**Table S1主要的PTM位点预测工具信息汇总**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **PTM type** | **Tool name** | **Year** | **Species** | **Feature information** | **Optimization** | **Algorithm** | **Web-server or source code** |
| Glycosylation | EnsembleGly | 2007 | Multi-species  (N-, O-, C-) | PSSM | No | SVM (Ensemble learning) | http://turing.cs.iastate.edu/EnsembleGly/\* |
| GlycoPP | 2012 | Multi-species  (N-, O-) | BE, SASA, PSSM | No | SVM | http:/www.imtech.res.in/raghava/glycopp/ |
| GPP | 2008 | Multi-species  (O-) | PW, SS, SASA | No | RF | http://comp.chem.nottingham.ac.uk/glyco/ |
| GlycoEP | 2013 | Multi-species  (N-, O-, C-) | BE, CPP, PSSM, SS, SASA | No | SVM | http://www.imtech.res.in/raghava/glycoep/ |
| OGTSite | 2015 | Multi-species  (O-) | HMM | K-means,  (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/OGTSite/ |
| PGlcS | 2015 | Multi-species  (O-) | SS, DS, AAindex, PSSM | RF | SVM | NO |
| GlycoMine | 2015 | Human  (N-, O-, C-) | AAindex, PSSM, FF, SS, CKSAAP, SASA, DS, FA | IG, mRMR | RF | http://www.structbioinfor.org/Lab/GlycoMine/\* |
| GlycoMinestruct | 2016 | Human  (N-, O-) | AAindex, PSSM, SASA, SS, LOR, DI, B-factor | Linear SVM | RF | http://glycomine.erc.monash.edu/Lab/GlycoMine\_Struct/ |
| O-GlcNAcPRED | 2013 | Multi-species  (O-) | ANBPB, CMV | No | SVM | No |
| O-GlcNAcPRED-II | 2018 | Multi-species  (O-) | AAC, DAAC, PSTAAP, BPB, DBPB, PSAAP, ANBPB | KPCA, FUS | RF, NB, KNN, SVM | http://121.42.167.206/OGlcPred/ |
| NGlycPred | 2012 | Multi-species  (N-) | SP, PA | No | RF | http://exon.niaid.nih.gov/nglycpred/ |
| CKSAAP\_OGlySite | 2008 | Multi-species  (O-) | CKSAAP | CC, IG | SVM | http://bioinformatics.cau.edu.cn/  zzd\_lab/CKSAAP\_OGlySite/\* |
| Acetylation | N-Ace | 2010 | Multi-species  （A,G,K, M, S, T） | PWM, SASA, PCP | No | SVM | http://N-Ace.mbc.NCTU.edu.tw/ |
| AceK | 2014 | Multi-species  (K) | BLOSUM62, AAPC | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/AceK/ |
| ASEB | 2012 | Multi-species  (K) | PPI | NO | EBM | http://cmbi.bjmu.edu.cn/huac\* |
| BRABSB-PHKA | 2012 | Human  (K) | BRABSB | No | SVM | http://www.bioinfo.bio.cuhk.edu.hk/bpbphka\* |
| PSKacePred | 2012 | Multi-species  (K) | BE, KNN, SASA | IG | SVM | http://bioinfo.ncu.edu.cn/inquiries\_PSKAcePred.aspx |
| LAcep | 2014 | Multi-species  (K) | PCP, TPM, PSSC | CfsSubsetEval, BestFirst | LR | http://www.scbit.org/iPTM/\* |
| LysAcet | 2009 | Multi-species  (K) | CP | CfsSubsetEval, BestFirst | SVM | http://www.biosino.org/LysAcet/\* |
| GPS-PAIL | 2016 | Human\_train  Other\_test  (K) | GPS | No | threshold determination | http://pail.biocuckoo.org |
| SSPKA | 2014 | Multi-species  (K) | PSSM, PCP, SS,FA, FF | mRMR | RF | http://www.structbioinfor.org/Lab/SSPKA\* |
| PLMLA | 2012 | Multi-species  (K) | SS, EBGW, PWAA, | No | SVM | http://bioinfo.ncu.edu.cn/inquiries\_PLMLA.aspx |
| Phosida | 2010 | Human  (K) | SC | No | SVM | http://www.phosida.com |
