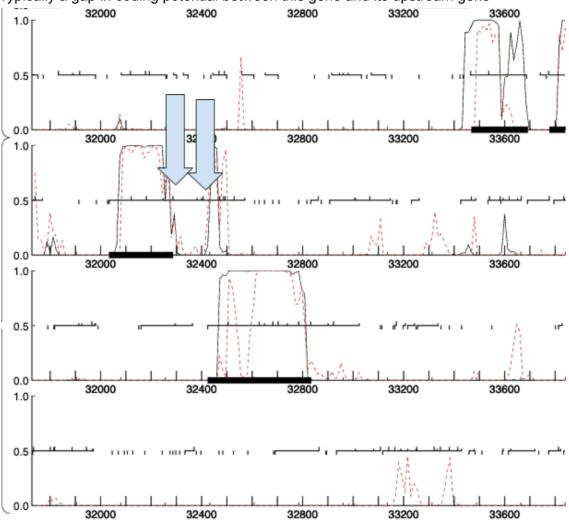
Cluster AY - IrrE-like metallopeptidase

Genes related to MidnightRain_54

Challenge/issue:

- Glimmer/GeneMark predictions often call starts in the middle of the peptidase domain, • calling into question whether the protein could function as a peptidase.
- Coding potential drops off, but does the ORF extend up to the upstream gene? •

Auto-annotation and coding potential



Typically a gap in coding potential between this gene and its upstream gene

Figure above: Genemark Sashimi genes 52, 53, & 54.

We will call the autoannotated start the SHORT start, or short protein. (~32300 above) We will call the start that closes the gap the LONG start, or the long protein. (~32400 above)

			Pham 16[224		
\$	18 9 10		2 p p	ŝ	3 ¹
1: Isolde 50 + 2					
	18 9 10	1,56	r r r		\$
2: Seahorse_54	18 9 10	196 18	1 ³ 1 ⁴		
B: Ragga 42	18 9 10	,50	1° 187 13	Ŷ	3
4: Auxilium_47	18 9 10	1,526	2° 189 - 12		3 3 ³
5: Hillester 54	18 9 191	1,526	r` 192		3
	18 9 191	,40	∿n???)*	30	3
	18 9 10	, ⁵² 0 ,9	n n		\$`
	18 3 10	126	v nor v		s`s`
	18 9 191	1,52,60	v`n₩ v*		
	18 9 10	, ¹ 2,0 ,8	12 N	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	3
6	18 9 1	1991	r nor r	<i>\$</i>	3
12: Tiff81_51	18 9 1	, ¹ 2,0 ,10	r r r	Ŷ	5 ⁵
13: Sashimi_52	18 9 191	, ⁵² 0	1 ²⁰ v		5
	18 9 1	150	v nite v		\$`
	18 9 191	, ⁵² 6	r nor v	\$ \$	5
	18 9 10	140	r ^a r r		5
	18 9 191	¹ ¹	n no no		3
	18 9 10	1,20 1,8	n v		3
19: YoungHarleezy_51	18 9 191	1,520	r r r		\$ \$

Figure above: Starterator for Gene 52 Sashimi

The short, autoannotated starts (right arrow) and the long starts (left arrow) are conserved across the pham.

HHPred alignments

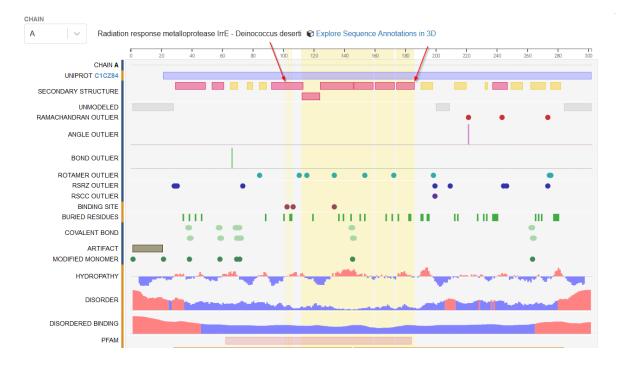
With the short protein:



