**Pse-in-One**: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences

Manual of stand-alone program of Pse-in-One

2018-12-01

Home-page: [http://bioinformatics.hitsz.edu.cn/Pse-in-One/](http://bioinformatics.hitsz.edu.cn/Pse-in-One/)
Contents

1. Introduction of Pse-in-One ................................................................. 2
2. Installation .......................................................................................... 2
3. Input/Output formats ......................................................................... 2
   3.1. Input format .................................................................................. 2
   3.2. Output format ................................................................................ 2
   3.3. Physicochemical Properties Selection .......................................... 3
   3.4. User-defined Physicochemical Properties ...................................... 3
4. Commands .......................................................................................... 3
   4.1 Command line parameters for kmer.py ....................................... 3
   4.2 Command line parameters for acc.py ......................................... 4
   4.3 Command line parameters for pse.py .......................................... 4
   4.4 Examples ..................................................................................... 5
Table 1. 14 modes of DNA sequences calculated by PseDAC-General .... 6
Table 2. 6 modes of RNA sequences calculated by PseRAC-General .......... 6
Table 3. 8 modes of protein sequences calculated by PseAAC-General ........ 7
Table 4. The names of the 148 physicochemical indices for dinucleotides .... 7
Table 5. The names of the 12 physicochemical indices for trinucleotides .... 8
Table 6. The names of the 6 physicochemical indices for dinucleotides ....  8
Table 7. The names of the 22 physicochemical indices for dinucleotides .... 8
Table 8. The names of the 547 physicochemical indices for amino acids. ... 9
References ............................................................................................ 11
1. Introduction of Pse-in-One

The **Pse-in-One** web server is able to generate totally 28 different modes of pseudo components for DNA, RNA, and protein sequences, including 14 modes for DNA sequences (**Table 1**), 6 modes for RNA sequences (**Table 2**), and 8 modes for protein sequences (**Table 3**).

To the best of our knowledge, **Pse-in-One** is so far the first web server that can generate all the possible pseudo components for DNA, RNA, and protein sequences, and even those defined by users themselves, and hence it is extremely flexible.

In order to handle large dataset, the stand-alone program of **Pse-in-One** is given, which is more powerful than the Pse-in-One web server, and will be introduced in the following parts of this manual.

2. Installation

The Python software should be first installed and configured. Python 2.7 64-bit is recommended, which can be downloaded from [https://www.python.org](https://www.python.org).

The **Pse-in-One** package can be run on Linux, Mac, and Windows systems. Download the package from [http://bioinformatics.hitsz.edu.cn/Pse-in-One/download](http://bioinformatics.hitsz.edu.cn/Pse-in-One/download) and extract it to a directory, for example, “~/usr”.

To execute the **Pse-in-One** in command line environment, navigate to the “~/usr/Pse-in-One-1.0/Pse-in-One” directory and you will find three python scripts, namely “kmer.py”, “acc.py” and “pse.py”. The “kmer.py” is used for calculating the modes in the category nucleic acid composition or amino acid composition; The “acc.py” is used for calculating the modes in autocorrelation category. The “pse.py” is used for calculating the modes in the category pseudo nucleotide composition or pseudo amino acid composition.

3. Input/Output formats

3.1. Input format

The input file should be a valid FASTA format that consists of a single initial line beginning with a greater-than symbol (“>”) in the first column, followed by lines of sequence data. The words right after the “>” symbol in the single initial line are optional and only used for the purpose of identification and description.

