

Inferência da função das proteínas em estudo

Tal como referido anteriormente, foram usadas duas formas para atingir o objetivo pretendido e obter a caracterização funcional das proteínas em estudo.

Assim sendo, a primeira delas passou pela análise dos registos da UniProt, permitindo melhorar as notas registadas no NCBI, ou até mesmo, em alguns casos, corrigir essas informações.

Após essa análise, teremos algumas proteínas com a sua função bem descrita (tipo de proteína a que pertence), podendo esses dados ser visualizados na tabela seguinte:

Tabela 1: Resultados da análise dos registos NCBI e UniProt para as proteínas em estudo.

Locus tag	UniprotID	Function
NGO0738	Q5F8N2	Belongs to the DNA polymerase type-Y family;Contains 1 umuC domain.
NGO0740	Q5F8N0	Belongs to the type-I 3-dehydroquinase family.
NGO0741	Q5F8M9	Belongs to the RecA family.
NGO0742	Q5F8M8	Belongs to the YbaB/EbfC family.
NGO0744	Q5F8M6	Belongs to the DNA mismatch repair MutL/HexB family.
NGO0760	Q5F8L2	Belongs to the RuvB family.
NGO0763	Q5F8K9	Belongs to the tRNA nucleotidyltransferase/poly(A) polymerase family. Bacterial CCA-adding enzyme type 1 subfamily.
NGO0767	Q5F8K5	Belongs to the RecR family.
NGO0770	Q5F8K2	Belongs to the ABC transporter superfamily. Lipoprotein translocase (TC 3.A.1.125) family.
NGO0786	Q5F8I7	Belongs to the uracil-DNA glycosylase family.
NGO0791	Q5F8I2	Belongs to the UPF0250 family.
NGO0792	Q5F8I1	Belongs to the LipB family.
NGO0793	Q5F8I0	Belongs to the radical SAM superfamily. Lipoyl synthase family.
NGO0804	Q5F8G9	Belongs to the NnrD/CARKD family.
NGO0809	Q5F8G6	Belongs to the IlvD/Edd family.
NGO0810	Q5F8G5	Belongs to the GlnD family.
NGO0813	Q5F8G2	Belongs to the radical SAM superfamily. Biotin synthase family.
NGO0820	Q5F8F6	Belongs to the tRNA(Ile)-lysine synthase family.
NGO0821	Q5F8F5	Belongs to the AccA family.
NGO0829	Q5F8E8	Belongs to the heat shock protein 70 family.
NGO0844	Q5F8D8	Belongs to the acetylglutamate kinase family.
NGO0846	Q5F8D6	Belongs to the Lgt family.
NGO0848	Q5F8D4	Belongs to the alpha-IPM synthase/homocitrate synthase family. LeuA type 1 subfamily.

NGO0850	Q5F8D3	Belongs to the gamma-glutamyl phosphate reductase family.
NGO0853	Q5F8D0	Belongs to the CrcB (TC 9.B.71) family.
NGO0858	Q5F8C7	Belongs to the PlsY family.
NGO0862	Q5F8C3	Belongs to the FBPase class 1 family.
NGO0866	Q5F8C0	Belongs to the SHMT family
NGO0872	Q5F8B4	Belongs to the anthranilate synthase component I family
NGO0900	Q5F889	Belongs to the EPSP synthase family.
NGO0907	Q5F882	Belongs to the PINc/VapC protein family.
NGO0913	Q5F878	Belongs to the succinate/malate CoA ligase beta subunit family.
NGO0928	Q5F863	Belongs to the vitamin-B12 independent methionine synthase family.
NGO0930	Q5F861	Belongs to the ribosomal protein L31P family. Type B subfamily.
NGO0933	Q5F858	Belongs to the AB hydrolase superfamily. HTA family.
NGO0936	Q5F856	Belongs to the elongation factor P family.
NGO0940	Q5F852	Belongs to the IPP transferase family.
NGO0947	Q5F849	Belongs to the DapA family.
NGO0958	Q5F840	Belongs to the RNase PH family.
NGO0962	Q5F836	Belongs to the NAPRTase family.
NGO0963	Q5F835	Belongs to the class-I aminoacyl-tRNA synthetase family.
NGO0970	Q5F831	Belongs to the ribose 5-phosphate isomerase family.

Para a inferência de proteínas sem função conhecida, torna-se necessária a sua análise recorrendo ao BLAST. Pelas proteínas homólogas encontradas é possível inferir a função das proteínas em estudo.

Para que esta análise seja mais correta, foi corrido o BLAST para as proteínas unicamente presentes na base de dados SwissProt, fazendo com que os resultados sejam o mais curado possível.

Tendo em conta que usando esta base de dados os resultados serão em muito menor número do que se tivéssemos recorrido a uma base de dados não redundante, usamos um limite de *e-value* de 1, ou seja, os resultados apresentados são apenas os que estão abaixo deste valor.

Uma vez que dentro dos resultados obtidos, nem sempre o valor com menor *e-value* deve ser o valor considerado, efetuar-se-á uma análise individual dos resultados para cada proteína de um determinado *locus_tag*, permitindo justificar a escolha do *hit* em que nos baseamos para a inferência.

Assim sendo, a nossa escolha do melhor resultado recai sempre no *hit* com menor *e-value* mas que ao mesmo tempo tenha uma cobertura da *query* mais alta, uma vez que podem

surgir *hits* com bom score e bom alinhamento em termos de *e-value* mas que no entanto não cobrem a *query* de forma significativa, comparando com o segundo ou terceiro *hit* do BLAST.

Essa análise encontra-se representada pelos *printscreens* dos distintos BLAST, onde o *hit* selecionado se encontra marcado a vermelho.

- NGO0729

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****Alinhamento****
####Proteína 0- locus_tag: NGO0729####
Sequencia: gi|51338674|sp|Q8BTY8.1|SCFD2_MOUSE RecName: Full=Sec1 family domain-containing protein 2; AltName: Full=Neuronal Sec1; AltName: Full=Syntaxin-binding protein 1-like 1 [Mus musculus]
Score: 31.187
e-value: 0.506956
Tamanho do alinhamento: 32
Cobertura da query: 0.457142857143
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- NGO0730

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****Alinhamento****
####Proteína 1- locus_tag: NGO0730####
Sequencia: gi|18202230|sp|O86236.1|Y132A_HAEIN RecName: Full=Uncharacterized transposase-like protein HI_1328.1 [Haemophilus influenzae Rd KW20]
Score: 119.013
e-value: 2.99628e-32
Tamanho do alinhamento: 113
Cobertura da query: 0.520737327189
****Alinhamento****
####Proteína 1- locus_tag: NGO0730####
Sequencia: gi|363548442|sp|Q6PBX5.2|MTND_DANRE RecName: Full=1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase; AltName: Full=Acireductone dioxygenase (Fe(2+)-requiring); Short=ARD; Short=Fe-ARD; AltName: Full=Membrane-type 1 matrix metalloproteinase cytoplasmic tail-binding protein 1; Short=MTCBP-1 [Danio rerio]
Score: 36.965
e-value: 0.0577594
Tamanho do alinhamento: 105
Cobertura da query: 0.483870967742
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- NGO0731

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****Alinhamento****
####Proteína 2- locus_tag: NGO0731####
Sequencia: gi|74996600|sp|Q54G57.1|HELIC1_DICDI RecName: Full=Activating signal co-integrator 1 complex subunit 3 [Dictyostelium discoideum]
Score: 31.5722
e-value: 0.708308
Tamanho do alinhamento: 31
Cobertura da query: 0.329787234043
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- NGO0732

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0734

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****Alinhamento****
####Proteína 4- locus_tag: NGO0734####
Sequencia: gi|11386823|sp|P57641.1|FENR_BUCAI RecName: Full=Ferredoxin--NADP reductase; Short=FNR; AltName: Full=Flavodoxin reductase; Short=FLDR; Short=FLXR [Buchnera aphidicola str. APS (Acyrtosiphon pisum)]
Score: 139.043
e-value: 7.28183e-38
Tamanho do alinhamento: 249
Cobertura da query: 0.96138996139
****Alinhamento****
####Proteína 4- locus_tag: NGO0734####
Sequencia: gi|3913664|sp|Q44532.3|FE|NR_AZOVI RecName: Full=Ferredoxin--NADP reductase; Short=FNR; Short=Protein X [Azotobacter vinelandii]
Score: 135.191
e-value: 2.45634e-36
Tamanho do alinhamento: 255
Cobertura da query: 0.984555984556
****Alinhamento****
####Proteína 4- locus_tag: NGO0734####
Sequencia: gi|8134461|sp|Q9Z615.1|FENR_BUCAP RecName: Full=Ferredoxin--NADP reductase; Short=FNR; AltName: Full=Flavodoxin reductase; Short=FLDR; Short=FLXR [Buchnera aphidicola str. Sg (Schizaphis graminum)]
Score: 130.568
e-value: 1.26121e-34
Tamanho do alinhamento: 232
Cobertura da query: 0.895752895753
****Alinhamento****
####Proteína 4- locus_tag: NGO0734####
Sequencia: gi|38604786|sp|Q89A28.1|FENR_BUCBP RecName: Full=Ferredoxin--NADP reductase; Short=FNR; AltName: Full=Flavodoxin reductase; Short=FLDR; Short=FLXR [Buchnera aphidicola str. Sg (Schizaphis graminum)]
Score: 129.568
e-value: 1.26121e-34
Tamanho do alinhamento: 232
Cobertura da query: 0.895752895753
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- NGO0735

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0736

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0739

****Alinhamento****

####Proteína 8- locus_tag: NGO0739####

Sequencia: gi|1172905|sp|P44804.1|REP_HAEIN RecName: Full=ATP-dependent DNA helicase Rep [Haemophilus influenzae Rd KW20]

Score: 604.749

e-value: 0.0

Tamanho do alinhamento: 641

Cobertura da query: 0.955290611028

****Alinhamento****

####Proteína 8- locus_tag: NGO0739####

Sequencia: gi|54041576|sp|P09980.3|REP_ECOLI RecName: Full=ATP-dependent DNA helicase Rep [Escherichia coli K-12]

Score: 583.563

e-value: 0.0

Tamanho do alinhamento: 641

Cobertura da query: 0.955290611028

****Alinhamento****

####Proteína 8- locus_tag: NGO0739####

Sequencia: gi|17865672|sp|Q9L6S1.1|REP_SALTY RecName: Full=ATP-dependent DNA helicase Rep [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

Score: 582.793

e-value: 0.0

Tamanho do alinhamento: 641

Cobertura da query: 0.955290611028

****Alinhamento****

####Proteína 8- locus_tag: NGO0739####

Sequencia: gi|11134339|sp|P57654.1|REP_BUCAI RecName: Full=ATP-dependent DNA helicase Rep [Buchnera aphidicola str. APS (Acyrthosiphon pisum)]

Score: 514.227

e-value: 2.10441e-172

Tamanho do alinhamento: 645

- NGO0743

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****Alinhamento****
####Proteína 12- locus_tag: NGO0743####
Sequencia: gi|118808|sp|P06710.1|DPO3X_ECOLI RecName: Full=DNA polymerase III subu
nit tau; AltName: Full=DNA polymerase III subunit gamma [Escherichia coli K-12]
Score: 421.809
e-value: 9.87337e-136
Tamanho do alinhamento: 361
Cobertura da query: 0.510608203678
****Alinhamento****
####Proteína 12- locus_tag: NGO0743####
Sequencia: gi|20141409|sp|P74876.2|DPO3X_SALTY RecName: Full=DNA polymerase III su
bunit tau; AltName: Full=DNA polymerase III subunit gamma [Salmonella enterica sub
sp. enterica serovar Typhimurium str. LT2]
Score: 415.231
e-value: 1.59173e-133
Tamanho do alinhamento: 394
Cobertura da query: 0.557284299859
****Alinhamento****
####Proteína 12- locus_tag: NGO0743####
Sequencia: gi|1169397|sp|P43746.1|DPO3X_HAEIN RecName: Full=DNA polymerase III sub
unit tau/gamma [Haemophilus influenzae Rd Kw20]
Score: 408.297
e-value: 2.85434e-130
Tamanho do alinhamento: 360
Cobertura da query: 0.509193776521
****Alinhamento****
####Proteína 12- locus_tag: NGO0743####
Sequencia: gi|31340040|sp|Q89A95.1|DPO3X_BUCBP RecName: Full=DNA polymerase III su
bunit gamma [Buchnera aphidicola str. Bp (Baizongia pistaciae)]
Score: 333.954
e-value: 5.89636e-106
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- NGO0745

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0746

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****Alinhamento****
####Proteina 15- locus_tag: NGO0746####
Sequencia: gi|74750472|sp|Q86VU5.1|CMTD1_HUMAN RecName: Full=Catechol O-methyltransferase domain-containing protein 1 [Homo sapiens]
Score: 162.54
e-value: 2.78699e-47
Tamanho do alinhamento: 210
Cobertura da query: 0.945945945946
****Alinhamento****
####Proteina 15- locus_tag: NGO0746####
Sequencia: gi|81873868|sp|Q8BIG7.1|CMTD1_MOUSE RecName: Full=Catechol O-methyltransferase domain-containing protein 1 [Mus musculus]
Score: 159.458
e-value: 4.25757e-46
Tamanho do alinhamento: 210
Cobertura da query: 0.945945945946
****Alinhamento****
####Proteina 15- locus_tag: NGO0746####
Sequencia: gi|75014085|sp|Q86IC9.1|CAMT1_DICDI RecName: Full=Probable caffeoyl-CoA O-methyltransferase 1; AltName: Full=O-methyltransferase 5 [Dictyostelium discoideum]
Score: 157.918
e-value: 8.03549e-46
Tamanho do alinhamento: 180
Cobertura da query: 0.810810810811
****Alinhamento****
####Proteina 15- locus_tag: NGO0746####
Sequencia: gi|75014084|sp|Q86IC8.1|CAMT2_DICDI RecName: Full=Probable caffeoyl-CoA O-methyltransferase 2; AltName: Full=O-methyltransferase 6 [Dictyostelium discoideum]
Score: 157.532
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○ NGO0747

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****Alinhamento****
####Proteina 16- locus_tag: NGO0747####
Sequencia: gi|18202649|sp|Q98KC1.1|BAMD_RHILO RecName: Full=Outer membrane protein
assembly factor BamD; Flags: Precursor [Mesorhizobium loti MAFF303099]
Score: 35.8094
e-value: 0.20617
Tamanho do alinhamento: 131
Cobertura da query: 0.552742616034
****Alinhamento****
####Proteina 16- locus_tag: NGO0747####
Sequencia: gi|18202811|sp|Q9CKA5.1|BAMD_PASMU RecName: Full=Outer membrane protein
assembly factor BamD; Flags: Precursor [Pasteurella multocida subsp. multocida str
. Pm70]
Score: 34.6538
e-value: 0.518835
Tamanho do alinhamento: 133
Cobertura da query: 0.561181434599
****Alinhamento****
####Proteina 16- locus_tag: NGO0747####
Sequencia: gi|261260096|sp|Q9QVC8.3|FKBP4_RAT RecName: Full=Peptidyl-prolyl cis-tr
ans isomerase FKBP4; Short=PPIase FKBP4; AltName: Full=52 kDa FK506-binding protei
n; Short=52 kDa FKBP; Short=FKBP-52; AltName: Full=59 kDa immunophilin; Short=p59;
AltName: Full=FK506-binding protein 4; Short=FKBP-4; AltName: Full=FKBP59; AltName
: Full=HSP-binding immunophilin; Short=HBI; AltName: Full=Immunophilin FKBP52; Alt
Name: Full=Rotamase; Contains: RecName: Full=Peptidyl-prolyl cis-trans isomerase F
KBP4, N-terminally processed [Rattus norvegicus]
Score: 34.6538
e-value: 0.634252
Tamanho do alinhamento: 44
Cobertura da query: 0.185654008439
****Alinhamento****
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○ NGO0748

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****Alinhamento****
####Proteina 17- locus_tag: NGO0748####
Sequencia: gi|131626|sp|P12044.1|PURE_BACSU RecName: Full=N5-carboxyaminoimidazole
ribonucleotide mutase; Short=N5-CAIR mutase; AltName: Full=5-(carboxyamino)imidazo
le ribonucleotide mutase [Bacillus subtilis subsp. subtilis str. 168]
Score: 206.838
e-value: 1.16922e-66
Tamanho do alinhamento: 151
Cobertura da query: 0.937888198758
****Alinhamento****
####Proteina 17- locus_tag: NGO0748####
Sequencia: gi|12230963|sp|P72157.2|PURE_PSEAE RecName: Full=N5-carboxyaminoimidazo
le ribonucleotide mutase; Short=N5-CAIR mutase; AltName: Full=5-(carboxyamino)imid
azole ribonucleotide mutase [Pseudomonas aeruginosa PA01]
Score: 200.675
e-value: 2.66879e-64
Tamanho do alinhamento: 152
Cobertura da query: 0.944099378882
****Alinhamento****
####Proteina 17- locus_tag: NGO0748####
Sequencia: gi|81174992|sp|Q87KE1.1|PURE_VIBPA RecName: Full=N5-carboxyaminoimidazo
le ribonucleotide mutase; Short=N5-CAIR mutase; AltName: Full=5-(carboxyamino)imid
azole ribonucleotide mutase [Vibrio parahaemolyticus RIMD 2210633]
Score: 198.364
e-value: 2.03882e-63
Tamanho do alinhamento: 153
Cobertura da query: 0.950310559006
****Alinhamento****
####Proteina 17- locus_tag: NGO0748####
Sequencia: gi|3914483|sp|O06456.1|PURE_SULSO RecName: Full=N5-carboxyaminoimidazol
e ribonucleotide mutase; Short=N5-CAIR mutase; AltName: Full=5-(carboxyamino)imida

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○ NGO0751

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****Alinhamento****
####Proteina 18- locus_tag: NGO0751####
Sequencia: gi|81622626|sp|Q9JMS3.1|YUAQ_ECOLI RecName: Full=Uncharacterized protei
n YuaQ [Escherichia coli K-12]
Score: 41.2022
e-value: 0.00907153
Tamanho do alinhamento: 67
Cobertura da query: 0.221854304636
****Alinhamento****
####Proteina 18- locus_tag: NGO0751####
Sequencia: gi|2506696|sp|P45508.2|YFAL_ECOLI RecName: Full=Uncharacterized protein
YfaL; Flags: Precursor [Escherichia coli K-12]
Score: 38.891
e-value: 0.0482025
Tamanho do alinhamento: 123
Cobertura da query: 0.407284768212

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○ NGO0752

****Alinhamento****

####Proteina 19- locus_tag: NGO0752####

Sequencia: gi|118438|sp|P13800.2|DEGU_BACSU RecName: Full=Transcriptional regulatory protein DegU; AltName: Full=Protease production enhancer protein [Bacillus subtilis subsp. subtilis str. 168]

Score: 172.555

e-value: 1.28858e-51

Tamanho do alinhamento: 219

Cobertura da query: 1.00458715596

****Alinhamento****

####Proteina 19- locus_tag: NGO0752####

Sequencia: gi|1706361|sp|P54662.1|DEGU_BREBE RecName: Full=Transcriptional regulatory protein DegU [Brevibacillus brevis]

Score: 162.54

e-value: 1.14569e-47

Tamanho do alinhamento: 221

Cobertura da query: 1.01376146789

****Alinhamento****

####Proteina 19- locus_tag: NGO0752####

Sequencia: gi|81696298|sp|Q6G850.1|VRAR_STAAS RecName: Full=Response regulator protein VraR [Staphylococcus aureus subsp. aureus MSSA476] >gi|81696461|sp|Q6GFH3.1|VRAR_STAAR RecName: Full=Response regulator protein VraR [Staphylococcus aureus subsp. aureus MRSA252] >gi|81704309|sp|Q7A0I0.1|VRAR_STAAS RecName: Full=Response regulator protein VraR [Staphylococcus aureus subsp. aureus MW2] >gi|81704831|sp|Q7A2Q1.1|VRAR_STAAM RecName: Full=Response regulator protein VraR [Staphylococcus aureus subsp. aureus Mu50] >gi|81705432|sp|Q7A4R9.1|VRAR_STAAN RecName: Full=Response regulator protein VraR [Staphylococcus aureus subsp. aureus N315] >gi|90116383|sp|P0C0Z1.1|VRAR_STAA1 RecName: Full=Response regulator protein VraR [Staphylococcus aureus subsp. aureus Mu3]

Score: 154.066

e-value: 1.10071e-44

○ NGO0753

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****Alinhamento****
####Proteína 20- locus_tag: NGO0753####
Sequencia: gi|127837|sp|P27896.1|NARQ_ECOLI RecName: Full=Nitrate/nitrite sensor p
rotein NarQ [Escherichia coli K-12]
Score: 159.458
e-value: 8.26274e-41
Tamanho do alinhamento: 578
Cobertura da query: 0.981324278438
****Alinhamento****
####Proteína 20- locus_tag: NGO0753####
Sequencia: gi|84028646|sp|P0AFA3.1|NARX_ECO57 RecName: Full=Nitrate/nitrite sensor
protein NarX [Escherichia coli O157:H7] >gi|84028647|sp|P0AFA2.1|NARX_ECOLI RecNam
e: Full=Nitrate/nitrite sensor protein NarX [Escherichia coli K-12] >gi|84028648|s
p|P0AFA4.1|NARX_SHIFL RecName: Full=Nitrate/nitrite sensor protein NarX [Shigella
Flexneri]
Score: 152.14
e-value: 2.98412e-38
Tamanho do alinhamento: 614
Cobertura da query: 1.04244482173
****Alinhamento****
####Proteína 20- locus_tag: NGO0753####
Sequencia: gi|1171657|sp|P44604.1|NARQ_HAEIN RecName: Full=Sensor protein NarQ hom
olog [Haemophilus influenzae Rd KW20]
Score: 150.984
e-value: 6.07897e-38
Tamanho do alinhamento: 597
Cobertura da query: 1.01358234295
****Alinhamento****
####Proteína 20- locus_tag: NGO0753####
Sequencia: gi|68566109|sp|P96685.1|YDFH_BACSU RecName: Full=Sensor histidine kinas
e YdfH [Bacillus subtilis subsp. subtilis str. 168]
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○ NGO0754

****Alinhamento****

####Proteína 21- locus_tag: NGO0754####

Sequencia: gi|20138930|sp|P58747.1|MOBA_NEIMB RecName: Full=Putative molybdenum cofactor guanylyltransferase; Short=MoCo guanylyltransferase; AltName: Full=GTP:molybdopterin guanylyltransferase; AltName: Full=Mo-MPT guanylyltransferase; AltName: Full=Molybdopterin guanylyltransferase; AltName: Full=Molybdopterin-guanine dinucleotide synthase; Short=MGD synthase [Neisseria meningitidis MC58]

Score: 373.244

e-value: 5.41957e-131

Tamanho do alinhamento: 192

Cobertura da query: 0.941176470588

****Alinhamento****

####Proteína 21- locus_tag: NGO0754####

Sequencia: gi|13124355|sp|Q9JUA5.1|MOBA_NEIMA RecName: Full=Molybdenum cofactor guanylyltransferase; Short=MoCo guanylyltransferase; AltName: Full=GTP:molybdopterin guanylyltransferase; AltName: Full=Mo-MPT guanylyltransferase; AltName: Full=Molybdopterin guanylyltransferase; AltName: Full=Molybdopterin-guanine dinucleotide synthase; Short=MGD synthase [Neisseria meningitidis Z2491]

Score: 371.318

e-value: 2.73196e-130

Tamanho do alinhamento: 192

Cobertura da query: 0.941176470588

****Alinhamento****

####Proteína 21- locus_tag: NGO0754####

Sequencia: gi|166218965|sp|A1KU57.1|MOBA_NEIMF RecName: Full=Molybdenum cofactor guanylyltransferase; Short=MoCo guanylyltransferase; AltName: Full=GTP:molybdopterin guanylyltransferase; AltName: Full=Mo-MPT guanylyltransferase; AltName: Full=Molybdopterin guanylyltransferase; AltName: Full=Molybdopterin-guanine dinucleotide synthase; Short=MGD synthase [Neisseria meningitidis FAM18]