Template alignment | Template 3D Structure | PDBe

3. 3DTE_A IrrE protein; Deinococcus, Radiotolerance, Gene regulation, Metallopeptidase, IrrE; HET: MSE; 2.6A {Deinococcus deserti} Probability: 99.22%, E-value: 1.1e-10, Score: 73.95, Aligned cols: 69, Identities: 22%, Similarity: 0.056, Template Neff: 9

	×					
Q ss_pred		CCHHHHH	hCCCCC	СННННННННННННННКСССНННННННКс-СССНННННННКССССНННННН		
Q Raph_50	1	MHELGHAH	YGHTGV	TGKQEALANRWAAYRLVNFDDVLALASV-EQSSSGVAAALEVMPDVLET	62 ((85)
Q Consensus	1	aHE1~H~~~	~~~~~	холоЕолалоfanolipлолологол-лолололалолу/лололол	62 ((85)
		++•	++	.+ +. +.+ + +++.+.+++. ++ +		
T Consensus	101	aHELgH~11	_~~~~~~~~~~~~~~~~~	E-eAn-FAa-LL-Pvvv-LavSa	180	(301)
T 3DTE_A	101	AHEISHAL		EGDRLEQVIETLCNVGAAALLMPAELIDDLLTRFGPTGRALAELARRADVSATSALY	180	(301)
T ss_dssp		ннннннн	ннсннннннннсо	синнинининининининыксинининининыксулинининининин		
T ss_pred		ннннннн	HhCCcchhhhhhHhha	сСссһНННННННННННҺҺССНННННННННСССНННННННннсСССННННН		
0						
Q ss_pred		нннннн				
Q Raph_50	63	YLQLLTR	69 (85)			
Q Consensus	63	Passasa	69 (85)			
		+				
T Consensus	181	R1~~~~~	187 (301)	2		
T 3DTE_A	181	ALAERTA	187 (301)	-		
T ss_dssp		ННННТСС				
T ss_pred		HHHHcCC				



Aligns with only part of the peptidase domain. The alignment begins with HExxH and ends with the three HTH helices (alignment boundaries shown with arrows). Note the PFAM box at bottom that annotates the metallopeptidase domain.

With the long protein as query:



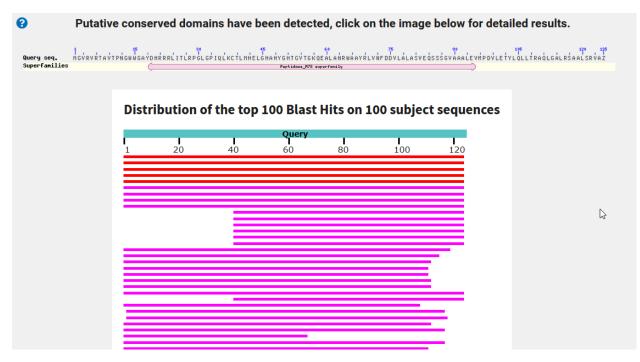
Template alignment Template 3D Structure PDBe 2. 3DTE_A IrrE protein; Deinococcus, Radiotolerance, Gene regulation, Metallopeptidase, IrrE; HET: MSE; 2.6A {Deinococcus deserti} Probability: 99.73%, E-value: 1e-15, Score: 103.96, Aligned cols: 107, Identities: 22%, Similarity: 0.153, Template Neff: 9 Q ss_pred СсееЕЕСССССсееЕЕЕСССССНИНИНИНИНИНИНИНИНИНИНИССССС------СһИНИНИНИНИНИНИ GVRVRTAVTPNGWNGAYDHRRRLITLRPGLGPIQLKCTLMHELGHAHYGHTGV-----TGKQEALANRWAA Q Raph_50long 2 67 (125) gi~i~~~~~~g~~~~~I~i~~~~~~I~hE1~H~~~~~~~ 0 Consensus 2 67 (125) ||.|...+++. ..|++..+.|+++.+.+.+++|+++||+||+++++....|.+||.||+ T Consensus gi~v~~~l~~-~~g~~~~~I~ln~~~~r~rFtlaHELgH~ll~~~~~ 141 (301) 63 ----E~eAn~FAa T 3DTE_A 63 GITLTFMPMGQ-RDGAYDPEHHVILINSQVRPERQRFTLAHEISHALLLGDDDLLSDLHDEYEGDRLEQVIETLCNVGAA 141 (301) T ss_dssp T_ss_pred Q ss_pred YRLVNFDDVLALASVEQ----SSSGVAAALEVMPDVLETYLQLLTR 109 (125) Q Raph_50long 68 ~11~p~~~~~~~~~~~~1a~~~~V~~~~~~r1~~~~~ 0 Consensus 68 109 (125) .+|||...+...+.... .+.+|++.|++|...+..|+.+++.. T Consensus 142 ~LL~P~~~~V~~La~~~vS~~a~~~Rl~~~~ 187 (301) T 3DTE_A 142 ALLMPAELIDDLLTRFGPTGRALAELARRADVSATSALYALAERTA 187 (301) T_ss_dssp T ss_pred

