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Comprehensive classification of nucleotidyltransferase fold proteins: identification of novel families and their representatives in human

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ABSTRACT

This article presents a comprehensive review of large and highly diverse superfamily of nucleotidyltransferase fold proteins by providing a global picture about their evolutionary history, sequence-structure diversity and fulfilled functional roles. Using top-of-the-line homology detection method combined with transitive searches and fold recognition, we revised the realm of these superfamily in numerous databases of catalogued protein families and structures, and identified 10 new families of nucleotidyltransferase fold. These families include hundreds of previously uncharacterized and various poorly annotated proteins such as Fukutin/LICD, NFAT, FAM46, Mab-21 and NRAP. Some of these proteins seem to play novel important roles, not observed before for this superfamily, such as regulation of gene expression or choline incorporation into cell membrane. Importantly, within newly detected families we identified 25 novel superfamily members in human genome. Among these newly assigned members are proteins known to be involved in congenital muscular dystrophy, neurological diseases and retinal pigmentosa what sheds some new light on the molecular background of these genetic disorders. Twelve of new human nucleotidyltransferase fold proteins belong to Mab-21 family known to be involved in organogenesis and development. The determination of specific biological functions of these newly detected proteins remains a challenging task.

INTRODUCTION

Nucleotidyltransferase (NTase) fold proteins constitute large and highly diverse superfamily of proteins (1). Almost all known members of this superfamily transfer nucleoside monophosphate (NMP) from nucleoside triphosphate (NTP) to an acceptor hydroxyl group belonging to protein, nucleic acid or small molecule. They are characterized by the presence of common α/β-fold structure composed of three-stranded, mixed β-sheet flanked by 4 α-helices with αβαβαβα topology. This common core corresponding to minimal NTase fold structure is usually decorated by various additional structural elements depending on the family (Figure 1). Sequence analyses of distinct members of this large superfamily revealed common sequence patterns that include conserved active site residues: hG[GS], [DE]h[DE]h and h[DE]h (h indicates a hydrophobic amino acid). Three conserved aspartate/glutamate are involved in coordination of divalent ions and activation of acceptor hydroxyl group of the substrate. Two of them (from [DE]h[DE]h motif) are located on the second core β-strand, while third carboxylate (from h[DE]h motif) is placed on the structurally adjacent third β-strand. The hG[GS] pattern is placed at the beginning of short, second core α-helix and have a crucial role in harboring of substrates within the active site (1).

Known members of NTase fold superfamily contribute to many important biological functions, such as: (i) RNA polyadenylation, (ii) RNA editing, (iii) DNA repair,

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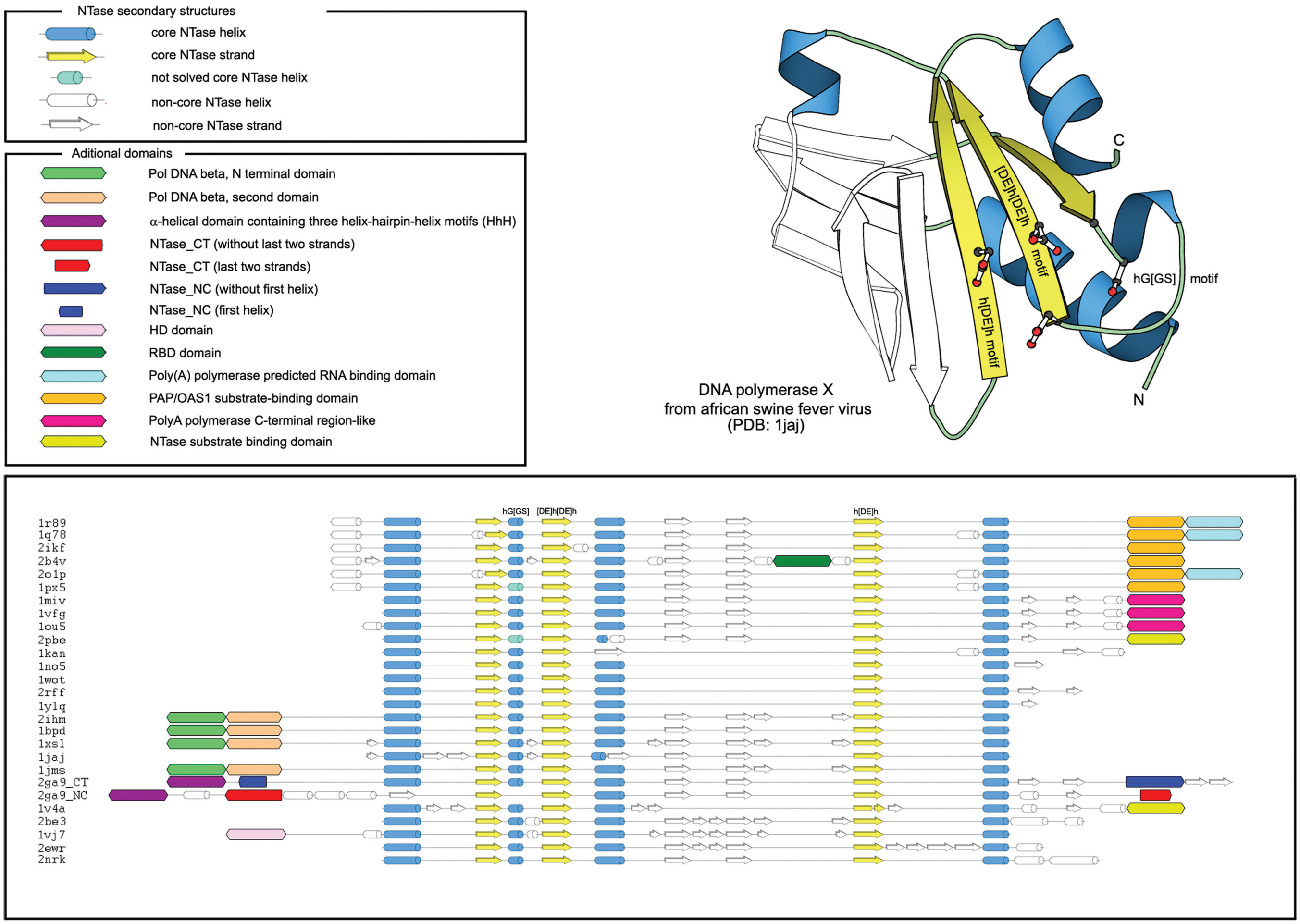

NTase secondary structures
core NTase helix
core NTase strand
not solved core NTase helix
non-core NTase helix
non-core NTase strand
Aditional domains
Pol DNA beta, N terminal domain
Pol DNA beta, second domain
α-helical domain containing three helix-hairpin-helix motifs (HhH)
NTase_CT (without last two strands)
NTase_CT (last two strands)
NTase_NC (without first helix)
NTase_NC (first helix)
HD domain
RBD domain
Poly(A) polymerase predicted RNA binding domain
PAP/OAS1 substrate-binding domain
PolyA polymerase C-terminal region-like
NTase substrate binding domain
C
[DE]h[DE]h motif
hG[GS] motif
h[DE]h motif
N
DNA polymerase X
from african swine fever virus
(PDB: 1jaj)
hG[GS]
[DE]h[DE]h
h[DE]h
1r89
1q78
2ikf
2b4v
2o1p
1px5
1miv
1vfg
1ou5
2pbe
1kan
1no5
1wot
2rff
1y1q
2ihm
1bpd
1xsl
1jaj
1jms
2ga9_CT
2ga9_NC
1v4a
2be3
1vj7
2ewr
2nrk

Figure 1. NTase fold superfamily structures. An example of NTase fold structure is presented together with the observed variation of secondary structure elements and additional domains in representative superfamily proteins of known structure. Positions of conserved active site motifs involved in catalysis ([DE]h[DE]h, h[DE]h) and substrate binding (hG[GS]) are marked above corresponding secondary structure elements. Side-chains of critical motifs residues (aspartates and serine) are shown as balls and sticks. Suffixes '_CT' and '_NC' refer to catalytic and non-catalytic NTase domains.

(iv) chromatin remodeling, (v) somatic recombination in the B cells, (vi) regulation of protein activity, (vii) antibiotic resistance and (viii) intracellular signal transduction (1,2). Specifically, they can bind and modify RNA (functional groups i-ii), DNA (iii–v), proteins (vi–vii), aminoglycosides (viii) and NTPs (viii). Proteins belonging to these functional groups are described shortly below.