Score: 366.311

e-value: 3.00181e-128

○ NGO0755

****Alinhamento****

####Proteína 22- locus_tag: NGO0755####

Sequencia: gi|84027900|sp|P0AFU8.1|RISA_ECOLI RecName: Full=Riboflavin synthase; Short=RS [Escherichia coli K-12] >gi|84027901|sp|P0AFU9.1|RISA_SHIFL RecName: Full=Riboflavin synthase; Short=RS [Shigella flexneri]
Score: 251.521

e-value: 7.49072e-83

Tamanho do alinhamento: 204

Cobertura da query: 0.99512195122

****Alinhamento****

####Proteína 22- locus_tag: NGO0755####

Sequencia: gi|1172947|sp|P45273.1|RISA_HAEIN RecName: Full=Riboflavin synthase; Short=RS [Haemophilus influenzae Rd KW20]
Score: 230.72

e-value: 1.10011e-74

Tamanho do alinhamento: 203

Cobertura da query: 0.990243902439

****Alinhamento****

####Proteína 22- locus_tag: NGO0755####

Sequencia: gi|25009063|sp|Q8KA22.1|RISA_BUCAP RecName: Full=Riboflavin synthase; Short=RS [Buchnera aphidicola str. Sg (Schizaphis graminum)]
Score: 186.422

e-value: 1.95259e-57

Tamanho do alinhamento: 202

Cobertura da query: 0.985365853659

****Alinhamento****

####Proteína 22- locus_tag: NGO0755####

Sequencia: gi|11387017|sp|P57212.1|RISA_BUCAI RecName: Full=Riboflavin synthase; Short=RS [Buchnera aphidicola str. APS (Acyrtosiphon pisum)]
Score: 180.259

e-value: 5.3733e-55

○ NGO0756

```

****Alinhamento****
####Proteina 23- locus_tag: NGO0756####
Sequencia: gi|81390271|sp|Q68XR2.1|CLPB_RICTY RecName: Full=Chaperone protein ClpB
[Rickettsia typhi str. Wilmington]
Score: 39.6614
e-value: 0.0227151
Tamanho do alinhamento: 107
Cobertura da query: 0.372822299652
****Alinhamento****
####Proteina 23- locus_tag: NGO0756####
Sequencia: gi|226739139|sp|A9A6N2.1|RFCL_METM6 RecName: Full=Replication factor C
large subunit; Short=RFC large subunit; AltName: Full=Clamp loader large subunit [
Methanococcus maripaludis C6]
Score: 39.2762
e-value: 0.0259492
Tamanho do alinhamento: 118
Cobertura da query: 0.411149825784
****Alinhamento****
####Proteina 23- locus_tag: NGO0756####
Sequencia: gi|54035883|sp|Q92JK8.1|CLPB_RICCN RecName: Full=Chaperone protein ClpB
[Rickettsia conorii str. Malish 7]
Score: 39.6614
e-value: 0.0270787
Tamanho do alinhamento: 107
Cobertura da query: 0.372822299652
****Alinhamento****
####Proteina 23- locus_tag: NGO0756####
Sequencia: gi|166977385|sp|A6VIW1.1|RFCL_METM7 RecName: Full=Replication factor C
large subunit; Short=RFC large subunit; AltName: Full=Clamp loader large subunit [
Methanococcus maripaludis C7]
Score: 38.891

```

○ NGO0757

```

****Alinhamento****
####Proteina 24- locus_tag: NGO0757####
Sequencia: gi|2498953|sp|P77754.1|SPY_ECOLI RecName: Full=Spheroplast protein Y; F
lags: Precursor [Escherichia coli K-12]
Score: 43.1282
e-value: 9.23065e-05
Tamanho do alinhamento: 102
Cobertura da query: 0.708333333333
****Alinhamento****
####Proteina 24- locus_tag: NGO0757####
Sequencia: gi|74607495|sp|Q6CWI2.1|IML1_KLULA RecName: Full=Vacuolar membrane-asso
ciated protein IML1 [Kluyveromyces lactis NRRL Y-1140]
Score: 33.4982
e-value: 0.558476
Tamanho do alinhamento: 77
Cobertura da query: 0.534722222222
>>>

```

○ NGO0758

****Alinhamento****

####Proteina 25- locus_tag: NGO0758####

Sequencia: gi|729235|sp|P40117.1|RPEC_CUPNH RecName: Full=Ribulose-phosphate 3-epimerase, chromosomal; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=R5P3E [Ralstonia eutropha H16]

Score: 322.013

e-value: 1.27929e-109

Tamanho do alinhamento: 224

Cobertura da query: 0.973913043478

****Alinhamento****

####Proteina 25- locus_tag: NGO0758####

Sequencia: gi|729236|sp|Q04539.1|RPEP_CUPNH RecName: Full=Ribulose-phosphate 3-epimerase, plasmid; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=R5P3E [Ralstonia eutropha H16]

Score: 316.235

e-value: 2.21364e-107

Tamanho do alinhamento: 221

Cobertura da query: 0.960869565217

****Alinhamento****

####Proteina 25- locus_tag: NGO0758####

Sequencia: gi|1169388|sp|P44756.1|RPE_HAEIN RecName: Full=Ribulose-phosphate 3-epimerase; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=R5P3E [Haemophilus influenzae Rd KW20]

Score: 311.997

e-value: 5.52961e-106

Tamanho do alinhamento: 223

Cobertura da query: 0.969565217391

****Alinhamento****

####Proteina 25- locus_tag: NGO0758####

Sequencia: gi|84028110|sp|P0AG09.1|RPE_EC057 RecName: Full=Ribulose-phosphate 3-epimerase; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=R

- NGO0759

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0761

```
****Alinhamento****
####Proteína 28- locus_tag: NGO0761####
Sequencia: gi|21759397|sp|Q8UIG8.2|RNPH_AGRT5 RecName: Full=Ribonuclease PH; Short
=RNase PH; AltName: Full=tRNA nucleotidyltransferase [Agrobacterium fabrum str. C5
8]
Score: 35.4242
e-value: 0.0304392
Tamanho do alinhamento: 101
Cobertura da query: 0.990196078431
****Alinhamento****
####Proteína 28- locus_tag: NGO0761####
Sequencia: gi|81342290|sp|O34313.1|NTPES_BACSU RecName: Full=Trifunctional nucleot
ide phosphoesterase protein YfkN; Includes: RecName: Full=2',3'-cyclic-nucleotide
2'-phosphodiesterase/3'-nucleotidase; Includes: RecName: Full=5'-nucleotidase; Fla
gs: Precursor [Bacillus subtilis subsp. subtilis str. 168]
Score: 33.113
e-value: 0.231807
Tamanho do alinhamento: 68
Cobertura da query: 0.666666666667
```


○ NGO0764

****Alinhamento****

####Proteina 31- locus_tag: NGO0764####

Sequencia: gi|71164824|sp|P0A9U5.1|YBIT_ECOS7 RecName: Full=Uncharacterized ABC transporter ATP-binding protein Ybit [Escherichia coli O157:H7] >gi|71164825|sp|P0A9U4.1|YBIT_ECOL6 RecName: Full=Uncharacterized ABC transporter ATP-binding protein Ybit [Escherichia coli CFT073] >gi|71164826|sp|P0A9U3.1|YBIT_ECOLI RecName: Full=Uncharacterized ABC transporter ATP-binding protein Ybit [Escherichia coli K-12]

Score: 723.391

e-value: 0.0

Tamanho do alinhamento: 542

Cobertura da query: 1.0

****Alinhamento****

####Proteina 31- locus_tag: NGO0764####

Sequencia: gi|81815543|sp|O31716.1|YKPA_BACSU RecName: Full=Uncharacterized ABC transporter ATP-binding protein YkpA [Bacillus subtilis subsp. subtilis str. 168]

Score: 496.123

e-value: 1.38762e-168

Tamanho do alinhamento: 543

Cobertura da query: 1.00184501845

****Alinhamento****

####Proteina 31- locus_tag: NGO0764####

Sequencia: gi|251757351|sp|O05519.2|YDIF_BACSU RecName: Full=Uncharacterized ABC transporter ATP-binding protein Ydif [Bacillus subtilis subsp. subtilis str. 168]

Score: 316.235

e-value: 1.10466e-97

Tamanho do alinhamento: 548

Cobertura da query: 1.0110701107

****Alinhamento****

####Proteina 31- locus_tag: NGO0764####

Sequencia: gi|238056737|sp|O34512.2|YFMM_BACSU RecName: Full=Uncharacterized ABC transporter ATP-binding protein YfmM [Bacillus subtilis subsp. subtilis str. 168]

○ NGO0765

****Alinhamento****

####Proteína 32- locus_tag: NGO0765####

Sequencia: gi|140642|sp|P24178.1|YFFB_ECOLI RecName: Full=Protein Yffb [Escherichia coli K-12]

Score: 90.8929

e-value: 9.65029e-23

Tamanho do alinhamento: 118

Cobertura da query: 0.951612903226

****Alinhamento****

####Proteína 32- locus_tag: NGO0765####

Sequencia: gi|1175963|sp|P44515.1|Y103_HAEIN RecName: Full=Uncharacterized protein HI_0103 [Haemophilus influenzae Rd KW20]

Score: 78.1814

e-value: 6.39402e-18

Tamanho do alinhamento: 115

Cobertura da query: 0.927419354839

****Alinhamento****

####Proteína 32- locus_tag: NGO0765####

Sequencia: gi|42560357|sp|P60376.1|SPX_LACLM RecName: Full=Regulatory protein Spx [Lactococcus lactis subsp. cremoris MG1363] >gi|42560360|sp|P60375.1|SPX2_LACLA RecName: Full=Regulatory protein Spx 2; AltName: Full=Thermoresistant insertional mutant protein A [Lactococcus lactis subsp. lactis I11403]

Score: 53.9138

e-value: 6.02046e-09

Tamanho do alinhamento: 111

Cobertura da query: 0.895161290323

****Alinhamento****

####Proteína 32- locus_tag: NGO0765####

Sequencia: gi|11136042|sp|O32175.1|YUSI_BACSU RecName: Full=Uncharacterized protein YusI [Bacillus subtilis subsp. subtilis str. 168]

Score: 53.5286

○ NGO0766

```

****Alinhamento****
####Proteina 33- locus_tag: NGO0766####
Sequencia: gi|83288412|sp|P0ADY2.1|PPID_ECOLI RecName: Full=Peptidyl-prolyl cis-trans isomerase D; Short=PPIase D; AltName: Full=Rotamase D [Escherichia coli CFT073]
>gi|83288413|sp|P0ADY1.1|PPID_ECOLI RecName: Full=Peptidyl-prolyl cis-trans isomerase D; Short=PPIase D; AltName: Full=Rotamase D [Escherichia coli K-12]
Score: 98.9821
e-value: 1.03211e-20
Tamanho do alinhamento: 619
Cobertura da query: 1.208984375
****Alinhamento****
####Proteina 33- locus_tag: NGO0766####
Sequencia: gi|3183576|sp|P44092.2|PPID_HAEIN RecName: Full=Peptidyl-prolyl cis-trans isomerase D; Short=PPIase D; AltName: Full=Rotamase D [Haemophilus influenzae Rd KW20]
Score: 90.8929
e-value: 4.12924e-18
Tamanho do alinhamento: 289
Cobertura da query: 0.564453125
****Alinhamento****
####Proteina 33- locus_tag: NGO0766####
Sequencia: gi|38605184|sp|Q7VKX4.1|PPID_HAEDU RecName: Full=Peptidyl-prolyl cis-trans isomerase D; Short=PPIase D; AltName: Full=Rotamase D [Haemophilus ducreyi 350 00HP]
Score: 69.3218
e-value: 2.59133e-11
Tamanho do alinhamento: 254
Cobertura da query: 0.49609375
****Alinhamento****
####Proteina 33- locus_tag: NGO0766####
Sequencia: gi|38605184|sp|Q7VKX4.1|PPID_HAEDU RecName: Full=Peptidyl-prolyl cis-trans isomerase D; Short=PPIase D; AltName: Full=Rotamase D [Haemophilus ducreyi 350 00HP]
Score: 69.3218
e-value: 2.59133e-11
Tamanho do alinhamento: 254
Cobertura da query: 0.49609375
****Alinhamento****

```

○ NGO0768

```

****Alinhamento****
####Proteina 35- locus_tag: NGO0768####
Sequencia: gi|13878933|sp|P34146.2|RAC1C_DICDI RecName: Full=Rho-related protein rac1C; Flags: Precursor [Dictyostelium discoideum]
Score: 31.9574
e-value: 0.302433
Tamanho do alinhamento: 31
Cobertura da query: 0.373493975904
****Alinhamento****
####Proteina 35- locus_tag: NGO0768####
Sequencia: gi|13878932|sp|P34144.2|RAC1A_DICDI RecName: Full=Rho-related protein rac1A; Flags: Precursor [Dictyostelium discoideum]
Score: 31.5722
e-value: 0.385332
Tamanho do alinhamento: 28
Cobertura da query: 0.33734939759

```

○ NGO0769

****Alinhamento****

####Proteína 36- locus_tag: NGO0769####

Sequencia: gi|9977671|sp|P57062.1|LOLC_NEIMB RecName: Full=Lipoprotein-releasing system transmembrane protein LolC [Neisseria meningitidis MC58]

Score: 825.854

e-value: 0.0

Tamanho do alinhamento: 415

Cobertura da query: 1.0

****Alinhamento****

####Proteína 36- locus_tag: NGO0769####

Sequencia: gi|9977668|sp|P57061.1|LOLC_NEIMA RecName: Full=Lipoprotein-releasing system transmembrane protein LolC [Neisseria meningitidis Z2491]

Score: 822.387

e-value: 0.0

Tamanho do alinhamento: 415

Cobertura da query: 1.0

****Alinhamento****

####Proteína 36- locus_tag: NGO0769####

Sequencia: gi|32129712|sp|Q87EF5.1|LOLC_XYLFT RecName: Full=Lipoprotein-releasing system transmembrane protein LolC [Xylella fastidiosa Temecula1]

Score: 377.867

e-value: 4.45631e-126

Tamanho do alinhamento: 416

Cobertura da query: 1.00240963855

****Alinhamento****

####Proteína 36- locus_tag: NGO0769####

Sequencia: gi|10720069|sp|Q9PEF2.1|LOLC_XYLFA RecName: Full=Lipoprotein-releasing system transmembrane protein LolC [Xylella fastidiosa 9a5c]

Score: 375.941

e-value: 2.38673e-125

○ NGO0771

```
****Alinhamento****
####Proteina 38- locus_tag: NGO0771####
Sequencia: gi|1169571|sp|P45158.1|RECD_HAEIN RecName: Full=RecBCD enzyme subunit R
ecD; AltName: Full=Exonuclease V subunit RecD; Short=ExoV subunit RecD; AltName: F
ull=Helicase/nuclease RecBCD subunit RecD [Haemophilus influenzae Rd KW20]
Score: 200.29
e-value: 2.4358e-54
Tamanho do alinhamento: 543
Cobertura da query: 0.934595524957
****Alinhamento****
####Proteina 38- locus_tag: NGO0771####
Sequencia: gi|2507018|sp|P04993.2|RECD_ECOLI RecName: Full=RecBCD enzyme subunit R
ecD; AltName: Full=Exodeoxyribonuclease V 67 kDa polypeptide; AltName: Full=Exodeo
xyribonuclease V alpha chain; AltName: Full=Exonuclease V subunit RecD; Short=ExoV
subunit RecD; AltName: Full=Helicase/nuclease RecBCD subunit RecD [Escherichia col
i K-12]
Score: 198.364
e-value: 7.65909e-54
Tamanho do alinhamento: 583
Cobertura da query: 1.00344234079
****Alinhamento****
####Proteina 38- locus_tag: NGO0771####
Sequencia: gi|614115553|sp|P9WHJ0.1|RECD_MYCTO RecName: Full=RecBCD enzyme subunit
RecD; AltName: Full=Exonuclease V subunit RecD; Short=ExoV subunit RecD; AltName:
Full=Helicase/nuclease RecBCD subunit RecD [Mycobacterium tuberculosis CDC1551] >g
i|614115556|sp|P9WHJ1.1|RECD_MYCTU RecName: Full=RecBCD enzyme subunit RecD; AltNa
me: Full=Exonuclease V subunit RecD; Short=ExoV subunit RecD; AltName: Full=Helica
se/nuclease RecBCD subunit RecD [Mycobacterium tuberculosis H37Rv]
Score: 190.274
```

○ NGO0773

```
****Alinhamento****
####Proteína 39- locus_tag: NGO0773####
Sequencia: gi|130250|sp|P20665.1|PIV_MORBO RecName: Full=Pilin gene-inverting prot
ein; AltName: Full=PIVML
Score: 160.999
e-value: 1.20294e-44
Tamanho do alinhamento: 321
Cobertura da query: 0.963963963964
****Alinhamento****
####Proteína 39- locus_tag: NGO0773####
Sequencia: gi|130251|sp|P19257.1|PIV_MORLA RecName: Full=Pilin gene-inverting prot
ein; AltName: Full=PIVML
Score: 159.073
e-value: 5.91291e-44
Tamanho do alinhamento: 321
Cobertura da query: 0.963963963964
****Alinhamento****
####Proteína 39- locus_tag: NGO0773####
Sequencia: gi|2497375|sp|P55615.1|Y4PF_RHISN RecName: Full=Putative transposase y4
pF/y4sB [Sinorhizobium fredii NGR234]
Score: 59.3066
e-value: 1.34496e-08
Tamanho do alinhamento: 148
Cobertura da query: 0.444444444444
****Alinhamento****
####Proteína 39- locus_tag: NGO0773####
Sequencia: gi|140939|sp|P19780.1|YIS1_STRCO RecName: Full=Insertion element IS110
uncharacterized 43.6 kDa protein [Streptomyces coelicolor A3(2)]
Score: 52.373
e-value: 2.06503e-06
Tamanho do alinhamento: 105
```

○ NGO0774

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0775

```

****Alinhamento****
####Proteina 41- locus_tag: NGO0775####
Sequencia: gi|29611938|sp|P74956.2|LON_VIBPA RecName: Full=Lon protease; AltName:
Full=ATP-dependent protease La [Vibrio parahaemolyticus RIMD 2210633]
Score: 1042.72
e-value: 0.0
Tamanho do alinhamento: 784
Cobertura da query: 0.956097560976
****Alinhamento****
####Proteina 41- locus_tag: NGO0775####
Sequencia: gi|71159411|sp|P0A9M1.1|LON_ECOL6 RecName: Full=Lon protease; AltName:
Full=ATP-dependent protease La [Escherichia coli CFT073] >gi|71159412|sp|P0A9M0.1|
LON_ECOLI RecName: Full=Lon protease; AltName: Full=ATP-dependent protease La [Esc
herichia coli K-12]
Score: 1037.71
e-value: 0.0
Tamanho do alinhamento: 784
Cobertura da query: 0.956097560976
****Alinhamento****
####Proteina 41- locus_tag: NGO0775####
Sequencia: gi|1170812|sp|P46067.1|LON_ERWAM RecName: Full=Lon protease; AltName: F
ull=ATP-dependent protease La [Erwinia amylovora]
Score: 1028.47
e-value: 0.0
Tamanho do alinhamento: 784
Cobertura da query: 0.956097560976
****Alinhamento****
####Proteina 41- locus_tag: NGO0775####
Sequencia: gi|123563421|sp|Q32JJ5.1|LON_SHIDS RecName: Full=Lon protease; AltName:
Full=ATP-dependent protease La [Shigella dysenteriae Sd197]

```

- NGO0777

```
****Alinhamento****
####Proteina 42- locus_tag: NGO0777####
Sequencia: gi|54036950|sp|P64389.1|DBHB_NEIMB RecName: Full=DNA-binding protein HU
-beta [Neisseria meningitidis MC58] >gi|54041019|sp|P64388.1|DBHB_NEIMA RecName: F
ull=DNA-binding protein HU-beta [Neisseria meningitidis Z2491]
Score: 171.4
e-value: 6.47224e-55
Tamanho do alinhamento: 89
Cobertura da query: 1.0
****Alinhamento****
####Proteina 42- locus_tag: NGO0777####
Sequencia: gi|14194646|sp|Q9JR30.1|DBHC_NEIMA RecName: Full=DNA-binding protein HU
-beta 2 [Neisseria meningitidis Z2491]
Score: 121.709
e-value: 2.01022e-35
Tamanho do alinhamento: 89
Cobertura da query: 1.0
****Alinhamento****
####Proteina 42- locus_tag: NGO0777####
Sequencia: gi|12643997|sp|P05384.3|DBHB_PSEAE RecName: Full=DNA-binding protein HU
-beta [Pseudomonas aeruginosa PA01]
Score: 119.783
e-value: 1.19296e-34
Tamanho do alinhamento: 89
Cobertura da query: 1.0
****Alinhamento****
####Proteina 42- locus_tag: NGO0777####
Sequencia: gi|60392171|sp|P0A1R8.1|DBHB_SALTY RecName: Full=DNA-binding protein HU
-beta; AltName: Full=HU-1; AltName: Full=NS1 [Salmonella enterica subsp. enterica
```

- NGO0778

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0779

```

****Alinhamento****
####Proteina 44- locus_tag: NGO0779####
Sequencia: gi|12230902|sp|P29365.2|DHOM_PSEAE RecName: Full=Homoserine dehydrogenase; Short=HDH [Pseudomonas aeruginosa PA01]
Score: 508.449
e-value: 1.00216e-176
Tamanho do alinhamento: 437
Cobertura da query: 1.00459770115
****Alinhamento****
####Proteina 44- locus_tag: NGO0779####
Sequencia: gi|585051|sp|P37144.1|DHON_METGL RecName: Full=Homoserine dehydrogenase; Short=HDH [Methylobacillus glycogenes]
Score: 393.66
e-value: 4.72926e-132
Tamanho do alinhamento: 435
Cobertura da query: 1.0
****Alinhamento****
####Proteina 44- locus_tag: NGO0779####
Sequencia: gi|11132649|sp|Q9ZL20.1|DHOM_HELPJ RecName: Full=Homoserine dehydrogenase; Short=HDH [Helicobacter pylori J99]
Score: 336.265
e-value: 1.36821e-109
Tamanho do alinhamento: 439
Cobertura da query: 1.0091954023
****Alinhamento****
####Proteina 44- locus_tag: NGO0779####
Sequencia: gi|3023647|sp|P56429.1|DHOM_HELPY RecName: Full=Homoserine dehydrogenase

```

○ NGO0780

```

****Alinhamento****
####Proteina 45- locus_tag: NGO0780####
Sequencia: gi|81906745|sp|Q9JKL4.1|NDUF3_MOUSE RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3; AltName: Full=Protein 2P1 [Mus musculus]
Score: 45.0542
e-value: 1.42545e-05
Tamanho do alinhamento: 57
Cobertura da query: 0.463414634146
****Alinhamento****
####Proteina 45- locus_tag: NGO0780####
Sequencia: gi|134035397|sp|A1L1F1.1|NDUF3_DANRE RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 [Danio rerio]
Score: 44.669
e-value: 2.1705e-05
Tamanho do alinhamento: 101
Cobertura da query: 0.821138211382
****Alinhamento****
####Proteina 45- locus_tag: NGO0780####
Sequencia: gi|81861023|sp|O08776.1|NDUF3_RAT RecName: Full=NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3; AltName: Full=Nuclear protein E3-3 [Rattus norvegicus]
Score: 41.5874
e-value: 0.000273603
Tamanho do alinhamento: 57
Cobertura da query: 0.463414634146
****Alinhamento****

```

- NGO0781

```

****Alinhamento****
####Proteína 46- locus_tag: NGO0781####
Sequencia: gi|54040347|sp|P63390.1|YHES_ECOS7 RecName: Full=Uncharacterized ABC tr
ansporter ATP-binding protein YheS [Escherichia coli O157:H7] >gi|54042344|sp|P633
89.1|YHES_ECOLI RecName: Full=Uncharacterized ABC transporter ATP-binding protein
YheS [Escherichia coli K-12]
Score: 668.692
e-value: 0.0
Tamanho do alinhamento: 634
Cobertura da query: 0.990625
****Alinhamento****
####Proteína 46- locus_tag: NGO0781####
Sequencia: gi|1176240|sp|P44808.1|Y658_HAEIN RecName: Full=Uncharacterized ABC tra
nsporter ATP-binding protein HI_0658 [Haemophilus influenzae Rd KW20]
Score: 640.188
e-value: 0.0
Tamanho do alinhamento: 640
Cobertura da query: 1.0
****Alinhamento****
####Proteína 46- locus_tag: NGO0781####
Sequencia: gi|75329083|sp|Q8H0V6.1|AB3F_ARATH RecName: Full=ABC transporter F fami
ly member 3; Short=ABC transporter ABCF.3; Short=AtABCF3; AltName: Full=GCN20-type
ATP-binding cassette protein GCN3 [Arabidopsis thaliana]
Score: 383.259
e-value: 2.87148e-121
Tamanho do alinhamento: 544
Cobertura da query: 0.85
****Alinhamento****
####Proteína 46- locus_tag: NGO0781####
Sequencia: gi|81914628|sp|Q8K268.1|ABCF3_MOUSE RecName: Full=ATP-binding cassette