CHAIN Α Radiation response metalloprotease IrrE - Deinococcus deserti P Explore Sequence Annotations in 3D \sim 80 12.0 140 160 1.80 200 220 240 CHAIN A UNIPROT C1CZ84 SECONDARY STRUCTURE UNMODELED RAMACHANDRAN OUTLIER ANGLE OUTLIER BOND OUTLIER ROTAMER OUTLIER RSRZ OUTLIER RSCC OUTLIER BINDING SITE BURIED RESIDUES ш 111 11 ш 111 1 11 ш COVALENT BOND ARTIFACT MODIFIED MONOMER HYDROPATHY DISORDER DISORDERED BINDING PFAM CATH ECOD MOLECULE PROCESSING ACTIVE SITE MUTAGENESIS REGION

Now, the HHPred alignment is across the whole peptidase domain in IrrE

Help

BLAST and **CDD**



Aligns across full length of the peptidase M78 domain

Conserved do Local query sequen	-	l Query_1706891] View	Standard R	esults 🗸 <table-cell></table-cell>
Protein Classifi	cation			?
		domain-containing protein(domain architecture ID 1522) main-containing protein which includes the catalytic domain of ImmA/IrrE family metallo-endopeptidase		
Graphical sumn	nary 🗌 Zoom te	p residue level show extra options »		2
Query seq. MGN Specific hits Non-specific hits Superfamilies	15 VRVRTAVTPNGUU	SAÝDHŘRRLÍ ITLRPŠL GPIQLKCTLHHELŠHAHVGHTGÝTGKQEŠLANRUÁAVŘLVNÝ POČVLÁLAŠVEQSSŠGVÄAALEVHPDVLETVLQLTRAQLGÁ POLIONS 778 Peptidase_M78 superfamily Search for similar domain architectures [27] Refine search [27]	120 LRSAALSRV	1125 1 2 2 2
List of domain l	hits			?
H Name	Accession	Description	Interval	E-value
[+] Peptidase_M78 [+] ImmA	pfam06114 COG2856	IrrE N-terminal-like domain; This entry includes the catalytic domain of the protein ImmA, Zn-dependent peptidase ImmA, M78 family [Posttranslational modification, protein turnover,	18-95 25-68	5.84e-07 6.26e-04
		Blast search parameters		
Data Source: User Options:		search RID = 68WF46DF015 2: CDSEARCH/cdd Low complexity filter: no Composition Based Adjustment: yes E-value threshold: 0.01 Maximum number of hits: 500		C

The peptidase domain alignments start at around 20aa or 24aa. The short start proteins start at about 40 aa on this alignment, which cuts out part of the peptidase conserved domain.

See Official Function List for naming. These examples hit IrrE-like metallopeptidases, which include a HTH domain.

DNA alignment shows sequence and reading frame conservation in the gap with no coding potential

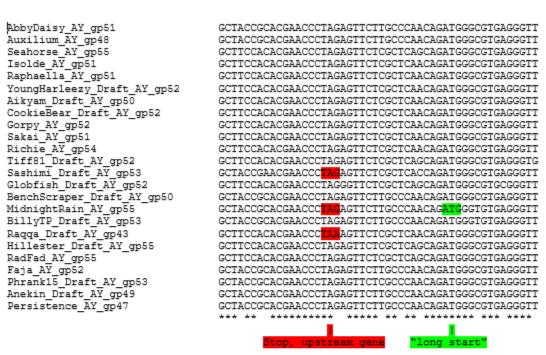
ClustalW close-up view, like Starterator

DNA sequences: Relatives of MidnightRain_55, plus 500 bp downstream of the stop codon, which includes the full length of the downstream gene, MidnightRain 54 and its relatives.

