Biomat_dBase: A Database on Biomaterials

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Abstract: Biomaterial science provides a platform for the development of bio-artificial implants. Growth or development of engineered tissues for the purpose of repairing, restoring and enhancing the function of a damaged tissue or organ needs designed biomaterials. The most studied tissue engineering strategy consists on using cells growth factors and temporary three-dimensional (3D) porous scaffolds. 3D scaffolds play a very important role in the success of tissue engineering and regenerative medicine. They provide structural support for cells to proliferate and maintain their differentiated phenotype and permit the convenient delivery of cells into the patients. Several features of scaffold can influence the cell growth and its functions. The artificial extracellular matrices can be produced from different biomaterials including ceramics, natural or synthetic polymers and composites. Recent discoveries and innovations in this emerging field adopt varieties of techniques ranging from biotechnology to material science and nanotechnology. The result is a huge amount of data. To maintain and keep updated, this would not be an easy task. New advances in computers and information technology help to create and organize the databases quite easy. Their contents can easily be accessed, managed and updated. A WWW interface benefits the users to search the different types of data based on the types of biomaterials, their abundance, structure and applications. This provides the scope and archive of information on this emerging field of biomaterials to the global scientific community. The database is freely accessible through http://dbbiomat.iitkgp.ernet.in.

Keywords: Biomaterials, BLAST, database, relational database, tissue engineering.

INTRODUCTION

Traditionally, biomaterials are intended to treat, deliver, augment or replace either the tissue or the function of body damaged either by disease or trauma [1-5]. Recently natural or synthetic nonviable biomaterials should not only promote an appropriate host response to the body, but also promote or inhibit specific cell activities. In the last few decades, with the combined advancement of biomaterials and biological sciences, the new field of “tissue engineering” and “regenerative medicine” has emerged creating unique opportunities to fabricate tissues in the laboratory. Biomaterials play a pivotal role in this field of science that is being used for producing new skin, connective tissues like bone and cartilage [6-9]. Strategies to provide smart capabilities to the biomaterials primarily seek to achieve matrices that are instructive/inductive to cells. They may help to stimulate/trigger target cell responses, which are crucial in the tissue regeneration processes [10]. The development of such a tissue engineered construct required the combination of engineered extracellular matrices (“scaffolds”), cells and biologically active molecules. Cells are the fundamental unit on this strategy because of their ability to proliferate differentiate, and deposit specific ECM [11, 12]. Biomaterials used in tissue engineering applications can be fabricated in different forms including films, scaffold, nanofibers, nanoparticles, and hydrogels. Films basically have a 2D architecture and are able to support the adhesion and proliferation of cells [13]. Scaffolds are considered as a microporous three dimensional structures, in which a cell suspension can be seeded, promoting proliferation, differentiation, migration and orientation of the cells [7 and 14-17]. The nanofibers are sub-microscopic range fibers, dimensionally similar to ECM, which provide the cues for cell survival, their organization and function [18-21]. On the other hand nanoparticles are sub-microscopic size particles applied for the delivery of drug, vaccines, plasmid DNA, and other bioactive molecules [22-27]. Hydrogels are 3D structures involving a network of structural, usually cross-linked molecules, within a water-based viscous matrix

#Available at: http://dbbiomat.iitkgp.ernet.in
Log in: database
Password: biomat321
employed for cell encapsulation, delivery of drugs and other molecule [28-32]. Different types of natural and synthetic biomaterials are utilized for the fabrication of the polymeric matrices including starch, collagen, gelatin, alginate, agarose, chitosan, hyaluronic acid, silk proteins, elastin and fibrin [33-35]. One promising feature of these polymers is their excellent ability to be processed into porous structures use for the cell transplantation and tissue regeneration. Moreover, these natural biopolymers show similarity to the ECM and other polymers of the body [12]. ECM is complex mixture of structural and functional proteins, glycoprotein and proteoglycans arranged in a unique tissue specific three-dimensional ultra structure, that provide mechanical stability and structural integrity to tissues and organs [34]. Natural based biomaterials are widely used for tissue engineering applications due to their excellent biodegradability, antimicrobial property [35], biocompatibility, oxygen permeability and nontoxic nature. Examples of their use includes applications for wound dressing [36-38], tissue engineering of bone [39, 40], cartilage [41, 42], ligament [43, 44], skin [45], tendon [43, 46], hepatic [47], reticular connective tissue [48] endothelial and blood vessels [49, 50]. Other example includes its use for vaccine design [51] and for the detection of brain activity [52]. Despite progress, currently there are a few tissue-engineering products available for clinical use especially synthetic ones. They can substitute soft and mechanically functional tissues such as muscle and connective tissue [53].

