List of Descriptors and Abbreviations

Amino Acid Composition (AAC): Total descriptor 20

AAC_A → Amino acid composition of Alanine

AAC_C → Amino acid composition of Cysteine

AAC_D → Amino acid composition of Aspartic acid

AAC_E → Amino acid composition of Glutamic acid

AAC_F → Amino acid composition of Phenylalanine

AAC_G → Amino acid composition of Glycine

AAC_H → Amino acid composition of Histidine

AAC_I → Amino acid composition of Isoleucine

AAC_K → Amino acid composition of Lysine

AAC_L → Amino acid composition of Leucine

AAC_M → Amino acid composition of Methionine

AAC_N → Amino acid composition of Asparagine

AAC_P → Amino acid composition of Proline

AAC_Q → Amino acid composition of Glutamine

AAC_R → Amino acid composition of Arginine

AAC_S → Amino acid composition of Serine

AAC_T → Amino acid composition of Threonine

AAC_V → Amino acid composition of Valine

AAC_W → Amino acid composition of Tryptophan

AAC_Y → Amino acid composition of Tyrosine

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Dipeptide Composition (order 1, traditional) : 400 dipeptide composition

DPC1_AA → Composition of Alanine-Alanine

DPC1_AC → Composition of Alanine-Cysteine

DPC1_YW → Composition of Alanine-Cysteine

DPC1_YY → Composition of Alanine-Cysteine

Dipeptide Composition (order 2, alternate) : 400 dipeptide composition

DPC2_AA → Composition of Alanine-Alanine

DPC2_AC → Composition of Alanine-Cysteine

DPC2_YW → Composition of Alanine-Cysteine

DPC2_YY → Composition of Alanine-Cysteine

Dipeptide Composition (order 3, with gap of 2 residues) : 400 dipeptide composition

DPC3_AA → Composition of Alanine-Alanine

DPC3_AC → Composition of Alanine-Cysteine

DPC3_YW → Composition of Alanine-Cysteine

DPC3_YY → Composition of Alanine-Cysteine

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Tripeptide Composition: 8000 tripeptide composition

TPC_AAA → Composition of Alanine-Alanine-Alanine

TPC_AAC → Composition of Alanine-Alanine-Cysteine

TPC_AAD → Composition of Alanine-Alanine-Aspartic acid

TPC_AAE → Composition of Alanine-Alanine-Glutamic acid

TPC_AAF → Composition of Alanine-Alanine-Phenylalanine

TPC_AAG → Composition of Alanine-Alanine-Glycine

TPC_AAH → Composition of Alanine-Alanine-Histidine

TPC_AAI → Composition of Alanine-Alanine-Isoleucine

TPC_AAK → Composition of Alanine-Alanine-Lysine

TPC_AAL → Composition of Alanine-Alanine-Leucine

TPC_YYM → Composition of Tyrosine-Tyrosine-Methionine

TPC_YYN → Composition of Tyrosine-Tyrosine-Asparagine

TPC_YYP → Composition of Tyrosine-Tyrosine-Proline

TPC_YYQ → Composition of Tyrosine-Tyrosine-Glutamine

TPC_YYR → Composition of Tyrosine-Tyrosine-Arginine

TPC_YYS → Composition of Tyrosine-Tyrosine-Serine

TPC_YYT → Composition of Tyrosine-Tyrosine-Threonine

TPC_YYV → Composition of Tyrosine-Tyrosine-Valine

TPC_YYW → Composition of Tyrosine-Tyrosine-Tryptophan

TPC_YYY → Composition of Tyrosine-Tyrosine- Tyrosine

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Atom Type Composition: 5 descriptors

ATC_C → Atomic Composition of Carbon

ATC_H → Atomic Composition of Hydrogen

ATC_N → Atomic Composition of Nitrogen

ATC_O → Atomic Composition of Oxygen

ATC_S → Atomic Composition of Sulphur

Bond Type Composition: 4 descriptors

BTC_T → Composition of total bonds

BTC_H → Composition of Hydrogen bonds

BTC_S → Composition of Single bonds

BTC_D → Composition of Double bonds

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Physico-chemical properties: 30 descriptors

PCP_PC → Composition of positively charged residues

PCP_NC → Composition of positively charged residues

PCP_NE → Composition of neutral charged residues

PCP_PO → Composition of polar residues

PCP_NP → Composition of non-polar residues

PCP_AL → Composition of residues having aliphatic side chain

PCP_CY → Composition of residues having cyclic side chain

PCP_AR → Composition of aromatic residues

PCP_AC → Composition of acidic residues

PCP_BS → Composition of basic residues

PCP_NE_ph → Composition of neutral residues based on pH

PCP_HB → Composition of hydrophobic residues

PCP_HL → Composition of hydrophilic residues

PCP_NT → Composition of neutral residues

PCP_HX → Composition of hydroxylic residues

PCP_SC → Composition of residues having sulphur content

PCP_SS_HE → Composition of residue in secondary structure (Helix)

PCP_SS_ST → Composition of residue in secondary structure (Strands)

PCP_SS_CO → Composition of residue in secondary structure (Coil)

PCP_SA_BU → Composition of residue in solvent accessibility (Buried)

PCP_SA_EX → Composition of residue in solvent accessibility (Exposed)

PCP_SA_IN → Composition of residue in solvent accessibility (Intermediate)

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

PCP_TN → Composition of tiny residues

PCP_SM → Composition of small residues

PCP_LR → Composition of large residues

PCP_Z1 → Composition of residues having Z1 advanced Physico-chemical properties

PCP_Z2 → Composition of residues having Z2 advanced Physico-chemical properties

PCP_Z3 → Composition of residues having Z3 advanced Physico-chemical properties

PCP_Z4 → Composition of residues having Z4 advanced Physico-chemical properties

PCP_Z5 → Composition of residues having Z5 advanced Physico-chemical properties

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Amino Acid Index: 553 type descriptors

AAI_ANDN920101 → Composition of index ANDN920101

AAI_ARGP820101 → Composition of index ARGP820101

AAI_ARGP820102 → Composition of index ARGP820102

AAI_ARGP820103 → Composition of index ARGP820103

AAI_BEGF750101 → Composition of index BEGF750101

AAI_BEGF750102 → Composition of index BEGF750102

AAI_BEGF750103 → Composition of index BEGF750103

AAI_BHAR880101 → Composition of index BHAR880101

AAI_BIGC670101 → Composition of index BIGC670101

AAI_BIOV880101 → Composition of index BIOV880101

AAI_KARS160113 → Composition of index KARS160113

AAI_KARS160114 → Composition of index KARS160114

AAI_KARS160115 → Composition of index KARS160115

AAI_KARS160116 → Composition of index KARS160116

AAI_KARS160117 → Composition of index KARS160117

AAI_KARS160118 → Composition of index KARS160118

AAI_KARS160119 → Composition of index KARS160119

AAI_KARS160120 → Composition of index KARS160120

AAI_KARS160121 → Composition of index KARS160121

AAI_KARS160122 → Composition of index KARS160122

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Residue Repeats Index: 20 descriptors