```

- NGO0782

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0783

```

****Alinhamento****
####Proteína 48- locus_tag: NGO0783####
Sequencia: gi|62510466|sp|Q9VT65.2|CANB_DROME RecName: Full=Calpain-B; AltName: Fu
ll=Calcium-activated neutral proteinase B; Short=CANP B; Contains: RecName: Full=C
alpain-B catalytic subunit 1; Contains: RecName: Full=Calpain-B catalytic subunit
2 [Drosophila melanogaster]
Score: 34.2686
e-value: 0.449378
Tamanho do alinhamento: 104
Cobertura da query: 0.611764705882

```

- NGO0784

```
****Alinhamento****
####Proteína 49- locus_tag: NGO0784####
Sequencia: gi|38372533|sp|P60005.1|USPE_PHOLL RecName: Full=Universal stress prote
in E [Photorhabdus luminescens subsp. laumondii TT01]
Score: 31.187
e-value: 0.397593
Tamanho do alinhamento: 43
Cobertura da query: 0.741379310345
>>>
```

- NGO0785

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0787

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0788

```
****Alinhamento****
####Proteína 53- locus_tag: NGO0788####
Sequencia: gi|60415944|sp|Q9UJZ1.1|STML2_HUMAN RecName: Full=Stomatin-like protein
2, mitochondrial; Short=SLP-2; AltName: Full=EPB72-like protein 2; AltName: Full=P
araprotein target 7; Short=Paratarg-7; Flags: Precursor [Homo sapiens]
Score: 272.322
e-value: 2.53254e-87
Tamanho do alinhamento: 288
Cobertura da query: 0.914285714286
****Alinhamento****
####Proteína 53- locus_tag: NGO0788####
Sequencia: gi|118573893|sp|Q32LL2.1|STML2_BOVIN RecName: Full=Stomatin-like protei
n 2, mitochondrial; Short=SLP-2; Flags: Precursor [Bos taurus]
Score: 271.166
e-value: 7.28153e-87
Tamanho do alinhamento: 288
Cobertura da query: 0.914285714286
****Alinhamento****
####Proteína 53- locus_tag: NGO0788####
Sequencia: gi|60415940|sp|Q99JB2.1|STML2_MOUSE RecName: Full=Stomatin-like protein
2, mitochondrial; Short=SLP-2; Short=mslp2; Flags: Precursor [Mus musculus]
Score: 270.011
e-value: 2.50599e-86
Tamanho do alinhamento: 289
Cobertura da query: 0.91746031746
****Alinhamento****
####Proteína 53- locus_tag: NGO0788####
Sequencia: gi|123781830|sp|Q4FZT0.1|STML2_RAT RecName: Full=Stomatin-like protein
2, mitochondrial; Short=SLP-2; Flags: Precursor [Rattus norvegicus]
Score: 269.626
```

○ NGO0789

```

****Alinhamento****
####Proteina 54- locus_tag: NGO0789####
Sequencia: gi|8928516|sp|Q9ZCT3.1|Y630_RICPR RecName: Full=UPF0118 membrane protei
n RP630 [Rickettsia prowazekii str. Madrid E]
Score: 174.096
e-value: 5.08843e-49
Tamanho do alinhamento: 353
Cobertura da query: 0.991573033708
****Alinhamento****
####Proteina 54- locus_tag: NGO0789####
Sequencia: gi|8928489|sp|O34472.1|YRRI_BACSU RecName: Full=UPF0118 membrane protei
n YrrI [Bacillus subtilis subsp. subtilis str. 168]
Score: 102.834
e-value: 1.52591e-23
Tamanho do alinhamento: 335
Cobertura da query: 0.941011235955
****Alinhamento****
####Proteina 54- locus_tag: NGO0789####
Sequencia: gi|2506918|sp|P43969.2|PERM_HAEIN RecName: Full=Putative permease PerM
homolog [Haemophilus influenzae Rd KW20]
Score: 99.7525
e-value: 1.66612e-22
Tamanho do alinhamento: 328
Cobertura da query: 0.921348314607
****Alinhamento****
####Proteina 54- locus_tag: NGO0789####
Sequencia: gi|8928521|sp|O32095.1|YUEF_BACSU RecName: Full=UPF0118 membrane protei
n YueF [Bacillus subtilis subsp. subtilis str. 168]
Score: 95.5153
e-value: 5.69474e-21

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○ NGO0794

```

****Alinhamento****
####Proteina 58- locus_tag: NGO0794####
Sequencia: gi|59799170|sp|P0A0R1.1|BFRA_NEIMB RecName: Full=Bacterioferritin A; Sh
ort=BFR A [Neisseria meningitidis MC58] >gi|59799171|sp|P0A0R2.1|BFRA_NEIGO RecNam
e: Full=Bacterioferritin A; Short=BFR A [Neisseria gonorrhoeae]
Score: 317.39
e-value: 2.29799e-110
Tamanho do alinhamento: 154
Cobertura da query: 1.0
****Alinhamento****
####Proteina 58- locus_tag: NGO0794####
Sequencia: gi|9910626|sp|P56998.1|BFRA_NEIMA RecName: Full=Bacterioferritin A; Sho
rt=BFR A [Neisseria meningitidis Z2491]
Score: 315.849
e-value: 7.3192e-110
Tamanho do alinhamento: 154
Cobertura da query: 1.0
****Alinhamento****
####Proteina 58- locus_tag: NGO0794####
Sequencia: gi|81783586|sp|Q9HWF9.1|BFR_PSEAE RecName: Full=Bacterioferritin; Short
=BFR [Pseudomonas aeruginosa PA01]
Score: 204.142
e-value: 8.22005e-66
Tamanho do alinhamento: 154
Cobertura da query: 1.0
****Alinhamento****
####Proteina 58- locus_tag: NGO0794####

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○ NGO0795

```

****Alinhamento****
####Proteína 59- locus_tag: NGO0795####
Sequencia: gi|54036801|sp|P63700.1|BFRB_NEIMB RecName: Full=Putative bacterioferritin B; Short=BFR B [Neisseria meningitidis MC58] >gi|54040862|sp|P63699.1|BFRB_NEIMA RecName: Full=Putative bacterioferritin B; Short=BFR B [Neisseria meningitidis Z2491]
Score: 314.309
e-value: 4.81538e-109
Tamanho do alinhamento: 157
Cobertura da query: 1.0
****Alinhamento****
####Proteína 59- locus_tag: NGO0795####
Sequencia: gi|2493292|sp|P77914.1|BFRB_NEIGO RecName: Full=Putative bacterioferritin B; Short=BFR B [Neisseria gonorrhoeae]
Score: 312.768
e-value: 1.60192e-108
Tamanho do alinhamento: 157
Cobertura da query: 1.0
****Alinhamento****
####Proteína 59- locus_tag: NGO0795####
Sequencia: gi|114931|sp|P22759.2|BFR_AZOVI RecName: Full=Bacterioferritin; Short=BFR; AltName: Full=Cytochrome b-557.5 [Azotobacter vinelandii]
Score: 185.652
e-value: 1.32396e-58
Tamanho do alinhamento: 156
Cobertura da query: 0.993630573248

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○ NGO0797

```

****Alinhamento****
####Proteína 60- locus_tag: NGO0797####
Sequencia: gi|116073|sp|P23939.1|CEBA_BACAM RecName: Full=BamHI control element [Bacillus acillus amyloliquefaciens]
Score: 57.5806
e-value: 1.56042e-10
Tamanho do alinhamento: 66
Cobertura da query: 0.628571428571
****Alinhamento****
####Proteína 60- locus_tag: NGO0797####
Sequencia: gi|141422|sp|P14307.1|YSMA_SERMA RecName: Full=Uncharacterized HTH-type transcriptional regulator in smaI restriction system 5'region [Serratia marcescens]
Score: 55.0694
e-value: 9.38502e-10
Tamanho do alinhamento: 65
Cobertura da query: 0.619047619048
****Alinhamento****
####Proteína 60- locus_tag: NGO0797####
Sequencia: gi|2495432|sp|P55409.1|Y4DJ_RHISN RecName: Full=Uncharacterized HTH-type transcriptional regulator y4dJ [Sinorhizobium fredii NGR234]
Score: 50.447
e-value: 4.16916e-08
Tamanho do alinhamento: 70
Cobertura da query: 0.666666666667
****Alinhamento****
####Proteína 60- locus_tag: NGO0797####
Sequencia: gi|1171067|sp|P43640.1|MUNC_MYCSP RecName: Full=Regulatory protein MunI [Mycoplasma sp.]
Score: 49.2914

```

○ NGO0798

****Alinhamento****

####Proteína 61- locus_tag: NGO0798####

Sequencia: gi|75356064|sp|Q5F8H5.1|GLND_NEIG1 RecName: Full=Bifunctional uridylyltransferase/uridylyl-removing enzyme; Short=UTase/UR; AltName: Full=Bifunctional [protein-PII] modification enzyme; AltName: Full=Bifunctional nitrogen sensor protein; Includes: RecName: Full=[Protein-PII] uridylyltransferase; Short=PII uridylyltransferase; Short=UTase; Includes: RecName: Full=[Protein-PII]-UMP uridylyl-removing enzyme; Short=UR [Neisseria gonorrhoeae FA 1090]

Score: 1763.43

e-value: 0.0

Tamanho do alinhamento: 852

Cobertura da query: 1.0

****Alinhamento****

####Proteína 61- locus_tag: NGO0798####

Sequencia: gi|238690198|sp|B4RLK3.1|GLND_NEIG2 RecName: Full=Bifunctional uridylyltransferase/uridylyl-removing enzyme; Short=UTase/UR; AltName: Full=Bifunctional [protein-PII] modification enzyme; AltName: Full=Bifunctional nitrogen sensor protein; Includes: RecName: Full=[Protein-PII] uridylyltransferase; Short=PII uridylyltransferase; Short=UTase; Includes: RecName: Full=[Protein-PII]-UMP uridylyl-removing enzyme; Short=UR [Neisseria gonorrhoeae NCCP11945]

Score: 1762.27

e-value: 0.0

Tamanho do alinhamento: 852

Cobertura da query: 1.0

****Alinhamento****

####Proteína 61- locus_tag: NGO0798####

Sequencia: gi|12644529|sp|Q9JZB4.1|GLND_NEIMB RecName: Full=Bifunctional uridylyltransferase/uridylyl-removing enzyme; Short=UTase/UR; AltName: Full=Bifunctional [protein-PII] modification enzyme; AltName: Full=Bifunctional nitrogen sensor protein; Includes: RecName: Full=[Protein-PII] uridylyltransferase; Short=PII uridylyltransferase; Short=UTase; Includes: RecName: Full=[Protein-PII]-UMP uridylyl-removing enzyme; Short=UR [Neisseria gonorrhoeae NCCP11945]

○ NGO0799

```

****Alinhamento****
####Proteina 62- locus_tag: NGO0799####
Sequencia: gi|400057|sp|P31002.1|IMDH_ACICA RecName: Full=Inosine-5'-monophosphate
dehydrogenase; Short=IMP dehydrogenase; Short=IMPD; Short=IMPDH [Acinetobacter cal
coaceticus]
Score: 631.713
e-value: 0.0
Tamanho do alinhamento: 488
Cobertura da query: 1.00205338809
****Alinhamento****
####Proteina 62- locus_tag: NGO0799####
Sequencia: gi|13959397|sp|Q9L6B7.1|IMDH_PASMU RecName: Full=Inosine-5'-monophospha
te dehydrogenase; Short=IMP dehydrogenase; Short=IMPD; Short=IMPDH [Pasteurella mu
ltocida subsp. multocida str. Pm70]
Score: 610.912
e-value: 0.0
Tamanho do alinhamento: 487
Cobertura da query: 1.0
****Alinhamento****
####Proteina 62- locus_tag: NGO0799####
Sequencia: gi|123150049|sp|Q0WD32.1|IMDH_YERPE RecName: Full=Inosine-5'-monophosph
ate dehydrogenase; Short=IMP dehydrogenase; Short=IMPD; Short=IMPDH [Yersinia pest
is]
Score: 601.282
e-value: 0.0
Tamanho do alinhamento: 486
Cobertura da query: 0.99794661191

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○ NGO0800

```

****Alinhamento****
####Proteina 63- locus_tag: NGO0800####
Sequencia: gi|205829224|sp|A8MQ27.1|NEU1B_HUMAN RecName: Full=E3 ubiquitin-protein
ligase NEURL1B; AltName: Full=Neuralized-2; Short=NEUR2; AltName: Full=Neuralized-
like protein 1B; AltName: Full=Neuralized-like protein 3 [Homo sapiens]
Score: 30.8018
e-value: 0.882743
Tamanho do alinhamento: 59
Cobertura da query: 0.719512195122
^^^

```

○ NGO0801

```

****Alinhamento****
####Proteina 64- locus_tag: NGO0801####
Sequencia: gi|731093|sp|P21499.2|RNR_ECOLI RecName: Full=Ribonuclease R; Short=RNA
se R; AltName: Full=Protein VacB [Escherichia coli K-12]
Score: 667.922
e-value: 0.0
Tamanho do alinhamento: 735
Cobertura da query: 0.929203539823
****Alinhamento****
####Proteina 64- locus_tag: NGO0801####
Sequencia: gi|27735249|sp|P30851.4|RNR_SHIFL RecName: Full=Ribonuclease R; Short=R
Nase R; AltName: Full=Protein VacB [Shigella flexneri]
Score: 667.152
e-value: 0.0
Tamanho do alinhamento: 735
Cobertura da query: 0.929203539823
****Alinhamento****
####Proteina 64- locus_tag: NGO0801####
Sequencia: gi|20139355|sp|Q9KNY1.1|RNR_VIBCH RecName: Full=Ribonuclease R; Short=R
Nase R [Vibrio cholerae O1 biovar El Tor str. N16961]
Score: 664.84
e-value: 0.0
Tamanho do alinhamento: 769
Cobertura da query: 0.97218710493
****Alinhamento****
####Proteina 64- locus_tag: NGO0801####
Sequencia: gi|1174933|sp|P44907.1|RNR_HAEIN RecName: Full=Ribonuclease R; Short=RN
ase R; AltName: Full=VacB protein homolog [Haemophilus influenzae Rd KW20]
Score: 661.374
e-value: 0.0

```

○ NGO0802

```

****Alinhamento****
####Proteina 65- locus_tag: NGO0802####
Sequencia: gi|152113093|sp|Q4WUK1.2|PFA5_AS PFU RecName: Full=Palmitoyltransferase
pfa5; AltName: Full=Protein fatty acyltransferase 5 [Aspergillus fumigatus Af293]
Score: 30.8018
e-value: 0.984991
Tamanho do alinhamento: 41
Cobertura da query: 0.460674157303
>>>

```


- NGO0803

```

****Alinhamento****
####Proteína 66- locus_tag: NGO0803####
Sequencia: gi|54042068|sp|P32132.2|TYPA_ECOLI RecName: Full=GTP-binding protein TypA/BipA; AltName: Full=Tyrosine phosphorylated protein A [Escherichia coli K-12] >
gi|61248986|sp|P0A3B1.1|TYPA_ECOL6 RecName: Full=GTP-binding protein TypA/BipA; AltName: Full=Tyrosine phosphorylated protein A [Escherichia coli CFT073] >gi|61248988|sp|P0A3B2.1|TYPA_ECO27 RecName: Full=GTP-binding protein TypA/BipA; AltName: Full=Tyrosine phosphorylated protein A [Escherichia coli O127:H6 str. E2348/69] >gi|61248990|sp|P0A3B3.1|TYPA_ECO57 RecName: Full=GTP-binding protein TypA/BipA; AltName: Full=Tyrosine phosphorylated protein A [Escherichia coli O157:H7] >gi|61248993|sp|P0A3B4.1|TYPA_SHIFL RecName: Full=GTP-binding protein TypA/BipA; AltName: Full=Tyrosine phosphorylated protein A [Shigella flexneri]
Score: 789.645
e-value: 0.0
Tamanho do alinhamento: 598
Cobertura da query: 0.991708126036
****Alinhamento****
####Proteína 66- locus_tag: NGO0803####
Sequencia: gi|1176325|sp|P44910.1|TYPA_HAEIN RecName: Full=GTP-binding protein TypA/BipA homolog [Haemophilus influenzae Rd KW20]
Score: 780.785
e-value: 0.0
Tamanho do alinhamento: 599
Cobertura da query: 0.993366500829
****Alinhamento****
####Proteína 66- locus_tag: NGO0803####
Sequencia: gi|38372576|sp|Q89AC9.2|TYPA_BUCBP RecName: Full=GTP-binding protein TypA/BipA homolog [Buchnera aphidicola str. Bp (Baizongia pistaciae)]
Score: 717.227
e-value: 0.0

```

- NGO0805

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0806

```

****Alinhamento****
####Proteína 69- locus_tag: NGO0806####
Sequencia: gi|9910653|sp|P57001.1|CYSG_NEIMA RecName: Full=Siroheme synthase; Includes: RecName: Full=Uroporphyrinogen-III C-methyltransferase; Short=Urogen III methylase; AltName: Full=SUMT; AltName: Full=Uroporphyrinogen III methylase; Short=UROM; Includes: RecName: Full=Precorrin-2 dehydrogenase; Includes: RecName: Full=Sirohydrochlorin ferrochelatase [Neisseria meningitidis Z2491]
Score: 324.709
e-value: 3.25539e-105
Tamanho do alinhamento: 164
Cobertura da query: 0.455555555556
****Alinhamento****
####Proteína 69- locus_tag: NGO0806####
Sequencia: gi|187471058|sp|A1KU10.1|CYSG_NEIMF RecName: Full=Siroheme synthase; Includes: RecName: Full=Uroporphyrinogen-III C-methyltransferase; Short=Urogen III methylase; AltName: Full=SUMT; AltName: Full=Uroporphyrinogen III methylase; Short=UROM; Includes: RecName: Full=Precorrin-2 dehydrogenase; Includes: RecName: Full=Sirohydrochlorin ferrochelatase [Neisseria meningitidis FAM18]
Score: 323.939
e-value: 4.49356e-105
Tamanho do alinhamento: 164
Cobertura da query: 0.455555555556
****Alinhamento****
####Proteína 69- locus_tag: NGO0806####
Sequencia: gi|9911082|sp|P95370.3|CYSG_NEIMB RecName: Full=Siroheme synthase; Includes: RecName: Full=Uroporphyrinogen-III C-methyltransferase; Short=Urogen III methylase; AltName: Full=SUMT; AltName: Full=Uroporphyrinogen III methylase; Short=UROM; Includes: RecName: Full=Precorrin-2 dehydrogenase; Includes: RecName: Full=Sirohydrochlorin ferrochelatase [Neisseria meningitidis FAM18]
Score: 323.939
e-value: 4.49356e-105
Tamanho do alinhamento: 164
Cobertura da query: 0.455555555556
****Alinhamento****

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- NGO0812

```

****Alinhamento****
####Proteína 72- locus_tag: NGO0812####
Sequencia: gi|2496748|sp|P55651.1|Y4SH_RHISN RecName: Full=Uncharacterized protein y4sH [Sinorhizobium fredii NGR234]
Score: 50.0618
e-value: 2.83781e-06
Tamanho do alinhamento: 96
Cobertura da query: 0.468292682927
****Alinhamento****
####Proteína 72- locus_tag: NGO0812####
Sequencia: gi|2496752|sp|Q53195.1|Y4UA_RHISN RecName: Full=Uncharacterized protein y4uA [Sinorhizobium fredii NGR234]
Score: 50.0618
e-value: 2.89194e-06
Tamanho do alinhamento: 96
Cobertura da query: 0.468292682927
****Alinhamento****
####Proteína 72- locus_tag: NGO0812####
Sequencia: gi|67460135|sp|P96738.1|CAPA_BACSU RecName: Full=PGA biosynthesis protein CapA [Bacillus subtilis subsp. subtilis str. 168]
Score: 45.8246
e-value: 8.83584e-05
Tamanho do alinhamento: 87
Cobertura da query: 0.424390243902
****Alinhamento****
####Proteína 72- locus_tag: NGO0812####
Sequencia: gi|618798120|sp|P9WM78.1|Y0574_MYCTO RecName: Full=Uncharacterized protein y0574 [Mycobacterium tuberculosis H37Rv]
Score: 45.8246
e-value: 8.83584e-05
Tamanho do alinhamento: 87
Cobertura da query: 0.424390243902
****Alinhamento****

```

- NGO0814

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0815

```
****Alinhamento****
####Proteína 75- locus_tag: NGO0815####
Sequencia: gi|3219995|sp|P37773.3|MPL_ECOLI RecName: Full=UDP-N-acetylmuramate:L-a
lanyl-gamma-D-glutamyl-meso-diaminopimelate ligase; AltName: Full=Murein peptide l
igase [Escherichia coli K-12]
Score: 497.664
e-value: 1.04825e-171
Tamanho do alinhamento: 457
Cobertura da query: 0.997816593886
****Alinhamento****
####Proteína 75- locus_tag: NGO0815####
Sequencia: gi|1176353|sp|P43948.1|MPL_HAEIN RecName: Full=UDP-N-acetylmuramate:L-a
lanyl-gamma-D-glutamyl-meso-diaminopimelate ligase; AltName: Full=Murein peptide l
igase [Haemophilus influenzae Rd KW20]
Score: 465.692
e-value: 3.22177e-159
Tamanho do alinhamento: 461
Cobertura da query: 1.00655021834
****Alinhamento****
####Proteína 75- locus_tag: NGO0815####
Sequencia: gi|123374163|sp|Q1D0T1.1|MURC_MYXXD RecName: Full=UDP-N-acetylmuramate-
-L-alanine ligase; AltName: Full=UDP-N-acetylmuramoyl-L-alanine synthetase [Myxoco
ccus xanthus DK 1622]
Score: 203.371
e-value: 8.83103e-58
Tamanho do alinhamento: 477
Cobertura da query: 1.04148471616
****Alinhamento****
####Proteína 75- locus_tag: NGO0815####
Sequencia: gi|23821878|sp|Q8R749.1|MURC_THETN RecName: Full=UDP-N-acetylmuramate--
-L-alanine ligase; AltName: Full=UDP-N-acetylmuramoyl-L-alanine synthetase [Caldana
```

- NGO0816

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0818

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0819

****Alinhamento****

####Proteína 78- locus_tag: NGO0819####

Sequencia: gi|81637729|sp|P94538.2|YSGA_BACSU RecName: Full=Uncharacterized tRNA/rRNA methyltransferase YsgA [Bacillus subtilis subsp. subtilis str. 168]

Score: 110.153

e-value: 3.86623e-27

Tamanho do alinhamento: 263

Cobertura da query: 1.00766283525

****Alinhamento****

####Proteína 78- locus_tag: NGO0819####

Sequencia: gi|3915481|sp|P74261.1|Y1673_SYNY3 RecName: Full=Uncharacterized tRNA/rRNA methyltransferase slr1673 [Synechocystis sp. PCC 6803 substr. Kazusa]

Score: 106.686

e-value: 1.115e-25

Tamanho do alinhamento: 263

Cobertura da query: 1.00766283525

****Alinhamento****

####Proteína 78- locus_tag: NGO0819####

Sequencia: gi|81889274|sp|Q5ND52.1|MRM3_MOUSE RecName: Full=rRNA methyltransferase 3, mitochondrial; AltName: Full=16S rRNA (guanosine(1370)-2'-O)-methyltransferase; AltName: Full=16S rRNA [Gm1370] 2'-O-methyltransferase; AltName: Full=RNA methyltransferase-like protein 1; Flags: Precursor [Mus musculus]

Score: 99.3673

e-value: 9.30054e-23

Tamanho do alinhamento: 293

Cobertura da query: 1.12260536398

****Alinhamento****

####Proteína 78- locus_tag: NGO0819####

○ NGO0822

****Alinhamento****

####Proteína 81- locus_tag: NGO0822####

Sequencia: gi|82592873|sp|P0ACH0.1|HSLR_EC057 RecName: Full=Heat shock protein 15; Short=HSP15 [Escherichia coli 0157:H7] >gi|82592874|sp|P0ACG9.1|HSLR_EC06 RecName: Full=Heat shock protein 15; Short=HSP15 [Escherichia coli CFT073] >gi|82592875|sp|P0ACG8.1|HSLR_EC06 RecName: Full=Heat shock protein 15; Short=HSP15 [Escherichia coli K-12]

Score: 112.849

e-value: 7.25896e-31

Tamanho do alinhamento: 132

Cobertura da query: 0.992481203008

****Alinhamento****

####Proteína 81- locus_tag: NGO0822####

Sequencia: gi|1176867|sp|P44754.1|HSLR_HAEIN RecName: Full=Heat shock protein 15 homolog; Short=HSP15 [Haemophilus influenzae Rd KW20]

Score: 108.227

e-value: 4.47999e-29

Tamanho do alinhamento: 123

Cobertura da query: 0.924812030075

****Alinhamento****

####Proteína 81- locus_tag: NGO0822####

Sequencia: gi|7387782|sp|Q44264.1|HSLR_AERSA RecName: Full=Heat shock protein 15 homolog; Short=HSP15 [Aeromonas salmonicida]

Score: 97.8265

e-value: 4.8498e-25

Tamanho do alinhamento: 124

Cobertura da query: 0.932330827068

****Alinhamento****

####Proteína 81- locus_tag: NGO0822####

Sequencia: gi|17433248|sp|Q9KGI8.1|Y073_BACHD RecName: Full=Uncharacterized protein

○ NGO0823

