CAMPO Apple Enzymes Extract
Index

CAMPO TOTAL APPLE’S ENZYMES EXTRACT

SPECIFICATIONS

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MATERIAL SAFETY DATA SHEETS

ENZYME: EC 2.1.2.1

LinkDB Search Result

ENZYME: EC 3.4.11.1

ENZYME: EC 3.1.1.3

ENZYME: EC 3.2.1.1

ENZYME: EC 2.6.1.1

ENZYME: EC 4.4.1.14

THE ROLE OF ENZYMES IN NUTRITION

THE ENZYME DATA BANK USER MANUAL
**TAXONOMY**

**Malus domestica**

*Taxonomy Id: 3750*

*Preferred common name: apple tree*

*Rank: species*

*Genetic Code: Standard [SGC0]*

*Mitochondrial genetic code: Standard [SGC0]*

*Other Names:*
  - Malus pumila [synonym], Malus x domestica [synonym], Malus domestica Broth [Synonym], apple [common name], apples [common name]

*Lineage (abbreviated):*
  - Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group;
  - Embryophyta; Magnoliophyta; Magnoliopsida; Rosales; Rosaceae; Malus.

<table>
<thead>
<tr>
<th>Nucleotide</th>
<th>Protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>(40)</td>
<td>(67)</td>
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</tbody>
</table>
GenBank (95.0/6/15/96).
Accession: U03294
GenBank (NCBI, Bethesda, Md. USA)

<table>
<thead>
<tr>
<th>LOCUS</th>
<th>MSU03294 1618bp mRNA PLN 17-NOV-1993</th>
</tr>
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<tbody>
<tr>
<td>DEFINITION</td>
<td>Malus sylvestris 1-aminocyclopropane-1-carboxylate synthase mRNA partial cds.</td>
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<tr>
<td>ACCESSION</td>
<td>U03294</td>
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<tr>
<td>NID</td>
<td>G417971</td>
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<tr>
<td>KEYWORDS</td>
<td>Malus sylvestris.</td>
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<tr>
<td>SOURCE</td>
<td>Malus sylvestris Eukaryotae: mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; Magnoliopsida; Rosales; Rosaceae; Malus;</td>
</tr>
<tr>
<td>ORGANISM</td>
<td></td>
</tr>
<tr>
<td>REFERENCE</td>
<td>1 (bases 1 to 1618)</td>
</tr>
<tr>
<td>AUTHORS</td>
<td>Dong, J.G., Kim, W.T. Yip, w.k., Thompson, G.A, Li, L., Bennett, A and Yang, S.F</td>
</tr>
<tr>
<td>TITLE</td>
<td>Cloning of a cDNA encoding 1-aminocyclopropane-1-carboxylate synthase and expression of its mRNA in ripening apple fruit</td>
</tr>
<tr>
<td>REFERENCE</td>
<td>2 (bases 1 to 1618)</td>
</tr>
<tr>
<td>AUTHORS</td>
<td>Dong, J. G.</td>
</tr>
<tr>
<td>TITLE</td>
<td>Direct submission</td>
</tr>
<tr>
<td>JOURNAL</td>
<td>Submitted (09-NOV-1993) Jian G. Dong, Vegetable Crops, University of California at Davis, Mann Lab, Davis, CA 95616-8631, USA</td>
</tr>
</tbody>
</table>
CAMPO TOTAL APPLE’S ENZYMES EXTRACT

Campo Total Apple’s Enzymes Extract is prepared from an assayed, free-dried preparation contains the following enzymes in a novel new non-human and non-animal protein matrix-Campo’s novel biotechnologic cloned vegetable matrix:

*Acid Phosphatase, Alanine Aminotransferase (ALT/GPT), \( \alpha \)-amylase, Aldolase, Alkaline Phosphatase, Aspartate Aminotransferase (AST/GOT), \( \gamma \)-Glutamyl Transpeptidase, \( \alpha \)-Hydroxybutyrate Dehydrogenase, Leucine Aminopeptidase, Lipase, Phosphohexose isomerase.*

The “Elevated Level” of our Total Apple’s Enzymes Extract is offered in a clear colorless liquid of diluted 10 x 3 biotechnologic -cloned vegetable matrix.

The elevated level does not cause irritation potential and discoloration or will not cause uncontrolled enzymatic, kinetic or endpoint functions in the end-formulations.

The **Total Apple’s Enzymes Extract** is unique novel configuration of stable blend in biotechnologic cloned vegetable protein matrix instead of animal or human protein matrix, as all enzymes when cloned and refined from the nucleic acid are unstable in any other matrices; while the cosmetic industry need special stable functional Enzymatic extract instead of the current Diagnostic Enzymes for Medical Diagnostic used now in Cosmetic formulations.

**For Best Functional Results:** Addition of Approx. 5% is suggested

**Types of Products:** Body-care, Colour Cosmetics and Special Treatment Hair Care for flaky scalp and brittle / dry hair.
SPECIFICATIONS

Plant species: Malus domestica
Plant part used: Fructus
INCI / CTFA Name (Proposed): Pyrus Malus (Apple) Fruit Extract (AND) Water
Appearance: Light Yellowish Brown Liquid
Odour: Slight Characteristic
PH Value (20°C): 6.9 - 7.4
Specific Gravity (20°C): 1.11 - 1.32
Refractive Index (20°C): 1.35 - 1.45
Dry Residue (160°C, 35 min.): 45% - 60%
Microbiology: Less than 100 germs / ml - Non-pathogens

Campo Research

INTERNATIONAL ENZYMES TEST METHODS & PROCEDURES NUMBER

<table>
<thead>
<tr>
<th>Int’l Procedure #</th>
<th>Enzymes</th>
<th>Test Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>104</td>
<td>Acid Phosphatase</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>505</td>
<td>Alanine Aminotransferase (ALT / GPT)</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>752</td>
<td>Aldolase</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>104</td>
<td>Alkaline Phosphatase</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>700</td>
<td>Amylase</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>505</td>
<td>Aspartate Aminotransferase (AST / GOT)</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>545</td>
<td>y-Glutamyl Transferees (y-GT)</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>500</td>
<td>Lactate Dehydrogenate (LD)</td>
<td>Calorimetric, Endpoint</td>
</tr>
<tr>
<td>340-UV</td>
<td>Lactate Dehydrogenate (LD-P)</td>
<td>UV-Kinetic</td>
</tr>
<tr>
<td>251</td>
<td>Leucine Aminopeptidase(LAP)</td>
<td>Calorimetric, Endpoint</td>
</tr>
</tbody>
</table>
CAMPO TOTAL APPLE’S ENZYMES EXTRACT

COMPOSITION

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acid Phosphates</td>
<td>0.0010%</td>
</tr>
<tr>
<td>Alanine Aminotransferase (ALT/GPT)</td>
<td>0.1030%</td>
</tr>
<tr>
<td>α-Amylase</td>
<td>0.3000%</td>
</tr>
<tr>
<td>Aldolase</td>
<td>2.0070%</td>
</tr>
<tr>
<td>Alkaline Phosphatase</td>
<td>1.8820%</td>
</tr>
<tr>
<td>Aspartate Aminotransferase (AST/GOT)</td>
<td>3.9000%</td>
</tr>
<tr>
<td>Y-Glutamyl transpeptidase</td>
<td>4.1000%</td>
</tr>
<tr>
<td>α-Hydroxybutyrate Dehydrogenase</td>
<td>5.0000%</td>
</tr>
<tr>
<td>Leucine Aminopeptidase</td>
<td>7.2001%</td>
</tr>
<tr>
<td>Lipase</td>
<td>10.0000%</td>
</tr>
<tr>
<td>Phosphohexose isomerase</td>
<td>1.0000%</td>
</tr>
<tr>
<td>Other Apple Fruit Enzymes &amp; Pro-Enzymes and Vegetal Protein Matrix Carrier Complex</td>
<td>20% - 24%</td>
</tr>
<tr>
<td>[Lactate Dehydrogenate (LD), Lactate Dehydrogenate (LD-P); Lucien Aminopeptidase (LAP); and Vegetal Peptides / Proteins, etc.]</td>
<td></td>
</tr>
</tbody>
</table>

The following blend / composition in a cosmetic formula will act as an enzymatic activator of aging skin rejuvenator that reverse aged skin to young skin via the enhanced enzymatic biosynthesis and pathway to increase the loss of enzymatic activity usually noted in aged skin conditions.

The fine lines will disappear and loss of water retention capacity will be reinstated as in the normal young skin.

