#### Contents

P	age
Supplementary Discussion	2
Supplementary Table 1. Data collection, phasing and refinement statistics	.11
Supplementary Table 2. Residues present in the model	.12
Supplementary Table 3. Statistics of structural alignment of subunits	
NuoL, M and N, their symmetry related domains and subunit NuoK	.13
Supplementary Table 4. Summary of analysis of interactions between subunits	.14
Supplementary Table 5. Residues forming putative proton translocation channels	.16
Supplementary Table 6. Mutations in the membrane domain of <i>E.coli</i> complex I	.17
Supplementary Table 7. Mutations in mitochondrially encoded complex I	
genes (subunits ND2-ND6) associated with human diseases	.23
Supplementary Table 8. Mutations in subunits A, D and C of Mrp antiporters	.25
Supplementary Figure 1. Electron density of E. coli complex I	
membrane domain	.27
Supplementary Figure 2. Crystal packing of E. coli complex I membrane domain	
in space group P1	.28
Supplementary Figure 3. Conservation of amino acid residues within	
the membrane domain of complex I (subunits NuoLMNAJK)	.29
Supplementary Figure 4. Surface charge distribution of E. coli complex I	
membrane domain	.30
Supplementary Figure 5. Overlay of the 14 conserved helices of three	
antiporter-like subunits	31
Supplementary Figure 6. Fold of subunits NuoK, NuoJ and NuoA	32
Supplementary Figure 7. Structure-based alignment of E. coli complex I	
subunits NuoL, M and N	.33
Supplementary Figure 8. Structure-based alignment of complex I subunits	
NuoL/M/N/A/J/K, using 30 representatives from all kingdoms of life	.34
Supplementary References	.43

doi:10.1038/nature10330

**RESEARCH** SUPPLEMENTARY INFORMATION

#### **Supplementary Discussion**

Please note: in the supplement the residues are listed with subunit name in the prefix; residues conserved between all three antiporter-like subunits are indicated by an asterisk.

#### 1. Description of proton-translocation pathways in antiporter-like subunits.

Possible pathways and intra-protein cavities were examined with programs  $CAVER^{61}$ ,  $HOLE^{62}$  and  $VOIDOO^{63}$ . None of the channels is solvent-accessible on both sides of the membrane, with either 1.4 or 1.2 Å<sup>62</sup> radius probes.

In the first channel (near TM7), the cavity surrounding LysTM7 is about 70  $Å^3$ , sufficient to hold up to two water molecules. One is observed in NuoN, near the Cterminus of TM7a. It is possible that less well-ordered water molecules are present in the similar positions in NuoL/M. In addition to LysTM7 and GluTM5, between 2 and 5 polar residues line this cavity (Fig. 4a-c and Supplementary Table 5). In all three subunits the channel is closed from the periplasm by a bulky residue just 'below' LysTM7 (LTrp143, <sub>M</sub>Trp143 and <sub>N</sub>Ile132), followed by a tightly packed layer of hydrophobic residues. In NuoM, the path to the cytoplasm from LysTM7 is open for the 1.2 Å probe, reaching the surface near Glu108 and His159 via Asp258 (Fig. 4b). In NuoN, the protonation pathway from LysTM7 to the cytoplasm could include a putative water molecule between Tyr159 and Ser239, reaching the surface via conserved Lys295 and nearby Asp355/Asp357 (Fig. 4c). In NuoL, connection to a small cavity near His100 and further on to the cytoplasm can be achieved via a cavity next to Thr257. Additionally, a large cavity (about 200 Å<sup>3</sup>) between NuoL and M is lined with polar residues. It is blocked from the periplasm by bulky hydrophobic residues, but is accessible to the cytoplasm via LArg115 or MHis441. Indeed, we observe a likely water molecule coordinated by invariant LArg175 and LGlu144. Thus, protonation of LysTM7 in NuoL may be achieved also by "side-entry" near GluTM5 (Fig. 4a). Unlike NuoM and N, NuoL contains another invariant charged residue between GluTM5 and LysTM7, Asp178, needed for full activity<sup>27</sup>. A cavity (about 100 Å<sup>3</sup>) between NuoM and N, near <sub>M</sub>GluTM5 and <sub>N</sub>LysTM12, is closed from the periplasm by hydrophobic residues. Access to the cytoplasm could be achieved if a water molecule is coordinated near MTyr151 and MThr172.

The cavity in the middle of the second channel, near Lys/GluTM12, is significantly larger and more polar than that in the first one. It is up to 200 Å<sup>3</sup> and is lined with about

ten polar residues (Fig. 4a-c and Supplementary Table 5). Two water molecules are observed in this cavity in NuoM and one in NuoN. Access to the cytoplasm from this cavity appears to be closed in all three subunits. However, the periplasm is accessible: in NuoL, Asp400 (conserved and important for proton pumping<sup>27</sup>) faces the cavity and can interact with Glu494, exposed at the likely lipid-periplasm interface. In NuoM, a path for the 1.2 Å probe is open *via* a small cavity lined with Ser414, Ser425 and Thr422, with only a short constriction near Thr332 at the surface. In NuoN, only Leu407 from the surface-exposed loop partly blocks the entrance to the channel, which is not likely to prevent access in the dynamic protein structure.

The connection between the two channels in each subunit is formed by many conserved charged and polar residues in the middle of the membrane (Fig. 4, Supplementary Fig. 8 and Table 5). The link between the channels is most obvious in NuoN: LysTM7 – W (observed water molecule) – Lys247 – W – His305 – W – LysTM12 (Fig. 4c). Although the distances between ionizable residues and resolved water molecules are 4-6 Å, there are no obstacles between them. Therefore, proton transfer is likely to be efficient, due to conformational flexibility and/or the presence of additional water molecules, probable due to the abundance of polar residues around this pathway. Some waters may be coordinated (also in NuoL/M) by the exposed backbone carbonyls from the  $\pi$ -bulge of TM8. Additionally, Tyr231 and Tyr333 nearby may participate in proton transfer, as suggested for a conserved tyrosine in cytochrome c  $oxidase^{64}$ . Importantly, central <sub>N</sub>Lys247 is invariant, essential for activity<sup>28</sup> and is found on the TM8  $\pi$ -bulge. In NuoM, Lys265 is in a similar position between the two channels, and is also invariant and essential<sup>30,31</sup>. The pathway between the channels in NuoM thus is likely to involve His248, Lys265, His348 and invariant His322, as well as resolved and putative water molecules (Fig. 4b). In NuoL, an analog of <sub>N</sub>Lys247 is absent, but in this area there is His254 and also Lys342, both invariant. Therefore, the pathway between the channels is likely to involve His254, Lys342, His338, His334 and putative water molecules (Fig. 4a).

Thus, in all antiporter-like subunits, two half-closed channels are linked in the middle of the membrane, forming a single continuous proton translocation pathway through each subunit. Similar to NuoL/M and NuoM/N cavities, the cavity at the NuoN/K/J interface might also be used for "side-entry" protonation of LysTM7 in NuoN *via* GluTM5. Thus, the additional input pathway to LysTM7 from the inter-subunit cavity

seems possible in all antiporter-like subunits. However, it is less likely compared to the first half-channel, since (in contrast to the NuoN/K/J interface) the NuoL/M and M/N interfaces are not extensive and so not well suited for active proton transport. The first half-channel also works better from the point of view of symmetry in conformational coupling, and residues lining it are more conserved than those at the interfaces. The overall architecture with two interacting anti-symmetrical half-channels may help achieve a high efficiency of coupling between the protein conformation and pmf, since nearly the entire subunit (rather than a single isolated channel of 3-4 helices) would be involved in proton translocation.

Overall, the periplasmic side of the protein is closed from the solvent more tightly, by bulky hydrophobic residues, probably because proton concentration here is higher compared to the cytoplasm. Large water-containing cavities in the second channel may serve to reduce the energy barrier for protons crossing the membrane, as observed in other proton pumps<sup>65</sup>.

# 2. Are there alternative possibilities for the proton-translocation pathway in antiporter-like subunits?

What are the alternatives to the proposed pathway through two connected halfchannels? A single fully functioning channel in only one of the two symmetry-related domains is unlikely, because the first channel, containing crucial LysTM7/GluTM5, is clearly functional and the second channel contains larger cavities with larger amount of conserved (some essential) polar residues, so must also be functional. A remote possibility is that GluTM5/LysTM7 act just as a conformational switch for the second channel. That is unlikely, since the first channel contains other polar residues and cavities linking it to the cytoplasm. Could both channels function as proton pumps? Then at least six protons would be translocated per cycle - such a stoichiometry is not thermodynamically feasible and has not been observed. Could one channel be used for proton transport and another for sodium (passive sodium antiport is suggested for complex I<sup>66</sup>, but remains controversial)? This is unlikely since many conserved (some essential) polar residues form a connection between the two channels, which is needed only if both channels are half-closed.

We built homology models (not shown) for the antiporter subunits MrpA and MrpD (NuoL and NuoM homologues respectively), which also suggest two half-closed channels

connected by charged residues. Effects of mutations are consistent (Supplementary Table 8), suggesting that Mrp antiporters employ similar pathways and mechanisms for proton translocation. They couple, probably also conformationally, proton influx into the cell (*i.e.* in the same direction as during reverse reaction in complex I) to sodium efflux<sup>26</sup>, with the sodium binding site possibly found in subunits MrpE-G or at the MrpA/D interface. Sequence conservation suggests that antiporter-like subunits in chloroplast Ndh complexes and membrane-bound hydrogenases are also likely to employ similar pathways.

# **3.** Description of the proposed mechanism of coupling between electron transfer and proton translocation.

We observed that upon reduction of the hydrophilic domain by NADH helix  $_{\rm B}$ H1 and the four-helix bundle from NuoD shift<sup>13</sup>. They are at the interface with the membrane domain and so can drive conformational changes there, in particular in subunits NuoA/J/K, through either direct contact (NuoD to NuoA) or *via* NuoH (Fig. 1c). Consistently, cross-links between NuoA and J disappear upon reduction of complex I<sup>67</sup>. Communication between the two domains may proceed in part *via* the long rigid helix TM1 of NuoH<sup>11</sup>, which approaches close to TMs 1-3 of NuoJ with one end (Fig. 1c) and, with another end, close to helix <sub>B</sub>H1 (which is linked to Fe-S cluster N2<sup>13</sup>). A short periplasmic helix of NuoJ, preceding <sub>J</sub>TM5, may provide a connection between <sub>H</sub>TM1 and the  $\beta$ H element (Fig. 3a).

Helix HL interacts with subunits NuoJ/K *via* LTM16, so it can be moved, piston rod-like, along the membrane domain surface. HL in turn contacts flexible (due to an intra-helical loop) <sub>LMN</sub>TM7, so it can change the environment of LysTM7, including the distance to GluTM5. Although lysine would be an unusual proton translocator due to its high pKa (~10), this value can be lowered by 3-4 pH units for a buried residue, as in the ApcT transporter<sup>68</sup>. Decrease in the distance between GluTM5 and LysTM7 will raise the pKa of lysine (due to approaching negative charge of carboxylate) and may result in its protonation (and *vice versa*, lysine deprotonation upon increase of distance).

Although helix HL is an obvious coupling element, it is likely to be not the only one. The  $\beta$ H element can interact with TM12 through the C-terminus of TM14 (linked to helix CH and hydrogen bonded to semi-conserved LTrp67 / MTrp71 from the hairpin).

TM14 can be mobile because it is short and highly tilted, resembling, together with helix CH, a broken TM helix (Fig. 3b). Additionally, interaction between the two half-channels from neighboring subunits is possible through an invariant proline in the TM12 intrahelical loop (MPro399\* and NPro387\*), which contacts GluTM5 from subunit NuoL and M, respectively. Conformational changes can push the proline against GluTM5, in turn changing its distance to LysTM7. The required flexibility of TM5 can be provided by another proline (conserved in NuoM, Pro149), which introduces a slight kink in the helix. Although this proline is absent in NuoL, LTM5 contains three conserved glycines.

Interaction between the two half-channels in the same subunit can be mediated by TM8. Invariant <sub>N</sub>Lys247, <sub>M</sub>Lys265 and <sub>L</sub>His254, connecting the two channels, are located on TM8 near its flexible kink. The  $\beta$ H element includes conserved (also in Mrp antiporters) salt bridges between the hairpin (<sub>M</sub>Asp84\*) and the C-terminus of TM8 (<sub>M</sub>Arg273\*, Fig. 3a). On the other hand, the N-terminus of TM8 is connected to TM7 by a very short rigid loop containing a conserved proline (<sub>M</sub>Pro252\*).

In NuoL, connecting helix CH is mostly unwound. However, LTM8 is one of the most conserved TM helices in the complex, suggesting that its role in coupling may be relatively greater in NuoL than in NuoM/N.

The conformational changes, driven by the βH element and TM8, can result in protonation/deprotonation of Lys/GluTM12 via interactions with the exposed C-terminus of TM12a or with nearby charged residues - <sub>N</sub>His305, invariant <sub>M</sub>His322 and invariant LHis334. The exposure of GluTM5 and Lys/GluTM12 to the inter-subunit cavities suggests an additional possibility. These residues may switch between the two conformations. In one, as observed in the current structure and probably representing the oxidised enzyme, GluTM5 is closer to LysTM7 of the same subunit. Upon enzyme reduction, it could approach closer to Lys/GluTM12 on the nearby subunit, increasing its pKa and leading to its protonation by the incoming proton from the first channel of that subunit. In this way, protonation of the crucial residue in the opposite half-channels would be achieved in different parts of the catalytic cycle, as required for the directionality of the pump. The distance from MGlu144 to MLys234 (5.4 Å) is only 2.8 Å shorter than the distance to  $_{\rm N}$ Lys395, so such a mechanism appears plausible. It is not exclusively necessary, as LysTM12 in NuoL clearly operates without such a partner. In NuoN, GluTM5 also does not face another antiporter-like subunit, although it may interact with KGlu72, at the beginning of the fourth proton pathway. Mutagenesis studies

support "switch" possibility – when GluTM5 in NuoM was shifted one helix turn up or down<sup>69</sup>, the activity was retained (Supplementary Table 6, E144A/F140E and E144A/L147E mutants). Only in these positions the residue mutated to glutamate is not only close to LysTM7, but is also at the interface with NuoN. In other cases activity was lost even if the residue is close to LysTM7 (E144A/M146E).

Since the reaction of complex I is fully reversible (pmf can drive reduction of NAD<sup>+</sup> by ubiquinol), oxidoreductase activity must be tightly coupled to the conformational changes. A possible explanation for such coupling is the necessity for ubiquinone to be moved, by conformational changes, 10-20 Å out of the membrane<sup>11</sup> in order to react with its electron donor, cluster N2. Conversely, such quinone movement may assist conformational changes, through interaction of charged (semi)quinone species with charged residues in the vicinity (and/or cluster N2). Therefore, if mutations of residues in the proton channels interfere with conformational changes, oxidoreductase activity would be affected also, as observed (Supplementary Tables 6 and 7). Two of the most common mutations causing human diseases involve residues near <sub>M</sub>TM7 and channel 4 (Supplementary Table 7).

Since the structure renders additional "direct" coupling unnecessary, it is unlikely that unusual disconnection of tandem coordinating cysteines from cluster N2 (observed upon reduction), will result in an additional translocated proton, as discussed previously<sup>13</sup>. However, such a change in N2 coordination helps to explain the reverse complex I reaction – pmf-driven conformational changes can shift helix H1 of NuoB, resulting in mechanical disconnection of the tandem cysteine(s), thus decreasing the redox potential of cluster N2 so that it can mediate reduction of NAD<sup>+</sup> *via* the chain of clusters. Conversely, in the forward reaction, disconnection of tandem cysteines upon N2 reduction will help drive conformational changes.

# 4. Are there any ubiquinone binding sites in the antiporter-like subunits, and is NuoN functionally different from NuoL/M?

In addition to the well-established ubiquinone-binding site at the interface of membrane and hydrophilic domains, quinone binding by antiporter-like subunits of complex I is also widely discussed in literature. On one hand, this is stimulated by photoaffinity labelling experiments with analogues of specific hydrophobic inhibitors, showing labelling of ND2<sup>70</sup>, ND4<sup>71</sup> and ND5<sup>36</sup> subunits of bovine complex I,

homologous to *E. coli* NuoN, M and L, respectively. On the other hand, the presence of the quinone-binding motif (L/A- $X_3$ -H- $X_{2/3}$ -L/T/S) in these subunits has been proposed by Fischer and Rich<sup>34</sup>. In this motif, the conserved histidine residue serves as a hydrogen bond donor to quinone carbonyl or hydroxyl moieties, while the quinone ring is usually flanked by aromatic and aliphatic residues.

The signature motif is quite weak and authors suggested that it can be more indicative of the true quinone-binding site when combined with high sequence conservation in the same region. Sequence motifs centred on LHis334, LHis338, MHis241, MHis322, MHis348 and NHis224 have been discussed as potential quinone binding sites<sup>27,28,34</sup>. In addition, Amarneh and Vik<sup>28</sup> observed inhibition of NADH oxidase activity by decylubiquinone in several mutants, including NHis224. The structure shows that the majority of these histidines are in fact buried deep inside the protein and are parts of putative proton translocation channels. Only MHis241 and NHis224 (structurally and sequentially conserved) are located on TM7b pointing outside the subunit. However, they interact directly with helix HL, which is the likely primary reason for their conservation. Importantly, inhibition (or lack of activation) with decylubiquinone were also observed for mutations<sup>28</sup> of other surface residues interacting with HL, <sub>N</sub>Lys158 and <sub>N</sub>Tyr300. Recently, analogous residues in NuoL and NuoM (Lys169, MLys173, LGln236 and <sub>M</sub>His241), all contacting HL (Fig. 3a and Supplementary Table 6), were mutated, with similar results for all three antiporter-like subunits<sup>38</sup>. Thus, the effect of these mutations cannot be attributed to disruption of any additional quinone binding sites. Rather, it occurs due to interference with conformational coupling, likely involving communication between helix HL and the quinone-binding site at the interface with the hydrophilic domain. Both proton-pumping and oxidoreductase activities were significantly affected in these mutants<sup>38</sup>, confirming essential coupling role of helix HL.

Thus, we do not see any potential quinone binding sites in antiporter-like subunits, either formed around these histidines or elsewhere. The labelling by photoaffinity inhibitor analogues may have been unspecific, for example due to the presence of hydrophobic crevices at the interfaces between subunits. Global conformational changes upon enzyme reduction or inhibitor binding would explain the effects observed on labelling<sup>36</sup>.

Also, one tightly bound quinone molecule<sup>72</sup>, as well as two semiquinone species, have been observed in bovine complex  $I^4$ . Fast-relaxing semiquinone ( $Q_{Nf}$ ) is sensitive to the membrane potential and interacts with cluster N2, whilst slow-relaxing semiquinone

 $(Q_{Ns})$  is not<sup>4,35</sup>. Additionally, mutations to GluTM5 in NuoN appear to affect activity less drastically than in NuoL/M<sup>28</sup>, and it was noted earlier<sup>15</sup> and discussed in detail recently<sup>73</sup> that TMs 1-3 are absent from NuoN in metazoans. These observations led to the proposals that subunit NuoN is functionally different from NuoL/M, does not pump protons and contains bound quinone acting as a cofactor  $(Q_{Ns})^{35,44,73}$ .

The structure indicates that this is unlikely, since TMs 1-3 are found at the periphery of antiporter-like subunits and only helices 4-13 form the functional core, which is very similar in NuoL, M and N. Also, the  $\beta$ -hairpin between TMs 2 and 3 is short in NuoN and its role in metazoans may be performed by supernumerary subunit(s). Additionally, TM1 is absent in NuoL from insects (*D. melanogaster*) and worms (*C. elegans*) (Supplementary Fig. 8).

Furthermore, although the NuoN environment is fully preserved in the structure (all subunits contacting it are present), we do not observe any bound cofactors. A likely explanation for the presence of two observed semiquinone species is that one of them  $(Q_{Ns})$  represents the population of quinone molecules bound as in the oxidised state of complex I, fully embedded in the membrane and thus far away from cluster N2. The other species  $(Q_{Nf})$  may represent quinone moved out of the membrane<sup>11</sup> by conformational changes, so that it can interact with cluster N2.

The difference in effects of GluTM5 mutations can be explained if inter-subunit interactions *via* GluTM5 are important to sustain conformational changes in antiporter-like subunits, as we describe for NuoL and M. However, in NuoN the equivalent <sub>N</sub>Glu133 does not face another antiporter-like subunit. Consequently, mutations may not impede overall conformational change and hence activity. Although proton pumping by NuoN is likely to be compromised by mutations, a drop in overall stoichiometry from 4 to 3 is difficult to measure experimentally. It was also noted that <sub>N</sub>Glu133 is not conserved in worms<sup>38,73</sup>. However, these species show other sequence deviations and lack also <sub>K</sub>Glu72 / <sub>J</sub>Tyr59 (Supplementary Fig. 8), so it is possible that channel 4, involving all three residues, is not functional in worms. On the other hand, all three crucial lysines (217, 247 and 395) are conserved in NuoN from these species, so this subunit is still likely involved in proton pumping, with the modulating role of <sub>N</sub>Glu133 taken over by other residue(s). Mutations of any of these lysines in NuoN completely abolish activity in *E. coli*<sup>28</sup>, supporting the notion that NuoN pumps protons similarly to NuoL/M.

In a recent publication<sup>37</sup> it was shown that when helix HL is truncated (or subunit NuoL removed completely), oxidoreductase activity remains, but proton-pumping is

diminished, confirming the essential coupling role of this helix. The proton-pumping assays were very qualitative, and any known quantitative measures<sup>42,74</sup> were not employed. Therefore, even though it was suggested that proton-pumping stoichiometry dropped from 4 to 2, this value is hardly reliable. Importantly, however, even if this estimation turns out to be correct, it does not mean that the 2 remaining protons are pumped via direct redox coupling involving two quinones and that NuoN does not pump protons, as the authors suggest<sup>37</sup>. Our structure shows that discontinuous helix TM7 in subunit NuoN contacts helix HL at its extremity, were HL is continued by LTM16, at the interface with subunits NuoAJK (Fig. 1ab). As we propose, conformational changes in NuoAJK drive LTM16 and HL, which then communicates with distal subunits NuoM/L. Truncation of HL will abolish this communication and so the translocation of two protons via NuoM/L. However, since TM7 in NuoN is in close contact with NuoAJK, NuoN can still perform proton translocation within our mechanism. The fourth proton channel is found at NuoN/K/J interface and so clearly may perform translocation without HL. So, in full agreement with our model, HL-truncated mutants can still translocate two protons per cycle.

In another recent proposal it is suggested that complex I contains only two functioning proton pump modules, one in each of the two halves of the membrane domain (divided as NuoHAJKN and NuoLM sub-complexes)<sup>75</sup>. During the catalytic cycle each pump would perform two "strokes", resulting in four protons translocated in total. This model implies that either NuoM or NuoL subunit is not functional, which appears highly unlikely in view of the many conserved and essential (Supplementary Table 6) charged residues found in the proton translocation channels in both subunits.

In summary, the structure does not provide support for the presence of any additional quinone-binding sites in antiporter-like subunits, nor for proposals that subunit NuoN is functionally different from NuoL/M. The presence of a single Q-site at the interface of the two main domains, involving subunit NuoH (Fig. 1c), is consistent with all available functional and mutagenesis data.

