

EMBL-EBI

Enter Text Here

Find

Terms of

Databases

Tools

Research

Training

Industry

About Us

Help

PDBsum entry l872

PDBsum

Go to PDB code: l872

go

Home

?

Top page

Protein


Prot-prot

Clefts


Protein-Protein interface: A}{B

PDB id

l872



Chains A and B highlighted
(click to view)

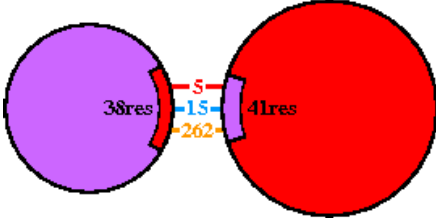


Interfaces

A}{B (38:41 res)

Chain A

Chain B



38res

41res

5

15

262

Key:

Salt bridges

Disulphide bonds

Hydrogen bonds

Non-bonded contacts

PDF

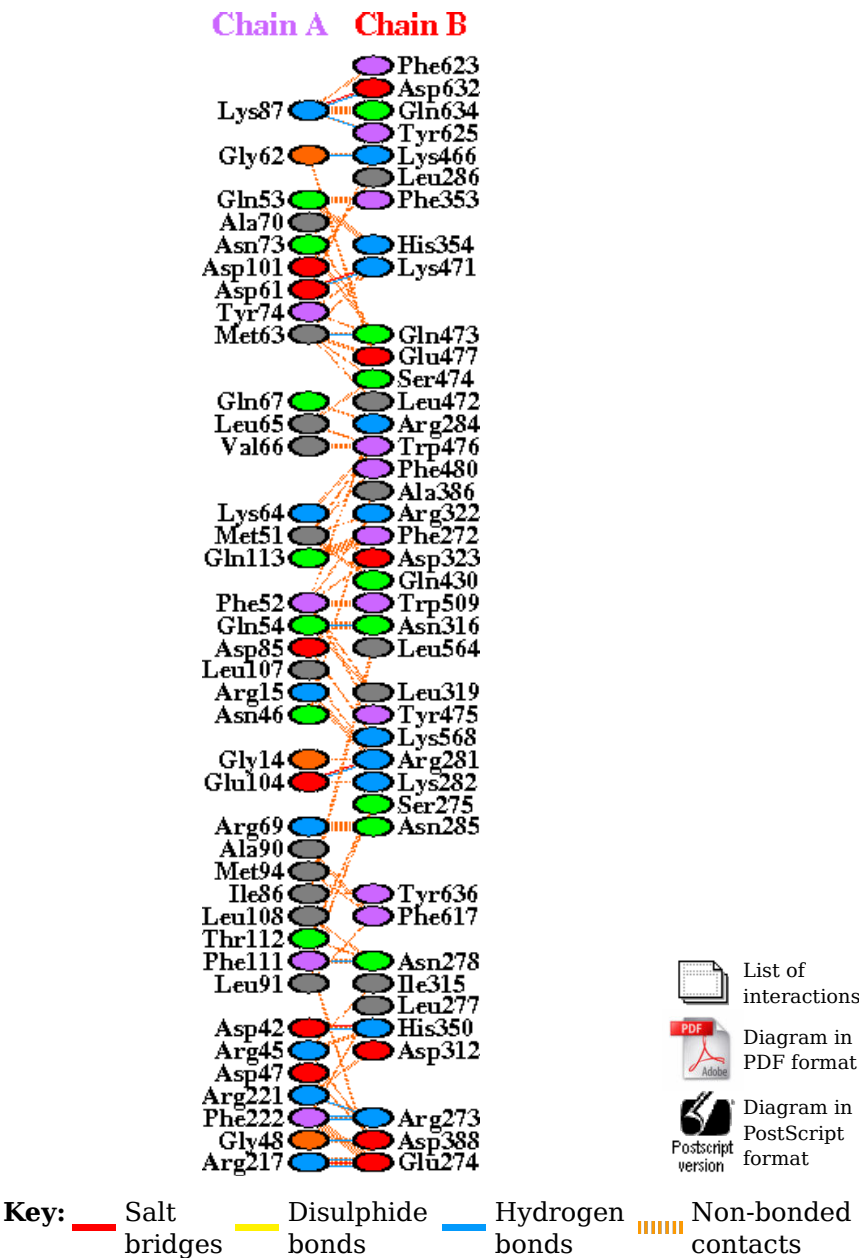
Postscript version

Schematic diagram of interactions between protein chains.

Interacting chains are joined by coloured lines, each representing a different type of interaction, as per the key above. The area of each circle is proportional to the surface area of the corresponding protein chain. The extent of the interface region on each chain is represented by the black wedge whose size signifies the interface surface area. Statistics for this interface are given below.

Interface statistics

Chain	No. of interface residues	Interface area (Å²)	No. of salt bridges	No. of disulphide bonds	No. of hydrogen bonds	No. of non-bonded contacts
A	38	2051	5	-	15	262
B	41	2023				



- List of interactions
- Diagram in PDF format
- Diagram in PostScript format

The number of H-bond lines between any two residues indicates the number of potential hydrogen bonds between them. For non-bonded contacts, which can be plentiful, the width of the striped line is proportional to the number of atomic contacts.

Residue colours: Positive (H,K,R); negative (D,E); S,T,N,Q = neutral; A,V,L,I,M = aliphatic; F,Y,W = aromatic; P,G = Pro&Gly; C = cysteine.