Anexos

Informações Genbank do genoma do S. aureus N315

Id: BA000018.3

Name: BA000018

Description: Staphylococcus aureus subsp. aureus N315 DNA, complete genome

Annotations:

- 'molecule_type': 'DNA' 'topology': 'circular',
- 'data_file_division': 'BCT',
- 'date': '07-OCT-2016',
- 'accessions': ['BA000018', 'AP003129-AP003138'],
- 'sequence_version': 3,
- 'keywords': [''],
- 'source': 'Staphylococcus aureus subsp. aureus N315',
- 'organism': 'Staphylococcus aureus subsp. aureus N315',
- 'taxonomy': ['Bacteria', 'Firmicutes', 'Bacilli', 'Bacillales', 'Staphylococcaceae', 'Staphylococcus'],
- 'references': [Reference(title='Whole genome sequencing of meticillin-resistant Staphylococcus aureus', ...), Reference(title='Direct Submission', ...)],
- 'comment': 'On or before Nov 5, 2004 this sequence version replaced AP003129.2,\nAP003130.2, AP003131.2, AP003132.2, AP003133.2, AP003134.2,\nAP003135.2, AP003136.2, AP003137.2, AP003138.2.'

DBXrefs: ['BioProject:PRJNA264', 'BioSample:SAMD00061099']

Genes essenciais (pelo modelo do Optflux) sem homologia no genoma humano (OrderedLocusNames e respetivo e-value)

[['SA0016', 0.253085],
['SA0176', 0.174251],
['SA0177', 0.0700738],
['SA0178', 0.0772464],
['SA0179', 0.309651],
['SA0344', 0.570958],
['SA0345', 0.123391],
['SA0346', 0.0883758],
['SA0419', 0.0869642],
['SA0439', 0.10084],
['SA0457', 0.267056],
['SA0473', 0.0911547],
['SA0474', 0.425756],
['SA0512', 0.285471],
['SA0547', 0.769982],
['SA0593', 0.733756],
['SA0594', 0.219757],
['SA0596', 0.0753623],
['SA0669', 0.08767],
['SA0670', 0.543606],
['SA0683', 0.128109],
['SA0693', 0.740484],
['SA0793', 0.288315],
['SA0794', 0.326249],
['SA0795', 0.0533705],
['SA0842', 0.0526714],
['SA0865', 0.201971],
['SA0910', 0.215554],
['SA0911', 0.116035],
['SA0913', 0.254344],
['SA0916', 0.408854],
['SA0919', 0.0633448],
['SA0920', 0.611704],
['SA0924', 0.14368],
['SA0938', 0.067339],
['SA0965', 0.0511052],
['SA0996', 0.747054],

['SA0997', 0.638148],
['SA1104', 0.205002],
['SA1115', 0.0699459],
['SA1164', 0.085164],
['SA1165', 0.245048],
['SA1177', 1.87107],
['SA1197', 0.289576],
['SA1199', 0.107574],
['SA1201', 0.23003],
['SA1202', 0.715529],
['SA1203', 0.163862]]
[['SA0016', 0.281624],
['SA0134', 0.0545394],
['SA0176', 0.901747],
['SA0178', 0.626128],
['SA0179', 0.0531147],
['SA0344', 0.0599982],
['SA0345', 0.160552],
['SA0346', 0.372101],
['SA0375', 0.277368],
['SA0376', 1.02961],
['SA0439', 0.0659293],
['SA0458', 0.0967526],
['SA0487', 0.350747],
['SA0547', 0.0598298],
['SA0548', 0.0506916],
['SA0549', 0.140952],
['SA0592', 0.13308],
['SA0593', 1.18195],
['SA0594', 0.889915],
['SA0597', 0.244495],
['SA0669', 0.359165],
['SA0670', 0.0679558],
['SA0793', 0.220178],
['SA0794', 0.0759321],
['SA0795', 1.44111],
['SA0796', 0.312388],

