

Supplementary information

Genetic and Proteomic characterization of Bile Salt Export Pump (BSEP) in Snake Liver

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1. Predicted ABCB/11 sequences from 3 known snakes

There are already predicted sequences of ABCB/11 from 3 snakes: *Ophiophagus Hannah*, *Thamnophis sirtalis* and *Python bivittatus*. Based on the shared sequences (conserved region), primers were designed and PCR amplified on the sample, which is exemplified as *Elaphe carinata-P*.

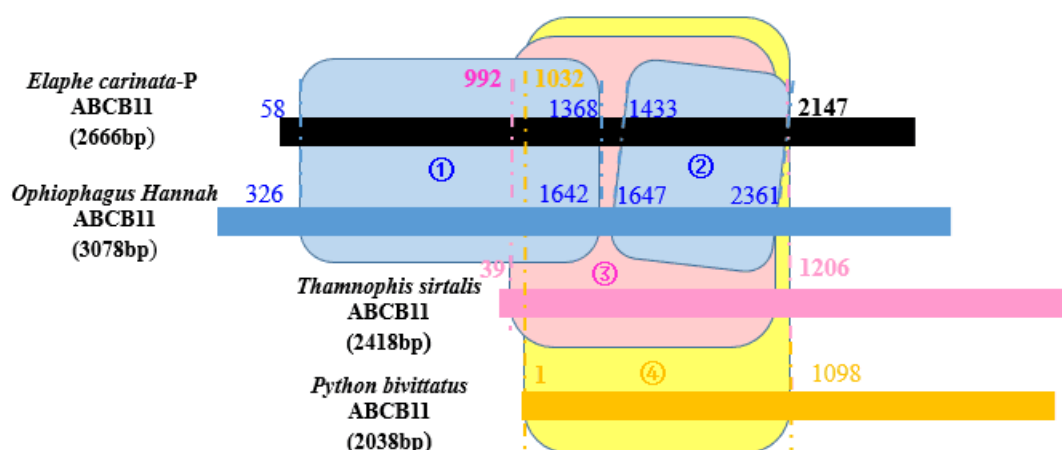


Fig. 1 Conserved region in predicted sequences between three different snakes. The colored square stands for shared sequences in different species. There were 2666bp identified from *Elaphe carinata-P*, which is detailed in the main text.

2. First sequences information:

Based on the conserved region of the three predicted snake ABCB/11 sequences, primers were designed and PCR amplification gives the sequences listed as below (red text is the primer sequences):

AGCAACTGACGCCTCTCAAGTTCAAGGGGCGACTGGCACACAGATAGGCATGATTGTGAATTCCTTCACCAATATCGGAGTCTC
CATTATTATCGCTTTCTACTTCAGCTGGAACTCAGCTTAGTCATAACCTGCTTCTTGCCTTTCTGGCTTTGTGAGGAATGGTTCA
GTCTCGAATGCTGACAGGC

3. Sequence information of later fragments:

Later fragment information were obtained based on the first sequences, detailed information were listed as below (red text is the primers):

Fragment 2

GAGCATCTTCTCGACAGCGTTCCAGATCTCAGTTGTCAAACATAGTCCCTGACCATCCAGCGTCAATTGTAGGATCCTATACAG
AGCGCAACTGTAGCATATCTCACTATGAAGAAGATGGAAGACCATTATGAAGGAACGGATTCATGAAAAGGATGAGGAAGAA
GTCGTACCTGCTAACGTGACCAGGATTTTGAAGTACAACGCTCCCGAATGGCCCTATATGGTGCTTGGATCCCTTGGGGCAGGG

GTCAATGGGGCAGTCAACCCCTCTCTATGCCCTGCTCTTCAGTCAAATTCTTGGAACCTTTTCGGTGCCTGATGAAGAAGAGCAA
AGAGCTCAGATCAACGGTGTCTGCTTGTCTTTGTGGTGGTTGGAATCGTATCATTCTTCACTCAGTTCTTACAGGGCTATACGTT
TGCAAAAGCCGGAGAATTGCTTACACGACGCTTAAGGAAAATTGGCTTCCAGGCGATGTTAGGCCAAGAAATTGGCTGGTTTG
ATGACCATAGAAACAGCCCAGGGGCCTTGACTACGAGACTA**GCAACTGACGCCTTCTCAAGT**

Fragment 3

TGAGGCTACCGTGCAAGAGACACCTTCCAAGGCTCGTTTTGGGCGCACCGCAATCTCCATAGCTCACCGTTGTCCACAGTGA
AATCTGCTGACATTATCGTTGGGTTGAGCATGGAAGAGCTGTGGAAAGAGGGAAACATGAAGAACTGATAGAACGGAAAGG
AGTGTATTTCACTGGTAACGTTGCAAAGCCAAGGCGACAAGGCACTCATGGAAAGCTCAATGCAAATATCTGACCCAAAACC
TGAAAAAATGCAGTCTTTCAGCAGGGGAAGCTATCAAGCAAGTTTACGAGCATCTCTCGACAGCGTTCAGATCTCAGTTGTC
AAACATAGTCCCTGACCATCCAGCGTCAATTGTAGGATCTATACAGAGCGCAACTGTAGCATATCTCACTATGAAGAAGATGGA
AGACCATTATGAAGGAACGGATTATGAAAAGGATGAGGAAGAAGTCGT**ACCTGCTAACGTGACCAGGA**

Fragment 4

GGACATTGGCTGGTTTGATTGTACATCAGTAGGGGAACCTCAATACCGCAATTTCTGAGATTGTGAGAGGCTGGAAGTTAACC
TTGGTTATTATCGCAGTCAGTCTCTAATTGGGATCGGAGCTGGCATAATTGGCCTGTCTGTAGCAAAGTTGACGGGTCTAGAGT
TAAAAGCTTATGCAAAAGCTGGGGCCATCGCTGATGAAGTCTCTCATCGATCCGAACCGTGGCTGCCTTTGGAGGAGAAAAA
AAAGAAGTTGAAAGATATGACAAAAACCTGGTGTTTGCTCAAACCTGGGGGATCAGAAAGGGAATCATTATGGGATTTTACA
GGCTACATTTGGTGATCATTTTCTGTGCTATGCACTGGCCTTCTGGTATGGCTCAAACTTGTCTTGAAGAAGAGGAATACT
CTGTGGCACCCCTTTTGCAGGTCTTTTCTCGGCGTCTAGTAGGTGCCTTAAATCTTGGTCAAGCAGCCCTTGCTTGAAGGCTT
TTGCAACAGGTCGAGGGGCTGCCACAAATATTTGAGACAATAGATGAAAAACCTAGAATTGACTGTATGTCAGAAGATGGCT
ACAACTGGACAAAGTCCGAGGTGACATTGAATCCATAATGTAACCTTCCATTACCCATCCAGGCCCGATGTTAAGATTTAGA
TCAACTCAGCATGATTATCAAGCCAGGTGAAACACAGCCTTTGTTGGCCCAAGCGGAGCAGGGAAAAAGTACCACAATTCAGC
TGATCCAGCGCTTCTATGACCCTACAGAAGGCATGGTTACCCTAGATGGACACGACATTCGTTCCCTTAACATTCACTGGCTGCG
TTCTTTGATGGGGGTGGTGGAGCAAGAACCTGTCTGTTGCCACCACTATAGCAGAAAACATTTCTACGGTCGGGAAGATG
CCACTATGGAAGACATCGTCAGAGCTTCAAAGAAGCCAATGCCTACAGCTTTATCATGGATCTGCCTTGCAATTCGACACCCT
TGTTGGAGAAGGTGGTGGCCAAATGAGCGGAGGCCAGAAGCAGCGAATTGCCATTGCTCGGGCTTTAGTTGCAAACCCCAA
ATCTGTTGCTGGACATGGCTACATCAGCACTGGACAATGAAAGTGAAGCTACTGCAATAAACTCGACCT

3'RACE results

When RACE was used to obtain the extra sequence information, different primers were used (see table. 1). The resulting sequences were listed below:

CGCTTTCTACTTCAGCTGGAAACTCAGCTTAGTCATAACCTGCTTCTTGCCTTTCTTGCTTTGTGAGGAATGGTTCAGCATTCA
ATGCAAATGGTGGCATTGAACTGTATTTCTACTGCTCCATCATCATCATCTCGCTCTCAATGATTCTGGGTGGTTACAACAA
TCAAAGAAATGACAATGAAATCAATAAAAAATGAAGAAAATGAAGATAAAGGATGGCAAGAGCGATGAAGTGAGGGATCTCTCT
CTCCCTTACCAAAGACCTTCCTTACCAAAGAGCCTGGTCTCCTAGCTTCTAAACAACAATAGAGTGGGGGACCACCCACATCTT
GGGAGACCCTTGCTCCAGAGGGCTGCAAGAGAGAAGGACGTATTCACCATATGATGGGGAATACCAGACGCTGATTCTTAC
ATCCATAAAAGAGCAATATTGAAACCTGACTCTGCGAATCTCTAGGGATTCTTATATATACAATGTCTTCTGTGTGAATGGTTC
TCTACGTAGTGTTCAAAGCACTTTGGCCAGATTACAAAATCCAATTATTCTATTCACTGCCA**TGA**AAAAAAAAAAAAAAAAAAAA
A

Table 1. Information of primers in 3' RACE

procedure	primers	Sequence (5'→3')
cDNA synthesis	3RACEP1	gcagtgggtatcaacgcagagtac- TTTTTTTTTTTTTTTTTTTTTTTTTVN
	Forward 1 (F1)	CCTTCACCAATATCGGAGTCTC
Nest PCR	Forward 2 (F2)	CGCTTTCTACTTCAGCTGGAAC
	R1=R2	
	=3RACEP2	gcagtgggtatcaacgcagagtac

4. Spliced whole sequences of BSEP from *Elaphe carinata*

Together, all the sequences were spliced in a single sequence, listed as below:

GGACATTGGCTGGTTTGATTGTACATCAGTAGGGGAACCTCAATACGCGAATTTCTGAGATTGTGAGAGGCTGGAAGTTAACCT
 TGGTTATTATCGCAGTCAGTCCTCTAATTGGGATCGGAGCTGGCATAATTGGCCTGTCTGTAGCAAAGTTGACGGGTCTAGAGTT
 AAAAGCTTATGCAAAAGCTGGGGCCATCGCTGATGAAGTGCTCTCATCGATCCGAACCGTGGCTGCCTTTGGAGGAGAAAAAA
 AAGAAGTTGAAAGATATGACAAAAACCTGGTGTGTTGCTCAAACTGGGGGATCAGAAAGGGAATCATTATGGGATTTTTCACAG
 GCTACATTTGGTGATCATTTTCTGTGCTATGCACTGGCCTTCTGGTATGGCTCAAACTTGCTCTGAAGAAGAGGAATACTCT
 GCTGGCACCCTTTTGAGGTCTTTTCTCGGCGTCTAGTAGGTGCCTTAAATCTTGGTCAAGCAGCCCCTTGCTTGAAGCTTTT
 GCAACAGGTCGAGGGGCTGCCACAAATATATTTGAGACAATAGATGAAAAACCTAGAATTGACTGTATGTCAGAAGATGGCTAC
 AAATGAGCAAAAGTCCGAGGTGACATTGAATTCATAATGTAACCTTCCATTACCCATCCAGGCCCGATGTTAAGATTTTAGATC
 AACTCAGCATGATTATCAAGCCAGGTGAAACCACAGCCTTGTGTTGGCCCAAGCGGAGCAGGGAAAAGTACCACAATTCAGCTG
 ATCCAGCGCTTCTATGACCCTACAGAAGGCATGGTTACCCTAGATGGACACGACATTCGTTCCCTTAACATTCAGTGGCTGCGTT
 CTTTGATGGGGGTGGTGGAGCAAGAACCTGTCTGTTGCCACCACTATAGCAGAAAACATTTCTACGGTCGGAAGATGCC
 ACTATGGAAGACATCGTCAGAGCTTCCAAAGAAGCCAATGCCTACAGCTTTATCATGGATCTGCCTCTGCAATTCGACACCCTTG
 TTGGAGAAGGTGGTGGCCAAATGAGCGGAGGCCAGAAGCAGCGAATTGCCATTGCTCGGGCTTTAGTTGAAACCCCAAAAT
 CCTGTTGCTGGACATGGCTACATCAGCACTGGACAATGAAAGTGAGGCTACCGTGCAAGAGACACTTTCAAGGCTCGTTTTG
 GGCGCACCGCAATCTCCATAGCTCACCGTTTGTCCACAGTGAAATCTGCTGACATTATCGTTGGGTTTGAAGCATGGAAGAGCTG
 TGGAAGAGGGGAAACATGAAGAACTGATAGAACGGAAGGAGTGATTTTCACTGGTAACGTTGCAAGCCAAGGCGACA
 AGGCACTCATGGAAAGCTCAATGCAAATATCTGACCCAAAACCTGAAAAAATGCAGTCTTTCAGCAGGGGAAGCTATCAAGCA
 AGTTTACGAGCATCTCTCGACAGCGTTCAGATCTCAGTTGTCAAACATAGTCCCTGACCATCCAGCGTCAATTGTAGGATCCT
 ATACAGAGCGCAACTGTAGCATATCTCACTATGAAGAAGATGGAAGACCATTTATGAAGGAACGATTATGAAAAGGATGAG
 GAAGAAGTCGTACCTGCTAACGTGACCAGGATTTTGAAGTACAACGCTCCGAATGGCCCTATATGGTGCTTGGATCCCTTGGG
 GCAGGGGTCAATGGGGCAGTCAACCTCTCTATGCCCTGCTCTTCACTCAAATCTTGGAACTTTTCGGTGCTGATGAAGAA
 GAGCAAAGAGCTCAGATCAACGGTGTCTGCTTGTGTTGGTGGTGAATCGTATCATTCTTCACTCAGTTCTTACAGGGCT
 ATACGTTTGCAAAGGCCGGAAGATTGCTTACACGACGCTTAAGGAAAATTGGCTTCCAGGCGATGTTAGGCCAAGAAATTGGC
 TGGTTTGATGACCATAGAAACAGCCAGGGGCTTGACTACGAGACTAGCAACTGACGCTCTCAAGTTCAAGGGGCGACTG
 GCACACAGATAGGCATGATTGTGAATTCCTTACCAATATCGGAGTCTCATTATTATCGCTTCTACTTCAGCTGGAACTCAGC

5. Blast result between resulting sequences and other species



[illegible]

Range	2: 3788 to 3888	GenBank	Graphics	Need Match	Previous Match	First Match
Score	Expect	Identities	Gaps		Strand	
50.0 bits(54)	0.031	71/100(71%)	0/100(0%)		Plus/Plus	
Query	1039	GGGGCCAGACAGGAGTGCATCTCTCTGGCCGCTTAGTCTGGAAAGCCAAAATCTGTT			1098	
Sbjct	3788	GGGGGGAAGAACACGACCATCTCATCTCTGGCCGACATGACGAGCATCTAAATCTTGC			3847	
Query	1099	TGCTGCATCGGTACATCAGCAGTCGCAATGAAGTGA		1138		
Sbjct	3848	TATAGAGAGGCATGCTCTCTTACAGACAGCAGTCA		3887		

Fig. 4 blast result of resulting sequences and *Homo sapiens*

Oryctolagus cuniculus ATP binding cassette subfamily B member 11 (ABCB11), mRNA
Sequence ID: NM_001082083.1 Length: 4664 Number of Matches: 2

Range 1: 746 to 2776		GenBank	Graphics	Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
1029 bits(1140)	0.0	1483/2081(71%)	64/2108(3%)	Plus/Plus	
Query 72	TGGAGGTTAACTGGTATTATATGACGTCAGTCTCTAATGGGATGGAGTGGCATA	131			
Sbjct 746	TGGAACTGACCTGGTATTATCTTCCTGACGCTCTCAATGGGATGGAGTGGCATA	805			
Query 132	ATTGGGCTGCTGTAGCAAGTTGACGGGCTCA-GAGTTAAAGCTTATGCAAGCTGG	190			
Sbjct 806	ATAGGTTGAGGCTGCTCAAGTTTACAGA-CTAGAGCTAAAGGCTATGCAAGCTGG	864			
Query 191	GGCATGCTGATGAGTGGCTCTCATGATCCAGACCTGGCTTGGAGGAG-333	250			
Sbjct 865	GTGCTAGCTGATGAGTCAATTCATCTATGCAAGCTGGCTTGGAGGAG-333	924			
Query 251	3333GAGTTGAAAGATATGCAAAAGCTGGTGTCTCTCAAGC-TGGGGATGCAAAA	309			
Sbjct 925	AAAGAGGTTGAAAGATATGCAAAAGCTGTATTGCTCAAGC-TGGGGATGCAAAA	984			
Query 310	GGGAATCATATTGGGATTTTCAAGGCTGACATTTGGTCAATTTTCTGCTATGCT	369			
Sbjct 985	AGTATAGTATGGGCTTCTTACTGATGACATGGTGTCTCACTTTTCTGCTATGCT	1044			
Query 370	ACTGGGCTTGGGATGAGTCTCAAAAGTGTCTGTGAAAGAGGAACTCTGCTGGAC	429			
Sbjct 1045	ATTGGGCTTGGGATGAGTCTCAAAAGTGTCTGTGAAAGAGGAACTCTGCTGGAC	1104			
Query 430	CTTTTGGAGGCTTTTCTGGGGTCTTAGTAGGTGCTTAAATCTTGGTCAAGGCTCC	489			
Sbjct 1105	CTTTTGGAGGCTTTTCTGGGGTCTTAGTAGGTGCTTAAATCTTGGTCAAGGCTCC	1163			
Query 490	CTTCTTGGAGGCTTTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCT	549			
Sbjct 1164	CTTCTTGGAGGCTTTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCT	1223			
Query 550	ATGAAAAAGCTAGATATGCTGATATGAGAGGATGCTTACAAAGTGGAGTGGAG	609			
Sbjct 1224	ACAGAGAAAGCTAGATATGCTGATATGAGAGGATGCTTACAAAGTGGAGTGGAG	1283			
Query 610	GTGAAATGAAATGATATGCTGATATGAGAGGATGCTTACAAAGTGGAGTGGAG	669			
Sbjct 1284	GTGAAATGAAATGATATGCTGATATGAGAGGATGCTTACAAAGTGGAGTGGAG	1343			
Query 670	TAGATCAACTGAGCATGATATGAGAGGATGCTTACAAAGTGGAGTGGAG	729			
Sbjct 1344	TAGATCAACTGAGCATGATATGAGAGGATGCTTACAAAGTGGAGTGGAG	1403			
Query 730	GAGCAGGGAAGGATGAGCAATGAGTGTGAGGCTTCTATGAGCTTACAGAGGCA	789			
Sbjct 1404	GAGCAGGGAAGGATGAGCAATGAGTGTGAGGCTTCTATGAGCTTACAGAGGCA	1463			
Query 790	TGGTACCTAGATGAGGACAGATGCTTCTTCAATGAGTGGCTGGCTTCTTGA	849			
Sbjct 1464	TGGTACCTAGATGAGGACAGATGCTTCTTCAATGAGTGGCTGGCTTCTTGA	1523			
Query 850	TGGGGGTGGTGGAGGAGGAGTGGTGTCTTCTTCTCAC-ACCATAGGAGAAAAATGCT	908			
Sbjct 1524	TGGGGGTGGTGGAGGAGGAGTGGTGTCTTCTTCTCAC-ACCATAGGAGAAAAATGCT	1582			
Query 909	TAGGCTGGAGATGAGGATGAGGAGGAGTGGTGTCTTCTTCTCAC-ACCATAGGAG	968			
Sbjct 1583	TAGGCTGGAGATGAGGATGAGGAGGAGTGGTGTCTTCTTCTCAC-ACCATAGGAG	1642			
Query 969	TAGAGCTTATCATGAGGAGGAGTGGTGTCTTCTTCTCAC-ACCATAGGAGGAGG	1028			
Sbjct 1643	TAGAGCTTATCATGAGGAGGAGTGGTGTCTTCTTCTCAC-ACCATAGGAGGAGG	1702			
Query 1029	CAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1088			
Sbjct 1703	CAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1762			

Query 1089	AAAATCTGTTGCTGGACATGCTACATGACACTGGACAAATGAAAGTGAAGGCTACGGT	1148			
Sbjct 1763	AAATCTGTTGCTGGACATGCTACATGACACTGGACAAATGAAAGTGAAGGCTACGGT	1822			
Query 1149	CAGAGAGACCTTCCAGGCTGGTTTGGGGGCAAGCAATCTCATAGCTCAAGCTTGG	1208			
Sbjct 1823	CAGAGAGACCTTCCAGGCTGGTTTGGGGGCAAGCAATCTCATAGCTCAAGCTTGG	1882			
Query 1209	TCCAGTGAAGATCTGACATTAATGCTGGTTGGAGCATGGAAGGCTGTGGAAGA	1268			
Sbjct 1883	TCCAGTGAAGATCTGACATTAATGCTGGTTGGAGCATGGAAGGCTGTGGAAGA	1942			
Query 1269	GGGAAACATGAAAGCTGATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1328			
Sbjct 1943	GGGAAACATGAAAGCTGATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2002			
Query 1329	AGCAGGAGGCA-CAGGAGCTCATG-GAAGGCTCA-ATCAAT-ATCTGAGCCA	1379			
Sbjct 2003	AGCAGGAGGCA-CAGGAGCTCATG-GAAGGCTCA-ATCAAT-ATCTGAGCCA	2059			
Query 1380	AAAGCTGAAAAAGTCAAGCTTCTTCCAGGAGGAGGCTATCAAGCAAGTTTAAAGGCTCT	1439			
Sbjct 2060	AAAGCTGAAAAAGTCAAGCTTCTTCCAGGAGGAGGCTATCAAGCAAGTTTAAAGGCTCT	2113			
Query 1440	CTTGGAGGCTTCCAGATCTAGTTTCAAGCATGTCCTCAAGCATGTCCTCAAGCTT	1499			
Sbjct 2114	CTTGGAGGCTTCCAGATCTAGTTTCAAGCATGTCCTCAAGCATGTCCTCAAGCTT	2173			
Query 1500	GAGGATGCTATACAGAGGCTCAAGCTTACATCTCACTATGAGAGGATGGAAG-CAC	1567			
Sbjct 2174	GAGGATGCTATACAGAGGCTCAAGCTTACATCTCACTATGAGAGGATGGAAG-CAC	2212			
Query 1558	CATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1617			
Sbjct 2213	CATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2265			
Query 1618	CGAGGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1677			
Sbjct 2256	CGAGGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2315			
Query 1678	CAGGGGTCAGTGGGGGAGTCAAGCTTCTATGAGGCTGCTTCTCACTCAAACTTGGAA	1737			
Sbjct 2316	CAGGGGTCAGTGGGGGAGTCAAGCTTCTATGAGGCTGCTTCTCACTCAAACTTGGAA	2375			
Query 1738	CTTTTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1797			
Sbjct 2378	CTTTTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2435			
Query 1798	TGTGGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1857			
Sbjct 2438	TGTGGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2495			
Query 1858	AGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1917			
Sbjct 2496	AGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2555			
Query 1918	AGGAGATGGCTGGTTTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1977			
Sbjct 2556	AGGAGATGGCTGGTTTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2615			
Query 1978	CAAGTGGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2037			
Sbjct 2616	CAAGTGGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2675			
Query 2038	CTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2097			
Sbjct 2678	CTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2735			
Query 2098	TAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2138			
Sbjct 2738	TAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2776			

Range 2: 3693 to 3792		GenBank	Graphics	Next Match	Previous Match	First Match
Score	Expect	Identities	Gaps	Strand		
55.4 bits(60)	7e-04	72/100(72%)	0/100(0%)	Plus/Plus		
Query 1039	GAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1098				
Sbjct 3693	GAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3752				
Query 1099	TGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1138				
Sbjct 3753	TGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3792				

Fig. 5 blast result of resulting sequences and *Oryctolagus cuniculus*

Rattus norvegicus ATP binding cassette subfamily B member 11 (Abcb11), mRNA
Sequence ID: NM_031760.1 Length: 5036 Number of Matches: 3
[See 1 more title\(s\)](#)

Range 1: 970 to 2261					Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand		
829 bits(918)	0.0	961/1293(74%)	2/1293(0%)	Plus/Plus		
Query 65	CAGAGGCTGGAGTTAACTTGGTTATTAATGACGAGTCTCTAAATTGGATGGAGC				124	
Sbjct 970	CAGGGGTTGGAAACTAACTTGGTTATCTCTGCTGTCAGGCTCTCATTTGGCATTGGGG				1029	
Query 126	TGGCATAATTGGCTCTCTGACCAAGTTGAGGGGTTAGAGTTAAAGCTTATGCAAA				184	
Sbjct 1030	AGGCTCATAGGCTCTGATATAGCCAGTTGAGGAGCTTGAATTCAGGGCTTATGCCAA				1089	
Query 186	AGCTGGGGCATGCTGATGAGTGTCTCATGATGCAAGGCTGGCTGGCTTGGAGG				244	
Sbjct 1090	AGCGGGGCTATTGCTGATGAGTGTCTCATCTATTGACAGTGGCGGCTTTGGTGG				1149	
Query 245	AGAAAAAGAAAGTTGAAGATATGACAAAAGCTGGTCTTTGCTCAA-CTGGGGAT				303	
Sbjct 1150	TGAGAACAAAGAGTTGAGGGTATGAGAAAGAAATCTTGTTTTCGCCAGGCTGGGAAAT				1209	
Query 304	CAGAAAGGAATCATATGGGATTTTTCACAGGCTACATTGGTGCAATTTTCTGTC				363	
Sbjct 1210	TGGAAAGGAATGGTGATGGGCTCTTCACAGGCTGAGTGGTGCTCATTTTCTCTG				1269	
Query 364	CTATGCCATGGGCTCTGGTATGGCTCAAACTTGTCTTGAAGAGAGGAATCTGTC				423	
Sbjct 1270	TTATGCCATGGGCTCTGGTATGGTTCACACTTGTCTTGAATGAGAGAGTATACAC				1329	
Query 424	TGGCAAGCTTTTGGAGGCTTTTCTGGGGTCTCTAGTGGTGGCTTAAATCTGGTCAAG				483	
Sbjct 1330	AGGACAGCTGGTCCAGAT-TTCTCTGTTGATATTAGCAGCTATGAATATGGCATG				1388	
Query 484	CAGGCGCTTCTGGAGGCTTTTGCACAGGTGGAGGGGCTGCCAAATATATTGAGA				543	
Sbjct 1389	CATCTCTGCTTGGAAATCTCTCCACAGGCTGGGTTTCAGCAGCTACCAATATTTTCAA				1448	
Query 544	CAATAGATGAAAAGCTAGAAATGAGTATGATGTCAGAGATGGCTACAACTGGCAAG				603	
Sbjct 1449	CAATAGACAGCAAGCTGTCAATGAGTGTGATGTCAGGAGAGGCTACAGCTAGACGAA				1508	
Query 604	TCCAGGCTGACATTGAATTCATAATGTAAGCTTCAATTAACATACAGGCGCATCTTA				663	
Sbjct 1509	TCAAGGCTGAATTTGAGTCCAGCAATGAGCTTCAATTAACATTAACATACAGGCGCAT				1568	
Query 664	AGATTTTAGATCAACTGAGCATGATTATCAAGCAGGTGAAAGCAGGCTTTGGTGGC				723	
Sbjct 1569	AGATTTTAGATAAGCTCAGCATGTTATCAAGCAGGTAAGGAGGCTCTGGTGGGAT				1628	
Query 724	CAGGCGAGCAGGAGAAAGTACACCAATTCAAGCTGATCAGAGGCTCTATAGGCTACAG				783	
Sbjct 1629	CCAGTGGGGCTGGGAGAGTACAGCAATTCAAGCTCAATTCAGAGATCTTATGAGGCTGTC				1688	
Query 784	AGGCTAGGTTACCTAGATGACACAGCAATGTTGCTTCACTACATGAGTGGCTGGTT				843	
Sbjct 1689	AGGCTAGGTTGACTCTGGAGGCGCATGACATGCTCTTAAACATCGGTTGGCTGAGAG				1748	
Query 844	CTTTGATGGGGTGGTGGAGCAAGAGCTGCTCTGTTTGGCAACACTATAGCAAAAMCA				903	
Sbjct 1749	ATCAAAATGGGATGGAGAGAGGAGGCGGCTCTGTTTCTCCAGCACTATGCAAAAMCA				1808	
Query 904	TTTCTAGGCTGGGAGGATGCAATTAAGAGACATGTCAGAGCTTCCAAAGAGGCCA				963	
Sbjct 1809	TTCGTTTGGGAGAGAGATGCAACATGAGACATGTCAGAGCTTCCAAAGAGGCTCA				1868	
Query 964	ATGGCTACAGCTTTATCATGGATCTGCTCTCAATTTGACAGCTTTGTTGGAGAGGGT				1023	
Sbjct 1869	ATGCATACAGCTTCAATTTATGGGCTTGGCGAGCAATTTGACAGCTTTGTTGGAGAGAG				1928	

Query 1024	CTGGCAAAATGAGCGGAGGCGAGAGGAGGAAATGGCATTCCTGGGCTTTAGTTGAAA	1083
Sbjct 1929	GAGGCCAGATGAGTGGTGGTCAGAGCAAGAGTAGCCATTGGCCGAGGCTCATAGGGA	1988
Query 1084	ACCCAAAAATCTGTTGCTGGACATGGCTACACAGCACTGGACAAATGAAGTGAAGCTA	1143
Sbjct 1989	ATCCAAAGATCTGCTCTGGATATGGCTACCTACAGCACTGGACAAATGAAGTGAAGCTA	2048
Query 1144	CGTGGCAGAGACACTTTCAGAGGCTGCTTTTGGGCGACAGCAATTCATAGCTCAAC	1203
Sbjct 2049	GAGTACAGAGCAATTAATAAGATCCACATGGGCAATCAATCATCTCAGTTGCCATC	2108
Query 1204	CTTTGCTCAGTCAAAATCTGCTGACATTATGCTGGGTTTGGACATGGAGAGCTGTGG	1263
Sbjct 2109	GCTCTCAGACAGTCAAGGCTCCAGATGTCATCATTTGGGTTTGGACATGGAGAGCTGTGG	2168
Query 1264	AAAGAGGAGAAATGAGAGAGTATAGAGCGAGAGAGAGTGTATTTCACACTGGTAAAGT	1323
Sbjct 2169	AAAGAGGAGAAATGAGAGAGTATAGAGCGAGAGAGTGTATTTCACACTGGTAAAGT	2228
Query 1324	TCCAAAGTCCAGGCGACAGGCACTCATGAAA 1366	
Sbjct 2229	TCCAAAGTCCAGGAGATATGCTACAAAGAAA 2261	

Range 2: 2458 to 3007					Next Match	Previous Match	First Match
Score	Expect	Identities	Gaps	Strand			
233 bits(258)	1e-57	384/551(70%)	2/551(0%)	Plus/Plus			
Query 1589	TGAGGAGAGTGGTACCTGTAACGTGACCAAGGATTTTGAAGTACAAAGCTCCGAAATG				1648		
Sbjct 2458	TGAGGAGAGTGGTACCTGTAACGTGACCAAGGATTTTGAAGTACAAAGCTCCGAAATG				2517		
Query 1649	GCCATATATGGTGGTATGCTTGGGCGAGGGTCAATGGGCGAGTCAAGCTCTCTA				1708		
Sbjct 2518	GCCATATATGGTGGTATGCTTGGGCGAGGGTCAATGGGCGAGTCAAGCTCTCTA				2577		
Query 1709	TGCGCTGCTCTCAGTCAAAATTTTGGAGGCTTTTGGTGGCTGATGAGAGAGGCAAG				1768		
Sbjct 2578	CTCGCTTTTATGCGCAGCTCTTGGAGCTTTTTCAGCTCTGATGATGAGAGAGGCAAG				2637		
Query 1769	AGCTGAGTCAAGGCTGCTGCTCTGCTTGGTGGTGGTGAATGATCACTCTCAC				1828		
Sbjct 2638	GTCAGAGATTCAGAGCATGTGCTGCTTTTGGTTCATCTGGGCTGTGATCATTTTAC				2697		
Query 1829	TCAGTCTTACAGGCTATAGCTTTCAGAGGCGGAGAAATGCTTACAC-AGGCTTAA				1887		
Sbjct 2698	ACAAATTCAGAGGCTTACAGCTTTCAGAGGCGGAGAAATGCTTACAC-AGGCTTAA				2756		
Query 1889	GGAAGATTGGCTTCCAGGCGATGTTAGGCGAGAAATTTGGCTGTTTGAATGACATGAA				1947		
Sbjct 2757	GGAAGATTGGCTTCCAGGCGATGTTAGGCGAGAAATTTGGCTGTTTGAATGACATGAA				2816		
Query 1948	ACAGGCGAGGCGCTTGAAGTACAGAGCTAGCACTGACGCTCTCAGTTCAAGGGGGA				2007		
Sbjct 2817	ATAATCTGAGAGTACAGAGCTAGGCTTCTACAGATGCTTCCAGGTTCAAGGGGCTA				2876		
Query 2008	CTGGCACAGATAGGCAATGTTGAAATCTCTCAACCAATATGAGGTCTGCATTTATTA				2067		
Sbjct 2877	CTGGCTCTCAGTTGGAAATGATGCTCAATCTTCACTACATCATTTGGGCTCTGCTGA				2936		
Query 2068	TGCGTCTTACTTCAAGTGGAAATCTAGCTTATGATCAATGCTGCTCTGCTCTTCTGG				2127		
Sbjct 2937	TGCGTCTTCTTCAAGTGGAAATCTAGCTTATGATCAATGCTGCTCTGCTCTTCTGG				2996		
Query 2128	CTTTGTCAGGA 2138						
Sbjct 2997	CTTTATGCGGA 3007						

Range 3: 3930 to 4023					Next Match	Previous Match	First Match
Score	Expect	Identities	Gaps	Strand			
57.2 bits(62)	2e-04	69/94(73%)	0/94(0%)	Plus/Plus			
Query 1045	AGAGCAGGGAATGCAATGCTCGGGCTTTAGTTGCAAGGCCCAAAATCTGTTGCTGG				1104		
Sbjct 3930	AGAGCAGGGAATGCAATGCTCGGGCAATTTGCGAGATCTTAAATCTTACTACTGG				3989		
Query 1105	ACATGGCTACATCAGCACTGCAATGAAGTGA 1138						
Sbjct 3990	ATGAGCTAGCTCTGCGCTAGACAGAGAGTGA 4023						

Fig. 6 blast result of resulting sequences and *Rattus norvegicus*

Range 1: 835 to 2105		GenBank	Graphics	Next Match	Previous Match
Score	Expect	Identities	Gaps	Strand	
794 bits(880)	0.0	941/1272(74%)	2/1272(0%)	Plus/Plus	

Query	65	CAGAGGCTGGAGATTAACCTGTGTTATATGACGACGACGCTCTCAATTGGGATGCGAGC	124
Subject	835	CAGGGGTTGGAAATTAACCTGGTGATCTGCTGTGCTGCTCTCATGGGATTGGGCA	894
Query	125	TGGCATTTGGGAGTCTGTACGAAGATTCAGGGGTTAGTAGTAAAGGATTCAGG	184
Subject	895	AGCTCTCATATGCTTGACCTGTGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG	954
Query	185	AGCTGGGAGGACGCTGCTGAAGGTCTCTCATGATCGACAAAGCTGCTGCTGCTGCTG	244
Subject	955	AGCTGGGCTATTGTGCGATGAAGCTCTCTCATCTATTGACGAAGCTGCTGCTGCTGCTG	1014
Query	245	AGAAAAAGGAGGTGAAGGATTATGCAAAAAAGCTGGTGTCTTCTCAAACTCGGGGAT	303
Subject	1015	TGTAATAATAGGGGTGAAGAGGTATGAAAAAATCTATGTTTCTGACGCGCTGGGGAAT	1074
Query	304	CAGAAAAAGGAATCATATGGGATTTTCTTACAGGCTCAATTTGTGCTCATCTCTG	363
Subject	1075	TTGAGAAAGGATGTGATGGGCTGCTCTGAGCTGGGTAATGCTGTGCTCTCTCTCTCTG	1134
Query	364	CATATCGATCGGCTCTGTGATGGCTCTAAAGCTCTGAGGAGAGAGAAATCTCTG	423
Subject	1135	TTATCGCATGGGCTCTGGTAAGGCTCGAGAGTCTGCTGGTGAAGGCGAGTACACAC	1194
Query	424	TGGCAAGCTCTGTCAGAGCTCTTCTGGGCGCTGATGATGGTGGCTCTAAATCTGCTGAG	483
Subject	1195	AGGCGAATCTGATCGAATTTCTCTCTGCTGATATACAGCATTAAGAAATGCGAATC	1253
Query	484	CAGCCCTTGCCTGGAAGGATTTTGCACAGGTGAGAGGGGCTGCCAAATATATTGAGA	543
Subject	1254	CATCTCTTCTTTGTGAAATCTCTCCACGGGTTCTGACAGGCTCTCGAATTTTCAAAA	603
Query	544	CAATGATGAAAAAGCTAGAAATGATCTATGTCAGAAAGATGCTCAAGATGCGAAG	1313
Subject	1314	CAGTACAGGCAAGGCAAGGCTCATGATGCTGCTGCTGAGGATGCTGTATGAGATGA	1373
Query	604	TCGAGAGGTACATTAATTCATTAATGATGTAACCTTATACCATTCAGAGCGGCTGA	663
Subject	1374	TCAAGGCGGAGGATGATGCTCCATATGTAAGCTTCCATATCTCTTGCAGCCAGGTTGA	1433
Query	664	AGATTTAGATCAACTCAGCATGATTATCAGGCGAGGTGAAGCACAGCTCTTGTGGCC	723
Subject	1434	AGATTTAAATCAACTCTGAGATGCTATTGACGCTAGGAGGAGAGCGGCTGCTGGGAT	1493
Query	724	CAGGCGAGAGGAGGAAAAGTACCAATATACAGTATCATGAGGACCTCTATGACCAATG	783
Subject	1494	CCAGTGGGCGAGGAGAGGACAGCAAGCATATGACATCTGATGATGATCTATTGACCGCT	1553
Query	784	AGGCGATGCTAGCTAGTGACAGGACGATCTGCTTCCGCTTAATCGGTGGCTGGT	843
Subject	1554	AGGCGATGGTATCTCTGGATGGCATGACTTGTCTCTTAACTCGGTGGCTGGAG	1613
Query	844	CTTTGATGGGGGTGGTGGAGCAGAAAGCTGCTCTTTTTCGACACCATATAGCAAAAAA	903
Subject	1614	ATCAAAATTTGCTGTAGAGAGGCGCAATGATGCTGCTCTCTCTGCTGCTGCTGCTG	1673
Query	904	TTTCTAGGCTGGGAGATTGCCATATGAGCAGATGCTGACGCTCTCCAGAGCA	963
Subject	1674	TCGCGCTGTGATAGAGAGGCGCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1733
Query	964	ATGCTTCACACCTATGATGATCTGGCTTGCATGATGCGACCTGTTGGAGAGGCT	1023
Subject	1734	ATGCTACACACCTATTATGGGCTGCGACAGCAATTTGACCTGCTTGGAGAGGCT	1793
Query	1024	TGGGCAAGGAGGAGGAGGAGCAGAGCAAGGAAATTCGCTATCTCGGGCTCTATCGGA	1083
Subject	1794	CGAGTGAAGATGATGCTGGGCAAGCAAGGATGCTGATCGGCGCGGCTCATACAAA	1853

Range 2: 2323 to 2872 GenBank Graphics			Next Match	Previous Match	First Match
Score	Expect	Identities	Gaps	Strand	
203 bits(224)	2e-48	375/550(68%)	0/550(0%)	Plus/Plus	

Range 3: 3795 to 3888		GenBank	Graphics	Next Match	Previous Match	First Match
Score	Expect	Identities	Gaps	Strand		
62.6 bits(68)	5e-06	70/94(74%)	0/94(0%)	Plus/Plus		

Fig. 7 blast result of resulting sequences and *Mus musculus*

6. Proteomic result of *Ophiophagus Hannah* liver proteins.

Shotgun proteomic was applied to protein extract of *Ophiophagus Hannah* liver, the resulting proteins were listed as below (start from next page):

N	Unused	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides (95%)	
1	230.29	230.29	83.87	53.78	49.19	tr V8PJW7	V8PJW7_OPHHA Myosin-10 (Fragment) OS=Ophiophagus hannah GN=Myh10 PE=	OPHHA	157	
2	191.36	191.36	83.1	57.67	52.15	tr V8PJJ1	V8PJJ1_OPHHA Spectrin beta chain, brain 1 (Fragment) OS=Ophiophagus	OPHHA	110	
3	172.61	172.61	65.48	48	44.99	tr V8P9W0	V8P9W0_OPHHA Filamin-A OS=Ophiophagus hannah GN=FLNA PE=4 SV=1	OPHHA	104	
4	171.18	204.26	80.03	50.84	47.64	tr V8PFF2	V8PFF2_OPHHA Myosin-9 (Fragment) OS=Ophiophagus hannah GN=MYH9 PE=4	OPHHA	140	
5	149.77	154.12	64.13	43.59	39.04	tr V8P4P2	V8P4P2_OPHHA Filamin-B (Fragment) OS=Ophiophagus hannah GN=FLNB PE=4	OPHHA	87	
6	116.36	116.36	62.53	47.73	44.06	tr V8P2J0	V8P2J0_OPHHA Clathrin heavy chain 1 (Fragment) OS=Ophiophagus hannah	OPHHA	71	
7	108.91	108.91	71.28	35.77	31.62	tr V8NH62	V8NH62_OPHHA Neuroblast differentiation-associated protein AHNAK (Fr	OPHHA	94	
8	101.77	101.77	46.72	30.28	28.12	tr V8P8N6	V8P8N6_OPHHA Fatty acid synthase (Fragment) OS=Ophiophagus hannah	GN=OPHHA	60	
9	101.56	101.56	61.38	29.17	22.64	tr V8NJK8	V8NJK8_OPHHA Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Ophiop	OPHHA	72	
10	100.03	100.03	44.67	15.63	13.03	tr V8NQB4	V8NQB4_OPHHA Apolipoprotein (Fragment) OS=Ophiophagus hannah GN=Apo	OPHHA	63	
11	94.85	94.85	72.87	37.27	31.52	tr V8P116	V8P116_OPHHA Kinectin OS=Ophiophagus hannah GN=KTN1 PE=4 SV=1	OPHHA	62	
12	92.85	92.85	58.1	26.84	22.12	tr V8NS95	V8NS95_OPHHA Utrrophin (Fragment) OS=Ophiophagus hannah GN=UTRN	PE=4 OPHHA	50	
13	89.46	89.46	47.78	24.47	19.87	tr V8PCU6	V8PCU6_OPHHA Low-density lipoprotein receptor-related protein 1 (Fra	OPHHA	59	
14	89.44	89.44	57.07	34.01	31.98	tr V8PGB5	V8PGB5_OPHHA Glycogen debranching enzyme (Fragment) OS=Ophiophagus	h OPHHA	54	
15	89.18	89.18	47.69	22.37	20.63	tr V8P3W1	V8P3W1_OPHHA Collagen alpha-1(XII) chain (Fragment) OS=Ophiophagus	h OPHHA	47	
16	88.47	88.47	54.36	33.98	28.93	tr V8P133	V8P133_OPHHA Ras GTPase-activating-like protein IQGAP2 OS=Ophiophagu	OPHHA	48	
17	84.5	84.5	83.97	61.78	56.84	tr V8P2D8	V8P2D8_OPHHA Alpha-actinin, sarcomeric (Fragment) OS=Ophiophagus	han OPHHA	57	
18	81.1	81.1	74.29	31.68	24.27	tr V8NTQ8	V8NTQ8_OPHHA Desmoplakin OS=Ophiophagus hannah GN=Dsp PE=4 SV=1	OPHHA	41	
19	80.59	80.59	61.68	48.47	42.69	tr V8P5F2	V8P5F2_OPHHA Endoplasmic (Fragment) OS=Ophiophagus hannah GN=HSP90B1	OPHHA	54	
20	79.47	79.47	89.69	63.91	62.97	tr V8P294	V8P294_OPHHA Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	GTP	58	
21	74.48	74.48	77.77	46.42	38.29	tr V8NVB7	V8NVB7_OPHHA Vinculin (Fragment) OS=Ophiophagus hannah GN=VCL PE=4	S OPHHA	42	
22	74.34	74.34	72.66	49.45	46.7	tr V8N9M0	V8N9M0_OPHHA Heat shock protein HSP 90-alpha (Fragment) OS=Ophiophag	OPHHA	46	
23	73	73	52.34	43.09	37.4	tr V8P0K4	V8P0K4_OPHHA AP-2 complex subunit beta (Fragment) OS=Ophiophagus	han OPHHA	37	
24	71.47	71.47	72.82	53.48	46.85	tr V8NX72	V8NX72_OPHHA Catenin alpha-1 OS=Ophiophagus hannah GN=CTNNA1	PE=4 SV OPHHA	37	
25	70.8	70.8	72.03	42.73	40.95	tr V8NWL5	V8NWL5_OPHHA C-1-tetrahydrofolate synthase, cytoplasmic (Fragment)	O OPHHA	44	
26	69.72	69.72	61.37	35.14	29.98	tr V8NJ00	V8NJ00_OPHHA Vigilin (Fragment) OS=Ophiophagus hannah GN=HDLBP	PE=4 OPHHA	41	
27	69.68	69.68	57.21	19.45	17.08	tr V8NV77	V8NV77_OPHHA Laminin subunit gamma-1 (Fragment) OS=Ophiophagus	hanna OPHHA	41	
28	66.37	66.37	66.25	26.91	20.37	tr V8P9J0	V8P9J0_OPHHA Eukaryotic translation initiation factor 3 subunit A	OS OPHHA	31	
29	66.28	66.28	45.26	21.28	18.6	tr V8NJM6	V8NJM6_OPHHA S-(hydroxymethyl)glutathione dehydrogenase (Fragment)	O OPHHA	44	
30	64.59	64.59	63.79	40.08	35.12	tr V8PFP1	V8PFP1_OPHHA Trifunctional purine biosynthetic protein adenosine-3	O OPHHA	46	
31	64.22	64.22	72.01	44.18	41.51	tr V8NQH5	V8NQH5_OPHHA Protein disulfide-isomerase A4 OS=Ophiophagus	hannah GN OPHHA	36	
32	64.2	64.2	34.83	21.79	19.74	tr V8P062	V8P062_OPHHA Fibronectin (Fragment) OS=Ophiophagus hannah GN=FN1	PE= OPHHA	37	
33	64.05	64.05	76.25	49.85	42.96	tr V8NXQ5	V8NXQ5_OPHHA Annexin (Fragment) OS=Ophiophagus hannah GN=ANXA6	PE=3 OPHHA	36	
34	62.1	62.1	73.4	44.83	41.54	tr V8NEC1	V8NEC1_OPHHA 78 kDa glucose-regulated protein OS=Ophiophagus	hannah OPHHA	48	
35	59.51	59.51	55.03	30.09	23.73	tr V8NYF2	V8NYF2_OPHHA UDP-glucose:glycoprotein glucosyltransferase 1 (Fragmen	OPHHA	30	
36	58.69	58.69	56.67	40.04	33.79	tr V8NUK3	V8NUK3_OPHHA AP-2 complex subunit alpha-2 (Fragment) OS=Ophiophagus	OPHHA	30	
37	58.69	58.69	76.15	50.71	50.71	tr V8NM23	V8NM23_OPHHA 60 kDa heat shock protein, mitochondrial OS=Ophiophagus	OPHHA	46	
38	58.4	58.4	79.66	50.75	50.75	tr V8NZT7	V8NZT7_OPHHA Bifunctional purine biosynthesis protein PURH	OS=Ophiop	OPHHA	41
39	57.79	57.79	85.07	76.8	76	tr V8P167	V8P167_OPHHA Actin, cytoplasmic 2 OS=Ophiophagus hannah GN=ACTG1	PE= OPHHA	47	
39	0	57.79	83.61	80	79.17	tr V8N8G6	V8N8G6_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus	hanna OPHHA	47	
40	57.72	57.72	50.79	14.09	12.97	tr V8P7Y8	V8P7Y8_OPHHA Collagen alpha-2(VI) chain (Fragment) OS=Ophiophagus	ha OPHHA	39	
41	56.54	56.54	58.95	43.35	34.16	tr V8NGV0	V8NGV0_OPHHA Regulator of nonsense transcripts 1 (Fragment) OS=Ophi	OPHHA	27	
42	55.46	55.46	56.26	37.87	29.55	tr V8NZD8	V8NZD8_OPHHA Sodium/potassium-transporting ATPase subunit alpha	OS=O OPHHA	29	
43	55.15	55.15	68.75	52.13	50.27	tr V8P2P2	V8P2P2_OPHHA Junction plakoglobin OS=Ophiophagus hannah GN=Jup	PE=4 OPHHA	33	
44	55.03	82.62	52.11	25.33	20.18	tr V8PCQ7	V8PCQ7_OPHHA Myosin-11 (Fragment) OS=Ophiophagus hannah GN=MYH11	PE= OPHHA	51	
45	54.96	54.97	69.26	43.77	40.66	tr V8P8K8	V8P8K8_OPHHA Protein disulfide-isomerase OS=Ophiophagus hannah GN=P4	OPHHA	37	
46	54.73	54.73	56.68	41.02	34.84	tr V8PAZ8	V8PAZ8_OPHHA Tensin (Fragment) OS=Ophiophagus hannah GN=TNS	PE=4 SV= OPHHA	29	
47	54.58	54.58	68.91	41.45	36.79	tr V8NA37	V8NA37_OPHHA Moesin (Fragment) OS=Ophiophagus hannah GN=Msn	PE=4 SV= OPHHA	27	
48	53.03	53.05	51.71	25.58	21.14	tr V8NFW1	V8NFW1_OPHHA Myosin-1c (Fragment) OS=Ophiophagus hannah GN=MYO1C	PE= OPHHA	25	
49	52.59	52.59	57.95	27.19	21.2	tr V8NPZ9	V8NPZ9_OPHHA Plexin-B2 (Fragment) OS=Ophiophagus hannah GN=PLXNB2	PE OPHHA	25	
50	52.13	52.13	50.64	20.12	15.88	tr V8NA23	V8NA23_OPHHA Translational activator GCN1 (Fragment) OS=Ophiophagus	OPHHA	26	
51	52.07	52.07	76.94	41.48	36.62	tr V8P9V0	V8P9V0_OPHHA Heat shock 70 kDa protein 4 (Fragment) OS=Ophiophagus	h OPHHA	25	
52	51.95	51.95	66.35	35.21	32.5	tr V8PEE5	V8PEE5_OPHHA Kinesin-like protein OS=Ophiophagus hannah GN=KIF5B	PE= OPHHA	28	
53	51.35	51.35	51.55	23.32	17.97	tr V8NBY3	V8NBY3_OPHHA Bifunctional aminoacyl-tRNA synthetase OS=Ophiophagus	h OPHHA	27	
54	51.27	51.27	71.28	41.29	36.1	tr V8NV43	V8NV43_OPHHA Transitional endoplasmic reticulum ATPase (Fragment)	OS OPHHA	27	
55	50.57	50.57	62.76	35.74	27.03	tr V8PCN4	V8PCN4_OPHHA 2-oxoglutarate dehydrogenase, mitochondrial OS=Ophi	OPHHA	21	
56	49.99	49.99	48.65	21.04	16.96	tr V8NJS6	V8NJS6_OPHHA Putative ubiquitin carboxyl-terminal hydrolase FAF-X	(F OPHHA	25	
57	49.93	49.93	45.69	36.42	34.77	tr V8P3P1	V8P3P1_OPHHA Aconitate hydratase, mitochondrial (Fragment) OS=Ophi	OPHHA	34	
58	49.88	49.88	51.02	32.85	23.72	tr V8NW73	V8NW73_OPHHA Cullin-associated NEDD8-dissociated protein 1 (Fragmen	OPHHA	22	
59	48.26	48.38	43.53	17.52	14.96	tr V8P209	V8P209_OPHHA Collagen alpha-3(VI) chain (Fragment) OS=Ophiophagus	ha OPHHA	30	
60	48.11	48.11	54.51	34.07	31.76	tr V8P0Q4	V8P0Q4_OPHHA Coatome subunit beta (Fragment) OS=Ophiophagus	hannah OPHHA	27	
61	47.84	47.84	71.3	22.93	19.97	tr V8NRT5	V8NRT5_OPHHA Early endosome antigen 1 (Fragment) OS=Ophiophagus	hann OPHHA	25	
62	47.62	47.62	55.02	21.8	17.06	tr V8NPB1	V8NPB1_OPHHA Serine/threonine-protein kinase MRCK beta (Fragment)	OS OPHHA	24	
63	47.57	57.36	65.96	21.25	16.8	tr V8PFR6	V8PFR6_OPHHA Spectrin beta chain, erythrocyte (Fragment) OS=Ophi	OPHHA	30	
64	47.24	47.24	54.87	21.48	14.47	tr V8NRP6	V8NRP6_OPHHA Kinesin-like protein (Fragment) OS=Ophiophagus	hannah GN OPHHA	21	
65	46.82	46.82	58.38	23.4	18.58	tr V8NNH1	V8NNH1_OPHHA Brefeldin A-inhibited guanine nucleotide-exchange	prote OPHHA	23	
66	46.69	46.69	77.11	37.19	30.79	tr V8N8J0	V8N8J0_OPHHA Elongation factor 2 (Fragment) OS=Ophiophagus	hannah GN OPHHA	25	
67	45.69	45.69	73.75	43.87	39.38	tr V8NWK2	V8NWK2_OPHHA T-complex protein 1 subunit epsilon (Fragment) OS=Ophi	OPHHA	21	
68	44.87	44.87	78.98	68.18	62.5	tr V8NY29	V8NY29_OPHHA Fructose-bisphosphate aldolase OS=Ophiophagus	hannah GN OPHHA	36	
69	44.83	44.83	70.46	49.32	44.99	tr V8PAD8	V8PAD8_OPHHA Phosphoserine aminotransferase OS=Ophiophagus	hannah GN OPHHA	33	
70	44.11	44.11	53.52	29.05	27.05	tr V8P459	V8P459_OPHHA Constitutive coactivator of PPAR-gamma-like protein	1-1 OPHHA	25	
71	43.68	43.68	70.6	51.81	43.86	tr V8NM39	V8NM39_OPHHA Isocitrate dehydrogenase [NADP] OS=Ophiophagus	hannah G NADP	26	
72	43.4	43.4	70.41	55.81	55.81	tr V8P1T3	V8P1T3_OPHHA ATP synthase subunit beta (Fragment) OS=Ophiophagus	hann OPHHA	37	
73	42.93	42.93	43.78	22.27	19.11	tr V8NT99	V8NT99_OPHHA Eukaryotic translation initiation factor 4 gamma	1 (Fra OPHHA	22	
74	42.67	42.67	47.26	17.47	13.15	tr V8POS2	V8POS2_OPHHA DnaJ-like subfamily C member 13 (Fragment) OS=Ophi	OPHHA	21	
75	42.56	42.56	74.47	48.36	45.07	tr V8PBR6	V8PBR6_OPHHA Serine hydroxymethyltransferase OS=Ophiophagus	hannah G OPHHA	23	
76	42.55	66.84	64.14	42.05	38.89	tr V8NTA5	V8NTA5_OPHHA Heat shock protein HSP 90-beta (Fragment) OS=Ophi	OPHHA	41	
77	42.36	42.36	66.89	21.57	16.78	tr V8NZ34	V8NZ34_OPHHA Rho-associated protein kinase 2 (Fragment) OS=Ophi	OPHHA	21	
78	42.32	42.32	69.31	45.73	37.8	tr V8PEI7	V8PEI7_OPHHA Arginyl-tRNA synthetase, cytoplasmic OS=Ophiophagus	han OPHHA	19	
79	42.15	42.15	49.7	29.58	28.74	tr V8P4E7	V8P4E7_OPHHA Aconitate hydratase (Fragment) OS=Ophiophagus	hannah GN OPHHA	24	
80	42.14	42.14	64.19	31.88	23.69	tr V8NSK8	V8NSK8_OPHHA Golgi apparatus protein 1 (Fragment) OS=Ophiophagus	han OPHHA	20	
81	42.09	42.09	66.94	37.57	29.64	tr V8PBT8	V8PBT8_OPHHA ATP-dependent RNA helicase DDX1 OS=Ophiophagus	hannah G OPHHA	21	
82	42.09	42.09	71.8	52.63	45.11	tr V8PGM9	V8PGM9_OPHHA Aspartyl-tRNA synthetase, cytoplasmic (Fragment)	OS=Oph OPHHA	22	
83	42.02	42.02	49.79	23.11	18.27	tr V8NM58	V8NM58_OPHHA Xanthine dehydrogenase/oxidase (Fragment) OS=Ophi	OPHHA	23	
84	41.74	41.74	58.22	42.43	37.83	tr V8P027	V8P027_OPHHA Dihydropyrimidinase-related protein 3 OS=Ophiophagus	ha OPHHA	26	
85	41.36	41.36	45.99	16.94	16.94	tr V8PF84	V8PF84_OPHHA Eukaryotic translation initiation factor 3 subunit	C OS OPHHA	22	
86	41.35	41.35	57.93	52.18	50.11	tr V8PB80	V8PB80_OPHHA Tubulin beta-4B chain (Fragment) OS=Ophiophagus	hannah OPHHA	33	
87	41.27	41.27	59.71	24.59	22.17	tr V8PCJ0	V8PCJ0_OPHHA Aldehyde dehydrogenase, mitochondrial OS=Ophiophagus	ha OPHHA	32	
88	41.09	41.09	64.29	26.85	22.33	tr V8P063	V8P063_OPHHA Structural maintenance of chromosomes			