RRI_A → Residue repeat index of Alanine

RRI_C → Residue repeat index of Cysteine

RRI_D → Residue repeat index of Aspartic acid

RRI_E → Residue repeat index of Glutamic acid

RRI_F → Residue repeat index of Phenylalanine

RRI_G → Residue repeat index of Glycine

RRI_H → Residue repeat index of Histidine

RRI_I → Residue repeat index of Isoleucine

RRI_K → Residue repeat index of Lysine

RRI_L → Residue repeat index of Leucine

RRI_M → Residue repeat index of Methionine

RRI_N → Residue repeat index of Asparagine

RRI_P → Residue repeat index of Proline

RRI_Q → Residue repeat index of Glutamine

RRI_R → Residue repeat index of Arginine

RRI_S → Residue repeat index of Serine

RRI_T → Residue repeat index of Threonine

RRI_V → Residue repeat index of Valine

RRI_W → Residue repeat index of Tryptophan

RRI_Y → Residue repeat index of Tyrosine

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Property Repeats Index: 25 descriptors corresponding to 25 physico-chemical properties

PRI_PC → Residue repeat index for positive charged residues

PRI_PC → Residue repeat index for negative charged residues

PRI_NE → Residue repeat index for neutral charged residues

PRI_PO → Residue repeat index for polar residues

PRI_NP → Residue repeat index for non-polar residues

PRI_AL → Residue repeat index for residues having aliphatic side chain

PRI_CY → Residue repeat index for residues having cyclic side chain

PRI_AR → Residue repeat index for aromatic residues

PRI_AC → Residue repeat index for acidic residues

PRI_BS → Residue repeat index for basic residues

PRI_NE → Residue repeat index for neutral residues based on pH

PRI_HB → Residue repeat index for hydrophobic residues

PRI_HL → Residue repeat index for hydrophilic residues

PRI_NT → Residue repeat index for neutral residues

PRI_HX → Residue repeat index for hydroxylic residues

PRI_SC → Residue repeat index for residues having sulphur content

PRI_SS_HE → Residue repeat index for residues in secondary structure (Helix)

PRI_SS_ST → Residue repeat index for residues in secondary structure (Strands)

PRI_SS_CO → Residue repeat index for residues in secondary structure (Coil)

PRI_SA_BU → Residue repeat index for residues in solvent accessibility (Buried)

PRI_SA_EX → Residue repeat index for residues in solvent accessibility (Exposed)

PRI_SA_IN → Residue repeat index for residues in solvent accessibility (Intermediate)

PRI_TN → Residue repeat index for tiny residues

PRI_SM → Residue repeat index for small residues

PRI_LR → Residue repeat index for large residues

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Distance Distribution of Repeats: 20 type of residues

DDR_A → Distribution of Alanine

DDR_C → Distribution of Cysteine

DDR_D → Distribution of Aspartic acid

DDR_E → Distribution of Glutamic acid

DDR_F → Distribution of Phenylalanine

DDR_G → Distribution of Glycine

DDR_H → Distribution of Histidine

DDR_I → Distribution of Isoleucine

DDR_K → Distribution of Lysine

DDR_L → Distribution of Leucine

DDR_M → Distribution of Methionine

DDR_N → Distribution of Asparagine

DDR_P → Distribution of Proline

DDR_Q → Distribution of Glutamine

DDR_R → Distribution of Arginine

DDR_S → Distribution of Serine

DDR_T → Distribution of Threonine

DDR_V → Distribution of Valine

DDR_W → Distribution of Tryptophan

DDR_Y → Distribution of Tyrosine

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Shannon Entropy of a Protein: 1 Descriptor

SEP → Shannon entropy of whole protein

Shannon Entropy of a Residue: 20 Descriptors

SER_A → Shannon entropy of Alanine

SER_C → Shannon entropy of Cysteine

SER_D → Shannon entropy of Aspartic acid

SER_E → Shannon entropy of Glutamic acid

SER_F → Shannon entropy of Phenylalanine

SER_G → Shannon entropy of Glycine

SER_H → Shannon entropy of Histidine

SER_I → Shannon entropy of Isoleucine

SER_K → Shannon entropy of Lysine

SER_L → Shannon entropy of Leucine

SER_M → Shannon entropy of Methionine

SER_N → Shannon entropy of Asparagine

SER_P → Shannon entropy of Proline

SER_Q → Shannon entropy of Glutamine

SER_R → Shannon entropy of Arginine

SER_S → Shannon entropy of Serine

SER_T → Shannon entropy of Threonine

SER_V → Shannon entropy of Valine

SER_W → Shannon entropy of Tryptophan

SER_Y → Shannon entropy of Tyrosine

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Shannon Entropy of Properties:25 features corresponding to 25 physicochemical properties

SEP_PC → Shannon entropy of positive charged residues

SEP_PC → Shannon entropy of negative charged residues

SEP_NE → Shannon entropy of neutral charged residues

SEP_PO → Shannon entropy of polar residues

SEP_NP → Shannon entropy of non-polar residues

SEP_AL → Shannon entropy of residues having aliphatic side chain

SEP_CY → Shannon entropy of residues having cyclic side chain

SEP_AR → Shannon entropy of aromatic residues

SEP_AC → Shannon entropy of acidic residues

SEP_BS → Shannon entropy of basic residues

SEP_NE → Shannon entropy of neutral residues based on pH

SEP_HB → Shannon entropy of hydrophobic residues

SEP_HL → Shannon entropy of hydrophilic residues

SEP_NT → Shannon entropy of neutral residues

SEP_HX → Shannon entropy of hydroxylic residues

SEP_SC → Shannon entropy of residues having sulphur content

SEP_SS_HE → Shannon entropy of residue in secondary structure (Helix)

SEP _SS_ST → Shannon entropy of residue in secondary structure (Strands)

SEP _SS_CO → Shannon entropy of residue in secondary structure (Coil)

SEP _SA_BU → Shannon entropy of residue in solvent accessibility (Buried)

SEP _SA_EX → Shannon entropy of residue in solvent accessibility (Exposed)

SEP _SA_IN → Shannon entropy of residue in solvent accessibility (Intermediate)

SEP_TN → Shannon entropy of tiny residues

SEP_SM → Shannon entropy of small residues

SEP_LR → Shannon entropy of large residues

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Autocorrelation : 3 descriptors (Dong, Jie, et al. *Journal of cheminformatics* (2018),10.1:16)