The actions of these natural established enzymes from apples are functional in natural facial skin peeling over a period of time via their (enzymes) enzymatic natural actions without blotches and irregular patches of skin peel instead of unlike the α-Hydroxy acids which harshly peel the facial skin in uneven; irregular or very unnatural skin peeling.

The flow of natural facial skin moisturizing factors will increase as the enzymatic actions will clear the clogged facial skin pores and these enzymatic cleaned skin pores will shrunked to natural sizes thereby enhancing the facial tightening and rejuvenation effect as experienced in young skins.

An important function of the enzymes is the mimic activity equivalent to human retinal A is experienced in facial skin, as the enzymatic actions will increase production of natural human vitamin A (Retinal A) in the facial skin as required by the young skin conditions.

The total activity of retinal A is increased in the aged skin thereby causing a “pronounced effect” in reversal activity to conditions as experienced in young skins.
These enzymes are very stable in storage or in cosmetic formulations and will give or act with “environment activity” i.e., will acts in the conditions or situation where the activity is required (on human skin).

The protein matrix carrier is of biotechnologic vegetal origin instead of human or animal protein matrix and will enhanced the proteins and lipids / collagen requirements in “firming” the sagging aged skin.

Campo Research
Singapore
# CAMPO RESEARCH Pte Ltd
## TECHNICAL SPECIFICATION

<table>
<thead>
<tr>
<th>PRODUCT Name (Campo Research)</th>
<th>CAMPO™ TOTAL APPLE’S ENZYMES EXTRACT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Other Trade Names (Campo Research)</td>
<td>CAMPO™ MALUS’ FRUCTUS EXTRACT, APPLES EXTRACT</td>
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<tr>
<td>CTFA TRADE NAME</td>
<td>TOTAL APPLE’S ENZYMES EXTRACT</td>
</tr>
<tr>
<td>Existing CTFA / INCI Name</td>
<td>Malus domestica/Pyrus Malus (Apple) Fruit Extract</td>
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<tr>
<td>Chinese Translation</td>
<td>苹果（PYRUS MALUS）果提取物</td>
</tr>
<tr>
<td>WATER (AQUA)</td>
<td></td>
</tr>
<tr>
<td>CAMPO PRODUCT #</td>
<td>96.3750</td>
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<tr>
<td>HS Code:</td>
<td>1302.19.0000</td>
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<tr>
<td>CTFA Monograph ID</td>
<td>8997 - Pyrus Malus (Apple) Fruit Extract</td>
</tr>
<tr>
<td>CAS #</td>
<td>85251-63-4 - Pyrus Malus (Apple) Fruit Extract</td>
</tr>
<tr>
<td>CAS # EU</td>
<td>89957-48-2 - Pyrus Malus Extract (EU)</td>
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<tr>
<td>EINECS Number and Name</td>
<td>286-475-7(1)- Malus domestica/ Pyrus Malus (Apple) Fruit Extract</td>
</tr>
<tr>
<td>EINECS # EU</td>
<td>289-567-5 - Pyrus Malus Extract (EU)</td>
</tr>
<tr>
<td>BATCH/LOT #</td>
<td>See COA Batch Lot</td>
</tr>
<tr>
<td>SPECIES</td>
<td>Malus domestica</td>
</tr>
<tr>
<td>Syn: Pyrus Malus (Apple) Fruit Extract</td>
<td></td>
</tr>
<tr>
<td>PARTS USED</td>
<td>Fructus</td>
</tr>
<tr>
<td>RAW MATERIAL - ORIGIN</td>
<td>Australia, New Zealand</td>
</tr>
<tr>
<td>CONCENTRATION</td>
<td></td>
</tr>
<tr>
<td>COMMENTS</td>
<td>*Please take note that all specifications are liable to changes without prior notice.</td>
</tr>
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</table>

<table>
<thead>
<tr>
<th>Specification Parameter Analysis</th>
<th>Specification Range</th>
<th>Results</th>
<th>Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>Physical Form</td>
<td>Liquid</td>
<td>Conforms</td>
<td>Visual</td>
</tr>
<tr>
<td>Color</td>
<td>Light Yellowish Brown</td>
<td>Conforms</td>
<td>Visual</td>
</tr>
<tr>
<td>Odor</td>
<td>Characteristic Slight</td>
<td>Conforms</td>
<td>Olfactory</td>
</tr>
<tr>
<td>Specific Gravity (20deg.C)</td>
<td>1.1100 - 1.3200</td>
<td>See COA</td>
<td>USP XXIV / Paar. DMA46</td>
</tr>
<tr>
<td>Refractive Index (20deg.C)</td>
<td>1.350 - 1.450</td>
<td>See COA</td>
<td>USP XXIV / DGF IV C (52)</td>
</tr>
<tr>
<td>pH(20deg.C.) (100% concentrate)</td>
<td>6.50-7.50</td>
<td>See COA</td>
<td>USP XXIV / DGF H III (92)</td>
</tr>
<tr>
<td>Dry Residue (160deg.C/35Min)</td>
<td>45% - 60%</td>
<td>See COA</td>
<td>Mettler 16d</td>
</tr>
<tr>
<td>Protein Matrix Content</td>
<td>-</td>
<td>See COA</td>
<td></td>
</tr>
<tr>
<td>Nitrogen Content</td>
<td>-</td>
<td>See COA</td>
<td></td>
</tr>
<tr>
<td>Sodium Content</td>
<td>-</td>
<td>See COA</td>
<td></td>
</tr>
<tr>
<td>Water Solubility</td>
<td>Soluble</td>
<td>Conforms</td>
<td></td>
</tr>
<tr>
<td>Viscosity @ 20deg.C(m PaS)</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Saponification Value BS684</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Decomposition Point</td>
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<td>-</td>
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<tr>
<td>Sulfated Ash Content</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Preservation</td>
<td>None</td>
<td>-</td>
<td>-</td>
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<tr>
<td>Pesticide Content</td>
<td>None</td>
<td>Conforms</td>
<td>Pflanzaniaschuttal 1989</td>
</tr>
<tr>
<td>Total Germs</td>
<td>&lt;100 CFU/ml - non-pathogenic</td>
<td>Conforms</td>
<td>USP XXIV/Ph.Eur.2.6.12(97)</td>
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<tr>
<td>Total Yeast/Mold</td>
<td>&lt;100 CFU/ml</td>
<td>Conforms</td>
<td>USP XXIV/Ph.Eur.2.6.12(97)</td>
</tr>
<tr>
<td>Heavy Metals(Total)As,Pb,Hg</td>
<td>&lt;0.05 ppm</td>
<td>Conforms</td>
<td>USP XXIV/Ph.Eur.2.6.12(97)</td>
</tr>
</tbody>
</table>

---

**CAMPO RESEARCH PTE LTD. SINGAPORE**
**CAMPO RESEARCH PVT LTD. MADRAS INDIA**
**CAMPO RESEARCH INC. SAN DIEGO CA. USA**
**CAMPO RESEARCH sro.,CZECH REPUBLIC**
**MATERIAL SAFETY & CONSUMER SAFETY TESTING LABS.**
**DIV. OF JTC KAMPOYAKI SINGAPORE**

**EMERGENCY MATERIAL SAFETY / ACCIDENTAL RELEASE CENTER Contact:**
Emergency Tel.no: +(65)-3833202/3833631(24hours) /3228551/3228503
Emergency Fax No: +(65)-3833632(24hours), 3824680, 3228558
**EMERGENCY PC-VIDEO-TELECONFERENCING: 3834024 / 3826650(24hours)**
**EMAILwebmaster@campo-research.com**
MATERIAL SAFETY DATA SHEETS

http://www.osha.gov/dsg/hazcom/ghs.html
http://www.unece.org/trans/danger/publi/ghs/ghs_welcome_e.html

| DATE OF FIRST ISSUE | February 10th 1996-Reviewer - Dr Balasubramaniam PhD |
| | February 10th 2012 – Reviewer=Joshua Teo |
| | February 5th 2013 – Reviewer = Balasubramaniam M PhD |

1 PRODUCT AND COMPANY IDENTIFICATION
COMMERCIAL NAME: CAMPO™ TOTAL APPLE’S ENZYMES EXTRACT
OTHER TRADE NAME: APPLES/MALUS FRUCTUS EXTRACT/ PYRUS MALUS (APPLE) FRUIT EXTRACT
INCI NAME: APPLES / MALUS FRUCTUS EXTRACT/ PYRUS MALUS FRUIT EXTRACT (AND) WATER

Chinese Translation
苹果（PYRUS MALUS）果提取物

INTERNATIONAL CHEMICAL IDENTIFICATION
(EC REGULATION NO#1272/2008 AMENDED NO#790/2009) and Compliant to the GHS

FDA NAME
MANUFACTURER: FRUIT EXTRACT
(cGMP MFG. FACILITIES): CAMPO RESEARCH Pte Ltd

EMERGENCY TELEPHONE NUMBERS: (65)-63833631/(65)-63228503 (Singapore)

2. HAZARDS IDENTIFICATION
NOT CLASSIFIED AS DANGEROUS ACCORDING TO DIRECTIVE 67/548/EEC OR ITS AMENDMENTS.

HAZARD CLASS and CATEGORY CODE(s) PICTOGRAM : NONE
HAZARD STATEMENT CODE(s) No GHS Pictogram (Totally Non-Hazardous Division 1.6; NO HAZARD STATEMENT

(Regulation (EC) No 1223/2009) and compliant to
the GHS
GHS CLASSIFICATION : No GHS Pictogram (Totally Non-Hazardous Division 1.6: No Hazard Statement.
To UN-GHS Criteria.

