# NamPRT and NNMT - key drivers of NAD-dependent signalling

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## Summary

Keywords

Highlights

### Introduction

NAD metabolism represents one of the most critical links that connect cellular signal transduction and energy metabolism. According to Kyoto Encyclopedia of genes and genomes KEGG (http://www.genome.jp/kegg/) approximately 25% of all biochemical reactions use NAD(P), mostly in redox reactions in which NAD(P)+ and NAD(P)H are reversibly interconverted. On the other hand, various signalling processes consume NAD+ by cleaving the molecule to nicotinamide (Nam) and ADP-ribose (Verdin, 2015). NAD+-dependend signalling reactions include poly- and mono ADP-ribosylation, NAD-dependent protein deacylation by sirtuins as well as the synthesis of calcium mobilizing molecules such as cyclic ADP-ribose (Opitz and Heiland, 2015). These NAD+-dependent signalling processes participate in the regulation of virtually all cellular activities. The enzymes involved in these processes are sensitive to the available NAD+ concentration (Ruggieri et al., 2015), which in turn is dependent on the NAD+/NADH redox ratio. Therefore, NAD+-depending signalling can act as a transmitter of changes in the cellular energy homeostasis, for example, to regulate gene expression or metabolic activity (Koch-Nolte et al., 2009).

The significance of NAD+-dependent signalling for NAD homeostasis has long been underestimated. However, it has now been established that inhibition of NAD biosynthesis in mammalian cells leads to a rapid decline in NAD concentration suggesting that NAD+-dependent signalling consumes substantial amounts of NAD (Ref?), that is why we later refer to them as NAD-consuming reactions. As it has been shown that NAD concentrations change in a circadian manner (Nakahata et al., 2009; Ramsey et al., 2009), the cellular NAD-pool is turned over at least once per day. To maintain the NAD concentration at physiological levels, NAD biosynthesis needs to proceed at an equally rapid rate. Imbalances in NAD-homeostasis have been linked to various, in particular, ageing-related diseases such as diabetes, neurodegenerative disorders and cancer (Chiarugi et al., 2012; Verdin, 2015). Various recent studies have demonstrated impressive health benefits of dietary supplementation with intermediates of NAD biosynthesis including NMN and nicotinamide riboside, NR (Belenky et al., 2007). Apparently, the exploitation of NAD biosynthetic routes, in addition to the use of nicotinamide as precursor (Fig. 1), results in increased NAD concentrations that stimulate NAD-dependent signalling processes, in particular, protein deacetylation by sirtuins.

In mammals, NAD biosynthesis predominantly relies on nicotinamide (Bogan and Brenner, 2008), a form of vitamin B3, as precursor. In the first step, Nam is converted to the mononucleotide, NMN by Nam phosphoribosyltransferase (NamPRT) using phosphoribosylpyrophosphate (PRPP) as co-substrate. The key role of this enzyme is related to the nature of NAD-dependent signalling reactions, namely, that in all these reactions Nam is cleaved off and potentially lost. If the released Nam were not recycled into NAD biosynthesis, humans would require a much higher daily vitamin B3 intake than the 15mg that are the current daily recommendation (ref). The nearly complete recycling of Nam is achieved by an extraordinary high affinity of NamPRT to Nam, the Km being in the low nM range (Burgos and Schramm, 2008). Despite the importance of its salvage, Nam can also be marked for excretion by methylation. Indeed, the presence of nicotinamide N-methyltransferase (NNMT) in vertebrates (Gossmann et al., 2012) is among the most enigmatic and counterintuitive features of NAD metabolism. Why is there one enzyme (NamPRT) seemingly optimized to recycle even the faintest amounts of Nam back into NAD synthesis, while at the same time there is another one (NNMT) that seems to have no metabolic function other than to remove Nam from NAD metabolism? This puzzle becomes even more intriguing when considering that the majority of lower organisms and plants deaminated Nam to nicotinic acid (NA) before it can enter NAD biosynthesis via the Preiss-Handler pathway (Fig. 1). Previous phylogenetic analysis show that the two Nam recycling pathways are both ancestral showing a scattered distribution in bacteria (Gazzaniga et al., 2009). In contrast, NNMT has so far only been found in animals (Gossmann et al., 2012). But analysis of the eukaryotic evolution pathway evolution has previously been limited by the low number of available genome sequences. A comprehensive evolutionary analysis is, however, needed to fully understand the phylogeny of NAD metabolism, in particular, Nam metabolizing enzymes and their relationship to signalling pathways.