95	40.12	40.12	66.42	38.02	36.54	tr V8NVZ0 V8NVZ0_OPNHA Multifunctional protein ADE2 (Fragment) OS=Ophiophagus OPNHA	24
96	40.06	40.06	76.44	24.73	16.54	tr V8PGR2 V8PGR2_OPNHA Structural maintenance of chromosomes protein 1A (Fragm OPNHA	17
97	39.95	39.95	54.95	39.59	34.13	tr V8NUY6 V8NUY6_OPNHA Histidine ammonia-lyase OS=Ophiophagus hannah GN=HAL PE OPNHA	23
98	39.88	41.48	54.02	17.28	17.18	tr V8N7V6 V8N7V6_OPNHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPNHA	28
99	39.66	39.66	59.02	38.2	34.59	tr V8PEL6 V8PEL6_OPNHA Methylmalonate-semialdehyde dehydrogenase [acylating], OPNHA	25
100	39.55	39.55	71.61	45.34	45.34	tr V8PG19 V8PG19_OPNHA T-complex protein 1 subunit theta OS=Ophiophagus hannah OPNHA	22
101	39.35	39.35	57.53	27.19	21.66	tr V8NN65 V8NN65_OPNHA Splicing factor 3B subunit 1 OS=Ophiophagus hannah GN=S OPNHA	19
102	39.29	39.29	49.53	25.99	25.06	tr V8P6J4 V8P6J4_OPNHA Microsomal triglyceride transfer protein large subunit OPNHA	21
103	38.9	38.9	54.14	30.81	29.09	tr V8NFY9 V8NFY9_OPNHA Ankyrin repeat and FYVE domain-containing protein 1 (Fr OPNHA	21
104	38.85	38.85	66.48	33.52	33.52	tr V8NCG3 V8NCG3_OPNHA Heterogeneous nuclear ribonucleoprotein U-like protein OPNHA	22
105	38.73	38.73	56.79	33.77	30.94	tr V8P1G2 V8P1G2_OPNHA Catalase (Fragment) OS=Ophiophagus hannah GN=CAT PE=3 S OPNHA	26
106	38.69	38.69	51	26.62	24.85	tr V8NZS0 V8NZS0_OPNHA Phenylalanine-4-hydroxylase (Fragment) OS=Ophiophagus h OPNHA	21
107	38.66	38.66	68.91	47.72	38.61	tr V8PBL7 V8PBL7_OPNHA tRNA-splicing ligase RtcB homolog OS=Ophiophagus hannah OPNHA	20
108	38.19	38.19	74.39	31.76	31.35	tr V8NZ73 V8NZ73_OPNHA Vimentin (Fragment) OS=Ophiophagus hannah GN=VIM PE=3 S OPNHA	25
109	38.14	38.14	68.18	31.17	28.05	tr V8PBQ3 V8PBQ3_OPNHA Propionyl-CoA carboxylase alpha chain, mitochondrial (F OPNHA	19
110	38.04	38.04	67.43	41.59	33.98	tr V8NQ25 V8NQ25_OPNHA T-complex protein 1 subunit alpha (Fragment) OS=Ophioph OPNHA	18
111	37.52	37.52	59.07	45.36	43.75	tr V8NJB3 V8NJB3_OPNHA Calcium-binding mitochondrial carrier protein Aralar2 (OPNHA	23
112	37.3	37.3	60.53	38.28	35.16	tr V8NM20 V8NM20_OPNHA GMP synthase [glutamine-hydrolyzing] (Fragment) OS=Ophi OPNHA	18
113	37.27	37.27	38.13	22.74	18.57	tr V8PG50 V8PG50_OPNHA NAD(P) transhydrogenase, mitochondrial (Fragment) OS=Op OPNHA	23
114	37.24	37.24	80.19	55.56	50.97	tr V8P7W6 V8P7W6_OPNHA 26S protease regulatory subunit 8 (Fragment) OS=Ophioph OPNHA	20
115	36.96	36.96	69.29	59.76	54.52	tr V8PAY9 V8PAY9_OPNHA 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial OPNHA	20
116	36.94	36.94	72.93	47.6	40.39	tr V8P2N0 V8P2N0_OPNHA Testin (Fragment) OS=Ophiophagus hannah GN=TES PE=4 SV= OPNHA	17
117	36.91	36.91	58.15	24.73	22.8	tr V8PJB1 V8PJB1_OPNHA Pleckstrin-like domain-containing family A member 6 (F OPNHA	19
118	36.88	36.88	56.47	30.01	23.96	tr V8P8G9 V8P8G9_OPNHA Alpha-1,4 glucan phosphorylase (Fragment) OS=Ophiophagu OPNHA	18
119	36.78	36.78	56.7	37.98	33.58	tr V8PA16 V8PA16_OPNHA Stress-70 protein, mitochondrial OS=Ophiophagus hannah OPNHA	20
120	36.73	36.73	60.14	45.98	39.69	tr V8NN23 V8NN23_OPNHA Serine/threonine-protein phosphatase 2A 65 kDa regulato OPNHA	18
121	36.67	36.67	53.06	32.6	24.74	tr V8NJ70 V8NJ70_OPNHA Dynamin-1 OS=Ophiophagus hannah GN=Dnm1 PE=3 SV=1 OPNHA	18
122	36.48	36.48	57.06	19.35	17.14	tr V8PGA0 V8PGA0_OPNHA Cytoplasmic FMRL-interacting protein 1 OS=Ophiophagus h OPNHA	19
123	36.24	36.24	65.77	51.21	46.63	tr V8NVK0 V8NVK0_OPNHA Amidophosphoribosyltransferase (Fragment) OS=Ophiophagu OPNHA	21
124	36.04	36.04	42.81	18.69	18.69	tr V8PEY3 V8PEY3_OPNHA Serine hydroxymethyltransferase (Fragment) OS=Ophiophag OPNHA	27
125	35.9	35.9	61.22	25.94	25.06	tr V8PIR9 V8PIR9_OPNHA 26S protease regulatory subunit 6A (Fragment) OS=Ophioph OPNHA	21
126	35.9	35.9	54.71	33	25.72	tr V8NRN1 V8NRN1_OPNHA NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochon OPNHA	17
127	35.89	35.9	68.62	40.27	38.09	tr V8PDE6 V8PDE6_OPNHA Plastin-3 OS=Ophiophagus hannah GN=PLS3 PE=4 SV=1 OPNHA	21
128	35.87	35.94	56.25	36.86	34.78	tr V8NIS2 V8NIS2_OPNHA Dolichyl-diphosphooligosaccharide--protein glycosyltran OPNHA	21
129	35.85	35.85	75.24	36.29	33.08	tr V8N601 V8N601_OPNHA Tyrosine--tRNA ligase (Fragment) OS=Ophiophagus hannah OPNHA	18
130	35.73	35.73	68.02	24.87	22.17	tr V8PO15 V8PO15_OPNHA Lamin-B1 OS=Ophiophagus hannah GN=Lmb1 PE=3 SV=1 OPNHA	20
131	35.51	35.51	53.65	35.21	33.43	tr V8P7D2 V8P7D2_OPNHA Signal transducer and activator of transcription (Fragm OPNHA	19
132	35.47	35.47	63.7	42.79	38.7	tr V8PGR3 V8PGR3_OPNHA Calreticulin OS=Ophiophagus hannah GN=CALR PE=3 SV=1 OPNHA	26
133	35.09	35.09	85.01	53.75	53.75	tr V8PFW0 V8PFW0_OPNHA Actin-related protein 3 OS=Ophiophagus hannah GN=ACTR3 OPNHA	21
134	35.03	35.03	62.2	19.35	13.79	tr V8PCT1 V8PCT1_OPNHA Afadin (Fragment) OS=Ophiophagus hannah GN=Mlt4 PE=4 S OPNHA	17
135	35.01	35.03	82.11	63.16	62.11	tr V8NI54 V8NI54_OPNHA Glutamate dehydrogenase 1, mitochondrial (Fragment) OS= OPNHA	27
136	34.93	34.93	79.09	62.36	56.27	tr V8P745 V8P745_OPNHA 40S ribosomal protein S4 OS=Ophiophagus hannah GN-RPS4 OPNHA	19
137	34.79	34.79	62.17	40.78	36.9	tr V8P708 V8P708_OPNHA Far upstream element-binding protein 1 OS=Ophiophagus h OPNHA	19
138	34.66	34.66	48.7	29.42	26.38	tr V8NSB9 V8NSB9_OPNHA NADPH-cytochrome reductase (Fragment) OS=Ophiophagus ha OPNHA	19
139	34.66	34.66	45.84	33.5	28.46	tr V8NUS4 V8NUS4_OPNHA Coatomer subunit gamma OS=Ophiophagus hannah GN=COPG PE OPNHA	17
140	34.65	34.65	41.44	21.55	18.88	tr V8P5Z1 V8P5Z1_OPNHA Nidogen-1 (Fragment) OS=Ophiophagus hannah GN=Nid1 PE=4 OPNHA	19
141	34.5	34.5	56.03	45.39	43.74	tr V8NGO4 V8NGO4_OPNHA ATP synthase subunit alpha OS=Ophiophagus hannah GN=Atp OPNHA	24
142	34.23	34.23	44.77	19.09	17.33	tr V8NB12 V8NB12_OPNHA Collagen alpha-6(VI) chain (Fragment) OS=Ophiophagus ha OPNHA	20
143	34.18	34.18	67.71	52.12	52.12	tr V8NFX8 V8NFX8_OPNHA Septin-7 (Fragment) OS=Ophiophagus hannah GN=sept7 PE=3 OPNHA	21
144	34.13	34.13	58.55	28.25	22.29	tr V8PEC5 V8PEC5_OPNHA Tight junction protein ZO-1 (Fragment) OS=Ophiophagus h OPNHA	17
145	34	34	62.18	31.49	28.48	tr V8NZ67 V8NZ67_OPNHA Vesicle-fusing ATPase (Fragment) OS=Ophiophagus hannah OPNHA	17
146	33.75	33.98	69.92	35.48	26.35	tr V8NZL6 V8NZL6_OPNHA Keratin, type II cytoskeletal 8 (Fragment) OS=Ophiophag OPNHA	26
147	33.54	33.54	56.04	23.29	21.26	tr V8P238 V8P238_OPNHA Sorbin and SH3 domain-containing protein 1 (Fragment) O OPNHA	17
148	33.42	33.71	55.31	29.66	29.66	tr V8NNT3 V8NNT3_OPNHA Hydroxymethylglutaryl-CoA synthase 1 (Fragment) OS=Ophi OPNHA	22
149	33.36	33.36	49.04	22.74	16.67	tr V8NXJ3 V8NXJ3_OPNHA Isoleucyl-tRNA synthetase, mitochondrial (Fragment) OS= OPNHA	14
150	33.25	33.25	79.35	54.84	47.53	tr V8P794 V8P794_OPNHA NADH dehydrogenase [ubiquinone] flavoprotein 1, mitocho OPNHA	17
151	33.25	33.25	92.55	68.24	63.53	tr V8P1F0 V8P1F0_OPNHA Phosphoglycerate mutase 1 OS=Ophiophagus hannah GN=Pgam OPNHA	25
152	33.24	33.24	40.75	12.05	10.76	tr V8NW16 V8NW16_OPNHA Long-chain specific acyl-CoA dehydrogenase, mitochondri OPNHA	22
153	33.2	33.2	62.84	33.65	30.94	tr V8NX18 V8NX18_OPNHA Mitochondrial import receptor subunit TOM70 (Fragment) OPNHA	18
154	33.12	33.27	53.11	30.49	26.39	tr V8PG08 V8PG08_OPNHA Putative ATP-dependent RNA helicase DDX17 OS=Ophiophagu OPNHA	16
155	32.92	32.92	42.36	21.89	19.45	tr V8P6U5 V8P6U5_OPNHA Echinoderm microtubule-associated protein-like 4 (Fragm OPNHA	17
156	32.87	32.87	58.81	23.12	13.58	tr V8PJ74 V8PJ74_OPNHA Pleckstrin-like domain-containing family A member 7 (F OPNHA	17
157	32.87	32.87	59.08	21.8	18.69	tr V8NZ52 V8NZ52_OPNHA Scavenger receptor cysteine-rich type 1 protein (Fragme OPNHA	20
158	32.85	32.85	66.46	31.99	30.91	tr V8PJ3 V8PJ3_OPNHA Chaperone activity of bcl complex-like, mitochondrial O OPNHA	19
159	32.78	32.78	56.3	26.54	20.74	tr V8NEA9 V8NEA9_OPNHA Programmed cell death 6-interacting protein OS=Ophioph OPNHA	15
160	32.68	32.68	41.27	32.45	30.86	tr V8N861 V8N861_OPNHA Aminopeptidase B (Fragment) OS=Ophiophagus hannah GN=Rn OPNHA	19
161	32.64	34.8	60.54	34.95	28.65	tr V8NEW1 V8NEW1_OPNHA Plastin-1 (Fragment) OS=Ophiophagus hannah GN=PLS1 PE=4 OPNHA	18
162	32.51	40.6	76.55	40.28	38.48	tr V8PDF5 V8PDF5_OPNHA Retinal dehydrogenase 1 OS=Ophiophagus hannah GN=ALDH1A OPNHA	26
163	32.49	32.49	55.74	32.91	29.59	tr V8NJM9 V8NJM9_OPNHA Long-chain-fatty-acid--CoA ligase 3 (Fragment) OS=Ophi OPNHA	17
164	32.36	32.36	48.05	27.62	26.9	tr V8NXA4 V8NXA4_OPNHA Importin-5 OS=Ophiophagus hannah GN=IPO5 PE=4 SV=1 OPNHA	17
165	32.33	32.33	58.01	32.21	29.89	tr V8NM08 V8NM08_OPNHA D-3-phosphoglycerate dehydrogenase OS=Ophiophagus hanna OPNHA	27
166	32.18	32.18	60.98	37.76	30.81	tr V8P6Z5 V8P6Z5_OPNHA Heterogeneous nuclear ribonucleoprotein R OS=Ophiophagu OPNHA	15
167	32.12	32.12	58.86	42.23	40.05	tr V8P4Q6 V8P4Q6_OPNHA Proliferation-associated protein 2G4 OS=Ophiophagus han OPNHA	17
168	32.09	32.09	42.23	17.25	9.865	tr V8NH58 V8NH58_OPNHA RNA-binding protein 12 OS=Ophiophagus hannah GN=RBM12 P OPNHA	14
169	31.89	31.89	84.84	51.62	51.62	tr V8NH00 V8NH00_OPNHA Enolase (Fragment) OS=Ophiophagus hannah GN=L345.12783 OPNHA	20
170	31.88	31.88	74.71	54.86	54.86	tr V8NXN9 V8NXN9_OPNHA Electron transfer flavoprotein subunit beta OS=Ophioph OPNHA	19
171	31.78	31.78	50.12	26.39	18.4	tr V8ND82 V8ND82_OPNHA Interleukin enhancer-binding factor 3 OS=Ophiophagus ha OPNHA	17
172	31.75	32.15	72.49	37.4	24.53	tr V8P127 V8P127_OPNHA Ribosomal protein S6 kinase 2 alpha (Fragment) OS=Ophi OPNHA	14
173	31.71	32.15	61.47	31.29	25.73	tr V8PB84 V8PB84_OPNHA Far upstream element-binding protein 2 (Fragment) OS=Op OPNHA	18
174	31.71	31.71	60.91	30.39	26.39	tr V8PE42 V8PE42_OPNHA Alpha-aminoacidic semialdehyde synthase, mitochondrial OPNHA	18
175	31.5	38.78	72.05	55.89	45.75	tr V8NZ18 V8NZ18_OPNHA Fructose-bisphosphate aldolase (Fragment) OS=Ophiophagu OPNHA	23
176	31.45	31.45	51.45	32	28.97	tr V8NQZ2 V8NQZ2_OPNHA Protein transport protein Sec23A OS=Ophiophagus hannah OPNHA	19
177	31.38	31.38	64.89	24.71	18.47	tr V8NHNO V8NHNO_OPNHA Amine sulfotransferase (Fragment) OS=Ophiophagus hannah OPNHA	22
178	31.26	31.26	71.13	44.57	41.8	tr V8ND58 V8ND58_OPNHA AP-2 complex subunit mu-1 OS=Ophiophagus hannah GN=AP2M OPNHA	19
179	31.2	31.2	48.79	37.74	31.13	tr V8PA47 V8PA47_OPNHA Coatomer subunit beta OS=Ophiophagus hannah GN=Copb2 PE OPNHA	18
180	31.13	31.13	59.7	29.04	27.03	tr V8NEY3 V8NEY3_OPNHA Alanine-tRNA synthetase, cytoplasmic (Fragment) OS=Ophi OPNHA	16
181	31.03	31.03	56.07	52.18	49.51	tr V8P9N2 V8P9N2_OPNHA Tubulin alpha-1A chain (Fragment) OS=Ophiophagus hannah OPNHA	22
182	30.94	30.94	60.35	23.57	23.57	tr V8NIM4 V8NIM4_OPNHA Oxysterol-binding protein (Fragment) OS=Ophiophagus han OPNHA	18
183	30.93	30.93	78.28	44.12	42.53	tr V8NJF1 V8NJF1_OPNHA Phosphoglycerate kinase (Fragment) OS=Ophiophagus hanna OPNHA	21
184	30.88	30.88	79.95	51.05	44.06	tr V8NRT1 V8NRT1_OPNHA Splicing factor, proline- and glutamine-rich OS=Ophioph OPNHA	14
185	30.85	31.18	56.98	31.01	25	tr V8NIH1 V8NIH1_OPNHA WD repeat-containing protein 11 (Fragment) OS=Ophiophag OPNHA	16
186	30.85	30.85	46.65	26.67	22.49	tr V8NY92 V8NY92_OPNHA Oxidation resistance protein 1 (Fragment) OS=Ophiophagu OPNHA	14
187	30.82	30.82	62.79	40.39	34.22	tr V8NVQ8 V8NVQ8_OPNHA Phosphoglucomutase-like protein 5 (Fragment) OS=Ophioph OPNHA	15
188	30.8	30.8	56.01	29.25	24.49	tr V8NYU2 V8NYU2_OPNHA Keratin, type I cytoskeletal 18 (Fragment) OS=Ophiophag OPNHA	19
189	30.71	30.71	47.59	35.31	33.77	tr V8P3W3 V8P3W3_OPNHA Elongation factor Tu OS=Ophiophagus hannah GN=TUFM PE=3 OPNHA	18
190	30.7	30.7	74.19	50	50	tr V8NTY1 V8NTY1_OPNHA Malate dehydrogenase (Fragment) OS=Ophiophagus hannah G OPNHA	19

191	30.66	39.17	56.67	33.51	25.65	tr V8NBZ7 V8NBZ7_OPHHA Catenin beta-1 (Fragment) OS=Ophiophagus hannah GN=CTNN OP	21
192	30.66	30.66	52.74	22.03	19.23	tr V8NXH8 V8NXH8_OPHHA Matrin-3 (Fragment) OS=Ophiophagus hannah GN=MATR3 PE=4 OP	15
193	30.57	30.57	58.56	22.01	16.85	tr V8NYV7 V8NYV7_OPHHA Leucyl-tRNA synthetase, cytoplasmic OS=Ophiophagus hann	15
194	30.54	30.54	41.74	14.21	12.6	tr V8NFB26 V8NFB26_OPHHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=	20
195	30.53	30.53	56.44	39.33	34	tr V8NQK3 V8NQK3_OPHHA Sulfide:quinone oxidoreductase, mitochondrial OS=Ophiop	18
196	30.51	30.51	43.05	16.65	12.95	tr V8NN56 V8NN56_OPHHA Transmembrane protein 2 (Fragment) OS=Ophiophagus hanna	14
197	30.32	30.32	49.45	24.24	24.24	tr V8N187 V8N187_OPHHA Peroxisomal multifunctional enzyme type 2 OS=Ophiophagu	22
198	30.28	36.43	56.77	27.71	20.32	tr V8NE95 V8NE95_OPHHA Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=	16
199	30.22	30.22	75.3	47.89	43.67	tr V8P6K5 V8P6K5_OPHHA L-lactate dehydrogenase OS=Ophiophagus hannah GN=L	19
200	30.16	30.16	54.87	17.37	16.5	tr V8NPK2 V8NPK2_OPHHA Caldesmon (Fragment) OS=Ophiophagus hannah GN=CALD1	17
201	30.12	30.12	68.12	43.32	43.32	tr V8N1X2 V8N1X2_OPHHA Flotillin-2 (Fragment) OS=Ophiophagus hannah GN=FL	15
202	30.1	30.1	50.09	32.07	27.89	tr V8P699 V8P699_OPHHA Calnexin (Fragment) OS=Ophiophagus hannah GN=CANX	17
203	30.09	30.1	62.58	39.35	36.34	tr V8N8U8 V8N8U8_OPHHA Sorting nexin-2 OS=Ophiophagus hannah GN=SNX2	17
204	29.97	29.97	44.37	15.42	12.72	tr V8PH64 V8PH64_OPHHA FAD-dependent oxidoreductase domain-containing protein	15
205	29.96	29.96	75.36	46.13	46.13	tr V8NCG0 V8NCG0_OPHHA Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Ophiophagu	17
206	29.78	29.78	83.87	61.29	56.85	tr V8PDX2 V8PDX2_OPHHA Triosephosphate isomerase OS=Ophiophagus hannah GN=	18
207	29.7	29.7	45.64	20.75	16.98	tr V8NFK2 V8NFK2_OPHHA DNA damage-binding protein 1 (Fragment) OS=Ophiophagu	14
208	29.6	29.6	50.43	35.58	29.88	tr V8P0Z6 V8P0Z6_OPHHA Hydroxyacid oxidase 1 (Fragment) OS=Ophiophagus hannah	16
209	29.52	29.52	63.78	42.6	34.69	tr V8PF03 V8PF03_OPHHA Succinate-semialdehyde dehydrogenase, mitochondrial (Fr	16
210	29.51	29.51	50.82	32.08	24.71	tr V8PCN6 V8PCN6_OPHHA Ubiquitin carboxyl-terminal hydrolase 5 OS=Ophiophagu	15
211	29.46	29.46	49.61	24.61	18.95	tr V8NL24 V8NL24_OPHHA Ubiquitin carboxyl-terminal hydrolase 7 (Fragment) OS=	14
212	29.13	29.13	48.07	28.04	27.89	tr V8P416 V8P416_OPHHA Prolyl endopeptidase (Fragment) OS=Ophiophagus hannah	14
213	29.08	29.08	65.67	29.85	25.37	tr V8NVZ1 V8NVZ1_OPHHA Amine oxidase [flavin-containing] A (Fragment) OS=Ophi	16
214	28.91	28.91	48.56	28.6	27.24	tr V8P4J6 V8P4J6_OPHHA Acyl-CoA synthetase short-chain family member 3, mitoch	15
215	28.84	28.84	48.95	18.96	14.57	tr V8NV23 V8NV23_OPHHA Eukaryotic translation initiation factor 5B (Fragment) OP	13
216	28.82	28.82	60.06	34.91	29.72	tr V8NZJ3 V8NZJ3_OPHHA BetA (Fragment) OS=Ophiophagus hannah GN=beta PE=3	15
217	28.62	28.62	73.19	28.4	24.87	tr V8P7H8 V8P7H8_OPHHA Cytoskeleton-associated protein 4 (Fragment) OS=Ophiop	23
218	28.49	28.49	45.22	30.82	26.24	tr V8P7P9 V8P7P9_OPHHA Signal transducer and activator of transcription (Fragm	14
219	28.31	28.31	69.87	29.99	28.94	tr V8NU45 V8NU45_OPHHA Succinate dehydrogenase (quinone) (Fragment) OS=Ophiop	15
220	28.18	28.18	52.77	25.44	21.41	tr V8PC38 V8PC38_OPHHA Extended synaptotagmin-1 (Fragment) OS=Ophiophagus hann	14
221	28.17	28.17	41.21	20.21	18.85	tr V8PON6 V8PON6_OPHHA Leukocyte elastase inhibitor (Fragment) OS=Ophiophagu	18
222	28.06	28.06	46.46	25.63	22.83	tr V8PE44 V8PE44_OPHHA Methylmalonyl-CoA mutase, mitochondrial OS=Ophiophagu	14
223	28.03	28.03	53.78	21.11	18.97	tr V8NL23 V8NL23_OPHHA MICOS complex subunit MIC60 OS=Ophiophagus hannah	15
224	28	28.37	54.06	21.24	15.6	tr V8PEZ1 V8PEZ1_OPHHA Lon protease homolog (Fragment) OS=Ophiophagus hannah	13
225	27.92	27.92	47.43	35.98	35.75	tr V8NWT5 V8NWT5_OPHHA Saccharopine dehydrogenase-like oxidoreductase OS=Ophi	15
226	27.91	27.91	68.25	49.5	41.5	tr V8NFD5 V8NFD5_OPHHA Guanine nucleotide-binding protein subunit beta-2-like	17
227	27.84	27.84	45.34	7.808	6.655	tr V8N8U7 V8N8U7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	17
228	27.79	27.79	48.5	33.88	30.74	tr V8NB65 V8NB65_OPHHA 26S proteasome non-ATPase regulatory subunit 2 OS=Ophi	15
229	27.74	27.74	54.32	23.13	23.13	tr V8NYG0 V8NYG0_OPHHA Major vault protein alpha (Fragment) OS=Ophiophagus han	15
230	27.71	29.79	62.21	33.4	31.3	tr V8N7M5 V8N7M5_OPHHA T-complex protein 1 subunit delta OS=Ophiophagus hannah	16
231	27.67	27.67	57.43	53.72	53.72	tr V8NDK0 V8NDK0_OPHHA 40S ribosomal protein SA OS=Ophiophagus hannah GN=	14
232	27.64	27.64	51.77	29.79	23.12	tr V8NJX7 V8NJX7_OPHHA Gamma-adducin OS=Ophiophagus hannah GN=ADD3 PE=4	13
233	27.63	27.63	60.51	42.96	34.18	tr V8PG75 V8PG75_OPHHA ATP-dependent RNA helicase DDX39A OS=Ophiophagus hannah	13
234	27.58	27.58	71.25	49.52	43.13	tr V8NGY4 V8NGY4_OPHHA Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Ophiopha	16
235	27.56	27.56	61.4	35.59	34.09	tr V8P718 V8P718_OPHHA Forminidoyltransferase-cyclodeaminase (Fragment) OS=Oph	20
236	27.32	27.32	86.7	62.23	58.8	tr V8NDW0 V8NDW0_OPHHA 14-3-3 protein epsilon OS=Ophiophagus hannah GN=	21
237	27.16	27.16	45.51	18.56	14.87	tr V8NMD0 V8NMD0_OPHHA SEC23-interacting protein (Fragment) OS=Ophiophagu	14
238	26.95	26.95	77.21	56.46	53.74	tr V8NKK1 V8NKK1_OPHHA Voltage-dependent anion-selective channel protein 3 OS=	23
239	26.91	26.91	26.2	11.44	11.44	tr V8PFH1 V8PFH1_OPHHA NADH-cytochrome b5 reductase 2 (Fragment) OS=Ophiopagu	18
240	26.89	48.97	53.66	34.45	27.85	tr V8PAD6 V8PAD6_OPHHA AP-2 complex subunit alpha-2 (Fragment) OS=Ophiophagu	23
241	26.68	26.68	57.65	21.42	21.42	tr V8NCP4 V8NCP4_OPHHA Complement C3 (Fragment) OS=Ophiophagus hannah GN=C	16
242	26.67	26.67	63.27	43.13	32.94	tr V8P016 V8P016_OPHHA 26S proteasome non-ATPase regulatory subunit 11 (Fragme	14
243	26.67	26.67	88.89	75.36	66.67	tr V8NJ44 V8NJ44_OPHHA Ras-related protein Rab-7a OS=Ophiophagus hannah GN=	14
244	26.62	26.62	83.53	53.41	53.01	tr V8P5H2 V8P5H2_OPHHA Proteasome subunit alpha type OS=Ophiophagus hannah	14
245	26.55	26.55	49.58	34.35	34.35	tr V8PG34 V8PG34_OPHHA Dehydrogenase/reductase SDR family member 7 (Fragment)	18
246	26.54	26.54	56.42	26.43	21.47	tr V8PFY6 V8PFY6_OPHHA Glycine dehydrogenase [decarboxylating], mitochondrial	12
247	26.42	26.42	59.95	44.03	32.89	tr V8PJ99 V8PJ99_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	13
248	26.4	26.4	44.66	18.65	16.39	tr V8NHT3 V8NHT3_OPHHA Aspartyl/asparaginyl beta-hydroxylase (Fragment) OS=Oph	12
249	26.4	26.4	68.35	36.5	33.54	tr V8P2C8 V8P2C8_OPHHA Pyruvate kinase OS=Ophiophagus hannah GN=PKM2	13
250	26.38	26.38	53.56	26.67	23.45	tr V8NQK7 V8NQK7_OPHHA Aspartate aminotransferase (Fragment) OS=Ophiophagus	16
251	26.36	26.36	27.36	10.71	9.695	tr V8NZA6 V8NZA6_OPHHA Host cell factor 1 OS=Ophiophagus hannah GN=HCFC1	13
252	26.3	26.3	38.73	10.96	7.416	tr V8NSQ9 V8NSQ9_OPHHA CCR4-NOT transcription complex subunit 1 OS=Ophiophagu	14
253	26.27	26.27	48.89	26	19.61	tr V8PGH4 V8PGH4_OPHHA Vacuolar protein sorting-associated protein 35 OS=Ophi	14
254	26.27	26.27	63.95	38.84	36.91	tr V8PBY1 V8PBY1_OPHHA Protein phosphatase 1B OS=Ophiophagus hannah GN=PPM1B	17
255	26.27	26.27	78.45	53.13	43.86	tr V8P3G8 V8P3G8_OPHHA NAD kinase domain-containing protein 1 (Fragment) OS=Op	15
256	26.23	26.23	60.62	27.23	21.38	tr V8PGZ0 V8PGZ0_OPHHA Signal recognition particle 68 kDa protein (Fragment) O	14
257	26.17	26.17	53.53	24.59	16.12	tr V8NNJ1 V8NNJ1_OPHHA Transcription intermediary factor 1-beta (Fragment) OS=	11
258	26.07	26.07	34.43	18.94	15.39	tr V8P7S7 V8P7S7_OPHHA Protein transport protein Sec24A (Fragment) OS=Ophiopha	13
259	25.96	25.96	66.2	13.35	11.12	tr V8NQD9 V8NQD9_OPHHA LIM domain only protein 7 (Fragment) OS=Ophiophagus	14
260	25.93	25.93	43.9	28.27	23.34	tr V8NDU4 V8NDU4_OPHHA Annexin (Fragment) OS=Ophiophagus hannah GN=Anx11	13
261	25.9	25.9	81.55	38.35	38.35	tr V8PGH6 V8PGH6_OPHHA Tropomyosin alpha-1 chain (Fragment) OS=Ophiophagu	15
262	25.85	25.85	41.52	13.29	11.26	tr V8NK36 V8NK36_OPHHA Murinoglobulin-2 OS=Ophiophagus hannah GN=Mug2	14
263	25.77	25.77	50.64	33.21	29.58	tr V8NK80 V8NK80_OPHHA Apoptosis-inducing factor 1, mitochondrial (Fragment) O	19
264	25.7	25.7	46.36	12.63	11.89	tr V8PD84 V8PD84_OPHHA Leucine-rich PPR motif-containing protein, mitochondria	14
265	25.69	25.69	48.59	36.01	27.55	tr V8P2T3 V8P2T3_OPHHA Asparaginyl-tRNA synthetase, cytoplasmic OS=Ophiophagu	12
266	25.67	25.67	67.82	50.99	47.03	tr V8PCC9 V8PCC9_OPHHA Acetyl-CoA acetyltransferase, mitochondrial OS=Ophiopha	14
267	25.66	25.66	48.64	23.19	23.19	tr V8NZD0 V8NZD0_OPHHA Transketolase (Fragment) OS=Ophiophagus hannah GN=Tkt	16
268	25.59	27.3	58.76	31.96	31.96	tr V8NWG5 V8NWG5_OPHHA Aldehyde dehydrogenase family 8 member A1 (Fragment) OS	15
269	25.55	25.96	53.15	23.94	14.24	tr V8PGP9 V8PGP9_OPHHA Myosin-Ib (Fragment) OS=Ophiophagus hannah GN=MYO1B	12
270	25.42	25.42	56.07	28.12	24.96	tr V8NWF0 V8NWF0_OPHHA Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synt	13
271	25.2	30.48	60.89	44.28	36.9	tr V8P6L3 V8P6L3_OPHHA Calcium-binding mitochondrial carrier protein Aralar1 O	14
272	25.2	27.28	74.04	47.3	33.93	tr V8PY86 V8PY86_OPHHA 26S protease regulatory subunit 4 OS=Ophiophagus hannah	13
273	25.18	25.18	56.01	19.64	10.68	tr V8P7Q5 V8P7Q5_OPHHA GRP1-associated protein 1 (Fragment) OS=Ophiophagus	11
274	25.18	25.18	61.36	31.96	23.3	tr V8PCY8 V8PCY8_OPHHA DCC-interacting protein 13-alpha OS=Ophiophagus hannah	11
275	25.11	25.11	72.95	35.7	35.7	tr V8NJV8 V8NJV8_OPHHA 2-hydroxyacyl-CoA lyase 1 (Fragment) OS=Ophiophagus	15
276	25.1	25.1	46.68	33.2	31.84	tr V8NNS8 V8NNS8_OPHHA Ubiquitin carboxyl-terminal hydrolase 14 OS=Ophiophagu	12
277	25.09	25.09	43.53	8.424	7.765	tr V8NSH6 V8NSH6_OPHHA Laminin subunit alpha-2 (Fragment) OS=Ophiophagus	13
278	25.01	25.01	63.27	37.79	36.09	tr V8P9F7 V8P9F7_OPHHA Putative aminopeptidase NPEPL1 (Fragment) OS=Ophiopagu	13
279	24.9	24.9	49.39	30.85	25.13	tr V8NML9 V8NML9_OPHHA Phenylalanyl-tRNA synthetase beta chain (Fragment) OS=	11
280	24.86	24.86	58.26	30.02	25.58	tr V8PAY8 V8PAY8_OPHHA Eukaryotic translation initiation factor 3 subunit L OS	14
281	24.81	24.81	66.34	29.77	25.49	tr V8PE54 V8PE54_OPHHA Seryl-tRNA synthetase, cytoplasmic OS=Ophiophagus	13
282	24.79	24.79	51	20.07	18.56	tr V8NLN2 V8NLN2_OPHHA Fructose-1,6-bisphosphatase isozyme 2 (Fragment) OS=Oph	25
283	24.77	24.77	72.28	41.57	41.57	tr V8NUJ3 V8NUJ3_OPHHA Inorganic pyrophosphatase (Fragment) OS=Ophiophagus	14
284	24.73	24.73	53.1	13.56	11.08	tr V8NNK8 V8NNK8_OPHHA Nuclear pore complex protein OS=Ophiophagus hannah	11
285	24.7	24.7	69.4	36.57	34.08	tr V8NHZ5 V8NHZ5_OPHHA Sorting nexin-4 OS=Ophiophagus hannah GN=SNX4	13
286	24.67	24.67	52.4	14.73	12.76	tr V8P4M7 V8P4M7_OPHHA Cordon-bleu protein-like 1 (Fragment) OS=Ophiophagus	12

