FIELDS of O07584  
catalytic activity: EC = 2.3.1.n4, a 1-acyl-sn-glycero-3-phosphate + a fatty acyl-[ACP] = a 1,2-diacyl-sn-glycero-3-phosphate + holo-[ACP]  
subcellular location: Cell membrane  
functional domains: Glycerol-3-phosphate (1)-acyltransferase, 1-acylglycerol-3-phosphate O-acyltransferase activity  
taxonomy: Bacteria, Bacillota, Bacilli  
protein size: 199 aa, 21923 KDa  
  
Summary  
> This protein is a 1-acyl-sn-glycero-3-phosphate acyltransferase, which is involved in the synthesis of phospholipids  
> It acts on a 1-acyl-sn-glycero-3-phosphate molecule and a fatty acyl-[ACP] (acyl carrier protein) molecule to produce a 1,2-diacyl-sn-glycero-3-phosphate molecule and holo-[ACP]  
> Its enzymatic activity is classified as EC = 2.3.1.n4  
> The protein is primarily located in the cell membrane  
> It contains functional domains such as Glycerol-3-phosphate (1)-acyltransferase and 1-acylglycerol-3-phosphate O-acyltransferase  
> This protein is found in bacteria, specifically in the Bacillota class of the Bacilli phylum  
> It has a size of 199 amino acids and a molecular weight of 21923 Daltons.  
  
QA  
> What is the catalytic activity of the protein? The catalytic activity of the protein is the conversion of a 1-acyl-sn-glycero-3-phosphate and a fatty acyl-[ACP] into a 1,2-diacyl-sn-glycero-3-phosphate and holo-[ACP].  
> Where is the protein primarily located? The protein is primarily located in the cell membrane.  
> What are the functional domains of the protein? The functional domains of the protein include Glycerol-3-phosphate (1)-acyltransferase and 1-acylglycerol-3-phosphate O-acyltransferase.  
> In which taxonomic groups is the protein found? The protein is found in bacteria, specifically in the Bacillota class of the Bacilli phylum.  
> What is the size of the protein? The protein has a size of 199 amino acids and a molecular weight of 21923 Daltons.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 199  
mw: 21923

FIELDS of P0A3T2  
functional domains: Periplasmic binding protein-like II  
taxonomy: Bacteria, Pseudomonadota, Alphaproteobacteria  
protein size: 329 aa, 34273 KDa  
  
Summary  
> This protein belongs to the functional domain called Periplasmic binding protein-like II  
> It is found in bacteria, specifically in the taxonomic groups Bacteria, Pseudomonadota, and Alphaproteobacteria  
> The protein has a size of 329 amino acids and a molecular weight of 34,273 KDa.  
  
QA  
> What is the functional domain of this protein? Periplasmic binding protein-like II.  
> In which taxonomic groups is this protein found? Bacteria, Pseudomonadota, Alphaproteobacteria.  
> What is the size of this protein in terms of amino acids? 329 amino acids.  
> What is the molecular weight of this protein? 34,273 KDa.  
> Is this protein an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 329  
mw: 34273

FIELDS of Q8TNY4  
catalytic activity: 2 ATP + H2O + hydrogencarbonate + L-glutamine = 2 ADP + carbamoyl phosphate + 2 H(+) + L-glutamate + phosphate, EC = 6.3.5.5  
cofactor: Mg(2+), Binds 4 Mg(2+) or Mn(2+) ions per subunit., Mn(2+)  
subunit: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate.  
functional domains: Carbamoyl phosphate synthetase, large subunit connection domain, PreATP-grasp domain, ATP-grasp fold, A domain, metal ion binding, Methylglyoxal synthase-like, Carbamoyl-phosphate synthetase, large subunit oligomerisation domain, ATP-grasp fold, B domain, carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity, Glutathione synthetase ATP-binding domain-like, Methylglyoxal synthase-like domain, ATP binding  
taxonomy: Archaea, Euryarchaeota, Stenosarchaea group  
protein size: 1070 aa, 118441 KDa  
  
Summary  
> This protein is a carbamoyl phosphate synthetase, involved in the synthesis of carbamoyl phosphate  
> It is composed of two subunits, a small (or glutamine) chain and a large (or ammonia) chain  
> The small chain promotes the hydrolysis of glutamine to ammonia, which is used by the large chain to synthesize carbamoyl phosphate  
> The protein requires the presence of four Mg(2+) or Mn(2+) ions per subunit as cofactors  
> It belongs to the Archaea domain, specifically to the Euryarchaeota group within the Stenosarchaea group  
> The protein has a size of 1070 amino acids and a molecular weight of 118441 KDa.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the conversion of 2 ATP, H2O, hydrogencarbonate, and L-glutamine into 2 ADP, carbamoyl phosphate, 2 H(+), L-glutamate, and phosphate.  
> What is the EC number of this protein? The EC number of this protein is 6.3.5.5.  
> What is the function of the small chain of this protein? The small chain promotes the hydrolysis of glutamine to ammonia.  
> How is carbamoyl phosphate synthesized in this protein? Carbamoyl phosphate is synthesized in this protein using ammonia, which is generated by the hydrolysis of glutamine.  
> What are the cofactors required by this protein? This protein requires the presence of four Mg(2+) or Mn(2+) ions per subunit as cofactors.  
> Which domain of this protein is involved in ATP binding? The ATP binding domain is involved in ATP binding.  
> What is the taxonomy of this protein? This protein belongs to the Archaea domain, specifically to the Euryarchaeota group within the Stenosarchaea group.  
> How big is this protein? This protein has a size of 1070 amino acids and a molecular weight of 118441 KDa.  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg(2+), mn(2+)  
length: 1070  
mw: 118441

FIELDS of Q92Z29  
catalytic activity: EC = 1.7.2.1, Fe(III)-[cytochrome c] + H2O + nitric oxide = Fe(II)-[cytochrome c] + 2 H(+) + nitrite  
cofactor: Cu(2+), Cu(+), Binds 1 Cu(2+) ion. The Cu(2+) ion is held by residues from each of 2 monomers of the trimer. Nitrite is bound to the Cu(2+) ion site. Pseudoazurin is the physiological electron donor for the Cu-NIR in vitro., FAD, Binds 1 Cu(+) ion. The Cu(+) ion is bound within a single monomer.  
subunit: Homotrimer.  
subcellular location: Periplasm  
functional domains: Cupredoxins, Cupredoxins - blue copper proteins, copper ion binding, nitrite reductase (NO-forming) activity  
taxonomy: Bacteria, Pseudomonadota, Alphaproteobacteria  
protein size: 376 aa, 40259 KDa  
  
Summary  
> This protein is a nitrite reductase (NO-forming) enzyme found in bacteria  
> It belongs to the Cupredoxins family and functions as a blue copper protein  
> The protein is a homotrimer, consisting of three identical subunits  
> It is localized in the periplasm, a region between the inner and outer membranes of bacterial cells  
> The protein has a size of 376 amino acids and a molecular weight of 40259 KDa  
> It binds two different metal cofactors, Cu(2+) and Cu(+), each playing distinct roles  
> The Cu(2+) ion is held by residues from each of the monomers, while the Cu(+) ion is bound within a single monomer  
> The protein's catalytic activity is described by the enzymatic reaction: Fe(III)-[cytochrome c] + H2O + nitric oxide = Fe(II)-[cytochrome c] + 2 H(+) + nitrite  
> Pseudoazurin is the physiological electron donor for the Cu-NIR in vitro  
> The presence of FAD further contributes to the protein's functionality.  
  
QA  
> What is the subunit composition of this protein? Homotrimer.  
> Where is this protein located within the bacterial cell? Periplasm.  
> What is the molecular weight of this protein? 40259 KDa. 4) Name one of the metal cofactors bound by this protein. Cu(2+).  
> How many amino acids does this protein consist of? 376 aa.  
> What is the enzymatic reaction catalyzed by this protein? Fe(III)-[cytochrome c] + H2O + nitric oxide = Fe(II)-[cytochrome c] + 2 H(+) + nitrite.  
> What is the physiological electron donor for the Cu-NIR in vitro? Pseudoazurin.  
> How many different metal ions does this protein bind? Two.  
> What is the functional family of this protein? Cupredoxins.  
> What is the role of FAD in this protein? It contributes to the protein's functionality.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: cu(2+),cu(+)  
length: 376  
mw: 40259

FIELDS of P19181  
functional domains: Immunoglobulins, Immunoglobulin  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 116 aa, 12808 KDa  
  
Summary  
> The provided protein is a eukaryotic protein with immunoglobulin domains  
> It has a size of 116 amino acids and a molecular weight of 12808 KDa  
> Immunoglobulins are involved in immune responses and are commonly found in chordates  
> They play a crucial role in recognizing and binding to antigens, initiating immune reactions, and facilitating the clearance of pathogens  
> The protein's immunoglobulin domains are responsible for the antigen-binding specificity, enabling the protein to recognize a wide range of antigens  
> With its unique structural properties, this protein participates in various immune-related processes, contributing to the defense mechanisms and overall protection against foreign substances.  
  
QA  
> What is the size of the protein? The protein has a size of 116 amino acids.  
> What is the molecular weight of the protein? The molecular weight of the protein is 12808 KDa.  
> What are the functional domains of the protein? The protein has immunoglobulin domains as its functional domains.  
> Which taxonomic groups does the protein belong to? The protein belongs to the taxonomic groups Eukaryota, Metazoa, and Chordata.  
> What is the role of immunoglobulins in the body? Immunoglobulins are involved in immune responses and play a crucial role in recognizing and binding to antigens.  
> What is the significance of the immunoglobulin domain in this protein? The immunoglobulin domain in this protein is responsible for its antigen-binding specificity, enabling it to recognize a wide range of antigens.  
> What processes does the protein participate in? The protein participates in various immune-related processes, contributing to defense mechanisms and protection against foreign substances.  
> Does this protein function as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 116  
mw: 12808

FIELDS of Q9FXB9  
subcellular location: Mitochondrion  
functional domains: Class II aaRS ABD-related, Tetratricopeptide repeat domain, zinc ion binding, RNA binding  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 704 aa, 79705 KDa  
  
Summary  
> This protein is found in the mitochondrion, a cellular organelle responsible for energy production  
> It contains several functional domains, including Class II aaRS ABD-related, tetratricopeptide repeat domain, zinc ion binding, and RNA binding  
> These domains enable the protein to perform specific functions within the cell  
> The protein is found in eukaryotes, specifically in the Viridiplantae group within the Streptophyta phylum  
> It has a size of 704 amino acids and a molecular weight of 79705 KDa.  
  
QA  
> Where is this protein located within the cell? It is located in the mitochondrion.  
> What are the functional domains present in this protein? The functional domains include Class II aaRS ABD-related, tetratricopeptide repeat domain, zinc ion binding, and RNA binding.  
> Which organisms can this protein be found in? It can be found in eukaryotes, specifically in the Viridiplantae group within the Streptophyta phylum.  
> What is the size of this protein? It has a size of 704 amino acids.  
> What is the molecular weight of this protein? The molecular weight is 79705 KDa.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: mitochondrion  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: True  
is\_enzyme: False  
length: 704  
mw: 79705

FIELDS of Q9SW75  
functional domains: Ribosomal protein L1, structural constituent of ribosome, RNA binding  
taxonomy: Eukaryota, Viridiplantae, Chlorophyta  
protein size: 213 aa, 23856 KDa  
  
Summary  
> Ribosomal protein L1 is a protein with functional domains that include being a structural constituent of the ribosome and having RNA binding properties  
> It is found in eukaryotes, specifically in the Viridiplantae kingdom, more specifically in the Chlorophyta class  
> The protein has a size of 213 amino acids and a molecular weight of 23856 KDa.  
  
QA  
> What are the functional domains of this protein? The functional domains of this protein include being a structural constituent of the ribosome and having RNA binding properties.  
> What is the taxonomy of this protein? This protein is found in eukaryotes, specifically in the Viridiplantae kingdom, more specifically in the Chlorophyta class.  
> How many amino acids make up this protein? This protein has a size of 213 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 23856 KDa.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 213  
mw: 23856

FIELDS of Q2LXN0  
catalytic activity: ATP + H2O + L-glutamine + L-glutamyl-tRNA(Gln) = ADP + H(+) + L-glutamate + L-glutaminyl-tRNA(Gln) + phosphate, ATP + H2O + L-aspartyl-tRNA(Asn) + L-glutamine = ADP + 2 H(+) + L-asparaginyl-tRNA(Asn) + L-glutamate + phosphate  
subunit: Heterotrimer of A, B and C subunits.  
functional domains: Glutamine synthetase/guanido kinase, asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity, glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity, GatB domain, N-terminal subdomain, GatB/YqeY motif, ATP binding  
taxonomy: Bacteria, Thermodesulfobacteriota, Syntrophia  
protein size: 476 aa, 53532 KDa  
  
Summary  
> Glutamine and asparagine are amino acids that play essential roles in various biological processes  
> A protein, found in bacteria of the Thermodesulfobacteriota group belonging to the Syntrophia genus, is responsible for the synthesis of both glutamine and asparagine  
> This protein is a heterotrimer composed of three subunits - A, B, and C  
> It exhibits several functional domains, including glutamine synthetase/guanido kinase, asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity, glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity  
> These functional domains facilitate the catalytic activities of the protein  
> One of the catalytic activities of this protein involves the hydrolysis of ATP, L-glutamine, and L-glutamyl-tRNA(Gln), resulting in the formation of ADP, H(+), L-glutamate, L-glutaminyl-tRNA(Gln), and phosphate  
> Another catalytic activity involves the hydrolysis of ATP, L-aspartyl-tRNA(Asn), and L-glutamine, leading to the production of ADP, 2 H(+), L-asparaginyl-tRNA(Asn), L-glutamate, and phosphate  
> These reactions highlight the role of this protein in the biosynthesis of glutamine and asparagine  
> The protein's subunit composition is important for its functioning, with each subunit contributing to its overall activity  
> Furthermore, the protein contains various functional domains, such as the GatB domain, N-terminal subdomain, GatB/YqeY motif, and ATP binding site, which are crucial for its enzymatic activities  
> Overall, this protein found in bacteria of the Thermodesulfobacteriota group, specifically Syntrophia genus, plays a vital role in the biosynthesis of glutamine and asparagine, exhibiting multiple catalytic activities and containing functional domains that contribute to its enzymatic functions.  
  
QA  
> What is the subunit composition of this protein? The protein is composed of A, B, and C subunits. It is a heterotrimer.  
> What are the catalytic activities of this protein? The protein exhibits catalytic activities involved in the hydrolysis of ATP, L-glutamine, and L-glutamyl-tRNA(Gln), as well as ATP, L-aspartyl-tRNA(Asn), and L-glutamine.  
> What are the functional domains of this protein? The functional domains of this protein include glutamine synthetase/guanido kinase, asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity, glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity, GatB domain, N-terminal subdomain, GatB/YqeY motif, and ATP binding site.  
> What is the taxonomy of this protein? This protein is found in bacteria of the Thermodesulfobacteriota group, specifically the Syntrophia genus.  
> What is the size of this protein? The protein has a size of 476 amino acids and a molecular weight of 53532 KDa.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 476  
mw: 53532

FIELDS of Q2LGZ2  
subunit: CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1), CF(0) has four main subunits: a, b, b' and c (By similarity)., F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel  
subcellular location: Chloroplast thylakoid membrane, Peripheral membrane protein, Plastid  
functional domains: ATP synthase (F1-ATPase), gamma subunit, proton-transporting ATP synthase activity, rotational mechanism  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 118 aa, 13024 KDa  
  
Summary  
> The protein discussed in the provided information is a subunit of the ATP synthase enzyme, specifically the CF(1) and CF(0) components of the F-type ATPases  
> CF(1) has five subunits, namely alpha(3), beta(3), gamma(1), delta(1), epsilon(1), while CF(0) consists of four main subunits: a, b, b', and c  
> The subcellular location of this protein is the chloroplast thylakoid membrane, and it is categorized as a peripheral membrane protein associated with plastids  
> The functional domains of this protein include ATP synthase (F1-ATPase), the gamma subunit, and proton-transporting ATP synthase activity involved in a rotational mechanism  
> In terms of taxonomy, this protein belongs to the Eukaryota domain, specifically the Viridiplantae kingdom within the Streptophyta phylum  
> The protein has a size of 118 amino acids and a molecular weight of 13024 kilodaltons.  
  
QA  
> What are the subunits of CF(1)? The subunits of CF(1) are alpha(3), beta(3), gamma(1), delta(1), and epsilon(1).  
> How many subunits does CF(0) have? CF(0) consists of four main subunits: a, b, b', and c.  
> Where is this protein located? This protein is located in the chloroplast thylakoid membrane.  
> What is the classification of this protein? This protein is classified as a peripheral membrane protein associated with plastids.  
> What are the functional domains of this protein? The functional domains of this protein include ATP synthase (F1-ATPase), the gamma subunit, and proton-transporting ATP synthase activity.  
> What is the taxonomy of this protein? This protein belongs to the Eukaryota domain, specifically the Viridiplantae kingdom within the Streptophyta phylum.  
> How large is this protein? This protein has a size of 118 amino acids and a molecular weight of 13024 kilodaltons.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 118  
mw: 13024

FIELDS of Q9PF89  
subunit: Forms oligomers.  
subcellular location: Cytoplasm, Nucleoid  
functional domains: AbrB/MazE/MraZ-like, Transcriptional regulator MraZ domain, DNA binding, DNA-binding transcription factor activity  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 148 aa, 16540 KDa  
  
Summary  
> This protein is a subunit that forms oligomers  
> It is found in the cytoplasm and nucleoid of bacterial cells, specifically within the taxonomic group of Gammaproteobacteria  
> The protein has functional domains including the AbrB/MazE/MraZ-like domain and the Transcriptional regulator MraZ domain  
> It possesses DNA binding capabilities and functions as a DNA-binding transcription factor  
> The protein has a size of 148 amino acids and a molecular weight of 16540 KDa.  
  
QA  
> What is the subcellular location of this protein? It is found in the cytoplasm and nucleoid.  
> What are the functional domains of this protein? It has the AbrB/MazE/MraZ-like domain and the Transcriptional regulator MraZ domain.  
> What is the size of this protein? It has a size of 148 amino acids.  
> What is the molecular weight of this protein? It has a molecular weight of 16540 KDa.  
> What is the taxonomic classification of this protein? It belongs to the taxonomic group of Gammaproteobacteria  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 148  
mw: 16540

FIELDS of Q9QYM2  
catalytic activity: EC = 3.2.1.143, [(1''->2')-ADP-alpha-D-ribose](n) + H2O = [(1''->2')-ADP-alpha-D-ribose](n-1) + ADP-D-ribose  
subcellular location: Nucleus  
functional domains: poly(ADP-ribose) glycohydrolase activity, chromatin binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 972 aa, 109003 KDa  
  
Summary  
> This protein is a poly(ADP-ribose) glycohydrolase that primarily functions in the nucleus  
> It has a catalytic activity of breaking down [(1''->2')-ADP-alpha-D-ribose], a type of ADP-ribose polymer, into smaller fragments  
> This reaction involves the hydrolysis of the glycosidic bond with the addition of a water molecule  
> The protein is involved in chromatin binding and is encoded by a gene found in eukaryotes, specifically in Metazoa (animals) and within the Chordata phylum  
> It has a size of 972 amino acids and a molecular weight of approximately 109,003 KDa.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein involves breaking down [(1''->2')-ADP-alpha-D-ribose] into smaller fragments.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: True  
length: 972  
mw: 109003

FIELDS of B5YE89  
catalytic activity: EC = 5.3.1.16, 1-(5-phospho-beta-D-ribosyl)-5-[(5-phospho-beta-D-ribosylamino)methylideneamino]imidazole-4-carboxamide = 5-[(5-phospho-1-deoxy-D-ribulos-1-ylimino)methylamino]-1-(5-phospho-beta-D-ribosyl)imidazole-4-carboxamide  
subcellular location: Cytoplasm  
functional domains: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity, Aldolase class I, Ribulose-phoshate binding barrel  
taxonomy: Bacteria, Dictyoglomota, Dictyoglomia  
protein size: 242 aa, 27654 KDa  
  
Summary  
> This protein is an enzyme with the catalytic activity EC = 5.3.1.16  
> It acts as a 1-(5-phospho-beta-D-ribosyl)-5-[(5-phospho-beta-D-ribosylamino)methylideneamino]imidazole-4-carboxamide isomerase, converting this compound into 5-[(5-phospho-1-deoxy-D-ribulos-1-ylimino)methylamino]-1-(5-phospho-beta-D-ribosyl)imidazole-4-carboxamide  
> The protein is primarily located in the cytoplasm  
> It possesses functional domains such as Aldolase class I and a Ribulose-phoshate binding barrel  
> The protein is found in bacterial organisms belonging to the Dictyoglomota class within the Dictyoglomia phylum  
> It has a length of 242 amino acids and a molecular weight of 27654 KDa.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is EC = 5.3.1.16.  
> What compound does this protein isomerase convert? This protein converts 1-(5-phospho-beta-D-ribosyl)-5-[(5-phospho-beta-D-ribosylamino)methylideneamino]imidazole-4-carboxamide into 5-[(5-phospho-1-deoxy-D-ribulos-1-ylimino)methylamino]-1-(5-phospho-beta-D-ribosyl)imidazole-4-carboxamide.  
> Where is this protein primarily located? This protein is primarily located in the cytoplasm.  
> Which functional domains does this protein possess? This protein possesses the functional domains of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity, Aldolase class I, and Ribulose-phoshate binding barrel.  
> What is the taxonomy of this protein? This protein belongs to the bacteria of the Dictyoglomota class within the Dictyoglomia phylum.  
> How long is this protein? This protein has a length of 242 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 27654 KDa.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 242  
mw: 27654

FIELDS of B8NLU5  
subcellular location: Nucleus  
functional domains: Leucine zipper domain, DNA binding, DNA-binding transcription factor activity  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 318 aa, 35914 KDa  
  
Summary  
> This protein is a DNA-binding transcription factor found in the nucleus of eukaryotic organisms, specifically in the fungi kingdom  
> It consists of 318 amino acids and has a molecular weight of approximately 35,914 kilodaltons  
> The protein contains functional domains, including a leucine zipper domain, which is involved in protein-protein interactions, and DNA-binding domains that allow it to bind to specific DNA sequences  
> Through its DNA-binding activity, this protein acts as a transcription factor, regulating the expression of target genes  
> Its presence in the nucleus and DNA-binding transcription factor activity suggest that it plays a role in transcriptional regulation, controlling various cellular processes in fungi.  
  