PolyA polymerases (PAPs) play a central role in posttranscriptional modifications of pre-mRNA by adding few or few dozens of adenosine monophosphates to its 3′-end (i). This modification protects maturated mRNA against degradation from its 3′-end. CCA-adding enzymes (CCases) and Terminal Uridil Transferases (TUTases) participate in RNA editing (ii). CCases catalyze non-template dependent transfer of two CMPs and one AMP onto the 3′ terminus of immature tRNAs. Adding triad of nucleotides by CCases is necessary for subsequenct aminoacylation and further interactions of tRNAs with the ribosome during protein synthesis (3). TUTases take part in insertion of uridine monophosphate in various RNAs and may have different specific functions. TUTase 1 (RET1) is a processive transferase involved in uridylylation of guide RNA (gRNA), while TUTase 2 (RET2) modifies mRNA by gRNA-dependent insertion of uridine (4,5). Various NTase fold proteins are involved in DNA processing by participating in DNA repair, chromatin remodeling or somatic recombination (iii–v). Specifically, polymerases Pol β, Pol λ, Pol μ and terminal deoxynucleotidyl-transferase (TdT) take part in numerous DNA repair processes (6). Pol λ and Pol μ fill shorts gaps in a template-dependent manner, while Pol μ has ability to catalyze template-independent synthesis (7). Additionally, Pol λ, Pol μ and TdT play an enormous role in creation changeability of antibodies (immunoglobulins), used by immune system to identify and neutralize antigens. Pol λ takes part in V(D)J recombination at immunoglobulin heavy-chain loci, Pol μ promotes accurate immunoglobulin κ light-chain recombination (7), while TdT is a template-independent DNA polymerase that synthesizes N regions (stretches of randomly added nucleotides) at junctions of immunoglobulin genes during somatic recombination. Other DNA polymerases belonging to NTase fold superfamily are TRF4/5 family proteins that possess a function related to DNA Topoisomerase I. The TRF enzymes are chromatin-associated NTases and are essential for condensation and segregation of chromatin in all eukaryotes. These proteins are required for repair of gaps that may be introduced as a result of topological manipulations during DNA condensation (1,2,8). Some members of NTase fold superfamily such as glutamine synthetase adenyltransferase can modulate activity of other proteins by either adding or removing of covalently bound NMP (vi) (9). Addition or removal of NMP to/from glutamine synthetase by glutamine synthetase adenyltransferase is crucial for assimilation of nitrogen in both prokaryotes and eukaryotes. Kanamycin nucleotidyltransferase (KNTase) and streptomycin nucleotidyltransferase are involved in metabolism of xenobiotics and are responsible for resistance of bacteria to antibiotics (vii). These plasmid encoded enzymes transfer a NMP to the hydroxyl group of aminoglycosides what weakens interactions of antibiotics with 30S subunit of ribosome (10). NTase fold proteins involved in intracellular signal transduction can be exemplified by bi-functional enzymes from Rel/Spo family (viii). Proteins belonging to this family enable bacteria to survive prolonged periods of nutrient limitation by taking part in metabolism of (p)ppGpp, important intracellular signaling alarmone. (p)ppGpp is associated with many biological processes such as quorum sensing, antibiotic synthesis, cell differentiation, bacteriocin production or virulence and stress-induced defense system. NTase fold superfamily also includes adenylate cyclases (ACs), which take part in synthesis of intracellular second messenger (cAMP) from ATP (1). ACs, through their ability to generate cAMP, regulate many cellular processes such as activation of protein kinases, modulation of calcium transport and regulation of gene activity. Another NTase fold proteins taking part in signal transduction are 2′–5′-oligoadenylate synthetases (OASes). These interferon-induced antiviral proteins participate in the regulation of apoptosis, cell growth and differentiation in vertebrates. OASes are activated through binding to dsRNA and then convert ATPs to 2′–5′-linked oligoadenylates (2–5A). 2–5A binds to a latent RNase L and triggers the formation of active dimeric enzyme, which degrades viral and cellular RNAs (2,11).

It should be noted that various members of NTase fold superfamily frequently display little sequence similarity, despite retaining a common core fold and few active site residues. The lack of significant sequence similarity between the families and presence of various insertions make homology inference a challenging task and hinders new family identification with traditional sequence-based approaches. Although this superfamily was thoroughly studied using standard *in silico* tools in recent years (1,2), many of the families have remained undiscovered due to their extreme sequence and structure divergence. To extend the realm of NTase fold proteins, we performed comprehensive searches in publicly available databases of protein families and structures using the state-of-the-art distant homology detection approaches. As a consequence we identified 10 new families of NTase fold and collected the most complete set of evolutionary related proteins that adopt this common fold. Presented paper thus offers an up-to-date review of this highly diverse superfamily of proteins, providing a global insight into their evolutionary history, sequence and structure diversity, and fulfilled functional roles.

MATERIALS AND METHODS

Detection of novel NTase fold proteins

Initially, known NTase fold families and structures were identified from literature and various protein databases such as PFAM (12), KOG (13), COG (14) and SCOP (15). This set encompassing collected PFAM, KOG and COG families and PDB (16) structures was then used for comprehensive searches for novel so far unknown members of NTase fold superfamily using a distant homology detection method Meta-BASIC (17). Meta-BASIC is a consensus meta profile alignment method capable of finding very distant similarity between proteins through a comparison of sequence profiles enriched by predicted secondary structures (meta profiles).

Identification of novel families of NTase fold was carried out using Gene Relational DataBase (GRDB) system, which included precalculated Meta-BASIC connections between 10 340 PFAM, 4852 KOG and 4872 COG families and 20 540 proteins of known structure (PDB90, representatives from PDB filtered at 90% of sequence identity). Each family and each structure in the system was represented by its sequence (for PDB90) or consensus sequence (for PFAM, COG and KOG), sequence profile generated with PSI-BLAST (18) using NCBI non-redundant (NR) protein sequence database derivative (NR70), and secondary structure profile predicted with PSI-PRED (19).

The search strategy was based on the transitivity concept, where each newly identified PFAM, KOG and COG family or PDB structure was used for further Meta-BASIC searches until no new additional hits were found. Moreover, the high divergence of some NTase fold families that is likely reflected as lower than threshold (<40) Meta-BASIC scores was also considered. According to rigorous structural criteria used in LiveBench benchmarks (http://meta.bioinfo.pl/results.pl?comp_name = livebench-2008.2), predictions with scores above 40 have less than 5% probability of being incorrect. Specifically, in addition to high scoring (>40) Meta-BASIC hits, all below threshold hits with scores >20 were also analyzed to detect correct predictions placed among unreliable or incorrect ones.

Selection of potentially correct predictions was based on two essential defining criteria for NTase fold proteins, that were verified manually. First, family profile should include correctly aligned conserved acidic residues from catalytic motifs (with the exception of families that might loose their catalytic function) in addition to the presence of hG[GS] motif (that in some cases can be also less conserved). Second, family profile should include all secondary structure elements that correspond to the evolutionary core of NTase fold (αβαβαβα) and conserved critical hydrophobic positions responsible for forming a hydrophobic core of the structure. To confirm difficult predictions, consensus sequences and selected representative members of families that met the above mentioned criteria were submitted to the Protein Structure Prediction Meta Server (http://meta.bioinfo.pl) that assembles various top-of-the-line fold recognition methods. Models generated by these methods were analyzed with 3D-Jury, a consensus approach that uses structural comparisons to select potentially the best predictions (20). 3D-Jury system was run with default settings that included five servers used for consensus building: FFAS03 (21), mGenTHREADER (22), INBGU (23), FUGUE-2 (24) and Meta-BASIC (17).

Grouping of families and structures

Collected NTase fold proteins were assembled into groups of closely related families and structures. Families and structures within single group share relatively high sequence similarity detectable with both PSI-BLAST and RPS-BLAST with confident *E*-value lower than 0.001. Proteins belonging to different groups are more diverse and can not be linked by these standard homology detections tools.

Generation of superfamily alignment

Initially, to collect sequences that belong to analyzed NTase fold families, PSI-BLAST searches were performed against NR database using consensus sequences of the families. For each family, multiple sequence alignment was generated using PCMA program (25) and where necessary followed by manual adjustments. Simultaneously, all identified NTase fold structures were superimposed to derive structure-based alignment of their sequences for the conserved core regions of the fold that encompass three β-strands and four α-helices (αβαβαβα topology). Final alignment for whole NTase fold superfamily in the conserved regions was assembled from sequence-to-structure mappings between NTase fold families and the closest structures. In majority of cases, the closest structures were identified as the most common templates appearing in high scoring 3D-Jury predictions. The family-structure mappings were built manually based on Meta-BASIC and 3D-Jury alignments, PSI-PRED secondary structure predictions and conservation of critical active site residues and hydrophobic patterns using consensus alignment and 3D assessment approach (26) for representative family proteins.

Domain architecture and genomic context analyses

To detect other protein domains in identified NTase fold families, collected family sequences were analyzed with Meta-BASIC after removal of the conserved NTase domain. Non-trivial assignments were further verified with 3D-Jury method. NTase fold proteins were also searched for transmembrane segments [TMHMM2 (27)], signal peptides [SignalP (28)], low compositional complexity [SEG (29)] and coiled coil regions [Coils2 (30)] using SMART server (31). Possible functional associations were investigated using genomic context analysis (neighborhood, co-occurrence, gene fusion and co-expression) with STRING database (32).

