

SUPPLEMENTARY INFORMATION

Sequence Analysis of Hypothetical Proteins from *Helicobacter pylori* 26695 to Identify Potential Virulence Factors

Ahmad Abu Turab Naqvi^{1§}, Farah Anjum^{2§}, Faez Iqbal Khan³, Asimul Islam¹,
Faizan Ahmad¹, Md. Imtaiyaz Hassan^{1*}

¹Center for Interdisciplinary Research in Basic Sciences, Jamia Millia Islamia, Jamia Nagar, New Delhi 110025, India, ²Female College of Applied Medical Science, Taif University, Al-Taif 21974, Kingdom of Saudi Arabia, ³School of Chemistry and Chemical Engineering, Henan University of Technology, Henan 450001, China

Supplementary Table 5. List of functionally annotated domain of 340 hypothetical proteins (HPs) from *Helicobacter pylori* by CATH, SUPERFAMILY, PANTHER, Pfam, CDART, SVMProt, and ProtoNet

No.	UniProt ID	CATH	SUPERFAMILY	PANTHER families (subfamily/family/superfamily)	Pfam (family/domain)	CDART	SVMProt (family)	ProtoNet Cluster (cluster name)
1	O24859	No result	No result	No result	CwfJ_C_1 (PF04677)	No result	EC 3.1 Hydrolases	Cluster 3627758 Proteobacteria
2	O24860	No result	No result	No result	TrbC/VIRB2 family	Transport secretion system IV, VirB2 protein	Transmembrane	Cluster 4547021 Conjugal transfer,TrbC
3	O24861	No result	No result	No result	Predicted membrane protein (DUF2079)	No result	Transmembrane	Cluster 4149736 Campylobacterales
4	O24863	No result	HCP-like	No result	No result	No result	No result	Cluster 3922017 Bacteria
5	O24869	No result	No result	No result	No result	No result	No result	Cluster 4074508 <i>Helicobacter pylori</i>
6	O24871	No result	No result	No result	Protein of unknown function (DUF1523)	Sporulation domain- containing protein	EC 2.4 Transferases- Glycosyltransferases	3869536 Protein of unknown function DUF1523
7	O24873	No result	No result	No result	No result	No result	DNA-binding	Cluster 4100399 <i>Helicobacter pylori</i>
8	P56066	E3 ubiquitin- protein ligase	ClpS-like superfamily	No result	ClpS	ATP-dependent Clp protease	Lipid-binding protein	Cluster 3969020 Adaptor protein

		UBR1-like domain				adaptor		ClpS, core
9	O24894	No result	His-Me finger endonucleases-like superfamily	No result	HNH endonuclease	No result	Zinc-binding	(Cluster) 3155256 HNH nuclease
10	O24898	No result	No result	No result	LPAM_1-like family	No result	Iron-binding	(Cluster) 4075984 <i>Helicobacter</i>
11	O24899	No result	Tropomyosin superfamily	SMC family (pthr18937)	No significant hit	No result	Lipid-binding proteins	(Cluster) 4040376 Prefoldin
12	O24900	Chaperone protein DnaK-like domain 1	Actin-like ATPase domain	No result	No result	No result	Zinc-binding	(Cluster) 3842857 Bacteria
13	O24901	No result	No result	No result	No result	No result	EC 3.1 Hydrolases - Acting on ester bonds	(Cluster) 3676170 <i>Helicobacter</i>
14	O24902	Uncharacterized family 60-like domain 1/2	HP0062-like superfamily	No result	No significant hit	WXG100 superfamily	Zinc-binding	(Cluster) 4058401 Protein of unknown function DUF909
15	O24903	No result	No result	No result	WHH family	SOAR Superfamily	Zinc-binding	(Cluster) 4131537 <i>Helicobacter</i>
16	O24904	Glucan synthesis regulatory protein-like domain	SMI1/KNR4-like superfamily	No result	SMI1/KNR4-like superfamily	SMI1/KNR4-like superfamily	Iron-binding	(Cluster) 4502027 Cell wall assembly and cell proliferation coordinating

17	O24905	No result	Aspartate receptor, ligand-binding domain	No result	No significant hit	No result	Magnesium-binding	protein, KNR4-like (Cluster) 17440 <i>Helicobacter pylori</i>
18	O24909	No result	No result	Neuropeptide-like protein 28-related	DUF1664 Family	RRM-Superfamily	Zinc-binding	(Cluster) 4102011 Campylobacterales
19	O24910	No result	No result	No result	No result	No result	No result	No result
20	P64651	No result	No result	No result	No result	Cyt_c_Oxidase_VIa superfamily	Transmembrane	(Cluster) 4104972 Helicobacteraceae
21	O24914	NLP/P60 family protein-like domain	Cysteine proteinases	No result	NLPC_P60 stabilising domain	NLPC_P60 superfamily	All lipid-binding proteins	(Cluster) 3921937 NLP/P60
22	O24921	No result	No result	No result	No significant hit	No result	mRNA-binding Proteins	(Cluster) 3877061 Helicobacteraceae
23	O24923	No result	No result	No result	No result	No result	EC 2.5. Transferases	(Cluster) 3637040 <i>Helicobacter</i>
24	O24926	No result	Adenine nucleotide alpha hydrolases-like superfamily	No result	DUF208 family	AANH_like superfamily	Zinc-binding	(Cluster) 4025260 Protein of unknown function DUF208
25	O24932	No result	No result	No result	No significant hit	No result	Zinc-binding	(Cluster) 4669317 Proteobacteria
26	O24934	Methylthioribulose-1-phosphate dehydratase-like domain	AraD/HMP-PK domain-like	Fuculose phosphate aldolase-like family	Aldolase_II family	Aldolase_II superfamily	Transmembrane	(Cluster) 3740371 L-fuculose-1-phosphate Aldolase

27	O24935	No result	No result	No result	No significant hit	No result	EC 3.6 Hydrolases	(Cluster) 4423557 Proteobacteria
28	O24936	No result	No result	No result	MAF_flag10 family	COG2604 superfamily	All DNA-binding	(Cluster) 3886733 Protein of unknown function DUF115
29	P56080	No result	Radical SAM enzymes superfamily	No result	Radical SAM superfamily 4Fe-4S single cluster domain	Radical_SAM superfamily	Iron-binding	(Cluster) 4068193 Radical SAM
30	O24937	No result	No result	Leucine zipper protein 4 subfamily	DUF874 family	No result	No result	(Cluster) 4085683 Protein of unknown function DUF874
31	O24938	No result	PEP carboxykinase- like	No result	DUF874 family	No result	Zinc-binding	(Cluster) 4085683 Protein of unknown function DUF874
32	O24939	No result	No result	No result	DUF874	Phage_Gp23 superfamily	Zinc-binding	(Cluster) 4085683 Protein of unknown function DUF874
33	P64653	No result	No result	No result	No significant hit	No result	No result	Cluster 3816596 <i>Helicobacter</i>
34	O24942	No result	No result	No result	No result	No result	No result	No result
35	O24943	No result	OmpH-like	No result	DUF1104 family	DUF1104 superfamily	Calcium-binding	(Cluster) 3995510 Protein of unknown function DUF1104
36	O24944	No result	No result	No result	No result	No result	DNA repair	(Cluster) 17510 <i>Helicobacter pylori</i>