	Native		SeMet	
Data collection				
Beamline	ID29		ID29	
Space group	P1		P1	
Cell dimensions				
a b c (Å)	95 59		93 67	
,, . ()	116 79		116.23	
	191 84		189.28	
$\alpha, \beta, \gamma$ (°)	98 40		98 31	
o, p, r ()	104 23		102.66	
	108.60		109.24	
	100100	Peak	Inflection	Remote
Wavelength (Å)	1.00	0 9789	0 9790	0.85
wavelength (11)	1.00	0.9709	0.9790	0.05
Scaling 1				
Resolution (Å)	30-3.2 (3.37-	30-3.5 (3.69-	30-3.60	30-3.7 (3.90-
	3.20)	3.50)	(3.79 - 3.60)	3.70)
$R_{\rm sym}$ or $R_{\rm merge}$ (%)	13.8 (73.2)	21.2 (101.9)	18.5	24.6 (100.1)
oyini inelge ( )		× /	(88.2)	× /
$R_{\rm nim}$ (%)	10.0 (55.2)	12.6 (60.4)	11.0	13.4 (54.7)
pini ( )	× /	· · · ·	(52.3)	· · · ·
Ι/σΙ	4.9 (1.3)	4.7 (1.3)	5.7 (1.5)	4.7 (1.5)
Completeness (%)	95 4 (96 1)	97 3 (97 7)	97.4	97 8 (98 0)
	<i>y</i> . ( <i>y</i> . ( <i>y</i> . ( <i>y</i> ))	<i>y</i> 1.5 ( <i>y</i> 1.1)	(97.7)	97.0 (90.0)
Redundancy	2.5	3.8	38	44
Sacling 2 (onigotronical	2.5 In transacted data	.)	5.0	
<b>Scaling 2</b> (allisotropical <b>D</b> esolution $\begin{pmatrix} \mathbf{\lambda} \end{pmatrix}$ )	20.20(2.16)	l)		
Resolution (A)	30-3.0 (3.10-			
$P \rightarrow P (0/)$	3.0)			
$R_{\rm sym}$ OI $R_{\rm merge}$ (%)	10.4(121.0) 12.0(02.0)			
$R_{\rm pim}$ (%)	12.0 (92.0)			
1/-1	4 1 (0 8)			
I/OI	4.1(0.8)			
Completeness (%)	95.5 (96.0)			
Redundancy	2.6 (2.6)			
Completeness after	86.5 (54.0)			
aniso truncation (%)				
Refinement				
Resolution (Å)	20-3.0			
No. reflections	126323			
$R_{\text{work}}/R_{\text{free}}$ (%)	23.19/28.16			
No. atoms	30310			
Protein	30002			
Ligand/ion	292			
Water	16			
Mean B-factors (Å <sup>-2</sup> )	76			
R.m.s deviations				
Bond lengths (Å)	0.016			
Bond angles (°)	1.070			

#### Supplementary Table 1. Data collection, phasing and refinement statistics.

\*Highest resolution shell is shown in parenthesis.

Scaling 1 and refinement to 3.2 Å were performed using all data as a control, yielding  $R_{work}/R_{free}=23.1/27.4$  %. The main refinement was performed with data anisotropically scaled and truncated to 3.4, 3.0 and 3.0 Å along  $a^*$ ,  $b^*$  and  $c^*$  axes respectively (Scaling 2).

Subunit	Number of residues in sequence	Residues built	Missing fragments
NuoL	613	1-612	C-terminus
NuoM	509	1-504	C-terminus
NuoN	485	1-191, 199-439, 445-485	Fragments of TM6 -TM7 loop and TM13 -TM14 loop
NuoK	100	1-100	None
NuoA	147	15-43, 61-126	Loop TM1-TM2, C and N termini
NuoJ	184	1-168	C-terminus

Supplementary Table 2. Residues present in the model.

**Supplementary Table 3.** Statistics of structural alignment of subunits NuoL, M and N, their symmetry related domains and subunit NuoK.

Subunits	RMSD Cα, Å	Length of alignment	Sequence Identity, %
NuoL-NuoM	1.73	437	22.0
NuoL-NuoN	2.15	421	20.2
NuoM-NuoN	2.16	418	19.4

a) Antiporter-like subunits, 14 conserved TM helices.

b) Symmetrical sets of five helices.

The letter signifies subunit, the number - set of helices: 1 - TM 4-8, 2 - TM 9-13.

Set of helices	RMSD Cα, Å	Length of alignment	Sequence Identity, %
L1-L2	2.22	136	10.3
M1-M2	3.09	137	9.5
N1-N2	2.91	148	12.2

c) Alignment of subunit NuoK with TM helices 4-6 (set 1) and 9-11 (set 2) of antiporter-like subunits. Naming convention as in table b.

Alignment	RMSD	Length of	Sequence
	Ca, A	angnment	Identity, 70
K-L1	2.66	85	18.7
K-L2	2.13	79	11.4
K-M1	2.20	78	10.3
K-M2	3.48	86	9.2
K-N1	1.95	88	17.0
K-N2	2.19	89	10.1

Supplementary Table 4. Summary of analysis of interactions between subunits.

a) Membrane domain assembly (subunits NuoLMNAJK)

Surface area, $Å^2$	62193.0	$\Delta G^{int}$ , kcal/mol	-322.3
Buried area, Å <sup>2</sup>	30535.0	$\Delta G^{diss}$ , kcal/mol	76.6

**b**) Individual subunits

Range	Surface area, Å <sup>2</sup>	Buried area, Å <sup>2</sup>	ΔG <sup>int</sup> kcal/mol	N <sub>HB</sub>	N <sub>SB</sub>
L	27186.8	4439.1	-44.63	19	3
М	18180.5	3981.5	-44.32	16	4
Ν	17841.3	6263.4	-66.26	24	7
K	7588.8	5846.4	-51.42	36	8
J	13595.9	7167.6	-85.47	25	6
А	8334.8	2837.0	-30.22	16	2

#### c) Pair-wise subunit interactions

Interfacing structures	Buried area, Å <sup>2</sup>	ΔG <sup>int</sup> , kcal/mol	N <sub>HB</sub>	N <sub>SB</sub>	
		A+J+K+N			
J + K	3347.2 (11%)	-63.9 (20%)	15 (22%)	3 (20%)	
J + A	2171.4 (7%)	-51.9 (16%)	8 (12%)	2 (13%)	
A + K	303.8 (1%)	-6.0 (2%)	5 (7%)	0 (0%)	
K + N	1724.8 (6%)	-32.0 (10%)	12 (18%)	3 (20%)	
A + N	361.7 (1%)	-7.5 (2%)	3 (4%)	0 (0%)	
J + N	1317.6 (4%)	-30.8 (10%)	2 (3%)	1 (7%)	
K + L	470.6 (2%)	-6.3 (2%)	4 (6%)	2 (13%)	
J + L	331.4 (1%)	-8.8 (3%)	0 (0%)	0 (0%)	
L+M+N					
M + L	2379.7 (8%)	-45.4 (14%)	12 (18%)[5]	1 (7%) [1]	
N + M	1601.8 (5%)	-39.5 (12%)	4 (6%)	3 (20%)	
N + L	1257.4 (4%)	-30.4 (9%)	3 (4%)	0 (0%)	

Analysis was performed using the PISA server at PDBe (<u>http://www.ebi.ac.uk/msd-srv/prot\_int/cgi-bin/piserver</u>).  $\Delta G^{int}$  indicates the solvation free energy gain upon formation of the assembly,  $\Delta G^{diss}$  indicates the free energy of assembly dissociation,  $N_{hb}$  – number of hydrogen bonds at the interface and  $N_{sb}$  – number of salt bridges at the interface. Numbers in square brackets indicate how many bonds between NuoM and NuoL are contributed by helix HL. All other subunits can contact NuoL only *via* HL and TM16.

Supplementary Table 4, continuation. Details of interactions between antiporter-like subunits. Contacts involving the  $\beta$ -hairpin are in blue, helix HL - in red. Potential weak hydrogen bonds are not included.

1		Dist, Å	Nuol		
rogen	bonds				
483[	NE2]	2.75	SER	69[	OG ]
479[	0]	2.88	TRP	67[	NE1]
483[	OE1]	2.99	SER	69[	OG ]
379[	OG ]	3.45	TYR	158[	ОН ]
416[	NE2]	2.99	ASN	190[	OD1]
433[	OG ]	3.15	ARG	175[	NE ]
416[	OE1]	3.63	TYR	189[	ОН ]
303[	NE1]	3.65	PHE	553[	0 ]
317[	OH ]	2.51	ASP	563[	OD1]
241[	NE2]	2.63	ASP	563[	OD2]
173[	NZ ]	2.79	ASN	566[	OD1]
300[	OH ]	3.30	LEU	565[	N ]
t brid	dges				
241[	NE2]	2.63	ASP	563[	OD2 ]
	483[ 479[ 483[ 479[ 483[ 379] 416[ 433[ 416[ 303[ 317[ 241[ 173[ 300] t brid 241[	A rogen bonds 483[ NE2] 479[ 0 ] 483[ OE1] 379[ OG ] 416[ NE2] 433[ OG ] 416[ OE1] 303[ NE1] 317[ OH ] 241[ NE2] 173[ NZ ] 300[ OH ] t bridges 241[ NE2]	A       Dist, Å         483[NE2]       2.75         479[0]       2.88         483[OE1]       2.99         379[OG]       3.45         416[NE2]       2.99         433[OG]       3.15         416[OE1]       3.63         303[NE1]       3.65         317[OH]       2.51         241[NE2]       2.63         tbridges       241[NE2]         241[NE2]       2.63	A       Dist, Å       Nuol         rogen bonds       2.75       SER         483[NE2]       2.75       SER         479[0]       2.88       TRP         483[OE1]       2.99       SER         379[OG]       3.45       TYR         416[NE2]       2.99       ASN         433[OG]       3.15       ARG         416[OE1]       3.63       TYR         303[NE1]       3.65       PHE         317[OH]       2.51       ASP         241[NE2]       2.63       ASP         173[NZ]       2.79       ASN         300[OH]       3.30       LEU         t       bridges       241[NE2]       2.63       ASP	A       Dist, Å       NuoL         rogen bonds       2.75       SER 69[         483[NE2]       2.75       SER 69[         479[O]       2.88       TRP 67[         483[OE1]       2.99       SER 69[         379[OG]       3.45       TYR 158[         416[NE2]       2.99       ASN 190[         433[OG]       3.15       ARG 175[         416[OE1]       3.63       TYR 189[         303[NE1]       3.65       PHE 553[         317[OH]       2.51       ASP 563[         241[NE2]       2.63       ASP 565[         tbridges       241[NE2]       2.63       ASP 563[

N+M					
NuoN		Dist, Å	NuoM		
Hydrogen	bonds				
VAL 469[	0 ]	3.19	TRP	71[	NE1]
GLN 472[	OE1]	3.14	ARG	74[	N ]
GLU 324[	OE2]	3.56	ARG	74[	NE ]
GLU 324[	OE1]	3.69	ARG	74[	NH2]
Salt brid	dges				
GLU 324[	OE2 ]	3.56	ARG	74[	NE ]
GLU 324[	OE1]	3.96	ARG	74[	NE ]
GLU 324[	OE1]	3.69	ARG	74[	NH2]
N+L					

NuoN			Dist, Å	NuoL
Hydr	ogen	bonds		
LYS	158[	NZ ]	3.60	TYR 594[ OH
ASP 2	229[	OD2 ]	2.52	TYR 594[ OH
PRO 2	222[	0]	3.31	SER 597[ OG

] ] ] **Supplementary Table 5.** Residues forming putative proton translocation channels, either directly or by coordinating water molecules. Essential residues are in bold. In channel 4 prefix indicates subunit.

Sub- unit		Channel	Residues
NuoL		Main cavity	<b>K229</b> , D178, T174, S150, <b>E144</b>
	1	Main link to cytoplasm	Т257, Т120, Н100
		Possible link at subunits' interface	R175, Y151, Y119, R115
		Connection	H254, K342, H338, T312, carbonyl O of A255
		Main cavity	<b>K399</b> , S398, T318, S314, Q315, T425, T428,
	2		S311, H334, T337, T429
		Link to periplasm	D400, S497, E494
NuoM		Main cavity	<b>K234</b> , T178, T266, <b>E144</b>
	1	Main link to cytoplasm	D258, S105, H117, E108, H159
		Possible link at subunits' interface	Q179, Y151, T172
		Connection	<b>K265</b> , H248, H348, S319,
		Connection	carbonyl O of A260 and G261
		Main cavity	<b>E407</b> , Q344, N403, S351, S321, H322, T395,
	2		T318, Y435, S436
		Link to periplasm	S414, S425, T422, T332
NuoN		Main cavity	<b>K217</b> , S136, S163, S167, S246, Y159, <b>E133</b>
	1	Main link to cytoplasm	S239, K295, D355, D357
		Possible link at subunits' interface	<sub>к</sub> Е72, Т160, S156
		Connection	<b>K247</b> , S219, T227, Y231, S302, Y333, S337
		Main cavity	<b>K395</b> , Y308, Y329, H305, S418, S382, S336,
	2		S304, N285, S301, Y425, Y424
		Link to periplasm	\$322
NuoN		Main channel	<sub>N</sub> S156, <sub>N</sub> T160, <sub>K</sub> E72, <sub>K</sub> E36, <sub>J</sub> Y59, <sub>K</sub> N40, <sub>J</sub> S35,
K/J/A	4		JE55, <sub>K</sub> Y62, <sub>K</sub> Q59, <sub>K</sub> S51
		Alternative link to periplasm	<sub>K</sub> S67, <sub>A</sub> Y84, <sub>A</sub> E81, <sub>J</sub> S145, <sub>J</sub> E142, <sub>A</sub> E102

**Supplementary Table 6.** Mutations in the membrane domain of *E.coli* complex I. Residues conserved between all antiporter-like subunits are in bold, those conserved within a single subunit in regular font and those not conserved in italic. Oxidoreductase activities were measured with either  $O_2$  or DQ as final acceptor and the range observed is shown. Proton pumping rates are very approximate. Abbreviations: SB - salt bridge, HB – hydrogen bond, HL – helix HL.

Mutation	Amino acid location		Effect		Reference
		Expression	Activity	Proton pumping	
D82A	β-hairpin - TM8 SB	normal	90%	80%	27
<b>D82N</b>		normal	75%	80%	27
D134N	surface, interacts with β-hairpin	normal	110%	70%	27
E144A	channel 1/ interface	reduced	20%	30%	27
E144Q	with NuoM	normal	15%	10%	27
K169C		normal	65%	decreased	38
K169E	TM6 – HL SB	normal	67%	decreased	38
K169R		normal	94%	decreased	38
D178A	channel 1	normal	95%	80%	27
D178N		normal	70%	50%	27
K229A	channel 1	low	10%	NA	27
K229R		normal	30%	NA	27
K229E		low	20%	NA	27
Q236H		normal	86%	NA	38
Q236K	TM7b – HL HB	normal	57%; DQ inhibition	significantly decreased	38
Q236C		normal	86%	NA	38
Q236E		normal	84%	NA	38
W238A		normal	80%	NA	27
W238Y	TM7b - TM7a HB	low	50%	NA	27
W238C		low	30%	NA	27
D303A	surface, interacts with	normal	110%	80%	27
D303N	TM11-12 loop	normal	100%	80%	27
H334A		low	50%	NA	27
H334Q	connecting	normal	120%	NA	27
H338A		normal	100%	NA	27
H338Q		normal	100%	NA	27
E359A	surface	normal	100%	normal	27
K399A	channel 2	low	20%	NA	27
K399E		low	15%	NA	27

#### a) Mutations in subunit NuoL

## **a)** Mutations in subunit **NuoL**, continuation.

Mutation	Amino acid location		Reference		
		Expression	Activity	Proton	
				pumping	
D400A	channel 2 / surface	normal	70%	50%	27
D400N		normal	90%	70%	27
D400E		normal	100%	90%	27
R431A	surface, near HL	low	10%	NA	27
R431H		normal	100%	NA	27

## **b)** Mutations in subunit **NuoM**

Mutation	Amino acid		Effect		Reference
	location	Expression	Activity	Proton pumping	
D84A	β-hairpin - TM8	normal	83%	NA	76
D84N	SB	normal	89%	NA	76
D135A	int	reduced	44%	normal	76
D135N	surface, interacts	normal	78%	normal	76
D135E	with p-nanpin	normal	87%	normal	76
E144A	channel 1 /	normal	2-10%	no pumping	76, 30, 69
E144Q	interface with	normal	2%	no pumping	76
E144D	NuoN	normal	89-100%	normal	76, 30
E144A/M145E		normal	3%	no pumping	69
E144A/W143E		normal	13%	~15%	69
E144A/V148E	channel 1 /	normal	3%	no pumping	69
E144A/F140E	interface with	normal	60%	~60%	69
E144A/F152E	NuoN	normal	3%	no pumping	69
E144A/F141E		normal	3%	no pumping	69
E144A/L147E		normal	45%	~50%	69
E144A/F139E		normal	2%	no pumping	69
E144A/F142E		normal	3%	no pumping	69
E144A/M146E		normal	2%	no pumping	69
E144A/P149E		normal	4%	no pumping	69
E144A/M150E		normal	2%	no pumping	69
E144A/Y151E		normal	3%	no pumping	69
E144A/L153E		normal	3%	no pumping	69
E144A/V127E		normal	3%	no pumping	69
E144A/I128E		normal	3%	no pumping	69
E144A/G129E		normal	5%	no pumping	69
E144A/I189E		normal	3%	no pumping	69
E144A/L190E		normal	2%	no pumping	69
E144A/A191E		normal	3%	no pumping	69

## b) Mutations in subunit NuoM, continuation

Mutation	Amino acid location		Reference		
		Expression	Activity	Proton	
				pumping	
K173C		normal	70%	decreased	38
K173E	TM6 – HL HB	normal	50%	decreased	38
K173R		normal	91%	decreased	38
H196A	surface	normal	79%	NA	76
K234A		normal	5-10%	significantly	76, 30
	channel 1			decreased	
K234R		slightly	5-20%	significantly	30
		reduced		decreased	
H241A		normal	88%	NA	76
H241E	TM7h - HI	normal	71%	NA	38
H241K	interaction	normal	40%; DQ	significantly	38
			inhibition	decreased	
H241R		normal	46%	NA	38
W243A		Normal/	103%	normal	76, 30
	TM7b – TM7a HB	decreased			
W243Y		normal	104%	NA	76
P245A	TM7b surface	normal	102%	NA	76
K265A	connecting	normal	35-80%	normal to	76, 30
				significantly	
R273A	TM8 - β-hairpin SB	normal	92%	NA	76
НЗЭЭЛ	channel ?	normal	100%	NA	76
11322A		normai	10070		70
H348A	connecting	normal	92%	NA	76
R365A	surface, SB TM11- TM14	normal	87%	NA	76
R369H	surface, HB to TM7b	normal	63%	normal	76
Y435A	channel 2	normal	99%	NA	76

## c) Mutations in subunit NuoN

Mutation	Amino acid location		Effect		Reference
		Expression	Activity	Proton	
				pumping	
M1H	N-terminus, surface	normal	20%	100%	28
M74K	surface	normal	90%	100%	28
C88S	TM3, interior	normal	100%	100%	28
C88V		normal	100%	100%	28
E104C	surface, near NuoJ	normal	90%	100%	28
E133A	channel 1 / interface with	normal	70%	100%	28
E133C	NuoK	normal	70%	100%	28
E133D		normal	80%	100%	28
R151C	surface	normal	90%	100%	28
E154C	surface, interacts with NuoK N-terminus	normal	70%	90%	28
K158C	TM6 – HL HB	normal	50%; DQ inhibition	80%	28, 38
K158R		normal	70%	80%	28, 38
K158E		normal	47%	reduced	38
T160I	interface with NuoK	normal	80%	NA	28
K217C	channel 1	No	NA	NA	28
K217R		normal	40%	80%	28
H224A		normal	100%	100%	28
H224Y	TM7b - HL interaction	normal	90%	100%	28
112211		normal	400/+ DO	700/	20
H224K		normai	inhibition	/0%	28
H224E	TM7b - HL interaction	normal	67%	NA	38
H224R		normal	32%	NA	38
W226C	TM7b – TM7a HB	normal	90%	100%	28
D229C	$TM7b{L}TM16$ and HL interaction	normal	70%	100%	28
K247C	connecting	normal	0-7%	50%	28
K247R		normal	80%	100%	28
K295C	channel 1 ?	normal	80%	70%	28
K295R		normal	90%	80%	28
Y300C	TM10 - HL interaction	normal	70%; DQ±	80%	28
Y300S		normal	50%; DQ±	80%	28
G391S	near channel 2	normal	90%	NA	28
K395C	channel 2	normal	5%	NA	28
K395R		normal	30%	NA	28
Y424C	channel 2	normal	90%	NA	28
M482C	surface	normal	100%	NA	28

## d) Mutations in subunit NuoK

Mutation	Amino acid location	Effect			Reference
		Expression	Activity	Proton	]
				pumping	
F15A	interface with NuoN	normal	90%	NA	32
G21V	interface with NuoJ	normal	61%	NA	32
R25A	HBs to backbone of	normal	26%	~30%	32
R25K	JTM1 C-terminus	normal	28-31%	NA	32
R26A	surface, near LTM16	normal	39%	~40%	32
R26K		normal	100%	NA	32
R25A/R26A		normal	14%	~30%	32
E36A		normal	1-7%	NA	32
E36Q	channel 4, interface	normal	3-8%	no	33, 32
	with NuoJ			pumping	
E36D		normal	120%	normal	33
I39D	interface with NuoN	normal	140%	normal	33
A69D	opposite E36	normal	119%	normal	33
E36Q/E72Q		normal	5%	impaired	33
E36Q/I39D		normal	21%	impaired	33
E36Q/A69D		normal	91%	normal	33
E72A	channel 4, interface	normal	43-48%	~50%	32
E72Q	with NuoN	normal	22-77%	~20%	33, 32
E72D		normal	100%	normal	33
E72Q/I39D		normal	180%	normal	33
E72Q/A69D		normal	77%	impaired	33
E72Q/G34D		normal	77%	impaired	33
E36Q/I39D/		normal	200%	impaired	33
A69D/E72Q					
R85A	surface	normal	100%	NA	32
R85K		normal	98%	NA	32
R87A	surface	normal	99%	NA	32
<i>R87K</i>	1	normal	100%	NA	32

## e) Mutations in subunit NuoA

Mutation	Amino acid location		Effect			
		Expression	Activity	Proton		
				pumping		
K46A	TM1-TM2 loop, not	normal	94-100%	NA	77	
	in the structure					
E51A	TM1-TM2 loop, not	normal	30%	NA	77	
	in the structure					
D79A	interface between	normal	86-95%	NA	77	
D79N	JTM3 and NuoH	normal	37-44%	NA	77	
E81A	alternative channel 4,	normal	~40%	NA	77	
	interface with NuoJ					
E81Q		normal	50-77%	NA	77	
D79N/E81Q		normal	2-10%	NA	77	

## f) Mutations in subunit NuoJ

Mutation	Amino acid location		Reference		
		Expression	Activity	Proton	
				pumping	
Y59C	channel 4, interface with	normal	57-93%	normal	40, 41
Y59F	NuoK	normal	44-50%	normal	40, 41
G61V	TM3 kink, interface with	normal	48-53%	normal	40
G61L	NuoA	normal	69-72%	normal	40
M64V	near channel 4	normal	78-89%	~60%	40, 41
M64C		normal	47%	NA	41
M64I		normal	100%	normal	40, 41
V65G	near TM3 kink, interface	normal	3-13%	No	40, 41
	with NuoA			pumping	
V65L		normal	21-23%	reduced	40
F67A	near channel 4	normal	~85%	100%	40
M72V	interface with NuoA/H	NA	38%	NA	41
M72A		NA	74%	NA	41
M72C		NA	50%	NA	41
M64V/M		NA	92%	NA	41
72A					
E80Q	surface, interacts with NuoK	normal	100%,	normal	40
E80A		normal	~90%	reduced	40
Y109F	surface	NA	96%	NA	41

Supplementary Table 7. Mutations in mitochondrially encoded complex I genes (subunits ND2-ND6) associated with human diseases. The most common disease associated mutations are in bold. Abbreviations: LHON - Leber Hereditary Optic Neuropathy; MELAS - Mitochondrial Encephalopathy, Lactic Acidosis and Stroke-like episodes; HB – hydrogen bond.