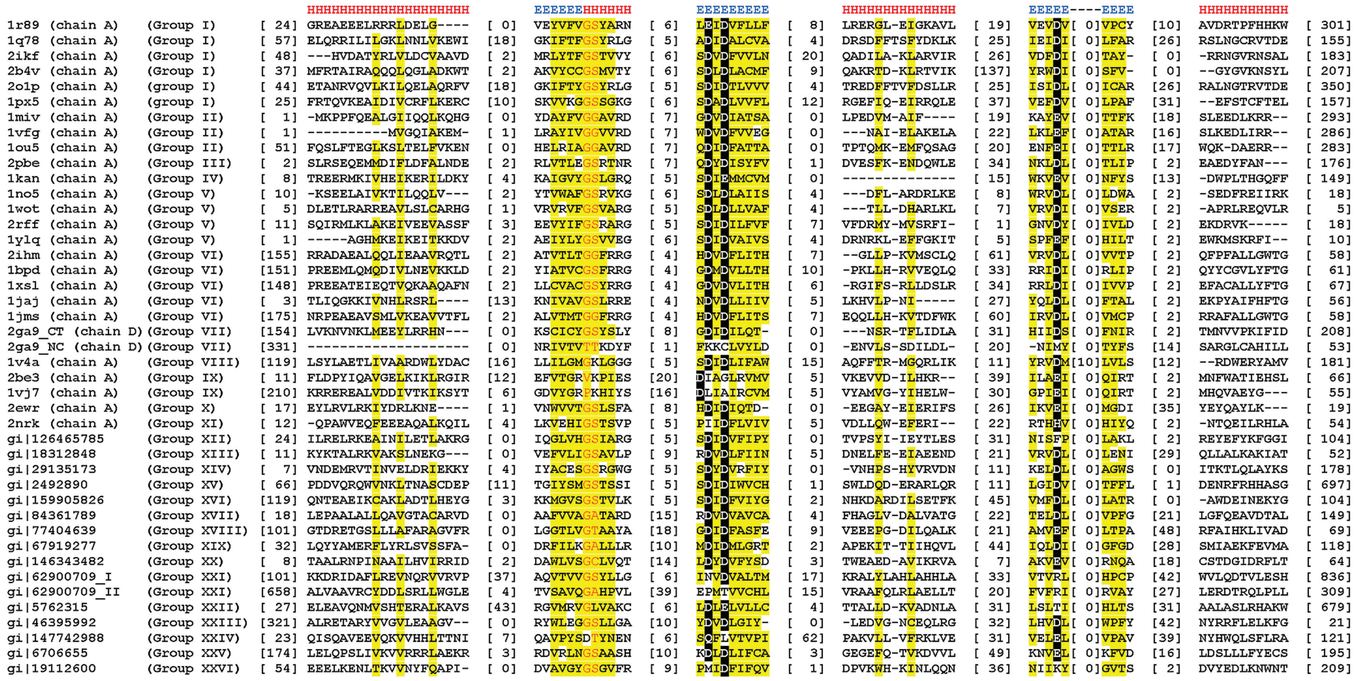
Identification of human superfamily members and associated genetic diseases

To identify human members of NTase fold superfamily, 43 570 human proteins (human proteome from ENSEMBL database) were included in the GRDB system. Similar search strategy was applied to that described above, starting with all known and newly identified families of NTase fold. Genetic disorders associated with genes encoding NTase fold proteins were identified using OMIM database (33). For selected human proteins high-quality 3D models were built with Modeller (34) followed by mapping of mutations observed in analyzed genetic disorders.

RESULTS AND DISCUSSION

In this study we applied similar approach to that used in our recent work where we identified a number of novel but highly diverged PD-(D/E)XK nuclease families (35). The initial set of known NTase fold proteins was used as the starting point for transitive Meta-BASIC searches for new superfamily members among all PFAM, KOG and COG families and PDB structures. To consider the observed high sequence divergence in NTase fold superfamily that is likely reflected in lower than confidence cut-off Meta-BASIC scores, we analyzed also below threshold hits. This resulted in identification of many novel families of NTase fold that escape detection with standard homology search methods. These potentially novel superfamily members were subjected to further extensive analyses including fold recognition with 3D Jury to confirm initial predictions. Final selection of correct but highly non-trivial assignments was based on a consistency of a predicted secondary structure pattern with that of NTase fold, general conservation of critical hydrophobic residues and—for potentially active enzymes—presence of active site motifs critical for maintaining of NTase function (Figure 2).

On the basis of their sequence similarity (evolutionary distance), all collected NTase fold families and structures were assembled into 26 distinct groups (Table 1). Families within single group can be easily linked both with PSI-BLAST and RPS-BLAST (closely related), in contrast to those belonging to different groups that can not be connected with these standard homology detection methods (distantly related). Figure 3 illustrates detected similarity network for NTase fold families and structures using Meta-BASIC method. It should be noted that the Meta-BASIC connections between diverse members of this superfamily were established transitively. This shows clearly the importance of the concept of transitivity applied in our approach, where newly identified families were used for detection of other novel families of NTase fold in further searches. Moreover, many established connections between families of unknown structure are



