Supplementary Materials

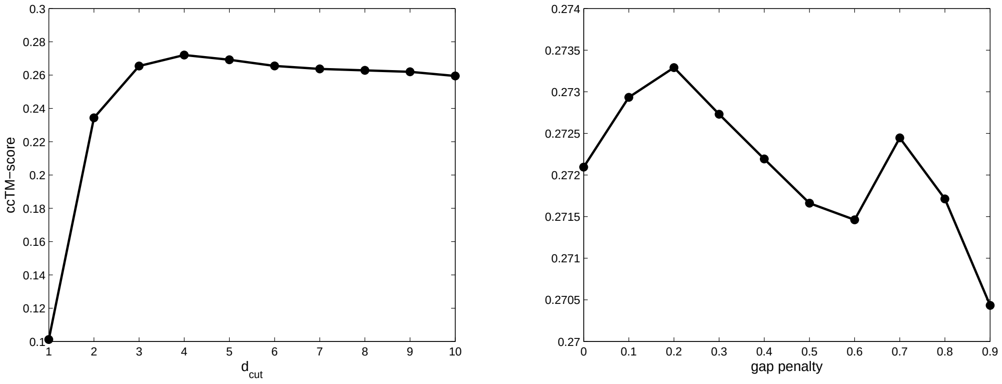

Figure S1. Selection of the optimal values for d_{cut} and gap penalty. The experiments were done on 50% randomly selected groups from the SABmark_twi dataset. The gap penalty on the left panel is 0 and the d_{cut} on the right panel is 4.

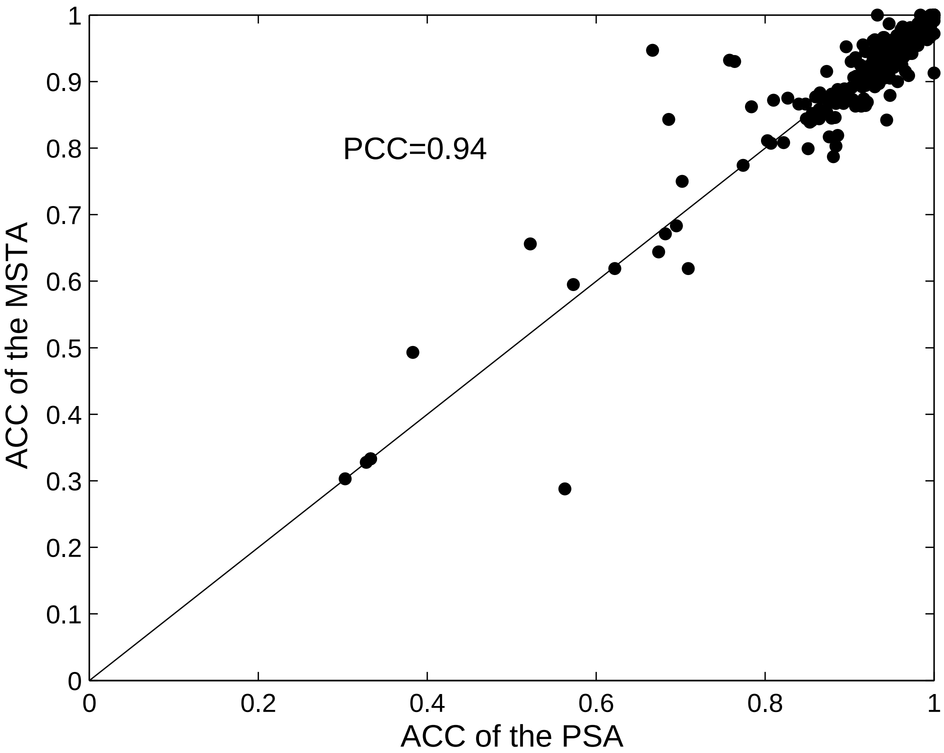

Figure S2. The correlation between the accuracy of the PSA and the MSTA. The data used in this figure are available in Table S5.

Table S1. The influence of TM-score normalization. TM-score_s/TM-score_b is the mean TM-score normalized by the size of the smaller/bigger protein. ccTM-score_s and ccTM-score_b are the mean common core TM-scores of the corresponding MSTA.