Subunit Human ( <i>E. coli</i> )	Human mutation: Amino acid (Nucleotide)	<i>E. coli</i> residue	<i>E. coli</i> structural location	Human disease	Effect on complex I: H – human, E – <i>E. coli</i>	Refe- rence
ND3 (NuoA)	Ser45Pro (T10191C)	Gly58	TM1-2 loop, not in structure,	multiple neuro- degenerative symptoms	H: reduced activity	78, 79
	Ser34Pro (T10158C)	Asn47	interface with NuoD	mitochondrial encephalopathy	H: reduced activity	79
ND6 (NuoJ)	Ile26Met (T14596A)	Val26	surface, possibly near Q-site	LHON	H: severe cxI deficiency	80
	Gly36Ser (C14568T)	Leu36	near channel 4	LHON, secondary mutation	NA	81
	Tyr59Cys (C14498T)	Tyr59	TM3, channel 4, interface with NuoK	LHON	E: 57-93% activity	40, 81, 41
	Leu60Ser (A14495G)	Ala60	TM3, near channel 4	LHON	NA	82
	Met64Val (T14484C)	Met64	TM3, near channel 4	LHON	H: increased inhibitor sensitivity E: 78-89% activity	40, 83
	Met64Ile (C14482A) (C14482G)				E: 100% activity	40, 84
	Ala72Val (G14459A)	Met72	TM3, interface to NuoA/H	LHON / Leigh disease / dystonia	H: cxI deficiency	85
	Ala74Val (G14453A)	Leu74	TM3, near surface	MELAS	H: reduced activity	86
	Pro25Leu (G14600A)	Pro25	N-terminus of TM2	LHON / MELAS	H: cxI deficiency	87

Subunit Human	Human mutation: Amino acid	<i>E. coli</i> residue	<i>E. coli</i> structural location	Human disease	Effect on complex I: H – human,	Refe- rence
(E. coli)	(Nucleotide)				$E - E. \ coli$	
ND5 (NuoL)	Phe124Leu (T12706C)	Phe123	near channel 1	Leigh disease	H: cxI deficiency	88
	Glu145Gly (A12770G)	Glu144	channel 1/ interface with NuoM	MELAS	NA	89
	Met237Leu (A13045C)	Met243	TM7b, interior	MELAS / LHON / Leigh disease	NA	89
	Ala458Thr (A13708G)	Ile462	lipid-facing surface	LHON	NA	90
	Asn505His (A13849C)	Trp512	TM15- TM13 HB	MELAS, secondary	NA	91
	Asp393Asn (G13513A)	Asp400	channel 2 / surface	Leigh disease	H: normal activity E: 90% activity, 70% pumping	92, 93, 94, 27
	Val243Ile (G13063A)	Val249	TM8, interior	mitochondrial disorder	H: normal assembly, reduced activity	87
	Ala236Thr (G13042A)	Ala242	TM7b, interior	LHON	NA	95
	Ala171Val (A12848T)	Ala170	near channel 1	LHON	NA	96
	Ser250Cys (A13084T)	Ala256	TM8, interior	MELAS / Leigh disease	H: cxI deficiency	97
ND4 (NuoM)	Arg340His (G11778A)	Arg369	surface, HB to TM7b	LHON	H: resistance to rotenone E: 63% activity, rotenone and UQ- binding affected	76, 98, 99
ND2 (NuoN)	Gly259Ser (A5244G)	Gly391	near channel 2	LHON, secondary	E: 90% activity	90, 28
	Asn150Asp (A4917G)	Ile269	near <sub>L</sub> TM16	LHON	NA	100

Organism	Sub- unit	Mutation	<i>E. coli</i> residue	Expressed	Growth in high NaCl	Antiport activity	Refe- rence
Bacillus	MrpD	D75A		+	+/-	<25%	101
subtilis	1	D75E	<sub>M</sub> D84	+	+	87%	101
		D75N		+	+	97%	101
		D128A		+	_/+	10%	101
		D128E	<sub>M</sub> D135	+	+	81%	101
		D128N		+	+	100%	101
		E137A		+	-	7%	101,102
		E137D	<sub>M</sub> E144	+	+	48%	101
		E137Q		+	-	0%	101
	MrpA	D50E		+	+/-	40%	101, 102
		D50A	<sub>L</sub> D82	+	+	0-60%	102
		D50N		+	+	56%	101, 102
		D103A		+	+/-	20-60%	102
		D103E	<sub>L</sub> D134	+	_/+	64%	101, 102
		D103N		+	+	76%	101, 102
		E113A		+	-	0-30%	102
		E113D	<sub>L</sub> E144	+	_/+	60%	101, 102
		E113Q		+	-	20%	101, 102
		E657A		+	-	<20%	102
		E657D	<sub>L</sub> N537	+	+	100%	101, 102
		E657Q		+	_/+	48%	101, 102
		D743A	Outside	+	-	NA	101, 102
		D743E	align-	+	+	120%	101, 102
		D743N	ment	+	-	16%	101, 102
		E747A	Outside	+	-	NA	101, 102
		E747D	align-	+	_/+	36%	101, 102
		E747Q	ment	+	-	4%	101, 102
Bacillus	MrpA	E140A	<sub>L</sub> E144	+	-	10%	26
pseudo-		K223A	LK229	+	-	3%	26
firmus		K299A	<sub>L</sub> K305	+	-	10%	26
		G392R	LG382	+	-	8%	26
		H230K	<sub>L</sub> Q236	+	+/-	72%, hNa <i>K</i> ,,*	26
		H700A		+	+	20%, hNa $K_{\rm m}^*$	26
		H700K	<sub>L</sub> V550	+	+	64%, hNaK <sub>m</sub> *	26
		H700W		+	+	70%, hNaK <sub>m</sub> *	26
		Y136A	<sub>L</sub> Y140	+	+	100%	26

# **Supplementary Table 8.** Mutations in subunits A, D and C of Mrp antiporters.

\*  $hNaK_m$  - high  $K_m$  for Na

Organism	Sub- unit	Mutation	<i>E. coli</i> residue	Expressed	Growth in high NaCl	Antiport activity	Refe- rence
		H230A	LQ236	+	+	100%	26
		W232A	<sub>L</sub> W238	+	+	100%	26
		Y258A	<sub>L</sub> Y264	+	+	100%	26
	MrpA	H345A	<sub>L</sub> H334	+	+	100%	26
		G392A	LG382	+	+	100%	26
		F405A	<sub>L</sub> F396	+	+	100%	26
		F135A	<sub>M</sub> F142	+	+	100%	26
		F136T	<sub>M</sub> W143	+	+	80%	26
		F136G		+	+/-	40%, hNaK <sub>m</sub> *	26
Bacillus	MrpD	F136A		+	+	80%	26
pseudo-		F136E		+	+	80%	26
firmus		E137A		+	-	2%	26
		E137Q	<sub>M</sub> E144	No growth	NA	NA	26
		E137D		+	+/-	100%, hNa <i>K</i> <sub>m</sub> *	26
		K219A	<sub>M</sub> K234	+	-	2%	26
		W228A	<sub>M</sub> W243	+	+	90%	26
		Q70A	кҮ62	+	+	80%	26
		G82I	<sub>K</sub> S74	+	+	50%	26
	MrpC	T75A	<sub>K</sub> S67	+	_/+	100%	26
		G82P	<sub>K</sub> S74	+	+	90%	26



**Supplementary Figure 1.** Electron density of *E. coli* complex I membrane domain. **a**, Anomalous difference density map calculated using structure factors (from 20 to 3.5 Å resolution) collected at Se peak wavelength and weighted phases from the final model, shown at the level of 4  $\sigma$ . **b**, Experimental map after multi-crystal (four datasets) density averaging and modification, contoured at 1  $\sigma$  and overlaid on the final model. **c**, The same map displayed around the model of helix HL and surface representation of the rest of the model. **d**, Example of 2Fo-Fc map, contoured at 1.5  $\sigma$ . **e**, Examples of 2Fo-Fc density corresponding to aliphatic lipid chains and a cymal-7 detergent molecule (indicated by an arrow), shown at 0.8  $\sigma$  over the surface of protein. Helix HL is shown in cartoon representation. **f**, Examples of 2Fo-Fc (blue, contoured at 0.9  $\sigma$ ) and Fo-Fc (green, contoured at 2.7  $\sigma$ ) omit density around water molecules (red spheres). For density calculations, the structure was refined and density calculated without water molecules.



**Supplementary Figure 2.** Crystal packing of E. coli complex I membrane domain in space group P1. Projections along crystallographic axes a (**a**) and b (**b**). Close view of crystallographic contacts between solvent exposed loops (**c**) and membrane embedded TM16 of NuoL (**d**). No protein-protein contacts are observed along axis a.



**Supplementary Figure 3.** Conservation of amino acid residues within the membrane domain of complex I (subunits NuoLMNAJK). Conservation degree decreases from blue (most conserved) to red (least conserved). **a**, View from the cytoplasm into membrane. Points of contact between helix HL and the main body of the domain are indicated by arrows. Highly conserved TM3 of NuoJ is indicated. **b**, Side view, similar to main text Figure 1a. The conservation degree was calculated using ConSurf server<sup>103</sup> and structure-based alignments of 30 sequences of complex I subunits from organisms representative of all kingdoms of life (Supplementary Fig. 7).



**Supplementary Figure 4.** Surface charge distribution of E. coli complex I membrane domain. **a**, View from the cytosol, **b**, Side view, cytosolic side up, **c**, View from the periplasm. Protein surface is shown coloured red for negative, white for neutral and blue for positive surface charges. **d**, Side view, periplasmic side up, with surface residues coloured according to the Eisenberg hydrophobicity scale<sup>104</sup> from white (hydrophobic) to red (hydrophilic). Surface-exposed Tyr and Trp residues are shown in green. The expected position of the lipid bilayer is indicated by black lines.



**Supplementary Figure 5.** Overlay of the 14 conserved helices of three antiporter-like subunits. **a**, Side view, cytoplasmic side up, centred on TM12. **b**, Side view centred on TM7. **c**, View from the cytoplasm into the membrane, with TM helices numbered. Coloured blue to red from N to C terminus. Essential charged residues are shown as sticks (GluTM5 and LysTM7 from channel one, GluTM12 from channel two and connecting <sub>M</sub>Lys<sup>265</sup> from TM8). Conserved prolines from intra-helical loops are also shown.



**Supplementary Figure 6.** Fold of subunits NuoK (a), NuoJ (b) and NuoA (c). Each subunit is highlighted in cartoon representation, coloured blue to red from N to C terminus, with TM helices numbered. Other subunits are shown as ribbons of the same colour as in Fig. 1. View in the membrane plane, cytoplasmic side up, from the interface with the hydrophilic domain. Conserved essential residues are shown as sticks ( ${}_{\rm K}{\rm Glu}^{36}$ ,  ${}_{\rm K}{\rm Glu}^{72}$  and  ${}_{\rm J}{\rm Tyr}^{59}$ ).



Supplementary Figure 7. Structure-based alignment of *E. coli* complex I subunits NuoL, M and N. The C-terminus of NuoL is omitted. Helices and  $\beta$ -strands are indicated, with TM helices labelled. The residues are coloured by conservation in Jalview<sup>105</sup>, using Clustalx colour scheme. GluTM5, LysTM7 and Lys/GluTM12 are indicated by the asterisks.

**Supplementary Figure 8**. Structure-based alignment of complex I subunits NuoL/M/N/A/J/K, using 30 representatives from all kingdoms of life. Helices and  $\beta$ -strands are indicated, with TM helices labelled. The residues are coloured by conservation in Jalview<sup>105</sup>, using Clustalx colour scheme. In subunits NuoL/M/N, GluTM5, LysTM7 and Lys/GluTM12 are indicated by the asterisks. Note that sequences in worms (three last sequences in the alignment) show many deviations, e.g. lacking conserved <sub>N</sub>Glu<sup>133</sup>, <sub>K</sub>Glu<sup>72</sup> and <sub>J</sub>Tyr<sup>59</sup>.

#### a) Subunit NuoK.

	TM	1ТА	12	TM3	
F					C 100
E.coli K.pneumoniae	1 MIPLQHGLILAAILF	LGLTGLVIRR - NLLFMLIGLEIMIN LGLTGLVIRR - NLLFMLISLEIMIN	AS AL AF VVAGSYWGQTDGQVMYIL AAAL AF VVAGSYWGQADGQIMYIL	A I S L A A A E A S I G L A L L L Q L H R R R Q N L N I D S V S E MR A I S L A A A E A S I G L A L L L Q L H R R R Q N L N I D S V S E L R	G 100
T.thermophilus	1 MSYLLTSALLF	LGVYGVLTRR - TAILVFLSIELMLN	AANLSLVGFARAYG-LDGQVAALM	VIAVAAAEVAVGLGLIVAIFRHRESTAVDDLSELR	G 95
R.marinus	1 · · · · · · · · · · · · MEITLNWYLALGVVLF	LGVLGVLFRR - NAIVILMSVELMLN	AVNLTLVALSQAMGDVSGQVLVFF	VISVAAAEAAVGLAIVIALFRKKVTVDVGEFNLFK	Y 101
A.aeolicus M.tuberculosis	1 MKTIPLEAFLTVSMILFO	LGLIGIIARR - NLVTVLMSLELALN IGASGVLLRR - NAIVMFMCVELMLN	AVN I AL VG ADHYLGL AEGQIFALF AVN LAFVTFAR MHGHLDAOMIAFF	IIALAATEAAVGLGIIIAIFRLKKVESTDEIRELR TMVVAACEVVVGLAIIMTIFRTRKSASVDDANLLK	G 102
S.coelicolor	1 MN P VNY LY LAALLF1	IGATGVLIRR - NAIVVFMCIELMLN	ACNLAFVAFSRMHGNLDGQIIAFF	TMVVAAAEVVVGLAIIVSLER SRHSASVDDASLMK	L 99
P.denitrificans R.capsulatus	1 MIGLTHYLVVGAILF1 1 MTIGLEHYLAVAAILF1	TGIFGIFVNR KNVIVILMSIELMLL	A VN I N F V A F S T H L G D L A G Q V F T M F A VN I N M V A F S T H L G D L V G Q V F T M F	VLTVAAAEAAIGLAILVVFFRNRGTIAVEDVNVMK VLTVAAAEAAIGLAILVVFFRNRGTIAVEDVNVMK	G 101
R.prowazekii	1 MLKILNMNEYISLNHYLILSSLVF1	IGMFGLFMNRKNIINILMSIELMLL	AVN INFVAFSVY MQELSGQIFSII	ILT VAAAETAIGLAILLIYFRNKGSIKITDINKMR	G 110
N.crassa	1 · · · · · · · · · · · · · · · · · · ·	IGILGFVLNR KNIILMLISIEIMLL	AITFLILVSSLNMDDIIGQTYAIY	IIV VAGAESAIGLAILVAFYRLRGSITIEYK	- 89
Y.lipolytica P.pastoris	1 MFIGTIL	L S F L G F V F N R R N I I L A F I C L E T M L L	GINLILLRNSVLFDDISGSLFAIV GCTVNTIYSASLDNDMIGLIYSLI	I I I L AG VES A I GL S L L V SYY R L R G V I N SY G I O I I I AG VES A I GL S I L VNYNR I R N S E I E N E	- 89
A.thaliana	1 MDLIKYFTFSMIIF	LGIWGILLNRRNILIMLMSIELMLL	AVNSNFLVFSVSLDDMMGQVFALL	VLTVAAAESAIGLAIFVITFR VRGTIAVEFINSIQ	G 100
B.vulgaris N.tabacum	1 MD S I KY F T F SMIT F	SGIRGILLNRRNIPIMSMPIESMLL	AVN LNFLVFSVSLDDMMGQLFALL AVN SNFLVFSVSSDDMMGQSFASL	V T V AAAE SAIGLAIFVITFR VRGTIAVEFINSIQ V P T V AAAE SAIGLAIFVITFR VRGTIAVESINSIQ	G 100
Taestivum X laevis	1 TDPIKYFTFSMIIS	LGIRGILLNRRNILIMSMPIESMLL	AVN LNFLVFSVSLDDMMGQSFASL	VPT VAAAESAIGLAIFVITFRVRGTIAVESINCIQ	G 100
G.gallus	1 MSPLHFSFYSAF1	FSSLGLAFHRTHLISALLCLESMML	SMFIPLSIWPVENQTPSFALVPIL	MLAFSACEAGTGLAMLVASARTHGSDHLHNLNLLQ	C 98
S.scrofa B.taurus	1 MPL VY MN I I MAFT 1 MSMVY MN I MMAFT	V S L V G L L MY R SH L M S S L L C L E G MML	SLFIMSTLIVLNTHFTLANMMPII SLFVMAALTILNSHFTLASMMPII	LLVF AACEAALGLSLLVMVSNTYGTDY VQNLNLLQ LLVF AACEAALGLSLLVMVSNTYGTDY VQNLNLLQ	C 98
H.sapiens A ausita	1 MPLIYMNIMLAF1	I S L L G M L VY R SH L M S S L L C L E G MM L	SL FIMATLMTLNTHSLLANIVPIA	MLVF AACEAAVGLALLVSISNTYGLDYVHNLNLLQ	C 98
D.melanogaster	1 MIMILYWSLPMILF	LGLFCFVSNRKHLLSMLLSLEFIVL	MLFFMLFIYLNMLNYESYFSMM	FLTFSVCEGALGLSILVSMIRTHGNDYFQSFSIM-	- 96
A.pisum C.elegans	1 MN L F I L V V MF ML I	SGVLFYIFNFNHLLMMLLGLEYLLL VSLFMFIFKWORLIFILISLEFMML	ILSLLFLMNLMMF I KQY ILLLV SLFLKFSYVLGEMMFFY	FFIFCISESVLGLTILILMVR MYGNDYMKSLMVLQ FMCFSVISSILGMVVMVGNMKFFGSDNCIF	C 96
Concophora	1 M1 F M1	VSLMMFLFKWYRFIFILIALEFLMM	S L F V S F MN N I V E MM F F Y	FMC FSVISSIVGMVIMVTSVKFYGNDYCIY	- 77
T.spiralis	1 MVEVLVEN	VGLIKIVFSLKSIIVELISMELLSL	ALMCLCWGCYWVYGVW	FLMVMVVHSVIGMLVLLWVIRYFGGDKVGSFV	- 81
<b>b)</b> Si	ibunit NuoA				
<b>b</b> ) 50					
			TM1		
				A CARACTER AND A CARACTER AND A CARACTER	
E.coli K poeumoolae	1		FLIVAIGLCCLMLVGGWFLGGRAR	A R S K N V P F E S G I D S V G S A R L A R S K N T P F E S G I D S V G S A R L	R 63
T.thermophilus		MAPIQEY VGTL1	VGVALFIGVAALLVGALLGPKKP	G R A K L M P Y E S G N D P A G E V K -	R 56
D.radiodurans R.marinus	1 MSVLQIRLTPDRLSFFAVVRASFH	E L S Q E R E R L E S G G R K T I V Q Y A N F L I I	M L L V G I G I G I L A I V V S G L L G P K K A M I V L A A G L A F S L L K L A E I L G P H R P I	T R T K L M A Y E S G N D P E R G G V G T G Q N P I K R M P Y E S G M D P V G S A R E	R 97 R 55
A.aeolicus M.tubarculoria		MEY   ALG	GLLVALL I ALGQAF VND I LGTR KRI	D PLEDY PY ECG VPLYDP E ARG	T 54
S.coelicolor	1	MN AY AP I L V	LG ALG AG F AI F S V VMATLIGPKRY	N · · · · R AK LE AY ECGIEPTYTP · · · · · · · · AGGG	R 56
P.denitrificans R.capsulatus	1		F L G M A S A L A I V L I L A A A V I A V R N P I L L A M A I G L A L I L I P P A A I I A Y R N P I	D P E K V S A Y E C G F N A F D D A R M D P E K V S A Y E C G F N A F D D A R M	K 58 K 63
R.prowazekii	1	MLQN SELLQEY LP   A1	F F G I A V L L S V L I M I L P N L L S T K K Y I	N K D K L E P <mark>Y E C G</mark> F E P F S D AR S	K 61
C.reinhardtii N.crassa_ND3	124 PMQQSVRGYNAWSPAQRYFVEGDH	VVTAEASR TFQFTGLDSGSFY PY VI	A T V I A T A I S T V F I V A P L V I A P S R VI F I L F V S I I A L L F L L I N L V F A P H I P I	D L D K S S AY EC G F D A F G E AR Q Y Q E K N S E F EC G F H S F H Q T R F	T 217 P 51
Y.lipolytica		MI OD I SNNX VI I VC	FILLIPI VGFALLAVNILLAVY KP	Y · · · · NEKLGAFECGLTSFNQ · · · · · · · · · TRL	A 51
Athaliana	1		LVISLLVSLILLGVPFLFASNSS	TY PEKLSAY ECGFDPFGD ARS	R 56
B.vulgaris N.tabacum			Y L V I S L L V S L I L L G V P F L F S S N T S Y L V I S P L V S L L P L G L P F L F S S N S S	T Y P E K L S A Y E C G F D P F G D A R S T Y P E K L S A Y E C G F D P S G D A R S	R 55 R 55
T.aestivum	1	· · · · · · · · · · · · · · · · · MLEFAPICI	Y L V I S L L V S L I L L G V P F L F A S N S S	T Y P E K L S A Y EC G F D P F G D AR SI	R 55
G.gallus	1		MLSLSFLLSAALTTMNFWLAQMAP	D TEKLSPYECGFDPLGS ARL	P 51
S.scrofa B.taurus	1		T L F T N V T L A S L L V L I A F WL P Q L N T I A L L T N F T L A T L L V I I A F WL P Q L N VI	Y S E K T S P Y E C G F D P MG S A R L Y S E K T S P Y E C G F D P MG S A R L	P 50 P 50
H.sapiens	1		ILMINTLLALLLMIITFWLPQLNG	Y ME K S T P <mark>Y E C G</mark> F D P M S P A R V	P 50
A.aurita D.melanogaster	1		I ALLILL ITTIVMFLASILSKKAL	D R E K V S V Y EC G F A P Y D N P G N I D R E K S S P F EC G F D P K S S	P 56 P 52
A.pisum	1	MINL I S	MLMMIIILMILFLIMILINMKMKF	N · · · · Y N K S A P F EC G F D P F N K · · · · · · · · · · · S R I	P 53
Concophora	1		VVLITLVL LVLLYVLSFVISMKKS	E L L K V S T F E S G F V S L S K VQN	\$ 51
T.spiralis	1	• • • • • • • • • • • • • • • • MS PMI MF FY	LIFFGLIVTLLMILLRSILSMSYLI	N T T F S F E C G F E S Y K MN R L	P 52
	TM2	-	TM3		
E.coli	64 LSAKFYLVAMFFVIFDVEALYLFA	WSTSIRE SGWVGFVEAAIFI	FVLLAGLVYLVRIGALDWTPARSRI	R E R M N P E T N S I A N R Q R • • • • • • • • • • • • • • • • •	147
K.pneumoniae	64 LSAKFYLVAMFFVIFDVEALYLYA	WS T S I R E S G W V G F V E A A I F I	L V L L AG L VY L VR I G A L D WT P AR SRI	R T L VN P E T D S P T N R H MQ	148
D.radiodurans	98 FPVHFYLVAMLFIVFDIETAFFYP	LAVAYQKLPQFAFFEALTFV	LLLLVGY VY VLKKKVLEWA ·····		160
R.marinus A.aeolicus	56 YTVKFYLVAMIFIVFDVEIVFLYP 55 FKOGYYLLGLLLILFDIEAAYLFP	WA V S Y R D F L E AG AG L G V L A V V V F F L WA V V F E E I G I Y G L I E V I V F V	IILAVGLLYDIKKGGLEFD		123
M.tuberculosis	101 FPIKYYLTAMLFIVFDIEIVFLYP	WAVSYDS LGTFALVEMAIFM	L T V F V A Y A Y V WR R G G L T WD		163
S.coelicolor P.denitrificans	57 FPIKTYLTAMLFIIFDIETVFLTP 59 FDVRFYLVSILFIIFDLEVAFLFP	WAVIFDALGIFGLVEMLLFV WAVSFASLSDVAFWGMMVFL	A V L T V G F A Y E WK KG A L E WA		115
R.capsulatus R.orowatekii	64 FDVR FYLVSILFIISDLEVAFLFP	WAVAFGD MSMTAFWSMMVFL	S V L T V G F AY E WK K G AL E WA		126
C.reinhardtii	218 F S V S F Y L V S I MY L L F D I E I AY L F P	AMTHASLPMY WTMNLFL	AILVAG FAY EWG MGALEWRE		275
N.crassa_ND3 Y.lipolytica	52 FDSPIAAQAICFVILDLEIFTMFP 52 FNAAFILVAILFLPFDLEISTLLP	Y VG S L G I N + + + + + T F Y S L V V I L G F M Y VM S I Y L + + + + + V S N Y G F T I V L L F L	F V V S AG F V F E L G K G A L K I D S K Q N M L I L I I G F V Y E I N T N A L K I N K H N K P	G G D S T H L E L K N L K D I S S L N L C P P S A F K N N T D S L I Y K L	147
P.pastoris	64 IPIAFILVALLFLPFDLEVSSMLP	YIVSIYSVGIYGLIIFILFL	LILIVGFIYEFNTKSLSITTILHK	KN K A L V KN L Y	141
A.thaliana B.vulgaris	57 FDIRFYLVSILFLIFDLEVTFFFP 56 FDIRFYLVSILFIIFDLEVTFFFP	WAVSLNK I D L F G F WS MMA F L WAVSLNK I D L F G F WS MMA F L	FILTIGFLYEWKRGALDWE		115
N.tabacum T.aestiyum	56 FDIRFYLVSILFIIPDPEVTFSFP	WAV P P N K I D P F G S WS MMA F L			118
X.laevis	50 F S MR F F LI AIL F LL F D LEI ALLLP	FPWAAQLN + · TPSIVILWAALIL	TLLTLGLIY EWLQGGLEWAE · · · ·		114
G.gallus S.scrofa	52 F S I R F F L V A I L F L L F D L E I A L L L P S1 F S M K F F L V A I T F L L F D L E I A L L L P	L P W A I Q L A H P M M T L T W A T T I I L P W A S Q T N N L K T M L T M A L F L L	ALLTFGLIYEWTQGGLEWAE TLLAASLAYEWTOKGLEWTE		116
B.taurus	51 FSMKFFLVAITFLLFDLEIALLLP	L PWASQT AN LNTML TMALFLI	ILLAVSLAYEWTOKGLEWTEYGT-		118
H.sapiens A.aurita	57 I SIRFFLIGILFLVFDLEIALLLP	WS V S S H L I S L P G I WL I F I F V	FILTWGLLYEWIKGGLEWE		115
D.melanogaster A nisum	53 FSLRFFLITIIFLIFDVEIALILP	MIIIMKYSNIMIWTITSIIFI MIMNEKISNMEYENIMEMIEE	LILLIGLYHEWNQGMLNWSN		117
Celegans	52 FSTHFFTMMLMFVTFDLETVMFLG	ILVSDLSSYISFLMMF	IFILGGFY MEWWYGKLVWVI		111
Concophora T.spiralis	52 F S I H F F V I ML M F V I F D L E I V M F L G 53 F S I N F F M V S L I F V L F D L E I I I L I A	¥ I PNMTS L T L L S Y I T AMS F L	F F T MMG F Y ME WWY G K L I WV I Y L F ML L S L ML E WALG K L S WI F		112

