

S.No.	Name of the Function	Command
1	Amino-acid Composition	<pre>aac_wp.py -i inputfile -o outputfile . i – input . o – output</pre>
2	Amino-acid Composition of N-Terminal	<pre>aac_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of N-Terminal residues</pre>
3	Amino-acid Composition of C-Terminal	<pre>aac_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of C-Terminal residues</pre>
4	Amino-acid Composition of Rest	<pre>aac_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues</pre>
5	Amino-acid Composition of split	<pre>aac_st.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of splits</pre>
6	Dipeptide Composition	<pre>dpc_wp.py -i inputfile -o outputfile -q order . i – input . o – output . q – order of dipeptide</pre>
7	Dipeptide Composition of N-Terminal	<pre>dpc_nt.py -i inputfile -o outputfile -n number -q order . i – input . o – output . n - number of N-Terminal residues . q – order of dipeptide</pre>

8	Dipeptide Composition of C-Terminal	dpc_ct.py -i inputfile -o outputfile -n number -q order . i – input . o – output . c - number of C-Terminal residues . q – order of dipeptide
9	Dipeptide Composition of Rest	dpc_rt.py -i inputfile -o outputfile -m number1 -n number2 -q order . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues . q – order of dipeptide
10	Dipeptide Composition (dpc_split_comp)	dpc_st.py -i inputfile -o outputfile -l lambda -n Number_of_splits . i – input . o – output . l - value of lambda . n – number of splits
11	Atom Composition	atc_wp.py -i inputfile -o outputfile . i – input . o – output
12	Atom Composition of N-Terminal	atc_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
13	Atom Composition of C-Terminal	atc_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
14	Atom Composition of Rest	atc_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
15	Atom Composition of split	atc_st.py -i inputfile -o outputfile -n number . i: input . o: output . n: number of splits

16	Bond Composition	boc.py -i inputfile -o outputfile . i – input . o – output
17	Bond Composition of N-Terminal	boc_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
18	Bond Composition of C-Terminal	boc_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
19	Bond Composition of Rest	boc_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
20	Bond Composition of split	boc_st.py -i inputfile -o outputfile -n number . i: input . o: output . n: number of splits
21	Atom & Bond	abc_wp.py -i inputfile -o outputfile . i – input . o – output
22	Atom & Bond of N-Terminal	abc_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
23	Atom & Bond of C-Terminal	abc_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues

24	Atom & Bond of Rest	abc_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
25	Atom & Bond of split	abc_st.py -i inputfile -o outputfile -n number . i: input . o: output . n: number of splits
26	Physicochemical Property composition	pcp_wp.py -i inputfile -o outputfile . i – input . o – output
27	Physicochemical Property composition of N-Terminal	pcp_nt.py -i inputfile -o outputfile -m number . i – input . o – output . n - number of N-Terminal residues
28	Physicochemical Property composition of C-Terminal	pcp_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
29	Physicochemical Property composition of rest	pcp_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
30	Physicochemical Property composition of split	pcp_st.py -i inputfile -o outputfile -n number . i: input . o: output . n: number of splits
31	Repetitive Residue Information (RRI)	rri_wp.py -i inputfile -o outputfile . i – input . o – output

32	Repetitive Residue Information of N-Terminal (RRI_nt)	rri_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
33	Repetitive Residue Information of C-Terminal (RRI_ct)	rri_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
34	Repetitive Residue Information of Rest (RRI_rest)	rri_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
35	Repetitive Residue Information (RRI_split)	rri_st.py -i inputfile -o outputfile -n number . i: input file in single line format . o: output file . n: number of splits
36	Distance Distribution of Residues	ddor_wp.py -i inputfile -o outputfile . i – input . o – output
37	Shannon Entropy of Physicochemical Property	sep_wp.py -i inputfile -o outputfile . i – input . o – output
38	Shannon Entropy of Physicochemical Property for C-Terminal	sep_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
39	Shannon Entropy of Physicochemical Property for N-Terminal	sep_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues

