

*48'th Annual Meeting of the Biophysical Society of Japan
at Tohoku University, on September 21, 2010*

Tutorials for PDBj 【1】



Haruki Nakamura

***Institute for Protein Research,
Osaka University***

<http://www.protein.osaka-u.ac.jp/rcsfp/pi/>

<http://www.pdbj.org/>

Tutorials 【1】: How to view structures?

(1) Keyword Search → View Structure

→ Download Coordinates

→ Examine Several Information

→ Other Advanced Usages and Links

(2) Search by PDBID

(3) Search by Author Names

(4) Search by Sequence

(5) Advanced Search

Tutorials 【1】: How to view structures?

(1) Keyword Search → View Structure

- Download Coordinates**
- Examine Several Information**
- Other Advanced Usages and Links**

**Let's Search “アスパラギン合成酵素”
or “Asparagine Synthetase”
using the Keyword Search**

Get Entry Data from browser, PDBj Mine

Access to <http://www.pdbj.org/>

The screenshot displays the PDBj Mine website interface. At the top, there is a header with the PDBj logo and navigation links for English, Japanese, simplified Chinese, traditional Chinese, and Korean. Below the header, the main content area is divided into several sections:

- Home**: A section with links to Data Deposition, Search, and Service and Software.
- Data Deposition**: A section with links to ADIT: PDB Deposition and ADIT-NMR.
- Search**: A section with links to Search PDB (Mine/xPSS), Latest Released Search, Sequence-Navigator, Structure-Navigator, SeSAW, Ligand Binding Sites (GIRAF), EM Navigator, Search NMR Data (BMRB), and Status Search.
- Service and Software**: A section with links to JV: Graphic Viewer, Protein Globe, ASH, MAFFTash, Structure Prediction, CRNPRED, Spanner, and SFAS.
- Derived database**: A section with links to eF-site/eF-seek/eF-surf, eProtS, ProMode, and Molecule of the Month.
- Download**: A section with links to PDB Archive/Snapshot Archive.
- Links**: A section with links to various resources.

The main content area also features a search bar with a dropdown menu for "PDB ID or Keyword" and a "Go" button. Below the search bar, there is a section for "Mine" with a link to "Mine日本語ページについて".

The sidebar on the right contains several logos and links, including CPDB, eProtS, Protein Globe, DBCLS, Tanpaku.org, and Bioinformatics Research and Development (BIRD).

Get Entry Data from our browser, PD Bj Mine

(1) Keyword search in Japanese

The screenshot shows the PDBj Mine website interface in Japanese. The top navigation bar includes links for English, Japanese, simplified Chinese, traditional Chinese, and Korean. The main content area is divided into several sections:

- トップページ (Top Page):** Includes links for Data Registration (ADIT: PDB Deposition, ADIT-NMR), Search (Search PDB (Mine/xPSSS), Latest Released Search, Sequence-Navigator, Structure-Navigator, SeSAW, Ligand Binding Sites (GIRAF), EM Navigator, Search NMR Data (BMRB), Status Search), Services & Software (jV: Graphic Viewer, Protein Globe, ASH, MAFFTash, Structure Prediction >> CRNPRED, Spanner, SFAS), Secondary Databases (ePDB/ePDB-seek/ePDB-surf, eProtS, ProMode, Molecule of the Month), Downloads (PDB Archive/Snapshot Archive), and Links.
- データ登録 (Data Registration):** Includes a link for Data Registration (データ登録のご案内 >>).
- 検索 (Search):** Features a search bar with the text "PDB検索 Mine" and "Mine日本語ページについて". Below the search bar is a dropdown menu for "PDB ID or Keyword" and a "Go" button. A link for "詳細条件検索 >>" is also present.
- 最新情報 (Latest Information):** Lists recent updates, including the 48th Annual Meeting of the Japanese Biophysical Society (2010/8/25), a PDF format structure validation report (2010/8/19), and the release of the jV3.8 software (2010/6/30).

A red circle highlights the search input field and the "Go" button in the search section.

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese



The screenshot shows the PDBj Mine search page. At the top, there is a green header bar with the text "検索" (Search). Below this, the "PDB検索 Mine" logo is displayed, with "PDBj" in small red text above "Mine". Under the logo, there is a link "Mine日本語ページについて" (About the PDBj Mine Japanese page). The search input area contains the text "アスパラギン合成酵素" (Asparagine synthetase) in the first field and "PDB ID or Keyword" in the second field, with a dropdown arrow. To the right of the input fields is a "Go" button, which is circled in red. Below the input fields, there is a link "詳細条件検索 >>" (Advanced search conditions >>).

検索

PDB検索 *Mine* PDBj

Mine日本語ページについて

アスパラギン合成酵素 PDB ID or Keyword ▼

Go

詳細条件検索 >>

Get Entry Data from our browser, PDBe Mine

(1) Keyword search in Japanese

Japanese [統計情報](#) [ヘルプ](#) [FAQ](#) [お問い合わせ](#)

[トップページ](#)

データ登録 >>

ADIT: PDB Deposition

ADIT-NMR

検索 >>

Search PDB (Mine/xPSSS)

Latest Released Search

Sequence-Navigator

Structure-Navigator

SeSAW

Ligand Binding Sites (GIRAF)

EM Navigator

Search NMR Data (BMRB)

Status Search

サービス&ソフトウェア >>

jV: Graphic Viewer

Protein Globe

ASH

MAFFTash

Structure Prediction >>

CRNPRED

Spanner

SFAS

二次データベース >>

eF-site/eF-seek/eF-surf

eProtS

Pro Mode

Molecule of the Month

ダウンロード >>

PDB Archive/Snapshot Archive

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBeと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

Mine

検索結果ページ

(PDB-IDをクリックすると、詳細情報をご覧いただけます)

1 - 16/ 44

クエリ: アスパラギン合成酵素 PDB ID or Keyword 表示順: 一件数

変換クエリ: (asparagine synthase) | (asparagine synthetase)

リセット 検索

1ct9		分子名称 タイトル 著者 実験手法 登録日 公開日	: ASPARAGINE SYNTHETASE B (E.C.6.3.5.4) : CRYSTAL STRUCTURE OF ASPARAGINE SYNTHETASE B FROM ESCHERICHIA COLI : Larsen, T.M., Boehlein, S.K., Schuster, S.M., Richards, N.G.J., Thoden, J.B., Holden, H.M., Rayment, I. : X-RAY DIFFRACTION : 1999-08-20 : 1999-12-15
11as		分子名称 タイトル 著者 実験手法 登録日 公開日	: ASPARAGINE SYNTHETASE, L-ASPARAGINE : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE : Nakatsu, T., Kato, H., Oda, J. : X-RAY DIFFRACTION : 1997-12-02 : 1998-12-30
12as		分子名称 タイトル 著者 実験手法 登録日 公開日	: ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP : Nakatsu, T., Kato, H., Oda, J. : X-RAY DIFFRACTION : 1997-12-02 : 1998-12-30

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

Japanese [統計情報](#) [ヘルプ](#) [FAQ](#) [お問い合わせ](#)

[トップページ](#)

データ登録 >>

ADIT: PDB Deposition

ADIT-NMR

検索 >>

Search PDB (Mine/xPSSS)

Latest Released Search

Sequence-Navigator

Structure-Navigator

SeSAW

Ligand Binding Sites (GIRAF)

EM Navigator

Search NMR Data (BMRB)

Status Search

サービス&ソフトウェア >>

JV: Graphic Viewer

Protein Globe

ASH

MAFFTash

Structure Prediction >>

CRNPRED

Spanner

SFAS

二次データベース >>

eF-site/eF-seek/eF-surf

eProtS

ProMode

Molecule of the Month

[ダウンロード >>](#)

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBeと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

Mine

検索結果ページ

(PDB-IDをクリックすると、詳細情報をご覧いただけます)

1 - 2 / 2

クエリ: アスパラギン合成酵素 Oda PDB ID or Keyword 表示順: 一件数

変換クエリ: ((asparagine synthase)) (asparagine synthetase)) Oda

[リセット](#) [検索](#)

11as		分子名称 : ASPARAGINE SYNTHETASE, L-ASPARAGINE タイトル : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE 著者 : Nakatsu, T., Kato, H., Oda, J. 実験手法 : X-RAY DIFFRACTION 登録日 : 1997-12-02 公開日 : 1998-12-30
ダウンロード		
12as		分子名称 : ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE タイトル : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP 著者 : Nakatsu, T., Kato, H., Oda, J. 実験手法 : X-RAY DIFFRACTION 登録日 : 1997-12-02 公開日 : 1998-12-30
ダウンロード		

クエリ: アスパラギン合成酵素 Oda PDB ID or Keyword 表示順: 一件数

変換クエリ: ((asparagine synthase)) (asparagine synthetase)) Oda

[リセット](#) [検索](#)

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

PDBj
Japanese 統計情報 ヘルプ FAQ お問い合わせ

トップページ
データ登録 >>
ADIT: PDB Deposition
ADIT-NMR

検索 >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

サービス&ソフトウェア >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

二次データベース >>
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

ダウンロード >>
PDB Archive/Snapshot Archive

リンク集

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBeと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

