

Supplementary Table S1. Proteins with similarity between fish and parasites. E-values were obtained from the alignment of the sequences of *R. viridisi* against sequences from different taxa using the NCBI database.

Protein ID	Teleostei E-value	Lophotrochozoa E-value	Platyhelminthes E-value
DN106_c0_g1_i4.p14	2e-21 peptidase inhibitor	3e-23 protein BOX15	1e-23 protein BOX15
DN5221_c0_g1_i2.p1	3e-15 C-type lectin	5e-14 lectin/receptor	4e-07 protein BOX15
DN12056_c0_g1_i1.p1	4e-07 protocadherin	3e-08 protocadherin	1e-08 protocadherin
DN5544_c0_g1_i11.p6	3e-09 C-type lectin	8e-07 C-type lectin	3e-07 C-type lectin
DN4578_c0_g2_i10.p1	3e-83 cathepsin	2e-87 cathepsin	2e-87 cathepsin
DN51_c2_g1_i1.p1	6e-29 disintegrin and metalloproteinase domain	4e-25 disintegrin and metalloproteinase domain	2e-24 BOX15
DN59_c0_g2_i1.p4	1e-40 diphosphomevalonate decarboxylase	7e-48 diphosphomevalonate decarboxylase	1e-40 diphosphomevalonate decarboxylase
DN700_c0_g1_i10.p1	2e-09 macrophage mannose receptor	2e-09 macrophage mannose receptor	8e-06 C-type lectin
DN70202_c0_g1_i1.p1	2e-104 cathepsin	2e-104 cathepsin	7e-105 BOX15/cathepsin
DN7233_c0_g1_i15.p5	5e-12 nuclear pore complex protein	2e-10 BOX15	8e-11 BOX15
DN75_c0_g1_i1.p2	5e-04 serine protease	2e-06 chymotrypsinogen	0.018 BOX15
DN890_c0_g1_i12.p4	6e-07 stromal interaction molecule	7e-08 stromal interaction molecule	7e-08 BOX15
DN1020_c0_g1_i6.p4	3e-31 C-type lectin	4e-41 C-type lectin	5e-39 C-type lectin
DN1169_c1_g1_i8.p1	3e-09 serine protease	8e-10 chymotrypsin-like elastase	4e-08 peptidase/serine protease
DN1300_c0_g1_i5.p2	3e-22 secretory phospholipase A2	4e-26 phospholipase A2	2e-21 BOX15/phospholipase A2
DN1349_c0_g1_i9.p4	1e-20 endoplasmic reticulum oxidoreductin 1 (ERO1)-like protein	1e-22 ERO1-like protein	8e-19 ERO1-like protein
DN13993_c0_g1_i3.p1	8e-11 C-type mannose receptor	6e-10 galactose-specific lectin	7e-09 lectin
DN5361_c0_g1_i3.p1	4e-37 frizzled-8-like	2e-40 frizzled-8	8e-41 frizzled-8

Supplementary Table S2. Possible multifunctional proteins found in predicted ES proteins of *R. viridisi*.

Protein ID	Pfam ID	Description	Reported in MultitaskProtDB
DN116_c0_g1_i15.p1	PF02225.23	Protease A domain	
	PF01532.21	Glycosyl hydrolase family 47	
DN1289_c0_g1_i2.p1	PF04777.14	Erv1 / Alr family (mitochondrial sulfhydryl oxidase)	Thioredoxin (<i>Escherichia coli</i>)
	PF00085.21	Thioredoxin (reduction of other proteins by cysteine thiol-disulfide exchange)	
DN2691_c0_g1_i1.p1	PF06468.14	Spondin_N (involved in patterning axonal growth trajectory)	Thrombospondin 1 (<i>Homo sapiens</i>)
	PF00090.20	Thrombospondin type@2 (Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Binds heparin.)	
	PF00014.24	Kunitz inhibitor domain (protease inhibitor)	
DN2999_c0_g1_i1.p1	PF01549.25	ShK domain-like (Stichodactyla toxin that blocks potassium channels)	
	PF00094.26	von Willebrand factor type D domain (growth regulator/binding domain)	
DN30683_c0_g2_i14.p2	PF14543.7	Xylanase inhibitor N-terminal	
	PF00026.24	Eukaryotic aspartyl protease	
DN466_c0_g1_i12.p1	PF01186.18	Lysyl oxidase	
	PF00530.19	Scavenger receptor cysteine-rich domain (endocytic receptors that mediate non-opsonic phagocytosis in response to foreign ligands)	

Supplementary Table S3. Adhesion proteins identified in *R. viridisi*.