Dataset	HOMSTRAD	SABmark_sup	SABmark_twi	SISY-multiple
Number of groups	398	425	209	86
Mean length difference	17.5	34.1	43.4	65.2
Pairwise TM-score_s	0.810	0.683	0.575	0.692
Pairwise TM-score_b	0.756	0.597	0.476	0.571
No. of different trees	176	280	152	57
ccTM-score_s	0.674	0.426	0.273	0.422
ccTM-score_b	0.673	0.425	0.272	0.418

Table S2. The comparison of the mTM-align results for different parameter optimization methods. The numbers before and after '/' are for the optimization with ccTM-score and ACC, respectively. The best results are highlighted in bold type.

Metrics	HOMSTRAD	SABmark_sup	SABmark_twi	SISY-multiple
ACC	0.934/**0.946**	NA	NA	NA
L_{core}	**146.6**/142.6	**72.9**/68.9	**38.1**/35	**80.5**/76.5
ccRMSD	1.3/**1.29**	1.43/**1.4**	1.39/**1.32**	**1.33**/1.33
ccTM-score	**0.674**/0.659	**0.426**/0.407	**0.273**/0.255	**0.422**/0.405
L_{ali}	**173.8**/171.7	**112.9**/110.7	**76.1**/74.5	**135.5**/133
RMSD	**1.46**/1.48	**1.8**/1.84	**2.04**/2.08	**1.74**/1.79
TM-score	**0.784**/0.775	**0.627**/0.616	**0.486**/0.476	**0.629**/0.619

Table S3. The impact of PSA to mTM-align. Def. represents the default alignment from TM-align. The best results are highlighted in bold type.

Dataset	Metrics	Def	IA1	IA2	IA3	IA4	IA5
HOMSTRAD	TM-score of the PSAs	**0.81**	0.805	0.805	0.81	0.799	0.796
	ccTM-score of the MSTAs	**0.674**	0.669	0.666	0.673	0.664	0.66
	TM-score of the MSTAs	**0.784**	0.78	0.778	0.783	0.776	0.775
SABmark_sup	TM-score of the PSAs	**0.683**	0.664	0.662	0.679	0.666	0.646
	ccTM-score of the MSTAs	**0.426**	0.407	0.402	0.42	0.408	0.388
	TM-score of the MSTAs	**0.627**	0.611	0.611	0.623	0.612	0.597
SABmark_twi	TM-score of the PSAs	**0.575**	0.54	0.536	0.566	0.554	0.52
	ccTM-score of the MSTAs	**0.273**	0.246	0.233	0.267	0.249	0.227
	TM-score of the MSTAs	**0.486**	0.456	0.447	0.478	0.466	0.436
SISY-multiple	TM-score of the PSAs	**0.692**	0.669	0.665	0.685	0.672	0.637
	ccTM-score of the MSTAs	**0.422**	0.378	0.361	0.405	0.403	0.36
	TM-score of the MSTAs	**0.629**	0.596	0.591	0.620	0.616	0.581

Table S4. The impact of phylogenetic tree to mTM-align. The best results are highlighted in bold type.

Dataset	Metrics	UPGMA	NJ	Random
HOMSTRAD	ccTM-score of the MSTAs	**0.674**	0.669	0.668
	TM-score of the MSTAs	**0.784**	0.782	0.781
SABmark_sup	ccTM-score of the MSTAs	**0.426**	0.416	0.415
	TM-score of the MSTAs	**0.627**	0.620	0.620
SABmark_twi	ccTM-score of the MSTAs	**0.273**	0.265	0.262
	TM-score of the MSTAs	**0.486**	0.477	0.476
SISY-multiple	ccTM-score of the MSTAs	**0.422**	0.419	0.414
	TM-score of the MSTAs	**0.629**	0.627	0.622

Table S5. The accuracy of the PSA and the MSTA on the HOMSTRAD dataset. These are the data used to draw Figure S2.