#### c) Subunit NuoJ.

	TM1	TM2	TM3	TM4
E.coli	1 ·····MEFAFYICGLIAILATLRVITH	TNPVHALLYLI IS LLAIS GVFFSLG	AYFAGALEIIVYAGAIMYLFVFVVMM	LNLGGSE IE QE RQWLKPQVWIGPAILSAIML 104
K.pneumoniae	1 ·····MEFAFYICGLIAILATLRVVTH	TNPVHALLYLIISLLAIAGVFFSLG	AYFAGALE I IVYAGA I MVLFVFVVMMI	LNLGGSEIEQERKWLQPGIWIGPAILSAVLL 104
T.thermophilus D.radiodurans	1 ····································	KNATHAALAL TUNF UV LAGVYVALD	ARF LGF TQV TVYAGA TVVLF LFV IMLI	LFAAQGE IGEDELVRSRELAALLALGVAGIL 104
R.marinus	1 · · · · · · · · · · · · · · · MIAQLLFFLLAVTA I AAALGMLIA	RNPVSSALWLVLNLFCIAGLYLTLQ	ASFLOVIQULIYAGAIMVLFLFVIML	LNLEALPHPRQIDWGKVLAFVVTMIVLAQLV 106
A.aeolicus	1 ·····	KNP I HV MLFFLSSLLAMAGLFLSLG	AE LLAGLQLI IYAVA IVVFYVLA ITT	IPWEKIKRFEGVYKTEILTASPILLVLFL 103
M.tuberculosis	1 MTAV LAS DV I VR TS TGE AV MF WV LS A LALLGAV GVV LA	VNAVYSAMFLAMTMIILAVFYMAQD	ALF LGVVQVVVY TGAVMMLF LFVLML	I GV DS AE S LKE T LKG QR V AAV L TGV GF GV LL 120
P.denitrificans	1 MTF AF Y LF A I S ACVAGF MVV IG	RNPVHSVLWLILAFLSAAGLFVLQG	AEFVAMLLVVVVVGAVAVLFLFVVMM	LDVDFAELKGELARYLPLALVIGVVLLAQLG 104
R.capsulatus	1 ·····AFYLFAVVAVVAGLMVVLS	KNPVHAVLWLILTFLSAAGLFVLMG	AEFVAMLLIIVYV <mark>GAVAVLFLF</mark> VVMM	LDIDFAALRGQLVRYAPVGGLIALVMLAQLA 107
R.prowazekii	1 MP IFFYLFTTLIIISSLCVVLS	KNSVYSVLWLIFTFINGSGLMILLG	AEF LAMLLIVIYVGAVAVLFLFVIMMI	LDINFNQAITKLRENLSLSIFITLIMFADLV 104
N.crassa	1 MNS LF LINESF TNGY ISSVLDI IS I LA IFCG ISVIVN	KNP I I SV LF LIGLF AS VS SY LI LLG	LSF IGLAY LIVY IGAIS ILF LF ILML	IN IRISE LOSNTNNS IPLTIILGIS LSYSLF 119
Y.lipolytica	1 ·····	KNP MVSILYMIALFVIAAMYLYLIG	LGIFSLLYIMIYIGAIAVLFLFIITLI	LDINSTELSVKSNIRDLPLVLISLIVLTISG 108
P.pastoris	1 MNLEILDLSILGFYSLIS	SNSFESIAILVATIMPVITELWYNY	SQLFALLYTL IYVGAVVILEVEILSV	INEKEEYEYEGLFILILVLLLDDLDDNES 100
A.thaiiana B.vulgaris	1MILSVLSSLALVSGLMVVRA	KNPVHSVLFF LLVFCDTSGLLLLLG	LDFF AMIF LVVY IGA LAV LF LFVV MM	FHIQIAE THEEVLRYLPVSGTTGLTFWWENF 102
N.tabacum	1 ·····MILSVLSSPALVSGLMVVRA	KNPVHSVLFLIPVFRNTSGLLLLLG	LDFFAMIFPVVYIGAIAVSFLFVVMM	FHIQIAE IHEEVLRYLPVSGIIGLLFWWEMF 102
T.aestivum	1 MR L LAP AF KF HF K GGRR TM I LS V LS S P A L V S G LMV V R A	KNPVHSVLFPILVFCDTSGLLILLG	L D F S A M I S P V V H I G A I A V S F L F V V MMF	FNIQIAEIHEEVLRYLPVSGIIGLIFWWEMF 120
G.gallus	1 MTYFV IFLGICFMLGVLAVASN	PSPFTAALGLVLAAGAGCLVTVSFG	VSFVSLALFLVYLGGMLVVFATSAAR	A A D P Y P E AWGSWS V V F Y V L V Y L I G V L V WY L F L 104 A A D P Y P E AWGDWR V V G Y G L G F V L V V WMG V V L 104
S.scrofa	1 MTMY   AF   LS T   F V   GF V GF S S K	PSPIYGGLGLIVSGGVGCGIVLNFG	GSFLGLMVFL IYLGGMLVVFGYTTAM	A TE MY PE VWV S NK TV F G A F V S G L MME F C MV Y 105
B.taurus	1 MMLY IVF ILSV IFV MGF VGF 5 5 K	PSPIYGGLGLIVSGGVGCGIVLNFG	GSFLGLMVFLIYLGGMMVVFGYTTAM	A TE QYPE IWLS NKAVLGAFVTGLLMEFF MVY 105
H.sapiens A aurita	1	PSP 1YGGLVL IVS GVVGCV I I LNF GO	3 GY MGL MVFL I Y LGGMVVVFGYTTAM	A LEEYPEAWGSGVEVLVSVLVGLAMEVGLVL 104
D.melanogaster	1 MIQLMLYSLIITTSIIFLNMI	HP LALGLTLL QT IF VCLLTGLMTK	SFWYSYILFLIFLGGMLVLFIYVTSL/	AS NEMENLS MKLTLESSLILIEMLILSE IND 103
A.pisum	1 MLK     ML TN L   MA     L TMMK	SPISSNLIILIQTMTLTMMINLINK	TAWISFMIFILY IGGLMI IFLY ISS I/	AFNELNINKNYKNMIYKIIFMSLMLYYFKMY 102
C.elegans	1 ····· MVKVFFVLAVLSSIISYIN	I DP MKSSFFLIFSLLFSMPVISMSM	HIWESYEICLLELS GIEVILVYESSLS	SKINVVKSYMAVFLLLLSMLYFSPTVLTYSS 101
T.spiralis	1 ····································	PLWISTLVFLLSIITAIHKFYSVHNI	NS MF GY LF V MIYS GGL LIMLTY ISS L	TPSTTTNKLPIKIMIMIPITYLFTWTMTKHN 103
13	TMA		TI	45
E H		NDOCLOCI		
E.coli Koneumoniae	105 VV I V I A I LGV	NDOGIDGA	A INAKEVGIALEGPY -VLAVELASML	LAGLVVAFHIGREERAGEVLSNRVDDSAKR 1/8
T.thermophilus	105 AAGLWGLDLAF T	QDLK	GGLPQALGPLLYGDW-LFVLLAVGFL	LMAATVVAVALVEPGKASRAKEAEKREEVAR 176
D.radiodurans	105 VTLALTYQDPRP-L	AESVQALR	GGAAGAVGETLLTRF - LLPFEAVSIL	LLVAIVGSVTLVQRPVPQPDGVTDETGAELP 181
A aeolicus	107 Y V A LGLDV LP TFV	FAEPSGVVI	KDNVEAVGRTLETSY - LEPFEVASVI	LVANVGATLLARKEE 162
M.tuberculosis	121 ISTIGQVATRG F	AGLTVANA	NGNVEGLAALIFSRY - LWAFELTSAL	LI TAAVGAMV LAHRERFERRK TQRE LS QERF 196
5.coelicolor	123 I AG I GNAS VS EF	TGLAQANA	NGNVEGIASLIFTKY - VFAFEITGAL	LITAAVGAMVLTHRERTERARTQRELSEQRI 198
P.denitrincans R.capsulatus	105 TAPS GWTPS DQAES	LRAAP V DAA	VENTAALGMILYDRY - LYLFOGAGLV	LVAMIGATULTINH HRKDVKRQNVLEQMWRD 183
R.prowazekii	105 I T I I L S T K N I N Y S S N	ISFAIANN	ISNTKAIGNVLYTEF - MLPFQIAGLI	LEVAMISCITLTLKKRDRIKHQDIRKQLSHN 183
C.reinhardtii	104 TP S MGP R G I I TG	LPG	AESITNLGHALYLYF - ADLLILNSLV	LTVALFGRFAIAPVRTTGR 162
N.crassa V linolutica	120 QLLPYDIAILSNESSNINNNLYNLSMNKQNNGNEGINTTP 109 LMLYSNDSILINKILEAEGNDYN	AVS LQPKNNDLLFVTSKTWDGNLAE	TTIITTIGNVMYSNY - STWLFLASFT	LLLAMVGSTVTTMKSNASWGGALPNTRETKT 240
P.pastoris	101 NDNDYNNYY I TD	YADWF NNY N	ESDLSVIGNLLF TEY -ALLLLIISFI	LLMS     GL   L   VKKD 161
A.thaliana	103 FILDNES IPLLPTQRNTTSLRY	TVYAGKVR51	NTNLE TL <mark>G</mark> NLLY TYY - F VWF LVP S L I	L L V A M I G A I V L T MHR T T K V K R Q D V F R R N A I D 189
B.vulgaris	103 F I LDNE T I P L LP TORN TTS LRY	TVYAGKVRSV	WTNLETLGNLLYTYY - FVWFLVSSLI	LUAMIGATVLTMHRTTKVKRQDVFRRNAID 189
Laestivum	121 FILDNETIPLLPTHRNTTSLRY	TVYAGKVRS	WTNLETLGNLLYTYY - SVWF LVSSLI	LVAMIGATVLTMHRTTKVKRQDVFRRNALD 207
X.laevis	105 GGVEVDGMNKS5	ELGSY	V MR GDWV GV A L MY S CWWV I I V YWWV S	I I N F V C G I W V N S K S MWWE S S C V 170
G.gallus	105 GGLVDFWKVGVVTVD	GGGVSI	ARLDFSGVAVFYSCGVGLFLVAGWG	LLLALFVVLELVRGLSRGAIRAV 173
B.taurus	106 YVLKDKEVEVVFEFNGLG	······································	FSEEAMGIAALYSYGTWLVIVIGWS	LIGVVVIMETTRGN ······ 175
H.sapiens	105 VKEYDGVVVVNFNSVG	••••••SWMIYEGEGLG	LIREDPIGAGALYDYGRWLVVVTGWT	LFVGVYIVIEIARGN174
A.aurita	103 GLEYSNINDPE	·····VEEILIKE	LLDIQTIGFQLYNSY - APHLIVASLI	LLVAMIGATILTLQPHLAAKRQDNFIQITRD 177
D.melanogaster A nisum	104 K 1555 LF LMNN		EDNEYLLNMEMMPNN - + ILLYMIMEL	LEF MULTUR WILKINK GPIROKNN 164
C.elegans	102 Y L G · · · · · · · · · · · · · · · · · ·		LSGFYYS IYWF IFCF ILVCL	LFF MNFSSYFLNFSGALRKV 144
C.oncophora	102 VFLS		LNVFYYSLYWIVLIYVILML	L I F MN F V S Y F L N F S G A L R K V 145
T.spiralis	104 F NE NY NY NE LN		MITTY LMS SPLINAV LTELTTSFC	LISSLESQEKYPIRSL
22 W				
E.coli K poeumoniae	1/9 K TEEHA			184
T.thermophilus				
<b>D</b> .radiodurans	182 P A P R AWRE GQS A P A L N S E P L K E R A			205
R.marinus	***************************************			
M.tuberculosis	197 RPGGHP TPLPNPGVYARHNAVDVAALLPDGSYSELSVPRM	ILR TRGADGLQTPSPGAVSGSLEGGA	5	262
S.coelicolor	199 RDGKHLPPLPAPGVYARHNAVDIAGLLPDGTPSELTVSKT	LRERGQIRDVS MEALGDLKALEQRA	E DR LE R K A V GP DNS K QS E E A S K	285
P.denitrificans	184 PAKTMELKDVKPGQGL			199
R.capsulatus R.prowazekii	18/ PARALEMVDVRPGQGL			202
C.reinhardtii				
N.crassa	241 E GR	••••••		243
Y.lipolytica P.nastoris				
A.thaliana	190 F R R T I MR R T T D P L T I Y			205
<b>B.vulgaris</b>	190 F R R T I MK R T T D P L T I Y			205
N.tabacum T.aestivum	190 SKKIIMRRTTOPLTTIRKSSGSNPHRETRTVWRSTDKCY- 208 SRSHIMNRTISPEGHSHRRSESSGAGGDDDNVKETEKAMU			228
X.laevis				247
G.gallus	• • • • • • • • • • • • • • • • • • • •			
S.scrofa B.taurur				
Hsapiens				
A.aurita	178 F HN I S K S HNNS S S • • • • • • • • • • • • • • • •			190
D.melanogaster				
Celegans				
C.oncophora				
T.spiralis				

