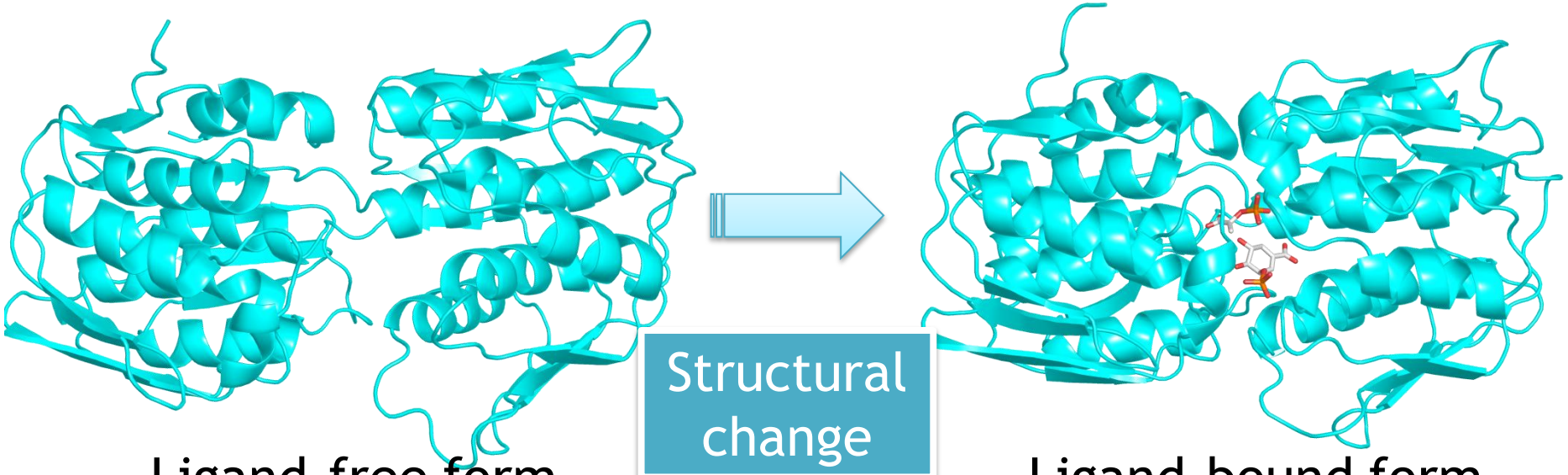
PSCDB : a database for protein structural change upon ligand binding

T. Amemiya[1], R. Koike[1], A. Kidera[2,3] and M. Ota[1]

1) Grad. Schl. of Info. Sci., Nagoya Univ.
2) Grad. Schl. of Nanobioscience, Yokohama City Univ.
3) Comput. Sci. Research Program, RIKEN

