

CAMPO

Apple Enzymes

Extract



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CAMPO® Multi-Purpose Cosmetic Base Chemicals & Active Ingredients

CAMPO® Novel Functional Active Cosmetic Ingredient & Raw Materials

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IMPORTANT NOTICE

Specifications may change without prior notice. Information contained in this technical literature is believed to be accurate and is offered in good faith for the benefit of the customer. The company, however, cannot assume any liability or risk involved in the use of its natural products or their derivatives, since the conditions of use are beyond our control. Statements concerning the possible use are not intended as recommendations to use our products in the infringement of any patent. We make no warranty of any kind; expressed or implied, other than that the material conforms to the applicable standard specifications.

Ask about our Herbal Natural Products Chemistry Consultancy Services – Product Registration EEC/UK New Drug Development (NDA-US); Quasi-Drug Topicals (MOHW_Japan); Development of Standards, Analysis & Profiles of Phytochemicals; Literature searches, Cultivation of Medicinal Plants, Clinical-Trials, Development of new uses for Phytochemicals and Extracts; Contract Research and Development Work in Natural Products for Novel Drugs, New Cosmetic Active Ingredients for Active Topica/OTC Cosmetic with functionality and Consumer-perceivable immediate-results, New Food Ingredients for Nutraceuticals & Functional Foods.

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IMPORTANT NOTICE

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[Ask about our Herbal Natural Products Chemistry Consultancy Services – Product Registration EEC/UK New Drug Development \(NDA-US\); Quasi-Drug Topicals \(MOHW_Japan\); Development of Standards, Analysis & Profiles of Phytochemicals; Literature searches, Cultivation of Medicinal Plants, Clinical-Trials, Development of new uses for Phytochemicals and Extracts; Contract Research and Development Work in Natural Products for Novel Drugs, New Cosmetic Active Ingredients for Active Topica/OTC Cosmetic with functionality and Consumer-perceivable immediate-results, New Food Ingredients for Nutraceuticals & Functional Foods.](#)

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福 CAMPO RESEARCH
ACTIVE INGREDIENTS

24 hrs. campo@publ.ipn.vocaltec.com support@campo-research.com

Campo Novel Active Cosmetic Ingredients. The Ingredients That Impart Consumer Precievable Functional Activities To Your Cosmetic End Products !!!

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.

Nucleotide (40)

Protein (67)

GenBank (95.0,6/15/96).

Accession: U03294

GenBank (NCBI, Bethesda, Md. USA)

LOCUS MSU03294 1618bp mRNA PLN 17-NOV-1993
DEFINITION Malus sylvestris 1-aminocyclopropane-1-carboxylate synthase mRNA partial cds.
ACCESSION U03294
NID G417971
KEYWORDS
SOURCE Malus sylvestris.
ORGANISM Malus sylvestris
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta;
Magnoliophyta; Magnoliopsida; Rosales; Rosaceae; Malus;
REFERENCE 1 (bases 1 to 1618)
AUTHORS Dong, J.G., Kim, W.T. Yip, w.k., Thompson, G.A, Li, L.,
Bennett,A and Yang, S.F
TITLE Cloning of a cDNA encoding 1-aminocyclopropane-1-
carboxylate synthase and expression of its mRNA in ripening
apple fruit
JOURNAL Planta 185, 38-45 (1991)
REFERENCE 2 (bases 1 to 1618)
AUTHORS Dong, J. G.
TITLE Direct submission
JOURNAL Submitted (09-NOV-1993) Jian G. Dong, Vegetable Crops,
University of California at Davis, Mann Lab, Davis, CA 95616-
8631, USA

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), α -amylase, Aldolase, Alkaline Phosphatase, Aspartate Aminotransferase (AST/GOT), γ -Glutamyl Transpeptidase, α -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 / Pyrus Malus
Plant part used	Fructus
INCI / CTFA Name (Proposed)	Pyrus Malus (Apple) Fruit Extract (AND) Malus Domestica 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

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INTERNATIONAL ENZYMES TEST METHODS & PROCEDURES NUMBER

Int'l Procedure #	Enzymes	Test Methods
104	Acid Phosphatase	<i>Calorimetric, Endpoint</i>
505	Alanine Aminotransferase (ALT / GPT)	<i>Calorimetric, Endpoint</i>
752	Aldolase	<i>Calorimetric, Endpoint</i>
104	Alkaline Phosphatase	<i>Calorimetric, Endpoint</i>
700	Amylase	<i>Calorimetric, Endpoint</i>
505	Aspartate Aminotransferase (AST / GOT)	<i>Calorimetric, Endpoint</i>
545	γ-Glutamyl Transferees (γ-GT)	<i>Calorimetric, Endpoint</i>
500	Lactate Dehydrogenate (LD)	<i>Calorimetric, Endpoint</i>
340-UV	Lactate Dehydrogenate (LD-P)	<i>UV-Kinetic</i>
251	Leucine Aminopeptidase(LAP)	<i>Calorimetric, Endpoint</i>

CAMPO TOTAL APPLE'S ENZYMES EXTRACT

COMPOSITION

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

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 shrink 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

PRODUCT Name (Campo Research) Other Trade Names (Campo Research)	CAMPO™ TOTAL APPLE'S ENZYMES EXTRACT CAMPO™ MALUS FRUCTUS EXTRACT, APPLES EXTRACT
CTFA TRADE NAME Existing CTFA / INCI Name	TOTAL APPLE'S ENZYMES EXTRACT Malus domestica/Pyrus Malus (Apple) Fruit Extract
Chinese Translation	苹果 (PYRUS MALUS) 果提取物 苹果 (MALUS DOMESTICA) 果提取物 水 AQUA (WATER)
CAMPO PRODUCT # HS Code:	96.3750 1302.19.0000
CTFA Monograph ID	8997 – Pyrus Malus (Apple) Fruit Extract 21160 – Malus Domestica Fruit Extract 9423 – Aqua
CAS # CAS # EU	N/A – Pyrus Malus (Apple) Fruit Extract 85251-63-4 (EU) – Pyrus Malus Fruit Extract 89957-48-2 – Malus Domestica Fruit Extract N/A (EU) – Malus Domestica Fruit Extract 7732-18-5 – Aqua (Water)
EINECS Number and Name EINECS # EU	N/A – Pyrus Malus (Apple) Fruit Extract 286-475-7 (EU) – Pyrus Malus Fruit Extract 289-567-5 (1) – Malus Domestica Fruit Extract N/A (EU) – Malus Domestica Fruit Extract 231-791-2(1) – Aqua (Water)
EINECS Number and Name EINECS # EU European Commission–Health & Consumer Cosmetics–Cosing	Pyrus Malus (Apple) Fruit Extract http://ec.europa.eu/consumers/cosmetics/cosing/index.cfm?fuseaction=search.details_v2&id=58863 Pyrus Malus Fruit Extract – 286-475-7 (EU) Malus Domestica Fruit Extract http://ec.europa.eu/consumers/cosmetics/cosing/index.cfm?fuseaction=search.details_v2&id=83460 Malus Domestica Fruit Extract – N/A (EU) Aqua (Water) http://ec.europa.eu/consumers/cosmetics/cosing/index.cfm?fuseaction=search.details_v2&id=31959 Aqua – 231-791-2 (EU)
BATCH/LOT #	See COA Batch Lot
SPECIES	Malus domestica Syn: Pyrus Malus (Apple) Fruit Extract
PARTS USED	Fructus
RAW MATERIAL - ORIGIN	Australia, New Zealand
CONCENTRATION	
COMMENTS	A Quality Management System, compliant to the International Standard ISO 9001, was used to manufacture and test this material *Please take note that all specifications are liable to changes without prior notice.