Mine 概要[12as]

日本語ページについて
PDBj Mineについて
更新情報

概要 構造情報 実験情報 機能情報 相同蛋白質 ダウンロード/画面表示 外部データベース

PDB ID or Keyword 検索

分子名称	ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE
タイトル	ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP
機能のキーワード	LIGASE, ASPARAGINE SYNTHETASE, NITROGEN FIXATION
由来する生物種	Escherichia coli K12
細胞内の位置	[UNP - ASNA_ECOLI] Cytoplasm
ポリマー鎖の合計数	2
分子量の合計	74226 (詳細は 構造情報のページ)
著者	Nakatsu, T., Kato, H., Oda, J. (登録日: 1997-12-02, 公開日: 1998-12-30)
引用文献	Nakatsu, T., Kato, H., Oda, J. Crystal structure of asparagine synthetase reveals a close evolutionary relationship to class II aminoacyl-tRNA synthetase. <i>Nature Struct. Biol.</i> , 5:15 - 19, 1998.(PubMed: 9437423) (DOI: 10.1038/nsb0198-15)
実験手法	X-RAY DIFFRACTION (2.2[Å])
他のデータベース情報	CATH, CE, FSSP, SCOP, VAST, UniProt (UNP - P00963), eF-site, KEGG (EC 6.3.1.1), GDB, EzCatDB

3次元構造ビューア
jv3 Jmol
jv3とJmolには
Java(TM)Plug in 1.5以上が必要です。

x軸周りに90度回転
250X250 500X500

y軸周りに90度回転
250X250 500X500

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

PDBj
Japanese

[トップページ](#)
[データ登録 >>](#)
ADIT: PDB Deposition
ADIT-NMR

[検索 >>](#)
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

[サービス&ソフトウェア >>](#)
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

[二次データベース >>](#)
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

[ダウンロード >>](#)
PDB Archive/Snapshot
Archive

[リンク集](#)

日本蛋白質構造データバンク(PDB) 生体高分子の立体構造データベース

Mine

概要 構造情報 実験情報

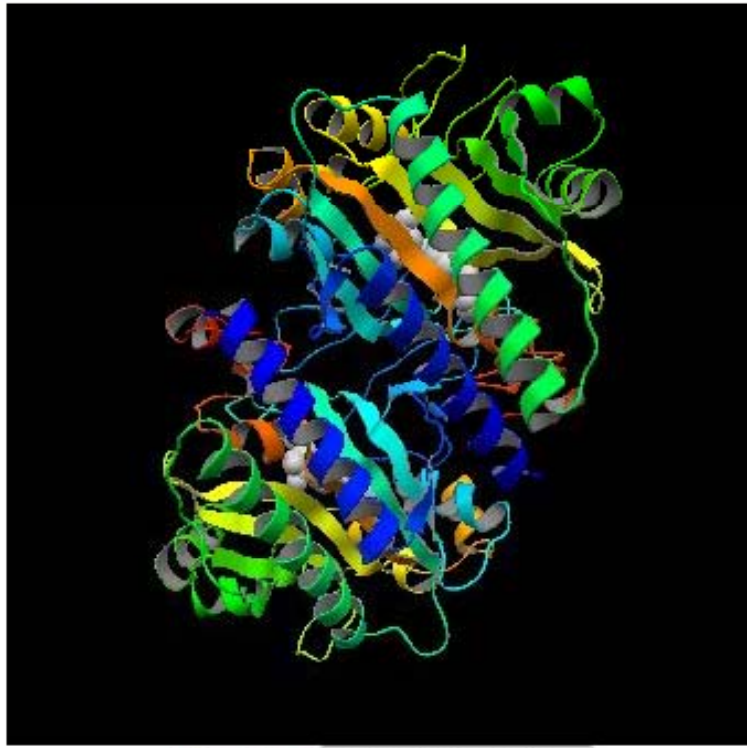
3次元構造ビューア
jv3 / Jmol
jv3 と Jmol には
Java(TM) Plug in 1.5以上が必要です。

x軸周りに90度回転
250X250 500X500

y軸周りに90度回転
250X250 500X500

PDBj Mine jV3 (Applet-Launcher) : 12as - Mozilla Firefox

<http://service.pdbj.org/mine/Detail2?PDBID=12AS&PAGEID=Interactive3&CAR>



jv version 3 アプレットランチャーバージョン

スタイル: ☒ Default ☐ Cartoon ☐ Wireframe ☐ CPK_without_water ☐ CPK

色: ☒ Default ☐ group ☐ chain ☐ atom

[コマンドエリアを表示する](#)

完了

Graphic viewer: jV version 3.8

Access to <http://www.pdbj.org/jV/>

PDBjViewer (jV)

[\[Introduction\]](#) | [Basic Usage](#) | [Graphics Examples](#) | [Download & Install](#) | [Acknowledgment](#) | [jV wiki](#) | [PDBj Home](#)]

Introduction

PDBjViewer (jV, for short) is a program to display molecular graphics of proteins and nucleic acids. jV supports the following features:

- jV can read and display PDBML files, the canonical XML format for the Protein Data Bank.
- Of course, jV can read and display the traditional PDB format files, too.
- RasMol-like usability.
- jV can process more than one molecules.
- jV can display polygons specified by XML. ([XML Schema for polygons](#) is available.)
- Multiple polygons can be processed simultaneously, and be superimposed onto molecular images.
- Animation can be realized. (Each frame of an animation is made of a single MODEL entity of the traditional PDB format file.)
- jV runs on the Java Runtime Environment ([JRE](#)) so that it can work as a stand-alone application as well as [an applet](#).
- The graphics of jV is based on OpenGL (JOGL), thereby producing [fairly beautiful](#) pictures.

[\[Page top\]](#) | [Introduction](#) | [Basic Usage](#) | [Graphics Examples](#) | [Download & Install](#) | [Acknowledgment](#) | [jV wiki](#) | [PDBj Home](#)]


Basic Usage

You can execute basic operations such as rotation and translation with mouse action. Major actions are described in the following table:

Action	Mouse Operation	
	Windows, Linux	Mac OS X
rotate around X (horizontal) axis rotate around Y (vertical) axis	left drag	drag
rotate around Z (anteroposterior) axis	Shift + right drag (move horizontally)	Shift + Command + drag (move horizontally)
translate along X axis (horizontally) translate along Y axis (vertically)	right drag	Command + drag
translate along Z axis (zoom in/out)	Shift + left drag	Shift + drag

Graphic viewer: *jV* version 3.8

Access to *jV* wiki



[page](#) [discussion](#) [view source](#) [history](#)

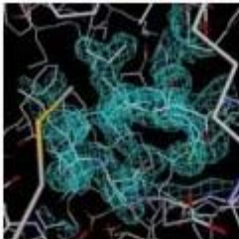
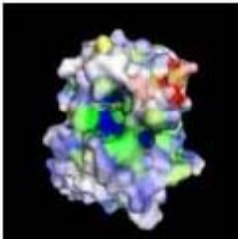
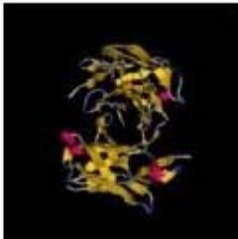
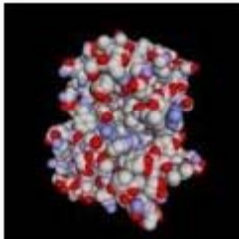
Main Page

Welcome to jV wiki.

jV version 3 (formerly known as PDBjViewer) is a program to display molecular graphics of protein and nucleic acids. jV supports the following features:

- jV can read and display PDBML files, the canonical XML format for the Protein Data Bank.
- Of course, jV can read and display the traditional PDB format files, too.
- RasMol-like usability.
- jV can process more than one molecules.
- jV can display polygons specified by XML. ([XML Schema for polygons](#) is available.)
- Multiple polygons can be processed simultaneously, and be superimposed onto molecular images.
- Animation can be realized.
- jV runs on the Java Runtime Environment ([JRE](#)) so that it can work as a stand-alone application as well as an applet.
- The graphics of jV is based on OpenGL ([JOGL](#)), thereby producing fairly beautiful pictures.