Protein ID	Uniprot ID	Annotation
DN100674_c1_g2_i1.p1	Q5RJH3	Cadherin-12
*DN919_c0_g1_i11.p6	Q9Y5E4	Protocadherin beta-5
DN76720_c0_g1_i2.p5	Q96JQ0	Protocadherin-16
*DN2904_c1_g1_i10.p1	Q96JQ0	Protocadherin-16
*DN3831_c0_g1_i12.p2	Q9Y5G1	Protocadherin gamma-B3
*DN76720_c0_g1_i1.p1	Q9Y5F6	Protocadherin gamma-C5
*DN76720_c0_g1_i1.p2	P58365	Cadherin-23
*DN46_c0_g1_i1.p1	Q91Y11	Protocadherin alpha-9
*DN1162_c0_g1_i11.p1	Q08174	Protocadherin-1
*DN3858_c0_g2_i1.p1	Q08174	Protocadherin-1
*DN3291_c0_g2_i1.p1	Q2PZL6	Protocadherin Fat 4
*DN12056_c0_g1_i1.p1	Q9Y5G0	Protocadherin gamma-B5
*DN1190_c0_g1_i3.p1	Q9Y5G8	Protocadherin gamma-A5
DN522_c1_g1_i6.p1	Q6WYY1	Protocadherin-11 X-linked
DN7461_c0_g3_i2.p1	Q5DRF1	Protocadherin alpha-13
DN1457_c0_g1_i1.p1	Q6KEQ9	Protocadherin-11 X-linked
DN3273_c0_g2_i1.p1	Q5DRC1	Protocadherin gamma-A10
DN25713_c0_g1_i5.p4	Q9H251	Cadherin-23
DN134_c0_g1_i1.p2	A5Z1X6	Integrin beta-1
*DN1069_c0_g1_i11.p1	P05107	Integrin beta-2
*DN2351_c0_g1_i1.p1	Q06274	Integrin alpha-5
DN20_c0_g1_i2.p1	P33730	E-selectin
**DN2061_c0_g1_i12.p2	Q18823	Laminin-like protein lam-2
DN3022_c0_g1_i1.p1	Q29058	Galectin-4
*DN7800_c0_g1_i1.p1	Q24292	Protein dachsous/ protocadherin-16/23
* DN602_c1_g1_i1.p1	Q9VW71	Fat-like cadherin-related tumor suppressor homolog/ protocadherin Fat
* DN191_c0_g1_i4.p2	O89026	Roundabout homolog 1
* DN6333_c0_g4_i2.p1	G5EBF1	Protein sax-3
* DN721_c0_g1_i1.p1	Q9HCK4	Roundabout homolog 2
**DN2063_c0_g1_i13.p1	Q9UQP3	Tenascin-N
**DN557_c0_g1_i3.p1	P08120	Collagen alpha-1(IV) chain
**DN725_c0_g1_i1.p1	P02466	Collagen alpha-2(I) chain
**DN725_c0_g1_i2.p1	P02466	Collagen alpha-2(I) chain
**DN1296_c0_g1_i5.p1	P02466	Collagen alpha-2(I) chain

*KEGG BRITE, object “cell adhesion molecules” [ko04515]; **KEGG “focal adhesion” [PATH:ko04510]

Supplementary Table S4. Families of carbohydrate-active enzymes (CAZymes) in predicted ES proteins of *R. viridisi*.

Protein ID	HMMER E-value	Coverage	HMM Profile
DN116_c0_g1_i15.p1	3.2e-138	0.99	GH47: Glycoside Hydrolase Family 47 (Activity: α -mannosidase (EC 3.2.1.113))
DN1423_c0_g1_i10.p2	7.3e-61	0.63	GH5_27: Glycoside Hydrolase Family 5 / Subf 27 (Activity: β -glucosidase (EC 3.2.1.21); β -mannosidase (EC 3.2.1.25))
DN1977_c0_g1_i14.p1	1.1e-154	0.99	GH31: Glycoside Hydrolase Family 31 (Activity: α -glucosidase (EC 3.2.1.20); α -galactosidase (EC 3.2.1.22); α -mannosidase (EC 3.2.1.24))
DN2542_c2_g1_i1.p1	1.6e-89	0.97	GH20: Glycoside Hydrolase Family 20 (Activity: β -hexosaminidase (EC 3.2.1.52); β -1,6-N-acetylglucosaminidase (EC 3.2.1.-))
DN3756_c0_g1_i1.p1	5.8e-39	0.98	GT31: Glycosyl Transferase Family 31 (Activity: chondroitin β -1,3-glucuronyltransferase (EC 2.4.1.226); chondroitin β -1,4-N-acetylgalactosaminyltransferase (EC 2.4.1.-))
DN502_c0_g1_i1.p5	6.8e-38	0.98	GT31
DN6559_c0_g1_i2.p1	4.8e-21	0.73	GT4: GlycosylTransferase Family 4 (Activity: α -glucosyltransferase (EC 2.4.1.52))
DN716_c0_g2_i12.p1	2.5e-129	0.99	GH47
DN834_c0_g1_i18.p2	1.6e-47	0.62	GT27: GlycosylTransferase Family 27 (Activity: polypeptide α -N-acetylgalactosaminyltransferase (EC 2.4.1.41))
DN151_c2_g1_i1.p2	DIAMOND		GT0
DN3825_c0_g1_i5.p1	Hotpep		PL0
DN725_c0_g1_i2.p1	Hotpep		PL0