['SA0843', 0.240757],
['SA0910', 0.0793319],
['SA0911', 0.808787],
['SA0916', 0.429948],
['SA0919', 0.247518],
['SA0920', 0.0971463],
['SA0921', 0.112943],
['SA0923', 0.252724],
['SA0924', 0.955198],
['SA0925', 0.102962],
['SA0926', 0.145853],
['SA0937', 0.0758166],
['SA0965', 1.24871],
['SA0994', 0.588693],
['SA0996', 0.274383],
['SA1065', 0.588667],
['SA1088', 0.0849591],
['SA1104', 1.25614],
['SA1115', 0.30158],
['SA1126', 0.391652],
['SA1150', 0.539172],
['SA1165', 0.280725],
['SA1177', 0.603203],
['SA1197', 0.558275],
['SA1199', 0.454343],
['SA1201', 0.512763],
['SA1203', 0.138754]]
['SA1204', 0.281624]
['SA1205', 0.0545394]
['SA1226', 0.901747]
['SA1228', 0.626128]
['SA1229', 0.0531147]
['SA1245', 0.0599982]
['SA1250', 0.160552]
['SA1259', 0.372101]
['SA1298', 0.277368]
['SA1299', 1.02961]

['SA1306', 0.0659293]   ['SA1650', 0.0793319]   ['SA2341', 1.25614]

['SA1346', 0.0967526]   ['SA1651', 0.808787]   ['SA2347', 0.30158]

['SA1397', 0.350747]   ['SA1728', 0.429948]   ['SA2406', 0.391652]

['SA1424', 0.0598298]   ['SA1735', 0.247518]   ['SA2412', 0.539172]

['SA1427', 0.0506916]   ['SA1749', 0.0971463]   ['SA2456', 0.280725]

['SA1439', 0.140952]   ['SA1858', 0.112943]   ['SA2465', 0.603203]

['SA1461', 0.13308]   ['SA1861', 0.252724]   ['SA2466', 0.558275]

['SA1487', 1.18195]   ['SA1863', 0.955198]   ['SA2467', 0.454343]

['SA1492', 0.889915]   ['SA1864', 0.102962]   ['SA2468', 0.512763]

['SA1494', 0.244495]   ['SA1865', 0.145853]   ['SA2471', 0.138754]

['SA1496', 0.359165]   ['SA1938', 0.0758166]

['SA1522', 0.0679558]   ['SA1965', 1.24871]

['SA1571', 0.220178]   ['SA2027', 0.588693]

['SA1585', 0.0759321]   ['SA2136', 0.274383]

['SA1587', 0.312388]   ['SA2288', 0.588667]

['SA1589', 0.240757]   ['SA2333', 0.0849591]

Genes essenciais tanto para o Optflux e para o DEG Sem Homologia com o genoma Humano

'SA0179', 0.309651   'SA1177', 1.87107   'SA1728', 0.429948

'SA0457', 0.267056   'SA1204', 0.281624   'SA2027', 0.588693

'SA0924', 0.14368   'SA1259', 0.372101   'SA2406', 0.391652

'SA0997', 0.638148   'SA1492', 0.889915   'SA1522', 0.0679558

'SA1104', 0.205002   'SA1494', 0.244495   'SA1346', 0.096752

Dihidrofolato redutase - UniProt

accessions : ['P99079', 'P10167']

annotation_update : ('05-DEC-2018', 89)

comments : ['FUNCTION: Key enzyme in folate metabolism. Catalyzes an essential reaction for de novo glycine and purine synthesis, and for DNA precursor synthesis (By similarity). {ECO:0000250}.', 'CATALYTIC ACTIVITY: Reaction=(6S)-5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-   dihydrofolate + H(+) + NADPH; Xref=Rhea:RHEA:15009,   ChEBI:CHEBI:15378, ChEBI:CHEBI:57451, ChEBI:CHEBI:57453,   ChEBI:CHEBI:57783, ChEBI:CHEBI:58349; EC=1.5.1.3; Evidence={ECO:0000255|PROSITE-ProRule:PRU00660};', 'PATHWAY: Cofactor biosynthesis; tetrahydrofolate biosynthesis; 5,6,7,8-tetrahydrofolate from 7,8-dihydrofolate: step 1/1.', 'SIMILARITY: Belongs to the dihydrofolate reductase family. {ECO:0000305}.']