The program 'jV' has been developed by [Kengo Kinoshita](#) ([Graduate School of Information Sciences](#), [Tohoku University](#)) and [Haruki Nakamura](#) ([Institute for Protein Research](#), [Osaka University](#)), with the support from [JST-BIRD](#).



contents

- [How to use](#)
- [Installation](#)
- [Trouble shooting](#)
- [Links](#)
- [Old version](#)

navigation

- [Main page](#)
- [Community portal](#)
- [Current events](#)
- [Recent changes](#)
- [Random page](#)
- [Help](#)

search

toolbox

- [What links here](#)
- [Related changes](#)
- [Special pages](#)
- [Printable version](#)
- [Permanent link](#)

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

PDBj
Japanese 統計情報 ヘルプ FAQ お問い合わせ

トップページ
データ登録 >>
ADIT: PDB Deposition
ADIT-NMR

検索 >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

サービス&ソフトウェア >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

二次データベース >>
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

ダウンロード >>
PDB Archive/Snapshot Archive

リンク集

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBeと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

Mine 概要[12as]

日本語ページについて
PDBj Mineについて
更新情報

概要 構造情報 実験情報 機能情報 相同蛋白質 ダウンロード/画面表示 外部データベース

PDB ID or Keyword 検索

3次元構造ビューア
JV3 / Jmol
JV3とJmolには
Java(TM)Plug in 1.5以上が必要です。

x軸周りに90度回転
250X250 500X500

y軸周りに90度回転
250X250 500X500

エントリー ID (PDB ID)	12as 配列情報 (FASTA形式) PDBファイルのダウンロード
分子名称	ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE
タイトル	ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP
機能のキーワード	LIGASE, ASPARAGINE SYNTHETASE, NITROGEN FIXATION
由来する生物種	Escherichia coli K12
細胞内の位置	[UNP - ASNA_ECOLI] Cytoplasm
ポリマー鎖の合計数	2
分子量の合計	74226 (詳細は 構造情報のページ)
著者	Nakatsu, T., Kato, H., Oda, J. (登録日: 1997-12-02, 公開日: 1998-12-30)
引用文献	Nakatsu, T., Kato, H., Oda, J. Crystal structure of asparagine synthetase reveals a close evolutionary relationship to class II aminoacyl-tRNA synthetase. <i>Nature Struct. Biol.</i> , 5:15 - 19, 1998.(PubMed: 9437423) (DOI: 10.1038/nsb0198-15)
実験手法	X-RAY DIFFRACTION (2.2[Å])
他のデータベース情報	CATH, CE, FSSP, SCOP, VAST, UniProt (UNP - P00963), eF-site, KEGG (EC 6.3.1.1), GDB, EzCatDB

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

PDBj
Japanese

[トップページ](#)
[データ登録 >>](#)
ADIT: PDB Deposition
ADIT-NMR

[検索 >>](#)
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

[サービス&ソフトウェア >>](#)
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

[二次データベース >>](#)
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

[ダウンロード >>](#)
PDB Archive/Snapshot Archive

[リンク集](#)

日本蛋白質構造データバンク(PDBj)
生体高分子の立体構造データベース

Mine

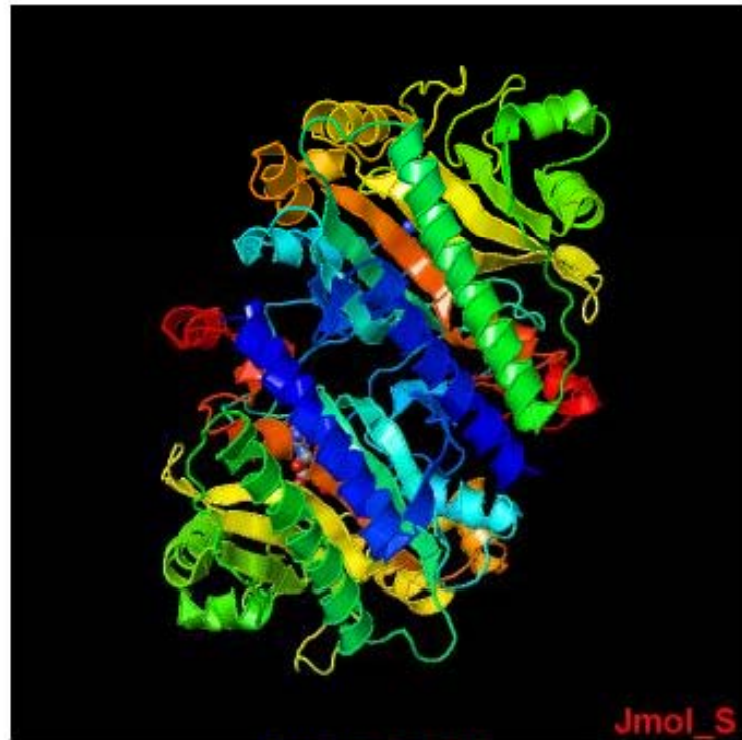
概要 構造情報 実験情報

3次元構造ビューア
jv3 / Jmol
jv3 と Jmol には
Java(TM) Plug in 1.5以上が必要です。

x軸周りに90度回転
250X250 500X500

y軸周りに90度回転
250X250 500X500

PDBj Mine Jmol : 12as - Mozilla Firefox



Jmol version 12.0

Style: ☒ Default ☐ Cartoon ☐ Rocket ☐ Wire frame ☐ CPK_without_water ☐ CPK

Color: ☒ Default ☐ Group ☐ Chain ☐ Atom

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

PDBj
Japanese

統計情報 ヘルプ FAQ お問い合わせ

トップページ
データ登録 >>
ADIT: PDB Deposition
ADIT-NMR

検索 >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

サービス&ソフトウェア >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash

Structure Prediction >>
CRNPRED
Spanner
SFAS

二次データベース >>
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

ダウンロード >>
PDB Archive/Snapshot Archive

リンク集

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、EMBL、および欧州PDBと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

Mine 概要[12as]

日本語ページについて
PDBj Mineについて
更新情報

概要 構造情報 実験情報 機能情報 相同蛋白質 ダウンロード/画面表示 外部データベース

PDB ID or Keyword 検索

3次元構造ビューア
JV3 / Jmol
JV3 と Jmol には
Java(TM) Plug in 1.5以上が必要です。

x軸周りに90度回転
250X250 500X500

y軸周りに90度回転
250X250 500X500

エントリー ID (PDB ID) 12as 配列情報 (FASTA形式) PDBファイルのダウンロード

分子名称 ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE

タイトル ASPARAGINE SYNTHETASE MUTANT C51A, C315A

機能のキーワード
由来する生物
細胞内の位置
ポリマー鎖の
分子量の合計
著者
引用文献
実験手法
他のデータ

>12AS: ASPARAGINE SYNTHETASE
MKTAYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVG
ALPDAQFEVVHSLAKWKQRQLTGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDG
RVMGDGERQFSTLKSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHVHSQELLSE
DAKGRERAI AKDLGAVFLVGIGGKLSGHRHDV RAPDYDDWSTPSELGHAGLNGDI
PVLEDAFELSSMGIRVDADTLKHQLALTGDEDRLLEWHQALLRGEMPQTIGGGIG
TMLLLQLPHIGQVQAGVWPAAVRESVPSLL

>12ASB: ASPARAGINE SYNTHETASE
MKTAYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVG
ALPDAQFEVVHSLAKWKQRQLTGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDG
RVMGDGERQFSTLKSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHVHSQELLSE
DAKGRFRATAKDI GAVEL VGIGGKI SDGHRHDV RAPDYDDWSTPSEL GHAGI NGDI

Get Entry Data from our browser, PDBj Mine

(1) Keyword search in Japanese

PDBj
Japanese

統計情報 ヘルプ FAQ お問い合わせ

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、[IUCr-BIRD](#)の支援を受け、[米国RCSB](#) [EMBL](#) および[欧州PDB](#)と協力して

[トップページ](#)

[データ登録 >>](#)

ADIT: PDB Depos

ADIT-NMR

[検索 >>](#)

Search PDB
(Mine/xPSSS)

Latest Released S

Sequence-Naviga

Structure-Navigat

SeSAW

Ligand Binding S
(GIRAF)

EM Navigator

Search NMR Data
(BMRB)

Status Search

[サービス&ソフトウェア](#)

JV: Graphic Views

Protein Globe

ASH

MAFFTash

Structure Predict

CRNPRED

Spanner

SFAS

[二次データベース >>](#)

eF-site/eF-seek/e

eProtS

ProMode


Molecule of the M

[ダウンロード >>](#)

PDB Archive/Sns

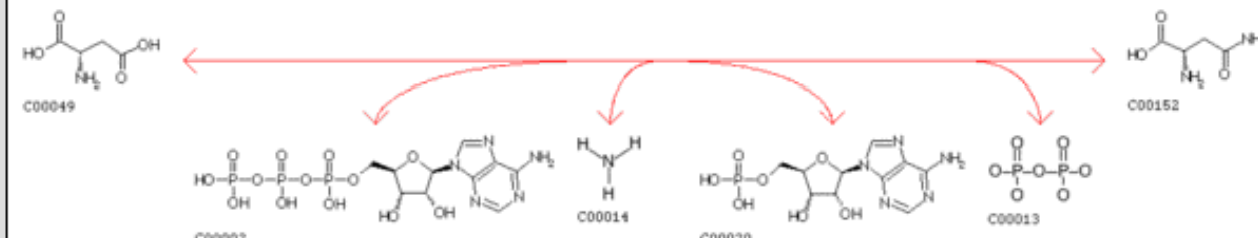
Archive

[リンク集](#)



REACTION: R00483

[Help](#)

Entry	R00483
Name	L-Aspartate:ammonia ligase (AMP-forming)
Definition	ATP + L-Aspartate + NH3 <=> AMP + Pyrophosphate + L-Asparagine
Equation	C00002 + C00049 + C00014 <=> C00020 + C00013 + C00152
	
RPair	RP: A00116 C00049_C00152 main
Pathway	PATH: rn00252 Alanine and aspartate metabolism PATH: rn00460 Cyanoamino acid metabolism PATH: rn00910 Nitrogen metabolism
Enzyme	6.3.1.1
Ortholog	KO: K01914 aspartate--ammonia ligase
LinkDB	All DBs

=> [Original format](#)

DBGET integrated database retrieval system, [GenomeNet](#)

Several Information for each Entry: Structural Details

PDBj English Statistics Help Contact Us

Home

Data Deposition >>

ADIT: PDB
Deposition
ADIT-NMR

Search >>

Search PDB
(Mine/xPSSS)
Latest Released
Search
Sequence-
Navigator
Structure-
Navigator
SeSAW
Ligand Binding
Sites (GIRAF)
EM Navigator
Search NMR Data
(BMRB)
Status Search

Service and Software >>

JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure
Prediction >>

CRNPRED
Spanner
SFAS

Derived database >>

eF-site/eF-
seek/eF-surf
eProtS
ProMode
Molecule of the
Month

Download >>

PDB

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.