This may also help to unravel, how biosynthesis and signalling are coupled and influence each other, as this is not well understood so far. It is widely assumed that a major driving force of NAD-consuming signalling reactions is the cellular NAD concentration. On the other hand, most enzymes using NAD in signalling reactions that have been characterized in detail, especially most sirtuins and PARPs, are subject to inhibition by nicotinamide (Borra et al., 2004; Ko and Ren, 2012). Thus, to promote NAD-dependent signalling reactions, the balance between elevated NAD levels and accumulating nicotinamide concentrations needs to be kept such that the inhibitory effect of Nam does not override the kinetic stimulation by high NAD levels. Given the complex nature of the NAD metabolome, it is not trivial to predict the optimal conditions for efficient NAD dependent signalling. However, it is obvious that Nam-converting enzymes must play a key role in this regard.

In the present study, we have conducted a comprehensive phylogenetic analysis of the genes that encode Nam-converting enzymes. The most surprising result was that with the emergence of deuterostomes, there has been a strong selection for the co-existence of NamPRT and NNMT. Moreover, this selection for the co-existence of NamPRT and NNMT was accompanied by a marked increase in the number of genes encoding NAD-consuming signalling reactions. To explain this observation, we build a kinetic model of NAD metabolism based on available kinetic parameters. This mathematical model provided a powerful tool to analyse the relationship between NAD biosynthetic and signalling fluxes when different subsets of Nam-utilizing enzymes are present. The model demonstrated that NNMT has a critical role to maintain high NAD consuming signalling fluxes by preventing accumulation of inhibitory Nam. At lower Nam concentrations, the impact of NNMT is minimal, because of the very high affinity of NamPRT. Taken together, our analyses suggest that the co-existence of NamPRT and NNMT has been a prerequisite to enable the evolutionary development of versatile NAD-dependent signalling mechanisms present in vertebrates.

## Results

As shown in Fig. 1,

Even though the latter pathway seems to be very inefficient, it is the pathway preferentially used by most bacteria, fungi and plants (see Figure 2A), whereas most metazoan recycle Nam using NamPRT. Analysing the phylogeney of the NAD recycling enzymes in metazoan in more detail reveals that not only does NamPRT replace NADA, but in most organisms, especially in deuterostomia, NamPRT is found together with the NAM methyltransferase NNMT (Figure 2B). NNMT methylates Nam to methyl-Nam that is in mammals excreted with the urine, thus removing Nam from recycling. NNMT seems to have arisen *de novo* in the common ancestor of ecdysozoa and lophotrochozoa, as we could not find any gene with considerable similarity in fungi or plants. Nematodes are the only organisms where we find NNMT together with NADA without NamPRT being present. In Deuterostomia the only large class that does only have NamPRT and seems to have lost NNMT again are sauropsida and here especially birds. The reason why a lot of birds do not encode NNMT remains unclear, as the appearance is quite scattered (not shown). It might be related to the excretion system, as the product of NNMT methyl-nicotinamide is in mammals excreted with the urine. There are some species where we could not find NamPRT or NADA but NNMT, we assume that this is due to incomplete genomes in the database.

In addition to the phylogenetic distribution of the two Nam salvage enzymes NADA and NamPRT, we looked at phylogenetic diversity of enzymes catalysing NAD dependent signalling reactions. To do so we used the previously established classification into 10 different families (Gossmann et al., 2012) (For details the materials and methods and supplementary information). The numbers in Figure 2B denote the average number of NAD- dependent signalling enzyme families we found in each taxa. With the exception of cnidaria and lophotrochozoa we find in proteostoia on average 3 to 4 families, whereas most deuterostomia have on average more than 8 families with an increasing diversification of enzymes within at least some of these families (Gossmann and Ziegler, 2014).

