

Supplemental Table S1. List of *P. gingivalis* AOP (Acylpeptidyl oligopeptidase) related proteins

Bacteria	Fungi	Plants
Archaea	Protists	Animals

Orthologs were searched by KEGG SSDB (Sequence Similarity DataBase) with "best-best" and threshold above 400.

Genes described in the text

KEGG Organism cord	Entry	Definition	Length	SW-score (margin)	bits	Identity	Organism	Category	Remarks
pgn	PGN_1349	dipeptidyl aminopeptidase	759			1	Porphyromonas gingivalis ATCC 33277	Bacteroidetes	periodontopathic
pgi	PGI004	prolyl oligopeptidase	759	4986 (4544)	1142	0.997	Porphyromonas gingivalis W83	Bacteroidetes	periodontopathic
pgt	PGTDC60_0926	putative dipeptidyl aminopeptidase	744	4892 (4447)	1121	0.996	Porphyromonas gingivalis TDC60	Bacteroidetes	periodontopathic
cao	Celal_0665	dipeptidyl aminopeptidase	753	3355 (-)	771	0.628	Cellulophaga algicola	Bacteroidetes, Flavobacteriaceae	isolated from the surfaces of Antarctic algae sea-ice-derived psychrophilic bacterium, synthesize the polyunsaturated fatty acids eicosapentaenoic acid (20:5 omega 3) and arachidonic acid (20:4 omega 6)
ptq	P700755_000784	amino/aminoacylpeptidase, esterase	756	3272 (2379)	752	0.612	Psychroflexus torquus	Bacteroidetes	
gfo	GFO_3212	prolyl oligopeptidase	765	2988 (2067)	687	0.566	Gramella forsetii	Bacteroidetes	marine heterotrophic bacterioplankton
asl	Aeqsu_1292	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	756	2936 (1982)	675	0.563	Aequorivita sublithincola	Bacteroidetes	isolated from Antarctic winter sea water, sea-ice algal assemblages and quartz stone subliths
zpr	ZPR_0124	prolyl oligopeptidase	720	2917 (-)	671	0.577	Zunongwangia profunda	Bacteroidetes, Flavobacteriaceae	aerobic, deep-sea bacterium
opi	Cpin_5159	peptidase S9 prolyl oligopeptidase active site domain protein	666	2768 (2309)	637	0.616	Chitinophaga pinensis	Bacteroidetes, Chitinophagaceae	degraded gelatin, cellulose and chitin, vary in shape between filaments and spherical bodies
kdi	Krodi_1034	secreted prolyl oligopeptidase family pr	678	2700 (-)	621	0.564	Krokinobacter sp. 4H-3-7-5	Bacteroidetes	isolated from subseafloor sediments at Suruga Bay (Japan), degrading complex polymeric substrates in marine habitats
ash	AL1_11090	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	643	1763 (-)	408	0.437	Alistipes shahii	Bacteroidetes	strictly anaerobic
lgy	T479_19275	peptidase	758	1749 (1021)	405	0.449	Lysinibacillus sp. GY32	Firmicutes - Bacilli	Bacillus subtilis lysine
sbr	SY1_01710	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	636	1753 (1333)	405	0.436	Freitibacterium fastidiosum	Synergistetes	isolated from the human mouth
dat	HRM2_48810	putative dipeptidyl aminopeptidase	638	1737 (-)	402	0.437	Desulfobacterium autotrophicum	Deltaproteobacteria	Desulfobacteraceae, strictly anaerobe, mesophilic sulfate-reducing bacterium
sgn	SGRA_1238	putative dipeptidyl aminopeptidase	644	1727 (-)	400	0.42	Saprosira grandis	Bacteroidetes	coastal marine bacterium that can capture and prey upon other marine bacteria using a mechanism known as 'ixotrophy'
tped	TPE_2272	peptidase S9 prolyl oligopeptidase active site domain protein	634	1720 (-)	398	0.435	Treponema pedis	Spirochaetes	Bovine digital dermatitis
afd	Alfi_1272	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	643	1704 (-)	394	0.423	Alistipes finegoldii	Bacteroidetes	isolated from appendiceal tissue samples in children with acute appendicitis and from perirectal and brain abscess material
lsp	Bsph_0460	dipeptidyl peptidase	756	1690 (-)	391	0.441	Lysinibacillus sphaericus	Firmicutes - Bacilli	formerly known as Bacillus sphaericus, insect pathogen
cvi	CV_1270	dipeptidyl aminopeptidase	634	1675 (-)	388	0.426	Chromobacterium violaceum	Betaproteobacteria	part of the normal flora of water and soil of tropical and sub-tropical regions
aco	Amico_1880	peptidase S9 prolyl oligopeptidase active site domain protein	636	1650 (-)	382	0.426	Aminobacterium colombiense	Synergistetes	strictly anaerobic, grow by fermentation of a limited range of amino acids but not carbohydrates
bpy	Bphyt_6730	peptidase S9 prolyl oligopeptidase active site domain protein	632	1644 (-)	381	0.407	Burkholderia phytofirmans	Betaproteobacteria	plant-associated bacterium with plant-beneficial properties
vca	M892_18080	peptidase	655	1637 (803)	379	0.423	Vibrio campbellii	Gammaproteobacteria - Others	an emerging pathogen in aquatic organisms
vha	VIBHAR_06914	prolyl oligopeptidase	655	1637 (803)	379	0.423	Vibrio harveyi	Gammaproteobacteria - Others	natural inhabitant of seawater
bbe	BBR47_36510	peptidase precursor	779	1612 (990)	373	0.417	Brevibacillus brevis	Firmicutes - Bacilli	G(+), aerobic, spore-forming bacillus
vex	VEA_000910	peptidase	640	1601 (-)	371	0.413	Vibrio sp. Ex25	Gammaproteobacteria - Others	
bgd	bgla_2g13570	peptidase S9	630	1594 (-)	369	0.411	Burkholderia gladioli	Betaproteobacteria	a plant pathogen, involved in human infections, especially in patients with cystic fibrosis
dsa	Desal_2454	peptidase S9 prolyl oligopeptidase active site domain protein	642	1595 (-)	369	0.414	Desulfovibrio salexigens	Deltaproteobacteria	anaerobic, marine sulfate reducer
bho	D560_2792	alpha/beta hydrolase fold family protein	638	1567 (-)	363	0.405	Bordetella holmesii	Betaproteobacteria	invasive infections (bacteraemia, meningitis, endocarditis, pericarditis, pneumonia, and arthritis) and pertussis-like symptoms
bav	BAV2037	peptidase	642	1564 (-)	362	0.405	Bordetella avium	Betaproteobacteria	
bgj	bgli_2g13370	peptidase S9 prolyl oligopeptidase active site domain protein	632	1563 (-)	362	0.405	Burkholderia glumae	Betaproteobacteria	
dhy	DESAM_22595	peptidase S9 prolyl oligopeptidase active site domain protein	646	1562 (-)	362	0.405	Desulfovibrio hydrothermalis	Deltaproteobacteria	
glo	Glov_2643	peptidase S9 prolyl oligopeptidase active site domain protein	644	1555 (-)	360	0.402	Geobacter lovleyi	Deltaproteobacteria	
bbh	BN112_0898	peptidase	637	1541 (-)	357	0.391	Bordetella bronchiseptica 253	Betaproteobacteria	
bpa	BPP1632	peptidase	637	1541 (-)	357	0.391	Bordetella parapertussis 12822	Betaproteobacteria	
bpc	BPTD_0902	putative peptidase	637	1541 (-)	357	0.391	Bordetella pertussis CS	Betaproteobacteria	pertussis
dac	Daci_1350	peptidase S9 prolyl oligopeptidase active site domain protein	655	1539 (-)	357	0.396	Delftia acidovorans	Betaproteobacteria	
axn	AX27061_2140	putative peptidase	639	1533 (-)	355	0.402	Achromobacter xylosoxidans NBRC 15126 = ATCC 27061	Betaproteobacteria	community-acquired pneumonia and bacteremia
siv	SSIL_0535	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	752	1527 (831)	354	0.408	Solibacillus silvestris	Firmicutes - Bacilli	
del	DelCs14_5163	peptidase S9 prolyl oligopeptidase	639	1514 (-)	351	0.405	Delftia sp. Cs1-4	Betaproteobacteria	
rge	RGE_14610	peptidase S9C family protein	652	1484 (853)	344	0.382	Rubrivivax gelatinosus	Betaproteobacteria	
bpt	Bpet2621	peptidase	623	1479 (-)	343	0.385	Bordetella petrii	Betaproteobacteria	
put	PT7_1170	peptidase	618	1468 (-)	340	0.397	Pusillimonas sp. T7-7	Betaproteobacteria	
scn	Solca_3344	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	628	1466 (-)	340	0.370	Solitalea canadensis	Bacteroidetes	greenhouse soil