37	O24945	No result	No result	No result	No result	No result	No result	No result	No result
38	P64655	No result	No result	No result	No result	No result	No result	No result	(Cluster) 373662 <i>Helicobacter pylori</i>
39	O24949	No result	NagB/RpiA/CoA transferase-like	Family not named	DUF162 family	DUF162 superfamily	Nuclear receptors	(Cluster) 4148786	Protein of unknown function DUF162
40	O24951	No result	No result	Uncharacterized protein ykge family	Cysteine-rich domain	CCG superfamily	Zinc-binding	(Cluster) 4016070	Glycolate oxidase, iron-sulphur subunit
41	O24959	No result	YdgH-like superfamily	No result	DUF4006 family	DUF4006 superfamily	Transmembrane	(Cluster) 17507	<i>Helicobacter pylori</i>
42	O24960	No result	No result	No result	No result	No result	Transmembrane	(Cluster) 3696015	Helicobacteraceae
43	O24961	No result	No result	No result	No result	No result	Transmembrane	(Cluster) 4136246	Epsilonproteobacteria
44	O24963	No result	Periplasmic binding protein-like II	No result	VitK2_biosynth family	VitK2_biosynth superfamily	Zinc-binding	(Cluster) 4062694	Protein of unknown function DUF191
45	O24964	No result	Spectrin repeat superfamily	No result	No significant hit	DivIC superfamily	Zinc-binding	(Cluster) 4095413	Epsilonproteobacteria
46	O24965	No result	No result	No result	AMIN family	AMIN Superfamily	EC 2.4. Transferases	(Cluster) 3805106	Epsilonproteobacteria

47	O24974	No result	No result	No result	No result	No result	Repressor	(Cluster) 4109733 Campylobacterales
48	O24975	Ogt protein-like domain	TPR-like superfamily	No result	No significant hit	No result	EC 3.6 Hydrolases	(Cluster) 4142353 Epsilonproteobacteria
49	O24976	Protein phosphatase CheZ-like domain	Chemotaxis phosphatase CheZ	No result	No significant hit	No result	Zinc-binding	(Cluster) 3634750 Campylobacterales
50	O24979	No result	No result	No result	EI24 family	Etoposide-induced protein 2.4 (EI24) superfamily	Transmembrane	(Cluster) 3985687 Protein of unknown function DUF540
51	O24984	Uncharacterized family 6-like domain	Prim-pol domain superfamily	No result	DUF1882 family	AE_Prim_S_like superfamily	Zinc-binding	(Cluster) 4572805 Region of unknown function DUF1882
52	O24985	No result	Sporulation related repeat superfamily	No result	No significant hit	No result	Zinc-binding	(Cluster) 4054004 Sporulation related repeat
53	O24986	No result	Plasmid maintenance system epsilon superfamily	No result	DUF1524 family	DUF1524 superfamily	TC 3.A.5 Type II (general) secretory pathway (IISP) family	(Cluster) 4146795 Protein of unknown function DUF262
54	O24989	No result	No result	No result	UPF0114 family	UPF0114 superfamily	Transmembrane	(Cluster) 4036464 Uncharacterized protein family UPF0114
55	P56117	Cardiolipin	Phospholipase	Phospholipase D	PLDc_2 family	PLDc_SF	Transmembrane	(Cluster) 4154050

		synthase-like domain	D/nuclease superfamily	endonuclease superfamily		superfamily		Phospholipase D/transphosphatidylase
56	O24992	No result	No result	No result	No significant hit	No result	DNA repair	(Cluster) 4085973
57	O24996	No result	No result	No result	No result	No result	All lipid-binding proteins	Campylobacterales (Cluster) 4125920
58	O25010	No result	Ribbon-helix-helix superfamily	No result	RHH_1 superfamily	No result	All DNA-binding	Proteobacteria (Cluster) 4044890
59	O25018	No result	No result	No result	No significant hit	PRK04081 superfamily	Zinc-binding	2K10 (Cluster) 3753466
60	O25022	Cytochrome c-like domain	Cytochrome c superfamily	No result	Cytochrome_CB B3 family	Cytochrom_C superfamily	All lipid-binding proteins	Epsilonproteobacteria (Cluster) 3874393
61	O25024	No result	Spermadhesin, CUB domain superfamily	No result	No result	No result	Lipoprotein	Cytochrome c (Cluster) 4176989
62	O25025	Uncharacterized family 34-like domain	HP0242-like superfamily	No result	DUF2018 family	DUF2018 superfamily	EC 3.6 Hydrolases	Campylobacterales (Cluster) 4078249
63	P64657	No result	No result	No result	Rod-binding	No result	All DNA-binding	Domain of unknown function DUF2018 (Cluster) 4023798
64	O25031	No result	No result	No result	DUF2393 family	DUF2393 superfamily	Transmembrane	Uncharacterized conserved protein UCP007248 (Cluster) 4178372

65	O25038	No result	MgtE N-terminal domain-like	No result	MgtE_N family	COG3334 superfamily	Actin binding	(Cluster) 3889916 Magnesium transporter, MgtE intracellular region
66	O25041	No result	No result	No result	No significant hit	No result	Zinc-binding	(Cluster) 4052098 Complete proteome
67	O25042	No result	No result	No result	EcoRII-C family	No result	No result	(Cluster) 4141954 Complete proteome
68	O25047	No result	No result	No result	No result	No result	DNA repair	(Cluster) 4111420 Epsilonproteobacteria
69	O25048	No result	No result	No result	DUF374 family	LPLAT superfamily	Lipid-binding protein	(Cluster) 4164839 Protein of unknown function DUF374
70	O25049	No result	No result	No result	No result	No result	EC 3.6 Hydrolases	(Cluster) 4261616 Campylobacterales
71	O25051	No result	No result	No result	No result	No result	EC 3.1 Hydrolases	(Cluster) 4015997 Campylobacterales
72	P56132	No result	No result	No result	Putative zinc- or iron-chelating domain	CxxCxxCC superfamily	Zinc-binding	(Cluster) 4132922 Uncharacterized protein family UPF0153
73	O25053	Delta-aminolevulinic acid dehydratase-like domain	Ribulose-phosphate binding barrel	No result	Indole-3-glycerol phosphate synthase family	TIM_phosphate_binding Superfamily	Cobalt-binding	(Cluster) 4080894 Ribulose-phosphate binding barrel
74	O25058	No result	TrkA C-terminal	No result	TrkA-C domain	TrkA_C	Zinc-binding	(Cluster) 3441447

