

Supplementary table 3. PRAT motif in prokaryotic proteins

No.	Entry Name	Position	Description
1	<a href="#">ebi:EbC_44000</a>	242..272	bscC; cellulose synthase operon protein C
2	<a href="#">xcc:XCC2930</a>	626..656	yoaA; ATP-dependent helicase
3	<a href="#">xcb:XC_1178</a>	626..656	ATP-dependent helicase
4	<a href="#">xca:xcc-b100_1222</a>	626..656	putative ATP-dependent DNA helicase
5	<a href="#">xtn:FD63_04990</a>	623..653	helicase
6	<a href="#">sml:Smlt0528</a>	709..739	putative NHL repeat protein
7	<a href="#">smt:Smal_0408</a>	135..165	SMP-30/Gluconolactonase/LRE domain protein
8	<a href="#">buj:BurJV3_0430</a>	135..165	NHL repeat containing protein
9	<a href="#">buj:BurJV3_0875</a>	182..212	OmpA/MotB domain protein
10	<a href="#">smz:SMD_0447</a>	94..124	NHL repeat protein
11	<a href="#">smz:SMD_0961</a>	182..212	OmpA domain protein
12	<a href="#">psd:DSC_05750</a>	162..192	thiamine biosynthesis protein
13	<a href="#">psd:DSC_13310</a>	295..325	hemE; uroporphyrinogen decarboxylase
14	<a href="#">psk:U771_21305</a>	212..242	ABC transporter ATP-binding protein
15	<a href="#">slo:Shew_2313</a>	121..151	Fe-S protein assembly chaperone HscA
16	<a href="#">pseo:OM33_08005</a>	368..398	cytochrome C biogenesis protein
17	<a href="#">maq:Maqu_3023</a>	88..118	chaperone DnaJ domain protein
18	<a href="#">mhc:MARHY2962</a>	88..118	cbpA; curved DNA-binding protein, analogue of the DnaJ, co-chaperone of DnaK (Hsp40 family)
19	<a href="#">mad:HP15_2909</a>	93..123	heat shock protein DnaJ domain protein
20	<a href="#">msr:AU15_20210</a>	28..58	hypothetical protein
21	<a href="#">mari:ACP86_04740</a>	88..118	cytochrome C biogenesis protein
22	<a href="#">tvi:Thivi_3349</a>	612..642	DNA helicase, Rad3
23	<a href="#">mpur:MARPU_07805</a>	106..136	methyl-accepting chemotaxis protein
24	<a href="#">aeh:MIg_1232</a>	671..701	putative membrane protein; K07288 uncharacterized membrane protein
25	<a href="#">mpc:Mar181_2354</a>	346..376	porin gram-negative type
26	<a href="#">but:X994_6345</a>	501..531	phage integrase family protein
27	<a href="#">bph:Bphy_2047</a>	247..277	protein of unknown function DUF477
28	<a href="#">bpy:Bphyt_4736</a>	176..206	hypothetical protein
29	<a href="#">bue:BRPE67_ACDS01190</a>	56..86	uncharacterized protein
30	<a href="#">bue:BRPE67_CCDS11140</a>	249..279	uncharacterized protein precursor
31	<a href="#">axy:AXYL_03112</a>	137..167	Tat pathway signal sequence domain protein 15
32	<a href="#">axo:NH44784_041941</a>	241..271	TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins
33	<a href="#">axo:NH44784_053511</a>	29..59	hypothetical protein
34	<a href="#">axn:AX27061_2371</a>	241..271	TonB-dependent receptor
35	<a href="#">axn:AX27061_3580</a>	29..59	hypothetical protein
36	<a href="#">axs:LH59_16440</a>	29..59	hypothetical protein
37	<a href="#">dac:Daci_4352</a>	494..524	multi-sensor hybrid histidine kinase (EC:2.7.13.3)
38	<a href="#">vap:Vapar_4522</a>	513..543	Polypeptide-transport-associated domain protein ShlB-type
39	<a href="#">vap:Vapar_6356</a>	494..524	Polypeptide-transport-associated domain protein ShlB-type
40	<a href="#">vpe:Varpa_2158</a>	512..542	polypeptide-transport-associated domain-containing protein shlB-type