glj	GKIL_3505	peptidase S9 prolyl oligopeptidase	651	1388 (127)	322	0.376	Gloeobacter sp. JS	Cyanobacteria	

riv	Riv7116_2074	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	698	1379 (777)	320	0.389	Rivularia sp. PCC 7116	Cyanobacteria	
plp	Ple7327_1527	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	631	1349 (918)	313	0.374	Pleurocapsa sp. PCC 7327	Cyanobacteria	
dsf	Dacsa_2858	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	633	1339 (-)	311	0.369	Dactylococcopsis salina	Cyanobacteria	
pbs	Plabr_3043	peptidase S9 prolyl oligopeptidase activ	686	1338 (-)	311	0.375	Planctomyces brasiliensis	Planctomycetes	
hao	PCC7418_0724	peptidase S9 prolyl oligopeptidase	633	1330 (901)	309	0.365	Halothece sp. PCC 7418	Cyanobacteria	
amr	AM1_4305	dipeptidyl aminopeptidase family protein	675	1300 (-)	302	0.385	Acaryochloris marina	Cyanobacteria	
gvi	glr0581	acylamino acid-releasing enzyme	668	1293 (671)	301	0.363	Gloeobacter violaceus	Cyanobacteria	
hoh	Hoch_3201	peptidase S9 prolyl oligopeptidase active site domain protein	924	1295 (455)	301	0.378	Haliangium ochraceum	Deltaproteobacteria	
ter	Tery_2052	peptidase S9, prolyl oligopeptidase activ	630	1291 (878)	300	0.361	Trichodesmium erythraeum	Cyanobacteria	
mic	Mic7113_1845	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	633	1270 (844)	295	0.344	Microcoleus sp. PCC 7113	Cyanobacteria	
npu	Npun_F0933	peptidase S9 prolyl oligopeptidase (EC:3.4.19.1)	628	1270 (844)	295	0.358	Nostoc punctiforme	Cyanobacteria	
glp	Glo7428_0294	peptidase S9 prolyl oligopeptidase	632	1245 (-)	290	0.352	Gloeocapsa sp. PCC 7428	Cyanobacteria	
rmr	Rmar_2049	peptidase S9 prolyl oligopeptidase active site domain protein	907	1241 (-)	289	0.352	Rhodothermus marinus DSM 4252	Bacteroidetes	
pcu	pc0225	hypothetical protein	649	1237 (-)	288	0.349	Candidatus Protochlamydia amoebophila	Chlamydiae	
rmg	Rhom172_0817	peptidase S9 prolyl oligopeptidase active site domain protein	907	1232 (-)	287	0.353	Rhodothermus marinus SG0.5JP17-172	Bacteroidetes	
cthe	Chro_4292	peptidase S9 prolyl oligopeptidase	633	1223 (-)	285	0.344	Chroococcidiopsis thermalis	Cyanobacteria	
oni	Osc7112_2337	peptidase S9 prolyl oligopeptidase	637	1224 (768)	285	0.345	Oscillatoria nigro-viridis	Cyanobacteria	
opr	Ocepr_0153	peptidase S9 prolyl oligopeptidase active site domain protein	603	1218 (708)	283	0.340	Oceanithermus profundus	Deinococcus-Thermus	
shg	Sph21_1568	peptidase S9 prolyl oligopeptidase active site domain protein	628	1205 (749)	281	0.330	Sphingobacterium sp. 21	Bacteroidetes	
ctm	Cabther_A1198	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	909	1203 (701)	280	0.360	Candidatus Chloracidobacterium thermophilum B	Acidobacteria	inhabits microbial mats of alkaline siliceous hot springs
aba	Acid345_1930	peptidase S9, prolyl oligopeptidase	646	1189 (694)	277	0.330	Candidatus Koribacter versatilis	Acidobacteria	
mgj	Mflv_4393	peptidase S9 prolyl oligopeptidase	626	1184 (761)	276	0.331	Mycobacterium gilvum PYR-GCK	Actinobacteria	
msp	Mspyr1_37430	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	626	1186 (766)	276	0.329	Mycobacterium gilvum Spyr1	Actinobacteria	utilize a wide range of PAH substrates as sole sources of carbon and energy
msd	MYST1_01603	S9C family peptidase	660	1179 (533)	275	0.345	Myxococcus stipitatus	Deltaproteobacteria	
nda	Ndas_1266	peptidase S9 prolyl oligopeptidase active site domain protein	631	1181 (73)	275	0.348	Nocardiosis dassonvillei	Actinobacteria	
acm	Acix9_4597	prolyl oligopeptidase	611	1177 (18)	274	0.360	Granulicella tudricola	Acidobacteria	
mne	D174_22515	peptidase	625	1172 (-)	273	0.336	Mycobacterium neoaurum	Actinobacteria	
nbr	O3l_007365	hypothetical protein	638	1171 (-)	273	0.343	Nocardia brasiliensis	Actinobacteria	
phe	Phep_0365	peptidase S9 prolyl oligopeptidase active site domain protein	632	1173 (-)	273	0.323	Pedobacter heparinus	Bacteroidetes	
acr	Acry_0766	peptidase S9 prolyl oligopeptidase	641	1162 (-)	271	0.344	Acidiphilium cryptum	Alphaproteobacteria	
sro	Sros_8147	hypothetical protein	634	1164 (687)	271	0.348	Streptosporangium roseum	Actinobacteria	
tkm	TK90_1646	peptidase S9 prolyl oligopeptidase active site domain protein	705	1165 (-)	271	0.333	Thioalkalivibrio sp. K90mix	Gammaproteobacteria - Others	
amv	ACMV_11060	putative peptidase S9	641	1160 (-)	270	0.344	Acidiphilium multivorum	Alphaproteobacteria	
mabb	MASS_4758	peptidase S9 prolyl oligopeptidase active site domain protein	622	1159 (-)	270	0.343	Mycobacterium abscessus subsp. bolletii 5051	Actinobacteria	
rce	RC1_4088	dipeptidyl aminopeptidase (EC:3.4.-.-)	682	1158 (624)	270	0.348	Rhodospirillum centenum	Alphaproteobacteria	
afw	Anae109_0952	peptidase S9 prolyl oligopeptidase	706	1154 (636)	269	0.347	Anaeromyxobacter sp. Fw109-5	Deltaproteobacteria	
mab	MAB_4725	Probable peptidase	622	1149 (-)	268	0.339	Mycobacterium abscessus ATCC 19977	Actinobacteria	
tni	TVNIR_3664	putative peptidase	672	1150 (-)	268	0.329	Thioalkalivibrio nitratireducens	Gammaproteobacteria - Others	
tpr	Tpau_1353	peptidase S9 prolyl oligopeptidase active site domain protein	629	1150 (-)	268	0.329	Tsakumurella paurometabola	Actinobacteria	
tps	THAPSDRAFT_8	hypothetical protein	715	1144 (727)	267	0.350	Thalassiosira pseudonana	Protists	marine centric diatom
gma	Acix8_0700	peptidase S9 prolyl oligopeptidase	680	1135 (734)	265	0.347	Granulicella mallensis	Actinobacteria	
salb	XNR_2671	Peptidase S9	629	1137 (737)	265	0.342	Streptomyces albus	Actinobacteria	
msg	MSME1_5371	peptidase S9 prolyl oligopeptidase active site domain protein	617	1133 (723)	264	0.324	Mycobacterium smegmatis MC2 155	Actinobacteria	
mva	Mvan_5922	peptidase S9 prolyl oligopeptidase	626	1131 (712)	264	0.332	Mycobacterium vanbaalenii	Actinobacteria	
ote	Oter_0706	peptidase S9 prolyl oligopeptidase	656	1133 (72)	264	0.335	Opitutus terrae	Verrucomicrobia	
gba	J421_5769	peptidase S9 prolyl oligopeptidase	626	1126 (673)	263	0.325	Gemmatimonadetes bacterium KBS708	Gemmatimonadetes	
rcm	AIE_03175	acylamino-acid-releasing enzyme	679	1130 (-)	263	0.337	Rickettsia canadensis McKiel	Alphaproteobacteria	
gsl	Gasu_08620	acylamino-acid-releasing enzyme isoform	643	1105 (54)	258	0.339	Idiomarina loihiensis GSL 199	Gammaproteobacteria - Others	
ssx	SACTE_5529	peptidase S9 prolyl oligopeptidase active site domain protein	629	1105 (697)	258	0.333	Streptomyces sp. SirexAA-E	Actinobacteria	
msl	Msil_1886	peptidase S9 prolyl oligopeptidase active site domain protein	636	1101 (-)	257	0.339	Methylocella silvestris	Alphaproteobacteria	
mhi	Mhar_2099	putative aminopeptidase	684	1093 (-)	255	0.322	Methanoseta harundinacea	Euryarchaeota	acetate-scavenging methanogen
psn	Pedsa_2606	peptidase S9 prolyl oligopeptidase active site domain protein	639	1091 (-)	255	0.308	Pedobacter saltans	Bacteroidetes, Sphingobacteria	
ram	MCE_03915	acylamino-acid-releasing protein	678	1076 (-)	251	0.333	Candidatus Rickettsia amblyommii	Alphaproteobacteria	
ilo	IL1172	secreted dipeptidyl aminopeptidase	649	1072 (582)	250	0.321	Idiomarina loihiensis L2TR	Gammaproteobacteria - Others	
rbo	AI1_01085	acylamino acid-releasing protein	678	1073 (176)	250	0.336	Rickettsia bellii OSU 85-389	Alphaproteobacteria	