Family name	PSA	MSTA
ATPase family associated with various cellular activities (AAA)	0.849	0.844
bacterial extracellular solute-binding proteins, family 3	0.881	0.787
amino acid dehydrogenase	0.966	0.915
aminotransferases class-I	0.956	0.952
ABC transporter	0.883	0.846
alpha beta-hydrolase	0.965	0.957
Acetyltransferase (GNAT) family	0.967	0.971
Histidine acid phosphatase	0.959	0.936
4'-phosphopantetheinyl transferase superfamily	0.907	0.936
actin/heat-shock cognate	0.962	0.940
Adenovirus fiber protein head domain (knob domain)	0.977	0.973
Adenylosuccinate synthetase	0.998	0.994
actin-depolymerizing proteins	0.992	0.987
alcohol dehydrogenase	0.998	0.996
nucleotide kinase	0.948	0.931
AhpC/TSA family	0.989	0.982
albumin	0.899	0.876
Aldehyde oxidase and xanthine dehydrogenase, domains 1-2	0.988	0.989
Aldehyde oxidase and xanthine dehydrogenase, domains 3-4	0.971	0.969
Aldehyde dehydrogenase	0.986	0.974
fructose-1,6-bisphosphate aldolase	0.985	0.979
aldo/keto reductase	0.982	0.978
Alpha amylase, catalytic domain	0.953	0.945
Alpha amylase, C-terminal domain	0.886	0.888
Alpha amylase, catalytic and C-terminal domains	0.929	0.924
ankyrin repeats	0.985	0.988
annexin	0.994	0.983
Antifreeze protein	0.995	0.995
AP endonuclease family 2	0.893	0.867
bacterial exopeptidases	0.928	0.961
Armadillo/beta-catenin-like repeats	0.333	0.333
aspartic proteinase	0.975	0.964
Asp/Glu/Hydontoin racemase domain	0.827	0.875
tRNA synthetases class II (D and K)	0.963	0.982
ATP-guanido phosphotransferase	0.954	0.945
ATP synthase	0.944	0.842

B domain	0.963	0.963
Bulb-type mannose-specific lectin	1.000	1.000
Bacterial DNA-binding protein	0.974	0.942
Bacterial luciferase	0.947	0.962
Bacteriorhodopsin	0.984	0.992
PQQ enzyme	0.985	0.994
FERM domain (Band 4.1 family), region 2	0.963	0.953
FERM domain (Band 4.1 family), region 1	0.972	0.981
FERM and ERM domains (Band 4.1 family)	0.996	0.983
Apoptosis regulator proteins, Bcl-2 family	0.913	0.925
Clostridial binary toxin A	0.967	0.951
Biotin-requiring enzymes	0.904	0.873
Inhibitor of Apoptosis domain	0.902	0.930
beta-lactamase	0.994	0.982
Metallo-beta-lactamase superfamily	0.935	0.950
serine proteinase inhibitor -- Bowman-Birk-type	0.917	0.874
Bromodomain	0.989	0.992
plant virus coat protein	0.674	0.644
Protein kinase C conserved region 1 (C1) domains (Cysteine-rich domains)	0.978	0.970
Protein kinase C conserved region 2 (CalB)	0.982	0.976
Eukaryotic-type carbonic anhydrase	0.965	0.972
CoA-dependent acetyltransferase	0.944	0.925
carbohydrate binding module family 3	0.979	0.971
carbohydrate binding module family 12	0.966	0.950
Starch binding domain	0.941	0.966
calcium-binding protein -- calmodulin-like	0.383	0.493
CBS domain	0.877	0.870
complement control protein module (SUSHI) (SCR)	0.940	0.944
cadherin	0.958	0.942
Calponin homology domain	0.973	0.948
chorismate binding enzyme	0.990	0.986
chromo (CHRomatin Organization MOdifier domain)	0.873	0.915
Chitin binding domain	0.987	0.985
Citrate synthase	0.973	0.963
cyclin-dependent kinases regulatory subunit	0.945	0.945
Colicin pore forming domain	0.970	0.959
Colicin immunity protein / pyocin immunity protein	0.996	0.996
GMC oxidoreductase	0.948	0.950
Cytochrome C oxidase subunit II	0.979	0.973