QA  
> Where is this protein located within a cell? It is located in the nucleus.  
> What are the functional domains of this protein? It has a leucine zipper domain and DNA binding domain/s.  
> What is the taxonomy of this protein? It belongs to the kingdom Fungi within the larger group Dikarya in the domain Eukaryota.  
> How many amino acids does this protein consist of? It has 318 amino acids.  
> What is the approximate molecular weight of this protein? It weighs around 35,914 kilodaltons.  
> What is the main activity of this protein? It functions as a DNA-binding transcription factor, regulating gene expression.  
> What is the specific DNA-binding activity of this protein? It binds to specific DNA sequences through its DNA-binding domains.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: False  
length: 318  
mw: 35914

FIELDS of Q9M2S9  
subcellular location: Peripheral membrane protein, Cell wall, Secreted, Membrane  
functional domains: PHL pollen allergen, Expansin, cellulose-binding-like domain, Barwin-like endoglucanases, RlpA-like domain  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 260 aa, 28162 KDa  
  
Summary  
> This protein is a peripheral membrane protein that can be found in various subcellular locations, including the cell wall, secreted form, and membrane  
> It contains several functional domains, such as PHL pollen allergen, Expansin, cellulose-binding-like domain, Barwin-like endoglucanases, and RlpA-like domain  
> The protein belongs to the taxonomic group Eukaryota, specifically within the kingdom Viridiplantae and the phylum Streptophyta  
> It has a size of 260 amino acids and a molecular weight of 28162 KDa.  
  
QA  
> What is the subcellular location of this protein? This protein can be found in the peripheral membrane, cell wall, secreted form, and membrane.  
> What are the functional domains present in this protein? This protein contains several functional domains including PHL pollen allergen, Expansin, cellulose-binding-like domain, Barwin-like endoglucanases, and RlpA-like domain.  
> Which taxonomic group does this protein belong to? This protein belongs to the taxonomic group Eukaryota.  
> What is the size of this protein in terms of amino acids? This protein has a size of 260 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 28162 KDa.  
> Which kingdom does this protein belong to? This protein belongs to the kingdom Viridiplantae.  
> In which phylum is this protein classified? This protein is classified in the phylum Streptophyta.  
> Does this protein function as an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 260  
mw: 28162

FIELDS of B1L7A5  
subcellular location: Cytoplasm  
functional domains: RNA binding, ribosome binding, Translation proteins SH3-like domain, translation initiation factor activity, Nucleic acid-binding proteins, translation elongation factor activity  
taxonomy: Archaea, Candidatus Korarchaeota, Candidatus Korarchaeum  
protein size: 134 aa, 14821 KDa  
  
Summary  
> This protein is a molecular entity that is located in the cytoplasm  
> It possesses several functional domains including RNA binding, ribosome binding, Translation proteins SH3-like domain, translation initiation factor activity, Nucleic acid-binding proteins, and translation elongation factor activity  
> Based on the provided taxonomy information, it is found in the domain Archaea, specifically in the Candidatus Korarchaeota, Candidatus Korarchaeum lineage  
> The protein has a size of 134 amino acids and a molecular weight of 14821 kilodaltons.  
  
QA  
> What is the subcellular localization of this protein? The protein is located in the cytoplasm.  
> What are the functional domains of this protein? The functional domains of this protein include RNA binding, ribosome binding, Translation proteins SH3-like domain, translation initiation factor activity, and Nucleic acid-binding proteins.  
> What is the taxonomic classification of this protein? The protein belongs to the domain Archaea, specifically to the Candidatus Korarchaeota, Candidatus Korarchaeum lineage.  
> How large is this protein in terms of amino acid length? The protein has a size of 134 amino acids.  
> What is the molecular weight of this protein? The protein has a molecular weight of 14821 kilodaltons.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 134  
mw: 14821

FIELDS of Q9USP7  
subcellular location: Cytoplasm  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 397 aa, 44018 KDa  
  
Summary  
> The protein is a eukaryotic protein that is located in the cytoplasm  
> It belongs to the taxonomic classification of fungi, specifically within the Dikarya group  
> The protein has a size of 397 amino acids and a molecular weight of 44018 KDa.  
  
QA  
> What is the subcellular location of the protein? The protein is located in the cytoplasm.  
> What is the taxonomic classification of the protein? The protein belongs to the group called Dikarya within the fungi kingdom.  
> How many amino acids does the protein have? The protein has a size of 397 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of 44018 KDa.  
> Can this protein act as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 397  
mw: 44018

FIELDS of Q9VU02  
subcellular location: Cytosol, Nucleus, Cytoplasm  
functional domains: Sm-like ribonucleoproteins, RNA binding  
taxonomy: Eukaryota, Metazoa, Ecdysozoa  
protein size: 124 aa, 13796 KDa  
  
Summary  
> This protein is found in the cytosol, nucleus, and cytoplasm  
> It belongs to the Sm-like ribonucleoproteins family and is involved in RNA binding  
> With a size of 124 amino acids, this protein has a molecular weight of 13796 KDa  
> It is found in the eukaryotic domain, specifically in the metazoan and ecdysozoan taxa.  
  
QA  
> What are the subcellular locations of this protein? This protein is found in the cytosol, nucleus, and cytoplasm.  
> What functional domains does this protein belong to? This protein belongs to the Sm-like ribonucleoproteins and has RNA binding ability.  
> What is the size of this protein? This protein has a size of 124 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 13796 KDa.  
> In which taxonomic groups is this protein found? This protein is found in the eukaryotic domain, specifically in the metazoan and ecdysozoan taxa.  
> Is this protein an enzyme? No  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: False  
length: 124  
mw: 13796

FIELDS of Q0TTA0  
catalytic activity: EC = 4.2.3.4, 7-phospho-2-dehydro-3-deoxy-D-arabino-heptonate = 3-dehydroquinate + phosphate  
cofactor: Zn(2+), Binds 1 divalent metal cation per subunit. Can use either Co(2+) or Zn(2+)., NAD(+), Co(2+)  
subcellular location: Cytoplasm  
functional domains: metal ion binding, 3-dehydroquinate synthase activity, nucleotide binding, Dehydroquinate synthase-like, Dehydroquinate synthase-like - alpha domain  
taxonomy: Bacteria, Bacillota, Clostridia  
protein size: 350 aa, 39123 KDa  
  
Summary  
> This protein is a 3-dehydroquinate synthase enzyme found in the cytoplasm of bacteria  
> It has a catalytic activity (EC = 4.2.3.4) that involves converting 7-phospho-2-dehydro-3-deoxy-D-arabino-heptonate into 3-dehydroquinate and phosphate  
> The protein requires a divalent metal cation for its function, with zinc (Zn2+) and cobalt (Co2+) being suitable cofactors  
> It also binds to NAD(+) for its activity  
> The protein is composed of several functional domains, including metal ion binding, 3-dehydroquinate synthase activity, nucleotide binding, and two Dehydroquinate synthase-like domains  
> It belongs to the bacteria taxonomic group, specifically within the Bacillota and Clostridia classes  
> The protein has a size of 350 amino acids and a mass of 39123 kilodaltons.  
  
QA  
> What type of enzyme is this protein? This protein is a 3-dehydroquinate synthase enzyme.  
> Where is this protein located within the cell? This protein is found in the cytoplasm.  
> What is the catalytic activity of this protein? The catalytic activity of this protein is converting 7-phospho-2-dehydro-3-deoxy-D-arabino-heptonate into 3-dehydroquinate and phosphate.  
> What are the possible cofactors for this protein? The possible cofactors for this protein are zinc (Zn2+) and cobalt (Co2+).  
> What is the size of this protein? This protein has a size of 350 amino acids.  
> Which taxonomic groups does this protein belong to? This protein belongs to the bacteria taxonomic group, specifically within the Bacillota and Clostridia classes.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: zinc (zn2+), cobalt (co2+)  
length: 350  
mw: 39123

FIELDS of Q4R6V2  
subcellular location: Cytoskeleton, Microtubule organizing center, Centrosome, Cytoplasm  
functional domains: unfolded protein binding, mRNA 3'-UTR binding, ATP hydrolysis activity, GroEL-like equatorial domain, GroEL apical domain-like, beta-tubulin binding, GroEL equatorial domain-like, ATP-dependent protein folding chaperone, GroEL-intermediate domain like, TCP-1-like chaperonin intermediate domain, mRNA 5'-UTR binding, G-protein beta-subunit binding, GroEL, ATP binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 541 aa, 59671 KDa  
  
Summary  
> This protein is found in various subcellular locations including the cytoskeleton, microtubule organizing center, centrosome, and cytoplasm  
> It has several functional domains involved in various activities such as unfolded protein binding, mRNA 3'-UTR binding, ATP hydrolysis, beta-tubulin binding, and ATP-dependent protein folding chaperone  
> The protein is classified in the taxonomy of eukaryotes, more specifically in the metazoan group within the chordata  
> It has a protein size of 541 amino acids and a molecular weight of approximately 59,671 kilodaltons.  
  
QA  
> What are the subcellular locations where this protein can be found? This protein can be found in the cytoskeleton, microtubule organizing center, centrosome, and cytoplasm.  
> What are the functional domains of this protein? The functional domains of this protein include unfolded protein binding, mRNA 3'-UTR binding, ATP hydrolysis activity, GroEL-like equatorial domain, GroEL apical domain-like, beta-tubulin binding, GroEL equatorial domain-like, ATP-dependent protein folding chaperone, GroEL-intermediate domain like, TCP-1-like chaperonin intermediate domain, mRNA 5'-UTR binding, G-protein beta-subunit binding, GroEL, and ATP binding.  
> In which taxonomic group does this protein belong? This protein belongs to the taxonomic group of eukaryotes, specifically within the metazoan group in the chordata.  
> What is the size of this protein? This protein has a size of 541 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is approximately 59,671 kilodaltons.  
> Does this protein function as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 541  
mw: 59671

FIELDS of P45183  
functional domains: MOP-like  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 69 aa, 7122 KDa  
  
Summary  
> This protein is a member of the MOP-like functional domain and is found in bacteria, specifically within the phylum Pseudomonadota of the class Gammaproteobacteria  
> It has a small size, consisting of only 69 amino acids, but has a relatively high molecular weight of 7122 kilodaltons.  
  
QA  
> What is the functional domain of this protein? The functional domain of this protein is MOP-like.  
> In which taxonomic groups can this protein be found? This protein can be found in bacteria, specifically within the phylum Pseudomonadota of the class Gammaproteobacteria.  
> How many amino acids does this protein contain? This protein contains 69 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 7122 kilodaltons.  
> Can this protein act as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 69  
mw: 7122

FIELDS of A5GVY8  
subunit: Part of the 50S ribosomal subunit.  
functional domains: L28p-like, rRNA binding, structural constituent of ribosome, Ribosomal protein L31  
taxonomy: Bacteria, Cyanobacteriota, Cyanophyceae  
protein size: 92 aa, 10050 KDa  
  
Summary  
> This protein is a component of the 50S ribosomal subunit found in bacteria, specifically in the phylum Cyanobacteriota and class Cyanophyceae  
> It has a size of 92 amino acids and a molecular weight of 10,050 KDa  
> The protein has several functional domains, including being a structural constituent of the ribosome, having rRNA binding capabilities, and being similar to a protein called L28p  
> It is classified as Ribosomal protein L31.  
  
QA  
> What is the localization of this protein? It is part of the 50S ribosomal subunit.  
> What are the functional domains of this protein? Its functional domains include being a structural constituent of the ribosome, having rRNA binding capabilities, and being similar to a protein called L28p.  
> What is the taxonomy of this protein? It belongs to the phylum Cyanobacteriota and class Cyanophyceae.  
> How large is this protein? It has a size of 92 amino acids and a molecular weight of 10,050 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 92  
mw: 10050

FIELDS of P15969  
subunit: Heterodimer of two subunits, a major chain and a minor chain, linked by a disulfide bond.  
subcellular location: Secreted  
functional domains: calcium channel regulator activity, toxin activity  
taxonomy: Eukaryota, Metazoa, Ecdysozoa  
protein size: 112 aa, 12808 KDa  
  
Summary  
> This protein is a heterodimer composed of a major chain and a minor chain, connected by a disulfide bond  
> It is primarily located in the extracellular space  
> The protein has two functional domains, calcium channel regulator activity and toxin activity  
> In terms of taxonomy, it belongs to the eukaryotic group, specifically the metazoan subgroup within the larger ecdysozoa category  
> It has a relatively small size, consisting of 112 amino acids and a molecular weight of 12808 KDa.  
  
QA  
> What kind of bond links the major and minor chains of the protein? A disulfide bond.  
> Where is this protein primarily located? In the extracellular space.  
> What are the functional domains of this protein? Calcium channel regulator activity and toxin activity.  
> Which taxonomic groups does this protein belong to? Eukaryota, Metazoa, Ecdysozoa.  
> How many amino acids does this protein consist of? It consists of 112 amino acids.  
> What is the molecular weight of this protein? The molecular weight is 12808 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 112  
mw: 12808

FIELDS of Q14CH1  
catalytic activity: EC = 2.8.1.9, AH2 + L-cysteine + Mo-molybdopterin = A + H2O + L-alanine + thio-Mo-molybdopterin  
cofactor: pyridoxal 5'-phosphate  
functional domains: Mo-molybdopterin cofactor sulfurase activity, molybdenum cofactor sulfurtransferase activity, lyase activity, molybdenum ion binding, Type I PLP-dependent aspartate aminotransferase-like (Major domain), pyridoxal phosphate binding, PLP-dependent transferases, MOSC N-terminal domain-like, PK beta-barrel domain-like  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 862 aa, 95013 KDa  
  
Summary  
> This protein, belonging to the Eukaryota kingdom and Metazoa phylum, is involved in various biochemical reactions  
> It has a size of 862 amino acids and a molecular weight of 95013 KDa  
> It possesses several functional domains, which include Mo-molybdopterin cofactor sulfurase activity, molybdenum cofactor sulfurtransferase activity, lyase activity, molybdenum ion binding, Type I PLP-dependent aspartate aminotransferase-like domain, pyridoxal phosphate binding, PLP-dependent transferases, MOSC N-terminal domain-like, and PK beta-barrel domain-like  
> The catalytic activity of this protein involves the conversion of AH2, L-cysteine, and Mo-molybdopterin into A, H2O, L-alanine, and thio-Mo-molybdopterin  
> The protein utilizes pyridoxal 5'-phosphate as a cofactor.  
  
QA  
> What is the size of the protein? It has a size of 862 amino acids.  
> What is the molecular weight of the protein? It has a molecular weight of 95013 KDa.  
> What are the functional domains of the protein? The functional domains include Mo-molybdopterin cofactor sulfurase activity, molybdenum cofactor sulfurtransferase activity, lyase activity, molybdenum ion binding, Type I PLP-dependent aspartate aminotransferase-like domain, pyridoxal phosphate binding, PLP-dependent transferases, MOSC N-terminal domain-like, and PK beta-barrel domain-like.  
> What is the catalytic activity of the protein? The catalytic activity of the protein involves the conversion of AH2, L-cysteine, and Mo-molybdopterin into A, H2O, L-alanine, and thio-Mo-molybdopterin.  
> What is the cofactor utilized by the protein? The protein utilizes pyridoxal 5'-phosphate as a cofactor.  
> To which taxonomy group does the protein belong? It belongs to the Eukaryota kingdom and Metazoa phylum.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: pyridoxal 5'-phosphate  
length: 862  
mw: 95013  
  
FIELDS of P62995  
subunit: Binds to A3 enhancer proteins SFRS4, SFRS5, SFRS6 and SFRS9  
subcellular location: Nucleus  
functional domains: protein domain specific binding, RNA binding, mRNA binding, pre-mRNA binding, RNA-binding domain, RBD, identical protein binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 288 aa, 33666 KDa  
  
Summary  
> This protein is found in the nucleus of eukaryotic organisms, specifically in metazoans belonging to the chordata group  
> It has a size of 288 amino acids, corresponding to a molecular weight of 33666 KDa  
> The protein is known to bind to various enhancer proteins (SFRS4, SFRS5, SFRS6, and SFRS9) that are involved in the regulation of gene expression  
> It contains several functional domains, including protein domain specific binding, RNA binding, mRNA binding, pre-mRNA binding, RNA-binding domain (RBD), and identical protein binding  
> These domains suggest that the protein is involved in interactions with other proteins as well as RNA molecules, potentially playing a role in RNA processing and gene regulation processes.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is in the nucleus.  
> Which taxa does this protein belong to? This protein belongs to the eukaryotic taxa, specifically metazoans within the Chordata group.  
> What is the size of this protein? The size of this protein is 288 amino acids, corresponding to a molecular weight of 33666 KDa.  
> What proteins does this protein bind to? This protein binds to enhancer proteins SFRS4, SFRS5, SFRS6, and SFRS9.  
> What are the functional domains of this protein? The functional domains of this protein include protein domain specific binding, RNA binding, mRNA binding, pre-mRNA binding, RNA-binding domain (RBD), and identical protein binding.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: False  
length: 288  
mw: 33666

FIELDS of B3PDE5  
catalytic activity: EC = 3.1.1.72, Deacetylation of xylans and xylo-oligosaccharides.  
subcellular location: Secreted  
functional domains: SGNH hydrolase, Galactose-binding domain-like, acetylxylan esterase activity, hydrolase activity, acting on glycosyl bonds  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 360 aa, 40063 KDa  
  
Summary  
> This protein is a secreted enzyme that belongs to the SGNH hydrolase family  
> It is primarily found in bacteria of the phylum Pseudomonadota, specifically in the class Gammaproteobacteria  
> With a size of 360 amino acids and a molecular weight of 40063 Da, this protein exhibits deacetylation activity towards xylans and xylo-oligosaccharides  
> It possesses functional domains related to galactose binding and acetylxylan esterase activity  
> Additionally, it performs hydrolase activity, specifically targeting glycosyl bonds.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the deacetylation of xylans and xylo-oligosaccharides.  
> Where is this protein located within the cell? This protein is secreted.  
> Which taxonomic groups does this protein belong to? This protein belongs to the taxonomic groups of Bacteria, Pseudomonadota, and Gammaproteobacteria.  
> What is the size of this protein? This protein has a size of 360 amino acids and a molecular weight of 40063 Da.  
> What are the functional domains of this protein? This protein has functional domains related to SGNH hydrolase, Galactose-binding domain-like, and acetylxylan esterase activity.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 360  
mw: 40063

FIELDS of P67875  
subcellular location: Secreted  
functional domains: RNA nuclease activity, IgE binding, RNA endonuclease activity, RNA binding, Microbial ribonucleases  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 176 aa, 19595 KDa  
  
Summary  
> The protein is a secreted protein found in Eukaryota, specifically in the fungi group called Dikarya  
> It has a protein size of 176 amino acids, weighing approximately 19595 KDa  
> The protein possesses various functional domains, including RNA nuclease activity, IgE binding, RNA endonuclease activity, RNA binding, and microbial ribonucleases.  
  
QA  
> What is the subcellular location of the protein? The protein is secreted.  
> What are the functional domains of the protein? The functional domains are RNA nuclease activity, IgE binding, RNA endonuclease activity, RNA binding, and microbial ribonucleases.  
> Which taxonomic group does the protein belong to? The protein belongs to the taxonomic group Eukaryota, specifically in the fungi group called Dikarya.  
> What is the size of the protein? The protein has a size of 176 amino acids, weighing approximately 19595 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 176  
mw: 19595

FIELDS of P29562  
catalytic activity: EC = 3.6.4.13, ATP + H2O = ADP + H(+) + phosphate  
subunit: It is composed of at least EIF4A, EIF4E and EIF4G1/EIF4G3  
functional domains: P-loop containing nucleotide triphosphate hydrolases, RNA binding, ATP hydrolysis activity, RNA helicase activity, P-loop containing nucleoside triphosphate hydrolases, translation initiation factor activity, ATP binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 398 aa, 45291 KDa  
  
Summary  
> This protein belongs to the eukaryotic translation initiation factor family and is involved in protein synthesis  
> It is composed of multiple subunits, including EIF4A, EIF4E, and EIF4G1/EIF4G3  
> The protein has several functional domains, including P-loop containing nucleotide triphosphate hydrolases, RNA binding, ATP hydrolysis activity, RNA helicase activity, P-loop containing nucleoside triphosphate hydrolases, translation initiation factor activity, and ATP binding  
> It has a catalytic activity of ATP hydrolysis, converting ATP and water into ADP, a proton (H+), and inorganic phosphate  
> This protein is found in eukaryotes, specifically in the metazoan and chordate taxa  
> It has a protein size of 398 amino acids and a molecular weight of 45291 kilodaltons.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is ATP hydrolysis, converting ATP and water into ADP, a proton (H+), and inorganic phosphate.  
> What are the functional domains of this protein? The functional domains of this protein include P-loop containing nucleotide triphosphate hydrolases, RNA binding, ATP hydrolysis activity, RNA helicase activity, P-loop containing nucleoside triphosphate hydrolases, translation initiation factor activity, and ATP binding.  
> What subunits compose this protein? This protein is composed of at least EIF4A, EIF4E, and EIF4G1/EIF4G3.  
> In which taxa is this protein found? This protein is found in eukaryotes, specifically in the metazoan and chordate taxa.  
> What is the size of this protein? This protein has a size of 398 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 45291 kilodaltons.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 398  
mw: 45291

FIELDS of O67730  
catalytic activity: EC = 2.5.1.72, dihydroxyacetone phosphate + iminosuccinate = H(+) + 2 H2O + phosphate + quinolinate  
cofactor: [4Fe-4S] cluster, Binds 1 [4Fe-4S] cluster per subunit.  
subcellular location: Cytoplasm  
functional domains: quinolinate synthetase A activity, NadA-like, 4 iron, 4 sulfur cluster binding, metal ion binding  
taxonomy: Bacteria, Aquificota, Aquificae  
protein size: 322 aa, 36804 KDa  
  
Summary  
> This protein belongs to the quinolinate synthetase family and is involved in the biosynthesis of quinolinic acid, an important intermediate in the de novo synthesis of NAD+  
> It is found in the cytoplasm of bacterial cells belonging to the Aquificae class within the Aquificota phylum  
> The protein has a size of 322 amino acids and a molecular weight of 36804 KDa  
> It possesses several functional domains, including quinolinate synthetase A activity, NadA-like domain, and domains involved in binding a [4Fe-4S] cluster and metal ions  
> The catalytic activity of the protein involves the conversion of dihydroxyacetone phosphate and iminosuccinate into hydrogen ions, water, phosphate, and quinolinate  
> It utilizes a [4Fe-4S] cluster as a cofactor, with one cluster binding per subunit.  
  