			domain-like superfamily			superfamily		Regulator of K+ conductance, C- terminal (Cluster) 4105483 Epsilonproteobacte ria
75	O25061	Homoserine O- acetyltransferase - like domain	Alpha/beta- hydrolases superfamily	No result	No result	No result	Transferases - Transferring phosphorus- containing groups	
76	O25065	No result	Acyl-CoA N- acyltransferases (Nat) superfamily	No result	Uncharacterized conserved protein (DUF2156) family	Uncharacterized conserved protein (DUF2156) superfamily	Zinc-binding	Cluster 4032884
77	O25075	Alginate lyase- like domain	Chondroitin AC/alginate lyase superfamily	No result	Alginate lyase family	AlgLyase superfamily	Transferases - Acyltransferases	(Cluster) 17559 Chondroitin AC/alginate lyase
78	O25076	No result	No result	No result	YceI family	No result	Transferases - Glycosyltransferases	(Cluster) 4045420 Campylobacterales
79	O25081	No result	No result	No result	No result	No result	Metal-binding	(Cluster) 4053038 Proteobacteria
80	O25085	No result	No result	No result	No significant hit	No result	Zinc binding	(Cluster) 3945908 <i>Helicobacter pylori</i>
81	O25104	No result	No result	No result	No significant hit	Phosphonate-bd superfamily	All DNA binding	(Cluster) 17549 <i>Helicobacter pylori</i>
82	O25105	No result	No result	No result	No result	No result	Transmembrane	Cluster 17548 <i>Helicobacter pylori</i>
83	O25107	No result	No result	No result	No significant hit	No result	All lipid binding	Cluster 4115740

								proteins	Glycoside hydrolase, family 24
84	O25108	No result	No result	No result	No result	No result	No result	No result	No result
85	O25109	No result	No result	No result	DUF1294 family	DUF1294 superfamily	TC 1.E. Channels/Pores - Holins	Cluster 4027041 Protein of unknown function DUF1294	
86	O25123	No result	No result	No result	DUF3883 family	DUF3883 superfamily	Zinc-binding	Cluster 4203048 Bacteria	
87	O25131	No result	No result	No result	No significant hit	No result	Zinc-binding	Cluster 17719 <i>Helicobacter pylori</i>	
88	O25145	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 17723 <i>Helicobacter pylori</i>	
89	O25146	No result	No result	No result	SPOR family	SPOR superfamily	No result	Cluster 2952387 Sporulation/cell division region, bacteria	
90	O25147	No result	No result	No result	No significant hit	No result	DNA repair	Cluster 4001135 <i>Helicobacter</i>	
91	P64659	No result	No result	No result	No result	No result	All lipid-binding proteins	Cluster 4187511 Helicobacteraceae	
92	O25155	No result	Metallo- dependent phosphatases	No result	Metallophos family	MPP_superfamily superfamily	Zinc-binding	Cluster 3982959 Metallophosphoest erase	
93	O25156	Alanine	PLP-binding	Proline synthetase	Ala_racemase_N	Predicted	Transferases -	Cluster 4106519	

		racemase-like domain	barrel	co-transcribed bacterial homolog protein	family	pyridoxal phosphate-dependent enzyme, YBL036C type	Transferring alkyl or aryl groups, other than methyl groups	Predicted pyridoxal phosphate-dependent enzyme, YBL036C type
94	O25159	No result	No result	No result	No result	No result	Magnesium-binding	Cluster 4140410
95	O25162	No result	No result	No result	Protein of unknown function (DUF3972)	Nucleotide-binding domain of the sugar kinase/HSP70/act in superfamily	Isomerases - Intramolecular oxidoreductases	Cluster 3573427
96	O25164	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 17730
97	O25172	No result	MurE/MurF N-terminal domain	No result	No result	No result	Zinc-binding	Cluster 3898021
98	O25174	CATH Domain 3lwgB00	Thioesterase/thiol ester dehydrase-isomerase	No result	Thioesterase superfamily	Hot_dog superfamily	Hydrolases - Acting on ester bonds	Cluster 4073243 Thioesterase superfamily
99	O34995	No result	No result	No result	No result	No result	Zinc-binding	Cluster 3101745
100	O34461	No result	Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment	No result	No result	No result	DNA replication	Cluster 4100399
101	O25177	No result	DHH phosphoesterases	No result	DHH family	DHH superfamily	Iron-binding	Cluster 17822 Cluster Name: Phosphoesterase, RecJ-like

								<i>Helicobacter pylori</i>
113	Q9WXL 5	No result	No result	No result	No significant hit	No result	All lipid-binding proteins	Cluster 544375 <i>Helicobacter pylori</i>
114	O25200	No result	No result	No result	No result	DUF2357 superfamily	Zinc-binding	Cluster 4491885 Bacteria
115	O25201	MKIAA1413 protein-like domain	P-loop containing nucleoside triphosphate hydrolases superfamily	Uncharacterized family	AAA_33 family	No result	Zinc-binding	Cluster 4033294 Smr protein/MutS2 C-terminal
116	O25203	No result	No result	No result	No result	No result	Transmembrane	Cluster 2937914 <i>Helicobacter</i>
117	K4NBS7	No result	No result	No result	No result	No result	Metal-binding	Cluster 485464
118	O25204	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 4149736 Campylobacteriales
119	O25205	No result	No result	No result	No result	No result	rRNA-binding Proteins	Cluster 4353258 Helicobacteraceae
120	O25212	Uncharacterized family 94-like domain	No result	No result	MAF_flag10 family	COG2604 Superfamily	All DNA-binding	Cluster 4146788 Protein of unknown function DUF115
121	O25213	TerB-like	TerB-like superfamily	No result	TerB family	TerB_like superfamily	Outer membrane	Cluster 3520815 <i>Helicobacter</i>
122	O25214	No result	No result	No result	No significant hit	Fer2_3 superfamily	EC 4.1 Lyases	Cluster 3999000 2Fe-2S ferredoxin-

123	O25215	No result	No result	No result	No result	No result	Repressor	like Cluster 3886650 Epsilonproteobacteria
124	O25228	No result	No result	No result	No significant hit	No result	Zinc-binding	Cluster 3277025 Complete proteome
125	O34410	No result	No result	No result	DUF3519 family DUF3519 family	DUF3519 superfamily DUF3519 superfamily	Zinc-binding	Cluster 4571442 Campylobacteriales
126	O25232	No result	No result	No result	No significant hit	PRK14471 superfamily	Transmembrane	Cluster 3226815 <i>Helicobacter pylori</i>
127	O25237	UPF0250 protein MCA0107-like domain	YbeD/HP0495- like superfamily	No result	DUF493 family	DUF493 superfamily	All DNA-binding	Cluster 4127012 Protein of unknown function DUF493
128	O25251	No result	No result	No result	No result	No result	No result	Cluster 4075984 <i>Helicobacter</i>
129	O25252	No result	No result	No result	DUF262 family DUF1524 family	DUF1524 superfamily DUF1524 superfamily COG3586 Superfamily	Lipid-binding protein	Cluster 4147588 Protein of unknown function DUF1524 RloF
130	O25255	ErfK / YbiS / YcfS / YnhG	NTF2-like superfamily	No result	YkuD family	NTF2_like superfamily	Lipid-binding protein	Cluster 3894011 YkuD domain