<u>Specification Parameter Analysis</u>	<u>Specification Range</u>	<u>Results</u>	<u>Methods</u>
Physical Form	Liquid	Conforms	Visual
Color	Light Yellowish Brown	Conforms	Visual

Odor	Characteristic Slight	Conforms	Olfactory
Specific Gravity (20deg.C)	1.1100 - 1.3200	See COA	USP XXIX / Paar. DMA46
Refractive Index (20deg.C)	1.350 - 1.450	See COA	USP XXIX / DGF IV C (52)
pH(20deg.C.) (100% concentrate)	6.50- 7.50	See COA	USP XXIX / DGF H III (92)
Dry Residue (160deg.C/35Min)	45% - 60%	See COA	Mettler 16J
Protein Matrix Content	-	See COA	
Nitrogen Content	-	See COA	
Sodium Content	-	See COA	
Water Solubility	Soluble	Conforms	
Viscosity @ 20deg.C(m PaS)	-	-	-
Saponification Value BS684	-		
Decomposition Point	-		
Sulfated Ash Content	-		
Preservation	None		
Pesticide Content	None		Pflanzaniaschuttal 1989
Total Germs	<100 CFU/ml - non-pathogenic	Conforms	USP XXIX/Ph.Eur.2.6.12(97)
Total Yeast/Mold	<100 CFU/ml	Conforms	USP XXIX/Ph.Eur.2.6.12(97)
Heavy Metals(Total)As,Pb,Hg	<0.05 ppm	Conforms	USP XXIX/Ph.Eur.2.6.12(97)

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 CAMPO RESEARCH USA, INC SAN DEIGO CA 92111, & Manhattan, New York City, USA
 CAMPO RESEARCH s.r.o., Brno, Czech Republic
 CAMPO RESEARCH Pvt. Ltd, CHENNAI , INDIA
 CAMPO RESEARCH CANADA LTD, TORONTO, CANADA

MATERIAL SAFETY & CONSUMER SAFETY TESTING LABS.
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EMAIL: msds911@campo-research.com

Campo Total Apple’s Enzymes Extract ©.

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“(SAFETY DATA SHEET – compliant to GHS)”
CONFIRMS TO EC DIRECTIVE 91/155/EEC, EC REGULATION NO#1272/2008, AMENDED EC REGULATION NO#790/2009 and Complies to The EU Cosmetic Products Regulation (Regulation (EC) No 1223/2009) effective on July 2013., and to EU Commission Regulation No.358/2014/9 of 9th April 2014 amending Annexes II and V, to EU Regulation No No.1223/2009 of The European Parliament and of The Council on Cosmetic products, (Effective Date 31st October 2014) AND to US DEPT.OF LABOR-Occupational Safety & Health Admin directives and compliant to Globally Harmonized System of Classification and Labeling of Chemicals (hereinafter referred to as “the GHS”)., and Complies and Confirms to the Requirements of State of California Proposition 65.

A Quality Management System, compliant to the International Standard ISO 9001, was used to manufacture and test this material

<http://www.osha.gov/dsg/hazcom/ghs.html>

http://www.unece.org/trans/danger/publi/ghs/ghs_welcome_e.html

<http://www.hc-sc.gc.ca/ahc-asc/intactiv/ghs-sgh/index-eng.php>

DATE OF FIRST ISSUE	February 10th 1996-Reviewer - Dr Balasubramaniam PhD
DATE OF LATEST REVISION	Dec. 19th 1996- Rev`wer- Dr Fergus Jes .G.Velasquez Bsc. Med Tech, MD February 10th 2012 – Reviewer=Joshua Teo February 5 th 2013 – Reviewer = Balasubramaniam M PhD 12th February 2015 - Joshua Teo BSc. Chem, Balasubramaniam M PhD & Oksana Nemchenko MD 15th May 2016 - Joshua Teo BSc. Chem, Balasubramaniam M PhD & Oksana Nemchenko MD
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:	<i>Pyrus Malus (Apple) Fruit Extract (AND) Malus Domestica Fruit Extract (AND) Water</i>
Chinese Translation	苹果 (PYRUS MALUS) 果提取物 苹果 (MALUS DOMESTICA) 果提取物 水 AQUA (WATER)
INTERNATIONAL CHEMICAL IDENTIFICATION <i>(EC REGULATION NO#1272/2008 AMENDED NO#790/2009)and Compliant to the GHS</i>	PYRUS MALUS FRUIT (APPLE) EXTRACT MALUS DOMESTICA FUIT EXTRACT AQUA (WATER)
FDA NAME	FRUIT EXTRACT
MANUFACTURER :	CAMPO RESEARCH Pte Ltd