QA  
> What is the subcellular location of the protein? The protein is located in the cytoplasm.  
> What is the size of the protein? The protein has a size of 322 amino acids.  
> What is the catalytic activity of the protein? The protein catalyzes the conversion of dihydroxyacetone phosphate and iminosuccinate into hydrogen ions, water, phosphate, and quinolinate.  
> What is the cofactor of the protein? The protein binds a [4Fe-4S] cluster as a cofactor, with one cluster binding per subunit.  
> What are the functional domains of the protein? The protein possesses domains involved in quinolinate synthetase A activity, NadA-like functions, and binding a [4Fe-4S] cluster and metal ions.  
> What is the taxonomy of the protein? The protein belongs to the Aquificae class within the Aquificota phylum.  
> Is this protein an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 322  
mw: 36804

FIELDS of P78283  
subunit: The heterotrimers can form oligomers, although 1 heterotrimer is thought to be able to translocate proteins, Heterotrimer consisting of SecY, SecE and SecG subunits  
subcellular location: Cell inner membrane, Multi-pass membrane protein  
functional domains: signal sequence binding, SecY subunit domain, Preprotein translocase SecY subunit, protein transmembrane transporter activity  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 444 aa, 48664 KDa  
  
Summary  
> This protein is a heterotrimer consisting of three subunits: SecY, SecE, and SecG  
> It is located in the cell inner membrane and belongs to the bacteria taxonomy, specifically in the Pseudomonadota group within the Gammaproteobacteria class  
> The protein has multiple functional domains, including signal sequence binding, the SecY subunit domain, and the Preprotein translocase SecY subunit  
> It exhibits protein transmembrane transporter activity  
> The protein has a size of 444 amino acids and a molecular weight of 48664 Kilodaltons.  
  
QA  
> What is the composition of the protein? The protein consists of three subunits: SecY, SecE, and SecG.  
> Where is the protein located? The protein is located in the cell inner membrane.  
> What is the taxonomic classification of the protein? The protein belongs to the bacteria taxonomy and is specifically classified in the Pseudomonadota group within the Gammaproteobacteria class.  
> What are the functional domains of the protein? The protein has functional domains including signal sequence binding, the SecY subunit domain, and the Preprotein translocase SecY subunit.  
> What activity does the protein exhibit? The protein exhibits protein transmembrane transporter activity.  
> What is the size of the protein? The protein has a size of 444 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of 48664 Kilodaltons.  
> Is this protein an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 444  
mw: 48664

FIELDS of Q2NGH3  
catalytic activity: 5-(2-hydroxyethyl)-4-methylthiazole + ATP = 4-methyl-5-(2-phosphooxyethyl)-thiazole + ADP + H(+), EC = 2.7.1.50  
cofactor: Mg(2+)  
functional domains: Ribokinase-like, hydroxyethylthiazole kinase activity, ATP binding, magnesium ion binding  
taxonomy: Archaea, Euryarchaeota, Methanomada group  
protein size: 285 aa, 30378 KDa  
  
Summary  
> This protein is involved in a specific catalytic activity that results in the conversion of 5-(2-hydroxyethyl)-4-methylthiazole and ATP into 4-methyl-5-(2-phosphooxyethyl)-thiazole, ADP, and a hydrogen ion  
> It possesses a ribokinase-like functional domain and exhibits hydroxyethylthiazole kinase activity  
> Furthermore, it binds to ATP and magnesium ions  
> The protein is found in Archaea, specifically in the Euryarchaeota group within the Methanomada category  
> It has a size of 285 amino acids and a molecular weight of 30378 KDa.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the conversion of 5-(2-hydroxyethyl)-4-methylthiazole and ATP into 4-methyl-5-(2-phosphooxyethyl)-thiazole, ADP, and a hydrogen ion.  
> What are the functional domains of this protein? The functional domains of this protein include a ribokinase-like domain and a domain that exhibits hydroxyethylthiazole kinase activity.  
> What does this protein bind to? This protein binds to ATP and magnesium ions.  
> In which taxonomic groups is this protein found? This protein is found in the Archaea domain, specifically in the Euryarchaeota group within the Methanomada category.  
> What is the size of this protein? This protein has a size of 285 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 30378 KDa.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg ions  
length: 285  
mw: 30378

FIELDS of Q5QXJ5  
catalytic activity: ATP + hydrogencarbonate + L-threonine = diphosphate + H2O + L-threonylcarbamoyladenylate, EC = 2.7.7.87  
subcellular location: Cytoplasm  
functional domains: DHBP synthase, L-threonylcarbamoyladenylate synthase, YrdC/RibB, double-stranded RNA binding, ATP binding  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 186 aa, 20040 KDa  
  
Summary  
> This protein is a multi-functional enzyme with a variety of biochemical and structural properties  
> It has a catalytic activity that involves the conversion of ATP, hydrogencarbonate, and L-threonine into diphosphate, water, and L-threonylcarbamoyladenylate  
> This reaction is classified as EC = 2.7.7.87  
> The protein is located in the cytoplasm of cells  
> Structurally, it contains different functional domains, including DHBP synthase, L-threonylcarbamoyladenylate synthase, YrdC/RibB, double-stranded RNA binding, and ATP binding domains  
> The protein has a size of 186 amino acids and a molecular weight of 20040 KDa  
> It is found in bacteria, specifically within the phylum Pseudomonadota, subclass Gammaproteobacteria.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein involves the conversion of ATP, hydrogencarbonate, and L-threonine into diphosphate, water, and L-threonylcarbamoyladenylate.  
> Where is this protein located? This protein is located in the cytoplasm.  
> What are the functional domains of this protein? The functional domains of this protein include DHBP synthase, L-threonylcarbamoyladenylate synthase, YrdC/RibB, double-stranded RNA binding, and ATP binding domains.  
> What is the taxonomy of this protein? This protein is found in bacteria, specifically within the phylum Pseudomonadota, subclass Gammaproteobacteria.  
> What is the size of this protein? This protein has a size of 186 amino acids and a molecular weight of 20040 KDa.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 186  
mw: 20040

FIELDS of Q5V1I9  
catalytic activity: (4aS,6R)-4a-hydroxy-L-erythro-5,6,7,8-tetrahydrobiopterin = (6R)-L-erythro-6,7-dihydrobiopterin + H2O, EC = 4.2.1.96  
functional domains: Transcriptional coactivator/pterin dehydratase, PCD-like, 4-alpha-hydroxytetrahydrobiopterin dehydratase activity  
taxonomy: Archaea, Euryarchaeota, Stenosarchaea group  
protein size: 92 aa, 10340 KDa  
  
Summary  
> This protein is a transcriptional coactivator/pterin dehydratase with a size of 92 amino acids and a molecular weight of 10340 Da  
> It exhibits a catalytic activity, specifically the conversion of (4aS,6R)-4a-hydroxy-L-erythro-5,6,7,8-tetrahydrobiopterin into (6R)-L-erythro-6,7-dihydrobiopterin and water  
> This enzymatic reaction is classified under the EC number 4.2.1.96  
> The protein belongs to the Stenosarchaea group within the Archaea domain, specifically the Euryarchaeota phylum.  
  
QA  
> What is the molecular weight of this protein? The molecular weight of this protein is 10340 Da.  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the conversion of (4aS,6R)-4a-hydroxy-L-erythro-5,6,7,8-tetrahydrobiopterin into (6R)-L-erythro-6,7-dihydrobiopterin and water.  
> Which domain does this protein belong to? This protein belongs to the transcriptional coactivator/pterin dehydratase domain.  
> What is the size of this protein? This protein has a size of 92 amino acids.  
> In which taxonomic group does this protein belong? This protein belongs to the Stenosarchaea group within the Archaea domain and the Euryarchaeota phylum.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 92  
mw: 10340

FIELDS of A5D5J2  
subunit: Contacts protein L29, and trigger factor when it is bound to the ribosome., Part of the 50S ribosomal subunit  
functional domains: Ribosomal proteins S24e, L23 and L15e, rRNA binding, structural constituent of ribosome  
taxonomy: Bacteria, Bacillota, Clostridia  
protein size: 95 aa, 11085 KDa  
  
Summary  
> This protein is a subunit of the ribosome in bacteria belonging to the Clostridia class  
> It interacts with other proteins such as L29 and trigger factor when it is bound to the ribosome  
> It consists of ribosomal proteins S24e, L23, and L15e, and plays a role in binding to ribosomal RNA  
> Additionally, it serves as a structural component of the ribosome  
> The protein has a size of 95 amino acids and a molecular weight of 11085 KDa.  
  
QA  
> What proteins does this subunit of the ribosome interact with? This subunit interacts with protein L29 and trigger factor when it is bound to the ribosome.  
> What is the role of this protein in the ribosome? This protein serves as a structural constituent of the ribosome and is involved in binding to ribosomal RNA.  
> What is the size of this protein? This protein has a size of 95 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 11085 KDa.  
> What is the taxonomy of this protein? This protein belongs to the class Clostridia within the bacteria taxonomic group.  
> What functional domains does this protein possess? This protein has ribosomal proteins S24e, L23, and L15e as its functional domains.  
> What ribosomal subunit does this protein belong to? This protein is part of the 50S ribosomal subunit.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 95  
mw: 11085

FIELDS of Q5WLZ7  
catalytic activity: EC = 3.4.21.92, Hydrolysis of proteins to small peptides in the presence of ATP and magnesium. alpha-casein is the usual test substrate. In the absence of ATP, only oligopeptides shorter than five residues are hydrolyzed (such as succinyl-Leu-Tyr-|-NHMec, and Leu-Tyr-Leu-|-Tyr-Trp, in which cleavage of the -Tyr-|-Leu- and -Tyr-|-Trp bonds also occurs).  
subunit: Fourteen ClpP subunits assemble into 2 heptameric rings which stack back to back to give a disk-like structure with a central cavity, resembling the structure of eukaryotic proteasomes.  
subcellular location: Cytoplasm  
functional domains: serine-type endopeptidase activity, ATP-dependent peptidase activity, ClpP/crotonase  
taxonomy: Bacteria, Bacillota, Bacilli  
protein size: 193 aa, 21309 KDa  
  
Summary  
> This protein is a serine-type endopeptidase that belongs to the ClpP/crotonase family  
> It is found in bacteria, specifically in the subcellular location cytoplasm  
> The protein has a catalytic activity with EC number 3.4.21.92, which involves hydrolyzing proteins into small peptides  
> This hydrolysis process requires the presence of ATP and magnesium  
> The usual test substrate for this protein is alpha-casein, and it can also hydrolyze oligopeptides shorter than five residues  
> The protein functions as a complex composed of fourteen ClpP subunits, which assemble into two heptameric rings stacked back to back, forming a disk-like structure with a central cavity  
> This structure is reminiscent of the eukaryotic proteasomes  
> The protein has a size of 193 amino acids and a molecular weight of 21309 KDa.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein involves hydrolyzing proteins to small peptides in the presence of ATP and magnesium.  
> What is the subunit composition of this protein? This protein is composed of fourteen ClpP subunits, which assemble into two heptameric rings.  
> In which subcellular location is this protein found? This protein is found in the cytoplasm.  
> What is the functional domain of this protein? The functional domains of this protein include serine-type endopeptidase activity, ATP-dependent peptidase activity, and ClpP/crotonase.  
> What is the taxonomy of this protein? This protein belongs to the Bacteria domain, Bacillota phylum, and Bacilli class.  
> What is the size and molecular weight of this protein? This protein has a size of 193 amino acids, with a molecular weight of 21309 KDa.  
> What is the usual test substrate for this protein? The usual test substrate for this protein is alpha-casein.  
> Does this protein hydrolyze oligopeptides shorter than five residues? Yes, in the absence of ATP, this protein can hydrolyze oligopeptides shorter than five residues, such as succinyl-Leu-Tyr-|-NHMec and Leu-Tyr-Leu-|-Tyr-Trp, and cleavage of specific bonds also occurs.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: atp, magnesium  
length: 193  
mw: 21309

FIELDS of F7EZ75  
catalytic activity: H2O + N(6)-succinyl-L-lysyl-[protein] + NAD(+) = 2''-O-succinyl-ADP-D-ribose + L-lysyl-[protein] + nicotinamide, H2O + N(6)-glutaryl-L-lysyl-[protein] + NAD(+) = 2''-O-glutaryl-ADP-D-ribose + L-lysyl-[protein] + nicotinamide, H2O + N(6)-malonyl-L-lysyl-[protein] + NAD(+) = 2''-O-malonyl-ADP-D-ribose + L-lysyl-[protein] + nicotinamide  
cofactor: Zn(2+), Binds 1 zinc ion per subunit.  
subunit: Homodimer, Monomer  
subcellular location: Mitochondrion, Cytosol, Cytoplasm, Nucleus  
functional domains: SIR2/SIRT2 'Small Domain, transferase activity, zinc ion binding, protein-malonyllysine demalonylase activity, DHS-like NAD/FAD-binding domain, protein-glutaryllysine deglutarylase activity, protein-succinyllysine desuccinylase activity, TPP-binding domain, NAD-dependent protein deacetylase activity, NAD+ binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 310 aa, 33881 KDa  
  
Summary  
> This protein is a functional enzyme that exhibits catalytic activity involving the addition or removal of chemical groups from other proteins  
> It is involved in several enzymatic reactions, including the addition of succinyl, glutaryl, or malonyl groups to lysine residues on target proteins, utilizing NAD(+) as a co-substrate  
> This results in the formation of succinyl-ADP-D-ribose, glutaryl-ADP-D-ribose, or malonyl-ADP-D-ribose, respectively  
> The catalytic activity of this protein is reliant on the presence of a zinc ion, as it binds one zinc ion per subunit  
> The protein exists as either a homodimer or a monomer, and it can be found in various subcellular locations, including the mitochondrion, cytosol, cytoplasm, and nucleus  
> It is widespread across different eukaryotic organisms, specifically within the metazoan phylum of chordates  
> The protein consists of 310 amino acids and has a molecular weight of 33881 kilodaltons.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein involves the addition or removal of chemical groups, such as succinyl, glutaryl, or malonyl, from lysine residues on target proteins.  
> What cofactor does this protein require? This protein requires a zinc ion as a cofactor.  
> What are the possible subunit forms of this protein? This protein can exist as either a homodimer or a monomer.  
> In which cellular locations can this protein be found? This protein can be found in the mitochondrion, cytosol, cytoplasm, and nucleus.  
> What is the taxonomy classification of this protein? This protein belongs to the taxonomic groups of Eukaryota, Metazoa, and Chordata.  
> What is the size of this protein? This protein consists of 310 amino acids and has a molecular weight of 33881 kilodaltons.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
localization: mitochondrion  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: True  
is\_enzyme: True  
cofactor: zinc  
length: 310  
mw: 33881

FIELDS of B5G2S6  
subcellular location: Golgi apparatus membrane, Single-pass type I membrane protein  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 72 aa, 8022 KDa  
  
Summary  
> This protein is a single-pass type I membrane protein located in the Golgi apparatus membrane  
> It is found in eukaryotes, specifically in metazoans belonging to the chordata phylum  
> With a size of 72 amino acids, this protein has a molecular weight of 8022 kilodaltons.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is the Golgi apparatus membrane.  
> Is this protein a membrane protein? Yes, this protein is a membrane protein.  
> What type of membrane protein is it? It is a single-pass type I membrane protein.  
> In which taxonomic groups is this protein found? This protein is found in eukaryotes and specifically in metazoans belonging to the chordata phylum.  
> How many amino acids does this protein comprise? This protein comprises 72 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 8022 kilodaltons.  
> Can this protein act as an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 72  
mw: 8022

FIELDS of Q6DJI4  
subunit: Component of the mitochondrial ribosome large subunit (39S) which comprises a 16S rRNA and about 50 distinct proteins.  
subcellular location: Mitochondrion  
functional domains: structural constituent of ribosome  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 135 aa, 15126 KDa  
  
Summary  
> The protein in question is a component of the mitochondrial ribosome large subunit (39S), which consists of a 16S rRNA and approximately 50 distinct proteins  
> It is primarily localized in the mitochondrion, a membrane-bound organelle found in eukaryotic cells  
> The protein functions as a structural constituent of the ribosome, playing a crucial role in protein synthesis within the mitochondria  
> It is found in eukaryotic organisms belonging to the Metazoa kingdom, specifically in Chordata, and has a size of 135 amino acids and a molecular weight of 15,126 KDa.  
  
QA  
> What is the subunit composition of the mitochondrial ribosome large subunit? The mitochondrial ribosome large subunit consists of a 16S rRNA and approximately 50 distinct proteins.  
> Where is the protein primarily localized? The protein is primarily localized in the mitochondrion.  
> What is the functional role of the protein? The protein functions as a structural constituent of the ribosome.  
> What is the taxonomy of organisms that possess this protein? Organisms belonging to the Eukaryota kingdom, specifically in Chordata, possess this protein.  
> What is the size of the protein? The protein has a size of 135 amino acids and a molecular weight of 15,126 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
localization: mitochondrion  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: True  
is\_enzyme: False  
length: 135  
mw: 15126

FIELDS of B4SPH3  
catalytic activity: guanosine(37) in tRNA + S-adenosyl-L-methionine = H(+) + N(1)-methylguanosine(37) in tRNA + S-adenosyl-L-homocysteine, EC = 2.1.1.228  
subunit: Homodimer.  
subcellular location: Cytoplasm  
functional domains: tRNA (guanine(37)-N(1))-methyltransferase activity, tRNA(m1g37)methyltransferase, domain 2, alpha/beta knot  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 252 aa, 27465 KDa  
  
Summary  
> This protein is a guanine-N1 methyltransferase enzyme involved in tRNA modification  
> It is a homodimeric protein with a subcellular location in the cytoplasm  
> The catalytic activity of this protein involves the transfer of a methyl group from S-adenosyl-L-methionine to guanosine at position 37 in tRNA, resulting in the formation of N1-methylguanosine  
> This enzymatic reaction is described by the EC number 2.1.1.228  
> The protein consists of 252 amino acids and has a molecular weight of 27465 KDa  
> It contains functional domains including tRNA (guanine(37)-N(1))-methyltransferase activity and tRNA(m1g37)methyltransferase  
> The structure of this protein includes a domain 2, alpha/beta knot configuration  
> Taxonomically, this protein is found in bacteria, specifically in the Pseudomonadota phylum of the Gammaproteobacteria class.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the methylation of guanosine at position 37 in tRNA using S-adenosyl-L-methionine as a methyl group donor.  
> Where is this protein located within the cell? This protein is located in the cytoplasm.  
> What is the subunit composition of this protein? This protein consists of homodimers.  
> How does this protein modify tRNA? This protein methylates guanosine at position 37 in tRNA, resulting in the formation of N1-methylguanosine.  
> What is the molecular weight and size of this protein? This protein has a molecular weight of 27465 KDa and consists of 252 amino acids.  
> What functional domains does this protein possess? This protein possesses functional domains including tRNA (guanine(37)-N(1))-methyltransferase activity and tRNA(m1g37)methyltransferase.  
> In what taxonomic group is this protein found? This protein is found in bacteria, specifically in the Pseudomonadota phylum of the Gammaproteobacteria class.  
> What is the EC number associated with the catalytic activity of this protein? The EC number associated with the catalytic activity of this protein is 2.1.1.228.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 252  
mw: 27465

FIELDS of Q5UQL7  
subcellular location: Virion  
functional domains: Group II dsDNA viruses VP, structural molecule activity, Major capsid protein Vp54, Adenovirus Type 2 Hexon, domain 4  
taxonomy: Viruses, Varidnaviria, Bamfordvirae  
protein size: 593 aa, 67260 KDa  
  
Summary  
> This protein is a major capsid protein Vp54 found in Group II dsDNA viruses  
> It has a size of 593 amino acids, with a molecular weight of 67260 KDa  
> The protein is primarily localized in the virion, which is the viral particle  
> It is involved in structural molecule activity, specifically in the formation of the viral capsid  
> The protein belongs to the taxonomic group of Varidnaviria, within the larger classification of viruses known as Bamfordvirae.  
  
QA  
> What is the subcellular location of the protein? The protein is localized in the virion.  
> What are the functional domains of the protein? The functional domains of the protein include Group II dsDNA viruses VP and Adenovirus Type 2 Hexon domain 4.  
> What is the size of the protein in terms of amino acids? The protein has a size of 593 amino acids.  
> What is the molecular weight of the protein? The molecular weight of the protein is 67260 KDa.  
> What is the primary role of the protein? The protein is involved in structural molecule activity, particularly in the formation of the viral capsid.  
> What is the taxonomic classification of the protein? The protein belongs to the taxonomic group of Varidnaviria within the larger group of viruses known as Bamfordvirae.  
> Can this protein act as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 593  
mw: 67260

FIELDS of B9KZK4  
catalytic activity: ATP + H2O + L-glutamine + L-glutamyl-tRNA(Gln) = ADP + H(+) + L-glutamate + L-glutaminyl-tRNA(Gln) + phosphate, ATP + H2O + L-aspartyl-tRNA(Asn) + L-glutamine = ADP + 2 H(+) + L-asparaginyl-tRNA(Asn) + L-glutamate + phosphate  
subunit: Heterotrimer of A, B and C subunits.  
functional domains: Glutamine synthetase/guanido kinase, asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity, glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity, GatB domain, N-terminal subdomain, GatB/YqeY motif, ATP binding  
taxonomy: Bacteria, Thermomicrobiota, Thermomicrobia  
protein size: 483 aa, 54102 KDa  
  
Summary  
> Glutamine synthetase (GS) is a protein found in bacteria belonging to the order Thermomicrobia in the class Thermomicrobiota  
> It functions as a heterotrimer composed of A, B, and C subunits  
> The protein has various functional domains, including glutamine synthetase/guanido kinase, asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity, glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity, GatB domain, N-terminal subdomain, GatB/YqeY motif, and ATP binding  
> The protein has a size of 483 amino acids and a molecular weight of 54102 KDa  
> It demonstrates catalytic activity involving ATP, H2O, L-glutamine, L-glutamyl-tRNA(Gln), L-aspartyl-tRNA(Asn), and phosphate, resulting in the formation of ADP, H(+), L-glutamate, L-glutaminyl-tRNA(Gln), L-asparaginyl-tRNA(Asn), and phosphate  
> The specific enzymatic reactions catalyzed by the protein involve the conversion of ATP, H2O, L-glutamine, and L-glutamy-tRNA(Gln) into ADP, H(+), L-glutamate, L-glutaminyl-tRNA(Gln), and phosphate, as well as the conversion of ATP, H2O, L-aspartyl-tRNA(Asn), and L-glutamine into ADP, H(+), L-asparaginyl-tRNA(Asn), L-glutamate, and phosphate.  
  
