

# Data retrieval using DBGET



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# Database retrieval system

- DBGET/LinkDB is an integrated database retrieval system, developed by the Institute for Chemical Research, Kyoto University, and the Human Genome Center of the University of Tokyo<sup>7</sup> , that is available through GenomeNet.
- DBGET provides access to about 20 databases. After querying one of these databases, DBGET presents links to associated information in addition to the list of results.
- The LinkDB database can also be searched directly with a specific entry and provides a list of links to all of the database entries with information about the entry.
- Another unique feature of DBGET is its connection with the Kyoto Encyclopedia of Genes and Genomes (KEGG) database<sup>8</sup> , which is a database of metabolic and regulatory pathways that has been developed by the same group.



# Aim-

To retrieve data using DBGET.

## PROCEDURE



### DBGET Search

DBGET
LinkDB
KEGG2

Search KEGG ENZYME for rubisco large subunit Go Clear

**DBGET** is an integrated database retrieval system for major biological databases, which are classified into five categories:

Category	Main commands			Remark
	bget	bfind	blink	
1. KEGG databases in DBGET	yes	yes	yes	Mirrored at GenomeNet
2. Other DBGET databases	yes	yes	yes	
3. Searchable databases on the Web	no	yes	yes	Used as Web resources
4. Link-only databases on the Web	no	no	yes	
5. PubMed database	yes	no	yes	

Databases in the third category are integrated for keyword search, but the actual data are to be obtained from the original sites. Databases in the fourth category are available only in the LinkDB system. PubMed is a link-only database, but the bget page is generated using the NCBI service in order to better integrate with KEGG and other DBGET databases. DBGET search targets are described on [this page](#).

**1. KEGG Databases in DBGET (19+1 databases)**

Database name		Abbreviation	Content	Remark
	<b>pathway</b>	path	KEGG pathways	See <a href="#">KEGG PATHWAY</a>
	<b>brite</b>	br	Functional hierarchies	See <a href="#">KEGG BRITE</a>
	<b>module</b>	md	KEGG modules	See <a href="#">KEGG MODULE</a>
	<b>orthology</b>	ko	KEGG orthology	See <a href="#">KEGG ORTHOLOGY</a>
<b>genomes</b>	<b>genome</b>	gn	KEGG organisms	See <a href="#">KEGG GENOME</a>
	<b>mgenome</b>	mgnm	Metagenomes	
<b>genes</b>	Complete genomes	org code	Gene catalogs in high-quality genomes	See <a href="#">KEGG GENES</a>



# GenomeNet

Search  for

Database: ENZYME - Search term: rubisco large subunit (Total 2 hits)

2.1.1.127

Click here

[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase; rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase N-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit epsilonN-methyltransferase; S-a ...

2.1.1.259

[fructose-bisphosphate aldolase]-lysine N-methyltransferase; rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase N-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit epsilonN-methyltransferase; S-aden ...

DBGET integrated database retrieval system

Put the name of an organism, protein or enzymes

Select the desired data bases





# ENZYME: 2.1.1.127

[Help](#)

<b>Entry</b>	EC 2.1.1.127 Enzyme
<b>Name</b>	[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase; rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase N-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit epsilonN-methyltransferase; S-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine 6-N-methyltransferase; RuBisCO methyltransferase; RuBisCO LSMT
<b>Class</b>	Transferases; Transferring one-carbon groups; Methyltransferases <a href="#">BRITe hierarchy</a>
<b>Sysname</b>	S-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine N6-methyltransferase
<b>Reaction(IUBMB)</b>	3 S-adenosyl-L-methionine + [ribulose-1,5-bisphosphate carboxylase]-L-lysine = 3 S-adenosyl-L-homocysteine + [ribulose-1,5-bisphosphate carboxylase]-N6,N6,N6-trimethyl-L-lysine [RN:R05179]
<b>Reaction(KEGG)</b>	R05179 <a href="#">Reaction</a>
<b>Substrate</b>	S-adenosyl-L-methionine [CPD:C00019]; [ribulose-1,5-bisphosphate carboxylase]-L-lysine [CPD:C06403]
<b>Product</b>	S-adenosyl-L-homocysteine [CPD:C00021]; [ribulose-1,5-bisphosphate carboxylase]-N6,N6,N6-trimethyl-L-lysine [CPD:C06404]
<b>Comment</b>	The enzyme catalyses three successive methylations of Lys-14 in the large subunits of hexadecameric higher plant ribulose-bisphosphate-carboxylase (EC 4.1.1.39). Only the three methylated form is observed [3]. The enzyme from pea ( <i>Pisum sativum</i> ) also three-methylates a specific lysine in the chloroplastic isoforms of fructose-bisphosphate aldolase (EC 4.1.2.13) [5].
<b>History</b>	EC 2.1.1.127 created 1999, modified 2012
<b>Orthology</b>	K00592 [ribulose-bisphosphate carboxylase]/[fructose-bisphosphate aldolase]-lysine N-methyltransferase
<b>Genes</b>	PDAM: 113668217