Supplementary table 3. PRAT motif in prokaryotic proteins

41	<a href="#">vpe:Varpa_3931</a>	502..532	polypeptide-transport-associated domain-containing protein shlb-type
42	<a href="#">vpd:VAPA_2c07470</a>	520..550	shlB1; putative hemolysin transporter protein ShlB
43	<a href="#">vpd:VAPA_2c09540</a>	509..539	shlB2; putative hemolysin transporter protein ShlB
44	<a href="#">mpt:Mpe_A1216</a>	148..178	thiamine biosynthesis lipoprotein
45	<a href="#">mms:mma_3616</a>	176..206	apbE; thiamine biosynthesis lipoprotein
46	<a href="#">rge:RGE_07540</a>	179..209	hypothetical protein
47	<a href="#">nis:NIS_1752</a>	66..96	hypothetical protein
48	<a href="#">gur:Gura_2011</a>	143..173	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase, FabA/FabZ
49	<a href="#">gbm:Gbem_1975</a>	184..214	modC-1; molybdate ABC transporter, ATP-binding protein
50	<a href="#">gbm:Gbem_2437</a>	302..332	cell division protein, SpoIID family, putative
51	<a href="#">geo:Geob_3148</a>	143..173	polyketide synthase
52	<a href="#">geb:GM18_2234</a>	184..214	molybdate ABC transporter, ATPase subunit
53	<a href="#">ppd:Ppro_2603</a>	26..56	uncharacterized domain 1
54	<a href="#">dpi:BN4_11679</a>	80..110	hypothetical protein
55	<a href="#">dgg:DGI_1393</a>	450..480	putative multi-sensor hybrid histidine kinase
56	<a href="#">ade:Adeh_0117</a>	34..64	SSU ribosomal protein S18P
57	<a href="#">acp:A2cp1_0135</a>	32..62	ribosomal protein S18
58	<a href="#">ank:Anaek_0124</a>	34..64	rpsR; 30S ribosomal protein S18
59	<a href="#">ank:Anaek_1325</a>	1212..1242	hypothetical protein
60	<a href="#">mym:A176_005302</a>	164..194	Outer membrane vitamin B12 receptor BtuB
61	<a href="#">vin:AKJ08_2310</a>	73..103	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
62	<a href="#">scl:sce9355</a>	1768..1798	cellulose synthase 1 operon protein C
63	<a href="#">scu:SCE1572_23355</a>	125..155	hypothetical protein
64	<a href="#">scu:SCE1572_43460</a>	288..318	hypothetical protein
65	<a href="#">hoh:Hoch_6735</a>	79..109	hypothetical protein
66	<a href="#">hoe:IMCC20628_03022</a>	479..509	pseudouridine synthase family protein (EC:5.4.99.22)
67	<a href="#">rec:RHECIAT_CH0000375</a>	441..471	putative carboxypeptidase-related protein (EC:3.4.16.-)
68	<a href="#">rle:RL0352</a>	441..471	putative exported peptidase
69	<a href="#">rtl:Rleg2_4351</a>	442..472	peptidase S10 serine carboxypeptidase
70	<a href="#">rlg:Rleg_4619</a>	443..473	peptidase S10 serine carboxypeptidase
71	<a href="#">rhl:LPU83_pLPU83d0946</a>	165..195	putative secreted protein
72	<a href="#">mor:MOC_1747</a>	70..100	Catalase (EC:1.11.1.6)
73	<a href="#">rva:Rvan_1086</a>	12..42	hypothetical protein
74	<a href="#">rva:Rvan_2815</a>	12..42	hypothetical protein
75	<a href="#">rli:RLO149_c031200</a>	2437..2467	hypothetical protein
76	<a href="#">malg:MALG_01407</a>	171..201	Precorrin-6x reductase (EC:1.3.1.54)
77	<a href="#">mmr:Mmar10_0227</a>	108..138	PfkB domain protein
78	<a href="#">sphm:G432_09150</a>	141..171	hopanoid biosynthesis associated RND transporter-like protein HpnN
79	<a href="#">ssan:NX02_17690</a>	325..355	hypothetical protein
80	<a href="#">rpm:RSPPHO_03231</a>	3..33	Chemotaxis sensory transducer
81	<a href="#">baco:OXB_0786</a>	582..612	hypothetical protein
82	<a href="#">paeh:H70357_32940</a>	257..287	translation factor
83	<a href="#">lpl:lp_3363</a>	378..408	copB; copper transporting ATPase
84	<a href="#">lpi:JDM1_2696</a>	378..408	copB; copper transporting ATPase
85	<a href="#">lpt:zj316_0024</a>	378..408	copB; Copper transporting ATPase (EC:3.6.3.4)
86	<a href="#">lps:LPST_C2765</a>	378..408	copB; copper transporting ATPase
87	<a href="#">lpr:LBP_cg2691</a>	378..408	copB; Copper transporting ATPase
88	<a href="#">lpz:Lp16_2647</a>	378..408	copper transporting ATPase
89	<a href="#">ljb:SH83_13980</a>	378..408	ATPase
90	<a href="#">sth:STH3159</a>	134..164	conserved domain protein