Cytochrome c oxidase subunit III	0.987	0.988
zinc carboxypeptidases	0.996	0.995
TCP-1/cpn60 chaperonin family, apical domain	0.933	0.934
Biotin carboxylase/Carbamoyl phosphate synthetase	0.890	0.873
Carbamoyl-phosphate synthase L chain and Phosphoribosylglycinamide synthetase, N-terminal domain	0.851	0.799
beta/gamma crystallins	0.573	0.595
cold-shock DNA-binding domain	0.990	0.985
Copper amine oxidase	0.978	0.975
Plastocyanin-like domain	0.951	0.959
copper-containing nitrite reductase	0.999	1.000
Domain first found in C1r, C1s, uEGF, and bone morphogenetic protein.	0.984	0.990
Cyclin	0.953	0.922
cyclophilin (peptidylprolyl isomerase)	0.982	0.977
Cyclodextrin glycosyltransferase	0.995	0.994
Cyclotide family	0.879	0.881
Papain family cysteine proteinase	0.977	0.971
3C cysteine protease (picornain 3C)	0.947	0.987
Cystathionine synthase	0.992	0.963
cystatin	0.919	0.894
cytochrome-c3	0.962	0.960
cytochrome-c5	0.932	0.912
cytochrome b5	0.970	0.960
cytochrome c	0.986	0.983
cytokine -- granulocyte colony stimulating factor	1.000	1.000
cytochrome c'	0.982	0.983
DAHP synthetase I family	0.969	0.958
Cytidine and deoxycytidylate deaminase zinc-binding region	0.968	0.964
subset of the extended AAA-ATPase domain family including DEAD/DEAH box helicases	0.928	0.933
DEATH domain, found in proteins involved in cell death (apoptosis)	0.914	0.863
dihydrofolate reductase	0.961	0.973
DHH family	0.996	0.996
DHHA2 domain	1.000	1.000
Dihydroorotate dehydrogenase	0.971	0.960
Homologues of snake disintegrins	0.822	0.808
6,7-dimethyl-8-ribityllumazine synthase	0.965	0.961
DNA polymerase III beta subunit	0.970	0.961
DNA polymerase processivity factor	0.865	0.883
DNA polymerase I	0.961	0.930
Double-stranded RNA binding motif	0.945	0.956

ThiS family	0.963	0.950
deoxyuridine 5'-triphosphate nucleotidohydrolase	0.964	0.937
E2 (early) protein, C terminal	0.991	0.991
enoyl-CoA hydratase	0.976	0.973
Elongation factor TS, dimerization domain	0.667	0.947
EF-1 guanine nucleotide exchange domain	0.957	0.900
Elongation factor Tu (EF-Tu), domain 2	0.990	0.992
Elongation factor Tu (EF-Tu), C-terminal domain	1.000	1.000
epidermal growth factor-like domain	0.840	0.866
Laminin-type epidermal growth factor-like domain	0.972	0.972
ENTH domain	0.960	0.928
NAD dependent epimerase/dehydratase family	0.977	0.965
ETS domain	0.930	0.963
Extradiol ring-cleavage dioxygenase	0.985	0.984
Fatty acid binding protein-like	0.980	0.965
FAD linked oxidases, C-terminal domain	0.764	0.930
FAD linked oxidases	0.886	0.819
FAD binding domain	0.904	0.872
Formamidopyrimidine-DNA glycosylase	0.978	0.976
fructose-1,6-bisphosphatase	0.995	0.997
ferredoxin (2Fe-2S)	0.944	0.931
ferredoxin (4Fe-4S)	0.884	0.867
ferritin	1.000	1.000
Fibrinogen beta and gamma chains, C-terminal globular domain	0.977	0.972
Filamin/ABP280 repeat	0.907	0.863
FKBP-type peptidyl-prolyl cis-trans isomerase	0.995	0.995
flavodoxin	0.958	0.953
Fibronectin type 1 domain	0.970	0.909
fibronectin type III domain	0.894	0.889
Fork head domain	0.875	0.870
GAF domain	0.959	0.944
GAL4-like Zn(II)2Cys6 (or C6 zinc) binuclear cluster DNA-binding domain	1.000	1.000
heterotrimeric G proteins - alpha subunit	0.997	0.991
GATA zinc finger	0.884	0.803
Glutamine amidotransferase class-I	0.961	0.978
Glutamine amidotransferases class-II	0.975	0.964
Paralytic/GBP/PSP peptide	0.944	0.944
Gelsolin homology domain	0.955	0.939
glycosyl hydrolase family 1	0.978	0.979