CLUSTAL 2.1 multiple sequence alignment

Faja_AY_gp52

Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 MidnightRain_AY_gp55 BillyTP_Draft_AY_gp53 RadFad_AY_gp55 Faja_AY_gp52 Phrank15_Draft_AY_gp53 Anekin_Draft_AY_gp49 Persistence_AY_gp47



 AbbyDaisy_AY_gp51
 CGGACGGCTGTCACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG

 Auxilium_AY_gp48
 CGGACGGCTGTCACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG

 Seahorse_AY_gp55
 AGACAGCTGTCACACCCTAACGGATGGTGGGGCGCGTACGATCACAGGCG

 Isolde_AY_gp51
 CGAACAGCCGTGACCCCTAATGGATGGTGGGGCGCGTACGATCACAGGCG

 YoungHarleezy_Draft_AY_gp52
 CGAACAGCCGTGACCCCTAATGGATGGTGGGGCGCGTACGATCACAGGCG

 Aikyam_Draft_AY_gp50
 CGAACAGCCGTGACCCCTAACGGATGGTGGGGCGCGTACGATCACAGGCG

 CookieBear_Draft_AY_gp52
 CGAACAGCCGTGACCCCTAACGGATGGTGGGGCGCGATACGATCACAGGCG

 SabaitArgg51
 CGAACAGCCGTGACCCCTAACGGATGGTGGGGGCGCATACGATCACAGGCG

 CookieBear_Draft_AY_gp52
 CGAACAGCCGTGACCCCTAACGGGTGGGGGGCGCATACGATCACAGGCG

 Gorpy_AY_gp52
 CGAACAGCCGTGACCCCTAATGGATGGTGGGGCGCATACGATCACAGGCG

 SabaitArg
 CGAACAGCCGTGACCCCTAATGGATGGTGGGGCCCATACGATCACAGGCG

 CGAACAGCCGTGACCCCTAATGGATGGTGGGGGCGCATACGATCACAGGCG CGAACAGCCGTGACCCCTAACGGATGGTGGGGTGCATACGATCACAGGCG
 Richie_AY_gp54
 CGAACAGCCGTGACCCCTAACGGATGGTGGGGGGGCATACGATCACAGGCG

 Tiff81_Draft_AY_gp52
 CGAACAGCCGTGACCACCGCGCATGGTGGGGGGCGCGTACGATCACAGGCG

 Sashimi_Draft_AY_gp53
 CGGACAGCTGTCACACCGCGCATGGTGGGGGGCGCGTACGATCACAGGCG

 Globfish_Draft_AY_gp52
 CGGACGCTGTCACACCGCACCGTACGGAGGGCGCGTACGATCACAGGCG

 BenchScraper_Draft_AY_gp50
 CGGACGCTGTCACACCTAACGGAGGGGGGCGCGTACGATCACACGGCG

 WidpightBain_AY_gm55
 CGGACGCCTGTTACACACGCATCGCGCGCCGTACGATCACACGGCG
 CGGACGGCTGTTACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG CGGACGGCTGTTACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG CGAACGGCTGTCACACCGAATGGTTGGTGGGGCGCGTACGATCACAGGCG CGGACGGCTGTCACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG CGAACAGCTGTCACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG CGGACGGCTGTCACACCTAACGGATGGTGGGGCGCGTACGATCACAGGCG CGGACGGCTGTCACACCTAACGGATGGTGGGGCGCATACGATCACAGGCG - -- -- -- -- -- -- ------ -- -------