## d) Subunit NuoN, part 1.

		TM1	TM2	TM3
Ecoli K, pneumoniae T, thermophilus Dradiodurans R, marinus A, aeolicus M, tuberculosis S, coelicolor P, denitrificans R, prowazekii N, craissa Y, Ilipolytica P, pastoris A, thaliana B, vulgaris N, tabacum T, aestivum	1 MT I T PONL I AL 1 MT I T POQLI AL 1 MT I T POQLI AL 1	LPLLIVGLTVVVVMLSIAWRR LPLLIVGLTVVVVMLSIAWRR ILPLLIVGLTVVVMLSIAWRR ILQLIVGAIVSTLGFVLP LWAAFPLVLTAVVGLVLVVWD LPRAILAIGILTVFILEFELE APMLIVSVAVAGVLAEAFLP SPVLIVLGAAIIGILVEAFVP LPEVLLAGALIGILVEAFVP LPEVLLAGALIGILVEAFVF IPEVLLAIVAMGVLIFGVWTG LPEVLLAIVAMGVLIFGVWTG LPEULLAIVAMGVLIFGVWTG IVCILHDTMSLSIISKGVGLH AIISLITFVSMSKLSDNRAII LLIIVYGSLVMKSHLLTKLIN FPEIFIINATFILLIHGVVFS SPEIFIINATFILLIHGVVFS	NHFLNATLSVIGLNAALVSLWFVGQ NHFLNATLSVIGLNAALVSLWFVGQ QGVKRATLLGLALALASLLLTWGKP RTLTALNILFVLASGASLVWLWGG AFWNDAPPIPWVAAGTLALALIWELF NKWRYGAQVTLALGGSAVALIAVIV RWRYGAQVTLALGGSAVALIAVIV RKRYYAQMFVSAVALVAAFAAIVA KORVARTLLWTVAAFLVVAAMYGL KORVARTLWVTVAAFLVVAAMYGL KORVAKPILWASAVTMLALALIIGL VKNRIJYNIVILCIISIFLTFKYS GGLHITNITQVFQIFIFLISILLI SGLUHITNITQVFQIFIFLISILLI SGLUHITNITQVFQIFIFLISILLI SGLUHITNITQVFQIFIFLISILLI SGLUHITNITQVFQIFIFLISILLI SGLUHITNITQVFQIFIFLUSIL SKKYDYPPLSSNVGWLGLLSVLIT TSKKYDYPPLVSNVGWLGLLSVLIT	AG AMD
X.laevis G.gallus	•••••••••••••••••••••••••••••••••••••••			•••••••••••••
S.scrota B.taurus H.sapiens				
A.aurita D.melanogaster A.pisum C.elegans	1	MLYNYY EVL L L T V L I A	SLVLKVTKKLFNILMFLTITFLLLS	VKSAGG
T.spiralis				
E.coli K.pneumoniae	<b>TM3</b> 77 TGLVLLASLATCTFAY PWLEGYN		TM4	TM5 LLAN ANHLASLFLGTELISLPLFGLVGYA 146 LLAGANHLAALFLGTELISLPLFGLVGYA 146
T.thermophilu D.radiodurans R.marinus A.aeolicus M.tuberculosi S.coelicolor P.denitrificans R.capsulatus	63 TLLALLGALLWTVGLVR SG 7 GGTVLLGALLTLVSLDTAYR AR 84 NAIILASGLLTIALS VPVLKRIR 73 KLFILAVTGFVLLSSVDYFSKKN 86 QGTVLLVTIMAVVFMAER SAR VSPQRQNTLAV/ 108 QGTILLTSLVGLFTFAERRLDPEQHG 76 KVVTLVAAGVLMKSADYMQRRN 77 KVVLLVSAAAVLAMSSDYNQRRN 77 KVVLLVSAAAVLAMSSDYNQRRN 78 KVVTLUSSAAVLAMSSDYNQRRN	IR L PG L D S F T PQ A S A V PG S D A E - • NR V D S F A AQ A A A V PG S E S E	R F F F Y LL V L Y A A L GMH - V S F A F F D ALL MY A V T G C L - H LH G E V Y AL L L F A T V G M I - S Q Y G E L P Y L Y L I A T L G L M R Q A E R A G T T T E V F P L L F A V A G M L - M L F F F P I L I V A L A V L G M - L L R F E F P I L I V A L A V L G M - L L R F E F P I L I V A L A V L G M - T Y E F F I M I S U G I F	L L A STR H L L IM, V A L E A L S L P L Y A L A T
C.reinhardtii N.crassa Y.lipolytica P.pastoris A.thaliana B.vulgaris N.tabacum T.aestivum X.laevis	55         LT VVLLQS           111         PLS 51QAVLKDYLFK1QGFNKEH           114         PLS 51QAVLKDYLFK1QGFNKEH           76         FINIVISLTGYNLYNNLYKTLFE           76         FICILLS FANTIGLS IDNLN           97         QIFLLIS TAGTISMCFDFFDQER           86         QILLLLS TAGTISMCFDFFQER           86         QILLLIS TAGTISMCFDFFQER           86         QILLLIS TAGTISMCFDFFERER           1         1		<ul> <li>FHSFEALLFLLLAYIGQL</li> <li>LKI EVPLLLFVICGAV</li> <li>PKKELIFLINIGAL</li> <li>YSKRTFIVIVLFLINIGAL</li> <li>FDAFEFIVLILLSTCGML</li> <li>FDAFEFIVLILLSTCSML</li> <li>FDAFEFIVLIPLPTRGML</li> <li>FDASEFIVLIPLPTRSML</li> </ul>	Y MMH SCNLVSFY VCLEAQTLCVVVLCGLLAR 111 LMSTNDLVSFLSELQSYGLHTSST1Y 180 LIVHSNDFTTFYA ELGSYSIYLLTAIY 144 LLPLVNDIMILF1TELQSYSLYLLTAIY 144 LLPLVNDIMILF1TELQSYSLYLLTAIF 146 FMISAYDLIAMYLA ELGSLCFYVIAASK 155 FMISAYDSIAMYLA ELGSLCFYVIAASK 155 LMIPAHDLIAMYLA ELGSLCFYVIAASK 155
G.gallus S.scrofa B.taurus H.sapiens A.aurita D.melanogaster A.pisum C.elegans C.oncophora T.spiralis	1 5 5 7 K I F C V L I G V I V I N S NR AR I F D S S 1 1		- MN PH AKL IC T V SL I MG TS - MN PI I Y TI L MT VMSG TM - MN PI I FI I LL TI MLG TI - MN PL AQ PV I Y ST I F AGTL - NV LLC V I LC V I LS I - MF N Y SK I LF I TI MI G TL - MI VF I SL FT LF LT L - ML AF MF MMV FF FG L - MX SF VWG I FY V I V VM	I T I S S N H W I L AWT G L E I N T L AI I P L I S K S - 47 U M I S S H W L I W I G F E M N L AM I P V L M K N - 47 I V M I S S H W L L W I G F E M N M L AI I P I M M K N - 47 I T A L S H W F F T W G L E M N M L AF I P V L T K K - 47 U M S T T M N M L I V L C I E U S L S I F I L I A Q E - 120 I T V T S N S W G A W M G L E I N L L S F I P L S S N - 48 L S I L T N V I V W Y S I F L L M T V F I L L M K S S - 43 M C L M N N I L I W S V F L M M T L L F V M N K M N - 43 U S F T M N N L S M W M G L E T T W M W V I I V E - 44
	TM6		TM7a	TM7b TM8
E.coli K.pneumoniae T.thermophilu Dradiodurans Rmarinus A.aeolicus M tuberculosi S.coelicolor P.denitrificans R.capsulatus R.prowazekii C.reinhardtii N.crassa Y.lipolytica P.pastoris A.thaliana B.vulgaris N.tabacum T.aestivum X.laevis G.gallus S.scrofa B.taurus H.surus A.aurita D.melanogaster A.pisum C.elegans C.oncophora T.spiralis	147 - FRQKRSLEASIKYTILSAAASSFLLFGMALVY           147 - FRQKRSLEASIKYTILSAAASSFLLFGMALVY           147 - FRQKRSLEASIKYTILSAAASSFLLFGMALVY           124 - WRRGQGLEAALKYFLLGSALAAFFLYGAALFY           156 - QDSRS QEAGLKYFLLGSAVGASILLYGLAFLY           154 - REDVGAGEAALKYFLLGAFLYGFLYGAALFY           155 - QDSRSLASALKYFLLGAVKYFLLGAFLYGFLYGIALLY           158 - RRSLSSEGALKYFLLGAFLYGFLYGIALLY           159 - NRRLLSQEAANKYFLLGAFLYGFLYGIALLY           150 - NRRLLSQEAANKYFLLGAFLYGFLYGIALLY           150 - NRRLLSQEAANKYFLLGAFLYGFLYGIALLY           150 - NRRLLSQEAANKYFLLGAFLYGTLYGIALY           150 - NRRLLSQEAANKYFLLGAFLYGLYGLYGASLY           147 - NSSYSEAGLKYFVLGSLSSGLLLYGASLY           147 - NSSYSEAGLKYFVLGSLSSGLLYGASLY           148 - ROSYNSESAGLKYFVLGSLSSGLLYGASLY           149 - NSSYKASKASMLYFFUGSLSSGLLYGASLY           149 - NSSYKASKASMLYFFWGGLSSGLLFGCSMIY           150 - RKSEFSTEAGLKYLLLGAFSGLLFGCSMIY           150 - RKSEFSTEAGSKYLLGAFSGLLFGCSMIY           150 - RKSEFSTEAGSKYLLGAFSGLLFGCSMIY </td <td>AQ SG D L S F V A L G K N L G D G - M- AN SG N L S F L A L G K S L A D N - M- G AT G L I V A G I A Q V S A L D P- G AT G T I M Y A G I A Q V Y S A L D P- G AT G T I M Y P Q MAAH L A E G- S A S G S M Y G T I A Q V D G T V Q N G F A G T T G F E G I I S T I E A G G F A G T T G F D L L H Q L N D Q R T G S L D M V G AN S G T S L D D L L H Q L N D Q R T G S L D M V G AN S G T S L D D L L H Q L N D G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T U T G E Y G I D L H P L Y S Q W I T Q L M P L Y S Q W T T X M F N M F S G Q W T M K L F N M L S G Q W T M K L F N M L S G Q W T M T T N I H S G S C E I T L I T Q E Y F P LL K I N M N N LL F I N NO</td> <td>LNE PLULAG FGLMI VG LH FPLULAG LGLMI VG PLY AL ALGULL VG ONI GI LUY TGTLLVLSG AH PI MFWAG VALLLI Q NT UT GTLLVLSG AH PI MFWAG VALLI AVG TDDS MALAG VALLA VG HISLGVIFGLVFNLVG HLSLGVIFGLVFNLVG SEI KPGLIIGI VFLSS QET FWILLV DN- MTSWY KSYLNFSLLIFS VG SAR SSG IF MGILFI AVG G- AR SSG IF MGILFI AVG C- AR SSG IF M</td> <td>LG F K L S L V P F H L WT P D V Y GG AP AP V S T F L AT 244 LG F K L S L V P F H L WT P D V Y GG AP AP V S T F L AT 244 LG F K AA L AP F H F WT P D V Y GG S P T P V L F MAT 213 F V F AA L AP F H F WT P D V Y GG AP T V V S L F L S T 254 F L F V G AV P F H WT P D V Y GG AP T T L T S V T S T F L S T 254 L F V G AV P F H WT P D V Y GG AP T T L T S V T S T F S T 233 L F V G AV P F H WT P D V Y GG AP T P T G F MAA 216 L F V G AV P F H WT P D V Y GG AP T P T G F MAA 216 L F V G AV P F H WT P D V Y GG AP T P V T G F MAA 216 L F V G AV P F H WT P D V Y GG AP T P V T G F MAA 216 L F F V G AV P F H WT P D V Y G S P T P V T AF F AT 244 L F F V G AV P F H WT P D V Y G S P T V T AF F AT 244 L F F V G AV P F H WT P D V Y G S P T P V T AF F AT 244 L F F L A SS P I H F W I P D V Y G S P T P V T AF F AT 244 L F F V S AV P F H WT P D V Y G S P T P V T AF F AT 244 L F F V S AV P F H WW T P D V Y G S P T V T AF F AT 244 L F F V S AV P F H WW T P U Y I S S P T V T AF F AT 245 L F F I G I AP L H K W L S I Y F N I I I T T Y I S L 238 F L F I T AV P F H WW AP D I Y G S P T P V T AF L S I 267 L F I T AV P F H WW AP D I Y G S P T P V T AF L S I 267 L F I T AV P F H WW AP D I Y G S P T P V T AF L S I 267 L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H W P F V L G S S L I T ALL S T 132 L AM L G M A P H F W P F V L G S S L I T ALL S T 132 L AM L G M A P H F W P F V L G G S S L I T ALL S T 132 L AM L G M A P H F W P F V L G G S S L T ALL S T 132 L AM L G M A P H F W P F V L G G S S L I T ALL S T 132 L M L G M A P H F W P F V L G G S S N N T L L L G T 209 L L L S G A A P H F W P F N W F Y T G G T P V T AF L S C 1 11 L L M L S L M P H W P M W P Y T G G T P V T AF L S T 132 L M L G M A P H F W P M W P Y T G G T N M S C L M M T 11 L M L S L M P H W W P M W F N M M S U M M S L L M T 11 L M L S L M P H W W P M Y N Y N S Y N S Y M S C L M M T 1 10 L M</td>	AQ SG D L S F V A L G K N L G D G - M- AN SG N L S F L A L G K S L A D N - M- G AT G L I V A G I A Q V S A L D P- G AT G T I M Y A G I A Q V Y S A L D P- G AT G T I M Y P Q MAAH L A E G- S A S G S M Y G T I A Q V D G T V Q N G F A G T T G F E G I I S T I E A G G F A G T T G F D L L H Q L N D Q R T G S L D M V G AN S G T S L D D L L H Q L N D Q R T G S L D M V G AN S G T S L D D L L H Q L N D G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T G S T G A T H F D Q L A K I L T G Y E I T U T G E Y G I D L H P L Y S Q W I T Q L M P L Y S Q W T T X M F N M F S G Q W T M K L F N M L S G Q W T M K L F N M L S G Q W T M T T N I H S G S C E I T L I T Q E Y F P LL K I N M N N LL F I N NO	LNE PLULAG FGLMI VG LH FPLULAG LGLMI VG PLY AL ALGULL VG ONI GI LUY TGTLLVLSG AH PI MFWAG VALLLI Q NT UT GTLLVLSG AH PI MFWAG VALLI AVG TDDS MALAG VALLA VG HISLGVIFGLVFNLVG HLSLGVIFGLVFNLVG SEI KPGLIIGI VFLSS QET FWILLV DN- MTSWY KSYLNFSLLIFS VG SAR SSG IF MGILFI AVG G- AR SSG IF MGILFI AVG C- AR SSG IF M	LG F K L S L V P F H L WT P D V Y GG AP AP V S T F L AT 244 LG F K L S L V P F H L WT P D V Y GG AP AP V S T F L AT 244 LG F K AA L AP F H F WT P D V Y GG S P T P V L F MAT 213 F V F AA L AP F H F WT P D V Y GG AP T V V S L F L S T 254 F L F V G AV P F H WT P D V Y GG AP T T L T S V T S T F L S T 254 L F V G AV P F H WT P D V Y GG AP T T L T S V T S T F S T 233 L F V G AV P F H WT P D V Y GG AP T P T G F MAA 216 L F V G AV P F H WT P D V Y GG AP T P T G F MAA 216 L F V G AV P F H WT P D V Y GG AP T P V T G F MAA 216 L F V G AV P F H WT P D V Y GG AP T P V T G F MAA 216 L F F V G AV P F H WT P D V Y G S P T P V T AF F AT 244 L F F V G AV P F H WT P D V Y G S P T V T AF F AT 244 L F F V G AV P F H WT P D V Y G S P T P V T AF F AT 244 L F F L A SS P I H F W I P D V Y G S P T P V T AF F AT 244 L F F V S AV P F H WT P D V Y G S P T P V T AF F AT 244 L F F V S AV P F H WW T P D V Y G S P T V T AF F AT 244 L F F V S AV P F H WW T P U Y I S S P T V T AF F AT 245 L F F I G I AP L H K W L S I Y F N I I I T T Y I S L 238 F L F I T AV P F H WW AP D I Y G S P T P V T AF L S I 267 L F I T AV P F H WW AP D I Y G S P T P V T AF L S I 267 L F I T AV P F H WW AP D I Y G S P T P V T AF L S I 267 L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H WW AP D I Y G S S T T V T AF L S I 256 F L F I T AV P F H W P F V L G S S L I T ALL S T 132 L AM L G M A P H F W P F V L G S S L I T ALL S T 132 L AM L G M A P H F W P F V L G G S S L I T ALL S T 132 L AM L G M A P H F W P F V L G G S S L T ALL S T 132 L AM L G M A P H F W P F V L G G S S L I T ALL S T 132 L M L G M A P H F W P F V L G G S S N N T L L L G T 209 L L L S G A A P H F W P F N W F Y T G G T P V T AF L S C 1 11 L L M L S L M P H W P M W P Y T G G T P V T AF L S T 132 L M L G M A P H F W P M W P Y T G G T N M S C L M M T 11 L M L S L M P H W W P M W F N M M S U M M S L L M T 11 L M L S L M P H W W P M Y N Y N S Y N S Y M S C L M M T 1 10 L M

# d) Subunit NuoN, part 2.

	TM8	TM9	TM10	TM11
Ecoli Kpneumoniae Tathermophilu Dradiodvans Rmarinus Aaeolicus Mtuberculosi Scoelicolor Pdenitrificans Rcapsulatus Rgrowazekii Creinhardtii Ncrassa Njipolytica Papastoris Athaliana Bvulgaris Ntabacum Taestivum Xlaevis Ggallus Sscrofa Blaurus H sapiens Aaurita Dmelanogaster Apisum Celegans Concophora Tapiralis	245 A S C I A I F G V W R L F L Y A P V G D S E 245 A S C I A I F G V W R L F L Y M P V G N S E 214 S V X A A A F A A L R V A P 251 A S V A A A F A A L R V F G - A L A A O P 251 A S V A A F A G A L R V Y D A A L P A E B 252 Y V Y A A F G A L L R V Y D A A L P A E B 252 A T P V A A F G A L L R V Y V A L P L H D 317 A T V A A F G A L R I L Y V V D A L P A E B 254 A P V A A F A G A L R V Y D A F G H V I G 244 A P L A A M A L I A R V H D A F G H V I G 245 A P V V A A M A L I A R V H D A F G H V I G 246 A P L A A M A L I A R V H D A F G V I G 247 A P L A A M A L I A R V H D A F G V I G 248 A S L G M V I V L I N I S K L I G N Y P 195 A P L S L S T T F W A S S W H 239 M P L S L S T T F W A S S W H 230 M P L S I L T L I Y I M H Y I N I Y N Y 257 A P I S I S A N I S N Y S I Y A S Y G A T 257 A P I S I S A N I S N Y S I Y A S Y G A T 257 A P I S I S A N I S N Y S I Y A S Y G A T 257 A P I S I S A N I S N Y S I Y A S Y G A T 257 A P I S I S A N I S N Y S I Y A S Y G T 133 W Q L A P M A I L Y O I Y A S Y G T 133 W Q L A P I S I H N I I M Y I N Y I N Y I 134 W C L A P I S I H N I M Y I N Y I S S 133 W Q L A P I S I S A N I S Y I Y S Y S S T 133 W Q L A P I S I Y N Y S I Y S S S T 133 W Q L A P I S I Y N Y S I Y S S S T 134 W Q L A P I S I Y N Y S I Y S S S T 135 W Q L A P I S I Y N Y S S T 135 W Q I A A S S Y I Y S Y N Y S S S S S S S S S S S S S S S	- A IR V V L A I IA F AS II F GN L MA LS OT T - A VR V V L A I IA F AS II F GN L MA LS OT T P E AL ALL VA LS VV VG NL AALAOK - GWH S V LO IL VALT LV IG NA AALV QO - WOLLLAL VAL V TMV AG NV LALV QO - WOLLLAL VAL V TMV AG NV LALV QO - WOLL LALV LAV L TMV AG NV LALV QO - WOR P VLWAI AI L TMT VG T V TAVN OT T - DWR V VWM LAV LS WF G S I AG IG OT - WOLL ALAVAS MY LG AI AG IG Q T - E WOQ IL AALAU AS MY LG AI AG IG Q T - E WOQ IL AALAU XS WF LG S I AG IG QT - WOY S V V V ALAV MY LG AI AG IG QT - DY S V V S V F IL F S MF IG S I GG AY G P - INS VI S IL AI LTLL VG S VGGLLO T - LQ IF FFC S I AS MI LG AL AAMAO T - LQ IF FFC S I AS MI LG AL AAMAO T - LQ IF FFC S I AS MI LG AL AAMAO T - UQ IF FFC S I AS MI LG AL AAMAO T - UQ IF FFC S I AS MI LG AL AAMAO T - NY NL IK TMAMALS I I GG WGGLNO T - INT PLIL IL GL ST TLI GG WGGLNO T - INT NL ILTL LG LS TS LI GG WGGLNO T - INT NL TL LG LS TS LI GG WGGLNO T - NK LV V AT I F SLI I GG WGGLNO T - NK LV V VAT I F SLI I GG WGGLNO T - NK LV V VAT I F SLI I GG WGGLNO T - NK LV LV AT I F SLI I G GW GGLNO T - NK LV LV AT I F SLI I G GW GGLNO T - NK LV LV AT I F SLI I G GW GGLNO T - NK LV LV AT I F SLI I G GW GGLNO T - NK LV LV AT I F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G GW GGLNO T - NK LV LV AT IF F SLI I G LV CV Y S I LW SV F S Y W V S - Y LI G V CV Y S I LW SV F S Y W V S - Y LI G V CV Y S I LW SV F S Y W V S	NIKRLEGY SISHLGYLLVALIAL NIKRLEGY SISHLGYLLVALIAL NIKRLEGY SISHLGYLLVALIAL NIKRLEGY SISHLGYLLVALIAL NIKRLEGY SISHLGYLLVALIAL NIKRLAY SIAHAGY LTGLAAG SIKRLAY SIAHAGYLTALTAV NVKRMLAY SIAHAGYLLGAAG SIKRLAY SIAHAGYLLGLAAG SIKRLAY SIAHAGFLLGLAAG SIKRLAY SIAHAGFLLGLAAG SIKRLAY SIAHAGFLLGLAAG SIKRLAY SIAHAGFLLALVGLAAG SIKRLAY SIAHAGFLLALVGLAAG SIKRLAY SIAHAGFLLALVGLAAG SIKRLAY SIAHAGFLLALVGLAAG SIKRLAY SIAHAGFLLALVGLAAG SIKRLAY SISHMGFGLLGLAAG SIKRLAY SIGHYGYLGGFSGG CVKRLAY SIGHYGYICIGFSGG CVKRLAY SIGHYGYICIGFSGG CVKRLAY SIGHYGYICIGFSGG CVKRLAY SIGHYGYICIGFSGG CVKRLAY SIGHYGYICIGFSGG CVKRLAY SIAHAGYMLSIGHYGYICIGFSGS SIRKLAY SIAHAGWISILPS SIRKLAY SIAHGWMINISIPS SIRKLAY SIAHGWMIXLPYN SIRKLAY SIAHGWMIXLPYN SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLAY SINTMGYMALSINIS SIRKLLAY SINTMGYMALSINIS SIRKLISSINNTWILSYN SIRKLISSINNTWILSYN SIRKLLISSISNWILASSDL	Q T G E M S M E A V G V Y L A G Y L F S S L G A F G V V S L M S S P Y 351 Q S G E M S M E A V G V Y L A G Y L F S S L G A F G V Y S L M S S P Y 351 N A Q A L G F Y L L T Y L A T G L A F A V L S Q I 5 303 T P E G Y A G A L F Y L L Y V L M Y V G A L A V V A A L O R A
			TM12a TM	12b TM13
Ecoli Kpneumoniae T.thermophilu D.radiodurans R.marinus A.aeolicus M.tuberculosi S.coelicolo P.denitrificans R.rapsulatus R.prowazekii C.reinhardtii N.rassa Y.lipolytica P.pastoris A.thaliana B.vulgaris N.tabacum T.aestivum X.laevis G.gallus S.scrofa B.tarrus H.sapiens A.aurita D.melanogaster A.pisum C.elegans C.oncophora T.spiralis	352 352 353 354 357 354 359 349 340 342 350 349 343 387 398 349 343 349 343 349 343 349 344 345 346 347 346 347 346 347 346 347 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 347 348 348 347 348 347 348 348 347 348 347 348 347 348 347 348 347 348 347 347 348 347 348 347 348 347 348 347 347 348 347 348 347 348 348 347 348 347 348 347 348 348 348 348 348 348 348 348		AVM TVMMLSLAGIPMTLGFIG FY AVM TVMMLSLAGIPMTLGFIG FY AVM TVMMLSLAGIPMTLGFIG FY LAFLYAMLSLIGLPFLAGFWG WJ LAFLYAMLSLIGLPFLAGFWG WJ VAMAFFMFSLTGFPLAGFAFAVFG MLSMFLLAFAGIPLTSGFSWFA AVFAVFLAFAGIPLTSGFSWFA AVFAVFLAFAGIPLTSGFSWFA LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVLMFSLAGVPTLGFFAGFG LAMLVTLSLAGUPTGFW LSALTISST SLATTISSTAGIPPLAGFCSFY WTFSITMFSYAGIPPLAGFCSFY WTFSITMFSYAGIPPLAGFCSFY WTFSITMFSYAGIPPLAGFCSFY WTFSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFSYAGIPPLAGFCSFY VMTSSITMFY VLILSLGGLPPLSGFW VMTSSITMFY VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGLPPLSGFW VMT VILLATLSNGGUPPLSGFW VMT VILLATLSNGGUPPLSGFW VMT VILLATLSNGGUPPLSGFW VMT VILLATLSNGGUPPLSGFW VMT VILLATLSNGGUPPLSGFW VMT VILLATLSNGV VMT VILLATLSNGV VMT VILLATLSNGV VMT VILLATLSNGV VMT VILLATLSNGV VMT VILLATLSNGV VMT VILLATLSNGV VMT VMT VMT VMT VMT VMT VMT VMT VMT VM	V L AVG VQ AH L WWL VG AV VVG S A I G L Y YY L R V AVS L Y L 43 AF AE AR AG AWG YL V A AV VVG S A I G L Y YY L R V AVS L Y L 43 AF AE AR AG AWG YL V L AL VT S AVS AVY Y L G L G L AVF A 38 AF AE AR AG AWG YL VI S VL AV VS S V S AL VYY L R VVY VF WM 43 F G L YK D M ALG L T L Y I V V VF VL R V VY VF WM 43 F G L YK D MF ALG L F AI A S L I S AYY Y L R V VY VF WM 43 F G L YK D MF ALG L F AI A S L I S AYY Y L R V VY VF WM 43 F G L YK D MF ALG L F AI A S L I S AYY Y L R V VY VF WM 43 F G L YK D MF ALG L F AI A S L I S AYY Y L R V VY VF WM 43 F G L YK V W F Y A A S AG AVP L V VG V I G V I S AY A AF F YI R V I V V WF WF 43 VF R AA AS G A AP L V I VG V I S S G V A AF F Y I R V I VY MF F 43 V F R AA AS G A P L V I VG V I S S G V A AF F Y I R V I VY MF 7 43 V T AA VD AG MGWL AV L G V I AS V I G AF YY L R I VY MY F 43 V I K AA I G G F VW V P V AV AV V AS V I G AF YY L R I VY K MY F 43 L F Y A AI N K E F T L AY G I F T S VV A AF YY L K V V K AMY F 42 L F Y A AL G G F VW P V AV V V V I A L I L T S V VG A YY L N I I K E I F F 43 L F A AL G G AY F L A VG V I Y S V I G C F Y I R L VK MF F 44 L F F A AL G C G AY F L A VG V VT S V I G C F YY I R L VK MF F 43 L F F A AL G C G AY F L A VG V VT S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A VG V VT S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG V Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG W Y T S V I G R F YY I R L AK MF F 43 L F F A AL G C G AY F L A P VG W Y T S V I G R F YY I R L AK MF F 43 L G E T T N S I I P T M AT T I T M L L M Y F W L Y S S L O Y Y C V V I Y C V Y C V Y C V Y C V Y C Y C Y C Y Y C Y C
		<u></u>	M14	
Ecoli K.pneumoniae T.thermophilu D.radiodurans R.marinus A.aeolicus M.tuberculosi S.coelicolor P.denitrificans R.capsulatus R.prowazekii	435         M A P E Q P G R D A P S N WQ           435         A A P E Q L N R D A P S N WQ           386         R P E E T P F R P G P           397         P D R T P A R E Y A H G - Q           437         K S P D E A P E A V R QQ A F P           419         Y G E V R H G Q T T V S           438         T E E S CO T PH V A A P           503         S E P R F E G P T V A V P           431         G E S E C M T S M M G           430         G E E S E G M T S M M G           430         G E E S C M T S M M G           434         T A I I K L P M O Y G		LISALLVLVLGVWPOPLISIVRLA LISALLVLVGOWPOPLISIVQLA KASIGIVLLALGLPGLVLPALAAG ALSIGIVVGGLPPKUWYGWASP VVCVVLIVLGVLPGLLEVTASFF LGTAFLVIFFGLFPHVVLDFILRA AVGTVVTVVLGIAPOPVLDLADOA AVGTVVTVVLGIAPOPVLDLADOA AVGTVVTVVLGVPOVLDAAGA LVLAAVAMLGGAINMAGVEGAAOA LULAVLVGFLFGSTILF	MP L M
Creinhardtii N.crassa Y.lipolytica P. pastoris	344 A P V H T A A S F T G A P 494 Y S P R H K L K T V D V E N T WP F P V K R D 423 D K N N I L I N S N E T V S 456 D T I S F K D I I S N L I I N	NQT >L K L N D S N A F S I S Y D R Y T V S S P L S S G Y 	T L T S AC AV AL AF AP VML V K P F V I - T I S S P F S I T I S I I T I V I L F I F MN L S S L I I L I T F G F I Y N S L I I D I F N V F I S N V I S V V I S S T L I I L I I I D V	38. KEWLSMGTIMVQVLFST
A.thaliana B.vulgaris N.tabacum T.aestiwum	450 DT PR TWILY E PMD 439 DT PR TWILY E PMD 439 DT PR TWILY E PMD 430 DT PR TWILY E PMD	RNKSLLL RDKSLLL RDKSLLL RDKSLLL	AMTSFFITLFLLYPSPLFSVTHQN AMTSSFITLFFLYPSPLFSVTHQN AMTSSFITSFPYPSPLFSVTHQN AMTSSFITSFPYPSPLFSVTHQN	49 ALSLYL
X.laevis G.gallus S.scrofa	303 T 5 5 P N T S N A S L T WR 303 T L P P N S S N H M K L WR T N 303 T M F P S T N N M K M K WQ F 303 T M F P S T N N M K M K WQ F	HHSKQPTL KTLNTPT EHTKQMK	LLSIALILSSFIIPISPLTLT AILTALSTTLLPLSPLIITML LLPTMIVLSTLILPMTPALSSLN- FIPTMVVISTMIPITPMICVI	
A.aurita A.aurita D.melanogaster	303 T LL P M S N N V K M K WQ F	EHTKPTP EHTKPTPIQATIL SINYNM	FLPTLIALTTLLLPISPFMLMIL GMLLYSVTFILVCPQILWKPIHYG YMIMTFFSIFGLFLISLFYFMF••	34. 34 V L S L F
A.pisum C.elegans C.oncophora T.coiralis	250 N F N L F N K WY L H I K	KNN	T N F I MMMN F F S L F F S Y L F I Y 	22: 28: 27: 27: 27: 27: 27:

