^{107}A$

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIAGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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Double mutations (Fig. S1)

$E^{45}A$, $D^{62}A$

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVAYTMQLSGEYLVRLYLVALILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$D^{72}A$, $E^{93}A$

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWAAYAYRAYKSGDPAGYVKKTLYAIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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S4 arginine mutations (Fig. 4)

5R→5Q

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLIISQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVQLLQFLQILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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5R→5K

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLIISKSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFKLVKLLKFLKILLLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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5R→5D

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N186:
MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAIADAADKIRFYHLFGAVMLTVLYGASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N182: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAIADAADKIRFYHLFGAVMLTVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N178: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAIADAADKIRFYHLFGAVSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N174: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAIADAADKIRFYHLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N170: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAIADAADKIRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLIISDSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N150: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFDLVDLLDFLDIILLSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$R^{117}Q$

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N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVRLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVRLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVRLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFQLVRLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$R^{120}Q$

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N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVQLLRFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVQLLRFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVQLLRFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVQLLRFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$R^{123}Q$

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N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLQFLRILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLQFLRILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLQFLRILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLQFLRILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$R^{126}Q$

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N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLQILLIISRGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLQILLIISRGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLQILLIISRGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLQILLIISRSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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$R^{133}Q$

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N166: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISQGSKFLSAIADAASGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N162: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISQGSKFLSAISGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N158: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISQGSKFSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
N154: MAGGRVRNIGDVMEHPLVELGVSYAALLSVIVVVVEYTMQLSGEYLVRLYLVDLILVIILWADYAYRAYKSGDPAGYVKKTLYEIPALVPAGLLALIEGHLAGLGLFRLVRLLRFLRILLIISQSGMGYPYDVPDYAFSTPVWISQAQGIRAGPGSSDKQEGEWPTGLRLSRIGGIH
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