created : ('01-MAR-2005', 0)

cross_references : [('EMBL', 'BA000018', 'BAB42519.1', '-', 'Genomic_DNA'), ('RefSeq', 'WP_000175746.1', 'NC_002745.2'), ('ProteinModelPortal', 'P99079', '-'), ('SMR', 'P99079', '-'), ('SWISS-2DPAGE', 'P99079', '-'), ('EnsemblBacteria', 'BAB42519', 'BAB42519', 'BAB42519'), ('KEGG', 'sau:SA1259', '-'), ('HOGENOM', 'HOG000040233', '-'), ('KO', 'K00287', '-'), ('OMA', 'RDNQLPW', '-'), ('BioCyc', 'SAUR158879:G1G21-1440-MONOMER', '-'), ('UniPathway', 'UPA00077', 'UER00158'), ('Proteomes', 'UP000000751', 'Chromosome'), ('GO', 'GO:0004146', 'F:dihydrofolate reductase activity', 'IEA:UniProtKB-EC'), ('GO', 'GO:0050661', 'F:NADP binding', 'IEA:InterPro'), ('GO', 'GO:0006545', 'P:glycine biosynthetic process', 'IEA:InterPro'), ('GO', 'GO:0006730', 'P:one-carbon metabolic process', 'IEA:UniProtKB-KW'), ('GO', 'GO:0046654', 'P:tetrahydrofolate biosynthetic process', 'IEA:UniProtKB-UniPathway'), ('CDD', 'cd00209', 'DHFR', '1'), ('Gene3D', '3.40.430.10', '-', '1'), ('InterPro', 'IPR012259', 'DHFR'), ('InterPro', 'IPR024072', 'DHFR-like_dom_sf'), ('InterPro', 'IPR017925', 'DHFR_CS'), ('InterPro', 'IPR001796', 'DHFR_dom'), ('PANTHER', 'PTHR22778:SF16', 'PTHR22778:SF16', '1'), ('Pfam', 'PF00186', 'DHFR_1', '1'), ('PIRSF', 'PIRSF000194', 'DHFR', '1'), ('SUPFAM', 'SSF53597', 'SSF53597', '1'), ('PROSITE', 'PS00075', 'DHFR_1', '1'), ('PROSITE', 'PS51330', 'DHFR_2', '1')]

data_class : Reviewed

description : RecName: Full=Dihydrofolate reductase; Short=DHFR; EC=1.5.1.3;

entry_name : DYR_STAAN

features : [('INIT_MET', 1, 1, 'Removed. {ECO:0000250}.', ''), ('CHAIN', 2, 159, 'Dihydrofolate reductase.', 'PRO_0000186408'), ('DOMAIN', 2, 157, 'DHFR. {ECO:0000255|PROSITE- ProRule:PRU00660}.', ''), ('NP_BIND', 7, 8, 'NADP. {ECO:0000250}.', ''), ('NP_BIND', 15, 20, 'NADP. {ECO:0000250}.', ''), ('NP_BIND', 44, 47, 'NADP. {ECO:0000250}.', ''), ('NP_BIND', 63, 66, 'NADP. {ECO:0000250}.', ''), ('NP_BIND', 93, 98, 'NADP. {ECO:0000250}.', ''), ('REGION', 6, 8, 'Substrate binding. {ECO:0000250}.', ''), ('BINDING', 28, 28, 'Substrate. {ECO:0000250}.', ''), ('BINDING', 58, 58, 'Substrate. {ECO:0000250}.', ''), ('BINDING', 112, 112, 'Substrate. {ECO:0000250}.', '')]

gene_name : Name=folA; OrderedLocusNames=SA1259;

host_organism : []

host_taxonomy_id : []

keywords : ['Complete proteome', 'NADP', 'One-carbon metabolism', 'Oxidoreductase']

molecule_type : None

organelle :

organism : Staphylococcus aureus (strain N315).