## e) Subunit NuoM, part 1.

-4

	TM1		TM2
	Manna Manna		
E.coli	1MLLPWLILIPFIGGFLCWQTERFGV		KVPRWIALITMGLTLALSLQLWLQGGYSL54
T.thermophilus	1 MVVLAVLLPVVFGALLLLGLPRALG		
D.radiodurans	1 MTNLMLYLPLLGALLVLVAPVKWR		+ E E V AG F F A A AT LG AG LWL WR LG 46
Aaeolicus	1METLLNVAIFLPLVGALLVAVIRNEIFA		KVASILIGAVVALISLVLFVNFDF52
M.tuberculosis S.coelicolor	1 MNN V PWL S V L WL V P L AG A V L I I L L P P G R R		LAKWAGMVVSVLTLAVSIVVAAE FKP56
P.denitrificans	1MTNLLSIITFLPIVAAIIMALFLRGQDEAA		R N A KWL A L L T T A T F V I S L F V L F R F D P 58
R.capsulatus R.prowazekii	1MQNLLSIITFLPLAAAAVLAVVSRGSGPAA	)	RNAKWVALTATVVTFLVSLLLLAG FDP58
C.reinhardtii	1 MFISVLLILFALCVTLIPEAHYHMVR		
N.crassa Y.lipolytica	1 MKKEFLMFLFALLIIPIIGIFIIWSTQFYSKMYQ 1	PFYYMPY PFKKVVITEG AN SCMLKDG SWSQVVLTD SDDMFI	QN E T A P K V V A F I I S I L N L M V S L L V Y I L F D F 106 N V K H F Y L F A S N L L L F I V V L Y I N F N T 48
P.pastoris	1 MLVQNLIIFNIIGIVLLVLLNNNNG		I LN KKSLLT I KNELKLKQ I GLI I S I I N I L55
A.thaliana B.vulgaris	1 MLEHFCECY FNLSGLILCPVLGSIILLFIPNSRIR 1 MLEHFCECY FDLSGLILCPVLGSIILLFIPNSRIR		LIRLIGLCASLITFLYSLVLWIQFDS61 LIRLIGLCASLITFLYSLVLWIQFDP61
N.tabacum	1 MLEHFCECYSDLSGLILCPVLGSITPLFIPNSRIR		PIRLIGLCASLITFLYPPVLRIQ FDP61
X.laevis	1 MLKILLPTLMLIPSTWLTNKKWLWPS		
G.gallus Secreta	1MLKIILPTIMLLPTALLSPAKSMWTN		TTMY SLLIASISLHWLTPSY YPT49
B.taurus	1 · · · · · · · · · · · · · · · · · · ·		·····STAHSLLISFTSLLLMNQFGDN - 48
H.sapiens A aurita	1MLKLIVPTIMLLPLTWLSKKHMIWIN		
D.melanogaster	1 MLKIIFFLLFLIPFCFINNMYWMVQ1		+
A.pisum C.elegans	1 ML I I F S M I F F S L K I K S WWL AQN		
C.oncophora	1 • • • • • • • • • • • • • • • • • • •		••••••••••••••••••••••••••••••••••••••
1.spiralis	1 MMSNEGSVLVEMAEG		·····
		TM3	TM4
E.coli K.pneumoniae	55 TQSAGIPQWQSEFDMPWIPRFGISIHLAIDGLS 55 TQSAGIPQWQSEFVLPWIPRFGISIHLAIDGLS	L M V V L T G L L G V L A V L C S W K E I E K Y	QGFFHLNLMWILGGVIGVFL132
T.thermophilus	43 H P G G V A H A F Q A P L L P G A G V Y W A F G L D G L S	ALFFLTIALTVFLGALVARVEGR	FLGLALLMEGLLLGLFA111
D.radiodurans R.marinus	47 G E G L S V L PWV P P L G V T Y A V E L N G V G 55 A G S P A Q P Q F V D R I T G W F P G L D I Q Y Y V G I D G L G	. A F A L V T A F M T L M A V WY A A R R V P N P	
Aaeolicus	53 SKKG - FQFETYVPW IKTLGIGYHVGVDGMA	SLILMTSILFLAAYIWSWKIEDR	PSLYFALFLALETACIGVFA125
M.tuberculosis S.coelicolor	56 DGDR YQLTESHSWIA DFGVRYELGVDGIA	ALIALTALLIPFIILAGWHDADPLETGSS	R WR PTQG F F AL I L AVE AMV I I S F E138
P.denitrificans	59 AN TG FQ F V EDH AW I MG LR Y KMG VDG I S 59 AN PG MO E V EDB AW I MG LH Y KI G VDG I S	/ L F V L L T T F MMP L T I L S T WQ V Q D K	
R.prowazekii	60 SNNT YQFVERYTW LDKIGLEFHVGVDGIA	FFVVLTSFLTLICIIGSLFTIKKY ······	I KEY LVC FLLMESLC I G A F T 133
C.reinhardtii N.crassa	50 SGHG - LQMLVILGR SHLAFGIDGVA 107 SNNO - FOFIOEHYD LSFYDIYLGVDGIS	S L M L L T T V L F P I C MM L L R T V AG	
Y.lipolytica	49 F S N S F Q F N F E L F N S L N P F G L S N S D I S N G L L F G I D G L S	TFILLTVLLIPLTLLGNWYNINFN	SNLYYTLVLAIGLVILLNFW130
P.pastoris A thaliana	56 1 1 1 ENWIGFNSNYYGFQN I ERFLNIYWGIDGIS 62 STAK FOFVESLRW LPYENINFYLGIDGIS	. L L V L L T L I L G P I A I L S N WK N L K G Y	
B.vulgaris	62 STAK FQFVESLRW L PYENIH FYLGIDGIS	. F F V I L T T F L I P I C I L V G W S G M R S Y	GKEY     AFL   C E FLM   AV FC 135
N.tabacum T.aestivum	62 STAK SQFVESLRWLPYENINFYLGIDGIS 62 STAK FQFVESLRWLPYENIHLYMGIDGLS	.FFVILTTFLIPICILVGWSGMRSY	GKEY I TAFLI KEFTMI AVFC 135
X.laevis	45NY LMT I DQ I S	PLLILTCWLLPLMLIASQNHLSNEP	ISRQRTFITMLVFLQLSLIMAF5111
G.gallus S.scrofa	49	APLLVLTTWLLPLMLMASQSHLSKETTTR	······································
B.taurus	49SLNFSLLFFSDSLS	PLLILTMWLLPLMLMASQHHLSKENLTR	KKLFITMLISLQLFLIMTFT111
Aaurita	52 ESLFYSNIITGWLASV PLSTDWGSLYFGVDHLS	PFILLTAILTPICIIISWNSITYL	·····VKEFLVFLLAIHLLLIGVFT129
D.melanogaster A nisum	47 E I S Y F L G C D M L S 44	G L I L L S L W I C S L M L L A S E M I N K H N N	YKNLFLLNIIILLLLLILTF S105
C.elegans	33F \$ WGGLFLVLD \$ Y \$	I L L I VMS L F I L G I I V I S E KNNN	LLILSEILVFICIIFF186
C.oncophora T.spiralis	33	L L L I MMML F I Y GMVMI S E KNMN	
	This	Thac	TN7-
	TIM5	IMO	
E.coli	133 AIDMELEFEEWEMMLVPMYELIALWGH	SKTR I TAAT KEEIYTQASGL VML I AI LAL VEVHYNATG VW	TFNY EELLNT - PMS SGVEYLLMLGFFI A230
Kpneumoniae	133 AIDMELEFEEWEMMLVPMYFLIALWGHKASD	SKTRITAATKFFIYTQAS <mark>GLVML</mark> IAILALAFVHFNATG VW	TFNY EDLLKT - PMSHGVEYLLMLGFFI A230
D.radiodurans	116 AR DLILFYVFFEWALIPSLLMLAVYG	SPHRMR ALVKFAAYTLLGSLFMLLSFIGYKWLGGSPTFALPD	LL AH P VGG V AQ TWLY LG F L A 204
R.marinus A apolicus	132 AY DLILFYIFFELTLIPMYFIIGIWG	SEDRIY AAVKEVLYTLVGSLLMLVGILYLGFAAGDAVNGGVF	TTDY FKLLAY - NVPLAAQGWLFFVFALA226
M.tuberculosis	160 ALDVLLFYVFFEAMLIPMYFLIGGFGQ	AGR SR AAVKFLLYNLFGGLIMLAAVIGLYVVTAQYDSGTFD	FREIVAG VAAGRYGADPAVFKALFLGFMFA258
S.coelicolor P.denitrificans	139 ATDVFLFYIFFEAMLIPLYFLIGGFGDRAHEHGEKTA 130 ALDLVLFYLFFEAGLIPMFLIIGIWG	A T Q R S Y A A V K F L L Y N L AG G L I M L A A V I G L Y V V A G N F S L T E I A S K D R I Y A S F K F F L Y T F L G S V L M L V AM I AMY R M A G T T D I P T L L	E AR AN G S L D M A T S T E R W L F L G F F F A 242 T F D F P S E N F R L L G M - T V V G G M O M L L F L A F F A 5 228
R.capsulatus	130 ALDLVLFYLFFEAGLIPMFLIIGIWG	SKERIY AAFKFFLYTFLG SVLML VAMVAMYMMAGTTDIVTLN	IS F D F P H A D L P F L G WWT L T G G V Q T L L F L A F F A S 229
R.prowazekii C.reinhardtii	134 SINLLLFYLFFEAILVPMYITIGVWG	SONR I Y AALKEFLY TEEGS VEELLAL I Y I Y SKIHSEDL TN I L Y G S L E AAY KI VLY TMAG SL VLL PTLEMIY SECGTTN VLYMT	E L I G N I P L F AQ K I L WWA I F I A222 C AY N H Q T V L G WG L L A V 195
N.crassa	179 VLDILLFYIFFESILPPLFILIGLFG	S S N K V R A S F Y I F L Y T L L G S L F L L S I L T M S S I MG T T Y F D A L L	K S N F DY T I Q I F L F C G I F I A265
P.pastoris	134 CLDLVSFYILFESTLAPLFLLIGIYG	ANN KNKAAYY VLIYTLASSLEMLLSIVIYIYIIINSTDYIYIN	NIILSINLQSLLFIGIIIG220
A.thaliana B.vulnarir	136 MLDLLLFYVFPESVLIPMFIIIGVWG	ROR KIKAAYQFFLYTLLGSLFMLLAILLILFQTGTTDLQILL	TTEF
N.tabacum	136 MLDLLLFYVLPESVLIPMFIIIGVWG	QR KIKAAYQLFLYTLLGSVFMLLAILLILLQTGTTDLQISL	TTEFSERRQIFLWIASFA 5 223
T.aestivum X.laevis	136 MLDLLLFYVFFESVLIPMFIIIGVWG	QR KIKAAYQFFLYTLLGSVFMLLAILLILLQTGTTDLQILL	TTEFSERRQILLWIAFFAS223
G.gallus	112 ATELMLFYISFEATLIPTLILITRWGN	QPERLS AGIYLLFYTLISSLPLLVSILYLHTNTGTLHLPIIK	L TH PN L P A S WT S L L S S L A L L M A 202
S.scrofa B.taurus	112 ATELILFYILFEATLYPTLIIITRWGN	2 T E R L N AG LY F L F Y T L AG S L P L L V A L VY I Q N T T G S L N F L I I H 2 T E R L N AG LY F L F Y T L AG S L P L L V A L I Y I O N T V G S L N F L M L O	Y WS H P L S N S WS N I F MWL AC I MA202 Y WV Q P V HN S WS N V F MWL AC MMA202
H.saplens	112 ATELIMFYIFFETTLIPTLAIITRWGN	2 PERLNAGTY FLFYTLVG SLPLLIALIY THNTLG SLNILLLT	L T AQ E L S N S WANN L MWL AY T MA202
A.aurita D.melanogaster	130 S L N I L L FY I M F EG I L I PM F L M I G I WG S 106 S M S L F M FY L F F E S S L I P T L F L I L G WG Y	K K E K E R A A F Y F F F F T L A G S L F M L L G I F T I Y K H T G T L D Y T I L S D P E R L Q A G L Y L L F Y T L L V S L P M L I G I F L L M N K I G S M N F Y L M N	- LQT LPSELQFWVF IGFFL5217 NFMFN YDLLYFCLLCA190
A.pisum	100 SNNFLLFYIFYEINLIPVIILIYGWGY	Y E E F K AG F Y L F VY M I F F S L P F F C L L S L N N F K F M F M Y Y F D Y	L N N L N
C.elegans C.oncophora	87 SSNLLMLYMFFELSLFPILVMILGFGS	I EKINSGYYLLFY ASLCSFPFLYVYKSNFMLSLCYFDFFN	S WEM

## e) Subunit NuoM, part 2.

	TM7a	TM7b	TM8		TM9	TM10	TM11
E.coli	231 FAVEMPVVPLH	GWL PD AH SQ AP 1	TAGSVOLAGILL	SLPLFPNASAEFAPI	AMWLGVIGIFYGAWMAFA	QTDIKRLIAY TSVSHMGFVLIA	Y TG 5 - Q L AY QG 340
K.pneumoniae T.thermophilus	231 FAVEMPVVPLH 201 FAIETPLEPLH	GWL PD AH SQ AP 1 AWL PP FHQENHE	T A G S V D L A G I L L E T A A Y G L L R F P S G L A D A L G T L Y K V G V F A F F R F	ALPLFPNASAEFAPI AIPLAPEGFAQAQGL	AMWLGVIGIFYGAWMAFA LLFLAALSALYGAWVAFA	QTDIKRLIAY TSVSHMGFVLIA AKDFKTLLAY AGLSHMGVAALG	I Y T G S - Q L A Y Q G 340 V F S G T - P E G A M G 310
D.radiodurans R.marinus	205 MAVELPLWPLH 227 FAIKVPLFPLH	AWL PDFHEQNHE	E S G I P D V M G T L Y K V G G Y G I F V F I G G S V I L A G V L L K M G T Y G L V R F	GLTLFPDASLELRPV CLPFFPNAATDYALW	L M A L A A F T A L Y A A W I A F G L A V L A V V G I V Y G A L V S R V	Q T N WKR L L AY AG L S H MG F V A L G Q A D A K K L V AY S S V S H L G F V V L G	L F S MN - E T A V I G 314 I F A F T - V E A MQ G 336
A.aeolicus M.tuberculosis	219 FAVELPMWPFH 259 FALEAPLWPFH	TWL PDAHVEAPT	TAG S V I L AG V L L K MG T Y G F V R F P A T A V L MMA V MD K V G T F G M L R Y	SLPFFPEASKYYIPL CLQLFPDPSTYFRPL	F T L S V V A V I Y A AMMA I A   V T L A I I G V I Y G A I V A I G	QTHMKRLIAY SSISHMGLVTLG QTDMMRLIAY TSISHFGFIIAG	T F A M N - S D A L N <mark>G</mark> 328 I F V M T - T Q G Q S <mark>G</mark> 368
S.coelicolor P.depitrificano	243 FAVKAPLFPLH 229 FAVKMPMWPVH	TWL PN AMGEST	APVAVLITAVVD KVGTFAMLRF	CLQLFPEASKWATPV SLPMFPVASGVAOPY	I L V <mark>L</mark> A V I S I I Y G A L L A V G V F W L S A I A I V Y T <b>S</b> L V A L A	QRDIKRLIAY ASISH FGFIIMG OSDMKKVIAY SSVAHMGYVTMG	I F AMT - S Q G Q S G 352 V F A AN - O I G V D G 338
R.capsulatus	230 FAVKMPMWPVH	TWL PDAHVQAPT	AGSVVLAAVLLKMGGYGFLRF	SL PMF PVG AETMTTF	VFILSAVAIVYTSLVALA	QEDMKKLIAY SSVAHMGYVTMG	F A AN - Q Q G V D G 339
C.reinhardtii	196 LAVKIPLMPVH		G S V L AG V L K L G G I G F L R F	ML P V V P E F C V S V F P L	VSTLCLVSFLFSTLSTLR	QIDLKKIVAY SSIAHMSMVTLA TTDIKELIAY SSVSHAAVYLIG	F S Q S - E F S A Y S 305
Y.lipolytica	218 I MVKTPLFPIH	VWL PVVHSESPI	AG SMILAGLILKLALY AT LR L	LL PLLCEAQILY TPM	IYIISLLTIILTSLATLR	QIDLKVIIAY SSISHMGIAILG	VC SNT - SLG I Y G 327
A.thaliana		I WL PEAHVEAPT	AGSVILAGILLEFGTYGFLRF	SIPMEPEATLCETPE	1 Y T L S A I A I I Y T S L T T L R	QIDLKKIIAY SSVAHMNLVTIG	MF S PN - 1 QG I GG 333
N.tabacum				SIPMEPEATLCSTPE		QIDLKKIIAY SSVAHMNLVTIG	MF S PN - 1 QG 1 GG 333
X.laevis	203 FMV AMPLYGTH		AGSMVLAAILLELGGYGIIRI	SIT-LSPSMKELAYP	FLILSLWGIIMTSSICLR	QTDLKSMIAY SSVSHMGLVISA	SNNQTPMKALTG312
S.scrofa	203 FMV KMPLYGLH		AG S M V L A A V L L K L G G Y G MMR I	T - TILNPLTNYMAYP		QTDLKSLIAY SSVSHMALVIVA	I M I Q T - P WS F MG 311
H.sapiens	203 FMVXMPLYGLH		AG S M V L A A V L L K L G G Y G MMR L	TL - ILNPLTKHMAYP		QTDLKSLIAY SSISHMALVVTA	L I Q T - PWS F T G 311
D.melanogaster			SGSMILAGIMLELGGYGMLEV	IS-FLQLMNLKYSFV	NISISLVGGVLVSLVCLR	QTDL KALIAY SSVAHMGIVLSG	LLTMT - YWGLCG299
C.elegans	167 FMMX FPIYFLH	LWLPKAHVEAPT	TASMLLAGLLLELGTAGFLRI	LG SL SF VHNNV	NILIAFLGMILGSFCCVF	QSDSKALAAY SSVTHMSFLLLS	L V F I T - MS S K I S 272
C.oncophora T.spiralis	163 FVVXLPVYLFH	LWLPKAHVEAP	LGSMILASILLETGGYGLVKV	SG LNVGSGCVFG	LVGLLLFLSLLSAVTTVV	QNDLKKFVAY SSVTHMTMVLGL	V V MG F - E V L D S A 269
	TM1	1		TM12a	TM12b	TM13	
E.coli	341 AVIQMIAHGES	AAGLEILCG-QI	Y ER I H TR DMR MMGGL WS KMKV	VL P AL S L F F A V A T L GM	PGTGNEVGEEMILEGSEO	VVPVITVISTEGLVEASV	SLAMLHR AY FG446
K.pneumoniae T.thermophilus	341 AVIQMIAHGES 311 GLYLLAASGVY	AAGLFILCG-QI	L Y E R L H T R D M R Q M G <mark>G</mark> L W S K I K V L Y E R T G T L E I G R Y R G L A Q S A P G	VL P AMS MF F A V A T L G M G L A A L A L I L F L AMVG L	P <mark>G T G N F V G E F M I L F G S Y K</mark> P G L S G F P G E F L T L L G A Y K	V V P V I T V I S T F G L V F A S V A S P W L A A L A F L S V I A S A A	S L S M L H R A Y F G 446 A L T A F Q K T F W E 416
D.radiodurans R.marinus	315 AMYLLAFQNLY 337 AIIQMINHGLS	TGALFMAVG M	NLQER VGSLDTR VG <mark>G</mark> VMNQAGA LYERRHTRLMEEFGGIAR VMPV	ALGGLTLALWFASIAV VFAFFLVFTALASAGL	PGLAGFVGEFSILLGAYQ PGLNGFVGEFMILLGSFK	VS PWLTFIAGLTTIAAAA SALVGHPLLIALATSGVILAAV	ALTAFQKTFWE419
A.aeolicus M.tuberculosis	329 AIYLMIAHGLS 369 STLYMLNHGLS	SAALFLGAG - F	I Y D R I H S Y H M D D L G <mark>G L</mark> A R Y I P Y L I A R R G S R S I A D Y G G V O K V A P I	FTFAFFLAVLAGIAF	PGFASFVSEFLILLGIFE PGLAPFISEFLVLLGTFS	KF P V W A F V A G I G M V L G A A R Y WL A A A F G V T A L V L S A V	S L Y M F R K V M L E 434 M L W L Y O R V M T G 474
S.coelicolor P.denitrificans	353 ATLYMVNHGI 5 339 AIFQMLSHGFI	TAVLMLIAG - FI	L	LAGTELIGGLATLSL AY AAVEMEETMAN VGL	PGLAPFVSEFLVLVGTFT PGTSGFVGEFLTLMGVFR	R Y P V I G I I AT L G I V L AAL VD T W V A L V AT S G V I L S A A	T L V L Y Q R T M T G 458 A L W L Y R R V T L G 444
R.capsulatus R.prowazekii	340 AIFQMLSHGFI 333 AIFQMLSHGII	SGALFLCVG-V SSSLFLIVG-TI	I Y DR MH TR E I A AY G <mark>G</mark> L VNR MP A L Y ER L H T KE I A KY G <b>G</b> V AN KMP I	AY ALIFMFFTMANVGL	PGTSGFV <mark>GE</mark> FLT <mark>LLG</mark> IFQ PSTSGFIGEFLSLLGIYK	VN TWVAL FATSGVILSAA VN VVTAFIAALGIILGAV	A L W L Y R R V V F G 445 M L K L Y K E V M L G 438
C.reinhardtii N.crassa	306 5 5 F L M I A H G L I 376 G I L L G L A H G F T	SPALFLIVG-II	L Y D R AH T K F I L Y F S <mark>G</mark> L G A S M P I L Y D R S G T R L I H Y Y K G I A Q M A P L	G S T L F F L F T L G N L A F . L S L L F F I F S L ANC G V	PLFPNFIAEVLCMVSIFA PLTLNFVGEFMSLYGVFE	VH E L L AY V F C V C Q V L G A A R L P L L G L L A S S S I V F S A A	G F W A F N R V V H G 411 Y S I F L F N R V A F G 482
Y.lipolytica P.pastoris	328 SIVLGVAHGFV 331 SLILCLAHGFV	SPALFLIVGGII	. Y DR Y H I R I VN Y Y K <mark>G</mark> L T T Y MPC . Y DR Y H N R L I N Y Y QG L S T F MP I	LATYIIILSFANIGT FSIYLVVFSFCNTGT	PLTGNFTGEFLSLQGGFI PLSGNFVGEFLSITGAVI	R N P I I G G I S C I S V L L A A I R H P I I G S L T A A S V L L S A C	QLKLTNKLTGG434 QMKLTNRLTGS437
A.thaliana B.vulgaris	334 SILLMLSHGLV 334 SILLMLSHGLV	SSALFLCVG-VI	LY DR H K T R L V R Y Y G G L V S T M P N LY D R H K T R L V R Y Y G G L V S T M P N	F S T I F F S F T L AN M S L	PGTSSFIGEFLILVGAFQ PGTSSFIGEFLILVGAFQ	RN SLVATLAALGMILGAA RN SLVATLAALGMILGAA	S L WL Y N R V V S G 439 S L WL Y N R V V S G 439
N.tabacum T.aestiyum	334 SILPMSSHGLV	SSALFLCVG-VI	Y DR H K TR L VR Y Y G G S V S T M P N	L S T I F F S S T L AN MS S	PGTSSFIGEFLILVGAFQ	RN SLVATLAALGMILGAA	SLWLYNR AVSG439
X.laevis G.gallus	313 AMILNTSDGLT 312 AMILMISHGLT	HSALCCLAKYQ	SY ER TH SR ALLL SR <mark>G</mark> LET I LP L NY ER TH SR I LI LTR GLOP LLP L	MGTWWLISNLANMAL MSVWWLLANLTNMAL	P P S P N WMG E I T I M T A L F N P P T T N L MAE L T I M V A L F N	WS SWT I I L TD LGTLL TAS	SLYMFLMTQRG419
S.scrofa B.taurus	312 AT AL MI AHGLT	SSMLFCLAN - TH	Y ER VH SR TMIL AR GLQTLLPL	MATWWLMASLTNLAL	P P S I N L I G E L F I I T A S F S P P T I N L I G E L F V V M S T F S	W5 N   T     L MG MN MM   T A L W5 N   T     L MG VN MV   T A L	SLYMLIITQRG417
H.sapiens A.aurita	312 AVILMIAHGLT	SSLLFCLAN - SI	Y ER TH SHIMILSQGLQTLLPL	MAFWWLLASLANLAL	P P T I N L L G E L S V L V T T F S P I S MN F V G E F MS I L S A L O	WS N I T L L T G L N M L V T A L	SLYMFTTTQWG417
D.melanogaster	300 SYTLMIAHGLC	SSGLECISN-10	SY ER LG SR SML INKGLLNFMPS	MTLWWFLLSSANMAA	P P T L N L L G E I S L L N S I V S	WS WI SMILLSFLSFFSAA	TLYLYSFSQHG405
C.elegans	273 SVMLMLAHGYT	STLMFYLIG-EI	FYHTSGSRMIY FMSSFFSSSMI	MGILFSVVFLSNSGV	PPSLSFLSEFLVISNSML	1 S K S M F V M I F I Y F V V S F Y	SLFLITSSLMG378
T.spiralis	270 VVCLMLSHGVL	SNSMFFMVG-MI	L S G S S K T R L L F K Q Q G L L R L S P V	VWFFLVFLLFMGSSV	PSVGMVGEVSVVVCCVS	VC SVNLVLLVLLFVVLLY	PLWFVCMLAVG375
			TM14		*		
E coll							500
K.pneumoniae	447 KA KSEIA	AKALPGMSLREI	SIILLVVLLVLLGFFPQPIL	DTSHAAMSNIQQWFVI	N S V S T T R P		509
D.radiodurans	417 EG PLG	AVRVPDLRGTEN	VL VL GL PLL AAL F F G V Y S A P V L	N L MQ P A VR A A L S L VG	5Q · · · · · · · · · · · · · · · · · · ·		409
A.aeolicus	447 PTQKEVN 435 EESIPEERVEK	WKKLKDLELHH	AIPFALIIGMALVMGIYPYPFV	KIVEHTSKLVFGG		ARLEVSEGEIVRIANP	534
M.tuberculosis S.coelicolor	475 PVAEG 459 PVKAE	VNGMPDLR VREI	. V V V A P L V A L L I F L G V F P K P V L	DIVNPAVENTMITTIG	2 H D P A P S V A H P V P A V G A S K T D P Q P E V E A A K	К ТАЕ G Р Н Р	553
P.denitrificans R.capsulatus	445 QL I KESL 446 EL V KESL	- KSITDMTPREN - KTISDMTTREN	CALFAPL VAMTLLLGVY PSL VT	DLIGPSVAHLVQDYN	Q S Q P A A P V A T A Q A S H A D L G T L A Q A T A G N		513
R.prowazekii C.reinhardtii	439 EI TN TEI 412 L P	- KH FR DLY KY EI - R G P AD V TR TE F	HTVLPLLIGAVWLGIKPMA	NVFHLSVENLLIKF -			491 443
N.crassa Y.lipolytica	483 G S F S K F F 435 I S S I Y	ENSIIDLTKREF MHRTNDVTIREF	Y ALIFLGVLVVFLGTYPSIIL (FIMNILIISTLIIGICPQIMY	. D G L H Y N V S S L I Y S Y G I N L L Y WT V N N Y I Y I I -	C K F C L G		543 486
P.pastoris A.thaliana	438 V F S Q Y 440 N L K P D F L	- H K F S D L N G R E V	F L L N W L L I P T I I I G I Y P S F V T / F I F I P F L V G L V W M G V Y P K V F L	N I L N L A S S T L I Y S V L D C MH T S V S N L V Q H G K	Г • • • • • • • • • • • • • • • • • • •		491 495
B.vulgaris N.tabacum	440 NL KPDFL 440 NL KPDFL	- H K F S D L N G R E V - H K F S D P N G R E V	/ F I F I P F L VG V V WMG V Y P K V F L / S I F I P F L VG V V R MG V H P K V F P	DCMHTSVSNLVQHGK DRMHTSVSNLVQHGK	F H		495 495
T.aestivum X.laevis	440 NL KPDFL 420 MT PEH	- Y K F S D L N G R E V L N A I N P T H T R E F	/ FIFL PFL VG V VWMG V Y PK V FL I TL M T M H L I PII PL MM K PEL I V	. D C MH T S V S N L V Q H G K VG L F F	F H • • • • • • • • • • • • • • • • • •		495 461
G.gallus S.scrofa	418 T L P S H 418 K Y T H H	I T T T P N S N T R E F I N N I K P S F T R E M	ILLMTLHIIPMLTLILKPELIS IALMALHILPLLLLTLNPKMIL	G T P L			459
B.taurus H.sapiens	418 KY TYH 418 SLT HH	I N N I S P S F T R E N I N N M K P S F T R E N	ALMSLHILPLLLLTLNPKIIL ATLMFMHLSPILLLSLNPDIIT	G P L Y			459
A.aurita D.melanogaster	434YPSSF 406 KLFSG	LQFARDVNRREI VYSFSSGKIREY	.WPPLLLIVLTITEGVMPTCLD LLMLLHWLPLNLLILKSESFN	0 L T L C L P Y I Y			480 447
A.pisum C.elegans	399 KLFFN	MNYLVYINLTEY YHNFNTWNVGF	LLLFMHWLPLNLIFLIMELFC				436
C.oncophora T.spiralis	379 KY	MLNFNNNYGLS - SLVVGWTLCDI	L F M I V M M Y N I F W L T M F F . V V S G W M P C L V L L Y W F N S A L L V	,			409 411