AbbyDaisy AY gp51	CCGGCTGATAACTCTTAGGCCAGGTCTTGGTCCGATCCAGTTGAAGTGCA
Auxilium AY gp48	CCGGCTGATAACTCTTAGGCCAGGTCTTGGTCCGATCCAATTGAAGTGCA
Seahorse AY gp55	CCGGCTGATCACTCTTCGCCCAGGTCTTGGTCCTATTCAATTGAAATGCA
Isolde AY gp51	CCGGCTGATCACTCTGCGCCCAGGTCTCGGTCCTATTCAATTGAAGTGCA
Raphaella AY gp51	CCGGCTGATCACTCTGCGCCCAGGTCTCGGTCCTATTCAATTGAAGTGCA
YoungHarleezy_Draft_AY_gp52	CCGGCTGATCACTCTGCGCCCAGGTCTCGGTCCGATTCAATACAAGTGCA
loungharieezy_brait_Ar_gpsz	CCGGCTGATCACTCTCGCCCAGGTCTCGGTCCTATTCAATACAAGTGCA
Aikyam_Draft_AY_gp50	
CookieBear_Draft_AY_gp52	CCGGCTGATCACTCTGCGCCCAGGTCTCGGTCCTATTCAATTGAAGTGCA
Gorpy_AY_gp52	CCGGCTGATCACTCTTCGCCCAGGTCTCGGTCCCATTCAATACAAGTGCA
Sakai_AY_gp51	CCGGCTGATCACTCTTCGCCCAGGTCTCGGTCCCATTCAATACAAGTGCA
Richie_AY_gp54	CCGACTGATCACTCTTCGCCCAGGTCTCGGTCCCATTCAATACAAGTGCA
Tiff81_Draft_AY_gp52	CCGGCTGATAACTCTTAGGCCAGGTCTTGGCCCGATCCAGTTGAAGTGCA
Sashimi_Draft_AY_gp53	CCGGCTGATCACTCTTCGCCCAGGTCTAGGACCGATTCAATTGAAGTGCA
Globfish_Draft_AY_gp52	CCGGCTGATCACTCTTCGCCCAGGTCTCGGGCCTATTCAATTGAAGTGCA
BenchScraper Draft AY gp50	CCGGCTGATAACTCTTAGGCCTGGTCTTGGTCCGATTCAATACAAGTGCA
MidnightRain AY gp55	CCGGCTGATAACTCTTAGGCCAGGTCTTGGTCCGATCCAGTTGAAGTGCA
BillyTP Draft AY gp53	CCGGCTGATAACTCTTAGGCCAGGTCTTGGTCCGATCCAGTTGAAGTGCA
Ragga Draft AY gp43	CCGGCTGATCACTCTTCGCCCAGGTCTCGGTCCCATTCAATACAAGTGCA
Hillester Draft AY gp55	CCGGCTGATCACTCTTCGCCCCGGTCTTGGTCCGATTCAATTGAAGTGCA
RadFad AY gp55	CCGGCTGATCACTCTTCGCCCCGGTCTTGGTCCGATTCAATTGAAGTGCA
Faja AY gp52	CCGGCTGATAACTCTTAGGCCAGGTCTTGGTCCTATTCAATTGAAGTGCA
Phrank15 Draft AY gp53	CCGGCTGATCACTCTTAGGCCAGGTCTTGGTCCGATCCAGTTGAAGTGCA
Anekin Draft AY gp49	CCGGCTGATAACTCTTAGGCCAGGTCTTGGCCCGATTCAGTTGAAGTGCA
Persistence AY gp47	CCGGCTGATCACTCTTAGACCAGGTCTTGGCCCGATTCAGTTGAAGTGCA
Persiscence_RI_gp4/	*** ***** ***** * ** ***** ** ** ** **
AbbyDaisy AY gp51	CTTTGATGCACGAGCTAGGTCACGCTCACTACGGTCATACGGGTGTGACG
	CTTTCITCII CCI CCTTCCCCCI CCCTCI CTICCCCCII TI CCCCCCCTCI CC
Auxilium_AY_gp48	CTTTGATGCACGAGCTTGGCCACGCTCACTACGGTCATACGGGCGTGACG
Seahorse AY gp55	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCATTATGGTCATACGGGTGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCATTATGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGCCATACGGGTGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCATTATGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCATTATGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGCCATACGGGTGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCATTATGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGTGGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp52 Sashimi_Draft_AY_gp53	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCATTATGGTCATACGGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGGTGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp52 Sashimi_Draft_AY_gp53 Globfish_Draft_AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCTCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCACGCGTGGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCACGCGTGGACG CTCTGATGCACGAGCTAGGCCACGCCAC
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp52 Sashimi_Draft_AY_gp53 Globfish_Draft_AY_gp52 BenchScraper_Draft_AY_gp50	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCTCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGGATGCACGAGCTGGCCCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGTGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGTGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp52 BenchScraper_Draft_AY_gp50 MidnightRain_AY_gp55	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCTCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTTGGCCACGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGTGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGCCATGCCCACTACGGTCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp52 BenchScraper_Draft_AY_gp50 MidnightRain_AY_gp53	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTTGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCACGCGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCACGCGCGTGACG CTTTGATGCACGAGCTAGGCCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGCCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGCCATGCCCACTACGGTCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp55 