ACR1_MB → Normalized Moreau-Broto autocorrelation descriptor with lag 1

ACR1_MO → Morgan autocorrelation descriptor with lag 1

ACR1_GE → Geary autocorrelation descriptor with lag 1

Conjoint Triad Descriptors: 343 descriptors (Dong, Jie, et al. *Journal of cheminformatics* (2018),10.1:16)

Group 1: A, G, V

Group 2: I, L, F, P

Group 3: Y, M, T, S

Group 4: H, N, Q, W

Group 5: R, K

Group 6: D, E

Group 7: C

CTC_111 → Normalize frequency of group1-group1-group1 (tri-group)

CTC_112 → Normalize frequency of group1-group1-group2 (tri-group)

CTC_113→ Normalize frequency of group1-group1-group3 (tri-group)

CTC_775 → Normalize frequency of group7-group7-group5 (tri-group)

CTC_776 → Normalize frequency of group7-group7-group6 (tri-group)

CCT_777 → Normalize frequency of group7-group7-group7 (tri-group)

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Composition enhanced Transition and Distribution: 189 descriptors (Dubchak I, et al. *Proceedings of the National Academy of Sciences of the United States of America*)

Attributes	Group1	Group 2	Group 3
Hydrophobicity	R,K,E,D,Q,N	G,A,S,T,P,H,Y	C,L,V,I,M,F,W
Normalized Vander Waals volume	G,A,S,T,P,D	N,V,E,Q,I,L	M,H,K,F,R,Y,W
Polarity	L,I,F,W,C,M,V,Y	P,A,T,G,S	H,Q,R,K,N,E,D
Polarizability	G,A,S,D,T	C,P,N,V,E,Q,I,L	K,M,H,F,R,Y,W
Charge	K,R	A,N,C,Q,G,H,I,L,M,F,P,S,T,W,Y,V	D,E
Secondary structure	E,A,L,M,Q,K,R,H	V,I,Y,C,W,F,T	G,N,P,S,D
Solvent accessibility	A,L,F,C,G,I,V,W	R,K,Q,E,N,D	M,S P,T,H,Y

- **Composition:** 21 Descriptors

  CeTD_HB1 → Composition of group 1 residues for hydrophobicity attribute

  CeTD_HB2 → Composition of group 2 residues for hydrophobicity attribute

  CeTD_HB3 → Composition of group 3 residues for hydrophobicity attribute

  CeTD_VW1 → Composition of group 1 residues for normalized vander waals volume attribute

  CeTD_VW2 → Composition of group 2 residues for normalized vander waals volume attribute

  CeTD_VW3 → Composition of group 2 residues for normalized vander waals volume attribute

  CeTD_PO1 → Composition of group 1 residues for polarity attribute

  CeTD_PO2 → Composition of group 2 residues for polarity attribute

  CeTD_PO3 → Composition of group 3 residues for polarity attribute

  CeTD_PZ1 → Composition of group 1 residues for polarizability attribute

  CeTD_PZ2 → Composition of group 2 residues for polarizability attribute

  CeTD_PZ3 → Composition of group 3 residues for polarizability attribute

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

CeTD_CH1 → Composition of group 1 residues for charge attribute

CeTD_CH2 → Composition of group 2 residues for charge attribute

CeTD_CH3 → Composition of group 3 residues for charge attribute

CeTD_SS1 → Composition of group 1 residues for secondary structure attribute

CeTD_SS2 → Composition of group 2 residues for secondary structure attribute

CeTD_SS3 → Composition of group 3 residues for secondary structure attribute

CeTD_SA1 → Composition of group 1 residues for solvent accessibility attribute

CeTD_SA2 → Composition of group 2 residues for solvent accessibility attribute

CeTD_SA3 → Composition of group 3 residues for solvent accessibility attribute

- **Transition:** 63 Descriptors

CeTD_11_HB → Number of transitions takes place from group 1 residues to group 1 residues for hydrophobicity attribute

CeTD_11_VW → Number of transitions takes place from group 1 residues to group 1 residues for normalized vander waals volume attribute

CeTD_11_PO → Number of transitions takes place from group 1 residues to group 1 residues for polarity attribute

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CeTD_12_HB → Number of transitions takes place from group 1 residues to group 2 residues for hydrophobicity attribute

CeTD_12_VW → Number of transitions takes place from group 1 residues to group 2 residues for normalized vander waals volume attribute

CeTD_12_PO → Number of transitions takes place from group 1 residues to group 2 residues for polarity attribute

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CeTD_33_CH → Number of transitions takes place from group 3 residues to group 3 residues for charge attribute

CeTD_33_SS → Number of transitions takes place from group 3 residues to group 3 residues for secondary structure attribute

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

CeTD_33_SA → Number of transitions takes place from group 3 residues to group 3 residues for solvent accessibility attribute

- **Distribution:** 105 Descriptors

CeTD_0_p_HB1 → Number of group 1 residues for hydrophobicity present in 0% quartile

CeTD_25_p_HB1 → Number of group 1 residues for hydrophobicity present in 25% quartile

CeTD_50_p_HB1 → Number of group 1 residues for hydrophobicity present in 50% quartile

CeTD_75_p_HB1 → Number of group 1 residues for hydrophobicity present in 75% quartile

CeTD_100_p_HB1 → Number of group 1 residues for hydrophobicity present in 100% quartile

CeTD_0_p_VW1 → Number of group 1 residues for normalized vander waals volume present in 0% quartile

CeTD_25_p_VW1 → Number of group 1 residues for normalized vander waals volume present in 25% quartile

CeTD_50_p_VW1 → Number of group 1 residues for normalized vander waals volume present in 50% quartile

CeTD_75_p_VW1 → Number of group 1 residues for normalized vander waals volume present in 75% quartile

CeTD_100_p_VW1 → Number of group 1 residues for normalized vander waals volume present in 100% quartile

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CeTD_0_p_HB2 → Number of group 2 residues for hydrophobicity present in 0% quartile

CeTD_25_p_HB2 → Number of group 2 residues for hydrophobicity present in 25% quartile

CeTD_50_p_HB2 → Number of group 2 residues for hydrophobicity present in 50% quartile

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

CeTD_75_p_HB2 → Number of group 2 residues for hydrophobicity present in 75% quartile

CeTD_100_p_HB2 → Number of group 2 residues for hydrophobicity present in 100% quartile

CeTD_0_p_VW2 → Number of group 2 residues for normalized vander waals volume present in 0% quartile

CeTD_25_p_VW2 → Number of group 2 residues for normalized vander waals volume present in 25% quartile

CeTD_50_p_VW2 → Number of group 2 residues for normalized vander waals volume present in 50% quartile

CeTD_75_p_VW2 → Number of group 2 residues for normalized vander waals volume present in 75% quartile

CeTD_100_p_VW2 → Number of group 2 residues for normalized vander waals volume present in 100% quartile

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CeTD_0_p_SA3 → Number of group 2 residues for solvent accessibility present in 0% quartile