A large number of discoveries and innovations have occurred in this field and thus a huge amount of data has been created. The management and updating of such a huge data is not an easy task. Thus, development of an appropriate biomaterial database is the need of the hour, which would allow the scientific community to be benefitted by the information given about the recent developments, prevents wasteful duplication of research and increase the faculty of knowledge for taking appropriate decision before initiation of new research. Based on these criteria, we have developed a database on biomaterials. It is available at http://dbbiomat.iitkgp.ernet.in. This derived database mainly focuses on the natural based biomaterials (protein and polysaccharides), site of occurrence of the biomaterials, structures and their applications.

**MATERIALS AND METHODS**

Biomaterial database is created using relational database management system (RDBMS) [54, 55] and operated in Red Hat Enterprise Linux 4. The web interface is developed in HTML/CSS; PHP and Java scripts are used for retrieving the stored data. The Basic Local Alignment Search Tools (BLAST) explore web interface and its scripts are implemented in PHP, based on [56-58]. The overall structure of the biomaterial database is shown in Fig. (1). The protein sequence corresponds to the biomaterials data collected from the protein data bank at www.rcsb.org/pdb. All the sequences are downloaded in a FASTA format and saved in a common database flat file. Then the database file is converted into a format acceptable by BLAST, using the Formatdb program [59]. The stand-alone version of the BLAST program is downloaded from the NCBI/BLAST web site (ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/LAST-TEST/). To begin the search, an input parameter called
threshold has to be defined by the user. In the Biomat_dBase server, the input for the BLAST is provided in the text box in standard FASTA format. The input may also be uploaded from the client’s local machine. The server takes the query from the input page and searches for similar homology sequences against the biomaterial database by using the BLASTP program. Finally, the similar protein sequences, which are obtained under the given threshold value is displayed in the new window. Data redundancy can be checked by the use of secondary structure matching tool (EBI-SSM) and Root Mean Squire Deviation (RMSD) to prevent the unnecessary duplication and redundancy in the database. The pictures of silk biomaterials are created on the webpage by using cascade style sheet (CSS) and java script.

**DATABASE ACCESS AND INTERFACE**

Biomaterial database is developed using relational database management system (RDBMS) and interfaced through the custom designed web interface by utilising Hypertext pre-processor (PHP), Hypertext Mark-up language (HTML) and JavaScript. The database is housed in a Sun Fire v880 Server running Solaris 9 (Sun Microsystems). The BLAST search, available in the Biomaterial database utilizes the formatted sequence data available in the relational database. The biomaterial database is freely available at a web based user interface site (http://dbbiomat.iitkgp.ernet.in). It allows users to explore the website and fetch the data corresponding to their queries. It also provides the information related to biomaterials, their sequence homology, percent sequence identity, information about the protein and polysaccharide biomaterials, their occurrences, structures and applications.

The structural component of biomaterial is solved using bioinformatics tools. The PDB ID of the related biomaterials is obtained from the Protein Data Bank (PDB) [60] from http://www.rcsb.org/pdb. On the basis of their structure they are classified and stored in the RDBMS. It provides the following information about the description of a particular biomaterial:

a) How its structure is solved experimentally (X-RAY crystallography, NMR spectroscopy or Fiber diffraction method),

b) Resolution of the structure

c) Group of the protein or polysaccharide biomaterials (hydrolyses or celluloses etc),

d) Assembly type (whether DNA or RNA bound, protein chain and number of residues),

e) Nucleotide chain and number of residues, and

f) References of the structure.

**RESULTS AND DISCUSSION**

The main objective of this work is to construct a database for biomaterials. Currently there is no such database on this emerging field. In order to develop this, we use a relational database system. For example, we consider the basic local alignment and search tool (BLAST) for protein and polysaccharide database, to store the sequence in the sequence database and to implement the BLAST algorithms within the database system for the retrieval and analysis of sequence information [61]. BLAST is the most widely used algorithm for comparing biological sequences such as amino acids or nucleotides [62]. The query sequence is compared against a large database or library at a very high speed and produces the statistical significance of matching sequences. In addition, the program finds the regions of local similarity during the sequence alignment. Several variants of the BLAST program exist, of which the protein-protein BLAST (BLASTp) program is used for identifying a query of amino acid sequence and for finding similar sequences in protein databases. Thus, the BLAST can be used to infer functional and evolutionary relationships between sequences. In general, the BLAST output tends to be large and need to be processed to gain meaningful information. Several programs are developed to aid this process, which include the MuSeqBox [63], BioParser [64], the Nuclear BLAST program [65] and the PLAN web server [66]. All these programs aid in data mining of the BLAST results to generate more comprehensive outputs as required by the users.