organism_classification : ['Bacteria', 'Firmicutes', 'Bacilli', 'Bacillales', 'Staphylococcaceae', 'Staphylococcus']

protein_existence : 1

references :

> Authors: Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.
>
> comments: [('STRAIN', 'N315')]
>
> location: Lancet 357:1225-1240(2001).
>
> number: 1

positions: ['NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].']

references: [('PubMed', '11418146'), ('DOI', '10.1016/S0140-6736(00)04403-2')]

title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

Authors: Scherl A., Francois P., Bento M., Deshusses J.M., Charbonnier Y., Converset V., Huyghe A., Walter N., Hoogland C., Appel R.D., Sanchez J.-C., Zimmermann-Ivol C.G., Corthals G.L., Hochstrasser D.F., Schrenzel J.

comments: [('STRAIN', 'N315')]

location: J. Microbiol. Methods 60:247-257(2005).

number: 2

positions: ['IDENTIFICATION BY MASS SPECTROMETRY.']

references: [('PubMed', '15590099'), ('DOI', '10.1016/j.mimet.2004.09.017')]

title: Correlation of proteomic and transcriptomic profiles of Staphylococcus aureus during the post-exponential phase of growth.

Authors: Vaezzadeh A.R., Deshusses J., Lescuyer P., Hochstrasser D.F.

comments: [('STRAIN', 'N315')]

location: Submitted (OCT-2007) to UniProtKB.

number: 3

positions: ['IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].']

references: []

title: Shotgun proteomic analysis of total and membrane protein extracts of S. aureus strain N315.

seqinfo : (159, 18251, '811898409FEAFAAB'

sequence :
MTLSILVAHDLQRVIGFENQLPWHLPNDLKHVKKLSTGHTLVMGRKTFESIGKPLPNRRNVVLTSDTSFNVEGVDVIHSIEDIYQLPGHVFIFGGQTLFEE
MIDKVDDMYITVIEGKFRGDTFFPPYTFEDWEVASSVEGKLDEKNTIPHTFLHLIRKK

sequence_length : 159

sequence_update : ('23-JAN-2007', 2)

taxonomy_id : ['158879']

Glutamate racemase - UniProt

accessions : ['P63638', 'Q99UV6']

annotation_update : ('05-DEC-2018', 85)

comments : ['FUNCTION: Provides the (R)-glutamate required for cell wall biosynthesis. {ECO:0000255|HAMAP-Rule:MF_00258}.', 'CATALYTIC ACTIVITY: Reaction=L-glutamate = D-glutamate; Xref=Rhea:RHEA:12813,   ChEBI:CHEBI:29985, ChEBI:CHEBI:29986; EC=5.1.1.3; Evidence={ECO:0000255|HAMAP-Rule:MF_00258};', 'PATHWAY: Cell wall biogenesis; peptidoglycan biosynthesis. {ECO:0000255|HAMAP-Rule:MF_00258}.', 'SIMILARITY: Belongs to the aspartate/glutamate racemases family. {ECO:0000255|HAMAP-Rule:MF_00258}.']

created : ('11-OCT-2004', 0)

cross_references : [('EMBL', 'BA000018', 'BAB42246.1', '-', 'Genomic_DNA'), ('PIR', 'B89886', 'B89886'), ('RefSeq', 'WP_001039659.1', 'NC_002745.2'), ('ProteinModelPortal', 'P63638', '-'), ('SMR', 'P63638', '-'), ('EnsemblBacteria', 'BAB42246', 'BAB42246', 'BAB42246'), ('KEGG', 'sau:SA0997', '-'), ('HOGENOM', 'HOG000262396', '-'), ('KO', 'K01776', '-'), ('OMA', 'VYGCTHY', '-'), ('BioCyc', 'SAUR158879:G1G21-1138-MONOMER', '-'), ('UniPathway', 'UPA00219', '-'), ('Proteomes', 'UP000000751', 'Chromosome'), ('GO', 'GO:0008881', 'F:glutamate racemase activity', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0071555', 'P:cell wall organization', 'IEA:UniProtKB-KW'), ('GO', 'GO:0009252', 'P:peptidoglycan biosynthetic process', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0008360', 'P:regulation of cell shape', 'IEA:UniProtKB-KW'), ('HAMAP', 'MF_00258', 'Glu_racemase', '1'), ('InterPro', 'IPR015942', 'Asp/Glu/hydantoin_racemase'), ('InterPro', 'IPR001920', 'Asp/Glu_race'), ('InterPro', 'IPR018187', 'Asp/Glu_racemase_AS_1'), ('InterPro', 'IPR033134', 'Asp/Glu_racemase_AS_2'), ('InterPro', 'IPR004391', 'Glu_race'), ('PANTHER', 'PTHR21198:SF2', 'PTHR21198:SF2', '1'), ('Pfam', 'PF01177', 'Asp_Glu_race', '1'), ('SUPFAM', 'SSF53681', 'SSF53681', '2'), ('TIGRFAMs', 'TIGR00067', 'glut_race', '1'), ('PROSITE', 'PS00923', 'ASP_GLU_RACEMASE_1', '1'), ('PROSITE', 'PS00924', 'ASP_GLU_RACEMASE_2', '1')]

