Prosite pattern	**Description**
PS00001	N-glycosylation site.
PS00002	Glycosaminoglycan attachment site.
PS00003	Tyrosine sulfation site.
PS00004	cAMP- and cGMP-dependent protein kinase phosphorylation site.
PS00005	Protein kinase C phosphorylation site.
PS00006	Casein kinase II phosphorylation site.
PS00007	Tyrosine kinase phosphorylation site.
PS00008	N-myristoylation site.
PS00009	Amidation site.
PS00012	Phosphopantetheine attachment site.
PS00013	Prokaryotic membrane lipoprotein lipid attachment site.
PS00015	Bipartite nuclear targeting sequence.
PS00016	Cell attachment sequence.
PS00017	ATP/GTP-binding site motif A (P-loop).
PS00018	EF-hand calcium-binding domain.
PS00029	Leucine zipper pattern.
PS00030	Eukaryotic RNA Recognition Motif (RRM) RNP-1 region signature.
PS00037	Myb DNA-binding domain repeat signature 1.
PS00038	Myc-type, 'helix-loop-helix' dimerization domain signature.
PS00061	Short-chain dehydrogenases/reductases family signature.
PS00063	Aldo/keto reductase family putative active site signature.
PS00070	Aldehyde dehydrogenases cysteine active site.
PS00086	Cytochrome P450 cysteine heme-iron ligand signature.
PS00107	Protein kinases ATP-binding region signature.
PS00133	Zinc carboxypeptidases, zinc-binding region 2 signature.
PS00134	Serine proteases, trypsin family, histidine active site.
PS00135	Serine proteases, trypsin family, serine active site.
PS00136	Serine proteases, subtilase family, aspartic acid active site.
PS00139	Eukaryotic thiol (cysteine) proteases cysteine active site.
PS00141	Eukaryotic and viral aspartyl proteases active site.
PS00142	Neutral zinc metallopeptidases, zinc-binding region signature.
PS00178	Aminoacyl-transfer RNA synthetases class-I signature.
PS00190	Cytochrome c family heme-binding site signature.
PS00211	ABC transporters family signature.
PS00213	Lipocalin signature.
PS00215	Mitochondrial energy transfer proteins signature.
PS00216	Sugar transport proteins signature 1.
PS00225	Crystallins beta and gamma 'Greek key' motif signature.
PS00237	G-protein coupled receptors family 1 signature.
PS00290	Immunoglobulins and major histocompatibility complex proteins signature.
PS00294	Prenyl group binding site (CAAX box).
PS00342	Microbodies C-terminal targeting signal.
PS00402	Binding-protein-dependent transport systems inner membrane comp. sign.
PS00430	TonB-dependent receptor proteins signature 1.
PS00435	Peroxidases proximal heme-ligand signature.
PS00589	PTS HPR component serine phosphorylation site signature.
PS00599	Aminotransferases class-II pyridoxal-phosphate attachment site.
PS00626	Regulator of chromosome condensation (RCC1) signature 2.
PS00639	Eukaryotic thiol (cysteine) proteases histidine active site.
PS00678	Trp-Asp (WD) repeats signature.
PS00687	Aldehyde dehydrogenases glutamic acid active site.

PS00867	Carbamoyl-phosphate synthase subdomain signature 2.
PS50099	Proline-rich region profile.
PS50240	Serine proteases, trypsin domain profile.
PS50310	Alanine-rich region profile.
PS50311	Cysteine-rich region profile.
PS50312	Aspartic acid-rich region profile.
PS50313	Glutamic acid-rich region profile.
PS50315	Glycine-rich region profile.
PS50316	Histidine-rich region profile.
PS50317	Isoleucine-rich region profile.
PS50318	Lysine-rich region profile.
PS50321	Asparagine-rich region profile.
PS50322	Glutamine-rich region profile.
PS50323	Arginine-rich region profile.
PS50324	Serine-rich region profile.
PS50325	Threonine-rich region profile.

Number of 4 digit EC numbers
1735
94
1460
1352
1847
1853
1462
1857
1229
44
118
537
614
437
45
395
42
20
38
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128
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83
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