CeTD_25_p_ SA3 → Number of group 2 residues for solvent accessibility present in 25% quartile

CeTD_50_p_ SA3 → Number of group 2 residues for solvent accessibility present in 50% quartile

CeTD_75_p_ SA3 → Number of group 2 residues for solvent accessibility present in 75% quartile

CeTD_100_p_ SA3 → Number of group 2 residues for solvent accessibility present in 100% quartile

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Pseudo Amino Acid Composition (order 1, traditional): 21 descriptors (Chou KC, 2001, *Proteins*)

PAAC1_A → Pseudo amino acid composition of Alanine

PAAC1_C → Pseudo amino acid composition of Cysteine

PAAC1_D → Pseudo amino acid composition of Aspartic acid

PAAC1_E → Pseudo amino acid composition of Glutamic acid

PAAC1_F → Pseudo amino acid composition of Phenylalanine

PAAC1_G → Pseudo amino acid composition of Glycine

PAAC1_H → Pseudo amino acid composition of Histidine

PAAC1_I → Pseudo amino acid composition of Isoleucine

PAAC1_K → Pseudo amino acid composition of Lysine

PAAC1_L → Pseudo amino acid composition of Leucine

PAAC1_M → Pseudo amino acid composition of Methionine

PAAC1_N → Pseudo amino acid composition of Asparagine

PAAC1_P → Pseudo amino acid composition of Proline

PAAC1_Q → Pseudo amino acid composition of Glutamine

PAAC1_R → Pseudo amino acid composition of Arginine

PAAC1_S → Pseudo amino acid composition of Serine

PAAC1_T → Pseudo amino acid composition of Threonine

PAAC1_V → Pseudo amino acid composition of Valine

PAAC1_W → Pseudo amino acid composition of Tryptophan

PAAC1_Y → Pseudo amino acid composition of Tyrosine

PAAC1_lam1 → Sequence correlation factor for lambda 1

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Pseudo Amino Acid Composition (order 2, alternate): 22 descriptors

PAAC2_A → Pseudo amino acid composition of Alanine

PAAC2_C → Pseudo amino acid composition of Cysteine

PAAC2_D → Pseudo amino acid composition of Aspartic acid

PAAC2_E → Pseudo amino acid composition of Glutamic acid

PAAC2_F → Pseudo amino acid composition of Phenylalanine

PAAC2_G → Pseudo amino acid composition of Glycine

PAAC2_H → Pseudo amino acid composition of Histidine

PAAC2_I → Pseudo amino acid composition of Isoleucine

PAAC2_K → Pseudo amino acid composition of Lysine

PAAC2_L → Pseudo amino acid composition of Leucine

PAAC2_M → Pseudo amino acid composition of Methionine

PAAC2_N → Pseudo amino acid composition of Asparagine

PAAC2_P → Pseudo amino acid composition of Proline

PAAC2_Q → Pseudo amino acid composition of Glutamine

PAAC2_R → Pseudo amino acid composition of Arginine

PAAC2_S → Pseudo amino acid composition of Serine

PAAC2_T → Pseudo amino acid composition of Threonine

PAAC2_V → Pseudo amino acid composition of Valine

PAAC2_W → Pseudo amino acid composition of Tryptophan

PAAC2_Y → Pseudo amino acid composition of Tyrosine

PAAC2_lam1 → Sequence correlation factor for lambda 1

PAAC2_lam2 → Sequence correlation factor for lambda 2

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Pseudo Amino Acid Composition (order 3, With gap of 2 residues): 23 descriptors

PAAC3_A → Pseudo amino acid composition of Alanine

PAAC3_C → Pseudo amino acid composition of Cysteine

PAAC3_D → Pseudo amino acid composition of Aspartic acid

PAAC3_E → Pseudo amino acid composition of Glutamic acid

PAAC3_F → Pseudo amino acid composition of Phenylalanine

PAAC3_G → Pseudo amino acid composition of Glycine

PAAC3_H → Pseudo amino acid composition of Histidine

PAAC3_I → Pseudo amino acid composition of Isoleucine

PAAC3_K → Pseudo amino acid composition of Lysine

PAAC3_L → Pseudo amino acid composition of Leucine

PAAC3_M → Pseudo amino acid composition of Methionine

PAAC3_N → Pseudo amino acid composition of Asparagine

PAAC3_P → Pseudo amino acid composition of Proline

PAAC3_Q → Pseudo amino acid composition of Glutamine

PAAC3_R → Pseudo amino acid composition of Arginine

PAAC3_S → Pseudo amino acid composition of Serine

PAAC3_T → Pseudo amino acid composition of Threonine

PAAC3_V → Pseudo amino acid composition of Valine

PAAC3_W → Pseudo amino acid composition of Tryptophan

PAAC3_Y → Pseudo amino acid composition of Tyrosine

PAAC3_lam1 → Sequence correlation factor for lambda 1

PAAC3_lam2 → Sequence correlation factor for lambda 2

PAAC3_lam3 → Sequence correlation factor for lambda 3

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Amphiphilic Pseudo Amino Acid Composition (order 1, traditional): 23 descriptors

APAAC1_A → Amphiphilic pseudo amino acid composition of Alanine

APAAC1_C → Amphiphilic pseudo amino acid composition of Cysteine

APAAC1_D → Amphiphilic pseudo amino acid composition of Aspartic acid

APAAC1_E → Amphiphilic pseudo amino acid composition of Glutamic acid

APAAC1_F → Amphiphilic pseudo amino acid composition of Phenylalanine

APAAC1_G → Amphiphilic pseudo amino acid composition of Glycine

APAAC1_H → Amphiphilic pseudo amino acid composition of Histidine

APAAC1_I → Amphiphilic pseudo amino acid composition of Isoleucine

APAAC1_K → Amphiphilic pseudo amino acid composition of Lysine

APAAC1_L → Amphiphilic pseudo amino acid composition of Leucine

APAAC1_M → Amphiphilic pseudo amino acid composition of Methionine

APAAC1_N → Amphiphilic pseudo amino acid composition of Asparagine

APAAC1_P → Amphiphilic pseudo amino acid composition of Proline

APAAC1_Q → Amphiphilic pseudo amino acid composition of Glutamine

APAAC1_R → Amphiphilic pseudo amino acid composition of Arginine

APAAC1_S → Amphiphilic pseudo amino acid composition of Serine

APAAC1_T → Amphiphilic pseudo amino acid composition of Threonine

APAAC1_V → Amphiphilic pseudo amino acid composition of Valine

APAAC1_W → Amphiphilic pseudo amino acid composition of Tryptophan

APAAC1_Y → Amphiphilic pseudo amino acid composition of Tyrosine

APAAC1_HB_lam1 → Sequence correlation factor for hydrophobicity with lambda 1

APAAC1_HL_lam1 → Sequence correlation factor for hydrophilicity with lambda 1

APAAC1_SC_lam1 → Sequence correlation factor for side chain mass with lambda 1

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Pseudo Amino Acid Composition (order 2, alternate): 26 descriptors