(cGMP MFG. FACILITIES) :	Hudson Industrial Bldg., #05-02, 14,New Industrial Road, Singapore 536203
EMERGENCY TELEPHONE NUMBERS:	(65)-63833631/(65)-63228503 (Singapore)
2. HAZARDS IDENTIFICATION	
NOT CLASSIFIED AS DANGEROUS ACCORDING TO DIRECTIVE 67/548/EEC OR ITS AMENDMENTS.	DIVISION 1.6; NON-HAZARDOUS NO HAZARD STATEMENT
HAZARD CLASS and CATEGORY CODE(s)	PICTOGRAM : NONE
HAZARD STATEMENT CODE(s) <i>(EC REGULATION NO#1272/2008 AMENDED NO#790/2009) and compliant to the GHS</i>	No GHS Pictogram (Totally Non-Hazardous) Division 1.6; NO HAZARD STATEMENT
GHS CLASSIFICATION : This material is Non-hazardous according To UN-GHS Criteria.	PICTOGRAM : NONE No GHS Pictogram (Totally Non-Hazardous) Division 1.6: No Hazard Statement.
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 (Apple) Fruit Extract 21160 – Malus Domestica Fruit Extract 9423 – Aqua
CAS # CAS # EU	N/A – Pyrus Malus (Apple) Fruit Extract 85251-63-4 (EU) – Pyrus Malus Fruit Extract 89957-48-2 – Malus Domestica Fruit Extract N/A (EU) – Malus Domestica Fruit Extract 7732-18-5 – Aqua (Water)
CAS NO# (CAS Name) <i>(EC REGULATION NO#1272/2008 AMENDED NO#790/2009)and compliant to the GHS</i>	85251-63-4 – Pyrus Malus Fruit Extract (EU) 7732-18-5 – Water (Aqua)
EINECS Name and Number EINECS# EU	N/A – Pyrus Malus (Apple) Fruit Extract 286-475-7 (EU) – Pyrus Malus Fruit Extract 289-567-5 (1) – Malus Domestica Fruit Extract N/A (EU) – Malus Domestica Fruit Extract 231-791-2(1) – Aqua (Water)
EINECS# (EINECS Name) <i>(EC REGULATION NO#1272/2008 AMENDED NO#790/2009) and compliant to the GHS</i>	286-475-7 – Pyrus Malus Fruit Extract (EU) 231-791-2(1) – Water (Aqua)
EINECS Name and Number EINECS# EU European Commission–Health & Consumer Cosmetics–Cosing	Pyrus Malus (Apple) Fruit Extract http://ec.europa.eu/consumers/cosmetics/cosing/index.cfm?fuseaction=search.details_v2&id=58863 Pyrus Malus Fruit Extract – 286-475-7 (EU) Malus Domestica Fruit Extract http://ec.europa.eu/consumers/cosmetics/cosing/index.cfm?fuseaction=search.details_v2&id=58863

	<p>cfm?fuseaction=search.details_v2&id=83460 Malus Domestica Fruit Extract – N/A (EU)</p> <p>Aqua (Water) http://ec.europa.eu/consumers/cosmetics/cosing/index.cfm?fuseaction=search.details_v2&id=31959 Aqua – 231-791-2 (EU)</p>
RISK PHRASES	None
SAFETY PHRASES 25-26	Not mandatory
<u>GHS CLASSIFICATION :</u> This material is Non-hazardous according To UN-GHS Criteria.	PICTOGRAM : NONE
<u>GHS LABEL ELEMENTS:</u>	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.
ORAL INGESTATION:	Essentially edible in small quantities
SKIN CONTACT:	Contact will probably cause no more than a temporary slight irritation. Wash off in flowing water or shower.
5 FIRE FIGHTING MEASURES	
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	
PHYSICAL FORM:	Liquid
COLOUR:	Light Yellowish Brown
ODOUR:	Characteristic- slight
BOILING POINT:	90 deg. cent.
MELTING POINT:	-
VISCOSITY:	-
FLASH POINT:	closed cup
FLAMMABILITY SOLID/GAS:	N/A
AUTO FLAMMABILITY:	N/A
SPECIFIC REFRACTIVE:	1.350 - 1.450
EXPLOSIVE PROPERTIES:	N/A
pH: (100% Concentrate)	6.50 – 7.50
OXIDIZING PROPERTIES:	N/A
VAPOUR PRESSURE:	0.90
DENSITY: (20 deg. Cent.)	1.110 - 1.320
WATER SOLUBILITY:	COMPLETE

OTHER SOLUBILITY:	In most cosmetic solvents
RESIDUE ON DRYING (160 deg C Mettler):	45-75 %
PARTITION COEFFICIENT: (OCTANOL/WATER)	-
EXPLOSIVE LIMITS:	-
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
ORAL:	LD 50> 8,000 mg/kg (Body weight) Rat Essentially Non-Toxic and Edible in Small Quantity. Expected To Be Essentially Non Toxic
DERMAL:	N/A
INHALATION:	8,000 MG/KG (Body Wt.); CATEGORY 5 Essentially Non-Toxic and Edible in Small Quantity.
SPECIFIC CONCENTRATION LIMITS M-FACTORS (EC REGULATION NO#1272/2008 AMENDED NO#790/2009) compliant to the GHS.	
TOXIC EFFECTS:	
SKIN:	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 Human repeated patch test 48 hours: 50/50 completely non-irritating/ non-erythema causing ingredient at 100% concentrate in water on 50 human volunteers.
EYE:	Very mild / minimal- not a transient conjunctival irritant at 10% concentrate in water (Eyetex Classification). <i>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.</i>
12 ECOLOGICAL INFORMATION	
BIODEGRATION:	Expected to be ultimately biodegradable.
FISH TOXICITY:	No data
BACTERIAL & VIRAL TOXICITY:	No data
WGK CLASS:	WGK (Self Classification)
13 DISPOSAL CONDITIONS	
DISPOSE OFF ACCORDING TO A RECOGNISED METHOD OF CHEMICAL WASTE DISPOSAL.	
14 TRANSPORT INFORMATION	
UN NUMBER# :	N/A
UN NAME:	Not Assigned
IMDG CODE/CLASS:	Not Hazardous
IMDG CODE PAGE NO.	N/A
ICAO/IATA AIR CLASS:	Non-Hazardous
ICAO/IATA AIR CLASS PACKING GROUP:	N/A
RID/ADR CLASS:	Non-Hazardous
ADNR CLASS:	Non-Hazardous
LABELLING: (EC REGULATION NO#1272/2008 AMENDED NO#790/2009) and compliant to	

<i>the GHS.</i>	
PICTOGRAM SIGNAL WORD CODE(s):	No GHS Pictograms (Totally Non-Hazardous)
HAZARD STATEMENT CODE(s):	Division 1.6; No Hazard Statement
SUPPLEMENTARY HAZARD STATEMENT CODE(s):	Similar Division 1.6; No Hazard Statement
15 REGULATORY INFORMATION	
OCCUPATIONAL EXPOSURE LIMITS:	N/A
U.S. State of California Proposition 65 INGREDIENTS Presence	None (Exempted from CA Prop 65 Register)
EU Commission Regulation No.358/2014/9 of 9th April 2014 amending Annexes II and V, to EU Regulation No No.1223/2009 of The European Parliament and of The Council on Cosmetic products	“Contains No Parabens and nor contains any Branched Chain Parabens”. (EU Regulation No.358/2014/9 of 9 th April 2014)
16 OTHER INFORMATION	
USES AS A COSMETIC ADDITIVE	1.0 - 5.0 %
	*Please take note that all specifications are liable to changes without prior notice.
Campo jtc ph	

Campo Total Apple’s Enzymes Extract ©.