| EnsemblePail | 2010 | Multi-species  (K) | PWM | No | SVM (Ensemble learning) | http://www.aporc.org/EnsemblePail/ |
| KA-predictor | 2016 | Multi-species  (K) | LC, PWAA, EBGW, CKSAAP, KNN, ACF, PseAAC, PCP, SS, SASA, DS, HSE, PSSM, HH | PCC | SVM | http://sourceforge.net/p/kapredictor\* |
| iAcet-Sumo | 2018 | Human  (K) | BE | (OSS)1 | SVM, binary relevance, multi-class classification | http://app.aporc.org/iAcetSumo/\* |
| BPBPHKA | 2012 | Human  (K) | BRABSB | No | SVM | http://www.bioinfo.bio.cuhk.edu.hk/bpbphka\* |
| KAcePred(26) | 2013 | Human  (K) | PSSM, PCP | No | SVM | http://bioinfo.ncu.edu.cn/AcetylAAVs\_Home.aspx |
| Methylation | BPB-PPMS | 2009 | Multi-species | BPB | No | SVM | http://www.bioinfo.bio.cuhk.edu.hk/bpbppms\* |
| CKSAAP\_methsite | 2013 | Multi-species | CKSAAP | No | SVM | http://202.198.129.219:8080/cksaap\_methsite\* |
| iMethyl-PseAAC | 2014 | Multi-species | PseAAC | No | SVM | http://www.jci-bioinfo.cn/iMethyl-PseAAC |
| MASA | 2009 | Multi-species | PWM, SASA | No | SVM | http://MASA.mbc.nctu.edu.tw/ |
| MethK | 2014 | Multi-species | AAC, SASA, BE, AAPC, DS | No | SVM | http://csb.cse.yzu.edu.tw/MethK/ |
| PMes | 2012 | Multi-species | SPC, VDWV, PWAA, SASA | No | SVM | http://bioinfo.ncu.edu.cn/inquiries\_PMeS\* |
| PSSMe | 2016 | Multi-species | AAC, KNN, PCP | IG | SVM | http://bioinfo.ncu.edu.cn/PSSMe.aspx |
| PRmePRed | 2017 | Multi-species | Atchley factors, AAC, SASA, DS, VDWV, Total charge, isoelectric point pI | IG | SVM | http://bioinfo.icgeb.res.in/PRmePRed/ |
| MePred-RF | 2017 | Multi-species | H, RE, IGS, OP, BE, TOBF, SDCF, CTF | MRMD | RF | http://server.malab.cn/MePred-RF |
| Phosphorylation | CKSAAP\_PhSite | 2012 | Multi-species | CKSAAP | IG | SVM | http://59.73.198.144/cksaap\_phsite/\* |
| CRPhos | 2008 | Multi-species | PCP | No | CRF | http://www.ptools.ua.ac.be/CRPhos/ |
| GPS2.1 | 2010 | Multi-species | GPS | No | threshold determination | http://gps.biocuckoo.org/index.php |
| GPS2.0 | 2008 | Multi-species | GPS | No | threshold determination | http://gps.biocuckoo.org/index.php |
| MetaPredPS | 2008 | Multi-species | element predictors | No | weighted voting strategy | http://MetaPred.umn.edu/MetaPredPS/\* |
| Musite | 2010 | Multi-species | KNN, DS, AAC, | (Bootstrap)1 | SVM | http://musite.sourceforge.net/ |
| phos\_pred | 2014 | Human | GO, BE, PPI | mRMR | RF | http://bioinformatics.ustc.edu.cn/phos\_pred/ |
| Phos3D | 2009 | Multi-species | PCP, 3D | PCA | SVM | http://phos3d.mpimp-golm.mpg.de |
| PhoScan | 2008 | Human\_train,  Multi-species  \_test | FAAC, SAAPSF | No | Log-odds ratio | http://bioinfo.au.tsinghua.edu.cn/phoscan/ |
| PHOSFER | 2013 | Multi-species  (Plants) | AAindex (Hydrophobicity, Composition, PCP ) | No | RF | http://saphire.usask.ca |
| PhosK3D | 2013 | Multi-species | PWM, SASA, SS, 3DS | No | SVM | http://csb.cse.yzu.edu.tw/  PhosK3D/ |
| PhosphoRice | 2012 | Rice | element predictors | No | weighted voting strategy | http://bioinformatics.fafu.edu.cn/PhosphoRice\* |