QA  
> What are the functional domains of this protein? The functional domains of this protein include glutamine synthetase/guanido kinase, asparaginyl-tRNA synthase (glutamine-hydrolyzing) activity, glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity, GatB domain, N-terminal subdomain, GatB/YqeY motif, and ATP binding.  
> What is the size of this protein? This protein has a size of 483 amino acids.  
> What is the catalytic activity of this protein? This protein catalyzes the reactions involving ATP, H2O, L-glutamine, L-glutamyl-tRNA(Gln), L-aspartyl-tRNA(Asn), and phosphate, resulting in the formation of ADP, H(+), L-glutamate, L-glutaminyl-tRNA(Gln), L-asparaginyl-tRNA(Asn), and phosphate.  
> In what organisms is this protein found? This protein is found in bacteria belonging to the order Thermomicrobia in the class Thermomicrobiota.  
> How is this protein composed? This protein is composed of heterotrimer subunits A, B, and C.  
> What is the molecular weight of this protein? This protein has a molecular weight of 54102 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 483  
mw: 54102

FIELDS of P06922  
subcellular location: Host cytoplasm, Host nucleus  
taxonomy: Viruses, Monodnaviria, Shotokuvirae  
protein size: 92 aa, 10075 KDa  
  
Summary  
> This protein is found in the cytoplasm and nucleus of the host cell  
> It belongs to the taxonomic group of viruses known as Monodnaviria within the larger group Shotokuvirae  
> The protein has a size of 92 amino acids and a molecular weight of 10075 KDa.  
  
QA  
> Where is this protein localized within the host cell? This protein is found in the cytoplasm and nucleus of the host cell.  
> What taxonomic group does this protein belong to? This protein belongs to the group of viruses known as Monodnaviria.  
> What is the size of this protein? The size of this protein is 92 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 10075 KDa.  
> Is this protein an enzyme? No  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: False  
length: 92  
mw: 10075

FIELDS of A0A2S3R7M0  
catalytic activity: hexadecanoyl-CoA + L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein] = CoA + H(+) + N(6)-hexadecanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], dodecanoyl-CoA + L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein] = CoA + H(+) + N(6)-dodecanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], decanoyl-CoA + L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein] = CoA + H(+) + N(6)-decanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein]  
cofactor: Mg(2+), Binds 2 Mg(2+) ions per subunit. Mg(2+) is required for actin cross-linking activity. Can also use Mn(2+) ions instead of Mg(2+).  
functional domains: ligase activity, cysteine-type peptidase activity, Galactose-binding domain-like, alpha/beta-Hydrolases, metal ion binding, EreA/ChaN-like, alpha/beta hydrolase, lipid binding, acyltransferase activity, toxin activity, PMT central region-like, beta-Roll  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 5206 aa, 556341 KDa  
  
Summary  
> The protein in question is an enzyme with catalytic activity  
> It is involved in reactions that convert hexadecanoyl-CoA, dodecanoyl-CoA, and decanoyl-CoA, together with L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], into CoA, H(+), and N(6)-hexadecanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], N(6)-dodecanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], and N(6)-decanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein]  
> This protein requires Mg(2+) ions, which can be replaced by Mn(2+) ions, as a cofactor  
> It possesses various functional domains, including ligase activity, cysteine-type peptidase activity, Galactose-binding domain-like, alpha/beta-Hydrolases, metal ion binding, EreA/ChaN-like, alpha/beta hydrolase, lipid binding, acyltransferase activity, toxin activity, PMT central region-like, beta-Roll  
> It is classified taxonomically as Bacteria, Pseudomonadota, Gammaproteobacteria  
> The protein is large, consisting of 5206 amino acids, with a mass of 556341 KDa.  
  
QA  
> What are the substrates for this protein's catalytic activity? The substrates for this protein's catalytic activity are hexadecanoyl-CoA, dodecanoyl-CoA, and decanoyl-CoA, alongside L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein].  
> What are the products generated by the enzymatic reactions? The enzymatic reactions produce CoA, H(+), N(6)-hexadecanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], N(6)-dodecanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein], and N(6)-decanoyl-L-lysyl-/S-(2E,6E,10E)-geranylgeranyl-L-cysteinyl-[protein].  
> What are the cofactors required for this protein's activity? This protein requires Mg(2+) ions as cofactors, which can alternatively be replaced by Mn(2+) ions.  
> What are the key functional domains present in this protein? The key functional domains include ligase activity, cysteine-type peptidase activity, Galactose-binding domain-like, alpha/beta-Hydrolases, metal ion binding, EreA/ChaN-like, alpha/beta hydrolase, lipid binding, acyltransferase activity, toxin activity, PMT central region-like, beta-Roll.  
> In which taxonomic groups is this protein classified? This protein is taxonomically classified as Bacteria, Pseudomonadota, Gammaproteobacteria.  
> How large is this protein in terms of amino acid count and mass? This protein consists of 5206 amino acids and has a mass of 556341 KDa.  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg(2+), mn(2+)  
length: 5206  
mw: 556341

FIELDS of P27868  
catalytic activity: EC = 2.2.1.6, H(+) + 2 pyruvate = (2S)-2-acetolactate + CO2  
cofactor: Binds 1 Mg(2+) ion per subunit., Mg(2+), thiamine diphosphate, Binds 1 thiamine pyrophosphate per subunit.  
functional domains: acetolactate synthase activity, Thiamin diphosphate-binding fold (THDP-binding), DHS-like NAD/FAD-binding domain, flavin adenine dinucleotide binding, TPP-binding domain, thiamine pyrophosphate binding, magnesium ion binding  
taxonomy: Bacteria, Cyanobacteriota, Cyanophyceae  
protein size: 579 aa, 63440 KDa  
  
Summary  
> This protein is a large enzyme found in bacteria, specifically in the Cyanobacteriota class of Cyanophyceae  
> It has a size of 579 amino acids and a molecular weight of 63440 KDa  
> The protein performs catalytic activity with the enzyme classification EC = 2.2.1.6  
> It catalyzes the reaction between H(+) and two molecules of pyruvate to form (2S)-2-acetolactate and CO2  
> The protein binds various cofactors, including 1 Mg(2+) ion and 1 thiamine diphosphate (TPP) per subunit  
> It contains functional domains such as acetolactate synthase activity, THDP-binding fold (THDP-binding), DHS-like NAD/FAD-binding domain, flavin adenine dinucleotide binding, TPP-binding domain, thiamine pyrophosphate binding, and magnesium ion binding.  
  
QA  
> What is the classification of the enzyme activity performed by this protein? EC = 2.2.1.6  
> What are the cofactors bound by this protein? It binds 1 Mg(2+) ion per subunit and 1 thiamine diphosphate (TPP) per subunit.  
> What are the functional domains of this protein? It has acetolactate synthase activity, THDP-binding fold (THDP-binding), DHS-like NAD/FAD-binding domain, flavin adenine dinucleotide binding, TPP-binding domain, thiamine pyrophosphate binding, and magnesium ion binding.  
> In which organisms is this protein found? It is found in bacteria, specifically in the Cyanobacteriota class of Cyanophyceae.  
> How large is this protein? It has a size of 579 amino acids and a molecular weight of 63440 KDa.  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg(2+), thiamine diphosphate (tpp)  
length: 579  
mw: 63440

FIELDS of Q6FT36  
subcellular location: Nucleus, Cytoplasm  
functional domains: JAB1/MPN domain, Cytidine Deaminase, domain 2, metalloendopeptidase activity, metal ion binding  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 465 aa, 53521 KDa  
  
Summary  
> This protein is found in the cytoplasm and nucleus of eukaryotic organisms, specifically within the fungi group known as Dikarya  
> It has a size of 465 amino acids and a molecular weight of 53521 kilodaltons  
> The protein possesses several functional domains, including Cytidine Deaminase domain 2 and JAB1/MPN domain  
> It exhibits metalloendopeptidase activity and binds to metal ions.  
  
QA  
> Where is this protein located? It is found in the cytoplasm and nucleus.  
> What is the size of this protein? It has a size of 465 amino acids.  
> What is the molecular weight of this protein? It has a molecular weight of 53521 kilodaltons.  
> What are the functional domains of this protein? It has Cytidine Deaminase domain 2 and JAB1/MPN domain.  
> What activity does this protein exhibit? It exhibits metalloendopeptidase activity.  
> What does this protein bind to? It binds to metal ions.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: True  
length: 465  
mw: 53521

FIELDS of A9MN11  
functional domains: YehU-like  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 72 aa, 8338 KDa  
  
Summary  
> This protein belongs to the functional domain known as YehU-like  
> It is found in Bacteria, specifically in the phylum Pseudomonadota within the class Gammaproteobacteria  
> The protein has a size of 72 amino acids and a molecular weight of 8338 KDa.  
  
QA  
> What is the functional domain of this protein? The functional domain of this protein is YehU-like.  
> In which taxonomic groups is this protein found? This protein is found in the taxonomic groups Bacteria, Pseudomonadota, and Gammaproteobacteria.  
> What is the size of this protein? This protein has a size of 72 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 8338 KDa.  
> Does this protein function as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 72  
mw: 8338

FIELDS of Q06J59  
subunit: Part of the 30S ribosomal subunit.  
subcellular location: Chloroplast, Plastid  
functional domains: rRNA binding, Ribosomal protein S3, C-terminal domain, Ribosomal protein S3 C-terminal domain, Prokaryotic type KH domain (KH-domain type II), structural constituent of ribosome  
taxonomy: Eukaryota, Sar, Rhizaria  
protein size: 246 aa, 28193 KDa  
  
Summary  
> This protein is a subunit of the 30S ribosomal subunit  
> It is localized in chloroplasts and plastids  
> The protein consists of several functional domains, including rRNA binding, Ribosomal protein S3, C-terminal domain, Ribosomal protein S3 C-terminal domain, and Prokaryotic type KH domain (KH-domain type II)  
> It serves as a structural constituent of the ribosome  
> In terms of taxonomy, this protein is found in eukaryotes, specifically in the SAR supergroup and the Rhizaria subphylum  
> It has a size of 246 amino acids and a molecular weight of 28193 kilodaltons.  
  
QA  
> What is the subcellular location of this protein? It is localized in Chloroplast and Plastid.  
> What are the functional domains of this protein? The functional domains include rRNA binding, Ribosomal protein S3, C-terminal domain, Ribosomal protein S3 C-terminal domain, and Prokaryotic type KH domain (KH-domain type II).  
> What is the structural role of this protein? It serves as a structural constituent of the ribosome.  
> In which taxonomic groups is this protein found? It is found in Eukaryota, specifically in the SAR supergroup and the Rhizaria subphylum.  
> What is the size of this protein? It has a size of 246 amino acids.  
> What is the molecular weight of this protein? The molecular weight is 28193 kilodaltons.  
> Is this protein an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 246  
mw: 28193

FIELDS of Q9BHU1  
functional domains: structural constituent of ribosome, Ribosomal protein S26e  
taxonomy: Eukaryota, Sar, Alveolata  
protein size: 125 aa, 14444 KDa  
  
Summary  
> This protein is a ribosomal protein S26e and serves as a structural constituent of the ribosome  
> It is found in eukaryotic organisms belonging to the taxa Eukaryota, Sar, and Alveolata  
> With a protein size of 125 amino acids, it has a molecular weight of 14444 KDa  
> Ribosomal protein S26e is a crucial component of the ribosome, the cellular organelle responsible for protein synthesis  
> It plays a role in stabilizing the structure of the ribosome and is involved in various stages of translation, including initiation, elongation, and termination.  
  
QA  
> What is the function of this protein? It serves as a structural constituent of the ribosome.  
> What is the taxonomic classification of this protein? Eukaryota, Sar, Alveolata.  
> How many amino acids comprise this protein? It consists of 125 amino acids.  
> What is the molecular weight of this protein? It has a molecular weight of 14444 KDa.  
> What is the role of this protein in translation? It is involved in various stages of translation, including initiation, elongation, and termination.  
> What is the primary cellular location of this protein? It is primarily localized to the ribosome.  
> Can this protein act as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 125  
mw: 14444

FIELDS of Q54J73  
catalytic activity: EC = 2.7.7.19, ATP + RNA(n) = diphosphate + RNA(n)-3'-adenine ribonucleotide  
cofactor: Mg(2+), Binds 2 magnesium ions. Also active with manganese., Mn(2+)  
subcellular location: Nucleus  
functional domains: Poly(A) polymerase predicted RNA binding domain, Nucleotidyltransferase, RNA binding, metal ion binding, PAP/OAS1 substrate-binding domain, poly(A) RNA polymerase activity, PAP/Archaeal CCA-adding enzyme, C-terminal domain, Beta Polymerase, domain 2, ATP binding  
taxonomy: Eukaryota, Amoebozoa, Evosea  
protein size: 809 aa, 88686 KDa  
  
Summary  
> This protein is a nucleotidyltransferase with a subcellular location in the nucleus  
> It belongs to the Eukaryota domain, specifically the Amoebozoa phylum in the Evosea class  
> The protein has a size of 809 amino acids and a molecular weight of 88686 KDa  
> In terms of functional domains, it contains the Nucleotidyltransferase, PAP/Archaeal CCA-adding enzyme C-terminal domain, ATP binding, Poly(A) polymerase predicted RNA binding domain, RNA binding, PAP/OAS1 substrate-binding domain, metal ion binding, and Beta Polymerase domain 2  
> The protein also exhibits catalytic activity with the enzymatic reaction involving ATP and RNA, resulting in the formation of diphosphate and RNA with a 3'-adenine ribonucleotide  
> The enzyme has an EC number of 2.7.7.19  
> It requires the presence of cofactors, specifically binding to two magnesium ions and being active with both manganese and magnesium.  
  
QA  
> What is the subcellular location of the protein? The protein is located in the nucleus.  
> What is the taxonomy of the protein? The protein belongs to the Eukaryota domain, Amoebozoa phylum, and Evosea class.  
> What is the size of the protein? The protein has a size of 809 amino acids and a molecular weight of 88686 KDa.  
> What are the functional domains of the protein? The functional domains include Nucleotidyltransferase, PAP/Archaeal CCA-adding enzyme C-terminal domain, ATP binding, Poly(A) polymerase predicted RNA binding domain, RNA binding, PAP/OAS1 substrate-binding domain, metal ion binding, and Beta Polymerase domain 2.  
> What is the catalytic activity of the protein? The protein catalyzes the reaction between ATP and RNA to form diphosphate and RNA with a 3'-adenine ribonucleotide.  
> What is the EC number of the enzyme? The enzyme has an EC number of 2.7.7.19.  
> What are the cofactors required by the protein? The protein binds two magnesium ions and is active with both manganese and magnesium.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: magnesium, manganese  
length: 809  
mw: 88686

FIELDS of Q9L290  
subunit: HJ DNA is sandwiched between 2 RuvA tetramers; dsDNA enters through RuvA and exits via RuvB, An RuvB hexamer assembles on each DNA strand where it exits the tetramer, Homotetramer  
subcellular location: Cytoplasm  
functional domains: 5' to 3' exonuclease, C-terminal subdomain, four-way junction helicase activity, DNA helicase RuvA subunit, C-terminal domain, RuvA domain 2-like, Nucleic acid-binding proteins, four-way junction DNA binding, ATP binding  
taxonomy: Bacteria, Actinomycetota, Actinomycetes  
protein size: 201 aa, 20551 KDa  
  
Summary  
> This protein is a homotetramer consisting of 201 amino acids, with a molecular weight of 20551 KDa  
> It is localized in the cytoplasm of bacterial cells  
> The functional domains of this protein include a 5' to 3' exonuclease domain, a C-terminal subdomain, a four-way junction helicase activity domain, a DNA helicase RuvA subunit domain, a C-terminal domain, a RuvA domain 2-like domain, and nucleic acid-binding proteins  
> In terms of structure, the DNA is sandwiched between two RuvA tetramers, with the double-stranded DNA entering through RuvA and exiting via RuvB  
> An RuvB hexamer assembles on each DNA strand as it exits the tetramer.  
  
QA  
> What is the subunit composition of this protein? The protein is composed of a homotetramer.  
> Where is this protein localized within the cell? It is localized in the cytoplasm.  
> What are the functional domains of this protein? The functional domains include a 5' to 3' exonuclease domain, a C-terminal subdomain, a four-way junction helicase activity domain, a DNA helicase RuvA subunit domain, a C-terminal domain, a RuvA domain 2-like domain, and nucleic acid-binding proteins.  
> How is the DNA structured in relation to this protein? The DNA is sandwiched between two RuvA tetramers.  
> How does the double-stranded DNA enter and exit the protein complex? The double-stranded DNA enters through RuvA and exits via RuvB.  
> What assembles on each DNA strand as it exits the tetramer? An RuvB hexamer assembles on each DNA strand as it exits the tetramer.  
> What is the size of this protein? The protein consists of 201 amino acids and has a molecular weight of 20551 KDa.  
> What is the taxonomy of this protein? It belongs to the bacterial taxonomy hierarchy, specifically under Bacteria, Actinomycetota, and Actinomycetes.  
> Does this protein function as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 201  
mw: 20551

FIELDS of Q8WZA1  
catalytic activity: 3-O-(alpha-D-mannosyl)-L-threonyl-[protein] + UDP-N-acetyl-alpha-D-glucosamine = 3-O-(N-acetyl-beta-D-glucosaminyl-(1->2)-alpha-D-mannosyl)-L-threonyl-[protein] + H(+) + UDP  
cofactor: The manganese ion interacts primarily with the substrate UDP-N-acetylglucosamine., Mn(2+)  
pH dependence: Optimum pH is 6.0.  
subcellular location: Golgi apparatus membrane, Single-pass type II membrane protein  
functional domains: Nucleotide-diphospho-sugar transferases, manganese ion binding, beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase activity, acetylglucosaminyltransferase activity  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 660 aa, 75252 KDa  
  
Summary  
> This protein is a eukaryotic enzyme belonging to the nucleotide-diphospho-sugar transferases functional domain  
> It is primarily located in the Golgi apparatus membrane and is a single-pass type II membrane protein  
> The protein has a size of 660 amino acids and a molecular weight of 75252 KDa  
> It exhibits two enzymatic activities: beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase activity and acetylglucosaminyltransferase activity  
> The protein requires a manganese ion as a cofactor, which interacts mainly with the substrate UDP-N-acetylglucosamine  
> Its catalytic activity involves transferring an alpha-D-mannosyl group from 3-O-(alpha-D-mannosyl)-L-threonyl-[protein] to UDP-N-acetyl-alpha-D-glucosamine, resulting in the formation of 3-O-(N-acetyl-beta-D-glucosaminyl-(1->2)-alpha-D-mannosyl)-L-threonyl-[protein], a hydrogen ion, and UDP  
> The protein demonstrates an optimum pH of 6.0.  
  
QA  
> What is the functional domain of this protein? Nucleotide-diphospho-sugar transferases  
> Where is this protein primarily located? Golgi apparatus membrane  
> How many amino acids does this protein have? 660  
> What is the molecular weight of this protein? 75252 KDa  
> What are the enzymatic activities of this protein? beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase activity and acetylglucosaminyltransferase activity  
> Which ion acts as a cofactor for this protein? Manganese ion  
> What does the cofactor primarily interact with? The substrate UDP-N-acetylglucosamine  
> What is the catalytic activity of this protein? 3-O-(alpha-D-mannosyl)-L-threonyl-[protein] + UDP-N-acetyl-alpha-D-glucosamine = 3-O-(N-acetyl-beta-D-glucosaminyl-(1->2)-alpha-D-mannosyl)-L-threonyl-[protein] + H(+) + UDP  
> What is the optimum pH for this protein? 6.0  
> Is this protein an enzyme? Yes  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: manganese  
length: 660  
mw: 75252

FIELDS of A4VQX9  
catalytic activity: EC = 2.5.1.3, 2-[(2R,5Z)-2-carboxy-4-methylthiazol-5(2H)-ylidene]ethyl phosphate + 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 2 H(+) = CO2 + diphosphate + thiamine phosphate, 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 4-methyl-5-(2-phosphooxyethyl)-thiazole + H(+) = diphosphate + thiamine phosphate, 2-(2-carboxy-4-methylthiazol-5-yl)ethyl phosphate + 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 2 H(+) = CO2 + diphosphate + thiamine phosphate  
cofactor: Binds 1 Mg(2+) ion per subunit., Mg(2+)  
functional domains: thiamine-phosphate diphosphorylase activity, Aldolase class I, magnesium ion binding, Thiamin phosphate synthase  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 213 aa, 22683 KDa  
  
Summary  
> This protein is involved in catalytic activities related to the synthesis of thiamine phosphate, an important coenzyme in many metabolic reactions  
> It functions as a thiamine phosphate synthase, catalyzing the conversion of various substrates into thiamine phosphate  
> The protein has a molecular weight of 22683 KDa and a size of 213 amino acids  
> It belongs to the Aldolase class I functional domain and has a magnesium ion binding site  
> It is found in bacteria, specifically in the Pseudomonadota phylum of Gammaproteobacteria.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein involves the synthesis of thiamine phosphate through reactions involving various substrates and the release of CO2 and diphosphate.  
> What cofactor is bound by this protein? This protein binds to one Mg(2+) ion per subunit.  
> What are the functional domains of this protein? The functional domains of this protein include thiamine-phosphate diphosphorylase activity, Aldolase class I, magnesium ion binding, and Thiamin phosphate synthase.  
> What is the taxonomy of organisms that contain this protein? This protein is found in bacteria, specifically in the Pseudomonadota phylum of Gammaproteobacteria.  
> What is the size of this protein? This protein has a size of 213 amino acids and a molecular weight of 22683 KDa.  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg(2+)  
length: 213  
mw: 22683

FIELDS of Q10452  
catalytic activity: ATP + L-seryl-[protein] = ADP + H(+) + O-phospho-L-seryl-[protein], ATP + L-threonyl-[protein] = ADP + H(+) + O-phospho-L-threonyl-[protein], EC = 2.7.11.1  
subcellular location: Nucleus, Cytoplasm  
functional domains: protein serine kinase activity, protein serine/threonine/tyrosine kinase activity, Protein kinase-like (PK-like), protein tyrosine kinase activity, protein kinase activity, Transferase(Phosphotransferase) domain 1, protein serine/threonine kinase activity, ATP binding  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 387 aa, 44165 KDa  
  
Summary  
> This protein is a kinase enzyme involved in phosphorylation reactions  
> It has multiple functional domains, including protein serine kinase activity, protein serine/threonine/tyrosine kinase activity, Protein kinase-like (PK-like), and protein tyrosine kinase activity  
> The protein is involved in transferase (phosphotransferase) reactions, specifically catalyzing the transfer of phosphate groups from ATP to serine or threonine residues of other proteins  
> It also possesses ATP binding activity  
> The protein is found in the nucleus and cytoplasm of eukaryotic organisms, specifically within the fungi kingdom  
> It has a size of 387 amino acids and a molecular weight of 44165 kilodaltons.  
  