Taken together, we found that the presence of NamPRT and NNMT coincides with an increased diversification of NAD-dependent signalling. That is surprising as intuitively, one would expect that a decrease in precursor concentration caused by the precursor removal through NNMT, should cause a decrease of NAD availability and consequently less active NAD dependent signalling. So why does the diversity of NAD dependent signalling increase and goes along with the disappearance of NADA and the coexistence of NamPRT and NNMT. Why is NADA on the other hand predominantly used in bacteria, plants and fungi even though the pathway is seemingly less efficient? Given the complexity of the NAD-metabolic network, this question is difficult to be comprehensively address experimentally. Thus, to answer these questions we built a kinetic model of NAD metabolism using existing kinetic data from the literature (details se materials and methods and supplementary material).

To be able to compare metabolic feature of evolutionary quite different systems in our simulations, and as we have limited information about expression levels of enzymes or changes of kinetic constants during evolution, we initially used the kinetic constants found for yeast or human enzymes for all systems analysed and used equal amounts of enzymes for all reactions. Wherever possible we did, however, not only include substrate affinities but also known product inhibition or inhibition by downstream metabolites. In addition, we did simulate different growth rates (cell division rates) and Nam availability (Nam import rates) as these parameters vary considerably between organisms. As we can see in Figure 3A-B the yeast-like pathway using NADA and recycling Nam via NA is superior both in terms of steady state NAD concentration and NAD consumption flux (representing the activity of NAD dependent signalling) in the absence of NNMT. In the presence of NNMT, the picture is slightly different (Figure 3C-D), even though NADA is still superior to NamPRT under most conditions. Only if Nam availability is very low, NamPRT is performing better because of its high substrate affinity. The disadvantage of NamPRT at equal amounts of enzyme, can, however, be compensated by an increased expression of NamPRT. Although, to reach similar NAD-concentrations in our model, NamPRT expression has to be 10fold higher than the expression of NADA (Figure S1). This might provide an explanation why we find NADA predominantly in bacteria, yeast and plants, organisms that show high division rates. Under these conditions protein expression costs are assumed to have a high impact on metabolic performance and thus pathways where low enzyme expression suffices, might be favourable, even though the yeast-like pathway has a lower efficiency. In addition, nitrogen is more readily available to most of these organisms, thus making the loss of nitrogen due to the initial deamination of Nam less critical.

But why do we find NamPRT predominantly in combination with NNMT, and how does this affect NAD consumption flux. When we simulate the presence and absence of NNMT in the presence of either NADA or NamPRT, we see that the impact of NNMT on NAD-concentration is quite strong in the presence of NADA but minor in the presence of NamPRT (Figure 4b and D). When we now simulate the effect on the NAD consumption flux, we see that that NNMT increases the NAD consumption flux under most conditions in the presence of NamPRT, whereas this is only true for high Nam availability in the presence of NADA. NAD consumption flux can be further increased by increasing the expression NamPRT, which also compensates the slight reduction in NAD-concentration in the presence of NNMT (see Figure S2). These effects are due to two independent properties of the pathways.

These findings can be explained when looking in more detail into the kinetic parameters of NamPRT and NAD consuming enzymes such as Sirt1p. The ability to maintain high NAD-concentration in the presence of NNMT and at low Nam availability, is due to the very high affinity of NamPRT for its substrate, having a half saturation constant (Km) in the low nM rage. The increase of NAD consumption flux, however, is caused by the fact that most NAD consuming enzymes are inhibited by their product Nam. Providing the reason why the presence of NNMT enables higher NAD-consumption fluxes.

As the substrate affinity and thus the half saturation constant Km of NamPRT for Nam is extremely high (in the low nM range) and as this might not have been the case throughout evolution, we next analysed the effect of the NamPRT-Km on NAD steady state concentration and NAD consumption flux, leaving all other kinetic parameters constant. In the absence of NNMT (Figure 5A-B) the Km has very little effect on steady state NAD concentration and NAD consumption flux. Without NNMT NAD concentration and consumption flux are both considerably affected by cell division rates at least if the enzyme expression is kept constant. This is of course an artificial scenario, as one would assume organisms to regulate enzyme expression to achieve similar levels of metabolite concentrations instead. In the absence of NNMT there appears furthermore to be a trade-off between achievable steady state NAD concentration and NAD consumption flux.

In the presence of NNMT, NAD-consumption flux and NAD concentration, increases with decreasing Km values (Figure 5A-D). And we note, that both the NAD steady state concentration and the consumption flux is relatively stable over a wide range of cell division rates even at constant expression levels of the involved enzymes, suggesting that NNMT might have an important role to maintain homeostasis of NAD-metabolism.