rms	RMA_0618	acylamino-acid-releasing protein	678	1069 (-)	250	0.332	Rickettsia massiliae MTU5	Alphaproteobacteria	
rpp	MCI_03405	acylamino acid-releasing protein	676	1071 (-)	250	0.330	Rickettsia parkeri	Alphaproteobacteria	
tra	Trad_0952	peptidase S9 prolyl oligopeptidase active site domain protein	648	1070 (-)	250	0.330	Truepera radiovictrix	Deinococcus-Thermus	
ngd	NGA_0474200	peptidase S9 prolyl oligopeptidase	766	1066 (-)	249	0.324	Nannochloropsis gaditana	Eukaryota:Chromalveolata	alga
raf	RAF_ORF0563	Acylamino-acid-releasing enzyme	676	1066 (-)	249	0.332	Rickettsia africana	Alphaproteobacteria	
rco	RC0603	acylamino acid-releasing enzyme	676	1068 (-)	249	0.330	Rickettsia conorii	Alphaproteobacteria	Boutonnuise fever
rpk	RPR_00630	acylamino-acid-releasing enzyme	682	1066 (-)	249	0.329	Rickettsia peacockii	Alphaproteobacteria	
rsv	Rsl_701	Acylamino-acid-releasing enzyme	676	1068 (-)	249	0.330	Rickettsia slovacica 13-B	Alphaproteobacteria	
xax	XACM_0248	dipeptidyl aminopeptidase	694	1066 (240)	249	0.325	Xanthomonas axonopodis pv. citrumelo F1	Gammaproteobacteria - Others	citrus canker disease

rak	A1C_03230	acylamino-acid-releasing protein	678	1062 (-)	248	0.331	Rickettsia akari	Alphaproteobacteria	
rau	MC5_04845	acylamino-acid-releasing protein	678	1061 (-)	248	0.334	Rickettsia australis	Alphaproteobacteria	
rfe	RF_0667	acylamino acid-releasing protein	678	1062 (-)	248	0.329	Rickettsia felis	Alphaproteobacteria	
rmi	RMB_05005	acylamino-acid-releasing protein	697	1061 (-)	248	0.333	Rickettsia massiliae AZT80	Alphaproteobacteria	
rph	RSA_03345	acylamino-acid-releasing enzyme	676	1062 (-)	248	0.329	Rickettsia philipii	Alphaproteobacteria	
rrj	Rl0wa_0719	acylamino-acid-releasing enzyme (EC:3.4.19.1)	676	1062 (-)	248	0.329	Rickettsia rickettsii Iowa	Alphaproteobacteria	Rocky Mountain spotted fever
nal	B005_4419	alpha/beta hydrolase fold family protein	634	1060 (656)	247	0.308	Nocardiopsis alba	Actinobacteria	
rbe	RBE_1233	acylamino acid-releasing protein	678	1059 (169)	247	0.334	Rickettsia bellii RML369-C	Alphaproteobacteria	
rhe	Rh054_03400	acylamino-acid-releasing protein	678	1057 (-)	247	0.325	Rickettsia heilongjiangensis	Alphaproteobacteria	
rja	RJP_0467	acylamino-acid-releasing enzyme	678	1058 (-)	247	0.325	Rickettsia japonica	Alphaproteobacteria	
rmo	MCL_00120	acylamino-acid-releasing protein	678	1056 (-)	247	0.327	Rickettsia montanensis	Alphaproteobacteria	
rre	MCC_03930	acylamino-acid-releasing protein	678	1060 (-)	247	0.330	Rickettsia rhipicephali	Alphaproteobacteria	
sen	SACE_2791	peptidase S9, prolyl oligopeptidase	627	1057 (521)	247	0.322	Saccharopolyspora erythraea	Actinobacteria	
cse	Cseg_1265	peptidase S9	679	1052 (331)	246	0.325	Caulobacter segnis	Alphaproteobacteria	
mcj	MCON_0004	acylamino-acid-releasing enzyme (EC:3.4.14.-)	694	1053 (-)	246	0.320	Methanoseta concilii	Euryarchaeota	obligately anaerobic, gram-negative, nonmotile rods
mrd	Mrad2831_4772	peptidase S9 prolyl oligopeptidase	632	1055 (-)	246	0.328	Methylobacterium radiotolerans	Alphaproteobacteria	
fbf	Fbal_2218	peptidase S9 prolyl oligopeptidase active site domain protein	678	1050 (75)	245	0.314	Ferrimonas balearica	Gammaproteobacteria - Others	
sse	Ssed_0476	peptidase S9 prolyl oligopeptidase	688	1047 (114)	245	0.316	Shewanella sediminis	Gammaproteobacteria - Others	
xcb	XC_0253	dipeptidyl aminopeptidase	697	1048 (297)	245	0.318	Xanthomonas campestris pv. campestris 8004	Gammaproteobacteria - Others	
swd	Swoo_4483	peptidase S9 prolyl oligopeptidase	682	1045 (46)	244	0.322	Shewanella woodyi	Gammaproteobacteria - Others	
mmn	midl_01208	dipeptidyl aminopeptidases/acylaminoacyl-peptidasepeptidase	639	1039 (-)	243	0.313	Candidatus Midichloria mitochondrii	Alphaproteobacteria	
psl	Psta_4769	peptidase S9 prolyl oligopeptidase active site domain protein	707	1041 (440)	243	0.319	Pirellula staleyi	Firmicutes - Bacilli	
xcj	XCAW_00662	Dipeptidyl aminopeptidase	694	1039 (221)	243	0.321	Xanthomonas citri	Gammaproteobacteria - Others	
xom	XOO_4120	dipeptidyl aminopeptidase	694	1041 (255)	243	0.321	Xanthomonas oryzae pv. oryzae MAFF311018	Gammaproteobacteria - Others	causing a serious blight of rice
eli	ELI_01715	dipeptidyl aminopeptidase	654	1037 (356)	242	0.327	Erythrobacter litoralis	Alphaproteobacteria	
mpo	Mpop_0377	peptidase S9 prolyl oligopeptidase active site domain protein	626	1036 (-)	242	0.320	Methylobacterium populi	Alphaproteobacteria	
pat	Patl_1803	peptidase S9, prolyl oligopeptidase activ	731	1030 (433)	241	0.307	Pseudoalteromonas atlantica	Gammaproteobacteria - Others	
mex	Mext_0301	peptidase S9 prolyl oligopeptidase	626	1027 (-)	240	0.319	Methylobacterium extorquens PA1	Alphaproteobacteria	
ppp	PHYPADRAFT_1	hypothetical protein	659	1027 (-)	240	0.311	Physcomitrella patens subsp. patens	Mosses	model organism
shn	Shewana3_0482	peptidase S9 prolyl oligopeptidase	686	1021 (121)	239	0.302	Shewanella sp. ANA-3	Gammaproteobacteria - Others	
bba	Bd2519	dipeptidyl aminopeptidase	659	1001 (-)	234	0.310	Bdellovibrio bacteriovorus HD100	Deltaproteobacteria	
scu	SCE1572_37960	peptidase S9	704	1000 (446)	234	0.311	Sorangium cellulosum So0157-2	Deltaproteobacteria	
gag	Glaag_1786	peptidase S9, prolyl oligopeptidase acti	689	995 (76)	233	0.302	Glaciicola sp. 4H-3-7+YE-5	Gammaproteobacteria - Others	
scl	sce6409	peptidase	712	995 (467)	233	0.316	Sorangium cellulosum So ce 56	Deltaproteobacteria	
aaa	Acav_2279	hypothetical protein	935	994 (-)	232	0.311	Acidovorax avenae	Betaproteobacteria	
spl	Spea_3841	peptidase S9 prolyl oligopeptidase	654	992 (129)	232	0.309	Shewanella pealeana	Gammaproteobacteria - Others	
alt	ambt_02545	peptidase S9, prolyl oligopeptidase acti	686	988 (244)	231	0.301	Alteromonas sp. SN2	Gammaproteobacteria - Others	
bra	BRAD03729	dipeptidyl aminopeptidase (EC:3.4.19.1)	652	981 (-)	229	0.315	Bradyrhizobium sp. ORS 278	Alphaproteobacteria	
shl	Shal_0425	peptidase S9 prolyl oligopeptidase	654	975 (565)	228	0.310	Shewanella halifaxensis	Gammaproteobacteria - Others	
bbat	Bdt_2457	dipeptidyl aminopeptidase	659	971 (-)	227	0.307	Bdellovibrio bacteriovorus Tiberius	Deltaproteobacteria	
psf	PSE_4388	prolyl oligopeptidase family	591	968 (-)	226	0.314	Pseudovibrio sp. FO-BEG1	Alphaproteobacteria	
actn	LD83_4216	peptidase S9 prolyl oligopeptidase active site domain protein	605	962 (435)	225	0.312	Actinoplanes sp. N902-109	Actinobacteria	
sfc	Spiaf_0906	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	637	961 (-)	225	0.303	Spirochaeta africana	Spirochaetes	
bfo	BRAFLDRAFT_1	hypothetical protein	653	404 (-)	98	0.323	Branchiostoma floridae (Florida lancelet)	Animalia: Chordata	Lancelets
sli	Slin_0469	peptidase S9 prolyl oligopeptidase active site domain protein	638	951 (532)	223	0.308	Spirosoma linguale	Bacteroidetes	
slo	Shew_3485	peptidase S9 prolyl oligopeptidase	654	951 (476)	223	0.311	Shewanella loihica	Gammaproteobacteria - Others	
aol	S58_42330	dipeptidyl aminopeptidase	652	948 (-)	222	0.293	Bradyrhizobium oligotrophica	Alphaproteobacteria	
kko	Kkor_2063	peptidase S9 prolyl oligopeptidase active site domain protein	655	943 (468)	221	0.300	Kangiella koreensis	Gammaproteobacteria - Others	
atu	Atu5193	peptidase	633	939 (-)	220	0.295	Agrobacterium fabrum	Alphaproteobacteria	