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                                                   HHHHHHHHHHHHHHHHHHHH         EEEEEEHHHHHH         EEEEEEEEE         HHHHHHHHHHHHHH          EEEEE----EEEE          HHHHHHHHHHH
1r89 (chain A)     (Group I)       [ 24] GREAEEELRRRLDELG----  [ 0]  VEYVFVGSYARN  [ 6]  LEIDVFLLF  [  8]  LRERGL-EIGKAVL  [ 19]  VEVDV[ 0]VPCY  [10]  AVDRTPFHHKW  [ 301]
1q78 (chain A)     (Group I)       [ 57] ELQRRILILGKLNNLVKEWI  [18]  GKIFTFGSYRLG  [ 5]  ADIDALCVA  [  4]  DRSDFFTSFYDKLK  [ 25]  IEIDI[ 0]LFAR  [26]  RSLNGCRVTDE  [ 155]
2ikf (chain A)     (Group I)       [ 48] ---HVDATYRLVLDCVAAVD  [ 2]  MRLYTFGSTVVY  [ 6]  SDVDFVVLN  [ 20]  QADILA-KLARVIR  [ 26]  VDFDI[ 0]TAY-  [ 0]  -RRNGVRNSAL  [ 183]
2b4v (chain A)     (Group I)       [ 37] MFRTAIRAQQQLQGLADKWT  [ 2]  AKVYCCGSMVTY  [ 6]  SDLDLACMF  [  9]  QAKRTD-KLRTVIK  [137]  YRWDI[ 0]SFV-  [ 0]  --GYGVKNSYL  [ 207]
2o1p (chain A)     (group I)       [ 44] ETANRVQVLKILQELAQRFV  [18]  GKIFTYGSYRLG  [ 5]  SDIDTLVVV  [  4]  TREDFFTVFDSLLR  [ 25]  ISIDL[ 0]ICAR  [26]  RALNGTRVTDE  [ 350]
1px5 (chain A)     (group I)       [ 25] FRTQVKEAIDIVCRFLKERC  [10]  SKVVKGGSSGKG  [ 6]  SDADLVVFL  [ 12]  RGEFIQ-EIRRQLE  [ 37]  VEFDV[ 0]LPAF  [31]  --EFSTCFTEL  [ 157]
1miv (chain A)     (Group II)      [  1] -MKPPFQEALGIIQQLKQHG  [ 0]  YDAYFVGGAVRD  [ 7]  GDVDIATSA  [  0]  LPEDVM-AIF----  [ 19]  KAYEV[ 0]TTFK  [18]  SLEEDLKRR--  [ 293]
1vfg (chain A)     (Group II)      [  1] ----------MVGQIAKEM-  [ 1]  LRAYIVGGVVRD  [ 7]  WDVDFVVEG  [  0]  ---NAI-ELAKELA  [ 22]  LKLEF[ 0]ATAR  [16]  SLKEDLIRR--  [ 286]
1ou5 (chain A)     (Group II)      [ 51] FQSLFTEGLKSLTELFVKEN  [ 0]  HELRIAGGAVRD  [ 7]  QDIDFATTA  [  0]  TPTQMK-EMFQSAG  [ 20]  ENFEI[ 0]TTLR  [17]  WQK-DAERR--  [ 283]
2pbe (chain A)     (Group III)     [  2] SLRSEQEMMDIFLDFALNDE  [ 2]  RLVTLEGSRTNR  [ 7]  QDYDISYFV  [  1]  DVESFK-ENDQWLE  [ 34]  NKLDL[ 0]TLIP  [ 2]  EAEDYFAN---  [ 176]
1kan (chain A)     (Group IV)      [  8] TREERMKIVHEIKERILDKY  [ 4]  KAIGVYGSLGRQ  [ 5]  SDIEMMCVM  [  0]  --------------  [ 15]  WKVEV[ 0]NFYS  [13]  -DWPLTHGQFF  [ 149]
1no5 (chain A)     (Group V)       [ 10] -KSEELAIVKTILQQLV---  [ 2]  YTVWAFGSRVKG  [ 6]  SDLDLAIIS  [  4]  ---DFL-ARDRLKE  [  8]  WRVDL[ 0]LDWA  [ 2]  -SEDFREIIRK  [  18]
1wot (chain A)     (Group V)       [  5] DLETLRARREAVLSLCARHG  [ 1]  VRVRVFGSVARG  [ 5]  SDLDLLVAF  [  4]  ---TLL-DHARLKL  [  7]  VRVDI[ 0]VSER  [ 2]  -APRLREQVLR  [   5]
2rff (chain A)     (Group V)       [ 11] SQIRMLKLAKEIVEEVASSF  [ 3]  EEVYIFGSRARG  [ 5]  SDIDILFVF  [  7]  VFDRMY-MVSRFI-  [  1]  GNVDY[ 0]IVLD  [ 2]  EKDRVK-----  [  18]
1ylq (chain A)     (Group V)       [  1] -----AGHMKEIKEITKKDV  [ 2]  AEIYLYGSVVEG  [ 6]  SDIDVAIVS  [  4]  DRNRKL-EFFGKIT  [  5]  SPFEF[ 0]HILT  [ 2]  EWKMSKRFI--  [  10]
2ihm (chain A)     (Group VI)      [155] RRADAEALQQLIEAAVRQTL  [ 2]  ATVTLTGGFRRG  [ 4]  HDVDFLITH  [  7]  --GLLP-KVMSCLQ  [ 61]  VRVDL[ 0]VVTP  [ 2]  QFPFALLGWTG  [  58]
1bpd (chain A)     (Group VI)      [151] PREEMLQMQDIVLNEVKKLD  [ 2]  YIATVCGSFRRG  [ 4]  GDMDVLLTH  [ 10]  -PKLLH-RVVEQLQ  [ 33]  RRIDI[ 0]RLIP  [ 2]  QYYCGVLYFTG  [  61]
1xsl (chain A)     (Group VI)      [148] PREEATEIEQTVQKAAQAFN  [ 2]  LLCVACGSYRRG  [ 4]  GDVDVLITH  [  6]  -RGIFS-RLLDSLR  [ 34]  RRLDI[ 0]IVVP  [ 2]  EFACALLYFTG  [  67]
1jaj (chain A)     (Group VI)      [  3] TLIQGKKIVNHLRSRL----  [13]  KNIVAVGSLRRE  [ 4]  NDVDLLIIV  [  5]  LKHVLP-NI-----  [ 27]  YQLDL[ 0]FTAL  [ 2]  EKPYAIFHFTG  [  56]
1jms (chain A)     (Group VI)      [175] NRPEAEAVSMLVKEAVVTFL  [ 2]  ALVTMTGGFRRG  [ 4]  HDVDFLITS  [  7]  EQQLLH-KVTDFWK  [ 60]  IRVDL[ 0]VMCP  [ 2]  RRAFALLGWTG  [  58]
2ga9_CT (chain D)  (Group VII)     [154] LVKNVNKLMEEYLRRHN---  [ 0]  KSCICYGSYSLY  [ 8]  GDIDILQT-  [  0]  ---NSR-TFLIDLA  [ 31]  HIIDS[ 0]FNIR  [ 2]  TMNVVPKIFID  [ 208]
2ga9_NC (chain D)  (Group VII)     [331] --------------------  [ 0]  NRIVTVTTKDYF  [ 1]  FKKCLVYLD  [  0]  -ENVLS-SDILDL-  [ 20]  -NIMY[ 0]TYFS  [14]  SARGLCAHILL  [  53]
1v4a (chain A)     (Group VIII)    [119] LSYLAETLIVAARDWLYDAC  [16]  LLILGMGKLGGG  [ 5]  SDIDLIFAW  [ 15]  AQFFTR-MGQRLIK  [ 11]  YRVDM[10]LVLS  [12]  --RDWERYAMV  [ 181]
2be3 (chain A)     (Group IX)      [ 11] FLDPYIQAVGELKIKLRGIR  [12]  EFVTGRVKPIES  [20]  DIAGLRVMV  [  5]  VKEVVD-ILHKR--  [ 39]  ILAEI[ 0]QIRT  [ 2]  MNFWATIEHSL  [  66]
1vj7 (chain A)     (Group IX)      [210] KRREREALVDDIVTKIKSYT  [ 6]  GDVYGRPKHIYS  [16]  DLIAIRCVM  [  5]  VYAMVG-YIHELW-  [ 30]  GPIEI[ 0]QIRT  [ 2]  MHQVAEYG---  [  55]
2ewr (chain A)     (Group X)       [ 17] EYLRVLRKIYDRLKNE----  [ 1]  VNWVVTGSLSFA  [ 8]  HDIDIQTD-  [  0]  -EEGAY-EIERIFS  [ 26]  IKVEI[ 0]MGDI  [35]  YEYQAYLK---  [  19]
2nrk (chain A)     (Group XI)      [ 12] -QPAWVEQFEEEAQALKQIL  [ 4]  LKVEHIGSTSVP  [ 5]  PIIDFLVIV  [  5]  VDLLQW-EFERI--  [ 22]  RTHHV[ 0]HIYQ  [ 2]  -NTQEILRHLA  [  54]
gi|126465785       (Group XII)     [ 24] ILRELRKEAINILETLAKRG  [ 0]  IQGLVHGSIARG  [ 5]  SDIDVFIPY  [  0]  TVPSYI-IEYTLES  [ 31]  NISFP[ 0]LAKL  [ 2]  REYEFYKFGGI  [ 104]
gi|18312848        (Group XIII)    [ 11] KYKTALRKVAKSLNEKG---  [ 0]  VEFVLIGSAVLP  [ 9]  RDVDLFIIN  [  5]  DNELFE-EIAEEND  [ 21]  VRVDL[ 0]LENI  [29]  QLLALKAKIAT  [  52]
gi|29135173        (Group XIV)     [  7] VNDEMRVTINVELDRIEKKY  [ 4]  IYACESGSRGWG  [ 5]  SDYDVRFIY  [  0]  -VNHPS-HYVRVDN  [ 11]  KELDL[ 0]AGWS  [ 0]  ITKTLQLAYKS  [ 178]
gi|2492890         (Group XV)      [ 66] PDDVQRQWVNKLTNASCDEP  [11]  TGIYSMGSTSSI  [ 5]  SDIDIWVCH  [  1]  SWLDQD-ERARLQR  [ 11]  LGIDV[ 0]TFFL  [ 1]  DENRFRHHASG  [ 697]
gi|159905826       (Group XVI)     [119] QNTEAEIKCAKLADTLHEYG  [ 3]  KKMGVSGSTVLK  [ 5]  SDIDFVIYG  [  2]  NHKDARDILSETFK  [ 45]  VMFDL[ 0]LATR  [ 0]  -AWDEINEKYG  [ 104]
gi|84361789        (Group XVII)    [ 18] LEPAALALLQAVGTACARVD  [ 0]  AAFVVAGATARD  [15]  RDVDVAVCA  [  4]  FHAGLV-DALVATG  [ 22]  TELDL[ 0]VPFG  [21]  LGFQEAVDTAL  [ 149]
gi|77404639        (Group XVIII)   [101] GTDRETGSLLLAFARAGVFR  [ 0]  LGGTLVGTAAYA  [18]  GDIDFASFE  [  9]  VEEEPG-DILQALK  [ 21]  AMVEF[ 0]LTPA  [48]  RFAIHKLIVAD  [  69]
gi|67919277        (Group XIX)     [ 32] LQYYAMERFLYRLSVSSFA-  [ 0]  DRFILKGALLLR  [10]  MDIDMLGRT  [  2]  APEKIT-TIIHQVL  [ 44]  IQLDI[ 0]GFGD  [28]  SMIAEKFEVMA  [ 118]
gi|146343482       (Group XX)      [  8] TAALRNPINAAILHVIRRID  [ 2]  DAWLVSGCLVQT  [14]  LDYDVFYSD  [  3]  TWEAED-AVIKRVA  [  7]  AKVEV[ 0]RNQA  [18]  CSTDGIDRFLT  [  64]
gi|62900709_I      (Group XXI)     [101] KKDRIDAFLREVNQRVVRVP  [37]  AQVTVVGSYLLG  [ 6]  INVDVALTM  [ 17]  KRALYLAHLAHHLA  [ 33]  VTVRL[ 0]HPCP  [42]  WVLQDTVLESH  [ 836]
gi|62900709_II     (Group XXI)     [658] ALVAAVRCYDDLSRLLWGLE  [ 4]  TVSAVQGAHPVL  [39]  EPMTVVCHL  [ 15]  VRAAFQLRLAELLT  [ 20]  FVFRI[ 0]RVAY  [27]  LERDTRQLPLL  [ 309]
gi|5762315         (Group XXII)    [ 27] ELEAVQNMVSHTERALKAVS  [43]  RGVMRVGLVAKC  [ 6]  LDLELVLLC  [  4]  TTALLD-KVADNLA  [ 31]  LSLTI[ 0]HLTS  [31]  AALASLRHAKW  [ 679]
gi|46395992        (Group XXIII)   [321] ALRETARYVVGVLEAAGV--  [ 0]  RYWLEGGSLLGA  [10]  YDVDLGIY-  [  0]  -LEDVG-NCEQLRG  [ 32]  LHVDL[ 0]WPFY  [42]  NYRRFLELKFG  [  21]
gi|147742988       (Group XXIV)    [ 23] QISQAVEEVQKVVHHLTTNI  [ 7]  QAVPYSDTYNEN  [ 6]  SQFLVTVPI  [ 62]  PAKVLL-VFRKLVE  [ 31]  VELEL[ 0]VPAV  [39]  NYHWQLSFLRA  [ 121]
gi|6706655         (Group XXV)     [174] LELQPSLIVKVVRRRLAEKR  [ 3]  RDVRLNGSAASH  [10]  KDLDLIFCA  [  3]  GEGEFQ-TVKDVVL  [ 49]  KNVEL[ 0]KFVD  [16]  LDSLLLFYECS  [ 195]
gi|19112600        (Group XXVI)    [ 54] EEELKENLTKVVNYFQAPI-  [ 0]  DVAVGYGSGVFR  [ 9]  PMIDFIFQV  [  1]  DPVKWH-KINLQQN  [ 36]  NIIKY[ 0]GVTS  [ 2]  DVYEDLKNWNT  [ 209]
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Figure 2. Multiple sequence alignment for NTase fold superfamily. Only conserved regions of the fold core are shown for representative proteins of known structure and single representative sequences for groups lacking experimentally solved structure. Sequences are labeled according to PDB code or NCBI gene identification (gi) number and the number of group they belong to (XVII–XXVI, newly detected NTase fold proteins). Multiple NTase fold domains occurring in some proteins are denoted by consecutive roman numbers. The numbers of excluded residues are specified in square brackets. Conservation of residues is denoted with the following scheme: uncharged, highlighted in yellow; small, letters in red; critical active site aspartates/glutamates, highlighted in black. Locations of secondary structure elements (E, β-strand; H, α-helix) are marked above sequences.

not detectable even with advanced fold recognition methods that require a known reference protein structure. In addition, by considering Meta-BASIC hits also with scores below a confident threshold of 40, we were able to identify the most divergent sequence groups. Although we investigated all Meta-BASIC predictions with scores above 20, subsequent analysis revealed that a more stringent cutoff of 28 would be sufficient to identify transitively all members of NTase fold superfamily (Figure 3).