287	24.67	24.67	61.17	25.96	24.14	tr V8P046 V8P046_OPPIHA Fibrinogen beta chain OS=Ophiophagus hannah GN=FGB PE=4 OPPIHA	20
288	24.61	24.61	46.93	26.61	21.93	tr V8P826 V8P826_OPPIHA Acetyl-coenzyme A synthetase 2-like, mitochondrial (Fra OPPIHA	11
289	24.56	24.56	59.91	39.66	29.42	tr V8P198 V8P198_OPPIHA Programmed cell death protein 4 OS=Ophiophagus hannah G OPPIHA	12
290	24.55	24.55	42.77	24.96	18.69	tr V8PA91 V8PA91_OPPIHA Acetyl-coenzyme A synthetase OS=Ophiophagus hannah GN=A OPPIHA	10
291	24.54	24.54	74.16	40.55	29.41	tr V8PFA7 V8PFA7_OPPIHA V-type proton ATPase subunit H OS=Ophiophagus hannah GN OPPIHA	13
292	24.48	24.48	54.98	36.43	35.75	tr V8NDL7 V8NDL7_OPPIHA V-type proton ATPase subunit B (Fragment) OS=Ophiophagu OPPIHA	13
293	24.27	24.27	67.19	36.75	30.71	tr V8NNL1 V8NNL1_OPPIHA 60S ribosomal protein L4 (Fragment) OS=Ophiophagus hann OPPIHA	14
294	24.25	24.25	75.1	50.59	49.8	tr V8NXD2 V8NXD2_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_0 OPPIHA	15
295	24.23	26.51	46.95	22.89	17.22	tr V8PHH0 V8PHH0_OPPIHA U5 small nuclear ribonucleoprotein component (Fragment) OPPIHA	12
296	24.23	24.23	50.4	29.12	24.7	tr V8P9H1 V8P9H1_OPPIHA UTP--glucose-1-phosphate uridylyltransferase OS=Ophioph OPPIHA	14
297	24.21	52.72	69.16	20.88	17.94	tr V8PFG8 V8PFG8_OPPIHA Myosin-10 OS=Ophiophagus hannah GN=MYH10 PE=4 SV=1 OPPIHA	29
298	24.07	31.06	73.29	36.06	33.22	tr V8P075 V8P075_OPPIHA Heterogeneous nuclear ribonucleoprotein Q (Fragment) OS OPPIHA	16
299	24.06	24.06	68	17.27	15.57	tr V8NP17 V8NP17_OPPIHA Collagen alpha-2(I) chain (Fragment) OS=Ophiophagus han OPPIHA	15
300	24.05	24.05	64.73	52.71	52.71	tr V8NWC0 V8NWC0_OPPIHA Ribose-phosphate pyrophosphokinase 2 (Fragment) OS=Ophi OPPIHA	22
301	23.98	23.98	48.45	24	19.63	tr V8NG27 V8NG27_OPPIHA Nodal modulator 1 OS=Ophiophagus hannah GN=NOM01 PE=4 S OPPIHA	11
302	23.94	23.94	62.94	56.35	46.7	tr V8NWQ9 V8NWQ9_OPPIHA Peroxiredoxin-6 (Fragment) OS=Ophiophagus hannah GN=PRD OPPIHA	11
303	23.85	26.14	82.86	56.33	53.06	tr V8P7V9 V8P7V9_OPPIHA 14-3-3 protein theta OS=Ophiophagus hannah GN=YWHAQ PE= OPPIHA	17
304	23.83	23.83	63.51	11.34	9.026	tr V8PCL4 V8PCL4_OPPIHA Band 4.1-like protein 1 (Fragment) OS=Ophiophagus hanna OPPIHA	13
305	23.8	23.8	65.4	27.68	23.72	tr V8P3Y7 V8P3Y7_OPPIHA V-type proton ATPase catalytic subunit A OS=Ophiophagus OPPIHA	15
306	23.73	23.73	55.02	13.08	12.09	tr V8PE26 V8PE26_OPPIHA Sickle tail protein OS=Ophiophagus hannah GN=Skt PE=4 S OPPIHA	15
307	23.69	23.69	52.8	21.51	17.02	tr V8NGE4 V8NGE4_OPPIHA Ubiquitin-like modifier-activating enzyme 6 (Fragment) OPPIHA	12
308	23.68	23.68	64.44	40.63	40.63	tr V8PB09 V8PB09_OPPIHA Peroxiredoxin-4 (Fragment) OS=Ophiophagus hannah GN=Prd OPPIHA	17
309	23.59	23.59	36.59	10.84	8.13	tr V8NI08 V8NI08_OPPIHA DENN domain-containing protein 4C (Fragment) OS=Ophioph OPPIHA	11
310	23.56	23.56	64.94	59.74	51.3	tr V8P7S0 V8P7S0_OPPIHA Eukaryotic translation initiation factor 5A OS=Ophioph OPPIHA	17
311	23.47	23.47	59.72	30.49	27.17	tr V8PGK1 V8PGK1_OPPIHA Coiled-coil domain-containing protein 22 OS=Ophiophagus OPPIHA	15
312	23.45	23.45	51.08	24.46	22.03	tr V8NVE6 V8NVE6_OPPIHA 6-phosphofructokinase, liver type OS=Ophiophagus hannah OPPIHA	11
313	23.42	23.42	42.39	7.954	6.698	tr V8POX6 V8POX6_OPPIHA Lysine--tRNA ligase OS=Ophiophagus hannah GN=KARS PE=3 OPPIHA	15
314	23.4	23.4	59.42	44.81	42.21	tr V8NX80 V8NX80_OPPIHA 3' (2'),5'-bisphosphate nucleotidase 1 OS=Ophiophagus ha OPPIHA	15
315	23.35	26.39	61.9	30.09	22.51	tr V8NRX1 V8NRX1_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	14
316	23.29	23.29	47.81	29.33	25.71	tr V8NQJ7 V8NQJ7_OPPIHA Methionyl-tRNA synthetase, cytoplasmic OS=Ophiophagus h OPPIHA	11
317	23.24	23.24	46.32	16.73	13.79	tr V8P6S8 V8P6S8_OPPIHA Protein transport protein Sec24D (Fragment) OS=Ophioph OPPIHA	11
318	23.16	26.53	62.82	26.99	25.64	tr V8NKM4 V8NKM4_OPPIHA ATP-dependent RNA helicase DDX3X OS=Ophiophagus hannah OPPIHA	14
319	23.12	23.12	42.58	16.08	12.72	tr V8NZF2 V8NZF2_OPPIHA Splicing factor 3B subunit 3 OS=Ophiophagus hannah GN=S OPPIHA	11
320	23.12	23.12	55.82	18.32	15.36	tr V8NGJ6 V8NGJ6_OPPIHA Hephaestin-like protein 1 OS=Ophiophagus hannah GN=HEPH OPPIHA	15
321	23.07	23.07	34.72	10.78	8.492	tr V8P7E4 V8P7E4_OPPIHA Protein furry-like-like protein (Fragment) OS=Ophiophag OPPIHA	15
322	23.06	23.06	45.99	20.11	17.97	tr V8POU3 V8POU3_OPPIHA Serine/threonine-protein phosphatase 4 regulatory subun OPPIHA	12
323	23.04	23.04	69.38	38.52	36.54	tr V8P8K0 V8P8K0_OPPIHA Aminomethyltransferase OS=Ophiophagus hannah GN=AMT PE= OPPIHA	15
324	23.03	23.03	57.43	23.14	21.62	tr V8NCQ7 V8NCQ7_OPPIHA Methylcrotonoyl-CoA carboxylase subunit alpha, mitochon OPPIHA	13
325	23.02	23.02	59.65	24.56	22.06	tr V8PBY8 V8PBY8_OPPIHA Vacuolar protein sorting-associated protein 45 OS=Ophioph OPPIHA	11
326	23.01	23.01	54.32	12.42	10.72	tr V8PHD2 V8PHD2_OPPIHA Sulfurtransferase OS=Ophiophagus hannah GN=Tst PE=4 SV= OPPIHA	16
327	22.98	22.98	49.75	19.34	16.79	tr V8PF80 V8PF80_OPPIHA Exocyst complex component 7 OS=Ophiophagus hannah GN=EX OPPIHA	11
328	22.9	22.9	57.25	15.15	14.31	tr V8P8H5 V8P8H5_OPPIHA Putative helicase MOV-10 (Fragment) OS=Ophiophagus hannah OPPIHA	13
329	22.9	22.9	54.7	16	12.56	tr V8NY20 V8NY20_OPPIHA ATP-dependent RNA helicase SUPV3L1, mitochondrial (Frag OPPIHA	10
330	22.84	22.84	67.69	21.25	19.21	tr V8NXB4 V8NXB4_OPPIHA Kinesin light chain 4 (Fragment) OS=Ophiophagus hannah OPPIHA	11
331	22.78	22.78	60.94	36.71	36.71	tr V8P364 V8P364_OPPIHA Perilipin OS=Ophiophagus hannah GN=PLIN2 PE=3 SV=1 OPPIHA	11
332	22.72	22.72	35.23	6.917	6.472	tr V8P7J4 V8P7J4_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	12
333	22.69	22.69	43.6	23.51	17.26	tr V8NIE2 V8NIE2_OPPIHA Heterogeneous nuclear ribonucleoprotein U-like protein OPPIHA	11
334	22.59	22.59	62.36	32.1	24.71	tr V8P5J0 V8P5J0_OPPIHA Eukaryotic translation initiation factor 5 OS=Ophiophag OPPIHA	12
335	22.57	22.57	68.16	30.13	27.78	tr V8N4L4 V8N4L4_OPPIHA Acyl-CoA dehydrogenase family member 9, mitochondrial (OPPIHA	10
336	22.56	22.56	38.24	16.59	12.68	tr V8P6M9 V8P6M9_OPPIHA Bile salt export pump (Fragment) OS=Ophiophagus hannah OPPIHA	11
337	22.52	22.52	73.48	53.03	46.97	tr V8PA97 V8PA97_OPPIHA 40S ribosomal protein S3a OS=Ophiophagus hannah GN=RP53 OPPIHA	13
338	22.51	22.51	69.49	29.66	27.4	tr V8P9B0 V8P9B0_OPPIHA Reticulocalbin-1 (Fragment) OS=Ophiophagus hannah GN=RC OPPIHA	13
339	22.46	22.46	58.1	29.18	26.43	tr V8P8H9 V8P8H9_OPPIHA Heterogeneous nuclear ribonucleoprotein A1 (Fragment) O OPPIHA	12
340	22.46	22.46	56.16	27.03	27.03	tr V8NE43 V8NE43_OPPIHA Eukaryotic translation initiation factor 2 subunit 2 OS OPPIHA	14
341	22.45	22.45	58.52	26.51	18.41	tr V8NMH5 V8NMH5_OPPIHA Cysteinylyl-tRNA synthetase, cytoplasmic (Fragment) OS=Op OPPIHA	10
342	22.44	22.44	48.56	33.41	31.01	tr V8P9Q5 V8P9Q5_OPPIHA Eukaryotic peptide chain release factor subunit 1 (Frag OPPIHA	12
343	22.42	22.42	44.9	18.01	15.26	tr V8NTN6 V8NTN6_OPPIHA Plasma membrane calcium-transporting ATPase 4 (Fragment) OPPIHA	11
344	22.39	22.39	44.68	5.573	3.791	tr V8PIE2 V8PIE2_OPPIHA Ankyrin-3 (Fragment) OS=Ophiophagus hannah GN=ANK3 PE=4 OPPIHA	15
345	22.36	22.36	80.97	39.53	32.98	tr V8POE7 V8POE7_OPPIHA Methyl-CpG-binding protein 2 (Fragment) OS=Ophiophagus OPPIHA	12
346	22.36	22.36	55	19.73	17.57	tr V8NIG3 V8NIG3_OPPIHA Beta,beta-carotene 9',10'-oxygenase (Fragment) OS=Ophi OPPIHA	15
347	22.28	22.57	45.02	23	14.45	tr V8NZ17 V8NZ17_OPPIHA Urocanate hydratase (Fragment) OS=Ophiophagus hannah GN OPPIHA	17
348	22.26	22.26	47.14	19.03	15.8	tr V8NCP1 V8NCP1_OPPIHA Integrin beta OS=Ophiophagus hannah GN=ITGB1 PE=3 SV=1 OPPIHA	13
349	22.26	22.26	62.79	41.86	41.86	tr V8NNK5 V8NNK5_OPPIHA Eukaryotic initiation factor 4A-II OS=Ophiophagus hanna OPPIHA	12
350	22.24	22.24	48.56	26.95	25.51	tr V8NW58 V8NW58_OPPIHA Leukotriene A-4 hydrolase (Fragment) OS=Ophiophagus han OPPIHA	13
351	22.22	22.22	53.71	14.01	8.204	tr V8NV83 V8NV83_OPPIHA GRIP and coiled-coil domain-containing protein 2 (Fragm OPPIHA	11
352	22.21	22.21	55.72	14.79	10.71	tr V8NH83 V8NH83_OPPIHA Dynamin-like protein (Fragment) OS=Ophiophagus hannah G OPPIHA	9
353	22.2	22.2	54.51	30.02	28.73	tr V8NTJ5 V8NTJ5_OPPIHA Fumarate hydratase, mitochondrial (Fragment) OS=Ophioph OPPIHA	19
354	22.14	22.14	52.29	34.7	26.27	tr V8PDB7 V8PDB7_OPPIHA Citrate synthase OS=Ophiophagus hannah GN=CS PE=3 SV=1 OPPIHA	11
355	22.13	22.13	80.26	66.95	57.08	tr V8NZ26 V8NZ26_OPPIHA 40S ribosomal protein S3 (Fragment) OS=Ophiophagus hann OPPIHA	12
356	22	22	67.64	44	44	tr V8NTRI V8NTRI_OPPIHA 40S ribosomal protein S2 OS=Ophiophagus hannah GN=RP52 OPPIHA	13
357	21.99	21.99	62.37	49.13	47.04	tr V8PAT0 V8PAT0_OPPIHA Glucosamine-6-phosphate isomerase OS=Ophiophagus hannah OPPIHA	11
358	21.97	21.97	49.1	39.43	39.43	tr V8PGE9 V8PGE9_OPPIHA Proteasome subunit alpha type (Fragment) OS=Ophiophagus OPPIHA	15
359	21.95	21.95	58.95	21.33	15.19	tr V8POG9 V8POG9_OPPIHA Protein phosphatase 1 regulatory subunit 12A (Fragment) OPPIHA	12
360	21.94	21.94	40.08	24.05	16.03	tr V8NVU5 V8NVU5_OPPIHA Ubiquitin carboxyl-terminal hydrolase 10 (Fragment) OS= OPPIHA	10
361	21.92	21.92	58.2	25.08	20.16	tr V8P2R9 V8P2R9_OPPIHA Threonyl-tRNA synthetase, cytoplasmic (Fragment) OS=Oph OPPIHA	11
362	21.91	21.91	47.13	7.583	5.589	tr V8PC53 V8PC53_OPPIHA RANBP2-like and GRIP domain-containing protein 5/6 (Fra OPPIHA	12
363	21.91	21.91	62.65	32.83	29.52	tr V8PG26 V8PG26_OPPIHA Glutaredoxin-3 OS=Ophiophagus hannah GN=GLRX3 PE=4 SV=1 OPPIHA	11
364	21.87	21.87	57.62	22.98	15	tr V8PJ82 V8PJ82_OPPIHA Putative ATP-dependent RNA helicase DDX23 (Fragment) OS OPPIHA	11
365	21.83	21.83	63.48	19.5	15.03	tr V8PBX6 V8PBX6_OPPIHA E3 ubiquitin-protein ligase HECTD3 (Fragment) OS=Ophi OPPIHA	10
366	21.83	21.83	69.95	24.35	21.93	tr V8P4U2 V8P4U2_OPPIHA Heterogeneous nuclear ribonucleoprotein U (Fragment) OS OPPIHA	13
367	21.8	21.85	66.23	34.43	24.34	tr V8NWQ4 V8NWQ4_OPPIHA 26S proteasome non-ATPase regulatory subunit 12 (Fragme OPPIHA	11
368	21.76	21.76	45.8	21.09	20.1	tr V8P9C3 V8P9C3_OPPIHA Carnitine O-palmitoyltransferase 2, mitochondrial (Frag OPPIHA	13
369	21.71	21.71	69.02	34.63	30.73	tr V8P437 V8P437_OPPIHA Lissencephaly-1 homolog OS=Ophiophagus hannah GN=PAFAH1 OPPIHA	11
370	21.7	21.7	48.79	31.35	30.68	tr V8NLC9 V8NLC9_OPPIHA Actin-related protein 2 (Fragment) OS=Ophiophagus hanna OPPIHA	17
371	21.7	21.7	83.5	54.05	41.1	tr V8NKD1 V8NKD1_OPPIHA Serine/threonine-protein phosphatase OS=Ophiophagus han OPPIHA	11
371	0	19.61	82.61	55.8	41.3	tr V8P7S2 V8P7S2_OPPIHA Serine/threonine-protein phosphatase (Fragment) OS=Ophi OPPIHA	10
372	21.68	21.68	45.6	12.36	10.14	tr V8PB91 V8PB91_OPPIHA Ubiquitin carboxyl-terminal hydrolase 47 (Fragment) OS= OPPIHA	12
373	21.67	21.67	58.03	26.83	20.9	tr V8NDQ0 V8NDQ0_OPPIHA Actin-related protein 2/3 complex subunit 1B (Fragment) OPPIHA	12
374	21.55	21.6	49.84	11.07	10.42	tr V8NQG3 V8NQG3_OPPIHA Sorbin and SH3 domain-containing protein 2 (Fragment) O OPPIHA	11
375	21.55	21.55	46.12	17.17	16	tr V8PG17 V8PG17_OPPIHA Fibronectin type III domain-containing protein 3B OS=Op OPPIHA	12
376	21.5	21.5	70.94	57.81	49.38	tr V8PBR7 V8PBR7_OPPIHA Protein SEC13-like protein OS=Ophiophagus hannah GN=Sec OPPIHA	12
377	21.49	21.5	57.8	47.98	40.17	tr V8NGN2 V8NGN2_OPPIHA 26S proteasome non-ATPase regulatory subunit 13 (Fragme OPPIHA	10
378	21.45	21.52	73.66	43.89	38.17	tr V8P8W0 V8P8W0_OPPIHA Annexin (Fragment) OS=Ophiophagus hannah GN=ANXA5 PE=3 OPPIHA	11
379	21.43	21.43	43.5	12.84	8.784	tr V8P298 V8P298_OPPIHA Tripeptidyl-peptidase 2 (Fragment) OS=Ophiophagus hanna OPPIHA	10
380	21.43	21.43	50.11	20.59	18.76	tr V8NMW3 V8NMW3_OPPIHA Non-specific lipid-transfer protein OS=Ophiophagus hann OPPIHA	17
381	21.4	21.4	51.13	39.8	30.73	tr V8NPL9 V8NPL9_OPPIHA S-adenosylmethionine synthase (Fragment) OS=Ophiophagus OPPIHA	12

382	21.4	21.4	58.75	43.89	40.92	tr	V8P0L1	V8P0L1_OPHHA	Guanine nucleotide-binding protein G(I) subunit alpha-2 OPHHA	14
383	21.31	21.31	55.28	17.61	13.45	tr	V8P931	V8P931_OPHHA	Presequence protease, mitochondrial (Fragment) OS=Ophio OPHHA	9
384	21.25	21.25	54.73	33.85	29.89	tr	V8NU21	V8NU21_OPHHA	Glucose-6-phosphate isomerase (Fragment) OS=Ophiophagus OPHHA	17
385	21.23	21.23	41.49	11.26	7.638	tr	V8P091	V8P091_OPHHA	Ubiquitin carboxyl-terminal hydrolase 24 OS=Ophiophagus OPHHA	9
386	21.18	21.18	39.8	16.71	16.71	tr	V8PH33	V8PH33_OPHHA	Integrin beta (Fragment) OS=Ophiophagus hannah GN=ITGB3 OPHHA	12
387	21.16	21.69	43.07	22.91	17.18	tr	V8NZC8	V8NZC8_OPHHA	Protein transport protein Sec24C (Fragment) OS=Ophiophaga OPHHA	10
388	21.16	21.16	54.86	24.76	24.76	tr	V8P2W6	V8P2W6_OPHHA	Protein LYRIC (Fragment) OS=Ophiophagus hannah GN=MTDH OPHHA	15
389	21.06	21.06	52.58	21.67	18.83	tr	V8P7C3	V8P7C3_OPHHA	Beta-ureidopropionase (Fragment) OS=Ophiophagus hannah OPHHA	14
390	21.03	21.03	38.57	28.48	28.48	tr	V8PBJ8	V8PBJ8_OPHHA	EGF-containing fibulin-like extracellular matrix protei OPHHA	11
391	21	21	60.1	22.54	19.3	tr	V8PC88	V8PC88_OPHHA	Cell division cycle 5-like protein (Fragment) OS=Ophiop OPHHA	10
392	20.99	20.99	55.46	27.84	26.06	tr	V8PA64	V8PA64_OPHHA	26S proteasome non-ATPase regulatory subunit 6 (Fragmen OPHHA	12
393	20.94	20.94	27.76	8.1	6.611	tr	V8PAX2	V8PAX2_OPHHA	Fibrillin-1 (Fragment) OS=Ophiophagus hannah GN=FBNI PE OPHHA	16
394	20.9	20.9	63.17	26.18	14.46	tr	V8POH5	V8POH5_OPHHA	Cullin-3 (Fragment) OS=Ophiophagus hannah GN=CUL3 PE=3 OPHHA	8
395	20.89	20.89	60.33	20.93	19.97	tr	V8PFC9	V8PFC9_OPHHA	Disintegrin and metalloproteinase domain-containing pro OPHHA	12
396	20.89	20.89	51.5	33.5	32.75	tr	V8NQ70	V8NQ70_OPHHA	PDZ and LIM domain protein 3 OS=Ophiophagus hannah GN=P OPHHA	15
397	20.84	20.84	54.02	26.32	22.22	tr	V8NN80	V8NN80_OPHHA	Sorting nexin OS=Ophiophagus hannah GN=Snx9 PE=3 SV=1 OPHHA	11
398	20.8	20.8	56.76	28.38	24.87	tr	V8PEA8	V8PEA8_OPHHA	Transforming growth factor-beta-induced protein ig-h3 (OPHHA	12
399	20.79	20.8	67.33	64.85	64.85	tr	V8P8Q7	V8P8Q7_OPHHA	Ras-related protein R-Ras2 OS=Ophiophagus hannah GN=RRA OPHHA	12
400	20.77	20.77	63.69	45.85	40.92	tr	V8P7Q0	V8P7Q0_OPHHA	Purine nucleoside phosphorylase (Fragment) OS=Ophiophag OPHHA	11
401	20.76	20.76	67.41	31.6	27.41	tr	V8PGK3	V8PGK3_OPHHA	Transducin beta-like protein 2 (Fragment) OS=Ophiophagu OPHHA	11
402	20.71	20.71	67.93	11.44	8.14	tr	V8PA14	V8PA14_OPHHA	TRIO and F-actin-binding protein (Fragment) OS=Ophiopha OPHHA	10
403	20.65	20.65	50.99	19.34	17.35	tr	V8NX23	V8NX23_OPHHA	Zyxin (Fragment) OS=Ophiophagus hannah GN=ZXY PE=4 SV=1 OPHHA	11
404	20.6	20.6	59.82	32.59	27.9	tr	V8PC74	V8PC74_OPHHA	Septin-10 (Fragment) OS=Ophiophagus hannah GN=SEPT10 PE OPHHA	10
405	20.54	20.54	51.87	31.17	28.18	tr	V8NN25	V8NN25_OPHHA	AidB (Fragment) OS=Ophiophagus hannah GN=aidB PE=3 SV=1 OPHHA	13
406	20.49	30.88	49.1	14.93	13.25	tr	V8NIG4	V8NIG4_OPHHA	Filamin-C (Fragment) OS=Ophiophagus hannah GN=Flnc PE=4 OPHHA	17
407	20.49	20.49	54.32	16.69	12.37	tr	V8P862	V8P862_OPHHA	Deubiquitinating protein (Fragment) OS=Ophiophagus hann OPHHA	10
408	20.48	20.48	50.06	18.96	13.53	tr	V8NGK5	V8NGK5_OPHHA	RNA-binding protein 4 (Fragment) OS=Ophiophagus hannah OPHHA	10
409	20.48	20.48	59.58	31.37	26.95	tr	V8PG00	V8PG00_OPHHA	Succinyl-CoA ligase subunit beta OS=Ophiophagus hannah OPHHA	10
410	20.47	20.47	63.76	31.65	29.59	tr	V8NSK0	V8NSK0_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	12
411	20.44	20.44	50.63	23.22	23.22	tr	V8N120	V8N120_OPHHA	Acetyl-CoA carboxylase 1 (Fragment) OS=Ophiophagus hann OPHHA	12
412	20.4	20.4	70.75	59.91	56.6	tr	V8P4D1	V8P4D1_OPHHA	Ras-related protein Rab-2A OS=Ophiophagus hannah GN=RAB OPHHA	13
413	20.39	20.39	76.67	48.79	39.39	tr	V8PG15	V8PG15_OPHHA	Serine/threonine-protein phosphatase OS=Ophiophagus han OPHHA	10
414	20.36	20.36	86.57	62.19	61.69	tr	V8NDS9	V8NDS9_OPHHA	Ras-related protein Rab-14 OS=Ophiophagus hannah GN=RAB OPHHA	11
415	20.35	20.35	44.29	15.6	10.58	tr	V8PEN0	V8PEN0_OPHHA	Protein flightless-1-like protein OS=Ophiophagus hannah OPHHA	10
416	20.32	20.32	45.36	19.1	13.93	tr	V8N949	V8N949_OPHHA	GDH/6PGL endoplasmic bifunctional protein (Fragment) OS OPHHA	11
417	20.26	20.26	56.7	21.58	15.66	tr	V8PJG1	V8PJG1_OPHHA	Nuclear migration protein nudC (Fragment) OS=Ophiophagu OPHHA	10
418	20.25	20.25	42.2	14.51	11.93	tr	V8P5K5	V8P5K5_OPHHA	AP-3 complex subunit delta-1 OS=Ophiophagus hannah GN=A OPHHA	10
419	20.24	20.24	67.93	34.3	31.4	tr	V8P3C8	V8P3C8_OPHHA	Dihydropyrimidine dehydrogenase [NADP+] (Fragment) OS=O NADP+	11
420	20.2	20.2	62.94	26.03	21.64	tr	V8PC41	V8PC41_OPHHA	LETM1 and EF-hand domain-containing protein 1, mitochon OPHHA	10
421	20.11	20.11	55.47	25.59	25.59	tr	V8POZ0	V8POZ0_OPHHA	Fibrinogen gamma chain (Fragment) OS=Ophiophagus hannah OPHHA	11
422	20.1	20.1	66.15	32.3	23.21	tr	V8PCE3	V8PCE3_OPHHA	MAGUK p55 subfamily member 6 (Fragment) OS=Ophiophagus OPHHA	10
423	20.08	20.08	57.28	32.18	27.59	tr	V8PG98	V8PG98_OPHHA	T-complex protein 1 subunit zeta OS=Ophiophagus hannah OPHHA	10
424	20.07	20.07	50.71	17.17	10.87	tr	V8PIQ3	V8PIQ3_OPHHA	Insulin-degrading enzyme (Fragment) OS=Ophiophagus hann OPHHA	9
425	20.04	20.18	84.53	55.8	55.8	tr	V8NNE3	V8NNE3_OPHHA	Nucleoside diphosphate kinase (Fragment) OS=Ophiophagus OPHHA	14
426	20.04	20.04	52.78	44.44	30.56	tr	V8PGJ1	V8PGJ1_OPHHA	Histone H4 (Fragment) OS=Ophiophagus hannah GN=H4-VIII OPHHA	11
426	0	18.32	58.25	54.37	53.4	tr	V8N8S2	V8N8S2_OPHHA	Histone H4 (Fragment) OS=Ophiophagus hannah GN=L345_010 OPHHA	11
427	19.99	22.04	69.9	41.1	38.51	tr	V8PHF4	V8PHF4_OPHHA	Glycerol-3-phosphate dehydrogenase [NAD(+)] (Fragment) NAD(+) OPHHA	19
428	19.96	22.23	80.69	51.74	48.65	tr	V8PHQ7	V8PHQ7_OPHHA	14-3-3 protein zeta/delta (Fragment) OS=Ophiophagus han OPHHA	14
429	19.92	19.92	85.95	44.12	35.95	tr	V8P625	V8P625_OPHHA	Mitochondrial import receptor subunit TOM34 OS=Ophiopha OPHHA	9
430	19.91	31.3	57.33	49.33	41.33	tr	V8NQ19	V8NQ19_OPHHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345_1 OPHHA	22
431	19.91	19.91	70.77	49.3	44.01	tr	V8PFV1	V8PFV1_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	10
432	19.85	19.85	37.75	10.58	9.75	tr	V8NQP0	V8NQP0_OPHHA	Tankyrase-1-binding protein (Fragment) OS=Ophiophagus h OPHHA	10
433	19.85	19.85	37.58	23.23	21.62	tr	V8NNB1	V8NNB1_OPHHA	Peroxisomal acyl-coenzyme A oxidase 2 OS=Ophiophagus ha OPHHA	11
434	19.8	19.8	75.14	61.88	61.88	tr	V8PEH4	V8PEH4_OPHHA	ADP-ribosylation factor 1 OS=Ophiophagus hannah GN=ARF1 OPHHA	13
434	0	19.77	69.61	61.88	61.88	tr	V8PHQ3	V8PHQ3_OPHHA	ADP-ribosylation factor 3 OS=Ophiophagus hannah GN=ARF3 OPHHA	13
435	19.76	20.01	51.93	20.63	15.47	tr	V8NQA6	V8NQA6_OPHHA	Band 4.1-like protein 1 (Fragment) OS=Ophiophagus hanna OPHHA	11
436	19.76	19.76	55.8	21.91	16.49	tr	V8NQX6	V8NQX6_OPHHA	Cullin-1 OS=Ophiophagus hannah GN=Cull PE=3 SV=1 OPHHA	10
437	19.75	19.75	35.29	8.551	6.812	tr	V8NCC0	V8NCC0_OPHHA	von Willebrand factor (Fragment) OS=Ophiophagus hannah OPHHA	10
438	19.71	19.71	53.5	27.81	26.54	tr	V8NGN8	V8NGN8_OPHHA	APOBEC1 complementation factor (Fragment) OS=Ophiophagu OPHHA	10
439	19.69	19.69	61.36	28.21	24.18	tr	V8P7I2	V8P7I2_OPHHA	Methylcrotonoyl-CoA carboxylase beta chain, mitochondri OPHHA	10
440	19.63	19.63	52.35	36.05	33.83	tr	V8NBS9	V8NBS9_OPHHA	Endoplasmic reticulum resident protein 44 OS=Ophiophagu OPHHA	12
441	19.6	19.6	51.63	20.55	16.64	tr	V8NR64	V8NR64_OPHHA	E3 UFM1-protein ligase 1 (Fragment) OS=Ophiophagus hann OPHHA	11
442	19.54	19.54	57.85	25.59	16.77	tr	V8NV19	V8NV19_OPHHA	Stress-induced-phosphoprotein 1 (Fragment) OS=Ophiophag OPHHA	11
443	19.54	19.54	74.48	51.38	44.14	tr	V8N135	V8N135_OPHHA	Septin-2 (Fragment) OS=Ophiophagus hannah GN=Sept2 PE=4 OPHHA	9
444	19.53	19.53	51.58	32.11	26.58	tr	V8P9S5	V8P9S5_OPHHA	Aminoacylase-1 OS=Ophiophagus hannah GN=ACY1 PE=4 SV=1 OPHHA	10
445	19.52	19.52	59.77	18.63	15.01	tr	V8NM62	V8NM62_OPHHA	Cytosol aminopeptidase (Fragment) OS=Ophiophagus hannah OPHHA	9
446	19.5	19.5	50.16	27.06	19.94	tr	V8P5D0	V8P5D0_OPHHA	Sec1 family domain-containing protein 1 OS=Ophiophagus OPHHA	9
447	19.49	19.49	58.78	25	25	tr	V8PEJ1	V8PEJ1_OPHHA	Myosin light polypeptide 6 (Fragment) OS=Ophiophagus ha OPHHA	19
448	19.47	19.47	46.31	19.72	16.03	tr	V8P997	V8P997_OPHHA	Glucocorticoid receptor (Fragment) OS=Ophiophagus hanna OPHHA	9
449	19.47	19.47	42.62	15.04	15.04	tr	V8PFM2	V8PFM2_OPHHA	Delta-1-pyrroline-5-carboxylate synthase (Fragment) OS= OPHHA	11
450	19.44	19.44	57.01	38.51	38.51	tr	V8P8G5	V8P8G5_OPHHA	Malate dehydrogenase OS=Ophiophagus hannah GN=MDH1 PE=3 OPHHA	17
451	19.43	19.43	64.74	33.61	23.42	tr	V8NAS7	V8NAS7_OPHHA	Sorting nexin-6 (Fragment) OS=Ophiophagus hannah GN=SNX OPHHA	10
452	19.42	19.42	45.31	16.49	16.49	tr	V8NLY2	V8NLY2_OPHHA	Serine/threonine-protein phosphatase 6 regulatory subun OPHHA	10
453	19.4	19.4	52.12	24.6	24.45	tr	V8NKS8	V8NKS8_OPHHA	Calpain-2 catalytic subunit (Fragment) OS=Ophiophagus h OPHHA	12
454	19.38	19.38	48.87	25.5	25.5	tr	V8NYY1	V8NYY1_OPHHA	Gelsolin OS=Ophiophagus hannah GN=GSN PE=4 SV=1 OPHHA	12
455	19.38	19.38	58.66	36.74	23.38	tr	V8PH14	V8PH14_OPHHA	Rho GTPase-activating protein 1 (Fragment) OS=Ophiophag OPHHA	8
456	19.37	19.38	45.92	22.96	19.79	tr	V8NLC1	V8NLC1_OPHHA	Acyl-coenzyme A oxidase OS=Ophiophagus hannah GN=ACOX1 OPHHA	11
457	19.33	20.66	71.29	28.55	18.18	tr	V8PDF3	V8PDF3_OPHHA	Coiled-coil domain-containing protein 93 (Fragment) OS= OPHHA	10
458	19.32	19.44	68.19	21.54	17.97	tr	V8P4M9	V8P4M9_OPHHA	RUN and FYVE domain-containing protein 1 OS=Ophiophagus OPHHA	10
459	19.3	19.3	56.99	26.1	19.21	tr	V8NUX0	V8NUX0_OPHHA	Putative adenosylhomocysteinase 2 (Fragment) OS=Ophioph OPHHA	8
460	19.3	19.3	65.88	32.94	32.94	tr	V8P9T9	V8P9T9_OPHHA	Citrate lyase subunit beta-like protein, mitochondrial OPHHA	11
461	19.19	19.19	54.74	16.34	8.357	tr	V8NTV6	V8NTV6_OPHHA	Thrombospondin-1 (Fragment) OS=Ophiophagus hannah GN=TH OPHHA	8
462	19.18	19.18	51.2	29.19	27.67	tr	V8P8L3	V8P8L3_OPHHA	THO complex subunit 4 OS=Ophiophagus hannah GN=THOC4 PE OPHHA	12
463	19.15	19.15	47.93	23.65	21.58	tr	V8NTB5	V8NTB5_OPHHA	Protein kinase C and casein kinase substrate in neurons OPHHA	10
464	19.03	19.08	52.7	22.37	18.02	tr	V8NLV9	V8NLV9_OPHHA	Band 4.1-like protein 2 (Fragment) OS=Ophiophagus hanna OPHHA	9
465	19.02	21.07	84.44	35.24	35.24	tr	V8PAL4	V8PAL4_OPHHA	Glycerol-3-phosphate dehydrogenase [NAD(+)] (Fragment) NAD(+) OPHHA	12
466	18.99	19.07	55.26	19.19	9.942	tr	V8NZ22	V8NZ22_OPHHA	N-alpha-acetyltransferase 15, NatA auxiliary subunit OS OPHHA	8
467	18.94	18.94	79.94	33.53	31.14	tr	V8NHE8	V8NHE8_OPHHA	Coatomer subunit epsilon (Fragment) OS=Ophiophagus hann OPHHA	11
468	18.93	18.93	52.82	28.01	22.93	tr	V8P1U0	V8P1U0_OPHHA	Zinc finger protein OS=Ophiophagus hannah GN=Znf326 PE= OPHHA	9
469	18.9	18.9	51.28	9.946	7.925	tr	V8NQD7	V8NQD7_OPHHA	Acyl-coenzyme A synthetase ACSM4, mitochondrial (Fragme OPHHA	10
470	18.9	18.9	46.7	26.2	22.99	tr	V8POU1	V8POU1_OPHHA	ATP-binding cassette sub-family B member 7, mitochondri OPHHA	12
471	18.9	18.9	62.07	33.05	30.17	tr	V8PFS2	V8PFS2_OPHHA	Protein phosphatase 1 regulatory subunit 7 OS=Ophiophag OPHHA	10
472	18.89	18.89	51.42	39.62	39.62	tr	V8PGL2	V8PGL2_OPHHA	ATP synthase subunit 0, mitochondrial OS=Ophiophagus ha OPHHA	15
473	18.86	18.86	46.45	9.747	8.205	tr	V8PF25	V8PF25_OPHHA	Intersectin-1 (Fragment) OS=Ophiophagus hannah GN=ITSN1 OPHHA	10
474	18.86	18.86	48.79	36.39	29.65	tr	V8NS48	V8NS48_OPHHA	Dimethylaniline monooxygenase [N-oxide-forming] 3 (Frag N-oxide-1 OPHHA	10
475	18.84	18.84	57.43	25.08	19.2	tr	V8PA12	V8PA12_OPHHA	Long-chain fatty acid transport protein 1 OS=Ophiophagu OPHHA	10

476	18.8	18.8	56.65	29.23	20.16	tr V8NVN6 V8NVN6_OPHHA E3 ubiquitin-protein ligase ARIH2 OS=Ophiophagus hannah OPHHA	8
477	18.76	18.76	49.17	11.93	9.873	tr V8NYV1 V8NYV1_OPHHA Transcription elongation regulator 1 (Fragment) OS=Ophiophagus hannah OPHHA	9
478	18.75	18.75	67.55	30.41	22.24	tr V8NAJ8 V8NAJ8_OPHHA Cytoplasmic dynein 1 heavy chain 1 OS=Ophiophagus hannah OPHHA	8
479	18.61	18.61	77.34	34.64	24.4	tr V8PDR5 V8PDR5_OPHHA Tyrosine-protein phosphatase non-receptor type 6 (Fragment) OPHHA	9
480	18.61	18.61	67.53	45.36	34.02	tr V8PFB9 V8PFB9_OPHHA 40S ribosomal protein S9 OS=Ophiophagus hannah GN=RPS9 OPHHA	11
481	18.6	18.6	57.84	30.35	26.88	tr V8NLC5 V8NLC5_OPHHA Methionine aminopeptidase 2 OS=Ophiophagus hannah GN=ME OPHHA	10
482	18.58	18.58	56.05	21.63	20.23	tr V8P1F7 V8P1F7_OPHHA Synapse-associated protein 1 (Fragment) OS=Ophiophagus hannah OPHHA	10
483	18.56	18.56	77.13	46.12	42.64	tr V8PFL3 V8PFL3_OPHHA Carbonic anhydrase 2 OS=Ophiophagus hannah GN=CA2 PE=4 OPHHA	11
484	18.56	18.56	48.16	29.48	29.48	tr V8PAD7 V8PAD7_OPHHA Zinc-binding alcohol dehydrogenase domain-containing protein OPHHA	10
485	18.51	18.51	60	28.53	26.4	tr V8PGG6 V8PGG6_OPHHA cAMP-dependent protein kinase type I-alpha regulatory subunit OPHHA	9
486	18.47	18.47	48.04	15.12	13.44	tr V8N9M1 V8N9M1_OPHHA Disks large-like 1 (Fragment) OS=Ophiophagus hannah GN= OPHHA	9
487	18.47	18.47	63.03	21.41	21.41	tr V8NT83 V8NT83_OPHHA Heterogeneous nuclear ribonucleoprotein D0 OS=Ophiophagus hannah OPHHA	10
488	18.47	18.47	51.23	32.6	30.68	tr V8NQ34 V8NQ34_OPHHA Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OPHHA	9
489	18.46	18.46	55.41	20.23	12.63	tr V8NXE2 V8NXE2_OPHHA Plakophilin-2 OS=Ophiophagus hannah GN=PKP2 PE=4 SV=1 OPHHA	9
490	18.42	18.42	51.19	14.08	11.77	tr V8PE43 V8PE43_OPHHA Myosin-VI (Fragment) OS=Ophiophagus hannah GN=MYO6 PE=4 OPHHA	9
491	18.38	18.38	48.52	27.75	25.64	tr V8PA08 V8PA08_OPHHA Aspartyl aminopeptidase OS=Ophiophagus hannah GN=DNPEP OPHHA	9
492	18.33	18.33	68.59	26.04	20.48	tr V8PDY1 V8PDY1_OPHHA Protein kinase C and casein kinase substrate in neurons OPHHA	9
493	18.32	18.32	45.17	22.15	15.54	tr V8NPY3 V8NPY3_OPHHA Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (Fragment) OPHHA	9
494	18.28	18.28	70.69	32.89	24.61	tr V8PGL9 V8PGL9_OPHHA Signal recognition particle 54 kDa protein OS=Ophiophagus hannah OPHHA	10
495	18.25	18.25	76.1	48.9	36.4	tr V8PIK7 V8PIK7_OPHHA Dephospho-CoA kinase domain-containing protein (Fragment) OPHHA	9
496	18.24	18.24	55.66	27.26	20.15	tr V8P215 V8P215_OPHHA Double-strand-break repair protein rad21-like protein OPHHA	8
497	18.22	18.75	57.08	9.67	7.642	tr V8NLY0 V8NLY0_OPHHA Myosin phosphatase Rho-interacting protein (Fragment) OPHHA	12
498	18.21	18.21	60.8	34.13	32.27	tr V8NM87 V8NM87_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	10
499	18.19	18.19	58.41	29.52	27.3	tr V8POE5 V8POE5_OPHHA Alcohol dehydrogenase [NADP+] (Fragment) OS=Ophiophagus hannah OPHHA	9
500	18.14	18.14	49.26	28.33	26.6	tr V8NRY3 V8NRY3_OPHHA N-acetylglucosamine 2-epimerase OS=Ophiophagus hannah GN= OPHHA	11
501	18.07	18.07	36.12	16.72	9.179	tr V8P3H3 V8P3H3_OPHHA Nuclear pore complex protein OS=Ophiophagus hannah GN=N OPHHA	9
502	18.05	18.05	57.84	19.78	15.92	tr V8POY3 V8POY3_OPHHA Cold shock domain-containing protein E1 (Fragment) OS=Ophiophagus hannah OPHHA	10
503	17.98	17.98	60.5	27.9	25.71	tr V8NVB9 V8NVB9_OPHHA Glyceraldehyde-3-phosphate dehydrogenase OS=Ophiophagus hannah OPHHA	14
504	17.95	17.95	33.52	12.71	7.555	tr V8P6B4 V8P6B4_OPHHA Stablin-2 OS=Ophiophagus hannah GN=Stab2 PE=4 SV=1 OPHHA	10
505	17.85	17.85	54.58	15.44	10.76	tr V8P1B5 V8P1B5_OPHHA Rab GTPase-activating protein 1 (Fragment) OS=Ophiophagus hannah OPHHA	8
506	17.83	17.83	52.75	28.64	22.49	tr V8P866 V8P866_OPHHA 1,4-alpha-glucan-branching enzyme (Fragment) OPHHA	9
507	17.83	17.83	70.49	39.93	34.72	tr V8N9K6 V8N9K6_OPHHA EH domain-containing protein 1 (Fragment) OS=Ophiophagus hannah OPHHA	10
508	17.81	17.81	42.5	10.75	7.906	tr V8P7L1 V8P7L1_OPHHA Putative E3 ubiquitin-protein ligase TRIP12 OS=Ophiophagus hannah OPHHA	9
509	17.81	17.81	65.43	51.44	47.74	tr V8P9M3 V8P9M3_OPHHA N-alpha-acetyltransferase 10 OS=Ophiophagus hannah GN=N OPHHA	9
510	17.79	17.92	32.67	19.57	13.56	tr V8PBX9 V8PBX9_OPHHA Clathrin coat assembly protein OS=Ophiophagus hannah GN= OPHHA	11
511	17.76	17.76	73.76	59.28	58.82	tr V8PB57 V8PB57_OPHHA Inorganic pyrophosphatase 2, mitochondrial (Fragment) OPHHA	10
512	17.71	17.71	56.19	44.76	44.76	tr V8P9V2 V8P9V2_OPHHA Abhydrolase domain-containing protein 14B OS=Ophiophagus hannah OPHHA	9
513	17.69	17.69	45.43	16.52	11.89	tr V8P2K1 V8P2K1_OPHHA Endoplasmic reticulum aminopeptidase 1 (Fragment) OS=Ophiophagus hannah OPHHA	8
514	17.65	17.65	45.57	16.05	13.74	tr V8P9C4 V8P9C4_OPHHA ATP-binding cassette sub-family F member 1 OS=Ophiophagus hannah OPHHA	10
515	17.65	17.65	45.29	30.53	27.99	tr V8NC48 V8NC48_OPHHA Nucleosome assembly protein 1-like 1 OS=Ophiophagus hannah OPHHA	10
516	17.63	17.63	50.44	33.72	31.09	tr V8PC58 V8PC58_OPHHA Serine/threonine-protein kinase MST4 (Fragment) OS=Ophiophagus hannah OPHHA	9
517	17.63	17.63	60.33	34.1	32.79	tr V8PEF3 V8PEF3_OPHHA Argininosuccinate lyase (Fragment) OS=Ophiophagus hannah OPHHA	11
518	17.58	17.58	52.61	31.7	31.7	tr V8PGZ7 V8PGZ7_OPHHA 60S ribosomal protein L5 (Fragment) OS=Ophiophagus hannah OPHHA	16
519	17.56	17.56	35.99	10.47	7.9	tr V8P4N3 V8P4N3_OPHHA TBC1 domain family member 9B (Fragment) OS=Ophiophagus hannah OPHHA	8
520	17.56	17.56	67.37	33.95	29.44	tr V8NVF6 V8NVF6_OPHHA Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Ophiophagus hannah OPHHA	10
521	17.53	17.66	62.83	31.09	27.61	tr V8NNU0 V8NNU0_OPHHA Eukaryotic translation initiation factor 2 subunit 3 OS=Ophiophagus hannah OPHHA	10
522	17.53	17.53	59.9	10.54	6.299	tr V8NRH5 V8NRH5_OPHHA Pinin OS=Ophiophagus hannah GN=PNN PE=4 SV=1 OPHHA	10
523	17.51	17.84	44.84	14.17	10.69	tr V8PB17 V8PB17_OPHHA AP-3 complex subunit beta-1 (Fragment) OS=Ophiophagus hannah OPHHA	8
524	17.5	17.53	51.04	28.13	28.13	tr V8N986 V8N986_OPHHA Chloride intracellular channel protein 1 OS=Ophiophagus hannah OPHHA	11
525	17.48	17.48	40.4	20.03	18.53	tr V8NN16 V8NN16_OPHHA Very long-chain acyl-CoA synthetase (Fragment) OS=Ophiophagus hannah OPHHA	11
526	17.45	17.45	50.09	29.23	17.78	tr V8NKF4 V8NKF4_OPHHA Eukaryotic translation initiation factor 2A OS=Ophiophagus hannah OPHHA	8
527	17.42	17.42	62.09	36.9	28.24	tr V8NVR5 V8NVR5_OPHHA Eukaryotic translation initiation factor 3 subunit E OS=Ophiophagus hannah OPHHA	9
528	17.4	17.4	54.86	31.42	31.42	tr V8NKC0 V8NKC0_OPHHA Serine-threonine kinase receptor-associated protein (Fragment) OPHHA	9
529	17.38	17.38	35.44	8.053	6.598	tr V8NWU3 V8NWU3_OPHHA Zinc finger ZZ-type and EF-hand domain-containing protein OPHHA	12
530	17.24	17.24	42.83	6.921	3.938	tr V8PEE2 V8PEE2_OPHHA Microtubule-actin cross-linking factor 1, isoforms 1/2 OPHHA	14
531	17.23	17.23	51	11.67	10.91	tr V8NXV0 V8NXV0_OPHHA WASH complex subunit strumpellin OS=Ophiophagus hannah OPHHA	9
532	17.23	17.23	48.67	20.25	17.27	tr V8P1P7 V8P1P7_OPHHA CD2-associated protein OS=Ophiophagus hannah GN=CD2AP P OPHHA	8
533	17.22	17.22	58.99	32.46	30.26	tr V8P2Y9 V8P2Y9_OPHHA DNA helicase (Fragment) OS=Ophiophagus hannah GN=RUVBL1 OPHHA	9
534	17.2	18.37	61.81	20.69	11.63	tr V8NTV0 V8NTV0_OPHHA Protein 4.1 (Fragment) OS=Ophiophagus hannah GN=EPB41 P OPHHA	7
535	17.18	16.65	61.32	27.7	21.96	tr V8P156 V8P156_OPHHA Radixin (Fragment) OS=Ophiophagus hannah GN=RDX PE=4 SV OPHHA	17
536	17.14	17.14	73.77	15.63	14.3	tr V8NDX8 V8NDX8_OPHHA ELKS/Rab6-interacting/CAST family member 1 (Fragment) OPHHA	10
537	17.12	17.12	57.46	16.67	11.44	tr V8P8A3 V8P8A3_OPHHA FACT complex subunit SPT16 (Fragment) OS=Ophiophagus hannah OPHHA	8
538	17.12	17.12	87.63	36.56	36.56	tr V8PBW2 V8PBW2_OPHHA Tumor protein D52 OS=Ophiophagus hannah GN=TPD52 PE=4 OPHHA	10
539	17.11	17.11	33.56	7.458	6.621	tr V8PCMO V8PCMO_OPHHA N-alpha-acetyltransferase 25, NatB auxiliary subunit (Fragment) OPHHA	12
540	17.1	17.1	59.33	13.43	11.57	tr V8P9X4 V8P9X4_OPHHA Exocyst complex component 2 (Fragment) OS=Ophiophagus hannah OPHHA	8
541	17.09	17.1	52.6	16.31	14.89	tr V8N612 V8N612_OPHHA Myosin-Ie (Fragment) OS=Ophiophagus hannah GN=MYO1 PE= OPHHA	9
542	17.06	17.06	75.29	38.4	34.98	tr V8P2P8 V8P2P8_OPHHA Serine/arginine-rich splicing factor 5 OS=Ophiophagus hannah OPHHA	11
543	17.03	17.03	65.93	33.19	33.19	tr V8NQNO V8NQNO_OPHHA Superoxide dismutase (Fragment) OS=Ophiophagus hannah OPHHA	13
544	17.01	17.01	100	53.33	48.48	tr V8PBL8 V8PBL8_OPHHA Peptidyl-prolyl cis-trans isomerase A OS=Ophiophagus hannah OPHHA	17
545	16.98	17.77	41.32	23.74	13.01	tr V8N8G4 V8N8G4_OPHHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPHHA	8
546	16.98	16.98	45.65	14.35	14.24	tr V8P6N9 V8P6N9_OPHHA cAMP-specific 3',5'-cyclic phosphodiesterase (Fragment) OPHHA	9
547	16.97	16.97	62.31	16.88	14.33	tr V8NMR0 V8NMR0_OPHHA Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OPHHA	8
548	16.95	16.95	57.87	37.07	22.93	tr V8P1T5 V8P1T5_OPHHA Eukaryotic translation initiation factor 3 subunit M OS=Ophiophagus hannah OPHHA	8
549	16.85	16.85	42.51	17.68	12.3	tr V8NWD0 V8NWD0_OPHHA Valyl-tRNA synthetase OS=Ophiophagus hannah GN=Vars PE= OPHHA	7
550	16.85	16.85	32.44	27.06	21.69	tr V8PFW4 V8PFW4_OPHHA Importin subunit alpha OS=Ophiophagus hannah GN=KPNA4 P OPHHA	9
551	16.82	16.85	57.42	5.488	4.25	tr V8P6K4 V8P6K4_OPHHA Dyx11 (Fragment) OS=Ophiophagus hannah GN=DST PE=4 OPHHA	11
552	16.82	16.82	66.48	13.91	11.28	tr V8P909 V8P909_OPHHA Tyrosine-protein kinase OS=Ophiophagus hannah GN=JAK1 P OPHHA	9
553	16.82	16.82	40	23.8	19.71	tr V8NAV0 V8NAV0_OPHHA Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Ophiophagus hannah OPHHA	9
554	16.82	16.82	59.08	32.62	32.62	tr V8NFB9 V8NFB9_OPHHA Enoyl-CoA hydratase, mitochondrial (Fragment) OS=Ophiophagus hannah OPHHA	11
555	16.82	16.82	50.12	27.74	21.68	tr V8NAW1 V8NAW1_OPHHA T-complex protein 1 subunit eta (Fragment) OS=Ophiophagus hannah OPHHA	9
556	16.79	16.79	50.71	27.4	17.95	tr V8P244 V8P244_OPHHA Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylglucosaminyl transferase (Fragment) OPHHA	9
557	16.78	16.78	49.01	41.06	41.06	tr V8PBD2 V8PBD2_OPHHA 40S ribosomal protein S14 OS=Ophiophagus hannah GN=RPS1 OPHHA	11
558	16.76	16.86	47.7	19.37	15.38	tr V8NCB6 V8NCB6_OPHHA GTPase-activating protein and VPS9 domain-containing protein OPHHA	9
559	16.75	18.34	50.62	6.234	4.541	tr V8P8L1 V8P8L1_OPHHA Keratin, type I cytoskeletal 19 (Fragment) OS=Ophiophagus hannah OPHHA	13
560	16.75	16.75	66.36	29.44	26.17	tr V8POB9 V8POB9_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	8
561	16.73	16.73	56.85	46.89	43.57	tr V8NWH3 V8NWH3_OPHHA GTP-binding protein Sar1a (Fragment) OS=Ophiophagus hannah OPHHA	9
562	16.72	16.78	47.79	12	12	tr V8P3B6 V8P3B6_OPHHA Vacuolar protein sorting-associated protein 18-like protein OPHHA	9
563	16.7	16.7	56.82	28.41	21.73	tr V8NEW4 V8NEW4_OPHHA Gamma-soluble NSF attachment protein (Fragment) OS=Ophiophagus hannah OPHHA	9
564	16.69	16.69	61.64	14.47	12.26	tr V8NM38 V8NM38_OPHHA La-related protein 1 (Fragment) OS=Ophiophagus hannah OPHHA	9
565	16.65	16.65	50.96	27.6	23.99	tr V8P1Q2 V8P1Q2_OPHHA Coiled-coil domain-containing protein 6 (Fragment) OS=Ophiophagus hannah OPHHA	10
566	16.62	16.73	76.03	19.28	14.88	tr V8NZ46 V8NZ46_OPHHA Golgin subfamily A member 5 (Fragment) OS=Ophiophagus hannah OPHHA	8
567	16.54	16.54	57.14	6.785	4.712	tr V8P1J1 V8P1J1_OPHHA Dyx11 (Fragment) OS=Ophiophagus hannah GN=DST PE=4 OPHHA	10
568	16.53	16.53	28.8	11.7	10.67	tr V8N855 V8N855_OPHHA Cytochrome protein OS=Ophiophagus hannah GN=CYP3A29 PE= OPHHA	12
569	16.52	16.52	42.78	19.51	14.82	tr V8PCA2 V8PCA2_OPHHA Coronin (Fragment) OS=Ophiophagus hannah GN=CORO1C PE=3 OPHHA	9
570	16.51	16.51	60.06	37.42	24.84	tr V8NLS7 V8NLS7_OPHHA Aminoacyl tRNA synthase complex-interacting multifunctional protein OPHHA	11
571	16.49	16.49	69.17	45	40.83	tr V8NUD5 V8NUD5_OPHHA Catechol O-methyltransferase OS=Ophiophagus hannah GN=COMT OPHHA	10