```
****Alinhamento****
####Proteina 82- locus_tag: NGO0823####
Sequencia: gi|81475251|sp|Q8FF46.1|ISCX_ECOL6 RecName: Full=Protein IscX [Escheric
hia coli CFT073]
Score: 73.9442
e-value: 1.27286e-17
Tamanho do alinhamento: 65
Cobertura da query: 1.0
****Alinhamento****
####Proteina 82- locus_tag: NGO0823####
Sequencia: gi|1175984|sp|P44668.1|ISCX_HAEIN RecName: Full=Protein IscX [Haemophil
us influenzae Rd KW20]
Score: 71.2478
e-value: 1.63942e-16
Tamanho do alinhamento: 65
Cobertura da query: 1.0
****Alinhamento****
####Proteina 82- locus_tag: NGO0823####
Sequencia: gi|82592924|sp|P0C0M0.1|ISCX_EC057 RecName: Full=Protein IscX [Escheric
hia coli O157:H7] >gi|82592925|sp|P0C0L9.1|ISCX_ECOLI RecName: Full=Protein IscX [
Escherichia coli K-12] >gi|82592926|sp|P0C0M1.1|ISCX_SHIFL RecName: Full=Protein I
scX [Shigella flexneri]
Score: 70.8626
e-value: 2.51069e-16
Tamanho do alinhamento: 65
Cobertura da query: 1.0
****Alinhamento****
####Proteina 82- locus_tag: NGO0823####
Sequencia: gi|2495641|sp|Q51384.1|Y3808_PSEAE RecName: Full=Uncharacterized protei
```

○ NGO0825

****Alinhamento****

####Proteina 83- locus_tag: NGO0825####

Sequencia: gi|12230890|sp|Q51383.2|FER_PSEAE RecName: Full=2Fe-2S ferredoxin [Pseudomonas aeruginosa PA01]

Score: 159.844

e-value: 1.11237e-49

Tamanho do alinhamento: 113

Cobertura da query: 1.0

****Alinhamento****

####Proteina 83- locus_tag: NGO0825####

Sequencia: gi|71152752|sp|P0A9R5.2|FER_EC057 RecName: Full=2Fe-2S ferredoxin [Escherichia coli O157:H7] >gi|71152753|sp|P0A9R4.2|FER_EC01 RecName: Full=2Fe-2S ferredoxin [Escherichia coli K-12] >gi|71152754|sp|P0A9R6.2|FER_SHIFL RecName: Full=2Fe-2S ferredoxin [Shigella flexneri]

Score: 158.688

e-value: 3.16471e-49

Tamanho do alinhamento: 111

Cobertura da query: 0.982300884956

****Alinhamento****

####Proteina 83- locus_tag: NGO0825####

Sequencia: gi|1169674|sp|P44428.2|FER_HAEIN RecName: Full=2Fe-2S ferredoxin [Haemophilus influenzae Rd KW20]

Score: 146.747

e-value: 1.27782e-44

Tamanho do alinhamento: 111

Cobertura da query: 0.982300884956

****Alinhamento****

####Proteina 83- locus_tag: NGO0825####

Sequencia: gi|4033381|sp|O51882.1|FER_BUCAP RecName: Full=2Fe-2S ferredoxin [Buchnera aphidicola str. Sg (Schizaphis graminum)]

Score: 130.954

- NGO0826

```
****Alinhamento****
####Proteína 84- locus_tag: NGO0826####
Sequencia: gi|25453339|sp|Q9JUF2.2|Y1343_NEIMA RecName: Full=Putative ankyrin repe
at protein NMA1343 [Neisseria meningitidis 72491]
Score: 506.523
e-value: 0.0
Tamanho do alinhamento: 252
Cobertura da query: 1.0
****Alinhamento****
####Proteína 84- locus_tag: NGO0826####
Sequencia: gi|25453336|sp|Q9JRZ6.1|Y1133_NEIMB RecName: Full=Putative ankyrin repe
at protein NMB1133/NMB1171 [Neisseria meningitidis MC58]
Score: 501.901
e-value: 5.93438e-180
Tamanho do alinhamento: 252
Cobertura da query: 1.0
****Alinhamento****
####Proteína 84- locus_tag: NGO0826####
Sequencia: gi|13878869|sp|P76394.1|YEGJ_ECOLI RecName: Full=Uncharacterized protei
n YegJ [Escherichia coli K-12]
Score: 60.077
e-value: 3.18314e-10
Tamanho do alinhamento: 93
Cobertura da query: 0.369047619048
****Alinhamento****
####Proteína 84- locus_tag: NGO0826####
Sequencia: gi|387912917|sp|Q01484.4|ANK2_HUMAN RecName: Full=Ankyrin-2; Short=ANK-
2; AltName: Full=Ankyrin-B; AltName: Full=Brain ankyrin; AltName: Full=Non-erythro
id ankyrin [Homo sapiens]
```

- NGO0827

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0828

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0730

```

****Alinhamento****
####Proteína 88- locus_tag: NGO0830####
Sequencia: gi|585010|sp|P37294.1|CRTB_SYNY3 RecName: Full=All-trans-phytoene synthase; Short=PSase [Synechocystis sp. PCC 6803 substr. Kazusa]
Score: 151.754
e-value: 1.32603e-41
Tamanho do alinhamento: 288
Cobertura da query: 0.993103448276
****Alinhamento****
####Proteína 88- locus_tag: NGO0830####
Sequencia: gi|3913360|sp|O07333.1|CRTY_ARTPT RecName: Full=Phytoene synthase [Arthrospira platensis]
Score: 144.821
e-value: 3.19116e-39
Tamanho do alinhamento: 279
Cobertura da query: 0.962068965517
****Alinhamento****
####Proteína 88- locus_tag: NGO0830####
Sequencia: gi|75282669|sp|Q52QW5.1|PSY_ONCHC RecName: Full=Phytoene synthase, chloroplastic; Short=OgPSY; Flags: Precursor [Oncidium hybrid cultivar]
Score: 145.591
e-value: 1.12535e-38
Tamanho do alinhamento: 263
Cobertura da query: 0.906896551724
****Alinhamento****
####Proteína 88- locus_tag: NGO0830####
Sequencia: gi|8928282|sp|Q9SSU8.1|PSY_DAUCA RecName: Full=Phytoene synthase, chlor

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○ NGO0831

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****Alinhamento****
####Proteína 89- locus_tag: NGO0831####
Sequencia: gi|2496575|sp|P55349.1|Y4AB_RHISN RecName: Full=Uncharacterized protein Y4aB [Sinorhizobium fredii NGR234]
Score: 75.485
e-value: 1.53636e-13
Tamanho do alinhamento: 433
Cobertura da query: 0.947483588621
****Alinhamento****
####Proteína 89- locus_tag: NGO0831####
Sequencia: gi|17367814|sp|Q9SMJ3.1|ZDS_CAPAN RecName: Full=Zeta-carotene desaturase, chloroplastic/chromoplastic; AltName: Full=9,9'-di-cis-zeta-carotene desaturase; AltName: Full=Carotene 7,8-desaturase; Flags: Precursor [Capsicum annuum]
Score: 75.485
e-value: 2.64914e-13
Tamanho do alinhamento: 328
Cobertura da query: 0.71772428884
****Alinhamento****
####Proteína 89- locus_tag: NGO0831####
Sequencia: gi|17367809|sp|Q9SE20.1|ZDS_SOLLC RecName: Full=Zeta-carotene desaturase, chloroplastic/chromoplastic; AltName: Full=9,9'-di-cis-zeta-carotene desaturase; AltName: Full=Carotene 7,8-desaturase; Flags: Precursor [Solanum lycopersicum]
Score: 70.8626
e-value: 6.97257e-12
Tamanho do alinhamento: 331
Cobertura da query: 0.724288840263

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○ NGO0832

```

****Alinhamento****
####Proteína 90- locus_tag: NGO0832####
Sequencia: gi|2506151|sp|P31808.3|YCIK_ECOLI RecName: Full=Uncharacterized oxidoreductase YciK [Escherichia coli K-12]
Score: 132.105
e-value: 1.47992e-35
Tamanho do alinhamento: 231
Cobertura da query: 0.966527196653
****Alinhamento****
####Proteína 90- locus_tag: NGO0832####
Sequencia: gi|20141366|sp|P37694.2|HETN_NOSS1 RecName: Full=Ketoacyl reductase HetN [Nostoc sp. PCC 7120]
Score: 78.9518
e-value: 2.63145e-16
Tamanho do alinhamento: 169
Cobertura da query: 0.707112970711
****Alinhamento****
####Proteína 90- locus_tag: NGO0832####
Sequencia: gi|82193364|sp|Q566S6.1|DRS7B_DANRE RecName: Full=Dehydrogenase/reductase SDR family member 7B [Danio rerio]
Score: 77.0258
e-value: 1.95075e-15
Tamanho do alinhamento: 210
Cobertura da query: 0.878661087866
****Alinhamento****
####Proteína 90- locus_tag: NGO0832####
Sequencia: gi|61249469|sp|P0A2D1.1|UCPA_SALTY RecName: Full=Oxidoreductase UcpA [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2] >gi|61249472|sp|P0A2D2.1|UCPA_SALTI RecName: Full=Oxidoreductase UcpA [Salmonella enterica subsp. enterica serovar Typhi]
Score: 75.485

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○ NGO0834

```

****Alinhamento****
####Proteína 91- locus_tag: NGO0834####
Sequencia: gi|81707197|sp|Q7DDH4.1|Y1126_NEIMB RecName: Full=Putative lipoprotein NMB1126/NMB1164; Flags: Precursor [Neisseria meningitidis MC58]
Score: 403.675
e-value: 3.14163e-142
Tamanho do alinhamento: 223
Cobertura da query: 1.0

```

○ NGO0835

```

****Alinhamento****
####Proteína 92- locus_tag: NGO0835####
Sequencia: gi|81707192|sp|Q7DDE8.1|Y1124_NEIMB RecName: Full=Putative lipoprotein NMB1124/NMB1162; Flags: Precursor [Neisseria meningitidis MC58]
Score: 426.017
e-value: 2.70295e-151
Tamanho do alinhamento: 215
Cobertura da query: 1.0

```

- NGO0836

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0841

```
****Alinhamento****
####Proteína 94- locus_tag: NGO0841####
Sequencia: gi|269969361|sp|B4EY85.1|HDA_PROMH RecName: Full=DnaA regulatory inacti
vator Hda [Proteus mirabilis HI4320]
Score: 118.627
e-value: 9.37388e-31
Tamanho do alinhamento: 228
Cobertura da query: 1.02702702703
****Alinhamento****
####Proteína 94- locus_tag: NGO0841####
Sequencia: gi|269969359|sp|B5XNQ6.1|HDA_KLEP3 RecName: Full=DnaA regulatory inacti
vator Hda [Klebsiella pneumoniae 342] >gi|269969360|sp|A6TCA8.1|HDA_KLEP7 RecName:
Full=DnaA regulatory inactivator Hda [Klebsiella pneumoniae subsp. pneumoniae MGH
78578]
Score: 117.087
e-value: 2.56648e-30
Tamanho do alinhamento: 218
Cobertura da query: 0.981981981982
****Alinhamento****
####Proteína 94- locus_tag: NGO0841####
Sequencia: gi|189042483|sp|A9MHP3.1|HDA_SALAR RecName: Full=DnaA regulatory inacti
vator Hda [Salmonella enterica subsp. arizonae serovar 62:z4,z23:-]
Score: 117.087
e-value: 3.93591e-30
Tamanho do alinhamento: 227
Cobertura da query: 1.02252252252
****Alinhamento****
```

○ NGO0842

****Alinhamento****

####Proteína 95- locus_tag: NGO0842####

Sequencia: gi|6225563|sp|O33611.1|IMD_STRAJ RecName: Full=Inhibition of morphological differentiation protein [Streptomyces azureus]

Score: 99.7525

e-value: 1.23503e-23

Tamanho do alinhamento: 227

Cobertura da query: 1.02252252252

****Alinhamento****

####Proteína 95- locus_tag: NGO0842####

Sequencia: gi|614101647|sp|P9WGJ0.1|Y3661_MYCTO RecName: Full=Uncharacterized protein MT3761 [Mycobacterium tuberculosis CDC1551] >gi|614101653|sp|P9WGJ1.1|Y3661_MYCTU RecName: Full=Uncharacterized protein Rv3661 [Mycobacterium tuberculosis H37Rv]

Score: 99.3673

e-value: 2.30234e-23

Tamanho do alinhamento: 223

Cobertura da query: 1.0045045045

****Alinhamento****

####Proteína 95- locus_tag: NGO0842####

Sequencia: gi|54039947|sp|P66802.1|Y517_MYCBO RecName: Full=Putative hydrolase Mb0517c [Mycobacterium bovis AF2122/97] >gi|614102121|sp|P9WGJ2.1|Y505_MYCTO RecName: Full=Putative hydrolase MT0526 [Mycobacterium tuberculosis CDC1551] >gi|614102125|sp|P9WGJ3.1|Y505_MYCTU RecName: Full=Putative hydrolase Rv0505c [Mycobacterium tuberculosis H37Rv]

Score: 89.7373

e-value: 4.55616e-20

Tamanho do alinhamento: 224

Cobertura da query: 1.00900900901

○ NGO0845

****Alinhamento****

####Proteína 97- locus_tag: NGO0845####

Sequencia: gi|59803087|sp|P30795.2|Y1242_ZYMMO RecName: Full=Uncharacterized protein ZM01242 [Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821]

Score: 359.377

e-value: 6.6835e-120

Tamanho do alinhamento: 374

Cobertura da query: 0.994680851064

****Alinhamento****

####Proteína 97- locus_tag: NGO0845####

Sequencia: gi|114152918|sp|Q09296.2|CBPC6_CAEEL RecName: Full=Cytosolic carboxypeptidase 6; AltName: Full=ATP/GTP-binding protein-like 4 homolog; Short=CeAGBL4 [Caenorhabditis elegans]

Score: 106.301

e-value: 3.97823e-24

Tamanho do alinhamento: 405

Cobertura da query: 1.07712765957

****Alinhamento****

####Proteína 97- locus_tag: NGO0845####

Sequencia: gi|160017458|sp|Q641K1.2|CBPC1_MOUSE RecName: Full=Cytosolic carboxypeptidase 1; AltName: Full=ATP/GTP-binding protein 1; AltName: Full=Nervous system nuclear protein induced by axotomy protein 1 [Mus musculus]

Score: 107.457

e-value: 7.19207e-24

Tamanho do alinhamento: 358

Cobertura da query: 0.952127659574

****Alinhamento****

○ NGO0847

```

****Alinhamento****
####Proteina 99- locus_tag: NGO0847####
Sequencia: gi|82583794|sp|P0AD05.1|YECA_ECOLI RecName: Full=Uncharacterized protein YecA [Escherichia coli K-12] >gi|82583795|sp|P0AD06.1|YECA_SHIFL RecName: Full=Uncharacterized protein YecA [Shigella flexneri]
Score: 76.6406
e-value: 9.29503e-16
Tamanho do alinhamento: 228
Cobertura da query: 1.03636363636
****Alinhamento****
####Proteina 99- locus_tag: NGO0847####
Sequencia: gi|166919158|sp|Q2LTP4.2|SECA_SYNAS RecName: Full=Protein translocase subunit SecA [Syntrophus aciditrophicus SB]
Score: 66.6254
e-value: 1.6968e-11
Tamanho do alinhamento: 35
Cobertura da query: 0.159090909091
****Alinhamento****
####Proteina 99- locus_tag: NGO0847####
Sequencia: gi|122298420|sp|Q07WJ3.1|SECA_SHEFN RecName: Full=Protein translocase subunit SecA [Shewanella frigidimarina NCIMB 400]
Score: 65.0846
e-value: 5.97326e-11
Tamanho do alinhamento: 34
Cobertura da query: 0.154545454545
****Alinhamento****
####Proteina 99- locus_tag: NGO0847####

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○ NGO0851

```

****Alinhamento****
####Proteina 102- locus_tag: NGO0851####
Sequencia: gi|34395724|sp|Q9JZG4.1|FTSK2_NEIMB RecName: Full=DNA translocase FtsK 2 [Neisseria meningitidis MC58]
Score: 2004.95
e-value: 0.0
Tamanho do alinhamento: 1014
Cobertura da query: 1.0
****Alinhamento****
####Proteina 102- locus_tag: NGO0851####
Sequencia: gi|34395722|sp|Q9JUK9.1|FTSK2_NEIMA RecName: Full=DNA translocase FtsK 2 [Neisseria meningitidis Z2491]
Score: 1994.55
e-value: 0.0
Tamanho do alinhamento: 1014
Cobertura da query: 1.0
****Alinhamento****
####Proteina 102- locus_tag: NGO0851####
Sequencia: gi|34395694|sp|Q8XRH0.1|FTSK1_RALSO RecName: Full=DNA translocase FtsK 1 [Ralstonia solanacearum GMI1000]
Score: 711.835
e-value: 0.0
Tamanho do alinhamento: 466
Cobertura da query: 0.459566074951
****Alinhamento****
####Proteina 102- locus_tag: NGO0851####
Sequencia: gi|34395695|sp|Q8XWX9.1|FTSK2_RALSO RecName: Full=DNA translocase FtsK

```

- NGO0852

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0854

```
****Alinhamento****
####Proteína 105- locus_tag: NGO0854####
Sequencia: gi|238693335|sp|B4S8A8.1|COBQ_PROA2 RecName: Full=Cobyric acid synthase
[Prosthecochloris aestuarii DSM 271]
Score: 50.4188
e-value: 0.641106
Tamanho do alinhamento: 28
Cobertura da query: 0.622222222222
```

- NGO0857

```
****Alinhamento****
####Proteína 106- locus_tag: NGO0857####
Sequencia: gi|81175298|sp|P0AC17.1|FOLB_ECOL6 RecName: Full=Dihydroneopterin aldol
ase; Short=DHNA [Escherichia coli CFT073] >gi|81175299|sp|P0AC16.1|FOLB_ECOLI RecN
ame: Full=Dihydroneopterin aldolase; Short=DHNA [Escherichia coli K-12] >gi|811753
00|sp|P0AC18.1|FOLB_SHIFL RecName: Full=Dihydroneopterin aldolase; Short=DHNA [Shi
gella flexneri]
Score: 89.3521
e-value: 4.21265e-22
Tamanho do alinhamento: 117
Cobertura da query: 0.991525423729
****Alinhamento****
####Proteína 106- locus_tag: NGO0857####
Sequencia: gi|1176105|sp|P46362.1|FOLB_HAEIN RecName: Full=Dihydroneopterin aldola
se; Short=DHNA [Haemophilus influenzae Rd KW20]
Score: 70.4774
e-value: 5.19545e-15
Tamanho do alinhamento: 115
Cobertura da query: 0.974576271186
****Alinhamento****
####Proteína 106- locus_tag: NGO0857####
Sequencia: gi|61224073|sp|P0A3E2.1|FOLB_STRP8 RecName: Full=Dihydroneopterin aldol
ase; Short=DHNA [Streptococcus pyogenes MGAS8232] >gi|81175301|sp|P0C0G5.1|FOLB_ST
RP1 RecName: Full=Dihydroneopterin aldolase; Short=DHNA [Streptococcus pyogenes se
rotype M1]
Score: 58.5362
e-value: 1.21253e-10
Tamanho do alinhamento: 119
Cobertura da query: 1.00847457627
****Alinhamento****
####Proteína 106- locus_tag: NGO0857####
Sequencia: gi|141435|sp|P28823.1|FOLB_BACSU RecName: Full=Dihydroneopterin aldolas
e; Short=DHNA [Bacillus subtilis subsp. subtilis str. 168]
Score: 57.7658
e-value: 2.5135e-10
```


- NGO0859

```

****Alinhamento****
####Proteína 108- locus_tag: NGO0859####
Sequencia: gi|401675|sp|P31777.1|RLMJ_HAEIN RecName: Full=Ribosomal RNA large subu
nit methyltransferase J; AltName: Full=23S rRNA (adenine(2030)-N6)-methyltransfera
se; AltName: Full=23S rRNA m6A2030 methyltransferase; AltName: Full=ORFJ [Haemophi
lus influenzae Rd KW20]
Score: 209.534
e-value: 2.33473e-64
Tamanho do alinhamento: 270
Cobertura da query: 0.960854092527
****Alinhamento****
####Proteína 108- locus_tag: NGO0859####
Sequencia: gi|586675|sp|P37634.1|RLMJ_ECOLI RecName: Full=Ribosomal RNA large subu
nit methyltransferase J; AltName: Full=23S rRNA (adenine(2030)-N6)-methyltransfera
se; AltName: Full=23S rRNA m6A2030 methyltransferase [Escherichia coli K-12]
Score: 207.994
e-value: 8.7665e-64
Tamanho do alinhamento: 264
Cobertura da query: 0.939501779359
>>>

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- NGO0861

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0863

```

****Alinhamento****
####Proteína 111- locus_tag: NGO0863####
Sequencia: gi|166989578|sp|A8GKU7.1|GLGA_SERP5 RecName: Full=Glycogen synthase; Al
tName: Full=Starch [bacterial glycogen] synthase [Serratia proteamaculans 568]
Score: 32.3426
e-value: 0.256399
Tamanho do alinhamento: 70
Cobertura da query: 0.972222222222
****Alinhamento****
####Proteína 111- locus_tag: NGO0863####
Sequencia: gi|127773|sp|P24733.1|MYS_ARGIR RecName: Full=Myosin heavy chain, stria
ted muscle [Argopecten irradians]
Score: 31.9574
e-value: 0.329049
Tamanho do alinhamento: 73
Cobertura da query: 1.01388888889
****Alinhamento****
####Proteína 111- locus_tag: NGO0863####
Sequencia: gi|129051|sp|P26268.1|ODPT_ASCSU RecName: Full=Pyruvate dehydrogenase E
1 component subunit alpha type II, mitochondrial; Short=PDHA2; Short=PDHE1-A; Flag
s: Precursor, partial [Ascaris suum]
Score: 30.4166
e-value: 0.950045
Tamanho do alinhamento: 39
Cobertura da query: 0.541666666667
>>>

```


○ NGO0865