PDB ID for protein and polysaccharide biomaterials is obtained from the Protein Data Bank. While creating a database, data redundancy becomes the biggest problem, where same data value is stored more than once in a table. This increases the size of data base unnecessarily, and leads to multiple display of search results leading to confusion and clutter in the database. Database redundancy can be checked by the use of secondary structure matching tool (EBI-SSM) for pair wise comparison and 3D alignment of the structures. Sequences that have higher sequence identity and best Root-mean-square deviation (RMSD) values are chosen. Those having lowest sequence identity and worst RMSD values are discarded. When multiple entry of a given structure is available in the PDB, we retain the one with the best resolution value. Between wild type and mutant proteins or polysaccharides, we kept the wild types to reduce the redundancy in the database.

The homepage of the database has modules for different matrices, classifications, search and references related to biomaterials. The homepage module provides information related to the concept of biomaterials, their design criteria and classifications. A typical homepage module is presented in Fig. (2A). Modules for the matrices provide information on different types of fabricated biomaterial structures in the form of scaffolds, nanofibers, nanoparticles, hydrogels and films used for potential applications of different tissue engineering and regenerative medicine. Classification modules segregate the biomaterials into those of natural and synthetic origin are in Fig. (2B) and (2C) respectively. The natural biomaterials are further classified into proteins and polysaccharides on the basis of their occurrence, structure and applications. We have provided the detail list for synthetic biomaterials and their applications in a tabular form on the web page.

The search tool option has a drop down list box on biomaterials including silk, starch, agarose, alginate, carrageenans, cellulose, chitosan, collagen, elastin, fibrin, gelatin, hyaluronic acid, arabinogalactane, and glycosaminoglycan. They are structurally classified on the basis of their PDB ID, sequence of the related biomaterials...
Fig. (2). (A). Home page representation of Biomat_dBase (B) classification of biomaterials (C) a drop down list box represents the structural classifications of biomaterials.

Fig. (3). (A). Represents homology search tool based on BLASTp (B) depicting the overall representation of BLAST result.
Table 1. Structural Classifications of Starch Biomaterial (as an Example)