GHS LABEL ELEMENTS: No GHS Pictogram (Totally Non-Hazardous Division 1.6: No Hazard Statement.

3 COMPOSITION / INFORMATION ON INGREDIENTS

STANDARDIZED PLANT EXTRACT IN WATER
Acid phosphatase, Alanine aminotransferase, α-amylase, Aldolase, Alkaline Phosphatase, Aspartate Aminotransferase, γ-Glutamyl Transpeptidase, α-Hydroxybutyrate Dehydrogenase, Leucine Aminopeptidase, Lipase, Phosphohexose Isomerase.

CTFA Monograph ID 8997 - Pyrus Malus Fruit (Apple) Extract
CAS # 85251-63-4 - Pyrus Malus (Apple) Extract
CAS # EU 89957-48-2 - Pyrus Malus Extract (EU)
CAS NO# (CAS Name) 7732-18-5 – Water (Aqua)

CAS NO# (CAS Name)
(EC REGULATION NO#1272/2008 AMENDED NO#790/2009) and compliant to the GHS
EINECS Name and Number 286-475-7(1) - Malus domestica/ Pyrus Malus (Apple) Fruit Ext
EINECS# EU 289-567-5 - Pyrus Malus Extract (EU)
231-791-2(1) – Water (Aqua)

EINECS# (EINECS Name)
(EC REGULATION NO#1272/2008 AMENDED NO#790/2009) and compliant to the GHS
RISK PHRASES None
SAFETY PHRASES 25-26 Not mandatory

GHS CLASSIFICATION : No GHS Pictogram (Totally Non-Hazardous Division 1.6: No Hazard Statement.
To UN-GHS Criteria.

GHS LABEL ELEMENTS: No GHS Pictogram (Totally Non-Hazardous Division 1.6: No Hazard Statement.

4 FIRST AID MEASURES

EYE CONTACT: Irrigation of the eye immediately with flowing water for 5 minutes is a good safety practice. Seek medical advice, if irritation occur and persist. Essentially edible in small quantities

ORAL INGESTATION: Contact will probably cause no more than a temporary slight irritation. Wash off in flowing water or shower.

SKIN CONTACT: Contact will probably cause no more than a temporary slight irritation. Wash off in flowing water or shower.

5 FIRE FIGHTING MEASURERS

COMBUSTIBLE BUT PRESENTS NO SPECIAL FIRE HAZARD.

EXTINGUISHING MEDIA: CO2, dry foam, dry chemical or skilled use of water spray.

PROTECTIVE EQUIPMENTS FOR FIGHTERS: Standard Equipments.

6 ACCIDENTAL RELEASE MEASURES
COVER WITH ABSORBENT MATERIAL (USE APPROPRIATE SAFETY EQUIPMENT) SOAK AND SWEEP INTO A DRUM.

7 HANDLING AND STORAGE
STORE IN SEALED CONTAINERS UNDER NORMAL COOL, DRY WAREHOUSING CONDITIONS.

8 EXPOSURE AND PERSONAL PROTECTION
IN ACCORDANCE WITH GOOD INDUSTRIAL PRACTICE AND HANDLING USING STANDARD EYE PROTECTION.

9 PHYSICAL AND CHEMICAL PROPERTIES

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>PHYSICAL FORM:</td>
<td>Liquid</td>
</tr>
<tr>
<td>COLOUR:</td>
<td>Light Yellowish Brown</td>
</tr>
<tr>
<td>ODOUR:</td>
<td>Characteristic- slight</td>
</tr>
<tr>
<td>BOILING POINT:</td>
<td>90 deg. cent.</td>
</tr>
<tr>
<td>MELTING POINT:</td>
<td>-</td>
</tr>
<tr>
<td>VISCOSITY:</td>
<td>-</td>
</tr>
<tr>
<td>FLASH POINT:</td>
<td>closed cup</td>
</tr>
<tr>
<td>FLAMMABILITY SOLID/GAS:</td>
<td>N/A</td>
</tr>
<tr>
<td>AUTO FLAMMABILITY:</td>
<td>N/A</td>
</tr>
<tr>
<td>SPECIFIC REFRACTIVE:</td>
<td>1.350 - 1.450</td>
</tr>
<tr>
<td>EXPLOSIVE PROPERTIES:</td>
<td>N/A</td>
</tr>
<tr>
<td>pH: (100% Concentrate)</td>
<td>6.50 – 7.50</td>
</tr>
<tr>
<td>OXIDIZING PROPERTIES:</td>
<td>N/A</td>
</tr>
<tr>
<td>VAPOUR PRESSURE:</td>
<td>0.90</td>
</tr>
<tr>
<td>DENSITY: (20 deg. Cent.)</td>
<td>1.110 - 1.320</td>
</tr>
<tr>
<td>WATER SOLUBILITY:</td>
<td>COMPLETE</td>
</tr>
<tr>
<td>OTHER SOLUBILITY:</td>
<td>In most cosmetic solvents</td>
</tr>
<tr>
<td>RESIDUE ON DRYING (160 deg C Mettler):</td>
<td>45-75 %</td>
</tr>
<tr>
<td>PARTITION COEFFICIENT:</td>
<td>-</td>
</tr>
<tr>
<td>(OCTANOL/WATER)</td>
<td>-</td>
</tr>
<tr>
<td>EXPLOSIVE LIMITS:</td>
<td>-</td>
</tr>
</tbody>
</table>

10 STABILITY AND REACTIVITY
THERMAL DECOMPOSITION: Stable under normal conditions of use

11 TOXICOLOGICAL DATA
Animal Tests Last Done 1992, as requirements of the then EC DIRECTIVE 91/155/EEC compliant to the GHS.

<table>
<thead>
<tr>
<th>Route</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>ORAL:</td>
<td>LD 50&gt; 8,000 mg/kg (Body weight) Rat Essentially Non-Toxic and Edible in Small Quantity.</td>
</tr>
<tr>
<td>DERMAL:</td>
<td>Expected To Be Essentially Non Toxic</td>
</tr>
<tr>
<td>INHALATION:</td>
<td>N/A</td>
</tr>
<tr>
<td>SPECIFIC CONCENTRATION LIMITS M-FACTORS (EC REGULATION NO#1272/2008 AMENDED NO#790/2009) compliant to the GHS.</td>
<td>8,000 MG/KG (Body Wt.); CATEGORY 5 Essentially Non-Toxic and Edible in Small Quantity.</td>
</tr>
<tr>
<td>SKIN:</td>
<td>Primarily Irritation Index (PII) = 0.0 (Non-Irritating - Skintex ), Not a Primarily Irritant. Non-irritant/ Non-sensitizer as per repeated patch insult test on 50 human volunteers</td>
</tr>
<tr>
<td></td>
<td>Human repeated patch test 48 hours: 50/50 completely non-irritating/ non-erythema causing ingredient at 100% concentrate in water on 50 human volunteers</td>
</tr>
<tr>
<td>EYE:</td>
<td>Very mild / minimal- not a transient conjunctival irritant at 10% concentrate in water (Eyetex Classification).</td>
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</table>
Summarized toxicological data as shown here are formation bounded under Non-Disclosure Agreement with various clients as when these Toxicological Data were established or their exclusive uses.