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ENZYME: EC 2.1.2.1

Official Name:

GLYCINE HYDROXYMETHYLTRANSFERASE

Alternative Names:

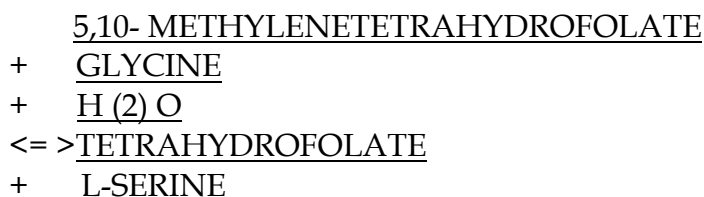
SERINE HYDROXYMETHYLTRANSFERASE

SERINE ALDOLASE

THREONINE ALDOLASE

SERINE HYDROXYMETHYLASE

Reaction catalyzed:



Co-factor(s): PYRIDOXAL PHOSPHATE

Comment(s):

- ALSO CATALYSES THE REACTION OF GLYCINE WITH ACETALDEHYDE TO FORM L-THREONINE, AND WITH 4-TRIMETHYLAMMONIIBUTANAL 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;

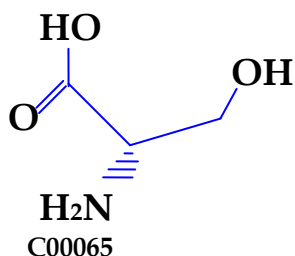
P07511, GLYC RABIT;

P37291, GLYC YEAST;

P34899, GLYM PEA ;

P49358, GLYN FLAPR;

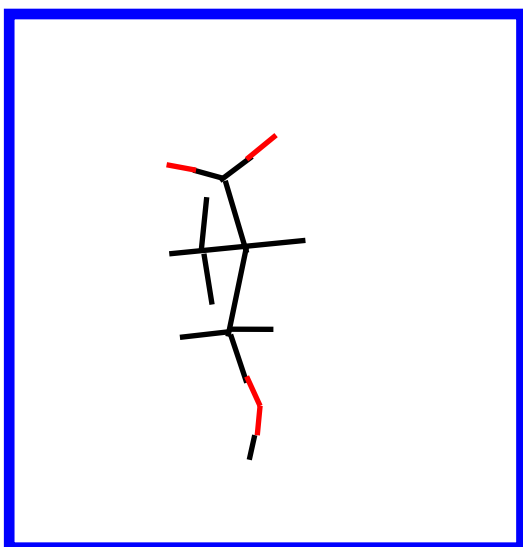
ENTRY **C00065**
 NAME **L-Serine**
 FORMULA **C3H7NO3**



DBLINKS CAS: 56-45-1

EC: 1.4.1.7	1.5.1.17	2.1.2.1	2.3.1.30	2.3.1.50
2.6.1.44	2.6.1.45	2.6.1.51	2.6.1.58	2.7.1.80
2.7.8.4	2.7.8.8	2.8.1.4	3.1.3.3	3.2.1.110
3.5.1.61	4.2.1.13	4.2.1.16	4.2.1.20	4.2.1.22
4.2.1.50	6.1.1.11	6.3.2.14		

L-serine (KLM0000340)



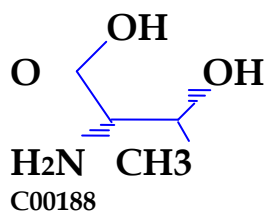
Config Rule:

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



DBLINKS CAS: 72-19-5

EC:	<u>1.1.1.103</u>	<u>1.5.1.17</u>	<u>2.1.2.1</u>	<u>4.1.2.5</u>	<u>4.2.1.16</u>
	<u>4.2.99.2</u>	<u>5.1.1.6</u>	<u>6.1.1.3</u>		

LinkDB Search Result

Database: LinkDB

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

COMPOUND : C00018 - RELATED ENTRIES (Total 242 hits.):

Database	Entry	Link type
1. ENZYME	<u>1.1.1.65</u>	original
2. ENZYME	<u>1.4.3.5</u>	original
3. ENZYME	<u>1.4.4.2</u>	original
4. ENZYME	<u>2.1.2.1</u>	original
5. ENZYME	<u>2.1.2.5</u>	original
6. ENZYME	<u>2.1.2.6</u>	original
7. ENZYME	<u>2.3.1.29</u>	original
8. ENZYME	<u>2.3.1.37</u>	original
9. ENZYME	<u>2.3.1.47</u>	original
10. ENZYME	<u>2.3.1.50</u>	original
11. ENZYME	<u>2.4.1.1</u>	original
12. ENZYME	<u>2.6.1.1</u>	original
13. ENZYME	<u>2.6.1.10</u>	original
14. ENZYME	<u>2.6.1.11</u>	original
15. ENZYME	<u>2.6.1.12</u>	original
16. ENZYME	<u>2.6.1.13</u>	original
17. ENZYME	<u>2.6.1.14</u>	original
18. ENZYME	<u>2.6.1.15</u>	original
19. ENZYME	<u>2.6.1.17</u>	original
20. ENZYME	<u>2.6.1.18</u>	original
21. ENZYME	<u>2.6.1.19</u>	original
22. ENZYME	<u>2.6.1.2</u>	original
23. ENZYME	<u>2.6.1.20</u>	original
24. ENZYME	<u>2.6.1.21</u>	original
25. ENZYME	<u>2.6.1.24</u>	original
26. ENZYME	<u>2.6.1.25</u>	original
27. ENZYME	<u>2.6.1.26</u>	original
28. ENZYME	<u>2.6.1.27</u>	original
29. ENZYME	<u>2.6.1.3</u>	original
30. ENZYME	<u>2.6.1.33</u>	original
31. ENZYME	<u>2.6.1.34</u>	original
32. ENZYME	<u>2.6.1.35</u>	original
33. ENZYME	<u>2.6.1.36</u>	original
34. ENZYME	<u>2.6.1.37</u>	original
35. ENZYME	<u>2.6.1.39</u>	original

PROSITE: PDOC00090 (Documentation)

{ PDOC00090 }

{ PS00096; SHMT }

Serine hydroxymethyltransferase pyridoxal - phosphate attachment site

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 is 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]

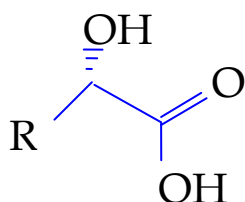
- Sequences known to belong to this class detected by the pattern: ALL
- Other sequence(s) detected in SWISS-PROT: None
- Last update: June 1994 / Pattern and text revised.

[1] Usha R., Savithri H.S., Rao N. A.
 Biochem. Biophys. Acta 1204: 75 83 (1994).