| PDB ID | Descriptor | Method | Resolution | Keywords | References | Assembly Type | Bound to RNA or DNA | Protein Chains and No. of Residues | Nucleotide Chains and a No. of Residues |
|--------|------------|--------|------------|----------|------------|---------------|-------------------|-------------------------------------|---------------------------------------|
| 1ACO   | Glucoamylase, granular starch-binding domain complex with cyclooctatin, NMR, minimized average structure | X-Ray | 2.05 | Hydrolase | Lauble et al., J Mol Biol. (1994) 237:437-51 | Monomer | No | A, 754 aa | 0 |
| 1ACZ   | Glucoamylase, granular starch-binding domain complex with cyclooctatin, NMR, 5 structures | NMR | | Hydrolase | Sorimachi et al., J Mol Biol. (1994) 259 (5):645-661 | Monomer | No | A, 108 aa | 0 |
| 1AMY   | Crystal and molecular structure of barley alpha-amylose | X-RAY | 2.80 | Hydrolase (O-Glycosyl) | Kadziola et al., J Mol Biol. (1985) 239:104-121 | Monomer | No | A, 403 aa | 0 |
| 1B90   | Bacillus cereus BETA-amylase Apo form | X-Ray | 2.50 | Hydrolase | Mikami et al., Biochemistry (1999) 38 (22):7050-61 | Monomer | No | A, 516 aa | 0 |
| 1BG9   | Barley alpha-amylose with substrate analogue acarbose | X-RAY | 2.80 | Hydrolase | Kadziola, J Mol Biol. (1998) 278: 205-217 | Monomer | No | A, 403 aa | 0 |
| 1BLI   | Bacillus licheniformis alpha-amylose | X-RAY | 1.90 | Hydrolase | Machius et al., Structure (1998) 6(3):281-292 | Monomer | No | A, 483 aa | 0 |
| 1CQY   | Starch binding domain of Bacillus cereus beta-amylose | X-RAY | 1.95 | Hydrolase | Yoon et al., J Micro. Biol. (1999) 9:619-623 | Monomer | No | A, 99 aa | 0 |
| 1GAI   | Glucoamylase-47I complexed with d-glucodihydrocarbocerol | X-RAY | 1.700 | Hydrolase | Aleshin et al., Biochemistry (1996) 35 (25): 8319-8328 | Monomer | No | A, 472 aa | 0 |
| 1GCY   | High resolution crystal structure of maltotetraose-forming exo-amylose | X-RAY | 1.60 | Hydrolase | Mezaki et al., Biosci Biotechnol Biochem. (2001) 65(1):222-5 | Monomer | No | A, 527 aa | 0 |
| 1HVX   | Bacillus steathermophilus alpha-amylose | X-RAY | 2.00 | Hydrolase | Savd et al., J Biochem. (2001) 129 (3):461-8 | Monomer | No | A, 515 aa | 0 |
| 1GI1   | Beta-amylose from Bacillus cereus var. mycoides in complex with alpha-EPG | X-RAY | 2.00 | Hydrolase | Hemmi et al., J Biochem. (2001) 129(3):461-8 | Monomer | No | A, 102 aa | 0 |
| 1KUL   | Glucoamylase, granular starch-binding domain, NMR, 5 structures | NMR | | Hydrolase | Sorimachi et al., J Mol Biol. (1996) 259(5):970-987 | Monomer | No | A, 108 aa | 0 |
| 1OB0   | kinetic stabilization of bacillus licheniformis-amylose through introduction of hydrophobic residues at the surface | X-RAY | 1.83 | Hydrolase | Machius et al., J Mol Biol. (1996) 259: 970-987 | Monomer | No | A, 483 aa | 0 |
| 1PEZ   | Bacillus circulans strain 251 mutant A230V | X-RAY | 2.32 | Transferase | Leemhuis et al., Biochemistry (2003) 42:7518-26 | Monomer | No | A, 686 aa | 0 |
| 1QHP   | Five-domain alpha-amylose from Bacillus steathermophilus, maltose complex | X-RAY | 1.70 | Hydrolase | Dauter et al., Biochemistry (1999) 38:8385 -8392 | Monomer | No | A, 686 aa | 0 |
| 1RZU   | Crystal structure of the glycogen synthase from A. tumefaciens in complex with ADP | X-Ray | 2.30 | Transferase | Buschiazzo et al., J EMBO (2004) 23(16):3196-205 | Monomer | No | A, B, 485 aa | 0 |
Table 1. contd…