Protein structural change upon ligand binding

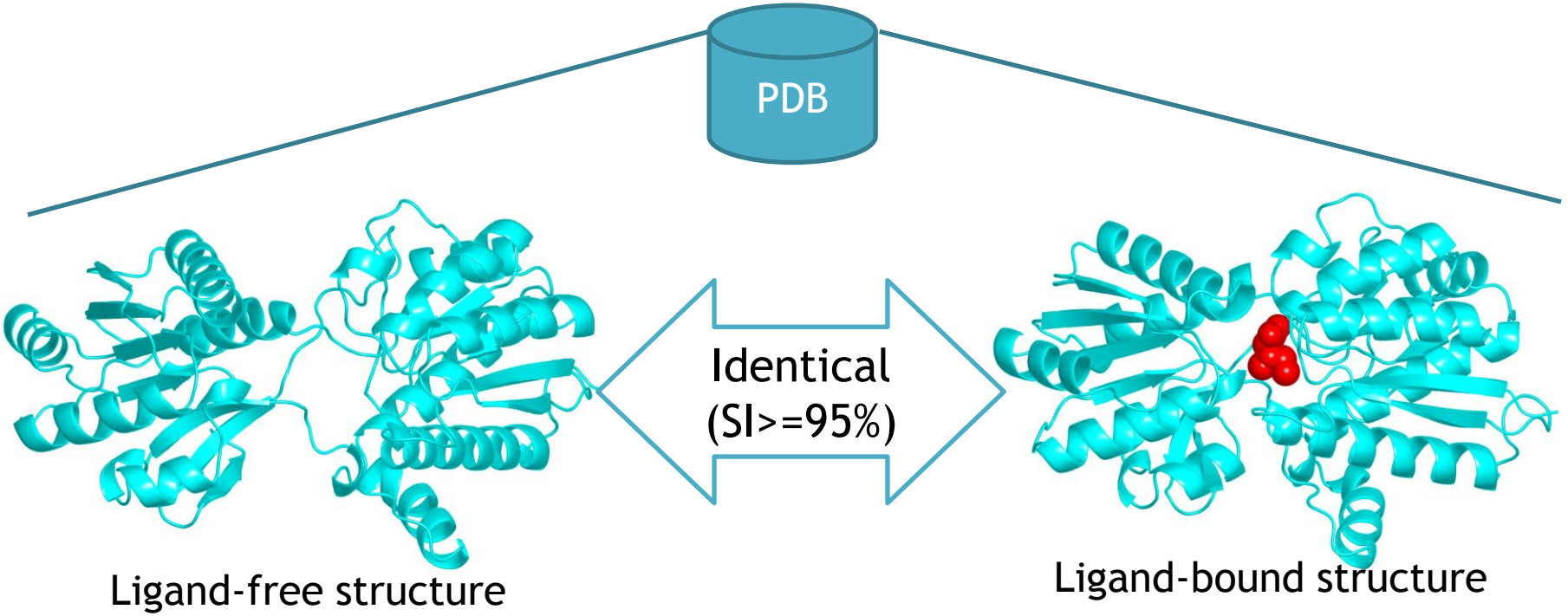
Structural change is the fundamental for protein function



CD.9 3-phosphoshikimate 1-carboxyvinyltransferase

To establish the comprehensive view of protein structural changes and functions, the database of protein structural changes is required.

Data in Protein Structural Change DataBase (PSCDB)



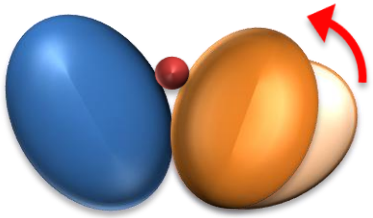
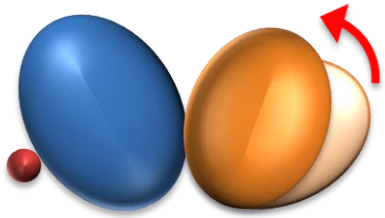
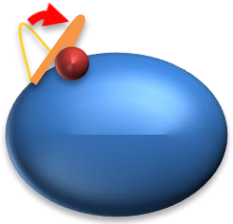
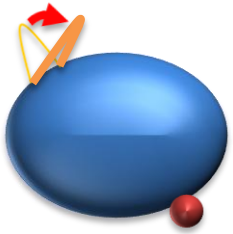
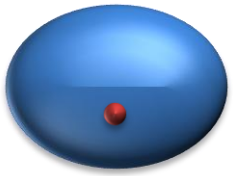
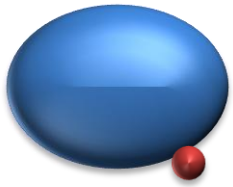
We selected the representative pairs according to mainly the SCOP family.

We extracted non-redundant 839 structural changes of monomeric or homo-dimeric proteins