ENTRY	EC <u>1.1.1.27</u>
NAME	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

DISEASE PATH: MAP00620 Pyruvate and acetyl-CoA metabolism
 PATH: MAP00640 Propanoate metabolism
 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
 2LDB 2LDX 3LDH 5LDH 6LDH 8LDH 9LDB
 9LDT
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



C04096

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](#);

P00727, [AMPL BOVIN](#);

P47707, [AMPL MYCSA](#);

P31427, [AMPL SOLTU](#);

P45334, [AMPA HAEIN](#);

P28838, [AMPL HUMAN](#);

P28839, [AMPL PIG](#);

P14904, [AMPL YEAST](#);

P30184, [AMPL ARATH](#);

P47631, [AMPL MYCGE](#);

P27888, [AMPL RICPR](#);

ENTRY	EC <u>3.4.11.1</u>
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	<u>Peptide</u> <u>H₂O</u>
PRODUCT	<u>N-Terminal amino acid</u> <u>Peptide</u>
INHIBITOR	<u>Amastatin</u>
COFACTOR	<u>Zinc</u>
EFFECTOR	<u>Heavy metal ion</u>
COMMENT	A zinc enzyme isolated from pig kidney and cattle lens; activated By heavy metal ions formerly EC <u>3.4.1.1</u> Inhibited by Amastatin {H. Kim and W.N. Lipscomb, Biochemistry, 32, 8465-8478 (1993) }.
MOTIF	PS: <u>PS00631</u> N-T-D-A-E-G-R-L
DBLINKS	University of Geneva ENZYME DATA BANK: <u>3.4.11.1</u> PDB: <u>1BLL</u> <u>1BPM</u> <u>1BPN</u> <u>1LAM</u> <u>1LAN</u> <u>1LAP</u> <u>1LCP</u> PIR: <u>A33879</u> <u>A40631</u> <u>A42432</u> <u>A48788</u> <u>APBOL</u> <u>APECA</u> <u>PQ0470</u> <u>PT0429</u> <u>PT0430</u> <u>PT0431</u> <u>S22399</u>

///

DBGET integrated database retrieval system, GenomeNet (Kyoto Center)

PROSITE: PDOC00548 (Documentation)

{ PDOC00548 }

{ PS00631; CYTOSOL AP }

CYTOSOL AMINOPEPTIDASE

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.

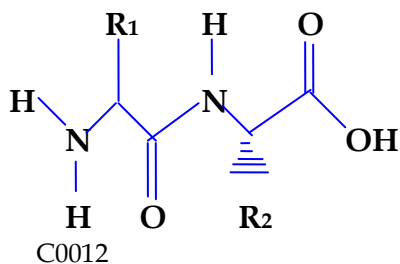
Cytosol aminopeptidase is highly similar to *Escherichia coli* pepA, a manganese dependent aminopeptidase. Residues involved in zinc ion-binding [2] in the mammalian enzyme are absolutely conserved in pepA where they presumably bind manganese.

A cytosol aminopeptidase from *Rickettsia prowazekii* [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].

ENTRY **C00012**
NAME **peptide**



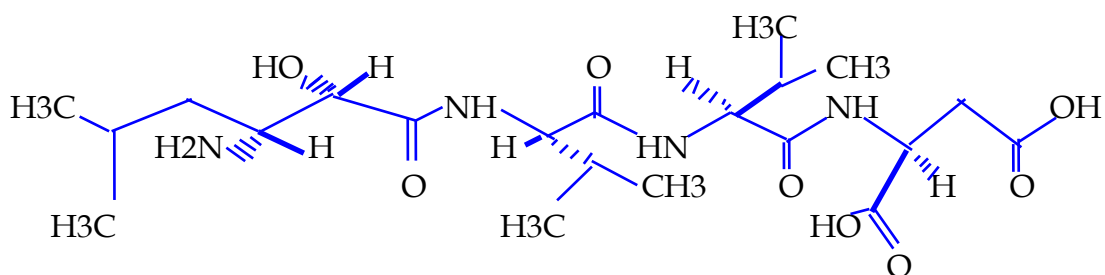
DBLINKS	EC:	2.3.1.88	2.3.2.2	3.4.11.1	3.4.11.2	3.4.11.5
		3.4.11.7	3.4.11.9	3.4.11.10	3.4.11.12	3.4.11.13
		3.4.11.14	3.4.11.15	3.4.11.16	3.4.11.17	3.4.11.18
		3.4.14.1	3.4.14.4	3.4.14.5	3.4.14.9	3.4.15.1
		3.4.15.4	3.4.16.1	3.4.16.2	3.4.16.4	3.4.17.1
		3.4.17.2	3.4.17.3	3.4.17.4	3.4.17.6	3.4.17.10
		3.4.17.11	3.4.17.12	3.4.17.15	3.4.17.16	3.4.17.17
		3.4.17.18	3.4.17.19	3.4.18.1	3.4.19.1	3.4.19.2
		3.4.19.3	3.4.19.5	3.4.19.7	3.4.19.9	3.4.19.10
		3.4.21.1	3.4.21.2	3.4.21.3	3.4.21.4	3.4.21.5
		3.4.21.6	3.4.21.7	3.4.21.10	3.4.21.12	3.4.21.13
		3.4.21.14	3.4.21.15	3.4.21.16	3.4.21.17	3.4.21.18
		3.4.21.19	3.4.21.20	3.4.21.25	3.4.21.26	3.4.21.32
		3.4.21.36	3.4.21.37	3.4.21.39	3.4.21.40	3.4.21.43
		3.4.21.44	3.4.21.47	3.4.21.49	3.4.21.50	3.4.21.51
		3.4.21.52	3.4.21.53	3.4.21.57	3.4.21.58	3.4.21.59
		3.4.21.61	3.4.21.62	3.4.21.63	3.4.21.64	3.4.21.65
		3.4.21.66	3.4.21.67	3.4.21.69	3.4.21.70	3.4.21.71
		3.4.21.72	3.4.22.1	3.4.22.2	3.4.22.3	3.4.22.4
		3.4.22.5	3.4.22.6	3.4.22.7	3.4.22.8	3.4.22.10
		3.4.22.11	3.4.22.12	3.4.22.13	3.4.22.14	3.4.22.15
		3.4.22.16	3.4.22.17	3.4.22.24	3.4.22.25	3.4.22.27
		3.4.22.30	3.4.22.31	3.4.22.32	3.4.22.33	3.4.22.34
		3.4.22.35	3.4.22.36	3.4.22.37	3.4.23.1	3.4.23.3
		3.4.23.4	3.4.23.5	3.4.23.12	3.4.23.13	3.4.23.14
		3.4.23.16	3.4.23.17	3.4.23.18	3.4.23.19	3.4.23.20
		3.4.23.21	3.4.23.22	3.4.23.23	3.4.23.24	3.4.23.25
		3.4.23.26	3.4.23.27	3.4.23.28	3.4.23.29	3.4.23.30
		3.4.23.31	3.4.23.32	3.4.23.33	3.4.23.34	3.4.23.35
		3.4.23.36	3.4.23.37	3.4.23.38	3.4.23.39	3.4.24.1
		3.4.24.3	3.4.24.4	3.4.24.5	3.4.24.6	3.4.24.7
		3.4.24.11	3.4.24.12	3.4.24.14	3.4.24.15	3.4.24.16
		3.4.24.17	3.4.24.18	3.4.24.19	3.4.24.20	3.4.24.21
		3.4.24.22	3.4.24.23	3.4.24.24	3.4.24.25	3.4.24.26
		3.4.24.27	3.4.24.28	3.4.24.29	3.4.24.30	3.4.24.31
		3.4.24.32	3.4.24.33	3.4.24.34	3.4.24.35	3.4.24.36
		3.4.24.37	3.4.24.38	3.4.24.39	3.4.24.40	3.4.24.41
		3.4.24.42	3.4.24.43	3.4.24.44	3.4.24.45	3.4.24.46