3.2. Output format

The output file formats support three choices that are suitable for downstream computational analyses, such as machine learning. The first and the default choice is the tab format. In this format, all data is separated by TABs. The second one is the LIBSVM’s sparse data format. For this format, each line contains an instance and is ended by a ‘n’ character, like `<label> <index1>:<value1> <index2>:<value2> ...` . The `<label>` is a category label of the sequence. The pair `<index>:<value>` gives a feature (attribute) value: `<index>` is an integer starting from 1 and `<value>` is a real
number. The third output format is the csv format. This format is similar to the tab format. The only difference is the separation characters between data are commas.
3.3. Physicochemical Properties Selection

The Physicochemical Properties Selection file is a text file that contains a list of property names used for generating the modes in categories: autocorrelation, pseudo nucleotide composition/ pseudo amino acid composition. For example, if you want to use the “Rise”, “Tilt” and “Shift” of DNA dinucleotide for calculating, the Physicochemical Properties Selection file should be written as follows:

| Rise   |
|--------|
| Tilt   |
| Shift  |

After saving this file as “propChosen.txt” and specifying it using the command “-i propChosen.txt”, or just “I propChosen.txt”, the above three properties will be used in calculations. Meanwhile, you can also use the command “-a True” to select all the built-in physicochemical properties for the corresponding sequence type, which can be selected by using parameter DNA, RNA or PROTEIN.

The complete lists of physicochemical properties for DNA, RNA and protein sequences used in the stand-alone program are provided in Table 4-8.

3.4. User-defined Physicochemical Properties

In the user-defined physicochemical index files, each index should be represented in three lines. The first line must start with a greater-than symbol (">") in the first column. The words right after the " >" symbol in the single initial line are optional and only used for the purpose of identification and description of the index. The second line lists the names of the sequence compositions (i.e. amino acids, nucleotides, dinucleotides, or trinucleotides, etc), which should be sorted in the alphabet order, such as 'A' 'C' ... 'AA' 'AC'. All the elements in this line should be separated by TAB. The corresponding values of these sequence compositions are listed in the third line, which are separated by TAB.

For example, if you defined a physicochemical property “user_property”, the user-defined physicochemical index file should be written as follows,

```
> user_property
A   C   ... AA AC ...
0.21 0.12  ... 0.37 0.15  ...
```

After saving this file as “user_defined.txt” and specifying it using the command “-e user_defined.txt”, or just “E user_defined.txt”, the properties defined by user will be used in calculations.

4. Commands

### 4.1 Command line parameters for kmer.py

| Options      | Interpretations                     |
|--------------|-------------------------------------|
| inputfile    | The input file in FASTA format.     |
| outputfile   | The output file stored results.     |
| {DNA, RNA, Protein} | The sequence type.                |
### 4.2 Command line parameters for acc.py

| Options         | Interpretations                                                                 |
|-----------------|---------------------------------------------------------------------------------|
| inputfile       | The input file, in FASTA format.                                                |
| outputfile      | The output file stored results.                                                 |
| \{DNA, RNA, Protein\} | The sequence type.                                                             |
| method          | The method name of autocorrelation.                                            |
| -h, --help      | show this help message and exit.                                               |
| -lag LAG        | The value of lag.                                                              |
| -i I            | The index file user chosen.                                                     |
| -e E            | The user-defined index file.                                                    |
| -all_index      | Choose all physicochemical indices.                                             |
| -no_all_index   | Do not choose all physicochemical indices, default.                            |
| -f \{tab, svm, csv\} | The output format (default = tab).                               |
|                | tab -- Simple format, delimited by TAB.                                          |
|                | svm -- The LIBSVM training data format.                                         |
|                | csv -- The format that can be loaded into a spreadsheet program.                |
| -l \{+1,-1\}   | The libSVM output file label.                                                   |