APAAC2_A → Amphiphilic pseudo amino acid composition of Alanine

APAAC2_C → Amphiphilic pseudo amino acid composition of Cysteine

APAAC2_D → Amphiphilic pseudo amino acid composition of Aspartic acid

APAAC2_E → Amphiphilic pseudo amino acid composition of Glutamic acid

APAAC2_F → Amphiphilic pseudo amino acid composition of Phenylalanine

APAAC2_G → Amphiphilic pseudo amino acid composition of Glycine

APAAC2_H → Amphiphilic pseudo amino acid composition of Histidine

APAAC2_I → Amphiphilic pseudo amino acid composition of Isoleucine

APAAC2_K → Amphiphilic pseudo amino acid composition of Lysine

APAAC2_L → Amphiphilic pseudo amino acid composition of Leucine

APAAC2_M → Amphiphilic pseudo amino acid composition of Methionine

APAAC2_N → Amphiphilic pseudo amino acid composition of Asparagine

APAAC2_P → Amphiphilic pseudo amino acid composition of Proline

APAAC2_Q → Amphiphilic pseudo amino acid composition of Glutamine

APAAC2_R → Amphiphilic pseudo amino acid composition of Arginine

APAAC2_S → Amphiphilic pseudo amino acid composition of Serine

APAAC2_T → Amphiphilic pseudo amino acid composition of Threonine

APAAC2_V → Amphiphilic pseudo amino acid composition of Valine

APAAC2_W → Amphiphilic pseudo amino acid composition of Tryptophan

APAAC2_Y → Amphiphilic pseudo amino acid composition of Tyrosine

APAAC2_HB_lam1 → Sequence correlation factor for hydrophobicity with lambda 1

APAAC2_HL_lam1 → Sequence correlation factor for hydrophilicity with lambda 1

APAAC2_SC_lam1 → Sequence correlation factor for side chain mass with lambda 1

APAAC2_HB_lam2 → Sequence correlation factor for hydrophobicity with lambda 2

APAAC2_HL_lam2 → Sequence correlation factor for hydrophilicity with lambda 2

APAAC2_SC_lam2 → Sequence correlation factor for side chain mass with lambda 2

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Pseudo Amino Acid Composition (order 3, With gap of 2 residues): 29 descriptors

APAAC3_A → Amphiphilic pseudo amino acid composition of Alanine

APAAC3_C → Amphiphilic pseudo amino acid composition of Cysteine

APAAC3_D → Amphiphilic pseudo amino acid composition of Aspartic acid

APAAC3_E → Amphiphilic pseudo amino acid composition of Glutamic acid

APAAC3_F → Amphiphilic pseudo amino acid composition of Phenylalanine

APAAC3_G → Amphiphilic pseudo amino acid composition of Glycine

APAAC3_H → Amphiphilic pseudo amino acid composition of Histidine

APAAC3_I → Amphiphilic pseudo amino acid composition of Isoleucine

APAAC3_K → Amphiphilic pseudo amino acid composition of Lysine

APAAC3_L → Amphiphilic pseudo amino acid composition of Leucine

APAAC3_M → Amphiphilic pseudo amino acid composition of Methionine

APAAC3_N → Amphiphilic pseudo amino acid composition of Asparagine

APAAC3_P → Amphiphilic pseudo amino acid composition of Proline

APAAC3_Q → Amphiphilic pseudo amino acid composition of Glutamine

APAAC3_R → Amphiphilic pseudo amino acid composition of Arginine

APAAC3_S → Amphiphilic pseudo amino acid composition of Serine

APAAC3_T → Amphiphilic pseudo amino acid composition of Threonine

APAAC3_V → Amphiphilic pseudo amino acid composition of Valine

APAAC3_W → Amphiphilic pseudo amino acid composition of Tryptophan

APAAC3_Y → Amphiphilic pseudo amino acid composition of Tyrosine

APAAC3_HB_lam1 → Sequence correlation factor for hydrophobicity with lambda 1

APAAC3_HL_lam1 → Sequence correlation factor for hydrophilicity with lambda 1

APAAC3_SC_lam1 → Sequence correlation factor for side chain mass with lambda 1

APAAC3_HB_lam2 → Sequence correlation factor for hydrophobicity with lambda 2

APAAC3_HL_lam2 → Sequence correlation factor for hydrophilicity with lambda 2

APAAC3_SC_lam2 → Sequence correlation factor for side chain mass with lambda 2

APAAC3_HB_lam3 → Sequence correlation factor for hydrophobicity with lambda 3

APAAC3_HL_lam3 → Sequence correlation factor for hydrophilicity with lambda 3

APAAC3_SC_lam3 → Sequence correlation factor for side chain mass with lambda 3

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Quasi-Sequence Order (order 1, traditional): 42 Descriptors (Chou KC, 2000, Biochemical and Biophysical Research Communications)