<table>
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<th>12 ECOLOGICAL INFORMATION</th>
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<td>BIODEGRATION:</td>
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*Please take note that all specifications are liable to changes without prior notice.
ENZYME: EC 2.1.2.1

Official Name:
GLYCINE HYDROXYMETHYLTRANSFERASE

Alternative Names:
SERINE HYDROXYMETHYLTRANSFERASE
SERINE ALDOLASE
THREONINE ALDOLASE
SERINE HYDROXYMETHYLASE

Reaction catalyzed:

\[
\begin{align*}
5,10- \text{METHYLENETETRAHYDROFOLATE} \\
+ \quad \text{GLYCINE} \\
+ \quad \text{H (2) O} \\
\leq \quad \text{TETRAHYDROFOLATE} \\
+ \quad \text{L-SERINE}
\end{align*}
\]

Co-factor(s): PYRIDOXAL PHOSPHATE

Comment(s):
- ALSO CATALYSES THE REACTION OF GLYCINE WITH ACETALDEHYDE TO FORM L-THREONINE, AND WITH 4-TRIMETHYLAMMONIOBUTANAL TO FORM 3-HYDROXY-N6, N6, N6-TRIMETHYL-L-LYSINE.

Cross Reference(s):

- PROSITE: PDOC00090
- EMP/PUMA: 2.1.2.1
- KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE: 2.1.2.1
- SWISS-PROT:

  - P34894, GLYA ACTAC;
  - P24531, GLYA CAMJE;
  - P34895, GLYA HYPME;
  - P34896, GLYC HUMAN;
  - Q10104, GLYC SCHPO;
  - P49357, GLYM FLAPR;
  - P14519, GLYM RABIT;
  - P39148, GLYA BACSU;
  - P00477, GLYA ECOLI;
  - P47634, GLYA MYCGE;
  - P34898, GLYC NEUCR;
  - P35623, GLYC SHEEP;
  - P34897, GLYM HUMAN;
  - P37292, GLYM YEAST;
  - P24060, GLYA BRAJA;
  - P43844, GLYA HAEIN;
  - P06192, GLYA SALTY;
  - P07511, GLYC RABIT;
  - P37291, GLYC YEAST;
  - P34899, GLYM PEA;
  - P49358, GLYN FLAPR;
ENTRY    C00065
NAME    L-Serine
FORMULA    C3H7NO3

L-serine (KLM0000340)

Config Rule:

config ('L-serine', [substituent (aminoacid_L_backbone), substituent (hydroxymethyl), linkage (from (aminoacid_L_backbone, car (1)), to (hydroxymethyl, car (1)), down, single ) ]).

%%% Substituent Config Rules for compound 'L-serine

config (aminoacid_L_backbone, [Left (amino), Right (hyd), Top (carboxyl), Center (car (1))].

ENTRY    C00188
NAME    L-Threonine
FORMULA C₄H₉NO₃

\[
\begin{align*}
&\text{O} & \text{OH} & \text{OH} \\
&\text{H}_2\text{N} & \text{CH}_3
\end{align*}
\]

DBLINKS CAS: 72-19-5

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## LinkDB Search Result

Database: LinkDB

Link Database
Release 96-06-22, Jun 96
Institute for Chemical Research, Kyoto University
2, 119, 344 entries

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Serine hydroxymethyltransferase (EC 2.1.2.1) (SHMT) [1] catalyzes the transfer of the hydroxymethyl group of serine to tetrahydrofolate to form 5-methylenetetrahydrofolate and glycine. In vertebrates, it exists in cytoplasmic and a mitochondrial form whereas only one form if found in prokaryotes. Serine hydroxymethyltransferase is a periodical-phosphate-containing enzyme. The pyridoxal-P group is attached to a lysine residue around which the sequence is highly conserved in all forms of the enzyme.

- Consensus pattern: [ST] (4) - H- K- [ST] - L - x - G - x - R [GSA] (2)
  [ K is the pyridoxal-P attachment site]
  - Sequences known to belong to this class detected by the pattern: ALL
  - Other sequence(s) detected in SWISS-PROT: None
  - Last update: June 1994 / Pattern and text revised.


ENTRY
NAME  EC 1.1.1.27
L-Lactate dehydrogenate
Lactic acid dehydrogenate
CLASS Oxidoreductases
Acting as the CH-OH group of donors
With NAD+ or NADP+ as acceptor
SYS NAME (S) Lactate NAD+ Oxidoreductase
REACTION (S) - Lactate + NAD+ - Pyruvate + NADH
SUBSTRATE (S) - Lactate
(S) - 2 - Hydroxymonocarboxylic acid
NAD+
PRODUCT Pyruvate
NADH
COMMENT Also oxidizes other (S)-2-hydroxy-monocarboxylic acids.
NADP - also acts more slowly with the animal, but not the Bacterial enzyme
PATHWAY PATH: MAP00010 Glycolysis / Gluconeogenesis
PATH: MAP00260 Glycine, serine and threonine metabolism
PATH: MAP00360 Phenylalanine and tyrosine metabolism (2)
PATH: MAP00380 Tryptophan metabolism
PATH: MAP00620 Pyruvate and acetyl-CoA metabolism
PATH: MAP00640 Propanoate metabolism
DISEASE
MIM: 150000  Exertional myoglobinuria due to deficiency of LDH.

MOTIF
PS: PS00064

DBLINKS
University of Geneva ENZYME DATA BANK: 1.1.1.27
PDB: 1HYH  1LDB  1LDM  1LDN  1LLC  1LLD
1LTH

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PIR:
A20629  A21986  A23083  A24999  A25805  A26053  A32430
A32957  A36070  A36957  A37334  A38231  A40488  A43598
A45246  A47180  B27246  B29704  B32957  B36070  B40885
C49904  DEBSLF  DEBSLM  DECHLH  DECHLM  DEDFLM  DEHULC
DEHULH  DEHULM  DELBLA  DEMSLC  DEMSLM  DEPGLH  DEPGLM
G43868  H64250  JC2312  JC2432  JN0449  JQ0183  JQ2222
JX0090  PA0103  S00019  S06290  S08182  S08183  S09954
S12151  S22492  S33362  S33453  S36863  S36864

ENTRY
C04096

NAME
(S) - 2 - Hydroxymonocarboxylic acid

\[
\text{OH} \quad \text{R} \quad \text{OH} \\
\text{OH} \quad \text{O} \\
\]

DBLINKS
EC: 1.1.1.27
ENZYME: EC 3.4.11.1

Official Name:
LEUCYL AMINOPEPTIDASE

Alternative Name(s):
CYTOSOL AMINOPEPTIDASE
LEUCINE AMINOPEPTIDASE
PEPTIDASES

Reaction catalyzed:
RELEASE OF AN N-TERMINAL AMINO ACID, XAA—XBB−, IN WHICH XAA IS PREFERABLY LEU, BUT MAY BE OTHER AMINO ACIDS INCLUDING PRO ALTHOUGH NOT ARG OR LYS, AND XBB MAY BE PRO.

Cofactor(s): ZINC

Comment(s):
• AMINO ACID AMIDES AND METHYL ESTERS ARE ALSO READILY HYDROLYSED, BUT RATES ON ARYLAMIDES ARE EXCEEDINGLY SLOW.
• IS ACTIVATED BY HEAVY METAL IONS.

Cross-reference(s):
• PROSITE: PDOC00548
• EMP/PUMA: 3.4.11.1
• KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE: 3.4.11.1
• SWISS-PROT:
  P11648, AMPA ECOLI;  P45334, AMPA HAEIN;  P30184, AMPL ARATH;
  P00727, AMPL BOVIN;  P28838, AMPL HUMAN;  P47631, AMPL MYCGE;
  P47707, AMPL MYCSA;  P28839, AMPL PIG;  P27888, AMPL RICPR;
  P31427, AMPL SOLTU;  P14904, AMPL YEAST;
<table>
<thead>
<tr>
<th><strong>ENTRY</strong></th>
<th><strong>EC 3.4.11.1</strong></th>
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</thead>
</table>
| **NAME** | Leucyl aminopeptidase  
Leucine aminopeptidase  
Leucyl peptidase  
Peptidase S  
Cytosol aminopeptidase |
| **CLASS** | Hydrolases  
Acting on peptide bonds (peptidases)  
Aminopeptidases |
| **REACTION** | Release of an N-terminal amino acid, Xaa + Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro. Amino acid amides and methyl esters are also readily hydrolyzed, but rates on arylamides are exceedingly low. |
| **SUBSTRATE** | Peptide  
H2O |
| **PRODUCT** | N-Terminal amino acid  
Peptide |
| **INHIBITOR** | Amastatin |
| **COFACTOR** | Zinc |
| **EFFECTOR** | Heavy metal ion |
| **COMMENT** | A zinc enzyme isolated from pig kidney and cattle lens; activated by heavy metal ions formerly EC 3.4.1.1  
Inhibited by Amastatin {H. Kim and W.N. Lipscomb, Biochemistry, 32, 8465-8478 (1993) } |
| **MOTIF** | PS: PS00631  
N-T-D-A-E-G-R-L |
| **DBLINKS** | University of Geneva ENZYME DATA BANK: 3.4.11.1  
PDB: 1BLL  
1BPM  
1BN  
1LAM  
1LAN  
1LAP  
1LCP  
PIR: A33879  
A40631  
A42432  
A48788  
APBOL  
APECA  
PQ0470  
PT0429  
PT0430  
PT0431  
S22399  

// //  
DBGET integrated database retrieval system, GenomeNet (Kyoto Center)
Cytosol aminopeptidase is an eukaryotic cytosolic zinc-dependent exoptidase that catalyzes the removal of unsubstituted amino-acid residues from the N-terminus of proteins. This enzyme is often known as Lucien aminopeptidase (EC 3.4.11.1) (LAP) but has been shown [1] to be identical with prolyl aminopeptidase (EC 3.4.11.5). Cytosol aminopeptidase is a hexamer of identical chains, each of which binds two zinc ions.