Supplementary table 3. PRAT motif in prokaryotic proteins

91	<a href="#">mas:Mahau_2082</a>	71..101	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
92	<a href="#">mtu:Rv3313c</a>	221..251	add; adenosine deaminase
93	<a href="#">mtv:RVBD_3313c</a>	221..251	adenosine deaminase Add
94	<a href="#">mra:MRA_3355</a>	221..251	add; adenosine deaminase (EC:3.5.4.4)
95	<a href="#">mf:TBF3G_13344</a>	221..251	adenosine deaminase add (adenosine aminohydrolase)
96	<a href="#">mtb:TBMG_03362</a>	221..251	adenosine deaminase
97	<a href="#">mtk:TBSG_03385</a>	221..251	adenosine deaminase add
98	<a href="#">mtz:TBXG_003342</a>	221..251	adenosine deaminase add
99	<a href="#">mtg:MRGA327_20415</a>	221..251	adenosine deaminase (EC:3.5.4.4)
100	<a href="#">mti:MRGA423_20825</a>	221..251	adenosine deaminase (EC:3.5.4.4)
101	<a href="#">mte:CCDC5079_3062</a>	221..251	adenosine deaminase add
102	<a href="#">mtur:CFBS_3506</a>	221..251	add; adenosine deaminase
103	<a href="#">mtl:CCDC5180_3023</a>	221..251	adenosine deaminase add
104	<a href="#">mto:MTCTRI2_3381</a>	221..251	add; adenosine deaminase
105	<a href="#">mtd:UDA_3313c</a>	221..251	add; hypothetical protein
106	<a href="#">mtn:ERDMAN_3631</a>	221..251	add; adenosine deaminase
107	<a href="#">mtj:J112_17805</a>	221..251	adenosine deaminase (EC:3.5.4.4)
108	<a href="#">mtub:MT7199_3356</a>	221..251	putative ADENOSINE DEAMINASE ADD (ADENOSINE AMINOHYDROLASE) (EC:3.5.4.4)
109	<a href="#">mtuc:J113_23150</a>	219..249	adenosine deaminase (EC:3.5.4.4)
110	<a href="#">mtue:J114_17770</a>	221..251	adenosine deaminase (EC:3.5.4.4)
111	<a href="#">mtx:M943_17125</a>	221..251	adenosine deaminase
112	<a href="#">mtul:TBHG_03250</a>	221..251	adenosine deaminase Add
113	<a href="#">mtut:HKBT1_3493</a>	221..251	add; adenosine deaminase
114	<a href="#">mtuu:HKBT2_3500</a>	221..251	add; adenosine deaminase
115	<a href="#">mtg:HKBS1_3503</a>	221..251	add; adenosine deaminase
116	<a href="#">mbo:Mb3342c</a>	221..251	add; adenosine deaminase (EC:3.5.4.4)
117	<a href="#">mbb:BCG_3379c</a>	221..251	add; adenosine deaminase (EC:3.5.4.4)
118	<a href="#">mbt:JTY_3339</a>	221..251	add_1; adenosine deaminase (EC:3.5.4.4)
119	<a href="#">mbt:JTY_3359</a>	221..251	add_2; adenosine deaminase (EC:3.5.4.4)
120	<a href="#">mbt:JTY_3379</a>	221..251	add_3; adenosine deaminase (EC:3.5.4.4)
121	<a href="#">mbm:BCGMEX_3377c</a>	221..251	add; Adenosine deaminase (EC:3.5.4.4)
122	<a href="#">mbk:K60_034450</a>	221..251	adenosine deaminase add
123	<a href="#">mbx:BCGT_3177</a>	221..251	Adenosine deaminase (EC:3.5.4.4)
124	<a href="#">mbz:LH58_18015</a>	221..251	adenosine deaminase
125	<a href="#">maf:MAF_33250</a>	221..251	add; adenosine deaminase (EC:3.5.4.4)
126	<a href="#">mce:MCAN_33391</a>	221..251	add; putative adenosine deaminase ADD (adenosine aminohydrolase)
127	<a href="#">mcg:BN44_70108</a>	221..251	add; Putative adenosine deaminase Add (adenosine aminohydrolase) (EC:3.5.4.4)
128	<a href="#">mcv:BN43_60332</a>	221..251	add; Putative adenosine deaminase Add (adenosine aminohydrolase) (EC:3.5.4.4)
129	<a href="#">mcx:BN42_41374</a>	221..251	add; Putative adenosine deaminase Add (adenosine aminohydrolase) (EC:3.5.4.4)
130	<a href="#">mcz:BN45_60354</a>	221..251	add; Putative adenosine deaminase Add (adenosine aminohydrolase) (EC:3.5.4.4)
131	<a href="#">mle:ML0700</a>	221..251	add; adenosine deaminase (EC:3.5.4.4)
132	<a href="#">mlb:MLBr_00700</a>	221..251	add; adenosine deaminase
133	<a href="#">mul:MUL_4210</a>	123..153	galE1; UDP-glucose 4-epimerase GalE1
134	<a href="#">mgi:Mflv_3124</a>	73..103	conserved hypothetical protein
135	<a href="#">mgi:Mflv_4841</a>	221..251	adenosine deaminase (EC:3.5.4.4)
136	<a href="#">msp:Mspyr1_24410</a>	73..103	hypothetical protein
137	<a href="#">msp:Mspyr1_42510</a>	221..251	adenosine deaminase (EC:3.5.4.4)
138	<a href="#">mab:MAB_3890c</a>	198..228	Probable histidine kinase response regulator
139	<a href="#">mabb:MASS_3902</a>	198..228	two-component histidine kinase DevS
140	<a href="#">mmv:MYCMA_2153</a>	198..228	histidine kinase

