

GENSCAN Output

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GENSCAN 1.0 Date run: 18-Aug-124 Time: 09:40:56

Sequence /tmp/08_18_24-09:40:56.fasta : 2815 bp : 52.82% C+G : Isochore 3 (51 - 57 C+G%)

Parameter matrix: HumanIso.smat

Predicted genes/exons:

Gn.Ex	Type	S	.Begin	...End	.Len	Fr	Ph	I/Ac	Do/T	CodRg	P....	Tscr..
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1.01	Init	+	221	406	186	1	0	94	105	207	0.703	22.03
1.02	Intr	+	1013	1058	46	1	1	106	89	4	0.929	0.77
1.03	Intr	+	1246	1293	48	2	0	140	82	25	0.987	6.24
1.04	Term	+	1595	2016	422	0	2	132	55	518	0.985	48.73
1.05	PlyA	+	2792	2797	6							1.05

Suboptimal exons with probability > 0.010

Exnum	Type	S	.Begin	...End	.Len	Fr	Ph	B/Ac	Do/T	CodRg	P....	Tscr..
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S.001	Intr	+	215	406	192	1	0	65	105	210	0.258	20.61
S.002	Init	+	236	406	171	1	0	68	105	186	0.035	17.71
S.003	Intr	+	971	1058	88	1	1	57	89	0	0.070	-2.96
S.004	Intr	+	1595	2012	418	0	1	132	48	511	0.012	45.15

Predicted peptide sequence(s):

>/tmp/08_18_24-09:40:56.fasta|GENSCAN_predicted_peptide_1|233_aa

MSTESMIRDVELAEEALPKKTGGPQGSRRCLFSLFSFLIVAGATTLFCLLHFGVIGPQR

EEFPRDLSLISPLAQAVRSSRTPSDKPVAVVAVNPQAEGQLQWLNRANALLANGVELR

DNQLVVPSEGLYLIYSQVLFKGQGPCSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRE

TPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL

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