data_class : Reviewed

description : RecName: Full=Glutamate racemase {ECO:0000255|HAMAP-Rule:MF_00258}; EC=5.1.1.3 {ECO:0000255|HAMAP-Rule:MF_00258};

entry_name : MURI_STAAN

features : [('CHAIN', 1, 266, 'Glutamate racemase.', 'PRO_0000095509'), ('REGION', 9, 10, 'Substrate binding. {ECO:0000255|HAMAP- Rule:MF_00258}.', ''), ('REGION', 41, 42, 'Substrate binding. {ECO:0000255|HAMAP- Rule:MF_00258}.', ''), ('REGION', 73, 74, 'Substrate binding. {ECO:0000255|HAMAP- Rule:MF_00258}.', ''), ('REGION', 185, 186, 'Substrate binding. {ECO:0000255|HAMAP- Rule:MF_00258}.', ''), ('ACT_SITE', 72, 72, 'Proton donor/acceptor. {ECO:0000255|HAMAP- Rule:MF_00258}.', ''), ('ACT_SITE', 184, 184, 'Proton donor/acceptor. {ECO:0000255|HAMAP-Rule:MF_00258}.', '')]

gene_name : Name=murI {ECO:0000255|HAMAP-Rule:MF_00258}; OrderedLocusNames=SA0997;

host_organism : []

host_taxonomy_id : []

keywords : ['Cell shape', 'Cell wall biogenesis/degradation', 'Complete proteome', 'Isomerase', 'Peptidoglycan synthesis']

molecule_type : None

organelle :

organism : Staphylococcus aureus (strain N315).

organism_classification : ['Bacteria', 'Firmicutes', 'Bacilli', 'Bacillales', 'Staphylococcaceae', 'Staphylococcus']

protein_existence : 1

references :

Authors: Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.

comments: [('STRAIN', 'N315')]

location: Lancet 357:1225-1240(2001).

number: 1

positions: ['NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].']

references: [('PubMed', '11418146'), ('DOI', '10.1016/S0140-6736(00)04403-2')]

title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

Authors: Vaezzadeh A.R., Deshusses J., Lescuyer P., Hochstrasser D.F.

comments: [('STRAIN', 'N315')]

location: Submitted (OCT-2007) to UniProtKB.

number: 2

positions: ['IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].']

references: []

title: Shotgun proteomic analysis of total and membrane protein extracts of S. aureus strain N315.

seqinfo : (266, 29698, '93BC35DB4A2C7B0E')

sequence :
MNKPIGVIDSGVGGLTVAKEIMRQLPNETIYYLGDIGRCPYGPRPGEQVKQYTVEIARKLMEFDIKMLVIACNTATAVALEYLQKTLSIPVIGVIEPGART
AIMTTRNQNVLVLGTEGTIKSEAYRTHIKRINPHVEVHGVACPGFVPLVEQMRYSDPTITSIVIHQTLKRWRNSESDTVILGCTHYPLLYKPIYDYFGGKKT
VISSGLETAREVSALLTFSNEHASYTEHPDHRFFATGDPTHITNIIKEWLNLSVNVERISVND

sequence_length : 266

sequence_update : ('11-OCT-2004', 1)

taxonomy_id : ['158879']