Supplementary table 3. PRAT motif in prokaryotic proteins

141	<a href="#">may:LA62_19745</a>	198..228	histidine kinase
142	<a href="#">mabo:NF82_19480</a>	198..228	histidine kinase
143	<a href="#">mabl:MMASJCM_3907</a>	198..228	putative sensor kinase
144	<a href="#">maz:LA61_19645</a>	198..228	histidine kinase
145	<a href="#">mak:LH56_04740</a>	198..228	histidine kinase
146	<a href="#">mys:NF92_04800</a>	198..228	histidine kinase
147	<a href="#">myc:NF90_04795</a>	198..228	histidine kinase
148	<a href="#">mmi:MMAR_5133</a>	123..153	galE1; UDP-glucose 4-epimerase GalE1
149	<a href="#">mli:MULP_05396</a>	123..153	galE1; UDP-glucose 4-epimerase GalE1 (EC:5.1.3.2)
150	<a href="#">mkn:MKAN_05520</a>	63..93	hypothetical protein
151	<a href="#">mkn:MKAN_20790</a>	221..251	adenosine deaminase
152	<a href="#">mks:LG40_05460</a>	43..73	hypothetical protein
153	<a href="#">mks:LG40_20605</a>	221..251	adenosine deaminase
154	<a href="#">mki:LH54_05465</a>	43..73	hypothetical protein
155	<a href="#">mki:LH54_20720</a>	221..251	adenosine deaminase
156	<a href="#">cik:ik0046</a>	131..161	putative ThiJ/Pfpl family protein
157	<a href="#">car:cauri_0738</a>	131..161	ThiJ/Pfpl family protein
158	<a href="#">ckp:ckrop_2062</a>	114..144	putative ThiJ/Pfpl family protein
159	<a href="#">cii:CIMIT_03240</a>	40..70	oxidoreductase
160	<a href="#">cii:CIMIT_07450</a>	131..161	thiamine biosynthesis protein ThiJ
161	<a href="#">coa:DR71_1702</a>	133..163	DJ-1/Pfpl family protein
162	<a href="#">csx:CSING_04185</a>	131..161	Putative amidotransferase
163	<a href="#">csx:CSING_07665</a>	132..162	tdcG; L-serine dehydratase, iron-sulfur-dependent, single chain form (EC:4.3.1.17)
164	<a href="#">cmv:CMUST_01965</a>	4..34	putative DUF1266 family protein
165	<a href="#">rer:RER_20480</a>	220..250	add; adenosine deaminase (EC:3.5.4.4)
166	<a href="#">rev:Q5Y_09845</a>	220..250	adenosine deaminase (EC:3.5.4.4)
167	<a href="#">reb:XU06_10080</a>	220..250	adenosine deaminase
168	<a href="#">gbr:Gbro_4631</a>	96..126	SNARE associated Golgi protein-like protein
169	<a href="#">srt:Strot_0620</a>	69..99	preprotein translocase subunit SecG
170	<a href="#">src:M271_08210</a>	47..77	hypothetical protein
171	<a href="#">lxx:Lxx18130</a>	476..506	two-component system, sensor protein
172	<a href="#">mim:AKG07_07185</a>	127..157	4-diphosphocytidyl-2C-methyl-D-erythritol kinase (EC:2.7.1.148)
173	<a href="#">mio:AOA12_01215</a>	502..532	cytochrome C biogenesis protein