40	Shannon Entropy of Physicochemical Property for Rest	sep_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
41	Shannon Entropy of Physicochemical Property	sep_st.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of splits
42	Autocorrelation	acr_wp.py -i inputfile -o outputfile -d lag . i – input . o – output . d - lag
43	Autocorrelation of C-Terminal	acr_ct.py -i inputfile -o outputfile -n number -d lag . i – input . o – output . n - number of C-Terminal residues . d - lag
44	Autocorrelation of N-Terminal	acr_nt.py -i inputfile -o outputfile -n number -d lag . i – input . o – output . n - number of N-Terminal residues . d - lag
45	Autocorrelation of Rest	acr_rt.py -i inputfile -o outputfile -m number1 -n number2 -d lag . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues . d - lag
46	Autocorrelation	acr_st.py -i inputfile -o outputfile -n number -d lag . i – input . o – output . n - number of splits . d - lag
47	Pseudo Amino-acid Composition	paac_wp.py -i inputfile -o outputfile -l lamda -w weight . i – input . o – output . l - lamda value (gap) . w - weight

48	Pseudo Amino-acid Composition of N-Terminal	paac_nt.py -i inputfile -o outputfile -n number -l lamda -w weight . i – input . o – output . n – number of N-Terminal Residues . l - lamda value (gap) . w - weight
49	Pseudo Amino-acid Composition of C-Terminal	paac_ct.py -i inputfile -o outputfile -n number -l lamda -w weight . i – input . o – output . n – number of C-Terminal Residues . l - lamda value (gap) . w - weight
50	Pseudo Amino-acid Composition of Rest	paac_rt.py -i inputfile -o outputfile -m number1 -n number2 -l lamda -w weight . i – input . o – output . m – number of N-Terminal Residues . n – number of C-Terminal Residues . l - lamda value (gap) . w - weight
51	Pseudo Amino-acid Composition of split	paac_st.py -i inputfile -o outputfile -l lambda -n number . i – input . o – output . l - lamda value (gap) . n - number of splits
52	Amphiphilic Pseudo Amino-acid Composition	apaac_wp.py -i inputfile -o outputfile -l lamda -w weight . i – input . o – output . l - lamda value (gap) . w - weight
53	Amphiphilic Pseudo Amino-acid Composition of N-Terminal	apaac_nt.py -i inputfile -o outputfile -n number -l lamda -w weight . i – input . o – output . n – number of N-Terminal Residues . l - lamda value (gap) . w - weight
54	Amphiphilic Pseudo Amino-acid Composition of C-Terminal	apaac_ct.py -i inputfile -o outputfile -n number -l lamda -w weight . i – input . o – output . n – number of C-Terminal Residues . l - lamda value (gap) . w - weight

55	Amphiphilic Pseudo Amino-acid Composition of Rest	apaac_rt.py -i inputfile -o outputfile -m number1 -n number2 -l lamda -w weight . i – input . o – output . m – number of N-Terminal Residues . n – number of C-Terminal Residues . l - lamda value (gap) . w - weight
56	Amphiphilic Pseudo Amino-acid Composition of split	apaac_st.py -i inputfile -o outputfile -m number1 -n number2 -l lamda -w weight . i – input . o – output . l - lamda value (gap) . n - number of splits
57	Quasi-Sequence Order (QOS)	qos_wp.py -i inputfile -o outputfile -g gap -w weight . i – input . o – output . g - gap . w - weight
58	Quasi-Sequence Order of C-Terminal	qos_ct.py -i inputfile -o outputfile -g gap -n number -w weight . i – input . o – output . n – number of N-Terminal Residues . g - gap . w - weight
59	Quasi-Sequence Order of N-Terminal	qos_nt.py -i inputfile -o outputfile -g gap -n number -w weight . i – input . o – output . n – number of C-Terminal Residues . g - gap . w - weight
60	Quasi-Sequence Order of Rest	qos_rt.py -i inputfile -o outputfile -g gap -m number1 -n number2 -w weight . i – input . o – output . m – number of N-Terminal Residues . n – number of C-Terminal Residues . g - lamda value gap . w - weight
61	Quasi-Sequence Order of split	qos_st.py -i inputfile -o outputfile -g gap -n Number_of_splits -w weight . i – input . o – output . g – gap value . n – number of splits . w – weight