### 4.3 Command line parameters for pse.py

| Options        | Interpretations                                                                 |
|----------------|---------------------------------------------------------------------------------|
| inputfile      | The input file, in valid FASTA format.                                          |
| outputfile     | The outputfile stored results.                                                  |
| \{DNA, RNA, Protein\} | The sequence type.                                                            |
| method         | The method name of pseudo components.                                          |
| -h, --help     | show this help message and exit.                                               |
| -lamada LAMADA | The value of lamada. default=2.                                                 |
| -w W           | The value of weight. default=0.1.                                               |
| -i I           | The index file user chosen.                                                     |
| -k K           | The value of kmer, it works only with PseKNC method.                            |
| -e E           | The user-defined index file, this parameter only needs to be set for PC-PseDNC-General, PC-PseTNC-General, SC-PseDNC-General, SC-PseTNC-General, PC-PseAAC-General or SC-PseAAC-General. |
| -all_index     | Choose all physicochemical indices.                                             |
-no_all_index  Do not choose all physicochemical indices, default.
-f {tab, svm, csv}  The output format (default = tab).
            tab -- Simple format, delimited by TAB.
            svm -- The LIBSVM format.
            csv -- The format that can be loaded into a spreadsheet
            program.
-l {+1,-1}  The libSVM output file label.

## 4.4 Examples

For user’s convenience, some examples of how to process a query sequence
using command line are given below.

**Example 1:** Calculate the kmer composition feature vector of the query sequence
and output the results in LIBSVM format.

```bash
ekmer.py test.txt output_kmer.txt DNA -k 2 -f svm
```

After running the above command, the following results will be found
in “output_kmer.txt” file.

```
0 1:0.023 2:0.034 3:0.053 4:0.023 5:0.045 6:0.086 7:0.143 8:0.06 9:0.049 10:0.15
11:0.124 12:0.049 13:0.015 14:0.064 15:0.053 16:0.03
```

**Example 2:** Calculate the auto covariance feature vector of the query sequence
and output the results in LIBSVM format.

```bash
acc.py test.txt output_acc.txt DNA TAC -l -a -f svm
```

After running the above command, the following results will be found
in “output_acc.txt” file.

```
0 1:-0.057 2:0.057 3:0.647 4:0.381 5:0.057 6:0.057 7:-0.051 8:-0.06 9:0.021
10:0.021 11:0.379 12:0.374 13:0.033 14:-0.011 15:0.413 16:0.019 17:-0.009
18:-0.009 19:-0.024 20:0.032 21:0.105 22:0.105 23:0.021 24:0.024 25:-0.008
26:-0.056 27:0.09 28:-0.088 29:-0.056 30:-0.056 31:-0.011 32:-0.008 33:-0.002
34:-0.002 35:-0.087 36:-0.085
```

**Example 3:** Calculate the PseDNC feature vector of the query sequence
and output the results in CSV format.

```bash
pse.py test.txt output_pse.csv DNA PseDNC -l -a -w 0.2
```

After running the above command, the following results will be found
in “output_pse.csv” file.

```
0.01,0.016,0.024,0.01,0.021,0.04,0.066,0.028,0.023,0.069,0.057,0.023,0.007,0.02
9,0.024,0.014,0.217,0.152,0.17
```

**Example 4:** Calculate the PC-PseDNC-General feature vector of the query sequence
using user-defined physicochemical index file and output the results in the CSV

```bash
```
format.

```
pse.py test.txt output_pse2.csv DNA PC-PseDNC-General –lamada 3 –w 0.2 -e user_indices.txt -f csv
```

After running the above command, the following results will be found in “outut_pse2.csv” file.

```
0.011,0.016,0.025,0.011,0.021,0.041,0.068,0.028,0.023,0.071,0.059,0.023,0.007,
0.03,0.025,0.014,0.213,0.153,0.161
```

The content of the file “test.txt” is listed as follow:

```
misc_ppid_8090
CTTCGCCAGCCACTCTTAGTCCGCCAGCGCGTGCGGCGGAGGCCGAGCGTCTCTATGATCCTGGCTTCTGGCAACGTCATCGTCACGCGCCGGATCC
AACCCCCAACACTTTAGCCAGCTCTAGAGGCGCGCGTGGCCGGGACG
GAAGTGCGCGCGGGTGTCGCCGGGAGTGCGCGCTCCTCTGGCTGACG
GGCGGGCCGGGCATGCGCCGGGGCGTTTTGGCGGGAAGCGCGGGGC
GGGCCGGACAATGAGAGTGTCCGCCTCC
```