Classification

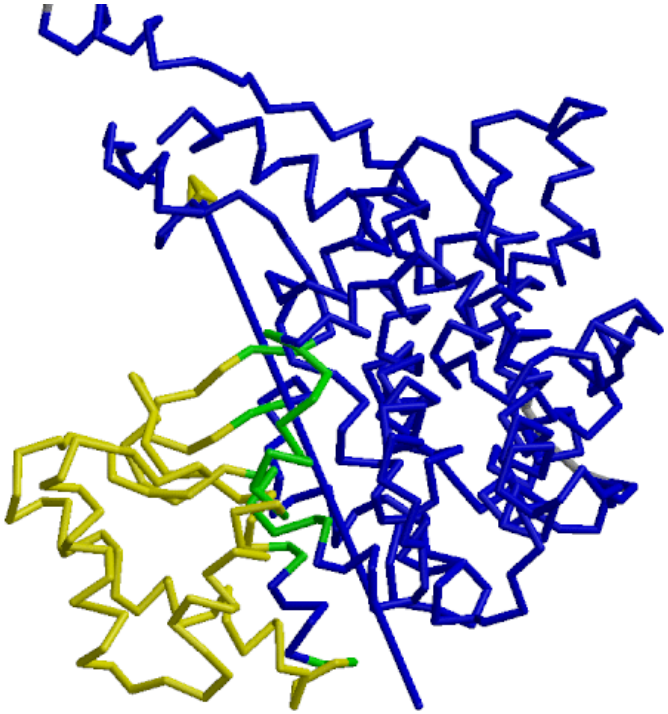
2. Relationship with ligand binding

1. Motion

	Coupled	Independent
Domain		
	Coupled domain motion (CD) : 59	Independent domain motion (ID) : 70
Local		
	Coupled Local motion (CL) : 125	Independent Local motion (IL) : 135
Small		
	Burying ligand motion (B) : 104	No significant motion (N) : 311