Mine Structural Details [12as] About PDBj Mine Update Information

Summary Structural Details Experimental Details Functional Details Sequence Neighbor Download/Display Link

PDB ID or Keyword search

Entity

Chain ID	Description	Type	DB Name (Accession)	Formula weight	Number of molecules	Biological source	Descriptive key words
A,B	ASPARAGINE SYNTHETASE sequence information (FASTA format)	polymer	UniProt (P00963)	36633.7	2	Escherichia coli K12	L-ASPARTATE:AMMONIA LIGASE (AMP-FORMING)
	ASPARAGINE	non-polymer	PDBChem (ASN) Chem.Comp.(ASN)	132.1	2		
	ADENOSINE MONOPHOSPHATE	non-polymer	PDBChem (AMP) Chem.Comp.(AMP)	347.2	2		
	water	water	PDBChem (HOH) Chem.Comp.(HOH)	18.0	203		

Display chain - A, B, All (in new window)

Chain-A: [polypeptide(L)] L-ASPARTATE:AMMONIA LIGASE (AMP-FORMING)

Number: 1
Sequence: MKTAYIAKQRIISFVKSHFSKOLEERLGLIEVQAPILSRVGCQTQDNLGSAEKAVQVKVLPDQAFEVVHSLAKMKRQLGQNDHFSAGE
Structure: xxx
Site:

91 101 111 121 131 141 151 161 171 181
GLYTHMKALRPDEDRLSPHSVTVDDQDHEVMGCGERQFSTLKSIVAEIMAGIKATEAAVSEEFGLAPFLPDQIHVHVSQELLRYHPDLDAKGRERATA

191 201 211 221 231 241 251 261 271 281
KDLGAVFLVGGGKLSDGHRHDVRAFDYDDNSTPSLGHAGLNGDILVNNPVLDAFELSSMOIRVDATLKHQLALTGDEDRLELHQAALLRGEMPQT

Details of the structure

- Name of the molecule(s)
- Molecular weight(s)
- Keywords
- Secondary structures, etc.

Several Information for each Entry: Experimental Details

PDBj English [Statistics](#) [Help](#) [Contact Us](#)

Home

Data Deposition >>

ADIT: PDB Deposition
ADIT-NMR

Search >>

Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

Service and Software >>

JV: Graphic Viewer
Protein Globe
ASH
MAFFTach

Structure Prediction >>

CRNPRED
Spanner
SFAS

Derived database >>

eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

Download >>

PDB Archive/Snapshot Archive

Links

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.

Mine **Experimental Details (X-Ray) [12as]** [About PDBj Mine](#) [Update Information](#)

[Summary](#) [Structural Details](#) **[Experimental Details](#)** [Functional Details](#) [Sequence Neighbor](#) [Download/Display](#) [Link](#)

[PDB ID or Keyword](#)

Refinement Statistics

Cell axes [Å]	53.000	126.130	52.860
Cell angles [degree]	90.00	105.59	90.00
Spacegroup	P 1 21 1		
Resolution limits [Å]	10.0 - 2.2 (2.30 - 2.20)		
R-work	0.164 (0.244)		
R-free	0.287 (0.345)		
RMSD bond length [Å]	0.008		
RMSD bond angle [degree]	1.25		

Values in parentheses refer to the highest resolution shell.

Data Collection Statistics

Resolution limits [Å]	2.2 (2.25 - 2.2)
Number of reflections	25168
Number of measurements	71426 ^{*4}
Rmerge I_obs	0.112 (0.238)
Completeness [%]	72.1 (53.4) ^{*4}
Redundancy	2.8 (1.7)
I/sigma(I)	1.

Values in parentheses refer to the highest resolution shell.

Crystallization Conditions

method	pH	temperature
Vapor diffusion, sitting drop ^{*1}	7.5	293 (K) ^{*1}

Details of the experiment

- Experimental method
(X-ray, NMR, EM, Neutron)
- Parameters for the crystal
- Crystallization conditions
- etc.

Several Information for each Entry: Functional Details

Details of the function

- Gene ontology information
- Ligand binding
- Functional site
- etc.

PDBj English [Statistics](#) [Help](#) [Contact Us](#)

Home

Data Deposition >>

ADIT: PDB Deposition
ADIT-NMR

Search >>

Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

Service and Software >>

/V: Graphic Viewer
Protein Globe
ASH
MAFFTash

Structure Prediction >>

CRNPRED
Spanner
SFAS

Derived database >>

eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

Download >>

PDB Archive/Snapshot Archive

Links

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the [RCSB](#) in USA and the [PDBe](#) in EU. PDBj is supported by JST-BIRD.

Mine **Functional Details [12as]** [About PDBj Mine](#) [Update Information](#)

[Summary](#) [Structural Details](#) [Experimental Details](#) **[Functional Details](#)** [Sequence Neighbor](#) [Download/Display](#) [Link](#)

[about Functional Details Page](#)

Functional Information from PDB Data

site_id	type	Number of Residues	Details
NU1	SITE	1	AMP BINDING (CATALYTIC) SITE (CHAIN A).
NU2	SITE	1	AMP BINDING (CATALYTIC) SITE (CHAIN B).
AC1	SITE	13	BINDING SITE FOR RESIDUE ASN A 331
AC2	SITE	13	BINDING SITE FOR RESIDUE ASN B 331
AC3	SITE	17	BINDING SITE FOR RESIDUE AMP A 332
AC4	SITE	15	BINDING SITE FOR RESIDUE AMP B 332

[\(More PDB information ...\)](#)

Functional Information from PDB atom coordinates for the "HETATM" binding sites

site_id	type	Number of Residues	Details
ASN_12as_A_331	binding site	17	ASPARAGINE binding site
AMP_12as_A_332	binding site	21	ADENOSINE MONOPHOSPHATE binding site
ASN_12as_B_331	binding site	19	ASPARAGINE binding site
AMP_12as_B_332	binding site	20	ADENOSINE MONOPHOSPHATE binding site

[\(More HETATOM information ...\)](#)

Catalytic Information from CSA

site_id	type	Number of Residues	Details
CSA1	catalytic site	3	a catalytic site defined by CSA, Medline 9437423
CSA2	catalytic site	3	a catalytic site defined by CSA, Medline 9437423

Several Information for each Entry: Sequence Neighbor

PDBID list of homologs

- Result of BLAST search
- Sequence Navigator is used.

PDBj English [Statistics](#) [Help](#) [Contact Us](#)

Home

Data Deposition >>

ADIT: PDB
Deposition
ADIT-NMR

Search >>

Search PDB
(Mine/XPSSS)
Latest Released
Search
Sequence-
Navigator
Structure-
Navigator
SeSAW
Ligand Binding Sites
(GIRAF)
EM Navigator
Search NMR Data
(BMRB)
Status Search

Service and Software >>

JV: Graphic Viewer
Protein Globe
ASH
MAFFTash

Structure Prediction >>

CRNPRED
Spanner
SFAS

Derived database >>

eF-site/eF-seek/eF-
surf
eProtS
ProMode
Molecule of the
Month

Download >>

PDB

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.