The content of the file “user_indices.txt” is listed as follow:

```
>user_defined_property
AA AC AG AT CA CC CG CT GA GC GG GT TA TC TG TT
0.063 1.502 0.783 1.071 -1.376 0.063 -1.664 0.783 -
0.081 -0.081 0.063 1.502 -1.233 -0.081 -1.376 0.063-
```

Table 1. 14 modes of DNA sequences calculated by PseDAC-General.

| Category                  | Mode    | Description                                           |
|---------------------------|---------|-------------------------------------------------------|
| Nucleic acid Composition  | Kmer    | Basic kmer (1)                                        |
|                           | RevKmer | Reverse complementary kmer (2,3)                      |
|                           | DAC     | Dinucleotide-based auto covariance (4,5)              |
|                           | DCC     | Dinucleotide-based cross covariance (4,5)             |
|                           | DACC    | Dinucleotide-based auto-cross covariance (4,5)        |
| Autocorrelation           | TAC     | Trinucleotide-based auto covariance (5)               |
|                           | TCC     | Trinucleotide-based cross covariance (5)              |
|                           | TACC    | Trinucleotide-based auto-cross covariance (5)         |
|                           | PseDNC  | Pseudo dinucleotide composition (6)                   |
|                           | PseKNC  | Pseudo k-tuple nucleotide composition (7,8)           |
|                           | PC-PseDNC-General | General parallel correlation pseudo dinucleotide composition (9) |
|                           | SC-PseDNC-General | General series correlation pseudo dinucleotide composition (9) |
|                           | PC-PseTNC-General | General parallel correlation pseudo trinucleotide composition (9) |
|                           | SC-PseTNC-General | General series correlation pseudo trinucleotide composition (9) |
Table 2. 6 modes of RNA sequences calculated by PseRAC-General.

| Category                  | Mode       | Description                                                                 |
|---------------------------|------------|-----------------------------------------------------------------------------|
| Nucleic acid composition  | Kmer       | Basic kmer (10)                                                             |
| Autocorrelation           | DAC        | Dinucleotide-based auto covariance (4,5,11)                                 |
|                           | DCC        | Dinucleotide-based cross covariance (4,5,11)                                 |
|                           | DACC       | Dinucleotide-based auto-cross covariance (4,5,11)                            |
| Pseudo nucleotide         | PC-PseDNC- | General parallel correlation pseudo dinucleotide composition (4,12)         |
| composition               | General    |                                                                             |
|                           | SC-PseDNC- | General series correlation pseudo dinucleotide composition (4,12)           |
|                           | General    |                                                                             |
Table 3. 8 modes of protein sequences calculated by PseAAC-General.

| Category                  | Mode               | Description                                      |
|---------------------------|--------------------|--------------------------------------------------|
| Amino acid composition    | Kmer               | Basic kmer (13)                                  |
| Autocorrelation           | AC                 | Auto covariance (5,11)                           |
|                           | CC                 | Cross covariance (5,11)                          |
|                           | ACC                | Auto-cross covariance (5,11)                     |
| Pseudo amino acid composition | PC-PseAAC          | Parallel correlation pseudo amino acid composition (14) |
|                           | SC-PseAAC          | Series correlation pseudo amino acid composition (15) |
|                           | PC-PseAAC-General  | General parallel correlation pseudo amino acid composition (14,16) |
|                           | SC-PseAAC-General  | General series correlation pseudo amino acid composition (15,16) |

Table 4. The names of the 148 physicochemical indices for dinucleotides.