## f) Subunit NuoL, part 1.

	TM1		TM2		TM3
Ecoli Kpneumoniae T.shermophilus Dradiodurans Rmarinus Aaeolicus Msuberculosis S.coelicolor P.denitificans Rcapsulatus Rprowazekii C.reinhandtii N.crassa Y.lipodytica P.pastoris Athaliana B.vulgaris Ntabacum X.laevis G.gallus S.acrofa B.taurus H.lapiens Aaurta D.melanogaster Apismi C.aensphere B.taurus H.lapiens Aaurta D.melanogaster Apismi	1         MNMLALTIILPLIGFVLLA           1         MNMLALTIILPLIGFVLLA           1         MALGTILLPLIGFVLLA           1         MALGTILPLIGFLGFALLM           1         MMTTUVLIPLLPLLGFLGFALLM           1         MMNTTUVLIPLIPLLGFALGFALLM           1         MMNTTUVGUIFTPLIAFLGFALLM           1         MMNTTUVGUIFTPLIAFLGFALLM           1         MMNTTUVGUIFTPLIAFLGFALLM           1         MMNTUVGUIFTPLIAFLGFALLM           1         MENTALUVAPLGAGAILL           1         MENTIALUVAPLGGLGAVIL           1         MENTIALUVAPLGGLGAVIL           1         MENTIALUVAPLGGLUNG           1         MELSVFPLLGGLUNG           1         MFLIGSUNG           1         MILGSUNG           1         MILGSUNGSUNG           1         MILGSUNGSUNG           1         MILGSUNGSUNG           1         MILGSUNGSUNG           1         MILLVESUNGSUNG           1         MILLSUNGSUNG           1         MILLVESUNGSUNG           1         MILLVESUNGSUNG           1         MILLVESUNGSUNG           1         MILLVESUNGSUNG           1         MILLVELLGSUNG	FSRGRWS         ENVSAIVGVG           FSRGRWS         ENLSATVGMG           LFGKRMR         ENLSATVGMG           LFGKRMR         ENLSATVGMG           LFGKRMR         ENLSATVGMG           LFGRRIG         CKSGSWLATV           LGGLAFRGLARGKVLIGALATL         CSGMRLD           LGGCGRRLD         NGKHUIGTL           LGGRRLD         RVGHWIGTL           LGWRAIG         RVGHWIGTL           LGWRAIG         KKAAQYLTTG           FGRRKQ         VSGAQLITCL           FFGRRGLG         VSGAQLITCL           FFGRRGLG         VSGAQLITCL           FFGRFLG         SEGSAIMTT           FFGRFLG         SEGSAIMTT           FFGRFLG         SEGSAIMTT           LMSTFNMN         INNLHHLIKT           LMSTFNMN         NNLHHLIKT           LMSTFNMN         NNLHNYK           NSNIYK         NVPYVKT           MSNIYK         NVPYVKT           MCSISFV         MKEVSKWNLI           MRVYSMWLI         MNLVSLV	S VGL AAL VT AF I G VD F S VGL AAL VT AF I G VD F S VGL AAL VT AF VG VD F L VL AS F LL GAGLL S G WVL S F AV AVMR Y L GO AV A VP F VL AL YL FL TY G GA L TT L FS L VV AL KA AAL AF G VG AML ADM L AAY S F VG AML ADM L AAY S F VG VL F AD L FL S C I S WV F FL S F L FL S C I S WV F FL S F L FL S C I S WV F FL S F V F FL S AL F S L V A L KA S V I T T G L A I L A F F F V C N V A F I S S V I Y F VG S V I T T G L A I L A F F F V C V S F S S I L S L I A F F F V C V S F S S I L S L I A F F F V C V S F S S I S L I A F F F V S V F T S S I F S L I A F F Y E S V K T A F L I S L I P T I F T K T A F L S L I P T I F T K T A F L S L I P T I F M S F S I S C F L S L Y P L M A F I S S I S C F L S L Y P L M M I S M S C F L S L Y M V V M S F I S L S F L S L Y M V V M S F I S L S F L S L Y M V V M S F I S L S F L S H F T M M F M S S C F L S L Y M V V I S M S C F L S L Y M V V I S M S C F L S L Y M V V I S M S C F L S L Y M V V M S F I S L S F L S F L S M W M F F I V L M L F L A E A L V G V V V V W V V V V V V V V V V V V V	FAN G EQ TY SQ P L WTW FAN G KQ AV SV P L WTW GAR FQA EW L P GG F P L L AR F F TW GG F P L L AR F F TW LG SG A ED T I TQ H L TW W F MG Y P R H I P V L DW TL VG Y P R H I P V L DW Y F MG	MS VGD F N I G F N L VL D G L S L T ML S VV T G VG MS VGD F N I G F N L VL D G L S L T ML S VV T G VG MS VGD F N I G F N L VL D G L S L T ML S VV T G VG MA AN - AN L S VG F VL D L S S L MT L I T T G G I A A G L E L A F Q Y I D E L S L MT L I T T G G I P A G G L Q D F G L Q I D Q L S M F F VL I T G VG I P A G G Q VD F G L Q I D Q L S M F F VL I T G VG I P A G G Q VD F G L Q I D Q L S M F F VL I T G VG I P A G G Q VD F G L Q I D Q L S M F F VL I T G VG I P A G G Q VD F G L Q I D Q L S M F F VL I T G VG I P A G G Q VD F G L Q I D Q L S M F F VL I T G VG I P A G G Q VD F G L Q I D Q L S M F F VL I T G VG I F S VG F H A G W F N F D L T A I M L I V T T V S I F F N L Q VN WS I V D Q L T S M F I A V T F V S I S S MF D A S W G F I P S L T V A ML I P V L I S I S S MF D A S W G F I P S L T V A ML I P V U T S I S S MF D A S W G F I P S L T V ML I V T T S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I S S MF D A S W G F I P S L T V ML I V T F S I T T T T T L S L S F K MD Y S M F I P V A I F V T 9 I T T T T T L S L S F K MD Y S M F I P V A I F V T 9 I T T T T T S S F N S L S S K M D Y S M F I F V A I F V T 9 S Y S L S MS I L S S K M D Y S M S I F M S F V M S S M I S S S MF D A S W T I L D W S L M F S F V S L S S S F F F S C M V Y V M I L L D W S L M F I S F V L S S Z F F S S S S F D A S S F D A S S S F F F N S L S S F D A S S S F S F S S S F S F S S S S S S S
	TM3	TM4	TM5		TM6
Ecoli Kpneumoniae Tahermophilus Dradiodurans Rmarinus Aaeolicus Mutuberculosis Scoelicolor P denitrificans Rcapsulatus Rcapsulatus Rcapsulatus Rcapsulatus Rcapsulatus Rcapsulatus Rcapsulatus Athaliana 8.vulgaris	97 FLI H MI A SW MR G E E			L I G F Y T D L I G F W T D L I G F WY KN L I G F WY KN L I G F WY KSG N S E A SD KD L I G WY E Q L I G WY H C L I G WY H K L I G WY G L I G L I G L I G WY G L I G L I G L I G WY G L I	P K NG A A AMK A F V Y T P K NG A A AMK A F V Y T Y G D V F P K NG A A AMK A F Y Y T Y G D V F P K NG A A AMK A F Y Y T Y G D V F P K NG A A AMK A F Y Y T Y G D V F F K N S K A A N K A F I V K T G D L G F K N S K A A A K A F I V K T G D L G P S A T A A K K A F I V K Y G D M G P S A T A A K K A F I V K Y G D M G P S A T A A K K A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D M G P S A T A A K X A F I V K Y G D F G P S A T A A K X A F I V K Y G D F G P S A T A A K X A F I V K Y G D F G P S A T A A K X A F I V K Y G D F G P S A T A A K X A F I V K Y G D F G P S A T A A K X A I X A M I V K Y G D F G F T Y L Q A D K A A I K A M I V K Y G D F G T L Q A D K A A I K A M I V K Y G D F G T L Q A D K A A I K A M I V K Y G D F G T L Q A D K A A I K A M I V K Y G D F G T L Q A D K A A I K A M I V K Y G D F G T L Q A D K A A I K A M I V K Y G D F G T L Q A D K A A I K A M I V K Y G D F G T D A T A L Q A I I Y K I G D I G T D A T A L Q A I I Y K I G D I G T D A T A L Q A I I Y K I G D I G T D A T A A L Q A I I Y K I G D I G T D A T A A L Q A I I Y K I G D I G T D A T A A L Q A I I Y K I G D I G T D A T A A L Q A I I Y K I G D I A T A D A N T A A L Q A I I Y K I G D A T A D A N T A A L Q A I I Y K I G D A T A C A N T A A L Q A I I Y K I G D A T C N S S A M T I I M K I G O F F A I C N S S A M T I I M K I Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C N S S A M T I I M K Y G D F A I C
	TM6	Т	M7a *	TM7b	TM8
Ecoli Kpneumoniae Tihermophilus Dradiodurans R.marinus Aaeolicus S.coelicolor P.denitrificans R.prowazeki C.reinhardtii N.crassa Yiloptytica P.pastoris A.thaliana B.vulgaris N.tabacum T.aestivum X.bevis G.gallus S.scrofa B.taurus H.Sapiens Aurita D.melanogaster A.pinalis	181         LAFALFILYNELGTLNFREMVELAP           181         LAFALFILYNELGTLNFREMVELAP           182         FLIGTLYNELGTLNFREMVELAP           196         FMLGMFLLYNELGTLNFREMVELAP           196         FMLGMFLLYKLYGTLSIFELAGOAA           186         FLLAMFLLFREVGSLDFGALLADPA           186         FLLAMFLLFREVGSLDFGALLADPA           186         FLLAMFLLFREVGSLDFGALLADPA           187         FLGITYSFVLFKTLEITOIFPKVE           188         FALGITGIYWLTGSVQFDEIFRQVP           183         FLGITGIFFYVLTGSVQFDEIFRQVP           183         FLGITGIFFYVLTGSVQFDEIFRQVP           183         FLGUTTVYGSNYNYTYFALS           178         LAGGILGCFTLFQTVDFSTIFACAS           178         LAGILGCFTLFQTVDFSTIFACAS           178         LAGILGCFTLFQTVDFSTIFACAS           184         FLLAMAWLASSLMWEQQTFMINS           185         FLLAMAWFLTNLNYWDQOIFMLNN           186         FLLAMAWFLTNNNWDFQOIFMLNN           187         LAGUTAWWNYGSINFLSVLPIS           188         LISMAWVANNLNSWMQOYFMLNS           189         LAGUTAWWNYGSINFLSVLPIS           180         LINKNWNYGSINFLSVLPIS           181         LISMAWFLTNNNWDQOIFMLNN           182         LAMAWLASSLYNWNY WWNLQOYFMLNN	AHF ADG         NNMLMWATLI           2NF ANG         STILQWATLI           2NF ANG         STILQWATLI           ALPSG         VLALAGLI           STR VA         QSAIELACLI           ALPSG         VVAAAVLI           EVDKY         ALGVATWI           ALGVATWI         ALGVATWI           ALGVATMI         ALGVATWI           ALGVATMI         ALGVATWI           LAGITEMFELWEDWN AANLLGY         LISNTXIFYH           SGFVG         LI           YINSD         IATIIGII           YINSD         IATIIGII           YOPRN SWIFCN         MALNAISLICI           PYRNSWIFCN         MRLNAISLICI           PYRNSWIFCN         MRLNAITLICI           PYRNSWIFCN         MRLNAITLICI           PYRNSWIFCN         MRLNAITLICI           PYRNSWIFCN         MRLNAITLICI           PYRNSWIFCN         MRLNAITLICI           PYRNSWIFCN         LI           PYRNSWIFCN         LI           PYRNSWIFCN         LI           PYRNSWIFCN         LI           PYRNSWIFCN         LI           PYLP         LI           PYLFIS         LI           VYMFLG         VI <td>MILLGGAYGKSAQLPLQ MILGGAYGKSAQLPLQ LLFLGAYGKSQLPLT LLFLGAYGKSQLPLT LLFLGAYGKSQCPLLPLT LLFGAYGKSQCPLLPLT LLFGGAYGKSQCPLL MILLGACAKSAQVPLQ MILLGACAKSAQVPLQ LLFVGAMGKSQCPLLLH LLFIGAGKSAQLLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGAYGKSQCVLLH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLLAATGKSQCVLLGSH LLLAATGKSQCVLLGSH LLLAATGKSQCVLLGSH LLLAASGSSQCVLLSQCVLLS MIMIASLTKSQCVPMS</td> <td>T WL AD AM AG P T P V A L I T WL AD AM AG P T P V A L I T WL PD AM AG P T P V A L I T WL PD AM AG P T P V A L I T WL PD AM AG P T P V AL I T WL PD AM AG P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM A AM G P T P V AL I S WL P L AM AA P T P V S L V S WL P L AM AA P T P V S L V S WL P I M AA P T P V S L V</td> <td>A A T MU T A G VY L I A R TH G L F L MT P E V L H L 282 A A T MU T A G VY L I A R TH G L F L MT P E V L H L 282 A A T MU T A G VY L I A R S F L Y S V L P U S Y A 299 A A T MU T A G VY L V T R S F L Y S V L P U S Y A 299 A A T MU T A G VY L V T R S F L Y S V L P U S Y A 299 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G V L L V R S P L F Y A P L A X M Y T A G V L U V R S P L F Y A P L X M Y T A G Y L U L R S P L F Y A P L X M Y T A G Y L L L R S S P L I E Y S T V L L 276 A A T MU T A G VY L L L R S A N L L E Y T P T V L L 276 A A T MU T A G VY L L L R S S P L I E Y S T V L L 276 A A T MU T A G Y L L L R S S P L I E Y S T X L L 276 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A T MU T A G Y E L L R S S P L I E Y S T X L V 285 A T MU T A G Y E L L R S S P L I E Y S T X L V 285 A T MU Y A G Y F L L R S P L F Y P S A L I V 285 S T MU Y A G I F L L I R T H P F L S S N K A L T T 276 S S T MU Y A G I F L L I R T H P F L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T M Y A G I F L L I R T H P T L S N K T A L T T 276 S S T M Y A G I F L L I R T H P L A S N Y L U Y M Y Z Y Z Y L Y A G Y V L I I R S N Y N S N Y L Y L Y M Y L Y A G Y Y L U R S N Y L Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y M</td>	MILLGGAYGKSAQLPLQ MILGGAYGKSAQLPLQ LLFLGAYGKSQLPLT LLFLGAYGKSQLPLT LLFLGAYGKSQCPLLPLT LLFGAYGKSQCPLLPLT LLFGGAYGKSQCPLL MILLGACAKSAQVPLQ MILLGACAKSAQVPLQ LLFVGAMGKSQCPLLLH LLFIGAGKSAQLLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGCMGKSQCVLLH LLFIGAYGKSQCVLLH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLFIGAYGKSQCVLLGSH LLLAATGKSQCVLLGSH LLLAATGKSQCVLLGSH LLLAATGKSQCVLLGSH LLLAASGSSQCVLLSQCVLLS MIMIASLTKSQCVPMS	T WL AD AM AG P T P V A L I T WL AD AM AG P T P V A L I T WL PD AM AG P T P V A L I T WL PD AM AG P T P V A L I T WL PD AM AG P T P V AL I T WL PD AM AG P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL PD AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I T WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM G P T P V AL I P WL P AM A AM G P T P V AL I S WL P L AM AA P T P V S L V S WL P L AM AA P T P V S L V S WL P I M AA P T P V S L V	A A T MU T A G VY L I A R TH G L F L MT P E V L H L 282 A A T MU T A G VY L I A R TH G L F L MT P E V L H L 282 A A T MU T A G VY L I A R S F L Y S V L P U S Y A 299 A A T MU T A G VY L V T R S F L Y S V L P U S Y A 299 A A T MU T A G VY L V T R S F L Y S V L P U S Y A 299 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G VY L V R S G P L Y N L A P T A Q L A 286 A A T MU T A G V L L V R S P L F Y A P L A X M Y T A G V L U V R S P L F Y A P L X M Y T A G Y L U L R S P L F Y A P L X M Y T A G Y L L L R S S P L I E Y S T V L L 276 A A T MU T A G VY L L L R S A N L L E Y T P T V L L 276 A A T MU T A G VY L L L R S S P L I E Y S T V L L 276 A A T MU T A G Y L L L R S S P L I E Y S T X L L 276 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A A T MU T A G Y E L L R S S P L I E Y S T X L L 275 A T MU T A G Y E L L R S S P L I E Y S T X L V 285 A T MU T A G Y E L L R S S P L I E Y S T X L V 285 A T MU Y A G Y F L L R S P L F Y P S A L I V 285 S T MU Y A G I F L L I R T H P F L S S N K A L T T 276 S S T MU Y A G I F L L I R T H P F L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T MU Y A G I F L L I R T H P T L S N K T A L T T 276 S S T M Y A G I F L L I R T H P T L S N K T A L T T 276 S S T M Y A G I F L L I R T H P L A S N Y L U Y M Y Z Y Z Y L Y A G Y V L I I R S N Y N S N Y L Y L Y M Y L Y A G Y Y L U R S N Y L Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y L Y M Y M