QA  
> What type of enzymatic activity does this protein possess? It has protein serine kinase activity, protein serine/threonine/tyrosine kinase activity, Protein kinase-like (PK-like), and protein tyrosine kinase activity.  
> What is the subcellular location of this protein? It is found in the nucleus and cytoplasm.  
> What is the taxonomy of this protein? It belongs to the Eukaryota domain, Fungi kingdom, and Dikarya phylum.  
> How many amino acids are present in this protein? It has 387 amino acids.  
> What is the molecular weight of this protein? Its molecular weight is 44165 kilodaltons.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: True  
length: 387  
mw: 44165

FIELDS of E9Q4Z2  
catalytic activity: EC = 6.4.1.2, acetyl-CoA + ATP + hydrogencarbonate = ADP + H(+) + malonyl-CoA + phosphate  
cofactor: Mg(2+), biotin, Mn(2+), Binds 2 magnesium or manganese ions per subunit.  
subunit: Monomer, homodimer, and homotetramer, Forms filamentous polymers  
subcellular location: Mitochondrion  
functional domains: PreATP-grasp domain, ATP-grasp fold, A domain, metal ion binding, Biotin dependent carboxylase carboxyltransferase, ClpP/crotonase, acetyl-CoA carboxylase activity, ATP-grasp fold, B domain, biotin binding, Glutathione synthetase ATP-binding domain-like, Rudiment single hybrid motif, identical protein binding, ATP binding, Single hybrid motif  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 2448 aa, 275750 KDa  
  
Summary  
> This protein is an enzyme involved in a specific catalytic activity  
> It belongs to the eukaryotic organisms, specifically Metazoa within the Chordata kingdom  
> It is primarily found in the mitochondrion within the cell  
> The protein functions as a catalyst and is responsible for a specific biochemical reaction involving the molecules acetyl-CoA, ATP, hydrogencarbonate, ADP, H(+), malonyl-CoA, and phosphate  
> It requires several cofactors, including magnesium ions, manganese ions, and biotin  
> The protein has multiple functional domains, such as the PreATP-grasp domain, ATP-grasp fold, A domain, metal ion binding domain, Biotin dependent carboxylase carboxyltransferase domain, and ClpP/crotonase domain  
> Additionally, it exhibits activities including acetyl-CoA carboxylase activity and binds ATP  
> The protein can exist as a monomer, homodimer, and homotetramer, and has the ability to form filamentous polymers  
> It has a size of 2448 amino acids and a molecular weight of 275750 KDa.  
  
QA  
> What is the subcellular location of this protein? Mitochondrion.  
> What is the catalytic activity of this protein? acetyl-CoA + ATP + hydrogencarbonate = ADP + H(+) + malonyl-CoA + phosphate.  
> What are the cofactors required by this protein? Magnesium ions, manganese ions, and biotin.  
> What are some of the functional domains of this protein? PreATP-grasp domain, ATP-grasp fold, A domain, metal ion binding domain, Biotin dependent carboxylase carboxyltransferase domain, and ClpP/crotonase domain.  
> What is the taxonomy of this protein? Eukaryota, Metazoa, Chordata.  
> What is the size of this protein in terms of amino acids? 2448 amino acids.  
> What is the molecular weight of this protein? 275750 KDa.  
> Is this protein an enzyme? Yes  
  
METRICS  
localization: mitochondrion  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: True  
is\_enzyme: True  
cofactor: magnesium ions, manganese ions, biotin  
length: 2448  
mw: 275750

FIELDS of P9WLP2  
functional domains: nmb1532 protein domain like  
taxonomy: Bacteria, Actinomycetota, Actinomycetes  
protein size: 255 aa, 28073 KDa  
  
Summary  
> The protein in question is a domain-like protein with the specific functional domain labeled as nmb1532  
> It is found in the bacterial phylum Actinomycetes, which is a subgroup of Actinomycetota  
> The protein has a size of 255 amino acids and a molecular weight of approximately 28,073 kilodaltons.  
  
QA  
> What is the specific functional domain of the protein? The specific functional domain of the protein is nmb1532.  
> In which bacterial phylum is the protein found? The protein is found in the phylum Actinomycetes.  
> What is the size of the protein in terms of amino acids? The protein has a size of 255 amino acids.  
> What is the molecular weight of the protein? The molecular weight of the protein is approximately 28,073 kilodaltons.  
> Can this protein act as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 255  
mw: 28073

FIELDS of Q9HKM7  
catalytic activity: AMP + ATP = 2 ADP, EC = 2.7.4.3  
functional domains: P-loop containing nucleotide triphosphate hydrolases, adenylate kinase activity, ATP hydrolysis activity, P-loop containing nucleoside triphosphate hydrolases, ATP binding  
taxonomy: Archaea, Candidatus Thermoplasmatota, Thermoplasmata  
protein size: 148 aa, 16263 KDa  
  
Summary  
> This protein is involved in catalytic activity, specifically the conversion of AMP and ATP into 2 ADP molecules  
> It belongs to the enzyme classification EC 2.7.4.3  
> The protein possesses several functional domains, including P-loop containing nucleotide triphosphate hydrolases, adenylate kinase activity, ATP hydrolysis activity, and ATP binding  
> It has been found in Archaea, specifically within the Candidatus Thermoplasmatota and Thermoplasmata taxa  
> The protein has a size of 148 amino acids and a molecular weight of 16263 KDa.  
  
QA  
> What is the specific catalytic activity of this protein? The specific catalytic activity of this protein is the conversion of AMP and ATP into 2 ADP molecules.  
> What is the enzyme classification for this protein? The enzyme classification for this protein is EC 2.7.4.3.  
> What functional domains are present in this protein? The functional domains present in this protein include P-loop containing nucleotide triphosphate hydrolases, adenylate kinase activity, ATP hydrolysis activity, and ATP binding.  
> In which taxa has this protein been found? This protein has been found in Archaea within the Candidatus Thermoplasmatota and Thermoplasmata taxa.  
> What is the size of this protein? This protein has a size of 148 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 16263 KDa.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 148  
mw: 16263

FIELDS of P00508  
catalytic activity: 2-oxoglutarate + L-kynurenine = H2O + kynurenate + L-glutamate, EC = 2.6.1.1, 2-oxoglutarate + L-aspartate = L-glutamate + oxaloacetate, EC = 2.6.1.7  
cofactor: pyridoxal 5'-phosphate  
subunit: Homodimer.  
subcellular location: Mitochondrion matrix  
functional domains: Aspartate Aminotransferase, domain 1, kynurenine-oxoglutarate transaminase activity, Type I PLP-dependent aspartate aminotransferase-like (Major domain), pyridoxal phosphate binding, protein homodimerization activity, L-aspartate:2-oxoglutarate aminotransferase activity, PLP-dependent transferases  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 423 aa, 47241 KDa  
  
Summary  
> This protein is a homodimeric enzyme found in the mitochondrion matrix of eukaryotic organisms  
> It functions as a pyridoxal 5'-phosphate (PLP) dependent aspartate aminotransferase, specifically involved in the interconversion of various amino acids and keto acids  
> The protein consists of 423 amino acids with a molecular weight of 47,241 KDa  
> It contains multiple functional domains, including the aspartate aminotransferase domain 1 and a type I PLP-dependent aspartate aminotransferase-like major domain  
> The protein catalyzes two important reactions: (1) the conversion of 2-oxoglutarate and L-kynurenine into kynurenate, L-glutamate, and water, and (2) the conversion of 2-oxoglutarate and L-aspartate into L-glutamate and oxaloacetate  
> Overall, this protein plays a crucial role in amino acid metabolism within the mitochondria.  
  
QA  
> What is the specific catalytic activity of this protein? The specific catalytic activity of this protein is the interconversion of 2-oxoglutarate and L-kynurenine into kynurenate, L-glutamate, and water, as well as the interconversion of 2-oxoglutarate and L-aspartate into L-glutamate and oxaloacetate.  
> What is the cofactor required for the enzymatic activity of this protein? The cofactor required for the enzymatic activity of this protein is pyridoxal 5'-phosphate (PLP).  
> What is the subunit composition of this protein? This protein consists of homodimers, indicating that each functional unit is composed of two identical subunits.  
> Where is this protein located within the cell? This protein is located in the mitochondrion matrix.  
> What are the functional domains present in this protein? The functional domains present in this protein include the aspartate aminotransferase domain 1, a type I PLP-dependent aspartate aminotransferase-like major domain, pyridoxal phosphate binding domain, and protein homodimerization domain.  
> What is the taxonomy of this protein? This protein belongs to the taxonomic groups Eukaryota, Metazoa, and Chordata.  
> What is the size of this protein in terms of amino acids and molecular weight? This protein consists of 423 amino acids with a molecular weight of 47,241 KDa.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
localization: mitochondrion  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: True  
is\_enzyme: True  
cofactor: pyridoxal 5'-phosphate (plp)  
length: 423  
mw: 47241

FIELDS of P05994  
catalytic activity: Preferential cleavage: Gly-|-Xaa, in proteins and in small molecule substrates., EC = 3.4.22.25  
functional domains: cysteine-type peptidase activity, Cysteine proteinases  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 348 aa, 39024 KDa  
  
Summary  
> This protein is a cysteine-type peptidase with a preferential cleavage activity of Gly-Xaa residues in both proteins and small molecule substrates  
> It belongs to the EC 3.4.22.25 enzyme class  
> With a size of 348 amino acids and a weight of 39024 KDa, it is found in eukaryotes, specifically in the Viridiplantae kingdom, within the Streptophyta group.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the preferential cleavage of Gly-Xaa residues in proteins and small molecule substrates.  
> What enzyme class does this protein belong to? This protein belongs to the EC 3.4.22.25 enzyme class.  
> How many amino acids does this protein have? This protein has a size of 348 amino acids.  
> What is the weight of this protein? The weight of this protein is 39024 KDa.  
> In which kingdom is this protein found? This protein is found in the Viridiplantae kingdom.  
> To which group within the Viridiplantae kingdom does this protein belong? This protein belongs to the Streptophyta group.  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 348  
mw: 39024

FIELDS of Q65EB6  
subcellular location: Cytoplasm  
functional domains: BH3618-like  
taxonomy: Bacteria, Bacillota, Bacilli  
protein size: 143 aa, 16045 KDa  
  
Summary  
> This protein is found in the cytoplasm of bacteria belonging to the Bacilli class  
> It has a size of 143 amino acids and a molecular weight of 16045 KDa  
> The protein contains functional domains known as BH3618-like.  
  
QA  
> Where is this protein found? This protein is found in the cytoplasm.  
> What are the functional domains of this protein? The functional domains of this protein are BH3618-like.  
> What is the taxonomy of bacteria this protein belongs to? This protein belongs to the Bacteria domain, specifically the Bacillota class and Bacilli order.  
> How many amino acids does this protein consist of? This protein consists of 143 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 16045 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 143  
mw: 16045

FIELDS of Q8ZTY5  
subunit: Heterotrimer composed of an alpha, a beta and a gamma chain.  
functional domains: RNA binding, ribosome binding, translation initiation factor activity, EIF\_2\_alpha, eIF2alpha middle domain-like, Nucleic acid-binding proteins, eIF-2-alpha, C-terminal domain  
taxonomy: Archaea, Thermoproteota, Thermoprotei  
protein size: 265 aa, 30561 KDa  
  
Summary  
> This protein is a heterotrimer composed of an alpha, a beta, and a gamma chain  
> It belongs to the RNA binding protein family and plays a role in translation initiation  
> It has functional domains including RNA binding, ribosome binding, and translation initiation factor activity  
> Specifically, it contains the EIF\_2\_alpha, eIF2alpha middle domain-like, and Nucleic acid-binding protein domains  
> This protein is found in the Archaea domain, specifically belonging to the Thermoproteota class and Thermoprotei order  
> It has a protein size of 265 amino acids and a molecular weight of 30561 KDa.  
  
QA  
> What are the subunits of this protein? It is composed of an alpha, a beta, and a gamma chain.  
> What are the functional domains of this protein? Its functional domains include RNA binding, ribosome binding, translation initiation factor activity, EIF\_2\_alpha, eIF2alpha middle domain-like, Nucleic acid-binding proteins, and the eIF-2-alpha C-terminal domain.  
> In which domain is this protein found? It is found in the Archaea domain.  
> What is the protein size of this protein? It has a protein size of 265 amino acids.  
> What is the molecular weight of this protein? It has a molecular weight of 30561 KDa.  
> Does this protein function as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 265  
mw: 30561

FIELDS of Q62130  
catalytic activity: EC = 3.1.3.48, H2O + O-phospho-L-tyrosyl-[protein] = L-tyrosyl-[protein] + phosphate  
subcellular location: Cytoskeleton, Nucleus, Cytoplasm  
functional domains: Pleckstrin-homology domain (PH domain)/Phosphotyrosine-binding domain (PTB), Ubiquitin-like, protein tyrosine phosphatase activity, Protein tyrosine phosphatase superfamily, receptor tyrosine kinase binding, transcription coregulator activity, (Phosphotyrosine protein) phosphatases II, PH domain-like, Second domain of FERM  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 1189 aa, 135042 KDa  
  
Summary  
> This protein, found in eukaryotic organisms belonging to the Chordata phylum, is a multi-functional enzyme that is involved in various cellular processes  
> With a size of 1189 amino acids and a molecular weight of 135042 KDa, it consists of several functional domains including the Pleckstrin-homology domain (PH domain)/Phosphotyrosine-binding domain (PTB), Ubiquitin-like domain, and PH domain-like domain  
> The protein is primarily located in the cytoskeleton, nucleus, and cytoplasm  
> The protein exhibits protein tyrosine phosphatase activity, specifically belonging to the Phosphotyrosine protein phosphatases II group within the broader category of the Protein tyrosine phosphatase superfamily  
> It functions by catalyzing the hydrolysis reaction that removes phosphate groups from O-phospho-L-tyrosyl residues in proteins, resulting in the formation of L-tyrosyl residues and free phosphate ions  
> This catalytic activity is characterized by the enzyme classification number EC = 3.1.3.48  
> Furthermore, the protein shows interactions with receptor tyrosine kinases and functions as a transcription coregulator  
> These roles imply its involvement in signal transduction pathways and gene regulation within the cell  
> In summary, this protein is a multifunctional enzyme with protein tyrosine phosphatase activity, located in the cytoskeleton, nucleus, and cytoplasm of eukaryotic organisms  
> It contains various functional domains, including PH domain/PTB and Ubiquitin-like domains  
> Its catalytic activity involves the removal of phosphate groups from O-phospho-L-tyrosyl residues in proteins  
> Additionally, it interacts with receptor tyrosine kinases and acts as a transcription coregulator.  
  
QA  
> What is the enzymatic activity of this protein? The enzymatic activity of this protein is protein tyrosine phosphatase activity.  
> Where is this protein predominantly located within the cell? This protein is predominantly located in the cytoskeleton, nucleus, and cytoplasm.  
> What is the size of this protein? This protein has a size of 1189 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 135042 KDa.  
> Which functional domains are present in this protein? This protein contains the Pleckstrin-homology domain (PH domain)/Phosphotyrosine-binding domain (PTB), Ubiquitin-like domain, and PH domain-like domain.  
> What is the catalytic reaction of this protein? The catalytic reaction of this protein involves the hydrolysis of O-phospho-L-tyrosyl residues in proteins, resulting in the formation of L-tyrosyl residues and phosphate ions.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: True  
length: 1189  
mw: 135042

FIELDS of Q57CE9  
catalytic activity: 2 H(+) + H2O + urea = CO2 + 2 NH4(+), EC = 3.5.1.5  
subunit: Heterotrimer of UreA (gamma), UreB (beta) and UreC (alpha) subunits  
subcellular location: Cytoplasm  
functional domains: Urease, beta-subunit, urease activity, Urease, beta subunit  
taxonomy: Bacteria, Pseudomonadota, Alphaproteobacteria  
protein size: 159 aa, 17763 KDa  
  
Summary  
> This protein is a urease enzyme involved in the catalytic breakdown of urea  
> It is composed of three subunits, UreA (gamma), UreB (beta), and UreC (alpha), forming a heterotrimeric structure  
> The protein is found in the cytoplasm of bacteria, specifically within the Pseudomonadota phylum of Alphaproteobacteria  
> With a size of 159 amino acids and a weight of 17763 KDa, this protein possesses catalytic activity as it mediates the conversion of urea into carbon dioxide (CO2) and ammonium ions (NH4(+))  
> This reaction is attributed to its enzymatic activity, referred to as EC = 3.5.1.5.  
  
QA  
> What is the composition of this protein? The protein is composed of UreA (gamma), UreB (beta), and UreC (alpha) subunits.  
> Where is this protein located within the cell? This protein is localized in the cytoplasm.  
> Which taxonomic groups does this protein belong to? This protein belongs to the Bacteria domain, Pseudomonadota phylum, and Alphaproteobacteria class.  
> What is the size of this protein? This protein has a size of 159 amino acids.  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the conversion of 2 H(+) + H2O + urea into CO2 and 2 NH4(+).  
> What is the enzymatic activity of this protein? The enzymatic activity of this protein is referred to as EC = 3.5.1.5.  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 159  
mw: 17763

FIELDS of Q9BGY6  
subcellular location: Single-pass membrane protein, Membrane  
functional domains: L domain-like, Ribonuclease Inhibitor  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 510 aa, 56496 KDa  
  
Summary  
> This protein is a single-pass membrane protein with a subcellular location on the membrane  
> It contains two functional domains, namely the L domain-like and Ribonuclease Inhibitor domains  
> The protein is found in organisms belonging to the Eukaryota kingdom, specifically in the Metazoa phylum, and more specifically in the Chordata class  
> It has a size of 510 amino acids and a molecular weight of 56496 Kilodaltons.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is the membrane.  
> How many functional domains does this protein have? This protein has two functional domains, which are the L domain-like and Ribonuclease Inhibitor domains.  
> What is the taxonomy of this protein? This protein belongs to the Eukaryota kingdom, Metazoa phylum, and Chordata class.  
> What is the size of this protein? The protein has a size of 510 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 56496 Kilodaltons.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 510  
mw: 56496

FIELDS of Q8BGB2  
subcellular location: Cytoplasm, Cell membrane  
functional domains: Tetratricopeptide repeat domain, TPR-like  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 858 aa, 96156 KDa  
  
Summary  
> This protein is found in eukaryotic organisms, specifically in metazoans belonging to the Chordata phylum  
> It has two functional domains known as TPR-like and tetratricopeptide repeat domains  
> The protein has a size of 858 amino acids and a molecular weight of 96156 KDa  
> It is localized in the cytoplasm and on the cell membrane.  
  
QA  
> What are the subcellular locations of this protein? The subcellular locations of this protein are the cytoplasm and the cell membrane. 2) Describe the functional domains of this protein. The functional domains of this protein include a TPR-like domain and a tetratricopeptide repeat domain.  
> What is the taxonomy of this protein? This protein belongs to the domain Eukaryota, the kingdom Metazoa, and the phylum Chordata.  
> How large is this protein? This protein has a size of 858 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 96156 KDa.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 858  
mw: 96156

FIELDS of Q9V9S7  
subcellular location: Presynapse  
functional domains: C2 domain, GTPase activator activity, C2 domain (Calcium/lipid-binding domain, CaLB), Rho GTPase activation protein, GTPase activation domain, GAP, PDZ domain-like  
taxonomy: Eukaryota, Metazoa, Ecdysozoa  
protein size: 1866 aa, 198298 KDa  
  
Summary  
> This protein is a large protein found in the subcellular location of the presynapse  
> It exhibits various functional domains including the C2 domain, GTPase activator activity, CaLB domain, Rho GTPase activation protein, GAP, and PDZ domain-like  
> The protein is widespread in eukaryotes, specifically in the metazoan and ecdysozoan taxa  
> It has a large size of 1866 amino acids and a molecular weight of 198298 KDa.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is the presynapse.  
> What are the functional domains present in this protein? The functional domains present in this protein are the C2 domain, GTPase activator activity, CaLB domain, Rho GTPase activation protein, GAP, and PDZ domain-like.  
> In which taxa is this protein found? This protein is found in eukaryotes, specifically in the metazoan and ecdysozoan taxa.  
> What is the size of this protein in amino acids? The size of this protein in amino acids is 1866.  
> What is the molecular weight of this protein? The molecular weight of this protein is 198298 KDa.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 1866  
mw: 198298

FIELDS of P54144  
subcellular location: Multi-pass membrane protein, Cell membrane  
functional domains: protein self-association, Ammonium transporter AmtB like domains, ammonium transmembrane transporter activity, Ammonium transporter  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 501 aa, 53577 KDa  
  
Summary  
> This protein is a multi-pass membrane protein located in the cell membrane  
> It contains functional domains such as protein self-association, Ammonium transporter AmtB-like domains, and exhibits ammonium transmembrane transporter activity  
> It is classified as an ammonium transporter  
> Based on the provided taxonomy information, it belongs to the eukaryotic group called Viridiplantae within the larger group of Streptophyta  
> The protein has a size of 501 amino acids and a molecular weight of 53577 KDa.  
  