		family protein-like domain	L,D-transpeptidase catalytic domain-like superfamily						
131	O25280	No result	No result	No result	No significant hit	No result	DNA repair	Cluster 4124997 Epsilonproteobacteria	
132	O25282	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 17591 <i>Helicobacter pylori</i>	
133	O25287	No result	No result	No result	No result	No result	Transmembrane	Cluster 4179165 Bacteria	
134	O25288	No result	Ribbon-helix-helix superfamily	No result	No result	No result	All DNA-binding	Cluster 4044890 2K1O	
135	O25292	No result	Radical SAM enzymes superfamily	No result	SPASM family	SPASM superfamily	Zinc-binding	Cluster 3822153 Radical SAM	
136	O25301	Phosphoglycerol transferase I-like domain	Alkaline phosphatase-like	No result	Sulfatase family	Exosortase_EpsH superfamily Sulfatase superfamily	Transmembrane	Cluster 3653580 Sulfatase	
137	O25305	No result	No result	No result	No significant hit	No result	TC 2.C. Electrochemical Potential-driven transporters	Cluster 2642957 <i>Helicobacter pylori</i>	

138	K4NB13	No result	Family A G protein-coupled receptor-like	No result	No result	No result	Iron-binding	Cluster 4221499 ABC transporter-like
139	O25308	No result	No result	No result	DUF3971 family AsmA_1 family	DUF3971 superfamily AsmA_1 superfamily	EC 2.7 Transferases	Cluster 4564890 Proteobacteria
140	O25309	No results	No results	No results	YceG-like family	Aminodeoxychorismate lyase	Iron Binding	Aminodeoxychorismate lyase
141	O25316	No result	No result	No result	No significant hit	No result	Zinc-binding	Cluster 3991180 Campylobacteriales
142	O25317	Disulfide bond formation protein B-like domain	No result	DsbB-like superfamily	DsbB family	DsbB superfamily	Transmembrane	Cluster 3979316 Disulphide bond formation protein DsbB
143	O25324	No result	No result	No result	No result	No result	Transmembrane	Cluster 4573274 Complete proteome
144	O25333	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 17552 GPCR, family 2, secretin-like
145	O25346	No result	No result	No result	DUF262 family DUF1524 family	DUF1524 superfamily	Zinc-binding	Cluster 4146795 Protein of unknown function DUF262
146	O25354	No result	No result	No result	No result	No result	Zinc-binding	Cluster 17567
147	O25358	No result	No result	3-hydroxyisobutyrate	No result	NAD_binding_11 Superfamily	EC 4.1. Lyases	Cluster 3846509 Complete proteome

148	O25364	No result	No result	dehydrogenase-related family No result	No significant hit	No result	Transmembrane	Cluster 3984657 <i>Helicobacter</i>
149	O25373	No result	Triger factor/SurA peptide-binding domain-like family	No result	SurA_N family	SurA_N superfamily	Zinc-binding	Cluster 3819568 SurA N-terminal
150	O25374	Mitochondria fission 1 protein-like domain	TPR-like family	No result	No significant hit	Chaperonin_like superfamily	Zinc-binding	Cluster 3784117 Tetratricopeptide region
151	P64663	No result	No result	No result	DUF2603 family	DUF2603 Superfamily	snRNA-binding proteins	Cluster 4080017 Epsilonproteobacteria
152	O25381	No result	No result	No result	No result	No result	EC 2.7 Transferases	Cluster 2026332 <i>Helicobacter pylori</i>
153	O25392	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 3636954 <i>Helicobacter pylori</i>
154	O25406	No result	No result	No result	No result	No result	Iron-binding	Cluster 4265527 <i>Helicobacter</i>
155	O25407	No result	No result	No result	No result	No result	Transmembrane	Cluster 4151559 <i>Helicobacter</i>
156	O25408	P-loop containing	P-loop containing	Transcriptional	Response	REC family	Zinc-binding	Cluster 4204544

		nucleotide triphosphate hydrolases	nucleoside triphosphate hydrolases	regulatory protein TyrR	regulator receiver domain	Signal receiver domain		Helix-turn-helix, Fis-type
157	O25412	No result	No result	No result	Exo70 family	No result	Zinc-binding	Cluster 4031958 Campylobacterales
158	O25423	No result	No result	No result	DUF1104 family	DUF1104 Superfamily TroA-like superfamily	rRNA-binding proteins	Cluster 3995510 Protein of unknown function DUF1104
159	O25429	No result	No result	No result	No result	No result	Zinc-binding	Cluster 4475939 Campylobacterales
160	O25430	No result	No result	No result	No significant hit	DRE_TIM_metallolyase superfamily	All DNA-binding	Cluster 4006672 <i>Helicobacter</i>
161	O25431	Mx1 protein-like domain	P-loop containing nucleoside triphosphate hydrolases superfamily	No result	MMR_HSR1 family	Ras_like_GTPase superfamily	Zinc-binding	Cluster 3150500 GTP-binding protein, HSR1-related
162	O25442	No result	Fibronectin type III superfamily	Cell adhesion molecule family	fn3 family	fn3 superfamily	Manganese-binding	Cluster 3586958 Fibronectin type III
163	O25450	NAD(P)-binding Rossmann-like Domain	Activating enzymes of the ubiquitin-like proteins	Ubiquitin-activating enzyme e1	ThiF family	Superfamily of activating enzymes (E1) of the ubiquitin-like proteins	Hydrolases-acting on ester bonds	Cluster 4090928
164	O25451	No result	No result	No result	No result	VID27	No result	No result

165	O25456	Lactate utilization protein B-like domain	NagB/RpiA/CoA transferase-like family	ATPase inhibitor/5-formyltetrahydrofolate cyclo-ligase family	5-FTHF_cyc-lig family	5-FTHF_cyc-lig superfamily	DNA repair	Cluster 3987246 5-formyltetrahydrofolate cyclo-ligase
166	O25457	No result	No result	No result	No significant hit	No result	Nuclear receptors	Cluster 17626 <i>Helicobacter pylori</i>
167	O25459	No result	No result	No result	CxxCxxCC family	CxxCxxCC superfamily	Zinc-binding	Cluster 4026871 Bacteria
168	O25460	No result	No result	No result	No significant hit	No result	All lipid-binding proteins	Cluster 4026871 Bacteria
169	O25461	No result	No result	No result	No significant hit	No result	Manganese-binding	Cluster 3525750
170	O25468	Ionotropic receptor 8a-like domain	Periplasmic binding protein-like II superfamily	No result	VitK2_biosynth family	VitK2_biosynth superfamily	DNA recombination	Cluster 4300500 Protein of unknown function DUF178
171	O25469	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 3845397 <i>Helicobacter pylori</i>
172	O25470	No result	No result	No result	No significant hit	DDE_5 superfamily	Transmembrane	Cluster 3987614 Campylobacteriales
173	O25472	No result	No result	No result	No result	No result	Outer membrane	Cluster 17617 <i>Helicobacter pylori</i>
174	O25478	No result	No result	No result	No result	No result	No result	Cluster 4149146 Restriction endonuclease, type