62	Sequence Order Coupling	soc_wp.py -i inputfile -o outputfile -g gap . i – input . o – output . g – gap
63	Sequence Order Coupling for C-Terminal	soc_ct.py -i inputfile -o outputfile -g gap -n number . i – input . o – output . n – number of N-Terminal Residues . g – gap
64	Sequence Order Coupling for N-Terminal	soc_nt.py -i inputfile -o outputfile -g gap -n number . i – input . o – output . n – number of C-Terminal Residues . g - gap
65	Sequence Order Coupling for Rest	soc_rt.py -i inputfile -o outputfile -g gap -m number1 -n number2 . i – input . o – output . m – number of N-Terminal Residues . n – number of C-Terminal Residues . g - lamda value gap
66	Sequence Order Coupling of split	soc_st.py -i inputfile -o outputfile -g gap -n Number_of_splits . i – input . o – output . g – gap value . n – number of splits
67	Binary Profile of amino acid	bin_aa_wp.py -i inputfile -o outputfile . i – input . o – output
68	Binary Profile of C-Terminal of amino acid	bin_aa_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of C-Terminal residues
69	Binary Profile of N-Terminal amino acid	bin_aa_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of N-Terminal residues

70	Binary Profile of rest of amino acid	bin_aa_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
71	Binary Profile of split of amino acid	bin_aa_st.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of splits
72	Binary Profile of Dipeptide	bin_di_wp.py -i inputfile -o outputfile -q order . i – input . o – output . q – order of dipeptide
73	Binary Profile of C-Terminal of Dipeptide	bin_di_ct.py -i inputfile -o outputfile -n number -q order . i – input . o – output . n - number of C-Terminal residues . q – order of dipeptide
74	Binary Profile of N-Terminal of Dipeptide	bin_di_nt.py -i inputfile -o outputfile -n number -q order . i – input . o – output . n - number of N-Terminal residues . q – order of dipeptide
75	Binary Profile of rest of Dipeptide	bin_di_rt.py -i inputfile -o outputfile -m number1 -n number2 -q order . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues . q – order of dipeptide
76	Binary Profile of split of Dipeptide	bin_di_st.py -i inputfile -o outputfile -l lag -n Number_of_splits . i - Input file in single line format . o - Output file . l - order of dipeptide . n - Number of splits
77	Binary Profile of atom	bin_at_wp.py -i inputfile -o outputfile . i – input . o – output

78	Binary Profile of C-Terminal of atom	bin_at_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
79	Binary Profile of N-Terminal of atom	bin_at_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
80	Binary Profile of rest of atom	bin_at_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
81	Binary Profile of split of atom	bin_at_st.py -i inputfile -o outputfile -n Number_of_splits . i - Input file in single line format . o - Output file . n - Number of splits
82	Binary Profile of bond	bin_bo_wp.py -i inputfile -o outputfile . i – input . o – output
83	Binary Profile of C-Terminal of bond	bin_bo_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
84	Binary Profile of N-Terminal of bond	bin_bo_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
85	Binary Profile of rest of bond	bin_bo_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues

86	Binary Profile of split of bond	bin_bo_st.py -i inputfile -o outputfile -n Number_of_splits . i - Input file in single line format . o - Output file . n - Number of splits
87	Binary Profile of atom & bond	bin_ab_wp.py -i inputfile -o outputfile . i – input . o – output
88	Binary Profile of C-Terminal of atom & bond	bin_ab_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of C-Terminal residues
89	Binary Profile of N-Terminal of atom & bond	bin_ab_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n - number of N-Terminal residues
90	Binary Profile of rest of atom & bond	bin_ab_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n - number of C-Terminal residues
91	Binary Profile of split of atom & bond	bin_ab_st.py -i inputfile -o outputfile -n Number_of_splits . i - Input file in single line format . o - Output file . n - Number of splits
92	Conjoint Triad Calculation	ctc_wp.py -i inputfile -o outputfile . i – input . o – output
93	Conjoint Triad Calculation for C-Terminal	ctc_ct.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of C-Terminal residues

94	Conjoint Triad Calculation for N-Terminal	ctc_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of N-Terminal residues
95	Conjoint Triad Calculation for Rest	ctc_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
96	Conjoint Triad Calculation for split	ctc_st.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of splits
97	Composition enhanced Transition Distribution	ctd_wp.py -i inputfile -o outputfile . i – input . o – output
98	Composition enhanced Transition Distribution of N-Terminal	ctd_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of N-Terminal residues
99	Composition enhanced Transition Distribution of C-Terminal	ctc_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of C-Terminal residues
100	Composition enhanced Transition Distribution of Rest	ctd_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
101	Composition enhanced Transition Distribution of splits	ctd_st.py -i inputfile -o outputfile -n number . i: input . o: output . n: number of splits