UDP-N-acetylglucosamine – UniProt

accessions : ['Q7A7B4']

annotation_update : ('05-DEC-2018', 102)

comments : ['FUNCTION: Catalyzes the last two sequential reactions in the de novo biosynthetic pathway for UDP-N-acetylglucosamine (UDP- GlcNAc). The C-terminal domain catalyzes the transfer of acetyl group from acetyl coenzyme A to glucosamine-1-phosphate (GlcN-1-P) to produce N-acetylglucosamine-1-phosphate (GlcNAc-1-P), which is converted into UDP-GlcNAc by the transfer of uridine 5- monophosphate (from uridine 5-triphosphate), a reaction catalyzed by the N-terminal domain. {ECO:0000255|HAMAP-Rule:MF_01631}.', 'CATALYTIC ACTIVITY: Reaction=acetyl-CoA + alpha-D-glucosamine 1-phosphate = CoA + H(+) + N-acetyl-alpha-D-glucosamine 1-phosphate; Xref=Rhea:RHEA:13725, ChEBI:CHEBI:15378, ChEBI:CHEBI:57287, ChEBI:CHEBI:57288, ChEBI:CHEBI:57776, ChEBI:CHEBI:58516; EC=2.3.1.157; Evidence={ECO:0000255|HAMAP-Rule:MF_01631};', 'CATALYTIC ACTIVITY: Reaction=H(+) + N-acetyl-alpha-D-glucosamine 1-phosphate + UTP = diphosphate + UDP-N-acetyl-alpha-D-glucosamine; Xref=Rhea:RHEA:13509, ChEBI:CHEBI:15378, ChEBI:CHEBI:33019, ChEBI:CHEBI:46398, ChEBI:CHEBI:57705, ChEBI:CHEBI:57776; EC=2.7.7.23; Evidence={ECO:0000255|HAMAP-Rule:MF_01631};', 'COFACTOR: Name=Mg(2+); Xref=ChEBI:CHEBI:18420; Evidence={ECO:0000255|HAMAP-Rule:MF_01631}; Note=Binds 1 Mg(2+) ion per subunit. {ECO:0000255|HAMAP- Rule:MF_01631};', 'PATHWAY: Nucleotide-sugar biosynthesis; UDP-N-acetyl-alpha-D- glucosamine biosynthesis; N-acetyl-alpha-D-glucosamine 1-phosphate from alpha-D-glucosamine 6-phosphate (route II): step 2/2. {ECO:0000255|HAMAP-Rule:MF_01631}.', 'PATHWAY: Nucleotide-sugar biosynthesis; UDP-N-acetyl-alpha-D- glucosamine biosynthesis; UDP-N-acetyl-alpha-D-glucosamine from N- acetyl-alpha-D-glucosamine 1-phosphate: step 1/1. {ECO:0000255|HAMAP-Rule:MF_01631}.', 'PATHWAY: Bacterial outer membrane biogenesis; LPS lipid A biosynthesis. {ECO:0000255|HAMAP-Rule:MF_01631}.', 'SUBUNIT: Homotrimer. {ECO:0000255|HAMAP-Rule:MF_01631}.', 'SUBCELLULAR LOCATION: Cytoplasm {ECO:0000255|HAMAP-Rule:MF_01631}.', 'SIMILARITY: In the N-terminal section; belongs to the N-acetylglucosamine-1-phosphate uridyltransferase family. {ECO:0000255|HAMAP-Rule:MF_01631}.', 'SIMILARITY: In the C-terminal section; belongs to the transferase hexapeptide repeat family. {ECO:0000255|HAMAP-Rule:MF_01631}.']