572	16.47	16.47	37.98	17.08	15.42	tr	V8NP25	V8NP25_OPPIHA Protein numb-like protein OS=Ophiophagus hannah GN=NUMB OPPIHA	9
573	16.42	16.51	43.74	14.29	13.29	tr	V8PIK1	V8PIK1_OPPIHA Cytosolic non-specific dipeptidase (Fragment) OS=Ophiophagus hannah GN=POF1B OPPIHA	8
574	16.39	16.39	46.35	16.73	11.21	tr	V8NC92	V8NC92_OPPIHA IQ motif and SEC7 domain-containing protein 1 (Fragment) OPPIHA	9
575	16.37	16.37	74.95	23.75	22.44	tr	V8NRG3	V8NRG3_OPPIHA Protein POF1B (Fragment) OS=Ophiophagus hannah GN=POF1B OPPIHA	8
576	16.28	16.28	50.38	12.06	10.55	tr	V8PIR5	V8PIR5_OPPIHA Multimerin-1 (Fragment) OS=Ophiophagus hannah GN=MMRN1 OPPIHA	9
577	16.23	16.55	56.49	12.08	7.361	tr	V8NZF4	V8NZF4_OPPIHA Tight junction protein ZO-2 (Fragment) OS=Ophiophagus hannah GN=ZO2 OPPIHA	8
578	16.23	16.23	69.57	27.11	21.99	tr	V8NP16	V8NP16_OPPIHA Sorting nexin-7 OS=Ophiophagus hannah GN=SNX7 PE=4 SV=1 OPPIHA	8
579	16.21	18.22	58.6	34.71	32.48	tr	V8NV77	V8NV77_OPPIHA 4-trimethylaminobutyraldehyde dehydrogenase (Fragment) OPPIHA	15
580	16.18	16.18	51.42	10.08	6.616	tr	V8PAH4	V8PAH4_OPPIHA TATA element modulatory factor (Fragment) OS=Ophiophagus hannah GN=ASRG OPPIHA	8
581	16.18	16.18	73.6	41.2	32	tr	V8NV58	V8NV58_OPPIHA Carbonyl reductase [NADPH] 1 (Fragment) OS=Ophiophagus hannah GN=NADPH OPPIHA	8
582	16.17	16.17	33.08	22.82	20.26	tr	V8NAR9	V8NAR9_OPPIHA Interleukin enhancer-binding factor 2 OS=Ophiophagus hannah GN=IL6 OPPIHA	8
583	16.13	16.13	65.82	33.76	33.76	tr	V8PF77	V8PF77_OPPIHA Methylglutaconyl-CoA hydratase, mitochondrial (Fragment) OPPIHA	9
584	16.12	16.12	36.11	10.97	7.89	tr	V8NNV7	V8NNV7_OPPIHA Inositol 1,4,5-trisphosphate receptor type 1 (Fragment) OPPIHA	10
585	16.12	16.12	62.94	27.27	22.38	tr	V8NZV7	V8NZV7_OPPIHA Actin-related protein 2/3 complex subunit 2 (Fragment) OPPIHA	9
586	16.11	16.23	38.7	19.48	8.312	tr	V8PIU6	V8PIU6_OPPIHA AP-1 complex subunit gamma-1 OS=Ophiophagus hannah GN=AP1 OPPIHA	6
587	16.11	16.11	73.64	34.96	28.08	tr	V8NLY8	V8NLY8_OPPIHA Phosphotriesterase-related protein OS=Ophiophagus hannah GN=PTER OPPIHA	9
588	16.1	16.11	40.25	23.54	23.54	tr	V8NA47	V8NA47_OPPIHA Cytochrome b-c1 complex subunit 2, mitochondrial (Fragment) OPPIHA	10
589	16.08	16.08	40.9	12.7	11.72	tr	V8NU38	V8NU38_OPPIHA Protein FAM91A1 (Fragment) OS=Ophiophagus hannah GN=FAM91A1 OPPIHA	9
590	16.08	16.08	37.75	14.48	10.55	tr	V8NKX1	V8NKX1_OPPIHA Cleavage and polyadenylation specificity factor subunit 1 OPPIHA	9
591	16.08	16.08	77.07	29.6	29.6	tr	V8NDE2	V8NDE2_OPPIHA L-asparaginase (Fragment) OS=Ophiophagus hannah GN=ASRG OPPIHA	9
592	16.04	16.08	39.73	7.797	6.773	tr	V8PFW1	V8PFW1_OPPIHA Laminin subunit alpha-4 (Fragment) OS=Ophiophagus hannah GN=LN4 OPPIHA	9
593	16.04	16.04	59.57	51.49	51.06	tr	V8PFX9	V8PFX9_OPPIHA Protein phosphatase 1 regulatory subunit 1B OS=Ophiophagus hannah GN=PPP1R1B OPPIHA	9
594	16.01	17.89	64.26	17.95	13.59	tr	V8NJD4	V8NJD4_OPPIHA Dynamin-1 (Fragment) OS=Ophiophagus hannah GN=DNM1 PE=4 OPPIHA	9
595	16	16.01	43.68	22.2	22.2	tr	V8NZM8	V8NZM8_OPPIHA Protein disulfide-isomerase A6 (Fragment) OS=Ophiophagus hannah GN=PDIA6 OPPIHA	10
596	15.97	15.97	41.06	18.25	16.61	tr	V8NGC4	V8NGC4_OPPIHA Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Ophiophagus hannah GN=PUF60 OPPIHA	8
597	15.93	15.93	67.41	37.7	31.31	tr	V8NVA0	V8NVA0_OPPIHA Glutamyl-tRNA synthetase (Fragment) OS=Ophiophagus hannah GN=GLYRS OPPIHA	8
598	15.92	15.92	52.31	16.37	16.19	tr	V8P2S3	V8P2S3_OPPIHA Apoptosis inhibitor 5 (Fragment) OS=Ophiophagus hannah GN=AI5 OPPIHA	10
599	15.92	15.92	72.85	20.81	20.81	tr	V8PI87	V8PI87_OPPIHA Glutathione S-transferase 2 OS=Ophiophagus hannah GN=GSTA2 OPPIHA	8
600	15.9	15.9	55.42	25.78	23.61	tr	V8P4S2	V8P4S2_OPPIHA TAR DNA-binding protein 43 OS=Ophiophagus hannah GN=TAR OPPIHA	8
601	15.86	15.86	51.87	22.86	19.12	tr	V8PHM3	V8PHM3_OPPIHA Ribonuclease inhibitor OS=Ophiophagus hannah GN=RNI1 PE OPPIHA	9
602	15.84	15.84	58.3	29.79	20.21	tr	V8P4B2	V8P4B2_OPPIHA ERO1-like protein beta OS=Ophiophagus hannah GN=ERO1L2 OPPIHA	7
603	15.83	15.83	55.5	29.36	27.98	tr	V8P678	V8P678_OPPIHA Heterogeneous nuclear ribonucleoprotein H OS=Ophiophagus hannah GN=HNRNP_H OPPIHA	11
604	15.82	15.82	69.64	51.79	47.77	tr	V8NQR3	V8NQR3_OPPIHA Elongation factor 1-beta OS=Ophiophagus hannah GN=EEF1B OPPIHA	9
605	15.79	15.83	66.35	9.563	8.737	tr	V8PGH1	V8PGH1_OPPIHA SAFB-like transcription modulator OS=Ophiophagus hannah GN=SAFB OPPIHA	8
606	15.78	15.78	50.1	22.74	21.13	tr	V8PBN0	V8PBN0_OPPIHA Carbohydrate kinase domain-containing protein (Fragment) OPPIHA	8
607	15.73	15.73	74.93	33.9	29.06	tr	V8P425	V8P425_OPPIHA LIM and cysteine-rich domains protein 1 (Fragment) OS=Ophiophagus hannah GN=LIM1 OPPIHA	8
608	15.72	15.72	83.61	44.26	40.98	tr	V8NJ95	V8NJ95_OPPIHA Glutathione S-transferase Mu 7 (Fragment) OS=Ophiophagus hannah GN=GSTM7 OPPIHA	12
609	15.69	15.69	41.52	10.68	6.59	tr	V8NQD2	V8NQD2_OPPIHA Laminin subunit beta-1 (Fragment) OS=Ophiophagus hannah GN=LAMB1 OPPIHA	7
610	15.68	15.68	54.23	23.91	23.91	tr	V8NXC3	V8NXC3_OPPIHA DnaJ-like subfamily B member 11 OS=Ophiophagus hannah GN=DNAJ11 OPPIHA	8
611	15.66	15.66	43.58	15.14	10.78	tr	V8NTU0	V8NTU0_OPPIHA Transportin-1 (Fragment) OS=Ophiophagus hannah GN=TNPO1 OPPIHA	8
612	15.64	15.64	40.55	19.53	16.56	tr	V8NJI3	V8NJI3_OPPIHA Protein transport protein Sec31A (Fragment) OS=Ophiophagus hannah GN=SEC31A OPPIHA	10
613	15.59	15.59	77.81	28.94	21.22	tr	V8PAB0	V8PAB0_OPPIHA LIM and SH3 domain protein 1 (Fragment) OS=Ophiophagus hannah GN=LIM1 OPPIHA	12
614	15.59	15.59	68.86	33.33	33.33	tr	V8NRV2	V8NRV2_OPPIHA Acetyl-CoA carboxylase (Fragment) OS=Ophiophagus hannah GN=ACC OPPIHA	9
615	15.56	15.56	35.27	11.37	9.984	tr	V8PHH1	V8PHH1_OPPIHA Acylamino-acid-releasing enzyme (Fragment) OS=Ophiophagus hannah GN=ACRE OPPIHA	8
616	15.55	15.55	54.99	25.06	19.95	tr	V8NGU6	V8NGU6_OPPIHA Signal recognition particle receptor subunit beta OS=Ophiophagus hannah GN=SRP OPPIHA	8
617	15.55	15.55	62.75	40.39	32.94	tr	V8NIG9	V8NIG9_OPPIHA NADH-cytochrome b5 reductase 3 (Fragment) OS=Ophiophagus hannah GN=NADH OPPIHA	8
618	15.53	15.53	54.21	28.22	28.22	tr	V8NJU8	V8NJU8_OPPIHA Alpha-amino acid semialdehyde dehydrogenase OS=Ophiophagus hannah GN=ALDH OPPIHA	10
619	15.53	15.53	70.83	40.83	37.08	tr	V8P224	V8P224_OPPIHA Prohibitin OS=Ophiophagus hannah GN=PHB PE=4 SV=1 OPPIHA	8
620	15.5	15.72	68.82	41.76	38.24	tr	V8P2E0	V8P2E0_OPPIHA Guanine nucleotide-binding protein subunit beta-4 OS=Ophiophagus hannah GN=GNB4 OPPIHA	8
621	15.48	15.48	51.19	42.46	41.67	tr	V8PAU7	V8PAU7_OPPIHA 6-phosphogluconolactonase (Fragment) OS=Ophiophagus hannah GN=6PG OPPIHA	9
622	15.45	15.45	61.64	18.51	13.43	tr	V8NKM7	V8NKM7_OPPIHA Cullin-4B (Fragment) OS=Ophiophagus hannah GN=CUL4B PE= OPPIHA	8
623	15.44	15.44	64.33	17.68	13.87	tr	V8NSX8	V8NSX8_OPPIHA Nucleolin (Fragment) OS=Ophiophagus hannah GN=NCL PE=4 OPPIHA	9
624	15.42	15.42	50.84	15.23	9.979	tr	V8PHR6	V8PHR6_OPPIHA Ras-interacting protein 1 (Fragment) OS=Ophiophagus hannah GN=RI1 OPPIHA	7
625	15.4	15.4	61.54	47.01	43.59	tr	V8NJ09	V8NJ09_OPPIHA Cysteine desulfurase, mitochondrial OS=Ophiophagus hannah GN=CSDH OPPIHA	8
626	15.39	15.39	62.3	25.2	25.2	tr	V8NDX6	V8NDX6_OPPIHA Translocation protein SEC63-like protein (Fragment) OS=Ophiophagus hannah GN=SEC63 OPPIHA	9
627	15.38	15.38	42.64	6.498	5.322	tr	V8NYY0	V8NYY0_OPPIHA Branched-chain-amino-acid aminotransferase, mitochondrial OS=Ophiophagus hannah GN=BCAT OPPIHA	11
628	15.35	15.35	67.92	21.97	21.97	tr	V8NP09	V8NP09_OPPIHA ATP synthase mitochondrial F1 complex assembly factor 1 OPPIHA	9
629	15.35	15.35	67.78	56.67	38.89	tr	V8P961	V8P961_OPPIHA Calmodulin (Fragment) OS=Ophiophagus hannah GN=CALM PE= OPPIHA	10
629	0	15.14	70	48.89	38.89	tr	V8NW64	V8NW64_OPPIHA Calmodulin (Fragment) OS=Ophiophagus hannah GN=CALM PE= OPPIHA	10
630	15.32	15.32	55.43	18.99	18.99	tr	V8NC60	V8NC60_OPPIHA Glutathione S-transferase (Fragment) OS=Ophiophagus hannah GN=GSTM OPPIHA	8
631	15.3	15.3	65.47	33.98	24.31	tr	V8NP28	V8NP28_OPPIHA Serine/threonine-protein kinase OSR1 (Fragment) OS=Ophiophagus hannah GN=OSR1 OPPIHA	8
632	15.26	43.79	60.73	56.5	56.5	tr	V8NKE3	V8NKE3_OPPIHA Actin, aortic smooth muscle OS=Ophiophagus hannah GN=ACTA1 OPPIHA	35
632	0	43.79	65.52	57.47	57.47	tr	V8NYT7	V8NYT7_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=UNCL345_0 OPPIHA	36
633	15.23	15.23	47.08	7.985	6.871	tr	V8P6V6	V8P6V6_OPPIHA Aldehyde dehydrogenase family 16 member A1 (Fragment) OS=Ophiophagus hannah GN=ALDH16A1 OPPIHA	8
634	15.21	18.12	59.6	26.27	20.29	tr	V8PEM1	V8PEM1_OPPIHA Acetyl-coenzyme A synthetase 2-like, mitochondrial (Fragment) OPPIHA	8
635	15.17	15.17	50.87	16.76	15.46	tr	V8NBV6	V8NBV6_OPPIHA Ecocyst complex component 8 (Fragment) OS=Ophiophagus hannah GN=ECOC8 OPPIHA	8
636	15.17	15.17	73.49	62.65	57.83	tr	V8NZX4	V8NZX4_OPPIHA Succinyl-CoA ligase GDP-forming subunit beta (Fragment) OPPIHA	9
637	15.16	15.16	54.06	13.14	11.89	tr	V8PBI1	V8PBI1_OPPIHA Ubiquitin-protein ligase E3A OS=Ophiophagus hannah GN=UOPBI1 OPPIHA	7
638	15.16	15.16	44.96	30.58	26.98	tr	V8NEC7	V8NEC7_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCL345_0 OPPIHA	7
639	15.15	15.15	60.79	25.75	21.81	tr	V8PAV2	V8PAV2_OPPIHA Hydroxysteroid dehydrogenase-like protein 2 OS=Ophiophagus hannah GN=HSD17B4 OPPIHA	9
640	15.13	15.13	39.14	6.549	5.592	tr	V8NTJ9	V8NTJ9_OPPIHA 5'-3' exoribonuclease 1 (Fragment) OS=Ophiophagus hannah GN=5-3 OPPIHA	10
641	15.13	15.13	31.24	24.72	24.72	tr	V8NP28	V8NP28_OPPIHA Ubiquinone biosynthesis monooxygenase COQ6 (Fragment) OS=Ophiophagus hannah GN=COQ6 OPPIHA	9
642	15.11	15.11	60.17	42.62	28.41	tr	V8PDG5	V8PDG5_OPPIHA Guanine deaminase (Fragment) OS=Ophiophagus hannah GN=GDH OPPIHA	8
643	15.06	15.06	72.57	23	17.3	tr	V8PB76	V8PB76_OPPIHA Glutathione synthetase OS=Ophiophagus hannah GN=GSS PE= OPPIHA	7
644	15.06	15.06	47.88	20.44	17.66	tr	V8NNX0	V8NNX0_OPPIHA Glycyl-tRNA synthetase (Fragment) OS=Ophiophagus hannah GN=GYS OPPIHA	12
645	15.06	15.06	72.86	28.02	23.3	tr	V8PIE1	V8PIE1_OPPIHA Hsp90 co-chaperone Cdc37 OS=Ophiophagus hannah GN=CDC37 OPPIHA	7
646	15.03	19.05	47.6	6.286	5.831	tr	V8PBC0	V8PBC0_OPPIHA Acetyl-CoA carboxylase 2 (Fragment) OS=Ophiophagus hannah GN=ACC2 OPPIHA	12
647	14.99	14.99	67.92	23.08	20.08	tr	V8NVJ4	V8NVJ4_OPPIHA Nuclear pore protein 58 (Fragment) OS=Ophiophagus hannah GN=NUP58 OPPIHA	8
648	14.98	14.98	67.3	18.56	12.81	tr	V8PA01	V8PA01_OPPIHA Polyribonucleotide nucleotidyltransferase 1, mitochondrial OPPIHA	7
649	14.97	14.97	45.44	16.49	14.74	tr	V8NYP3	V8NYP3_OPPIHA Complement component C8 beta chain (Fragment) OS=Ophiophagus hannah GN=C8B OPPIHA	8
650	14.95	14.95	27.17	13.7	11.46	tr	V8NRX3	V8NRX3_OPPIHA Anion exchange protein (Fragment) OS=Ophiophagus hannah GN=ANX OPPIHA	8
651	14.95	14.95	68	31.56	20.89	tr	V8NB73	V8NB73_OPPIHA Putative signal peptidase complex subunit 2 (Fragment) OPPIHA	8
652	14.94	14.94	77.36	36.49	32.43	tr	V8NMA9	V8NMA9_OPPIHA Sulfotransferase (Fragment) OS=Ophiophagus hannah GN=SU OPPIHA	11
653	14.91	23.38	42.17	17.22	14.96	tr	V8NT90	V8NT90_OPPIHA Cytoplasmic FMR1-interacting protein 2 (Fragment) OS=Ophiophagus hannah GN=CFIP2 OPPIHA	13
654	14.91	14.91	32.96	7.431	6.22	tr	V8NKA6	V8NKA6_OPPIHA Angiotensin-converting enzyme OS=Ophiophagus hannah GN=ACE OPPIHA	8
655	14.9	14.91	63.45	16.24	16.24	tr	V8NP00	V8NP00_OPPIHA Thyroid hormone receptor-associated protein 3 OS=Ophiophagus hannah GN=TRAP3 OPPIHA	8
656	14.89	14.89	63.81	33.98	22.65	tr	V8PH70	V8PH70_OPPIHA V-type proton ATPase subunit C1 OS=Ophiophagus hannah GN=V-ATPase OPPIHA	7
657	14.82	14.82	48.36	12.72	9.351	tr	V8PF53	V8PF53_OPPIHA Partitioning defective 3-like protein (Fragment) OS=Ophiophagus hannah GN=PD3 OPPIHA	7
658	14.82	14.82	62.16	53.28	49.81	tr	V8NEA4	V8NEA4_OPPIHA WD repeat-containing protein 1 OS=Ophiophagus hannah GN=WD1 OPPIHA	8
659	14.8	14.8	82.53	30.14	21.92	tr	V8NN02	V8NN02_OPPIHA Pyruvate dehydrogenase E1 component subunit alpha, soma OPPIHA	7
660	14.79	15.68	40.06	11.62	11.09	tr	V8PFQ6	V8PFQ6_OPPIHA Nuclear pore complex protein (Fragment) OS=Ophiophagus hannah GN=NUP OPPIHA	8
661	14.79	14.79	73.98	36.73	32.14	tr	V8P6H0	V8P6H0_OPPIHA V-type proton ATPase subunit E1 OS=Ophiophagus hannah GN=V-ATPase OPPIHA	8
662	14.78	14.79	53.61	21.29	17.87	tr	V8PT10	V8PT10_OPPIHA COP9 signalosome complex subunit 1 (Fragment) OS=Ophiophagus hannah GN=COP9 OPPIHA	7
663	14.75	14.77	41.41	5.482	3.346	tr	V8PET1	V8PET1_OPPIHA Vacuolar protein sorting-associated protein 13C (Fragment) OPPIHA	8
664	14.73	14.73	56.67	18.74	16.16	tr	V8NTJ2	V8NTJ2_OPPIHA Isovaleryl-CoA dehydrogenase, mitochondrial OS=Ophiophagus hannah GN=IVD OPPIHA	10
665	14.69	14.72	73.71	36.31	21.68	tr	V8PBF5	V8PBF5_OPPIHA Obg-like ATPase 1 (Fragment) OS=Ophiophagus hannah GN=OBG1 OPPIHA	7

666	14.68	14.68	61.3	38.31	34.87	tr V8NY12 V8NY12_OPPIHA	Proteasome subunit alpha type (Fragment) OS=Ophiophagus OPPIHA	9
667	14.67	23.11	39.14	23.03	21.54	tr V8N9E0 V8N9E0_OPPIHA	AP-1 complex subunit beta-1 OS=Ophiophagus hannah GN=AP OPPIHA	16
668	14.67	14.67	65.28	25.23	19.44	tr V8NVT0 V8NVT0_OPPIHA	Putative imidazolonepropionase (Fragment) OS=Ophiophagu OPPIHA	8
669	14.63	14.63	45.27	19.67	12.86	tr V8NCH8 V8NCH8_OPPIHA	E3 ubiquitin-protein ligase UBR4 (Fragment) OS=Ophioph OPPIHA	7
670	14.63	14.63	52.3	25.38	16.52	tr V8NHH5 V8NHH5_OPPIHA	Xaa-Pro aminopeptidase 1 OS=Ophiophagus hannah GN=XNPPE OPPIHA	7
671	14.62	14.62	55.89	21.37	21.37	tr V8NZ64 V8NZ64_OPPIHA	Serin H1 (Fragment) OS=Ophiophagus hannah GN=SERPINH1 OPPIHA	8
672	14.61	14.61	81.93	52.1	52.1	tr V8P3M5 V8P3M5_OPPIHA	Brain acid soluble protein l-like protein (Fragment) OS=OPPIHA	11
673	14.59	14.59	43.66	30.28	21.48	tr V8NVV2 V8NVV2_OPPIHA	Polypyrimidine tract-binding protein 2 (Fragment) OS=Op OPPIHA	9
674	14.57	14.58	66.45	43.87	34.19	tr V8NGR3 V8NGR3_OPPIHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345 1 OPPIHA	8
675	14.56	14.57	35.86	11.81	8.793	tr V8NFU9 V8NFU9_OPPIHA	Sortilin-related receptor (Fragment) OS=Ophiophagus han OPPIHA	7
676	14.54	14.54	58.02	50.62	40.74	tr V8NP41 V8NP41_OPPIHA	Ras suppressor protein 1 (Fragment) OS=Ophiophagus hann OPPIHA	7
677	14.53	14.53	69.96	42.15	31.39	tr V8NHZ3 V8NHZ3_OPPIHA	GrpE protein homolog OS=Ophiophagus hannah GN=GRPEL1 PE OPPIHA	7
678	14.52	16.74	44.13	23.32	16.61	tr V8NPT8 V8NPT8_OPPIHA	Ankyrin-1 (Fragment) OS=Ophiophagus hannah GN=Ankl PE=4 OPPIHA	8
679	14.51	29.57	61.05	20.27	17.53	tr V8P5W8 V8P5W8_OPPIHA	Alpha-actinin-2 OS=Ophiophagus hannah GN=ACTN2 PE=4 SV= OPPIHA	14
680	14.48	14.48	41.4	28.34	22.29	tr V8P3J3 V8P3J3_OPPIHA	Autophagy-related protein 3 OS=Ophiophagus hannah GN=AT OPPIHA	7
681	14.47	14.47	42.86	6.707	5.834	tr V8NZ98 V8NZ98_OPPIHA	DNA-directed RNA polymerase (Fragment) OS=Ophiophagus h OPPIHA	7
682	14.45	14.45	56.18	49.44	49.44	tr V8NSV1 V8NSV1_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	12
683	14.44	15.33	57.1	31.88	27.54	tr V8NRH4 V8NRH4_OPPIHA	Beta-1-syntrophin OS=Ophiophagus hannah GN=SENTB1 PE=4 S OPPIHA	8
684	14.4	14.42	37.5	4.923	3	tr V8P932 V8P932_OPPIHA	Kalirin (Fragment) OS=Ophiophagus hannah GN=Kalrn PE=4 OPPIHA	8
685	14.4	14.4	57.34	20.94	14.68	tr V8PEP3 V8PEP3_OPPIHA	PDZ and LIM domain protein 7 (Fragment) OS=Ophiophagus OPPIHA	7
686	14.37	14.37	37.86	13.69	6.667	tr V8PCV3 V8PCV3_OPPIHA	PDZ and LIM domain protein 5 (Fragment) OS=Ophiophagus OPPIHA	6
687	14.34	14.34	70.9	26.72	22.75	tr V8NQW5 V8NQW5_OPPIHA	Heterogeneous nuclear ribonucleoprotein G OS=Ophiophagu OPPIHA	8
688	14.31	14.38	67.26	25	22.92	tr V8P4Y1 V8P4Y1_OPPIHA	Annexin OS=Ophiophagus hannah GN=ANXA1 PE=3 SV=1 OPPIHA	9
689	14.3	14.4	66.79	32.86	27.14	tr V8N7X5 V8N7X5_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	8
690	14.27	14.27	51.94	42.23	38.35	tr V8P4Z8 V8P4Z8_OPPIHA	Membrane-associated progesterone receptor component 2 O OPPIHA	8
691	14.27	14.27	45.99	26.64	26.64	tr V8PID6 V8PID6_OPPIHA	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, OPPIHA	8
692	14.24	18.64	71.63	35.46	29.55	tr V8PHS9 V8PHS9_OPPIHA	Protein phosphatase 1A (Fragment) OS=Ophiophagus hannah OPPIHA	11
693	14.24	14.24	81.37	28.6	27.27	tr V8PGX0 V8PGX0_OPPIHA	Glutaryl-CoA dehydrogenase, mitochondrial (Fragment) OS=OPPIHA	9
694	14.23	14.23	51.79	44.62	41.04	tr V8NLH8 V8NLH8_OPPIHA	Calponin OS=Ophiophagus hannah GN=CNN3 PE=3 SV=1 OPPIHA	11
695	14.22	14.22	60.95	12.88	8.194	tr V8P1T7 V8P1T7_OPPIHA	Liprin-alpha-1 (Fragment) OS=Ophiophagus hannah GN=PPF1 OPPIHA	7
696	14.22	14.22	43.3	15.82	12.73	tr V8PAJ0 V8PAJ0_OPPIHA	Conserved oligomeric Golgi complex subunit 3 (Fragment) OPPIHA	7
697	14.21	14.21	49.11	18.83	18.83	tr V8P2F3 V8P2F3_OPPIHA	Coagulation factor XIII A chain OS=Ophiophagus hannah G OPPIHA	9
698	14.2	14.2	64.24	10.66	8.197	tr V8PJ09 V8PJ09_OPPIHA	ATP-dependent RNA helicase DDX42 (Fragment) OS=Ophioph OPPIHA	7
699	14.2	14.2	54.55	32.21	27.01	tr V8NAG5 V8NAG5_OPPIHA	Dihydrolipoyl dehydrogenase, mitochondrial (Fragment) O OPPIHA	8
700	14.17	14.76	49.84	16.25	12.66	tr V8NDP3 V8NDP3_OPPIHA	C-factor (Fragment) OS=Ophiophagus hannah GN=csaG PE=4 OPPIHA	9
701	14.17	14.17	76.21	24.48	20.34	tr V8NZU9 V8NZU9_OPPIHA	Eukaryotic translation initiation factor 4B (Fragment) OPPIHA	7
702	14.17	14.17	38.41	24.68	22.75	tr V8PC91 V8PC91_OPPIHA	Malic enzyme OS=Ophiophagus hannah GN=ME1 PE=3 SV=1 OPPIHA	7
703	14.15	14.15	71.38	23.1	23.1	tr V8NSZ3 V8NSZ3_OPPIHA	Proteasome subunit beta type (Fragment) OS=Ophiophagus OPPIHA	7
704	14.13	14.13	64.78	20.53	18.83	tr V8NGY3 V8NGY3_OPPIHA	UDP-N-acetylhexosamine pyrophosphorylase (Fragment) OS= OPPIHA	8
705	14.13	14.13	49.51	20.91	17.16	tr V8NWA8 V8NWA8_OPPIHA	NEDD8-activating enzyme E1 regulatory subunit (Fragment OPPIHA	7
706	14.13	14.13	53.15	21.4	21.4	tr V8NXE6 V8NXE6_OPPIHA	Hydroxyacylglutathione hydrolase, mitochondrial (Fragme OPPIHA	8
707	14.13	14.13	59.51	38.65	38.65	tr V8PF33 V8PF33_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	12
708	14.08	14.14	57.89	33.87	27.69	tr V8P9H4 V8P9H4_OPPIHA	FAS-associated factor 2 OS=Ophiophagus hannah GN=FAF2 P OPPIHA	8
709	14.04	14.04	47.28	18.56	18.56	tr V8NN61 V8NN61_OPPIHA	Lamina-associated polypeptide 2, isoforms alpha/zeta (F OPPIHA	9
710	14.03	14.03	56.54	34.28	34.28	tr V8NXE1 V8NXE1_OPPIHA	Pyridoxal kinase (Fragment) OS=Ophiophagus hannah GN=PD OPPIHA	11
711	14.03	14.03	48.77	43.83	43.83	tr V8N5V3 V8N5V3_OPPIHA	Peptidyl-prolyl cis-trans isomerase OS=Ophiophagus hann OPPIHA	9
712	14	14	63.21	39.38	35.23	tr V8P9H5 V8P9H5_OPPIHA	Rho-related GTP-binding protein RhoC OS=Ophiophagus han OPPIHA	10
713	13.97	13.97	41.67	10.82	6.817	tr V8NXS9 V8NXS9_OPPIHA	Myoferlin (Fragment) OS=Ophiophagus hannah GN=Myof PE=4 OPPIHA	7
714	13.96	13.96	43.5	7.357	5.709	tr V8NBL5 V8NBL5_OPPIHA	Collagen alpha-4(VI) chain (Fragment) OS=Ophiophagus ha OPPIHA	7
715	13.95	14.18	58.09	9.243	6.135	tr V8NLN1 V8NLN1_OPPIHA	C-Jun-amino-terminal kinase-interacting protein 4 (Frag OPPIHA	6
716	13.94	13.94	46.75	18.04	12.84	tr V8P1G3 V8P1G3_OPPIHA	FACT complex subunit SSRP1 (Fragment) OS=Ophiophagus ha OPPIHA	7
717	13.91	13.91	69.37	10.62	6.288	tr V8NPY9 V8NPY9_OPPIHA	Thyroid receptor-interacting protein 11 (Fragment) OS=O OPPIHA	6
718	13.89	13.89	50.49	28.68	24.75	tr V8P7L6 V8P7L6_OPPIHA	Serine/threonine-protein kinase 4 (Fragment) OS=Ophioph OPPIHA	7
719	13.89	13.89	92.06	60.32	54.76	tr V8P013 V8P013_OPPIHA	Histidine triad nucleotide-binding protein 1 OS=Ophioph OPPIHA	7
720	13.88	13.88	35.42	14.58	12.88	tr V8NDA3 V8NDA3_OPPIHA	Eukaryotic peptide chain release factor GTP-binding sub OPPIHA	7
721	13.88	13.88	44.02	16.79	16.79	tr V8P9Y0 V8P9Y0_OPPIHA	Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragmen OPPIHA	8
722	13.86	17.1	39.01	15.1	13	tr V8NB69 V8NB69_OPPIHA	Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	10
723	13.86	13.86	58.91	31.72	31.72	tr V8P151 V8P151_OPPIHA	Twinfilin-2 (Fragment) OS=Ophiophagus hannah GN=TWf2 PE OPPIHA	8
724	13.86	13.86	55.14	29.91	23.05	tr V8NTD6 V8NTD6_OPPIHA	Epidermal retinol dehydrogenase 2 OS=Ophiophagus hannah OPPIHA	6
725	13.85	13.88	64.34	39.34	35.25	tr V8P9B2 V8P9B2_OPPIHA	Thioredoxin-dependent peroxide reductase, mitochondrial OPPIHA	10
726	13.84	13.84	54.49	25.75	22.16	tr V8PEA3 V8PEA3_OPPIHA	Histone H2A (Fragment) OS=Ophiophagus hannah GN=H2AFY P OPPIHA	8
727	13.83	13.83	55.26	42.11	39.47	tr V8P8N1 V8P8N1_OPPIHA	Actin-related protein 2/3 complex subunit 5 (Fragment) OPPIHA	8
728	13.82	13.82	73.29	55.48	43.15	tr V8NVJ6 V8NVJ6_OPPIHA	40S ribosomal protein S16 OS=Ophiophagus hannah GN=RP51 OPPIHA	8
729	13.82	13.82	43.77	35.46	29.07	tr V8PDC3 V8PDC3_OPPIHA	5'-AMP-activated protein kinase subunit gamma-1 OS=Ophi OPPIHA	8
730	13.8	13.8	60.37	33.64	27.65	tr V8NMV9 V8NMV9_OPPIHA	Ribosomal protein OS=Ophiophagus hannah GN=RPL10A PE=3 OPPIHA	7
731	13.79	13.79	49.36	37.77	31.76	tr V8NS71 V8NS71_OPPIHA	Alpha-soluble NSF attachment protein (Fragment) OS=Ophi OPPIHA	8
732	13.78	13.78	39.51	14.81	14.81	tr V8NR60 V8NR60_OPPIHA	Clathrin interactor 1 (Fragment) OS=Ophiophagus hannah OPPIHA	7
733	13.76	16.01	57.53	29.04	24.66	tr V8P617 V8P617_OPPIHA	Eukaryotic initiation factor 4A-III OS=Ophiophagus hann OPPIHA	9
734	13.76	13.76	45.66	18.28	9.091	tr V8NI19 V8NI19_OPPIHA	Trafficking protein particle complex subunit 10 (Fragme OPPIHA	6
735	13.7	13.7	48.94	30.85	20	tr V8PFK4 V8PFK4_OPPIHA	Ubiquitin-like modifier-activating enzyme ATG7 (Fragmen OPPIHA	7
736	13.66	13.66	46.28	28.67	28.67	tr V8P934 V8P934_OPPIHA	Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS= OPPIHA	9
737	13.63	13.63	52.67	18.85	10.29	tr V8PCG2 V8PCG2_OPPIHA	Cullin-5 (Fragment) OS=Ophiophagus hannah GN=CUL5 PE=3 OPPIHA	7
738	13.62	13.62	63.36	23.14	15.7	tr V8P8Y4 V8P8Y4_OPPIHA	Ethanolamine-phosphate cytidylyltransferase OS=Ophioph OPPIHA	6
739	13.59	13.59	49.14	25	25	tr V8N4Z5 V8N4Z5_OPPIHA	Short-chain dehydrogenase/reductase family 9C member 7 OPPIHA	9
740	13.56	13.56	57.54	39.11	35.2	tr V8P180 V8P180_OPPIHA	Sorcin OS=Ophiophagus hannah GN=SRI PE=4 SV=1 OPPIHA	10
741	13.55	13.55	44.75	13.78	11.55	tr V8PG97 V8PG97_OPPIHA	AMP deaminase 2 (Fragment) OS=Ophiophagus hannah GN=AMP OPPIHA	7
742	13.53	13.55	23.32	15.55	15.55	tr V8P319 V8P319_OPPIHA	Protein transport protein Sec61 subunit alpha isoform 1 OPPIHA	7
743	13.53	13.53	43.79	16.5	12.91	tr V8NHHA V8NHHA_OPPIHA	Peroxisomal carnitine O-octanoyltransferase OS=Ophioph OPPIHA	7
744	13.53	13.53	62.26	36.78	29.09	tr V8NBL1 V8NBL1_OPPIHA	Delta-l-pyrroline-5-carboxylate dehydrogenase, mitochon OPPIHA	10
745	13.53	13.53	66.8	34.43	34.43	tr V8NWH1 V8NWH1_OPPIHA	Vesicle-associated membrane protein-associated protein OPPIHA	8
746	13.52	13.55	59.47	36.32	26.58	tr V8PGY1 V8PGY1_OPPIHA	Sorting and assembly machinery component 50-like protei OPPIHA	6
747	13.52	13.52	41.76	20.59	20.59	tr V8NXN6 V8NXN6_OPPIHA	Fumarylacetoacetase (Fragment) OS=Ophiophagus hannah GN OPPIHA	10
748	13.46	13.46	52.73	19.21	14.31	tr V8PHP9 V8PHP9_OPPIHA	Bridging integrator 2 (Fragment) OS=Ophiophagus hannah OPPIHA	7
749	13.42	13.42	83.27	39.78	36.06	tr V8NKP2 V8NKP2_OPPIHA	COP9 signalosome complex subunit 4 (Fragment) OS=Ophioph OPPIHA	7
750	13.4	13.55	41.49	7.635	7.23	tr V8NZ18 V8NZ18_OPPIHA	Canalicular multispecific organic anion transporter 1 (OPPIHA	7
751	13.38	13.43	50.9	21.1	16.37	tr V8NYY8 V8NYY8_OPPIHA	Dystrobrevin alpha (Fragment) OS=Ophiophagus hannah GN= OPPIHA	7
752	13.37	13.37	64.02	19	15.31	tr V8NKS7 V8NKS7_OPPIHA	Prolyl 4-hydroxylase subunit alpha-1 (Fragment) OS=Ophi OPPIHA	7
753	13.36	13.36	40.22	12.62	12.62	tr V8NRG5 V8NRG5_OPPIHA	von Willebrand factor A domain-containing protein 5A (F OPPIHA	8
754	13.35	13.35	35.03	9.189	5.599	tr V8P808 V8P808_OPPIHA	Telomerase protein component 1 (Fragment) OS=Ophiophagu OPPIHA	6
755	13.35	13.35	89.84	50	50	tr V8NR18 V8NR18_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	8
756	13.34	13.34	87.58	46.58	46.58	tr V8NCG9 V8NCG9_OPPIHA	Serine/arginine-rich splicing factor 9 (Fragment) OS=Op OPPIHA	9
757	13.33	13.33	46.6	11.22	8.927	tr V8NLW9 V8NLW9_OPPIHA	Rho GTPase-activating protein 35 (Fragment) OS=Ophioph OPPIHA	8
758	13.33	13.33	50.66	18.09	18.09	tr V8NKY2 V8NKY2_OPPIHA	Serine/threonine-protein phosphatase (Fragment) OS=Ophi OPPIHA	7
759	13.3	13.3	57.85	14.19	10.74	tr V8P629 V8P629_OPPIHA	Beta-adrenergic receptor kinase 1 (Fragment) OS=Ophioph OPPIHA	7
760	13.28	13.28	74.39	21.68	17.57	tr V8P229 V8P229_OPPIHA	Src substrate cactactin (Fragment) OS=Ophiophagus hanna OPPIHA	7
761	13.28	13.28	47.74	30.97	28.71	tr V8PB68 V8PB68_OPPIHA	26S proteasome non-ATPase regulatory subunit 14 OS=Ophi OPPIHA	7

762	13.25	18.43	42.72	34.95	29.77	tr	V8NIF8	V8NIF8_OPHHA	L-lactate dehydrogenase OS=Ophiophagus hannah GN=LDB P OPHHA	13
763	13.23	13.23	54.71	46.47	46.47	tr	V8P3X6	V8P3X6_OPHHA	N-alpha-acetyltransferase 50 OS=Ophiophagus hannah GN=N OPHHA	7
764	13.21	13.21	39.93	21.32	16.07	tr	V8NVS4	V8NVS4_OPHHA	CTP synthase OS=Ophiophagus hannah GN=CTPS PE=3 SV=1 OPHHA	7
765	13.2	13.2	53.16	32.28	29.11	tr	V8P7L4	V8P7L4_OPHHA	Pyrroline-5-carboxylate reductase OS=Ophiophagus hannah OPHHA	8
766	13.19	13.39	40.44	9.737	7.178	tr	V8P8T3	V8P8T3_OPHHA	Protein VPRBP OS=Ophiophagus hannah GN=VPRBP PE=4 SV=1 OPHHA	6
767	13.18	13.18	43.12	14.34	7.415	tr	V8N9N8	V8N9N8_OPHHA	Small nuclear ribonucleoprotein helicase (Fragment) OS= OPHHA	6
768	13.17	13.17	52.62	9.927	5.165	tr	V8NZ25	V8NZ25_OPHHA	Nuclear mitotic apparatus protein 1 (Fragment) OS=Ophio OPHHA	6
769	13.16	13.16	57.05	6.686	4.759	tr	V8P082	V8P082_OPHHA	Melanoma inhibitory activity protein 3 OS=Ophiophagus h OPHHA	8
770	13.16	13.16	76.28	44.65	32.56	tr	V8NTQ2	V8NTQ2_OPHHA	Vesicle-trafficking protein SEC22b OS=Ophiophagus hanna OPHHA	9
771	13.15	13.15	42.18	10.14	9.467	tr	V8NML1	V8NML1_OPHHA	Phosphorylase b kinase regulatory subunit alpha, liver OPHHA	7
772	13.11	13.11	49.82	18.79	14.54	tr	V8PCX9	V8PCX9_OPHHA	Drebrin-like protein (Fragment) OS=Ophiophagus hannah G OPHHA	9
773	13.05	13.05	41.88	11.37	6.961	tr	V8NTS6	V8NTS6_OPHHA	Glutamyl aminopeptidase (Fragment) OS=Ophiophagus hanna OPHHA	6
774	13.04	25.61	52.85	15.72	12.52	tr	V8NFI6	V8NFI6_OPHHA	Brefeldin A-inhibited guanine nucleotide-exchange prote OPHHA	12
775	13.03	13.03	74.05	25.14	24.86	tr	V8NND4	V8NND4_OPHHA	Serine/threonine-protein phosphatase 2A 55 kDa regulato OPHHA	7
776	13.01	13.01	55.01	15.99	13.86	tr	V8PH40	V8PH40_OPHHA	Paraspeckle component 1 OS=Ophiophagus hannah GN=PSPC1 OPHHA	6
777	13	13	24.62	7.859	6.09	tr	V8NAV5	V8NAV5_OPHHA	ATP-binding cassette sub-family A member 8-A (Fragment) OPHHA	7
778	12.99	12.99	62.56	38.86	38.86	tr	V8P6V7	V8P6V7_OPHHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345 O OPHHA	8
779	12.97	12.97	40.38	7.258	6.203	tr	V8P819	V8P819_OPHHA	N-acetyltransferase 10 (Fragment) OS=Ophiophagus hannah OPHHA	7
780	12.97	12.97	34.49	11.07	8.794	tr	V8NFG3	V8NFG3_OPHHA	Agrin (Fragment) OS=Ophiophagus hannah GN=AGRN PE=4 SV= OPHHA	8
781	12.96	13.39	67.63	13.89	8.855	tr	V8NDC6	V8NDC6_OPHHA	N-alpha-acetyltransferase 16, NatA auxiliary subunit (F OPHHA	6
782	12.96	12.96	57.05	19.96	14.97	tr	V8P3S0	V8P3S0_OPHHA	Protein kinase C alpha type (Fragment) OS=Ophiophagus h OPHHA	6
783	12.95	12.95	25.94	14.09	12.29	tr	V8PEG3	V8PEG3_OPHHA	Dolichyl-diphosphooligosaccharide--protein glycosyltran OPHHA	7
784	12.88	12.88	41.89	22.76	22.52	tr	V8PDK4	V8PDK4_OPHHA	Mannose-1-phosphate guanylttransferase alpha-A OS=Ophio OPHHA	7
785	12.87	12.87	51.04	19.73	13.66	tr	V8POK3	V8POK3_OPHHA	Asparagine synthetase [glutamine-hydrolyzing] OS=Ophio OPHHA	6
786	12.83	12.83	24.65	7.567	5.94	tr	V8NM36	V8NM36_OPHHA	Protein MON2-like protein OS=Ophiophagus hannah GN=mon2 OPHHA	6
787	12.82	12.82	31.66	12.57	10.01	tr	V8NK75	V8NK75_OPHHA	Nuclear pore complex protein OS=Ophiophagus hannah GN=N OPHHA	7
788	12.8	12.8	50.51	34.81	22.53	tr	V8P8Z3	V8P8Z3_OPHHA	Mitochondrial dicarboxylate carrier (Fragment) OS=Ophio OPHHA	7
789	12.78	12.78	37.56	19.38	17.46	tr	V8NL87	V8NL87_OPHHA	Nucleosome assembly protein 1-like 4 (Fragment) OS=Ophi OPHHA	7
790	12.74	12.74	62.23	18.25	15.33	tr	V8NAE4	V8NAE4_OPHHA	Sarcolemmal membrane-associated protein OS=Ophiophagus OPHHA	6
791	12.7	12.7	53.17	27.07	25.37	tr	V8NV76	V8NV76_OPHHA	Biglycan (Fragment) OS=Ophiophagus hannah GN=BGV PE=4 S OPHHA	6
792	12.68	12.68	59.45	37.4	32.28	tr	V8NLD4	V8NLD4_OPHHA	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, OPHHA	8
793	12.67	12.67	79.26	24.07	24.07	tr	V8N9W8	V8N9W8_OPHHA	Alpha-2-macroglobulin receptor-associated protein (Frag OPHHA	8
794	12.66	12.66	66.46	16.67	16.67	tr	V8NQ28	V8NQ28_OPHHA	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 4 OPHHA	8
795	12.65	12.65	52.27	11.25	9.619	tr	V8NBW6	V8NBW6_OPHHA	Glutamate--cysteine ligase catalytic subunit OS=Ophio OPHHA	6
796	12.63	12.63	69.97	34.98	26.07	tr	V8NZ44	V8NZ44_OPHHA	LIM and senescent cell antigen-like-containing domain p OPHHA	9
797	12.6	12.6	58.69	44.13	40.38	tr	V8P9G7	V8P9G7_OPHHA	Dolichol-phosphate mannosyltransferase (Fragment) OS=Op OPHHA	8
798	12.59	12.59	51.8	8.546	6.522	tr	V8P5I0	V8P5I0_OPHHA	Poly [ADP-ribose] polymerase OS=Ophiophagus hannah GN=P ADP-ribo: OPHHA	6
799	12.59	12.59	35.7	9.974	8.924	tr	V8P7C1	V8P7C1_OPHHA	Nuclear pore complex protein OS=Ophiophagus hannah GN=N OPHHA	7
800	12.52	12.52	62.27	37.27	34.55	tr	V8P4E3	V8P4E3_OPHHA	Maleylacetoacetate isomerase OS=Ophiophagus hannah GN=G OPHHA	11
801	12.52	12.52	78.26	56.52	51.3	tr	V8P297	V8P297_OPHHA	60S ribosomal protein L30 OS=Ophiophagus hannah GN=RPL3 OPHHA	6
802	12.5	12.5	36.27	19.57	14.18	tr	V8NAG9	V8NAG9_OPHHA	Bifunctional coenzyme A synthase OS=Ophiophagus hannah OPHHA	6
803	12.49	12.49	54.78	40.44	23.9	tr	V8PC26	V8PC26_OPHHA	Synaptic vesicle membrane protein VAT-1-like protein (F OPHHA	7
804	12.45	12.45	55.52	16.93	11.76	tr	V8PCK1	V8PCK1_OPHHA	Protein OS-9 (Fragment) OS=Ophiophagus hannah GN=OS9 PE OPHHA	6
805	12.44	12.44	41.35	7.275	6.509	tr	V8NRY5	V8NRY5_OPHHA	alpha-1,2-Mannosidase OS=Ophiophagus hannah GN=EDEM3 PE OPHHA	7
806	12.44	12.44	45.93	12.22	10.41	tr	V8PBD9	V8PBD9_OPHHA	A-kinase anchor protein 2 (Fragment) OS=Ophiophagus han OPHHA	7
807	12.42	12.42	32.53	5.459	3.817	tr	V8NUB4	V8NUB4_OPHHA	Protein dopey-2 (Fragment) OS=Ophiophagus hannah GN=DOP OPHHA	6
808	12.41	12.41	53.59	13.11	6.557	tr	V8P312	V8P312_OPHHA	Putative ATP-dependent RNA helicase DDX46 (Fragment) OS OPHHA	5
809	12.41	12.41	50.34	40.69	36.55	tr	V8N7G7	V8N7G7_OPHHA	Cytochrome c oxidase subunit 5A, mitochondrial (Fragmen OPHHA	8
810	12.4	12.4	45.04	15.63	15.63	tr	V8PBM4	V8PBM4_OPHHA	WD repeat-containing protein 44 (Fragment) OS=Ophiophag OPHHA	9
811	12.4	12.4	42.59	17.64	17.07	tr	V8P2R3	V8P2R3_OPHHA	Dynactin subunit 4 (Fragment) OS=Ophiophagus hannah GN= OPHHA	7
812	12.35	14.51	76.42	34.93	25.97	tr	V8NRN4	V8NRN4_OPHHA	Septin-9 OS=Ophiophagus hannah GN=SEPT9 PE=3 SV=1 OPHHA	9
813	12.35	12.35	48.24	10.47	8.588	tr	V8P4D8	V8P4D8_OPHHA	Glucosamine--fructose-6-phosphate aminotransferase [iso OPHHA	7
814	12.34	12.34	79.17	41.67	41.67	tr	V8P478	V8P478_OPHHA	14 kDa phosphohistidine phosphatase (Fragment) OS=Ophio OPHHA	6
815	12.33	12.33	46.85	9.321	6.623	tr	V8PC22	V8PC22_OPHHA	SWI/SNF complex subunit SMARCC2 (Fragment) OS=Ophiophag OPHHA	6
816	12.32	12.32	67.78	27.22	27.22	tr	V8NU77	V8NU77_OPHHA	[Pyruvate dehydrogenase [lipaoamide]] kinase isozyme 1, Pyruvate OPHHA	6
817	12.32	12.32	32.34	28.19	24.04	tr	V8P2Q0	V8P2Q0_OPHHA	Glycogenin-1 OS=Ophiophagus hannah GN=Gygl PE=4 SV=1 OPHHA	6
818	12.3	12.3	31.32	13.01	9.228	tr	V8P1N3	V8P1N3_OPHHA	Plasminogen (Fragment) OS=Ophiophagus hannah GN=PLG PE= OPHHA	6
819	12.29	12.29	38.56	9.804	8.235	tr	V8P8L8	V8P8L8_OPHHA	Hepatocyte growth factor-regulated tyrosine kinase subs OPHHA	6
820	12.28	12.28	47.53	9.801	8.326	tr	V8PIC9	V8PIC9_OPHHA	Diacylglycerol kinase (Fragment) OS=Ophiophagus hannah OPHHA	6
821	12.26	12.33	51.41	12.1	7.56	tr	V8NW59	V8NW59_OPHHA	PERK amino acid-rich with GYF domain-containing protein OPHHA	6
822	12.26	12.26	65	25.25	22	tr	V8NZ75	V8NZ75_OPHHA	Putative RNA-binding protein Luc7-like 2 OS=Ophiophagus OPHHA	7
823	12.23	12.23	36.92	34.05	31.18	tr	V8NA13	V8NA13_OPHHA	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS= OPHHA	7
824	12.21	12.21	82.3	29.19	29.19	tr	V8P4E1	V8P4E1_OPHHA	Ferrochelatase, mitochondrial (Fragment) OS=Ophiophagus OPHHA	7
825	12.19	12.46	61.81	19.23	14.84	tr	V8PFN4	V8PFN4_OPHHA	HCLS1-binding protein 3 (Fragment) OS=Ophiophagus hanna OPHHA	6
826	12.19	12.19	38.3	5.133	4.393	tr	V8PIE8	V8PIE8_OPHHA	M-phase phosphoprotein 8 (Fragment) OS=Ophiophagus hann OPHHA	9
827	12.18	12.18	72.44	48.03	40.94	tr	V8NNR3	V8NNR3_OPHHA	Serine/arginine-rich splicing factor 3 OS=Ophiophagus h OPHHA	8
828	12.16	12.16	42.57	9.979	8.599	tr	V8NT00	V8NT00_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	8
829	12.14	12.14	93.07	66.34	59.41	tr	V8P1H5	V8P1H5_OPHHA	Pterin-4-alpha-carbinolamine dehydratase 2 (Fragment) O OPHHA	9
830	12.12	12.12	70.45	39.2	39.2	tr	V8N8Y4	V8N8Y4_OPHHA	Proteasome subunit alpha type-2 (Fragment) OS=Ophiophag OPHHA	8
831	12.11	12.11	47.39	9.13	8.261	tr	V8NGB9	V8NGB9_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	8
832	12.09	13.66	48.93	10.81	6.518	tr	V8P5N6	V8P5N6_OPHHA	Clustered mitochondria protein homolog OS=Ophiophagus h OPHHA	6
833	12.09	12.09	58.22	25.91	25.91	tr	V8P110	V8P110_OPHHA	Sialic acid synthase OS=Ophiophagus hannah GN=NANS PE=4 OPHHA	8
834	12.08	12.08	42.86	20.48	17.86	tr	V8NZM4	V8NZM4_OPHHA	Angio-associated migratory cell protein OS=Ophiophagus OPHHA	6
835	12.08	12.08	53.99	29.58	25.35	tr	V8PIE5	V8PIE5_OPHHA	40S ribosomal protein S7 OS=Ophiophagus hannah GN=rps7 OPHHA	7
836	12.06	12.06	43.27	19.93	18.85	tr	V8N4T2	V8N4T2_OPHHA	Inter-alpha-trypsin inhibitor heavy chain H3 (Fragment) OPHHA	7
837	12.06	12.06	82	70	70	tr	V8NQ30	V8NQ30_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	9
838	12.05	12.05	52.15	11.37	9.349	tr	V8NNT9	V8NNT9_OPHHA	Alpha-mannosidase OS=Ophiophagus hannah GN=MAN2A1 PE=3 OPHHA	7
839	12.05	12.05	40	16.31	12.87	tr	V8PBL4	V8PBL4_OPHHA	Protein sel-1-like 1 (Fragment) OS=Ophiophagus hannah G OPHHA	6
840	12.05	12.05	53.43	28.36	22.69	tr	V8NV38	V8NV38_OPHHA	DnaJ-like subfamily B member 1 OS=Ophiophagus hannah GN OPHHA	7
841	12.05	12.05	51.85	22.9	20.88	tr	V8N9J7	V8N9J7_OPHHA	60S acidic ribosomal protein P0 OS=Ophiophagus hannah G OPHHA	6
842	12.03	12.03	64.18	25.75	25.75	tr	V8NG17	V8NG17_OPHHA	Putative methyltransferase (Fragment) OS=Ophiophagus ha OPHHA	6
843	12.02	14.34	52.24	22.08	22.08	tr	V8P534	V8P534_OPHHA	Polypyrimidine tract-binding protein 1 OS=Ophiophagus h OPHHA	10
844	12.02	14.15	62.96	29.01	24.38	tr	V8NS12	V8NS12_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	7
845	12.02	12.02	58.31	25.76	23.39	tr	V8NIU2	V8NIU2_OPHHA	Flotillin-1 (Fragment) OS=Ophiophagus hannah GN=flotl P OPHHA	7
846	12.01	12.24	51.79	15.54	9.96	tr	V8NP10	V8NP10_OPHHA	Monofunctional C1-tetrahydrofolate synthase, mitochondr OPHHA	6
847	12.01	12.01	52.04	23.43	20.16	tr	V8PAE4	V8PAE4_OPHHA	Mannose-1-phosphate guanylttransferase beta-A (Fragment) OPHHA	7
848	12	12	48.9	15.76	13.11	tr	V8P6C7	V8P6C7_OPHHA	Trafficking protein particle complex subunit 9 (Fragmen OPHHA	7
849	12	12	68.52	33.8	33.8	tr	V8NTB0	V8NTB0_OPHHA	Ras-related protein Rab-5A OS=Ophiophagus hannah GN=RAB OPHHA	6
850	11.99	11.99	55.39	16.82	14.56	tr	V8N7X3	V8N7X3_OPHHA	Mitofusin-2 (Fragment) OS=Ophiophagus hannah GN=Mfn2 PE OPHHA	6
851	11.98	11.98	66.23	53.25	28.57	tr	V8NY31	V8NY31_OPHHA	Protein-L-isoaspartate O-methyltransferase OS=Ophiophag OPHHA	7
852	11.96	11.96	52.93	13.41	6.039	tr	V8PAM2	V8PAM2_OPHHA	Acyl-CoA dehydrogenase family member 11 OS=Ophiophagus OPHHA	6
853	11.96	11.96	75.4	38.1	38.1	tr	V8N341	V8N341_OPHHA	Histone H2B (Fragment) OS=Ophiophagus hannah GN=H2B-1 P OPHHA	11
854	11.95	11.95	44.86	24.29	17.07	tr	V8P4K3	V8P4K3_OPHHA	Selenocysteine-specific elongation factor (Fragment) OS=Ophio OPHHA	6
855	11.94	11.94	53.36	8.734	7.948	tr	V8NZ20	V8NZ20_OPHHA	DENN domain-containing protein 2C (Fragment) OS=Ophioph OPHHA	6
856	11.92	11.92	51.03	41.03	35.86	tr	V8N717	V8N717_OPHHA	Nicotinamide phosphoribosyltransferase (Fragment) OS=Op OPHHA	6
857	11.91	11.91	53.89	24.44	24.44	tr	V8P7P5	V8P7P5_OPHHA	Mesencephalic astrocyte-derived neurotrophic factor (Fr OPHHA	7