According to our classification, 16 groups (Groups I–XVI, for a brief description of these groups see Supplementary Data) include well-known members of NTase fold superfamily while, importantly, remaining 10 groups of proteins (Groups XVII–XXVI) encompasses novel families of NTase fold that we identified among uncharacterized and poorly annotated proteins. Some of them probably do not exhibit NTase function as they lack important catalytic residues. Their specific function is not clear but we speculate that some of them may participate in signaling pathways or regulation of gene expression. To hint at additional functional information, both domain architecture (Supplementary Figure S1) and genomic context were derived for all NTase fold families. Newly identified NTase fold proteins are described in more details below.

Newly detected NTase fold superfamily members

Groups XVII–XX (uncharacterized proteins). Four new groups of proteins of so far unknown structure and function that we assigned to NTase fold superfamily encompass: group XVII (uncharacterized protein conserved in bacteria COG4849), group XVIII (uncharacterized conserved protein COG5397), group XIX [uncharacterized conserved protein COG2253 and domain of unknown function DUF1814 (PF08843)], group XX [uncharacterized protein conserved in bacteria COG3575 and bacterial protein of unknown function DUF925 (PF06042)]. All these proteins have only single NTase domain and are probably active NTases, as they posses conserved catalytic acidic residues and hG[GS] motif. Unfortunately, no specific functions could be assigned for those enzymes through bioinformatics analyses and because of lack of any experimental data.

Group XXI (NRAP). Nucleolar RNA-associated proteins (NRAP) (KOG2054 and PF03813) belong to another group of newly detected divergent members of NTase fold superfamily. High expression of NRAP is observed in tissues with most abundant ribosome biogenesis such as spleen, kidney, colon and testis. Usually, proteins from this group posses duplicated inactive NTase domain (lack of conserved catalytic amino acids), each followed by C-terminal PAP/OAS1 substrate binding domain, which is also found in OAS family proteins, TRF4/5 polymerases, trypanosomal urydylytransferases, poly(A) polymerases and archeal CCA-adding enzymes. The most probably both non-catalytic NTase and PAP/OAS1 substrate binding domains take part in nucleic acid binding. Accordingly, NRAP appears to be

Table 1. NTase fold groups, their representatives in human and connections to genetic diseases

Group	PDB90	COG	KOG	PFAM	Human gene location	ENSEMBL	Diseases	Description
Known superfamily members								
I	2O1P	COG5186	KOG2245	PF04928	Chr14: 96038471–96103178	ENSP00000216277		• Poly(A) polymerase
	1Q78	COG5260	KOG1906		Chr2: 60836887–6087960	ENSP00000238714		• TUTase
	2IKF	COG1746	KOG2277		Chr10: 30641765–30703376	ENSP00000263063		• DNA polymerase
	2B4V				Chr16: 48745280–48820909	ENSP00000350054		• tRNA nucleotidyltransferase
	1R89				Chr5: 78944152–79018227	ENSP00000369637		(CCA-adding enzyme)
	1PX5				Chr5: 6767718–6810161	ENSP00000230859		• 2′–5′-oligoadenylate synthetase
					Chr11: 62098756–62115592	ENSP00000278279		• TRF4/5 nucleotidyltransferase
					Chr9: 88092468–88159198	ENSP00000365128		
					Chr1: 52661535–52791360	ENSP00000360596		
					Chr12: 111900657–111933911	ENSP00000342278		
					Chr12: 111860540–111895433	ENSP00000228928		
					Chr12: 111829122–111854374	ENSP00000202917	Type 1 diabetes	
					Chr12: 119942478–119961164	ENSP00000257570		
II	1MIV	COG0617	KOG2159	PF01743	Chr3: 3107800–3131722	ENSP00000354999		• tRNA nucleotidyltransferase
	1VFG							• Poly(A) polymerase
	1OU5							
III	2PBE			PF04439				• Streptomycin adenylyltransferase
IV	1KAN							• Kanamycin nucleotidyltransferase
V	1WOT	COG1669		PF01909				• Predicted nucleotidyltransferase
	1NO5	COG1708						
	2RFF							
	1YLQ							
VI	1BPD	COG1796	KOG2534		Chr10: 103328629–103338004	ENSP00000359187		• DNA polymerase
	1XSL				Chr10: 98054075–98088290	ENSP00000360216		
	1JMS				Chr7: 44078374–44088607	ENSP00000242248		
	2IHM				Chr8: 42315131–42348482	ENSP00000265421		
	1JAJ							
VII	2GA9			PF03296				• Poxvirus poly(A) polymerase
VIII	1V4A	COG2844		PF03710				• Glutamine synthetase
		COG1391		PF03445				adenylyltransferase
		COG2905						• Putative nucleotidyltransferase
IX	1VJ7	COG0317	KOG1157	PF04607				• Guanosine polyphosphate
	2BE3	COG2357						pyrophosphohydrolase/synthetase
X	2EWR							• Predicted nucleotidyltranferase
XI	2NRK	COG2320		PF04229				• Predicted nucleotidyltransferase
XII		COG2413						• Predicted nucleotidyltransferase
XIII		COG4914						• Predicted nucleotidyltransferase
XIV		COG3541						• Predicted nucleotidyltransferase
XV		COG3072		PF01295				• Adenylate cyclase
XVI		COG1665						• Predicted nucleotidyltransferase

Novel superfamily members								
XVII		COG4849						• Uncharacterized conserved protein
XVIII		COG5397						• Uncharacterized conserved protein
XIX		COG2253		PF08843				• Uncharacterized conserved protein
XX		COG3575		PF06042				• Uncharacterized conserved protein
XXI			KOG2054	PF03813	Chr9: 33451354–33463941	ENSP00000368784		• NRAP
XXII			KOG3792	PF07528	Chr19: 3755022–3785924	ENSP00000262961		• NFAT
			KOG3793		Chr5: 32390214–32480601	ENSP00000371560		• Predicted nucleotidyltransferase
					Chr9: 124926811–125070676	ENSP00000362742		
					Chr19: 10642282–10656141	ENSP00000250241		
					Chr1: 151900905–151910148	ENSP00000355011		
XXIII		COG3475		PF06828	Chr9: 107360232–107443220	ENSP00000223528	Fukuyama-type congenital muscular dystrophy	• LICD
				PF04991				• Fukutin-related proteins
					Chr19: 51943121–51953581	ENSP00000326570	Congenital muscular dystrophy type 1C	
XXIV			KOG3963	PF03281	Chr2: 241474139–241484087	ENSP00000373586		• Mab-21
					Chr4: 151722699–151725262	ENSP00000324701	Neurologic disorders	
					Chr13: 34946319–34948830	ENSP00000369251	Neurologic disorders	
					Chr3: 193997301–194118644	ENSP00000314252		
					Chr10: 106061884–106088152	ENSP00000350915		
					Chr16: 19033206–19034943	ENSP00000370849		
					Chr22: 38228230–38244079	ENSP00000327124		
					Chr2: 96355688–96357806	ENSP00000355121		
					Chr17: 18104594–18109818	ENSP00000323591		
					Chr6: 74179959–74218720	ENSP00000296913		
					Chr17: 7279486–7281722	ENSP00000315387		
					Chr1: 116455899–116479384	ENSP00000358512		
XXV			KOG3852	PF07984	Chr1: 117950079–117972517	ENSP00000358458		• FAM46
					Chr6: 82512166–82519210	ENSP00000358771	Retinal pigmentosa	
					Chr1: 27204098–27212049	ENSP00000351491		
					ChrX: 79477659–79587466	ENSP00000342730		
XXVI			KOG2986	PF09139	Chr3: 11806920–11863355	ENSP00000273037		• MMP37

Proteins belonging to single group share relatively high sequence similarity detectable by both PSI-BLAST and RPS-BLAST. The columns provide: the group number (column 'Group'); representative proteins (at 90% seq id) with solved structure (column 'PDB90'); protein families catalogued in COG, KOG and PFAM databases (columns 'COG', 'KOG' and 'PFAM', respectively); human members in ENSEMBL database and their gene loci (columns 'ENSEMBL' and 'Human gene location', respectively), human genetic diseases associated with mutations found in corresponding genes (column 'Diseases') and functional description of the families (column 'Description').