| PDB ID | Descriptor | Method | Resolution | Keywords | References | Assembly Type | Bound to RNA or DNA | Protein Chains and No. of Residues | Nucleotide Chains and a No. of Residues |
|--------|------------|--------|------------|----------|------------|---------------|-------------------|-----------------------------------|----------------------------------------|
| 1TCM   | Cyclodextrin glycosyltransferase w616a mutant from *Bacillus circulans* strain 251 | X-RAY | 2.20       | Glycosyl Transferase  | Penninga et al., J Mol Biol. (1996) 276:3277-84 | Monomer | No | A, B, 686 aa | 0 |
| 1UH4   | Thermaactinomyces vulgaris R-47 alpha-amylase 1/malto-tridecose complex | X-RAY | 1.80       | Hydrolase | Abe et al., J Mol Biol. (2004) 335:811-822 | Monomer | No | A, 637 aa | 0 |
| 2C4M   | Structure of iodinated cbm25 from *Bacillus halodurans* amylase | X-RAY | 1.39       | Carbohydrate binding module | Boraston et al., J Mol Biol. (2006) 281:587 | Monomer | No | A, 102 aa B, 102 aa | 0 |
| 2C4M   | Starch phosphorylase: structural studies explain oxyanion-dependent kinetic stability and regulatory control | X-RAY | 1.90       | Transferase | Purvis et al., (2009) (submitted to PDB) | Dimer | No | A, B, C, D 796 aa | 0 |
| 2DJM   | Solution structure of N-terminal starch-binding domain of glucoamylase from *Rhizopus oryzae* | NMR |           | Sugar binding protein | Liu et al., Biochimica et Biophysica Acta Gene Regulatory Mechanisms (2007) 403:21-30 | Monomer | No | A, 106 aa | 0 |
| 2FBA   | Glucoamylase from *Saccharomyces fibuligera* at atomic resolution | X-RAY | 1.10       | Hydrolase | Sevcik et al., FEBS J. (2006) 273: 2161-2171 | Monomer | No | A, 492 aa | 0 |
| 2QZS   | Crystal Structure of Wild-type *E.coli* GS in complex with ADP and Glucose(wtGSb) | X-RAY | 2.20       | Transferase | Sheng et al., J Biol Chem. (2009) 284: 17796-17807 | Monomer | No | A, 485 aa | 0 |
| 2Q4V   | Carbohydrate-binding of the starch binding domain of *Rhizopus oryzae* glucoamylase in complex with beta-cyclodextrin and maltoheptaose | X-RAY | 1.25       | Hydrolase | Tung et al., J Biochem. (2008) 416(1):27-36 | Monomer | No | A, 106 aa | 0 |
| 2WAN   | Pullulanase from *Bacillus acidopullulyticus* | X-RAY | 1.65       | Hydrolase | Turkenburg et al., Proteins (2009) 76(2):516-9 | Monomer | No | A, 921 aa | 0 |
| 2XHM   | Crystal structure of the *Gracillariopsis lemaneiformis* alpha-1,4-glucan lyase | X-RAY | 1.06       | Lyase | Rozeboom et al. (2009) (submitted to PDB) | Monomer | No | A, B, C, D 1027 aa | 0 |
| 2XFR   | Crystal structure of barley beta-amylase at atomic resolution | X-RAY | 0.97       | Hydrolase | Rejzek, M, Mol Biosyst (2011) 7: 718 | Monomer | No | A, 535 aa | 0 |
| 2Y5E   | Barley limit dextrinase in complex with beta-cyclodextrin | X-RAY | 2.10       | Hydrolase | Vester-Christensen et al., J Mol Biol. (2010) 403(5):739-50 | Monomer | No | A, 858 aa | 0 |
| 3BC9   | Crystal structure of CBM20 domain of human putative glycerophosphodiester phosphodiesterase 5 (KIAA1434) | X-RAY | 2.0        | Hydrolase | Tan et al., J Mol Biol (2008) 378: 850-868 | Monomer | No | A, 599 aa | 0 |
| 3BCD   | Alpha-amylase B in complex with acarbose | X-RAY | 1.35       | Hydrolase | Tan et al., J Mol Biol (2008) 378: 850-868 | Monomer | No | A, 599 aa | 0 |
### Table 1. contd…

| PDB ID | Descriptor | Method | Resolution | Keywords | References | Assembly Type | Bound to RNA or DNA | Protein Chains and No. of Residues | Nucleotide Chains and a No. of Residues |
|--------|------------|--------|------------|----------|------------|---------------|-------------------|------------------------------|--------------------------------------|
| 3CK7   | Structure of cycloextrin glycosyltransferase complexed with its main product beta-cycloextrin | X-RAY | 2.40 | Glycosyltransferase | Schmidt et al., Biochemistry (1998) 37 (17): 3909-15 | Monomer | No | A, B, C, D | 527 aa | 0 |
| 3COP   | B. thetaiotaomicron SusD | X-RAY | 1.50 | Sugar binding protein | Koropatkin et al., Structure (2008) 16(7): 1105-15 | Monomer | No | A, 485 aa | 0 |
| 3D1J   | Crystal Structure of E.coli GS mutant E377A in complex with ADP and oligosaccharides | X-RAY | 2.29 | Transferase | Sheng et al., J Biol Chem. (2009) 284: 17796-17807 | Monomer | No | A, 477 | 0 |
| 3K8L   | Crystal structure of SusG | X-RAY | 2.20 | Membrane Protein | Koropatkin et al., Structure (2008) 17(7): 1105-15 | Monomer | No | A, B, 669 aa | 0 |
| 3NCH   | Glucose-6-Phosphate activated form of Yeast Glycogen Synthase | X-RAY | 2.41 | Transferase | Baskaran et al., Proc Natl Acad Sci. (2010) 107: 17563-17568 | Tetramer | No | A, B, C, D, 725 aa | 0 |
| 3O3C   | Structure of a plant phosphatase | X-RAY | 2.40 | Hydrolase | Baskaran et al., Proc Natl Acad Sci. (2010) 107: 17563-17568 | Tetramer | No | A, B, C, D, 725 aa | 0 |
| 3O7Z   | Crystal Structure of E.coli Branching Enzyme in complex with linear oligosaccharides | X-RAY | 2.41 | Transferase | Feng et al., Biochemistry (2011) 50 (14): 2919-30 | Tetramer | No | A, B, C, D, 612 aa | 0 |
| 5BCA   | Deletion mutant delta (145-150), f151d of cycloextrin glycosyltransferase | X-RAY | 2.60 | Glycosyltransferase | Oyama et al., J Biochem. (1999) 125: 1120-1130 | Monomer | No | A, B, C, D, 516 aa | 0 |
| 5CGT   | Beta-amylose from Bacillus cereus var. mycoides | X-RAY | 2.20 | Hydrolase | Pasieglia et al., Eur J Biochem (1998) 255: 710-717 | Monomer | No | A, 684 aa | 0 |