BenchScraper_Draft_AY_gp55 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp43	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTTGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCACGCCGCGCGCACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGCCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp52 BenchScraper_Draft_AY_gp50 MidnightRain_AY_gp53 Raqqa_Draft_AY_gp43 Hillester_Draft_AY_gp55	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGGGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGGGTGTGACG CTCTGATGCACGAGCTTGGCCATGCCCACTACGGCCACGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCACGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTTGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 BenchScraper_Draft_AY_gp53 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp55 RadFad_AY_gp55	CTCTTATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGGTGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCACGCGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCACGCGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCACGCGGCGTGACG CTTTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGCGTGACG CTTTGATGCACGAGCTAGGCCACGCCAC
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp55 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp43 Hillester_Draft_AY_gp55 RadFad_AY_gp52	CTCTTATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCACGCGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCACGCGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCACGCGGCGTGACG CTTTGATGCACGAGCTAGGCCACGCCCACTACGGCCACGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGCCATACGGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGCCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG
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Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp53 BenchScraper_Draft_AY_gp55 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp53 Raqa_Draft_AY_gp55 Faja_AY_gp52 Phrank15_Draft_AY_gp53 Anekin_Draft_AY_gp49	CTCTTATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCAC
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp53 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp55 RadFad_AY_gp55 Faja_AY_gp52 Phrank15 Draft_AY_gp53	CTCTTATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGACATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCAC
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp53 BenchScraper_Draft_AY_gp55 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp53 Raqa_Draft_AY_gp55 Faja_AY_gp52 Phrank15_Draft_AY_gp53 Anekin_Draft_AY_gp49	CTCTTATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCAC
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp53 BenchScraper_Draft_AY_gp55 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp53 Raqa_Draft_AY_gp55 Faja_AY_gp52 Phrank15_Draft_AY_gp53 Anekin_Draft_AY_gp49	CTCTTATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCATGCCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCACGCGGGGGACA CTCTGATGCACGAGCTGGCCACGCCCACTACGGCCACGCGGGGGACA CTCTGATGCACGAGCTGGCCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTGGCCCACGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCATGCCCACTACGGTCATACGGGCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG CTTTGATGCACGAGCTAGGTCACGCCACTACGGTCATACGGCCGTGACG
Seahorse_AY_gp55 Isolde_AY_gp51 Raphaella_AY_gp51 YoungHarleezy_Draft_AY_gp52 Aikyam_Draft_AY_gp50 CookieBear_Draft_AY_gp52 Gorpy_AY_gp52 Sakai_AY_gp51 Richie_AY_gp54 Tiff81_Draft_AY_gp53 Globfish_Draft_AY_gp53 Globfish_Draft_AY_gp53 BenchScraper_Draft_AY_gp55 BillyTP_Draft_AY_gp53 Raqqa_Draft_AY_gp53 Raqa_Draft_AY_gp55 Faja_AY_gp52 Phrank15_Draft_AY_gp53 Anekin_Draft_AY_gp49	CTCTTATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGTCACGCCACTACGGCCATACGGGCGTGACG CTCTGATGCACGAGCTAGGCCACGCCAC

Conserved DNA sequence between "long start" and "short start" - no frameshifts. It appears that natural selection may be keeping this region intact, and potentially translatable.

The AA sequence in this region aligns with IrrE peptidase domain, so does not appear to be random DNA sequence, despite the minimal coding potential signal.