azl	AZL_e02370	dipeptidyl aminopeptidase	647	938 (-)	220	0.290	Azospirillum sp. B510	Alphaproteobacteria	
phd	102326605	dipeptidyl peptidase family member 6-like	688	959 (529)	224	0.314	Pantholops hodgsonii (chiru)	Vertebrates	
kol	Kole_1169	peptidase S9 prolyl oligopeptidase active site domain protein	605	938 (464)	220	0.302	Kosmotoga olearia	Thermotogae	
sfr	Sfri_3832	peptidase S9 prolyl oligopeptidase	659	940 (20)	220	0.307	Shewanella frigidimarina	Gammaproteobacteria - Others	
syx	SynWH7803_232	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	673	929 (-)	218	0.300	Synechococcus sp. WH7803	Cyanobacteria	
cbr	CBG22967	C. briggsae CBR-DPF-6 protein	735	938 (476)	220	0.298	Caenorhabditis briggsae	Nematodes	
mmv	MYCMA_2595	peptidase YuxL	405	928 (-)	217	0.398	Mycobacterium massiliense	Actinobacteria	
sbb	Sbal175_3867	peptidase S9 prolyl oligopeptidase	662	927 (135)	217	0.312	Shewanella baltica BA175	Gammaproteobacteria - Others	
shp	Sput200_0326	peptidase S9 prolyl oligopeptidase	662	927 (476)	217	0.316	Shewanella putrefaciens 200	Gammaproteobacteria - Others	
svo	SVI_4063	prolyl oligopeptidase family protein	654	928 (21)	217	0.304	Shewanella violacea	Gammaproteobacteria - Others	
psm	PSM_A1098	peptidase	647	921 (377)	216	0.289	Pseudoalteromonas sp. SM9913	Gammaproteobacteria - Others	
pha	PSHAa1953	peptidase (EC:3.4.-.-)	646	919 (13)	215	0.294	Pseudoalteromonas haloplanktis	Gammaproteobacteria - Others	
ccx	COCOR_01391	S9C family peptidase	657	915 (330)	214	0.300	Corallocooccus coralloides	Deltaproteobacteria	
saz	Sama_0323	prolyl oligopeptidase family protein	649	914 (12)	214	0.293	Shewanella amazonensis	Gammaproteobacteria - Others	
pmf	P9303_17781	hypothetical protein	681	907 (-)	213	0.290	Prochlorococcus marinus MIT 9303	Cyanobacteria	
amac	MASE_10025	prolyl oligopeptidase	654	898 (219)	211	0.304	Alteromonas macleodii ATCC 27126	Gammaproteobacteria - Others	

swp	swp_2199	peptidase S9, prolyl oligopeptidase active site region	655	900 (73)	211	0.289	Shewanella piezotolerans	Gammaproteobacteria - Others
she	Shewmr4_3601	peptidase S9 prolyl oligopeptidase	661	897 (89)	210	0.309	Shewanella sp. MR-4	Gammaproteobacteria - Others
son	SO_4252	subfamily S9C unassigned peptidase	662	893 (48)	209	0.306	Shewanella oneidensis	Gammaproteobacteria - Others
hhy	Halhy_0603	secreted prolyl oligopeptidase	636	888 (42)	208	0.286	Halicomonobacter hydrossis	Bacteroidetes
mtt	Ftrac_3409	prolyl oligopeptidase	632	885 (458)	208	0.3	Marivirga tractuosa	Bacteroidetes
sur	STAU_2909	peptidase, s9 prolyl oligopeptidase	645	883 (130)	207	0.288	Stigmatella aurantiaca	Deltaproteobacteria
shm	Shewmr7_0355	peptidase S9 prolyl oligopeptidase	662	880 (458)	206	0.307	Shewanella sp. MR-7	Gammaproteobacteria - Others
cfu	CFU_2991	putative dipeptidyl aminopeptidase (EC:3.4.19.1)	681	874 (-)	205	0.299	Collimonas fungivorans	Betaproteobacteria
mpg	Theba_1360	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	597	873 (-)	205	0.293	Mesotoga prima	Thermotogae
nko	Niako_5191	secreted prolyl oligopeptidase family protein	633	875 (-)	205	0.297	Niastella koreensis	Bacteroidetes
sdn	Sden_0322	peptidase S9, prolyl oligopeptidase activ	653	872 (-)	205	0.284	Shewanella denitrificans	Gammaproteobacteria - Others
mxn	MXAN_5299	S9C family peptidase (EC:3.4.-.-)	711	865 (-)	203	0.302	Myxococcus xanthus	Deltaproteobacteria
nmu	Nmul_A2303	peptidase S9, prolyl oligopeptidase active site region	615	857 (-)	201	0.29	Nitrosospora multiformis	Betaproteobacteria
psu	Psesu_2690	prolyl oligopeptidase family protein	655	854 (326)	201	0.289	Pseudoxanthomonas suwonensis	Gammaproteobacteria - Others
pzu	PHZ_c2763	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	654	852 (162)	200	0.295	Phenylobacterium zucineum	Alphaproteobacteria
nde	NIDE2169	putative prolyl oligopeptidase (EC:3.4.-.-)	695	843 (140)	198	0.292	Candidatus Nitrospira defluvii	Nitrospirae
rhd	R2APBS1_0898	dipeptidyl aminopeptidase/acylaminoacyl	663	845 (45)	198	0.265	Rhodanobacter denitrificans	Gammaproteobacteria - Others
sng	SNE_A14730	peptidase S9, prolyl oligopeptidase active site region	625	842 (405)	198	0.297	Simkania negevensis	Chlamydiae
tsp	Tsp_06698	dipeptidyl peptidase family member 6	674	834 (43)	196	0.296	Trichinella spiralis	Nematodes
puv	PUV_15680	dipeptidyl peptidase family member 6	636	828 (-)	195	0.289	Parachlamydia acanthamoebae	Chlamydiae
dji	CH75_03080	prolyl oligopeptidase	663	825 (402)	194	0.288	Dyella jiangningensis	Gammaproteobacteria - Others
cps	CPS_3511	prolyl oligopeptidase (EC:3.4.21.26)	638	815 (89)	192	0.296	Colwellia psychrerythraea	Gammaproteobacteria - Others
sth	STH2102	acylamino acid-releasing protein	610	807 (346)	190	0.29	Symbiobacterium thermophilum	Firmicutes - Clostridia
mmr	Mmar10_0602	peptidase S9 prolyl oligopeptidase	653	790 (32)	186	0.256	Maricaulis maris	Alphaproteobacteria
sjp	SJA_C1-18850	putative dipeptidyl aminopeptidase	575	787 (121)	185	0.305	Sphingobium japonicum	Alphaproteobacteria
vpd	VAPA_1c26650	putative peptidase, S9A/B/C family	688	779 (-)	183	0.28	Variovorax paradoxus B4	Betaproteobacteria
gau	GAU_3499	putative peptidase	704	763 (303)	180	0.257	Gemmatimonas aurantiaca	Gemmatimonadetes
rsh	Rsph17029_3714	peptidase S9 prolyl oligopeptidase	650	763 (-)	180	0.288	Rhodobacter sphaeroides ATCC 17029	Alphaproteobacteria
ack	C380_18670	peptidase S9 prolyl oligopeptidase	350	754 (-)	178	0.385	Acidovorax sp. KKS102	Betaproteobacteria
smz	SMD_1159	prolyl oligopeptidase family protein	662	756 (196)	178	0.279	Stenotrophomonas maltophilia D457	Gammaproteobacteria - Others
htu	Htur_3188	peptidase S9 prolyl oligopeptidase active site domain protein	612	745 (-)	176	0.286	Haloterrigena turkmenica	Euryarchaeota
ttu	TERTU_3768	dipeptidyl aminopeptidase	654	744 (43)	175	0.279	Teredinibacter turnerae	Gammaproteobacteria - Others
nou	Natoc_2100	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	608	739 (-)	174	0.278	Natronococcus occultus	Euryarchaeota
hmu	Hmuk_3141	peptidase S9 prolyl oligopeptidase active site domain protein	596	732 (179)	173	0.265	Halomicrobium mukohataei	Euryarchaeota
ttr	Tter_1709	peptidase S9 prolyl oligopeptidase active site domain protein	594	735 (243)	173	0.258	Thermobaculum terrenum	Unclassified (Bacteria)
aex	Astex_2784	prolyl oligopeptidase family protein	663	731 (40)	172	0.278	Asticcacaulis excentricus	Alphaproteobacteria
cak	Caul_1195	peptidase S9 prolyl oligopeptidase	645	727 (67)	172	0.268	Caulobacter sp. K31	Alphaproteobacteria
tbo	Thebr_2291	peptidase S9 prolyl oligopeptidase	597	728 (-)	172	0.275	Thermoanaerobacter brockii	Firmicutes - Clostridia
tex	Teth514_2353	peptidase S9 prolyl oligopeptidase	597	728 (-)	172	0.275	Thermoanaerobacter sp. X514	Firmicutes - Clostridia
thx	The_2401	peptidase S9 prolyl oligopeptidase	597	728 (-)	172	0.275	Thermoanaerobacter sp. X513	Firmicutes - Clostridia
tpd	Teth39_2247	peptidase S9 prolyl oligopeptidase	597	729 (-)	172	0.275	Thermoanaerobacter pseudethanolicus	Firmicutes - Clostridia
gni	GNIT_3583	peptidase S9 prolyl oligopeptidase	639	723 (56)	171	0.256	Glaciecola nitratireducens	Gammaproteobacteria - Others
nat	NJ7G_2593	WD40-like beta Propeller containing prote	603	723 (-)	171	0.276	Natrinema sp. J7-2	Euryarchaeota