| Base stacking                | Protein induced deformability | B-DNA twist                                      |
|------------------------------|-------------------------------|--------------------------------------------------|
| Propeller twist              | Duplex stability:(freeenergy) | Duplex tability(disruptenergy)                   |
| Protein DNA twist            | Stabilising energy of Z-DNA   | Aida_BA_transition                               |
| Breslauer_dS                 | Electron_interaction          | Hartman_trans_free_energy                        |
| Lisser_BZ_transition         | Polar_interaction             | SantaLucia_dG                                    |
| Sarai_flexibility            | Stability                     | Stacking_energy                                  |
| Sugimoto_dS                  | Watson-Crick_interaction      | Twist                                            |
| Shift                        | Slide                         | Rise                                             |
| Twist stiffness              | Tilt stiffness                | Shift_rise                                       |
| Twist_shift                  | Enthalpy1                     | Twist_twist                                      |
| Shift2                       | Tilt3                         | Tilt1                                            |
| Slide (DNA-protein complex)1 | Tilt_shift                    | Twist_tilt                                       |
| Roll_rise                    | Stacking energy               | Stacking energy1                                 |
| Propeller Twist              | Roll11                        | Rise (DNA-protein complex)                       |
| Roll2                        | Roll3                         | Roll1                                            |
| Slide_slide                  | Enthalpy                      | Shift_shift                                      |
| Flexibility_slide            | Minor Groove Distance         | Rise (DNA-protein complex)1                     |
| Roll (DNA-protein complex)1  | Entropy                       | Cytosine content                                 |
| Major Groove Distance        | Twist (DNA-protein complex)   | Purine (AG) content                              |
| Tilt_slide                   | Major Groove Width            | Major Groove Depth                               |
| Free energy6                 | Free energy7                  | Free energy4                                     |
| Free energy3                 | Free energy1                  | Twist_roll                                       |
| Flexibility_shift            | Shift (DNA-protein complex)1  | Thymine content                                  |
| Tip                          | Keto (GT) content             | Roll stiffness                                   |
| Entropy1                     | Roll_slide                    | Slide (DNA-protein complex)                      |
| Twist2                       | Twist5                        | Twist4                                           |
| Tilt (DNA-protein complex)1  | Twist_slide                   | Minor Groove Depth                               |
| Persistance Length           | Rise3                         | Shift stiffness                                  |
| Slide3                       | Slide2                        | Slide1                                           |
| Rise1                        | Rise stiffness                | Mobility to bend towards minor                   |
| Parameter                                      | Value                                                                 |
|-----------------------------------------------|-----------------------------------------------------------------------|
| Groove                                        | A-philicity                                                           |
| DNA denaturation                              | Bending stiffness                                                    |
| Breslauer_dG                                  | Breslauer_dH                                                          |
| Helix-Coil transition                         | Ivanov_BA_transition                                                 |
| SantaLucia_dH                                 | SantaLucia_dS                                                         |
| Sugimoto_dG                                   | Sugimoto_dH                                                           |
| Tilt                                          | Roll                                                                  |
| Clash Strength                                | Roll_roll                                                             |
| Adenine content                               | Direction                                                             |
| Roll_shift                                    | Shift_slide                                                           |
| Tilt4                                         | Shift1                                                                |
| Twist (DNA-protein complex)                   | Tilt_rise                                                             |
| Stacking energy2                              | Rise_rise                                                             |
| Tilt_tilt                                     | Roll4                                                                 |
| Minor Groove Size                             | GC content                                                            |
| Slide stiffness                               | Melting Temperature                                                  |
| Tilt (DNA-protein complex)                    | Guanine content                                                       |
| Major Groove Size                             | Twist_rise                                                            |
| Melting Temperature                           | Free energy                                                           |
| Bend                                          | Mobility to bend towards major groove                                 |

**Table 5.** The names of the 12 physicochemical indices for trinucleotides.

| Parameter                                      | Value                                                                 |
|-----------------------------------------------|-----------------------------------------------------------------------|
| Bendability (DNAse)                           | Bendability (consensus)                                               |
| Consensus 롤                                           | Consensus-Rigid                                                      |
| MW-Daltons                                     | MW-kg                                                                |
| Nucleosome positioning                        | Dnase I-Rigid                                                        |

**Table 6.** The names of the 6 physicochemical indices for dinucleotides.

| Parameter                                      | Value                                                                 |
|-----------------------------------------------|-----------------------------------------------------------------------|
| Twist                                         | Tilt                                                                  |
| Shift                                         | Slide                                                                  |