| PhosphoSVM | 2014 | Multi-species | H, RE, SS, DS, SASA, OP, ACH, KNN | No | SVM | http://sysbio.unl.edu/PhosphoSVM/ |
| PKIS | 2013 | Human | CMS | No | SVM | http://bioinformatics.ustc.edu.cn/pkis |
| PlantPhos | 2011 | *A. thaliana* | HMM | (K-means clustering)1  (MDDLogo-clustering)1 | HMMsearch | http://csb.cse.yzu.edu.tw/PlantPhos/ |
| PostMod | 2010 | Multi-species | BLOSUM62, PSSM, | NO | noise-reducing  algorithm | http://pbil.kaist.ac.kr/PostMod/ |
| PPRED | 2010 | Multi-species | PSSM | No | SVM | http://www.cse.univdhaka.edu/~ashis/ppred/index.php\* |
| PPSP | 2006 | Multi-species | BLOSUM62 | No | BDT | http://bioinformatics.lcdustc.org/PPSP\* |
| Predikin | 2008 | Multi-species | DS, SS | No | HMM | http://predikin.biosci.uq.edu.au/ |
| PTMPred | 2013 | Multi-species | PSPM | No | SVM | http://www.aporc.org/doc/wiki/PTMPred |
| ViralPhos | 2013 | virus | PWM | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/ViralPhos/ |
| RF-Phos | 2016 | Multi-species | H, RE, IGS, SASA, OP, ACH, BE, CTD, SOCN, QSO | Gini impurity | RF | http://bcb.ncat.edu/RF\_Phos/ |
| MusiteDeep | 2017 | *H. sapiens* | BE | NO | Multi-layer CNN | https://github.com/duolinwang/MusiteDeep |
| PhosPred-RF | 2017 | Multi-species | H, RE, IGS, OP, BE, TOBF, SkipF | No | RF | http://server.malab.cn/PhosPred-RF |
| PhosphoPredict | 2017 | *H. sapiens* | BE, SS, SASA, DS | mRMR | RF | http://phosphopredict.erc.monash.edu/ |
| PhosContext2vec | 2018 | Multi-species | H, RE, DS, SS, OP, ACH,  context2vecadd, context2vecinference | No | SVM | http://phoscontext2vec.erc.monash.edu/ |
| Quokka | 2018 | Human | NNS, AAF, WLS, BSI, KNN | No | LR | http://quokka.erc.monash.edu/ |
| S-sulfenylation | SOHSite | 2016 | Multi-species | PSSM, PCP | *F-score* | SVM | No |
| MDD-SOH | 2015 | Multi-species | PSSM, BLOSUM62 | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/MDDSOH/ |
| PRESS | 2016 | Multi-species | sequence, spatial, SASA, SS | No | SVM | http://press-sulfenylation.cse.uoi.gr/ |
| iSulf-Cys | 2016 | Human | BE, PSAAP, PCP | No | SVM | http://app.aporc.org/iSulf-Cys/ |
| SOHPRED | 2016 | Human | PSAAP, HQI, CKSAAP, PSSM | No | NB, RF, SVM  Ensemble-learning | http://genomics.fzu.edu.cn/SOHPRED\* |
| S-SulfPred | 2017 | *H. sapiens* | PSAAP, PCP | OSSU-SMOTEO | SVM | No |
| SulCysSite | 2017 | Multi-species | PCP, BE, PSSM, pCKSAAP | No | RF | http://kurata14.bio.kyutech.ac.jp/SulCysSite/ |
| SVM-SulfoSite | 2018 | Human | BE, PCP, CKSAAP, AAC, HQI | ( randomly replicates data )1 | SVM | https://github.com/HussamAlbarakati/SVM-Sulfosite |
| Palmitoylation | CSS-Palm | 2008 | Multi-species | CSS | No | threshold determination | http://bioinformatics.lcd-ustc.org/css\_palm\* |
| CKSAAP-Palm | 2009 | Multi-species | CKSAAP, | No | SVM | http://www.aporc.org/doc/wiki/  CKSAAP-Palm |
| SeqPalm | 2015 | Multi-species | AAC, PWM, CKSAAP, ACPCPC | RF method,  (SMOTE)1 | RF | http://lishuyan.lzu.edu.cn/seqpalm |