QSO1_SC_A → Quasi-sequence order with Schneider matrix for Alanine

QSO1_SC_C → Quasi-sequence order with Schneider matrix for Cysteine

QSO1_SC_D → Quasi-sequence order with Schneider matrix for Aspartic acid

QSO1_SC_E → Quasi-sequence order with Schneider matrix for Glutamic acid

QSO1_SC_F → Quasi-sequence order with Schneider matrix for Phenylalanine

QSO1_SC_G → Quasi-sequence order with Schneider matrix for Glycine

QSO1_SC_H → Quasi-sequence order with Schneider matrix for Histidine

QSO1_SC_I → Quasi-sequence order with Schneider matrix for Isoleucine

QSO1_SC_K → Quasi-sequence order with Schneider matrix for Lysine

QSO1_SC_L → Quasi-sequence order with Schneider matrix for Leucine

QSO1_SC_M → Quasi-sequence order with Schneider matrix for Methionine

QSO1_SC_N → Quasi-sequence order with Schneider matrix for Asparagine

QSO1_SC_P → Quasi-sequence order with Schneider matrix for Proline

QSO1_SC_Q → Quasi-sequence order with Schneider matrix for Glutamine

QSO1_SC_R → Quasi-sequence order with Schneider matrix for Arginine

QSO1_SC_S → Quasi-sequence order with Schneider matrix for Serine

QSO1_SC_T → Quasi-sequence order with Schneider matrix for Threonine

QSO1_SC_V → Quasi-sequence order with Schneider matrix for Valine

QSO1_SC_W → Quasi-sequence order with Schneider matrix for Tryptophan

QSO1_SC_Y → Quasi-sequence order with Schneider matrix for Tyrosine

QSO1_G_A → Quasi-sequence order with Grantham matrix for Alanine

QSO1_G_C → Quasi-sequence order with Grantham matrix for Cysteine

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

QSO1_G_D → Quasi-sequence order with Grantham matrix for Aspartic acid

QSO1_G_E → Quasi-sequence order with Grantham matrix for Glutamic acid

QSO1_G_F → Quasi-sequence order with Grantham matrix for Phenylalanine

QSO1_G_G → Quasi-sequence order with Grantham matrix for Glycine

QSO1_G_H → Quasi-sequence order with Grantham matrix for Histidine

QSO1_G_I → Quasi-sequence order with Grantham matrix for Isoleucine

QSO1_G_K → Quasi-sequence order with Grantham matrix for Lysine

QSO1_G_L → Quasi-sequence order with Grantham matrix for Leucine

QSO1_G_M → Quasi-sequence order with Grantham matrix for Methionine

QSO1_G_N → Quasi-sequence order with Grantham matrix for Asparagine

QSO1_G_P → Quasi-sequence order with Grantham matrix for Proline

QSO1_G_Q → Quasi-sequence order with Grantham matrix for Glutamine

QSO1_G_R → Quasi-sequence order with Grantham matrix for Arginine

QSO1_G_S → Quasi-sequence order with Grantham matrix for Serine

QSO1_G_T → Quasi-sequence order with Grantham matrix for Threonine

QSO1_G_V → Quasi-sequence order with Grantham matrix for Valine

QSO1_G_W → Quasi-sequence order with Grantham matrix for Tryptophan

QSO1_G_Y → Quasi-sequence order with Grantham matrix for Tyrosine

QSO1_SC1 → Quasi-sequence order with Schneider matrix with lag 1

QSO1_G1 → Quasi-sequence order with Grantham matrix with lag 1

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Quasi-Sequence Order (order 2, alternate): 44 Descriptors

QSO2_SCA → Quasi-sequence order with Schneider matrix for Alanine

QSO2_SCC → Quasi-sequence order with Schneider matrix for Cysteine

QSO2_SCD → Quasi-sequence order with Schneider matrix for Aspartic acid

QSO2_SCE → Quasi-sequence order with Schneider matrix for Glutamic acid

QSO2_SCF → Quasi-sequence order with Schneider matrix for Phenylalanine

QSO2_SCG → Quasi-sequence order with Schneider matrix for Glycine

QSO2_SCH → Quasi-sequence order with Schneider matrix for Histidine

QSO2_SCI → Quasi-sequence order with Schneider matrix for Isoleucine

QSO2_SCK → Quasi-sequence order with Schneider matrix for Lysine

QSO2_SCL → Quasi-sequence order with Schneider matrix for Leucine

QSO2_SCM → Quasi-sequence order with Schneider matrix for Methionine

QSO2_SCN → Quasi-sequence order with Schneider matrix for Asparagine

QSO2_SCP → Quasi-sequence order with Schneider matrix for Proline

QSO2_SCQ → Quasi-sequence order with Schneider matrix for Glutamine

QSO2_SCR → Quasi-sequence order with Schneider matrix for Arginine

QSO2_SCS → Quasi-sequence order with Schneider matrix for Serine

QSO2_SCT → Quasi-sequence order with Schneider matrix for Threonine

QSO2_SCV → Quasi-sequence order with Schneider matrix for Valine

QSO2_SCW → Quasi-sequence order with Schneider matrix for Tryptophan

QSO2_SCY → Quasi-sequence order with Schneider matrix for Tyrosine

QSO2_GA → Quasi-sequence order with Grantham matrix for Alanine

QSO2_GC → Quasi-sequence order with Grantham matrix for Cysteine

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

QSO2_GD → Quasi-sequence order with Grantham matrix for Aspartic acid

QSO2_GE → Quasi-sequence order with Grantham matrix for Glutamic acid

QSO2_GF → Quasi-sequence order with Grantham matrix for Phenylalanine

QSO2_GG → Quasi-sequence order with Grantham matrix for Glycine

QSO2_GH → Quasi-sequence order with Grantham matrix for Histidine

QSO2_GI → Quasi-sequence order with Grantham matrix for Isoleucine

QSO2_GK → Quasi-sequence order with Grantham matrix for Lysine

QSO2_GL → Quasi-sequence order with Grantham matrix for Leucine

QSO2_GM → Quasi-sequence order with Grantham matrix for Methionine

QSO2_GN → Quasi-sequence order with Grantham matrix for Asparagine

QSO2_GP → Quasi-sequence order with Grantham matrix for Proline

QSO2_GQ → Quasi-sequence order with Grantham matrix for Glutamine

QSO2_GR → Quasi-sequence order with Grantham matrix for Arginine

QSO2_GS → Quasi-sequence order with Grantham matrix for Serine

QSO2_GT → Quasi-sequence order with Grantham matrix for Threonine

QSO2_GV → Quasi-sequence order with Grantham matrix for Valine

QSO2_GW → Quasi-sequence order with Grantham matrix for Tryptophan

QSO2_GY → Quasi-sequence order with Grantham matrix for Tyrosine

QSO2_SC1 → Quasi-sequence order with Schneider matrix with lag 1

QSO2_G1 → Quasi-sequence order with Grantham matrix with lag 1

QSO2_SC2 → Quasi-sequence order with Schneider matrix with lag 2

QSO2_G2 → Quasi-sequence order with Grantham matrix with lag 2

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Quasi-Sequence Order (order 3, with gap of 2 residues): 46 Descriptors