**Table 7.** The names of the 22 physicochemical indices for dinucleotides.
Table 8. The names of the 547 physicochemical indices for amino acids.

| Hydrophobicity | Hydrophilicity | Mass | ANDN920101 |
|----------------|----------------|------|------------|
| ARG820101      | ARGP820102     | ARGP820103 | BEGF750101 |
| BEGF750102     | BEGF750103     | BHAR880101 | BICO670101 |
| BIOV880101     | BIOV880102     | BROC820101 | BROC820102 |
| BULH740101     | BULH740102     | BUNA790101 | BUNA790102 |
| BUNA790103     | BUNA790104     | BUNA790103 | BUNA790104 |
| CHAM820101     | CHAM820102     | CHAM820103 | CHAM820104 |
| CHAM830103     | CHAM830104     | CHAM830105 | CHAM830106 |
| CHAM830107     | CHAM830108     | CHAM830109 | CHAM830110 |
| CHOP780201     | CHOP780202     | CHOP780203 | CHOP780204 |
| CHOP780205     | CHOP780206     | CHOP780207 | CHOP780208 |
| CHOP780209     | CHOP780210     | CHOP780211 | CHOP780212 |
| CHOP780213     | CHOP780214     | CHOP780215 | CHOP780216 |
| CIDH920101     | CIDH920102     | CIDH920103 | CIDH920104 |
| CIDH920105     | COHE340101     | CRAJ730101 | CRAJ730102 |
| CRAW730103     | DAWD720101     | DAWD720102 | DAWD720103 |
| DESM900101     | DESM900102     | EISD840101 | EISD860101 |
| EISD860102     | EISD860103     | FASG760101 | FASG760102 |
| EISD860103     | FASG760104     | FASG760105 | FAUJ830101 |
| EISD860104     | FASG760105     | FASG760106 | FAUJ830102 |
| FAUJ830101     | FAUJ830102     | FAUJ830103 | FAUJ830104 |
| FAUJ830105     | FAUJ830106     | FAUJ830107 | FAUJ830108 |
| FAUJ830109     | FAUJ830110     | FAUJ830111 | FAUJ830112 |
| FAUJ830113     | FINA770101     | FINA910101 | FINA910102 |
| FINA910103     | FINA910104     | GARJ730101 | GEIM800101 |
| GEIM800102     | GEIM800103     | GEIM800104 | GEIM800105 |
| GEIM800106     | GEIM800107     | GEIM800108 | GEIM800109 |
| GEIM800110     | GEIM800111     | GOLD730101 | GOLD730102 |
| GRAR740101     | GRAR740102     | GRAR740103 | GRAR740104 |
| HOPA770101     | HOPA780101     | HOPA780102 | HOPA780103 |
| HUTJ700103     | ISOY800101     | ISOY800102 | ISOY800103 |
| ISOY800104     | ISOY800105     | ISOY800106 | ISOY800107 |
| ISOY800108     | JANJ780101     | JANJ780102 | JANJ780103 |
| JANJ790101     | JANJ790102     | JANJ790103 | JANJ790104 |
| JOND920101     | JOND920102     | JOND920103 | JOND920104 |
| KANM800101     | KANM800102     | KANM800103 | KANM800104 |
| KAPR850101     | KAPR850102     | KAPR850103 | KAPR850104 |
| KLEP780101     | KRIW870101     | KRIW870102 | KRIW870103 |
| KRIW870103     | KYTJ820101     | LAWE840101 | LEVM760101 |
| LEVM760102     | LEVM760103     | LEVM760104 | LEVM760105 |
| LEVM760106     | LEVM760107     | LEVM760108 | LEVM760109 |
| LEVM780103     | LEVM780104     | LEVM780105 | LEVM780106 |
| LEWM710101     | LEWM710102     | LEWM710103 | LEWM710104 |
| MAXF760101     | MAXF760102     | MAXF760103 | MAXF760104 |
| MAXF760105     | MAXF760106     | MAXF760107 | MAXF760108 |