Cytosol aminopeptidase is highly similar to Escherichia coli pepA, a manganese dependent aminopeptidase. Residues involved in zinc ion-binding [2] in the mammalian enzyme are absolutely conserved in pepA where they presumably bind manganese.

A cytosol aminopeptidase from Rickettsia prowazekki [3] and one from Arabidopsis thaliana belong to this family.

As a signature pattern for these enzymes, we selected a perfectly conserved octapeptide, which contains two residues involved in binding metal ions: an aspartate and a glutamate.

- Consensus pattern: N-T-D-A-E-G-R-L
  [ The D and the E are Zinc/ Manganese ligands]
- Sequences known to belong to this class detected by the pattern: ALL
- Other sequence(s) detected in SWISS-PROT: NONE.
- Note: these proteins belong to family M17 in the classification of peptidases [4,E1].
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DBGET integrated database retrieval system, GenomeNet (Kyoto center)

**ENTRY C01552**
**NAME** Amastatin
**FORMULA** C21 H38 N4 O8

![Chemical structure of Amastatin](image)

C01552

**DBLINKS**
CAS: 67655-94-1
EC: 3.4.11.1

**ENTRY C00038**
**NAME** Zinc
**FORMULA** Zn

**DBLINKS**
CAS: 7440-66-6
ENZYME: EC 3.1.1.3

Official Name:
TRIACYLGLYCEROL LIPASE

Alternative Name(s):
LIPASE
TRIGLYCERIDE LIPASE
TRIBUTYRASE

Reaction catalyzed:

TRIACYLGLYCEROL
+ H(2)O
<=> DIACYLGLYCEROL
+ A FATTY ACID ANION

Comment(s):
● THE PANCREATIC ENZYME ACTS ONLY ON AN ESTER-WATER INTERFACE; THE OUTER ESTER LINKS ARE PREFERENTIALLY HYDROLYSED

Human Genetic Disease(s):
HEPATIC LIPASE DEFICIENCY; MIM: 15670
CONGENITAL LIPASE DEFICIENCY; MIM: 246600
WOLMAN DISEASE; MIM: 278000.

cross-reference(s):
● PROSITE: PDOC00110, PDOC00112.
● EMP / PUMA: 3.1.1.3
● KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE: 3.1.1.3
● SWISS-PROT
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![Chemical structure of Diacylglycerol](attachment:image_url)

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Lipase’s, serine active site

Triglyceride lipases (EC3.1.1.3) [1] are lipolytic enzymes that hydrolyze the ester bond of triglycerides. Lipases are widely distributed in animals, plants and prokaryotes. In higher vertebrates there are at least three tissue-specific isozymes: pancreatic, hepatic, and gastric / lingual. These three types of lipases are closely related to each other as well as to lipoprotein lipase (EC 3.1.1.34) [2], which hydrolyzes triglycerides of chylomicrons and very low-density lipoproteins (VLDL).

The most conserved region in all these proteins is centered around a serine residue which has been shown [3] to participate, with an histidine and an aspartic acid residue, to a charge relay system. Such a region is also present in lipases of prokaryotic origin and in lecithin-cholesterol acyltransferase (EC 2.3.1.43) (LCAT) [4], which catalyzes fatty acid transfer between phosphatidylcholine and cholesterol. We have built a pattern from that region.

  [ S is the active site residue]
- Sequences known to belong to this class detected by the pattern : ALL.

- Other sequence(s) detected in SWISS-PROT: 16.
- Note: Drosophila vittellogenins are also related to lipases [5], but they have lost their active site serine
ENTRY          EC 3.1.1.34
NAME            Lipoprotein lipase
                Clearing factor lipase
                Diglyceride lipase
CLASS           Hydrolyses
                Acting on ester bonds
                Carboxylic ester hydrolyses
SYSNAME         Triglycerol-protein acylhydrolase
REACTION        Triacylgllycerol  +  water  =  Diacylglycerol  +  a-carboxylate
SUBSTRATE       Triacylglycerol
                Water
PRODUCT         Diacylglycerol
                Carboxylate
COMMENT         Hydrolyses triacylglycerols in chylomicrons and low-density lipoproteins. Also hydrolyses diacylglycerol.
DISEASE         MIM: 238600  Hyperlipoproteinemia I
MOTIF           PS: PS00120 [LIV]-X-[LIVFY]- [LIVST]-G- [HYWV]-S-x-G-[GSTAC]
DBLINKS         University of Geneva ENZYME DATA BANK: 3.1.1.34

Triacylglycerol Related Enzymes
( Total 4 listed )
1. 2.3.1.20  Diacylglycerol O-acyltransferase
2. 2.3.1.77  Triacylglycerol-sterol O-acyltransferase
3. 3.1.1.3   Triacylglycerol lipase
4. 3.1.1.34  Lipoprotein lipase
ENTRY C00001
NAME H2O
FORMULA H2O

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</tr>
<tr>
<td></td>
<td>Serine aldolase</td>
</tr>
<tr>
<td></td>
<td>Threonine aldolase</td>
</tr>
<tr>
<td></td>
<td>Serine hydroxymethylase</td>
</tr>
<tr>
<td>CLASS</td>
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</tr>
<tr>
<td></td>
<td>Transferring one-carbon groups</td>
</tr>
<tr>
<td></td>
<td>Hydroxymethyl-, formyl- and related transverses</td>
</tr>
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<td>SYSNAME</td>
<td>5,10- Methylenetetrahydrofolate : glycine hydroxymethyltransferase</td>
</tr>
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<td>REACTION</td>
<td>5,10- Methylene tetrahydrofolate + Glycine + H2O = Tetrahydrofolate + L-Serine</td>
</tr>
<tr>
<td>SUBSTRATE</td>
<td>5,10- Methylene tetrahydrofolate</td>
</tr>
<tr>
<td></td>
<td>Acetaldehyde</td>
</tr>
<tr>
<td></td>
<td>4-Trimethylammoniobutanal</td>
</tr>
<tr>
<td></td>
<td>Glycine</td>
</tr>
<tr>
<td></td>
<td>H2O</td>
</tr>
<tr>
<td>PRODUCT</td>
<td>Tetrahydrofolate</td>
</tr>
<tr>
<td></td>
<td>L-Serine</td>
</tr>
<tr>
<td></td>
<td>L-Threonine</td>
</tr>
<tr>
<td></td>
<td>3-hydroxy-N6, N6-trimethyl-L-lysine</td>
</tr>
<tr>
<td>COFACTOR</td>
<td>Pyridoxal phosphate</td>
</tr>
<tr>
<td>COMMENT</td>
<td>A pyridoxal-phosphate protein. Also catalyses the reaction of glycine with acetaldehyde to form L-threonine, and with 4-trimethylammoniobutanal to form 3-hydroxy-N6, N6,N6-trimethyl-L-lysine.</td>
</tr>
<tr>
<td>PATHWAY</td>
<td>PATH: MAP00260 Glycine, serine and threonine metabolism</td>
</tr>
<tr>
<td></td>
<td>PATH: MAP00460 Cyanoamino acid metabolism</td>
</tr>
<tr>
<td></td>
<td>PATH: MAP00670 One carbon pool by folate</td>
</tr>
<tr>
<td></td>
<td>PATH: MAP00680 Methane metabolism</td>
</tr>
<tr>
<td></td>
<td>PATH: MAP00700 Glyoxylate cycle</td>
</tr>
<tr>
<td></td>
<td>PATH: MAP00750 Vitamin B6 metabolism</td>
</tr>
<tr>
<td>MOTIF</td>
<td>PS: PS00096 [ST] (4) -H-K-[ST]-L-x-G-x-R- [GSA] (2)</td>
</tr>
<tr>
<td>DBLINKS</td>
<td>University of Geneva ENZYME DATA BANK: 2.1.2.1</td>
</tr>
</tbody>
</table>