QA  
> It is a multi-pass membrane protein located in which cellular compartment? Answer: The protein is located in the cell membrane.  
> What types of domains does it contain? Answer: It contains functional domains such as protein self-association and Ammonium transporter AmtB-like domains.  
> What kind of transporter activity does it have? Answer: It exhibits ammonium transmembrane transporter activity.  
> Which groups does it belong to? Answer: It belongs to the eukaryotic group called Viridiplantae within the larger group of Streptophyta.  
> How many amino acids does it consist of? Answer: The protein has a size of 501 amino acids.  
> How much does it weigh? Answer: The protein has a molecular weight of 53577 KDa.  
> Can this protein act as an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 501  
mw: 53577

FIELDS of Q8R3F9  
catalytic activity: EC = 2.7.7.19, ATP + RNA(n) = diphosphate + RNA(n)-3'-adenine ribonucleotide, EC = 2.7.7.52, RNA(n) + UTP = diphosphate + RNA(n)-3'-uridine ribonucleotide  
cofactor: Mg(2+), Binds 1 divalent cation per subunit., Mn(2+)  
subcellular location: Nucleolus, Nucleus, Nucleus speckle  
functional domains: Nucleotidyltransferase, zinc ion binding, mRNA 3'-UTR binding, RNA binding, enzyme-substrate adaptor activity, RNA uridylyltransferase activity, PAP/OAS1 substrate-binding domain, beta-beta-alpha zinc fingers, U6 snRNA binding, poly(A) RNA polymerase activity, RNA-binding domain, RBD, ATP binding, Beta Polymerase, domain 2, enzyme binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 869 aa, 94603 KDa  
  
Summary  
> This protein is a nucleotidyltransferase with a variety of functional domains involved in RNA processing and modification  
> It has catalytic activity, specifically as an ATP-dependent RNA uridylyltransferase  
> It catalyzes two enzymatic reactions, one involving the addition of diphosphate to RNA-adenine ribonucleotide and the other involving the addition of diphosphate to RNA-uridine ribonucleotide  
> The protein requires divalent cations like Mg(2+) or Mn(2+) as cofactors  
> It is found in the nucleolus, nucleus, and nucleus speckles within the cell  
> The protein is relatively large, consisting of 869 amino acids and having a molecular weight of 94603 KDa  
> It is present in eukaryotes, specifically in metazoans belonging to the Chordata phylum.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein includes ATP-dependent RNA uridylyltransferase activity.  
> What are the cofactors required by this protein? This protein requires divalent cations such as Mg(2+) or Mn(2+) as cofactors.  
> Where is this protein localized within the cell? This protein is found in the nucleolus, nucleus, and nucleus speckles.  
> What is the size of this protein? This protein consists of 869 amino acids and has a molecular weight of 94603 KDa.  
> What is the taxonomy of this protein? This protein is present in eukaryotes, specifically in metazoans belonging to the Chordata phylum.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg(2+), mn(2+)  
length: 869  
mw: 94603

FIELDS of Q4FNV6  
catalytic activity: adenosine(37) in tRNA + L-threonylcarbamoyladenylate = AMP + H(+) + N(6)-L-threonylcarbamoyladenosine(37) in tRNA, EC = 2.3.1.234  
cofactor: Binds 1 Fe(2+) ion per subunit., Fe(2+)  
subcellular location: Cytoplasm  
functional domains: N(6)-L-threonylcarbamoyladenine synthase activity, iron ion binding, Actin-like ATPase domain  
taxonomy: Bacteria, Pseudomonadota, Alphaproteobacteria  
protein size: 357 aa, 38795 KDa  
  
Summary  
> This protein is a functional enzyme involved in the synthesis of N(6)-L-threonylcarbamoyladenosine(37) in tRNA  
> It is found in the cytoplasm of bacteria belonging to the Alphaproteobacteria class of the Pseudomonadota phylum  
> The protein consists of 357 amino acids and has a molecular weight of 38795 KDa  
> It possesses an actin-like ATPase domain, which suggests a role in energy-dependent processes  
> Additionally, it exhibits iron ion binding properties, indicating a requirement for Fe(2+) as a cofactor  
> The catalytic activity of the protein involves the conversion of adenosine(37) in tRNA to AMP, H(+), and N(6)-L-threonylcarbamoyladenosine(37) in tRNA with an EC number of 2.3.1.234.  
  
QA  
> What is the subcellular location of this protein? The protein is localized in the cytoplasm.  
> What are the functional domains of this protein? The protein possesses an actin-like ATPase domain.  
> What is the size of this protein? The protein is composed of 357 amino acids and has a molecular weight of 38795 KDa.  
> What is the specific catalytic activity of this protein? The protein catalyzes the conversion of adenosine(37) in tRNA to AMP, H(+), and N(6)-L-threonylcarbamoyladenosine(37) in tRNA.  
> What is the cofactor required by this protein? The protein requires Fe(2+) as a cofactor for its activity.  
> What is the taxonomic classification of bacteria that harbor this protein? The protein is found in bacteria belonging to the Alphaproteobacteria class of the Pseudomonadota phylum.  
> What is the enzymatic classification of this protein? The protein is classified with EC number 2.3.1.234.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: fe(2+)  
length: 357  
mw: 38795

FIELDS of Q8R4L0  
subcellular location: Cytoplasmic vesicle, Cytoplasm, Late endosome, Cell membrane  
functional domains: SH2 domain, signaling adaptor activity, 1-phosphatidylinositol-3-kinase regulator activity, SH3-domain, SH3 Domains  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 259 aa, 28476 KDa  
  
Summary  
> The protein described is a eukaryotic protein found in various subcellular locations including the cytoplasm, cell membrane, cytoplasmic vesicles, and late endosomes  
> It belongs to the domain of signaling adaptor activity and possesses functional domains such as SH2 and SH3 domains  
> Additionally, it exhibits 1-phosphatidylinositol-3-kinase regulator activity  
> The protein is present in metazoans, specifically within the chordata phylum  
> It has a size of 259 amino acids and a molecular weight of approximately 28,476 kilodaltons.  
  
QA  
> What are the subcellular locations where the protein is found? The protein is found in the cytoplasm, cell membrane, cytoplasmic vesicles, and late endosomes.  
> What functional domains does the protein possess? The protein possesses SH2 and SH3 domains.  
> What activity does the protein exhibit as a regulator? The protein exhibits 1-phosphatidylinositol-3-kinase regulator activity.  
> In which taxonomical classification is the protein found? The protein is found within the metazoan group, specifically within the chordata phylum.  
> What is the size of the protein? The protein has a size of 259 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of approximately 28,476 kilodaltons.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 259  
mw: 28476

FIELDS of P39793  
catalytic activity: Preferential cleavage: (Ac)2-L-Lys-D-Ala-|-D-Ala. Also transpeptidation of peptidyl-alanyl moieties that are N-acyl substituents of D-alanine., EC = 3.4.16.4, [GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)](n)-di-trans,octa-cis-undecaprenyl diphosphate + beta-D-GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-di-trans,octa-cis-undecaprenyl diphosphate = [GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)](n+1)-di-trans-octa-cis-undecaprenyl diphosphate + di-trans,octa-cis-undecaprenyl diphosphate + H(+), EC = 2.4.1.129  
subcellular location: Forespore inner membrane, Cell membrane, Single-pass type II membrane protein  
functional domains: Immunoglobulins, Biosynthetic peptidoglycan transglycosylase-like, penicillin binding, DD-peptidase/beta-lactamase superfamily, serine-type D-Ala-D-Ala carboxypeptidase activity, beta-lactamase/transpeptidase-like, Fibronectin type III, Lysozyme-like, peptidoglycan glycosyltransferase activity  
taxonomy: Bacteria, Bacillota, Bacilli  
protein size: 914 aa, 99562 KDa  
  
Summary  
> This protein is a large enzyme found in bacteria with a size of 914 amino acids or 99,562 kilodaltons  
> It is primarily located in the cell membrane and forespore inner membrane  
> Structurally, it contains various functional domains such as immunoglobulins, DD-peptidase/beta-lactamase superfamily, penicillin binding, biosynthetic peptidoglycan transglycosylase-like, lysozyme-like, beta-lactamase/transpeptidase-like, peptidoglycan glycosyltransferase activity, serine-type D-Ala-D-Ala carboxypeptidase activity, and Fibronectin type III  
> The protein is classified under the taxonomy of Bacteria, specifically belonging to the class Bacilli.  
  
QA  
> What is the size of this protein? The size of this protein is 914 amino acids or 99,562 kilodaltons.  
> Where is this protein primarily located? This protein is primarily located in the cell membrane and forespore inner membrane.  
> What are the functional domains present in this protein? The functional domains of this protein include immunoglobulins, DD-peptidase/beta-lactamase superfamily, penicillin binding, biosynthetic peptidoglycan transglycosylase-like, lysozyme-like, beta-lactamase/transpeptidase-like, peptidoglycan glycosyltransferase activity, serine-type D-Ala-D-Ala carboxypeptidase activity, and Fibronectin type III.  
> Under which taxonomy is this protein classified? This protein is classified under the taxonomy of Bacteria, specifically belonging to the class Bacilli.  
> What is the catalytic activity of this protein? The catalytic activity of this protein involves the cleavage and transpeptidation of specific substrates, such as [GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)](n)-di-trans,octa-cis-undecaprenyl diphosphate.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 914  
mw: 99562

FIELDS of Q7P0M1  
catalytic activity: EC = 3.5.4.10, EC = 2.1.2.3, H2O + IMP = 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide, (6S)-10-formyltetrahydrofolate + 5-amino-1-(5-phospho-beta-D-ribosyl)imidazole-4-carboxamide = (6S)-5,6,7,8-tetrahydrofolate + 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide  
functional domains: Methylglyoxal synthase-like, IMP cyclohydrolase activity, Cytidine deaminase-like, phosphoribosylaminoimidazolecarboxamide formyltransferase activity, Methylglyoxal synthase-like domain  
taxonomy: Bacteria, Pseudomonadota, Betaproteobacteria  
protein size: 525 aa, 56042 KDa  
  
Summary  
> This protein is a catalytic enzyme with multiple functional domains  
> It plays a role in various biochemical reactions and is found in bacteria belonging to the taxonomic group Betaproteobacteria  
> The protein has a size of 525 amino acids and a molecular weight of 56042 KDa.  
  
QA  
> What are the catalytic activities of the protein? The protein has catalytic activities with EC numbers 3.5.4.10 and 2.1.2.It catalyzes the conversion of H2O and IMP into 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide, as well as the conversion of (6S)-10-formyltetrahydrofolate and 5-amino-1-(5-phospho-beta-D-ribosyl)imidazole-4-carboxamide into (6S)-5,6,7,8-tetrahydrofolate and 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide.  
> What are the functional domains of the protein? The protein has functional domains including Methylglyoxal synthase-like, IMP cyclohydrolase activity, Cytidine deaminase-like, phosphoribosylaminoimidazolecarboxamide formyltransferase activity, and Methylglyoxal synthase-like domain.  
> What is the taxonomic classification of bacteria where this protein is found? This protein is found in bacteria belonging to the taxonomic group Betaproteobacteria within the broader group of Pseudomonadota.  
> How large is the protein in terms of amino acids and molecular weight? The protein has a size of 525 amino acids and a molecular weight of 56042 KDa.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 525  
mw: 56042

FIELDS of Q6F999  
catalytic activity: EC = 2.7.7.1, ATP + H(+) + nicotinate beta-D-ribonucleotide = deamido-NAD(+) + diphosphate, ATP + beta-nicotinamide D-ribonucleotide + H(+) = diphosphate + NAD(+), EC = 2.7.7.18  
functional domains: Nucleotidylyl transferase, nicotinate-nucleotide adenylyltransferase activity, HUPs, nicotinamide-nucleotide adenylyltransferase activity, ATP binding  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 188 aa, 22079 KDa  
  
Summary  
> This protein is a nucleotidylyl transferase with various functional domains, including nicotinate-nucleotide adenylyltransferase activity and HUPs (hypoxanthine and uracil phosphoribosyltransferases) domain  
> It is involved in catalytic activities such as the conversion of ATP, nicotinate beta-D-ribonucleotide, and H(+) into deamido-NAD(+), and the conversion of ATP, beta-nicotinamide D-ribonucleotide, and H(+) into diphosphate and NAD(+)  
> The protein is found in bacteria, specifically in the Pseudomonadota phylum of the Gammaproteobacteria class  
> It has a size of 188 amino acids and a molecular weight of 22079 KDa.  
  
QA  
> What are the catalytic activities of this protein? The catalytic activities of this protein include the conversion of ATP, nicotinate beta-D-ribonucleotide, and H(+) into deamido-NAD(+), and the conversion of ATP, beta-nicotinamide D-ribonucleotide, and H(+) into diphosphate and NAD(+).  
> What are the functional domains of this protein? The functional domains of this protein include nucleotidylyl transferase, nicotinate-nucleotide adenylyltransferase activity, HUPs, and nicotinamide-nucleotide adenylyltransferase activity.  
> In which taxonomic group is this protein found? This protein is found in bacteria, specifically in the Pseudomonadota phylum of the Gammaproteobacteria class.  
> What is the size of this protein? This protein has a size of 188 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 22079 KDa.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 188  
mw: 22079

FIELDS of O54982  
subunit: Homotetramer; which constitutes the calcium-activated potassium channel  
subcellular location: Multi-pass membrane protein, Cell membrane  
functional domains: Voltage-gated potassium channels, potassium channel activity, voltage-gated monoatomic ion channel activity, NAD(P)-binding Rossmann-like Domain  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 1121 aa, 126870 KDa  
  
Summary  
> This protein is a calcium-activated potassium channel that functions as a homotetramer  
> It is primarily located in the cell membrane and is classified as a multi-pass membrane protein  
> The protein has functional domains including voltage-gated monoatomic ion channel activity, voltage-gated potassium channel activity, and a NAD(P)-binding Rossmann-like domain  
> In terms of taxonomy, this protein belongs to the Eukaryota kingdom, Metazoa phylum, and Chordata subphylum  
> It has a protein size of 1121 amino acids and a molecular weight of 126870 Kilodaltons.  
  
QA  
> What is the subunit composition of this protein? The subunit composition of this protein is a homotetramer.  
> Where is this protein primarily located? This protein is primarily located in the cell membrane.  
> What are the functional domains of this protein? The functional domains of this protein include voltage-gated monoatomic ion channel activity, voltage-gated potassium channel activity, and a NAD(P)-binding Rossmann-like domain.  
> What is the taxonomy of this protein? This protein belongs to the Eukaryota kingdom, Metazoa phylum, and Chordata subphylum.  
> What is the size of this protein in amino acids and molecular weight? This protein has a size of 1121 amino acids and a molecular weight of 126870 Kilodaltons.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 1121  
mw: 126870

FIELDS of B0TWS3  
subunit: F(0) has three main subunits: a(1), b(2) and c(10-14), F(1) is attached to F(0) by a central stalk formed by the gamma and epsilon chains, while a peripheral stalk is formed by the delta and b chains., F(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1), F-type ATPases have 2 components, F(1) - the catalytic core - and F(0) - the membrane proton channel, The alpha and beta chains form an alternating ring which encloses part of the gamma chain  
subcellular location: Cell inner membrane, Single-pass membrane protein  
functional domains: F1F0 ATP synthase subunit B, membrane domain, proton-transporting ATP synthase activity, rotational mechanism  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 156 aa, 17414 KDa  
  
Summary  
> F-type ATPases are enzymes that play a crucial role in the synthesis of ATP in various organisms  
> These ATPases consist of two main components: F(1) and F(0)  
> F(1) is the catalytic core, composed of five subunits: alpha(3), beta(3), gamma(1), delta(1), and epsilon(1)  
> It forms an alternating ring structure, encasing part of the gamma chain  
> F(0) is the membrane proton channel and consists of three main subunits: a(1), b(2), and c(10-14)  
> The F(1) component is attached to F(0) through a central stalk formed by the gamma and epsilon chains, while a peripheral stalk is formed by the delta and b chains  
> F-type ATPases are found in the cell inner membrane and are classified in the taxonomic groups Bacteria, Pseudomonadota, and Gammaproteobacteria  
> These ATPases exhibit proton-transporting ATP synthase activity and utilize a rotational mechanism  
> The specific functional domain related to these ATPases is the F1F0 ATP synthase subunit B, membrane domain  
> The protein size of this ATPase is approximately 156 amino acids, with a molecular weight of 17414 KDa.  
  
QA  
> What are the components of F-type ATPases? F-type ATPases have two components: F(1) (the catalytic core) and F(0) (the membrane proton channel).  
> How many subunits are present in the F(1) component of F-type ATPases? The F(1) component of F-type ATPases has five subunits: alpha(3), beta(3), gamma(1), delta(1), and epsilon(1).  
> What are the main subunits of the F(0) component of F-type ATPases? The main subunits of the F(0) component of F-type ATPases are a(1), b(2), and c(10-14).  
> How is the F(1) component of F-type ATPases connected to the F(0) component? The F(1) component of F-type ATPases is attached to the F(0) component by a central stalk formed by the gamma and epsilon chains, and a peripheral stalk formed by the delta and b chains.  
> Where are F-type ATPases located in the cell? F-type ATPases are found in the cell inner membrane.  
> What is the functional domain associated with F-type ATPases? The specific functional domain related to F-type ATPases is the F1F0 ATP synthase subunit B, membrane domain.  
> What is the size of this protein? The protein size of this ATPase is approximately 156 amino acids with a molecular weight of 17414 KDa.  
> What is the taxonomic classification of F-type ATPases? F-type ATPases are classified in the taxonomic groups Bacteria, Pseudomonadota, and Gammaproteobacteria.  
> What is the main activity of F-type ATPases? F-type ATPases exhibit proton-transporting ATP synthase activity through a rotational mechanism.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
localization: mitochondrion  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: True  
is\_enzyme: True  
length: 156  
mw: 17414

FIELDS of Q2FFX3  
catalytic activity: EC = 2.5.1.78, (2S)-2-hydroxy-3-oxobutyl phosphate + 5-amino-6-(D-ribitylamino)uracil = 6,7-dimethyl-8-(1-D-ribityl)lumazine + H(+) + 2 H2O + phosphate  
subunit: Forms an icosahedral capsid composed of 60 subunits, arranged as a dodecamer of pentamers.  
functional domains: 6,7-dimethyl-8-ribityllumazine synthase activity, Lumazine/riboflavin synthase, Lumazine synthase  
taxonomy: Bacteria, Bacillota, Bacilli  
protein size: 154 aa, 16396 KDa  
  
Summary  
> This protein is a lumazine synthase enzyme found in bacteria  
> It has a catalytic activity represented by the EC number 2.5.1.78, where it catalyzes the reaction between (2S)-2-hydroxy-3-oxobutyl phosphate and 5-amino-6-(D-ribitylamino)uracil to produce 6,7-dimethyl-8-(1-D-ribityl)lumazine along with a release of H(+), phosphate, and two molecules of water  
> It functions as a part of an icosahedral capsid composed of 60 subunits, organized in a dodecamer of pentamers  
> The functional domains of this protein include 6,7-dimethyl-8-ribityllumazine synthase activity, Lumazine/riboflavin synthase, and Lumazine synthase  
> This protein is classified under the bacterial taxonomy, specifically in the Bacillota and Bacilli phyla  
> It has a protein size of 154 amino acids and a mass of 16396 KDa.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is represented by the EC number 2.5.1.78, where it converts (2S)-2-hydroxy-3-oxobutyl phosphate and 5-amino-6-(D-ribitylamino)uracil into 6,7-dimethyl-8-(1-D-ribityl)lumazine, H(+), phosphate, and two molecules of water.  
> How is this protein organized? This protein is part of an icosahedral capsid composed of 60 subunits, arranged as a dodecamer of pentamers.  
> What are the functional domains of this protein? The functional domains of this protein include 6,7-dimethyl-8-ribityllumazine synthase activity, Lumazine/riboflavin synthase, and Lumazine synthase.  
> What is the taxonomy of this protein? This protein belongs to the Bacteria domain, specifically in the Bacillota and Bacilli phyla.  
> What is the size of this protein? This protein has a size of 154 amino acids and a mass of 16396 KDa.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 154  
mw: 16396

FIELDS of Q9BDR0  
subunit: Heteromultimer with KCNC2  
subcellular location: Single-pass type I membrane protein, Apical cell membrane, Cell membrane, Single-pass membrane protein  
functional domains: voltage-gated potassium channel activity, potassium channel regulator activity  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 71 aa, 8557 KDa  
  
Summary  
> This protein is a heteromultimer with KCNC2 and belongs to the family of voltage-gated potassium channels  
> It is a type I membrane protein located primarily on the apical cell membrane and cell membrane  
> The protein consists of 71 amino acids and has a molecular weight of 8557 KDa  
> It possesses functional domains involved in both voltage-gated potassium channel activity and potassium channel regulator activity  
> The protein is found in a variety of eukaryotic organisms, specifically within the Metazoa and Chordata taxa.  
  
QA  
> The protein forms a heteromultimer with which other protein? It forms a heteromultimer with KCNC2.  
> Where is this protein located within the cell? It is primarily located on the apical cell membrane and the cell membrane.  
> What is the size of this protein in terms of amino acids and molecular weight? It consists of 71 amino acids and has a molecular weight of 8557 KDa.  
> What functional activities does this protein possess? It has functional domains involved in voltage-gated potassium channel activity and potassium channel regulator activity.  
> Which taxonomic groups is this protein found in? It is found within the Eukaryota domain, specifically within the Metazoa and Chordata taxa.  
> Is this protein an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 71  
mw: 8557

FIELDS of Q8ZTU2  
functional domains: Ribosomal protein L31e, structural constituent of ribosome  
taxonomy: Archaea, Thermoproteota, Thermoprotei  
protein size: 91 aa, 10579 KDa  
  
Summary  
> The provided protein is a ribosomal protein L31e, which serves as a structural constituent of the ribosome  
> This protein is found in Archaea, specifically within the Thermoproteota class of the Thermoprotei phylum  
> It has a size of 91 amino acids, with a molecular weight of 10579 KDa.  
  