102	Shannon Entropy of Residue Level	ser_wp.py -i inputfile -o outputfile . i – input . o – output
103	Shannon Entropy of Residue Level for N-Terminal	ser_nt.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of N-Terminal residues
104	Shannon Entropy of Residue Level for C-Terminal	ser_ct.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of C-Terminal residues
105	Shannon Entropy of Residue Level for Rest	ser_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
106	Shannon Entropy of Residue Level for split	ser_st.py -i inputfile -o outputfile -n number . i - input . o - output . n - number of splits
107	Shannon Entropy	se_wp.py -i inputfile -o outputfile . i – input . o – output
108	Shannon Entropy of N-Terminal	se_nt.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of N-Terminal residues
109	Shannon Entropy of C-Terminal	se_ct.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of C-Terminal residues

110	Shannon Entropy of rest	se_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
111	Shannon Entropy of split	se_st.py -i inputfile -o outputfile -n number . i - input . o - output . n - number of splits
112	Tripeptide Composition	tpc_wp.py -i inputfile -o outputfile . i – input . o – output
113	Binary Profile of Physicochemical Property	bin_pc_wp.py -i inputfile -o outputfile . i – input . o – output
114	Binary Profile of Physicochemical Property of N-Terminal	bin_pc_nt.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of N-Terminal residues
115	Binary Profile of Physicochemical Property of C-Terminal	bin_pc_ct.py -i inputfile -o outputfile –n number . i – input . o – output . n – number of C-Terminal residues
116	Binary Profile of Physicochemical Property of rest	bin_pc_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
117	AAIndex for whole sequence	aai_wp.py -i inputfile -o outputfile . i – input . o – output

118	AAIndex of N-Terminal	aai_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of N-Terminal residues
119	AAIndex of C-Terminal	aai_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of C-Terminal residues
120	AAIndex of Rest	aai_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues
121	AAIndex of split	aai_st.py -i inputfile -o outputfile -n number . i - input . o - output . n - number of splits
122	Binary Profile of AAIndex	bin_aai_wp.py -i inputfile -o outputfile . i – input . o – output
123	Binary Profile of AAIndex of N-Terminal	bin_aai_nt.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of N-Terminal residues
124	Binary Profile of AAIndex of C-Terminal	bin_aai_ct.py -i inputfile -o outputfile -n number . i – input . o – output . n – number of C-Terminal residues
125	Binary Profile of AAIndex of rest	bin_aai_rt.py -i inputfile -o outputfile -m number1 -n number2 . i – input . o – output . m - number of N-Terminal residues . n – number of C-Terminal residues



126	PSSM Normalization using method 1	pssm_n1.py -i inputfile -o outputfile . i – PSSM file of peptide/protein sequences . o – output
127	PSSM Normalization using method 2	pssm_n2.py -i inputfile -o outputfile . i – PSSM file of peptide/protein sequences . o – output
128	PSSM Normalization using method 3	pssm_n3.py -i inputfile -o outputfile . i – PSSM file of peptide/protein sequences . o – output
129	PSSM Normalization using method 4	pssm_n4.py -i inputfile -o outputfile . i – PSSM file of peptide/protein sequences . o – output
130	PSSM Composition	pssm_comp.py -i inputfile -o outputfile . i – PSSM file of peptide/protein sequences . o – output
131	Binary profiles for patterns	pat_bin.py -i inputfile -w window_size -o outputfile . i – input . w– size of the window . o – output
132	Patters for csv file	pat_csv.py -i inputfile -w window_size -o outputfile . i – file in the .csv format . w– size of the window . o – output
133	Patters for strings	pat_str.py -i inputfile -w window_size -x extension -o outputfile . i – input file . w– size of the window . x– [y n] extension of X needed or not . o – output

134	Patterns for Standard Physicochemical properties composition	pat_pcc.py -i inputfile -w window_size -o outputfile . i – input . w– size of the window . o – output
135	Patterns for amino acid index composition	pat_aai.py -i inputfile -a file_of_aaindices -w window_size -o outputfile . i – input . a – File having the list of amino acid indices name . w– size of the window . o – output