175	O25483	No result	Cytochrome c oxidase subunit I-like	No result	Domain of unknown function (DUF3943)	OM_channels superfamily	Lipid-binding protein	I, EcoRI, R subunit Cluster 4070624
176	O25491	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 4070139
177	O25495	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 17610
178	O25498	No result	No result	No result	No result	No result	RNA-binding Protein	Cluster 17703
179	O25499	No result	Restriction endonuclease-like superfamily	No result	UPF0102 family	UPF0102 superfamily	All lipid-binding proteins	Cluster 4311920 Uncharacterised protein family UPF0102
180	O25504	No result	No result	No result	No result	No result	Zinc-binding	Cluster 2867122
181	O25509	No result	No result	No result	No result	No result	mRNA-binding	Cluster 3948858
182	O25510	Outer membrane protein transport protein (OMPP1/FadL/TodX)	Outer membrane protein transport protein	Long-chain fatty acid transport protein	Outer membrane protein transport protein (OMPP1/FadL/TodX)	OM_channels superfamily	Lipid-binding protein	Cluster 3999419 Membrane protein, aromatic hydrocarbon degradation
183	O25513	No result	No result	No result	No result	No result	Hydrolase-acting on ester bonds	Cluster 4091591
184	O25520	DNA methylase specificity domains	DNA methylase specificity domain	No result	No result	No result	Calcium-binding	Cluster 951039
185	O25523	No result	No result	No result	No result	HARE-HTH	Zinc-binding	Cluster 4124124

186	O25527	No result	No result	No result	No result	No result	superfamily No result	Transferases - Glycosyltransferases	Cluster 3970162
187	O25535	No result	Sec63 N-terminal domain-like	No result	No result	No result	No result	DNA-binding	Cluster 4049026
188	O25538	No result	No result	No result	No result	No result	No result	Calcium-binding	Cluster 17694
189	O25542	No result	Inosine monophosphate dehydrogenase (IMPDH)	No result	No result	No result	No result	Zinc-binding	Cluster 17692
190	O25545	No result	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 3871452
191	O25546	No result	No result	No result	NYN domain	LabA_like superfamily	No result	Chlorophyll biosynthesis	Cluster 3871452
192	O25547	General control protein GCN4 (amino acid biosynthesis regulatory protein)	Tropomyosin	No result	No result	No result	No result	Lipid-binding protein	Cluster 1013393
193	O25548	No result	No result	No result	No result	No result	No result	No result	No result
194	O25550	No result	No result	No result	No result	No result	No result	Zinc-binding	Cluster 4090514
195	O25553	No result	No result	No result	No result	No result	No result	DNA repair	Cluster 4120620
196	O25555	No result	t-snare proteins	No result	No result	No result	No result	Zinc-binding	Cluster 4375583
197	O25557	No result	The spindle assembly checkpoint	No result	No result	No result	No result	Zinc-binding	Cluster 2955406 Cytosolic fatty-acid binding

198	O25562	Jelly Rolls	protein mad2 RmlC-like cupins	No result	Cupin domain	Alpha-mannosidase binding domain	Iron-binding	Cluster 4386616 Cupin, RmlC-type
199	O25564	No result	No result	No result	Flagellar hook-length control protein FliK	Flagellar hook-length control protein FliK	Zinc-binding	Cluster 4091836 Flagellar hook-length control protein
200	O25567	No result	No result	No result	No result	No result	DNA replication	Cluster 3095818 Catalytic activity
201	O25576	DHBP synthase	YrdC/RibB	No result	No result	Sua5_yciO_yrdC Superfamily	rRNA-binding Proteins	Cluster 3787688 DHBP synthase RibB-like alpha/beta domain
202	O25579	No result	Autotransporter	No result	Putative vacuolating cytotoxin	Putative vacuolating cytotoxin	P-type ATPase (P-ATPase) family	Cluster 4073891 Vacuolating cytotoxin
203	O25589	Aminopeptidase	Acyl-CoA N-acyltransferases (Nat)	N-terminal acetyltransferase	Acetyltransferase (GNAT) family	N-Acyltransferase superfamily	P-type ATPase (P-ATPase) family	Cluster 4131589 N-acetyltransferase activity
204	O25592	No result	No result	No result	Protein of unknown function DUF262	HNH nucleases	DNA repair	Cluster 3986941
205	O25601	No result	No result	No result	No result	No result	Metal-binding	Cluster 4648314
206	O25602	No result	No result	No result	No result	Radical SAM superfamily.	Hydrolases - Acting on ester bonds	Cluster 4064501
207	O25607	No result	No result	No result	No result	No result	Transferases -	Cluster 4149356

208	O25616	P-loop containing nucleotide triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	No result	50S ribosome-binding GTPase	ATP-binding cassette transporter nucleotide-binding domain	Glycosyltransferases Transferases - Glycosyltransferases	Cluster 4013695
209	O25617	Single alpha-helices involved in coiled-coils or other helix-helix interfaces	Bacterial hemolysins	No result	No result	No result	DNA-binding	Cluster 4075673 Dynamin, GTPase region
210	O25618	P-loop containing nucleotide triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	No result	Dynamin family	ATP-binding cassette transporter nucleotide-binding domain	Zinc-binding	Cluster 4075673 Dynamin, GTPase region
211	O25619	P-loop containing nucleoside triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	Mitogen-activated protein kinase kinase 7-related	Dynamin family	ATP-binding cassette transporter nucleotide-binding domain	DNA-binding	Cluster 4102010
212	O25624	Outer membrane efflux proteins (OEP)	Outer membrane efflux proteins (OEP)	Outer membrane cation efflux protein	Outer membrane efflux protein	Outer membrane efflux protein	DNA-binding	Cluster 3164161 Outer membrane efflux protein
213	O25625	No result	No result	No result	No result	No result	DNA-binding	Cluster 4106197
214	O25630	No result	No result	No result	Peptidase family M50	Site-2 protease (S2P) class of	Lipid-binding protein	Cluster 4147222 Peptidase M50,

							zinc metalloproteases (MEROPS family M50)		putative membrane-associated zinc metallopeptidase
215	O25632	No result	No result	No result	No result	No result	No result	Transmembrane	Cluster 4446324
216	O25635	No result	CHY zinc finger-like	No result	No result	No result	No result	Transmembrane	Cluster 1077083
217	O25636	tRNA Endonuclease; Chain: A, domain 1	Restriction endonuclease-like	No result	Domain of unknown function (DUF1887)	Domain of unknown function (DUF1887)		Hydrolases - Acting on Ester Bonds	Cluster 3328895
218	O25637	No result	No result	No result	No result	Relaxase/Mobilisation nuclease domain		rRNA-binding Protein	Cluster 3610304 Endonuclease relaxase, MobA/VirD2
219	O25641	No result	No result	No result	No result	No result	No result	Hormone	Cluster 3955371
220	O25642	No result	No result	No result	Nucleotidyl transferase of unknown function (DUF1814)	Nucleotidyl transferase of unknown function (DUF1814)		Manganese-binding	Cluster 4002051 DUF1814
221	O25644	No result	No result	No result	No result	Relaxase/Mobilisation nuclease domain		Zinc-binding	Cluster 3610304 Endonuclease relaxase, MobA/VirD2
222	O25647	No result	No result	No result	No result	No result	No result	No result	Cluster 4018938
223	O25648	No result	No result	No result	No result	No result	No result	Zinc-binding	Cluster 4159822
224	O25651	No result	No result	No result	No result	No result	No result	DNA-binding	Cluster 4120620