```

****Alinhamento****
####Proteina 112- locus_tag: NGO0865####
Sequencia: gi|110832730|sp|Q60WT2.2|ACASE_CAEBR RecName: Full=Alkaline ceramidase;
Short=AlkCDase; AltName: Full=Alkaline N-acylsphingosine amidohydrolase; AltName:
Full=Alkaline acylsphingosine deacylase [Caenorhabditis briggsae]
Score: 30.8018
e-value: 0.733593
Tamanho do alinhamento: 24
Cobertura da query: 0.3
****Alinhamento****
####Proteina 112- locus_tag: NGO0865####
Sequencia: gi|74958979|sp|O45145.2|ACASE_CAEL RecName: Full=Alkaline ceramidase;
Short=AlkCDase; AltName: Full=Alkaline N-acylsphingosine amidohydrolase; AltName:
Full=Alkaline acylsphingosine deacylase [Caenorhabditis elegans]
Score: 30.8018
e-value: 0.754655
Tamanho do alinhamento: 24
Cobertura da query: 0.3

```

○ NGO0867

```

****Alinhamento****
####Proteina 114- locus_tag: NGO0867####
Sequencia: gi|1175808|sp|P44204.1|Y1458_HAEIN RecName: Full=Uncharacterized protein HI_1458 [Haemophilus influenzae Rd KW20]
Score: 56.9954
e-value: 2.68258e-10
Tamanho do alinhamento: 79
Cobertura da query: 0.612403100775
****Alinhamento****
####Proteina 114- locus_tag: NGO0867####
Sequencia: gi|116927|sp|P24716.1|COPR_STRAG RecName: Full=Plasmid copy control protein CopR [Streptococcus agalactiae]
Score: 36.1946
e-value: 0.010691
Tamanho do alinhamento: 43
Cobertura da query: 0.333333333333
****Alinhamento****
####Proteina 114- locus_tag: NGO0867####
Sequencia: gi|81620431|sp|Q97QZ2.1|PEZA_STRPN RecName: Full=Antitoxin PezA [Streptococcus pneumoniae TIGR4]
Score: 37.3502
e-value: 0.0111776
Tamanho do alinhamento: 58
Cobertura da query: 0.449612403101
****Alinhamento****
####Proteina 114- locus_tag: NGO0867####
Sequencia: gi|160358932|sp|A6U5H5.1|Y045_SINMW RecName: Full=Uncharacterized HTH-type transcriptional regulator Smed_0045 [Sinorhizobium medicae WSM419] >gi|160358955|sp|P0C5S2.1|Y410_RHIME RecName: Full=Uncharacterized HTH-type transcriptional regulator R00410 [Sinorhizobium meliloti 1021]
Score: 36.5798
e-value: 0.0143061
Tamanho do alinhamento: 71
Cobertura da query: 0.550387596899
****Alinhamento****
####Proteina 114- locus_tag: NGO0867####
Sequencia: gi|81342368|sp|O34647.1|VORD_BACSI RecName: Full=Uncharacterized HTH-type

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- NGO0868

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0869

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****Alinhamento****
####Proteína 116- locus_tag: NGO0869####
Sequencia: gi|81175261|sp|P0ABP7.1|DEDA_EC057 RecName: Full=Protein DedA; AltName:
Full=Protein DSG-1 [Escherichia coli O157:H7] >gi|81175262|sp|P0ABP6.1|DEDA_EC057
RecName: Full=Protein DedA; AltName: Full=Protein DSG-1 [Escherichia coli K-12]
Score: 293.123
e-value: 7.03469e-99
Tamanho do alinhamento: 203
Cobertura da query: 0.948598130841
****Alinhamento****
####Proteína 116- locus_tag: NGO0869####
Sequencia: gi|8928459|sp|O69601.1|Y287_MYCLE RecName: Full=Uncharacterized membran
e protein ML0287 [Mycobacterium leprae TN]
Score: 144.05
e-value: 1.08743e-40
Tamanho do alinhamento: 169
Cobertura da query: 0.789719626168
****Alinhamento****
####Proteína 116- locus_tag: NGO0869####
Sequencia: gi|614101606|sp|P9WP08.1|Y364_MYCTO RecName: Full=Uncharacterized membr
ane protein MT0380 [Mycobacterium tuberculosis CDC1551] >gi|614101612|sp|P9WP09.1|
Y364_MYCTU RecName: Full=Uncharacterized membrane protein Rv0364 [Mycobacterium tu
berculosis H37Rv]
Score: 135.191
e-value: 2.63928e-37
Tamanho do alinhamento: 200
Cobertura da query: 0.934579439252
****Alinhamento****
####Proteína 116- locus_tag: NGO0869####
Sequencia: gi|76363850|sp|P0AA63.1|YQJA_EC057 RecName: Full=Inner membrane protein
YqjA [Escherichia coli K-12] >gi|85681277|sp|P0AA64.1|YQJA_EC057 RecName: Full=Inn
er membrane protein YqjA [Escherichia coli CFT073] >gi|85681278|sp|P0AA66.1|YQJA_S
HIFL RecName: Full=Inner membrane protein YqjA [Shigella flexneri] >gi|85700303|sp
|P0AA65.1|YQJA_EC057 RecName: Full=Inner membrane protein YqjA [Escherichia coli O
```

○ NGO0870

****Alinhamento****

####Proteína 117- locus_tag: NGO0870####

Sequencia: gi|2833489|sp|Q57242.1|UUP1_HAEIN RecName: Full=ABC transporter ATP-binding protein uup-1 [Haemophilus influenzae Rd KW20]

Score: 572.778

e-value: 0.0

Tamanho do alinhamento: 648

Cobertura da query: 1.01886792453

****Alinhamento****

####Proteína 117- locus_tag: NGO0870####

Sequencia: gi|2506112|sp|P43672.2|UUP_ECOLI RecName: Full=ABC transporter ATP-binding protein uup [Escherichia coli K-12]

Score: 540.036

e-value: 0.0

Tamanho do alinhamento: 634

Cobertura da query: 0.996855345912

****Alinhamento****

####Proteína 117- locus_tag: NGO0870####

Sequencia: gi|25009547|sp|Q8K9I3.1|UUP_BUCAP RecName: Full=ABC transporter ATP-binding protein uup [Buchnera aphidicola str. Sg (Schizaphis graminum)]

Score: 412.149

e-value: 6.62633e-134

Tamanho do alinhamento: 632

Cobertura da query: 0.993710691824

****Alinhamento****

####Proteína 117- locus_tag: NGO0870####

Sequencia: gi|11387131|sp|P57445.1|UUP_BUCAI RecName: Full=ABC transporter ATP-binding protein uup [Buchnera aphidicola str. APS (Acyrtosiphon pisum)]

Score: 410.994

e-value: 2.15575e-133

Tamanho do alinhamento: 633

Cobertura da query: 0.995283018868

****Alinhamento****

####Proteína 117- locus_tag: NGO0870####

Sequencia: gi|1175738|sp|P45167.1|UUP2_HAEIN RecName: Full=ABC transporter ATP-binding protein uup-2 [Haemophilus influenzae Rd KW20]

○ NGO0873

****Alinhamento****

####Proteína 119- locus_tag: NGO0873####

Sequencia: gi|400287|sp|P31033.1|MTM4_NEIGO RecName: Full=Modification methylase NgoMIV; Short=M.NgoMIV; AltName: Full=Cytosine-specific methyltransferase NgoMIV [Neisseria gonorrhoeae]

Score: 556.214

e-value: 0.0

Tamanho do alinhamento: 315

Cobertura da query: 1.00961538462

****Alinhamento****

####Proteína 119- locus_tag: NGO0873####

Sequencia: gi|1709163|sp|P50188.1|MTN1_NOCAE RecName: Full=Modification methylase NaeI; Short=M.NaeI; AltName: Full=Cytosine-specific methyltransferase NaeI [Neisseria aerocolonigenes]

Score: 349.747

e-value: 9.15884e-117

Tamanho do alinhamento: 312

Cobertura da query: 1.0

****Alinhamento****

####Proteína 119- locus_tag: NGO0873####

Sequencia: gi|1709155|sp|P50196.1|MTE8_ECOLX RecName: Full=Modification methylase Eco47II; Short=M.Eco47II; AltName: Full=Cytosine-specific methyltransferase Eco47II [Escherichia coli]

Score: 176.792

e-value: 6.60173e-50

Tamanho do alinhamento: 344

Cobertura da query: 1.10256410256

****Alinhamento****

####Proteína 119- locus_tag: NGO0873####

Sequencia: gi|1709158|sp|P50192.1|MTHA_HAEPH RecName: Full=Modification methylase HphIA; Short=M.HphIA; AltName: Full=Cytosine-specific methyltransferase HphIA; AltName: Full=M.Hphi(C) [Haemophilus parahaemolyticus]

Score: 169.859

e-value: 1.00553e-47

Tamanho do alinhamento: 335

Cobertura da query: 1.07371794872

○ NGO0874

****Alinhamento****

####Proteína 120- locus_tag: NGO0874####

Sequencia: gi|401149|sp|P31032.1|T2M4_NEIGO RecName: Full=Type-2 restriction enzyme NgoMIV; Short=R.NgoMIV; AltName: Full=Endonuclease NgoMIV; AltName: Full=Type II restriction enzyme NgoMIV [Neisseria gonorrhoeae]

Score: 584.334

e-value: 0.0

Tamanho do alinhamento: 285

Cobertura da query: 0.996503496503

- NGO0875

```

****Alinhamento****
####Proteína 121- locus_tag: NGO0875####
Sequencia: gi|251757316|sp|P12045.2|PURK_BACSU RecName: Full=N5-carboxyaminoimidazole ribonucleotide synthase; Short=N5-CAIR synthase; AltName: Full=5-(carboxyamino)imidazole ribonucleotide synthetase [Bacillus subtilis subsp. subtilis str. 168]
Score: 293.893
e-value: 2.27631e-94
Tamanho do alinhamento: 374
Cobertura da query: 0.989417989418
****Alinhamento****
####Proteína 121- locus_tag: NGO0875####
Sequencia: gi|20141763|sp|P52559.2|PURK_BRUME RecName: Full=N5-carboxyaminoimidazole ribonucleotide synthase; Short=N5-CAIR synthase; AltName: Full=5-(carboxyamino)imidazole ribonucleotide synthetase [Brucella melitensis bv. 1 str. 16M]
Score: 259.225
e-value: 3.09653e-81
Tamanho do alinhamento: 345
Cobertura da query: 0.912698412698
****Alinhamento****
####Proteína 121- locus_tag: NGO0875####
Sequencia: gi|81859608|sp|Q5HH19.1|PURK_STAAC RecName: Full=N5-carboxyaminoimidazole ribonucleotide synthase; Short=N5-CAIR synthase; AltName: Full=5-(carboxyamino)imidazole ribonucleotide synthetase [Staphylococcus aureus subsp. aureus COL]
Score: 236.113
e-value: 3.49221e-72
Tamanho do alinhamento: 359
Cobertura da query: 0.949735449735
****Alinhamento****
####Proteína 121- locus_tag: NGO0875####
Sequencia: gi|81827873|sp|Q6GAE8.1|PURK_STAAS RecName: Full=N5-carboxyaminoimidazole ribonucleotide synthase; Short=N5-CAIR synthase; AltName: Full=5-(carboxyamino)imidazole ribonucleotide synthetase [Staphylococcus aureus subsp. aureus MSSA476]
>gi|81847829|sp|Q8NX94.1|PURK_STAAW RecName: Full=N5-carboxyaminoimidazole ribonucleotide synthase; Short=N5-CAIR synthase; AltName: Full=5-(carboxyamino)imidazole ribonucleotide synthetase [Staphylococcus aureus subsp. aureus MW2]
Score: 236.113
e-value: 4.0972e-72
Tamanho do alinhamento: 359
Cobertura da query: 0.949735449735

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- NGO0876

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0879

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0880

****Alinhamento****

####Proteína 124- locus_tag: NGO0880####

Sequencia: gi|226701204|sp|B6EII1.1|Y2166_ALISL RecName: Full=UPF0115 protein VSAL_I2166 [Aliivibrio salmonicida LFI1238]

Score: 75.9442

e-value: 3.90212e-15

Tamanho do alinhamento: 126

Cobertura da query: 0.626865671642

****Alinhamento****

####Proteína 124- locus_tag: NGO0880####

Sequencia: gi|254799898|sp|B8D704.1|Y097_BUCAT RecName: Full=UPF0115 protein BUAPT UC7_097 [Buchnera aphidicola str. Tuc7 (Acyrtosiphon pisum)]

Score: 73.1738

e-value: 7.80864e-15

Tamanho do alinhamento: 113

Cobertura da query: 0.562189054726

****Alinhamento****

####Proteína 124- locus_tag: NGO0880####

Sequencia: gi|11387268|sp|P57199.1|Y098_BUCAI RecName: Full=UPF0115 protein BU098 [Buchnera aphidicola str. APS (Acyrtosiphon pisum)] >gi|254799897|sp|B8D8Q0.1|Y096_BUCA5 RecName: Full=UPF0115 protein BUAP5A_096 [Buchnera aphidicola str. 5A (Acyrtosiphon pisum)]

Score: 73.1738

e-value: 8.1117e-15

Tamanho do alinhamento: 113

Cobertura da query: 0.562189054726

****Alinhamento****

####Proteína 124- locus_tag: NGO0880####

Sequencia: gi|189039821|sp|A7MS57.1|Y3116_VIBCB RecName: Full=UPF0115 protein VIBH AR_03116 [Vibrio campbellii ATCC BAA-1116]

Score: 72.7886

e-value: 8.62011e-15

- NGO0881

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****Alinhamento****
####Proteína 125- locus_tag: NGO0881####
Sequencia: gi|109940089|sp|P19769.2|INSK_ECOLI RecName: Full=Putative transposase
InsK for insertion sequence element IS150 [Escherichia coli K-12]
Score: 313.153
e-value: 8.30594e-105
Tamanho do alinhamento: 263
Cobertura da query: 0.96336996337
****Alinhamento****
####Proteína 125- locus_tag: NGO0881####
Sequencia: gi|2497400|sp|O05086.1|Y1721_HAEIN RecName: Full=Uncharacterized transp
osase-like protein HI_1721 [Haemophilus influenzae Rd KW20]
Score: 240.35
e-value: 2.29923e-77
Tamanho do alinhamento: 208
Cobertura da query: 0.761904761905
****Alinhamento****
####Proteína 125- locus_tag: NGO0881####
Sequencia: gi|75521059|sp|Q79CE8.1|T1353_SHIFL RecName: Full=Probable transposase
for insertion sequence element IS1353 [Shigella flexneri]
Score: 191.045
e-value: 4.7301e-55
Tamanho do alinhamento: 268
Cobertura da query: 0.981684981685
****Alinhamento****
####Proteína 125- locus_tag: NGO0881####
Sequencia: gi|140940|sp|P16940.1|YIS2_SHISO RecName: Full=Insertion element IS600
uncharacterized 31 kDa protein; AltName: Full=ISO-S3 31 kDa protein [Shigella sonnei]
Score: 139.428
e-value: 9.67485e-38
Tamanho do alinhamento: 265
Cobertura da query: 0.970695970696
****Alinhamento****
####Proteína 125- locus_tag: NGO0881####

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- NGO0883

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****Alinhamento****
####Proteína 126- locus_tag: NGO0883####
Sequencia: gi|21759462|sp|Q92WB5.1|UXUA_RHIME RecName: Full=Mannonate dehydratase;
AltName: Full=D-mannonate hydro-lyase [Sinorhizobium meliloti 1021]
Score: 32.7278
e-value: 0.391125
Tamanho do alinhamento: 45
Cobertura da query: 0.416666666667

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- NGO0884

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0885

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****Alinhamento****
####Proteina 128- locus_tag: NGO0885####
Sequencia: gi|1173328|sp|P42453.1|RUBR_ACIAD RecName: Full=Rubredoxin; Short=Rdxs
[Acinetobacter sp. ADP1]
Score: 73.9442
e-value: 7.46265e-18
Tamanho do alinhamento: 54
Cobertura da query: 0.964285714286
****Alinhamento****
####Proteina 128- locus_tag: NGO0885####
Sequencia: gi|29336560|sp|Q9FDN6.1|HRB_MOOTA RecName: Full=High molecular weight r
ubredoxin; AltName: Full=Nitric oxide reductase NADH:FprA oxidoreductase [Moorella
thermoacetica ATCC 39073]
Score: 74.7146
e-value: 5.9534e-17
Tamanho do alinhamento: 47
Cobertura da query: 0.839285714286
****Alinhamento****
####Proteina 128- locus_tag: NGO0885####
Sequencia: gi|134111|sp|P19500.1|RUBR_THETC RecName: Full=Rubredoxin; Short=Rd [Th
ermoanaerobacterium thermosaccharolyticum DSM 571]
Score: 70.4774
e-value: 1.69777e-16
Tamanho do alinhamento: 49
Cobertura da query: 0.875
****Alinhamento****
####Proteina 128- locus_tag: NGO0885####
Sequencia: gi|134110|sp|P23474.1|RUBR_CLOSD RecName: Full=Rubredoxin; Short=Rd [[C
lostridium] sticklandii DSM 519]
Score: 70.4774
e-value: 1.71232e-16
Tamanho do alinhamento: 49
Cobertura da query: 0.875
****Alinhamento****
####Proteina 128- locus_tag: NGO0885####
Sequencia: gi|19857441|sp|P24297.2|RUBR_PYRFU RecName: Full=Rubredoxin; Short=Rd [
Pyrococcus furiosus DSM 3638]
Score: 70.0922
e-value: 2.25764e-16
```

○ NGO0886

****Alinhamento****

####Proteína 129- locus_tag: NGO0886####

Sequencia: gi|68565360|sp|Q5RBD5.1|IVD_PONAB RecName: Full=Isovaleryl-CoA dehydrogenase, mitochondrial; Short=IVD; Flags: Precursor [Pongo abelii]

Score: 70.4774

e-value: 4.07978e-12

Tamanho do alinhamento: 222

Cobertura da query: 0.616666666667

****Alinhamento****

####Proteína 129- locus_tag: NGO0886####

Sequencia: gi|125051|sp|P26440.1|IVD_HUMAN RecName: Full=Isovaleryl-CoA dehydrogenase, mitochondrial; Short=IVD; Flags: Precursor [Homo sapiens]

Score: 69.707

e-value: 6.7687e-12

Tamanho do alinhamento: 222

Cobertura da query: 0.616666666667

****Alinhamento****

####Proteína 129- locus_tag: NGO0886####

Sequencia: gi|81669137|sp|O34421.1|ACDC_BACSU RecName: Full=Probable acyl-CoA dehydrogenase YngJ [Bacillus subtilis subsp. subtilis str. 168]

Score: 68.9366

e-value: 1.02794e-11

Tamanho do alinhamento: 358

Cobertura da query: 0.994444444444

****Alinhamento****

####Proteína 129- locus_tag: NGO0886####

Sequencia: gi|125052|sp|P12007.2|IVD_RAT RecName: Full=Isovaleryl-CoA dehydrogenase, mitochondrial; Short=IVD; Flags: Precursor [Rattus norvegicus]

Score: 67.3958

e-value: 3.62118e-11

Tamanho do alinhamento: 223

Cobertura da query: 0.619444444444

****Alinhamento****

####Proteína 129- locus_tag: NGO0886####

Sequencia: gi|66773808|sp|Q9JHI5.1|IVD_MOUSE RecName: Full=Isovaleryl-CoA dehydrogenase, mitochondrial; Short=IVD; Flags: Precursor [Mus musculus]

Score: 67.3958

○ NGO0887

```

****Alinhamento****
####Proteína 130- locus_tag: NGO0887####
Sequencia: gi|81345945|sp|P96684.1|YDFG_BACSU RecName: Full=Uncharacterized protein Ydfg [Bacillus subtilis subsp. subtilis str. 168]
Score: 36.965
e-value: 0.0310865
Tamanho do alinhamento: 118
Cobertura da query: 0.648351648352
****Alinhamento****
####Proteína 130- locus_tag: NGO0887####
Sequencia: gi|122300718|sp|Q087J4.1|MIAB_SHEFN RecName: Full=tRNA-2-methylthio-N(6)-dimethylallyl-adenosine synthase; AltName: Full=(Dimethylallyl)adenosine tRNA methylthiotransferase MiaB; AltName: Full=tRNA-i(6)A37 methylthiotransferase [Shewanella frigidimarina NCIMB 400]
Score: 34.8556
e-value: 0.331361
Tamanho do alinhamento: 137
Cobertura da query: 0.752747252747
****Alinhamento****
####Proteína 130- locus_tag: NGO0887####
Sequencia: gi|229890653|sp|A8H7B6.1|MIAB_SHEPA RecName: Full=tRNA-2-methylthio-N(6)-dimethylallyl-adenosine synthase; AltName: Full=(Dimethylallyl)adenosine tRNA methylthiotransferase MiaB; AltName: Full=tRNA-i(6)A37 methylthiotransferase [Shewanella pealeana ATCC 700345]
Score: 34.2686
e-value: 0.43979
Tamanho do alinhamento: 137
Cobertura da query: 0.752747252747

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○ NGO0888

```

****Alinhamento****
####Proteína 131- locus_tag: NGO0888####
Sequencia: gi|74876153|sp|Q75JF3.1|CLCC_DICDI RecName: Full=Chloride channel protein C [Dictyostelium discoideum]
Score: 34.2686
e-value: 0.167592
Tamanho do alinhamento: 85
Cobertura da query: 0.691056910569
****Alinhamento****
####Proteína 131- locus_tag: NGO0888####
Sequencia: gi|6647917|sp|Q9ZDL0.1|Y318_RICPR RecName: Full=Uncharacterized protein RP318 [Rickettsia prowazekii str. Madrid E]
Score: 32.7278
e-value: 0.262535
Tamanho do alinhamento: 42
Cobertura da query: 0.341463414634

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- NGO0890

```

****Alinhamento****
####Proteína 132- locus_tag: NGO0890####
Sequencia: gi|1170737|sp|P45295.1|LDHD_HAEIN RecName: Full=D-lactate dehydrogenase
[Haemophilus influenzae Rd KW20]
Score: 908.672
e-value: 0.0
Tamanho do alinhamento: 564
Cobertura da query: 1.00177619893
****Alinhamento****
####Proteína 132- locus_tag: NGO0890####
Sequencia: gi|126035|sp|P06149.3|DLD_ECOLI RecName: Full=D-lactate dehydrogenase;
AltName: Full=Respiratory D-lactate dehydrogenase [Escherichia coli K-12]
Score: 744.962
e-value: 0.0
Tamanho do alinhamento: 558
Cobertura da query: 0.991119005329
****Alinhamento****
####Proteína 132- locus_tag: NGO0890####
Sequencia: gi|294956519|sp|O23240.3|D2HDH_ARATH RecName: Full=D-2-hydroxyglutarate
dehydrogenase, mitochondrial; Short=AtD-2HGDH; Flags: Precursor [Arabidopsis thali
ana]
Score: 50.8322
e-value: 2.25892e-05
Tamanho do alinhamento: 160
Cobertura da query: 0.284191829485
****Alinhamento****
####Proteína 132- locus_tag: NGO0890####
Sequencia: gi|205716814|sp|Q1JPD3.2|D2HDH_BOVIN RecName: Full=D-2-hydroxyglutarate
dehydrogenase, mitochondrial; Flags: Precursor [Bos taurus]
Score: 49.2914
e-value: 5.77139e-05
Tamanho do alinhamento: 145
Cobertura da query: 0.257548845471
****Alinhamento****
####Proteína 132- locus_tag: NGO0890####
Sequencia: gi|91208273|sp|Q8N465.3|D2HDH_HUMAN RecName: Full=D-2-hydroxyglutarate

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- NGO0891

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****Alinhamento****
####Proteína 133- locus_tag: NGO0891####
Sequencia: gi|384872661|sp|O14141.2|YEW3_SCHPO RecName: Full=Mat-like protein C3G6
.03c [Schizosaccharomyces pombe 972h-]
Score: 33.4982
e-value: 0.345012
Tamanho do alinhamento: 74
Cobertura da query: 0.532374100719