1. Motion

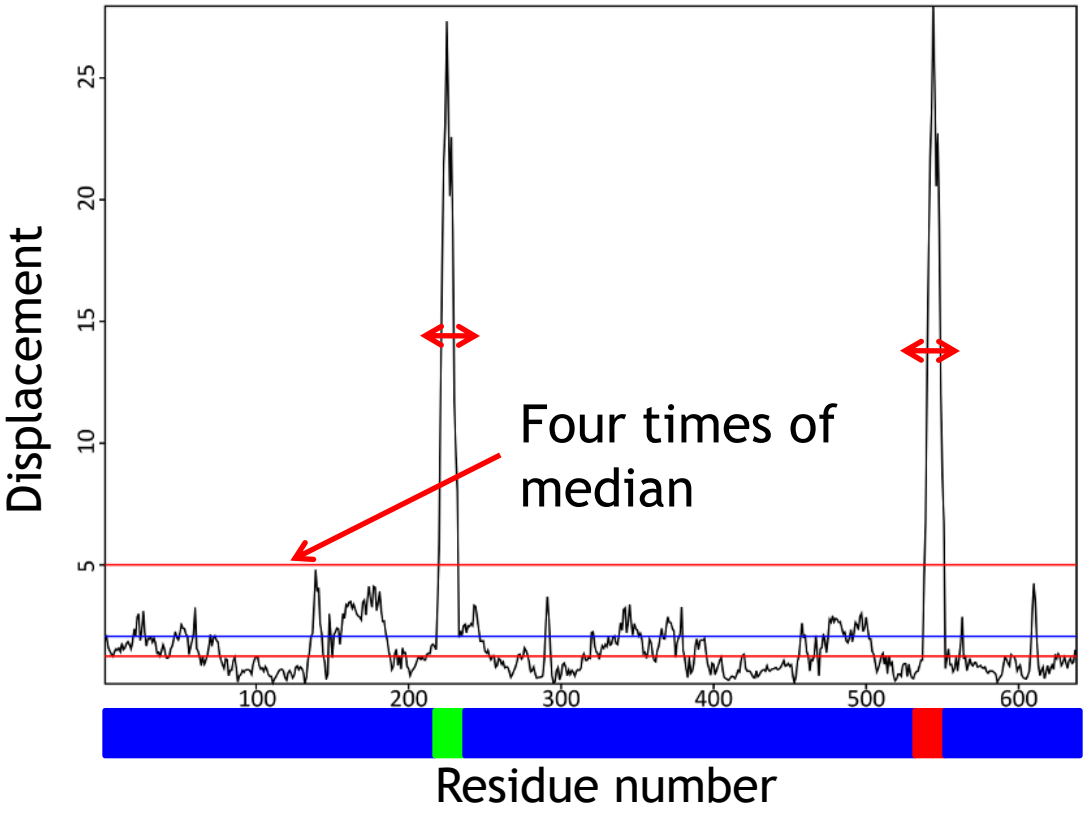
Domain motion

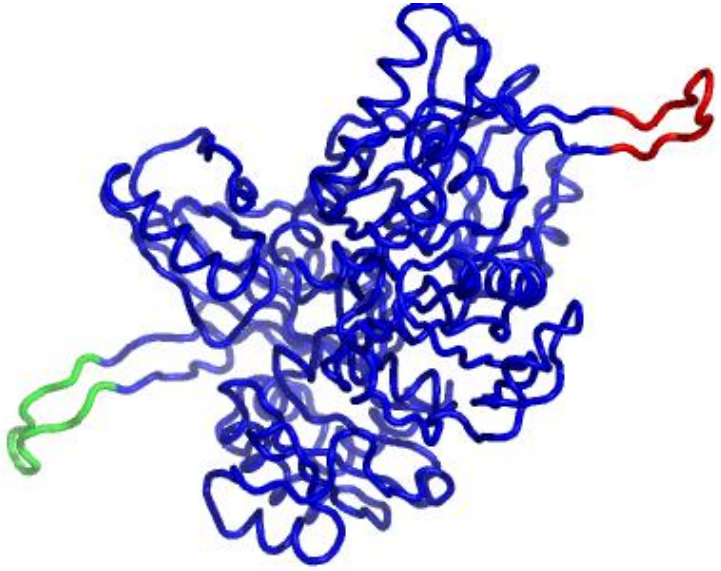


DynDom Program (Hayward *et al.*, (1998) *Proteins*)

1. Motion

Local motion



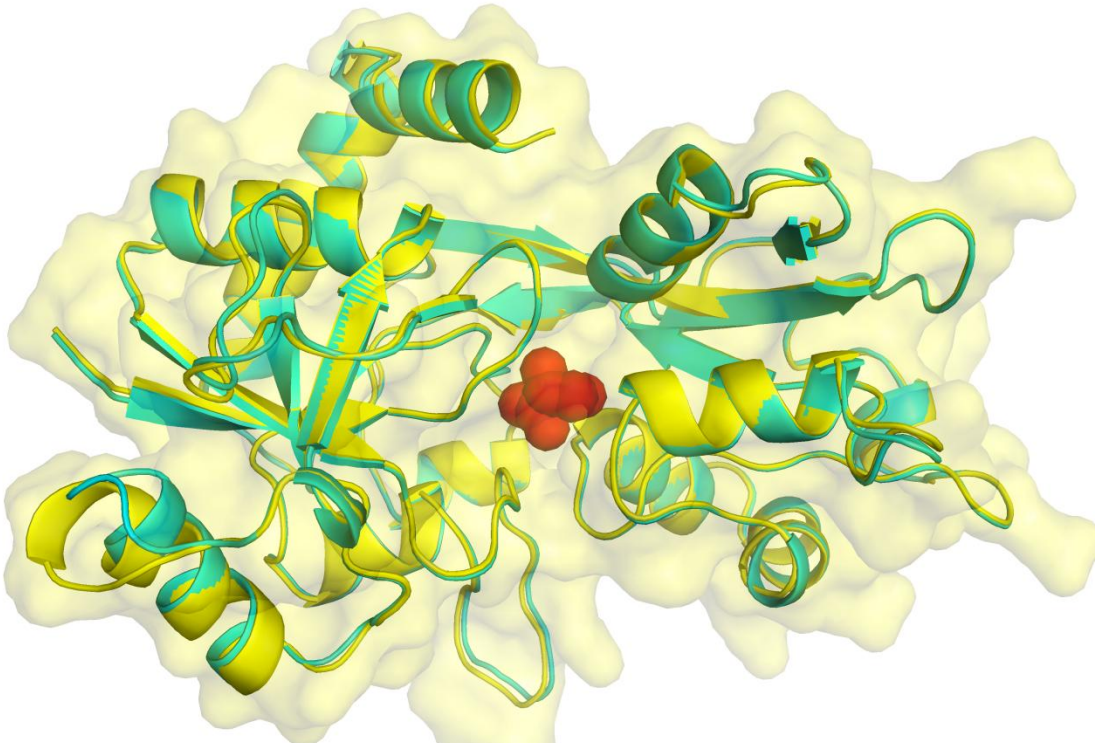


CL.58 D-alanine:D-alanine ligase

A local segment was composed of more than five residues with displacements more than four times of median or disorder-order transition residues.