174	<a href="#">iva:Isova_1057</a>	142..172	hypothetical protein
175	<a href="#">ars:ADJ73_06540</a>	23..53	enoyl reductase
176	<a href="#">ppc:HMPREF9154_2947</a>	281..311	hypothetical protein
177	<a href="#">fre:Franean1_7288</a>	551..581	serine/threonine protein kinase
178	<a href="#">fri:FraEul1c_7136</a>	544..574	serine/threonine protein kinase
179	<a href="#">fal:FRAAL3011</a>	720..750	LuxR family transcriptional regulator
180	<a href="#">bsd:BLASA_3360</a>	43..73	putative Dihydrofolate reductase
181	<a href="#">amd:AMED_4809</a>	157..187	MerR family transcriptional regulator
182	<a href="#">amn:RAM_24480</a>	157..187	MerR family transcriptional regulator
183	<a href="#">amm:AMES_4750</a>	157..187	MerR family transcriptional regulator
184	<a href="#">amz:B737_4750</a>	157..187	MerR family transcriptional regulator
185	<a href="#">kphy:AOZ06_32210</a>	515..545	hypothetical protein
186	<a href="#">afs:AFR_01450</a>	484..514	putative DEAD/DEAH box helicase
187	<a href="#">acq:AM609_06650</a>	132..162	thiamine biosynthesis protein ThiJ
188	<a href="#">rxy:Rxyl_0550</a>	88..118	hypothetical protein
189	<a href="#">gpa:GPA_30220</a>	268..298	hypothetical protein
190	<a href="#">apv:Apar_0409</a>	60..90	transcriptional regulator, LysR family

**Supplementary table 3.** PRAT motif in prokaryotic proteins

191	<a href="#">taz:TREAZ_2244</a>	617..647	peptidase, U32 family
192	<a href="#">gma:Acix8_3091</a>	94..124	cobalamin 5'-phosphate synthase
193	<a href="#">sus:Acid_1225</a>	495..525	NHL repeat containing protein
194	<a href="#">hao:PCC7418_0289</a>	288..318	photosystem I core protein PsaB
195	<a href="#">gei:GEI7407_1208</a>	986..1016	protein of unknown function DUF490
196	<a href="#">arp:NIES39_N00970</a>	158..188	hypothetical protein
197	<a href="#">pgi:PG1715</a>	759..789	hypothetical protein
198	<a href="#">pgn:PGN_0400</a>	798..828	hypothetical protein
199	<a href="#">pgt:PGTDC60_0586</a>	788..818	hypothetical protein
200	<a href="#">afd:Alfi_1149</a>	243..273	Acyl-protein synthetase, LuxE
201	<a href="#">ash:AL1_22280</a>	243..273	Acyl-protein synthetase, LuxE.
202	<a href="#">doi:FH5T_20350</a>	148..178	HupE / UreJ protein
203	<a href="#">hhy:Halhy_2969</a>	198..228	peptidase S8 and S53 subtilisin kexin sedolisin
204	<a href="#">hmu:Hmuk_1595</a>	352..382	oligopeptide/dipeptide ABC transporter, ATPase subunit
205	<a href="#">htu:Htur_5093</a>	223..253	hypothetical protein
206	<a href="#">hah:Halar_3531</a>	264..294	protein of unknown function DUF87