glycosyl hydrolases family 10	0.965	0.962
glycosyl hydrolase family 11	0.979	0.961
glycosyl hydrolase family 14 (beta-amylase)	0.995	0.987
glycosyl hydrolases family 18	0.876	0.817
glycosyl hydrolase family 22 (lysozyme)	0.985	0.975
glycosyl hydrolase family 33 (sialidases or neuraminidases)	0.951	0.937
glycosyl hydrolase family 34 (neuraminidase)	0.981	0.987
glycosyl hydrolase family 5	0.928	0.895
glycosyl hydrolases family 6	0.963	0.971
glycosyl hydrolase family 7	0.985	0.975
Domain containing Gla (gamma-carboxyglutamate) residues	0.948	0.905
glutaminase-asparagainase	0.995	0.994
glutathione S-transferase	0.984	0.972
Glycosyl hydrolases family 18, TIM barrel domain and insertion domain	0.969	0.977
Glycosyl hydrolases family 18, TIM barrel domain	0.977	0.971
Glycosyl hydrolases family 18, insertion domain	0.944	0.912
Glycosyl hydrolases family 2, immunoglobulin-like beta-sandwich domain	0.563	0.288
glyceraldehyde 3-phosphate dehydrogenase	0.977	0.980
glucose permease	0.989	0.991
pyridine nucleotide-disulphide oxidoreductases class-I	0.922	0.923
GTP-binding protein	0.957	0.940
Haloperoxidase	0.948	0.919
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	0.905	0.906
Helicase conserved C-terminal domain	0.853	0.839
Helicase	0.865	0.876
hemopexin-like	0.969	0.978
Bacterial transferase hexapeptide repeats	0.328	0.328
Hexokinase	0.995	0.966
Anticodon binding domain	0.979	0.969
high potential iron-sulfur protein	0.962	0.955
Nucleosome core histone H2A/H2B/H3/H4	0.906	0.895
histocompatibility antigen-binding domain	1.000	1.000
Helix-loop-helix DNA-binding domain	0.758	0.932
Heavy-metal-associated domain	0.958	0.958
HMG (high mobility group) box	0.848	0.866
DNA-binding homeodomain	0.984	0.981
Ligand-binding domain of nuclear hormone receptors	0.955	0.954
hormone receptor (DNA-binding domain)	0.958	0.955
Bacterial regulatory helix-turn-helix proteins, araC family, single structural repeat	0.938	0.917

Huristasin-like	0.908	0.908
isocitrate and isopropylmalate dehydrogenase	0.975	0.950
immunoglobulin domain -- C1 set - constant non immunoglobulin	0.978	0.978
immunoglobulin domain -- C1 set - constant immunoglobulin	0.951	0.938
immunoglobulin domain -- I set	0.929	0.924
tryptophan biosynthesis enzyme	0.866	0.877
immunoglobulin domain -- V set - variable non immunoglobulin	0.946	0.932
immunoglobulin domain -- V set - immunoglobulin heavy chain	0.994	0.988
immunoglobulin domain -- V set - immunoglobulin light chain	0.986	0.979
interleukin 8-like protein	0.860	0.877
Inositol monophosphatase family	0.929	0.936
insulin	0.907	0.902
integrin I-domain	0.975	0.977
interleukin 1-beta-like growth factor	0.941	0.941
invasin	0.948	0.933
Chalcone and stilbene synthases	0.969	0.950
serine proteinase inhibitor -- Kazal-type	0.930	0.946
serine carboxypeptidase	0.952	0.951
Serine/Threonine protein kinases, catalytic domain	0.949	0.919
Kinesin motor, catalytic domain ATPase	0.989	0.984
kringle domain	0.963	0.936
serine proteinase inhibitor -- Kunitz-type	0.930	0.909
Bacterial regulatory proteins, lacI family	0.919	0.864
maltoporin (LamB protein)	0.980	0.969
Laminin G domain	0.927	0.906
lactate/malate dehydrogenase	0.967	0.954
Low-density lipoprotein receptor domain class A	0.880	0.872
Leukocidin (pore-forming toxin)	1.000	1.000
Levivirus coat protein	0.984	0.963
CoA-ligase C-terminal domain	0.997	0.997
Zinc-binding domain present in Lin-11, Isl-1, Mec-3.	0.686	0.843
pancreatic lipase	0.996	0.995
fungal lipase	0.983	0.971
Lipocalin family	0.936	0.925
Low molecular weight phosphatase	0.995	0.998
ribonuclease inhibitor	0.333	0.333
heat-labile enterotoxin/cholera toxin, A subunit	0.993	0.996
heat-labile enterotoxin/cholera toxin, B subunit	0.996	0.984
legume lectin	0.983	0.984