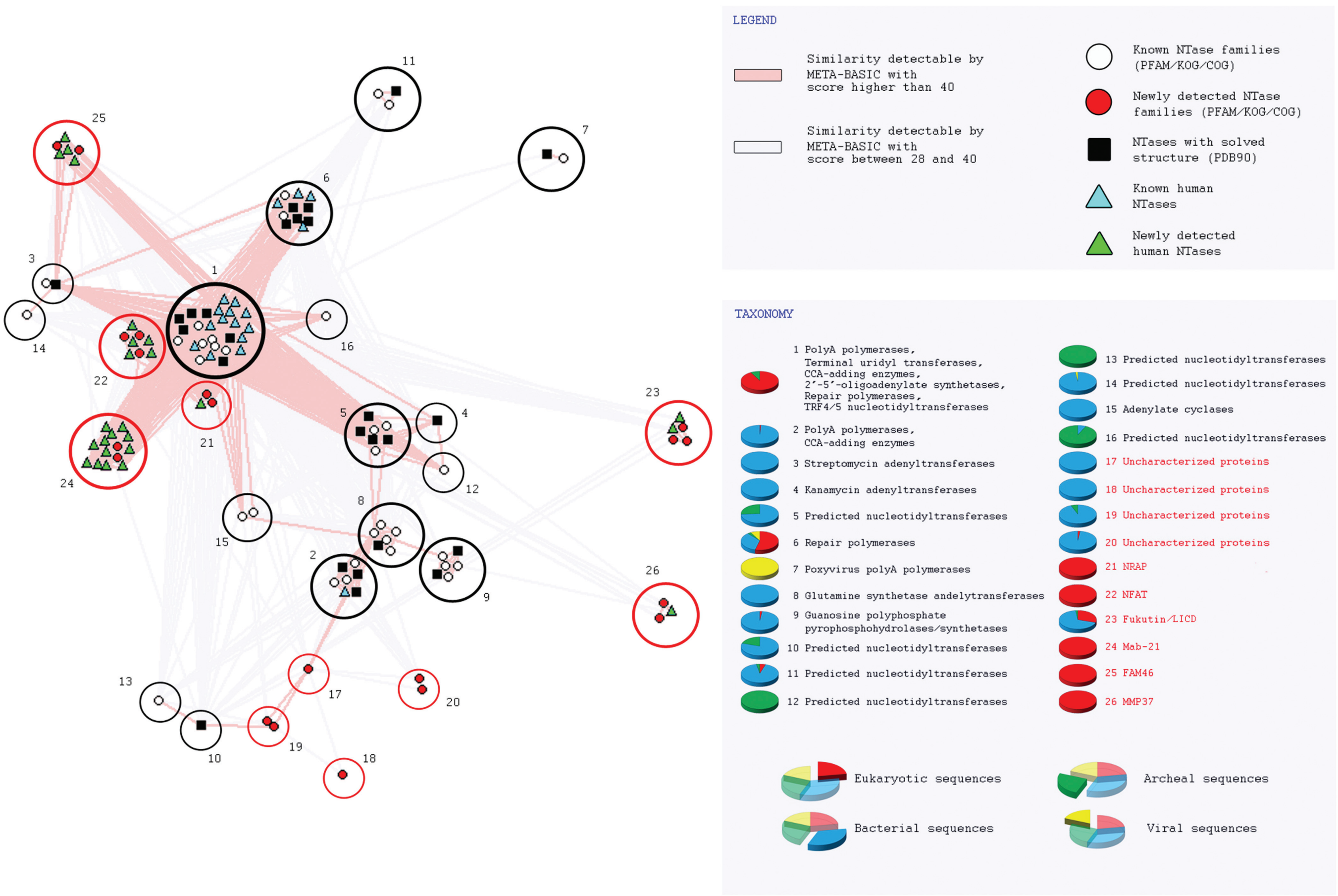
LEGEND
Similarity detectable by META-BASIC with score higher than 40
Similarity detectable by META-BASIC with score between 28 and 40
Known NTase families (PFAM/KOG/COG)
Newly detected NTase families (PFAM/KOG/COG)
NTases with solved structure (PDB90)
Known human NTases
Newly detected human NTases
TAXONOMY
1 PolyA polymerases, Terminal uridyl transferases, CCA-adding enzymes, 2'-5'-oligoadenylate synthetases, Repair polymerases, TRF4/5 nucleotidyltransferases
2 PolyA polymerases, CCA-adding enzymes
3 Streptomycin adenyltransferases
4 Kanamycin adenyltransferases
5 Predicted nucleotidyltransferases
6 Repair polymerases
7 Poxyvirus polyA polymerases
8 Glutamine synthetase andelyltransferases
9 Guanosine polyphosphate pyrophosphohydrolases/synthetases
10 Predicted nucleotidyltransferases
11 Predicted nucleotidyltransferases
12 Predicted nucleotidyltransferases
13 Predicted nucleotidyltransferases
14 Predicted nucleotidyltransferases
15 Adenylate cyclases
16 Predicted nucleotidyltransferases
17 Uncharacterized proteins
18 Uncharacterized proteins
19 Uncharacterized proteins
20 Uncharacterized proteins
21 NRAP
22 NFAT
23 Fukutin/LICD
24 Mab-21
25 FAM46
26 MMP37
Eukaryotic sequences
Archeal sequences
Bacterial sequences
Viral sequences
1
2
3
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Figure 3. Connectivity network for NTase fold superfamily. Groups of closely related proteins that can be linked by both PSI-BLAST and RPS-BLAST are surrounded by black (known members of NTase fold superfamily) and red (newly detected) circles. Detected Meta-BASIC connections between PFAM, KOG, COG families, PDB structures and human proteins are shown as lines colored according to the Meta-BASIC score: pink, confident scores above 40; grey, below threshold scores between 28 and 40. For each group short description and taxonomy distribution is provided.

involved in ribosome biogenesis by interacting with pre-rRNA primary transcript (36). In addition, some proteins belonging to group XXI are classified as U3 snoRNP involved in maturation of pre-18S rRNA according to existing descriptions in NR sequence database generated by automatic computational analysis of large-scale protein–protein interactions (36). All these data suggests that NRAP proteins may participate in rRNA splicing.

Group XXII (NFAT). Nuclear factor of activated T-cells (NFAT), subunits NF90 and NF45 (KOG3792 and KOG3793, respectively) together with DZF (PF07528) form a group of proteins newly assigned to NTase fold superfamily. These proteins are known to play an important role in regulation of antigen-response genes. Human NF45 (ILF2) and NF90 (ILF3) may contribute to RNA gene regulation at the levels of transcription, export and translocation (37,38). NF45 and NF90 also stabilize the association between the KU70, KU80 and the DNA-dependent protein kinase (DNA-PK). KU70, KU80 and DNA-PK each serve essential roles in development of lymphocytic immunity through their contributions to double-stranded DNA break repair and antibody and T-cell receptor diversity (38). Additionally, NF90 takes part in the formation of a circular conformation of the viral genomes, which is important for the coordination of viral translation and replication (39).

NTase domain in group XXII proteins is always followed by C-terminal PAP/OAS1 substrate binding domain, which is usually responsible for DNA or RNA binding. In addition to that, extra N-terminal (zinc finger domain) and C-terminal (double-stranded RNA binding motif—PF00035) domains may assist in binding nucleic acids. Importantly, only some proteins from this group [e.g. human proteins: spermatid perinuclear RNA-binding protein—STRBP and interleukin enhancer-binding factor 3 (ILF3)] share conserved [DE]h[DE]h motif in NTase domain and thus may have NTase activity. Similarly to DNA topoisomerase I—related function protein family, those NFAT proteins may function as a chromatin-associated NTases. Remaining proteins from group XXII that do not posses conserved amino acids responsible for catalysis could probably function as a transcription regulators. This is consistent with experimental data indicating that NFAT proteins may contribute to gene regulation (38).

Group XXIII (Fukutin/LICD). Group XXIII includes LPS biosynthesis proteins (COG3475), Fukutin-related proteins (PF06828) and LICD protein family (PF04991). Proteins from this group are known to participate mostly in glycosylation and posttranslational protein modification. LicD2 from *Streptococcus pneumoniae* takes part in addition of phosphocholine to lipoteichoic acid (LTA) using CDP-choline as a substrate. Choline is an essential growth factor, which in the form of phosphocholine is incorporated in the cell wall by its attachment to teichioc (TA) and lipoteichoic acids. Choline participates in pneumococcal cell separation, transformation, autolysis and interactions with the host cell surface and choline-binding proteins. In *Haemophilus influenzae* licD is cotranscribed with licA, licB and licC, which encode choline kinase, choline transferase and phosphocholine citidyl transferase, respectively (Supplementary Figure S2). In *S. pneumoniae*, in contrast to *H. influenzae*, licD2 and licD1 (both homologous to licD) are cotranscribed with sugar transporter, while licA, licB and licC are regulated together in other operon (40,41). Finally, the yeast MNN4 (LICD family member) transfers mannosyl phosphate from GDP-mannose to N- and O-linked oligsosaccharides in proteins (42,43).

Predicted NTase domain encoded by licD from *H. influenzae* and licD1 and licD2 from *S. pneumoniae* is the most likely to be active what suggest its direct role in incorporation of phosphocholine (ChoP) to the cell wall LTA and TA (alone or in cooperation with N-terminal glycosyl transferase domain, see below). Specifically, some proteins from group XXIII possess additional domains including NAD(P) binding domain and newly identified but probably non-active glycosyl transferase family 2 domain (PF00535) that lacks conserved catalytic amino acids. Detection of glycosyl transferase domain was highly non-trivial and was possible by applying consensus of fold recognition (3D-Jury). Active glycosyl transferases form glycosyl bonds by catalyzing the transfer of sugar moieties from donor molecules such as UDP-glucose, UDP-*N*-acetyl-galactosamine, GDP-mannose or CDP-abequose to specific acceptor molecules (44). Probably, the non-active glycosyl transferase domain in group XXIII proteins can recognize specific molecules (choline—LicD or sugar—Fukutin) bound to NDP, transfer of which is carried by NTase domain. Additional NAD(P) binding domain has Rossmann fold structure but its specific function is not known.