## f) Subunit NuoL, part 2.

	TM9	TM10	TN	W11	
8.1487.11 I					14040180000
E.coli K pneumoniae	283 VG I VG AVTLLLAGFAAL VQ TDI KR 283 VG I VG AVTLVLAGFAAL VOTDI KR	VLAY STMSOLGYMFLALG	VQ AWD AAT FHLMTHAFF	FRALLELASGSVILACH	5 1 372
T.thermophilus	270 I AVVGLLTAAYGALSAFGQTDIKK	VAY STISQLGY MFLAAG	VG AY WVAL FHVFTHAFF	F	HL 359
D.radiodurans	300 VAWVGGLTALYGALSALNQHDIKK	ILAY STVSQLGYMFMAVG	LG AY SAGVEHL LTHAFF	F K ALL F L C AG AV I H AL H E E Q D V R AMG G MR R I	FM 389
R.marinus	285 VALVGALTAFMAATIAVTQYDIKK	VLAY STVSQLGY MFMAAG	VG AFFVSIFHVLTHAFF	FKACLFLGSGSVIHAMHHVEHTLHERGHHGHLDPQDMRNMGGLGR I	FM 389
M.tuberculosis	287 VVIVGAVTLLFGALIGCAKDDIKR	ALAASTI SOLGY MYLAAG	LG PAGY AF ALMHELTHGFF	FRAGLELGSGAVIHAMH	AL 378
S.coelicolor	288 VTIVGAVTLLFGAIVGCAKDDIKK	A L A G S T M S Q I G Y M V L A A G	LGPIGYVFAIMHLVTHGFF	F K AG L F L G AG S V M H G M N D E V D M R R Y G G L R K '	YM 379
P.denitrificans	292 I VIIGATTAFFAATVGLVQNDIKR	VIAY STC SOL GYMFVAAG	VG VY SAAMFHLLTHAFF	F K AML F L G AG S V I H AMH H E Q D MR N Y G G L R K I	KI 381
R.capsulatus R.prowazekii	292 VVYVGAVTAFFAATVGLVQNUTAK	LIAY STC SOL GYMENACG	VS SYNSALFHL VTHAFF	FRANLFLGAGSVIHAMH	KI 381 KM 377
C.reinhardtli	267 VIIVGSLTAFMAGVEGATQSDLKR	VIAY STC SOLGY MMV SLG	L G E T G G E A S MGH L M T H A S F	F KAAL FL AAGMV I SGNG	5 A 358
N.crassa	277 CLWLGAITTVF55LIGLFQQDIKK	VIAY STMSQLGMMVIAIG	LSSYNVALFHLINHAFY	Y KALLFLG AG S V I H A V A D N Q D F R K F G G L K N '	r L 366
Y.lipolytica P pastoris	280 TEWIGAL TTESAGETATCSNOL FR		US AYNLALFHLLGHAFF	FRALLEMS AGST THSTENESQDTR TYGGELS	FL 370
Athaliana	286 ITSAGAMTSFLAATTGILQNDLKR	VIAY STC SQLGY MIFACG	ISNYSVSVFHLMNHAFF	F KALL F L S AG S V I H AMS D E QD MR K MGGL AS	SF 375
B.vulgaris	286 ITFAGAMTSFLAATTGILQNDLKR	V I AY <mark>S T</mark> C <mark>S Q L G Y</mark> M I F AC G	ISNYSVSVFHLMNHAFF	F K A L L F L S A G S V I H A M S D E Q D M R K M G G L A S :	SF 375
N.tabacum	286 ITFAGAMTSFLAATTGILONDLKR	VIAY STC SOLGY MIFACG		FRALLFLSAGSVIHAMS	SF 375
X.laevis	279 CLCLGAMTTLFTAACALTQNDIKK	VAFSTSSOLGLMMVTIG	LI FQLAFFHICNNAFF	F VYY FFC S G Y S S C L N DEQDIR KMG G L Q N	5 L 367
G.gallus	277 CLCLGALSTLFAATCALTQNDIKK	A F <mark>S T</mark> S <mark>S Q L G L MM V T I G</mark>	LD LPQLAFLHISTHAFF	FKAMLFLCSGLIIHSLNGEQDIRKMGCLQK	TL 366
S.scrofa B.tounur	277 TLCLGAITTLFTALCAITQNDIKK	VAFSTSSOLGLMMVTIG	IN QPHLAFLHICMHAFF	FKAMLEMCSGSTTHSLN	AM 366
H.sapiens	277 TLCLGAITTLFAAVCALTONDIKK	VAFSTSSQLGLMMVTIG	IN QPHLAFLHICTHAFF	FRAMLEMCSGSTINSEN	TM 366
Aaurita	274 TALVGSITALFAATIGLAQNDIKK	I I AY STC SOLGFMVLSCG	ISYYSVALFHLVNHAFF	FKALLFLGAGSIIHSML ······DEQDIRKMGGINI ···	TQ 363
D.melanogaster	244 MLLLSGLTMFMAGLGANFEFDLKK	I I ALSTL SOLGLMMSILS	MG FLKLAMFHLLTHALF	F KALL FMC AG AT THNMN N SQD I R LMGGL S I G I I	HM 335
Celegans	245 LMVLSVLTMFMAGLGACFEFDLKK	I ALST LSOLGLMMFSLS	MG MVKIALFHLLMHALF	FRALLEMS AGE VINGY KG	- L 334
C.oncophora	230 MLLIGVFTMFFSSITALVEEDMKK	VVALSTLSQMGFSMLTLG	LG LSFISFVHLVSHALF	FKSCLFMQVGYLIHCNX	FP 319
T.spiralis	233 LIVVGLLTSLYASLMAFFEFDLKK	I LAY STMSQVAMVMLMLL	SG MY SLMVMHIVNHALV	V K ALL EMN VG I I MSY MF ANQE VR MV TC VGY N -	- V 322
	THID	THEAT			
	TM12a	TM12b		TM13	
E.coli	373 PLVYLCFLVGGAALSALPLVT	·····AGFFSKDEILA	GAMAN GHINLMV	AGLVGAFMTSLYTFRMIFIVFHGKEQIH	444
T thermophilus	3/3 PLVTVCFLVGGAALSALPLTT	SGEWSEDALLA	ATL TYPE GGVGEYVC	GALL VAVI TAMY AMRWEVI VELGEERGH	432
D.radiodurans	390 P F T H V A A L MG V L A I S G I P I W		A A WAQ S P WLY V	IGLG VALL TAFY MGR WY FL VWR GEYR GQ V	460
R.marinus	390 PATRTTYLIATLAIAGFPLT	•••••• AGFF <mark>SK</mark> DEILF	K A F E Y G Y N G H A Y A W I A W I I	LG V V T A L L T A F Y MMR SY V L T F E G T P R W P M A D Q	470
Alaeolicus Mitubarculorir	372 PVTYVAFMIGALSLAGVFPFS	GEEEVOALLE	SMY EWSG VLGV	LGTIVAFITAYYAFHEGFLVFHGRERWREIYD	· · 445
S.coelicolor	380 PVTFVTFGLGYLALIGFPGL		AAFAKGG TEGWILGAG	CALLGAAITAY YMTRVMLMTFFGEER WRNAPTPSPAKPDVEPAAETR	GT 474
P.denitrificans	382 PLTEWAMMIGTEAITGVGIPLTHL	G F A G F L <mark>S K D</mark> A I I E	S AY AG	VL L V I A A C F T S F Y S W <mark>R</mark> L I F L T F Y G K P R G D H H A H	461
R.capsulatus R.capsulatus	382 PFTFAIMMIGTLAITGVGIPFFSI	G V P V G F AGY L S KD A I I E	SAFAS GNGFAFY	VLVAAAGMTSFYSWRLIFLTFYGEARGDHHKH	467
C.reinhardtii	359 MFTMLTLMVASLSLIGWPELS	GFYSKETILN	LAAICADP IADVAHTI	LLLLTAMLTS AY TTKLFYQC FMVDFSGSSVTP	- 436
N.crassa	367 PLTYSVMLIASLSLVAFPYM	T <mark>G F Y <mark>S K</mark>D F I L E</mark>	SAYGQFS FSGVAVY I	I AT I G A I F T T L Y S V K V L Y L T F L AN PNGY I H F Y R H F I L Y E R L Y V Y V S Y	TG 461
Y.lipolytica	371 PYTYICITIASLSLMAMPGL	TO EVEN DILLE	STYGSYSISNYVVYW	VI AY L S AVL TC VY SMKILY L TFY SN PNNNT I TY	448
P.pastoris A.thaliana	368 PLATICIFIASESLMATPGL	TGFYSKDVILE	L AY T KY T I SGN F A F WI	VIGSVSVLFTSVVSFRLLFLTFLVPTNSFGRDI	- 445
<b>B.vulgaris</b>	376 PFTY AMMLMGSLSLIGFPFL	· · · · · · · · TGFYSKDVILE	LAYTKYT ISGNFAFWI	VLGSVSVLFTSYYSFRLLFLTFLVPTNSFGRDI	453
N.tabacum	376 PFTYAMMLMGSLSLIGFPFL	· · · · · · · · TGFYSKOVILE	L AY T KY T I S G N F A F WI	VLGSVSVLFTSYVSFRSLFLTFLVPTNSFGRD1	453
T.aestivum X Iaevis	376 PLTY AMMLMGSLSLIGFPFL	AGEES FOALLE	LAYTKYTISGNFAFWI	1 T I I AT SET A I V SED VI EE ASMGH DR SN DI SP	453
G.gallus	367 PMTTSCLTIGNLALMGTPFL	AG F Y S KD L I I E	NLNTSYIN TWALS	LTLLATSFTATY SLEMTLLVQTGHTRTPAITP	442
S.scrofa	367 PFTTTALIIGSLALTGMPYLT	G F Y <mark>S K</mark> D L I I E	AANMSYTN AWALLM	MTLIATSLTAAYSTRIIFFAFLGQPRFPPLVL	442
B.taurus H.saniens	367 PETTTALIVGSLALTGMPELT	GEV SKOLITE	AANTSYTN AWALLA TANMSYTN AWALS	MTLIATSFTATYSTRIIFFALLGQPRFPTLVN	442
A.aurita	364 PISYVFIVIGSLSLAGFPFM	AGYY SKOLLLE	LSSQKYFVIFGFW	VLG I F AT L L T A L Y S F K L I L R S F L Q F Q N S P K I Y W	439
D.melanogaster	336 PLTSACFNVSNLALCGMPFLA	G F Y <mark>S K D</mark> M I L E	I V S I S N V N M F S F F I	LYYFSTGLTVS <mark>Y</mark> SF <mark>R</mark> LVYYSMTGDLNCGSLNM	411
A.pisum C elegans	320 PECGLIEMETLMSLCGEPEEC	GEV SKOL I FE	Y FLMMNLN FFFFF		395
C.oncophora	320 LFMQVQLLVTLFCLCGLIFSS		LFFLNNN YLLLSL	LFFVSIFLTFGYSYR LWKSLFVNFLKVXNNYS	395
T.spiralis	323 G F V L G S V I L C L V V M C G L T F T S		L S I K E D T L F H I	IL VN V V L F M S V M Y S L R M I Y V L MG G L S G K V F L N C	395
		*			
		TM14		TM15	
E.coli	445 AHAVK	GVTHSLPLIVLLILSTFV	G A L I V P P L C	QGVL PQTTEL AHGSMLTLEITSGVVAVVGILL	A A 509
Kpneumoniae	445 • • • • • • • • • • • • • • • • • •	GITHHLPLIVLLVLSTFV	GALIVPPLE	EGVLPQTTELAHGSVMTLEIASGIIAIAGILI	A A 509
T.thermophilus D.radiodurans	433	A P P V M L W P N H L L A L G S V L A D G L M R F P L G V L A A L A T L	GGELNIPAELPSIGI P	E P F L	LL 503
Rmarinus	471 · · · · · · · · · · · · · · · · · · ·	SPATMTLPLWVLAALSLV	GGFVGLPGVIAHGEWNLIF	HHYLGAS · · · · · · · · · · · · · · · · · · ·	L 1 550
A.aeolicus	446 • • • • • • • • • • • • • • • • • •	V E G V M T V P M G L L G F L T V L	TGLFGLWLEHWYVG	L I G G E E K G I H L S V A L V S L G V A I A G I W L	PW 511
M.tuberculosis	455 · · · · · · · · · · · · · · · · · ·	A P A VMTWPMILLAVGSVF	SGGLLAVGGTLF	RHWLQPVVGSHEEATHALPTWVATTLALGVVAV	G I 523
P.denitrificans	462 DH AH E	SPPVMTIPLGVLAIGAVE	AGMVWYGPFFGDHHK V1	T E Y F H I AG AH H E A A E G E E A E H A T A E A P V E H A V A D T A T A E G E A A A E A E I	H A 549
<b>R</b> .capsulatus	468 · · · · · · · · · · · · · · · · · · ·	S P A V M L A P L A L <mark>L</mark> A V G S V L	AGMVWYHSFFGDKVASFF	N L P A A A H G E A H G T E H A T E G H V P E A A M T A E A A H E A A M A G T M A M A E P A A	EH 557
R.prowazekii	452 KH AH E	P T K I MN N P L I L L V AG S F F	SGMIGYYLLSMDKPNGYFF	HESLFNLHIYKLLINHHPLYIKLLPMAVGIVGIII	GI 529
N.crassa	462 KEEFYLPKHMSKEINNLPRSVSGE	GGFFLSLPLVILALFSIF	FGFITKDIFIGLGSNFFIL	DNSLFIHPIHEIMIDTEFAVPTLFKLLPFIFTISFSLI	AL 561
Y.lipolytica	449 • • • • • • • • • • • • • • • • • •	S N I Y I T L P M F I <mark>L</mark> A I F A M F	AGWILKDIYLGVGTDFVGT	THILPNNFSYFDTEFSITQFYKLLPLISAILVSIL	IV 526
P.pastoris	446 · · · · · · · · · · · · · · · · · ·	NDIVLITPMIILTILSIF	GGYLLRDIYLGMGSP FN	NELFIHPN NLSLIETEFSLPSILKVLPLITGLGGGLI	LL 523
A.thailana B.vulgaris	454	APIPMAIPLILLALGSLF APIPMAIPLILLAFGSIF	VGYLAKDMMIGLGTNFWAM	NN SLLYLF	AY 533
N.tabacum	454 · · · · · · · · · · · · · · · · · ·	APIPMAIPLILLALGSLF	VGYLAKDMMIGLGTNFWAN	NSPFVLPKNEILAESEFAAPTITKLIPIPFSTSGAYV	AY 533
T.aestivum	454 · · · · · · · · · · · · · · · · · ·	APIPMAIPLILLALGSLF	VGYLAKDMMIGLGTNFWAM	IN S P F V L P K N E I L A E S E F A A P T I T K L I P I L F S T S G A S L	AY 533
G.gallus	443 · · · · · · · · · · · · · · · · · ·	NTPPAILPIMRLALGSIN	AGLLISSLILP	PKTPPMTMPTLAKQAATTVSVTGLT	AL 502
S.scrofa	443 · · · · · · · · · · · · · · · · · ·	NNPLLINSIKRLLIGSIF	AG F 1   S N N   P P		AL 502
B.taurus	443 · · · · · · · · · · · · · · · · · ·	NN P L L I N S I KR L L I G S L F	AGY 1   SNN   P P	TTIPQMTMPYYLKTTALIVTILGFIL	AL 502
H.sapiens A aurita	443 INE	NN PTLLN PIKRLAAGSLF	AGELIENP	TINNAVH DI DVSIKI DI DVSIKI DI VTACCTT	AL 502
D.melanogaster	412 · · · · · · · · · · · · · · · · · · ·	ESWIMLRGMMGLLIMSII	GGSMLNWLIFP	FPYMICLPIYMKLLTLFVCIVGGLF	GY 470
A.pisum	396 • • • • • • • • • • • • • • • • • • •	E S K I L I I S MM F I S F I M L F	FG S F F MWL MFY	KFDLILLEFKFKILSVLILFFSIWF	FF 455
Celegans	411 · · · · · · · · · · · · · · · · · ·	G WG L MM K S C V G L V V F S V F	FGALISWLVMD	ATLVSLPIHLKNLTLTVCFLGVIL	0 5 468
Concophora	370			- LEFT FE STELET BET SELECTION	

## f) Subunit NuoL, part 3.

	HIa	HID
E.coli	510 WLWL	LNSMM 569
K.pneumoniae	S10 WLWL GKRTLVTSIANSAPGRFFGTWWFHAWGFDWLYDKVFVKPFLGIAWLLKRD P	LNSLM 569
T.thermophilus	504 G WA G LWA G F VEF POR KV F PARYLAF E AAS REAFY VDR AY NALL I VN PL KALAE AL FYGD - RG	LLSGY 564
R.marinus	531 GLY WS WT AY REGLAY DDML & REFGATY & WAAKYY WO FY DRAIL VOPLL & FANGLAAFDO - KY	IDGAV 619
A.aeolicus	512 P VY V K	FIDGI 572
<b>M.tuberculosis</b>	524 A V A V R	VDGSV 587
S.coelicolor	546 A VAW	VDGVV 608
Reapsulatus	500 ELAR PUGGATI MIEDANI MUEANTAFAWAVSEPFAMVLGETTAWIETTANSEPRELANQUPALIRELENKWEFDETEFIFVREAKWEGREGKEWEGDG - AV	1 D G A 1 664
R.prowazekii	530 CLYKGSLSVQTLTNES	DRFGP 607
C.reinhardtii	492 A A V G	GL 538
N.crassa	562 VLSEK	ELLGP 626
Y.lipolytica P.pastoris	527 VINEF FAIVPNLINKYTNTYTSTPNQKLVSDQTLINHTTPKGLVTSQNTANHVDK.GSL	01 EGP 589
A.thaliana	534 N VN P	EILGP 599
B.vulgaris	534 N VN L	EILGP 599
N.tabacum	534 N VN P - · · · · · · · · · · · · · · · · · ·	EILGP 599
T.aestivum X Ianuir	534 N VN L VADQLQR AFQT STFCNR LY SFFNKR WFDQVLNDFL VR SFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFLR FGY SVSFE ALDRGA N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR N TY VNDGVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR WFDQVLNDFL VR SFFNKR N TY VNDGVLNDFL VR SFFNKR N TY VNDFL VR SFFNKR N TY VNDFL VR SFFNKR N TY VNDFL VR SFFNKR N	ETLGP 599
G.gallus	S03 ELSS	K K MG P 563
S.scrofa	503 ELNN	ETILP 563
B.taurus	503 E I S N MT K N L K Y H Y P S N A F K F S T L L G Y F P T I MH R L A P Y MN L S M S Q K S A S S L L D L I W L	EAILP 563
H.sapiens	503 DLNY - LTNKLKMKSPLCTFYFSNMLGFYPSITHRTIPYLGLLTSQNLPLLLLDITWL	EKLLP 563
D.melanogaster	JULE W TELEW TELEVIS START OF DATION TO A THE AND THE THE AND	Y FGGO 533
A.pisum	456 E L N N	YNFNS 516
C.elegans	469 F M S K S S Y N F S T F N F E WM V WM S G S MW F L P Y 1 S S Q P L V Y L P L T A G G A V S S L G D L G - WL	ELLGG 528
Concophora	446 IF 5Y - FVY KILFKELIY KFLVDY FAKNVIY KVKNLKFLDLWLNKIG	- FYGF 494
r apriaita	THE FER.	400
	HID TM16	
E.coli	570 N I PAVLSR FAGKGLLL - SENGY LR WY VASMS I GAV V VLALLMVLR	613
K.pneumoniae	570 N I P A I L S R F A G K G L L V - S E N G Y L R WY V A S M S I G A V V L A L L M V L R	613
T.thermophilus	565 FGLGGAARSLGQGLAR·LQTGYLRVYALLFVLGALLLLGVMRW-	606
D.radiodurans B marious	596 SG VARNAG AF GALFAR - NQ SG Y KAYALSM VLG TALI IG Y WALKMIGR GG I	645
A.aeolicus	53 VN ATY PIVELLG SVLKFF ON GRISWY VMGLATGLTIVLIFAITIRGGL	622
M.tuberculosis	588 N A L A T L V S Q T S N R L R Q - MQ T G F A R N Y A L S M L V G A V L V A A A L L V V Q L W	633
S.coelicolor	609 NG TAAS VGGLSGR MRR - LQNG FAR SY AVS MFGGAALL VAATLLMRAV	654
P.denitrificans R capsulatur	657 NG VAMGLIPRLTRAAVR VQSGYLFHYAFAMVLGIVGLLIWVMRGAH	703
R.prowazekii	608 NGFARVINYFCAVTCK-IOTGYIFNYTLYIVSFIVTISYFVLKNIY-	653
C.reinhardtii	539 L 5 V G N L R A	546
N.crassa	627 FGLEKVLIKWSKDIAS - LSTSIVTNY ALFILVGFILY VFTFISLLEGGLDLNLSLFILLLSLTSSTSSDSKEGKMIKKAV VSTKNKNIR	715
Y.lipolytica B postoric	590 VG INRLLNKASYNVIN - LSSNTRSSLSMNSMIILITIVSLLLVVVVVNVNFIIVIPVLISILYILFS	655
A.thaliana	500 YG SY TFRELAER ISO - LOSGF Y I YA FA MULGI TLF Y TFFC MWD SLSSW YD NR LSF I LI VSSFY TKSSOE	669
<b>B.vulgaris</b>	600 YG I SY TFR R L A ER I SQ - LQSG F VY HY A F AML LG L T L F V T F F C MWD F L S SW VD N R L S F I WI V S S F Y N N K S SQ E	670
N.tabacum	600 Y G I SY T FR R L A ER I S Q - L Q S G F VY H Y A F AML L G S T L F V T F S R MWD S L S S W V D N R S S F I WI V S S F Y N N K S S Q	669
Laestivum	600 Y G I SY TERRIAER I SQ - LQSG SVY HY AF AMLLGS TPFYTESR MWD SLS SWVD SR SS FILL V SS FLINKS SQE	670
G.gallus	305 QUMYNQQEPMIKITIN TQQQLIKITLIELMISATTTLE 564 EGLANLHITMIKISTT-LHTGLIKSYLGSFALTILTTILLIOK	605
S.scrofa	564 KTTSFIQMKMSIMVSN - QKGLIKLYFLSFLITIMISMMLFNYHE	606
B.taurus	564 KTISLAQMKASTLVTNQKGLIKLYFLSFLITILISMILFNFHE	606
H.sapiens A aurita	564 KTISQHQISTSIITST-QKGMIKLYFLSFFFPLVLTLLLIT-	603
D.melanogaster	200 RUNDINIYRTSSTISSIUSULTNTAITTILFESLFTLEFG- 534 HUYOKLSMYSKTIFLMHNNSLKIYLLLEFVENILLILLEFVENSLY-	605
A.pisum	517 GLIFFLKKMIGFSQNIFLNSYKVYILLFFLWFLIILLFNY	556
C.elegans	529 QG AN K S L MNY S L G L Q S - MS S S G L K V F I L V MWV V V I F ML F F	567
Concophora	495 NWIGMISNNFSYFMSTFKYNNVIFLIFLIFLL	527
i.spiralis	MAAFISFAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	518

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