PIR:

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<tr>
<th>A33696</th>
<th>A40202</th>
<th>A42241</th>
<th>A46746</th>
<th>A56662</th>
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<td>B53525</td>
<td>JQ1016</td>
<td>S15203</td>
<td>S29348</td>
<td>S34379</td>
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<tr>
<td>S40218</td>
<td>S61632</td>
<td>XYECS</td>
<td>XYRBCS</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Tetrahydrofolate (KLM0000566)

Synonyms:

- ‘tetrahydrofolic acid’
- tetrehydrofolic_acid
- ‘THF’

Confide Rule:

confide (tetrahydrofolate, [substituent (‘1-benzoyl-4-yl’), substituent (‘pteridin-N10-yl’), substituent (‘D-glutamate’ (1, peptide, end)), linkage (from (‘pteridin-N10-yl’, nit (10)), to (‘1-benzoyl-4-yl’, car (4)), right, single), linkage (from (‘1-benzoyl-4-yl’, car (7)),}
ENZYME : EC 3.2.1.1

Official Name:
ALPHA-AMYLASE

Alternative Name(s):
1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE.

Reaction catalyzed:
ENZYMATIC HYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

Comment(s):
- ACTS ON STARCH, GLYCOGEN AND RELATED POLYSACCHARIDES AND OLIGOSACCHARIDES IN A RANDOM MANNER; REDUCING GROUPS ARE LIBERATED IN THE ALPHA-CONFIGURATION.

cross-reference(s):
- EMP / PUMA: 3.2.1.1
- KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE: 3.2.1.1
- SWISS-PROT

P27935, AM2A ORYSA; P27939, AM3C ORYSA; P72940, AMC1 ORYSA; P09961, AMY1 DICTH; P17654, AMY1 DICTH; Q09840, AMY1 SCHPO; P04063, AMY2 HORVU; P04747, AMY3 HORVU; P04749, AMY5 HORVU; P10529, AMYA ASPOR; P21543, AMYB BACOP; P00688, AMYP MOUSE; P17692, AMYR BACS8; P29957, AMY ALTHA; P08137, AMY BACCI; P06279, AMY BACST ; P23671, AMY CLOAB ; P30270, AMY STRGR ; P09794, AMY STRLM; P29750, AMY TECU; P38939, APU THEET ; P16950, APU THETY;
ENTRY C00930
NAME Oligosaccharide

------

ENTRY C00420
NAME Polysaccharide

------

DBLINKS

ENTRY C00930
NAME Oligosaccharide

------

ENTRY C00420
NAME Polysaccharide

------

DBLINKS

ENTRY C00930
NAME Oligosaccharide

------

ENTRY C00420
NAME Polysaccharide

------

DBLINKS
<table>
<thead>
<tr>
<th>ENTRY</th>
<th>EC 3.2.1.1</th>
</tr>
</thead>
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| NAME    | alpha-Amylase  
          | Glycogenase  |
| CLASS   | Hydrolases  
          | Glycosidases  
          | Hydrolyzing O-glycosyl compounds  |
| SYSNAME | 1,4-alpha-D-Glucan glucanohydrolase  |
| REACTION| Endohydrolysis of 1,4-alpha-D-glucosidic linkages in polysaccharides containing three or more 1,4-alpha-linked D-glucose units  |
| SUBSTRATE| Starch  
            | Glycogen  
            | Water  
            | Polysaccharides  |
| PRODUCT | Oligosaccharides  |
| COMMENT | Acts on starch, glycogen and related polysaccharides and oligosaccharides in a random manner; reducing groups are liberated in the alpha-configuration.  |
| PATHWAY | PATH: MAP00500 Starch and sucrose metabolism  |
| MOTIF   | PS : PS00506  
          | PS : PS00679  
          | PS : PS01072  |
| DBLINKS | University of Geneva ENZYME data bank: 3.2.1.1  |
ENTRY C00182
NAME Glycogen

DBLINKS

DBGET integrated database retrieval system, GenomeNet (Kyoto Centre)
ENZYME: EC 2.6.1.1

Official Name:
ASPARTATE AMINOTRANSFERASE.

Alternative Name(s):
TRANSAMINASE A.
GLUTAMIC-OXALOACETIC TRANSAMINASE.

Reaction catalyzed:
L- ASPARTATE
- 2-OXOGLUTARATE
< > OXALOACETATE
L-GLUTAMATE

Cofactor(s) : PYRIDOXAL-PHOSPHATE

Comment(s):
- ALSO ACTS ON L-TYROSINE, L-PHENYLALANINE AND L-TRYPTOPHAN. THIS ACTIVITY CAN BE FORMED FROM EC 2.6.1.57 BY CONTROLLED PROTEOLYSIS.

cross-reference(s):
- PROSITE : PDOC00098
- EMP/PUMA : 2.6.1.1
- KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE: 2.6.1.1.
- SWISS-PROT:

P46643, AAT1 ARATH
P46644, AAT3 ARATH
Q06191, AATB RHIME
P28734, AATC DAUCA
P05201, AATC MOUSE
P12343, AATC RABIT
P46248, AATM ARATH
P08907, AATM HORSE
P05202, AATM MOUSE
P00507, AATM RAT
P39643, AAT BAQCSU
P36692, AAT STRGR
AAT1 MEDSA
AAT4 ARATH
AATC BOVINE
AATC HORSE
AATC ORYSN
AATC RAT
AATC BOVIN
AATM HUMAN
AATM PIG
AATM RABIT
AATM YEAST
AAT ECOLI
AAT SULSO

AAT2 ARATH
Q02635, AATA RHIME
P00504, AATC CHICK
P17174, AATC HUMAN
P00503, AATC PIG
P23542, AATC YEAST
P00508, AATM CHICK
P08907, AATM HORSE
P00505, AATM HUMAN
P26563, AATM LUPAN
P12345, AATM RABIT
P00506, AATM PIG
P12345, AATM RABIT
P23034, AAT BACSP
P44425, AAT HAEIN
PROSITE: PDOC0098 (documentation)

[PDOC00098]
[PS00105; AA TRANSFER CLASS1]

*******************************************************************************
Aminotransferases class-I pyridoxal-phosphate attachment site
*******************************************************************************

Aminotransferases share certain mechanistic features with other pyridoxal-phosphate-dependent enzymes, such as the covalent binding of the pyridoxal phosphate group to a lysine residue. On the basis of sequence similarity, these various enzymes can be grouped [1,2] into subfamilies. One of the called class-I, currently consists of the following enzymes:

- **Aspartate aminotransferase (AAT) (EC 2.6.1.1)**. AAT catalyzes the reversible transfer of the amino group from L-aspartate to 2-oxoglutarate to form oxaloacetate and L-glutamate. In eukaryotes, there are two AAT isozymes: one is located in the mitochondrial matrix, the second is cytoplasmic. In prokaryotes, only one form of AAT is found (gene aspC).
- **Tyrosine aminotransferase (EC 2.6.1.5)** which catalyzes the first step in tyrosine catabolism by reversibly transferring its amino group to oxoglutarate forming 4-Hydroxyphenylpyruvate and L-glutamate.
- **Aromatic aminotransferase (EC 2.6.1.57)** involved in the synthesis of Try, Asp and Leu (gene tyrB).
- **1-aminocyclopropane-1-carboxylate synthases (EC 4.4.1.14) (ACC synthases)** from plants. ACC synthases catalyze the first step in ethylene biosynthesis.
- **Pseudomonas denitrificans cob**, which is involved in cobalamin biosynthesis.
- **Yeast hypothetical protein YJL060w.**

The sequence around the pyridoxal-phosphate attachment site of this class enzyme is sufficiently conserved to allow the creation of a specific pattern.

- Consensus pattern: [GS]-[LIVMFYTAC]- [GSTA]-K-X(2)-[GSALVN]-LVMFA]-X-[GNZ X-R-[LIVMA]-[GA]  
  [k is the pyridoxal-pyridoxal-p attachment site]
- sequences known to belong to this class detected by the pattern: ALL.
- Other sequence(s) detected in SWISS-PROT: NONE.
- Last update: November 1995 / pattern and text revised.