GH: Glycoside Hydrolase, GT: Glycosyl Transferase, PL: Polysaccharide Lyase

Supplementary Table S5. Most antigenic ES proteins from *R. viridis* (VaxiJen score > 0.9).

Protein ID	Annotation	Score
DN725_c0_g1_i1.p1	Collagen alpha-2(I) chain	1.3983
DN18884_c0_g6_i2.p1	Unknown nigellin-1.1	1.3867
DN2184_c0_g1_i6.p6	Unknown fkbp-type peptidyl-prolyl cis-trans isomerase slyd	1.3846
DN725_c0_g1_i2.p1	Collagen alpha-2(I) chain	1.3310
DN146924_c0_g3_i1.p1	Unknown SH3-like barrel	1.2806
DN9007_c0_g1_i4.p2	Unknown protein phosphatase 1 regulatory subunit 3a	1.2422
DN8473_c0_g5_i3.p1	Unknown Ribosomal protein L14e	1.2028
DN1296_c0_g1_i5.p1	GTPase NRas	1.1934
DN557_c0_g1_i3.p1	Collagen alpha-2(IV) chain (Nematoda)	1.1569
DN93160_c0_g2_i1.p1	Unknown beta-Grasp (ubiquitin-like)	1.1100
DN102334_c1_g2_i1.p1	Unknown PA1123-like	1.1017
DN28732_c0_g3_i1.p1	Unknown Flavodoxin-like	1.0883
DN19332_c0_g1_i7.p1	Unknown patellamide protein	1.0872
DN49560_c0_g1_i1.p1	Beta-1,4-galactosyltransferase 2	1.0820
DN8509_c0_g1_i3.p1	unknown	1.0786
DN33919_c0_g3_i1.p1	unknown	1.0510
DN98968_c0_g3_i1.p1	unknown	1.0417
DN1329_c1_g1_i12.p5	Inactive histone-lysine N- methyltransferase 2E	1.0151
DN30584_c0_g1_i1.p1	unknown	1.0057
DN11034_c2_g2_i1.p1	unknown	1.0029
DN12500_c1_g2_i1.p1	unknown	1.0007
DN46661_c0_g1_i1.p1	unknown	0.9913
DN18130_c1_g1_i1.p1	unknown	0.9897
DN90688_c0_g3_i1.p2	unknown	0.9897
DN75293_c0_g1_i1.p1	unknown	0.9874
DN69511_c0_g1_i1.p1	unknown	0.9873
DN17841_c0_g1_i1.p2	unknown	0.9814
DN111655_c0_g4_i1.p1	unknown	0.9658
DN180090_c0_g1_i1.p1	unknown	0.9604
DN121379_c0_g3_i1.p1	unknown	0.9571
DN1001_c0_g1_i1.p4	Transcription factor 12	0.9432
DN15568_c3_g2_i1.p1	unknown	0.9359

DN18483_c0_g4_i3.p1	unknown	0.9352
DN16250_c1_g5_i1.p1	unknown	0.9179
DN140269_c1_g1_i2.p1	unknown	0.9158
DN1236_c1_g1_i10.p3	unknown	0.9147
DN15610_c0_g2_i1.p1	unknown	0.9105
DN5197_c0_g2_i3.p3	unknown	0.9075
DN29218_c0_g1_i1.p1	unknown	0.9035
DN51918_c0_g1_i1.p1	unknown	0.9025
DN7673_c0_g3_i1.p1	unknown	0.9025
DN98683_c0_g1_i1.p1	unknown	0.9017
DN1882_c0_g1_i10.p1	unknown	0.9006
DN43568_c0_g3_i1.p1	unknown	0.9000