| MEEJ800101     | MEEJ800102     | MEEJ800103 | MEEJ800104 |
| MEEJ800105     | MEEJ800106     | MEEJ800107 | MEEJ800108 |
| MEEJ800109     | MEEJ800110     | MEEJ800111 | MEEJ800112 |
| MEIH800101     | MEIH800102     | MEIH800103 | MEIH800104 |
| MIYS850101     | MIYS850102     | MIYS850103 | MIYS850104 |
| NAGK730101 | NAGK730102 | NAGK730103 | NAKH900101 |
|------------|------------|------------|------------|
| NAKH900102 | NAKH900103 | NAKH900104 | NAKH900105 |
| NAKH900106 | NAKH900107 | NAKH900108 | NAKH900109 |
| NAKH900110 | NAKH900111 | NAKH900112 | NAKH900113 |
| NAKH920101 | NAKH920102 | NAKH920103 | NAKH920104 |
| NAKH920105 | NAKH920106 | NAKH920107 | NAKH920108 |
| NISK800101 | NISK860101 | NOZY710101 | OOBM770101 |
| OOBM770102 | OOBM770103 | OOBM770104 | OOBM770105 |
| OOBM850101 | OOBM850102 | OOBM850103 | OOBM850104 |
| OOBM850105 | PALJ810101 | PALJ810102 | PALJ810103 |
| PALJ810104 | PALJ810105 | PALJ810106 | PALJ810107 |
| PALJ810108 | PALJ810109 | PALJ810110 | PALJ810111 |
| PALJ810112 | PALJ810113 | PALJ810114 | PALJ810115 |
| PALJ810116 | PARJ860101 | PLJV810101 | PONP800101 |
| PONP800102 | PONP800103 | PONP800104 | PONP800105 |
| PONP800106 | PONP800107 | PONP800108 | PRAM820101 |
| PRAM820102 | PRAM820103 | PRAM900101 | PRAM900102 |
| PRAM900103 | PRAM900104 | PTIO830101 | PTIO830102 |
| QIAN880101 | QIAN880102 | QIAN880103 | QIAN880104 |
| QIAN880105 | QIAN880106 | QIAN880107 | QIAN880108 |
| QIAN880109 | QIAN880110 | QIAN880111 | QIAN880112 |
| QIAN880113 | QIAN880114 | QIAN880115 | QIAN880116 |
| QIAN880117 | QIAN880118 | QIAN880119 | QIAN880120 |
| QIAN880121 | QIAN880122 | QIAN880123 | QIAN880124 |
| QIAN880125 | QIAN880126 | QIAN880127 | QIAN880128 |
| QIAN880129 | QIAN880130 | QIAN880131 | QIAN880132 |
| QIAN880133 | QIAN880134 | QIAN880135 | QIAN880136 |
| QIAN880137 | QIAN880138 | QIAN880139 | RACS770101 |
| RACS770102 | RACS770103 | RACS820101 | RACS820102 |
| RACS820103 | RACS820104 | RACS820105 | RACS820106 |
| RACS820107 | RACS820108 | RACS820109 | RACS820110 |
| RACS820111 | RACS820112 | RACS820113 | RACS820114 |
| RADA880101 | RADA880102 | RADA880103 | RADA880104 |
| RADA880105 | RADA880106 | RADA880107 | RADA880108 |
| RICI880101 | RICI880102 | RICI880103 | RICI880104 |
| RICI880105 | RICI880106 | RICI880107 | RICI880108 |
| RICI880109 | RICI880110 | RICI880111 | RICI880112 |
| RICI880113 | RICI880114 | RICI880115 | RICI880116 |
| RICI880117 | ROBB760101 | ROBB760102 | ROBB760103 |
| ROBB760104 | ROBB760105 | ROBB760106 | ROBB760107 |
| ROBB760108 | ROBB760109 | ROBB760110 | ROBB760111 |
| ROBB760112 | ROBB760113 | ROBB790101 | ROSG850101 |
| ROSG850102 | ROSM880101 | ROSM880102 | ROSM880103 |
| SIM760101 | SNEP660101 | SNEP660102 | SNEP660103 |
| SNEP660104 | SUEM840101 | SUEM840102 | SWER830101 |
| TANS770101 | TANS770102 | TANS770103 | TANS770104 |
| TANS770105 | TANS770106 | TANS770107 | TANS770108 |
| TANS770109 | TANS770110 | VASM830101 | VASM830102 |
| VASM830103 | VELV850101 | VENT840101 | VHEG790101 |
### References