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- NGO0892

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0893

```
****Alinhamento****
####Proteina 135- locus_tag: NGO0893####
Sequencia: gi|75165032|sp|Q94AX4.1|DLD_ARATH RecName: Full=D-lactate dehydrogenase
[cytochrome], mitochondrial; Short=AtD-LDH; AltName: Full=D-lactate ferricytochrom
e C oxidoreductase; AltName: Full=Glycolate deshydrogenase; Flags: Precursor [Arab
idopsis thaliana]
Score: 77.0258
e-value: 5.02924e-13
Tamanho do alinhamento: 421
Cobertura da query: 0.329678935004
****Alinhamento****
####Proteina 135- locus_tag: NGO0893####
Sequencia: gi|75165032|sp|Q94AX4.1|DLD_ARATH RecName: Full=D-lactate dehydrogenase
[cytochrome], mitochondrial; Short=AtD-LDH; AltName: Full=D-lactate ferricytochrom
e C oxidoreductase; AltName: Full=Glycolate deshydrogenase; Flags: Precursor [Arab
idopsis thaliana]
Score: 53.5286
e-value: 9.48554e-06
Tamanho do alinhamento: 96
Cobertura da query: 0.0751761942052
****Alinhamento****
####Proteina 135- locus_tag: NGO0893####
Sequencia: gi|81671645|sp|P94534.1|GLCF_BACSU RecName: Full=Probable glycolate oxi
dase iron-sulfur subunit [Bacillus subtilis subsp. subtilis str. 168]
Score: 72.4034
e-value: 9.42216e-12
Tamanho do alinhamento: 443
Cobertura da query: 0.346906812843
****Alinhamento****
####Proteina 135- locus_tag: NGO0893####
Sequencia: gi|74727712|sp|Q86WU2.1|LDHD_HUMAN RecName: Full=Probable D-lactate deh
ydrogenase, mitochondrial; Short=DLD; Short=Lactate dehydrogenase D; Flags: Precu
sor [Homo sapiens]
```

- NGO0894

```
****Alinhamento****
####Proteína 136- locus_tag: NGO0894####
Sequencia: gi|38605054|sp|Q9JUP6.1|DUSC_NEIMA RecName: Full=tRNA-dihydrouridine synthase C [Neisseria meningitidis Z2491]
Score: 667.152
e-value: 0.0
Tamanho do alinhamento: 333
Cobertura da query: 1.0
****Alinhamento****
####Proteína 136- locus_tag: NGO0894####
Sequencia: gi|38605055|sp|Q9JZL5.1|DUSC_NEIMB RecName: Full=tRNA-dihydrouridine synthase C [Neisseria meningitidis MC58]
Score: 647.506
e-value: 0.0
Tamanho do alinhamento: 332
Cobertura da query: 0.996996996997
****Alinhamento****
####Proteína 136- locus_tag: NGO0894####
Sequencia: gi|38605039|sp|Q9AMN9.1|DUSC_PSEAC RecName: Full=tRNA-dihydrouridine synthase C [Pseudomonas alcaligenes]
Score: 313.538
e-value: 1.10871e-103
Tamanho do alinhamento: 311
Cobertura da query: 0.933933933934
****Alinhamento****
####Proteína 136- locus_tag: NGO0894####
Sequencia: gi|38605051|sp|Q9HZ95.1|DUSC_PSEAE RecName: Full=tRNA-dihydrouridine synthase C [Pseudomonas aeruginosa PA01]
Score: 310.071
e-value: 3.25363e-102
Tamanho do alinhamento: 312
Cobertura da query: 0.936936936937
****Alinhamento****
####Proteína 136- locus tag: NGO0894####
```

- NGO0895

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0896

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0897

****Alinhamento****

####Proteina 139- locus_tag: NGO0897####

Sequencia: gi|332278231|sp|Q3KR16.3|PKHG6_HUMAN RecName: Full=Pleckstrin homology domain-containing family G member 6; Short=PH domain-containing family G member 6; AltName: Full=Myosin-interacting guanine nucleotide exchange factor; Short=MyoGEF

[Homo sapiens]

Score: 30.4166

e-value: 0.727344

Tamanho do alinhamento: 25

Cobertura da query: 0.462962962963

○ NGO0899

****Alinhamento****

####Proteina 140- locus_tag: NGO0899####

Sequencia: gi|25453011|sp|Q9JTT4.1|GRE_A_NEIMA RecName: Full=Transcription elongation factor GreA; AltName: Full=Transcript cleavage factor GreA [Neisseria meningitidis Z2491]

Score: 309.301

e-value: 3.63692e-107

Tamanho do alinhamento: 158

Cobertura da query: 1.0

****Alinhamento****

####Proteina 140- locus_tag: NGO0899####

Sequencia: gi|25453012|sp|Q9JYU3.1|GRE_A_NEIMB RecName: Full=Transcription elongation factor GreA; AltName: Full=Transcript cleavage factor GreA [Neisseria meningitidis MC58]

Score: 306.99

e-value: 3.12924e-106

Tamanho do alinhamento: 158

Cobertura da query: 1.0

****Alinhamento****

####Proteina 140- locus_tag: NGO0899####

Sequencia: gi|189042254|sp|A1WH11.1|GRE_A_VEREI RecName: Full=Transcription elongation factor GreA; AltName: Full=Transcript cleavage factor GreA [Verminephrobacter eiseniae EF01-2]

Score: 219.935

e-value: 5.55694e-72

Tamanho do alinhamento: 157

Cobertura da query: 0.993670886076

****Alinhamento****

####Proteina 140- locus_tag: NGO0899####

Sequencia: gi|122311293|sp|Q0A765.1|GRE_A_ALKEH RecName: Full=Transcription elongation factor GreA; AltName: Full=Transcript cleavage factor GreA [Alkalilimnicola ehrlichii MLHE-1]

Score: 218.009

e-value: 3.98188e-71

Tamanho do alinhamento: 157

Cobertura da query: 0.993670886076

****Alinhamento****

####Proteina 140- locus_tag: NGO0899####

Sequencia: gi|166200666|sp|A1WXX6.1|GRE_A_HALHL RecName: Full=Transcription elongat

○ NGO0901

```
****Alinhamento****
####Proteina 142- locus_tag: NGO0901####
Sequencia: gi|2495615|sp|P76190.1|MEPH_ECOLI RecName: Full=Murein DD-endopeptidase
MepH; AltName: Full=Murein hydrolase MepH; Flags: Precursor [Escherichia coli K-12
]
Score: 120.168
e-value: 1.04102e-31
Tamanho do alinhamento: 135
Cobertura da query: 0.762711864407
****Alinhamento****
####Proteina 142- locus_tag: NGO0901####
Sequencia: gi|2497706|sp|Q47151.1|YAFL_ECOLI RecName: Full=Probable endopeptidase
YafL; AltName: Full=Uncharacterized lipoprotein YafL; Flags: Precursor [Escherichi
a coli K-12]
Score: 110.153
e-value: 4.36162e-28
Tamanho do alinhamento: 126
Cobertura da query: 0.71186440678
****Alinhamento****
####Proteina 142- locus_tag: NGO0901####
Sequencia: gi|239938773|sp|O35010.2|YKFC_BACSU RecName: Full=Gamma-D-glutamyl-L-ly
sine endopeptidase; AltName: Full=Cell wall endopeptidase YkfC [Bacillus subtilis
subsp. subtilis str. 168]
Score: 90.1225
e-value: 1.38018e-20
Tamanho do alinhamento: 144
Cobertura da query: 0.813559322034
****Alinhamento****
####Proteina 142- locus_tag: NGO0901####
Sequencia: gi|30913478|sp|P96645.1|YDDH_BACSU RecName: Full=Probable endopeptidase
YddH; Flags: Precursor [Bacillus subtilis subsp. subtilis str. 168]
Score: 88.1965
e-value: 7.91985e-20
Tamanho do alinhamento: 101
Cobertura da query: 0.570621468927
****Alinhamento****
####Proteina 142- locus_tag: NGO0901####
Sequencia: gi|30913154|sp|P96740.2|PGDS_BACSU RecName: Full=Gamma-DL-glutamyl hydr
olase; AltName: Full=Poly-gamma-glutamate depolymerase; Short=PGA depolymerase; Fl
```

○ NGO0902

```
****Alinhamento****
####Proteina 143- locus_tag: NGO0902####
Sequencia: gi|160332301|sp|P75919.2|CLSC_ECOLI RecName: Full=Cardiolipin synthase
C; Short=CL synthase [Escherichia coli K-12]
Score: 421.779
e-value: 8.17445e-141
Tamanho do alinhamento: 461
Cobertura da query: 0.878095238095
****Alinhamento****
####Proteina 143- locus_tag: NGO0902####
Sequencia: gi|12230794|sp|Q9ZMP2.1|Y190_HELPJ RecName: Full=Uncharacterized protei
n jhp_0176 [Helicobacter pylori J99]
Score: 234.572
e-value: 1.55709e-68
Tamanho do alinhamento: 462
Cobertura da query: 0.88
****Alinhamento****
####Proteina 143- locus_tag: NGO0902####
Sequencia: gi|2493740|sp|P56117.1|Y190_HELPY RecName: Full=Uncharacterized protein
HP_0190 [Helicobacter pylori 26695]
Score: 233.802
e-value: 3.28816e-68
Tamanho do alinhamento: 422
Cobertura da query: 0.80380952381
****Alinhamento****
####Proteina 143- locus_tag: NGO0902####
Sequencia: gi|123461420|sp|A0ALI7.1|CLS_LISW6 RecName: Full=Cardiolipin synthase;
Short=CL synthase [Listeria welshimeri serovar 6b str. SLCC5334]
Score: 99.3673
e-value: 6.16047e-21
Tamanho do alinhamento: 394
Cobertura da query: 0.750476190476
****Alinhamento****
####Proteina 143- locus_tag: NGO0902####
Sequencia: gi|3025309|sp|P71040.2|CLSA_BACSU RecName: Full=Major cardiolipin synth
ase ClsA; Short=CL synthase 2 [Bacillus subtilis subsp. subtilis str. 168]
Score: 98.9821
```

○ NGO0903

****Alinhamento****

####Proteína 144- locus_tag: NGO0903####

Sequencia: gi|401630|sp|P31474.1|HSRA_ECOLI RecName: Full=Probable transport protein HsrA; AltName: Full=High-copy suppressor of rspA [Escherichia coli K-12]
Score: 359.377

e-value: 2.58911e-117

Tamanho do alinhamento: 454

Cobertura da query: 0.970085470085

****Alinhamento****

####Proteína 144- locus_tag: NGO0903####

Sequencia: gi|1176313|sp|P44903.1|HSRA_HAEIN RecName: Full=Probable transport protein HsrA [Haemophilus influenzae Rd KW20]
Score: 340.887

e-value: 3.07575e-110

Tamanho do alinhamento: 449

Cobertura da query: 0.959401709402

****Alinhamento****

####Proteína 144- locus_tag: NGO0903####

Sequencia: gi|81644351|sp|Q6D2A9.1|MDTD_PECAS RecName: Full=Putative multidrug resistance protein MdtD [Pectobacterium atrosepticum SCRI1043]
Score: 297.36

e-value: 1.9497e-93

Tamanho do alinhamento: 451

Cobertura da query: 0.963675213675

****Alinhamento****

####Proteína 144- locus_tag: NGO0903####

Sequencia: gi|224493140|sp|A8GHR1.1|MDTD_SERP5 RecName: Full=Putative multidrug resistance protein MdtD [Serratia proteamaculans 568]
Score: 296.975

e-value: 3.72937e-93

Tamanho do alinhamento: 471

Cobertura da query: 1.00641025641

****Alinhamento****

####Proteína 144- locus_tag: NGO0903####

○ NGO0904

```
****Alinhamento****
####Proteina 145- locus_tag: NGO0904####
Sequencia: gi|259495142|sp|A9VI76.1|LUTA1_BACWK RecName: Full=Lactate utilization
protein A 1 [Bacillus weihenstephanensis KBAB4]
Score: 177.563
e-value: 9.81064e-53
Tamanho do alinhamento: 245
Cobertura da query: 0.945945945946
****Alinhamento****
####Proteina 145- locus_tag: NGO0904####
Sequencia: gi|259495158|sp|C5D587.1|LUTA_GEOSW RecName: Full=Lactate utilization p
rotein A [Geobacillus sp. WCH70]
Score: 172.94
e-value: 5.27084e-51
Tamanho do alinhamento: 239
Cobertura da query: 0.92277992278
****Alinhamento****
####Proteina 145- locus_tag: NGO0904####
Sequencia: gi|81348195|sp|Q5L300.1|LUTA_GEOKA RecName: Full=Lactate utilization pr
otein A [Geobacillus kaustophilus HTA426]
Score: 170.244
e-value: 5.37994e-50
Tamanho do alinhamento: 239
Cobertura da query: 0.92277992278
****Alinhamento****
####Proteina 145- locus_tag: NGO0904####
Sequencia: gi|259495145|sp|B7JF51.1|LUTA2_BACC0 RecName: Full=Lactate utilization
protein A 2 [Bacillus cereus AH820]
Score: 167.162
e-value: 8.48861e-49
Tamanho do alinhamento: 235
Cobertura da query: 0.907335907336
****Alinhamento****
####Proteina 145- locus_tag: NGO0904####
Sequencia: gi|259495149|sp|B7GLD6.1|LUTA_ANOFW RecName: Full=Lactate utilization p
rotein A [Anoxybacillus flavithermus WK1]
```

○ NGO0905

```
****Alinhamento****
####Proteina 146- locus_tag: NGO0905####
Sequencia: gi|81784471|sp|Q9JYT7.1|Y1437_NEIMB RecName: Full=Uncharacterized prote
in NMB1437 [Neisseria meningitidis MC58]
Score: 469.544
e-value: 6.59518e-168
Tamanho do alinhamento: 233
Cobertura da query: 1.0
****Alinhamento****
####Proteina 146- locus_tag: NGO0905####
Sequencia: gi|81366817|sp|Q5WJD9.1|LUTC_BACSK RecName: Full=Lactate utilization pr
otein C [Bacillus clausii KSM-K16]
Score: 58.9214
e-value: 1.90995e-09
Tamanho do alinhamento: 92
Cobertura da query: 0.394849785408
****Alinhamento****
####Proteina 146- locus_tag: NGO0905####
Sequencia: gi|18271758|sp|P77433.2|YKGG_ECOLI RecName: Full=Uncharacterized protei
n YkgG [Escherichia coli K-12]
Score: 58.9214
e-value: 2.28447e-09
Tamanho do alinhamento: 104
Cobertura da query: 0.44635193133
****Alinhamento****
####Proteina 146- locus_tag: NGO0905####
Sequencia: gi|259495083|sp|C4L0S0.1|LUTC_EXISA RecName: Full=Lactate utilization p
rotein C [Exiguobacterium sp. AT1b]
Score: 56.6102
e-value: 1.25536e-08
Tamanho do alinhamento: 99
Cobertura da query: 0.424892703863
****Alinhamento****
####Proteina 146- locus_tag: NGO0905####
Sequencia: gi|81786962|sp|Q9KBU0.1|LUTC_BACHD RecName: Full=Lactate utilization pr
```

○ NGO0906

****Alinhamento****

####Proteína 147- locus_tag: NGO0906####

Sequencia: gi|259495067|sp|B9E9G9.1|LUTB_MACCJ RecName: Full=Lactate utilization p
rotein B [Macroccoccus caseolyticus JCSC5402]

Score: 352.443

e-value: 2.31989e-114

Tamanho do alinhamento: 409

Cobertura da query: 0.845041322314

****Alinhamento****

####Proteína 147- locus_tag: NGO0906####

Sequencia: gi|259495062|sp|A8FDN5.1|LUTB_BACP2 RecName: Full=Lactate utilization p
rotein B [Bacillus pumilus SAFR-032]

Score: 350.517

e-value: 9.98526e-114

Tamanho do alinhamento: 484

Cobertura da query: 1.0

****Alinhamento****

####Proteína 147- locus_tag: NGO0906####

Sequencia: gi|2494447|sp|P77536.1|YKGF_ECOLI RecName: Full=Uncharacterized electro
n transport protein YkgF [Escherichia coli K-12]

Score: 348.977

e-value: 4.1981e-113

Tamanho do alinhamento: 378

Cobertura da query: 0.780991735537

****Alinhamento****

####Proteína 147- locus_tag: NGO0906####

Sequencia: gi|81555738|sp|O07021.2|LUTB_BACSU RecName: Full=Lactate utilization pr
oteín B [Bacillus subtilis subsp. subtilis str. 168]

Score: 347.821

e-value: 1.29982e-112

Tamanho do alinhamento: 480

Cobertura da query: 0.99173553719

****Alinhamento****

####Proteína 147- locus_tag: NGO0906####

Sequencia: gi|259495064|sp|C5D586.1|LUTB_GEOSW RecName: Full=Lactate utilization p
rotein B [Geobacillus sp. WCH70]

Score: 343.969

○ NGO0908

****Alinhamento****

####Proteina 149- locus_tag: NGO0908####

Sequencia: gi|75432487|sp|Q5F881.1|FITA_NEIG1 RecName: Full=Antitoxin FitA; AltName: Full=Trafficking protein A [Neisseria gonorrhoeae FA 1090]

Score: 153.68

e-value: 2.89492e-48

Tamanho do alinhamento: 78

Cobertura da query: 1.0

****Alinhamento****

####Proteina 149- locus_tag: NGO0908####

Sequencia: gi|2496668|sp|P55510.1|Y4JJ_RHISN RecName: Full=Putative plasmid stability protein y4jJ [Sinorhizobium fredii NGR234]

Score: 66.6254

e-value: 1.93832e-14

Tamanho do alinhamento: 62

Cobertura da query: 0.794871794872

****Alinhamento****

####Proteina 149- locus_tag: NGO0908####

Sequencia: gi|29840856|sp|Q52561.2|STBC_PSESM RecName: Full=Plasmid stability protein StbC [Pseudomonas syringae pv. tomato str. DC3000]

Score: 62.7734

e-value: 7.70263e-13

Tamanho do alinhamento: 62

Cobertura da query: 0.794871794872

****Alinhamento****

####Proteina 149- locus_tag: NGO0908####

Sequencia: gi|160175296|sp|A1BD24.1|RPOC_CHLPD RecName: Full=DNA-directed RNA polymerase subunit beta'; Short=RNAP subunit beta'; AltName: Full=RNA polymerase subunit beta'; AltName: Full=Transcriptase subunit beta' [Chlorobium phaeobacteroides DSM 266]

Score: 33.113

e-value: 0.172877

Tamanho do alinhamento: 68

Cobertura da query: 0.871794871795

○ NGO0909

****Alinhamento****

####Proteina 150- locus_tag: NGO0909####

Sequencia: gi|109940089|sp|P19769.2|INSK_ECOLI RecName: Full=Putative transposase InSK for insertion sequence element IS150 [Escherichia coli K-12]

Score: 313.153

e-value: 8.30594e-105

Tamanho do alinhamento: 263

Cobertura da query: 0.96336996337

****Alinhamento****

####Proteina 150- locus_tag: NGO0909####

Sequencia: gi|2497400|sp|O05086.1|Y1721_HAEIN RecName: Full=Uncharacterized transposase-like protein HI_1721 [Haemophilus influenzae Rd KW20]

Score: 240.35

e-value: 2.29923e-77

Tamanho do alinhamento: 208

Cobertura da query: 0.761904761905

****Alinhamento****

####Proteina 150- locus_tag: NGO0909####

Sequencia: gi|75521059|sp|Q79CE8.1|T1353_SHIFL RecName: Full=Probable transposase for insertion sequence element IS1353 [Shigella flexneri]

Score: 191.045

e-value: 4.7301e-55

Tamanho do alinhamento: 268

Cobertura da query: 0.981684981685

****Alinhamento****

####Proteina 150- locus_tag: NGO0909####

Sequencia: gi|140940|sp|P16940.1|YIS2_SHISO RecName: Full=Insertion element IS600 uncharacterized 31 kDa protein; AltName: Full=ISO-S3 31 kDa protein [Shigella sonnei]

Score: 139.428

e-value: 9.67485e-38

Tamanho do alinhamento: 265

Cobertura da query: 0.970695970696

****Alinhamento****

####Proteina 150- locus_tag: NGO0909####

Sequencia: gi|549108|sp|P35878.1|T904_IACIA RecName: Full=Transposase for insertion

○ NGO0912

****Alinhamento****

####Proteina 151- locus_tag: NGO0912####

Sequencia: gi|12230978|sp|Q51567.2|SUCD_PSEAE RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha [Pseudomonas aeruginosa PA01]

Score: 441.425

e-value: 8.57747e-155

Tamanho do alinhamento: 289

Cobertura da query: 0.976351351351

****Alinhamento****

####Proteina 151- locus_tag: NGO0912####

Sequencia: gi|84027800|sp|P0AGF1.2|SUCD_EC057 RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha [Escherichia coli O157:H7] >gi|84027801|sp|P0AGF0.2|SUCD_EC06 RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha [Escherichia coli CFT073] >gi|84027802|sp|P0AGE9.2|SUCD_EC06 RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha [Escherichia coli K-12]

Score: 436.032

e-value: 1.21316e-152

Tamanho do alinhamento: 291

Cobertura da query: 0.983108108108

****Alinhamento****

####Proteina 151- locus_tag: NGO0912####

Sequencia: gi|30581056|sp|P53591.2|SUCD_COXBU RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha [Coxiella burnetii RSA 493]

Score: 428.328

e-value: 1.5975e-149

Tamanho do alinhamento: 288

Cobertura da query: 0.972972972973

****Alinhamento****

####Proteina 151- locus_tag: NGO0912####

Sequencia: gi|1174474|sp|P45102.1|SUCD_HAEIN RecName: Full=Succinyl-CoA ligase [ADP-forming] subunit alpha; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha [Haemophilus influenzae Rd KW20]

Score: 416.772

○ NGO0914

****Alinhamento****

####Proteina 153- locus_tag: NGO0914####

Sequencia: gi|74693643|sp|Q757K7.1|GPII18_ASHGO RecName: Full=GPI mannosyltransferase 2; AltName: Full=GPI mannosyltransferase II; Short=GPI-MT-II; AltName: Full=Glycosylphosphatidylinositol-anchor biosynthesis protein 18 [Ashbya gossypii ATCC 10895]

Score: 33.113

e-value: 0.21099

Tamanho do alinhamento: 56

Cobertura da query: 0.589473684211

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○ NGO0915

****Alinhamento****

####Proteina 154- locus_tag: NGO0915####

Sequencia: gi|124106279|sp|P52992.2|DLDH_CUPNH RecName: Full=Dihydrolipoyl dehydrogenase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of 2-oxoglutarate dehydrogenase complex [Ralstonia eutropha H16]

Score: 572.392

e-value: 0.0

Tamanho do alinhamento: 475

Cobertura da query: 0.995807127883

****Alinhamento****

####Proteina 154- locus_tag: NGO0915####

Sequencia: gi|118676|sp|P14218.3|DLDH_PSEFL RecName: Full=Dihydrolipoyl dehydrogenase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of 2-oxoglutarate dehydrogenase complex [Pseudomonas fluorescens]

Score: 500.36

e-value: 3.30737e-172

Tamanho do alinhamento: 478

Cobertura da query: 1.00209643606

****Alinhamento****

####Proteina 154- locus_tag: NGO0915####

Sequencia: gi|81541333|sp|Q9I3D1.1|DLDH2_PSEAE RecName: Full=Dihydrolipoyl dehydrogenase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of 2-oxoglutarate dehydrogenase complex; AltName: Full=Glycine oxidation system L-factor; AltName: Full=LPD-GLC [Pseudomonas aeruginosa PA01]

Score: 500.36

e-value: 3.45433e-172

Tamanho do alinhamento: 478

Cobertura da query: 1.00209643606

****Alinhamento****

####Proteina 154- locus_tag: NGO0915####

Sequencia: gi|1706442|sp|P31052.4|DLDH2_PSEPU RecName: Full=Dihydrolipoyl dehydrogenase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of 2-oxoglutarate dehydrogenase complex; AltName: Full=Glycine oxidation system L-factor; AltName: Full=LPD-GLC [Pseudomonas putida]

Score: 491.5

e-value: 1.08476e-168

Tamanho do alinhamento: 479

○ NGO0916

****Alinhamento****

####Proteina 155- locus_tag: NGO0916####

Sequencia: gi|1709441|sp|P52993.1|ODO2_CUPNH RecName: Full=Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex; AltName: Full=2-oxoglutarate dehydrogenase complex component E2; Short=OGDC-E2; AltName: Full=Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex [Ralstonia eutropha H16]

