Abbreviations
**Abbreviations:**

3dswap-pred*: Algorithm for prediction of 3D domain swapping from sequence information
3DSSwap*: Knowledgebase of 3D domain swapping
3PFBDB*: Database of best-representative PSSM profiles of protein families
AAINDEX: Database of amino acid indices, substitution matrices and pair-wise contact potentials
Ala: Alanine
ANN: artificial neural networks
API: Application Programming Interface
ARF: Auxin response factors
Arg: Arginine
Asn: Asparagine
Asp: Aspartate
ATP: Adenosine Triphosphate
bHLH: basic helix-loop-helix
BIND: Biomolecular Interaction Network Database
BLAST: Basic Local Alignment Search Tool
BLASTP: Basic Local Alignment Search Tool Proteins
BLOSUM: Blocks Substitution Matrix
BRP*: Best representative PSSM profile of a protein domain family
bZIP: basic region/leucine zipper motif
CD-HIT: program for clustering large protein database at high sequence identity threshold.
CD2: Cluster of Differentiation 2
CDART: Conserved Domain Architecture Retrieval Tool
CDD: Conserved Domain Database
CDK: Cyclin Dependent protein Kinases
CGI: Common Gateway Interface
COG: Clusters of Orthologous Groups
CPU: Central Processing Unit
CSA: Catalytic Site Atlas
Cys: Cysteine
DDJB: DNA Database of Japan
DEP: Domain found in Dishevelled, Egl-10, and Pleckstrin
DIAL: Domain Identification ALgorithm
DISOPRED: tool to predict disorder regions in protein sequences
DLAR: Drosophila Leukocyte Antigen Related Protein
DNA: Deoxyribonucleic acid
DNA: Deoxyribose Nucleic Acid
DO: Disease ontology
DOI: Document Object Identifier
DOMINE: Database of protein interactions
dsh: dishevelled
DT: decision tree
EBI: European Bioinformatics Institute
EREBP: ethylene-responsive element binding proteins
FASSM: Program for Function Association of protein sequence using Sequence & Structure Motifs
FN: False Negative
FP: False Positive
FU: Functional Unit
GA: genetic algorithms
gcc: GNU C compiler
Glu: Glutamine
Gly: Glycine
GO: Gene Ontology
GOA: Gene Ontology Annotations
GPCR: G-Protein Coupled Receptor
GRAVY: Grand Average of Hydropathy
GSEA: Gene Set Enrichment Analysis
GWAS: Genome-wide association studies
HARMONY: Tool for the assessment of protein structure quality
HBOND: Program for calculating hydrogen bond from PDB file, part of JOY suite
His: Histidine
HIV: Human Immunodeficiency Virus
HMM: Hidden Markov Model
HMMER: Software for biosequence analysis using profile hidden Markov models
HORI*: Tool for the computation of Higher Order Residue Interactions in proteins
HTTP: Hyper Text Transfer Protocol
IWS: Integrated Web Server
Jmol: Open source molecule viewer written in Java
JOY: Tool for protein sequence-structure representation and analysis
IG: Information Gain
KEGG: Kyoto Encyclopedia of genes and genomes
Leu: Leucine
Lys: Lysine
MALIGN: Multiple Alignment Program
MCC: Matthews Correlation Coefficient
MEA: Modular Enrichment Analysis
MODIP: Modelling of Disulphide bonds In Proteins
MOLSCRIPT: program for displaying molecular 3D structures, such as proteins, in both schematic and detailed representations.
mRNA: Messenger RNA
MSA: Multiple Sequence Alignment
MSigDB: Molecular Signatures Database
MView: Program to reformat the results of a sequence database search (BLAST, FASTA, etc) or a multiple alignment (MSF, PIR, CLUSTAL, etc) adding optional HTML markup to control coloring
and web page layout.

NCBI: National Centre for Biotechnology Information
NMR: Nucleic Magnetic Resonance
NPV: Negative Prediction Value
PAM: Point Accepted Mutation
PCA: Principal Component Analysis
PDB: Protein Data Bank
PDBSum: PDBsum provides an at-a-glance overview of every macromolecular structure deposited in the Protein Data Bank.
PDZ: PSD-95/Discs-Large/ZO-1
PeptideMine*: Web server for identification and analysis of peptides from interacting sequence space
PFAM: Protein Family Database
PHYLIP: Phylogeny Inference Package
PIR: Protein Information Resource
PPV: Positive Prediction Value
PRODOM: Protein Domain Database
PROSITE: Database of protein domains, families and functional sites
PSA: Program for solvent accessibility from PDB file, part of JOY suite
PSI-BLAST: Position Specific Iterated BLAST
PSIMOT: conserved motifs obtained from a given BRP using the PSIMOT routine of FASSM
PSIPRED: Protein secondary structure prediction program
PSSM: Position Specific Scoring Matrix
PSM: Position-specific Scoring Matrix
PTEN: phosphatase and tensin homolog
PTP: Protein Tyrosine Phosphatase
PURE: Algorithm for Prediction of Unassigned REgions in proteins
PyMOL: an open-source, user-sponsored, molecular visualization system
RBF: Radial Basis Function
RefSeq: Reference Sequence Database
REST: REpresentational State Transfer
RF: Random Forest
RGS: Regulators of G protein Signaling
RNA: Ribonucleic Acid
RNA: Ribonucleic acid
RNAi: RNA interference
RNase: Ribonuclease
ROC: Receiver Operating Characteristic
RPS-BLAST: Reverse Position-Specific BLAST
RPTP: Receptor Protein Tyrosine Phosphatase
RYMV: Resistance to rice yellow mottle virus
ScanProsite: Tool for scanning protein sequences to predict functional pattern using PROSITE database
SCOP: Structural Classification of Proteins
SEA: Singular Enrichment Analysis
SEQPLOT*: Tool for visualizing multiple amino acid indices derived from a given sequence
Ser: Serine
SH3: Src Homology 3
SI: swarm intelligence
SMART: Simple Modular Architecture Research Tool
SOAP: Simple Object Access Protocol
SOM: Self Organizing Map
Spo0A: Stage 0 sporulation protein A
SSE: Secondary structural element
SSTRUC: Program for calculating secondary structure from PDB file, part of JOY suite
STIF*: Hidden Markov Model based Stress responsive Transcription Factor prediction algorithm
STIFDB*: Stress responsive transcription factor database
STRING: Database of known and predicted protein-protein interactions
SVM: support vector machines
TAIR: The Arabidopsis Information Resource
TF: Transcription Factor
TFBS: Transcription Factor Binding Site
TFMap*: Transcription factor map
Thr: Threonine
TN: True Negative
TP: True Positive
TREMBL: Translated EMBL
Tyr: Tyrosine
UniProt: Universal Protein Resource
URL: Uniform Resource Locator
UTR: Untranslated Region
Val: Valine
VP1: Viviparous 1
XML: eXtensible Markup Language
* Abbreviations based on concepts introduced in this thesis