| MDD-palm | 2017 | Multi-species | AAC, PSSM | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/MDDPalm/ |
| Pupylation | GPS-PUP | 2011 | Multi-species | GPS | No | threshold determination | http://pup.biocuckoo.org |
| Ensemble Pup | 2013 | Multi-species | BPB | (bootstrap procedure)1 | SVM | http://210.47.24.217:8080/EnsemblePup/\* |
| PrePup | 2013 | Multi-species | PCP, PSSM, DS, SS, SASA | mRMR | SVM | No |
| iPUP | 2013 | *M. smegmatis*,  *M. tuberculosis*,  *E. coli* | CKSAAP | chi-square test | SVM | http://cwtung.kmu.edu.tw/ipup |
| PupPred | 2013 | Multi-species | BE, AAC, AAPC, GAAP, PCP, KNN, SS, PSSM | *F-score* | SVM | http://bioinfo.ncu.edu.cn/PupPred.aspx\* |
| pbPUP | 2015 | Multi-species | pbCKSAAP | chi-square test | SVM | http://protein.cau.edu.cn/pbPUP/ |
| PUL-PUP | 2016 | Multi-species | CKSAAP, | chi-square test,  (PUL-PUP)1 | SVM | https://pul-pup.github.io/ |
| IMP-PUP | 2016 | Multi-species | CKSAAP | *F-score*,  (IMP-PUP)1 | SVM | https://juzhe1120.github.io/ |
| EPuL | 2016 | Multi-species | CKSAAP | chi-square test,  (EPuL)1 | SVM | http://59.73.198.144:8080/EPuL\* |
| S-glutathionylation | GSHSite | 2015 | Mouse | BLOSUM62, AAPC | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/GSHSite/ |
| PGluS | 2015 | Multi-species | CKSAAP, PSSM, PCP, ACF, WAAC, EBGW, vDWV, AAC | MDA | SVM | http://59.73.198.144:8088/PGluS/\* |
| SSGlu | 2016 | *H. sapiens, M. musculus* | AAC, ACF, BE, PCP, PSSM | MDA | SVM | http://59.73.198.144:8080/SSGlu/\* |
| S-nitrosylation | GPS-SNO | 2010 | Multi-species | GPS 3.0 | No | threshold determination | http://sno.biocuckoo.org/ |
| iSNO-AAPair | 2013 | Human, Mouse | PseAAC | No | Similarity discrimination | http://app.aporc.org/iSNO-AAPair/ |
| iSNO-PseAAC | 2013 | Multi-species | PseAAC | No | threshold determination | http://app.aporc.org/iSNO-PseAAC/ |
| PSNO | 2014 | Multi-species | PSSM, SS, PCP | Relative Entropy | KNN | http://59.73.198.144:8088/PSNO/\* |
| SNOSite | 2011 | Mouse | PWM, AAC | *F-score*,  (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/SNOSite/ |
| iSNO-ANBPB | 2014 | Multi-species | ANBPB, SS, Electrostatic Charge | No | SVM | No |
| KSRC | 2014 | Multi-species | PSSM, PCP, SASA, AAC, DS | mRMR | KSRC | No |
| Succinylation | iSuc-PseAAC | 2015 | Multi-species | PSAAP | No | SVM | http://app.aporc.org/iSuc-PseAAC/ |
| iSuc-PseOpt | 2016 | Multi-species | PseAAC | (KNNC+IHTS)1 | RF | http://www.jci-bioinfo.cn/iSuc-PseOpt |
| Success | 2018 | Multi-species | SASA, PSSM, SS, Backbone torsion angles | (k-nearest neighbor strategy)1 | SVM | https://github.com/YosvanyLopez/Success |
| SucPred | 2015 | Multi-species | ACF, EBGW, VDWV, WAAC | (PSoL)1 | SVM | http://59.73.198. 144:8088/SucPred/\* |
| SuccFind | 2015 | Multi-species | AAC, CKSAAP, PCP | *F-score* | SVM | http://bioinfo.ncu.edu.cn/SuccFind.aspx |
| pSuc-Lys | 2016 | Multi-species | PseAAC | No | RFE | http://www.jci-bioinfo.cn/pSuc-Lys |