Group XXIV (Mab-21). This group contains small conserved eukaryotic family of ‘Male-abnormal 21’ (Mab-21) proteins (PF03281) and Mab-21-like cell fate specification proteins (KOG3963). They posses newly detected N-terminal NTase domain followed by C-terminal PAP/OAS1 substrate binding domain. In *Caenorhabditis elegans* Mab-21 protein is associated with cell fates and the formation of sensory organs in male nematodes, located in the tail and involved in copulation (45). D6 genes from *Danio rerio* and *Xenopus laevis* encode Mab-21 family proteins and are important during eye differentiation and neuronal development, respectively. In *Mus musculus* expression of the D6 genes is essential for development of the embryonic brain, eye, limbs and neural crest derivatives (46). Additionally, Mab-21 proteins are closely connected with signal transduction. In *C. elegans* Mab-21 is involved in transforming growth factor-β (TGF-β) signaling pathway (47), while human homologs interact with nuclear transducer SMAD1 in vertebrate bone morphogenetic protein 4 (BMP4) signaling pathway (46). It was shown that one of the human Mab-21 proteins (KIAA1754) may bind inositol 1,4,5-triphosphate (intracellular messanger) (48) and can act as a transcriptional repressor when targeted to a heterologous promoter (46). Our analyses indicate that only some Mab-21 family members have conserved catalytic residues in predicted NTase domain, while remaining homologs likely do not retain enzymatic function. On the basis of the presence of additional C-terminal domain (potentially responsible for nucleic acid binding) and available experimental data for the members of this family we hypothesize that Mab-21 proteins may act as a transcription regulators.

Group XXV (FAM46). Group XXV consists of uncharacterized conserved FAM46 (C6orf37) proteins (KOG3852 and PF07984) with newly detected NTase domain. These proteins are expressed in the neural retina, adult skeletal muscle, thymus, liver, lung and brain (49). Majority of FAM46 proteins, similarly to other superfamily members from groups I, XXI, XXII and XXIV, possess additional C-terminal PAP/OAS1 substrate binding domain. FAM46 proteins are known to have different functions in many tissues at various stages of development. For instance, in human FAM46A is a SMAD signaling pathway related protein, where SMADs are intercellular effectors of transforming growth factor-β (TGF-β) (50). Consequently, similarly to Mab-21, FAM46 proteins seem to be involved in TGF-β signaling pathway. In addition, the presence of predicted potential phosphorylation sites in FAM46A (in regions corresponding to NTase and C-terminal PAP/OAS1 substrate binding domains) may suggest post-translational activation or regulation of its function (49). The most importantly, FAM46 proteins share all critical catalytic amino acids and thus might be active NTases which carry out some NTase reaction potentially crucial for cellular signaling.

Group XXVI (MMP37). Another novel group of NTase fold proteins embraces uncharacterized conserved proteins (KOG2986) and mitochondrial matrix protein of 37 kDa (MMP37) family (PF09139). MMP37 family is involved in the translocation of proteins across the mitochondrial inner membrane *via* the TIM23-PAM complex. Gallas *et al.* hypothesized that MMP37 proteins enhance the early stages of the TIM23 matrix import pathway (51). Our analysis shows that although MMP37 proteins possess NTase fold, they have only one active site carboxylate (from [DE]h[DE]h motif) and thus probably are not able to carry out enzymatic reaction. These potentially non-active members of NTase fold superfamily may bind ATP, hydrolysis of which is necessary for the translocation of proteins through the membrane.

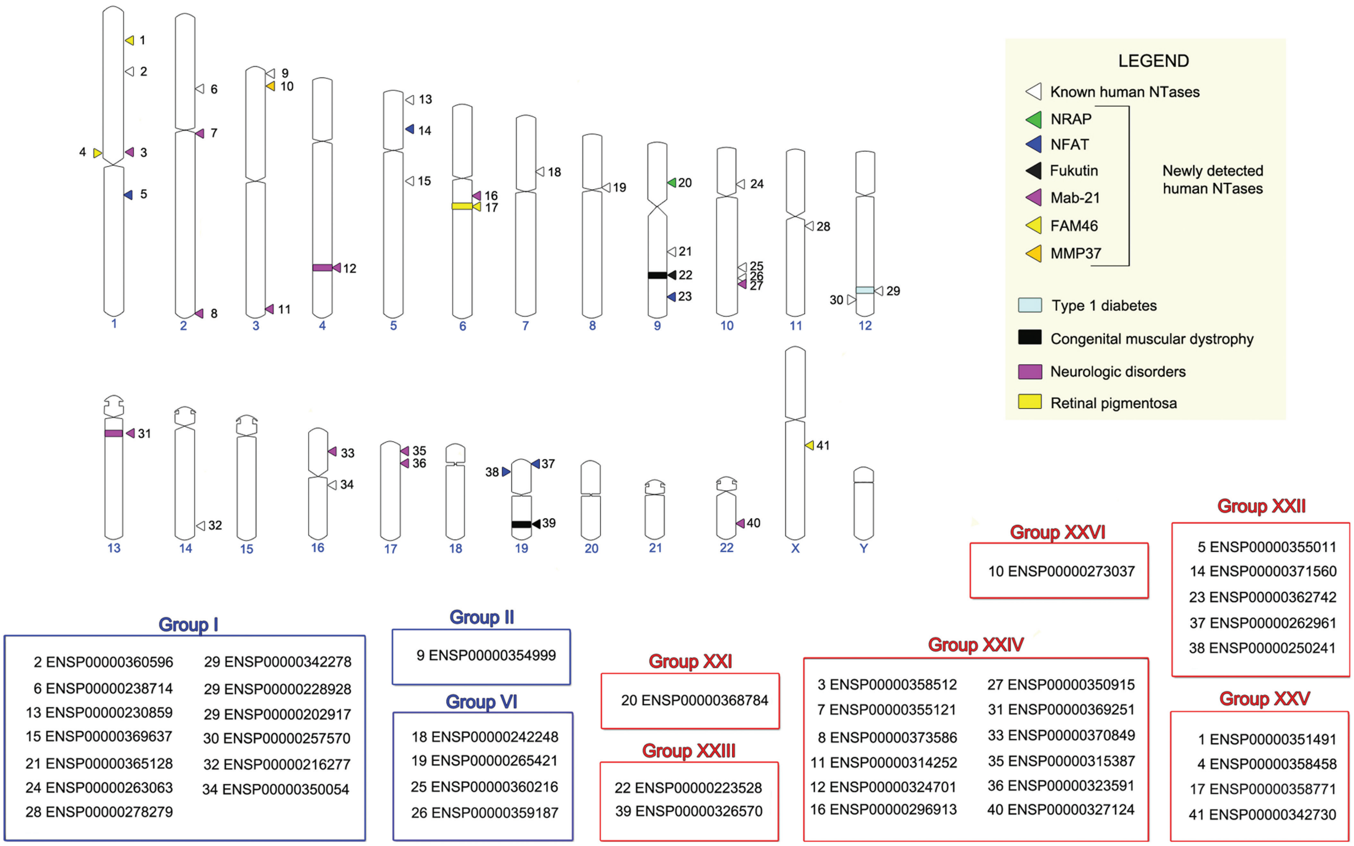

Figure 4. NTase fold proteins in human. Locations of genes encoding NTase fold proteins in human genome are marked with triangles, while rectangles correspond to known genetic diseases associated with mutations found in some of these genes. ENSEMBL identifiers are provided for each protein in blue and red boxes that correspond to known and newly identified groups in our classification, respectively.

This hypothesis is consistent with available experimental data and suggestions risen by Gallas *et al*.

Human NTase fold superfamily proteins

So far only 18 human proteins have been assigned to NTase fold superfamily. These NTases belong to three different groups: group I (PAPOLA, PAPOLG, PAPD1, PAPD5, PAPD4, POLS, TUT1, ZCCHC6, ZCCHC11, OAS1, OAS2, OAS3, OASL), group II (TRNT1) and group VI (POLB, POLM, POLL, DNTT). They participate in many important processes such as RNA maturation, transcription, translation and somatic recombination. Our comprehensive search in human proteome using Meta-BASIC and initiated with all classified above NTase fold families resulted in detection of 25 novel human superfamily members (Figure 4 and Supplementary Figure S3). These proteins of previously unknown structure and function have been placed in seven newly identified groups (Table 1): group XXI (one protein encoded by *NOL6*), group XXII (five proteins encoded by *KIAA1085*, *ZFR*, *STRBP*, *ILF3* and *ILF2*), group XXIII (two proteins encoded by *FKTN* and *FKTR*), group XXIV (12 proteins encoded by *C2ORF54*, *MAB21L2*, *MAB21L1*, *C3ORF59*, *KIAA1754*, *SMCR7L*, *SMCR7*, *C6ORF150*, *TMEM102*, *C1ORF161*, *ITPRIPL1* and *ITPRIPL2*), group XXV (four proteins encoded by *FAM46A*, *FAM46B*, *FAM46C* and *FAM46D*) and group XXVI (one protein encoded by C3ORF31). Assignment of these proteins to NTase fold superfamily combined with available experimental data allowed us to describe the molecular mechanisms of their action, e.g. in incorporation of choline into membrane or regulation of transcription and translation. It should be noted that genes encoding NTase fold proteins (43 human genes in total) are dispersed quite evenly in human genome and are located on majority of chromosomes with the exception of chromosomes 15, 18, 20, 21 and Y (Figure 4).