1. Motion

Small motion

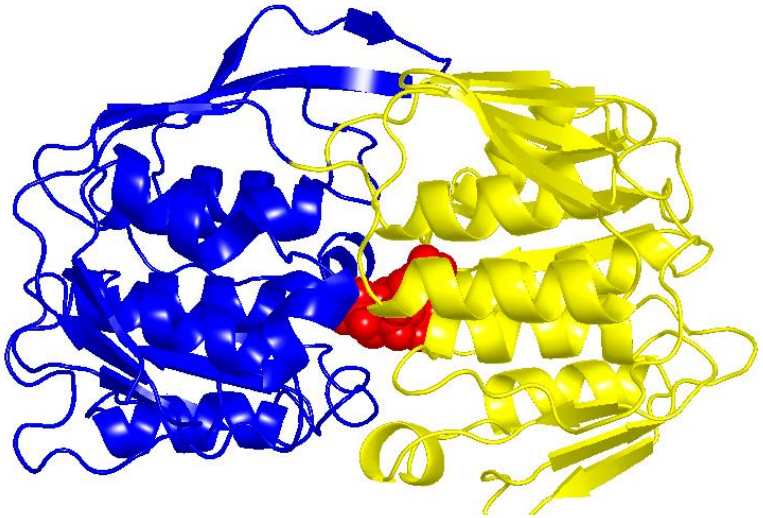


B.26 Glutamate NMDA recepter subunit 3B

RMSD < 1.0 Å

2. Relationship with ligand binding

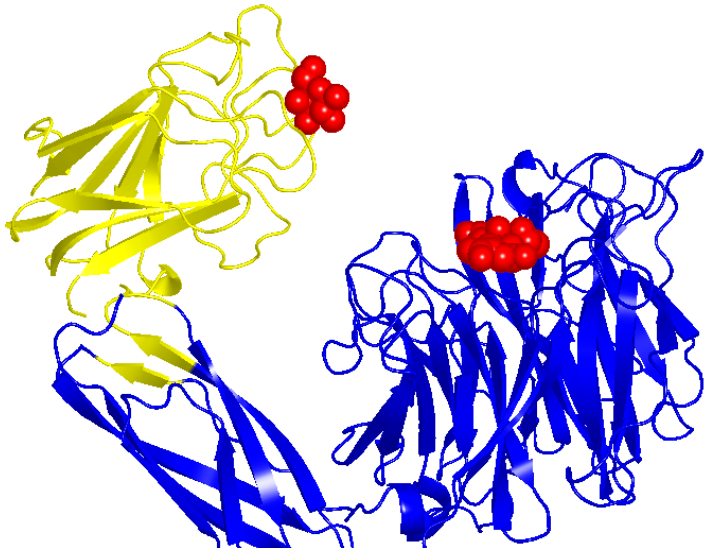
Domain motion



CD.15 3-phosphoshikimate 1-carboxyvinyltransferase

Coupled

Coupled domain motion



ID.38 Sialidase

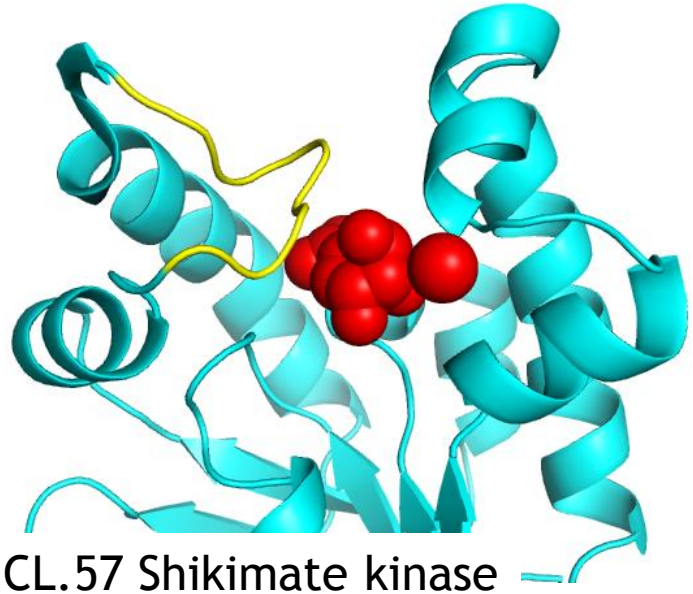
Independent

Independent domain motion

It was classified as “coupled” if both two domains contacted the ligand molecule. Otherwise, it was classified as “independent”.