Lumazine binding domain	0.984	0.980
LuxS protein	0.994	0.995
Lyase	0.965	0.944
Methyl-coenzyme M reductase alpha subunit, C-terminal domain	0.996	1.000
Methyl-coenzyme M reductase alpha subunit, N-terminal domain	0.990	0.992
Methyl-coenzyme M reductase alpha subunit	0.993	0.996
Methyl-coenzyme M reductase beta subunit, C-terminal domain	1.000	1.000
Methyl-coenzyme M reductase beta subunit, N-terminal domain	1.000	1.000
Methyl-coenzyme M reductase beta subunit	1.000	1.000
Methyl-coenzyme M reductase gamma subunit	0.997	0.996
acyl-CoA dehydrogenase	0.996	0.995
6-O-methylguanine DNA methyltransferase	0.864	0.844
Class II histocompatibility antigen, alpha chain	0.971	0.976
Class II histocompatibility antigen, beta chain	0.986	0.965
Class II histocompatibility antigen, C-terminal domain	0.984	0.977
Class II histocompatibility antigen, N-terminal domain	0.930	0.892
Macrophage migration inhibitory factor (MIF)	0.994	0.994
muconate lactonizing enzyme-like	0.993	0.979
Cobalamin (vitamin B12)-binding domain	0.856	0.852
Monooxygenase (hydroxylase) regulatory protein	0.695	0.683
lpha plus beta	0.991	0.990
Probable molybdopterin binding domain	0.957	0.950
nitrogenase molybdenum-iron protein, alpha and beta chains	0.962	0.925
Prokaryotic molybdopterin oxidoreductases	0.925	0.912
C-type lectin	0.941	0.905
metallothionein -- alpha-domain	1.000	1.000
metallothionein -- beta-domain	0.810	0.872
Mur ligase family, glutamate ligase domain	0.879	0.845
Myb-like DNA-binding domain	0.915	0.892
antibacterial protein	0.976	0.964
NAD(P)H dehydrogenase (quinone)	0.997	0.997
nucleotide diphosphate kinase	0.995	0.992
short-chain scorpion toxin	0.955	0.955
nerve growth factor	0.973	0.973
Nickel-dependent hydrogenases, large subunit	0.996	0.994
Nitroreductase	0.931	0.921
Nitric oxide synthase, oxygenase domain	0.999	0.998
Nucleotidyltransferase, domain 2	0.959	0.959
Nucleotidyl transferase	0.963	0.970

aminotransferase class-III	0.969	0.969
Pyridoxal-dependent decarboxylase, C-terminal sheet domain	0.981	0.987
Aspartate/ornithine carbamoyltransferase	0.988	0.968
NADH ubiquinone oxidoreductase, 20 Kd subunit	0.995	0.994
P or trefoil or TFF domain	0.984	1.000
cytochrome p450	0.935	0.897
Purple acid phosphatase	0.960	0.964
calcium-binding protein -- parvalbumin-like	0.997	0.996
PAS domain	0.954	0.944
thiamine pyrophosphate enzymes	0.932	0.902
PDZ Domain	0.974	0.961
Pectin/pectate lyase	0.957	0.965
PEP-utilizing enzyme, mobile domain	0.955	0.957
metallopeptidase family M24	0.976	0.975
Assemblin (Peptidase family S21)	0.977	0.967
peroxidase	0.980	0.978
Phosphoglycerate mutase	0.974	0.972
phosphoglycerate kinase	0.948	0.879
PH domain	0.929	0.926
Phage integrase	0.921	0.869
phycocyanin	0.984	0.979
ciliate pheromone	0.931	0.951
phospholipase A2	0.980	0.982
oligosaccharide phosphorylase	0.991	0.991
Pilin (bacterial filament)	0.702	0.750
Pyruvate kinase	0.971	0.942
plant lipid-transfer proteins	0.916	0.955
plant toxin	0.992	0.984
purine nucleoside phosphorylase	0.971	0.954
porin	0.964	0.959
serine proteinase inhibitor -- potato I-type	0.960	0.928
pancreatic hormone	0.303	0.303
inorganic pyrophospatase	0.974	0.976
Prokaryotic/plant carbonic anhydrase	0.972	0.969
profilin	0.979	0.963
Carboxypeptidase activation peptide	0.984	0.980
Proteasome A-type and B-type	0.976	0.968
immunoglobulin-binding domain	0.987	0.987
phosphoribosyltransferase	0.981	0.954