225	K4ND94	No result	No result	No result	No result	No result	Chlorophyll biosynthesis	Cluster 3831628
226	O25667	No result	No result	No result	No result	No result	lipid-binding protein	Cluster 3973416
227	O25672	No result	GyrA/ParC C-terminal domain-like	No result	Uncharacterized protein conserved in bacteria (DUF2147)	Uncharacterized protein conserved in bacteria (DUF2147)	lipid-binding protein	Cluster 3961404
228	O25673	Jelly Rolls	Clavamate synthase-like	Toxin-antitoxin biofilm protein TabA	Domain of unknown function (DUF386)	Domain of unknown function (DUF386)	Iron-binding	Cluster 3930640
229	O25689	YlxR-like	YlxR-like	No result	Protein of unknown function (DUF448)	YlxR homologs	mRNA-binding Protein	Cluster 4124916 YlxR-like
230	O25691	Nucleotidyltransferase; domain 5	Actin-like ATPase domain	No result	No result	Inactive homolog of metal-dependent proteases, putative molecular chaperone [Posttranslational modification, protein turnover, chaperones]	Iron-binding	Cluster 3916712
231	O25694	No result	Peptidoglycan hydrolase LytM	No result	No result	Peptidase family M23	Iron-binding	Cluster 3823076 Peptidase M23B
232	O25704	Metallothionein	Metallothionein	No result	No result	No result	Transferases -	Cluster 17532

		(MT)					Glycosyltransferases	
233	O25705	No result	No result	No result	No result	No result	lipid-binding protein	Cluster 4063447
234	O07680	No result	No result	No result	No result	No result	Transmembrane	Cluster 706754
235	O25707	No result	No result	No result	No result	No result	Zinc-binding	Cluster 4029186
236	O25708	Zn peptidases	Zn-dependent exopeptidases	No result	No result	M14 family of metallocarboxype ptidases and related proteins	Hydrolases - Acting on ester bonds	Cluster 3725983
237	O25709	No result	No result	No result	No result	No result	Nuclear receptor	Cluster 4139420
238	O25710	No result	No result	No result	No result	Topoisomerase- primase domain	Lipid-binding protein	Cluster 3871381
239	O25713	Putative neuraminylactose -binding hemagglutinin homolog like domain	NLBH-like	No result	No result	Neuraminylactos e-binding hemagglutinin precursor (NLBH)	Lipid-binding protein	Cluster 4371290
240	O25717	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 3758559
241	O25721	P-loop containing nucleotide triphosphate hydrolases	P-loop containing nucleotide triphosphate hydrolases	No result	PD-(D/E)XK nuclease superfamily	CRISPR/Cas system-associated protein Cas4	Zinc-binding	Cluster 4131750
242	O25726	No result	No result	No result	No result	No result	Hydrolases - Acting on ester bonds	Cluster 4124925 Nucleoside Triphosphate

								Pyrophosphohydrolyase
243	O25727	No result	No result	No result	No result	No result	No result	No result
244	O25734	No result	DNA-binding domain of EIN3-like	No result	No result	No result	Lipid-binding protein	Cluster 3563489
245	O25741	Apolipoprotein	Apolipoprotein A-I	No result	No result	Mitochondrial ATP synthase B chain precursor (ATP-synt_B)	Zinc-binding	Cluster 3226815
246	O34410	No result	No result	No result	No result	No result	Zinc-binding	Cluster 3942743
247	O25745	No result	No result	No result	No result	No result	Hydrolases - Acting on acid anhydrides	Cluster 4584687
248	O25747	No result	Anti-sigma factor FlgM	No result	Anti-sigma-28 factor, FlgM	Anti-sigma-28 factor, FlgM	Sodium-binding	Cluster 4085540 Anti-sigma-28 factor, FlgM
249	K4NFN1	No result	No result	No result	No result	No result	DNA-binding	Cluster 4089198
250	O25749	Hemolysin BL-binding component (Hemolysin BL-binding component HblA)	TPR-like	No result	Tetratricopeptide repeat	Phage lysis regulatory protein, LysB family	Zinc-binding	Cluster 3955134 Tetratricopeptide region
251	O25761	P-loop containing nucleotide triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	No result	AAA domain	ATP-binding cassette transporter nucleotide-	Zinc-binding	Cluster 4155788

252	O25762	No result	No result	No result	Uncharacterized protein conserved in bacteria (DUF2130)	binding domain lambda phage tail tape-measure protein (Tape_meas_lam_C)	Hydrolases - Acting on acid anhydrides	Cluster 3831088
253	O25768	GMP synthetase; Chain A, domain 3	Prokaryotic type KH domain (KH-domain type II)	No result	KH domain	K homology RNA-binding domain, type I	Hydrolases - Acting on ester bonds	Cluster 3939787
254	O25787	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 17790
255	O25799	No result	No result	No result	No result	No result	Zinc-binding	Cluster 4085683
256	O25803	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 3854408
257	K4NT00	No result	No result	No result	No result	No result	DNA-binding	Cluster 4046620
258	O25808	Bifunctional epoxide hydrolase 2	HAD-like	No result	Haloacid dehalogenase-like hydrolase	Haloacid dehalogenase-like hydrolases	Lipid-binding protein	Cluster 4144620 Haloacid dehalogenase-like hydrolase
259	O25816	No result	No result	No result	RDD family	RDD family	Transmembrane	Cluster 17783
260	O25818	No result	No result	No result	No result	No result	Outer membrane	Cluster 787162
261	O25831	No result	No result	No result	No result	No result	Transferases - Transferring phosphorus-containing groups	Cluster 4047493
262	O25834	No result	No result	No result	No result	No result	TC 3.A.5 Type II (general) secretory	Cluster 3987080

263	O25839	Syntaxin-1A homolog (uncoordinated protein 64)	t-SNARE proteins	No result	No result	Catalytic domain of the protein kinase superfamily	TC 3.A.5 Type II (general) secretory pathway (IISP) family	Cluster 4028448
264	O25843	Cell wall targeting domain of glycyglycine endopeptidase	No result	No result	Bacterial SH3 domain	Src Homology 3 domain superfamily	Repressor	Cluster 4144717 SH3, type 3
265	O25848	No result	No result	No result	RDD family	RDD family	Transmembrane	Cluster 3934759 RDD
266	O25854	No result	No result	No result	No result	No result	lipid-binding protein	Cluster 3747760 NADH dehydrogenase (ubiquinone)
267	O25855	No result	No result	No result	No result	No result	DNA-binding	Cluster 3961113 NADH dehydrogenase (ubiquinone) activity
268	O25864	Serine threonine protein phosphatase 5, tetratricopeptide repeat	TPR-like	Tetratricopeptide repeat protein, TPR	Tetratricopeptide repeat	No result	TC 2.C. Electrochemical potential-driven transporters - Ion-gradient-driven	Cluster 3560845 Serine threonine protein phosphatase 5, tetratricopeptide repeat