1. Lee, D., Karchin, R. and Beer, M.A. (2011) Discriminative prediction of mammalian enhancers from DNA sequence. *Genome research, 21*, 2167-2180.

2. Noble, W.S., Kuehn, S., Thurman, R., Yu, M. and Stamatoyannopoulos, J. (2005) Predicting the in vivo signature of human gene regulatory sequences. *Bioinformatics, 21 Suppl 1*, i338-343.
3. Gupta, S., Dennis, J., Thurman, R.E., Kingston, R., Stamatoyannopoulos, J.A. and Noble, W.S. (2008) Predicting human nucleosome occupancy from primary sequence. *PLoS computational biology*, 4, e1000134.

4. Friedel, M., Nikolajewa, S., Suhnel, J. and Wilhelm, T. (2008) DiProDB: a database for dinucleotide properties. *Nucleic Acids Res.*, 37, D37-D40.

5. Dong, Q., Zhou, S. and Guan, J. (2009) A new taxonomy-based protein fold recognition approach based on autocross-covariance transformation. *Bioinformatics*, 25, 2655-2662.

6. Chen, W., Feng, P.M., Lin, H. and Chou, K.C. (2013) iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. *Nucleic Acids Res.*, 41, e68.

7. Guo, S.H., Deng, E.Z., Xu, L.Q., Ding, H., Lin, H., Chen, W. and Chou, K.C. (2014) iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. *Bioinformatics*, 30, 1522-1529.

8. Lin, H., Deng, E.-Z., Ding, H., Chen, W. and Chou, K.-C. (2014) iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. *Bioinformatics*, 42, 12961-12972.

9. Chen, W., Lei, T.Y., Jin, D.C., Lin and H. and Chou, K.C. (2014) PseKNC: a flexible web server for generating pseudo K-tuple nucleotide composition. *Analytical biochemistry*, 456, 53-60.

10. Wei, L., Liao, M., Gao, Y., Ji, R., He, Z. and Zou, Q. (2014) Improved and Promising Identification of Human MicroRNAs by Incorporating a High-quality Negative Set. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 11, 192-201.

11. Guo, Y., Yu, L., Wen, Z. and Li, M. (2008) Using support vector machine combined with auto covariance to predict protein-protein interactions from protein sequences. *Nucleic Acids Research*, 36, 3025-3030.

12. Chen, W., Zhang, X., Brooker, J., Lin, H., Zhang, L. and Chou, K.-C. (2014) PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. *Bioinformatics*, DOI: 10.1093/bioinformatics/btu1602.

13. Liu, B., Wang, X., Lin, L., Dong, Q. and Wang, X. (2008) A Discriminative Method for Protein Remote Homology Detection and Fold Recognition Combining Top-n-grams and Latent Semantic Analysis. *BMC Bioinformatics*, 9, 510.

14. Chou, K.-C. (2001) Prediction of protein cellular attributes using pseudo-amino-acid-composition. *PROTEINS: Structure, Function, and Genetics*, 43, 246-255.

15. Chou, K.-C. (2005) Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. *Bioinformatics*, 21, 10-19.

16. Kawashima, S., Pokarowski, P., Pokarowska, M., Kolinski, A., Katayama, T. and Kanehisa, M. (2008) AAindex: amino acid index database, progress report 2008. *Nucleic Acids Res.*, 36, D202-D205.