| SuccinSite | 2016 | Multi-species | CKSAAP, BE, PCP | mRMR | RF | http://systbio.cau.edu.cn/SuccinSite/ |
| SucStruct | 2017 | Multi-species | SASA, SS, local backbone angles | IG,  (k-nearest neighbor strategy)1 | DT | https://github.com/YosvanyLopez/  SucStruct |
| PSSM-Suc | 2017 | Multi-species | PSSM | (k-nearest neighbor strategy)1 | DT | https://github.com/YosvanyLopez/PSSM-Suc |
| PSuccE | 2018 | Multi-species | AAC, BE, PCP, GPAAC | IG | SVM (Ensemble learning) | https://github.com/ningq669/PSuccE |
| SSEvol-Suc | 2018 | Multi-species | PSSM, SS | No | AdaBoost | https://github.com/YosvanyLopez/SSEvol-Suc |
| SUMOylation | SUMOsp | 2006 | Multi-species | GPS , MotifX | No | threshold determination | http://bioinformatics.lcdustc.org/sumosp/\* |
| SUMOpre | 2008 | Multi-species | amino acid position information | No | threshold determination | http://spg.biosci.tsinghua.edu.cn/service/sumoprd/predict.cgi\* |
| SUMOsp 2.0 | 2009 | Multi-species | Modified GPS | No | threshold determination | http://sumosp.biocuckoo.org/ |
| GPS-SUMO | 2014 | Multi-species | GPS | PSO | threshold determination | http://sumosp.biocuckoo.org |
| JASSA | 2015 | Multi-species | PFM | No | Scoring strategy | http://www.jassa.fr/ |
| SUMOhydro | 2012 | Multi-species | Hydrobinary | No | SVM | http://protein.cau.edu.cn/others/  SUMOhydro/ |
| SUMOplot | 2006 | Multi-species | hydrophobicity (PCP),  SS, SASA | No | MSE-test | http://www.sce.carleton.ca/faculty/green/green.php?page=webservers |
| SUMO\_LDA | 2016 | Multi-species | PCP, PSAAP, MCKSAAP | *F\_score* | LDA | No |
| pSumo-CD | 2016 | Multi-species | PseAAC | No | CD | http://www.jcibioinfo.cn/pSumo-CD\* |
| iAcet-Sumo | 2018 | *Human* | BE | (OSS)1 | SVM, binary relevance, multi-class classification | http://app.aporc.org/iAcetSumo/\* |
| Tyrosine sulfation | Sulfinator | 2002 | Multi-species | Multiple sequence alignment | No | HMM | https://web.expasy.org/sulfinator/ |
| SulfoSite | 2009 | Multi-species | PWM, SASA | No | SVM | http://SulfoSite.mbc.nctu.edu.tw/ |
| PredSulSite | 2012 | Multi-species | SS, EBGW, ACF | No | SVM | http://www.bioinfo.ncu.edu.cn/inquiries\_PredSulSite.aspx\* |
| SulfoTyrP | 2013 | Multi-species | BPBAA, HCMV | No | SVM | No |
| DFA-PTSs | 2016 | Multi-species | PSSM, SS, DS, PCP | RES+IFS | SVM | http://biolabxynu.zicp.net:9090/DFA PTSs/\* |
| TyrPred | 2018 | Multi-species | AAC, BE, CKSAAP, PWAA, KNN, EBGW | elastic net | SVM | http://computbiol.ncu.edu.cn/TyrPred |
| Ubiquitination | CKSAAP\_UbSite | 2011 | *S. cerevisiae* | CKSAAP, BE | CHI, IG | SVM | http://systbio.cau.edu.cn/cksaap\_ubsite/ |
| hCKSAAP\_UbSite | 2013 | *H. sapiens* | CKSAAP, BE, PCP，  Aggregation propensity | No | SVM | http://systbio.cau.edu.cn/cksaap\_ubsite/ |
| RUBI | 2014 | *H. sapiens* | Alignment, DS | No | SVM, BRNN | http://protein.bio.unipd.it/rubi/ |
| iUbiq-Lys | 2015 | Multi-species | PseAAC | No | SVM | http://www.jci-bioinfo.cn/iUbiq-Lys |