QSO3_SCA → Quasi-sequence order with Schneider matrix for Alanine

QSO3_SCC → Quasi-sequence order with Schneider matrix for Cysteine

QSO3_SCD → Quasi-sequence order with Schneider matrix for Aspartic acid

QSO3_SCE → Quasi-sequence order with Schneider matrix for Glutamic acid

QSO3_SCF → Quasi-sequence order with Schneider matrix for Phenylalanine

QSO3_SCG → Quasi-sequence order with Schneider matrix for Glycine

QSO3_SCH → Quasi-sequence order with Schneider matrix for Histidine

QSO3_SCI → Quasi-sequence order with Schneider matrix for Isoleucine

QSO3_SCK → Quasi-sequence order with Schneider matrix for Lysine

QSO3_SCL → Quasi-sequence order with Schneider matrix for Leucine

QSO3_SCM → Quasi-sequence order with Schneider matrix for Methionine

QSO3_SCN → Quasi-sequence order with Schneider matrix for Asparagine

QSO3_SCP → Quasi-sequence order with Schneider matrix for Proline

QSO3_SCQ → Quasi-sequence order with Schneider matrix for Glutamine

QSO3_SCR → Quasi-sequence order with Schneider matrix for Arginine

QSO3_SCS → Quasi-sequence order with Schneider matrix for Serine

QSO3_SCT → Quasi-sequence order with Schneider matrix for Threonine

QSO3_SCV → Quasi-sequence order with Schneider matrix for Valine

QSO3_SCW → Quasi-sequence order with Schneider matrix for Tryptophan

QSO3_SCY → Quasi-sequence order with Schneider matrix for Tyrosine

QSO3_GA → Quasi-sequence order with Grantham matrix for Alanine

QSO3_GC → Quasi-sequence order with Grantham matrix for Cysteine

QSO3_GD → Quasi-sequence order with Grantham matrix for Aspartic acid

QSO3_GE → Quasi-sequence order with Grantham matrix for Glutamic acid

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

QSO3_GF → Quasi-sequence order with Grantham matrix for Phenylalanine

QSO3_GG → Quasi-sequence order with Grantham matrix for Glycine

QSO3_GH → Quasi-sequence order with Grantham matrix for Histidine

QSO3_GI → Quasi-sequence order with Grantham matrix for Isoleucine

QSO3_GK → Quasi-sequence order with Grantham matrix for Lysine

QSO3_GL → Quasi-sequence order with Grantham matrix for Leucine

QSO3_GM → Quasi-sequence order with Grantham matrix for Methionine

QSO3_GN → Quasi-sequence order with Grantham matrix for Asparagine

QSO3_GP → Quasi-sequence order with Grantham matrix for Proline

QSO3_GQ → Quasi-sequence order with Grantham matrix for Glutamine

QSO3_GR → Quasi-sequence order with Grantham matrix for Arginine

QSO3_GS → Quasi-sequence order with Grantham matrix for Serine

QSO3_GT → Quasi-sequence order with Grantham matrix for Threonine

QSO3_GV → Quasi-sequence order with Grantham matrix for Valine

QSO3_GW → Quasi-sequence order with Grantham matrix for Tryptophan

QSO3_GY → Quasi-sequence order with Grantham matrix for Tyrosine

QSO3_SC1 → Quasi-sequence order with Schneider matrix with lag 1

QSO3_G1 → Quasi-sequence order with Grantham matrix with lag 1

QSO3_SC2 → Quasi-sequence order with Schneider matrix with lag 2

QSO3_G2 → Quasi-sequence order with Grantham matrix with lag 2

QSO3_SC3 → Quasi-sequence order with Schneider matrix with lag 3

QSO3_G3 → Quasi-sequence order with Grantham matrix with lag 3

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Sequence Order Coupling Number (order 1, traditional): 2 descriptors

SOC1_SC1 → Sequence order coupling number with Schneider matrix for lag 1

SOC1_G1 → Sequence order coupling number with Grantham matrix for lag 1

Sequence Order Coupling Number (order 2, alternate): 4 descriptors

SOC2_SC1 → Sequence order coupling number with Schneider matrix for lag 1

SOC2_G1 → Sequence order coupling number with Grantham matrix for lag 1

SOC2_SC2 → Sequence order coupling number with Schneider matrix for lag 2

SOC2_G2 → Sequence order coupling number with Grantham matrix for lag 2

Sequence Order Coupling Number (order 3, with gap of 2 residues): 6 descriptors

SOC3_SC1 → Sequence order coupling number with Schneider matrix for lag 1

SOC3_G1 → Sequence order coupling number with Grantham matrix for lag 1

SCO3_SC2 → Sequence order coupling number with Schneider matrix for lag 2

SOC3_G2 → Sequence order coupling number with Grantham matrix for lag 2

SOC3_SC3 → Sequence order coupling number with Schneider matrix for lag 3

SOC3_G3 → Sequence order coupling number with Grantham matrix for lag 3

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Binary Profile Descriptor

Binary profile of Amino acids : Total features 20* window/protein length (N)

A1 → Presence/Absence (1 or 0) for Alanine at position 1

C1 → Presence/Absence (1 or 0) for Cysteine at position 1

D1 → Presence/Absence (1 or 0) for Aspartic acid at position 1

E1 → Presence/Absence (1 or 0) for Glutamic acid at position 1

F1 → Presence/Absence (1 or 0) for Phenylalanine at position 1

A2 → Presence/Absence (1 or 0) for Alanine at position 2

C2 → Presence/Absence (1 or 0) for Cysteine at position 2

D2 → Presence/Absence (1 or 0) for Aspartic acid at position 2

E1 → Presence/Absence (1 or 0) for Glutamic acid at position 2

F2 → Presence/Absence (1 or 0) for Phenylalanine at position 2

An → Presence/Absence (1 or 0) for Alanine at position n

Cn → Presence/Absence (1 or 0) for Cysteine at position n

Dn → Presence/Absence (1 or 0) for Aspartic acid at position n

En→ Presence/Absence (1 or 0) for Glutamic acid at position n

Fn → Presence/Absence (1 or 0) for Phenylalanine at position n

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Dipeptide profile of amino acids : Total features 20*20*window/protein length(n)-q

AA1 → Presence/Absence (1 or 0) for Alanine-Alanine at position 1

AC1 → Presence/Absence (1 or 0) for Alanine-Cysteine at position 1

AD1 → Presence/Absence (1 or 0) for Alanine-Aspartic acid at position 1

AE1 → Presence/Absence (1 or 0) for Alanine-Glutamic acid at position 1

AA2 → Presence/Absence (1 or 0) for Alanine-Alanine at position 2

AC2 → Presence/Absence (1 or 0) for Alanine-Cysteine at position 2

AD2 → Presence/Absence (1 or 0) for Alanine-Aspartic acid at position 2

AE2 → Presence/Absence (1 or 0) for Alanine-Glutamic acid at position 2

AAn → Presence/Absence (1 or 0) for Alanine-Alanine at position n

ACn → Presence/Absence (1 or 0) for Alanine-Cysteine at position n

ADn → Presence/Absence (1 or 0) for Alanine-Aspartic acid at position n

AEn → Presence/Absence (1 or 0) for Alanine-Glutamic acid at position n

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Atom and Bond profile: Total features 5*total number of atoms (n) + 4*total number of bonds (m)