When we compare NAD consumption and NAD concentration with and without NNMT with two different substrate affinities of NamPRT, we see that at a Km of 100nM, which is in the range of the Km of NAPRT for its substrate, or the Km of NADA for Nam, we see that NAD consumption flux is only higher with NNMT at low cell division rates, whereas at high division rates higher NAD consumption fluxes are achieved without NNMT (Figure 5 E-F). This might explain why we do not find NNMT in organism that tend to have high growth rates. Our analysis also suggests that NNMT might have exerted an evolutionary driving force on the substrate affinity of NamPRT, explaining the extreme values found for the human enzyme.

But pathway dynamics are of course not solely dependent on one enzyme. Thus, what is the impact of the substrate affinity of NNMT that is competing with NamPRT for the same substrate? In Figure 6A we see that the substrate affinity values found in the human enzymes (indicated by the black stars) are actually optimal with respect to both achievable steady state NAD concentration and consumption fluxes. Thus, a further increase of the affinity of NamPRT for Nam would not provide any advantage.

**NAD-consumption without inhibition by Nam**

To see whether we can find evolutionary sequence variations in the protein sequence of NamPRT that indicate co-evolutionary changes of NamPRT upon the appearance of NNMT, we created a sorted alignment of a selected eukaryotic NamPRT sequence. As shown in Figure 7A (unresolved\_loop.png) and Supplementary Figure 3 deuterostomia that have only NamPRT and NNMT (indicated by the number 6 in parenthesis) have an insert of 10 amino acids corresponding to position 43 to 52 of the human enzyme. Looking at the crystal structure of human NamPRT this sequence insertion corresponds to a region that has not been structurally resolved in any of the currently available crystal structures (e.g.(Wang et al., 2006) structure visualisation Figure 7b). Tis unresolved loop structure overlaps with a predicted weak nuclear localisation signal, that is not present without the insertion. The loop is in addition connected to one of the beta-sheets involved in substrate binding, potentially affecting the affinity or turnover of the enzyme.

The observed evolutionary change in the primary sequence of NamPRT could therefore have had different effects, that we wanted to test experimentally. We first investigated whether or not the deletion of AS 43-52 has an effect on the localisation of the human enzyme. We could, however, not detect any changes in subcellular localisation (Figure 7C). Even though, it is still possible that due to dimerization and the presence of the wild type NamPRT in the experiments the deletion of the loop could not exert a dominant effect, we conclude that the partial nuclear localisation of NamPRT is not affected by the deletion.

Due to the extreme affinity of NamPRT it is very difficult to experimentally analyse potential differences in substrate affinity in the mutated enzyme….

### Comments and parts of old version not included yet

### Results:

### Most strikingly: with the emergence of NNMT in Deutersostomia NADA becomes minor 🡪 chordata: NADA disappears. These analyses also support the view that tunicates and branchiostoma are not part of the phylum chordata

In the evolutionary context and additional question arises: Why do only a few organisms, mostly less complex animals, express NADA in addition to NamPRT and NNMT. Including NADA into the simulations we see that the effect of NADA on NAD-consumption is very limited in the presence of NNMT (Figure 4F) even at high expression levels (see Suppl. Figure 1C and D) and could be compensated by increased expression of NamPRT (not shown).

Until this point we have neglected compartmentalisation of the pathway. We do however know from previous studies that in early vertebrate development a compartmentalisation of the pathway has occurred reflected by a gene triplication of NMNAT and the occurrence of compartment specific domains called ISTIDs (Lau et al., 2010). Looking at the evolutionary timepoint of appearance of NNMT and the gene triplication of NMNATs, we see that NNMT occurs prior to the gene triplication and the first occurrence of ISTIDs and we have confirmed this in our own analysis (not shown).

### Discussion

#### Evolutionary and physiological role of NNMT

The dynamic interaction between metabolism and signal transduction as well as gene regulation is still not very well understood. New approaches are required to disentangle the underlying network, helping us to understand how alterations affect human physiology. We here combine phylogenetic analysis and mathematical modelling of a central metabolic pathway supported by experimental analysis to reveal the likely evolutionary development of the NAD biosynthesis and consumption pathway and the physiological role of the methyltransferase NNMT.