269	O25866	No result	TPR-like	No result	Telomere-length maintenance and DNA damage repair	No result	energizers Metal-binding	Cluster 3936270
270	O25870	Glycogen phosphorylase B	UDP-Glycosyltransferase/glycogen phosphorylase	No result	Glycosyltransferase family 9 (heptosyltransferase)	Glycosyltransferase	Transferases - Glycosyltransferases	Cluster 3225644 Glycosyltransferase, family 9
271	O25872	Class B acid phosphatase (CBAP) (EC 3.1.3.2) (minor phosphate-irrepressible acid phosphatase)	HAD-like	HAD superfamily, subfamily IIIB acid phosphatase	HAD superfamily, subfamily IIIB (Acid phosphatase)	Haloacid dehalogenase-like hydrolase	Hydrolases - Acting on ester bonds	Cluster 4145093 5-nucleotidase lipoprotein e(P4)
272	O25873	YceI-like	YceI-like	Protein YceI	YceI-like domain	YceI-like domain	Lipid-binding protein	Cluster 4099186 Lipid/polyisoprenoid-binding, YceI-like
273	O25875	No result	No result	No result	No result	No result	Zinc-binding	Cluster 3636954
274	O25881	No result	No result	No result	No result	No result	Chlorophyll biosynthesis	Cluster 17763
275	O25882	No result	No result	No result	No result	No result	Magnesium-binding	Cluster 17762
276	O25884	No result	No result	No result	YtkA-like	FixH	lipid-binding protein	Cluster 3946806
277	O25886	OB fold (dihydrolipoamid	HlyD-like secretion proteins	Cation efflux system protein	HlyD family secretion protein	Biotinyl_lipoyl_domain	Hydrolases - Acting on acid anhydrides	Cluster 4017487 Secretion protein

		e acetyltransferase, E2P)						HlyD	
278	O25888	No result	No result	No result	Branched-chain amino acid transport protein (AzID)	Branched-chain amino acid transport protein (AzID)	Oxidoreductases - Acting on NADH or NADPH	Cluster 4096802 Branched-chain amino acid transport	
279	O25891	No result	Tropomyosin	No result	No result	No result	Zinc-binding	Cluster 17833	
280	O25892	5'-nuclease	PIN domain-like	No result	NYN domain	LabA_like proteins	DNA-binding	Cluster 4067770	
281	O25894	DnaJ-like protein subfamily C member 6	Chaperone J- domain	DnaJ (Hsp40) homolog, subfamily A, member 3A	DnaJ domain	DnaJ domain or J-domain	DNA-binding	Cluster 4194234 Heat shock protein DnaJ, N-terminal	
282	O25904	No result	No result	No result	No result	Src Homology 3 domain superfamily	Transmembrane	Cluster 3892393	
283	O25906	tRNA endonuclease; Chain: A, domain 1	Restriction endonuclease-like	No result	No result	No result	DNA condensation	Cluster 4157908 Endonuclease activity	
284	O25913	No result	No result	No result	No result	No result	Iron-binding	Cluster 4232875	
285	O25930	HTH-type transcriptional regulator MalT (ATP-dependent transcriptional activator MalT)	TPR-like	Outer membrane protein assembly factor BamD	Outer membrane lipoprotein	No result	Lipid-binding protein	Cluster 3755724	

286	O25932	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 4445056
287	O25933	Extracellular endonuclease, subunit A	His-Me finger endonucleases	No result	DNA/RNA non-specific endonuclease	DNA/RNA non-specific endonuclease	RNA-binding protein	Cluster 3881571 DNA/RNA non-specific endonuclease
288	O25934	DNA methylase specificity domains (type-1 restriction enzyme MjaXIP specificity protein (S.MjaXIP))	DNA methylase specificity domain	Type-1 restriction enzyme EcoKI specificity protein	Type I restriction modification DNA specificity domain	Type I restriction modification DNA specificity domain	Calcium-binding	Cluster 4139603 Restriction endonuclease, type I, S subunit, EcoBI
289	O25935	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 4115500
290	K4NT19	No result	No result	No result	No result	No result	Transmembrane	Cluster 4392168
291	O25938	No result	No result	No result	No result	No result	Hydrolases - Acting on ester bonds	Cluster 3409026
292	O25939	No result	No result	No result	No result	No result	DNA-binding	Cluster 4392168
293	O25940	No result	No result	No result	No result	No result	Zinc-binding	Cluster 1044505
294	O25941	No result	No result	No result	No result	No result	Hormone	Cluster 17858
295	O25942	Ibrinogen binding protein from staphylococcus aureus domain	No result	Nuclear export mediator factor NEMF	Fibronectin-binding protein A N-terminus (FbpA)	Adenine nucleotide alpha hydrolases superfamily	Zinc-binding	Cluster 4091562 Fibronectin-binding A, N-terminal
296	O34810	No result	No result	No result	Protein of unknown function	HNH nuclease	Zinc-binding	Cluster 4163036

					DUF262				
297	O34461	No result	No result	No result	No result	No result	DNA replication	Cluster 4100399	
298	O34995	No result	No result	No result	No result	No result	Zinc-binding	Cluster 3101745	
299	O25960	Beta polymerase, domain 2	Nucleotidyltransferase	Iojax superfamily ortholog	Oligomerization domain	Oligomerization domain	Nuclear receptors	Cluster 4100352 Iojax-related protein	
300	O25966	Uncharacterized protein ybcJ	Alpha-L RNA-binding motif	No result	S4 domain	S4/Hsp/tRNA synthetase RNA-binding domain	RNA-binding Protein	Cluster 4115647 RNA-binding S4	
301	O25967	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 17817	
302	O25974	Vaccinia virus protein VP39	S-adenosyl-L-methionine-dependent methyltransferase	No result	No result	No result	Zinc-binding	Cluster 3763341	
303	O25977	No result	No result	No result	No result	No result	Hydrolases - Acting on acid anhydrides	Cluster 4066082	
304	O25978	No result	Toll/Interleukin receptor TIR domain	No result	No result	TIR domain	DNA replication	Cluster 4638206	
305	O25979	Hemolysin BL-binding component	No result	No result	No result	No result	Hydrolases - Acting on ester bonds	Cluster 4006921	
306	O25981	No result	No result	No result	No result	No result	Transmembrane	Cluster 4096522	
307	O25990	GMP synthetase; chain A, domain 3	No result	No result	Jag N-terminus	Jag N-terminus	Transferases - Transferring phosphorus-	Cluster 3468167	

