Immunoinformatics-*Insilico* Prediction of Immunogenicity

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Abstract

With the escalating immunological data, immunoinformatics is rapidly growing subdiscipline of bioinformatics which plays a key role in the prediction of immunogenicity by employing biological databases of immune-related molecules and epitopes along with the usage of bioinformatics tools for analysis of T and B cell epitope, vaccine development, and molecular interactions.

Keywords: Kabat Database; JenPep; NetChop Prediction Server; BACTIBASE Database; CombiPRED

Introduction

With the increasing number of databases containing valuable immunological data, integration of computational tools was a necessity to improve our understanding of immune system and pathogens under immune responses [1,2]. Knowledge related to pathogens and cancer induced immune responses is valuable, identifying specific epitopes and epitope sequence specificity based on complete genetic typing of HLA-epitope [3]. Web-based methods enables the exploration of immunologically relevant data from a variety of perspectives including in silico designing of vaccines, immune system modelling, antigen-antibody interaction study etc. All these efforts saves time and is cost effective [4,5].

Given below is a huge list of different immunoinformatics related databases and informatics tools (Table 1).

S. No	Immunoinformatics databases /tools	Purpose
1	IMGT/LIGMDatabase	Database containing data on germline and rearranged immunoglobulin from vertebrates [6]
2	Kabat database	Contain protein sequences with immunological properties [7]
3	ExactAntigen	Database for searching monoclonal antibodies [8]
4	BoLA	Bovine leucocyte antigens database [9]
5	HLA Database	Uses data from IMGT/HLA database [10]
6	AntiJgen (an extension of JenPep)	Database providing data on immunological interactions [11]
7	MHCBN	Provides data on T cell epitopes and MH binding/non-binding peptides [12]
8	EpiPox Database	Integrated with Poxvirus Bioinformatics Resource Center database [13]
9	JenPep	Provides data on peptide binding [14]
10	EPIMHC	Curated database of MH ligands [15]
11	SiPeP	Nonsynonymous coding SNPs database [16]
12	Bcipep	Immunant dominant B cell epitopes based database [17]
13	CIDB	Cancer immunome database [18]
14	Epitome	Structure-inferred antigenic residues Immuno-complex [19]
15	HaptenDB	Provides data on anti-hapten antibodies, carrier proteins and haptens [20]
16	CED	Conformational epitope database [21]
17	SYFPEITHI	MH ligands and peptide motifs database [22]
18	SNPBinder	Histocompatibility antigens (mHAgs) and antigenic peptides database [2]
19	Food Allergen Sequences	Food safety database [23]
20	InformAll Database	Database of food allergens from plant origin [24]
21	SDAP	Database providing data on allergenic protein structures [25]
22	NetCTL	Predicts peptide binding to different HLA-A and HLA-B alleles [26]
23	BACTIBASE Database	Bacteriocin natural antimicrobial peptides based database [27]
24	Cybase	Cyclic peptides and cyclotides database [28]
25	DBAASP	Peptides structure and antimicrobial activity database [29]
26	Peptaibol Database	Peptaibols, antimicrobial peptides database [30]
27	PhytAMP	Database on plant antimicrobial peptides [31]
28	ImmunomeBase	Database for metazoan immunity genes and orthologs [32]
29	NetChop Prediction Server	Produces neural network predictions for cleavage sites of the human proteasome [33]
30	PAProC	Prediction algorithm for proteasomal cleavages [34]
31	CombiPRED	MH prediction tool [35]
32	nHLAPred	MH1 binding peptide prediction server based on neural network [36]
33	ProPred-I	Promiscuous MH1 binding peptide prediction server [37]
34	RANKPEP	Binding peptides database [38]
36	NetMHC	Prediction of peptide binding using neural networks and hidden Markov models [39]
37	SYFPEITHI T cell epitope prediction	Profiling based database [22]

Table 1: Immunoinformatics related databases and informatics tools.

Conclusion

Extensive clinical data has been deposited in several immunological databases. As a result immunoinformatics has appeared as a major asset to help understand the immune system and its components using bioinformatic approaches. It not only assists in utilizing the immunological data but also contributes in designing new propositions related to immune responses.

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