nge	Natgr_3653	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	627	723 (180)	171	0.257	Natronobacterium gregoryi	Euryarchaeota
cja	CJA_0136	phospholipase/carboxylesterase (EC:3.1.-.-)	653	718 (269)	170	0.246	Cellvibrio japonicus	Gammaproteobacteria - Others
hma	rrnAC0178	prolyl oligopeptidase	574	712 (171)	168	0.286	Haloarcula marismortui	Euryarchaeota
npe	Natpe_0482	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	605	712 (-)	168	0.279	Natrinema pellirubrum	Euryarchaeota
ehx	EMIHURAFT_1	hypothetical protein	523	709 (230)	167	0.312	Emiliana huxleyi	Protists
hhi	HAH_0927	prolyl oligopeptidase family protein	602	709 (106)	167	0.28	Haloarcula hispanica ATCC 33960	Euryarchaeota
hxa	Halxa_3746	peptidase S9 prolyl oligopeptidase active site domain protein	628	708 (-)	167	0.282	Halopiger xanaduensis	Euryarchaeota
nmg	Nmag_2538	peptidase S9 prolyl oligopeptidase active site domain protein	611	707 (162)	167	0.278	Natrialba magadii	Euryarchaeota
bif	N288_24340	peptidase S9	594	697 (65)	165	0.275	Bacillus infantis	Firmicutes - Bacilli
btg	BTB_c33010	acylamino-acid-releasing protein	596	697 (-)	165	0.279	Bacillus thuringiensis Bt407	Firmicutes - Bacilli
ccr	CC_1048	prolyl oligopeptidase	642	697 (32)	165	0.262	Caulobacter crescentus CB15	Alphaproteobacteria
rrd	RradSPS_0187	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	607	699 (270)	165	0.274	Rubrobacter radiotolerans	Actinobacteria
hme	HFX_0799	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	606	688 (123)	163	0.264	Halofexax mediterranei	Euryarchaeota
bcv	Bcav_0522	peptidase S9 prolyl oligopeptidase active site domain protein	610	684 (250)	162	0.263	Beutenbergia cavernae	Actinobacteria
hvo	HVO_0829	prolyl oligopeptidase family protein	608	685 (-)	162	0.272	Halofexax volcanii	Euryarchaeota
hbo	Hbor_23890	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	601	680 (-)	161	0.27	Halogeometricum borinquense	Euryarchaeota
sali	L593_01585	peptidase S9 prolyl oligopeptidase active site domain protein	629	682 (146)	161	0.27	Salinarchaeum sp. Harcht-Bsk1	Euryarchaeota
acj	ACAM_1532	acylamino-acid-releasing enzyme	596	665 (-)	157	0.275	Aeropyrum camini	Orenarchaeota
hru	Halru_2329	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	629	664 (107)	157	0.257	Halovivax ruber	Euryarchaeota
hah	Halar_3645	peptidase S9 prolyl oligopeptidase active site domain protein	601	660 (89)	156	0.265	Halophilic archaeon	Unclassified (Archaea)
oih	OB0234	acylamino-acid-releasing enzyme	598	660 (78)	156	0.254	Oceanobacillus iheyensis	Firmicutes - Bacilli
bli	BL03160	amine dehydrogenase	598	657 (242)	155	0.254	Bacillus licheniformis ATCC 14580	Firmicutes - Bacilli

sepsis of newborn infants, myocarditis

fba	FIC_01050	hypothetical protein	647	652 (-)	154	0.257	Flavobacteriaceae bacterium	Bacteroidetes	
aac	Aaci_0897	peptidase S9 prolyl oligopeptidase active site domain protein	600	646 (-)	153	0.275	Alicyclobacillus acidocaldarius subsp. acidoca	Firmicutes - Bacilli	
fco	FCOL_08560	hypothetical protein	647	646 (-)	153	0.257	Flavobacterium columnare	Bacteroidetes	Columnaris disease in fish
sphm	G432_04120	peptidase S9 prolyl oligopeptidase	655	645 (73)	153	0.283	Sphingomonas sp. MM-1	Alphaproteobacteria	
fau	Fraau_1535	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	719	639 (-)	152	0.23	Frateria aurantia	Gammaproteobacteria - Others	
rxv	Rxl_0312	peptidase S9, prolyl oligopeptidase activ	588	641 (237)	152	0.258	Rubrobacter xylanophilus	Actinobacteria	
swi	Swit_1112	peptidase S9 prolyl oligopeptidase	656	639 (64)	152	0.269	Sphingomonas wittichii	Alphaproteobacteria	
bsb	Bresu_0343	prolyl oligopeptidase family protein	663	632 (165)	150	0.267	Brevundimonas subvibrioides	Alphaproteobacteria	
ssy	SLG_29830	putative S9 family peptidase	653	631 (-)	150	0.277	Sphingobium sp. SYK-6	Alphaproteobacteria	
cep	Cri9333_0047	hypothetical protein	651	628 (165)	149	0.287	Crinalium epipsammum	Cyanobacteria	
bex	A11Q_1061	hypothetical protein	652	625 (-)	148	0.255	Bdellovibrio exovorius	Deltaproteobacteria	
gym	GYMC10_5064	peptidase S9 prolyl oligopeptidase active site domain protein	598	623 (-)	148	0.248	Paenibacillus sp. Y412MC10	Firmicutes - Bacilli	
hje	HajB3_13730	prolyl oligopeptidase family protein	611	622 (-)	148	0.268	Halalkalicoccus jeotgali	Euryarchaeota	
pseu	Pse7367_0048	hypothetical protein	670	618 (203)	147	0.271	Pseudanabaena sp. PCC 7367	Cyanobacteria	
rcu	RCOM_0196290	hypothetical protein	565	618 (200)	147	0.258	Ricinus communis (castor bean)	Eudicots	
bmx	BMS_2343	putative peptidase	645	615 (-)	146	0.271	Bacteriovorax marinus	Deltaproteobacteria	
ape	APE_2441.1	acylamino-acid-releasing enzyme	595	609 (-)	145	0.269	Aeropyrum pernix	Crenarchaeota	
hba	Hbal_3137	peptidase S9 prolyl oligopeptidase active site domain protein	644	604 (9)	144	0.256	Hirschia baltica	Alphaproteobacteria	
hla	Hlac_1688	peptidase S9 prolyl oligopeptidase active site domain protein	633	604 (1)	144	0.261	Halorubrum lacusprofundi	Euryarchaeota	
hne	HNE_1336	S9 family peptidase (EC.3.4.--)	673	604 (66)	144	0.263	Hyphomonas neptunium	Alphaproteobacteria	
kvl	KVU_PB0120	peptidase S9 prolyl oligopeptidase active site domain protein	608	593 (-)	141	0.248	Ketogulonicigenium vulgare WSH-001	Alphaproteobacteria	
oan	Oant_3086	peptidase S9 prolyl oligopeptidase	605	593 (-)	141	0.256	Ochrobactrum anthropi	Alphaproteobacteria	
acp	A2cp1_0843	peptidase S9 prolyl oligopeptidase active site domain protein	653	589 (165)	140	0.253	Anaeromyxobacter dehalogenans 2CP-1	Deltaproteobacteria	
saga	M5M_16300	prolyl oligopeptidase family protein	654	589 (134)	140	0.238	Simidiua agarivorans	Gammaproteobacteria - Others	
aho	Ahos_0960	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	548	584 (-)	139	0.26	Acidianus hospitalis	Crenarchaeota	
kfl	Kfla_0165	peptidase S9 prolyl oligopeptidase active site domain proteine	596	581 (-)	138	0.263	Kribbella flavida	Actinobacteria	
baci	B1NLA3E_10700	peptidase S9 prolyl oligopeptidase active site domain proteine	595	577 (-)	137	0.246	Bacillus sp. 1NLA3E	Firmicutes - Bacilli	
pcl	Pcal_0773	peptidase S9 prolyl oligopeptidase active site domain protein	571	575 (-)	137	0.255	Pyrobaculum calidifontis	Crenarchaeota	
npp	PP1Y_AT30886	peptidase S9 prolyl oligopeptidase	588	571 (-)	136	0.302	Novosphingobium sp. PP1Y	Alphaproteobacteria	
hal	VNG0409C	hypothetical protein	598	561 (-)	134	0.261	Halobacterium sp. NRC-1	Euryarchaeota	
hsl	OE1613R	acylaminoacyl peptidase (EC:3.4.19.1)	598	562 (-)	134	0.261	Halobacterium salinarum	Euryarchaeota	
rlg	Rleg_6348	peptidase S9 prolyl oligopeptidase active site domain protein	629	562 (-)	134	0.246	Rhizobium leguminosarum bv. trifolii WSM132	Alphaproteobacteria	
hwa	HQ2276A	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	629	557 (-)	133	0.241	Haloquadratum walsbyi DSM 16790	Euryarchaeota	
mpt	Mpe_A2193	hypothetical protein	674	558 (-)	133	0.265	Methylibium petroleiphilum	Betaproteobacteria	
hwc	Hqrw_2515	peptidase S9 family protein	629	555 (-)	132	0.241	Haloquadratum walsbyi C23	Euryarchaeota	
pbr	PB2503_11399	prolyl oligopeptidase	677	552 (-)	132	0.287	Parvularcula bermudensis	Alphaproteobacteria	
saci	Sinac_7018	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	648	551 (113)	131	0.268	Singulisphaera acidiphila	Planctomycetes	