created : ('10-JAN-2006', 0)

cross_references : [('EMBL', 'BA000018', 'BAB41687.1', '-', 'Genomic_DNA'), ('PIR', 'D89816', 'D89816'), ('RefSeq', 'WP_001252543.1', 'NC_002745.2'), ('ProteinModelPortal', 'Q7A7B4', '-'), ('SMR', 'Q7A7B4', '-'), ('EnsemblBacteria', 'BAB41687', 'BAB41687', 'BAB41687'), ('KEGG', 'sau:SA0457', '-'), ('HOGENOM', 'HOG000283476', '-'), ('KO', 'K04042', '-'), ('OMA', 'IEPQTHL', '-'), ('BioCyc', 'SAUR158879:G1G21-511-MONOMER', '-'), ('UniPathway', 'UPA00113', 'UER00532'), ('UniPathway', 'UPA00113', 'UER00533'), ('UniPathway', 'UPA00973', '-'), ('Proteomes', 'UP000000751', 'Chromosome'), ('GO', 'GO:0005737', 'C:cytoplasm', 'IEA:UniProtKB-SubCell'), ('GO', 'GO:0019134', 'F:glucosamine-1-phosphate N-acetyltransferase activity', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0000287', 'F:magnesium ion binding', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0003977', 'F:UDP-N-acetylglucosamine diphosphorylase activity', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0000902', 'P:cell morphogenesis', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0071555', 'P:cell wall organization', 'IEA:UniProtKB-KW'), ('GO', 'GO:0009245', 'P:lipid A biosynthetic process', 'IEA:UniProtKB-UniPathway'), ('GO', 'GO:0009103', 'P:lipopolysaccharide biosynthetic process', 'IEA:InterPro'), ('GO', 'GO:0009252', 'P:peptidoglycan biosynthetic process', 'IEA:UniProtKB-UniRule'), ('GO', 'GO:0008360', 'P:regulation of cell shape', 'IEA:UniProtKB-KW'), ('GO', 'GO:0006048', 'P:UDP-N-acetylglucosamine biosynthetic process', 'IEA:UniProtKB-UniPathway'), ('CDD', 'cd03353', 'LbH_GlmU_C', '1'), ('Gene3D', '3.90.550.10', '-', '1'), ('HAMAP', 'MF_01631', 'GlmU', '1'), ('InterPro', 'IPR005882', 'Bifunctional_GlmU'), ('InterPro', 'IPR038009', 'GlmU_C_LbH'), ('InterPro', 'IPR001451', 'Hexapep'), ('InterPro', 'IPR018357', 'Hexapep_transf_CS'), ('InterPro', 'IPR005835', 'NTP_transferase_dom'), ('InterPro', 'IPR029044', 'Nucleotide-diphossugar_trans'), ('InterPro', 'IPR011004', 'Trimer_LpxA-like_sf'), ('Pfam', 'PF00132', 'Hexapep', '3'), ('Pfam', 'PF00483', 'NTP_transferase', '1'), ('SUPFAM', 'SSF51161', 'SSF51161', '1'), ('SUPFAM', 'SSF53448', 'SSF53448', '1'), ('TIGRFAMs', 'TIGR01173', 'glmU', '1'), ('PROSITE', 'PS00101', 'HEXAPEP_TRANSFERASES', '1')]

data_class : Reviewed

description : RecName: Full=Bifunctional protein GlmU {ECO:0000255|HAMAP-Rule:MF_01631}; Includes: RecName: Full=UDP-N-acetylglucosamine pyrophosphorylase {ECO:0000255|HAMAP-Rule:MF_01631}; EC=2.7.7.23 {ECO:0000255|HAMAP-Rule:MF_01631}; AltName: Full=N-acetylglucosamine-1-phosphate uridyltransferase {ECO:0000255|HAMAP-Rule:MF_01631}; Includes: RecName: Full=Glucosamine-1-phosphate N-acetyltransferase {ECO:0000255|HAMAP-Rule:MF_01631}; EC=2.3.1.157 {ECO:0000255|HAMAP-Rule:MF_01631};

entry_name : GLMU_STAAN

features : [('CHAIN', 1, 450, 'Bifunctional protein GlmU.', 'PRO_0000068710'), ('REGION', 1, 229, 'Pyrophosphorylase. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('REGION', 8, 11, 'UDP-GlcNAc binding. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('REGION', 77, 78, 'UDP-GlcNAc binding. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('REGION', 230, 250, 'Linker. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('REGION', 251, 450, 'N-acetyltransferase. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('REGION', 385, 386, 'Acetyl-CoA binding. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('ACT_SITE', 362, 362, 'Proton acceptor. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('METAL', 102, 102, 'Magnesium. {ECO:0000255|HAMAP-