| UbiPred | 2008 | Multi-species | Amino acid identity, PSSM, PCP | IPMA | SVM | http://iclab.life.nctu.edu.tw/ubipred\* |
| UbiProber | 2013 | Multi/single-species | KNN, PCP, AAC | IG | SVM | http://bioinfo.ncu.edu.cn/UbiProber.aspx |
| UbPred | 2009 | *S. cerevisiae* | AAC, PCP, sequence complexity, protein properties, PSSM | t-test | RF | http://www.ubpred.org |
| UbiSite | 2016 | Multi-species | BE , AAC, AAPC, PWM, PSSM, SASA, SS | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/UbiSite/ |
| ESA-UbiSite | 2016 | *Human* | PCP | ESA | SVM | http://iclab.life.nctu.edu.tw/iclab\_webtools/ESAUbiSite/\* |
| Ubipredictor | 2016 | Multi-species | AAPC, PSSM, PCP, | LDA | LDA | http://chemdp.com/ubipredictor.php\* |
| MDDLogoSVM | 2017 | Multi-species | AAC, AAPC, PSSM | (MDDLogo-clustering)1 | SVM | No |
| Deep architecture | 2017 | Multi-species | One hot, PCP, PSSM | No | multimodal deep architecture | https://github.com/jiagenlee/deepUbiquitylation |
| Using UbiNets | 2018 | Multi-species | PCP | No | DenseNet | No |
| Carbonylation | CarSPred | 2014 | Multi-species  (K, R, T, P) | PSPAKSAP, DKMDI, KNN, HQI | mRMR | WSVM | https://sourceforge.net/projects/hqlstudio/files/CarSPred-1 |
|  | CarSite | 2017 | Human  (K, R, T, P) | PSAAP, CKSAAP, AAC, PCP | *F-score*  (OSS)1 | SVM | No |
|  | predCar-site | 2017 | Multi-species  (K, R, T, P) | PseAAC | (DEC)1 | SVM | http://research.ru.ac.bd/predCar-Site/ |
|  | CarSPred.Y | 2016 | Yeast  (K, R, T, P) | AAC, PSAAP, HQI | t-test | WSVM | https://sourceforge.net/projects/hqlstudio/ files/CarSpred.Y/\* |
|  | iCar-PseCp | 2016 | Human,  E. coli  (K, R, T, P) | PseAAC | (MC)1 | RF | http://www.jci-bioinfo.cn/iCar-PseCp |
|  | MDD-carb | 2017 | Multi-species  (K, R, T, P) | HMM | (MDDLogo-clustering)1 | SVM | http://csb.cse.yzu.edu.tw/MDDCarb/ |
| Hydroxylation | OH-PRED | 2017 | Multi-species  (P, K) | ANBPB, PCP | No | SVM | No |
|  | HydPred | 2016 | Multi-species  (P, K) | AAC, CKSAAP, ACPCP, PWM, BE | RF  (SMOTE)1 | RF | http://lishuyan.lzu.edu.cn/hydpred/ |
|  | PredHydroxy | 2015 | Multi-species  (P, K) | PWAA, HQI, | No | SVM | http://bioinfo.ncu.edu.cn/PredHydroxy.aspx |
|  | RF-Hydroxysite | 2016 | Multi-species  (P, K) | HQI, H, ACH | RF | RF | http://bcb.ncat.edu/RF\_hydroxy/ |
|  | iHyd-PseAAC | 2014 | Multi-species  (P, K) | PSDP | No | DF | http://app.aporc.org/iHyd-PseAAC/ |
|  | iHyd-PseCp | 2016 | Multi-species  (P, K) | PseAAC | No | RF | http://www.jci-bioinfo.cn/iHyd-PseCp |
|  | Hu’s method | 2010 | Multi-species  (P, K) | AAIndex, PSSM, DS, | mRMR | NNA | No |
| Malonylation | Mal-Lys | 2016 | Multi-species  (K) | k-mer, PSAAP, PCP | mRMR | SVM | http://app.aporc.org/Mal-Lys/ |
|  | MaloPred | 2016 | Multi-species  (K) | AAC, BE, EBGW, KNN, PSSM, | IG | SVM | http://bioinfo.ncu.edu.cn/MaloPred.aspx |
|  | SPRINT‐Mal | 2018 | Multi-species  (K) | PSSM, PCP, HSE | No | SVM | http://sparks-lab.org/server/SPRINT-Mal/ |