Mine **Sequence Neighbor [12as]** [About PDBj Mine](#) [Update Information](#)

[Summary](#) [Structural Details](#) [Experimental Details](#) [Functional Details](#) [Sequence Neighbor](#) [Download/Display](#) [Link](#)

Results (1-12) / 12

12ASA Exact Matches: 11ASA 12ASB 11ASB

Seq. Identity: 32% Seq. Positives: 43% E-value: 0.083 Score: 34 Compound: HYPOTHETICAL PROTEIN ATU1052

[New Search \[2GZ4A\]](#) [Structural Superposition](#)

12ASA	65	103	EVVNSLAK-----KQKQELGKDFSG-----ESLITM-KALAPDEIRLSPLKSVTVQKMKRVMGQDQFSLKSPVEAIWAGI-KATEAAVSEERGLAP
2GZ4A	28	103	DLAKGLAVARKKQKFGKDAKPTVAGKLLVETLFCRHCFOATPDENKHALLDAP-----ETVIGD-----NLSFKSVVGGGKTYVEGLEAAVGLKGLP

2GZ4A Exact Matches: 2GZ4B 2GZ4D 2GZ4C

Seq. Identity: 34% Seq. Positives: 59% E-value: 1.2 Score: 30 Compound: TBC1 DOMAIN FAMILY MEMBER 22A

[New Search \[2QFZA\]](#) [Structural Superposition](#)

12ASA	34	49	LSRVGDDPQGLSGAKDAVGVKYNALPDAQFEVVHSLAKKKGKTLQKD
2QFZA	159	49	MSKGLDGIQENTFFAGGIGQKYNMLE-----ELVSRIDEQVHGLQKRE

Seq. Identity: 34% Seq. Positives: 59% E-value: 1.2 Score: 30 Compound: TBC1 DOMAIN FAMILY MEMBER 22A

[New Search \[2QFZB\]](#) [Structural Superposition](#)

12ASA	34	49	LSRVGDDPQGLSGAKDAVGVKYNALPDAQFEVVHSLAKKKGKTLQKD
2QFZB	159	49	MSKGLDGIQENTFFAGGIGQKYNMLE-----ELVSRIDEQVHGLQKRE

Seq. Identity: 47% Seq. Positives: 47% E-value: 3.5 Score: 29 Compound: LYSYL-TRNA SYNTHETASE

[New Search \[3E9IA\]](#) [Structural Superposition](#)

12ASA	267	44	DEDFLEAELKHALLAGKHPQETIGGIGQKRYHGLLGLPVIQGV
3E9IA	439	44	DEDFLEA-----LEYQKQPTGGLGIGOVERLHGLNLSRSTIDV

3E9IA Exact Matches: 3E9HA 3E9HC 3E9IC 3E9HB 3E9IB 3E9HD 3E9ID

Seq. Identity: 46% Seq. Positives: 71% E-value: 2.7 Score: 29 Compound: TBC1 DOMAIN FAMILY MEMBER 22B

[New Search \[3DZXA\]](#) [Structural Superposition](#)

12ASA	34	28	LSRVGDDPQGLSGAKDAVGVKYNALPDAQFEVVHSLAKKKGKTLQKD
3DZXA	136	28	MSKGLDGIQENTFFAGGIGQKYNMLE

Several Information for each Entry: Download/Display

The screenshot shows the PDBj Mine website interface. The main heading is "Download / Display [12as]". Below this, there is a search bar with a dropdown menu for "PDB ID or Keyword" and a "search" button. The interface is divided into several sections: "Data Deposition >>", "Search >>", "Service and Software >>", "Derived database >>", and "Download >>". The "Search >>" section contains a table with columns for "file format", "file name", "Display", and "Download". The table lists various file formats and their corresponding file names, with buttons for "display" and "download" next to each entry.

file format	file name	Display	Download
PDB format	all	display	download
	header only	display	download
	mmCIF	display	download
XML	all	display	download
	no-atom	display	download
	PDBML	display	download
	PDBMLplus	display	download
ext-atom	display	download	

Download or display of the archival data

- Conventional PDB format
- Conventional PDB header
- mmCIF
- PDBML/PDBMLplus
- PDBML without coordinates
- PDBML for only coordinates
- Structure factor

Data Formats of PDB data

- **PDB (conventional and flat)**
- **PDB Exchange (mmCIF)**
 - **Mechanism for extension based on new demands**
- **PDBML**
 - **Derived from mmCIF**
 - **All entries converted to XML**
 - **Automatic translation from mmCIF data files and dictionaries**
 - **3-styles of translation released**

*(Westbrook, Ito, Nakamura, Henrick, Berman (2005)
Bioinformatics, 21, 988-992)*

Example of PDBML for an atom coordinate.

ATOM 1 N THR A 1 17.047 14.099 3.625 1.00 13.79

PDB-format

<PDBx:atom_siteCategory>

<PDBx:atom_site id="1">

<PDBx:group_PDB>ATOM</PDBx:group_PDB>

<PDBx:type_symbol>N</PDBx:type_symbol>

<PDBx:label_atom_id>N</PDBx:label_atom_id>

<PDBx:label_comp_id>THR</PDBx:label_comp_id>

<PDBx:label_asym_id>A</PDBx:label_asym_id>

<PDBx:label_entity_id>1</PDBx:label_entity_id>

<PDBx:label_seq_id>1</PDBx:label_seq_id>

<PDBx:Cartn_x>17.047</PDBx:Cartn_x>

<PDBx:Cartn_y>14.099</PDBx:Cartn_y>

<PDBx:Cartn_z>3.625</PDBx:Cartn_z>

<PDBx:occupancy>1.00</PDBx:occupancy>

<PDBx:B_iso_or_equiv>13.79</PDBx:B_iso_or_equiv>

<PDBx:auth_seq_id>1</PDBx:auth_seq_id>

<PDBx:auth_comp_id>THR</PDBx:auth_comp_id>

<PDBx:auth_asym_id>A</PDBx:auth_asym_id>

<PDBx:auth_atom_id>N</PDBx:auth_atom_id>

<PDBx:pdxb_PDB_model_num>1</PDBx:pdxb_PDB_model_num>

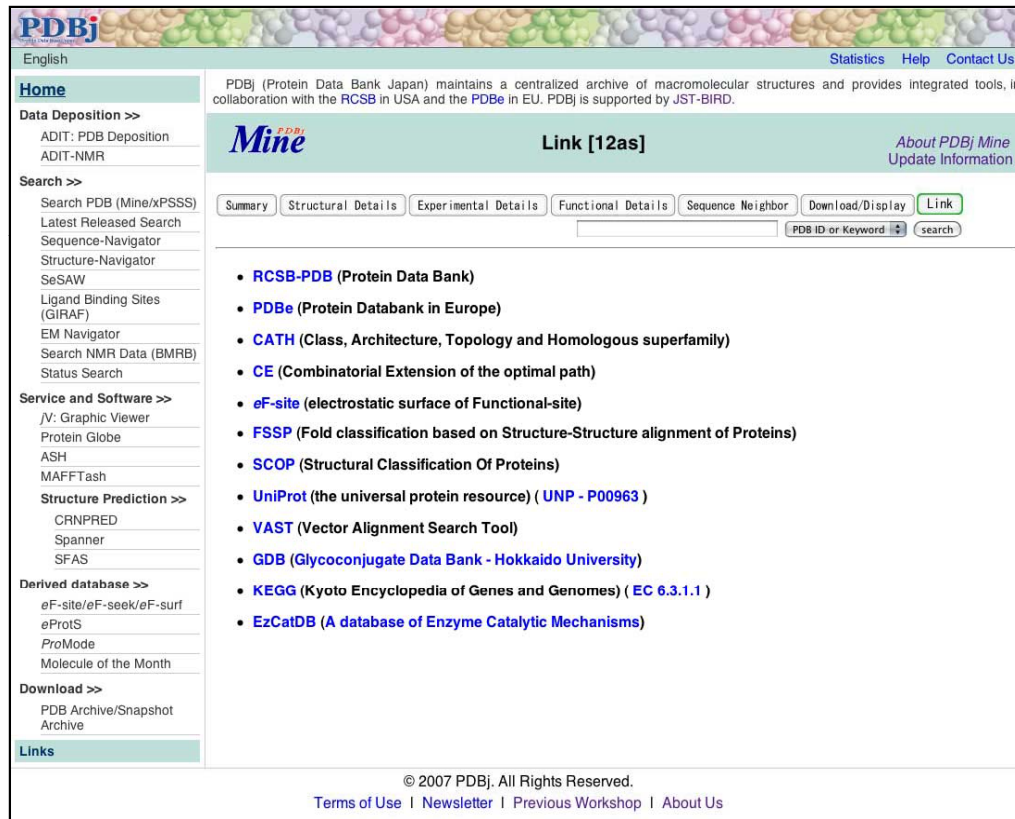
</PDBx:atom_site>

Full-tag description

Separated file for
coordinates

<atom_record id="1">ATOM 1 A A 1 1 ? . THR THR N N N 17.047 14.099 3.625 1.00 13.79</atom_record>

Several Information for each Entry: Link



The screenshot displays the PDBj Mine website. The header includes the PDBj logo, language selection (English), and navigation links (Statistics, Help, Contact Us). The main content area is titled 'Link [12as]' and features a search bar with a 'Link' button. Below the search bar, a list of links to other databases is provided, including RCSB-PDB, PDBe, CATH, CE, eF-site, FSSP, SCOP, UniProt, VAST, GDB, KEGG, and EzCatDB. The left sidebar contains various search and service options, and the footer includes copyright information and links to Terms of Use, Newsletter, Previous Workshop, and About Us.

English Statistics Help Contact Us

Home

Data Deposition >>

ADIT: PDB Deposition
ADIT-NMR

Search >>

Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

Service and Software >>

JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

Derived database >>

eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

Download >>

PDB Archive/Snapshot
Archive

Links

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.