C1 → Presence/Absence (1 or 0) for Carbon atom at position 1

H1 → Presence/Absence (1 or 0) for Hydrogen atom at position 1

N1 → Presence/Absence (1 or 0) for Nitrogen atom at position 1

O1 → Presence/Absence (1 or 0) for Oxygen atom at position 1

S1 → Presence/Absence (1 or 0) for Sulphur atom at position 1

C2 → Presence/Absence (1 or 0) for Carbon atom at position 2

H2 → Presence/Absence (1 or 0) for Hydrogen atom at position 2

N2 → Presence/Absence (1 or 0) for Nitrogen atom at position 2

O2 → Presence/Absence (1 or 0) for Oxygen atom at position 2

S2 → Presence/Absence (1 or 0) for Sulphur atom at position 2

C_n → Presence/Absence (1 or 0) for Carbon atom at n^{th} position

H_n → Presence/Absence (1 or 0) for Hydrogen atom at n^{th} position

N_n → Presence/Absence (1 or 0) for Nitrogen atom at n^{th} position

O_n → Presence/Absence (1 or 0) for Oxygen atom at n^{th} position

S_n → Presence/Absence (1 or 0) for Sulphur atom at n^{th} position

SI1 → Presence/Absence (1 or 0) for single bond at position 1

DO1 → Presence/Absence (1 or 0) for double bond at position 1

CY1 → Presence/Absence (1 or 0) for cyclic ring at position 1

BE1 → Presence/Absence (1 or 0) for benzene ring at position 1

SI2 → Presence/Absence (1 or 0) for single bond at position 2

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

DO2 → Presence/Absence (1 or 0) for double bond at position 2

CY2 → Presence/Absence (1 or 0) for cyclic ring at position 2

BE2 → Presence/Absence (1 or 0) for benzene ring at position 2

SI_m → Presence/Absence (1 or 0) for single bond at m^{th} position

DO_m → Presence/Absence (1 or 0) for double bond at m^{th} position

CY_m → Presence/Absence (1 or 0) for cyclic ring at m^{th} position

BE_m → Presence/Absence (1 or 0) for benzene ring at m^{th} position

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

Residue Properties Profile: Total features 25*window/protein length(n)

PC1 → Presence/Absence (1 or 0) for positively charged residues at position 1

NC1 → Presence/Absence (1 or 0) for positively charged residues at position 1

NE1 → Presence/Absence (1 or 0) for neutral charged residues at position 1

PO1 → Presence/Absence (1 or 0) for polar residues at position 1

NP1 → Presence/Absence (1 or 0) for non-polar residues at position 1

AL1 → Presence/Absence (1 or 0) for residues having aliphatic side chain at position 1

CY1 → Presence/Absence (1 or 0) for residues having cyclic side chain at position 1

AR1 → Presence/Absence (1 or 0) for aromatic residues at position 1

AC1 → Presence/Absence (1 or 0) for acidic residues at position 1

BS1 → Presence/Absence (1 or 0) for basic residues at position 1

NE1 → Presence/Absence (1 or 0) for neutral residues based on pH at position 1

HB1 → Presence/Absence (1 or 0) for hydrophobic residues at position 1

HL1 → Presence/Absence (1 or 0) for hydrophilic residues at position 1

NT1 → Presence/Absence (1 or 0) for neutral residues at position 1

HX1 → Presence/Absence (1 or 0) for hydroxylic residues at position 1

SC1 → Presence/Absence (1 or 0) for residues having sulphur content at position 1

SS_HE1 → Presence/Absence (1 or 0) for secondary structure (Helix) residues at position 1

SS_ST1 → Presence/Absence (1 or 0) for secondary structure (Strands) residues at position 1

SS_CO1 → Presence/Absence (1 or 0) for secondary structure (Coil) residues at position 1

SA_BU1→ Presence/Absence (1 or 0) for solvent accessibility (Buried) residues at position 1

SA_EX1 → Presence/Absence (1 or 0) for solvent accessibility (Exposed) residues at position 1

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

SA_IN1 → Presence/Absence (1 or 0) for solvent accessibility (Intermediate) residues at position 1

TN1 → Presence/Absence (1 or 0) for tiny residues at position 1

SM1 → Presence/Absence (1 or 0) for small residues at position 1

LR1 → Presence/Absence (1 or 0) for large residues at position 1

PC2 → Presence/Absence (1 or 0) for positively charged residues at position 2

NC2 → Presence/Absence (1 or 0) for positively charged residues at position 2

NE2 → Presence/Absence (1 or 0) for neutral charged residues at position 2

PO2 → Presence/Absence (1 or 0) for polar residues at position 2

NP2 → Presence/Absence (1 or 0) for non-polar residues at position 2

AL2 → Presence/Absence (1 or 0) for residues having aliphatic side chain at position 2

CY2 → Presence/Absence (1 or 0) for residues having cyclic side chain at position 2

AR2 → Presence/Absence (1 or 0) for aromatic residues at position 2

AC2 → Presence/Absence (1 or 0) for acidic residues at position 2

BS2 → Presence/Absence (1 or 0) for basic residues at position 2

NE2 → Presence/Absence (1 or 0) for neutral residues based on pH at position 2

HB2 → Presence/Absence (1 or 0) for hydrophobic residues at position 2

HL2 → Presence/Absence (1 or 0) for hydrophilic residues at position 2

NT2 → Presence/Absence (1 or 0) for neutral residues at position 2

HX2 → Presence/Absence (1 or 0) for hydroxylic residues at position 2

SC2 → Presence/Absence (1 or 0) for residues having sulphur content at position 2

SS_HE2 → Presence/Absence (1 or 0) for secondary structure (Helix) residues at position 2

SS_ST2 → Presence/Absence (1 or 0) for secondary structure (Strands) residues at position 2

SS_CO2 → Presence/Absence (1 or 0) for secondary structure (Coil) residues at position 2

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

SA_BU2→ Presence/Absence (1 or 0) for solvent accessibility (Buried) residues at position 2

SA_EX2 → Presence/Absence (1 or 0) for solvent accessibility (Exposed) residues at position 2

SA_IN2 → Presence/Absence (1 or 0) for solvent accessibility (Intermediate) residues at position 2

TN2 → Presence/Absence (1 or 0) for tiny residues at position 2

SM2 → Presence/Absence (1 or 0) for small residues at position 2

LR2 → Presence/Absence (1 or 0) for large residues at position 2

TNn → Presence/Absence (1 or 0) for tiny residues at position n

SMn → Presence/Absence (1 or 0) for small residues at position n

LRn → Presence/Absence (1 or 0) for large residues at position n

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.

AA Index profile: Total features 553*window/protein length(n)

ANDN920101_1 → Presence/Absence (1 or 0) for ANDN920101 at position 1

KARS160122_1 → Presence/Absence (1 or 0) for KARS160122 at position 1

ANDN920101_2 → Presence/Absence (1 or 0) for ANDN920101 at position 2

KARS160122_2 → Presence/Absence (1 or 0) for KARS160122 at position 2

ANDN920101_n → Presence/Absence (1 or 0) for ANDN920101 at position n

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KARS160122_2n→ Presence/Absence (1 or 0) for KARS160122 at position n

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Note: 'N' prefix is added to the header for choosing N-terminal residues, 'C' prefix is added to the header for choosing C-terminal residues, 'R' prefix is added to the header for choosing rest method, 'NC' prefix is added to the header if NC-terminal has chosen, 'RNC' prefix is added to the header if Rest after removing NC-terminal has chosen, and the suffix of '_sn,' where n is the number of splits, is added on choosing the split option.