

Name	Range	Type	Example	Description
			-14 to +14	
PSSM	20 x window	Numeric	-14_T_pssm	Evolutionary Profile; normalized absolute conservation of aa at specific positions
PERC	20 x window	Numeric	13_R_perc	Evolutionary Profile; relative conservation of AA at specific positions
infPP	1 x window	Numeric	4_infPP	Information per position; information content of specific positions in PSSM and PERC
relW	1 x window	Numeric	-5_relW	Relative weight; information content of specific positions in PSSM and PERC
disis_plus	1 x window	binary	12_disis_plus	DNA binding site predicted
disis_minus	1 x window	binary	12_disis_minus	no DNA binding site predicted
disis_raw	1 x window	Numeric	0_disis_raw	raw DNA binding site prediction score
isis_plus	1 x window	binary	12_isis_plus	PPI site predicted
isis_minus	1 x window	binary	12_isis_minus	no PP site predicted
isis_raw	1 x window	Numeric	0_isis_raw	raw PPI site prediction score
profbval_raw1	1 x window	Numeric	0_profbval_raw1	raw residue flexibility score
profbval_raw2	1 x window	Numeric	0_profbval_raw2	raw residue non-flexibility score
md_plus	1 x window	binary	9_md_plus	intrinsically disordered region predicted
md_minus	1 x window	binary	9_md_minus	no disordered region predicted
md_raw	1 x window	Numeric	5_md_raw	raw disorder prediction score
md_ri	1 x window	Numeric	5_md_ri	disorder prediction reliability score
helix	1 x window	binary	1_helix	helix predicted
strand	1 x window	binary	1_strand	strand predicted
loop	1 x window	binary	1_loop	loop predicted
OTH	1 x window	Numeric	-5_OTH	raw prediction output for Helix
OTE	1 x window	Numeric	-4_OTE	raw prediction output for Sheet
Otl	1 x window	Numeric	3_Otl	raw prediction output for Loop
ri_sec	1 x window	Numeric	6_ri_sec	reliability index of sec struct prediction, applies to helix, sheet, loop and oth, ote, otl
e	1 x window	binary	12_e	exposed predicted
i	1 x window	binary	12_i	intermediate predicted
b	1 x window	binary	12_b	buried predicted
rel_acc	1 x window	Numeric	13_rel_acc	predicted relative solvent accessibility in %
ri_acc	1 x window	Numeric	-11_ri_acc	reliability index of solvent accessibility prediction; applies to e,i,b and rel_acc
PSIC	20 x window	Numeric	-13_N_psic	Evolutionary Profile; position specific independent counts at specific positions
psic_numSeq	1 x window	Numeric	-6_psic_numSeq	Number of gapless sequences at this position; applies to PSIC
PFAM domain	1 x window	binary	5_pfam_within_domain	for each residue in the window: is it part of a pfam domain?
PFAM domain conservation	1 x window	0,0.5,1	9_pfam_domain_conservation	How well is the position conserved in this domain - in three bins
PFAM residue fit	1 x window	0,0.3,0.6,1	2_pfam_residue_fit	how well does the residue fit into this domain - in 4 bins
PFAM PP	1 x window	Numeric	-5_pfam_pp	posterior probability that this residue matches it's position in the domain
Mass	1 x window	Numeric	9_chemprop_mass	mass of the amino acid
Volume	1 x window	Numeric	2_chemprop_vol	volume of the amino acid (= size)
hydrophobicity	1 x window	Numeric	4_chemprop_hyd	hydrophobicity of the amino acid
c-beta branching	1 x window	binary	-13_chemprop_cbeta	aa is a c-beta branching aa
hbearer	1 x window	binary	8_chemprop_hbreaker	aa is a helix breaker (only true for proline)
charge	1 x window	0,0.5,1	-12_chemprop_charge	charge in 3 states
prosite	1 x window	binary	13_prosite	aa is part of a prosite pattern
AA composition	20 (global)	Numeric	5_composition	relative occurrence of an AA in the entire sequence
length	4 (global)	0,0.5,1	length_category1	protein length in 4 categories with each 3 states
sec struc composition	3 x 3 (global)	0,0.5,1	helix_composition1	for each helix, strand and loop the relative occurrence is given in 3 categories with each 3 states
solvent accessibility composition	3 x 3 (global)	0,0.5,1	buried_composition2	for each buried, intermediate, exposed the relative occurrence is given in 3 categories with each 3 states
Length categories:	1-60 61-120 121-180 181-			
Composition	-25 -50 -75			