call	Cal6303_2107	hypothetical protein	650	537 (-)	128	0.254	Calothrix sp. PCC 6303	Cyanobacteria	
ddr	Deide_02310	Dipeptidyl aminopeptidase	609	530 (-)	127	0.239	Deinococcus deserti	Deinococcus-Thermus	
pog	Pogu_2024	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	605	532 (-)	127	0.249	Pyrobaculum oguniense	Crenarchaeota	
gob	Gobs_2493	peptidase S9 prolyl oligopeptidase active site domain protein	607	527 (27)	126	0.271	Geodermatophilus obscurus	Actinobacteria	
afs	AFR_33195	yuxL-like peptidase	598	524 (-)	125	0.255	Actinoplanes friuliensis	Actinobacteria	
hau	Haur_2468	peptidase S9 prolyl oligopeptidase	628	517 (-)	124	0.256	Herpetosiphon aurantiacus	Chloroflexi	
pas	Pars_0382	peptidase S9 prolyl oligopeptidase	569	518 (-)	124	0.255	Pyrobaculum arsenaticum	Crenarchaeota	
sde	Sde_0061	peptidase S9, prolyl oligopeptidase active	653	514 (57)	123	0.245	Saccharophagus degradans	Gammaproteobacteria - Others	
pis	Pisl_1310	peptidase S9 prolyl oligopeptidase	588	511 (-)	122	0.254	Pyrobaculum islandicum	Crenarchaeota	
req	REQ_04650	serine peptidase	605	510 (-)	122	0.31	Rhodococcus equi	Actinobacteria	
sto	ST1737	acylamino acid-releasing enzyme	536	511 (-)	122	0.248	Sulfolobus tokodaii	Crenarchaeota	
pyr	P186_2578	acylamino-acid-releasing enzyme	579	503 (-)	121	0.254	Pyrobaculum sp. 1860	Crenarchaeota	
tne	Tneu_0240	peptidase S9 prolyl oligopeptidase	572	506 (-)	121	0.273	Pyrobaculum neutrophilum	Crenarchaeota	
pai	PAE1189	acylamino acid-releasing enzyme	570	502 (-)	120	0.264	Pyrobaculum aerophilum	Crenarchaeota	
pyn	PNA2_1210	hypothetical protein	623	501 (-)	120	0.255	Pyrococcus sp. NA2	Euryarchaeota	
sin	YN1551_2237	acylaminoacyl-peptidase (EC:3.4.19.1)	536	501 (-)	120	0.253	Sulfolobus islandicus Y.N.15.51	Crenarchaeota	
siy	YG5714_0524	acylaminoacyl-peptidase (EC:3.4.19.1)	537	501 (-)	120	0.249	Sulfolobus islandicus Y.G.57.14	Crenarchaeota	
sic	SiL_0560	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	536	496 (-)	119	0.253	Sulfolobus islandicus LAL14/1	Crenarchaeota	
ial	IALB_0609	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	678	493 (-)	118	0.219	Ignavibacterium album	Chlorobi	
sih	SiH_0806	acylaminoacyl-peptidase	536	492 (-)	118	0.253	Sulfolobus islandicus HVE10/4	Crenarchaeota	
sii	LD85_0588	acylaminoacyl-peptidase	536	492 (-)	118	0.247	Sulfolobus islandicus LD.8.5	Crenarchaeota	
sir	SiRe_0548	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	536	493 (-)	118	0.253	Sulfolobus islandicus REY15A	Crenarchaeota	
sis	LS215_1104	acylaminoacyl-peptidase (EC.3.4.19.1)	536	492 (-)	118	0.247	Sulfolobus islandicus L.S.2.15	Crenarchaeota	
sve	SVEN_0653	peptidase S9, prolyl oligopeptidase	688	490 (69)	118	0.347	Streptomyces venezuelae	Actinobacteria	
tsa	AcIPR4_1592	hypothetical protein	650	492 (39)	118	0.244	Terriglobus saanensis	Acidobacteria	
acan	ACA1_383640	peptidase S9, prolyl oligopeptidase	683	489 (73)	117	0.244	Acanthamoeba castellanii	Protists	
bth	BT_1838	alanyl dipeptidyl peptidase	840	488 (69)	117	0.238	Bacteroides thetaiotaomicron	Bacteroidetes	
pho	PH0594	hypothetical protein	622	489 (-)	117	0.25	Pyrococcus horikoshii	Euryarchaeota	

sid	M164_0582	acylaminoacyl-peptidase (EC:3.4.19.1)	536	486 (-)	117	0.251	Sulfolobus islandicus M.16.4	Crenarchaeota	
sim	M1627_0572	acylaminoacyl-peptidase (EC:3.4.19.1)	536	486 (-)	117	0.251	Sulfolobus islandicus M.16.27	Crenarchaeota	
abi	Aboo_1529	peptidase S9 prolyl oligopeptidase active site domain protein	622	484 (-)	116	0.248	Aciduliprofundum boonei	Euryarchaeota	
cgy	CGLY_04170	Putative acylamino-acid-releasing enzyme	599	483 (-)	116	0.275	Corynebacterium glycinophilum	Actinobacteria	
kal	KALB_237	peptidase S9 prolyl oligopeptidase active site domain protein	589	482 (-)	116	0.257	Kutzneria albidia	Actinobacteria	
pab	PAB1418	peptidase	632	484 (-)	116	0.254	Pyrococcus abyssi	Euryarchaeota	
pdx	Psed_1901	acylaminoacyl-peptidase	643	484 (75)	116	0.341	Pseudonocardia dioxanivorans	Actinobacteria	
tel	tir1685	peptidase	615	485 (-)	116	0.314	Thermosynechococcus elongatus	Cyanobacteria	
bfs	BF9343_3151	hypothetical protein	845	479 (-)	115	0.234	Bacteroides fragilis NCTC9343	Bacteroidetes	
cyn	Cyan7425_3959	peptidase S9 prolyl oligopeptidase active site domain protein	646	480 (-)	115	0.347	Cyanothece sp. PCC 7425	Cyanobacteria	
sia	M1425_0550	acylaminoacyl-peptidase (EC:3.4.19.1)	536	481 (-)	115	0.251	Sulfolobus islandicus M.14.25	Crenarchaeota	
sol	Ssol_2289	peptidase S9 prolyl oligopeptidase active site domain protein	536	480 (-)	115	0.246	Sulfolobus solfataricus 98/2	Crenarchaeota	
ss0	SSO1419	acylaminoacyl peptidase (EC:3.4.19.1)	536	480 (-)	115	0.246	Sulfolobus solfataricus P2	Crenarchaeota	
tuz	TUZN_0815	acylamino-acid-releasing enzyme	567	478 (-)	115	0.262	Thermoproteus uzoniensis	Crenarchaeota	
fli	Flei_0808	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	741	474 (-)	114	0.234	Flexibacter litoralis	Bacteroidetes	
gwc	GWCH70_0857	peptidase S9 prolyl oligopeptidase active site domain protein	670	476 (-)	114	0.238	Geobacillus sp. WCH70	Firmicutes - Bacilli	
pys	Py04_0613	peptidase	624	475 (-)	114	0.247	Pyrococcus sp. ST04	Euryarchaeota	
thn	NK55_05060	prolyl oligopeptidase family protein	620	475 (-)	114	0.304	Thermosynechococcus sp. NK55	Cyanobacteria	
ttn	TTX_0458	acylamino-acid releasing enzyme	568	474 (-)	114	0.272	Thermoproteus tenax	Crenarchaeota	
cyc	PCC7424_1335	peptidase S9 prolyl oligopeptidase act	643	470 (-)	113	0.311	Cyanothece sp. PCC 7424	Cyanobacteria	
sti	Sthe_1948	peptidase S9 prolyl oligopeptidase active site domain protein	652	469 (14)	113	0.299	Sphaerobacter thermophilus	Chloroflexi	G(+), aerobic thermophilic
dpd	Deipe_1257	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	613	464 (-)	112	0.231	Deinococcus perardilitoris	Deinococcus-Thermus	
kra	Krad_3393	peptidase S9 prolyl oligopeptidase	619	466 (50)	112	0.342	Kineococcus radiotolerans	Actinobacteria	
oac	Oscil6304_3095	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	644	465 (-)	112	0.297	Oscillatoria acuminata	Cyanobacteria	
atm	ANT_14760	putative S9 family peptidase (EC:3.4.--)	635	463 (21)	111	0.239	Anaerolinea thermophila	Chloroflexi	
fre	Franea1_2294	peptidase S9 prolyl oligopeptidase	776	462 (-)	111	0.346	Frankia sp. EAN1pec	Actinobacteria	
mph	MLP_33280	S9 family peptidase (EC:3.4.--)	641	461 (-)	111	0.325	Microlunatus phosphovorius	Actinobacteria	
sho	SHJGH_7943	putative acylaminoacyl-peptidase	739	462 (48)	111	0.333	Streptomyces hygroscopicus subsp. jinggange	Actinobacteria	produce sirolimus (also known as rapamycin)
shy	SHJG_8182	acylaminoacyl-peptidase	739	462 (48)	111	0.333	Streptomyces hygroscopicus subsp. jinggange	Actinobacteria	
trs	Terro_4215	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	711	463 (-)	111	0.353	Terriglobus roseus	Acidobacteria	soil bacterium, oligotrophic lifestyle
gps	C427_1209	hypothetical protein	675	458 (-)	110	0.297	Glaciecola psychrophila	Gammaproteobacteria - Others	
pdi	BDL0713	alanyl dipeptidyl peptidase	830	458 (-)	110	0.229	Parabacteroides distasonis	Bacteroidetes	
bhl	Bache_1118	alanyl dipeptidyl peptidase	845	451 (-)	109	0.242	Bacteroides helcogenes	Bacteroidetes	