[1] Bairoch A.  
J. Biol. Chem. 266:2567-2572 (1991)
ENZYME : EC 4. 4. 1. 14

Official Name:
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE

Sysname(s):
S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE

Co-factor(s):
PYRIDOXAL PHOSPHATE

Comment(s):
• A PYRIDOXAL-PHOSPHATE PROTEIN. THE ENZYME CATALYSES AN ALPHA, GAMMA-ELIMINATION.

Reaction:
• S-ADENOSYL-L-METHIONINE = 1-AMINOCYCLOPROPANE-1-CARBOXYLATE
  + METHYLTHIOADENOSINE

Substrate: S-ADENOSYL-L-METHIONINE

Product: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE;
         METHYLTHIOADENOSINE

Pathway:
PATH: MAP00640  PROPANOATE METABOLISM

Class:
LYASES; CARBON-SULFUR LYASES.

Motif:

DBLINKS:
UNIVERSITY OF GENEVA ENZYME DATA BANK: 4.4.1.14
ENTRY       C00018  
NAME        PYRIDOXAL PHOSPHATE  
FORMULA    C8H10NO6P  

DBLINKS     CAS: 54-47-7
Vitamin K-dependent carboxylation domain

Vitamin K-dependent carboxylation [1,2] is the post-translational modification of glutamic residues to form gamma-carboxyglutamate (Gla). Proteins known contain Gla are listed below.

- A number of plasma proteins involved in blood coagulation. These proteins are prothrombin coagulation factors VII, IX and X, proteins C, S.
- Two proteins that occur in calcified tissues: osteocalcin (also known as bone-Gla protein, BGP) and matrix Glu-protein (MGP).
- Cone snail venom peptides: conantokin-G and -T, and conotoxin GS [3].

With the exception of the snail toxins, all these proteins contain N-terminal module of about forty amino acids where the majority of the residues are carboxylated. This domain is responsible for the high-affinity of Calcium ions. The Gla-domain starts at the N-terminal extremity of the mature form of these proteins and ends with a conserved aromatic residue a conserved Gla-x (3) - Gla-x Cys motif [4] is found in the middle of the domain, which seems to be important for substrate recognition by the carboxylase.

- Consensus pattern: x (12)-E-x(3)-E-x-C-x (6)-[DEN]-x-[LIVMFY]-x(9)-[FYW]
- Sequences known to belong to this class detected by the pattern: ALL.
- Other sequence(s) detected in SWISS-PROT: 5.

- Note: all glutamic residues present in the domain are potential carboxylation sites; in coagulation proteins, all are modified to Gla, while in BGP and MGP some are not.

- Expert (s) to contact by e-mail: Price P.A : pprice@ucsd.edu
- Last update: December 1992/ Text revised
LinkDB Search Result
Database: LinkDB

Link Database
Release 96-06-22, Jun 96
Institute for Chemical Research, Kyoto University
2, 119, 344 entries

COMPOUND : C00182-related entries (Total 16 hits.):

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<td>3.2.1.3</td>
<td>original</td>
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<td>ENZYME</td>
<td>3.2.1.41</td>
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</tr>
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<td>reverse</td>
</tr>
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<td>3.2.1.68</td>
<td>reverse</td>
</tr>
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</table>

DBGET integrated database retrieval system, GenomeNet (Kyoto Centre)
THE ROLE OF ENZYMES IN NUTRITION

In 1932, Dr. Edward Howell, physician and researcher, discovered that all food in its fresh, raw state contains its own enzymes, which are able to digest raw food and deliver its nutrients. Dr. Howell’s research further revealed that a dramatic improvement in health and longevity is attained when food “self-digests”, using its own naturally occurring enzymes. Unfortunately, this is only possible when food is eaten raw, since cooking destroys enzymes.

In 1947, Dr William Hanson developed and patented the technology to extract plant and specific animal enzymes, which when added to the diet, have a unique ability to provide the same digestive activity as food enzymes in the human digestive tract. In addition to digestive assistance, these glandular extracts allow specific nutrients to be directed into specific human glands and organs, since the enzymes of bovine (cow), match identically, to those of the corresponding human organ or gland. A fine example is when we consume a Vitamin C called Adrenucleo, this nutrient goes directly to our adrenal glands. The adrenal glands are known as the stress or fatigue glands, collagen production, insulin resistance and more.

ENZYMES, THE SPARK OF LIFE

We are born because of enzymes and we die without them. Millions of enzymes are active in the body at all times, causing every chemical action and reaction including senses of sight, sound, thought, touch, digestion and cellular duplication. Our entire immune function relies on enzyme activity. Digestion in particular, the basis of immunity, relies upon specific enzymes secreted by cells in the digestive tract and pancreas, so as to release valuable nutrients from your food.

Nature has endowed all foods in their natural, uncooked form with enzymes to digest the protein, fiber, fat and carbohydrates in the food. Nutritional enzyme supplements taken with each meal will add to your body’s enzyme supply.

BECAUSE YOU EAT COOKED FOOD YOU NEED ENZYMES

When enzymes are missing from your food, the full burden of digestion, falls on your own digestive system. Nutritional enzymes can provide the same type of digestive activity as raw food enzymes. today’s typical diet of cooked, canned and convenience foods make it very important to take supplemental nutritional enzymes to relieve some of your body’s digestive stress.

A WELL BALANCED DIET PLUS VITAMIN SUPPLEMENTS ARE NOT ENOUGH. ENZYMES ARE ESSENTIAL.

You can eat the most nutritious foods and take the best vitamin and mineral supplements, but if you do not digest and absorb what you consume, you will not realize optimal health benefits. Even if you include raw food in your diet, most raw foods contain only enough enzymes to aid in their own digestion, with none left for the cooked foods in your diet.
Vitamins and minerals must team up with enzymes to perform the body’s basic functions. There is clinical evidence that nutritional enzymes can enhance the nutritional value of dietary supplements containing vitamins, minerals, herbs and whole food concentrates. If you are not experiencing the benefits you expected from you dietary supplements, you will want to add nutritional enzymes to your diet.

**LIFE’S DEMANDS DEplete your enzymes**

Cooked and processed food, caffeinated and alcoholic beverages, colds and fever, pregnancy, stress strenuous exercise and extreme weather conditions, are just a few of the things that use up your enzymes daily. Adding nutritional enzymes to your diet enables you to bring this constant drain on your valuable enzyme supply under control.

**A lack of enzymes in your dieT, RObs your immune system**

When your food is continually deficient in enzymes, the digestive organs become exhausted. Since the body puts a higher priority on digestion than on maintaining health, it will steal enzymes from the immune system and blood vessels that regulate cholesterol, to help with digestion. Thus, nutritional enzyme supplements can help take some of the stress off not only your digestive organs, but also your immune system and simultaneously assist in cholesterol maintenance.

**Cellular enzymes activity is influenced by small changes in PH.**

Maintaining alkalinity at the cell is the cornerstone of immunity, longevity and a healthy metabolism for all glands, organs and systems. Eating more raw fruit and raw vegetables will assist in reaching and maintaining alkalinity. When we are born, every cell in the body is alkaline. Raw food’s alkaline ash, mops acid ash deposits left by meat, chicken, and coffee and refined sugar products. It takes thirty glasses of water to neutralize the acid of one coke.

“*When cellular PH is optimal antioxidant enzyme activity is optimal, causing free radicals to be effectively neutralized.*”  
Vernon Mountcastle, M.D.
THE ENZYME DATA BANK USER MANUAL

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   3.2. The DE line 6
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   3.5. The CF line 8
   3.6. The CC line 8
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Appendix 1: Report form of the NC-IUBMB 10
INTRODUCTION

1.1) Definition of the scope of the data bank

The ‘ENZYME’ data bank contains the following data for each type of characterized enzyme for which an EC number has been provided:
- EC number
- Recommended name
- Alternative names (if any)
- Catalytic activity
- Cofactors (if any)
- Pointers to the SWISS-PROT entry/entries that correspond to the enzyme (if any)

The ENZYME data bank can be useful to anybody working with enzymes and that it can be of help in the development of computer programs involved with the manipulation of metabolic pathways.

1.2) Sources of the data

The main sources for the data in the ENZYME data bank comes from recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) [1] A minor part of the data has been extracted from the literature.


Assigning the EC numbers for newly characterized enzymes is the responsibility of the Nomenclature Committee of IUBMB (NC-IUBMB). To contact the committee one should write to:

Prof. K. Tipton
Department of Biochemistry
Trinity College
Dublin2
Republic of Ireland

He can also be contacted by electronic mail at the following address:
ktipton@vaxl.tcd.ie
By phone at the number:
+35-1+677 2400
CONVENTIONS USED IN THE DATA BANK

[NOTE: The data has been restructured for Sybase. This section describes the original flat-file structure.]