- ### All links
- Chemical substance (5)
    - KEGG COMPOUND (5)
  - Chemical reaction (2)
    - KEGG REACTION (1)
    - KEGG RCLASS (1)
  - Gene (641)
    - KEGG ORTHOLOGY (1)
    - KEGG GENES (133)
    - KEGG MGENES (109)
    - RefGene (398)
  - Protein sequence (167)
    - UniProt (131)** ←
    - SWISS-PROT (2)
    - RefSeq(pep) (13)
    - PDBSTR (21)
  - DNA sequence (389)
    - RefSeq(nuc) (23)
    - GenBank (219)
    - EMBL (147)
  - 3D Structure (7)
    - PDB (7)
  - Protein domain (5)
    - InterPro (4)
    - PROSITE(DOC) (1)
  - Others (4)
    - CCP (1)
    - JRE (1)
    - PEQ (1)
    - TCC (1)
  - All databases (1220)
- [Download RDF](#)





**Database: UniProt****Entry: A0A072UM69**LinkDB: [A0A072UM69](#)Original site: [A0A072UM69](#)

ID A0A072UM69\_MEDTR Unreviewed; 490 AA.  
AC A0A072UM69;  
DT 01-OCT-2014, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2014, sequence version 1.  
DT 07-OCT-2020, entry version 36.  
DE SubName: Full=Rubulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltr  
DE EC=2.1.1.127 {ECO:0000313|EMBL:RHN62002.1};  
DE EC=2.1.1.259 {ECO:0000313|EMBL:RHN62002.1};  
DE SubName: Full=Rubisco large subunit N-methyltransferase {ECO:0000313|EMBL:KEH30792.1};  
GN Name=25492966 {ECO:0000313|EnsemblPlants:KEH30792};  
GN OrderedLocusNames=MTR\_4g082305 {ECO:0000313|EMBL:KEH30792.1};  
GN ORFNames=MtrunA17\_Chr4g0042701 {ECO:0000313|EMBL:RHN62002.1};  
OS Medicago truncatula (Barrel medic) (Medicago tribuloides).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae; Pentapetalae;  
OC rosids; fabids; Fabales; Fabaceae; Papilionoideae; 50 kb inversion clade;  
OC NPAAA clade; Hologalegina; IRL clade; Trifolieae; Medicago.  
OX NCBI\_TaxID=3880 {ECO:0000313|EMBL:KEH30792.1, ECO:0000313|Proteomes:UP000002051};  
RN [1] {ECO:0000313|EMBL:KEH30792.1, ECO:0000313|EnsemblPlants:KEH30792, ECO:0000313|Prot  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=A17 {ECO:0000313|EMBL:KEH30792.1}, and cv. Jemalong A17  
RC {ECO:0000313|EnsemblPlants:KEH30792,  
RC ECO:0000313|Proteomes:UP000002051};  
RX PubMed=22089132; DOI=10.1038/nature10625;  
RA Young N.D., Debelle F., Oldroyd G.E.D., Geurts R., Cannon S.B.,  
RA Udvardi M.K., Benedito V.A., Mayer K.F.X., Gouzy J., Schoof H.,  
RA Van de Peer Y., Proost S., Cook D.R., Meyers B.C., Spannagl M., Cheung F.,  
RA De Mita S., Krishnakumar V., Gundlach H., Zhou S., Mudge J., Bharti A.K.,  
RA Murray J.D., Naoumkina M.A., Rosen B., Silverstein K.A.T., Tang H.,  
RA Rombauts S., Zhao P.X., Zhou P., Barbe V., Bardou P., Bechner M.,  
RA Bellec A., Berger A., Berges H., Bidwell S., Bisseling T., Choise N.,  
RA Couloux A., Denny R., Deshpande S., Dai X., Doyle J.J., Dudge A.-M.,  
RA Farmer A.D., Fouteau S., Franken C., Gibelin C., Gish J., Goldstein S.,  
RA Gonzalez A.J., Green P.J., Hallab A., Hartog M., Hua A., Humphray S.J.,  
RA Jeong D.-H., Jing Y., Jocker A., Kenton S.M., Kim D.-J., Klee K., Lai H.,  
RA Lang C., Lin S., Macmil S.L., Magdelenat G., Matthews L., McCorrison J.,  
RA Monaghan E.L., Mun J.-H., Najjar F.Z., Nicholson C., Noirot C.,  
RA O'Bleness M., Paule C.R., Poulain J., Prion F., Qin B., Qu C., Retzel E.F.,  
RA Riddle C., Sallet E., Samain S., Samson N., Sanders I., Saurat O.,  
RA Scarpelli C., Schiex T., Segurens B., Severin A.J., Sherrier D.J., Shi R.,  
..