QA  
> What is the role of this protein? This protein serves as a structural constituent of the ribosome.  
> What is the taxonomy of this protein? This protein belongs to the Archaea domain, Thermoproteota class, and Thermoprotei phylum.  
> How long is this protein? This protein consists of 91 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 10579 KDa.  
> Can this protein act as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 91  
mw: 10579

FIELDS of P0ABN5  
catalytic activity: fumarate(out) + 3 H(+)(out) = fumarate(in) + 3 H(+)(in), fumarate(in) + L-aspartate(out) = fumarate(out) + L-aspartate(in), (S)-malate(in) + succinate(out) = (S)-malate(out) + succinate(in), fumarate(in) + succinate(out) = fumarate(out) + succinate(in), L-aspartate(in) + succinate(out) = L-aspartate(out) + succinate(in)  
subcellular location: Cell inner membrane, Multi-pass membrane protein  
functional domains: C4-dicarboxylate transmembrane transporter activity, succinate:fumarate antiporter activity, symporter activity  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 433 aa, 45751 KDa  
  
Summary  
> This protein is a transmembrane transporter found in bacteria, specifically in the subcellular location of the cell inner membrane  
> It belongs to the functional domains of C4-dicarboxylate transmembrane transporter activity, succinate:fumarate antiporter activity, and symporter activity  
> With a protein size of 433 amino acids and a molecular weight of 45751 KDa, this protein plays a crucial role in catalyzing various reactions involving fumarate, L-aspartate, succinate, and (S)-malate  
> It catalyzes the exchange of these molecules between the interior and exterior of the cell, involving the transport of fumarate, succinate, and L-aspartate in both directions  
> The enzymatic reactions facilitated by this protein include the transport of fumarate and succinate in exchange for protons (H+), as well as the transport of L-aspartate and (S)-malate  
> This protein is essential for maintaining the balance and homeostasis of these molecules within the cell.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is the cell inner membrane.  
> What are the functional domains of this protein? The functional domains of this protein include C4-dicarboxylate transmembrane transporter activity, succinate:fumarate antiporter activity, and symporter activity.  
> What is the protein size and molecular weight of this protein? The protein size is 433 amino acids, and the molecular weight is 45751 KDa.  
> What are the enzymatic reactions catalyzed by this protein? This protein catalyzes the exchange of fumarate, L-aspartate, succinate, and (S)-malate between the interior and exterior of the cell. It facilitates the transport of fumarate and succinate in exchange for protons (H+), as well as the transport of L-aspartate and (S)-malate.  
> What is the taxonomy of this protein? This protein belongs to the Bacteria domain, specifically the Pseudomonadota phylum within the Gammaproteobacteria class.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 433  
mw: 45751

FIELDS of Q58130  
catalytic activity: (2R,3S)-3-methylmalate + NAD(+) = 2-oxobutanoate + CO2 + NADH, EC = 1.1.1.n5, EC = 1.1.1.85, (2R,3S)-3-isopropylmalate + NAD(+) = 4-methyl-2-oxopentanoate + CO2 + NADH, (R)-malate + NAD(+) = CO2 + NADH + pyruvate, EC = 1.1.1.83  
cofactor: Mg(2+), Mn(2+), Binds 1 Mg(2+) or Mn(2+) ion per subunit.  
temperature dependence: Loses 50% of its activity after heating at 80 degrees Celsius for 10 min.  
subunit: Homotetramer.  
subcellular location: Cytoplasm  
functional domains: Isocitrate/Isopropylmalate dehydrogenase-like, D-malate dehydrogenase (decarboxylating) activity, isocitrate dehydrogenase (NAD+) activity, 3-isopropylmalate dehydrogenase activity, NAD binding, magnesium ion binding, Isopropylmalate Dehydrogenase  
taxonomy: Archaea, Euryarchaeota, Methanomada group  
protein size: 333 aa, 36330 KDa  
  
Summary  
> This protein is a D-malate dehydrogenase (decarboxylating) with isopropylmalate dehydrogenase activity  
> It belongs to the Methanomada group, a subset of the Archaea domain within the Euryarchaeota phylum  
> The protein has a subunit structure consisting of a homotetramer  
> It is primarily localized in the cytoplasm  
> The protein has multiple functional domains, including isocitrate/ isopropylmalate dehydrogenase-like domains  
> It exhibits catalytic activity in various enzymatic reactions, such as converting (2R,3S)-3-isopropylmalate to 4-methyl-2-oxopentanoate, and (2R,3S)-3-methylmalate to 2-oxobutanoate  
> It can also convert (R)-malate to pyruvate and (2R,3S)-3-methylmalate to CO2  
> The protein requires a cofactor, either Mn(2+) or Mg(2+), with each subunit binding one Mg(2+) or Mn(2+) ion  
> Additionally, it is temperature-sensitive, losing 50% of its activity when heated at 80 degrees Celsius for 10 minutes.  
  
QA  
> What kind of enzymatic activity does this protein have? This protein has D-malate dehydrogenase (decarboxylating) and isopropylmalate dehydrogenase activity.  
> What is the subunit structure of this protein? The subunit structure of this protein is a homotetramer.  
> Where is this protein primarily located? This protein is primarily located in the cytoplasm.  
> What are the functional domains of this protein? The functional domains of this protein include isocitrate/isopropylmalate dehydrogenase-like domains.  
> What enzymatic reactions can this protein catalyze? This protein can catalyze reactions such as converting (2R,3S)-3-isopropylmalate to 4-methyl-2-oxopentanoate, (2R,3S)-3-methylmalate to 2-oxobutanoate, (R)-malate to pyruvate, and (2R,3S)-3-methylmalate to CO2.  
> What cofactor does this protein require? This protein requires either Mn(2+) or Mg(2+) as a cofactor.  
> What happens to the activity of this protein at high temperatures? The activity of this protein decreases by 50% when heated at 80 degrees Celsius for 10 minutes.  
> Does this protein function as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mn(2+), mg(2+)  
length: 333  
mw: 36330

FIELDS of Q08103  
subcellular location: Single-pass membrane protein, Membrane  
functional domains: Immunoglobulin  
taxonomy: Viruses, Duplodnaviria, Heunggongvirae  
protein size: 444 aa, 46708 KDa  
  
Summary  
> This protein is a single-pass membrane protein that belongs to the immunoglobulin functional domain family  
> It is found in viruses of the Duplodnaviria superphylum, specifically in the Heunggongvirae class  
> The protein has a size of 444 amino acids and a molecular weight of approximately 46708 KDa.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is the membrane.  
> What is the functional domain of this protein? The functional domain of this protein is the immunoglobulin domain.  
> Which taxonomy group does this protein belong to? This protein belongs to the Viruses group, specifically in the Duplodnaviria superphylum and Heunggongvirae class.  
> What is the size of this protein in terms of amino acids? This protein has a size of 444 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is approximately 46708 KDa.  
> Is this protein an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 444  
mw: 46708

FIELDS of E0SCY3  
subcellular location: Periplasm  
functional domains: transmembrane transporter activity, Periplasmic binding protein-like II  
taxonomy: Bacteria, Pseudomonadota, Gammaproteobacteria  
protein size: 332 aa, 36357 KDa  
  
Summary  
> This protein is found in the periplasm of bacteria, specifically in the taxonomic group Gammaproteobacteria within the phylum Pseudomonadota  
> It has a size of 332 amino acids (aa) and a molecular weight of 36357 Kilodaltons (KDa)  
> The protein is characterized by its functional domains, which include transmembrane transporter activity and a Periplasmic binding protein-like II domain.  
  
QA  
> Where is this protein located? This protein is located in the periplasm.  
> What are the functional domains of this protein? The functional domains of this protein include transmembrane transporter activity and a Periplasmic binding protein-like II domain.  
> What is the taxonomic group of bacteria that this protein belongs to? This protein belongs to the taxonomic group Gammaproteobacteria.  
> How long is this protein in terms of amino acids? This protein is 332 amino acids long.  
> What is the molecular weight of this protein? The molecular weight of this protein is 36357 Kilodaltons (KDa).  
> Does this protein function as an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 332  
mw: 36357

FIELDS of Q1LVN1  
subcellular location: Single-pass type I membrane protein, Golgi apparatus, Cell membrane  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 133 aa, 14877 KDa  
  
Summary  
> The protein under discussion is a single-pass type I membrane protein that is found in the Golgi apparatus and cell membrane  
> It is present in eukaryotic organisms and belongs to the Metazoa phylum within the Chordata subphylum  
> This protein has a relatively small size, consisting of 133 amino acids and has a molecular weight of 14877 KDa.  
  
QA  
> What is the subcellular location of the protein? The protein is found in the Golgi apparatus and the cell membrane.  
> Which domain does the protein belong to? The protein is a single-pass type I membrane protein.  
> To which taxonomic group does the protein belong? The protein belongs to the Chordata subphylum within the Metazoa phylum.  
> What is the size of the protein in terms of amino acids? The protein consists of 133 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of 14877 KDa.  
> Does this protein function as an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 133  
mw: 14877

FIELDS of O77780  
subunit: Heterodimer with ADAM1/fertilin subunit alpha.  
subcellular location: Single-pass type I membrane protein, Membrane  
functional domains: Metalloproteases ('zincins'), catalytic domain, metalloendopeptidase activity, Blood coagulation inhibitor (disintegrin), Disintegrin domain, Collagenase (Catalytic Domain)  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 745 aa, 83150 KDa  
  
Summary  
> This protein is a heterodimer consisting of two subunits, one of which is known as ADAM1/fertilin subunit alpha  
> It is a single-pass type I membrane protein that is located on various membranes  
> The protein contains several functional domains, including a disintegrin domain, a catalytic domain, and a blood coagulation inhibitor domain  
> The disintegrin domain helps in protein-protein interactions, while the catalytic domain possesses metalloendopeptidase and collagenase activities  
> As an enzyme, this protein is involved in various enzymatic reactions, but the specific details are not provided  
> The protein is found in eukaryotes and belongs to the taxonomic groups of Metazoa and Chordata  
> With a size of 745 amino acids, the protein has a molecular weight of 83150 KDa.  
  
QA  
> What is the subunit composition of this protein? Its subunit composition consists of a heterodimer with the ADAM1/fertilin subunit alpha.  
> What is the subcellular location of this protein? This protein is located on various membranes as a single-pass type I membrane protein.  
> What are the functional domains present in this protein? This protein contains a disintegrin domain, a catalytic domain (metal protease), and a blood coagulation inhibitor domain.  
> What is the taxonomy of this protein? This protein is found in eukaryotes and belongs to the taxonomic groups of Metazoa and Chordata.  
> What is the size of this protein? This protein is composed of 745 amino acids and has a molecular weight of 83150 KDa.  
> Can this protein be correctly termed an enzyme? Yes  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 745  
mw: 83150

FIELDS of Q9W3W8  
functional domains: Ribosomal protein L22/L17, structural constituent of ribosome, Ribosomal protein L22  
taxonomy: Eukaryota, Metazoa, Ecdysozoa  
protein size: 186 aa, 21593 KDa  
  
Summary  
> The protein under consideration is a ribosomal protein, specifically Ribosomal protein L22/L17  
> It functions as a structural constituent of the ribosome  
> This protein is found in eukaryotes, belonging to the taxonomic groups Eukaryota, Metazoa, and Ecdysozoa  
> It has a size of 186 amino acids and a molecular weight of 21593 kilodaltons.  
  
QA  
> What is the function of the protein? The protein functions as a structural constituent of the ribosome.  
> What are the functional domains of the protein? The protein contains Ribosomal protein L22/L17 domains.  
> What is the taxonomic classification of the protein? The protein belongs to the taxonomic groups Eukaryota, Metazoa, and Ecdysozoa.  
> What is the size of the protein? The protein has a size of 186 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of 21593 kilodaltons.  
> What is the specific name of the protein? The specific name of the protein is not provided in the given information.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 186  
mw: 21593

FIELDS of Q6ZVL6  
subcellular location: Single-pass membrane protein, Membrane  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 1849 aa, 198999 KDa  
  
Summary  
> This protein is a single-pass membrane protein that is primarily located in the membrane  
> It belongs to the taxonomy of Eukaryota, specifically the Metazoa phylum within the Chordata subphylum  
> It has a large protein size of 1849 amino acids, with a molecular weight of approximately 198,999 kilodaltons.  
  
QA  
> What is the subcellular location of this protein? The subcellular location of this protein is in the membrane.  
> Is this protein a membrane protein? Yes, this protein is a membrane protein.  
> Which kingdom does this protein belong to? This protein belongs to the kingdom Eukaryota.  
> What is the taxonomic classification of this protein? This protein is classified within the Metazoa phylum and the Chordata subphylum.  
> How many amino acids are in this protein? This protein contains 1849 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is approximately 198,999 kilodaltons.  
> Is this protein found in eukaryotes? Yes, this protein is found in eukaryotes.  
> Which phylum does this protein belong to? This protein belongs to the phylum Metazoa  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 1849  
mw: 198999

FIELDS of P42699  
cofactor: Cu(2+)  
subcellular location: Chloroplast thylakoid membrane, Peripheral membrane protein, Plastid  
functional domains: Cupredoxins - blue copper proteins, protein domain specific binding, electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II activity, Cupredoxins, copper ion binding  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 167 aa, 16984 KDa  
  
Summary  
> This protein is a Cupredoxin, which belongs to the blue copper protein family  
> It has a size of 167 amino acids and a molecular weight of 16984 kilodaltons  
> It is found in various subcellular locations, including the plastid and the peripheral membrane of the chloroplast thylakoid membrane  
> The protein is involved in electron transport, specifically transferring electrons from the cytochrome b6/f complex of photosystem II  
> It possesses functional domains that are important for its activity, such as cupredoxins and protein domain-specific binding  
> Additionally, it has a specific binding capability for copper ions  
> Based on its taxonomy, this protein is classified under the domain Eukaryota within the kingdom Viridiplantae and phylum Streptophyta.  
  
QA  
> What is the size of the protein? The protein has a size of 167 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of 16984 kilodaltons.  
> Where is the protein located within the cell? The protein is found in the plastid and the peripheral membrane of the chloroplast thylakoid membrane.  
> What is the function of the protein? The protein is involved in electron transport, specifically transferring electrons from the cytochrome b6/f complex of photosystem II.  
> What are the functional domains of the protein? The functional domains of the protein include cupredoxins and protein domain-specific binding.  
> What ions does the protein bind to? The protein specifically binds to copper ions.  
> How is the protein classified taxonomically? The protein belongs to the domain Eukaryota within the kingdom Viridiplantae and phylum Streptophyta.  
> Is this protein an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 167  
mw: 16984

FIELDS of P38589  
subunit: Homodimer.  
functional domains: High potential iron-sulphur protein, 4 iron, 4 sulfur cluster binding, metal ion binding, HIPIP (high potential iron protein), electron transfer activity  
taxonomy: Bacteria, Pseudomonadota, Alphaproteobacteria  
protein size: 57 aa, 6223 KDa  
  
Summary  
> This protein is a homodimer that belongs to the HIPIP family  
> It consists of 4 iron and 4 sulfur cluster binding domains, as well as metal ion binding domains  
> The protein is involved in electron transfer activity  
> It is relatively small, consisting of 57 amino acids, and has a molecular weight of 6223 KDa  
> This protein is found in bacteria, specifically in the Pseudomonadota phylum of Alphaproteobacteria.  
  
QA  
> What is the quaternary structure of this protein? It is a homodimer.  
> What are the functional domains of this protein? It has high potential iron-sulphur protein, 4 iron, 4 sulfur cluster binding, metal ion binding, and HIPIP domains.  
> What is the primary function of this protein? It is involved in electron transfer activity.  
> How many amino acids are present in this protein? It consists of 57 amino acids.  
> What is the molecular weight of this protein? It has a molecular weight of 6223 KDa.  
> In which taxonomic group is this protein found? It belongs to the phylum Alphaproteobacteria within the Pseudomonadota bacteria.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 57  
mw: 6223

FIELDS of Q8ET90  
functional domains: NagB/RpiA/CoA transferase-like  
taxonomy: Bacteria, Bacillota, Bacilli  
protein size: 233 aa, 25993 KDa  
  
Summary  
> The protein is a NagB/RpiA/CoA transferase-like protein found in bacteria, specifically in the class Bacilli  
> It consists of 233 amino acids and has a molecular weight of 25993 KDa  
> The protein contains functional domains that are similar to NagB/RpiA/CoA transferases.  
  
QA  
> What type of protein is this? The protein is a NagB/RpiA/CoA transferase-like protein.  
> Where is this protein found? This protein is found in bacteria, specifically in the class Bacilli.  
> How big is this protein? The protein consists of 233 amino acids and has a molecular weight of 25993 KDa.  
> What functional domains does this protein have? This protein contains functional domains that are similar to NagB/RpiA/CoA transferases.  
> Is this protein an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 233  
mw: 25993

FIELDS of Q6KHG5  
catalytic activity: EC = 2.7.8.7, apo-[ACP] + CoA = adenosine 3',5'-bisphosphate + H(+) + holo-[ACP]  
cofactor: Mg(2+)  
subcellular location: Cytoplasm  
functional domains: holo-[acyl-carrier-protein] synthase activity, 4'-phosphopantetheinyl transferase, 4'-phosphopantetheinyl transferase domain, magnesium ion binding  
taxonomy: Bacteria, Mycoplasmatota, Mollicutes  
protein size: 107 aa, 12968 KDa  
  
Summary  
> The protein under consideration is found in bacteria, specifically in the taxonomic groups Bacteria, Mycoplasmatota, and Mollicutes  
> It is a small protein with a size of 107 amino acids and a molecular weight of 12,968 Daltons  
> It is primarily located in the cytoplasm  
> The protein exhibits various functional domains, including holo-[acyl-carrier-protein] synthase activity and two 4'-phosphopantetheinyl transferase domains  
> Additionally, it possesses a significant capability for binding magnesium ions  
> The protein's catalytic activity involves the conversion of apo-[ACP] (acyl carrier protein lacking a prosthetic group) and CoA (coenzyme A) into adenosine 3',5'-bisphosphate, H(+) (proton), and holo-[ACP] (ACP with its prosthetic group attached)  
> The reaction is facilitated by the presence of magnesium ions as cofactors.  
  
QA  
> What is the catalytic activity of the protein? The catalytic activity of the protein is the conversion of apo-[ACP] and CoA into adenosine 3',5'-bisphosphate, H(+), and holo-[ACP].  
> What is the cofactor required for the protein's catalytic activity? The protein requires Mg(2+) as a cofactor for its catalytic activity.  
> Where is the protein primarily located? The protein is primarily located in the cytoplasm.  
> What are the functional domains of the protein? The protein has holo-[acyl-carrier-protein] synthase activity and two 4'-phosphopantetheinyl transferase domains.  
> What is the size of the protein? The protein has a size of 107 amino acids.  
> What is the taxonomy of the protein? The protein belongs to the taxonomic groups Bacteria, Mycoplasmatota, and Mollicutes.  
> What is the molecular weight of the protein? The protein has a molecular weight of 12,968 Daltons.  
> What is the product of the protein's catalytic activity? The product of the protein's catalytic activity is adenosine 3',5'-bisphosphate, H(+), and holo-[ACP].  
> Is this protein an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: mg(2+)  
length: 107  
mw: 12968

FIELDS of Q8RHA6  
catalytic activity: EC = 3.1.26.5, Endonucleolytic cleavage of RNA, removing 5'-extranucleotides from tRNA precursor.  
subunit: Consists of a catalytic RNA component (M1 or rnpB) and a protein subunit.  
functional domains: ribonuclease P activity, 3'-tRNA processing endoribonuclease activity, Ribosomal protein S5 domain 2-like, tRNA binding  
taxonomy: Bacteria, Fusobacteriota, Fusobacteriia  
protein size: 111 aa, 13363 KDa  
  
Summary  
> This protein is a ribonuclease involved in the processing of tRNA precursor molecules  
> It possesses endonucleolytic activity, specifically cleaving RNA and removing 5'-extranucleotides from tRNA precursor molecules  
> The protein consists of a catalytic RNA component (M1 or rnpB) and a protein subunit  
> It contains several functional domains including ribonuclease P activity, 3'-tRNA processing endoribonuclease activity, Ribosomal protein S5 domain 2-like, and a tRNA binding domain  
> The protein is found in bacteria, specifically in the taxonomic classes of Bacteria, Fusobacteriota, and Fusobacteriia  
> It has a relatively small size of 111 amino acids, with a molecular weight of 13,363 kilodaltons.  
  
QA  
> What is the catalytic activity of this protein? Its catalytic activity is the endonucleolytic cleavage of RNA, specifically removing 5'-extranucleotides from tRNA precursor molecules.  
> What are the subunits of this protein? It consists of a catalytic RNA component (M1 or rnpB) and a protein subunit.  
> What are the functional domains of this protein? The functional domains of this protein include ribonuclease P activity, 3'-tRNA processing endoribonuclease activity, Ribosomal protein S5 domain 2-like, and a tRNA binding domain.  
> In which taxonomic groups is this protein found? This protein is found in bacteria, specifically in the taxonomic classes of Bacteria, Fusobacteriota, and Fusobacteriia.  
> What is the size of this protein? It has a size of 111 amino acids and a molecular weight of 13,363 kilodaltons.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 111  
mw: 13363

FIELDS of Q4W945  
catalytic activity: atrochrysone carboxyl-[ACP] + H2O = atrochrysone carboxylate + H(+) + holo-[ACP]  
cofactor: Zn(2+), Binds 2 Zn(2+) ions per subunit.  
functional domains: metal ion binding, Metallo-hydrolase/oxidoreductase, Winged helix-like DNA-binding domain superfamily/Winged helix DNA-binding domain, hydrolase activity, Ribonuclease Z/Hydroxyacylglutathione hydrolase-like  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 315 aa, 35346 KDa  
  
Summary  
> This protein is a metallo-hydrolase/oxidoreductase found in eukaryotic fungi belonging to the Dikarya subkingdom  
> It has a size of 315 amino acids and a molecular weight of 35346 KDa  
> The protein exhibits hydrolase activity and contains functional domains such as metal ion binding and a Winged helix-like DNA-binding domain  
> It catalyzes the conversion of atrochrysone carboxyl-[ACP] and H2O into atrochrysone carboxylate, a proton (H+), and holo-[ACP]  
> The protein requires two Zn(2+) ions per subunit as cofactors.  
  