*Note*: \* link not working at the time of writing.  
Feature:

ACPCP: Autocorrelation of Amino Acid Physicochemical Properties.

KNN Feature: k nearest neighbor feature;

PCP (AAindex): physicochemical property;

AAC: amino acid composition;

FAAC：flexibility amino acid composition (F, Y, W, H, I, V, L, C)

AAPC: amino acid pairwise composition;

BE: Binary Encoding;

BPB: Bi-profile Bayes feature extraction

ANBPB: adapted normal distribution bi-profile Bayes

BRABSB: bi-relative adapted binomial score Bayes;

CMS: composition of monomer spectrum;

CP: protein coupling patterns;

CPP: Composition profile of patterns;

DKMDI: Increment of k-mer diversity;

FA: Functional Annotation (Domain, Nucleotide binding, Disulfide bond, Posttranslational modified residue, Glycosylation, Active site, Natural variant, Metal ion binding site, Binding site)

FF: Functional Features (Gene ontology, KEGG pathway, Pfam, InterPro, Protein-protein interaction)

GAAC: Grouping amino acid compositions

SS: secondary structure;

SC: sequence context;

SP: structural properties;

3D: 3D structural information

HQI: high-quality indices

HSE: Half Sphere Exposure

HH: Position-Specific Scoring Matrix by HHblits

IGS: Information Gain Score

PWM: positional weighted matrix;

PW: pattern weight;

PA: Pattern;

TPM: transition probability matrix

PSSM: position-specific scoring matrix (Evolutionary information);

PSSC: position-specific symbol composition

PSPAKSAP: position-specific propensity of amino acid and k-spaced amino acid pair

PFM: Position Frequency Matrix

SASA: solvent-accessible surface area;

LC: Location Coding;

LOR: Log-odds ratios;

DI: Depth Index;

SPC: Sparse property coding

H: Shannon Entropy

RE: Relative Entropy

OP: Overlapping Properties

ACH: Average Cumulative Hydrophobicity;

CTD: Composition, Transition, and Distribution

SOCN: Sequence Order Coupling Numbers

QSO: Quasi Sequence Order

EBGW: Encoding based on grouped weight;

ACF: Autocorrelation functions;

VDWV: normalized van der waals volume

WAAC: position weight amino acids composition

BPBAA: bi-profile Bayesian amino acid profile;

CMV: composition moment vectors;

MCKSAAP: modification of composition of k-space amino acid pair;

NNS: Nearest Neighbour Similarity

AAF: Amino Acid Frequency

WLS: WebLogo-based Sequence conservation

BSI: BLOSUM62 Substitution Index

CKSAAP(k-spaced): composition of k-spaced residue pairs

PSAAP: position-specific amino acid propensity

PSPM: position-specific propensity matrix

PSFM: position specific frequency matrix;

SAAPSF: position specific frequency of specific amino acids

GPAAC: Grey Pseudo Amino Acid Composition

Hydrobinary: combining amino acid hydrophobicity with the binary encoding scheme;

DS: disorder status;

TOBF: Twenty One-bit features

SkipF: Skip-n-gram Features

SDCF: Skip Dipeptide Composition Features

CTF: Conjoint Triad Features

Optimization (Feature selection):

CHI: Chi-Squared;

IG: Information Gain;

IPMA: informative physicochemical property mining algorithm;

ESA: evolutionary screening algorithm

LDA:  [Linear Discriminant Analysis](https://chinesesites.library.ingentaconnect.com/search?option1=keywords&value1=%27Linear+Discriminant+Analysis+(LDA)%27)

RES: Relative Entropy Selection

IFS: Incremental Feature Selection

OSS: One-sided selection

PCC: Pearson Correlation Coefficient

mRMR: ofMax-Relevance and Min-Redundancy

MRMD: Maximal‑Relevance‑Maximal‑Distance

CC: Correlation coefficient

Optimization (Resampling method)：

PSoL: Positive samples only learning

KPCA: K-means clustering algorithm and principal components analysis (PCA)

FUS: fuzzy undersampling method

DEC: Different Error Costs;

MC: Monte Carlo approach

Algorithm:

BRNNs: bidirectional recurrent neural networks;

DenseNet : Densely Connected Convolution Networks;

LDA: Linear discriminant analysis

CD: covariant discriminant;

DT: Decision tree;

LR: Logistic regression

EBM: enrichment based method

DF: discriminant function

NNA: Nearest neighbor algorithm;

Species:

*A. thaliana*: *Arabidopsis thaliana*

*H. sapiens*: *Homo sapiens*；

*S. cerevisiae*: *Saccharomyces cerevisiae*;

*M. smegmatis:* *Mycobacterium smegmatis*

*M. tuberculosis:* *Mycobacterium tuberculosis*

*E.coli*: *Escherichia coli*

*M. musculus: Mus musculus*