2.1) Structure of an entry
The entries in the database data file (ENZYME.DAT) are structured so as to be usable by human readers as well as by computer programs. Each entry in the database is composed of lines. Different types of lines, each with its own format, are used to record the various types of data, which make up the entry. The general structure of a line is the following:

<table>
<thead>
<tr>
<th>Characters</th>
<th>Content</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 to 2</td>
<td>Two-character line code. Indicates the type of information contained in the line.</td>
</tr>
<tr>
<td>3 to 5</td>
<td>Blank</td>
</tr>
<tr>
<td>6 up to 78</td>
<td>Data</td>
</tr>
</tbody>
</table>

The currently used line types, along with their respective line codes, are listed below:

- **ID**: Identification (begins each entry: 1 per entry)
- **ED**: Description (official name) (> = 1 per entry)
- **AN**: Alternate name(s) (> = 0 per entry)
- **CA**: Catalytic activity (> = 0 per entry)
- **CF**: Cofactor(s) (> = 0 per entry)
- **CC**: Comments (> = 0 per entry)
- **DI**: Disease(s) associated with the enzyme (> = 0 per entry)
- **DR**: Cross-references to SWISS-PROT (> = 0 per entry)
- **//**: Termination line (ends each entry; 1 per entry)

Some entries do not contain all of the line types, and some line types occur many times in a single entry. Each entry must begin with an identification line (ID) and end with a terminator line (//).

A detailed description of each line type is given in the next section of this document.

2.2) One sample entry

```
ID      1.14.17.3
DE      PETIDYLGLYCINE MONOOXYGENASE.
AN      PEPTIDYL ALPHA-AMIDATING ENZYME.
CA      DEHYDROASCORBATE+ H(2)O
CF      COPPER.
CC      -I- PEPTIDYLGLYCINES WITH A NEUTRAL AMINO ACID RESIDUE IN THE PENULTIMATE POSITION ARE THE BEST SUBSTRATES FOR THE ENZYME.
```
CC  - THE ENZYME ALSO CATALYZES THE DISMUTATION OF THE PRODUCT TO
   GLYOXYLATE AND THE CORRESPONDING DESGLYCINE PEPTIDE AMIDE.

DR  P10731, AMD BOVIN; AMD HUMAN; P14925, AMD-RAT;

DR  P08478, AMD1-XENLA; P12890, AMD2-XENLA;

3) THE DIFFERENT LINE TYPES

   This section describes in detail the format of each type of line used in the
   database.

3.1) The ID line
   The ID (Identification) line is always the first line of an entry. The format of the
   ID line is:

   ID  EC NUMBER

Examples:

   ID  1.1.1.1
   ID  6.3.2.1

3.2) The DE line
   The DE (Description) line(s) contain the NC-IUB recommended name for an
   enzyme. The format of the DE Line is:

   DE  DESCRIPTION.

Examples:

   DE  UDP-N ACETYLMURAMOYLALANYL -D GLUTAMYL-2,6-
   DE  DIAMINOPIMELATE—D—
   DE  ALANYL-D-ALANYL LIGASE.

Important note: Enzymes are sometimes deleted from the EC list, others are
   renumbered; however, the NC-IUBMB does not allocate the old numbers to new
   enzymes. Obsolete EC numbers are indicated in this data bank by the following
   DE line syntaxes. For deleted ENZYMES:

   DE  TRANSFERRED ENTRY:  x . x . x . x .
   and for renumbered enzymes:

   DE  TRANSFERRED ENTRY:  1 . 7 . 99 . 5 .
3.3) The AN line
The AN (Alternate Name) line(s) are used to indicate the different name(s), other than the NC-IUMB recommended name, that are used in the literature to describe an enzyme. The format of the AN line is:

AN NAME

As an example we list here both the DE and AN lines for the enzyme EC 2.7.7.31:

DE DNA NUCLEOTIDYLEXOTRANSFERASE
AN TERMINAL ADDITION ENZYME
AN TERMINAL TRANSFERASE
AN TERMINAL DEOXYRIBONUCLEOTIDYLTRANSFERASE

3.4) The CA line
The CA (Catalytic Activity) line(s) are used to indicate the reaction(s) catalyzed by an enzyme. The format of the CA line is:

CA REACTION.

Where the reaction is indicated following the recommendations of the NC-IUMB. The majority of the reactions are described using a standard chemical reaction format:

CA SUBSTRATE-11 + SUBSTRATE-12 [+ SUBSTRATE-1N...] = SUBSTRATE-21
CA SUBSTRATE-22 [+ SUBSTRATE-2N].

As shown in the following examples:

CA L-MALATE + NAD(+) = OXALOACETATE + NADH
CA 2 ATP + GLUTAMINE + CO(2) + H(2)O = 2ADP + ORTHOPHOSPHATE +
CA GLUTAMATE + CARBAMOYL PHOSPHATE.
In some cases free text is used to describe a reaction. As shown in the following examples:

CA DEGRADATES STARCH TO CYCLODEXTRINS BY FORMATION OF A 1,4-
CA ALPHA-D-GLUCOSIDIC BOND.

CA CLEAVES LEU- | -LEU BOND IN ANGIOTENSINOGEN TO GENERATE
CA ANGIOTENSIN I.

Notes
3.5) The CF line
The CF (Cofactor) line(s) are used to indicate which cofactor(s) an enzyme requires. The format of the CF line is:

CF COFACTOR 1; COFACTOR 2 OR COFACTOR 3 [; COFACTOR N...].

Examples:

CF PYRIDOXAL PHOSPHATE
CF MOLYBDENUM OR VANADIUM; IRON-SULPHUR.
CF IRON; ASCORBATE.

3.6) The CC line
The CC lines are free text comments on the entry, and may be used to convey any useful information.

Examples:

CC !- THE PRODUCT SPONTANEOUSLY ISOMERIZED TO L-ASCORBATE.

CC !- SOME MEMBERS OF THIS GROUP OXIDIZE ONLY PRIMARY ALCOHOL; OTHERS ACT ALSO ON SECONDARY ALCOHOLS.

3.7) The DI line
The DI (Disease) line(s) are used to indicate the known disease(s) associated with a deficiency of the enzyme. Currently this information is only given for human diseases listed in the MIM book [2].

Mendelian Inheritance in Man
Catalogs of autosomal dominant, autosomal recessive, and x-linked phenotypes
Tenth Edition

The format of the DI line is:

DI DISEASE NAME; MIM: NUMBER
Where “NUMBER” is the MIM catalog number of the disease (or phenotype).

Examples:

DI  XANTHINURIA; MIM: 278300
DI  PHENYLKETONURIA; MIM: 261600

3.8) The DR line
The DR (Data Bank Reference) line(s) are used as pointers to the SWISS-PROT entries that corresponds to the enzyme being described. The format of the DR line is:

DR  AC NB, ENTRY NAME;  AC NB, ENTRY NAME;  AC NB, ENTRY NAME;

where:
- ‘AC NB’ is the SWISS-PROT primary accession number of the entry to which reference is being made.
- ‘ENTRY NAME’ is the SWISS-PROT entry name.

Example:

DR  P00366, DHE3 BOVIN;  P00368, DHE3 CHICK;  P00367, DHE3 HUMAN;
DR  P10860, DHE3 RAT;

3.9) The termination line
The // (terminator) line contains no data or comments. It designates the end of an entry.

4.) RELEASE NOTES

The data bank is complete and up to date. Until new enzyme nomenclature data is published, there is only the plan to update the SWISS-PROT pointers at each release of the protein sequence data bank, correct eventual errors, and complete the information concerning synonyms and cofactors using the literature.
REPORT FORM ON AN ENZYME NOT INCLUDED IN THE CURRENT EDITION OF ENZYME NOMENCLATURE

The Nomenclature Committee of the International Union of Biochemistry intends to update the Enzyme List from time to time by the publication of Supplements, and ultimately by the production of a full new edition. The assistance of the biochemical community is sought in this task. This sheet can be used to draw the attention of the editor to enzymes missing from this list, or to errors in existing entries.

Reaction catalyzed:

Systematic and other names proposed by authors:

Subclass in Enzyme Nomenclature proposed (e.g. 2.7.7-):

Source of enzyme (e.g. yeast, horse liver. E.coli, etc.):

Brief comment on specificity:

Cofactor requirement(s):

References (if accepted by a journal but not yet published, give name of journal and date of acceptance; please enclose reprints if available):

Name and address of person submitting this report:

The completed form should be sent to:

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