QA  
> What is the catalytic activity of the protein? The protein catalytic activity is the conversion of atrochrysone carboxyl-[ACP] and H2O into atrochrysone carboxylate, a proton (H+), and holo-[ACP].  
> What is the size of the protein? The protein has a size of 315 amino acids.  
> What is the molecular weight of the protein? The protein has a molecular weight of 35346 KDa.  
> What are the functional domains of the protein? The functional domains of the protein include metal ion binding and a Winged helix-like DNA-binding domain.  
> What is the taxonomy of the protein? The protein belongs to the Eukaryota domain and the Fungi kingdom, specifically the Dikarya subkingdom.  
> What is the required cofactor for the protein? The protein requires two Zn(2+) ions per subunit as a cofactor.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: zn(2+) ions  
length: 315  
mw: 35346

FIELDS of P32344  
subunit: The 37S small subunit contains a 15S ribosomal RNA (15S mt-rRNA) and 34 different proteins, The 54S large subunit contains a 21S rRNA (21S mt-rRNA) and 46 different proteins., Mature yeast 74S mitochondrial ribosomes consist of a small (37S) and a large (54S) subunit, Component of the mitochondrial small ribosomal subunit (mt-SSU)  
subcellular location: Mitochondrion, Peripheral membrane protein, Mitochondrion inner membrane  
functional domains: structural constituent of ribosome  
taxonomy: Eukaryota, Fungi, Dikarya  
protein size: 111 aa, 12772 KDa  
  
Summary  
> This protein is a component of the mature yeast 74S mitochondrial ribosomes, which consist of a small (37S) and a large (54S) subunit  
> The small subunit (37S) contains a 15S ribosomal RNA (15S mt-rRNA) and 34 different proteins, while the large subunit (54S) contains a 21S rRNA (21S mt-rRNA) and 46 different proteins  
> It is a structural constituent of the ribosome and is located in the mitochondrion, particularly in the peripheral membrane and the inner membrane  
> According to taxonomy, this protein belongs to the Eukaryota domain, specifically the Fungi kingdom within the Dikarya phylum  
> It has a protein size of 111 amino acids and a molecular weight of 12772 KDa.  
  
QA  
> What are the components of the mature yeast 74S mitochondrial ribosomes? The mature yeast 74S mitochondrial ribosomes consist of a small (37S) and a large (54S) subunit.  
> What is the composition of the small subunit (37S) of the mitochondrial ribosomes? The small subunit (37S) contains a 15S ribosomal RNA (15S mt-rRNA) and 34 different proteins.  
> How many proteins are present in the large subunit (54S) of the mitochondrial ribosomes? The large subunit (54S) contains 46 different proteins.  
> What is the subcellular location of this protein? This protein is located in the mitochondrion, particularly in the peripheral membrane and the inner membrane.  
> What is the functional domain of this protein? The functional domain of this protein is the structural constituent of the ribosome.  
> Which domain does this protein belong to? This protein belongs to the Eukaryota domain.  
> Which kingdom does this protein belong to? This protein belongs to the Fungi kingdom.  
> What is the protein size of this protein? This protein has a size of 111 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 12772 KDa.  
> Can this protein act as an enzyme? No  
  
METRICS  
localization: mitochondrion  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: True  
is\_enzyme: False  
length: 111  
mw: 12772

FIELDS of Q3BCU4  
subunit: Homodimerization requires the C-terminus cytoplasmic region (By similarity), Homodimer  
subcellular location: Cell membrane, Membrane, Lateral cell membrane, Caveola, Sarcolemma, Cell junction, Multi-pass membrane protein, Tight junction  
functional domains: Jelly Rolls, cAMP binding, structural molecule activity, cAMP-binding domain-like  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 356 aa, 40860 KDa  
  
Summary  
> This protein is a homodimer consisting of two subunits  
> It is primarily located in the cell membrane, particularly in areas such as the lateral cell membrane, caveola, sarcolemma, cell junction, and tight junction  
> The protein has various functional domains, including jelly rolls and a cAMP-binding domain-like region  
> Its functional roles include structural molecule activity and cAMP binding  
> The protein is found in eukaryotes, specifically within the metazoan phylum Chordata  
> It has a size of 356 amino acids and a molecular weight of 40860 KDa.  
  
QA  
> What is the subunit composition of this protein? The protein is a homodimer consisting of two subunits.  
> Where is the primary location of this protein? The primary location of the protein is in the cell membrane, including areas such as the lateral cell membrane, caveola, sarcolemma, cell junction, and tight junction.  
> What are some functional domains of this protein? Some functional domains of this protein include jelly rolls and a cAMP-binding domain-like region.  
> What are the functional roles of this protein? The protein has structural molecule activity and is capable of binding to cAMP.  
> In which taxonomic groups can this protein be found? This protein can be found in eukaryotes, specifically within the metazoan phylum Chordata.  
> What is the size of this protein in terms of amino acids and molecular weight? The protein has a size of 356 amino acids and a molecular weight of 40860 KDa.  
> Is this protein an enzyme? No  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 356  
mw: 40860

FIELDS of Q4UJY2  
functional domains: Ankyrin repeat, Ankyrin repeat-containing domain  
taxonomy: Bacteria, Pseudomonadota, Alphaproteobacteria  
protein size: 380 aa, 42903 KDa  
  
Summary  
> The protein is a bacterial protein belonging to the domain Bacteria, specifically the phylum Pseudomonadota and class Alphaproteobacteria  
> It has a protein size of 380 amino acids and a molecular weight of 42,903 KDa  
> The protein contains functional domains known as Ankyrin repeats and an Ankyrin repeat-containing domain  
> The Ankyrin repeat is a common structural motif involved in protein-protein interactions and is responsible for numerous cellular functions.  
  
QA  
> The protein belongs to which domain, phylum, and class? The protein belongs to the domain Bacteria, specifically the phylum Pseudomonadota and class Alphaproteobacteria.  
> What is the size of this protein in terms of amino acids and molecular weight? The protein has a size of 380 amino acids and a molecular weight of 42,903 KDa.  
> What are the functional domains present in this protein? The protein contains Ankyrin repeats and an Ankyrin repeat-containing domain.  
> What is the role of the Ankyrin repeats in the protein? The Ankyrin repeats are involved in protein-protein interactions and mediate various cellular functions. 5) Provide a generalized overview of the protein's functional properties. The protein is involved in protein-protein interactions and likely plays a crucial role in cellular processes based on its Ankyrin repeat-containing domains.  
> Does this protein possess the characteristics of an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
length: 380  
mw: 42903

FIELDS of Q8IYB7  
cofactor: Mg(2+), Mn(2+)  
subcellular location: P-body, Cytoplasm  
functional domains: RNA nuclease activity, poly(U) RNA binding, Nucleic acid-binding proteins, 3'-5'-RNA exonuclease activity, magnesium ion binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 885 aa, 99279 KDa  
  
Summary  
> This protein is a nucleic acid-binding protein found in the subcellular locations known as P-body and cytoplasm  
> It has various functional domains, including RNA nuclease activity, poly(U) RNA binding, and 3'-5'-RNA exonuclease activity  
> It also has the capability to bind to magnesium ions  
> With a size of 885 amino acids and a molecular weight of 99279 Da, this protein is present in eukaryotes, specifically within the metazoan and chordate taxa.  
  
QA  
> What is the role of this protein in subcellular locations? This protein is found in P-body and cytoplasm.  
> What functional domains does this protein possess? This protein has RNA nuclease activity, poly(U) RNA binding, and 3'-5'-RNA exonuclease activity.  
> Which cofactors does this protein interact with? This protein interacts with Mg(2+) and Mn(2+) as cofactors.  
> What is the size of this protein in terms of amino acids? This protein has a size of 885 amino acids.  
> What is the molecular weight of this protein? This protein has a molecular weight of 99279 Da.  
> What is the taxonomy of this protein? This protein belongs to the Eukaryota, Metazoa, and Chordata taxa.  
> Does this protein function as an enzyme? No  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: False  
cofactor: mg(2+), mn(2+)  
length: 885  
mw: 99279

FIELDS of P12081  
catalytic activity: EC = 6.1.1.21, ATP + L-histidine + tRNA(His) = AMP + diphosphate + H(+) + L-histidyl-tRNA(His)  
subunit: Homodimer.  
subcellular location: Cytoplasm  
functional domains: Class II aaRS ABD-related, histidine-tRNA ligase activity, S15/NS1 RNA-binding domain, S15/NS1, RNA-binding, protein homodimerization activity, Anticodon-binding domain, Class II aaRS and biotin synthetases, identical protein binding, ATP binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 509 aa, 57411 KDa  
  
Summary  
> This protein is a histidine-tRNA ligase enzyme that catalyzes the formation of L-histidyl-tRNA(His) from L-histidine, ATP, and tRNA(His)  
> It is a homodimer and is localized in the cytoplasm  
> The protein consists of several functional domains, including a class II aminoacyl-tRNA synthetase (aaRS) ABD-related domain, a histidine-tRNA ligase activity domain, an S15/NS1 RNA-binding domain, an anticodon-binding domain, and a class II aaRS and biotin synthetases domain  
> It also exhibits protein homodimerization activity and identical protein binding  
> With a size of 509 amino acids and a molecular weight of 57411 kilodaltons, this protein is found in eukaryotes, specifically in metazoans belonging to the chordata phylum.  
  
QA  
> What is the catalytic activity of this protein? The catalytic activity of this protein is the formation of L-histidyl-tRNA(His) from L-histidine, ATP, and tRNA(His).  
> Where is this protein localized? This protein is localized in the cytoplasm.  
> How many functional domains does this protein possess? This protein possesses several functional domains, including a class II aaRS ABD-related domain, a histidine-tRNA ligase activity domain, an S15/NS1 RNA-binding domain, an anticodon-binding domain, and a class II aaRS and biotin synthetases domain.  
> What is the size of this protein? The size of this protein is 509 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 57411 kilodaltons.  
> In which taxonomic groups is this protein found? This protein is found in eukaryotes, specifically in metazoans belonging to the chordata phylum.  
> Does this protein possess the characteristics of an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 509  
mw: 57411

FIELDS of Q9ERV7  
subcellular location: Nucleus, Cytoplasm  
functional domains: L domain-like, endopeptidase activity, Death Domain, Fas, DEATH domain, Ribonuclease Inhibitor  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 915 aa, 101141 KDa  
  
Summary  
> This protein is found in the nucleus and cytoplasm of eukaryotic organisms, particularly within the metazoan group of chordates  
> It has a protein size of 915 amino acids and a molecular weight of 101141 KDa  
> The protein contains various functional domains, including L domain-like, endopeptidase activity, Death Domain, Fas, DEATH domain, and Ribonuclease Inhibitor.  
  
QA  
> What are the subcellular locations of this protein? The subcellular locations of this protein are the nucleus and cytoplasm.  
> What is the taxonomy of this protein? The taxonomy of this protein includes Eukaryota, Metazoa, and Chordata.  
> How many amino acids does this protein have? This protein has 915 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 101141 KDa.  
> What are some functional domains present in this protein? Some functional domains present in this protein are L domain-like, endopeptidase activity, Death Domain, Fas, DEATH domain, and Ribonuclease Inhibitor.  
> Can this protein be correctly termed an enzyme? No  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: False  
length: 915  
mw: 101141

FIELDS of A2XBT1  
catalytic activity: EC = 2.7.1.172, ATP + N(6)-D-ribulosyl-L-lysyl-[protein] = ADP + H(+) + N(6)-(3-O-phospho-D-ribulosyl)-L-lysyl-[protein], ATP + N(6)-(D-erythrulosyl)-L-lysyl-[protein] = ADP + H(+) + N(6)-(3-O-phospho-D-erythrulosyl)-L-lysyl-[protein]  
subcellular location: Chloroplast, Plastid  
functional domains: Protein kinase-like (PK-like), protein-ribulosamine 3-kinase activity, ATP binding, kinase activity  
taxonomy: Eukaryota, Viridiplantae, Streptophyta  
protein size: 342 aa, 37791 KDa  
  
Summary  
> This protein is involved in catalytic activity and is classified as a protein kinase-like enzyme  
> It plays a role in a specific enzymatic reaction within the cell  
> The protein acts as a kinase, which means it transfers a phosphate group from ATP to a specific amino acid residue in its target protein  
> In this case, the protein catalyzes the transfer of a phosphate group to the N(6)-D-ribulosyl-L-lysine residue of the target protein  
> This reaction results in the formation of ADP, a hydrogen ion, and the N(6)-(3-O-phospho-D-ribulosyl)-L-lysine residue  
> Additionally, the protein can also catalyze the transfer of a phosphate group to the N(6)-(D-erythrulosyl)-L-lysine residue of the target protein  
> This reaction leads to the formation of ADP, a hydrogen ion, and the N(6)-(3-O-phospho-D-erythrulosyl)-L-lysine residue  
> The protein is localized within the chloroplast and plastid, subcellular organelles found in eukaryotic cells  
> It possesses functional domains such as Protein kinase-like (PK-like) and protein-ribulosamine 3-kinase activity  
> The protein is capable of ATP binding and exhibits kinase activity  
> The protein has a size of 342 amino acids and weighs approximately 37,791 kilodaltons.  
  
QA  
> What is the catalytic activity of this protein? ADP + H(+) + N(6)-(3-O-phospho-D-ribulosyl)-L-lysyl-[protein]  
> What are the subcellular locations of this protein? Chloroplast, Plastid  
> What are the functional domains of this protein? Protein kinase-like (PK-like), protein-ribulosamine 3-kinase activity  
> What is the size of this protein? 342 amino acids, 37791 KDa  
> What is the enzymatic reaction catalyzed by this protein? ATP + N(6)-D-ribulosyl-L-lysyl-[protein] = ADP + H(+) + N(6)-(3-O-phospho-D-ribulosyl)-L-lysyl-[protein], ATP + N(6)-(D-erythrulosyl)-L-lysyl-[protein] = ADP + H(+) + N(6)-(3-O-phospho-D-erythrulosyl)-L-lysyl-[protein]  
> Can this protein act as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 342  
mw: 37791

FIELDS of B1ZVM5  
catalytic activity: adenosine(2503) in 23S rRNA + 2 reduced [2Fe-2S]-[ferredoxin] + 2 S-adenosyl-L-methionine = 2-methyladenosine(2503) in 23S rRNA + 5'-deoxyadenosine + L-methionine + 2 oxidized [2Fe-2S]-[ferredoxin] + S-adenosyl-L-homocysteine, EC = 2.1.1.192, adenosine(37) in tRNA + 2 reduced [2Fe-2S]-[ferredoxin] + 2 S-adenosyl-L-methionine = 2-methyladenosine(37) in tRNA + 5'-deoxyadenosine + L-methionine + 2 oxidized [2Fe-2S]-[ferredoxin] + S-adenosyl-L-homocysteine  
cofactor: [4Fe-4S] cluster, Binds 1 [4Fe-4S] cluster. The cluster is coordinated with 3 cysteines and an exchangeable S-adenosyl-L-methionine.  
subcellular location: Cytoplasm  
functional domains: tRNA (adenine-C2-)-methyltransferase activity, Radical SAM enzymes, rRNA binding, tRNA binding, 4 iron, 4 sulfur cluster binding, metal ion binding, rRNA (adenine-C2-)-methyltransferase activity, Aldolase class I  
taxonomy: Bacteria, Verrucomicrobiota, Opitutae  
protein size: 428 aa, 46782 KDa  
  
Summary  
> This protein is involved in catalytic activity and is responsible for methylating specific nucleotides in RNA molecules  
> It catalyzes the reaction between adenosine in the RNA molecule, reduced [2Fe-2S]-[ferredoxin], and S-adenosyl-L-methionine to produce modified nucleotides, 5'-deoxyadenosine, L-methionine, oxidized [2Fe-2S]-[ferredoxin], and S-adenosyl-L-homocysteine  
> This reaction occurs both in the 23S rRNA and in tRNA molecules  
> The protein utilizes a [4Fe-4S] cluster as a cofactor, which is coordinated with three cysteine residues and an exchangeable S-adenosyl-L-methionine  
> It is predominantly located in the cytoplasm  
> The protein possesses functional domains involved in tRNA (adenine-C2-)-methyltransferase activity, Radical SAM enzymes, rRNA binding, tRNA binding, 4 iron, 4 sulfur cluster binding, metal ion binding, rRNA (adenine-C2-)-methyltransferase activity, and Aldolase class I  
> It is found in bacteria specifically belonging to the Verrucomicrobiota class, Opitutae order  
> The protein has a size of 428 amino acids and a molecular weight of 46,782 Daltons.  
  
QA  
> What is the role of this protein? This protein is involved in catalytic activity and specifically catalyzes the methylation of adenosine in RNA molecules.  
> What are the substrates for the enzymatic reactions catalyzed by this protein? The substrates for the enzymatic reactions are adenosine in the RNA molecule, reduced [2Fe-2S]-[ferredoxin], and S-adenosyl-L-methionine.  
> What are the products of the enzymatic reactions catalyzed by this protein? The products include modified nucleotides (2-methyladenosine), 5'-deoxyadenosine, L-methionine, oxidized [2Fe-2S]-[ferredoxin], and S-adenosyl-L-homocysteine.  
> What is the cofactor associated with this protein? The cofactor is a [4Fe-4S] cluster, which is coordinated with three cysteine residues and an exchangeable S-adenosyl-L-methionine.  
> Where is this protein located within the cell? It is predominantly located in the cytoplasm.  
> What are the functional domains of this protein? The functional domains include tRNA (adenine-C2-)-methyltransferase activity, Radical SAM enzymes, rRNA binding, tRNA binding, 4 iron, 4 sulfur cluster binding, metal ion binding, rRNA (adenine-C2-)-methyltransferase activity, and Aldolase class I.  
> What is the taxonomy of the organisms that possess this protein? This protein is found in bacteria of the Verrucomicrobiota class, specifically the Opitutae order.  
> What is the size of this protein? It has a size of 428 amino acids and a molecular weight of 46,782 Daltons.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
in\_membrane: False  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
cofactor: [4fe-4s] cluster, s-adenosyl-l-methionine  
length: 428  
mw: 46782

FIELDS of Q3AQW9  
catalytic activity: Release of signal peptides from bacterial membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-(S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small, neutral side chains., EC = 3.4.23.36  
subcellular location: Cell inner membrane, Multi-pass membrane protein  
functional domains: aspartic-type endopeptidase activity  
taxonomy: Bacteria, Chlorobiota, Chlorobiia  
protein size: 163 aa, 18426 KDa  
  
Summary  
> The protein in question is a bacterial membrane prolipoprotein endopeptidase  
> It possesses aspartic-type endopeptidase activity and is involved in the catalytic cleavage of signal peptides from bacterial membrane prolipoproteins  
> Structurally, it is a multi-pass membrane protein located in the cell inner membrane  
> The protein is classified within the Bacteria kingdom, specifically within the Chlorobiota class and Chlorobiia order  
> It has a size of 163 amino acids, corresponding to a molecular weight of 18,426 KDa.  
  
QA  
> What is the function of the protein? It possesses aspartic-type endopeptidase activity and is involved in the catalytic cleavage of signal peptides from bacterial membrane prolipoproteins.  
> Where is the protein located in the cell? It is located in the cell inner membrane.  
> What is the taxonomy of the protein? It is classified within the Bacteria kingdom, specifically within the Chlorobiota class and Chlorobiia order.  
> What is the size of the protein? It has a size of 163 amino acids, corresponding to a molecular weight of 18,426 KDa.  
> What specific enzymatic activity does the protein exhibit? It exhibits the enzymatic activity of releasing signal peptides from bacterial membrane prolipoproteins.  
> What is the general structure of the protein? It is a multi-pass membrane protein.  
> What are the key properties of the protein? It has aspartic-type endopeptidase activity, is located in the cell inner membrane, and belongs to the Bacteria kingdom within the Chlorobiota class and Chlorobiia order.  
> What type of peptides does the protein hydrolyze? It hydrolyzes peptides in the -Xaa-Yaa-Zaa-|-(S,diacylglyceryl)Cysmotif, where Xaa is hydrophobic (preferably Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small, neutral side chains.  
> What is the enzymatic classification of the protein? Its enzymatic classification is EC = 3.4.23.36.  
> What is the general function of the protein in bacterial membranes? The protein plays a role in the cleavage of signal peptides from bacterial membrane prolipoproteins.  
> Can this protein act as an enzyme? Yes  
  
METRICS  
localization: membrane  
in\_membrane: True  
in\_nucleus: False  
in\_mitochondria: False  
is\_enzyme: True  
length: 163  
mw: 18426

FIELDS of Q9BXJ9  
subcellular location: Nucleus, Cytoplasm  
functional domains: ribosome binding, TPR-like, RNA binding  
taxonomy: Eukaryota, Metazoa, Chordata  
protein size: 866 aa, 101272 KDa  
  
Summary  
> This protein is found in the nucleus and cytoplasm of cells  
> It belongs to the Eukaryota domain, specifically the Metazoa phylum within the Chordata subphylum  
> The protein is composed of 866 amino acids and has a molecular weight of 101272 KDa  
> It possesses functional domains such as ribosome binding, TPR-like, and RNA binding.  
  
QA  
> What are the subcellular locations of this protein? The subcellular locations of this protein are the nucleus and cytoplasm.  
> What is the taxonomy of this protein? This protein belongs to the Eukaryota domain, the Metazoa phylum, and the Chordata subphylum.  
> How long is this protein in terms of amino acid length? This protein is composed of 866 amino acids.  
> What is the molecular weight of this protein? The molecular weight of this protein is 101272 KDa.  
> What are the functional domains of this protein? The functional domains of this protein include ribosome binding, TPR-like, and RNA binding.  
> Can this protein act as an enzyme? No  
  
METRICS  
localization: nucleus  
in\_membrane: False  
in\_nucleus: True  
in\_mitochondria: False  
is\_enzyme: False  
length: 866  
mw: 101272