Rule:MF_01631}.', ''), ('METAL', 227, 227, 'Magnesium. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 22, 22, 'UDP-GlcNAc. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 72, 72, 'UDP-GlcNAc. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('BINDING', 139, 139, 'UDP-GlcNAc; via amide nitrogen. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('BINDING', 154, 154, 'UDP-GlcNAc. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 227, 227, 'UDP-GlcNAc. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 332, 332, 'UDP-GlcNAc. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 350, 350, 'UDP-GlcNAc. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 365, 365, 'UDP-GlcNAc. {ECO:0000255|HAMAP- Rule:MF_01631}.', ''), ('BINDING', 376, 376, 'UDP-GlcNAc. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('BINDING', 422, 422, 'Acetyl-CoA; via amide nitrogen. {ECO:0000255|HAMAP-Rule:MF_01631}.', ''), ('BINDING', 439, 439, 'Acetyl-CoA. {ECO:0000255|HAMAP- Rule:MF_01631}.', '')]

gene_name : Name=glmU {ECO:0000255|HAMAP-Rule:MF_01631}; Synonyms=gcaD; OrderedLocusNames=SA0457;

host_organism : []

host_taxonomy_id : []

keywords : ['Acyltransferase', 'Cell shape', 'Cell wall biogenesis/degradation', 'Complete proteome', 'Cytoplasm', 'Magnesium', 'Metal-binding', 'Multifunctional enzyme', 'Nucleotidyltransferase', 'Peptidoglycan synthesis', 'Repeat', 'Transferase']

molecule_type : None

organelle :

organism : Staphylococcus aureus (strain N315).

organism_classification : ['Bacteria', 'Firmicutes', 'Bacilli', 'Bacillales', 'Staphylococcaceae', 'Staphylococcus']

protein_existence : 1

references :

Authors: Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.

comments: [('STRAIN', 'N315')]

location: Lancet 357:1225-1240(2001).

number: 1

positions: ['NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].']

references: [('PubMed', '11418146'), ('DOI', '10.1016/S0140-6736(00)04403-2')]

title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

Authors: Vaezzadeh A.R., Deshusses J., Lescuyer P., Hochstrasser D.F.

comments: [('STRAIN', 'N315')]

location: Submitted (OCT-2007) to UniProtKB.

number: 2

positions: ['IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].']

references: []

title: Shotgun proteomic analysis of total and membrane protein extracts of S. aureus strain N315.

seqinfo : (450, 48516, '9B741359A12DDE89'

sequence :
MRRHAIILAAGKGTRMKSKKYKVLHEVAGKPMVEHVLESVKGSGVDQVVTIVGHGAESVKGHLGERSLYSFQEKQLGTAHAVQMAKSHLEDKEGTTI
VVCGDTPLITKETLETLIAHHEDANAQATVLSASIQQPYGYGRIVRNASGRLERIVEEKDATQAEKDINEISSGIFAFNNKTLFEKLTQVKNDNAQGEYYLP
DVLSLILNDGGIVEVYRTNDVEEIMGVNDRVMLSQAEKAMQRRTNHYHMLNGVTIIDPDSTFIGPDVTIGSDTVIEPGVRINGRTEIGEDVVIGQYSEIN

NSTIENGACIQQSVVNDASVGANTKVGPFAQLRPGAQLGADVKVGNFVEIKKADLKDGAKVSHLSYIGDAVIGERTNIGCGTITVNYDGENKFKTIVGK
DSFVGCNVNLVAPVTIGDDVLVAAGSTITDDVPNDSLAVARARQTTKEGYRK

sequence_length : 450

sequence_update : ('05-JUL-2004', 1)

taxonomy_id : ['158879']