3.4.24.47	3.4.24.48	3.4.24.49	3.4.24.50	3.4.24.51
3.4.24.52	3.4.24.53	3.4.24.54	3.4.99.36	3.4.99.37
3.4.99.38	3.4.99.39	3.4.99.40	3.4.99.41	3.4.99.42
3.4.99.44	3.4.99.45	3.4.99.46	3.5.1.52	

///

DBGET integrated database retrieval system, GenomeNet (Kyoto center)

ENTRY C01552
NAME Amastatin
FORMULA C21 H38 N4 O8



C01552

DBLINKS CAS: 67655-94-1
 EC: [3.4.11.1](#)

ENTRY C00038
NAME Zinc
 Zn 2+
FORMULA Zn

Zn

C00038

DBLINKS CAS: 7440-66-6

ENZYME: EC 3.1.1.3

Official Name:

TRIACYLGLYCEROL LIPASE

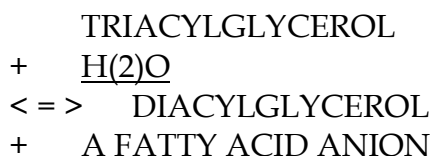
Alternative Name(s):

LIPASE

TRIGLYCERIDE LIPASE

TRIBUTYRASE

Reaction catalyzed:



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

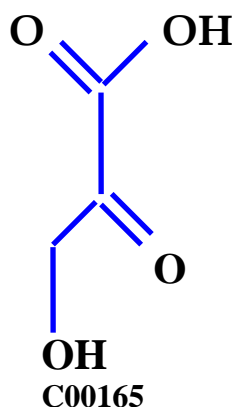
CONGENITAL LIPASE DEFICIENCY; MIM: 246600

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

ENTRY C00165
NAME Diacylglycerol
FORMULA C3H4O4



DBLINKS EC: 2.3.1.22 2.3.1.73 2.3.1.77 2.4.1.184 3.1.1.3
3.1.1.34 3.1.4.10 3.1.4.11

PROSITE: PDOC00110 (Documentation)

{ PDOC00110 }

{ PS00120; LIPASE SER }

Lipase's, serine active site

Triglyceride lipases (EC3.1.1.3) [1] are lipolytic enzymes that hydrolyzes 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.

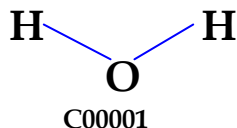
- Consensus pattern : [LIV] -x- [IVFY]- [LIVST] -G- [HYWV] -S-x-G- [GSTAC]
[S is the active site residue]
- Sequences known to belong to this class detected by the pattern : ALL.
- Other sequence(s) detected in SWISS-PROT: 16.
- Note: Drosophila vittellogenins are also related to lipases [5], but they 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	Triglycero-protein acylhydrolase
REACTION	Triacylglycerol + water = Diacylglycerol + a- carboxylate
SUBSTRATE	Triacylglycerol Water
PRODUCT	Diacylglycerol Carboxylate
COMMENT	Hydrolyses triacylglycerols in chylomicrons and low-density lipoproteins Also hydrolyses diacylglycerol.
DISEASE	<u>MIM: 238600</u> Hyperlipoproteinemia I
MOTIF	PS: <u>PS00120</u> [LIV]-X-[LIVFY]- [LIVST]-G- [HYWV]-S-x-G-[GSTAC]
DBLINKS	University of Geneva ENZYME DATA BANK: <u>3.1.1.34</u>

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
Water
FORMULA H2O



DBLINKS CAS: 7732-18-5

ENTRY EC 2.1.2.1
NAME Glycine hydroxymethyltransferase
 Serine aldolase
 Threonine aldolase
 Serine hydroxymethylase
CLASS Transverses
 Transferring one-carbon groups
 Hydroxymethyl-, formyl- and related transverses
SYSNAME 5,10- Methylene tetrahydrofolate : glycine hydroxymethyltransferase
REACTION 5,10- Methylene tetrahydrofolate + Glycine + H2O = Tetrahydrofolate + L- Serine
SUBSTRATE 5,10- Methylene tetrahydrofolate
 Acetaldehyde
 4-Trimethylammonio butanal
 Glycine
 H2O
PRODUCT Tetrahydrofolate
 L-Serine
 L-Threonine
 3-hydroxy-N6, N6-trimethyl-L-lysine
COFACTOR Pyridoxal phosphate
COMMENT A pyridoxal-phosphate protein. Also catalyses the reaction of glycine with acetaldehyde to form L-threonine, and with 4-trimethylammonio-butanal to form 3-hydroxy-N6, N6,N6-trimethyl-L-lysine.
PATHWAY PATH: MAP00260 Glycine, serine and threonine metabolism
 PATH: MAP00460 Cyanoamino acid metabolism
 PATH: MAP00670 One carbon pool by folate
 PATH: MAP00680 Methane metabolism
 PATH: MAP00700 Glyoxylate cycle
 PATH: MAP00750 Vitamin B6 metabolism
MOTIF PS: PS00096 [ST] (4) -H-K-[ST]-L-x-G-x-R- [GSA] (2)
DBLINKS University of Geneva ENZYME DATA BANK: 2.1.2.1
 PIR:
A33696 A40202 A42241 A46746 A56662 B46746 B48427

B53525

IQ1016

S15203

S29348

S34379

S40212

S40213

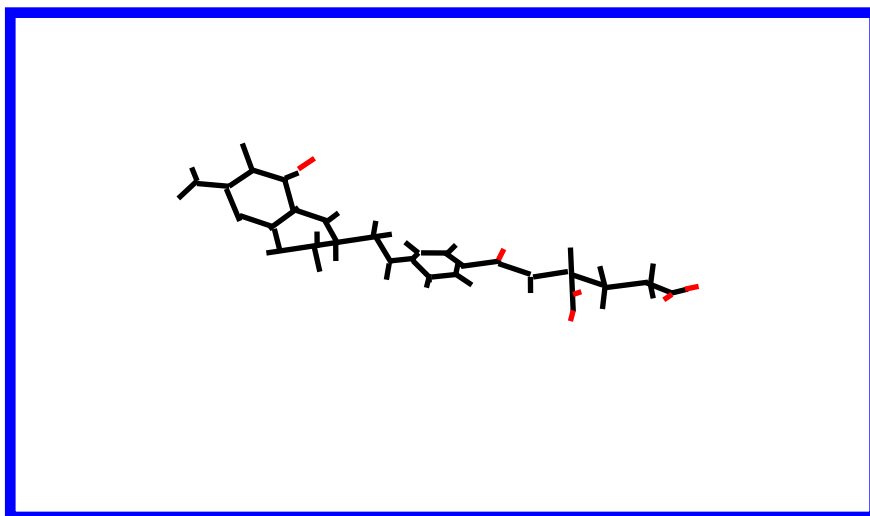
S40218

S61632

XYECS

XYRBSC

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:

ENDOXYDROLYSIS 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.