858	11.89	11.89	53.56	17.85	12.21	tr V8P9F3 V8P9F3_OPPIHA 6-phosphofructokinase type C OS=Ophiophagus hannah GN=P OPPIHA	5
859	11.89	11.89	69.17	37.5	30.42	tr V8P212 V8P212_OPPIHA Proteasome activator complex subunit 2 OS=Ophiophagus h OPPIHA	8
860	11.89	11.89	68.34	27.41	13.51	tr V8N9Y2 V8N9Y2_OPPIHA Tropomodulin-3 (Fragment) OS=Ophiophagus hannah GN=TMOD OPPIHA	5
861	11.86	11.86	44.13	22.54	20.66	tr V8N9Y6 V8N9Y6_OPPIHA Microtubule-associated protein RP/EB family member 2 (F OPPIHA	6
862	11.84	12.06	50.26	13.44	8.308	tr V8NLM7 V8NLM7_OPPIHA U2 snRNP-associated SURP motif-containing protein OS=Op OPPIHA	6
863	11.84	11.84	28.5	18.65	14.34	tr V8P9S8 V8P9S8_OPPIHA Beta-galactosidase-1-like protein (Fragment) OS=Ophioph OPPIHA	5
864	11.83	20.29	72.85	47.96	47.96	tr V8N5X4 V8N5X4_OPPIHA Eukaryotic initiation factor 4A-I (Fragment) OS=Ophioph OPPIHA	12
865	11.82	12.27	52.33	24.57	14.99	tr V8N5T1 V8N5T1_OPPIHA Amine oxidase [flavin-containing] A OS=Ophiophagus hann OPPIHA	6
866	11.82	11.82	52.77	19.5	12.7	tr V8P1U1 V8P1U1_OPPIHA ATP-binding cassette sub-family E member 1 OS=Ophiophag OPPIHA	5
867	11.81	11.81	48.48	16.45	11.98	tr V8P1J5 V8P1J5_OPPIHA Vacuolar protein sorting-associated protein 4A (Fragmen OPPIHA	6
868	11.8	11.8	42.71	36.68	36.68	tr V8NNY5 V8NNY5_OPPIHA Chromobox protein-like 3 (Fragment) OS=Ophiophagus hann OPPIHA	7
869	11.78	11.78	59.35	28.05	24.8	tr V8NDP5 V8NDP5_OPPIHA Annexin OS=Ophiophagus hannah GN=ANXA2 PE=3 SV=1 OPPIHA	6
870	11.77	14	75.41	43.03	39.75	tr V8P7Z6 V8P7Z6_OPPIHA 14-3-3 protein beta/alpha OS=Ophiophagus hannah GN=YWHA OPPIHA	8
871	11.77	11.77	38.35	9.519	7.706	tr V8NVMO V8NVMO_OPPIHA Lish domain and HEAT repeat-containing protein (Fragmen OPPIHA	7
872	11.75	11.86	48.55	16.91	11.99	tr V8NQL5 V8NQL5_OPPIHA Double-stranded RNA-binding protein Staufsen-like 1 OS=O OPPIHA	6
873	11.75	11.75	64.07	41.36	30.17	tr V8NZF0 V8NZF0_OPPIHA Syntenin-1 OS=Ophiophagus hannah GN=SDCBP PE=4 SV=1 OPPIHA	6
874	11.74	11.74	79.6	23.68	22.17	tr V8NZM6 V8NZM6_OPPIHA Heterogeneous nuclear ribonucleoprotein L-like protein OPPIHA	6
875	11.73	11.73	38.3	9.265	9.265	tr V8PCQ6 V8PCQ6_OPPIHA Adipocyte enhancer-binding protein 1 (Fragment) OS=Ophi OPPIHA	7
876	11.72	11.73	43.86	6.941	6.178	tr V8NPZ4 V8NPZ4_OPPIHA Guanylate cyclase soluble subunit beta-1 (Fragment) OS= OPPIHA	6
877	11.72	11.72	70.59	39.22	33.33	tr V8PD47 V8PD47_OPPIHA Sorting nexin-3 OS=Ophiophagus hannah GN=SNX3 PE=4 SV=1 OPPIHA	6
878	11.72	11.72	45.76	20.34	20.34	tr V8POC2 V8POC2_OPPIHA Transmembrane emp24 domain-containing protein 10 (Fragm OPPIHA	6
879	11.7	11.7	55.17	20	16.9	tr V8NNB0 V8NNB0_OPPIHA Small nuclear ribonucleoprotein Sm D2 (Fragment) OS=Ophi OPPIHA	6
880	11.68	11.68	53.58	8.734	8.636	tr V8PDA7 V8PDA7_OPPIHA DNA helicase OS=Ophiophagus hannah GN=mcms PE=3 SV=1 OPPIHA	6
881	11.67	11.68	62.97	23.68	17.38	tr V8P8E3 V8P8E3_OPPIHA Nucleobindin-1 OS=Ophiophagus hannah GN=Nucl1 PE=4 SV=1 OPPIHA	6
882	11.66	11.67	41.44	17.5	17.5	tr V8NH23 V8NH23_OPPIHA ATP-dependent Clp protease ATP-binding subunit clpX-lik OPPIHA	7
883	11.66	11.66	60.49	38.54	38.54	tr V8NWQ1 V8NWQ1_OPPIHA Ras-related protein Rab-18 OS=Ophiophagus hannah GN=RAB OPPIHA	7
884	11.63	12.9	58.25	31.65	29.29	tr V8PF66 V8PF66_OPPIHA Sulfurtransferase OS=Ophiophagus hannah GN=MPST PE=4 SV OPPIHA	9
885	11.63	11.63	56.48	12.96	7.673	tr V8P004 V8P004_OPPIHA Leucine-rich repeat-containing protein 39 (Fragment) OS OPPIHA	5
886	11.61	11.61	45.35	30.23	29.94	tr V8P4H8 V8P4H8_OPPIHA Mitotic checkpoint protein BUB3 (Fragment) OS=Ophiophag OPPIHA	7
887	11.6	11.6	57.76	11.45	11.45	tr V8NRC0 V8NRC0_OPPIHA Nucleolar transcription factor 1 OS=Ophiophagus hannah OPPIHA	6
888	11.6	11.6	54.95	13.7	10.72	tr V8PGV7 V8PGV7_OPPIHA Excyst complex component 5 (Fragment) OS=Ophiophagus h OPPIHA	6
889	11.59	13.97	48.35	7.302	4.381	tr V8NBU4 V8NBU4_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	8
890	11.59	11.59	61.18	10.93	10.93	tr V8P9S7 V8P9S7_OPPIHA Synaptopodin (Fragment) OS=Ophiophagus hannah GN=Synpo OPPIHA	6
891	11.59	11.59	50.32	25.95	25.95	tr V8PFV3 V8PFV3_OPPIHA Phosphoribosyl pyrophosphate synthase-associated protei OPPIHA	7
892	11.58	11.58	59.2	37.81	37.81	tr V8P641 V8P641_OPPIHA 39S ribosomal protein L46, mitochondrial (Fragment) OS= OPPIHA	6
893	11.57	11.57	81.61	35.25	18.77	tr V8NDR8 V8NDR8_OPPIHA Phosphatidylinositol transfer protein beta isoform (Fra OPPIHA	5
894	11.54	11.54	35.13	17.56	17.56	tr V8P5W4 V8P5W4_OPPIHA Putative serine carboxypeptidase CPVL OS=Ophiophagus ha OPPIHA	6
895	11.53	12.12	52.35	21.63	18.18	tr V8NVH7 V8NVH7_OPPIHA FCH domain only protein 2 (Fragment) OS=Ophiophagus han OPPIHA	6
896	11.52	11.52	44.75	15.45	8.283	tr V8P8D1 V8P8D1_OPPIHA KCH motif and ankyrin repeat domain-containing protein 4 OPPIHA	6
897	11.52	11.52	53.05	16.16	16.16	tr V8NWU9 V8NWU9_OPPIHA High mobility group protein B1 (Fragment) OS=Ophiophagu OPPIHA	7
898	11.49	11.49	41.79	21.07	21.07	tr V8NE81 V8NE81_OPPIHA 60S ribosomal protein L7a OS=Ophiophagus hannah GN=RPL7 OPPIHA	6
899	11.48	11.48	46.01	16.36	12.27	tr V8P8F7 V8P8F7_OPPIHA Myc box-dependent-interacting protein 1 (Fragment) OS=O OPPIHA	6
900	11.48	11.48	49.03	24.71	24.71	tr V8NPW0 V8NPW0_OPPIHA 15-hydroxyprostaglandin dehydrogenase [NAD+] OS=Ophiophag NAD+ OPPIHA	8
901	11.47	11.47	47.04	7.527	6.631	tr V8NRT2 V8NRT2_OPPIHA Apoptotic chromatin condensation inducer in the nucleus OPPIHA	6
902	11.47	11.47	37.12	14.71	7.981	tr V8NF17 V8NF17_OPPIHA Serine/threonine-protein phosphatase 6 regulatory ankyr OPPIHA	5
903	11.47	11.47	30.77	7.958	7.029	tr V8P9G9 V8P9G9_OPPIHA Dipeptidyl peptidase 4 OS=Ophiophagus hannah GN=DPP4 PE OPPIHA	6
904	11.46	11.59	48.41	18.69	12.34	tr V8NCM0 V8NCM0_OPPIHA Importin subunit alpha OS=Ophiophagus hannah GN=KPNA6 P OPPIHA	6
905	11.46	11.46	48.88	17.41	15.63	tr V8NXX6 V8NXX6_OPPIHA Cytoplasmic dynein 1 light intermediate chain 2 OS=Ophi OPPIHA	6
906	11.46	11.46	53.28	32.79	32.79	tr V8NRH7 V8NRH7_OPPIHA F-actin-capping protein subunit alpha-2 OS=Ophiophagus OPPIHA	9
907	11.44	11.44	47.95	8.709	7.45	tr V8NNP3 V8NNP3_OPPIHA Formin-like protein 3 (Fragment) OS=Ophiophagus hannah OPPIHA	6
908	11.44	11.44	36.54	11.04	8.528	tr V8NH27 V8NH27_OPPIHA Enhancer of mRNA-decapping protein 4 (Fragment) OS=Ophi OPPIHA	6
909	11.42	11.42	38.59	6.222	4.249	tr V8POM7 V8POM7_OPPIHA Dedicator of cytokinesis protein 8 (Fragment) OS=Ophiophag OPPIHA	7
910	11.42	11.42	52.61	42.57	35.34	tr V8PBB4 V8PBB4_OPPIHA Pleckstrin-likey domain-containing family F member 2 OS OPPIHA	7
911	11.41	11.41	78.41	35.23	30.11	tr V8NMW4 V8NMW4_OPPIHA 60S ribosomal protein L18a OS=Ophiophagus hannah GN=RPL OPPIHA	6
912	11.4	11.4	49.37	41.14	21.84	tr V8PHR8 V8PHR8_OPPIHA Hexaprenyldihydroxybenzoate methyltransferase, mitochon OPPIHA	5
913	11.39	11.39	41.15	16.53	14.5	tr V8PEM5 V8PEM5_OPPIHA 2',5'-phosphodiesterase 12 (Fragment) OS=Ophiophagus ha OPPIHA	6
914	11.38	11.38	36.73	14.66	12.19	tr V8P0W6 V8P0W6_OPPIHA Integrin alpha-1 (Fragment) OS=Ophiophagus hannah GN=It OPPIHA	6
915	11.37	11.37	60.06	23.84	16.41	tr V8NJF8 V8NJF8_OPPIHA Protein arginine N-methyltransferase 1 (Fragment) OS=Op OPPIHA	6
916	11.37	11.37	38.53	14.48	14.48	tr V8N972 V8N972_OPPIHA Acetolactate synthase-like protein (Fragment) OS=Ophioph OPPIHA	7
917	11.37	11.37	30.6	15.3	15.3	tr V8NQ66 V8NQ66_OPPIHA High mobility group protein B3 (Fragment) OS=Ophiophagu OPPIHA	6
918	11.35	11.35	46.67	14.23	14.23	tr V8NTW1 V8NTW1_OPPIHA Epidermal growth factor receptor kinase substrate 8 OS= OPPIHA	6
919	11.33	12.26	58.31	29.78	22.33	tr V8PB23 V8PB23_OPPIHA DnaJ-like subfamily A member 1 OS=Ophiophagus hannah GN OPPIHA	7
920	11.31	11.31	47.85	24.09	24.09	tr V8PCV2 V8PCV2_OPPIHA Epimerase family protein SDR39U1 (Fragment) OS=Ophiophag OPPIHA	6
921	11.27	13.6	50.25	34.07	17.16	tr V8NV16 V8NV16_OPPIHA Septin-6 (Fragment) OS=Ophiophagus hannah GN=SEPT6 PE=3 OPPIHA	7
922	11.26	11.26	53.22	13.14	10.99	tr V8NZ44 V8NZ44_OPPIHA Prospero homeobox protein 1 (Fragment) OS=Ophiophagus h OPPIHA	6
923	11.23	11.23	50.7	10.73	4.996	tr V8NVR9 V8NVR9_OPPIHA Laminin subunit alpha-5 OS=Ophiophagus hannah GN=LAMA5 OPPIHA	6
924	11.2	11.2	45.59	12.62	10.12	tr V8PCC6 V8PCC6_OPPIHA Exostosin-like 3 (Fragment) OS=Ophiophagus hannah GN=EX OPPIHA	6
925	11.18	11.18	46.99	16.64	10.77	tr V8NHT5 V8NHT5_OPPIHA Putative pre-mRNA-splicing factor ATP-dependent RNA hel OPPIHA	6
926	11.18	11.18	34.23	15.34	11.65	tr V8NU41 V8NU41_OPPIHA Threonine synthase-like 1 (Fragment) OS=Ophiophagus han OPPIHA	7
927	11.18	11.18	52.27	30.45	24.55	tr V8NWX7 V8NWX7_OPPIHA Peptidyl-prolyl cis-trans isomerase OS=Ophiophagus hann OPPIHA	9
928	11.16	11.16	35.68	5.704	3.58	tr V8P633 V8P633_OPPIHA Serine/threonine-protein kinase mTOR OS=Ophiophagus han OPPIHA	7
929	11.15	11.15	31.63	1.498	1.198	tr V8NT23 V8NT23_OPPIHA Cadherin EGF LAG seven-pass G-type receptor 1 (Fragment OPPIHA	7
930	11.15	11.15	39.61	8.425	7.659	tr V8P2Q3 V8P2Q3_OPPIHA Ataxin-2-like protein (Fragment) OS=Ophiophagus hannah OPPIHA	6
931	11.14	11.14	56.7	12.41	7.349	tr V8N8N0 V8N8N0_OPPIHA Rho guanine nucleotide exchange factor 12 OS=Ophiophagu OPPIHA	6
932	11.14	11.14	31.91	8.547	7.407	tr V8NZE9 V8NZE9_OPPIHA Microsomal triglyceride transfer protein large subunit OPPIHA	8
933	11.12	11.12	54.92	26.94	22.28	tr V8NP40 V8NP40_OPPIHA Delta-aminolevulinic acid dehydratase (Fragment) OS=Ophi OPPIHA	6
934	11.11	11.11	59.27	29.03	20.97	tr V8P120 V8P120_OPPIHA Proteasome subunit alpha type OS=Ophiophagus hannah GN= OPPIHA	5
935	11.1	18.74	39.63	15.71	7.496	tr V8PBG8 V8PBG8_OPPIHA Cullin-associated NEDD8-dissociated protein 1 (Fragment OPPIHA	7
936	11.1	11.3	57.64	9.807	6.029	tr V8NLM4 V8NLM4_OPPIHA Golgin subfamily A member 3 OS=Ophiophagus hannah GN=GO OPPIHA	6
937	11.08	11.08	60.45	34.33	34.33	tr V8NJY4 V8NJY4_OPPIHA 60S ribosomal protein L9 OS=Ophiophagus hannah GN=RPL9 OPPIHA	7
938	11.05	13.33	57.03	33.13	15.06	tr V8NG26 V8NG26_OPPIHA EH domain-containing protein 4 OS=Ophiophagus hannah GN OPPIHA	6
939	11.05	11.05	37.16	8.063	5.468	tr V8NDX1 V8NDX1_OPPIHA Protein diaphanous-like 1 (Fragment) OS=Ophiophagus han OPPIHA	5
940	11.05	11.05	79.79	34.2	30.57	tr V8PH65 V8PH65_OPPIHA Neurocalcin-delta (Fragment) OS=Ophiophagus hannah GN=N OPPIHA	7
941	11.05	11.05	88.68	47.17	47.17	tr V8NVW6 V8NVW6_OPPIHA Cysteine and glycine-rich protein 1 (Fragment) OS=Ophiophag OPPIHA	7
942	11.03	11.03	40.33	14.83	14.83	tr V8PJ77 V8PJ77_OPPIHA Sulfite oxidase (Fragment) OS=Ophiophagus hannah GN=SUO OPPIHA	7
943	11.01	11.01	62.56	21.5	15.7	tr V8N8N3 V8N8N3_OPPIHA Glutaminyl-tRNA synthetase (Fragment) OS=Ophiophagus ha OPPIHA	6
944	11.01	11.01	24.74	9.754	7.803	tr V8P260 V8P260_OPPIHA MMS19 nucleotide excision repair protein-like protein (OPPIHA	6
945	10.97	11.06	34.4	16	16	tr V8NQ39 V8NQ39_OPPIHA Transmembrane 9 superfamily member 2 (Fragment) OS=Ophi OPPIHA	7
946	10.97	10.97	37.54	11.5	11.5	tr V8NJ76 V8NJ76_OPPIHA Disabled-like 2 (Fragment) OS=Ophiophagus hannah GN=Dab OPPIHA	6
947	10.95	11.78	33.23	16.46	8.54	tr V8P2R2 V8P2R2_OPPIHA TBC1 domain family member 17 OS=Ophiophagus hannah GN=T OPPIHA	5
948	10.95	10.95	47.65	20.47	15.44	tr V8P4W7 V8P4W7_OPPIHA ADP/ATP translocase 1 OS=Ophiophagus hannah GN=SLC25A4 OPPIHA	5
949	10.95	10.95	52.36	30.55	24.36	tr V8PEB5 V8PEB5_OPPIHA Acylglycerol kinase, mitochondrial (Fragment) OS=Ophioph OPPIHA	5
950	10.95	10.95	68.57	55.24	55.24	tr V8P1H8 V8P1H8_OPPIHA Dynein light chain 2, cytoplasmic (Fragment) OS=Ophioph OPPIHA	8
951	10.92	12.17	51.42	13.21	9.375	tr V8NWY8 V8NWY8_OPPIHA Echinoderm microtubule-associated protein-like 1 (Fragm OPPIHA	5
952	10.92	11.03	64.63	26.19	16.67	tr V8NW74 V8NW74_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	5
953	10.92	10.92	56.42	22.57	14.6	tr V8NFN2 V8NFN2_OPPIHA Xylulose kinase (Fragment) OS=Ophiophagus hannah GN=Xyl OPPIHA	5

954	10.91	10.91	64.09	22.27	20	tr V8PB62 V8PB62_OPHHA	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Ophiophagu	OPHHA	6
955	10.91	10.91	29.71	20.42	15.92	tr V8NEY1 V8NEY1_OPHHA	Dolichyl-diphosphooligosaccharide--protein glycosyltran	OPHHA	5
956	10.9	10.9	61	12.02	8.504	tr V8NVQ4 V8NVQ4_OPHHA	Ladinin-1 OS=Ophiophagus hannah GN=Lad1 PE=4 SV=1	OPHHA	5
957	10.89	10.89	49.19	25.81	18.55	tr V8PCP5 V8PCP5_OPHHA	Macrophage-capping protein OS=Ophiophagus hannah GN=Cap	OPHHA	5
958	10.88	10.88	48.25	17.68	12.89	tr V8PBJ9 V8PBJ9_OPHHA	Methylcrotonoyl-CoA carboxylase beta chain, mitochondri	OPHHA	5
959	10.87	10.87	49.26	28.78	28.78	tr V8P6T1 V8P6T1_OPHHA	Nuclear pore glycoprotein p62 (Fragment) OS=Ophiophagus	OPHHA	6
960	10.84	18.85	67.78	67.78	63.33	tr V8PE16 V8PE16_OPHHA	ADP-ribosylation factor 4 OS=Ophiophagus hannah GN=ARF4	OPHHA	12
961	10.83	10.83	36.8	11.77	10.66	tr V8NNM2 V8NNM2_OPHHA	Protein enabled-like protein (Fragment) OS=Ophiophagus	OPHHA	7
962	10.82	10.84	41.37	5.325	4.207	tr V8NL45 V8NL45_OPHHA	Myotubularin-related protein 5 (Fragment) OS=Ophiophagu	OPHHA	6
963	10.82	10.83	62.58	12.05	7.928	tr V8NNU9 V8NNU9_OPHHA	Myosin-Ib (Fragment) OS=Ophiophagus hannah GN=MYO1D	PE= OPHHA	6
964	10.82	10.82	42.78	10.53	6.732	tr V8NWW4 V8NWW4_OPHHA	Toll-like receptor 3 (Fragment) OS=Ophiophagus hannah G	OPHHA	5
965	10.81	10.81	41.47	13.76	11.82	tr V8PHX6 V8PHX6_OPHHA	Coiled-coil domain-containing protein 47 (Fragment) OS=	OPHHA	5
966	10.79	16.9	67.01	26.53	26.53	tr V8PH67 V8PH67_OPHHA	Heterogeneous nuclear ribonucleoprotein A3 (Fragment) O	OPHHA	9
967	10.77	15.68	61.22	37.95	26.87	tr V8NYM0 V8NYM0_OPHHA	S-adenosylmethionine synthase isoform type-2 (Fragment)	OPHHA	8
968	10.77	12.04	31.99	13.35	11.18	tr V8N9W1 V8N9W1_OPHHA	Alpha-2-macroglobulin (Fragment) OS=Ophiophagus hannah	OPHHA	6
969	10.77	10.77	50.78	24.45	21	tr V8P111 V8P111_OPHHA	Dual specificity mitogen-activated protein kinase kinas	OPHHA	5
970	10.77	10.77	37.72	35.33	30.54	tr V8NZJ6 V8NZJ6_OPHHA	Proteasome subunit beta type-2 (Fragment) OS=Ophiophagu	OPHHA	7
971	10.76	10.76	29.54	8.475	6.295	tr V8PD87 V8PD87_OPHHA	1-aminocyclopropane-1-carboxylate synthase-like protein	OPHHA	5
972	10.76	10.76	34.41	16.1	15.9	tr V8N1A0 V8N1A0_OPHHA	Neutral alpha-glucosidase AB (Fragment) OS=Ophiophagus	OPHHA	6
973	10.76	10.76	81.25	62.5	51.25	tr V8N1C7 V8N1C7_OPHHA	Tropomyosin beta chain (Fragment) OS=Ophiophagus hannah	OPHHA	8
974	10.72	10.72	43.23	13.06	11.04	tr V8PID4 V8PID4_OPHHA	5-aminolevulinate synthase (Fragment) OS=Ophiophagus ha	OPHHA	5
975	10.71	10.71	56.15	7.282	6.634	tr V8PGN6 V8PGN6_OPHHA	Cingulin-like protein 1 (Fragment) OS=Ophiophagus hanna	OPHHA	6
976	10.7	10.7	64.09	17.41	13.29	tr V8PGX6 V8PGX6_OPHHA	Protein phosphatase 1 regulatory subunit 21 (Fragment)	OPHHA	6
977	10.69	10.69	38.94	26.84	22.42	tr V8N1J6 V8N1J6_OPHHA	Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=	OPHHA	6
978	10.66	12.53	78.89	30.15	24.62	tr V8NYS7 V8NYS7_OPHHA	GTPase KRas (Fragment) OS=Ophiophagus hannah GN=KRAS	PE= OPHHA	6
979	10.66	10.66	40.32	7.111	3.576	tr V8NXB9 V8NXB9_OPHHA	Cullin-9 OS=Ophiophagus hannah GN=CUL9 PE=3 SV=1	OPHHA	7
980	10.66	10.66	71.27	32.73	28.36	tr V8NE97 V8NE97_OPHHA	Crk-like protein (Fragment) OS=Ophiophagus hannah GN=Cr	OPHHA	5
981	10.65	10.65	67.1	27.69	18.24	tr V8P180 V8P180_OPHHA	ELKS/Rab6-interacting/CAST family member 1 OS=Ophiophag	OPHHA	5
982	10.65	10.65	48.6	25.86	25.55	tr V8PC36 V8PC36_OPHHA	Heme oxygenase 2 (Fragment) OS=Ophiophagus hannah GN=Hm	OPHHA	5
983	10.64	10.64	69.44	20.3	15.17	tr V8PDA4 V8PDA4_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	5
984	10.64	10.64	63.9	41.95	37.56	tr V8NGZ7 V8NGZ7_OPHHA	Ran-specific GTPase-activating protein (Fragment) OS=Op	OPHHA	5
985	10.64	10.64	65.14	28.57	28.57	tr V8NYF0 V8NYF0_OPHHA	Low molecular weight phosphotyrosine protein phosphatas	OPHHA	6
986	10.62	10.62	80.15	31.99	31.99	tr V8NVP2 V8NVP2_OPHHA	cAMP-dependent protein kinase type II-alpha regulatory	OPHHA	6
987	10.61	10.61	40.72	18.57	7.84	tr V8NTM4 V8NTM4_OPHHA	Tubulin--tyrosine ligase-like protein 12 (Fragment) OS=	OPHHA	4
988	10.59	10.71	58.67	22.38	14.92	tr V8PB17 V8PB17_OPHHA	WD40 repeat-containing protein SMU1 OS=Ophiophagus hann	OPHHA	6
989	10.57	13.29	39.14	16.44	14.87	tr V8PG83 V8PG83_OPHHA	Coronin OS=Ophiophagus hannah GN=Coro1b PE=3 SV=1	OPHHA	6
990	10.57	10.57	33.47	8.566	8.566	tr V8NIS7 V8NIS7_OPHHA	Glutathione reductase, mitochondrial (Fragment) OS=Ophi	OPHHA	6
991	10.56	10.56	43.41	12.52	9.683	tr V8PG77 V8PG77_OPHHA	cAMP-dependent protein kinase catalytic subunit alpha (	OPHHA	6
992	10.53	10.53	42.13	3	2.562	tr V8PHV8 V8PHV8_OPHHA	Laminin subunit alpha-3 (Fragment) OS=Ophiophagus hanna	OPHHA	6
993	10.52	10.52	60.3	24.12	15.33	tr V8NFU6 V8NFU6_OPHHA	Ornithine aminotransferase, mitochondrial OS=Ophiophagu	OPHHA	5
994	10.51	10.51	45.78	11.41	10.31	tr V8ND09 V8ND09_OPHHA	Alpha-fetoprotein (Fragment) OS=Ophiophagus hannah GN=A	OPHHA	6
995	10.49	10.49	68.35	22.78	21.01	tr V8NQ06 V8NQ06_OPHHA	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, Pyruvate	5	
996	10.46	10.46	57.03	19.63	15.15	tr V8P6A7 V8P6A7_OPHHA	Peptidylprolyl isomerase domain and WD repeat-containin	OPHHA	5
997	10.46	10.46	62.5	31.25	22.5	tr V8P7L5 V8P7L5_OPHHA	Clahtin light chain B (Fragment) OS=Ophiophagus hannah	OPHHA	5
998	10.45	10.45	43.93	10.47	6.769	tr V8NSD0 V8NSD0_OPHHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345_0	OPHHA	4
999	10.41	10.41	58.31	13.52	8.632	tr V8P6E1 V8P6E1_OPHHA	Nexilin OS=Ophiophagus hannah GN=NEXN PE=4 SV=1	OPHHA	6
1000	10.4	10.4	69.49	57.63	57.63	tr V8P2J2 V8P2J2_OPHHA	Myotrophin OS=Ophiophagus hannah GN=MTNP PE=4 SV=1	OPHHA	7
1001	10.39	10.39	54.6	17.77	16.48	tr V8NHK5 V8NHK5_OPHHA	Fragile X mental retardation syndrome-related protein 1	OPHHA	6
1002	10.38	10.38	44.85	20.39	15.88	tr V8PFF6 V8PFF6_OPHHA	Splicing factor U2AF 65 kDa subunit OS=Ophiophagus hann	OPHHA	5
1003	10.37	10.37	45.85	12.1	6.567	tr V8P5Q9 V8P5Q9_OPHHA	Epidermal growth factor receptor substrate 15-like 1 OS	OPHHA	5
1004	10.36	10.36	54.38	22.96	19.03	tr V8NA46 V8NA46_OPHHA	Long-chain-fatty-acid--CoA ligase 1 (Fragment) OS=Ophi	OPHHA	5
1005	10.35	10.35	41.24	12.21	10.06	tr V8POK6 V8POK6_OPHHA	GRB2-associated-binding protein 1 (Fragment) OS=Ophioph	OPHHA	5
1006	10.32	10.32	28.48	28.48	23.42	tr V8PH92 V8PH92_OPHHA	Transcription factor BTF3 OS=Ophiophagus hannah GN=BTF3	OPHHA	6
1007	10.31	12.27	47.09	6.757	4.938	tr V8P243 V8P243_OPHHA	Coagulation factor V OS=Ophiophagus hannah GN=F5 PE=4 S	OPHHA	7
1008	10.3	10.3	29.73	14.23	10.63	tr V8NHS0 V8NHS0_OPHHA	WW domain-binding protein 11 (Fragment) OS=Ophiophagus	OPHHA	5
1009	10.3	10.3	49.83	19.47	16.17	tr V8NZX6 V8NZX6_OPHHA	Methionine adenosyltransferase 2 subunit beta (Fragment)	OPHHA	5
1010	10.29	10.29	57.62	31.1	17.68	tr V8NTY6 V8NTY6_OPHHA	Calcium/calmodulin-dependent protein kinase type 1 OS=O	OPHHA	5
1011	10.28	14.71	37.27	14	11.58	tr V8PD88 V8PD88_OPHHA	Disks large-like 1 (Fragment) OS=Ophiophagus hannah GN=	OPHHA	7
1012	10.27	38.56	63.49	27.85	23.14	tr V8NH89 V8NH89_OPHHA	Elongation factor 2 OS=Ophiophagus hannah GN=EEF2 PE=4	OPHHA	19
1013	10.27	10.27	52.15	28.65	14.33	tr V8NW96 V8NW96_OPHHA	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma (F	OPHHA	5
1014	10.27	10.27	45.17	27.1	14.08	tr V8NBF0 V8NBF0_OPHHA	Basement membrane-specific heparan sulfate proteoglycan	OPHHA	4
1015	10.26	10.26	44.93	17.6	12.63	tr V8P4S1 V8P4S1_OPHHA	Ufm1-specific protease 2 OS=Ophiophagus hannah GN=UFS2	OPHHA	5
1016	10.26	10.26	43.01	22.43	13.19	tr V8NED4 V8NED4_OPHHA	COP9 signalosome complex subunit 5 (Fragment) OS=Ophi	OPHHA	6
1017	10.26	10.26	46.25	19.22	19.22	tr V8NJ04 V8NJ04_OPHHA	Toll-interacting protein (Fragment) OS=Ophiophagus hann	OPHHA	6
1018	10.25	10.25	42.01	18.26	17.35	tr V8PGD5 V8PGD5_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	6
1019	10.24	10.24	60.38	29.06	18.11	tr V8NDS4 V8NDS4_OPHHA	Transmembrane emp24 domain-containing protein 7 (Fragme	OPHHA	5
1020	10.21	10.21	44.8	19.89	13.8	tr V8NXB2 V8NXB2_OPHHA	WD repeat-containing protein 26 (Fragment) OS=Ophiophag	OPHHA	5
1021	10.21	10.21	53.2	23.23	19.53	tr V8NUX4 V8NUX4_OPHHA	Tetratricopeptide repeat protein 35 OS=Ophiophagus hann	OPHHA	5
1022	10.2	10.21	48.24	32.94	32.94	tr V8PFF0 V8PFF0_OPHHA	Glutamate--cysteine ligase regulatory subunit OS=Ophioph	OPHHA	5
1023	10.2	10.2	60	30.37	30.37	tr V8P1A5 V8P1A5_OPHHA	Alpha-aminoadipic semialdehyde dehydrogenase (Fragment)	OPHHA	9
1024	10.19	10.19	62.84	10.14	7.239	tr V8PGN4 V8PGN4_OPHHA	Sister chromatid cohesion protein PDS5-like B (Fragment)	OPHHA	5
1025	10.19	10.19	47.64	13.21	7.547	tr V8NPB4 V8NPB4_OPHHA	Nucleoporin p54 (Fragment) OS=Ophiophagus hannah GN=NUP	OPHHA	5
1026	10.18	10.18	44.79	17.08	15	tr V8NTB8 V8NTB8_OPHHA	Cleavage stimulation factor subunit 1 (Fragment) OS=Oph	OPHHA	5
1027	10.17	10.17	35.98	9.382	7.395	tr V8NZ10 V8NZ10_OPHHA	Serine/threonine-protein kinase Nek9 (Fragment) OS=Ophi	OPHHA	5
1028	10.17	10.17	52.16	19.85	17.3	tr V8P043 V8P043_OPHHA	Transmembrane protein 43 OS=Ophiophagus hannah GN=Tmem4	OPHHA	6
1029	10.16	10.16	52.35	19.71	17.06	tr V8NAX3 V8NAX3_OPHHA	Beta-1,4-galactosyltransferase 1 OS=Ophiophagus hannah	OPHHA	5
1030	10.14	10.14	60.91	28.81	28.81	tr V8NJA6 V8NJA6_OPHHA	rRNA 2'-O-methyltransferase fibrillarin OS=Ophiophagus	OPHHA	8
1031	10.14	10.14	45.28	26.95	20.49	tr V8PGR8 V8PGR8_OPHHA	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, Pyruvate	5	
1032	10.13	12.44	62.35	25.67	17.85	tr V8NEK3 V8NEK3_OPHHA	Ras GTPase-activating-like protein IQGAP3 (Fragment) OS	OPHHA	8
1033	10.13	10.13	43.09	23.58	17.07	tr V8NZW7 V8NZW7_OPHHA	Prolargin OS=Ophiophagus hannah GN=Prelp PE=4 SV=1	OPHHA	8
1034	10.13	10.13	38.98	12.47	10.24	tr V8P672 V8P672_OPHHA	Sequestosome-1 (Fragment) OS=Ophiophagus hannah GN=SQST	OPHHA	5
1035	10.12	10.28	49.59	35.66	31.97	tr V8NFP1 V8NFP1_OPHHA	Adapter molecule crk (Fragment) OS=Ophiophagus hannah G	OPHHA	6
1036	10.12	10.17	34.99	17.97	17.97	tr V8P1A7 V8P1A7_OPHHA	Kynurenine/alpha-aminoadipate aminotransferase, mitoch	OPHHA	5
1037	10.09	10.09	40.58	9.682	5.504	tr V8NXX4 V8NXX4_OPHHA	Tensin-like C1 domain-containing phosphatase (Fragment)	OPHHA	5
1038	10.08	10.09	43.65	6.781	3.375	tr V8N9B6 V8N9B6_OPHHA	Epiplakin (Fragment) OS=Ophiophagus hannah GN=Eppkl PE=	OPHHA	7
1039	10.07	10.07	31.9	9.348	4.803	tr V8PBP3 V8PBP3_OPHHA	Elongator complex protein 1 (Fragment) OS=Ophiophagus h	OPHHA	4
1040	10.06	10.06	46.86	20.42	17.28	tr V8NZW4 V8NZW4_OPHHA	E3 ubiquitin-protein ligase ARIH1 (Fragment) OS=Ophioph	OPHHA	6
1041	10.05	10.05	66.18	44.85	44.85	tr V8PAR8 V8PAR8_OPHHA	60S ribosomal protein L27 OS=Ophiophagus hannah GN=RPL2	OPHHA	6
1042	10.04	16.72	69.26	28.79	28.79	tr V8NL10 V8NL10_OPHHA	Ras-related protein Rap-1A OS=Ophiophagus hannah GN=RAP	OPHHA	8
1043	10.04	10.04							

1050	10	10.05	34.3	19.83	19.83	tr	V8NDL5	V8NDL5_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	8
1051	10	10.04	42.83	6.528	6.528	tr	V8PB93	V8PB93_OPHHA	Coiled-coil and C2 domain-containing protein 1A OS=Ophi OPHHA	5
1052	10	10	62.45	45.57	36.71	tr	V8P3W5	V8P3W5_OPHHA	Transcriptional activator protein Pur-alpha (Fragment) OPHHA	5
1053	10	10	46.15	21.28	21.28	tr	V8NC88	V8NC88_OPHHA	Protein NDRG1 (Fragment) OS=Ophiophagus hannah GN=NdrG1 OPHHA	10
1054	10	10	12.91	4.719	4.719	tr	V8NRB7	V8NRB7_OPHHA	Nascent polypeptide-associated complex subunit alpha, m OPHHA	6
1055	10	10	77.71	41.57	41.57	tr	V8PD17	V8PD17_OPHHA	Protein canopy-like 2 (Fragment) OS=Ophiophagus hannah OPHHA	5
1056	10	10	20.39	11.78	11.78	tr	V8NI55	V8NI55_OPHHA	Ubiquitin-4 (Fragment) OS=Ophiophagus hannah GN=UBQLN4 OPHHA	5
1057	10	10	83.33	71.93	71.93	tr	V8NA13	V8NA13_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	6
1058	10	10	35.09	35.09	35.09	tr	V8NE16	V8NE16_OPHHA	Cell division control protein 42-like protein OS=Ophiophagus hanna OPHHA	5
1059	9.98	10	47.98	16.83	11.68	tr	V8PGL4	V8PGL4_OPHHA	Glycerol-3-phosphate dehydrogenase (Fragment) OS=Ophiophagus hanna OPHHA	5
1060	9.98	10	57.19	30.48	20.55	tr	V8N9B0	V8N9B0_OPHHA	Glycerol kinase OS=Ophiophagus hannah GN=Gk PE=4 SV=1 OPHHA	5
1061	9.98	9.98	37.05	3.929	3.047	tr	V8PGR1	V8PGR1_OPHHA	Talin-2 (Fragment) OS=Ophiophagus hannah GN=TLN2 PE=4 S OPHHA	5
1062	9.96	9.96	64.31	6.403	6.403	tr	V8P7W2	V8P7W2_OPHHA	Leucine zipper protein 1 (Fragment) OS=Ophiophagus hanna OPHHA	6
1063	9.96	9.96	37.36	16.76	14.84	tr	V8NGJ3	V8NGJ3_OPHHA	3-hydroxybutyrate dehydrogenase type 2 (Fragment) OS=Op OPHHA	5
1064	9.95	9.95	62.82	19.55	16.03	tr	V8P8X3	V8P8X3_OPHHA	Oxidoreductase HTATIP2 (Fragment) OS=Ophiophagus hannah OPHHA	5
1065	9.92	9.92	54.8	13.18	9.975	tr	V8NFD1	V8NFD1_OPHHA	Rab3 GTPase-activating protein catalytic subunit (Frage OPHHA	6
1066	9.91	9.91	43.54	10.31	7.818	tr	V8NSV1	V8NSV1_OPHHA	SLIT-ROBO Rho GTPase-activating protein 2 OS=Ophiophagus hanna OPHHA	5
1067	9.9	9.9	47.04	7.928	6.66	tr	V8NAC4	V8NAC4_OPHHA	Myosin-If OS=Ophiophagus hannah GN=MYO1F PE=4 SV=1 OPHHA	5
1068	9.9	9.9	52.12	12.22	9.726	tr	V8NVH9	V8NVH9_OPHHA	Basic leucine zipper and W2 domain-containing protein 1 OPHHA	5
1069	9.9	9.9	66.17	35.34	17.67	tr	V8P5J2	V8P5J2_OPHHA	ADP-ribosylation factor-like protein 8A (Fragment) OS=O OPHHA	5
1070	9.89	9.89	58.24	24.18	20.51	tr	V8P9B8	V8P9B8_OPHHA	Arf-GAP with dual PH domain-containing protein 1 (Fragm OPHHA	5
1071	9.88	9.88	53.68	8.655	7.836	tr	V8P7D0	V8P7D0_OPHHA	Ras GTPase-activating protein 1 (Fragment) OS=Ophiophag OPHHA	5
1072	9.88	9.88	53.34	13.5	8.422	tr	V8PG40	V8PG40_OPHHA	Lon protease homolog (Fragment) OS=Ophiophagus hannah G OPHHA	5
1073	9.88	9.88	33	11.4	7.8	tr	V8NLA0	V8NLA0_OPHHA	Heparin cofactor 2 (Fragment) OS=Ophiophagus hannah GN= OPHHA	6
1074	9.88	9.88	49.45	22.18	16.36	tr	V8POG1	V8POG1_OPHHA	COP9 signalosome complex subunit 7a (Fragment) OS=Ophi OPHHA	5
1075	9.87	9.87	43.33	11.45	11.3	tr	V8PCW5	V8PCW5_OPHHA	Calcium/calmodulin-dependent protein kinase type II sub OPHHA	5
1076	9.87	9.87	47.12	19.11	14.66	tr	V8P6R7	V8P6R7_OPHHA	Golgi resident protein GCP60 (Fragment) OS=Ophiophagus OPHHA	6
1077	9.86	9.86	65.85	37.98	29.97	tr	V8P1U9	V8P1U9_OPHHA	Axin interactor, dorsalization-associated protein OS=Op OPHHA	6
1078	9.85	9.85	50.38	20.46	20.46	tr	V8P7A6	V8P7A6_OPHHA	SWI/SNF-related matrix-associated actin-dependent regul OPHHA	6
1079	9.85	9.85	69.15	23.4	22.87	tr	V8N7G8	V8N7G8_OPHHA	ATP synthase subunit gamma, mitochondrial (Fragment) OS OPHHA	7
1080	9.81	9.81	38.81	14.93	13.22	tr	V8NHC7	V8NHC7_OPHHA	Puromycin-sensitive aminopeptidase (Fragment) OS=Ophiophagus hanna OPHHA	8
1081	9.8	9.8	40.52	5.043	3.668	tr	V8NBP2	V8NBP2_OPHHA	Transcriptional repressor CTCF (Fragment) OS=Ophiophagu OPHHA	5
1082	9.79	9.79	47.84	24.46	15.29	tr	V8N597	V8N597_OPHHA	Glutamate carboxypeptidase 2 (Fragment) OS=Ophiophagus OPHHA	5
1083	9.79	9.79	31.94	17.37	17.17	tr	V8P6L6	V8P6L6_OPHHA	Golgi reassembly-stacking protein 2 (Fragment) OS=Ophi OPHHA	5
1084	9.77	9.77	62.07	35.47	21.18	tr	V8P8S4	V8P8S4_OPHHA	60S ribosomal protein L13a OS=Ophiophagus hannah GN=RPL OPHHA	5
1085	9.77	9.77	69.12	55.15	48.53	tr	V8NG47	V8NG47_OPHHA	Ubiquitin-conjugating enzyme E2 L3 OS=Ophiophagus hanna OPHHA	5
1086	9.76	9.76	63.18	17.81	10.93	tr	V8P470	V8P470_OPHHA	Pre-mRNA-splicing factor RBM22 (Fragment) OS=Ophiophagu OPHHA	5
1087	9.76	9.76	43.24	17.3	17.3	tr	V8N0M4	V8N0M4_OPHHA	3-hydroxyanthranilate 3,4-dioxygenase OS=Ophiophagus ha OPHHA	7
1088	9.74	9.74	30.14	19.39	13.55	tr	V8N830	V8N830_OPHHA	Tetratricopeptide repeat protein 39B (Fragment) OS=Ophi OPHHA	5
1089	9.74	9.74	41.4	32.36	27.41	tr	V8NST7	V8NST7_OPHHA	Geranylgeranyl transferase type-2 subunit alpha (Fragme OPHHA	6
1090	9.73	9.73	73.64	59.09	50.91	tr	V8NJ67	V8NJ67_OPHHA	Neutral alpha-glucosidase AB (Fragment) OS=Ophiophagus OPHHA	7
1091	9.72	9.72	48.43	17.66	17.66	tr	V8P772	V8P772_OPHHA	Hsc70-interacting protein OS=Ophiophagus hannah GN=ST13 OPHHA	5
1092	9.71	9.71	47.1	18.55	9.355	tr	V8P4E6	V8P4E6_OPHHA	Neurolysin, mitochondrial OS=Ophiophagus hannah GN=NLN OPHHA	4
1093	9.7	9.7	45.54	20.06	11.78	tr	V8P114	V8P114_OPHHA	Proteasome subunit alpha type-1 (Fragment) OS=Ophiophag OPHHA	7
1094	9.69	9.76	43.17	8.314	8.314	tr	V8NL22	V8NL22_OPHHA	Canalicular multispecific organic anion transporter 2 (OPHHA	5
1095	9.68	10.46	40.02	10.78	7.559	tr	V8P546	V8P546_OPHHA	Conserved oligomeric Golgi complex subunit 1 (Fragment) OPHHA	5
1096	9.68	9.68	53.02	31.03	27.16	tr	V8NN10	V8NN10_OPHHA	Coiled-coil domain-containing protein OS=Ophiophagus ha OPHHA	9
1097	9.67	9.67	49.82	18.6	18.6	tr	V8NNA3	V8NNA3_OPHHA	2,4-dienoyl-CoA reductase, mitochondrial OS=Ophiophagus OPHHA	7
1098	9.66	9.66	37.87	7.534	5.479	tr	V8PF71	V8PF71_OPHHA	Integrin alpha-3 (Fragment) OS=Ophiophagus hannah GN=It OPHHA	5
1099	9.66	9.66	60.85	20.11	18.25	tr	V8P612	V8P612_OPHHA	Adipocyte plasma membrane-associated protein (Fragment) OPHHA	8
1100	9.65	9.65	39.34	16.39	14.21	tr	V8P2J9	V8P2J9_OPHHA	Mitogen-activated protein kinase 9 (Fragment) OS=Ophiophagus hanna OPHHA	5
1101	9.65	9.65	58.96	39.15	33.96	tr	V8P2U4	V8P2U4_OPHHA	Dihydropyrimidine dehydrogenase [NADP+] (Fragment) OS=O NADP+	5
1102	9.62	9.66	64.43	5.023	2.91	tr	V8NRZ7	V8NRZ7_OPHHA	Golgin subfamily B member 1 OS=Ophiophagus hannah GN=GO OPHHA	6
1103	9.62	9.62	37.68	13.37	8.535	tr	V8NP36	V8NP36_OPHHA	NEDD8 ultimate buster 1 (Fragment) OS=Ophiophagus hanna OPHHA	4
1104	9.62	9.62	37.87	25.6	25.6	tr	V8NBA3	V8NBA3_OPHHA	Ubiquitin-like modifier-activating enzyme 5 OS=Ophiophagus hanna OPHHA	5
1105	9.6	9.6	40.8	19.4	15.67	tr	V8PAV4	V8PAV4_OPHHA	Arfaptin-1 OS=Ophiophagus hannah GN=ARF1P1 PE=4 SV=1 OPHHA	5
1106	9.58	11.97	61.36	13.45	11.59	tr	V8NLF1	V8NLF1_OPHHA	Rho-associated protein kinase 1 (Fragment) OS=Ophiophag OPHHA	7
1107	9.58	9.58	49.55	18.75	12.28	tr	V8P144	V8P144_OPHHA	Gamma-butyrobetaine dioxygenase (Fragment) OS=Ophiophag OPHHA	5
1108	9.57	9.57	53.88	18.93	18.93	tr	V8PAF7	V8PAF7_OPHHA	Ras-related protein Ral-B OS=Ophiophagus hannah GN=RALB OPHHA	5
1109	9.55	9.55	49.79	31.22	31.22	tr	V8PF10	V8PF10_OPHHA	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Ophiophagus h OPHHA	6
1110	9.51	9.51	86.07	55.74	55.74	tr	V8P885	V8P885_OPHHA	Mitochondrial peptide methionine sulfoxide reductase (F OPHHA	5
1111	9.5	9.5	88.18	25	25	tr	V8NDE5	V8NDE5_OPHHA	Protein CDV3-like protein (Fragment) OS=Ophiophagus han OPHHA	5
1112	9.49	9.49	43.97	17.59	11.45	tr	V8NNU3	V8NNU3_OPHHA	60 kDa SS-A/Ro ribonucleoprotein (Fragment) OS=Ophiophagus hanna OPHHA	4
1113	9.48	9.48	33.62	7.866	6.789	tr	V8NIV0	V8NIV0_OPHHA	Periodic tryptophan protein 2-like protein (Fragment) O OPHHA	4
1114	9.47	9.47	51.14	11.14	11.14	tr	V8NXA3	V8NXA3_OPHHA	Ephexin-1 (Fragment) OS=Ophiophagus hannah GN=NEEF PE=4 OPHHA	5
1115	9.47	9.47	42.16	18.38	11.8	tr	V8NJR5	V8NJR5_OPHHA	SUMO-activating enzyme subunit 2 (Fragment) OS=Ophiophagus hanna OPHHA	5
1116	9.47	9.47	61.26	20.95	20.95	tr	V8PGA4	V8PGA4_OPHHA	DnaJ-like subfamily A member 2 (Fragment) OS=Ophiophagu OPHHA	5
1117	9.46	9.46	48.42	19.72	10.04	tr	V8NUT2	V8NUT2_OPHHA	Beta-galactosidase (Fragment) OS=Ophiophagus hannah GN= OPHHA	4
1118	9.45	9.45	34.67	17.11	15.11	tr	V8NU48	V8NU48_OPHHA	Tubulin gamma chain (Fragment) OS=Ophiophagus hannah GN OPHHA	5
1119	9.44	9.44	49.59	4.508	3.864	tr	V8PF55	V8PF55_OPHHA	Nicotinamide N-methyltransferase (Fragment) OS=Ophiophagus hanna OPHHA	7
1120	9.43	9.43	82.57	51.38	47.71	tr	V8P9P7	V8P9P7_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	10
1121	9.4	9.4	44.65	33.49	21.86	tr	V8NA53	V8NA53_OPHHA	Tricarboxylate transport protein, mitochondrial (Fragme OPHHA	4
1122	9.4	9.4	38.76	25.73	23.45	tr	V8NLO8	V8NLO8_OPHHA	[Protein ADP-ribosylarginine] hydrolase (Fragment) OS=O Protein /	5
1123	9.36	9.36	42	8.243	7.556	tr	V8NS56	V8NS56_OPHHA	Complement component C6 (Fragment) OS=Ophiophagus hanna OPHHA	5
1124	9.36	9.36	29.71	11.21	11.21	tr	V8PC05	V8PC05_OPHHA	Carbonic anhydrase 14 (Fragment) OS=Ophiophagus hannah OPHHA	5
1125	9.36	9.36	39.88	24.86	21.39	tr	V8NJ50	V8NJ50_OPHHA	Enoyl-CoA delta isomerase 2, mitochondrial (Fragment) O OPHHA	6
1126	9.35	9.35	69.85	22.3	19.61	tr	V8NUE1	V8NUE1_OPHHA	ADP-ribosylation factor GTPase-activating protein 3 OS= OPHHA	6
1127	9.35	9.35	36.59	12.04	7.165	tr	V8NKJ4	V8NKJ4_OPHHA	Palladin (Fragment) OS=Ophiophagus hannah GN=PALLD PE=4 OPHHA	4
1128	9.33	9.33	50.96	18.26	12.74	tr	V8N966	V8N966_OPHHA	FAD synthase OS=Ophiophagus hannah GN=fladl PE=4 SV=1 OPHHA	4
1129	9.32	9.32	34.61	6.435	5.565	tr	V8NVE0	V8NVE0_OPHHA	Integrin alpha-6 (Fragment) OS=Ophiophagus hannah GN=IT OPHHA	5
1130	9.31	9.31	35.75	14.25	11.25	tr	V8NMK4	V8NMK4_OPHHA	Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPHHA	5
1131	9.31	9.31	85.85	62.26	62.26	tr	V8P334	V8P334_OPHHA	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OPHHA	5
1132	9.29	9.29	56.67	18.15	15.56	tr	V8NJT5	V8NJT5_OPHHA	Regulator of microtubule dynamics protein 1 (Fragment) OPHHA	5
1133	9.28	9.28	67.47	45.78	45.78	tr	V8N9Z2	V8N9Z2_OPHHA	40S ribosomal protein S21 OS=Ophiophagus hannah GN=RPS2 OPHHA	6
1134	9.26	9.26	42.15	12.65	7.728	tr	V8NE12	V8NE12_OPHHA	Elongation factor 1-gamma OS=Ophiophagus hannah GN=EEF1 OPHHA	5
1135	9.26	9.26	23.78	14.23	14.23	tr	V8P1B3	V8P1B3_OPHHA	Transmembrane 9 superfamily member 3 OS=Ophiophagus han OPHHA	6
1136	9.23	10.14	40.42	10.53	8.626	tr	V8PFG1	V8PFG1_OPHHA	Ubiquitin-protein ligase E3C (Fragment) OS=Ophiophagus OPHHA	6
1137	9.23	9.23	44.94	7.23	7.23	tr	V8NCV9	V8NCV9_OPHHA	Cytochrome protein OS=Ophiophagus hannah GN=CYP1A5 PE=4 OPHHA	6
1138	9.23	9.23	63.66	20.94	13.55	tr	V8P6T4	V8P6T4_OPHHA	G patch domain and KOW motifs-containing protein OS=Oph OPHHA	4
1139	9.22	9.23	46.74	9.309	6.046	tr	V8NR95	V8NR95_OPHHA	Exocyst complex component 1 (Fragment) OS=Ophiophagus h OPHHA	4
1140	9.22	9.22	41.74	11.41	9.933	tr	V8P4G1	V8P4G1_OPHHA	Oxysterol-binding protein OS=Ophiophagus hannah GN=OSBP OPHHA	5
1141	9.22	9.22	48.98	17.01	12.5	tr	V8PCU4	V8PCU4_OPHHA	ADP-ribosylation factor GTPase-activating protein 2 (Fr OPHHA	5
1142	9.21	9.21	55.74	23.83	17.87	tr	V8P358	V8P358_OPHHA	60S ribosomal protein L17 (Fragment) OS=Ophiophagus han OPHHA	5
1143	9.19	9.19	43.97	8.906	5.975	tr	V8P5G7	V8P5G7_OPHHA	Lymphocyte antigen 75 (Fragment) OS=Ophiophagus hannah OPHHA	4
1144	9.19	9.19	64.45	32.7	29.38	tr	V8NI36	V8NI36_OPHHA	Eukaryotic translation initiation factor 4E (Fragment) OPHHA	6
1145	9.18	9.18	59.37	25.94	14.12	tr	V8P218	V8P218_OPHHA	Eukaryotic translation initiation factor 3 subunit H OS OPHHA	4