							containing groups	
308	O25993	No result	No result	No result	No result	LPP20 lipoprotein	Lipid-binding protein	Cluster 4040893
309	O25994	No result	No result	No result	No result	No result	Metal-binding	Cluster 4161243
310	O25998	No result	No result	Heat shock protein HsIJ	META domain	META domain	Zinc-binding	Cluster 4025302 Meta and HsIJ
311	O25999	XCC0632-like	XCC0632-like	No result	Protein of unknown function (DUF330)	No result	Calcium-binding	Cluster 3954805
312	O26000	No result	No result	No result	MCE family	MCE Superfamily	EC 3.1 Hydrolases	Cluster 3804716. Mammalian cell entry related
313	O26006	DNA methylase specificity domains	DNA methylase specificity domain	No result	Type I restriction modification DNA specificity domain	Type I restriction modification DNA specificity domain	Zinc-binding	Cluster 4032542
314	O26007	Vaccinia virus protein VP39	S-adenosyl-L-methionine-dependent methyltransferase	No result	VRR-NUC domain	Restriction_endonuclease	Hydrolases - Acting on ester bonds	Cluster 3951495 N-6 DNA methylase
315	O26014	Bardet-Biedl syndrome 4 protein-like domain	TPR-like superfamily	Tetratricopeptide repeat protein, tpr family	TPR_2 TPR_9 TPR_11 family	TPR Superfamily	Zinc-binding	Cluster 4034294 Tetratricopeptide region
316	O26015	Apolipoprotein N-acyltransferase - like domain	Carbon-nitrogen hydrolase	N-Carbamoylputrescine amidase family	CN_hydrolase family	Nitrilase Superfamily	EC 2.4 Transferases	Cluster 3458100 Nitrilase/N-carbamoyl-D-

317	O26019	AT4G38090 protein -like domain	Ribosomal protein S5 domain 2-like superfamily	Impact family member yigz family	UPF0029 family	UPF0029 superfamily	All lipid-binding proteins	aminoacid amidohydrolase Cluster 4126851 Uncharacterized protein family UPF0029
318	O26020	No result	No result	Sub family not named	ABC2_membrane _3 family	ABC2_membrane Superfamily	Transmembrane	Cluster 3951276 ABC-2 type transporter
319	O26021	No result	No result	Membrane component of ABC transporter yhhJ- related	ABC2_membrane _3 family	ABC2_membrane Superfamily	Transmembrane	Cluster 3912464 ABC-2 type transporter
320	O26022	Outer membrane efflux proteins (OEP)	Outer membrane efflux proteins (OEP)	Outer membrane protein tolC	Outer membrane efflux protein	Outer membrane efflux protein	Transferases - Acyltransferases	Cluster 3798968 Outer membrane efflux protein
321	O26025	Fe-S cluster assembly (FSCA)	Fe-S cluster assembly (FSCA) domain-like	NifU-like protein 1, chloroplastic	NifU-like domain	NifU-like domain	Iron-binding	Cluster 4102718 NIF system FeS cluster assembly, NifU, C-terminal
322	O26026	No result	No result	No result	No significant hit	No result	Zinc-binding	Cluster 4243913 Campylobacterales
323	O26035	Cytidine Deaminase; domain 2	Cytidine deaminase-like	No result	Cytidine and deoxycytidylate deaminase zinc-	Cytidine and deoxycytidylate deaminase zinc-	Transferases - Transferring phosphorus-	Cluster 4121891 Diaminohydroxyph osphoribosylamino

					binding region	binding region	containing group	pyrimidine deaminase
324	O26041	No result	No result	No result	No result	No result	No result	Cluster 971010 <i>Helicobacter pylori</i>
325	O26042	Catecholate siderophore receptor Fiu (Ferric iron uptake protein) (TonB-dependent receptor Fiu)	Porins	Ferrichrome iron receptor-related	TonB-dependent Receptor Plug Domain	Porin superfamily	DNA repair	Cluster 3959756 Ferric hydroxamate uptake protein; chain A, domain 1
326	O26045	No result	No result	No result	No significant hit	No result	Transmembrane	Cluster 1813217. <i>Helicobacter pylori</i>
327	O26046	Vaccinia virus protein VP39	S-adenosyl-L-methionine-dependent methyltransferase	No result	Eco57I restriction-modification methylase	S-adenosylmethionine-dependent methyltransferases (SAM or AdoMet-MTase), class I	transferases - Transferring phosphorus-containing groups	Cluster 4172875 N6 adenine-specific DNA methyltransferase, N12 class
328	O26047	No result	No result	No result	No significant hit	No result	TC 3.A.5 Type II (general) secretory pathway (IISP) family	Cluster 4172875. N6 adenine-specific DNA methyltransferase, N12 class
329	O26055	No result	No result	No result	No result	No result	Zinc-binding	Cluster 3951569. <i>Helicobacter pylori</i>

330	O26058	5'-Methylthioadenosine/S-adenosylhomocysteine nucleosidase 1	Purine and uridine phosphorylases	No result	Phosphorylase superfamily	Phosphorylase superfamily	Transferases - Glycosyltransferases	Cluster 3659745 Nucleoside phosphorylase
331	P64665	No result	HP1531-like superfamily	No result	DUF2443 family	DUF2443 Superfamily	Metal-binding	Cluster 3777821. Helicobacter
332	O26063	No result	No result	No result	No significant hit	No result	EC 3.1 Hydrolases	Cluster 3712781. Complete proteome
333	O26088	LPS-assembly protein lptD -like domain	No result	No result	OstA family	OstA Superfamily	mRNA-binding Proteins	Cluster 3978895 OstA-like protein
334	O26089	No result	No result	No result	No result	No result	Lipid-binding protein	Cluster 4476062 Protein of unknown function DUF1239
335	O26095	No result	EscU C-terminal domain-like	Flagellar biosynthetic protein flhB	FlhB HrpN YscU SpaS Family	FlhB HrpN YscU SpaS Family	Zinc-binding	Cluster 4154428 Type III secretion exporter
336	O26099	No result	No result	No result	No significant hit	No result	EC 3.1 Hydrolases	Cluster 17845 Helicobacter pylori
337	O26100	Lipid phosphate phosphatase 1 - like domain	Acid phosphatase/Vanadium-dependent haloperoxidase superfamily	Sphingosine-1-phosphate phosphohydrolase	PAP2 superfamily	PAP2_like Superfamily	All lipid-binding proteins	Cluster 4064009 Acid phosphatase/Vanadium-dependent haloperoxidase
338	O26107	No result	No result	No result	DUF3944 family	COG4735	Zinc-binding	Cluster 3773525

					Ubiq_cyt_C_ Chap family	Superfamily DUF3944		Uncharacterised protein family UPF0174
339	K4NEW 8	No result	No result	No result	Ubiq_cyt_C_ Chap family	Superfamily COG4735	rRNA-binding proteins	Cluster 4746425 Uncharacterised protein family UPF0174
340	O26108	No result	No result	No result	DUF3944 family	COG4735 superfamily	No result	No result