2. Relationship with ligand binding

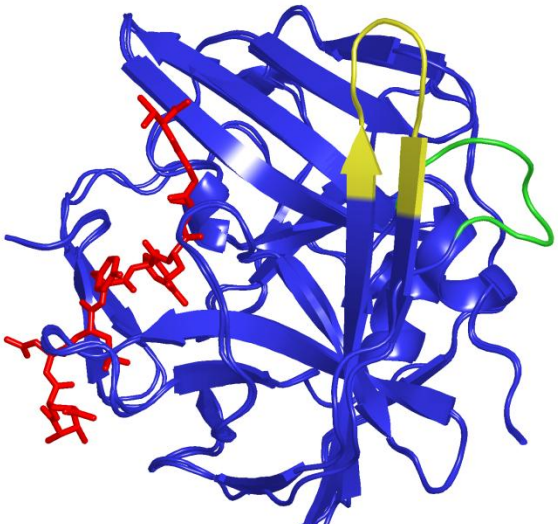
Local motion



CL.57 Shikimate kinase

Coupled

Coupled local motion



IL.69 Nuclear inclusion protein A

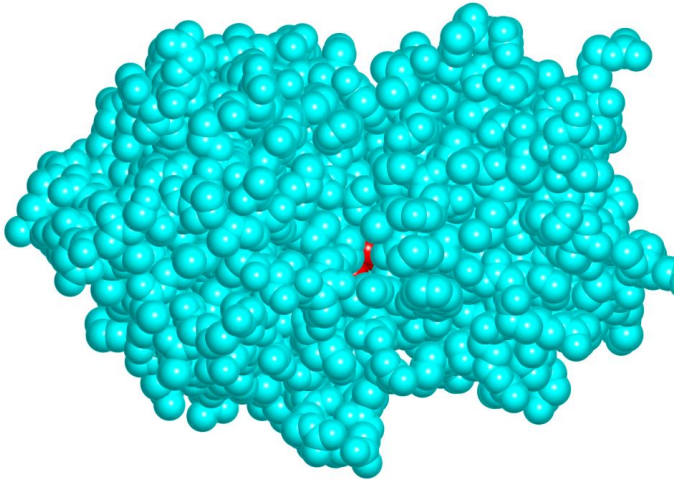
Independent

Independent local motion

It was classified as “coupled” if both core segment and local segments contacted the ligand molecule. Otherwise, it was classified as “independent”.

2. Relationship with ligand binding

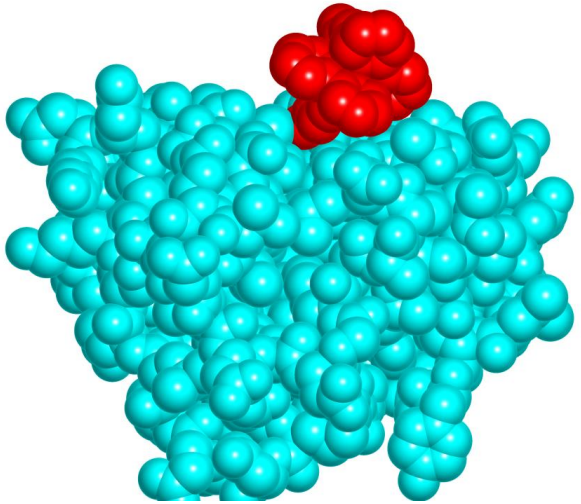
Small motion



B.26 Glutamate receptor subunit 3B

Coupled

Burying ligand motion



N.96 Adrenodoxin

Independent

No significant motion

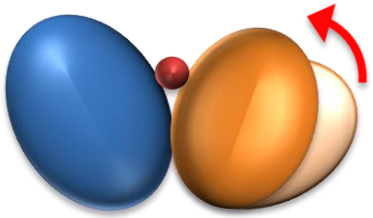
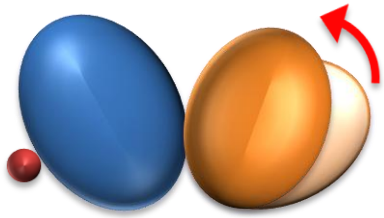
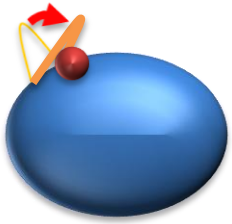
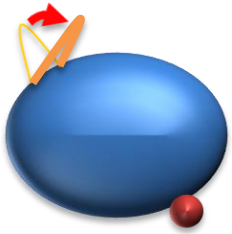
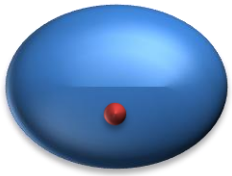
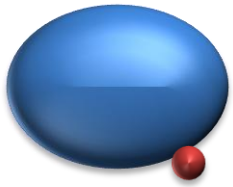
Relative accessible surface area >= 90%