1146	9.17	9.17	40.71	4.667	4.667	tr V8P5V6 V8P5V6_OPPIHA Elongation factor G, mitochondrial OS=Ophiophagus hanna OPPIHA	5
1147	9.15	10.13	41.48	5.89	4.574	tr V8NX99 V8NX99_OPPIHA Neutral alpha-glucosidase C (Fragment) OS=Ophiophagus h OPPIHA	6
1148	9.14	9.14	47.48	18.83	18.83	tr V8P4X0 V8P4X0_OPPIHA Ubiquitin-conjugating enzyme E2 variant 3 (Fragment) OS OPPIHA	5
1149	9.12	9.12	78.01	23.56	23.56	tr V8P2T8 V8P2T8_OPPIHA Adenylate kinase 2, mitochondrial OS=Ophiophagus hannah OPPIHA	6
1150	9.1	9.1	39.16	18.53	18.18	tr V8P9X8 V8P9X8_OPPIHA S-formylglutathione hydrolase (Fragment) OS=Ophiophagus OPPIHA	5
1151	9.09	9.12	35.32	8.66	6.36	tr V8NHA5 V8NHA5_OPPIHA Glycogen [starch] synthase, muscle OS=Ophiophagus hanna OPPIHA	4
1152	9.09	9.09	50.16	18.47	10.19	tr V8NF47 V8NF47_OPPIHA Ankyrin-1 OS=Ophiophagus hannah GN=ANK1 PE=4 SV=1 OPPIHA	4
1153	9.07	9.07	50.97	6.395	3.391	tr V8P992 V8P992_OPPIHA Interferon-induced helicase C domain-containing protein OPPIHA	4
1154	9.07	9.07	39.55	21.64	21.64	tr V8NRD3 V8NRD3_OPPIHA 5'-AMP-activated protein kinase catalytic subunit alpha OPPIHA	4
1155	9.06	9.06	39.9	15.15	15.15	tr V8NZA8 V8NZA8_OPPIHA Prostaglandin reductase 2 (Fragment) OS=Ophiophagus han OPPIHA	5
1156	9.05	9.05	45.68	13.53	11.47	tr V8NFR6 V8NFR6_OPPIHA Epidermal growth factor receptor OS=Ophiophagus hannah OPPIHA	5
1157	9.04	15.07	67.45	30.54	27.85	tr V8P7Q2 V8P7Q2_OPPIHA GTP-binding protein SAR1b (Fragment) OS=Ophiophagus han OPPIHA	9
1158	9.03	9.03	55.26	19.12	11.4	tr V8NQ87 V8NQ87_OPPIHA BAG family molecular chaperone regulator 3 OS=Ophiophag OPPIHA	4
1159	9.03	9.03	46.77	12.69	12.69	tr V8P8S1 V8P8S1_OPPIHA U1 small nuclear ribonucleoprotein 70 kDa (Fragment) OS OPPIHA	5
1160	9.02	9.02	56.18	14.54	11.16	tr V8NFC4 V8NFC4_OPPIHA Rho guanine nucleotide exchange factor 1 OS=Ophiophagus Rho	5
1161	9.02	9.02	66.93	19.79	12.76	tr V8P5T0 V8P5T0_OPPIHA Short/branched chain specific acyl-CoA dehydrogenase, m OPPIHA	5
1162	9	9	52.46	10.15	8.769	tr V8PFI8 V8PFI8_OPPIHA Cullin-2 (Fragment) OS=Ophiophagus hannah GN=CUL2 PE=3 OPPIHA	5
1163	8.99	9.05	57.08	11.92	9.677	tr V8PJC2 V8PJC2_OPPIHA Transcription initiation factor IIB OS=Ophiophagus hann OPPIHA	6
1164	8.99	8.99	55.86	24.32	24.32	tr V8PE61 V8PE61_OPPIHA Serine/arginine-rich splicing factor 6 OS=Ophiophagus h OPPIHA	8
1165	8.98	8.98	45.91	19.74	10.43	tr V8P618 V8P618_OPPIHA Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS OPPIHA	4
1166	8.98	8.98	58.45	50	32.39	tr V8NGY1 V8NGY1_OPPIHA Phosphatidylethanolamine-binding protein 1 (Fragment) O OPPIHA	4
1167	8.97	8.97	58.35	6.357	6.357	tr V8NIQ8 V8NIQ8_OPPIHA Replication factor C subunit 1 (Fragment) OS=Ophiophagu OPPIHA	5
1168	8.96	8.96	42.52	9.979	5.509	tr V8NQ84 V8NQ84_OPPIHA Papilin (Fragment) OS=Ophiophagus hannah GN=PAPLN PE=4 OPPIHA	5
1169	8.95	8.95	59.7	16.67	16.67	tr V8NJF6 V8NJF6_OPPIHA DnaJ-like subfamily C member 11 (Fragment) OS=Ophiophag OPPIHA	5
1170	8.95	8.95	43.5	23.16	17.51	tr V8P7N3 V8P7N3_OPPIHA Protein FAM45A OS=Ophiophagus hannah GN=FAM45A PE=4 SV= OPPIHA	5
1171	8.94	8.98	53.52	12.74	6.897	tr V8PIL3 V8PIL3_OPPIHA Serine/threonine-protein kinase N2 (Fragment) OS=Ophiop OPPIHA	4
1172	8.94	8.94	35.84	8.117	5.786	tr V8NMT5 V8NMT5_OPPIHA Apoptotic protease-activating factor 1 OS=Ophiophagus h OPPIHA	5
1173	8.94	8.94	44.61	22.68	20.45	tr V8N4R8 V8N4R8_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=L345 I OPPIHA	6
1174	8.93	8.93	36.91	18.06	15.45	tr V8NS44 V8NS44_OPPIHA LanC-like protein 1 OS=Ophiophagus hannah GN=LANCL1 PE= OPPIHA	5
1175	8.91	8.91	43.78	10.04	6.747	tr V8NJK7 V8NJK7_OPPIHA Golgi integral membrane protein 4 (Fragment) OS=Ophioph OPPIHA	4
1176	8.91	8.91	56.3	40.74	29.63	tr V8PBR9 V8PBR9_OPPIHA 60S ribosomal protein L32 OS=Ophiophagus hannah GN=RPL3 OPPIHA	4
1177	8.9	8.9	69.44	20.83	13.66	tr V8NSR1 V8NSR1_OPPIHA 60S ribosomal protein L3 (Fragment) OS=Ophiophagus hann OPPIHA	4
1178	8.88	11.12	82.4	37.77	25.75	tr V8PF48 V8PF48_OPPIHA 14-3-3 protein gamma (Fragment) OS=Ophiophagus hannah G OPPIHA	6
1179	8.87	8.98	42.77	6.423	5.766	tr V8NWE5 V8NWE5_OPPIHA COP9 signalosome complex subunit 2 (Fragment) OS=Ophiop OPPIHA	6
1180	8.87	8.89	54.78	13.04	12.61	tr V8NFT6 V8NFT6_OPPIHA Glutathione S-transferase OS=Ophiophagus hannah GN=L345 OPPIHA	4
1181	8.86	10.97	57.76	18.22	13.25	tr V8PH87 V8PH87_OPPIHA Dihydropyrimidinase (Fragment) OS=Ophiophagus hannah GN OPPIHA	6
1182	8.86	8.87	36.76	13.38	9.296	tr V8PBA8 V8PBA8_OPPIHA RalBP1-associated Eps domain-containing protein 1 OS=Op OPPIHA	6
1183	8.86	8.86	42.75	13.53	13.53	tr V8NLU3 V8NLU3_OPPIHA BRISC complex subunit Abrol OS=Ophiophagus hannah GN=FA OPPIHA	5
1184	8.85	8.86	49.87	4.068	4.068	tr V8NN36 V8NN36_OPPIHA Hydroxyindole O-methyltransferase (Fragment) OS=Ophioph OPPIHA	6
1185	8.85	8.85	48.82	7.649	6.637	tr V8NRD2 V8NRD2_OPPIHA Phosphoinositide phospholipase C (Fragment) OS=Ophioph OPPIHA	5
1186	8.85	8.85	42.25	23.47	23.47	tr V8NPQ0 V8NPQ0_OPPIHA Enoyl-CoA delta isomerase 2, mitochondrial OS=Ophiophag OPPIHA	6
1187	8.84	8.85	47.69	14.97	11.46	tr V8NMM0 V8NMM0_OPPIHA Mitochondrial Rho GTPase 2 OS=Ophiophagus hannah GN=RHO OPPIHA	6
1188	8.84	8.85	47.19	12.19	12.19	tr V8PFW5 V8PFW5_OPPIHA Collagen alpha-1(IV) chain OS=Ophiophagus hannah GN=COL OPPIHA	5
1189	8.84	8.85	43.5	10.77	10.77	tr V8NJP6 V8NJP6_OPPIHA KIF1-binding protein-like protein (Fragment) OS=Ophioph OPPIHA	5
1190	8.83	8.83	19.33	7.692	6.781	tr V8N8H0 V8N8H0_OPPIHA Nuclear pore complex protein Nup98-Nup96 OS=Ophiophagus OPPIHA	4
1191	8.83	8.83	34.53	16.21	10.53	tr V8P0J2 V8P0J2_OPPIHA Dihydrolypoyllysine-residue succinyltransferase compone OPPIHA	6
1192	8.82	8.82	58.52	26.92	20.05	tr V8NH71 V8NH71_OPPIHA Guanine nucleotide-binding protein subunit alpha-11 OS= OPPIHA	5
1193	8.81	8.81	38.47	12.52	9.223	tr V8P1F8 V8P1F8_OPPIHA HBS1-like protein (Fragment) OS=Ophiophagus hannah GN=H OPPIHA	5
1194	8.81	8.81	46.21	15.88	11.55	tr V8NKQ1 V8NKQ1_OPPIHA CWF19-like protein 1 (Fragment) OS=Ophiophagus hannah G OPPIHA	5
1195	8.79	8.8	42.88	5.742	4.773	tr V8NWL8 V8NWL8_OPPIHA Chromodomain-helicase-DNA-binding protein 2 (Fragment) OPPIHA	4
1196	8.79	8.79	64.83	11.31	8.966	tr V8NMY2 V8NMY2_OPPIHA Scaffold attachment factor B1 (Fragment) OS=Ophiophagus OPPIHA	4
1197	8.78	8.78	49.8	20.48	14.46	tr V8NHM5 V8NHM5_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	4
1198	8.78	8.78	41.26	15.38	15.38	tr V8P788 V8P788_OPPIHA Peroxisomal 2,4-dienoyl-CoA reductase OS=Ophiophagus ha OPPIHA	7
1199	8.75	8.75	45.44	8.87	7.898	tr V8NK59 V8NK59_OPPIHA Protein argonaute-1 (Fragment) OS=Ophiophagus hannah GN OPPIHA	5
1200	8.75	8.75	70.11	21.54	12.53	tr V8NI92 V8NI92_OPPIHA SAM domain and HD domain-containing protein 1 (Fragment OPPIHA	4
1201	8.75	8.75	36.19	21.27	18.66	tr V8NHH1 V8NHH1_OPPIHA Nucleophosmin (Fragment) OS=Ophiophagus hannah GN=NPM1 OPPIHA	5
1202	8.74	8.74	54.79	13.79	8.429	tr V8NEN0 V8NEN0_OPPIHA Transferrin receptor protein 1 (Fragment) OS=Ophiophagu OPPIHA	5
1203	8.72	8.73	78.43	48.04	42.16	tr V8NP18 V8NP18_OPPIHA High mobility group protein B1 (Fragment) OS=Ophiophagu OPPIHA	5
1204	8.71	8.71	48.39	10.75	9.677	tr V8NQ17 V8NQ17_OPPIHA Rab GTPase-binding effector protein 1 (Fragment) OS=Oph OPPIHA	6
1205	8.71	8.71	38.5	18.25	15.25	tr V8P760 V8P760_OPPIHA Monoacylglycerol lipase ABHD12 (Fragment) OS=Ophiophagu OPPIHA	4
1206	8.71	8.71	63.2	39.6	35.2	tr V8N7B1 V8N7B1_OPPIHA Guanine nucleotide-binding protein G(I)/G(S)/G(T) subun OPPIHA	5
1207	8.71	8.71	57.14	27.62	27.62	tr V8N8M0 V8N8M0_OPPIHA 60S ribosomal protein L23a (Fragment) OS=Ophiophagus ha OPPIHA	5
1208	8.7	8.86	56.1	15.02	7.981	tr V8NZF6 V8NZF6_OPPIHA WD repeat-containing protein mio (Fragment) OS=Ophioph OPPIHA	5
1209	8.7	8.7	68.23	19.86	17.33	tr V8PF79 V8PF79_OPPIHA Sulfotransferase OS=Ophiophagus hannah GN=SULT1B1 PE=3 OPPIHA	7
1210	8.7	8.7	80.77	33.17	28.37	tr V8NP90 V8NP90_OPPIHA EF-hand domain-containing family member A1 OS=Ophiophag OPPIHA	5
1211	8.67	8.67	42.57	24.57	15.43	tr V8P147 V8P147_OPPIHA Putative 4-hydroxy-2-oxoglutarate aldolase, mitochondri OPPIHA	6
1212	8.66	8.66	51.93	16.57	16.57	tr V8PGU9 V8PGU9_OPPIHA Selenide, water dikinase 1 (Fragment) OS=Ophiophagus ha OPPIHA	5
1213	8.63	8.63	18.69	8.923	5.556	tr V8PGS0 V8PGS0_OPPIHA Epsin-1 (Fragment) OS=Ophiophagus hannah GN=Epn1 PE=4 S OPPIHA	7
1214	8.62	8.62	38.49	11.29	6.022	tr V8PFM7 V8PFM7_OPPIHA Superkiller viralicidic activity 2-like 2 (Fragment) OS OPPIHA	4
1215	8.61	8.61	22.48	19.88	19.88	tr V8PB34 V8PB34_OPPIHA Translocating chain-associated membrane protein 1 (Frag OPPIHA	8
1216	8.59	8.6	58.42	12.63	11.4	tr V8P1V4 V8P1V4_OPPIHA Glycylpeptide N-tetradecanoyltransferase (Fragment) OS= OPPIHA	5
1217	8.58	8.58	54.39	8.667	6.501	tr V8NL95 V8NL95_OPPIHA Phosphatidylinositol 4-kinase alpha (Fragment) OS=Ophi OPPIHA	5
1218	8.58	8.58	46.07	16.57	11.8	tr V8P6H2 V8P6H2_OPPIHA Cat eye syndrome critical region protein 5 (Fragment) O OPPIHA	4
1219	8.57	8.73	41.62	9.714	5.524	tr V8PBU7 V8PBU7_OPPIHA Cystathionine beta-synthase (Fragment) OS=Ophiophagus h OPPIHA	5
1220	8.57	8.57	60.74	38.43	23.14	tr V8NBZ0 V8NBZ0_OPPIHA Ubiquitin thioesterase OTUB1 (Fragment) OS=Ophiophagus OPPIHA	4
1221	8.57	8.57	52.94	23.53	23.04	tr V8P869 V8P869_OPPIHA Serine/arginine-rich splicing factor 12 (Fragment) OS=O OPPIHA	5
1222	8.56	8.56	63.16	24.01	24.01	tr V8N8W5 V8N8W5_OPPIHA ELAV-like protein 1 (Fragment) OS=Ophiophagus hannah GN OPPIHA	6
1223	8.56	8.56	53.48	14.34	9.426	tr V8NEM7 V8NEM7_OPPIHA Target of Myb protein 1 OS=Ophiophagus hannah GN=TOM1 P OPPIHA	5
1224	8.55	8.58	45.03	6.277	3.656	tr V8PA85 V8PA85_OPPIHA Inad-like protein (Fragment) OS=Ophiophagus hannah GN=I OPPIHA	4
1225	8.54	8.57	63.79	5.212	4.587	tr V8NPP9 V8NPP9_OPPIHA FYVE and coiled-coil domain-containing protein 1 OS=Oph OPPIHA	6
1226	8.53	8.54	52.03	8.102	6.077	tr V8NY13 V8NY13_OPPIHA E3 ubiquitin-protein ligase BRE1A OS=Ophiophagus hannah OPPIHA	4
1227	8.53	8.53	45.76	19.56	17.34	tr V8NJJ7 V8NJJ7_OPPIHA Sulfotransferase (Fragment) OS=Ophiophagus hannah GN=Su OPPIHA	5
1228	8.52	8.52	55.9	28.13	19.79	tr V8NZN1 V8NZN1_OPPIHA Aldose 1-epimerase (Fragment) OS=Ophiophagus hannah GN= OPPIHA	4
1229	8.5	8.5	55.88	21.76	15.59	tr V8NDL2 V8NDL2_OPPIHA Vinexin (Fragment) OS=Ophiophagus hannah GN=SORBS3 PE=4 OPPIHA	4
1230	8.5	8.5	50.66	17.11	17.11	tr V8N1L4 V8N1L4_OPPIHA Putative deoxyribose-phosphate aldolase OS=Ophiophagus OPPIHA	5
1231	8.48	11.77	62.44	36.1	36.1	tr V8NN41 V8NN41_OPPIHA Ras-related protein Rab-1A OS=Ophiophagus hannah GN=RAB OPPIHA	9
1232	8.48	9.64	38.76	6.435	4.921	tr V8NEG2 V8NEG2_OPPIHA KN motif and ankyrin repeat domain-containing protein 1 OPPIHA	5
1233	8.47	8.47	78.73	35.29	25.34	tr V8P071 V8P071_OPPIHA Proteasome subunit beta type OS=Ophiophagus hannah GN=P OPPIHA	4
1234	8.46	8.57	29.53	6.345	5.076	tr V8NX16 V8NX16_OPPIHA Tyrosine-protein phosphatase non-receptor type 23 (Frag OPPIHA	5
1235	8.46	8.46	51.15	4.287	4.287	tr V8NVC6 V8NVC6_OPPIHA Collagen alpha-2(IV) chain (Fragment) OS=Ophiophagus ha OPPIHA	6
1236	8.45	8.45	71.12	22.09	12.38	tr V8NAS8 V8NAS8_OPPIHA Leucine-rich repeat flightless-interacting protein 2 (F OPPIHA	5
1237	8.45	8.45	31.98	19.77	15.99	tr V8P5D6 V8P5D6_OPPIHA Beta-1,3-glucosyltransferase (Fragment) OS=Ophiophagus OPPIHA	5
1238	8.44	8.44	52.31	18.46	16.15	tr V8NKR4 V8NKR4_OPPIHA Pyruvate dehydrogenase protein X component, mitochondri OPPIHA	4
1239	8.43	8.43	63.39	45.36	37.16	tr V8NR61 V8NR61_OPPIHA Lactoylglutathione lyase OS=Ophiophagus hannah GN=Glo1 OPPIHA	5
1240	8.43	8.43	46.52	24.6	19.79	tr V8P4F1 V8P4F1_OPPIHA Eukaryotic translation initiation factor 3 subunit J (F OPPIHA	4
1241	8.42	8.42	62.68	6.856	2.781	tr V8NQ79 V8NQ79_OPPIHA A-kinase anchor protein 9 (Fragment) OS=Ophiophagus han OPPIHA	4

1242	8.42	8.42	55.94	23.27	18.81	tr V8NYM1 V8NYM1_OPHPHA Trans-2,3-enoyl-CoA reductase (Fragment) OS=Ophiophagus OPHPHA	5
1243	8.41	9.29	37.14	13.93	6.786	tr V8P3P7 V8P3P7_OPHPHA TBC1 domain family member 15 (Fragment) OS=Ophiophagus OPHPHA	3
1244	8.41	8.41	39.03	4.865	3.106	tr V8P902 V8P902_OPHPHA Lipopolysaccharide-responsive and beige-like anchor pro OPHPHA	4
1245	8.41	8.41	39.55	7.872	4.568	tr V8NUS7 V8NUS7_OPHPHA Nuclear pore complex protein (Fragment) OS=Ophiophagus OPHPHA	4
1246	8.4	8.4	51.16	18.82	8.879	tr V8NRZ9 V8NRZ9_OPHPHA Tryptophanyl-tRNA synthetase, cytoplasmic OS=Ophiophagu OPHPHA	3
1247	8.4	8.4	43.09	19.29	14.79	tr V8N181 V8N181_OPHPHA Ferritin OS=Ophiophagus hannah GN=L345_I2574 PE=3 SV=1 OPHPHA	4
1248	8.39	8.48	59.47	27.24	14.95	tr V8NLNO V8NLNO_OPHPHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHPHA	5
1249	8.39	8.39	46.77	12.9	11.29	tr V8PAV1 V8PAV1_OPHPHA Putative carboxypeptidase PM20D1 (Fragment) OS=Ophiophag OPHPHA	4
1250	8.39	8.39	35.69	29.58	26.37	tr V8NQM7 V8NQM7_OPHPHA Acetyl-CoA acetyltransferase, cytosolic (Fragment) OS=O OPHPHA	6
1251	8.38	8.38	48.31	11.59	6.039	tr V8PBC4 V8PBC4_OPHPHA Rho guanine nucleotide exchange factor 7 (Fragment) OS= OPHPHA	4
1252	8.37	8.37	41.48	3.564	3.049	tr V8PHT2 V8PHT2_OPHPHA A-kinase anchor protein 13 (Fragment) OS=Ophiophagus ha OPHPHA	7
1253	8.37	8.37	55.56	13.07	12.75	tr V8NNV1 V8NNV1_OPHPHA Mitochondrial import inner membrane translocase subunit OPHPHA	4
1254	8.37	8.37	65.1	52.35	46.31	tr V8N8J8 V8N8J8_OPHPHA Dehydrogenase/reductase SDR family member 11 OS=Ophioph OPHPHA	4
1255	8.36	8.36	35.98	8.821	6.046	tr V8POZ2 V8POZ2_OPHPHA Acyl-coenzyme A thioesterase 1 (Fragment) OS=Ophiophagu OPHPHA	4
1256	8.35	13.25	49.23	6.12	3.989	tr V8N7A2 V8N7A2_OPHPHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHPHA	7
1257	8.35	8.68	28.76	6.352	5.15	tr V8P8E6 V8P8E6_OPHPHA GRE2-associated-binding protein 3 (Fragment) OS=Ophioph OPHPHA	5
1258	8.34	13.21	76.04	22.92	19.27	tr V8NE74 V8NE74_OPHPHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHPHA	6
1259	8.33	8.33	51.19	9.002	6.941	tr V8NQ00 V8NQ00_OPHPHA Transcription elongation factor SPT5 (Fragment) OS=Ophi OPHPHA	5
1260	8.33	8.33	58.86	21.43	14	tr V8PGQ0 V8PGQ0_OPHPHA Serine beta-lactamase-like protein LACTB, mitochondrial OPHPHA	4
1261	8.33	8.33	26.82	9.683	6.331	tr V8NGC2 V8NGC2_OPHPHA Acyl-coenzyme A amino acid N-acyltransferase 1 (Fragmen OPHPHA	4
1262	8.33	8.33	54.3	47.85	36.02	tr V8PCM1 V8PCM1_OPHPHA Erlin-2 OS=Ophiophagus hannah GN=ERLIN2 PE=4 SV=1 OPHPHA	4
1263	8.32	8.46	33.01	20	13.73	tr V8NNV0 V8NNV0_OPHPHA Glutamate-rich WD repeat-containing protein 1 OS=Ophioph OPHPHA	4
1264	8.31	8.31	33.22	5.217	5.217	tr V8NBS0 V8NBS0_OPHPHA Macrophage mannose receptor 1 (Fragment) OS=Ophiophagus OPHPHA	6
1265	8.3	9.87	64.89	37.02	29.01	tr V8P9E1 V8P9E1_OPHPHA F-actin-capping protein subunit alpha-1 (Fragment) OS=O OPHPHA	6
1266	8.3	8.3	54.89	11.65	8.459	tr V8PDS2 V8PDS2_OPHPHA Translation initiation factor eIF-2B subunit gamma OS=O OPHPHA	4
1267	8.29	10.6	61.38	13.23	9.846	tr V8PAY7 V8PAY7_OPHPHA Heat shock protein 75 kDa, mitochondrial OS=Ophiophagus OPHPHA	5
1268	8.28	8.29	17.84	10.8	8.291	tr V8NH26 V8NH26_OPHPHA Clef lip and palate transmembrane protein 1-like prote OPHPHA	4
1269	8.27	8.27	52.64	13.53	6.642	tr V8NPRO V8NPRO_OPHPHA Plakophilin-3 (Fragment) OS=Ophiophagus hannah GN=Pkp3 OPHPHA	4
1270	8.27	8.27	60.63	28.51	16.74	tr V8NA36 V8NA36_OPHPHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHPHA	4
1271	8.27	8.27	50	21.22	18.31	tr V8P857 V8P857_OPHPHA Methylosome protein 50 OS=Ophiophagus hannah GN=Wdr77 P OPHPHA	4
1272	8.26	8.26	38.26	9.266	6.606	tr V8POY8 V8POY8_OPHPHA Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP OPHPHA	5
1273	8.25	8.26	55.19	27.04	27.04	tr V8NZS4 V8NZS4_OPHPHA S-methyl-5'-thioadenosine phosphorylase (Fragment) OS=O OPHPHA	5
1274	8.24	8.24	41.84	14.54	11.87	tr V8PBE6 V8PBE6_OPHPHA Sulfotransferase OS=Ophiophagus hannah GN=Sult1a1 PE=3 OPHPHA	5
1275	8.23	27.16	52.72	49.75	45.05	tr V8P514 V8P514_OPHPHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_0 OPHPHA	16
1276	8.23	8.23	53.98	24.22	19.38	tr V8NT89 V8NT89_OPHPHA Ischorismatase domain-containing protein 1 (Fragment) OPHPHA	4
1277	8.23	8.23	51.5	23.18	14.59	tr V8P7N2 V8P7N2_OPHPHA UMP-CMP kinase OS=Ophiophagus hannah GN=CMKP1 PE=3 SV=1 OPHPHA	4
1278	8.22	8.22	34.97	24.04	20.49	tr V8P3U9 V8P3U9_OPHPHA Creatine kinase B-type (Fragment) OS=Ophiophagus hannah OPHPHA	4
1279	8.21	8.94	34.14	7.484	4.771	tr V8P9K2 V8P9K2_OPHPHA Cation-transporting ATPase (Fragment) OS=Ophiophagus ha OPHPHA	4
1280	8.21	8.21	51.08	12.77	11.04	tr V8NKTO V8NKTO_OPHPHA RNA-binding protein 47 (Fragment) OS=Ophiophagus hannah OPHPHA	5
1281	8.2	8.2	42.95	16.99	14.1	tr V8P513 V8P513_OPHPHA D-aspartate oxidase (Fragment) OS=Ophiophagus hannah GN OPHPHA	5
1282	8.19	8.19	51.03	46.9	46.9	tr V8NHR8 V8NHR8_OPHPHA Ubiquitin-conjugating enzyme E2 K (Fragment) OS=Ophioph OPHPHA	5
1283	8.18	8.33	28.83	19.68	11.21	tr V8NKN0 V8NKN0_OPHPHA Histone-binding protein RBBP4 (Fragment) OS=Ophiophagus OPHPHA	3
1284	8.17	8.18	62.95	29.79	21.5	tr V8NHF9 V8NHF9_OPHPHA Methionine aminopeptidase 1 OS=Ophiophagus hannah GN=ME OPHPHA	6
1285	8.17	8.17	47.3	12.45	10.17	tr V8NH29 V8NH29_OPHPHA Proactivator polypeptide OS=Ophiophagus hannah GN=PSAP OPHPHA	5
1286	8.16	8.16	27.43	27.43	27.43	tr V8NAC9 V8NAC9_OPHPHA NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Ophioph OPHPHA	4
1287	8.15	8.15	62.98	27.88	25	tr V8PEW2 V8PEW2_OPHPHA NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, OPHPHA	4
1288	8.13	8.22	56.8	17.24	11.76	tr V8P8U4 V8P8U4_OPHPHA DnaJ-like subfamily C member 3 (Fragment) OS=Ophiophagus OPHPHA	6
1289	8.13	8.13	47.77	4.738	2.428	tr V8NU88 V8NU88_OPHPHA Chromodomain-helicase-DNA-binding protein 4 OS=Ophiophag OPHPHA	5
1290	8.13	8.13	40.47	13.14	8.898	tr V8P2C1 V8P2C1_OPHPHA RNA-binding protein FUS OS=Ophiophagus hannah GN=FUS PE OPHPHA	5
1291	8.13	8.13	44.53	21.89	21.89	tr V8NHN6 V8NHN6_OPHPHA LanC-like protein 2 OS=Ophiophagus hannah GN=LANCL2 PE= OPHPHA	4
1292	8.12	8.12	44.99	17.72	15.85	tr V8N6Z1 V8N6Z1_OPHPHA Mannose-6-phosphate isomerase (Fragment) OS=Ophiophagus OPHPHA	4
1293	8.11	8.11	49.26	9.664	8.188	tr V8NZE8 V8NZE8_OPHPHA Conserved oligomeric Golgi complex subunit 4 (Fragment) OPHPHA	4
1294	8.11	8.11	41.31	11.96	11.96	tr V8PDD3 V8PDD3_OPHPHA Ran-binding protein 3 (Fragment) OS=Ophiophagus hannah OPHPHA	4
1295	8.1	8.1	42.38	18.29	15.85	tr V8P0J5 V8P0J5_OPHPHA Eukaryotic translation initiation factor 3 subunit F OS OPHPHA	4
1296	8.09	8.09	28.37	7.151	7.151	tr V8NLL4 V8NLL4_OPHPHA Furin OS=Ophiophagus hannah GN=FURIN PE=3 SV=1 OPHPHA	4
1297	8.09	8.09	55.71	21.92	21.92	tr V8POX8 V8POX8_OPHPHA Translin (Fragment) OS=Ophiophagus hannah GN=TSN PE=4 S OPHPHA	5
1298	8.09	8.09	65.12	32.56	32.56	tr V8NLG0 V8NLG0_OPHPHA 10 kDa heat shock protein, mitochondrial (Fragment) OS= OPHPHA	7
1299	8.08	8.15	54.5	8.882	5.702	tr V8NXS7 V8NXS7_OPHPHA DNA ligase (Fragment) OS=Ophiophagus hannah GN=LIG3 PE= OPHPHA	4
1300	8.07	8.09	34.61	12.93	10.93	tr V8NEF3 V8NEF3_OPHPHA Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Ophiophag OPHPHA	5
1301	8.06	8.06	43.42	10.44	10.44	tr V8NG15 V8NG15_OPHPHA Zinc transporter 9 (Fragment) OS=Ophiophagus hannah GN= OPHPHA	4
1302	8.05	8.05	51.74	10.99	10.99	tr V8P400 V8P400_OPHPHA X-ray repair cross-complementing protein 6 (Fragment) O OPHPHA	4
1303	8.04	8.04	41.28	7.11	7.11	tr V8NNW5 V8NNW5_OPHPHA Complement C5 (Fragment) OS=Ophiophagus hannah GN=C5 PE OPHPHA	4
1304	8.04	8.04	60.22	14.36	14.36	tr V8N6G5 V8N6G5_OPHPHA Protein-glutamine gamma-glutamyltransferase E (Fragment OPHPHA	4
1305	8.04	8.04	72.22	32.64	32.64	tr V8P783 V8P783_OPHPHA Nucleoside diphosphate kinase, mitochondrial (Fragment) OPHPHA	5
1306	8.04	8.04	39.87	23.59	21.26	tr V8PED8 V8PED8_OPHPHA Mitochondrial carrier-like 2 OS=Ophiophagus hannah GN=M OPHPHA	5
1307	8.02	14.94	29.27	11.28	10.28	tr V8P3H7 V8P3H7_OPHPHA Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS= OPHPHA	7
1308	8.02	10.31	59.46	34.05	34.05	tr V8PFI9 V8PFI9_OPHPHA Rho-related GTP-binding protein RhoB (Fragment) OS=Ophi OPHPHA	7
1309	8.02	8.54	38.38	14.39	14.39	tr V8P6E9 V8P6E9_OPHPHA Kynureninase (Fragment) OS=Ophiophagus hannah GN=KYNU P OPHPHA	5
1310	8.01	8.02	57.19	11.87	7.554	tr V8P8Y0 V8P8Y0_OPHPHA Procollagen galactosyltransferase 1 (Fragment) OS=Ophi OPHPHA	4
1311	8	13.35	85.71	45.58	45.58	tr V8N2E2 V8N2E2_OPHPHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHPHA	8
1312	8	8	37.1	4.708	4.708	tr V8P6C4 V8P6C4_OPHPHA Lymphocyte antigen 75 (Fragment) OS=Ophiophagus hannah OPHPHA	5
1313	8	8	43.49	12.82	12.82	tr V8PGK0 V8PGK0_OPHPHA D site-binding protein (Fragment) OS=Ophiophagus hannah OPHPHA	5
1314	8	8	62.03	31.01	31.01	tr V8NY64 V8NY64_OPHPHA Synaptosomal-associated protein 23 OS=Ophiophagus hanna OPHPHA	4
1315	8	8	64.29	44.05	44.05	tr V8PBL9 V8PBL9_OPHPHA Sorting nexin-12 (Fragment) OS=Ophiophagus hannah GN=SN OPHPHA	4
1316	8	8	75.19	20.93	20.93	tr V8NNW5 V8NNW5_OPHPHA 17-beta-hydroxysteroid dehydrogenase 13 (Fragment) OS=O OPHPHA	4
1317	7.99	8	73.19	21.18	19.03	tr V8NUW7 V8NUW7_OPHPHA Isocitrate dehydrogenase [NAD] subunit alpha, mitochond NAD	5
1318	7.99	7.99	63.51	7.74	7.74	tr V8NK84 V8NK84_OPHPHA Liprin-beta-1 OS=Ophiophagus hannah GN=PPF1BP1 PE=4 SV= OPHPHA	5
1319	7.99	7.99	73.33	40	34.81	tr V8NQT7 V8NQT7_OPHPHA Short-chain specific acyl-CoA dehydrogenase, mitochondr OPHPHA	5
1320	7.98	7.98	57.7	13.17	13.17	tr V8NSQ0 V8NSQ0_OPHPHA Torsin-1A-interacting protein 1 OS=Ophiophagus hannah G OPHPHA	4
1321	7.97	7.97	37.03	2.61	2.61	tr V8P8R8 V8P8R8_OPHPHA Autophagy-related protein 9A (Fragment) OS=Ophiophagus OPHPHA	4
1322	7.97	7.97	36.28	7.419	5.386	tr V8NEY4 V8NEY4_OPHPHA SCY1-like protein 2 (Fragment) OS=Ophiophagus hannah GN OPHPHA	4
1323	7.97	7.97	69.23	39.23	30	tr V8NAA6 V8NAA6_OPHPHA 40S ribosomal protein S15a OS=Ophiophagus hannah GN=RPS OPHPHA	4
1324	7.96	7.96	53.45	40.52	39.66	tr V8P4X6 V8P4X6_OPHPHA Eukaryotic translation initiation factor 1A, Y-chromoso OPHPHA	4
1325	7.96	7.96	39.61	12.96	12.96	tr V8NDI3 V8NDI3_OPHPHA Carboxylic ester hydrolase OS=Ophiophagus hannah GN=L34 OPHPHA	5
1326	7.96	7.96	39.59	20.41	16.33	tr V8PBD4 V8PBD4_OPHPHA Inositol monophosphatase 1 (Fragment) OS=Ophiophagus ha OPHPHA	4
1327	7.94	7.94	39.18	16.42	14.74	tr V8NX44 V8NX44_OPHPHA [Pyruvate dehydrogenase [acetyl-transferring]]-phosphat Pyruvate	5
1328	7.94	7.94	34.53	21.62	17.42	tr V8PD15 V8PD15_OPHPHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_0 OPHPHA	5
1329	7.93	8.45	71.81	32.21	22.15	tr V8N6H9 V8N6H9_OPHPHA Glycogen [starch] synthase, liver (Fragment) OS=Ophioph OPHPHA	5
1330	7.93	7.94	63.31	44.97	34.91	tr V8NHP6 V8NHP6_OPHPHA Regulation of nuclear pre-mRNA domain-containing protei OPHPHA	5
1331	7.93	7.93	85.43	32.39	28.34	tr V8POT1 V8POT1_OPHPHA PRKC apoptosis WTL regulator protein (Fragment) OS=Ophi OPHPHA	4
1332	7.92	7.92	33.12	16.03	9.916	tr V8NEJ7 V8NEJ7_OPHPHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHPHA	4
1333	7.92	7.92	39.36	17.02	17.02	tr V8P531 V8P531_OPHPHA Cytochrome b-c1 complex subunit 7 (Fragment) OS=Ophioph OPHPHA	5
1334	7.91	7.91	35.01	6.162	5.509	tr V8P2D7 V8P2D7_OPHPHA Zinc finger protein (Fragment) OS=Ophiophagus hannah GN OPHPHA	5
1335	7.91	7.91	56.15	14.12	9.302	tr V8PDL0 V8PDL0_OPHPHA WD repeat-containing protein 48 (Fragment) OS=Ophiophag OPHPHA	4
1336	7.91	7.91	18.03	3.72	3.72	tr V8P7P1 V8P7P1_OPHPHA Carboxylic ester hydrolase (Fragment) OS=Ophiophagus ha OPHPHA	6
1337	7.91	7.91	45	19.67	16.33	tr V8N8G8 V8N8G8_OPHPHA Very long-chain specific acyl-CoA dehydrogenase, mitoch OPHPHA	7