in FASTA formats, structure descriptions, methods of structural salvations and resolutions, keywords of the related proteins, assembly type of the proteins whether the proteins are bound to RNA or DNA, protein chains and number of residues, nucleotides and number of residues, and their related references as shown in the Fig. (2C). All the entries are displayed in a tabular format on the webpage. An example on starch biomaterial is shown in Table I.

The entry page of BLAST explore is a simple programme that receives only a single FASTA formatted query sequence as an input. This allows the selection of the BLASTP alignment algorithm. This will take the database sequences from the PDB, the selection of BLAST e-Value threshold, the option of filtering low complexity sequence segments and BLAST Matrix. Fig. (3A) represents the BLASTp homology search page. The BALST result page shows the bit score, e-value, sequence alignment and homology sequence with the biomaterial database. The BLAST output thus generated is represented in the form of a web shot as shown in Fig. (3B). Further, an input parameter, called threshold, should be defined by the users to start the search. The server takes the query from the input page, searches for similar protein and polysaccharide sequences against the biomaterial database using the BLASTP program. Finally, similar sequences which are obtained under the given threshold value are displayed in a new window.

We have put reference modules for the related biomaterials; interested users may also browse through it to retrieve the useful information from the literature. This will help researchers in designing their experiments.

**CONCLUSIONS**

A major feature of this biomaterial database is the ability to browse through the content. Most of the data are displayed in the form of RDBMS that are integrated in a hierarchical manner. This enables the browsers to display the required data by moving the mouse over it. Based on this, the database is designed for providing a platform for information on biomaterials. For avoiding the unnecessary duplication of research and for efficient utilization of resources and sharing of contents biomaterial database is necessary. This database is focused on the biomaterial types and their characteristics (occurrence, structure and applications). The search tool option provides information related to homology query sequences against all fifteen types of protein and polysaccharides biomaterials based on BLAST search tool.
For a particular protein or polysaccharide, RDBMS is designed to classify the data on the basis of their structures. BLAST explore provides a simple initiative and interactive graphical representation of the BLAST results. We have projected by pictorial diagram on the fabrication of different biomaterial matrices from silk protein biomaterials for different biomedical and tissue engineering applications as an example. This will be helpful for the researchers to get the initial idea how to proceed with the fabrication of biomaterial matrices. This database will help biologists and material scientists to build their own database for sequence similarity and for predicting homology of related query sequences. The users can retrieve the useful information related to natural and synthetic biomaterials from this database. We display some pictures of biomaterials obtained from silk proteins at web page as an example. The silk protein as a biomaterial mimics the natural material extremely well [67]. Biomaterial database is easily accessible and created by the optimization of data and development of common minimum standard for sharing such resources. Inspite of many efforts, still there is no standard protocol for developing a biomaterial database that caters to a specialized area. A continuous critical assessment in this field and dialogue among the academicians and programmers will contribute immensely in knowledge sharing and scientific advancement. The authors recognize this is a first step towards the organization of data integration. We also look forward to increasing network effect benefits for the entire biomaterials community as adoption accelerates and improves to the standard are implemented.

SUPPLEMENTARY DATA

Biomaterial database is freely available on the site http://dwbiomat.itikgp.ernet.in. Questions, comments and suggestions from the users are welcome for future up gradation.

CONFLICT OF INTEREST

The authors confirm that this article content has no conflicts of interest.

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