We show that the vitamin B3 degrading enzyme NNMT plays a vital role for the diversification of NAD dependent signalling reactions and potentially also for NAD homeostasis. Due to the fact that NamPRT has a very high affinity for Nam whereas NNMT has a rather low affinity for it, NNMT is able to remove excess Nam that would lead to inhibition of NAD depend signalling reactions while maintaining NAD-concentrations and even increasing NAD-consumption fluxes.

The affinities measured for the human enzymes seem to be optimal and further increase in NAD-consumption rates might only enabled by compartmentalisation of NAD biosynthesis

#### General applicability

It is of course impossible to extend our conclusions to other metabolic processes without analysing them in more detail, but we have noted that the metabolism of other vitamins, such as pyridoxal (vitamin B6) metabolism, also contains vitamin degrading enzymes, that might thus have similar roles. Degrading enzymes do in general not receive the same attention as biosynthetic enzymes, reflected by the observation that NNMT has only recently been analysed in more detail, beside the much earlier recognition of NNMT as potential marker for some types of cancer (e.g. Ref?) and routine clinical measurements of urine methyl-Nam concentrations in the context of different diseases (e.g. Ref? ). Our analysis show, however, that degrading enzymes do not solely modify substrates for better excretion, but can play a vital role both in for human physiology as well as in the evolutionary development of biological processes.

#### Limitations of our analysis and outlook

Among others we neglected the potential effects of the methyl donor S-adenosyl-methionin (SAM) and its precursor methionine in our analysis, although it is most likely contributing yet another regulatory level for Nam availability and thus an additional interaction point between gene regulation and metabolism. It has been shown earlier that in turn NNMT-expression influences protein methylation dependent on methionine availability (Ulanovskaya et al., 2013). One of the challenges in the analysis of this aspect is the availability of *in vivo* concentration measurements for SAM and the large amount of reactions using it as substrate. The same holds for the analysis of enzyme acetylation versus deacetylation that would enable prediction about enzyme activation or histone state if available.

### Experimental Procedure

#### Dynamic modelling

Kinetic parameters (substrate affinity (Km) and turnover rates (kcat), substrate and product inhibitions) were retrieved from the enzyme database BRENDA and additionally evaluated by checking the original literature especially with respect to measurement conditions. Parameter values from mammals were used if available. For yeasts specific enzymes, yeast values were used. The full list of kinetic parameter including reference to original literature can be found in Supplementary table 1. For NMNAT the previously developed rate law for substrate competition was used (Schauble et al., 2013). Despite these modifications, Henri-Michaelis-Menten kinetics were used for all reactions except the import and efflux of Nam, which were simulated using constant flux and mass action kinetics, respectively. All simulations were performed using the steady state calculation and parameter scan options provided by COPASI 4.22 (Hoops et al., 2006). The model will be available at the Biomodels database accession number #. Related figures were generated using gnuplot.

#### Phylogenetic Analysis

NADA, NamPRT, and NNMT enzymes or enzyme candidates were identified using Blastp with known enzymes against the non-redundant protein sequence database (nr). A list of functionally verified enzymes used as templates is given in supplementary table 2. This table also includes the length cut-offs for identified enzymes. The e-value cut-off was 1e-30 for all enzymes. We configure Blastp to yield maximum 20000 target sequences, using the BLOSUM62 matrix with a word size of 6 and gap opening and extension costs of 11 and 1, respectively. Low-complexity filtering was disabled. Obvious sequence contaminations were removed by manual inspection of the results. The taxonomy IDs of the species for each enzyme was derived from the accession2taxonomy database provided by NCBI. Scripts for creating, analysing, and visualising the phylogenetic tree were written in Python, using the ETE2 toolkit (Huerta-Cepas et al., 2010).

#### Cloning and mutation of NamPRT

#### Cell culture conditions and fluorescence imaging

### Figure Legends

#### Figure1

***Schematic overview of NAD-biosynthesis and consumption***. NAD can be synthesized using several routes from altogether three main precursors: tryptophan, nicotinamide (Nam) and nicotinic acid (NA). Nam and NA are together known as vitamin B3 or niacin. Alternatively, nicotinamide ribose (NR) can be used omitting the energetically unfavourable reaction of Nam phosphoribosyltransferase (NamPRT), requiring nicotinamide ribose kinase (NRK) instead (Bogan and Brenner, 2008). As in humans only 1% of the tryphtophan taken up with our diet is converted into NAD, vitamin B3 and to a lower extend NR are essential components of our diet, with Nam being the major NAD precursor in humans. Nam is furthermore the product of NAD consuming signalling reactions such as sirtuins (NAD-dependent histone deacetylases) or PARPs (poly ADP robosylases).