doi	FH5T_19635	peptidase S9 K01278	733	452 (-)	109	0.239	Draconibacterium orientale	Bacteroidetes	
rca	Rcas_3030	peptidase S9 prolyl oligopeptidase	644	451 (-)	109	0.324	Roseiflexus castenholzii	Chloroflexi	
shw	Sputw3181_2695	peptidase S9 prolyl oligopeptidase	676	451 (43)	109	0.273	Shewanella sp. W3-18-1	Gammaproteobacteria - Others	
aca	ACP_2431	S9A/B/C family peptidase (EC:3.4.--)	696	449 (-)	108	0.239	Acidobacterium capsulatum	Acidobacteria	
gmc	GY4MC1_2907	WD40-like beta Propeller containing pro	669	450 (-)	108	0.236	Geobacillus sp. Y4.1MC1	Firmicutes - Bacilli	
gor	KTR9_3721	dipeptidyl aminopeptidase / acylaminoacyl-peptidase	637	446 (-)	108	0.234	Gordonia sp. KTR9	Actinobacteria	
gth	Geoth_2932	acylaminoacyl-peptidase (EC:3.4.19.1)	669	450 (-)	108	0.236	Geobacillus thermoglucosidarius	Firmicutes - Bacilli	
mrh	MycrN_4084	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	625	450 (-)	108	0.314	Mycobacterium rhodesiae	Actinobacteria	
pfi	PFC_00665	acylaminoacyl peptidase	620	447 (-)	108	0.245	Pyrococcus furiosus COM1	Euryarchaeota	
pfu	PF0318	acylaminoacyl peptidase	620	447 (-)	108	0.245	Pyrococcus furiosus DSM 3638	Euryarchaeota	
rsi	Runs1_0908	peptidase S9 prolyl oligopeptidase active site domain protein	657	450 (-)	108	0.23	Runella slithyformis	Bacteroidetes	
scb	SCAB_6711	peptidase	784	448 (40)	108	0.303	Streptomyces scabiei	Actinobacteria	
swo	Swol_2498	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	867	449 (-)	108	0.26	Syntrophomonas wolfei	Firmicutes - Clostridia	
tit	OCC_08195	peptidase S9	632	447 (-)	108	0.255	Thermococcus litoralis	Euryarchaeota	
bid	Bind_0145	peptidase S9 prolyl oligopeptidase	693	443 (-)	107	0.317	Beijerinckia indica	Alphaproteobacteria	
bsd	BLASA_3700	peptidase, S9C (Acylaminoacyl-peptidase)	643	445 (-)	107	0.326	Blastococcus saxosidians	Actinobacteria	
fal	FRAAL4487	acylaminoacyl-peptidase	783	443 (-)	107	0.328	Frankia alni	Actinobacteria	symbiosis with actinorhizal plants
gpo	GPOL_c36210	prolyl oligopeptidase family protein	727	443 (-)	107	0.292	Gordonia polyisoprenivorans	Actinobacteria	
sap	Sulac_0970	peptidase S9 prolyl oligopeptidase	644	442 (-)	107	0.304	Sulfobacillus acidophilus DSM 10332	Firmicutes - Clostridia	
say	TPY_2918	peptidase, S9A/B/C family, catalytic domain-containing protein	644	442 (-)	107	0.304	Sulfobacillus acidophilus TPY	Firmicutes - Clostridia	
tko	TK2049	acylamino acid-releasing protein	622	443 (-)	107	0.234	Thermococcus kodakarensis	Euryarchaeota	
can	Cyan10605_2681	peptidase S9 prolyl oligopeptidase active site domain protein	630	438 (-)	106	0.29	Cyanobacterium aponinum	Cyanobacteria	
gif	M493_04925	peptidase	672	439 (-)	106	0.227	Geobacillus sp. JF8	Firmicutes - Bacilli	
nhl	Nhal_3185	peptidase S9 prolyl oligopeptidase active site domain protein	643	440 (-)	106	0.276	Nitrosococcus halophilus	Gammaproteobacteria - Others	
cel	CELE_F44B9.1	Protein DPF-6, isoform A	740	927 (478)	217	0.292	Caenorhabditis elegans	Nematodes	dpf6
sus	Acid_5430	peptidase S9 prolyl oligopeptidase	687	439 (27)	106	0.229	Candidatus Solibacter usitatus	Acidobacteria	
ths	TES1_1770	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	632	441 (39)	106	0.235	Thermococcus sp. ES1	Euryarchaeota	
cap	CLDAP_00480	peptidase S9 family protein	610	436 (-)	105	0.332	Caldilinea aerophila	Chloroflexi	
gya	GYMC52_0879	WD40-like beta Propeller containing protein	673	437 (-)	105	0.228	Geobacillus sp. Y412MC52	Firmicutes - Bacilli	
gyc	GYMC61_1753	peptidase S9 prolyl oligopeptidase active site domain protein	673	437 (-)	105	0.228	Geobacillus sp. Y412MC61	Firmicutes - Bacilli	
tfo	BFO_0313	peptidase, S9A/B/C family, catalytic domain-containing protein	846	435 (-)	105	0.24	Tannerella forsythia	Bacteroidetes	
tfu	Tfu_0806	acyl-peptide hydrolase	661	436 (-)	105	0.31	Thermobifida fusca	Actinobacteria	

arp	NIES39_L00850	probable peptidase	636	430 (-)	104	0.308	Arthrosira platensis	Cyanobacteria
clg	Calag_1053	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	639	429 (-)	104	0.236	Caldisphaera lagunensis	Crenarchaeota
eol	EmtoL2528	peptidase S9 prolyl oligopeptidase active site domain protein	785	431 (-)	104	0.259	Emticia oligotrophica	Bacteroidetes
fra	Francci3_2909	peptidase S9 prolyl oligopeptidase active site domain protein	735	430 (-)	104	0.303	Frankia sp. CcI3	Actinobacteria
gct	GC56T3_2594	peptidase S9 prolyl oligopeptidase active site domain protein	673	431 (-)	104	0.228	Geobacillus sp. C56-T3	Firmicutes - Bacilli
gxl	H845_3137	peptidase S9 prolyl oligopeptidase active site domain protein	665	430 (-)	104	0.317	Glucanacetobacter xilinus E25	Alphaproteobacteria
gxy	GLX_18240	peptidase S9	663	429 (-)	104	0.315	Glucanacetobacter medellinensis NBRC 3288	Alphaproteobacteria
bca	BCE_0191	prolyl oligopeptidase family protein, putative	652	426 (-)	103	0.235	Bacillus cereus ATCC 10987	Firmicutes - Bacilli
bpf	BpOF4_12245	peptidase S9 prolyl oligopeptidase active site domain protein	663	425 (-)	103	0.249	Bacillus pseudofirmus	Firmicutes - Bacilli
lby	Lbys_2150	peptidase s9b dipeptidylpeptidase iv domain-containing protein	718	427 (-)	103	0.235	Leadbetterella byssophila	Bacteroidetes
mjl	Mjls_3640	peptidase S9 prolyl oligopeptidase	652	426 (-)	103	0.298	Mycobacterium sp. JLS	Actinobacteria
mkm	Mkms_3708	peptidase S9 prolyl oligopeptidase	652	426 (-)	103	0.298	Mycobacterium sp. KMS	Actinobacteria
mmc	Mmcs_3635	peptidase S9 prolyl oligopeptidase active site domain protein	652	426 (-)	103	0.298	Mycobacterium sp. MCS	Actinobacteria
msa	Mycsm_04398	prolyl oligopeptidase family protein	613	428 (-)	103	0.284	Mycobacterium smegmatis JS623	Actinobacteria
nwa	Nwat_1862	peptidase S9 prolyl oligopeptidase active site domain protein	643	426 (-)	103	0.298	Nitrosococcus watsonii	Gammaproteobacteria - Others
ppl	POSPLDRAFT_8	hypothetical protein	621	426 (-)	103	0.335	Postia placenta	Basidiomycetes
pya	PYCH_10860	acylaminoacyl-peptidase	621	426 (-)	103	0.238	Pyrococcus yanosii	Euryarchaeota
tsi	TSIB_1049	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	633	426 (-)	103	0.242	Thermococcus sibiricus	Euryarchaeota
bco	Bcell_1306	WD40-like beta Propeller containing prot	666	422 (-)	102	0.233	Bacillus cellulolyticus	Firmicutes - Bacilli
bvu	BVU_4083	alanyl dipeptidyl peptidase	816	423 (-)	102	0.216	Bacteroides vulgatus	Bacteroidetes
ccz	CCALI_01862	ipeptidyl aminopeptidases/acylaminoacyl-peptidase	838	420 (9)	102	0.281	Chthonomonas calidirosea	Armatimonadetes
chn	A605_08045	putative prolyl oligopeptidase	621	420 (-)	102	0.27	Corynebacterium halotolerans	Actinobacteria
cya	CYA_1925	S9C family peptidase (EC:3.4.--)	644	421 (-)	102	0.331	Synechococcus sp. JA-3-3Ab	Cyanobacteria
cyb	CYB_2016	S9C family peptidase (EC:3.4.--)	642	420 (-)	102	0.335	Synechococcus sp. JA-2-3B'a(2-13)	Cyanobacteria
eus	EUTSA_v100244	hypothetical protein	770	420 (-)	102	0.315	Eutrema salsugineum	Eudicots former Arabidopsis salsugineum, halophytic plant
fgi	FGOP10_01521	FAD dependent oxidoreductase	678	422 (-)	102	0.298	Fimbriomonas ginsengisoli	Armatimonadetes
ipa	Isop_1893	acylaminoacyl-peptidase (EC:3.4.19.1)	734	421 (-)	102	0.235	Isosphaera pallida	Planctomycetes
ngr	NAEGRDRAFT_6	hypothetical protein	732	422 (13)	102	0.234	Naegleria gruberi	Heterolobosea