Score: 532.332

e-value: 0.0

Tamanho do alinhamento: 414

Cobertura da query: 1.0534351145

****Alinhamento****

####Proteina 155- locus_tag: NGO0916####

Sequencia: gi|1171887|sp|P45302.1|ODO2_HAEIN RecName: Full=Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex; AltName: Full=2-oxoglutarate dehydrogenase complex component E2; Short=OGDC-E2; AltName: Full=Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex [Haemophilus influenzae Rd KW20]

Score: 457.218

e-value: 1.15098e-157

Tamanho do alinhamento: 410

Cobertura da query: 1.04325699746

****Alinhamento****

####Proteina 155- locus_tag: NGO0916####

Sequencia: gi|84027823|sp|P0AFG7.2|ODO2_EC057 RecName: Full=Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex; AltName: Full=2-oxoglutarate dehydrogenase complex component E2; Short=OGDC-E2; AltName: Full=Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex [Escherichia coli O157:H7] >gi|84027824|sp|P0AFG6.2|ODO2_EC01 RecName: Full=Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex; AltName: Full=2-oxoglutarate dehydrogenase complex component E2; Short=OGDC-E2; AltName: Full=Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex [Escherichia coli K-12]

Score: 446.047

e-value: 2.25829e-153

Tamanho do alinhamento: 402

Cobertura da query: 1.02290076336

****Alinhamento****

####Proteina 155- locus_tag: NGO0916####

- NGO0917

****Alinhamento****

####Proteina 156- locus_tag: NGO0917####

Sequencia: gi|124106292|sp|Q59106.2|ODO1_CUPNH RecName: Full=2-oxoglutarate dehydrogenase E1 component; AltName: Full=Alpha-ketoglutarate dehydrogenase [Ralstonia eutropha H16]

Score: 1100.12

e-value: 0.0

Tamanho do alinhamento: 945

Cobertura da query: 1.00318471338

****Alinhamento****

####Proteina 156- locus_tag: NGO0917####

Sequencia: gi|129036|sp|P20707.1|ODO1_AZOVI RecName: Full=2-oxoglutarate dehydrogenase E1 component; AltName: Full=Alpha-ketoglutarate dehydrogenase [Azotobacter vinelandii]

Score: 971.844

e-value: 0.0

Tamanho do alinhamento: 951

Cobertura da query: 1.00955414013

****Alinhamento****

####Proteina 156- locus_tag: NGO0917####

Sequencia: gi|84027820|sp|P0AFG5.1|ODO1_EC057 RecName: Full=2-oxoglutarate dehydrogenase E1 component; AltName: Full=Alpha-ketoglutarate dehydrogenase [Escherichia coli O157:H7] >gi|84027821|sp|P0AFG4.1|ODO1_EC06 RecName: Full=2-oxoglutarate dehydrogenase E1 component; AltName: Full=Alpha-ketoglutarate dehydrogenase [Escherichia coli CFT073] >gi|84027822|sp|P0AFG3.1|ODO1_EC01 RecName: Full=2-oxoglutarate dehydrogenase E1 component; AltName: Full=Alpha-ketoglutarate dehydrogenase [Escherichia coli K-12]

Score: 949.888

e-value: 0.0

Tamanho do alinhamento: 939

Cobertura da query: 0.996815286624

****Alinhamento****

####Proteina 156- locus_tag: NGO0917####

Sequencia: gi|1171886|sp|P45303.1|ODO1_HAEIN RecName: Full=2-oxoglutarate dehydrogenase E1 component; AltName: Full=Alpha-ketoglutarate dehydrogenase [Haemophilus influenzae Rd KW20]

Score: 941.799

e-value: 0.0

○ NGO0918

```
****Alinhamento****
####Proteina 157- locus_tag: NGO0918####
Sequencia: gi|12230874|sp|P14165.2|CISY_PSEAE RecName: Full=Citrate synthase [Pseudomonas aeruginosa PA01]
Score: 634.41
e-value: 0.0
Tamanho do alinhamento: 427
Cobertura da query: 1.0
****Alinhamento****
####Proteina 157- locus_tag: NGO0918####
Sequencia: gi|116463|sp|P20902.2|CISY_ACIAN RecName: Full=Citrate synthase [Acinetobacter calcoaceticus subsp. anitratus]
Score: 608.986
e-value: 0.0
Tamanho do alinhamento: 419
Cobertura da query: 0.981264637002
****Alinhamento****
####Proteina 157- locus_tag: NGO0918####
Sequencia: gi|7387572|sp|O33915.2|CISY_RHIME RecName: Full=Citrate synthase [Sinorhizobium meliloti 1021]
Score: 607.06
e-value: 0.0
Tamanho do alinhamento: 427
Cobertura da query: 1.0
****Alinhamento****
####Proteina 157- locus_tag: NGO0918####
Sequencia: gi|30173515|sp|P94325.2|CISY_BRADU RecName: Full=Citrate synthase [Bradyrhizobium diazoefficiens USDA 110]
Score: 605.134
e-value: 0.0
Tamanho do alinhamento: 428
Cobertura da query: 1.00234192037
****Alinhamento****
####Proteina 157- locus_tag: NGO0918####
```


○ NGO0919

```
****Alinhamento****
####Proteina 158- locus_tag: NGO0919####
Sequencia: gi|81175076|sp|Q9KPA2.1|Y2471_VIBCH RecName: Full=Uncharacterized prote
in VC_2471 [Vibrio cholerae 01 biovar El Tor str. N16961]
Score: 56.225
e-value: 2.21565e-10
Tamanho do alinhamento: 71
Cobertura da query: 0.865853658537
****Alinhamento****
####Proteina 158- locus_tag: NGO0919####
Sequencia: gi|81175067|sp|Q8DC84.1|Y1557_VIBVU RecName: Full=Uncharacterized prote
in WV1_1557 [Vibrio vulnificus CMCP6]
Score: 55.0694
e-value: 6.28742e-10
Tamanho do alinhamento: 71
Cobertura da query: 0.865853658537
****Alinhamento****
####Proteina 158- locus_tag: NGO0919####
Sequencia: gi|81175078|sp|Q7MHM8.1|Y2841_VIBVY RecName: Full=Uncharacterized prote
in WV2841 [Vibrio vulnificus YJ016]
Score: 53.9138
e-value: 1.46394e-09
Tamanho do alinhamento: 71
Cobertura da query: 0.865853658537
****Alinhamento****
####Proteina 158- locus_tag: NGO0919####
Sequencia: gi|81175061|sp|Q8EH90.1|Y1339_SHEON RecName: Full=Uncharacterized prote
in SO_1339 [Shewanella oneidensis MR-1]
Score: 53.9138
e-value: 1.59322e-09
Tamanho do alinhamento: 70
Cobertura da query: 0.853658536585
****Alinhamento****
####Proteina 158- locus_tag: NGO0919####
Sequencia: gi|75353459|sp|Q5E305.1|Y2096_VIBF1 RecName: Full=Uncharacterized prote
in VF_2096 [Vibrio fischeri ES114]
```


○ NGO0920

****Alinhamento****

####Proteina 159- locus_tag: NGO0920####

Sequencia: gi|118615|sp|P07014.1|SDHB_ECOLI RecName: Full=Succinate dehydrogenase iron-sulfur subunit [Escherichia coli K-12]

Score: 333.569

e-value: 4.53497e-114

Tamanho do alinhamento: 235

Cobertura da query: 0.971074380165

****Alinhamento****

####Proteina 159- locus_tag: NGO0920####

Sequencia: gi|21362473|sp|Q8ZQU2.2|SDHB_SALTY RecName: Full=Succinate dehydrogenase iron-sulfur subunit [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

Score: 333.183

e-value: 7.90675e-114

Tamanho do alinhamento: 235

Cobertura da query: 0.971074380165

****Alinhamento****

####Proteina 159- locus_tag: NGO0920####

Sequencia: gi|20137875|sp|Q92JJ8.1|SDHB_RICCN RecName: Full=Succinate dehydrogenase iron-sulfur subunit [Rickettsia conorii str. Malish 7]

Score: 285.804

e-value: 7.00413e-95

Tamanho do alinhamento: 235

Cobertura da query: 0.971074380165

****Alinhamento****

####Proteina 159- locus_tag: NGO0920####

Sequencia: gi|81826336|sp|Q68XS0.1|SDHB_RICTY RecName: Full=Succinate dehydrogenase iron-sulfur subunit [Rickettsia typhi str. Wilmington]

Score: 285.034

e-value: 1.30108e-94

Tamanho do alinhamento: 235

Cobertura da query: 0.971074380165

****Alinhamento****

####Proteina 159- locus_tag: NGO0920####

Sequencia: gi|75537005|sp|Q4UN71.1|SDHB_RICFE RecName: Full=Succinate dehydrogenase iron-sulfur subunit [Rickettsia felis URRWXC12]

Score: 283.878

e-value: 3.8558e-94

○ NGO0921

```
****Alinhamento****
####Proteina 160- locus_tag: NGO0921####
Sequencia: gi|122425298|sp|Q1RHB9.1|SDHA_RICBR RecName: Full=Succinate dehydrogenase flavoprotein subunit [Rickettsia bellii RML369-C]
Score: 674.085
e-value: 0.0
Tamanho do alinhamento: 587
Cobertura da query: 1.0
****Alinhamento****
####Proteina 160- locus_tag: NGO0921####
Sequencia: gi|81826335|sp|Q68XN9.1|SDHA_RICTY RecName: Full=Succinate dehydrogenase flavoprotein subunit [Rickettsia typhi str. Wilmington]
Score: 669.463
e-value: 0.0
Tamanho do alinhamento: 587
Cobertura da query: 1.0
****Alinhamento****
####Proteina 160- locus_tag: NGO0921####
Sequencia: gi|20137871|sp|Q92J97.1|SDHA_RICCN RecName: Full=Succinate dehydrogenase flavoprotein subunit [Rickettsia conorii str. Malish 7]
Score: 669.078
e-value: 0.0
Tamanho do alinhamento: 587
Cobertura da query: 1.0
****Alinhamento****
####Proteina 160- locus_tag: NGO0921####
Sequencia: gi|75535803|sp|Q4UJM1.1|SDHA_RICFE RecName: Full=Succinate dehydrogenase flavoprotein subunit [Rickettsia felis URRWXCal2]
Score: 666.766
e-value: 0.0
Tamanho do alinhamento: 587
Cobertura da query: 1.0
****Alinhamento****
```

○ NGO0922

****Alinhamento****

####Proteína 161- locus_tag: NGO0922####

Sequencia: gi|218512006|sp|P51057.2|DHSD_COXBU RecName: Full=Succinate dehydrogenase hydrophobic membrane anchor subunit [Coxiella burnetii RSA 493]

Score: 72.7886

e-value: 5.6151e-16

Tamanho do alinhamento: 113

Cobertura da query: 1.0

****Alinhamento****

####Proteína 161- locus_tag: NGO0922####

Sequencia: gi|81175274|sp|P0AC45.1|DHSD_ECOL6 RecName: Full=Succinate dehydrogenase hydrophobic membrane anchor subunit [Escherichia coli CFT073] >gi|81175275|sp|P0AC44.1|DHSD_ECOLI RecName: Full=Succinate dehydrogenase hydrophobic membrane anchor subunit [Escherichia coli K-12] >gi|81175276|sp|P0AC46.1|DHSD_SHIFL RecName: Full=Succinate dehydrogenase hydrophobic membrane anchor subunit [Shigella flexneri]

Score: 69.3218

e-value: 1.30882e-14

Tamanho do alinhamento: 115

Cobertura da query: 1.01769911504

****Alinhamento****

####Proteína 161- locus_tag: NGO0922####

Sequencia: gi|81170423|sp|Q8X9A9.1|DHSD_EC057 RecName: Full=Succinate dehydrogenase hydrophobic membrane anchor subunit [Escherichia coli O157:H7]

Score: 65.855

e-value: 1.90865e-13

Tamanho do alinhamento: 115

Cobertura da query: 1.01769911504

^^^

- NGO0923

```

****Alinhamento****
####Proteína 162- locus_tag: NGO0923####
Sequencia: gi|60392191|sp|P69054.1|DHSC_ECOLI RecName: Full=Succinate dehydrogenas
e cytochrome b556 subunit; Short=Cytochrome b-556 [Escherichia coli K-12] >gi|6039
2192|sp|P69055.1|DHSC_EC057 RecName: Full=Succinate dehydrogenase cytochrome b556
subunit; Short=Cytochrome b-556 [Escherichia coli O157:H7]
Score: 85.8853
e-value: 1.34424e-20
Tamanho do alinhamento: 123
Cobertura da query: 0.984
****Alinhamento****
####Proteína 162- locus_tag: NGO0923####
Sequencia: gi|54036973|sp|P63726.1|DHSC_SALTI RecName: Full=Succinate dehydrogenas
e cytochrome b556 subunit; Short=Cytochrome b-556 [Salmonella enterica subsp. ente
rica serovar Typhi] >gi|54040872|sp|P63725.1|DHSC_SALTY RecName: Full=Succinate de
hydrogenase cytochrome b556 subunit; Short=Cytochrome b-556 [Salmonella enterica s
ubsp. enterica serovar Typhimurium str. LT2]
Score: 82.8037
e-value: 1.82039e-19
Tamanho do alinhamento: 123
Cobertura da query: 0.984
****Alinhamento****
####Proteína 162- locus_tag: NGO0923####
Sequencia: gi|2493412|sp|Q59659.1|DHSC_PARDE RecName: Full=Succinate dehydrogenase
cytochrome b556 subunit; Short=Cytochrome b-556 [Paracoccus denitrificans]
Score: 68.5514
e-value: 3.65518e-14
Tamanho do alinhamento: 113
Cobertura da query: 0.904
****Alinhamento****
####Proteína 162- locus_tag: NGO0923####
Sequencia: gi|1706427|sp|P51055.1|DHSC_COXBU RecName: Full=Succinate dehydrogenase
cytochrome b556 subunit; Short=Cytochrome b-556 [Coxiella burnetii RSA 493]
Score: 63.929
e-value: 1.62697e-12
Tamanho do alinhamento: 121

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- NGO0924

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0925

```

****Alinhamento****
####Proteina 164- locus_tag: NGO0925####
Sequencia: gi|118671|sp|P11959.2|DLDH1_GEOSE RecName: Full=Dihydrolipoyl dehydroge
nase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of
pyruvate complex [Geobacillus stearothermophilus]
Score: 181.03
e-value: 1.6477e-49
Tamanho do alinhamento: 458
Cobertura da query: 0.980728051392
****Alinhamento****
####Proteina 164- locus_tag: NGO0925####
Sequencia: gi|118672|sp|P21880.1|DLDH1_BACSU RecName: Full=Dihydrolipoyl dehydroge
nase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of
pyruvate complex; AltName: Full=S complex, 50 kDa subunit [Bacillus subtilis subsp
. subtilis str. 168]
Score: 178.333
e-value: 1.81461e-48
Tamanho do alinhamento: 455
Cobertura da query: 0.974304068522
****Alinhamento****
####Proteina 164- locus_tag: NGO0925####
Sequencia: gi|7531099|sp|O84561.1|DLDH_CHLTR RecName: Full=Dihydrolipoyl dehydroge
nase; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=E3 component of
2-oxoglutarate dehydrogenase complex [Chlamydia trachomatis D/UW-3/CX]
Score: 174.481
e-value: 4.35879e-47
Tamanho do alinhamento: 464
Cobertura da query: 0.993576017131
****Alinhamento****
####Proteina 164- locus_tag: NGO0925####
Sequencia: gi|300669691|sp|Q04829.3|DLDH_HALVD RecName: Full=Dihydrolipoyl dehydro
genase; AltName: Full=Dihydrolipoamide dehydrogenase [Haloferax volcanii DS2]
Score: 170.629
e-value: 1.21139e-45

```

○ NGO0926

****Alinhamento****

####Proteína 165- locus_tag: NGO0926####

Sequencia: gi|1723174|sp|P44758.1|PRX5_HAEIN RecName: Full=Hybrid peroxiredoxin hy Prx5; AltName: Full=Thioredoxin reductase [Haemophilus influenzae Rd KW20]

Score: 382.489

e-value: 3.35489e-133

Tamanho do alinhamento: 236

Cobertura da query: 0.963265306122

****Alinhamento****

####Proteína 165- locus_tag: NGO0926####

Sequencia: gi|387942496|sp|B3EWI1.1|GSPRX_MARGR RecName: Full=Glutathione amide-dependent peroxidase; Short=Prx/Grx [Marichromatium gracile]

Score: 315.464

e-value: 1.14324e-106

Tamanho do alinhamento: 242

Cobertura da query: 0.987755102041

****Alinhamento****

####Proteína 165- locus_tag: NGO0926####

Sequencia: gi|3915480|sp|P73728.1|Y1621_SYNY3 RecName: Full=Putative peroxiredoxin sll1621; AltName: Full=Thioredoxin reductase [Synechocystis sp. PCC 6803 substr. K azusa]

Score: 207.223

e-value: 3.53251e-65

Tamanho do alinhamento: 171

Cobertura da query: 0.697959183673

****Alinhamento****

####Proteína 165- locus_tag: NGO0926####

Sequencia: gi|38503409|sp|O69777.2|YRP2_RHIET RecName: Full=Putative peroxiredoxin in rpoN2 3'region; AltName: Full=Thioredoxin reductase [Rhizobium etli]

Score: 173.711

e-value: 2.97525e-52

Tamanho do alinhamento: 170

Cobertura da query: 0.69387755102

****Alinhamento****

####Proteína 165- locus_tag: NGO0926####

Sequencia: gi|2496756|sp|Q53212.1|Y4VD_RHISN RecName: Full=Putative peroxiredoxin

○ NGO0927

****Alinhamento****

####Proteína 166- locus_tag: NGO0927####

Sequencia: gi|74676436|sp|Q07351.2|STP4_YEAST RecName: Full=zinc finger protein STP4 [Saccharomyces cerevisiae S288c]

Score: 31.187

e-value: 0.354833

Tamanho do alinhamento: 47

Cobertura da query: 0.87037037037

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○ NGO0929

****Alinhamento****

####Proteina 168- locus_tag: NGO0929####

Sequencia: gi|81784704|sp|Q9JZQ3.1|METF_NEIMB RecName: Full=5,10-methylenetetrahydrofolate reductase [Neisseria meningitidis MC58]

Score: 597.045

e-value: 0.0

Tamanho do alinhamento: 292

Cobertura da query: 1.0

****Alinhamento****

####Proteina 168- locus_tag: NGO0929####

Sequencia: gi|1170934|sp|P45208.1|METF_HAEIN RecName: Full=5,10-methylenetetrahydrofolate reductase [Haemophilus influenzae Rd KW20]

Score: 516.153

e-value: 0.0

Tamanho do alinhamento: 292

Cobertura da query: 1.0

****Alinhamento****

####Proteina 168- locus_tag: NGO0929####

Sequencia: gi|84028093|sp|P0AEZ1.1|METF_ECOLI RecName: Full=5,10-methylenetetrahydrofolate reductase [Escherichia coli K-12] >gi|84028094|sp|P0AEZ2.1|METF_SHIFL RecName: Full=5,10-methylenetetrahydrofolate reductase [Shigella flexneri]

Score: 452.21

e-value: 5.00161e-159

Tamanho do alinhamento: 290

Cobertura da query: 0.993150684932

****Alinhamento****

####Proteina 168- locus_tag: NGO0929####

Sequencia: gi|20141497|sp|P11003.2|METF_SALTY RecName: Full=5,10-methylenetetrahydrofolate reductase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

Score: 450.284

e-value: 2.8881e-158

○ NGO0931

```

****Alinhamento****
####Proteina 170- locus_tag: NGO0931####
Sequencia: gi|75507370|sp|Q5F860.1|RL36_NEIG1 RecName: Full=50S ribosomal protein
L36 [Neisseria gonorrhoeae FA 1090] >gi|238690195|sp|B4RL58.1|RL36_NEIG2 RecName:
Full=50S ribosomal protein L36 [Neisseria gonorrhoeae NCCP11945]
Score: 83.1889
e-value: 7.8923e-22
Tamanho do alinhamento: 41
Cobertura da query: 1.0
****Alinhamento****
####Proteina 170- locus_tag: NGO0931####
Sequencia: gi|54039021|sp|P66295.1|RL362_NEIMB RecName: Full=50S ribosomal protein
L36 2 [Neisseria meningitidis MC58] >gi|54041912|sp|P66294.1|RL362_NEIMA RecName:
Full=50S ribosomal protein L36 2 [Neisseria meningitidis Z2491] >gi|205831045|sp|A
1KTL0.1|RL362_NEIMF RecName: Full=50S ribosomal protein L36 2 [Neisseria meningiti
dis FAM18]
Score: 82.4185
e-value: 1.69924e-21
Tamanho do alinhamento: 41
Cobertura da query: 1.0
****Alinhamento****
####Proteina 170- locus_tag: NGO0931####
Sequencia: gi|205831044|sp|A9M4E0.1|RL362_NEIM0 RecName: Full=50S ribosomal protei
n L36 2 [Neisseria meningitidis 053442]
Score: 81.6481
e-value: 3.94496e-21
Tamanho do alinhamento: 41
Cobertura da query: 1.0
****Alinhamento****
####Proteina 170- locus_tag: NGO0931####
Sequencia: gi|54039227|sp|P66310.1|RL36_XANCP RecName: Full=50S ribosomal protein
L36 [Xanthomonas campestris pv. campestris str. ATCC 33913] >gi|54041917|sp|P66309
.1|RL36_XANAC RecName: Full=50S ribosomal protein L36 [Xanthomonas axonopodis pv.
citri str. 306] >gi|81305782|sp|Q4UVD8.1|RL36_XANC8 RecName: Full=50S ribosomal pr
otein L36 [Xanthomonas campestris pv. campestris str. 8004] >gi|123522146|sp|Q2P3S

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○ NGO0932

```

****Alinhamento****
####Proteina 171- locus_tag: NGO0932####
Sequencia: gi|14916767|sp|O66814.1|Y532_AQUAE RecName: Full=Uncharacterized protei
n Y532; Flags: Precursor [Aquifex aeolicus VF5]
Score: 35.8094
e-value: 0.0622891
Tamanho do alinhamento: 86
Cobertura da query: 0.58904109589
****Alinhamento****
####Proteina 171- locus_tag: NGO0932####
Sequencia: gi|81670836|sp|P73658.1|IOJAP_SYNY3 RecName: Full=Ribosomal silencing f
actor Rsfs [Synechocystis sp. PCC 6803 substr. Kazusa]
Score: 32.7278
e-value: 0.609403
Tamanho do alinhamento: 43
Cobertura da query: 0.294520547945

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- NGO0934