1338	7.9	17.81	59.17	40.83	33.14	tr V8P7D3 V8P7D3.OPHHA Eukaryotic translation initiation factor 5A OS=Ophiophag	12
1339	7.9	7.9	36.22	22.76	18.59	tr V8P7N4 V8P7N4.OPHHA Lipid phosphate phosphohydrolase 3 (Fragment) OS=Ophiophag	4
1340	7.89	7.89	50.13	19.34	14.5	tr V8PCH4 V8PCH4.OPHHA Golgi-associated PDZ and coiled-coil motif-containing p	6
1341	7.89	7.89	64.65	21.34	18.47	tr V8P6Q2 V8P6Q2.OPHHA DNA-(apurinic or apyrimidinic site) lyase OS=Ophiophag	5
1342	7.88	7.91	45.07	2.9	1.801	tr V8NWK3 V8NWK3.OPHHA Nesprin-1 (Fragment) OS=Ophiophag hannah GN=SYNE1 PE=	8
1343	7.88	7.88	53.29	12.65	9.444	tr V8P6G2 V8P6G2.OPHHA Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Op	4
1344	7.87	10.23	51.22	11.89	8.566	tr V8PFS0 V8PFS0.OPHHA Tyrosine-protein kinase (Fragment) OS=Ophiophag hanna	5
1345	7.87	7.87	88.34	38.65	32.52	tr V8PGN0 V8PGN0.OPHHA Superoxide dismutase [Cu-Zn] OS=Ophiophag hannah GN=L	6
1346	7.86	7.88	28.47	12.73	10.42	tr V8NQJ4 V8NQJ4.OPHHA Cathepsin Z (Fragment) OS=Ophiophag hannah GN=CTSZ PE	4
1347	7.86	7.87	45.13	3.859	1.963	tr V8PGL6 V8PGL6.OPHHA Protein SON (Fragment) OS=Ophiophag hannah GN=SON PE=	5
1348	7.85	7.85	32.83	11.72	8.276	tr V8NT05 V8NT05.OPHHA Nuclear cap-binding protein subunit 1 (Fragment) OS=Oph	5
1349	7.85	7.85	40.41	21.51	17.15	tr V8P2W1 V8P2W1.OPHHA IST1-like protein OS=Ophiophag hannah GN=IST1 PE=4	5
1350	7.85	7.85	54.48	26.12	22.76	tr V8NS03 V8NS03.OPHHA TIP41-like protein (Fragment) OS=Ophiophag hannah GN=	4
1351	7.84	7.84	46.1	7.797	3.22	tr V8P4C3 V8P4C3.OPHHA Methionine synthase (Fragment) OS=Ophiophag hannah GN	3
1352	7.83	7.83	55.88	15.59	12.95	tr V8NRD0 V8NRD0.OPHHA Myoferlin (Fragment) OS=Ophiophag hannah GN=Myof PE=4	4
1353	7.81	7.81	72.87	32.45	27.13	tr V8PGJ5 V8PGJ5.OPHHA 60S ribosomal protein L18 OS=Ophiophag hannah GN=rp11	5
1354	7.81	7.81	47.6	22.75	22.75	tr V8P771 V8P771.OPHHA Protein FAM98B (Fragment) OS=Ophiophag hannah GN=Fam9	5
1355	7.8	8.49	56.86	8.007	7.026	tr V8PC11 V8PC11.OPHHA Peroxidase mlt-7 (Fragment) OS=Ophiophag hannah GN=ml	5
1356	7.8	7.8	43.87	35.48	35.48	tr V8PHT5 V8PHT5.OPHHA Proteasome subunit alpha type-5 (Fragment) OS=Ophiophag	5
1357	7.77	7.81	62.22	49.63	42.96	tr V8NXL1 V8NXL1.OPHHA ADP-ribosylation factor-like protein 1 OS=Ophiophag h	4
1358	7.77	7.79	44.05	5.712	4.93	tr V8NZY9 V8NZY9.OPHHA Cell division cycle and apoptosis regulator protein 1 (OPHHA	4
1359	7.77	7.77	41.2	24.65	15.85	tr V8PB08 V8PB08.OPHHA Nicotinate-nucleotide pyrophosphorylase [carboxylating] OPHHA	6
1360	7.76	7.76	58.61	13.86	13.86	tr V8PF88 V8PF88.OPHHA Nucleoporin Nup37 (Fragment) OS=Ophiophag hannah GN=N	5
1361	7.76	7.76	65.59	38.17	29.57	tr V8P763 V8P763.OPHHA Adenylate kinase isoenzyme 4, mitochondrial OS=Ophioph	5
1362	7.75	7.75	56.2	12.14	7.635	tr V8NYE4 V8NYE4.OPHHA Dynamin-1-like protein (Fragment) OS=Ophiophag hannah	5
1363	7.75	7.75	73.62	48.47	28.22	tr V8NPD8 V8NPD8.OPHHA Trafficking protein particle complex subunit 6B OS=Ophi	4
1364	7.74	7.74	23.35	14.97	12.38	tr V8PG41 V8PG41.OPHHA Poliovirus receptor-related protein 3 (Fragment) OS=Oph	4
1365	7.74	7.74	72.44	40.94	38.58	tr V8N702 V8N702.OPHHA Uncharacterized protein (Fragment) OS=Ophiophag hanna	4
1366	7.73	8.8	62.15	18.13	12.95	tr V8NCY7 V8NCY7.OPHHA Fermitin family-like 3 (Fragment) OS=Ophiophag hannah	5
1367	7.73	7.73	54.29	21.63	21.63	tr V8P1L5 V8P1L5.OPHHA Syntaxin-7 OS=Ophiophag hannah GN=STX7 PE=4 SV=1	4
1368	7.73	7.73	43.46	15.69	15.69	tr V8PCV0 V8PCV0.OPHHA Septin-1 (Fragment) OS=Ophiophag hannah GN=SEPT1 PE=3	4
1369	7.72	7.72	46.7	6.089	4.37	tr V8PJH0 V8PJH0.OPHHA Trafficking protein particle complex subunit 8 (Fragmen	5
1370	7.71	7.71	45.44	11.36	11.36	tr V8NQK0 V8NQK0.OPHHA Tryptophan 2,3-dioxygenase (Fragment) OS=Ophiophag ha	5
1371	7.71	7.71	55.29	18.25	15.61	tr V8N9K7 V8N9K7.OPHHA Collagen type IV alpha-3-binding protein (Fragment) OS=	6
1372	7.69	10.26	54.52	8.601	8.601	tr V8NSS1 V8NSS1.OPHHA DNA (Cytosine-5)-methyltransferase 3B (Fragment) OS=Oph	5
1373	7.68	7.68	57.54	8.432	8.432	tr V8PCK9 V8PCK9.OPHHA ADP topoisomerase 1 (Fragment) OS=Ophiophag hannah	5
1374	7.68	7.68	44.68	6.586	5.928	tr V8PAN8 V8PAN8.OPHHA Coronin (Fragment) OS=Ophiophag hannah GN=Coro7 PE=3	4
1375	7.67	7.67	65.21	13.82	13.82	tr V8NWA5 V8NWA5.OPHHA Protein kinase C and casein kinase substrate in neurons	5
1376	7.66	7.68	44.98	18.88	15.66	tr V8NGG6 V8NGG6.OPHHA 40S ribosomal protein S6 OS=Ophiophag hannah GN=RPS6	6
1377	7.66	7.66	66.49	24.05	24.05	tr V8NFU8 V8NFU8.OPHHA NAD-dependent deacetylase sirtuin-3, mitochondrial (Fra	6
1378	7.65	7.66	26.4	11.31	10.2	tr V8PD09 V8PD09.OPHHA Integrin alpha-5 (Fragment) OS=Ophiophag hannah GN=IT	4
1379	7.64	7.72	43.94	11.95	8.586	tr V8NW46 V8NW46.OPHHA Serine/threonine-protein phosphatase 2A 56 kDa regulato	4
1380	7.64	7.64	81.38	24.48	23.45	tr V8N4W5 V8N4W5.OPHHA Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, m	5
1381	7.63	7.63	82.39	24.53	18.24	tr V8N9S3 V8N9S3.OPHHA Cytochrome protein OS=Ophiophag hannah GN=Cyp2c23 PE=	5
1382	7.62	7.62	42.9	17.76	14.21	tr V8NQ63 V8NQ63.OPHHA Sphingosine-1-phosphate lyase 1 OS=Ophiophag hannah	4
1383	7.6	7.6	62.54	17.14	17.14	tr V8NWG8 V8NWG8.OPHHA Calcium uptake protein 1, mitochondrial (Fragment) OS=O	4
1384	7.59	7.59	42.72	10.73	9.387	tr V8P5X7 V8P5X7.OPHHA Ran GTPase-activating protein 1 OS=Ophiophag hannah	4
1385	7.58	7.58	50.92	8.067	4.79	tr V8N1V9 V8N1V9.OPHHA Transcription elongation factor SPT6 (Fragment) OS=Ophi	4
1386	7.58	7.58	55.36	19.72	19.72	tr V8NBS8 V8NBS8.OPHHA E3 ubiquitin-protein ligase UBR4 (Fragment) OS=Ophioph	4
1387	7.57	7.57	56.59	6.919	3.602	tr V8PCT0 V8PCT0.OPHHA Ankyrin (Fragment) OS=Ophiophag hannah GN=RA114 PE	3
1388	7.57	7.57	59.9	32.29	25	tr V8PJC8 V8PJC8.OPHHA SAP domain-containing ribonucleoprotein OS=Ophiophag	4
1389	7.57	7.57	31.56	21.25	18.44	tr V8NM79 V8NM79.OPHHA Serine/threonine-protein kinase PAK 2 (Fragment) OS=Oph	4
1390	7.56	7.56	34.44	4.06	3.077	tr V8P3K1 V8P3K1.OPHHA Lysine-specific demethylase 5B-B (Fragment) OS=Ophioph	6
1391	7.55	7.55	60.81	11.49	8.615	tr V8P1Q5 V8P1Q5.OPHHA Collagen alpha-3(VI) chain (Fragment) OS=Ophiophag ha	5
1392	7.55	7.55	49.59	15.45	15.45	tr V8P1P0 V8P1P0.OPHHA MAGUK p55 subfamily member 7 (Fragment) OS=Ophiophag	4
1393	7.55	7.55	44.75	31.05	22.83	tr V8P9G6 V8P9G6.OPHHA Grancalcin OS=Ophiophag hannah GN=Gca PE=4 SV=1	4
1394	7.55	7.55	52.17	28.99	28.99	tr V8N1T9 V8N1T9.OPHHA Putative oxidoreductase GLYR1 OS=Ophiophag hannah GN=	5
1395	7.54	7.54	45.75	12.71	6.519	tr V8P573 V8P573.OPHHA Bifunctional protein NCOAT OS=Ophiophag hannah GN=MGE	4
1396	7.54	7.54	74.89	30.14	24.66	tr V8NRL5 V8NRL5.OPHHA Protein Niban OS=Ophiophag hannah GN=FAM129A PE=4	6
1397	7.53	7.53	54.01	10.76	10.76	tr V8NPP3 V8NPP3.OPHHA ATP-binding cassette sub-family D member 3 OS=Ophiophag	4
1398	7.52	7.52	47.33	12.17	9	tr V8PB55 V8PB55.OPHHA LEM domain-containing protein 2 (Fragment) OS=Ophiophag	4
1399	7.52	7.52	56.17	17.28	14.2	tr V8NFZ5 V8NFZ5.OPHHA UDP-N-acetylhexosamine pyrophosphorylase-like protein	5
1400	7.52	7.52	87.94	40.43	33.33	tr V8P5L4 V8P5L4.OPHHA Tumor susceptibility protein (Fragment) OS=Ophiophag	4
1401	7.5	13.89	45.1	17.65	15.2	tr V8N5L7 V8N5L7.OPHHA Retinol dehydrogenase 16 (Fragment) OS=Ophiophag hannah	11
1402	7.5	7.5	38.94	6.673	4.753	tr V8NR19 V8NR19.OPHHA Strychnin gamma OS=Ophiophag hannah GN=SYNRG PE=4	4
1403	7.49	7.49	60.62	17.5	17.5	tr V8PCU2 V8PCU2.OPHHA 39S ribosomal protein L39, mitochondrial OS=Ophiophag	4
1404	7.48	7.48	39.3	26.87	19.9	tr V8PDK5 V8PDK5.OPHHA Ras-related protein Rab-9A OS=Ophiophag hannah GN=RAB	5
1405	7.47	7.47	35.78	8.687	5.791	tr V8PA33 V8PA33.OPHHA Trafficking protein particle complex subunit 11 OS=Ophi	4
1406	7.46	7.86	45.57	10.55	4.975	tr V8PF57 V8PF57.OPHHA Phosphorylase b kinase regulatory subunit beta OS=Ophi	4
1407	7.43	7.43	31.99	6.239	6.239	tr V8PJ25 V8PJ25.OPHHA PAB-dependent poly(A)-specific ribonuclease subunit 2 (OPHHA	4
1408	7.43	7.43	62.65	12.65	12.65	tr V8NM18 V8NM18.OPHHA Parafibromin (Fragment) OS=Ophiophag hannah GN=CD	4
1409	7.43	7.43	52.33	45.35	37.21	tr V8N6Z7 V8N6Z7.OPHHA Proteasome subunit alpha type-5 (Fragment) OS=Ophiophag	5
1410	7.42	8.89	70.63	43.65	34.92	tr V8NND9 V8NND9.OPHHA Pterin-4-alpha-carbinolamine dehydratase (Fragment) OS=	6
1411	7.42	7.44	47.3	14.7	7.939	tr V8PBW7 V8PBW7.OPHHA Histone-lysine N-methyltransferase setd3 OS=Ophiophag	4
1412	7.42	7.42	65.22	6.545	5.175	tr V8NXL6 V8NXL6.OPHHA Collagen alpha-1(I) chain OS=Ophiophag hannah GN=COL1	5
1413	7.41	8.76	69.62	32.28	32.28	tr V8PCQ9 V8PCQ9.OPHHA Single-stranded DNA-binding protein, mitochondrial OS=O	7
1414	7.4	7.4	56.58	15.79	15.79	tr V8PIM7 V8PIM7.OPHHA Cytoplasmic protein NCK2 OS=Ophiophag hannah GN=NCK2	5
1415	7.4	7.4	38.48	14.01	12.11	tr V8NBY5 V8NBY5.OPHHA N-acetylglucosamine-6-sulfatase (Fragment) OS=Ophiophag	4
1416	7.39	7.39	29.52	24.1	17.47	tr V8PJE4 V8PJE4.OPHHA Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Ophi	5
1417	7.38	7.44	61.93	19.54	10.91	tr V8NCH3 V8NCH3.OPHHA Tyrosine-protein kinase SYK (Fragment) OS=Ophiophag h	3
1418	7.38	7.38	77.27	38.18	30	tr V8P956 V8P956.OPHHA Protein BRICK1 (Fragment) OS=Ophiophag hannah GN=BRK1	5
1419	7.37	7.37	49.8	4.573	3.317	tr V8P1C1 V8P1C1.OPHHA Cytoskeleton-associated protein 5 (Fragment) OS=Ophiophag	6
1420	7.37	7.37	51.38	21.54	21.54	tr V8PH38 V8PH38.OPHHA Yorkie-like protein OS=Ophiophag hannah GN=YAP1 PE=4	4
1421	7.37	7.37	49.18	39.34	39.34	tr V8NJG3 V8NJG3.OPHHA Mitochondrial import inner membrane translocase subunit	4
1422	7.36	7.36	56.73	15.25	12.11	tr V8NFG1 V8NFG1.OPHHA Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosam	4
1423	7.35	7.35	32.62	3.19	2.286	tr V8PHJ2 V8PHJ2.OPHHA Desmoglein-2 OS=Ophiophag hannah GN=DSG2 PE=4 SV=1	4
1424	7.34	7.34	42.57	6.275	4.289	tr V8P8B7 V8P8B7.OPHHA Synaptopodin-2 (Fragment) OS=Ophiophag hannah GN=SYNP	4
1425	7.34	7.34	42.48	15.58	9.381	tr V8NU70 V8NU70.OPHHA ATP-dependent RNA helicase A (Fragment) OS=Ophiophag	4
1426	7.34	7.34	62.5	36.11	36.11	tr V8P5J1 V8P5J1.OPHHA Coiled-coil domain-containing protein 58 OS=Ophiophag	4
1427	7.33	7.33	55.33	19.8	19.8	tr V8NN75 V8NN75.OPHHA GTP-binding protein Rheb (Fragment) OS=Ophiophag hannah	5
1428	7.32	7.32	47.32	27.76	23.66	tr V8P5N7 V8P5N7.OPHHA mRNA export factor (Fragment) OS=Ophiophag hannah GN=	4
1429	7.31	7.31	48.04	8.096	6.05	tr V8P9L1 V8P9L1.OPHHA Tripartite motif-containing protein 2 (Fragment) OS=Oph	4
1430	7.29	7.39	28.65	8.26	7.206	tr V8PGW3 V8PGW3.OPHHA Lumican (Fragment) OS=Ophiophag hannah GN=LUM PE=4	5
1431	7.29	7.29	40.81	16.18	16.18	tr V8PFV7 V8PFV7.OPHHA Down syndrome critical region protein 3 OS=Ophiophag	4
1432	7.29	7.29	73.49	28.92	28.92	tr V8N3T9 V8N3T9.OPHHA Sulfotransferase (Fragment) OS=Ophiophag hannah GN=L3	6
1433	7.28	7.28	44.9	9.475	6.122	tr V8NEH4 V8NEH4.OPHHA Phospholipase A2 (Fragment) OS=Ophiophag hannah GN=PL	3

1434	7.28	7.28	26.78	6.345	6.345	tr V8PHD7 V8PHD7_OPPIHA Transmembrane protease serine 6 (Fragment) OS=Ophiophag	OPPIHA	4
1435	7.28	7.28	38.56	11.86	9.958	tr V8P995 V8P995_OPPIHA Selenoprotein 0 (Fragment) OS=Ophiophagus hannah GN=SEL	OPPIHA	4
1436	7.26	7.65	57.44	11.79	8.718	tr V8NLY3 V8NLY3_OPPIHA Erln-1 OS=Ophiophagus hannah GN=Erln1 PE=4 SV=1	OPPIHA	4
1437	7.26	7.28	26.75	8.618	6.686	tr V8NCK6 V8NCK6_OPPIHA Inter-alpha-trypsin inhibitor heavy chain H2 (Fragment) OPPIHA	4	4
1438	7.25	7.25	51.66	21.33	18.48	tr V8P3K9 V8P3K9_OPPIHA 60S ribosomal protein L13 OS=Ophiophagus hannah GN=RPL1	OPPIHA	4
1439	7.25	7.25	33.33	18.33	11.67	tr V8PBS5 V8PBS5_OPPIHA Proteasome subunit beta type (Fragment) OS=Ophiophagus	OPPIHA	4
1440	7.25	7.25	48.48	25.25	25.25	tr V8PHC5 V8PHC5_OPPIHA COMM domain-containing protein 9 (Fragment) OS=Ophiophag	OPPIHA	4
1441	7.24	7.24	34.54	4.067	3.422	tr V8P3Z1 V8P3Z1_OPPIHA Nuclear pore membrane glycoprotein (Fragment) OS=Ophiop	OPPIHA	4
1442	7.24	7.24	47.65	30	24.12	tr V8NPE9 V8NPE9_OPPIHA Peptidyl-prolyl cis-trans isomerase OS=Ophiophagus hann	OPPIHA	4
1443	7.24	7.24	55	40	34.44	tr V8NLU0 V8NLU0_OPPIHA ADP-ribosylation factor-like protein 3 (Fragment) OS=Op	OPPIHA	4
1444	7.22	7.22	86.28	26.71	20.94	tr V8P759 V8P759_OPPIHA DnaJ-like subfamily C member 7 (Fragment) OS=Ophiophag	OPPIHA	5
1445	7.21	7.21	43.92	12.85	8.507	tr V8P1L3 V8P1L3_OPPIHA RalA-binding protein 1 (Fragment) OS=Ophiophagus hannah	OPPIHA	4
1446	7.2	10.54	46.1	33.77	26.95	tr V8N9R5 V8N9R5_OPPIHA Coatomer subunit gamma-2 (Fragment) OS=Ophiophagus hann	OPPIHA	7
1447	7.2	7.2	40.57	25.71	25.71	tr V8P055 V8P055_OPPIHA NudC domain-containing protein 2 (Fragment) OS=Ophiophag	OPPIHA	4
1448	7.19	7.19	63.11	18.45	15.53	tr V8NNS7 V8NNS7_OPPIHA Guanine nucleotide-binding protein G(S) subunit alpha (OPPIHA	4	4
1449	7.19	7.19	28.26	12.06	6.522	tr V8P143 V8P143_OPPIHA Glycerate kinase (Fragment) OS=Ophiophagus hannah GN=G1	OPPIHA	4
1450	7.17	7.17	54.25	6.187	2.974	tr V8NQ11 V8NQ11_OPPIHA Signal-induced proliferation-associated 1-like protein OPPIHA	4	4
1451	7.17	7.17	34.07	11.72	7.724	tr V8P3K7 V8P3K7_OPPIHA Elongator complex protein 2 (Fragment) OS=Ophiophagus h	OPPIHA	3
1452	7.17	7.17	80.62	29.37	29.37	tr V8NJ20 V8NJ20_OPPIHA Programmed cell death protein 6 OS=Ophiophagus hannah G	OPPIHA	4
1453	7.16	7.16	44.84	26.98	26.98	tr V8PGJ2 V8PGJ2_OPPIHA Beta-parvin (Fragment) OS=Ophiophagus hannah GN=PARVB	OPPIHA	5
1454	7.13	9.24	60.58	19.23	12.82	tr V8P798 V8P798_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	4
1455	7.13	7.13	54.17	22.73	17.05	tr V8NL19 V8NL19_OPPIHA Phosphate carrier protein, mitochondrial OS=Ophiophagus	OPPIHA	4
1456	7.13	7.13	60.99	24.11	24.11	tr V8PDP7 V8PDP7_OPPIHA Tight junction protein ZO-1 (Fragment) OS=Ophiophagus h	OPPIHA	4
1457	7.12	7.12	44.54	4.476	4.476	tr V8NLK9 V8NLK9_OPPIHA Wings apart-like protein-like protein (Fragment) OS=Oph	OPPIHA	4
1458	7.12	7.12	52.45	24.51	24.51	tr V8PED7 V8PED7_OPPIHA Sickle tail protein-like protein (Fragment) OS=Ophiophag	OPPIHA	4
1459	7.11	7.11	41.91	9.553	8.012	tr V8P665 V8P665_OPPIHA Midline-1 OS=Ophiophagus hannah GN=MID1 PE=4 SV=1	OPPIHA	4
1460	7.11	7.11	44.57	11.02	7.508	tr V8NX30 V8NX30_OPPIHA ATP-dependent zinc metalloprotease YME1L1 OS=Ophiophag	OPPIHA	3
1461	7.11	7.11	36.59	15.94	15.94	tr V8PBK0 V8PBK0_OPPIHA ATP-dependent Clp protease proteolytic subunit (Fragmen	OPPIHA	5
1462	7.11	7.11	67.78	51.11	51.11	tr V8PJF5 V8PJF5_OPPIHA Non-histone chromosomal protein HMG-17 OS=Ophiophagus h	OPPIHA	4
1463	7.09	7.09	35.04	21.37	15.1	tr V8P5W7 V8P5W7_OPPIHA Endophilin-B1 (Fragment) OS=Ophiophagus hannah GN=SH3GL	OPPIHA	4
1464	7.09	7.09	53.73	28.86	28.86	tr V8NWZ5 V8NWZ5_OPPIHA Ras-related protein Rab-22A (Fragment) OS=Ophiophagus h	OPPIHA	4
1465	7.09	7.09	39.74	33.11	33.11	tr V8NKN1 V8NKN1_OPPIHA Malignant T cell-amplified sequence 1-A (Fragment) OS=O	OPPIHA	5
1466	7.08	7.08	66.06	17.69	13	tr V8N2C6 V8N2C6_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	5
1467	7.07	7.07	55.28	15.84	15.84	tr V8PFH9 V8PFH9_OPPIHA Rhomboid-like protein OS=Ophiophagus hannah GN=PARL	PE=OPPIHA	4
1468	7.06	7.06	86.36	35.35	16.67	tr V8NN24 V8NN24_OPPIHA 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (Fragm	OPPIHA	3
1469	7.06	7.06	90.26	42.86	42.86	tr V8NE40 V8NE40_OPPIHA 5'-AMP-activated protein kinase subunit beta-1 (Fragmen	OPPIHA	4
1470	7.06	7.06	65.29	38.02	31.4	tr V8N5P8 V8N5P8_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	4
1471	7.05	11.42	47.45	23.36	14.78	tr V8P9X6 V8P9X6_OPPIHA Regulator of differentiation 1 (Fragment) OS=Ophiophag	OPPIHA	6
1472	7.05	7.05	69.66	23.45	23.45	tr V8P1R5 V8P1R5_OPPIHA 60S ribosomal protein L26 OS=Ophiophagus hannah GN=RPL2	OPPIHA	4
1473	7.05	7.05	55.85	32.45	32.45	tr V8NU85 V8NU85_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=L345	O	5
1474	7.04	9.15	63.32	32.16	27.14	tr V8P064 V8P064_OPPIHA Peroxiredoxin-1 OS=Ophiophagus hannah GN=PRDX1	PE=4 SV=OPPIHA	5
1475	7.04	8.25	41.29	11.15	6.446	tr V8NEC5 V8NEC5_OPPIHA Very long-chain acyl-CoA synthetase (Fragment) OS=Ophiop	OPPIHA	4
1476	7.03	8.11	38.58	18.63	18.63	tr V8NZQ9 V8NZQ9_OPPIHA Thrombospondin-4 (Fragment) OS=Ophiophagus hannah GN=TH	OPPIHA	6
1477	7.03	7.03	51.92	16.38	16.38	tr V8PAP9 V8PAP9_OPPIHA 60S ribosomal protein L6 (Fragment) OS=Ophiophagus hann	OPPIHA	4
1478	7.03	7.03	52.73	21.22	18.65	tr V8PGN1 V8PGN1_OPPIHA Alpha-centractin (Fragment) OS=Ophiophagus hannah GN=AC	OPPIHA	4
1479	7.02	7.02	45.83	7.44	3.75	tr V8P6S2 V8P6S2_OPPIHA Receptor-type tyrosine-protein phosphatase F (Fragment)	OPPIHA	4
1480	7.02	7.02	59.42	10.18	8.663	tr V8NPB2 V8NPB2_OPPIHA E3 ubiquitin-protein ligase MIB2 (Fragment) OS=Ophiophag	OPPIHA	4
1481	7.02	7.02	23.55	3.85	3.85	tr V8P787 V8P787_OPPIHA Cysteine-rich with EGF-like domain protein 1 OS=Ophioph	OPPIHA	4
1482	7.01	7.01	34.73	19.46	19.46	tr V8P5X2 V8P5X2_OPPIHA Nuclear inhibitor of protein phosphatase 1 (Fragment) O	OPPIHA	4
1483	7	7	53.55	14.91	6.601	tr V8P2Z1 V8P2Z1_OPPIHA [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kin	OPPIHA	4
1484	6.99	7.66	56.9	10.03	5.208	tr V8P522 V8P522_OPPIHA Protein crooked neck (Fragment) OS=Ophiophagus hannah G	OPPIHA	3
1485	6.98	6.98	63.64	16.04	13.1	tr V8PDR0 V8PDR0_OPPIHA AII receptor-interacting protein (Fragment) OS=Ophiophag	OPPIHA	5
1486	6.96	9.58	45.25	29.41	19	tr V8P072 V8P072_OPPIHA Clathrin light chain A OS=Ophiophagus hannah GN=CLTA	PE	8
1487	6.96	6.96	44.91	9.768	5.438	tr V8PGU8 V8PGU8_OPPIHA Ankyrin repeat and SAM domain-containing protein 1A (Fr	OPPIHA	3
1488	6.96	6.96	36.48	8.863	8.863	tr V8NZ16 V8NZ16_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=	OPPIHA	7
1489	6.96	6.96	62.14	31.43	30.71	tr V8P1S6 V8P1S6_OPPIHA Ferritin OS=Ophiophagus hannah GN=FTTH PE=3 SV=1	OPPIHA	5
1490	6.95	6.95	29.87	4.659	4.659	tr V8NSF0 V8NSF0_OPPIHA Neogenin (Fragment) OS=Ophiophagus hannah GN=NEO1	PE=4	OPPIHA
1491	6.95	6.95	84.72	31.25	31.25	tr V8P2F2 V8P2F2_OPPIHA Ubiquitin-conjugating enzyme E2 variant 2 OS=Ophiophag	OPPIHA	5
1492	6.94	7.26	45.54	6.072	3.582	tr V8NNB3 V8NNB3_OPPIHA Cohesin subunit SA-2 (Fragment) OS=Ophiophagus hannah G	OPPIHA	4
1493	6.93	6.94	23.71	19.59	19.59	tr V8NEH2 V8NEH2_OPPIHA Ubiquinone biosynthesis protein COQ9, mitochondrial (Fr	OPPIHA	4
1494	6.93	6.93	45.06	14.1	11.51	tr V8NM18 V8NM18_OPPIHA D-glucuronyl C5-epimerase OS=Ophiophagus hannah GN=GLCE	OPPIHA	4
1495	6.93	6.93	33.63	30.97	30.97	tr V8NF24 V8NF24_OPPIHA Nicalin (Fragment) OS=Ophiophagus hannah GN=NCLN	PE=4 S	OPPIHA
1496	6.92	8.66	82.59	42.11	22.27	tr V8NED2 V8NED2_OPPIHA Phosphatidylinositol transfer protein alpha isoform (Fr	OPPIHA	4
1497	6.92	6.92	58.59	19.82	19.82	tr V8NQ12 V8NQ12_OPPIHA Hypoxanthine-guanine phosphoribosyltransferase (Fragmen	OPPIHA	5
1498	6.92	6.92	51.32	18.86	18.86	tr V8NAN7 V8NAN7_OPPIHA 2-methoxy-6-polypropenyl-1,4-benzoquinol methylase, mitoc	OPPIHA	4
1499	6.92	6.92	52.6	20.23	17.34	tr V8N2G3 V8N2G3_OPPIHA 40S ribosomal protein S25 (Fragment) OS=Ophiophagus h	OPPIHA	6
1500	6.9	6.93	33.92	5.019	3.726	tr V8P555 V8P555_OPPIHA Phosphorylase b kinase regulatory subunit alpha, skelet	OPPIHA	4
1501	6.9	6.9	62.7	24.6	24.6	tr V8NF52 V8NF52_OPPIHA Protein FAM49B (Fragment) OS=Ophiophagus hannah GN=FAM4	OPPIHA	4
1502	6.89	6.89	38.16	16.89	14.47	tr V8NTW8 V8NTW8_OPPIHA Splicing factor 1 (Fragment) OS=Ophiophagus hannah GN=S	OPPIHA	5
1503	6.89	6.89	54.82	28.92	24.1	tr V8NDF2 V8NDF2_OPPIHA Histone H2A (Fragment) OS=Ophiophagus hannah GN=H2AFV	P	OPPIHA
1504	6.89	6.89	42.22	32.22	32.22	tr V8NG16 V8NG16_OPPIHA Phosphomevalonate kinase (Fragment) OS=Ophiophagus hann	OPPIHA	5
1505	6.88	6.88	49.38	34.57	33.33	tr V8P2Y8 V8P2Y8_OPPIHA Eukaryotic translation initiation factor 1 (Fragment) O	OPPIHA	4
1506	6.87	6.87	24.44	23.7	22.22	tr V8N7D6 V8N7D6_OPPIHA Eukaryotic translation initiation factor 1b (Fragment)	OPPIHA	2
1507	6.87	6.87	33.27	6.518	4.28	tr V8NZZ8 V8NZZ8_OPPIHA L-fucose kinase (Fragment) OS=Ophiophagus hannah GN=FUK	OPPIHA	3
1508	6.87	6.87	51.96	26.96	26.96	tr V8NKC2 V8NKC2_OPPIHA Tumor protein D53-like protein (Fragment) OS=Ophiophagu	OPPIHA	6
1509	6.85	9.08	64.78	19.92	13.84	tr V8N1J1 V8N1J1_OPPIHA Copine-3 OS=Ophiophagus hannah GN=Cpne3	PE=4 SV=1	OPPIHA
1510	6.84	7.25	30.95	15.48	12.3	tr V8NNB5 V8NNB5_OPPIHA Heterogeneous nuclear ribonucleoproteins A2/B1 (Fragmen	OPPIHA	4
1511	6.83	6.83	51.55	8.044	6.307	tr V8NYZ6 V8NYZ6_OPPIHA FERM, RhoGEF and pleckstrin domain-containing protein 2	OPPIHA	4
1512	6.82	6.82	54.27	8.868	6.41	tr V8PJV5 V8PJV5_OPPIHA Oxysterol-binding protein (Fragment) OS=Ophiophagus han	OPPIHA	4
1513	6.82	6.82	41.31	10.37	6.86	tr V8P153 V8P153_OPPIHA Complement component C6 OS=Ophiophagus hannah GN=C6	PE=OPPIHA	3
1514	6.82	6.82	31.18	6.12	6.12	tr V8N7Y3 V8N7Y3_OPPIHA Vascular non-inflammatory molecule 2 (Fragment) OS=Ophi	OPPIHA	4
1515	6.82	6.82	22.52	10.9	10.9	tr V8NVC8 V8NVC8_OPPIHA Proteasomal ubiquitin receptor ADRM1 OS=Ophiophagus han	OPPIHA	4
1516	6.81	7.45	48.39	7.701	6.897	tr V8NSK5 V8NSK5_OPPIHA Protein phosphatase 1 regulatory subunit 12C (Fragment)	OPPIHA	4
1517	6.81	6.81	48.87	48.87	24.81	tr V8N975 V8N975_OPPIHA EH domain-containing protein 3 (Fragment) OS=Ophiophag	OPPIHA	4
1518	6.8	8.46	51.83	17.43	9.021	tr V8NM10 V8NM10_OPPIHA Alpha-adducin (Fragment) OS=Ophiophagus hannah GN=ADD1	OPPIHA	5
1519	6.8	6.8	74.12	55.29	55.29	tr V8NIS3 V8NIS3_OPPIHA Programmed cell death protein 5 OS=Ophiophagus hannah G	OPPIHA	5
1520	6.79	6.86	33.33	7.589	5.804	tr V8N9T4 V8N9T4_OPPIHA Amyloid beta A4 protein-binding family B member 1-inter	OPPIHA	4
1521	6.78	7.97	34.6	21.56	12.09	tr V8NG07 V8NG07_OPPIHA Actin-like protein 6A (Fragment) OS=Ophiophagus hannah	OPPIHA	5
1522	6.78	7.17	54.61	14.54	8.511	tr V8NCD9 V8NCD9_OPPIHA N-acetylneuraminatase lyase (Fragment) OS=Ophiophagus han	OPPIHA	4
1523	6.78	6.78	66.95	24.27	20.5	tr V8PC25 V8PC25_OPPIHA Ribose-5-phosphate isomerase (Fragment) OS=Ophiophagus	OPPIHA	5
1524	6.78	6.78	46.05	34.21	28.95	tr V8N1M7 V8N1M7_OPPIHA Protein C20orf11-like protein OS=Ophiophagus hannah GN=	OPPIHA	4
1525	6.77	6.77	62.95	6.906	5.046	tr V8NN62 V8NN62_OPPIHA LIM domain and actin-binding protein 1 OS=Ophiophagus h	OPPIHA	3
1526	6.77	6.77	39.05	12.19	12.19	tr V8N8V4 V8N8V4_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	4
1527	6.76	11.26	69.27	38.02	29.69	tr V8P053 V8P053_OPPIHA Serine/arginine-rich splicing factor 1 (Fragment) OS=Op	OPPIHA	5
1528	6.74	6.74	40.41	7.37	5.337	tr V8PBK8 V8PBK8_OPPIHA Sister chromatid cohesion protein PDS5-like A (Fragment)	OPPIHA	3
1528	6.74	6.74	45.8	20.17	12.18	tr V8NLA7 V8NLA7_OPPIHA Trafficking protein particle complex subunit 3 (Fragmen	OPPIHA	3

1529	6.74	6.74	68.54	23.97	23.97	tr V8PI86 V8PI86_OPHHA Zinc finger protein (Fragment) OS=Ophiophagus hannah GN OPHHA	5
1530	6.74	6.74	58.93	33.33	23.21	tr V8NIK8 V8NIK8_OPHHA Glutaredoxin-related protein 5, mitochondrial (Fragment OPHHA	5
1531	6.72	10.93	63.31	18.93	18.93	tr V8NG70 V8NG70_OPHHA Protein kinase C alpha type (Fragment) OS=Ophiophagus h OPHHA	7
1532	6.72	6.72	44.26	9.715	5.103	tr V8P913 V8P913_OPHHA Rho GTPase-activating protein 4 (Fragment) OS=Ophiophag OPHHA	4
1533	6.71	6.71	36.36	24.24	17.58	tr V8NFJ5 V8NFJ5_OPHHA Ras GTPase-activating-like protein IQGAP1 (Fragment) OS OPHHA	4
1534	6.7	6.75	50.96	11.27	6.235	tr V8NX10 V8NX10_OPHHA WD repeat and FYVE domain-containing protein 1 OS=Ophio OPHHA	4
1535	6.69	6.72	38.53	14.42	12.77	tr V8N3T6 V8N3T6_OPHHA Thimet oligopeptidase (Fragment) OS=Ophiophagus hannah OPHHA	4
1536	6.69	6.69	58.66	4.398	3.078	tr V8PJ36 V8PJ36_OPHHA 5-azacytidine-induced protein 1 OS=Ophiophagus hannah G OPHHA	3
1537	6.68	6.68	57.92	13.8	9.502	tr V8PDC5 V8PDC5_OPHHA Inositol polyphosphate 1-phosphatase (Fragment) OS=Ophi OPHHA	3
1538	6.68	6.68	46.52	16.96	9.13	tr V8NY27 V8NY27_OPHHA Peptidyl-prolyl cis-trans isomerase-like 4 OS=Ophiophag OPHHA	3
1539	6.66	6.66	53.59	16.99	11.48	tr V8NRM6 V8NRM6_OPHHA Delta(24)-sterol reductase OS=Ophiophagus hannah GN=Dhc OPHHA	4
1540	6.66	6.66	32.62	17.38	17.38	tr V8NC05 V8NC05_OPHHA Tetratricopeptide repeat protein 38 (Fragment) OS=Ophio OPHHA	5
1541	6.65	6.65	55.56	28.24	23.15	tr V8NJS7 V8NJS7_OPHHA Tyrosine-protein kinase CSK (Fragment) OS=Ophiophagus h OPHHA	3
1542	6.65	6.65	60.34	36.31	26.26	tr V8NAL6 V8NAL6_OPHHA 26S proteasome non-ATPase regulatory subunit 8 (Fragmen OPHHA	3
1543	6.64	7.61	44.71	14.18	12.02	tr V8NV52 V8NV52_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	5
1544	6.64	6.64	52.01	12.07	12.07	tr V8NIT0 V8NIT0_OPHHA Ras-related protein Rab-11B (Fragment) OS=Ophiophagus h OPHHA	4
1544	0.03	5.15	50.74	12.59	12.59	tr V8NJW9 V8NJW9_OPHHA Ras-related protein Rab-11B (Fragment) OS=Ophiophagus h OPHHA	3
1545	6.64	6.64	61.92	19.62	15.77	tr V8PH96 V8PH96_OPHHA Transcription elongation factor A protein 1 OS=Ophiophag OPHHA	4
1546	6.63	6.63	39.68	5.864	3.656	tr V8PIX6 V8PIX6_OPHHA Calmodulin-regulated spectrin-associated protein 3 OS=O OPHHA	3
1547	6.63	6.63	44.99	10.51	7.882	tr V8NVT2 V8NVT2_OPHHA Nuclear pore complex protein Nup93 OS=Ophiophagus hanna OPHHA	4
1548	6.63	6.63	55.78	27.21	16.33	tr V8NEG8 V8NEG8_OPHHA Cell differentiation protein RCD1-like protein OS=Ophio OPHHA	4
1549	6.62	6.62	48.62	15.69	12.92	tr V8PEC2 V8PEC2_OPHHA Replication factor C subunit 2 (Fragment) OS=Ophiophagu OPHHA	3
1550	6.61	6.61	46.83	18.25	11.11	tr V8NQQ7 V8NQQ7_OPHHA Malonyl-CoA decarboxylase, mitochondrial (Fragment) OS= OPHHA	3
1551	6.61	6.61	48.8	19.16	17.07	tr V8NR53 V8NR53_OPHHA Phytanoyl-CoA dioxygenase domain-containing protein 1 (OPHHA	3
1552	6.6	6.6	55.61	22.43	22.43	tr V8NG88 V8NG88_OPHHA 5'-AMP-activated protein kinase subunit beta-2 (Fragmen OPHHA	4
1553	6.59	6.59	45.83	12	8.833	tr V8NWP4 V8NWP4_OPHHA Inhibitor of nuclear factor kappa-B kinase subunit beta OPHHA	4
1554	6.59	6.59	29.04	6.933	3.507	tr V8NN87 V8NN87_OPHHA Antigen (Fragment) OS=Ophiophagus hannah GN=CD109 PE=4 OPHHA	3
1555	6.59	6.59	35.76	15.95	11.16	tr V8NMM7 V8NMM7_OPHHA Serine palmitoyltransferase 1 OS=Ophiophagus hannah GN= OPHHA	3
1556	6.56	6.56	39.5	11.27	6.88	tr V8PIF5 V8PIF5_OPHHA Diacylglycerol kinase (Fragment) OS=Ophiophagus hannah OPHHA	4
1557	6.56	6.56	46.72	12.09	10.66	tr V8PAZ5 V8PAZ5_OPHHA Phosphoacetylglucosamine mutase (Fragment) OS=Ophiophag OPHHA	4
1558	6.55	6.55	34.57	23.4	23.4	tr V8PSW4 V8PSW4_OPHHA PRAL family protein 3 OS=Ophiophagus hannah GN=ARL6IP5 OPHHA	4
1559	6.54	6.54	52.01	10.12	5.825	tr V8NMF8 V8NMF8_OPHHA Pre-mRNA-processing factor 40-like A (Fragment) OS=Ophi OPHHA	3
1560	6.53	6.53	45.17	17.76	12.77	tr V8NAB7 V8NAB7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	3
1561	6.52	6.52	57.87	12.06	7.168	tr V8ND02 V8ND02_OPHHA Dynactin subunit 1 (Fragment) OS=Ophiophagus hannah GN= OPHHA	3
1562	6.52	6.52	48.04	12.69	12.39	tr V8NVY1 V8NVY1_OPHHA PDZ domain-containing protein GIPC1 OS=Ophiophagus hann OPHHA	3
1563	6.51	6.53	42.47	4.61	2.766	tr V8PJ1 V8PJ1_OPHHA Arf-GAP with SH3 domain, ANK repeat and PH domain-conta OPHHA	3
1564	6.51	6.52	70.59	28.57	22.69	tr V8NSS7 V8NSS7_OPHHA 40S ribosomal protein S20 OS=Ophiophagus hannah GN=rps2 OPHHA	3
1565	6.5	6.5	43.77	13.13	9.259	tr V8PHM1 V8PHM1_OPHHA Nuclear protein localization protein 4-like protein (Fr OPHHA	3
1566	6.46	6.46	51.8	27.48	23.42	tr V8N9A4 V8N9A4_OPHHA Acetolactate synthase-like protein (Fragment) OS=Ophiop OPHHA	3
1567	6.46	6.46	29.13	24.27	19.42	tr V8POY4 V8POY4_OPHHA 26S proteasome non-ATPase regulatory subunit 7 (Fragmen OPHHA	3
1568	6.45	6.45	44.4	12.2	9.078	tr V8P5K0 V8P5K0_OPHHA Extended synaptotagmin-2-B (Fragment) OS=Ophiophagus ha OPHHA	4
1569	6.44	6.44	41.32	5.933	4.432	tr V8NY58 V8NY58_OPHHA Intron-binding protein aquarius OS=Ophiophagus hannah G OPHHA	4
1570	6.44	6.44	37.64	6.383	4.419	tr V8P2U1 V8P2U1_OPHHA Ornithine decarboxylase 2 (Fragment) OS=Ophiophagus han OPHHA	4
1571	6.44	6.44	48.84	12.79	7.752	tr V8PAK3 V8PAK3_OPHHA Pyridine nucleotide-disulfide oxidoreductase domain-con OPHHA	3
1572	6.44	6.44	37.29	20.34	15.59	tr V8P6F1 V8P6F1_OPHHA Poly(RC)-binding protein 3 (Fragment) OS=Ophiophagus ha OPHHA	4
1573	6.43	6.43	56	26.5	22	tr V8NB33 V8NB33_OPHHA UV excision repair protein RAD23-like B OS=Ophiophagus OPHHA	6
1574	6.42	17.74	61.26	16.23	15.05	tr V8NQ85 V8NQ85_OPHHA Kinesin light chain 1 (Fragment) OS=Ophiophagus hannah OPHHA	10
1575	6.42	7.72	49.87	6.774	2.879	tr V8P6U8 V8P6U8_OPHHA Vigilin OS=Ophiophagus hannah GN=HDLBP PE=4 SV=1 OPHHA	4
1576	6.42	6.42	73.71	29.38	20.62	tr V8PB12 V8PB12_OPHHA Synaptobrevin-like YKT6-B OS=Ophiophagus hannah GN=ykt6 OPHHA	3
1577	6.41	6.42	44.24	16.62	14.21	tr V8NI66 V8NI66_OPHHA Syntaxin-5 (Fragment) OS=Ophiophagus hannah GN=STX5 PE= OPHHA	4
1578	6.41	6.41	47.23	13.06	8.766	tr V8NC40 V8NC40_OPHHA Dipeptidyl peptidase 9 (Fragment) OS=Ophiophagus hannah OPHHA	4
1579	6.41	6.41	33.33	33.33	28.07	tr V8PF68 V8PF68_OPHHA Enhancer of rudimentary homolog OS=Ophiophagus hannah G OPHHA	5
1580	6.4	6.65	54.59	11.47	7.126	tr V8P1R2 V8P1R2_OPHHA Dystrobrevin alpha (Fragment) OS=Ophiophagus hannah GN= OPHHA	4
1581	6.4	6.52	67.27	20.36	18.55	tr V8PH30 V8PH30_OPHHA WD repeat-containing protein 82 (Fragment) OS=Ophiophag OPHHA	4
1582	6.4	6.4	44.87	3.865	2.415	tr V8P7S1 V8P7S1_OPHHA Cortactin-binding protein 2 OS=Ophiophagus hannah GN=CT OPHHA	4
1583	6.4	6.4	36.69	8.633	7.374	tr V8P2J8 V8P2J8_OPHHA Tyrosine aminotransferase OS=Ophiophagus hannah GN=Tat OPHHA	3
1584	6.4	6.4	32.23	15.67	12.36	tr V8NXS1 V8NXS1_OPHHA RNA-binding protein 42 (Fragment) OS=Ophiophagus hannah OPHHA	3
1585	6.39	11.16	50.74	25	16.09	tr V8NZ79 V8NZ79_OPHHA Serine/threonine-protein kinase 24 (Fragment) OS=Ophio OPHHA	5
1586	6.39	6.39	32.96	5.817	4.848	tr V8PJ40 V8PJ40_OPHHA Poly(A) polymerase alpha OS=Ophiophagus hannah GN=PAPOL OPHHA	3
1587	6.39	6.39	44.06	17.94	7.652	tr V8NKK0 V8NKK0_OPHHA Abl interactor 1 (Fragment) OS=Ophiophagus hannah GN=Ab OPHHA	3
1588	6.38	6.42	52.62	4.499	2.59	tr V8NJM4 V8NJM4_OPHHA DNA topoisomerase 2 (Fragment) OS=Ophiophagus hannah GN OPHHA	3
1589	6.38	6.38	38.04	20.25	15.03	tr V8PDL2 V8PDL2_OPHHA Uroporphyrinogen decarboxylase (Fragment) OS=Ophiophagu OPHHA	4
1590	6.38	6.38	56.04	17.22	13.92	tr V8PBS2 V8PBS2_OPHHA 60S ribosomal protein L23 OS=Ophiophagus hannah GN=RPL2 OPHHA	4
1591	6.37	6.37	29.26	7.882	4.138	tr V8NJ15 V8NJ15_OPHHA Apoptosis-stimulating of p53 protein 2 (Fragment) OS=Op OPHHA	3
1592	6.37	6.37	36.68	17.3	13.15	tr V8P4N4 V8P4N4_OPHHA Inosine-uridine preferring nucleoside hydrolase (Fragme OPHHA	4
1593	6.36	16.84	62.29	27.54	27.54	tr V8PDL7 V8PDL7_OPHHA Gamma-enolase (Fragment) OS=Ophiophagus hannah GN=ENO2 OPHHA	11
1594	6.36	6.36	29.38	6.623	6.623	tr V8NPL6 V8NPL6_OPHHA Serine/threonine-protein phosphatase 6 regulatory ankyr OPHHA	4
1595	6.35	6.55	32.78	7.851	4.024	tr V8P3F2 V8P3F2_OPHHA Pikachurin (Fragment) OS=Ophiophagus hannah GN=EGFLAM P OPHHA	3
1596	6.35	6.35	73.24	15.41	12.43	tr V8N5V9 V8N5V9_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	4
1597	6.34	6.34	84.38	31.87	27.5	tr V8PC39 V8PC39_OPHHA 60S ribosomal protein L21 OS=Ophiophagus hannah GN=RPL2 OPHHA	4
1598	6.34	6.34	30.37	20.25	17.48	tr V8PCR6 V8PCR6_OPHHA Cytosolic Fe-S cluster assembly factor NUBP1 OS=Ophioph OPHHA	3
1599	6.34	6.34	77.98	45.87	38.53	tr V8N801 V8N801_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	3
1600	6.33	6.33	67.65	30.88	21.57	tr V8N9Z3 V8N9Z3_OPHHA Ribosomal protein L15 OS=Ophiophagus hannah GN=RPL15 PE OPHHA	3
1601	6.33	6.33	47.04	13.24	11.11	tr V8NPQ8 V8NPQ8_OPHHA Laminin subunit alpha-5 (Fragment) OS=Ophiophagus hanna OPHHA	3
1602	6.33	6.33	31.58	19.65	16.14	tr V8PH42 V8PH42_OPHHA CCR4-NOT transcription complex subunit 7 (Fragment) OS= OPHHA	3
1603	6.32	6.32	59.79	17.99	16.4	tr V8P9N3 V8P9N3_OPHHA Thioredoxin domain-containing protein 5 OS=Ophiophagus OPHHA	3
1604	6.31	6.31	56.3	26.39	16.72	tr V8PAK1 V8PAK1_OPHHA Coiled-coil domain-containing protein OS=Ophiophagus ha OPHHA	3
1605	6.31	6.31	43.43	19.19	13.47	tr V8N5W2 V8N5W2_OPHHA Vinexin (Fragment) OS=Ophiophagus hannah GN=Sorbs3 PE=4 OPHHA	3
1606	6.3	6.3	41.77	3.836	3.069	tr V8P890 V8P890_OPHHA Plectstrin-likey domain-containing family A member 5 (F OPHHA	3
1607	6.3	6.3	33.86	20.63	20.11	tr V8PE08 V8PE08_OPHHA NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, OPHHA	5
1608	6.29	13.67	44.98	25.34	15.3	tr V8P9A2 V8P9A2_OPHHA Septin-11 (Fragment) OS=Ophiophagus hannah GN=SEPT11 PE OPHHA	6
1609	6.29	6.29	63.09	20.17	19.74	tr V8NYP1 V8NYP1_OPHHA Vesicle-associated membrane protein-associated protein OPHHA	6
1610	6.29	6.29	43.75	37.5	27.5	tr V8NA78 V8NA78_OPHHA Iron-sulfur cluster assembly l-like, mitochondrial (Fra OPHHA	3
1611	6.28	6.28	79.63	41.67	26.85	tr V8NQ20 V8NQ20_OPHHA CDGSH iron-sulfur domain-containing protein 1 OS=Ophio OPHHA	5
1612	6.26	6.29	42.47	6.365	3.794	tr V8P829 V8P829_OPHHA Plexin-A1 (Fragment) OS=Ophiophagus hannah GN=P1xna1 PE OPHHA	3
1612	0.02	5.53	48.31	2.753	2.753	tr V8NMA3 V8NMA3_OPHHA Plexin-A4 (Fragment) OS=Ophiophagus hannah GN=P1xna4 PE OPHHA	3
1613	6.26	6.26	62.57	13.71	10.86	tr V8N7E8 V8N7E8_OPHHA Dysferlin (Fragment) OS=Ophiophagus hannah GN=Dysf PE=4 OPHHA	3
1614	6.26	6.26	36.66	12.06	7.657	tr V8PBF0 V8PBF0_OPHHA Carboxymethylenebutenolidase-like protein (Fragment) OS OPHHA	4
1615	6.26	6.26	34.08	11.8	9.8	tr V8P5B6 V8P5B6_OPHHA Antigen (Fragment) OS=Ophiophagus hannah GN=ALCAM PE=4 OPHHA	3
1616	6.26	6.26	28.09	12.58	7.757	tr V8P270 V8P270_OPHHA Serine/threonine-protein phosphatase 2A 56 kDa regulato OPHHA	3
1617	6.26	6.26	79.81	37.5	27.88	tr V8P3S5 V8P3S5_OPHHA Ras-related protein Rab-21 OS=Ophiophagus hannah GN=Rab OPHHA	3
1618	6.25	6.27	42.32	4.159	2.481	tr V8PEU2 V8PEU2_OPHHA Sacsin (Fragment) OS=Ophiophagus hannah GN=SACS PE=4 SV OPHHA	7
1619	6.25	6.25	52.46	9.275	4.783	tr V8NE31 V8NE31_OPHHA Putative leucine-rich repeat-containing protein (Fragme OPHHA	3
1620	6.25	6.25	45.79	7.477	6.008	tr V8P4S3 V8P4S3_OPHHA Putative ATP-dependent RNA helicase DDX58 OS=Ophiophagu OPHHA	5
1621	6.25	6.25	65.8	28.5	28.5	tr V8NGD4 V8NGD4_OPHHA Cysteine and glycine-rich protein 2 OS=Ophiophagus hann OPHHA	4
1622	6.24	6.24	51.51	6.763	4.892	tr V8NAJ6 V8NAJ6_OPHHA Ena/VASP-like protein OS=Ophiophagus hannah GN=Evl PE=4 OPHHA	3