noc	Noc_1156	peptidase S9, prolyl oligopeptidase active	643	421 (-)	102	0.317	Nitrosococcus oceani	Gammaproteobacteria - Others
pah	Poras_0615	alanyl dipeptidyl peptidase	850	420 (-)	102	0.246	Porphyromonas asaccharolytica	Bacteroidetes
pmk	MDS_2931	peptidase S9 prolyl oligopeptidase	627	423 (-)	102	0.288	Pseudomonas mendocina NK-01	Gammaproteobacteria - Others
sal	Sala_2007	peptidase S9 prolyl oligopeptidase active site domain protein	720	421 (-)	102	0.252	Sphingopyxis alaskensis	Alphaproteobacteria
sdv	BN159_4170	peptide hydrolase	608	420 (-)	102	0.315	Streptomyces davawensis	Actinobacteria
the	GQS_07685	peptidase, prolyl oligopeptidase family protein	621	421 (-)	102	0.231	Thermococcus sp. 4557	Euryarchaeota
ure	UREG_02301	hypothetical protein	619	423 (-)	102	0.351	Uncinocarpus reesii	Fungi, Onygenaceae
xfa	XF2260	alanyl dipeptidyl peptidase	688	421 (-)	102	0.278	Xylella fastidiosa 9a5c	Gammaproteobacteria - Others
ace	Acel_1489	peptidase S9 prolyl oligopeptidase	646	416 (-)	101	0.27	Acidothermus cellulolyticus	Actinobacteria
bty	Btoyo_2873	Prolyl oligopeptidase family (Peptidase_S9)	652	417 (-)	101	0.228	Bacillus toyonensis	Firmicutes - Bacilli
cbg	CbuG_0482	prolyl oligopeptidase family protein	636	419 (-)	101	0.274	Coxiella burnetii CbuG_Q212	Gammaproteobacteria - Others
cmr	Cycma_1643	peptidase s9b dipeptidylpeptidase iv domain-containing protein	727	417 (-)	101	0.226	Cyclobacterium marinum	Bacteroidetes
gka	GK096	acylaminoacyl peptidase (EC:3.4.19.1)	673	417 (-)	101	0.221	Geobacillus kaustophilus	Firmicutes - Bacilli
rrs	RoseRS_205	peptidase S9 prolyl oligopeptidase	644	417 (-)	101	0.307	Roseiflexus sp. RS-1	Chloroflexi
sch	Sphch_1573	putative oligopeptidase	680	419 (-)	101	0.236	Sphingobium chlorophenolicum	Alphaproteobacteria
trn	BD01_1914	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	623	416 (-)	101	0.235	Thermococcus nautili	Euryarchaeota
xff	XFLM_00590	peptidase S9 prolyl oligopeptidase	688	417 (-)	101	0.278	Xylella fastidiosa subsp. fastidiosa GB514	Gammaproteobacteria - Others
xft	PD1300	alanyl dipeptidyl peptidase	688	417 (-)	101	0.278	Xylella fastidiosa Temecula1	Gammaproteobacteria - Others
ams	AMIS_65980	putative peptidase	633	412 (-)	100	0.329	Actinoplanes missouriensis	Actinobacteria
bbd	Belba_1253	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	726	415 (-)	100	0.237	Belliella baltica	Bacteroidetes
bxy	BXY_01510	dipeptidyl aminopeptidases/acylaminoacyl-peptidase	692	414 (8)	100	0.226	Bacteroides xylanisolvens	Bacteroidetes
dgo	DGo_CA0157	Peptidase S9, prolyl oligopeptidase acti	600	412 (-)	100	0.235	Deinococcus gobiensis	Deinococcus-Thermus
mcb	Mycch_3538	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	612	413 (-)	100	0.294	Mycobacterium chubuense	Actinobacteria
psc	A458_10360	prolyl oligopeptidase family protein	636	413 (-)	100	0.29	Pseudomonas stutzeri CCUG 29243	Gammaproteobacteria - Others
rey	O5Y_06260	hydrolase	646	413 (-)	100	0.288	Rhodococcus erythropolis CCM2595	Actinobacteria
scs	Sta7437_4364	WD40-like beta Propeller containing protein	642	412 (-)	100	0.253	Stanieria cyanosphaera	Cyanobacteria
sma	SAV_4564	peptidase	613	412 (-)	100	0.308	Streptomyces avermitilis	Actinobacteria
taf	THA_621	acylamino-acid-releasing enzyme	646	414 (-)	100	0.239	Thermosiphon africanus	Thermotogae
ton	TON_1543	acylamino acid-releasing protein	623	411 (-)	100	0.235	Thermococcus onnurineus	Euryarchaeota
crd	CRES_1792	putative prolyl oligopeptidase	619	407 (-)	99	0.254	Corynebacterium resistens	Actinobacteria
cyh	Cyan8802_0748	peptidase S9 prolyl oligopeptidase active site domain protein	644	409 (-)	99	0.305	Cyanotheca sp. PCC 8802	Cyanobacteria
cyp	PCC8801_0719	peptidase S9 prolyl oligopeptidase active site domain protein	644	408 (-)	99	0.305	Cyanotheca sp. PCC 8801	Cyanobacteria
goh	B932_1116	acyl-peptide hydrolase-like protein	639	410 (-)	99	0.302	Glucanobacter oxydans H24	Alphaproteobacteria
hsw	Hsw_0094	Putative dipeptidyl peptidase IV	736	408 (-)	99	0.231	Hymenobacter swuensis	Bacteroidetes
salu	DC74_4470	putative peptidase	644	408 (-)	99	0.227	Streptomyces albus	Actinobacteria
sci	B446_20210	peptide hydrolase	593	410 (-)	99	0.224	Streptomyces collinus	Actinobacteria
sgr	SGR_3367	peptidase	613	407 (-)	99	0.327	Streptomyces griseus	Actinobacteria

syc	syc2040_c	peptidase	643	409 (-)	99	0.308	<i>Synechococcus elongatus</i> PCC6301	Cyanobacteria
syf	Synpcc7942_205	peptidase	643	409 (-)	99	0.308	<i>Synechococcus elongatus</i> PCC7942	Cyanobacteria
tha	TAM4_1457	acylamino acid-releasing protein	623	409 (-)	99	0.23	<i>Thermococcus</i> sp. AM4	Euryarchaeota
apk	APA386B_1599	peptidase S9 prolyl oligopeptidase active site domain protein	675	403 (-)	98	0.31	<i>Acetobacter pasteurianus</i> 386B	Alphaproteobacteria
nve	NEMVE_v1g1636	hypothetical protein	656	440 (-)	106	0.289	<i>Nematostella vectensis</i> (sea anemone)	Cnidarians
cfn	CFAL_09325	peptidase S9	607	406 (-)	98	0.311	<i>Corynebacterium falsenii</i>	Actinobacteria
cmp	Cha6605_1018	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	641	404 (-)	98	0.307	<i>Chamaesiphon minutus</i>	Cyanobacteria
crb	CARUB_v100066	hypothetical protein	817	406 (-)	98	0.306	<i>Capsella rubella</i>	Eudicots
ggh	GHH_c08980	putative acylaminoacyl-peptidase (EC:3.4.21.-)	673	405 (-)	98	0.247	<i>Geobacillus</i> sp. GHH01	Firmicutes - Bacilli
gtn	GTNG_0849	acylaminoacyl peptidase	672	403 (-)	98	0.221	<i>Geobacillus thermodenitrificans</i>	Firmicutes - Bacilli
mad	HP15_3136	prolyl oligopeptidase family protein	594	405 (-)	98	0.302	<i>Marinobacter adhaerens</i>	Gammaproteobacteria - Others
osp	Odosp_0863	hypothetical protein	845	403 (-)	98	0.223	<i>Odoribacter splanchnicus</i>	Bacteroidetes
srm	SRM_02249	peptidase	690	403 (-)	98	0.239	<i>Salinibacter ruber</i> M8	Bacteroidetes
sru	SRU_2034	acyl-peptide hydrolase	690	403 (-)	98	0.239	<i>Salinibacter ruber</i> DSM 13855	Bacteroidetes
tba	TERMP_01779	acylamino-acid-releasing enzyme	632	405 (-)	98	0.227	<i>Thermococcus barophilus</i>	Euryarchaeota
tte	TTE1551	dipeptidyl aminopeptidase/acylaminoacyl-peptidase	632	404 (-)	98	0.228	<i>Thermoanaerobacter tengcongensis</i>	Firmicutes - Clostridia
bql	LL3_03301	hypothetical protein	694	400 (-)	97	0.231	<i>Bacillus amyloliquefaciens</i> LL3	Firmicutes - Bacilli
bsx	C663_3081	hypothetical protein	659	401 (-)	97	0.231	<i>Bacillus subtilis</i> XF-1	Firmicutes - Bacilli
bsy	I653_15530	hypothetical protein	657	401 (-)	97	0.231	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> BAB-1	Firmicutes - Bacilli
dto	TOL2_C08770	peptidase S9, prolyl oligopeptidase active site region	723	400 (-)	97	0.323	<i>Desulfobacula toluolica</i>	Deltaproteobacteria
fgr	FG00791.1	hypothetical protein	1109	400 (-)	97	0.301	<i>Fusarium graminearum</i>	Ascomycetes plant pathogen
mar	MAE_24600	peptidase, S9C (acylaminoacyl-peptidase)	640	400 (-)	97	0.309	<i>Microcystis aeruginosa</i>	Cyanobacteria
mro	MROS_0490	Dipeptidyl-peptidase 4	725	401 (-)	97	0.225	<i>Melioribacter roseus</i>	Chlorobi
sesp	BN6_27280	hypothetical protein	592	401 (-)	97	0.22	<i>Saccharothrix espanaensis</i>	Actinobacteria
tga	TGAM_0114	peptidase, prolyl oligopeptidase family protein	623	401 (-)	97	0.223	<i>Thermococcus gammatolerans</i>	Euryarchaeota