For the recycling of Nam two different pathways exist. The pathway found in yeast and many bacteria is using a four-step pathway starting with the deamination of Nam to nicotinic acid by Nam deamidase (NADA). The other three enzymes comprise the Preiss-Handler pathway that also exists in vertebrates. The recycling pathway found in mammals directly converts Nam into the corresponding mononucleotide (NMN) a reaction catalysed by NamPRT and driven by a non-stoichiometric ATP-hydrolysis. A similar reaction catalysed by an evolutionary related enzyme NAPRT, converts NA into the NA mononucleotide. NMN and NAMN are converted into dinucleotides by the Nam/NA adenylytransferases (NMNATs). The recycling pathway via NA finally requires an amination step catalysed by NADsynthase, driven by the conversion of ATP to AMP producing pyrophosphate.

#### Figure 2

***Evolutionary distribution of NADA, NNMT and NamPRT and their relation to the number of NAD-consumer*** A) Distribution of NADA,NNMT and NamPRT in the main taxa. NADA is dominant in Bacteria, Fungi and Plants, whereas NamPRT together with NNMT is dominant in deuterostomia.

B) The circle size indicates the number of genomes analysed in the particular taxon using a logarithmic scale. The numbers below the taxon names indicate the average number of NAD-consuming enzyme families found in all sub-taxa. Only selected sub-trees are shown. In total genomes or transcriptomes of 969 eukaryotic species are included.

#### Figure ?

***Comprehensive analysis of the potential evolutionary role of NNMT and the effect of different enzyme combinations on NAD-consumption and concentration*** If NNMT is absent (A-C) NAD-consumption fluxes and NAD-concentration are very dependent on the availability of Nam (Nam efflux/import ratio). Furthermore, affinity changes of NamPRT have only very little effect on NAD-consumption flux (A) and –concentration (B) or only under specific conditions. In the presence of NNMT (D-F) NAD-consumption flux (D and F) and-concentration (E) are relatively independent on the ratio between Nam efflux and import, in contrast affinity changes of NamPRT have a large effect. The addition of NADA has very little effect (C and F), especially in the presence of NNMT (F). The substrate affinity of NNMT and NamPRT have opposite effects on NAD-consumption(G) and –concentration (H), as would be expected. The affinities previously measured for human enzymes (indicated by the white star) appears to be close to optimal as further improvements would have little or no effect on NAD-consumption or –concentration. Further improvement of NAD-consumption rates can only be achieved by compartmentalisation (I), as NNMT is localised to the cytosol, cytosolic NAD-consumption rates are lower than nuclear NAD-consumption rates if NAD-biosynthesis and-consuming reactions are present in both compartments.

#### Figure 7

***Deuterostomia that encode NNMT show a sequence insertion in the N-terminal region of NamPRT that enables nuclear localisation.***

Multiple sequence alignment of NamPRT from selected deuterostomia clearly show a sequence insertion (A) in organisms that encode NamPRT and NNMT. (Species names are given and the number in parenthesis indicates the enzyme combination encoded in these species; 3 – NADA and NamPRT, 6 – NamPRT and NNMT, 7 – NADA, NamPRT and NNMT. The nuclear localisation signal (NLS) indicated was predicted using using cNLS-mapper (<http://nls-mapper.iab.keio.ac.jp/cgi-bin/NLS_Mapper_form.cgi> (Kosugi et al., 2009)). The inserted region is not resolved in crystal structures of human NamPRT and thus appears to be a flexible loop structure at the surface of the NamPRT-dimer. The visualisation is based on a structure prediction of SWISS-MODEL (Arnold et al., 2006; Biasini et al., 2014) of the sequence of the human NamPRT (P43490) using the model 2H3D as template (Wang et al., 2006). Deleting the respective sequence insertion results in a reduced nuclear localisation of GFP-labeled NamPRT in human cell lines. images C) wildtype NamPRT is distributed between cytosol and nucleus and the deletion of the insert sequence (NLS1) does not chance the localisation of the recombinant protein.

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