Mine Link [12as] About PDBj Mine Update Information

Summary Structural Details Experimental Details Functional Details Sequence Neighbor Download/Display **Link**

PDB ID or Keyword search

- **RCSB-PDB** (Protein Data Bank)
- **PDBe** (Protein Databank in Europe)
- **CATH** (Class, Architecture, Topology and Homologous superfamily)
- **CE** (Combinatorial Extension of the optimal path)
- **eF-site** (electrostatic surface of Functional-site)
- **FSSP** (Fold classification based on Structure-Structure alignment of Proteins)
- **SCOP** (Structural Classification Of Proteins)
- **UniProt** (the universal protein resource) ([UNP - P00963](#))
- **VAST** (Vector Alignment Search Tool)
- **GDB** (Glycoconjugate Data Bank - Hokkaido University)
- **KEGG** (Kyoto Encyclopedia of Genes and Genomes) ([EC 6.3.1.1](#))
- **EzCatDB** (A database of Enzyme Catalytic Mechanisms)

© 2007 PDBj. All Rights Reserved.
[Terms of Use](#) | [Newsletter](#) | [Previous Workshop](#) | [About Us](#)

Link to other databases

- RCSB-PDB, MSD-EBI
- CATH, SCOP, FSSP: folds
- UniProt: Sequences
- KEGG: Pathways
- EzCatDB: enzymes
- etc.

Tutorials 【1】: How to view structures?

(1) Keyword Search → View Structure

→ Download Coordinates

→ Examine Several Information

→ Other Advanced Usages and Links

(2) Search by PDBID (**PDBID: 12as**)

(3) Search by Author Names

(4) Search by Sequence

(5) Advanced Search

Get Entry Data from our browser, PDBj Mine

(2) PDBID search

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.

Deposition

Search

Search PDB Mine

12as PDB ID or Keyword

Go

What's new

24-Nov-2009
On November 25, 2009, our existing data viewer xPSSS will be integrated into PDBj Mine, which has recently been developed. ([more...](#))

22-Oct-2009
On October 22, 2009, PDBj main pages and deposition pages in "traditional Chinese" have been released.

9-Oct-2009
On October 14, 2009, the weekly data update will be made, in principle, at 9:00 AM (JST) of every Wednesday, which corresponds to 0:00 (UTC). This update is simultaneously made at every member of the wwPDB: RCSB-PDB, PDBe, and PDBj.

9-Oct-2009
On October 14, 2009, we will start to use a new data viewer, **PDBj Mine**, which has been recently developed by PDBj. Because PDBj Mine uses a relational database, XPath/XQuery is not available. Our XML-based database, xPSSS, is still available for another couple of months.

Summary [12as]

PDB ID 12as [sequence information \(FASTA format\)](#)

Descriptor ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE

Title ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP

Functional Keywords LIGASE, ASPARAGINE SYNTHETASE, NITROGEN FIXATION

Biological source Escherichia coli K12

Cellular location [UNP - ASNA_ECOLI] Cytoplasm

Total number of polymer chains 2

Total molecular weight 74226 (the details in [Structural Details Page](#))

Authors Nakatsu, T., Kato, H., Oda, J. (*deposition date* : 1997-12-02, *release date* : 1998-12-30)

Primary citation Nakatsu, T., Kato, H., Oda, J. Crystal structure of asparagine synthetase reveals a close evolutionary relationship to class II aminoacyl-tRNA synthetase. *Nature Struct. Biol.*, 5:15 - 19, 1998. ([PubMed](#) : 9437423) ([DOI](#): 10.1038/nsb0198-15)

Experimental method X-RAY DIFFRACTION (2.2Å)

Other Database Information CATH, CE, FSPP, SCOP, VAST, UniProt (UNP - P00963), eF-site, KEGG (EC 6.3.1.1), GDB, EzCaiDB

PDBID (e.g. 12as) should be input in a box and GO



Summary for each PDBID is displayed.

Tutorials 【1】: How to view structures?

(1) Keyword Search → View Structure

→ **Download Coordinates**

→ **Examine Several Information**

→ **Other Advanced Usages and Links**

(2) Search by PDBID

(3) Search by Author Names (Oda, J.**)**

(4) Search by Sequence

(5) Advanced Search

Get Entry Data from our browser, PDBj Mine

(3) Search by Author Name

検索

PDB検索 *PDBj Mine*

Mine日本語ページについて

("Family name, Initial of Given name") (e.g.) Ito, N.

詳細条件検索 >>

Get Entry Data from our browser, PDBj Mine

(3) Search by Author Name

[トップページ](#)
[データ登録 >>](#)
ADIT: PDB Deposition
ADIT-NMR
[検索 >>](#)
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search
[サービス&ソフトウェア >>](#)
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
[Structure Prediction >>](#)
CRNPRED
Spanner
SFAS
[二次データベース >>](#)
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month
[ダウンロード >>](#)
PDB Archive/Snapshot Archive
[リンク集](#)

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

PDBj Mine

検索結果ページ

(PDB-IDをクリックすると、詳細情報をご覧ください)

1 - 16/ 37

クエリ: Oda, J. PDB ID or Keyword 表示順: 一件件数

[リセット](#) [検索](#)

2glt	分子名称 タイトル 著者 実験手法 登録日 公開日	: GLUTATHIONE BIOSYNTHETIC LIGASE : STRUCTURE OF ESCHERICHIA COLI GLUTATHIONE SYNTHETASE AT PH 6.0. : Matsuda, K., Yamaguchi, H., Kato, H., Nishioka, T., Katsube, Y., Oda, J. : X-RAY DIFFRACTION : 1995-05-16 : 1995-07-31
ダウンロード		
1gsh	分子名称 タイトル 著者 実験手法 登録日 公開日	: GLUTATHIONE BIOSYNTHETIC LIGASE : STRUCTURE OF ESCHERICHIA COLI GLUTATHIONE SYNTHETASE AT PH 7.5 : Matsuda, K., Kato, H., Yamaguchi, H., Nishioka, T., Katsube, Y., Oda, J. : X-RAY DIFFRACTION : 1995-05-16 : 1996-07-11
ダウンロード		
1gsa	分子名称 タイトル 著者 実験手法 登録日 公開日	: GLUTATHIONE SYNTHETASE, ADENOSINE-5"-DIPHOSPHATE, GLUTATHIONE : STRUCTURE OF GLUTATHIONE SYNTHETASE COMPLEXED WITH ADP AND GLUTATHIONE : Hara, T., Kato, H., Nishioka, T., Katsube, Y., Oda, J. : X-RAY DIFFRACTION : 1995-06-08 : 1996-06-20
ダウンロード		
12as	分子名称 タイトル 著者 実験手法 登録日	: ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP : Nakatsu, T., Kato, H., Oda, J. : X-RAY DIFFRACTION : 1997-12-02
ダウンロード		

日本語ページについて

PDBj Mineについて

更新情報

Tutorials 【1】: How to view structures?

(1) Keyword Search → View Structure

→ Download Coordinates

→ Examine Several Information

→ Other Advanced Usages and Links

(2) Search by PDBID

(3) Search by Author Names

(4) Search by Sequence (**MKTAYIAKQRQISF**)

(5) Advanced Search

Get Entry Data from our browser, PDBj Mine

(4) Search by Sequence

検索

PDB検索

PDBj
Mine

Mine日本語ページについて

MKTAYIAKQRQISF

sequence ▼

Go

(longer than 5 residues) (e.g.) KGFEPLIQFA

詳細条件検索 >>

Get Entry Data from our browser, PDBj Mine

(4) Search by Sequence

PDBj
Japanese

統計情報 ヘルプ FAQ お問い合わせ

トップページ
データ登録 >>
ADIT: PDB Deposition
ADIT-NMR
検索 >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search
サービス&ソフトウェア >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS
二次データベース >>
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month
ダウンロード >>
PDB Archive/Snapshot Archive
リンク集

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

Mine 検索結果ページ
(PDB-IDをクリックすると、詳細情報をご覧いただけます)

日本語ページについて
PDBj Mineについて
更新情報

1 - 2 / 2

クエリ: MKTAYIAKQRQIS 配列 キーワードの追加: 表示順: 公開日の新しい順

リセット 検索

12as		分子名称 タイトル 著者 実験手法 登録日 公開日	: ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP : Nakatsu, T., Kato, H., Oda, J. : X-RAY DIFFRACTION : 1997-12-02 : 1998-12-30
ダウンロード			
11as		分子名称 タイトル 著者 実験手法 登録日 公開日	: ASPARAGINE SYNTHETASE, L-ASPARAGINE : ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE : Nakatsu, T., Kato, H., Oda, J. : X-RAY DIFFRACTION : 1997-12-02 : 1998-12-30
ダウンロード			

クエリ: MKTAYIAKQRQIS 配列 キーワードの追加: 表示順: 公開日の新しい順

リセット 検索

Tutorials 【1】: How to view structures?