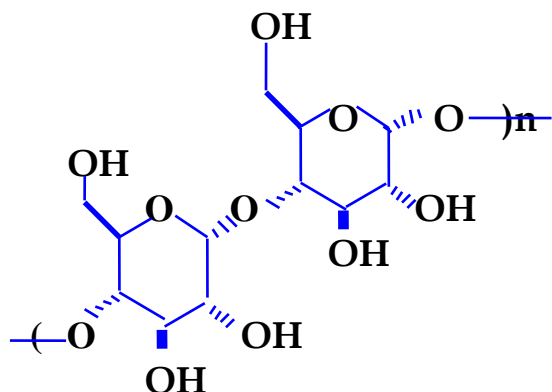
cross-reference(s):

- EMP / PUMA: [3.2.1.1](#)
- KYOTO UNIVERSITY LIGAND CHEMICAL DATABASE: [3.2.1.1](#)
- SWISS-PROT

P27935,	AM2A ORYSA;	P27932,	AM3A ORYSA;	P27937,	AM3B ORYSA;
P27939,	AM3C ORYSA;	P27933,	AM3D ORYSA;	P27934,	AM3E ORYSA;
P72940,	AMC1 ORYSA;	P97941,	AMC2 ORYSA;	P22630,	AMY1 AERHY;
PO9961,	AMY1 DICTH;	P25718,	AMY1 ECOLI;	P00693,	AMY1 HORVU;
P17654,	AMY1 DICTH;	P21567,	AMY1 SACFI;	P19269,	AMY1 SCHOC;
Q09840,	AMY1 SCHPO;	P14898,	AMY2 DICTH;	P26612,	AMY2 ECOLI;
P04063,	AMY2 HORVU;	P26613,	AMY2 SALTY;	P14899,	AMY3 DICTH;
P04747,	AMY3 HORVU;	P08117,	AMY3 WHEAT;	P04748,	AMY4 HORVU;
P04749,	AMY5 HORVU;	P04750,	AMY6 HORVU;	P41131,	AMYA AERHY;
P10529,	AMYA ASPOR;	P08144,	AMYA DROME;	P17859,	AMYA VIGMU;
P21543,	AMYB BACOP;	P19961;	AMYC HUMAN;	P04746,	AMYP HUMAN;
P00688,	AMYP MOUSE;	P00690,	AMYP PIG;	P00689,	AMYP RAT;
P17692,	AMYR BACS8;	P04745,	AMYS HUMAN;	P00687,	AMYP RAT ;
P29957,	AMY ALTHA;	P30292,	AMY ASPSH ;	P00692,	AMY BACAM ;
P08137,	AMY BACCL;	P06278,	AMY BAACL;	P20845,	AMY BACME ;
P06279,	AMY BACST ;	P00691,	AMY BACSU,	P30269,	AMY BUTFI ;
P23671,	AMY CLOAB ;	P49274,	AMY DERPT ;	P49067,	AMY PURFU;
P30270,	AMY STRGR ;	P08486,	AMY STRHY ;	Q05884,	AMY STRLI;
P09794,	AMY STRLM;	P27350,	AMY STRTL;	P22998,	AMY STRVL ;
P29750,	AMY TECU;	P26828,	AMY THETU;	P09107,	AMY TRICA;
P38939,	APU THEET ;	P36905,	APU THESA;	P38536,	APU THETU ;
P16950,	APU THETY;				

ENTRY C00930

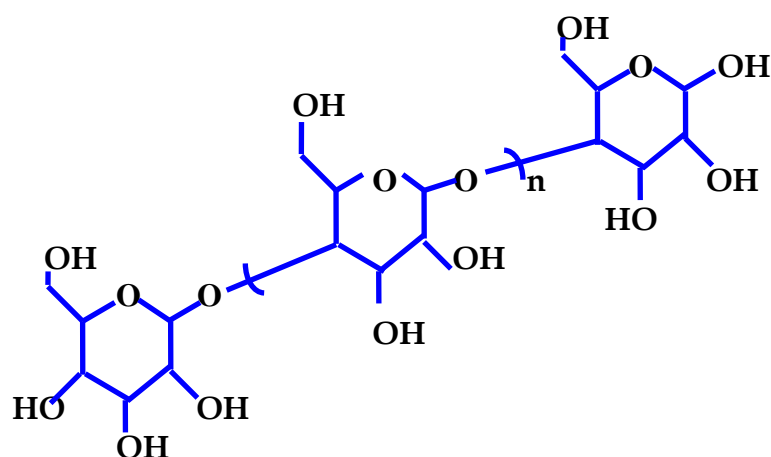
NAME Oligosaccharide



C00930

DBLINKS EC: 3.2.1.1 3.2.1.123
///

ENTRY C00420
NAME Polysaccharide



C00420

DBLINKS EC: 3.2.1.1 3.2.1.2 3.2.1.3 3.2.1.94

ENTRY **EC 3.2.1.1**

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

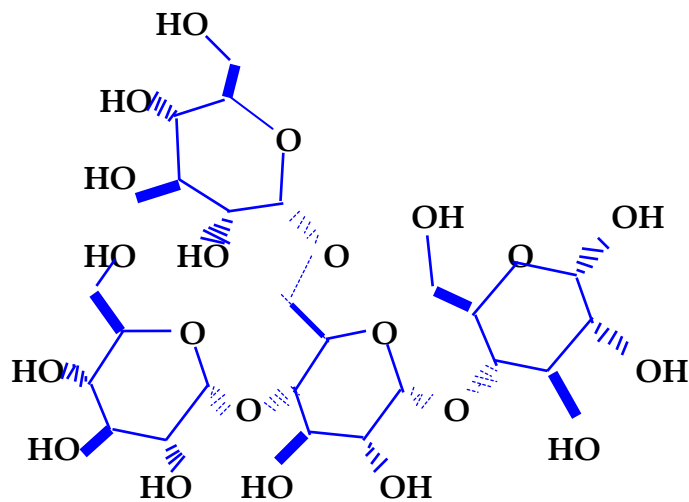
COMMENT Acts on starch, glycogen and related polysaccharides and
oligosaccharides in a random manner; reducing groups are
liberated in the alpha-configuration.