**All links**

Ontology (4)  
GO (4)  
Chemical reaction (2)  
KEGG ENZYME (2)  
Gene (3)  
KEGG ORTHOLOGY (1)  
KEGG GENES (1)  
NCBI-Gene (1)  
Protein sequence (1)  
RefSeq(pep) (1)  
DNA sequence (2)  
EMBL (2)  
Protein domain (9)  
InterPro (4)  
Pfam (2)  
PROSITE (2)  
SMART (1)  
Literature (3)  
PubMed (3)  
All databases (24)

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DR PROSITE; PS51583; SAM\_MTI27; 1.  
 DR PROSITE; PS50280; SET; 1.  
 PE 4: Predicted;  
 KW Methyltransferase {ECO:0000313|EMBL:KEH30792.1};  
 KW Reference proteome {ECO:0000313|Proteomes:UP000002051};  
 KW S-adenosyl-L-methionine {ECO:0000256|PIRSR:PIRSR009328-1};  
 KW Transferase {ECO:0000313|EMBL:KEH30792.1}.  
 FT DOMAIN 65..289  
 FT /note="SET"  
 FT /evidence="ECO:0000259|PROSITE:PS50280"  
 FT REGION 81..83  
 FT /note="S-adenosyl-L-methionine binding"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT REGION 243..244  
 FT /note="S-adenosyl-L-methionine binding"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT BINDING 223  
 FT /note="S-adenosyl-L-methionine"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT BINDING 223  
 FT /note="Substrate; via carbonyl oxygen"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT BINDING 227  
 FT /note="Substrate"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT BINDING 240  
 FT /note="Substrate; via carbonyl oxygen"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT BINDING 255  
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 FT BINDING 288  
 FT /note="Substrate"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 FT BINDING 301  
 FT /note="Substrate"  
 FT /evidence="ECO:0000256|PIRSR:PIRSR009328-1"  
 SQ SEQUENCE 490 AA; 55253 MW; FE3F1A790D92F835 CRC64;  
 MATIFSGGSV SLFPFHTNKG TSSFATKAPT LHLKKPFSVK SVASLGTEAS VSPAVQTFWK  
 WLQEEGVITA KTPVKASVVP EGLGLVALKD ISRNDVILQV PKRLWINPDA VASSEIGRVC  
 SKLTPWLSVM LFLIRERSRE DSVNKHVYFGI LPQETDSTIY WSEELQELQ GTQLLNTTLS  
 VKEYVKNELC KLEKEIILPN KKLFPSPVTL DDFFWAFGIL RSRAFSRLRN ENLVVIPLAD  
 LINHSARVTT DDHAYEVKGP AGLFSDWYLF SLRSPSVKA GEQVYIYQDL NKSNAELALD  
 YGFIEPNADR YAYTLTLGIS ESDPFFDDKV DVAESNGFSQ TAYFDIFYNR PLPEGMLPYL  
 RLVALGGTDA FLLLESLFRDS INGHLEVPMS RNEELVCKA VRDACKSALA GYHTTIEQDR  
 KLKLEANLESR LAIAVGIREG EKLILQQIDE IFEQKELELD QLEYVQERRL KDLGLCGESG  
 DVLGDLAKYF

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# Conclusion

- DBGET has simpler, but more limited, search methods than either SRS or Entrez. For DBGET, you can search the database of your choice using one of two commands. The bfind command allows searching based on text terms. In response, a list of entries that match the query is presented together with links to associated information about each entry. The bget command searches by entry name or accession number.



# Thank You