```
****Alinhamento****
####Proteína 173- locus_tag: NGO0934####
Sequencia: gi|166234753|sp|A7MTX1.1|UBIE_VIBCB RecName: Full=Ubiquinone/menaquinon
e biosynthesis C-methyltransferase UbiE; AltName: Full=2-methoxy-6-polyprenyl-1,4-
benzoquinol methylase; AltName: Full=Demethylmenaquinone methyltransferase [Vibrio
campbellii ATCC BAA-1116]
Score: 47.3654
e-value: 1.54068e-05
Tamanho do alinhamento: 100
Cobertura da query: 0.518134715026
****Alinhamento****
####Proteína 173- locus_tag: NGO0934####
Sequencia: gi|48474449|sp|Q8DDP9.1|UBIE_VIBVU RecName: Full=Ubiquinone/menaquinone
biosynthesis C-methyltransferase UbiE; AltName: Full=2-methoxy-6-polyprenyl-1,4-be
nzoquinol methylase; AltName: Full=Demethylmenaquinone methyltransferase [Vibrio v
ulnificus CMCP6] >gi|61217315|sp|Q7MQ33.1|UBIE_VIBVY RecName: Full=Ubiquinone/mena
quinone biosynthesis C-methyltransferase UbiE; AltName: Full=2-methoxy-6-polypreny
l-1,4-benzoquinol methylase; AltName: Full=Demethylmenaquinone methyltransferase [
Vibrio vulnificus YJ016]
Score: 46.9802
e-value: 2.66512e-05
Tamanho do alinhamento: 100
Cobertura da query: 0.518134715026
****Alinhamento****
####Proteína 173- locus_tag: NGO0934####
Sequencia: gi|48474408|sp|Q87TH4.1|UBIE_VIBPA RecName: Full=Ubiquinone/menaquinone
biosynthesis C-methyltransferase UbiE; AltName: Full=2-methoxy-6-polyprenyl-1,4-be
nzoquinol methylase; AltName: Full=Demethylmenaquinone methyltransferase [Vibrio p
arahaemolyticus RIMD 2210633]
Score: 46.2098
e-value: 4.12342e-05
Tamanho do alinhamento: 100
Cobertura da query: 0.518134715026
****Alinhamento****
####Proteína 173- locus_tag: NGO0934####
Sequencia: gi|61217193|sp|Q5QYG2.1|UBIE_IDILO RecName: Full=Ubiquinone/menaquinone
biosynthesis C-methyltransferase UbiE; AltName: Full=2-methoxy-6-polyprenyl-1,4-be
nzoquinol methylase; AltName: Full=Demethylmenaquinone methyltransferase [Idiomari
```

- NGO0937

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0938

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0939

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0941

****Alinhamento****

####Proteína 179- locus_tag: NGO0941####

Sequencia: gi|150421688|sp|P68398.2|TADA_ECOLI RecName: Full=tRNA-specific adenosine deaminase [Escherichia coli K-12] >gi|150421691|sp|P68397.2|TADA_SHIFL RecName: Full=tRNA-specific adenosine deaminase [Shigella flexneri]

Score: 136.346

e-value: 4.31111e-38

Tamanho do alinhamento: 145

Cobertura da query: 0.606694560669

****Alinhamento****

####Proteína 179- locus_tag: NGO0941####

Sequencia: gi|150421686|sp|Q8XA44.2|TADA_EC057 RecName: Full=tRNA-specific adenosine deaminase [Escherichia coli O157:H7] >gi|150421687|sp|Q8FF24.2|TADA_ECOL6 RecName: Full=tRNA-specific adenosine deaminase [Escherichia coli CFT073]

Score: 135.576

e-value: 8.87831e-38

Tamanho do alinhamento: 145

Cobertura da query: 0.606694560669

****Alinhamento****

####Proteína 179- locus_tag: NGO0941####

Sequencia: gi|1175980|sp|P44931.1|TADA_HAEIN RecName: Full=tRNA-specific adenosine deaminase [Haemophilus influenzae Rd KW20]

Score: 134.806

e-value: 2.19688e-37

Tamanho do alinhamento: 144

Cobertura da query: 0.602510460251

****Alinhamento****

####Proteína 179- locus_tag: NGO0941####

Sequencia: gi|150421689|sp|Q8XGY4.2|TADA_SALTI RecName: Full=tRNA-specific adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhi] >gi|150421690|sp|Q7CQ08.2|TADA_SALTY RecName: Full=tRNA-specific adenosine deaminase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]

Score: 132.88

e-value: 1.13031e-36

Tamanho do alinhamento: 145

Cobertura da query: 0.606694560669

****Alinhamento****

○ NGO0942

****Alinhamento****

####Proteína 180- locus_tag: NGO0942####

Sequencia: gi|1731014|sp|P54486.1|YQGC_BACSU RecName: Full=Uncharacterized protein YqgC [Bacillus subtilis subsp. subtilis str. 168]

Score: 65.855

e-value: 9.34029e-13

Tamanho do alinhamento: 145

Cobertura da query: 0.895061728395

○ NGO0942a

****Alinhamento****

####Proteina 181- locus_tag: NGO0942a####

Sequencia: gi|52783329|sp|Q9JZK3.1|RLMB_NEIMB RecName: Full=23S rRNA (guanosine-2'-O-)-methyltransferase RlmB; AltName: Full=23S rRNA (guanosine2251 2'-O)-methyltransferase; AltName: Full=23S rRNA Gm2251 2'-O-methyltransferase [Neisseria meningitidis MC58]

Score: 508.834

e-value: 0.0

Tamanho do alinhamento: 249

Cobertura da query: 0.996

****Alinhamento****

####Proteina 181- locus_tag: NGO0942a####

Sequencia: gi|52783328|sp|Q9JU08.2|RLMB_NEIMA RecName: Full=23S rRNA (guanosine-2'-O-)-methyltransferase RlmB; AltName: Full=23S rRNA (guanosine2251 2'-O)-methyltransferase; AltName: Full=23S rRNA Gm2251 2'-O-methyltransferase [Neisseria meningitidis Z2491]

Score: 508.064

e-value: 0.0

Tamanho do alinhamento: 250

Cobertura da query: 1.0

****Alinhamento****

####Proteina 181- locus_tag: NGO0942a####

Sequencia: gi|52783300|sp|Q7NYX3.1|RLMB_CHRVO RecName: Full=23S rRNA (guanosine-2'-O-)-methyltransferase RlmB; AltName: Full=23S rRNA (guanosine2251 2'-O)-methyltransferase; AltName: Full=23S rRNA Gm2251 2'-O-methyltransferase [Chromobacterium violaceum ATCC 12472]

Score: 382.104

e-value: 6.46991e-133

Tamanho do alinhamento: 246

Cobertura da query: 0.984

****Alinhamento****

####Proteina 181- locus_tag: NGO0942a####

Sequencia: gi|52783303|sp|Q7VTK4.1|RLMB_BORPE RecName: Full=23S rRNA (guanosine-2'-O-)-methyltransferase RlmB; AltName: Full=23S rRNA (guanosine2251 2'-O)-methyltransferase; AltName: Full=23S rRNA Gm2251 2'-O-methyltransferase [Bordetella pertussis Tohama I] >gi|52783304|sp|Q7W7I7.1|RLMB BORPA RecName: Full=23S rRNA (guanosine

○ NGO0948

****Alinhamento****

####Proteína 183- locus_tag: NGO0948####

Sequencia: gi|81784709|sp|Q9JZR5.1|Y928_NEIMB RecName: Full=Uncharacterized protein NMB0928 [Neisseria meningitidis MC58]

Score: 793.882

e-value: 0.0

Tamanho do alinhamento: 398

Cobertura da query: 1.0

****Alinhamento****

####Proteína 183- locus_tag: NGO0948####

Sequencia: gi|123731833|sp|Q35JU7.1|BAMC_THIDA RecName: Full=Outer membrane protein assembly factor BamC; Flags: Precursor [Thiobacillus denitrificans ATCC 25259]

Score: 239.58

e-value: 2.83968e-73

Tamanho do alinhamento: 367

Cobertura da query: 0.922110552764

****Alinhamento****

####Proteína 183- locus_tag: NGO0948####

Sequencia: gi|391737990|sp|C7RSI4.1|BAMC_ACCPU RecName: Full=Outer membrane protein assembly factor BamC; Flags: Precursor [Candidatus Accumolibacter phosphatis clade IIA str. UW-1]

Score: 226.868

e-value: 2.60149e-68

Tamanho do alinhamento: 371

Cobertura da query: 0.93216080402

****Alinhamento****

####Proteína 183- locus_tag: NGO0948####

Sequencia: gi|391737999|sp|A8FW15.1|BAMC_SHESH RecName: Full=Outer membrane protein assembly factor BamC; Flags: Precursor [Shewanella sediminis HAW-EB3]

Score: 37.3502

e-value: 0.186613

○ NGO0949

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****Alinhamento****
####Proteína 184- locus_tag: NGO0949####
Sequencia: gi|1172517|sp|P42786.1|PIP_NEIGO RecName: Full=Proline iminopeptidase;
Short=PIP; AltName: Full=Prolyl aminopeptidase; Short=PAP [Neisseria gonorrhoeae]
Score: 640.958
e-value: 0.0
Tamanho do alinhamento: 310
Cobertura da query: 1.0
****Alinhamento****
####Proteína 184- locus_tag: NGO0949####
Sequencia: gi|12230405|sp|Q9JZR6.1|PIP_NEIMB RecName: Full=Proline iminopeptidase;
Short=PIP; AltName: Full=Prolyl aminopeptidase; Short=PAP [Neisseria meningitidis
MC58]
Score: 621.698
e-value: 0.0
Tamanho do alinhamento: 310
Cobertura da query: 1.0
****Alinhamento****
####Proteína 184- locus_tag: NGO0949####
Sequencia: gi|12230404|sp|Q9JUV1.1|PIP_NEIMA RecName: Full=Proline iminopeptidase;
Short=PIP; AltName: Full=Prolyl aminopeptidase; Short=PAP [Neisseria meningitidis
Z2491]
Score: 618.616
e-value: 0.0
Tamanho do alinhamento: 310
Cobertura da query: 1.0
****Alinhamento****
####Proteína 184- locus_tag: NGO0949####
Sequencia: gi|148880081|sp|P93732.3|PIP_ARATH RecName: Full=Proline iminopeptidase
; Short=PIP; AltName: Full=Prolyl aminopeptidase; Short=PAP [Arabidopsis thaliana]
Score: 348.206
e-value: 1.26147e-116
Tamanho do alinhamento: 311
Cobertura da query: 1.00322580645
****Alinhamento****
####Proteína 184- locus_tag: NGO0949####
Sequencia: gi|12230400|sp|O32449.1|PIP_SERMA RecName: Full=Proline iminopeptidase;

```

○ NGO0950

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

○ NGO0950a

****Alinhamento****

####Proteina 186- locus_tag: NGO0950a####

Sequencia: gi|417412|sp|Q04884.1|OPAH_NEIGO RecName: Full=Opacity protein opA60; F
lags: Precursor, partial [Neisseria gonorrhoeae]

Score: 358.992

e-value: 2.99155e-124

Tamanho do alinhamento: 232

Cobertura da query: 1.0

****Alinhamento****

####Proteina 186- locus_tag: NGO0950a####

Sequencia: gi|129147|sp|P09888.2|OMPC_NEIGO RecName: Full=Outer membrane protein P
.IIC; Short=Protein IIC; Flags: Precursor [Neisseria gonorrhoeae]

Score: 355.525

e-value: 2.69969e-122

Tamanho do alinhamento: 237

Cobertura da query: 1.02155172414

****Alinhamento****

####Proteina 186- locus_tag: NGO0950a####

Sequencia: gi|129222|sp|P11297.1|OP28_NEIGO RecName: Full=Opacity protein V28; Fla
gs: Precursor, partial [Neisseria gonorrhoeae]

Score: 351.673

e-value: 2.07087e-121

Tamanho do alinhamento: 232

Cobertura da query: 1.0

****Alinhamento****

####Proteina 186- locus_tag: NGO0950a####

Sequencia: gi|417407|sp|Q04874.1|OPAB_NEIGO RecName: Full=Opacity protein opA51; F
lags: Precursor, partial [Neisseria gonorrhoeae]

Score: 347.436

e-value: 9.02688e-120

Tamanho do alinhamento: 232

Cobertura da query: 1.0

****Alinhamento****

####Proteina 186- locus_tag: NGO0950a####

Sequencia: gi|417409|sp|Q04878.1|OPAE_NEIGO RecName: Full=Opacity protein opA55; F

- NGO0952

```

****Alinhamento****
####Proteína 187- locus_tag: NGO0952####
Sequencia: gi|81832759|sp|Q7DDB6.1|Y1497_NEIMB RecName: Full=Probable TonB-depende
nt receptor NMB1497; Flags: Precursor [Neisseria meningitidis MC58]
Score: 1828.91
e-value: 0.0
Tamanho do alinhamento: 922
Cobertura da query: 1.0
****Alinhamento****
####Proteína 187- locus_tag: NGO0952####
Sequencia: gi|1175580|sp|P45114.1|Y1217_HAEIN RecName: Full=Probable TonB-dependen
t receptor HI_1217; Flags: Precursor [Haemophilus influenzae Rd KW20]
Score: 942.954
e-value: 0.0
Tamanho do alinhamento: 959
Cobertura da query: 1.04013015184
****Alinhamento****
####Proteína 187- locus_tag: NGO0952####
Sequencia: gi|417861|sp|Q01996.1|TBP1_NEIGO RecName: Full=Transferrin-binding prot
ein 1; Flags: Precursor [Neisseria gonorrhoeae]
Score: 57.7658
e-value: 3.81133e-07
Tamanho do alinhamento: 238
Cobertura da query: 0.258134490239
****Alinhamento****
####Proteína 187- locus_tag: NGO0952####
Sequencia: gi|730894|sp|Q09056.1|TBP11_NEIMI RecName: Full=Transferrin-binding pro
tein 1; Flags: Precursor [Neisseria meningitidis serogroup B]
Score: 57.3806
e-value: 4.36113e-07
Tamanho do alinhamento: 194
Cobertura da query: 0.210412147505
****Alinhamento****
####Proteína 187- locus_tag: NGO0952####
Sequencia: gi|81784983|sp|Q9K0U9.1|TBP1_NEIMB RecName: Full=Transferrin-binding pr
otein 1; Flags: Precursor [Neisseria meningitidis MC58]
Score: 56.225

```

- NGO0953

Para o *e-value* definido não existe nenhum resultado, logo não é possível inferir a função da proteína.

- NGO0955

```

****Alinhamento****
####Proteína 189- locus_tag: NGO0955####
Sequencia: gi|74948303|sp|Q9VP05.2|MEDI1_DROME RecName: Full=Mediator of RNA polyme
rase II transcription subunit 1; AltName: Full=Mediator complex subunit 1; AltName
: Full=dTRAP220 [Drosophila melanogaster]
Score: 30.8018
e-value: 0.592267
Tamanho do alinhamento: 37
Cobertura da query: 0.755102040816

```


○ NGO0956

```

****Alinhamento****
####Proteina 190- locus_tag: NGO0956####
Sequencia: gi|12229624|sp|O69077.2|AK_PSEAE RecName: Full=Aspartokinase; AltName:
Full=Aspartate kinase [Pseudomonas aeruginosa PAO1]
Score: 548.125
e-value: 0.0
Tamanho do alinhamento: 405
Cobertura da query: 1.0
****Alinhamento****
####Proteina 190- locus_tag: NGO0956####
Sequencia: gi|81840468|sp|Q88EI9.1|AK_PSEPK RecName: Full=Aspartate kinase; AltName:
Full=Aspartokinase [Pseudomonas putida KT2440]
Score: 536.954
e-value: 0.0
Tamanho do alinhamento: 404
Cobertura da query: 0.997530864198
****Alinhamento****
####Proteina 190- locus_tag: NGO0956####
Sequencia: gi|635552404|sp|A4VJB4.1|AKLYS_PSEU5 RecName: Full=Aspartate kinase Ask
_LysC; AltName: Full=Aspartokinase [Pseudomonas stutzeri A1501]
Score: 536.569
e-value: 0.0
Tamanho do alinhamento: 404
Cobertura da query: 0.997530864198
****Alinhamento****
####Proteina 190- locus_tag: NGO0956####
Sequencia: gi|635552405|sp|C3JXY0.1|AK_PSEFS RecName: Full=Aspartate kinase; AltName:
Full=Aspartokinase [Pseudomonas fluorescens SBW25]
Score: 533.487
e-value: 0.0
Tamanho do alinhamento: 406
Cobertura da query: 1.0024691358
****Alinhamento****
####Proteina 190- locus_tag: NGO0956####
Sequencia: gi|6225021|sp|O67221.1|AK_AQUAE RecName: Full=Aspartokinase; AltName: Full=
Aspartate kinase [Aquifex aeolicus VF5]
Score: 391.734
e-value: 9.91963e-132

```

○ NGO0957

```

****Alinhamento****
####Proteina 191- locus_tag: NGO0957####
Sequencia: gi|47117813|sp|O61735.3|CLOCK_DROME RecName: Full=Circadian locomotor o
utput cycles protein kaput; AltName: Full=dCLOCK; AltName: Full=dPAS1 [Drosophila
melanogaster]
Score: 30.8018
e-value: 0.615012
Tamanho do alinhamento: 37
Cobertura da query: 0.685185185185

```

○ NGO0959

```
****Alinhamento****
####Proteina 193- locus_tag: NGO0959####
Sequencia: gi|614085506|sp|P9WFC8.1|Y1636_MYCTO RecName: Full=Universal stress pro
tein MT1672 [Mycobacterium tuberculosis CDC1551] >gi|614085511|sp|P9WFC9.1|Y1636_M
YCTU RecName: Full=Universal stress protein Rv1636; Short=USP Rv1636 [Mycobacteriu
m tuberculosis H37Rv]
Score: 67.0106
e-value: 3.17349e-13
Tamanho do alinhamento: 146
Cobertura da query: 0.948051948052
****Alinhamento****
####Proteina 193- locus_tag: NGO0959####
Sequencia: gi|1177001|sp|P42297.1|YXIE_BACSU RecName: Full=Universal stress protei
n YxiE; Short=USP YxiE; Flags: Precursor [Bacillus subtilis subsp. subtilis str. 1
68]
Score: 63.929
e-value: 3.55235e-12
Tamanho do alinhamento: 156
Cobertura da query: 1.01298701299
****Alinhamento****
####Proteina 193- locus_tag: NGO0959####
Sequencia: gi|2501594|sp|Q57997.1|Y577_METJA RecName: Full=Universal stress protei
n MJ0577; Short=USP MJ0577 [Methanocaldococcus jannaschii DSM 2661]
Score: 63.929
e-value: 4.83233e-12
Tamanho do alinhamento: 161
Cobertura da query: 1.04545454545
****Alinhamento****
####Proteina 193- locus_tag: NGO0959####
Sequencia: gi|123761536|sp|Q49YE0.1|Y1056_STAS1 RecName: Full=Putative universal s
tress protein SSP1056 [Staphylococcus saprophyticus subsp. saprophyticus ATCC 1530
5]
Score: 57.7658
e-value: 6.84846e-10
```

○ NGO0960

```
****Alinhamento****
####Proteina 194- locus_tag: NGO0960####
Sequencia: gi|2495206|sp|Q46927.1|TCDA_ECOLI RecName: Full=tRNA threonylcarbamoyla
denosine dehydratase; AltName: Full=t(6)A37 dehydratase [Escherichia coli K-12]
Score: 262.307
e-value: 2.40046e-85
Tamanho do alinhamento: 253
Cobertura da query: 0.980620155039
****Alinhamento****
####Proteina 194- locus_tag: NGO0960####
Sequencia: gi|2495207|sp|Q57097.1|TCDA_HAEIN RecName: Full=tRNA threonylcarbamoyla
denosine dehydratase; AltName: Full=t(6)A37 dehydratase [Haemophilus influenzae Rd
KW20]
Score: 254.603
e-value: 1.71355e-82
Tamanho do alinhamento: 250
Cobertura da query: 0.968992248062
****Alinhamento****
####Proteina 194- locus_tag: NGO0960####
Sequencia: gi|281312490|sp|O32037.3|TCDA_BACSU RecName: Full=tRNA threonylcarbamoyl
adenosine dehydratase; AltName: Full=t(6)A37 dehydratase [Bacillus subtilis subsp
. subtilis str. 168]
Score: 125.176
e-value: 1.12022e-32
Tamanho do alinhamento: 147
Cobertura da query: 0.56976744186
****Alinhamento****
####Proteina 194- locus_tag: NGO0960####
Sequencia: gi|731629|sp|P38756.1|TCD1_YEAST RecName: Full=tRNA threonylcarbamoyla
denosine dehydratase 1; AltName: Full=t(6)A37 dehydratase 1 [Saccharomyces cerevisi
ae S288c]
Score: 88.5817
e-value: 7.96106e-19
```

○ NGO0961

****Alinhamento****

####Proteína 195- locus_tag: NGO0961####

Sequencia: gi|81438522|sp|Q87BI4.1|SCPA_XYLFT RecName: Full=Segregation and condensation protein A [Xylella fastidiosa Temecula1]

Score: 237.854

e-value: 6.02844e-75

Tamanho do alinhamento: 265

Cobertura da query: 0.933098591549

****Alinhamento****

####Proteína 195- locus_tag: NGO0961####

Sequencia: gi|158706360|sp|Q9PAP4.2|SCPA_XYLFA RecName: Full=Segregation and condensation protein A [Xylella fastidiosa 9a5c]

Score: 237.269

e-value: 8.50899e-75

Tamanho do alinhamento: 256

Cobertura da query: 0.901408450704

****Alinhamento****

####Proteína 195- locus_tag: NGO0961####

Sequencia: gi|81629001|sp|Q83CP8.1|SCPA_COXBU RecName: Full=Segregation and condensation protein A [Coxiella burnetii RSA 493]

Score: 222.246

e-value: 1.97223e-69

Tamanho do alinhamento: 247

Cobertura da query: 0.869718309859

****Alinhamento****

####Proteína 195- locus_tag: NGO0961####

Sequencia: gi|254767840|sp|C0ZC76.1|SCPA_BREBN RecName: Full=Segregation and condensation protein A [Brevibacillus brevis NBRC 100599]

Score: 146.747

e-value: 1.47302e-40

Tamanho do alinhamento: 254

Cobertura da query: 0.894366197183

****Alinhamento****

####Proteína 195- locus_tag: NGO0961####

○ NGO0968

****Alinhamento****

####Proteina 198- locus_tag: NGO0968####

Sequencia: gi|84028669|sp|P0AEQ8.1|GLNP_EC057 RecName: Full=Glutamine transport system permease protein GlnP [Escherichia coli O157:H7] >gi|84028670|sp|P0AEQ7.1|GLNP_EC06 RecName: Full=Glutamine transport system permease protein GlnP [Escherichia coli CFT073] >gi|84028671|sp|P0AEQ6.1|GLNP_EC01 RecName: Full=Glutamine transport system permease protein GlnP [Escherichia coli K-12] >gi|84028672|sp|P0AEQ9.1|GLNP_SHIFL RecName: Full=Glutamine transport system permease protein GlnP [Shigella flexneri]

Score: 128.257

e-value: 2.6394e-34

Tamanho do alinhamento: 246

Cobertura da query: 0.991935483871

****Alinhamento****

####Proteina 198- locus_tag: NGO0968####

Sequencia: gi|84027923|sp|P0AFT3.1|YECS_EC06 RecName: Full=Inner membrane amino-acid ABC transporter permease protein YecS [Escherichia coli CFT073] >gi|84027924|sp|P0AFT2.1|YECS_EC01 RecName: Full=Inner membrane amino-acid ABC transporter permease protein YecS [Escherichia coli K-12] >gi|84027925|sp|P0AFT4.1|YECS_SHIFL RecName: Full=Inner membrane amino-acid ABC transporter permease protein YecS [Shigella flexneri]

Score: 119.013

e-value: 8.33516e-31

Tamanho do alinhamento: 233

Cobertura da query: 0.939516129032

****Alinhamento****

####Proteina 198- locus_tag: NGO0968####

Sequencia: gi|81815748|sp|O34671.1|GLNM_BACSU RecName: Full=Probable glutamine ABC transporter permease protein GlnM [Bacillus subtilis subsp. subtilis str. 168]

Score: 115.546

e-value: 1.44285e-29

Tamanho do alinhamento: 242

Cobertura da query: 0.975806451613

****Alinhamento****

○ NGO0969

****Alinhamento****

####Proteina 199- locus_tag: NGO0969####

Sequencia: gi|50401478|sp|Q7BSX4.1|YFI3_EC057 RecName: Full=Uncharacterized endonuclease; Flags: Precursor [Escherichia coli O157:H7]

Score: 86.6557

e-value: 1.38402e-19

Tamanho do alinhamento: 136

Cobertura da query: 0.583690987124

****Alinhamento****

####Proteina 199- locus_tag: NGO0969####

Sequencia: gi|1175987|sp|Q99342.1|YFI3_ECOLX RecName: Full=Uncharacterized endonuclease; AltName: Full=ORFA; Flags: Precursor [Escherichia coli]

Score: 86.2705

e-value: 1.84737e-19

Tamanho do alinhamento: 136

Cobertura da query: 0.583690987124

****Alinhamento****

####Proteina 199- locus_tag: NGO0969####

Sequencia: gi|2501229|sp|Q57519.1|Y1296_HAEIN RecName: Full=Uncharacterized endonuclease HI_1296; Flags: Precursor [Haemophilus influenzae Rd KW20]

Score: 85.5001

e-value: 5.17532e-19

Tamanho do alinhamento: 145

Cobertura da query: 0.622317596567

****Alinhamento****

####Proteina 199- locus_tag: NGO0969####

Sequencia: gi|266681|sp|P29769.1|NUC_SHIFL RecName: Full=Micrococcal nuclease; Flags: Precursor [Shigella flexneri]

Score: 83.5741

e-value: 2.14626e-18

Tamanho do alinhamento: 160

Cobertura da query: 0.68669527897