(1) Keyword Search → View Structure

→ Download Coordinates

→ Examine Several Information

→ Other Advanced Usages and Links

(2) Search by PDBID

(3) Search by Author Names

(4) Search by Sequence

(5) Advanced Search

(5) Advanced Search

From "Advanced Search" on Top page

Data Deposition >>
ADIT: PDB
Deposition
ADIT-NMR

Search >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

Service and Software >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

Derived database >>
eF-site/eF-seek/eF-surf
eProtS
ProMode
Molecule of the Month

Download >>
PDB
Archive/Snapshot
Archive

Links

Mine **Advanced Search** [About PDBj Mine](#) [Update Information](#)

sorted by **release date descending** Display size per page **16** **reset** **search**

PDB ID:
Keyword:

Release Date: **after:** month day year **before:** month day year

Deposition Date: **after:** month day year **before:** month day year

Citation Author: and and ☐ primary

Journal: **Title:** **Name:**
Year: **Volume:**

Contains Chain Type:

	Yes	No	ignore
polypeptide(D)	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
polypeptide(L)	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
polydeoxyribonucleotide	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
polyribonucleotide	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
polysaccharide(D)	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
polysaccharide(L)	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
polydeoxyribonucleotide/polyribonucleotide hybrid	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
cyclic-pseudo-peptide	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
other	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>

Compound Information:
Title:
Other DB : **ID :**

Ligands and Prosthetic groups:
Number of Chains: (min) - (max)
Chain length: (min) - (max)

Experimental Technique:
Resolution: (min) - (max)
Source:
Host Species:

Search by many conditions

- Author names & Journal
- Experimental method
- Ligand name
- Residues
- Resolution
- Species
- etc.


[English](#)

[Statistics](#)
[Help](#)
[Contact Us](#)

[Home](#)

Data Deposition >>
[ADIT: PDB Deposition](#)
[ADIT-NMR](#)

Search >>
[Search PDB \(xPSSS\)](#)
[Sequence-Navigator](#)
[Structure-Navigator](#)
[EM Navigator](#)
[Search NMR Data \(BMRB\)](#)
[Status Search](#)

Service and Software >>
[Protein Globe](#)
[ASH](#)
[/V: Graphic Viewer](#)

Derived database >>
[eF-site/eF-seek/eF-surf](#)
[eProTS](#)
[ProMode](#)
[Molecule of the Month](#)

Download >>
[FTP Archive/sync Service](#)

About Remediation Data

[Links](#)

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the [RCSB](#) in USA and the [MSD-EBI](#) in EU. PDBj is supported by [JST-BIRD](#).

Sequence Navigator

About Sequence Navigator

Sequence Navigator Soap Service

To Enter Navigator, Input a PDB ID and Chain ID

OR Input an AA Sequence

Clustering Options

☒ No Clustering
 ☐ Cluster by E-value 10^{-4}


[English](#)

[Home](#)

Data Deposition >>
[ADIT: PDB Deposition](#)
[ADIT-NMR](#)


Search >>
[Search PDB \(xPSSS\)](#)
[Sequence-Navigator](#)

[PDBj \(Protein Data Bank Japan\) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the \[RCSB\]\(#\) in USA and the \[MSD-EBI\]\(#\) in EU. PDBj is supported by \[JST-BIRD\]\(#\).](#)

[Sequence Navigator](#)

[Superposition](#)

[Number of Amino Acids](#)



[English](#)

[Statistics](#)
[Help](#)
[Contact Us](#)

Home

Data Deposition >>

ADIT: PDB Deposition

ADIT-NMR

Search >>

Search PDB (xPSSS)

Sequence-Navigator

Structure-Navigator

EM Navigator

Search NMR Data (BMRB)

Status Search

Service and Software >>

Protein Globe

ASH

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the [RCSB](#) in USA and the [MSD-EBI](#) in EU. PDBj is supported by [JST-BIRD](#).

Sequence Navigator

Query ID: [1UAN]

Query Chain: [A]

Clustering Option: [No Clustering]

Re-Clustering Options

☒ No Clustering ☐ Cluster by E-value 10^*

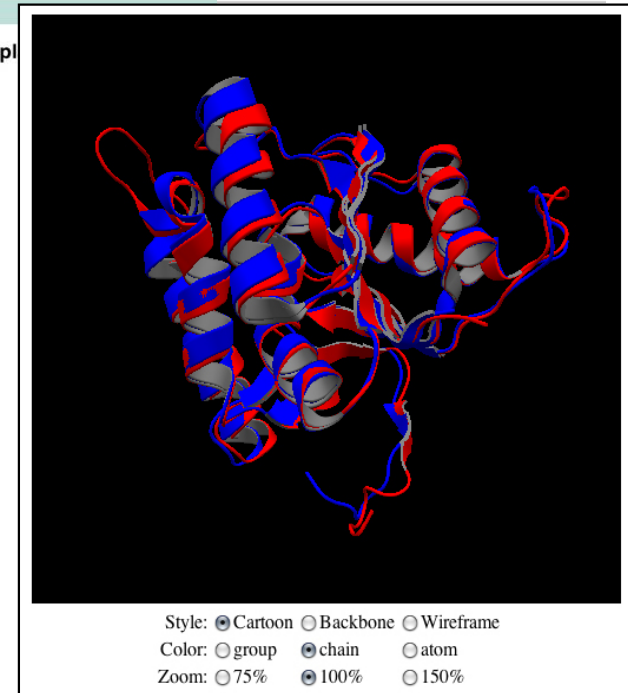
Find All Homologs

⊕ (more clusters)

⊖ (fewer clusters)

Results (1-15) / 15

KA EGLSTG ILDLTRGEMSGKTPEEREKEVAEASRILGLDFRGNLGFPDGI
KA EGLSTG ILDLTRGEMSGKTPEEREKEVAEASRILGLDFRGNLGFPDGI




PDBID or amino-acid sequence should be input and "Find All Homologs"



List of hit PDBIDs is displayed.

Search of Similar Structures: Structure Navigator



[English](#)
[Statistics](#)
[Help](#)
[Contact Us](#)

[Home](#)

Data Deposition >>

- ADIT: PDB Deposition
- ADIT-NMR

Search >>

- Search PDB (xPSSS)
- Sequence-Navigator
- Structure-Navigator
- EM Navigator
- Search NMR Data (BMRB)
- Status Search

Service and Software >>

- Protein Globe

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB in USA and the MSD-EBI in EU. PDBj is supported by JST-BIRD.

Structure Navigator

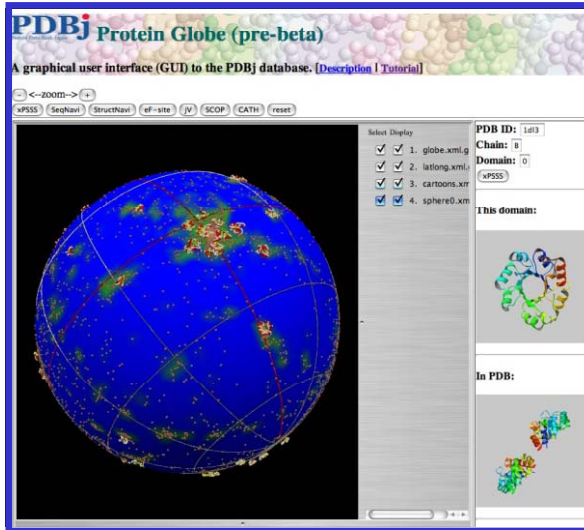
[Back to result summary page](#)

Templ	NER(4)	%NER(4)	%Seq ID	RMSD	Score	Domain	Details
1uanB	216	98	100	0.432	155		alignment
2ixdA	194	88	39	1.311	124		alignment
2ixdB	191	87	38	1.342	122		alignment
1q74C	153	69	25	2.034	83		alignment
1q74B	150	68					
1q74D	145	66					
1q74A	143	65					
1q7IB	142	64					

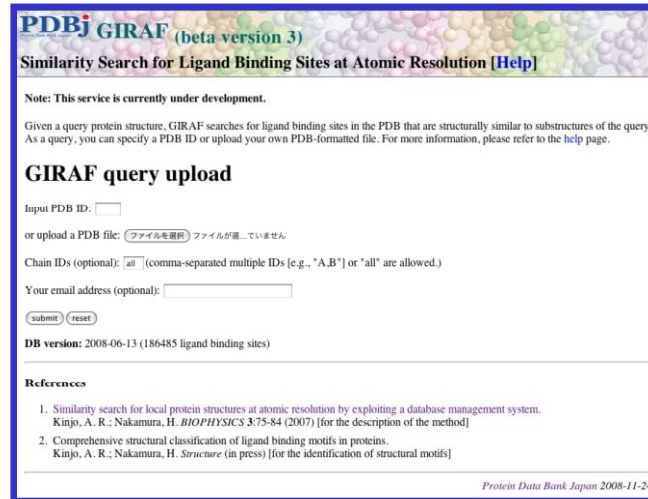
PDBID should be input and "Start Structure Navigator"

→ List of hit PDBIDs is displayed.