Finally, we have also analyzed genetic mutations in these human proteins found in various diseases using data collected from OMIM database and manual literature searches. In addition to known connection between OASes and type 1 diabetes (52), we have shown that members of NTase fold superfamily may be also involved in congenital muscular dystrophy, neurologic diseases and retinal pigmentosa, what sheds some new light on the molecular background of these diseases (Figure 4 and Table 1).

Congenital muscular dystrophy. The congenital muscular dystrophies (CMDs) constitute a heterogeneous group of autosomal recessive disorders (53). According to Muntoi

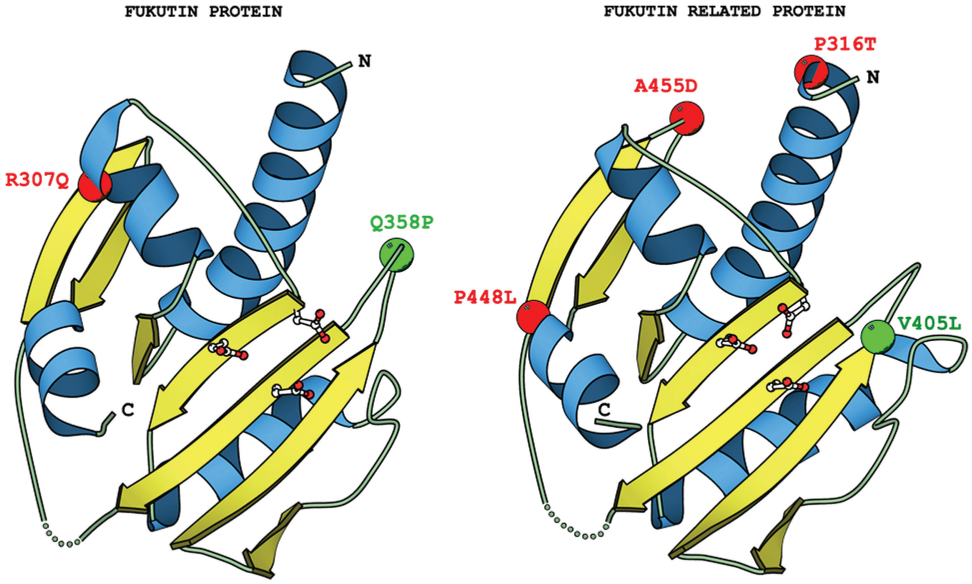

Figure 5. Genetic mutations in Fukutin and Fukutin related protein connected with congenital muscular dystrophy. Positions of single point mutations found in genes encoding Fukutin (in Fukuyama-type congenital muscular dystrophy, FCMD) and Fukutin related protein (in congenital muscular dystrophy type 1C, MDC1C) are shown as spheres on the respective 3D models of their structure. Mutations denoted with green spheres are clustered in the area of the active site and probably impede catalysis or substrate binding. Red spheres represent mutations grouped on the opposite side of the protein surface where they may impair protein–protein or protein–membrane interactions.

and Voit (54) there are three groups of proteins which take part in CMD disorder: extracellular proteins and/or receptors in extracellular matrix, *O*-mannosyl glycosyltransferases and endoplasmatic reticulum proteins. The second group includes *O*-mannosyl transferase, β1,2*N*-acetylglucosaminyltransferase, and Fukutin/Fukutin-related proteins which are newly predicted members of NTase fold superfamily.

Aravidin and Koonin observed that Fukutin (encoded by *FCMD*) and Fukutin related protein (encoded by *FKRP*) possess DxD motif and a distal aspartate residue suggesting that these proteins may coordinate a divalent cation similar to a number of NTases (43). Here we show that Fukutin-related protein is composed of N-terminal inactive glycosyltransferase domain followed by NTase domain, while Fukutin includes only NTase domain. It is possible that Fukutin and Fukutin-related protein possess enzymatic activity that contributes to the synthesis of the *O*-mannosyl glycans in α-dystroglycan. Our hypothesis is supported by experimental data which shows that CMD may be connected with reduction or abnormalities in glycosylated α-dystroglycan (55).

We analyzed all known mutations in FCMD and FKTR genes leading to Fukuyama-type congenital muscular dystrophy (FCMD) and congenital muscular dystrophy type 1C (MDC1C). MDC1C is caused by mutations in the gene encoding Fukutin-related protein (53), while retrotransposon insertion in the 3′ UTR of FCMD gene is known to lead to FCMD. Compounds heterozygotes have also been described with point mutations in one allele of the FCMD gene and the retrotransposon on the second allele. However, no patient had homozygous point mutations suggesting that the complete lack of functional Fukutin could result in embryonic lethality (53).

To analyze the role of single point mutations, we have built 3D models for NTase domain of Fukutin and Fukutin-related protein using the structure of putative NTase TM1012 from *Thermotoga maritima* (PDB: 2ewr) as the closest template identified by 3D-Jury. We have mapped analyzed mutations onto corresponding 3D models and found that they can be divided into two groups. First group includes mutations that cluster in the area of the active site (Q358P in FKTN and V405L in FKRP; green spheres on Figure 5) and probably impede catalysis or substrate binding. Remaining mutations (R307Q in FKTN and P316T, P448L, A455D in FKRP; red spheres on Figure 5) are also grouped on the surface but on the opposite side of the protein where they may impair protein–protein (e.g. with N-terminal substrate binding domain) or protein–membrane interactions. Specifically, these mutations may thus lead to improper orientation of NTase and N-terminal substrate binding domains and as a consequence may lead to misalignment of the bound substrate relative to the active site or alternatively weaken interaction of the protein with membrane.

Neurological disorders. All human proteins from Mab-21 family consist of N-terminal NTase domain followed by C-terminal PAP/OAS1 substrate-binding domain and as hypothesized above they may function as transcription regulators. Although the detailed role of this protein family remains as of now undiscovered, there is an evidence on specific function of these proteins in the broad range of neurological disorders. The various phenotypes associated with this group of genes is related to the nature of the pathogenic condition. It was shown that CAG-trinucleotides repeats in the 5′-untranslated region of two Mab-21 proteins (C2orf54/ENSP00000373586 and MAB21L2/ENSP00000324701, both seem to be active NTases) may undergo the span what can lead to the accumulation of altered proteins in neurons. Previous reports suggested the involvement of this condition in neurologic disorders, such as affective disorders (56), or mental retardation (57). By the analogy to the other neurodegenerative disorders the specific function of these Ntase fold proteins is not critical for the altered phenotype, but is a result of the loco-specific pattern of expression of aberrant gene products.

Retinal pigmentosa. Retinal pigmentosa (RP) is a group of genetic eye conditions encompassing retinal disorders connected with rod retina degeneration (58). FAM46A, located on chromosome 6, was reported to be responsible for various types of dominant and recessive retinal dystrophies. FAM46A may be involved in signal transduction and experimental data shows that it may be a partner in protein–protein interaction map of the SMAD signaling pathway, specifically of SARA, a key regulator of SMAD activation. One of the SMAD-associated factors, BMP7, is known to increase a number of other segments process in chick cultured photoreceptors, while others such as interleukin 2 and STAT-1 are associated with photoreceptor survival and retinal degradation (50). This data combined with our fold and function prediction indicate that FAM46A is an important NTase in signal transduction, and lack of this NTase activity may lead to retinal dysfunction.

CONCLUSION

In this work we combined the state-of-the-art distant homology detection method with transitive similarity searches and fold recognition to identify currently the most complete realm of NTase fold proteins. To fulfill this task we analyzed also lower than threshold predictions to identify novel protein families distantly related to other members of NTase fold superfamily in terms of sequence and structure space. Using this approach we significantly increased the number of known NTase fold proteins and identified 10 new groups which include hundreds of proteins of previously unreported structures and molecular functions. These results clearly suggest that such approach can push limits further for distant homology detection in the midnight zone of homology and allows to study those superfamilies that were exposed in evolution to higher sequence divergence.

The resulting comprehensive classification of NTase fold proteins provides a global picture of this superfamily and sheds some new light on sequence–structure–function relationships and evolution of these proteins that diverged from a common ancestor to adapt to various functional niches. Majority of NTase fold proteins are active NTase that participate in various important biological processes, including DNA repair, somatic recombination, intercellular signaling transduction, enzyme activity regulation and antibiotic resistance. Functional predictions for newly detected members of this superfamily suggest also novel, previously not observed activities such as regulation of gene expression or choline incorporation into cell membrane.

We also performed the systematic search of human proteome to detect 43 NTase fold proteins including 25 novel members of this superfamily. The new members belong to six of ten groups, with nearly a half of these (12) belonging to the group XXIV (Mab-21) in our classification. Some members of this family were reported to be actively involved in either transcription or secondary messenger signaling. Genetic data from OMIM database combined with sequence/structure analyses for newly detected human NTases and their inactive homologs, allowed to obtain a novel insight into molecular background of selected genetic disorders, including a congenital muscular dystrophy, retinal pigmentosa and neurological disorders. These data should inspire further experimental studies on predicted activity and potential substrates providing further insight into detailed biological roles of these highly important proteins in humans.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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