Photosystem I reaction centre subunit IV / PsaE	0.967	0.967
Phosphotyrosine-binding (PTB) domain, phosphotyrosine-interaction (PI) domain	0.952	0.921
protein-tyrosine phosphatase	0.991	0.984
Site-specific recombinases	0.774	0.774
reductases	0.952	0.935
DNA-binding repressor	0.985	0.982
Response regulator receiver domain	0.936	0.910
Regulator of G protein signaling domain	0.964	0.961
Rhodanese-like domain	0.943	0.937
picornavirus coat proteins	0.709	0.619
Ribosomal protein L1p/L10e family	0.807	0.807
Ribosomal protein L6 domain	0.969	0.950
Ribosomal protein L7Ae/L30e/S12e/Gadd45 family	0.924	0.920
Ribosome inactivating protein	0.971	0.967
Ring finger	0.784	0.862
Microbial ribonucleases	1.000	0.997
Ribonuclease HII	0.993	0.997
pancreatic ribonuclease	0.977	0.972
ribonuclease H	0.956	0.969
ribonucleotide-diphosphate reductase	0.965	0.957
Ribosome recycling factor	0.682	0.671
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	0.944	0.931
rubredoxin	1.000	1.000
Ribulose bisphosphate carboxylase large chain, catalytic domain	0.985	0.974
Ribulose bisphosphate carboxylase large chain, N-terminal domain	0.962	0.961
Ribulose bisphosphate carboxylase large chain	0.975	0.972
Ribulose bisphosphate carboxylase, small chain	0.997	0.995
retroviral proteinase	0.963	0.961
S4 domain	1.000	0.913
S-100/ICaBP type calcium binding protein	0.933	1.000
SAP domain	0.947	0.918
Bacterial extracellular solute-binding protein, family 1	0.903	0.891
long-chain scorpion toxin	0.955	0.954
short-chain dehydrogenases/reductases	0.958	0.943
sea anemone toxin	0.855	0.841
serine proteinase -- bacterial	0.985	0.983
serine proteinase - eukaryotic	0.984	0.978
serine proteinase inhibitor -- serpin-type	0.985	0.977
Src homology 2 domains	0.948	0.932

Src homology 3 domains	0.972	0.965
S-lectin	0.989	0.975
Sm protein	0.982	0.979
Cu/Zn superoxide dismutase	0.987	0.989
Fe/Mn superoxide dismutase	0.967	0.959
serine proteinase inhibitor -- squash-type	0.864	0.858
SRF-type transcription factor (DNA-binding and dimerisation domain)	0.967	0.961
Staphylococcal/Streptococcal toxin	0.957	0.950
soybean trypsin inhibitor (Kunitz)	0.969	0.961
subtilase	0.961	0.957
periplasmic binding protein -- sugar	0.958	0.934
Sulfotransferase protein	0.931	0.913
snake venom metalloproteinase	1.000	0.997
TATA-box binding protein, C-terminal domain	0.991	0.975
Transforming growth factor-beta (TGF-beta)	0.943	0.913
Thaumatin	0.980	0.976
thionin	0.963	0.963
thioredoxin	0.622	0.619
IPT/TIG domain	0.997	0.997
Serine protease inhibitors	0.803	0.811
triose phosphate isomerase	0.993	0.990
zinc metalloproteinase, thermolysin-like	0.982	0.983
thymidylate synthase	0.983	0.977
Tobacco mosaic virus coat	0.959	0.950
TNF(Tumor Necrosis Factor) family	0.982	0.970
Toprim domain	0.919	0.945
snake toxin	0.873	0.854
Scorpion short toxin	0.896	0.952
TPR Domain	0.522	0.656
Transketolase, pyridine binding domain	0.951	0.958
Transketolase, C-terminal domain	0.940	0.966
Transketolase, pyridine binding and C-terminal domains	0.964	0.964
Transthyretin (prealbumin)	1.000	0.991
transferrin	0.990	0.969
tRNA synthetases class I (I, L, M and V), catalytic and anticodon-binding domains	0.965	0.950
tRNA synthetases class II (G, H, P and S)	0.959	0.955
Putative tRNA binding domain	0.949	0.938
Cereal trypsin/alpha-amylase inhibitor family	0.920	0.905
Tyrosine kinase, catalytic domain	0.986	0.966

Ubiquitin homologues	1.000	1.000
ubiquitin conjugating enzyme	0.974	0.967
Ubiquinol cytochrome reductase transmembrane region	0.983	0.983
UcrQ family	0.917	0.917
uracil-DNA glycosylase	0.998	0.995
YjgF family	1.000	0.972
WW domain	0.933	0.934
xylose isomerase	0.991	0.989
Yersinia virulence determinant (YopE)	0.957	0.960
YgbB family	0.996	0.996
zinc finger -- CCHH-type	0.942	0.946