PSCDB

http://idp1.force.cs.is.nagoya-u.ac.jp/pscdb/

2. Relationship with ligand binding

1. Motion

	Coupled	Independent
Domain	 Coupled domain motion (CD) : 59	 Independent domain motion (ID) : 70
Local	 Coupled Local motion (CL) : 125	 Independent Local motion (IL) : 135
Small	 Burying ligand motion (B) : 104	 No significant motion (N) : 311

Other motion (O) : 35

An example of the entries

CD.1 HYPOTHETICAL OXIDORE

PDB

The ligand-free form
1nxu_AB [Alignment: 1 2]
The ligand-bound form
1s20_AB[Alignment: 1 2]

View

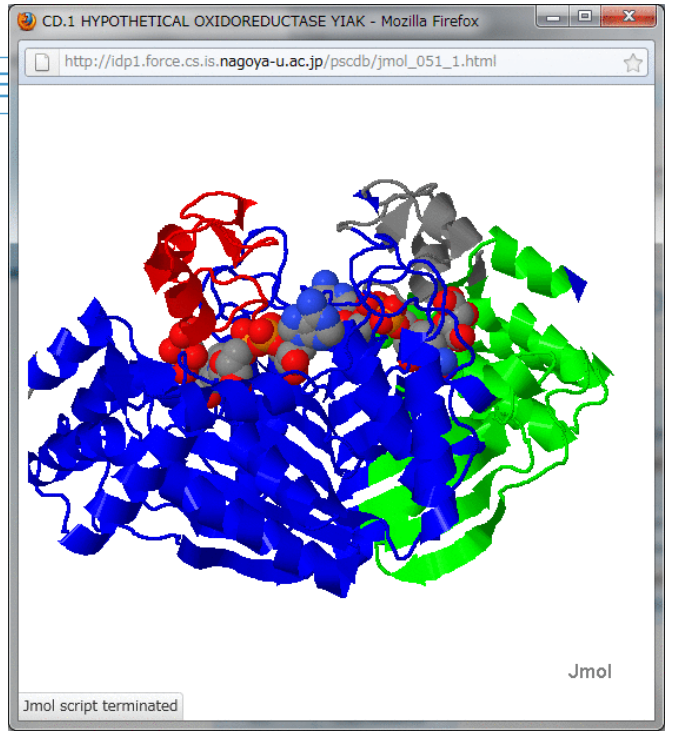
Animations of

Animation (D1 fixed)

An image of the result of the linear response theory

PNG Image (D1 fixed)

Generated by **PyMOL**



Function

EC*1	CSA distance*2
1.1.1.130	1.2

*1 Enzyme commission number.

*2 The distance between the active site annotated in CSA[23] and the ligand-binding sites.

Ligand*1

2xNAD,2xTLA

*1 Ligand name designated by the PDB identifiers.

Segments

Component No.	Fixed*1	Moving*1	Motion type	Ligand binding	Coupled motion type
1	D1(89A-90A,99A-106A,121A-136A,138A-176A,196A-197A,205A-205A,218A-247A,265A-307A,331A-332A,1B-175B,220B-230B)	D2(3A-88A,91A-98A,107A-120A,137A-137A,248A-264A,308A-330A)	Domain	Coupled	Opening
2	D1	D3(176B-219B)	Domain	Coupled	Opening

*1 The location of the fixed and moving segments indicated by the residue number assigned in the ligand-bound form.

By clicking to this “Animation” button, morphing animation can be viewed through JMOL

Summary

We created the PSCDB. PSCDB is available at http://idp1.force.cs.is.nagoya-u.ac.jp/pscdb/

(T. Amemiya *et al*. 2011, *Nucleic Acids Res*. (Submitted))

Future works

The selected motion may not represent the dominant motion of the protein family. We will examine all combinations of pairs of ligand-free and ligand-bound structures observed in a protein family.

We will also develop an automated pipeline to analyze and classify protein structural changes.

A liaison to the BLAST homology search program will also be available.

Acknowledgments

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Natsuko Hama

(Information and Mathematical Sci. Lab)