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**



C00182

DBLINKS EC [2.4.1.18](#) [2.4.1.161](#) [3.2.1.1](#) [3.2.1.2](#) [3.2.1.3](#)
 [3.2.1.33](#) [3.2.1.41](#) [3.2.1.68](#)

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,	<u>AAT1 ARATH ;</u>	P28011,	<u>AAT1 MEDSA ;</u>	P46645,	<u>AAT2 ARATH ;</u>
P46644,	<u>AAT3 ARATH ;</u>	P46646,	<u>AAT4 ARATH ;</u>	Q02635,	<u>AATA RHIME ;</u>
Q06191,	<u>AATB RHIME ;</u>	P33097,	<u>AATC BOVINE ;</u>	P00504,	<u>AATC CHICK ;</u>
P28734	<u>AATC DAUCA;</u>	P08906,	<u>AATC HORSE ;</u>	P17174,	<u>AATC HUMAN;</u>
P05201,	<u>AATC MOUSE ;</u>	P37833,	<u>AATC ORYSA ;</u>	P00503,	<u>AATC PIG _____ ;</u>
P12343,	<u>AATC RABIT ;</u>	P13221,	<u>AATC RAT _____ ;</u>	P23542,	<u>AATC YEAST _____ ;</u>
P46248,	<u>AATM ARATH;</u>	P12344,	<u>AATM BOVIN ;</u>	P00508,	<u>AATM CHICK ;</u>
P08907,	<u>AATM HORSE ;</u>	P00505,	<u>AATM HUMAN;</u>	P26563,	<u>AATM LUPAN ;</u>
P05202,	<u>AATM MOUSE;</u>	P00506,	<u>AATM PIG _____ ;</u>	P12345,	<u>AATM RABIT _____ ;</u>
P00507,	<u>AATM RAT _____ ;</u>	Q01802,	<u>AATM YEAST _____ ;</u>	P23034,	<u>AAT BACSP _____ ;</u>
P39643,	<u>AAT BAQCSU ;</u>	P00509,	<u>AAT ECOLI _____ ;</u>	P44425,	<u>AAT HAEIN _____ ;</u>
P36692,	<u>AAT STRGR _____ ;</u>	P14909,	<u>AAT SULSO _____ ;</u>		

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 similar 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 isozyme: 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 cobalamine 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]-LIVMFA]-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.

Unpublished observations (1992).

[2] Sung M. A , Tanizawa k., Tanaka H., Kurmitsu S., Kagmiyama H.,

Hirotsu K., Okamoto A., Higuchi T., soda K..

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.

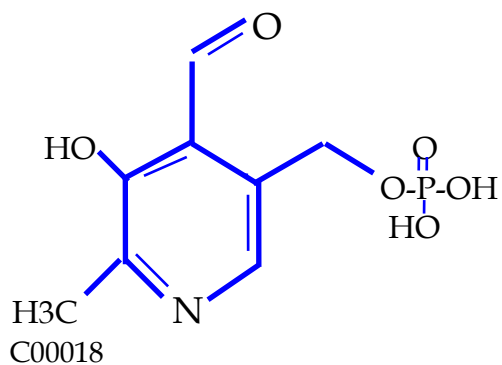
Motif:

PS: PS00105 [GS] - [LIVMFYTAC] - [GSTA] - K - x(2) - [GSALVN] - [LIVMFA] - x -
[GNAR] - x - R - [LIVMA] - [GA]

DBLINKS:

UNIVERSITY OF GENEVA ENZYME DATA BANK: 4.4.1.14

ENTRY C00018
NAME PYRIDOXAL PHOSPHATE
FORMULA C₈H₁₀NO₆P



DBLINKS CAS: 54-47-7

PROSITE; PDOC00011 (documentation)

{ PDOC00011 }

{ PS00011; GLU CARBOXYLATION }

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 Gla-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](mailto:pprice@ucsd.edu)

-Last update: December 1992/ Text revised

[1] Friedman P.A., Przysiecki C.T.

Int j. Biochem19: -7 (1987).

[2] Vermeer C.

Biochem. J. 266:625-636 (1990)

[3] Haack J.A., Rivier J.E., Parks T.N., Mena E.E., Cruz L. j., Olivera B.1,

J. Biol. Chem. 265: 6025-6029 (1990)

[4] Price P.A., Fraser J.D., Metz- Virca G.

Proc. Nat'l. Acad Sci. U.S.A. 84:8335-8339(1987)

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.):

	Database	Entry	Link type
1	ENZYME	<u>2.4.1.161</u>	original
2	ENZYME	<u>2.4.1.18</u>	original
3	ENZYME	<u>3.2.1.1</u>	original
4	ENZYME	<u>3.2.1.2</u>	original
5	ENZYME	<u>3.2.1.3</u>	original
6	ENZYME	<u>3.2.1.33</u>	original
7	ENZYME	<u>3.2.1.41</u>	original
8	ENZYME	<u>3.2.1.68</u>	original
9	LIGAND	<u>2.4.1.161</u>	reverse
10	LIGAND	<u>2.4.1.18</u>	reverse
11	LIGAND	<u>3.2.1.1</u>	reverse
12	LIGAND	<u>3.2.1.2</u>	reverse
13	LIGAND	<u>3.2.1.3</u>	reverse
14	LIGAND	<u>3.2.1.33</u>	reverse
15	LIGAND	<u>3.2.1.41</u>	reverse
16	LIGAND	<u>3.2.1.68</u>	reverse

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. Afire example is when we consume a Vitamin C called Adrenucleo, this nutrient goes directly to our adrenalglands. 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 your 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.

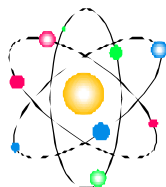
A LACK OF ENZYMES IN YOUR DIET, ROBS YOUR IMMUNE SYSTEM

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 MANNUAL

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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.

[1] Enzyme Nomenclature, NC-IUBMB, Academic Press, New York, (1992).

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:

ktiption@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:

Characters	Content
1 to 2	Two - Character line code. Indicates the type of information contained in the line.
3 to 5	Blank
6 up to 78	Data

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	- - PEPTIDYLGLYCINES WITH A NEUTRAL AMINO ACID RESIDUE IN THE
CC	PENULTIMATE POSITION ARE THE BEST SUBSTRATES FOR THE ENZYME.

CC -1- THE ENZYME ALSO CATALYZES THE DISMUTATION OF THE PRODUCT TO
CC 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-IIUB 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 DELETED ENTR

and for renumbered enzymes:

DE TRANSFERRED ENTRY: x.x.x.x.

where x.x.x.x. is the new, valid, EC number; as shown in the following example:

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 DEGRADES 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

- Subscript and superscript are indicated between brackets: for example NAD⁺ and NADP⁺ are indicated as NAD(+) and NADP(+), H₂O as H(2)O, co₂ as CO(2), etc.
- Greek letters are spelled out.

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
CC 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].

[2] McKusick V.A.
 Mendelian Inheritance in Man
 Catalogs of autosomal dominant, autosomal recessive, and x-linked phenotypes
 Tenth Edition
 John Hopkins University Press, Baltimore, (1991).

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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