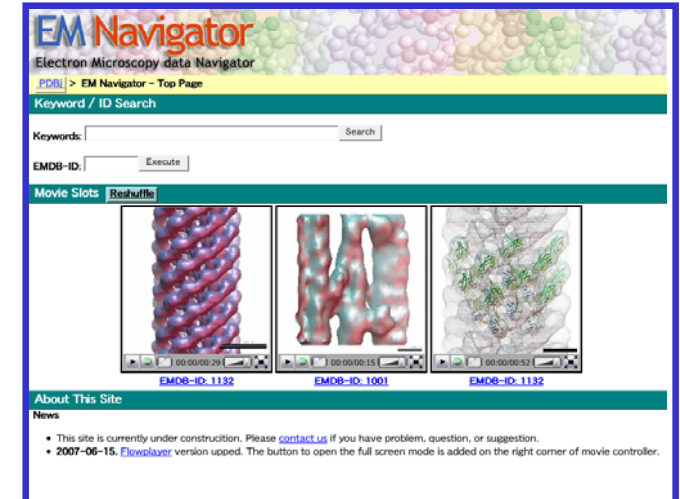
Development of other Databases and Services



Protein Folds Browser,
Protein Globe (Kinjo & Standley)



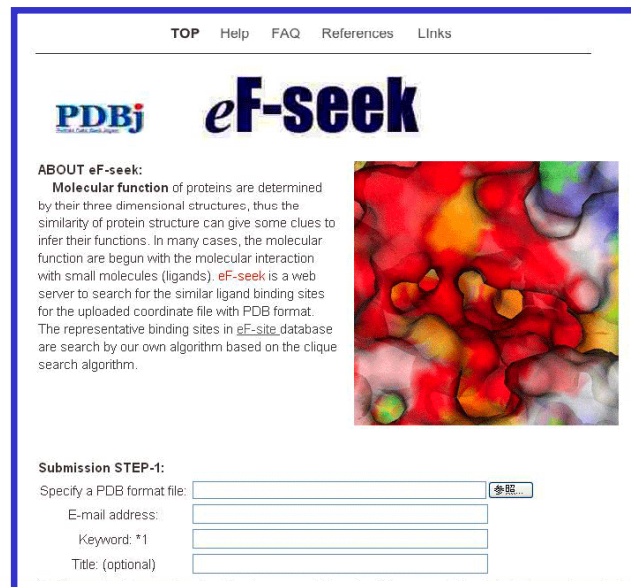
Ligand Binding Site Search,
GIRAF (Kinjo)



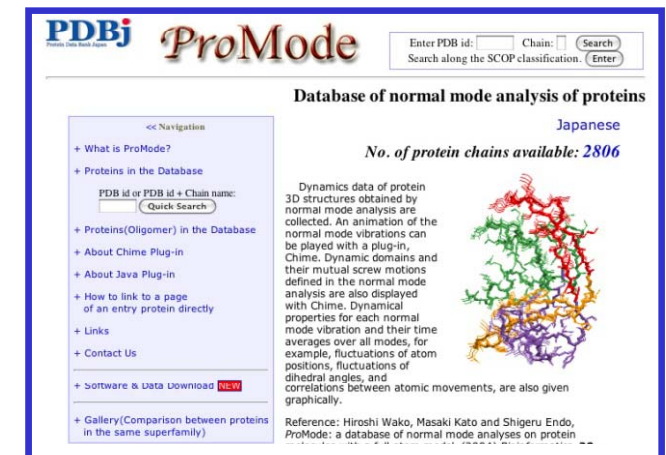
Electron Microscopy Navigator,
EM-Navi (Suzuki)



Protein Molecular Surface
Database, **eF-site**
(Kinoshita & Nakamura)



Search for Similar Surface, **eF-seek** (Kinoshita & Nakamura)



Protein Dynamics Database,
ProMode (Wako & Endo)

Development of other Databases and Services

Homolog protein search,
Sequence Navigator
(Standley)

Similar fold search,
Structure Navigator
(Standley & Toh)

Function Annotation from
Folds and Sequences,
SeSAW (Standley)

Alignment of Sequence and
Structures. **MAFFTash**
(Kato, Toh & Standley)

Encyclopedia of Protein
Structures, **eProtS**
(Kinjo, Kudo, & Ito)

Molecule of the Month, **MoM**
(Goodsell & Kudo)

Development of other Databases and Services

<http://www.pdbj.org/spanner/>

Spanner

Spanner is a structural homology modeling program—that is, it threads a specific amino-acid sequence onto a specific PDB structure, patching up the gaps as best it can.

To create a model, you must provide a template structure, as well as an alignment of the sequence you wish to model onto the template sequence. Spanner will replace matching residues, fill any gaps caused by inserted or deleted residues, and thermodynamically optimize the resulting structure.

The resulting PDB, as well as a log file, will be emailed to you when the modeling task finishes. If an error prevented a homology model from being generated (for example, when the alignment you provided does not match the template structure), the log file will explain which part of the modeling sequence failed.

Template PDB structure (PDB format):
 ファイルが選...ていません

Sequence alignment (FASTA format; first sequence is the template, second sequence is the query):
 ファイルが選...ていません

Model: ☐ (not necessary if PDB file contains only one model)

Chain: ☐ (not necessary if PDB file contains only one chain)

Email address for results:

© 2008–2009 Massachusetts Institute of Technology and Osaka University

*Homology modeling service
(Mieszko, Standley, Nakamura)*

<http://www.pdbj.org/sfas/>

PDBj **iFReC**
WPI Osaka University

Sequence to Function Annotation Server

Please enter your query

Name:

Sequence:

Or

Upload a FASTA-formatted sequence file: ファイルが選...ていません

Select Alignment methods

<input checked="" type="checkbox"/> Blast	<input type="radio"/> Whole PDB	<input checked="" type="radio"/> Rep. Domains
<input type="checkbox"/> PsiBlast	<input type="radio"/> Whole PDB	<input checked="" type="radio"/> Rep. Domains
<input type="checkbox"/> HHpred	<input checked="" type="radio"/> PDB + SCOP	

Send results to this email address

[Send feedback](#) [About SFAS](#)

**Function Annotation from
Sequences, SFAS (Standley)**

When you have any difficulties/troubles, please do not hesitate to ask us from:

The screenshot displays the PDBj (Protein Data Bank Japan) website. The top navigation bar includes links for English, Japanese, simplified Chinese, traditional Chinese, and Korean. The 'ヘルプ' (Help) link is circled in red. The main content area is titled 'お問い合わせ' (Contact Us) and includes a form for sending an email to the PDBj manager. The sidebar on the left contains links for 'トップページ' (Home), 'データ登録' (Data Submission), '検索' (Search), 'サービス&ソフトウェア' (Services & Software), '二次データベース' (Secondary Databases), 'ダウンロード' (Download), and 'リンク集' (Link Collection). The right sidebar shows the number of entries available (67981) and various logos including PDB, eProTS, Protein Globe, DBCLS, and Tanpaku.org.

English Japanese simplified Chinese traditional Chinese Korean 統計情報 **ヘルプ** FAQ お問い合わせ

トップページ 日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、BMRB、および欧州PDBと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。 **67981** entries available

データ登録 >>
ADIT: PDB Deposition
ADIT-NMR

検索 >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

サービス&ソフトウェア >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

二次データベース >>
eF-site/eF-seek/eF-surf
eProTS
ProMode
Molecule of the Month

ダウンロード >>
PDB Archive/Snapshot Archive

リンク集

English Japanese 統計情報 ヘルプ FAQ お問い合わせ

トップページ 日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSB、生物学的磁気共鳴データバンク(BMRB)、および欧州PDBと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

データ登録 >>
ADIT: PDB Deposition
ADIT-NMR

検索 >>
Search PDB (Mine/xPSSS)
Latest Released Search
Sequence-Navigator
Structure-Navigator
SeSAW
Ligand Binding Sites (GIRAF)
EM Navigator
Search NMR Data (BMRB)
Status Search

サービス&ソフトウェア >>
JV: Graphic Viewer
Protein Globe
ASH
MAFFTash
Structure Prediction >>
CRNPRED
Spanner
SFAS

二次データベース >>
eF-site/eF-seek/eF-surf
eProTS
ProMode
Molecule of the Month

ダウンロード >>
PDB Archive/Snapshot Archive

リンク集

お問い合わせ

PDBj管理者へメール送信

FAQページもご覧下さい。お探しの情報が見つからない場合、下記フォームからお問い合わせ下さい。

PDB登録・編集に関するお問い合わせには、

- 座標、構造因子/回折強度、NMR距離制限情報、ADITについては、「PDB登録・編集に関するお問い合わせ」をご利用ください
- NMR実験データ、ADIT-NMRについては、「BMRB登録・編集に関するお問い合わせ」をご利用ください

すべての入力項目が必須です。

URLを入力される場合、"http://"は入力しないでください。入力チェックがかり、エラーになります。

お名前:

メールアドレス:

件名: (64文字以内)

お問い合わせ内容:

電子メールアドレスが正しいことをご確認ください。「メール送信」ボタンを押して送信されると、お問い合わせ内容が送信者に電子メールで送信されます。お問い合わせ内容メールが届かない場合、電子メールアドレスを誤入力されたか、spam/junk/迷惑メールフォルダに移動された可能性があります。

67981 entries available on 15 Sep., 2010 00:00(UTC) / 09:00(JST)

WORLDWIDE PDB PROTEIN DATA BANK

eProTS 蛋白質構造データベース Encyclopedia of Protein Structures

Protein Globe

DBCLS Database Center for Life Science

Tanpaku.org

National Project on Protein Structural and Functional Analysis

BIRD