1623	6.23	6.23	54.64	9.731	7.934	tr V8PCF0 V8PCF0_OPPIHA Sulfotransferase 1C2 (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1624	6.23	6.23	55.36	16.31	16.31	tr V8NPG2 V8NPG2_OPPIHA THUMP domain-containing protein 1 (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1625	6.22	6.23	34.7	8.499	7.649	tr V8N6N4 V8N6N4_OPPIHA Antigen peptide transporter 1 (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1626	6.22	6.22	33.92	7.941	6.326	tr V8PAE9 V8PAE9_OPPIHA Ubiquitin-like modifier-activating enzyme 1 (Fragment) OPPIHA	5
1627	6.22	6.22	64.53	25.58	19.77	tr V8NJN7 V8NJN7_OPPIHA Proteasome subunit beta type-7 (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1628	6.21	6.21	28.54	7.029	5.857	tr V8NKG2 V8NKG2_OPPIHA Fibronectin type-III domain-containing protein 3a (Fragment) OPPIHA	3
1629	6.21	6.21	65.2	26.96	11.91	tr V8PE13 V8PE13_OPPIHA Developmentally-regulated GTP-binding protein 2 OS=Ophiophagus hannah G OPPIHA	3
1630	6.21	6.21	61.78	20.67	15.87	tr V8NHZ7 V8NHZ7_OPPIHA Paralemmin-1 (Fragment) OS=Ophiophagus hannah GN=PALM P OPPIHA	5
1631	6.2	6.2	36.56	6.503	4.745	tr V8PID1 V8PID1_OPPIHA CUGBP Elav-like family member 1 OS=Ophiophagus hannah G OPPIHA	3
1632	6.19	6.19	47.09	9.419	7.615	tr V8N9U9 V8N9U9_OPPIHA Atlastin-3 (Fragment) OS=Ophiophagus hannah GN=At13 PE= OPPIHA	4
1633	6.19	6.19	58.12	18.38	18.38	tr V8P2Q7 V8P2Q7_OPPIHA Proliferating cell nuclear antigen OS=Ophiophagus hannah G OPPIHA	3
1634	6.19	6.19	83.93	52.68	39.29	tr V8NH75 V8NH75_OPPIHA V-type proton ATPase subunit F (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1635	6.16	6.29	57.76	13.7	10.05	tr V8NME0 V8NME0_OPPIHA Luc7-like protein 3 OS=Ophiophagus hannah GN=LUC7L3 PE= OPPIHA	3
1636	6.16	6.16	45.07	4.876	4.179	tr V8PBX0 V8PBX0_OPPIHA Alpha-amylase (Fragment) OS=Ophiophagus hannah GN=Amy2 OPPIHA	3
1637	6.16	6.16	62.44	21.32	21.32	tr V8NQ62 V8NQ62_OPPIHA Prostaglandin E synthase 3 (Fragment) OS=Ophiophagus hannah G OPPIHA	6
1638	6.16	6.16	60.8	25.6	25.6	tr V8NQ46 V8NQ46_OPPIHA 60S ribosomal protein L31 OS=Ophiophagus hannah GN=RPL31 OPPIHA	3
1639	6.15	6.15	69.36	12.42	10.35	tr V8PA17 V8PA17_OPPIHA SURP and G-patch domain-containing protein 1 (Fragment) OPPIHA	4
1640	6.15	6.15	43.32	18.99	13.95	tr V8NEF5 V8NEF5_OPPIHA Dihydropyrimidinase-residue acetyltransferase component OPPIHA	3
1641	6.14	8.17	76.54	16.87	16.87	tr V8NF78 V8NF78_OPPIHA Decorin (Fragment) OS=Ophiophagus hannah GN=DCN PE=4 SV OPPIHA	4
1642	6.14	6.14	34.33	7.794	7.794	tr V8NDH0 V8NDH0_OPPIHA Eukaryotic translation initiation factor 4 gamma 3 (Fra OPPIHA	3
1643	6.14	6.14	58.22	21.05	14.8	tr V8NL73 V8NL73_OPPIHA Extracellular matrix protein 1 (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1644	6.12	6.13	38.39	7.1	5.415	tr V8PHB7 V8PHB7_OPPIHA Trafficking protein particle complex subunit 12 (Fragment) OPPIHA	3
1645	6.12	6.12	49.79	10.7	5.487	tr V8POS1 V8POS1_OPPIHA Leucine-rich repeat-containing protein 8D (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1646	6.12	6.12	54.79	12.79	9.589	tr V8ND66 V8ND66_OPPIHA Dynactin subunit 1 (Fragment) OS=Ophiophagus hannah GN= OPPIHA	4
1647	6.12	6.12	40.72	12.74	8.033	tr V8P695 V8P695_OPPIHA Protein XRP2 OS=Ophiophagus hannah GN=RP2 PE=3 SV=1 OPPIHA	3
1648	6.12	6.12	73.68	21.53	18.18	tr V8NRL8 V8NRL8_OPPIHA Malectin OS=Ophiophagus hannah GN=MLEC PE=4 SV=1 OPPIHA	3
1649	6.12	6.12	33.09	17.28	14.34	tr V8NP91 V8NP91_OPPIHA Serum paraoxonase/arylesterase 2 OS=Ophiophagus hannah G OPPIHA	6
1650	6.1	7.16	55.84	7.721	4.143	tr V8NQ88 V8NQ88_OPPIHA EH domain-binding protein 1 (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1651	6.1	6.12	37.06	5.637	5.637	tr V8PFU6 V8PFU6_OPPIHA C-Jun-amino-terminal kinase-interacting protein 4 OS=Ophiophagus hannah G OPPIHA	4
1652	6.1	6.1	60.19	13.79	13.79	tr V8NV08 V8NV08_OPPIHA ADP-ribose pyrophosphatase, mitochondrial OS=Ophiophagus hannah G OPPIHA	4
1653	6.1	6.1	48.1	12.36	12.36	tr V8NW84 V8NW84_OPPIHA Mothers against decapentaplegic homolog (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1654	6.09	6.09	58.19	11.34	11.34	tr V8P615 V8P615_OPPIHA Transmembrane and coiled-coil domains protein 3 (Fragment) OPPIHA	3
1655	6.09	6.09	38.63	8.155	8.155	tr V8P4R3 V8P4R3_OPPIHA Protein disulfide-isomerase TMX3 (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1656	6.08	6.11	50.64	8.227	3.291	tr V8P973 V8P973_OPPIHA Cytosolin-A OS=Ophiophagus hannah GN=SPECC1L PE=4 SV=1 OPPIHA	3
1657	6.08	6.08	53.01	9.452	6.849	tr V8P4A8 V8P4A8_OPPIHA Paraplegin (Fragment) OS=Ophiophagus hannah GN=Sp7 PE= OPPIHA	3
1658	6.08	6.08	56.45	18.82	18.82	tr V8P627 V8P627_OPPIHA Spermidine synthase (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1659	6.07	13.02	33.76	25.85	19.87	tr V8NGF1 V8NGF1_OPPIHA Importin subunit alpha-3 (Fragment) OS=Ophiophagus hannah G OPPIHA	6
1660	6.07	6.08	44.57	19.29	11.14	tr V8PFK0 V8PFK0_OPPIHA cGMP-dependent protein kinase 1 (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1661	6.07	6.07	32.29	5.643	5.016	tr V8P3L8 V8P3L8_OPPIHA Importin-11 (Fragment) OS=Ophiophagus hannah GN=IPO11 P OPPIHA	3
1662	6.07	6.07	20.24	5.283	3.199	tr V8NUW4 V8NUW4_OPPIHA Latent-transforming growth factor beta-binding protein OPPIHA	3
1663	6.07	6.07	42.95	10.07	10.07	tr V8POT8 V8POT8_OPPIHA Coagulation factor XIII A chain (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1664	6.07	6.07	31.93	14.71	14.71	tr V8NBH5 V8NBH5_OPPIHA Acyl-CoA dehydrogenase family member 11 OS=Ophiophagus hannah G OPPIHA	3
1665	6.06	7.63	28.72	10.24	10.24	tr V8PF08 V8PF08_OPPIHA Sodium/glucose cotransporter 5 (Fragment) OS=Ophiophagus hannah G OPPIHA	5
1666	6.06	6.06	77.87	13.73	10.92	tr V8NBC8 V8NBC8_OPPIHA Egl nine-like 1 (Fragment) OS=Ophiophagus hannah GN=EGF OPPIHA	3
1667	6.06	6.06	54.96	16.35	11.8	tr V8NQ83 V8NQ83_OPPIHA Long-chain-fatty-acid--CoA ligase 5 OS=Ophiophagus hannah G OPPIHA	4
1668	6.06	6.06	49.13	16.38	13.59	tr V8NUQ3 V8NUQ3_OPPIHA Mitochondrial-processing peptidase subunit alpha (Fragment) OPPIHA	3
1669	6.06	6.06	39.86	13.17	13.17	tr V8NE57 V8NE57_OPPIHA Serine/threonine-protein phosphatase (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1670	6.05	6.14	36.43	13.82	11.56	tr V8N9F0 V8N9F0_OPPIHA Protein TFG OS=Ophiophagus hannah GN=TFG PE=4 SV=1 OPPIHA	4
1671	6.05	6.06	53.99	12.55	9.506	tr V8NAJ7 V8NAJ7_OPPIHA 3-ketoacyl-CoA thiolase, mitochondrial (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1672	6.05	6.05	64.29	14.94	14.94	tr V8NUV3 V8NUV3_OPPIHA 40S ribosomal protein S23 (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1673	6.05	6.05	63.64	16.08	16.08	tr V8NW17 V8NW17_OPPIHA 40S ribosomal protein S23 OS=Ophiophagus hannah GN=RPS2 OPPIHA	3
1674	6.04	6.07	34.29	15.71	13.14	tr V8P7Q9 V8P7Q9_OPPIHA Complement component C8 alpha chain (Fragment) OS=Ophiophagus hannah G OPPIHA	5
1675	6.04	6.04	47.62	8.617	11.74	tr V8NUE2 V8NUE2_OPPIHA Enoyl-CoA hydratase domain-containing protein 1 (Fragment) OPPIHA	3
1676	6.04	6.04	53.33	21.28	8.617	tr V8NEZ7 V8NEZ7_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1677	6.04	6.04	90.84	35.88	12.82	tr V8P068 V8P068_OPPIHA Phosphorylated adapter RNA export protein (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1678	6.04	6.04	30.57	14.51	35.88	tr V8NGB8 V8NGB8_OPPIHA Succinate dehydrogenase [ubiquinone] iron-sulfur subunit OPPIHA	6
1679	6.03	30.74	60.56	47.5	14.51	tr V8PC01 V8PC01_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1680	6.03	10.1	45.42	29.01	47.5	tr V8N532 V8N532_OPPIHA Tubulin beta-2A chain OS=Ophiophagus hannah GN=TUBB2A P OPPIHA	24
1681	6.03	6.03	61.47	22.48	25.57	tr V8PGX8 V8PGX8_OPPIHA Guanine nucleotide-binding protein G(K) subunit alpha (Fragment) OPPIHA	5
1682	6.03	6.03	47.91	9.424	5.963	tr V8NT73 V8NT73_OPPIHA Coproporphyrinogen-III oxidase, mitochondrial (Fragment) OPPIHA	2
1683	6.03	6.03	59.73	30.87	9.424	tr V8PBB2 V8PBB2_OPPIHA Quinone oxidoreductase (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1684	6.03	6.03	51	37	30.87	tr V8NW79 V8NW79_OPPIHA Golgi-associated plant pathogenesis-related protein 1 (Fragment) OPPIHA	3
1685	6.02	6.25	72	44.8	37	tr V8NNB6 V8NNB6_OPPIHA MICOS complex subunit MIC13 OS=Ophiophagus hannah GN=qi OPPIHA	3
1686	6.02	6.03	64.81	17.41	36	tr V8NNX2 V8NNX2_OPPIHA Arginyl-tRNA synthetase, cytoplasmic (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1687	6.02	6.02	47.12	12.5	17.41	tr V8P3K8 V8P3K8_OPPIHA Integrin alpha-X (Fragment) OS=Ophiophagus hannah GN=IT OPPIHA	4
1688	6.02	6.02	67.96	29.28	10.19	tr V8P360 V8P360_OPPIHA Interferon regulatory factor 2-binding protein-like protein OPPIHA	3
1689	6.01	6.01	42.23	16.22	29.28	tr V8NS34 V8NS34_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1690	6.01	6.01	27.1	15.89	16.22	tr V8NT58 V8NT58_OPPIHA Integral membrane protein 2A (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1691	6	6.04	32.92	15	15.89	tr V8NMX5 V8NMX5_OPPIHA Acidic leucine-rich nuclear phosphoprotein 32 family member OPPIHA	3
1692	6	6	53.33	3.546	15	tr V8NXM1 V8NXM1_OPPIHA MOB kinase activator 1B (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1693	6	6	47.06	10.59	3.546	tr V8NM86 V8NM86_OPPIHA Collagen alpha-1(III) chain OS=Ophiophagus hannah GN=CO OPPIHA	3
1694	6	6	52	18	10.59	tr V8NGH9 V8NGH9_OPPIHA PDZ and LIM domain protein 2 OS=Ophiophagus hannah GN=P OPPIHA	3
1695	6	6	26.61	7.752	18	tr V8PFC0 V8PFC0_OPPIHA Prefoldin subunit 4 (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1696	6	6	66.2	35.92	7.752	tr V8P5D4 V8P5D4_OPPIHA Monoacylglycerol lipase ABHD6 (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1697	6	6	56.86	20.59	35.92	tr V8P037 V8P037_OPPIHA DNA-directed RNA polymerase II subunit RPB4 OS=Ophiophagus hannah G OPPIHA	3
1698	6	6	40.11	19.79	20.59	tr V8N8F7 V8N8F7_OPPIHA Bifunctional ATP-dependent dihydroxyacetone kinase/FAD- OPPIHA	3
1699	6	6	60.47	27.91	19.79	tr V8N9W6 V8N9W6_OPPIHA Glycine N-methyltransferase (Fragment) OS=Ophiophagus hannah G OPPIHA	4
1700	6	6	34.93	26.03	27.91	tr V8NJP1 V8NJP1_OPPIHA Galectin OS=Ophiophagus hannah GN=L345_11938 PE=4 SV=1 OPPIHA	6
1701	6	6	60.42	51.04	26.03	tr V8P5H9 V8P5H9_OPPIHA Cystatin-B OS=Ophiophagus hannah GN=CSTB PE=4 SV=1 OPPIHA	3
1702	5.96	5.96	81.3	15.27	51.04	tr V8NIV8 V8NIV8_OPPIHA Dynein light chain roadblock-type 2 OS=Ophiophagus hannah G OPPIHA	5
1703	5.96	5.96	78.85	18.06	15.27	tr V8NYC5 V8NYC5_OPPIHA Spindlin-2 (Fragment) OS=Ophiophagus hannah GN=SPIN2 PE OPPIHA	3
1704	5.95	6.13	29.03	5.963	18.06	tr V8NZW8 V8NZW8_OPPIHA Charged multivesicular body protein 4b OS=Ophiophagus hannah G OPPIHA	3
1705	5.95	6.06	36.8	8.696	3.91	tr V8NTN1 V8NTN1_OPPIHA Nuclear factor of activated T-cells, cytoplasmic 3 (Fra OPPIHA	3
1706	5.95	5.95	61.95	21.95	4.242	tr V8NRY4 V8NRY4_OPPIHA Solute carrier family 12 member 4 OS=Ophiophagus hannah G OPPIHA	3
1707	5.94	5.94	39.86	4.447	18.54	tr V8NC54 V8NC54_OPPIHA Biliverdin reductase A (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1708	5.94	5.94	43.42	5.156	2.921	tr V8NZY5 V8NZY5_OPPIHA F-box/LRR-repeat protein 3 (Fragment) OS=Ophiophagus hannah G OPPIHA	6
1709	5.94	5.94	34.59	9.412	2.307	tr V8PAQ4 V8PAQ4_OPPIHA Putative global transcription activator SMF2L2 (Fragment) OPPIHA	2
1710	5.93	5.93	27.03	22.07	7.529	tr V8P7Y1 V8P7Y1_OPPIHA Lysocardiolipin acyltransferase 1 OS=Ophiophagus hannah G OPPIHA	3
1711	5.93	5.93	69.23	21.54	22.07	tr V8P386 V8P386_OPPIHA Complement component 1 Q subcomponent-binding protein, OPPIHA	5
1712	5.91	5.93	39.34	16.63	21.54	tr V8P7R5 V8P7R5_OPPIHA Septin-11 (Fragment) OS=Ophiophagus hannah GN=SEPT11 PE OPPIHA	3
1713	5.91	5.91	52.84	8.295	10.54	tr V8PHL8 V8PHL8_OPPIHA Serum deprivation-response protein OS=Ophiophagus hannah G OPPIHA	4
1714	5.91	5.91	67.76	14.47	7.22	tr V8PDT9 V8PDT9_OPPIHA U4/U6 small nuclear ribonucleoprotein Prp3 (Fragment) OPPIHA	4
1715	5.91	5.91	50	40.28	11.51	tr V8P823 V8P823_OPPIHA Epithelial cell adhesion molecule OS=Ophiophagus hannah G OPPIHA	3
1716	5.9	5.9	38.9	15.85	30.56	tr V8NF61 V8NF61_OPPIHA 60S ribosomal protein L38 (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1717	5.89	5.89	33.33	17.62	15.85	tr V8N4C0 V8N4C0_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	3
					17.62	tr V8P6T5 V8P6T5_OPPIHA Syntaxin-12 OS=Ophiophagus hannah GN=STX12 PE=4 SV=1 OPPIHA	3

1718	5.88	5.88	25.97	7.759	4.31	tr	V8NWL2	V8NWL2_OPPIHA Alpha-mannosidase (Fragment) OS=Ophiophagus hannah GN=M OPPIHA	3
1719	5.88	5.88	51.08	13.85	13.85	tr	V8NYT0	V8NYT0_OPPIHA Protein CWC15-like protein OS=Ophiophagus hannah GN=CWC OPPIHA	4
1720	5.86	5.86	41.24	6.768	4.618	tr	V8P7D8	V8P7D8_OPPIHA Ankyrin repeat domain-containing protein 13D OS=Ophiophagus hannah GN=V8P7D8 OPPIHA	4
1721	5.86	5.86	55.74	7.916	5.008	tr	V8NFA2	V8NFA2_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=V8NFA2 OPPIHA	3
1722	5.86	5.86	60.73	7.287	7.287	tr	V8P4C6	V8P4C6_OPPIHA 40S ribosomal protein S18 (Fragment) OS=Ophiophagus hannah GN=V8P4C6 OPPIHA	3
1723	5.85	5.85	62.41	25.31	8.772	tr	V8N148	V8N148_OPPIHA Mitogen-activated protein kinase 3 (Fragment) OS=Ophiophagus hannah GN=V8N148 OPPIHA	3
1724	5.85	5.85	57.92	9.836	3.825	tr	V8P177	V8P177_OPPIHA Huntingtin-interacting protein 1 OS=Ophiophagus hannah GN=V8P177 OPPIHA	3
1725	5.85	5.85	60.28	20.09	9.112	tr	V8NWT9	V8NWT9_OPPIHA AP-3 complex subunit mu-1 (Fragment) OS=Ophiophagus hannah GN=V8NWT9 OPPIHA	3
1726	5.85	5.85	51.76	24.12	19.41	tr	V8NKK3	V8NKK3_OPPIHA 60S ribosomal protein L14 (Fragment) OS=Ophiophagus hannah GN=V8NKK3 OPPIHA	3
1727	5.85	5.85	26.12	5.683	5.683	tr	V8NZM7	V8NZM7_OPPIHA Cadherin-2 (Fragment) OS=Ophiophagus hannah GN=CDH2 PE= OPPIHA	3
1728	5.84	5.85	44.4	9.483	9.052	tr	V8N7T6	V8N7T6_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=V8N7T6 OPPIHA	3
1729	5.84	5.84	41.53	7.023	5.344	tr	V8P7T3	V8P7T3_OPPIHA Coagulation factor XIII B chain OS=Ophiophagus hannah GN=V8P7T3 OPPIHA	3
1730	5.84	5.84	57.94	11.18	11.18	tr	V8NYF8	V8NYF8_OPPIHA Nuclear receptor coactivator 5 OS=Ophiophagus hannah GN=V8NYF8 OPPIHA	3
1731	5.83	5.83	55.1	11.89	11.89	tr	V8P235	V8P235_OPPIHA Methylmalonic aciduria type A protein, mitochondrial (F) OPPIHA	3
1732	5.82	5.82	28.47	11.31	11.31	tr	V8N688	V8N688_OPPIHA ATP-binding cassette sub-family A member 8-B (Fragment) OPPIHA	3
1733	5.82	5.82	39.79	18.85	16.23	tr	V8N6N1	V8N6N1_OPPIHA Transmembrane protein 33 OS=Ophiophagus hannah GN=V8N6N1 OPPIHA	3
1734	5.82	5.82	89.83	72.88	72.88	tr	V8N290	V8N290_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=V8N290 OPPIHA	3
1735	5.81	5.83	59.62	13.53	6.977	tr	V8P9M4	V8P9M4_OPPIHA Calcium-binding mitochondrial carrier protein SCAAC-3 (OPPIHA	3
1736	5.81	5.81	38.19	9.055	9.055	tr	V8P9T6	V8P9T6_OPPIHA alpha-1,2-Mannosidase (Fragment) OS=Ophiophagus hannah GN=V8P9T6 OPPIHA	4
1737	5.8	18.58	66.37	23.19	17.17	tr	V8PGM8	V8PGM8_OPPIHA Putative ATP-dependent RNA helicase DDX5 (Fragment) OS= OPPIHA	10
1738	5.8	5.8	48.99	5.325	4.473	tr	V8P5A4	V8P5A4_OPPIHA TBC1 domain family member 8B (Fragment) OS=Ophiophagus hannah GN=V8P5A4 OPPIHA	4
1739	5.8	5.8	55.21	9.407	9.407	tr	V8P9S2	V8P9S2_OPPIHA Sterol 26-hydroxylase, mitochondrial (Fragment) OS=Ophiophagus hannah GN=V8P9S2 OPPIHA	4
1740	5.78	5.86	32.56	3.206	2.828	tr	V8NBL3	V8NBL3_OPPIHA Neurobeachin-like protein 1 (Fragment) OS=Ophiophagus hannah GN=V8NBL3 OPPIHA	3
1741	5.78	5.78	37.88	9.957	8.442	tr	V8NQ58	V8NQ58_OPPIHA Dihydropyrimidinase-related protein 2 (Fragment) OS=Ophiophagus hannah GN=V8NQ58 OPPIHA	3
1742	5.77	5.77	53.47	17.55	8.98	tr	V8NFB1	V8NFB1_OPPIHA H/ACA ribonucleoprotein complex subunit 4 OS=Ophiophagus hannah GN=V8NFB1 OPPIHA	3
1743	5.76	5.78	43.51	4.753	2.438	tr	V8P851	V8P851_OPPIHA General transcription factor II-I (Fragment) OS=Ophiophagus hannah GN=V8P851 OPPIHA	3
1744	5.76	5.76	37.71	9.482	3.197	tr	V8NGX1	V8NGX1_OPPIHA Nuclear factor NF-kappa-B subunit 1 (Fragment) OS=Ophiophagus hannah GN=V8NGX1 OPPIHA	3
1745	5.74	5.74	36.23	4.307	3.632	tr	V8NFG4	V8NFG4_OPPIHA Cleavage and polyadenylation specificity factor subunit 1 OPPIHA	3
1746	5.74	5.74	35.79	8.26	4.506	tr	V8NM19	V8NM19_OPPIHA La-related protein 4 (Fragment) OS=Ophiophagus hannah GN=V8NM19 OPPIHA	3
1747	5.74	5.74	33.78	6.634	6.634	tr	V8P246	V8P246_OPPIHA Mitogen-activated protein kinase kinase kinase MLT (Frag OPPIHA	4
1748	5.73	8.34	51.56	25	18.49	tr	V8P7Y0	V8P7Y0_OPPIHA DnaJ-like subfamily B member 4 (Fragment) OS=Ophiophagus hannah GN=V8P7Y0 OPPIHA	5
1749	5.73	6.91	67.46	28.99	28.99	tr	V8NAF2	V8NAF2_OPPIHA ADP-ribosylation factor 6 (Fragment) OS=Ophiophagus hannah GN=V8NAF2 OPPIHA	4
1750	5.73	5.73	64.69	6.755	3.787	tr	V8P6G6	V8P6G6_OPPIHA Putative global transcription activator SNF2L1 (Fragmen OPPIHA	3
1751	5.73	5.73	78.7	16.2	16.2	tr	V8P3P3	V8P3P3_OPPIHA Bcl-2-likeous antagonist/killer (Fragment) OS=Ophiophagus hannah GN=V8P3P3 OPPIHA	3
1752	5.72	5.72	59.93	6.568	5.255	tr	V8NTY9	V8NTY9_OPPIHA Cdc42-interacting protein 4 (Fragment) OS=Ophiophagus hannah GN=V8NTY9 OPPIHA	3
1753	5.72	5.72	37.53	7.087	7.087	tr	V8PDH1	V8PDH1_OPPIHA Neural cell adhesion molecule 1 (Fragment) OS=Ophiophagus hannah GN=V8PDH1 OPPIHA	3
1754	5.71	5.71	67.62	30.48	20	tr	V8PEY7	V8PEY7_OPPIHA 60S ribosomal protein L36 OS=Ophiophagus hannah GN=RPL3 OPPIHA	3
1755	5.71	5.71	58.96	19.08	19.08	tr	V8PC47	V8PC47_OPPIHA Enoyl-CoA delta isomerase 1, mitochondrial OS=Ophiophagus hannah GN=V8PC47 OPPIHA	3
1756	5.7	8.02	63.23	7.794	5.159	tr	V8NW57	V8NW57_OPPIHA E3 ubiquitin-protein ligase BRE1A OS=Ophiophagus hannah GN=V8NW57 OPPIHA	4
1757	5.69	5.69	41.92	20.82	18.08	tr	V8P5M6	V8P5M6_OPPIHA Regulator of chromosome condensation OS=Ophiophagus hannah GN=V8P5M6 OPPIHA	3
1758	5.68	5.72	65.83	21.67	21.67	tr	V8N543	V8N543_OPPIHA Mitochondrial import inner membrane translocase subunit OPPIHA	3
1759	5.68	5.68	71.29	23.27	23.27	tr	V8N486	V8N486_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=V8N486 OPPIHA	3
1760	5.68	5.68	30.07	14.05	11.11	tr	V8NG96	V8NG96_OPPIHA Magnesium transporter protein 1 (Fragment) OS=Ophiophagus hannah GN=V8NG96 OPPIHA	4
1761	5.67	7.57	74.74	35.26	26.32	tr	V8POS7	V8POS7_OPPIHA Hippocalcin-like protein 1 (Fragment) OS=Ophiophagus hannah GN=V8POS7 OPPIHA	4
1762	5.66	6.07	68.57	15.36	11.79	tr	V8NP56	V8NP56_OPPIHA Rho-associated protein kinase 1 (Fragment) OS=Ophiophagus hannah GN=V8NP56 OPPIHA	3
1763	5.66	5.72	35.71	9.857	5.429	tr	V8NR27	V8NR27_OPPIHA Nuclear pore complex protein Nup88 (Fragment) OS=Ophiophagus hannah GN=V8NR27 OPPIHA	4
1764	5.66	5.66	71.32	34.88	34.88	tr	V8PG53	V8PG53_OPPIHA Thioredoxin domain-containing protein 12 OS=Ophiophagus hannah GN=V8PG53 OPPIHA	3
1765	5.65	5.95	62.71	31.07	26.55	tr	V8N4N7	V8N4N7_OPPIHA EH domain-containing protein 2 (Fragment) OS=Ophiophagus hannah GN=V8N4N7 OPPIHA	4
1766	5.65	5.65	62.91	20.42	10.56	tr	V8P1K2	V8P1K2_OPPIHA Ras GTPase-activating protein-binding protein 1 (Fragme OPPIHA	3
1767	5.64	5.7	60.46	7.143	7.143	tr	V8P3S6	V8P3S6_OPPIHA mRNA cap guanine-N7 methyltransferase OS=Ophiophagus hannah GN=V8P3S6 OPPIHA	3
1768	5.63	5.63	50.73	16.13	10.85	tr	V8PAA0	V8PAA0_OPPIHA Myelin expression factor 2 OS=Ophiophagus hannah GN=V8PAA0 OPPIHA	3
1769	5.63	5.63	77.14	26.19	18.1	tr	V8PO10	V8PO10_OPPIHA Golgi SNAP receptor complex member 2 (Fragment) OS=Ophiophagus hannah GN=V8PO10 OPPIHA	3
1770	5.63	5.63	46.62	14.47	14.47	tr	V8PFY0	V8PFY0_OPPIHA Aspartoacylase-2 (Fragment) OS=Ophiophagus hannah GN=V8PFY0 OPPIHA	4
1771	5.62	5.62	44.4	16.4	16.4	tr	V8NKL8	V8NKL8_OPPIHA Ras-associated and pleckstrin-like domains-containing OPPIHA	3
1772	5.61	5.61	30.19	5.594	2.529	tr	V8P9T7	V8P9T7_OPPIHA Bromodomain-containing protein 4 (Fragment) OS=Ophiophagus hannah GN=V8P9T7 OPPIHA	3
1773	5.61	5.61	37.37	14.25	9.287	tr	V8NRG8	V8NRG8_OPPIHA Putative RNA-binding protein 23 (Fragment) OS=Ophiophagus hannah GN=V8NRG8 OPPIHA	3
1774	5.61	5.61	58.15	26.63	20.11	tr	V8N7Z7	V8N7Z7_OPPIHA U4/U6.5 tri-snRNP-associated protein 1 (Fragment) OS=Ophiophagus hannah GN=V8N7Z7 OPPIHA	3
1775	5.6	6.37	41.62	4.275	4.275	tr	V8P836	V8P836_OPPIHA Collagen alpha-6(IV) chain OS=Ophiophagus hannah GN=V8P836 OPPIHA	5
1776	5.59	5.59	37.24	4.368	2.805	tr	V8NS16	V8NS16_OPPIHA Transporter (Fragment) OS=Ophiophagus hannah GN=V8NS16 OPPIHA	4
1777	5.59	5.59	56.36	7.839	3.919	tr	V8P0D6	V8P0D6_OPPIHA Putative ATP-dependent RNA helicase DHX36 (Fragment) OS=Ophiophagus hannah GN=V8P0D6 OPPIHA	3
1778	5.58	5.6	51.12	14.51	9.821	tr	V8P1I3	V8P1I3_OPPIHA Growth arrest-specific protein 7 (Fragment) OS=Ophiophagus hannah GN=V8P1I3 OPPIHA	3
1779	5.57	5.69	50.35	2.481	2.149	tr	V8NGL1	V8NGL1_OPPIHA Nesprin-2 (Fragment) OS=Ophiophagus hannah GN=V8NGL1 OPPIHA	8
1780	5.57	5.57	63.68	29.85	17.41	tr	V8PAC8	V8PAC8_OPPIHA Nuclear factor 1 C-type (Fragment) OS=Ophiophagus hannah GN=V8PAC8 OPPIHA	3
1781	5.56	5.56	41.18	10.87	7.487	tr	V8NX47	V8NX47_OPPIHA Spartn OS=Ophiophagus hannah GN=V8NX47 OPPIHA	3
1782	5.56	5.56	32.62	22.32	12.45	tr	V8P3L9	V8P3L9_OPPIHA Autophagy protein 5 OS=Ophiophagus hannah GN=V8P3L9 OPPIHA	2
1783	5.55	5.55	48.67	25.33	14	tr	V8P9Z0	V8P9Z0_OPPIHA Mitochondrial ornithine transporter 1 (Fragment) OS=Ophiophagus hannah GN=V8P9Z0 OPPIHA	3
1784	5.54	7.7	41.17	15.53	10.87	tr	V8NU83	V8NU83_OPPIHA Signal transducing adapter molecule 2 OS=Ophiophagus hannah GN=V8NU83 OPPIHA	4
1785	5.52	5.53	31.1	4.146	4.024	tr	V8ND08	V8ND08_OPPIHA Cytochrome c1, heme protein, mitochondrial OS=Ophiophagus hannah GN=V8ND08 OPPIHA	4
1786	5.52	5.52	37.67	5.285	5.285	tr	V8PC2	V8PC2_OPPIHA Amyloid beta A4 protein (Fragment) OS=Ophiophagus hannah GN=V8PC2 OPPIHA	3
1787	5.52	5.52	41.46	6.402	6.402	tr	V8NY28	V8NY28_OPPIHA Protein PAT1-like 2 (Fragment) OS=Ophiophagus hannah GN=V8NY28 OPPIHA	4
1788	5.52	5.52	60.47	22.09	22.09	tr	V8P1S7	V8P1S7_OPPIHA Ras-related protein R-Ras2 (Fragment) OS=Ophiophagus hannah GN=V8P1S7 OPPIHA	3
1789	5.52	5.52	49.72	18.64	18.64	tr	V8N9G7	V8N9G7_OPPIHA 39S ribosomal protein L32, mitochondrial OS=Ophiophagus hannah GN=V8N9G7 OPPIHA	4
1790	5.51	7.84	49.09	32.73	24.09	tr	V8P5V2	V8P5V2_OPPIHA Ras-related protein Rab-3D OS=Ophiophagus hannah GN=V8P5V2 OPPIHA	4
1791	5.51	5.52	50	7.244	5.966	tr	V8NFI5	V8NFI5_OPPIHA Cleavage stimulation factor subunit 2 tau variant (Frag OPPIHA	3
1792	5.51	5.51	40	4.72	4.72	tr	V8NQ88	V8NQ88_OPPIHA Tetratricopeptide repeat protein 13 (Fragment) OS=Ophiophagus hannah GN=V8NQ88 OPPIHA	3
1793	5.51	5.51	34.58	18.75	18.75	tr	V8P494	V8P494_OPPIHA Eukaryotic translation initiation factor 6 (Fragment) OS=Ophiophagus hannah GN=V8P494 OPPIHA	3
1794	5.5	8.3	58.07	23.29	13.66	tr	V8PEZ8	V8PEZ8_OPPIHA Serine/arginine-rich splicing factor 5 (Fragment) OS=Ophiophagus hannah GN=V8PEZ8 OPPIHA	4
1795	5.5	5.5	46.83	4.736	3.514	tr	V8PCW9	V8PCW9_OPPIHA Tetratricopeptide repeat protein 37 (Fragment) OS=Ophiophagus hannah GN=V8PCW9 OPPIHA	3
1796	5.5	5.5	19.5	8.714	7.261	tr	V8P485	V8P485_OPPIHA Epoxide hydrolase 2 (Fragment) OS=Ophiophagus hannah GN=V8P485 OPPIHA	3
1797	5.49	5.49	40.53	7.84	6.509	tr	V8NGE1	V8NGE1_OPPIHA Putative GTP-binding protein Parf (Fragment) OS=Ophiophagus hannah GN=V8NGE1 OPPIHA	3
1798	5.49	5.49	52.29	12	12	tr	V8NVQ0	V8NVQ0_OPPIHA rRNA adenine N(6)-methyltransferase (Fragment) OS=Ophiophagus hannah GN=V8NVQ0 OPPIHA	3
1799	5.48	6.93	57.22	20	6.296	tr	V8P330	V8P330_OPPIHA Ribosomal protein S6 kinase alpha-3 (Fragment) OS=Ophiophagus hannah GN=V8P330 OPPIHA	3
1800	5.48	5.48	55.27	9.283	7.595	tr	V8P3W8	V8P3W8_OPPIHA Rab GTPase-binding effector protein 2 (Fragment) OS=Ophiophagus hannah GN=V8P3W8 OPPIHA	3
1801	5.48	5.48	51.45	12.5	9.884	tr	V8NS67	V8NS67_OPPIHA Eukaryotic translation initiation factor 3 subunit G OS=Ophiophagus hannah GN=V8NS67 OPPIHA	3
1802	5.48	5.48	21.51	10.98	8.009	tr	V8PG58	V8PG58_OPPIHA Interferon-related developmental regulator 2 OS=Ophiophagus hannah GN=V8PG58 OPPIHA	3
1803	5.47	5.48	33.55	7.947	7.947	tr	V8NQUS	V8NQUS_OPPIHA WD repeat-containing protein 37 (Fragment) OS=Ophiophagus hannah GN=V8NQUS OPPIHA	3
1804	5.46	6.38	50.82	25.14	19.67	tr	V8P4K0	V8P4K0_OPPIHA Protein lin-7-like A (Fragment) OS=Ophiophagus hannah GN=V8P4K0 OPPIHA	4
1805	5.46	5.46	34.47	2.872	1.996	tr	V8P498	V8P498_OPPIHA Autophagy-related protein 2-like B (Fragment) OS=Ophiophagus hannah GN=V8P498 OPPIHA	3
1806	5.46	5.46	52.7	10.64	6.383	tr	V8NC04	V8NC04_OPPIHA ATP-binding cassette sub-family B member 8, mitochondri OPPIHA	3
1807	5.46	5.46	75.4	15.08	8.73	tr	V8ND26	V8ND26_OPPIHA Prefoldin subunit 6 OS=Ophiophagus hannah GN=V8ND26 OPPIHA	3
1808	5.45	5.46	54.57	13.85	11.36	tr	V8PF59	V8PF59_OPPIHA Centromere/kinetochore protein zw10-like protein (Fragm OPPIHA	3
1809	5.45	5.45	49.81	14.37	9.195	tr	V8P5C1	V8P5C1_OPPIHA Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosam OPPIHA	3
1810	5.45	5.45	46.21	23.48	16.67	tr	V8P395	V8P395_OPPIHA Glutathione peroxidase (Fragment) OS=Ophiophagus hannah GN=V8P395 OPPIHA	3
1811	5.44	6.65	25.17	11.13	8.733	tr	V8POF7	V8POF7_OPPIHA Transketolase-like protein 2 (Fragment) OS=Ophiophagus hannah GN=V8POF7 OPPIHA	5
1812	5.43	5.43	44.21	14.88	14.46	tr	V8N837	V8N837_OPPIHA Dual specificity mitogen-activated protein kinase 1 (Fr OPPIHA	3
1813	5.42	5.42	35.43	16.27	11.02	tr	V8PGK8	V8PGK8_OPPIHA Thromboxane-A synthase (Fragment) OS=Ophiophagus hannah GN=V8PGK8 OPPIHA	3

1814	5.42	5.42	50.44	31.86	31.86	tr V8N3L4 V8N3L4_OPPIHA Complement C3 (Fragment) OS=Ophiophagus hannah GN=C3 PE OPPIHA	3
1815	5.41	13.83	54.43	36.29	33.33	tr V8P6N2 V8P6N2_OPPIHA Ribose-phosphate pyrophosphokinase 1 (Fragment) OS=Ophi OPPIHA	11
1816	5.41	5.41	61.44	26.8	26.8	tr V8NMY4 V8NMY4_OPPIHA Ubiquitin carboxyl-terminal hydrolase isozyme L5 (Fragm OPPIHA	3
1817	5.4	10.3	80.29	32.21	22.6	tr V8NQ74 V8NQ74_OPPIHA GTPase KRas OS=Ophiophagus hannah GN=KRAS PE=4 SV=1 OPPIHA	5
1817	0.01	11.77	68.66	29.85	24.38	tr V8NZX8 V8NZX8_OPPIHA GTPase NRas (Fragment) OS=Ophiophagus hannah GN=NRAS PE OPPIHA	6
1818	5.4	7.51	22.8	9.985	8.495	tr V8NUP4 V8NUP4_OPPIHA Transmembrane 9 superfamily member 2 (Fragment) OS=Ophi OPPIHA	5
1819	5.4	5.41	54	8.571	5.429	tr V8P3C4 V8P3C4_OPPIHA Calpastatin (Fragment) OS=Ophiophagus hannah GN=CAST PE OPPIHA	3
1820	5.4	5.4	49.42	5.922	2.427	tr V8NP52 V8NP52_OPPIHA Serine/threonine-protein kinase PRP4-like protein (Frag OPPIHA	2
1821	5.39	5.39	43.01	10.48	10.48	tr V8NZE5 V8NZE5_OPPIHA Protein O-glucosyltransferase 1 (Fragment) OS=Ophiophag OPPIHA	3
1822	5.39	5.39	48.65	11.58	8.88	tr V8NYF4 V8NYF4_OPPIHA Acylpyruvase FAHD1, mitochondrial (Fragment) OS=Ophioph OPPIHA	3
1823	5.38	5.38	49.21	13.1	7.341	tr V8NCY4 V8NCY4_OPPIHA Eukaryotic translation initiation factor 4 gamma 3 (Fra OPPIHA	2
1824	5.38	5.38	46.94	23.81	17.69	tr V8PEK8 V8PEK8_OPPIHA Ribokinase (Fragment) OS=Ophiophagus hannah GN=RBKS PE= OPPIHA	3
1825	5.38	5.38	29.19	17.84	17.3	tr V8P6T0 V8P6T0_OPPIHA 15 kDa selenoprotein (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1826	5.38	5.38	36.13	26.89	26.89	tr V8N418 V8N418_OPPIHA Beta-arrestin-2 (Fragment) OS=Ophiophagus hannah GN=ARR OPPIHA	3
1827	5.37	5.37	82.64	38.89	25.69	tr V8N7H8 V8N7H8_OPPIHA SLIT-ROBO Rho GTPase-activating protein 2 (Fragment) OS=OPPIHA	3
1828	5.36	5.76	55.12	9.537	4.488	tr V8PA50 V8PA50_OPPIHA Zinc phosphodiesterase ELAC protein 2 (Fragment) OS=Oph OPPIHA	2
1829	5.36	5.36	31.55	4.729	2.676	tr V8NLR3 V8NLR3_OPPIHA Exportin-T (Fragment) OS=Ophiophagus hannah GN=XPT PE= OPPIHA	3
1830	5.36	5.36	36.77	4.626	4.626	tr V8PIS5 V8PIS5_OPPIHA Transforming growth factor-beta receptor-associated pro OPPIHA	3
1831	5.36	5.36	60.66	23.77	14.75	tr V8NME7 V8NME7_OPPIHA Chloride intracellular channel protein 4 (Fragment) OS= OPPIHA	4
1832	5.36	5.36	38.83	35.92	34.95	tr V8NQN5 V8NQN5_OPPIHA LIM and senescent cell antigen-like-containing domain p OPPIHA	3
1833	5.35	5.35	54.06	9.219	3.594	tr V8NQC4 V8NQC4_OPPIHA Pre-mRNA-processing factor 39 OS=Ophiophagus hannah GN= OPPIHA	2
1834	5.35	5.35	46.85	12.59	10.14	tr V8P2L6 V8P2L6_OPPIHA Protein FAM54B OS=Ophiophagus hannah GN=FAM54B PE=4 SV= OPPIHA	3
1835	5.34	5.34	49.61	9.424	5.759	tr V8P918 V8P918_OPPIHA Phospholipase A-2-activating protein (Fragment) OS=Ophi OPPIHA	3
1836	5.34	5.34	51.67	11.94	11.67	tr V8NHU0 V8NHU0_OPPIHA Alpha-methylacyl-CoA racemase (Fragment) OS=Ophiophagus OPPIHA	4
1837	5.34	5.34	60.61	20.35	16.45	tr V8NJ71 V8NJ71_OPPIHA Proline synthase co-transcribed bacterial-like protein OPPIHA	3
1838	5.32	5.32	62.05	7.59	5.326	tr V8PA80 V8PA80_OPPIHA Pre-mRNA-splicing factor CWC25-like protein OS=Ophiophaga OPPIHA	3
1839	5.32	5.32	38.92	7.703	6.486	tr V8NJ63 V8NJ63_OPPIHA Signal transducer and activator of transcription OS=Oph OPPIHA	4
1840	5.32	5.32	26.17	7.799	5.026	tr V8NA49 V8NA49_OPPIHA Thioredoxin reductase 3 (Fragment) OS=Ophiophagus hanna OPPIHA	3
1841	5.3	5.3	46.09	2.02	2.02	tr V8NTJ8 V8NTJ8_OPPIHA Dedicator of cytokinesis protein 9 (Fragment) OS=Ophiop OPPIHA	3
1842	5.3	5.3	58.51	16.49	10.11	tr V8PBF2 V8PBF2_OPPIHA Guanine nucleotide-binding protein subunit alpha-13 (Fr OPPIHA	3
1843	5.3	5.3	58.78	36.64	29.01	tr V8PGJ8 V8PGJ8_OPPIHA Protein phosphatase 1 regulatory subunit 21 OS=Ophiopha OPPIHA	3
1844	5.29	5.31	27.1	5.048	2.673	tr V8NX18 V8NX18_OPPIHA Rab3 GTPase-activating protein non-catalytic subunit OS OPPIHA	3
1845	5.29	5.29	20.92	7.609	7.609	tr V8P1T2 V8P1T2_OPPIHA ABI family member 3 OS=Ophiophagus hannah GN=ABI3 PE=4 OPPIHA	3
1846	5.28	5.85	61.5	17.84	14.08	tr V8NGW1 V8NGW1_OPPIHA Retinol dehydrogenase 16 (Fragment) OS=Ophiophagus hann OPPIHA	4
1847	5.28	5.28	39.61	10.96	6.18	tr V8NYA8 V8NYA8_OPPIHA MOSC domain-containing protein 2, mitochondrial (Fragme OPPIHA	2
1848	5.28	5.28	43.92	8.685	8.685	tr V8POD2 V8POD2_OPPIHA RNA 3'-terminal phosphate cyclase (Fragment) OS=Ophioph OPPIHA	3
1849	5.27	5.27	49.64	6.569	6.569	tr V8NX22 V8NX22_OPPIHA Putative ATP-dependent RNA helicase DHX58 (Fragment) OS OPPIHA	3
1850	5.27	5.27	64.44	26.67	21.48	tr V8NDW1 V8NDW1_OPPIHA GDP-L-fucose synthase (Fragment) OS=Ophiophagus hannah OPPIHA	3
1851	5.27	5.23	13.01	10.5	8.447	tr V8NU92 V8NU92_OPPIHA Fibulin-5 (Fragment) OS=Ophiophagus hannah GN=FBLN5 PE= OPPIHA	3
1852	5.26	5.32	35.35	5.537	3.918	tr V8NNL8 V8NNL8_OPPIHA TBC1 domain family member 8 (Fragment) OS=Ophiophagus h OPPIHA	3
1853	5.26	5.26	46.84	11.14	9.367	tr V8N908 V8N908_OPPIHA Sorting nexin-8 (Fragment) OS=Ophiophagus hannah GN=SNX OPPIHA	3
1854	5.26	5.26	66.67	27.38	22.02	tr V8POPO V8POPO_OPPIHA Stathmin (Fragment) OS=Ophiophagus hannah GN=STMN1 PE=3 OPPIHA	4
1855	5.25	5.25	32.92	7.335	5.635	tr V8P8V9 V8P8V9_OPPIHA Histone deacetylase 6 (Fragment) OS=Ophiophagus hannah OPPIHA	4
1856	5.25	5.25	69.23	41.03	41.03	tr V8POX3 V8POX3_OPPIHA Succinyl-CoA ligase GDP-forming subunit beta (Fragment) OPPIHA	4
1857	5.24	5.24	27.54	22.16	15.57	tr V8P9M8 V8P9M8_OPPIHA Translocon-associated protein subunit delta OS=Ophiopha OPPIHA	5
1858	5.23	5.28	26.17	4.95	2.013	tr V8P1P1 V8P1P1_OPPIHA Macrophage-stimulating protein receptor (Fragment) OS=O OPPIHA	2
1859	5.23	5.23	59.85	20.2	10.1	tr V8NR50 V8NR50_OPPIHA Pre-mRNA-splicing regulator WTAP OS=Ophiophagus hannah OPPIHA	3
1860	5.23	5.23	26.38	4.341	4.341	tr V8ND78 V8ND78_OPPIHA Basement membrane-specific heparan sulfate proteoglycan OPPIHA	4
1861	5.22	5.22	29.64	7.972	5.893	tr V8PCJ8 V8PCJ8_OPPIHA GPI transamidase component PIG-T OS=Ophiophagus hannah OPPIHA	3
1862	5.21	5.21	28.26	8.203	8.073	tr V8P228 V8P228_OPPIHA SH2B adapter protein 2 (Fragment) OS=Ophiophagus hannah OPPIHA	4
1863	5.21	5.21	48.95	12.94	11.89	tr V8NKQ0 V8NKQ0_OPPIHA Microfibrillar-associated protein 1 (Fragment) OS=Ophio OPPIHA	3
1864	5.21	5.21	40.75	15.01	6.166	tr V8NH50 V8NH50_OPPIHA Actin-binding LIM protein 1 (Fragment) OS=Ophiophagus h OPPIHA	2
1865	5.21	5.21	39.92	13.04	13.04	tr V8NI61 V8NI61_OPPIHA Valacyclovir hydrolase (Fragment) OS=Ophiophagus hannah OPPIHA	3
1866	5.2	5.2	30.91	6.472	6.472	tr V8P8B5 V8P8B5_OPPIHA Cadherin-13 (Fragment) OS=Ophiophagus hannah GN=CDH13 P OPPIHA	4
1867	5.2	5.2	45.53	18.7	18.7	tr V8N726 V8N726_OPPIHA UBX domain-containing protein 1 (Fragment) OS=Ophiophag OPPIHA	3
1868	5.19	5.19	46.68	8.955	3.256	tr V8NGY4 V8NGY4_OPPIHA Histidyl-tRNA synthetase, cytoplasmic OS=Ophiophagus ha OPPIHA	2
1869	5.18	5.18	49.51	15.93	7.598	tr V8NPT7 V8NPT7_OPPIHA Cysteine protease ATG4B (Fragment) OS=Ophiophagus hanna OPPIHA	2
1870	5.17	5.17	40.82	11.59	7.005	tr V8NYL0 V8NYL0_OPPIHA Lysophosphatidic acid phosphatase type 6 OS=Ophiophagus OPPIHA	3
1871	5.17	5.17	54.22	36.75	30.72	tr V8NP04 V8NP04_OPPIHA Septin-2A (Fragment) OS=Ophiophagus hannah GN=sept-2-A P OPPIHA	3
1872	5.16	10.32	47.67	11.37	11.37	tr V8NS63 V8NS63_OPPIHA Long-chain-fatty-acid-CoA ligase 4 (Fragment) OS=Ophio OPPIHA	6
1873	5.16	5.16	48.07	10.83	5.138	tr V8N7L5 V8N7L5_OPPIHA Metastasis-associated protein MTA2 (Fragment) OS=Ophiop OPPIHA	3
1874	5.15	5.15	48.04	2.399	1.897	tr V8P219 V8P219_OPPIHA Microtubule-actin cross-linking factor 1 (Fragment) OS= OPPIHA	7
1875	5.15	5.15	68.17	11.41	5.255	tr V8NF56 V8NF56_OPPIHA RNA polymerase II-associated protein 3 (Fragment) OS=Op OPPIHA	3
1876	5.15	5.15	52.17	16.43	9.179	tr V8NXU7 V8NXU7_OPPIHA Myc-associated zinc finger protein (Fragment) OS=Ophiop OPPIHA	3
1877	5.15	5.15	47.35	9.412	9.412	tr V8NLE1 V8NLE1_OPPIHA Cathepsin L1 OS=Ophiophagus hannah GN=CTSL1 PE=3 SV=1 OPPIHA	4
1878	5.15	5.15	43.54	7.555	7.555	tr V8N4X6 V8N4X6_OPPIHA ATP-binding cassette sub-family B member 9 (Fragment) O OPPIHA	3
1879	5.13	5.13	31.64	4.127	3.175	tr V8NIQ5 V8NIQ5_OPPIHA Zinc finger and BTB domain-containing protein 2 (Fragme OPPIHA	3
1880	5.13	5.13	42.62	20.77	20.77	tr V8PCW3 V8PCW3_OPPIHA Transmembrane protein 85 OS=Ophiophagus hannah GN=Tmem8 OPPIHA	3
1881	5.12	5.13	51.32	16.12	14.14	tr V8P5Y4 V8P5Y4_OPPIHA Small glutamine-rich tetratricopeptide repeat-containin OPPIHA	3
1882	5.12	5.12	53.6	14.86	14.86	tr V8NTK8 V8NTK8_OPPIHA Histone Hlx (Fragment) OS=Ophiophagus hannah GN=HlFX PE OPPIHA	3
1883	5.12	5.12	33.81	18.71	15.11	tr V8NLS3 V8NLS3_OPPIHA Peroxisomal membrane protein PEX14 (Fragment) OS=Ophi OPPIHA	3
1884	5.12	5.12	64.94	37.66	37.66	tr V8N9B2 V8N9B2_OPPIHA Rab GDP dissociation inhibitor alpha (Fragment) OS=Ophi OPPIHA	3
1885	5.11	8.96	55.56	16.02	10.08	tr V8PJF0 V8PJF0_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	7
1886	5.11	5.11	28.73	3.861	2.008	tr V8NSV2 V8NSV2_OPPIHA Disco-interacting protein 2-like B (Fragment) OS=Ophiop OPPIHA	2
1887	5.11	5.11	43.15	18.95	16.13	tr V8PBS7 V8PBS7_OPPIHA ERI1 exoribonuclease 3 (Fragment) OS=Ophiophagus hannah OPPIHA	3
1888	5.1	5.1	40.52	28.45	28.45	tr V8PHT6 V8PHT6_OPPIHA Ubiquitin-40S ribosomal protein S27a (Fragment) OS=Ophi OPPIHA	4
1889	5.1	5.1	27.84	15.46	15.46	tr V8P6K8 V8P6K8_OPPIHA Corticosteroid 11-beta-dehydrogenase isozyme 1 (Fragmen OPPIHA	3
1890	5.09	5.09	75.15	30.3	30.3	tr V8PHO4 V8PHO4_OPPIHA Cold-inducible RNA-binding protein (Fragment) OS=Ophiop OPPIHA	3
1891	5.09	5.09	61.31	20.44	20.44	tr V8P254 V8P254_OPPIHA Osteoclast-stimulating factor 1 (Fragment) OS=Ophiophag OPPIHA	3
1892	5.08	5.08	76.92	16.78	13.29	tr V8N8H1 V8N8H1_OPPIHA Protein RUFY3 (Fragment) OS=Ophiophagus hannah GN=RUFY3 OPPIHA	3
1893	5.08	5.08	52.63	7.105	7.105	tr V8PHX7 V8PHX7_OPPIHA Prothrombin (Fragment) OS=Ophiophagus hannah GN=F2 PE=3 OPPIHA	4
1894	5.07	5.07	68.26	28.26	21.74	tr V8P407 V8P407_OPPIHA Calcium-binding protein p22 (Fragment) OS=Ophiophagus h OPPIHA	4
1895	5.06	5.06	44.66	13.55	6.298	tr V8PAD3 V8PAD3_OPPIHA Alpha-1-syntrophin (Fragment) OS=Ophiophagus hannah GN= OPPIHA	3
1896	5.06	5.06	52.51	20.95	10.06	tr V8P9G2 V8P9G2_OPPIHA Adenyllyltransferase and sulfurtransferase MOCS3 (Fragme OPPIHA	3
1897	5.06	5.06	80.49	42.68	42.68	tr V8PD19 V8PD19_OPPIHA Acylphosphatase-2 OS=Ophiophagus hannah GN=ACYP2 PE=3 S OPPIHA	3
1898	5.06	5.06	65.33	52	52	tr V8P5X1 V8P5X1_OPPIHA Homogentisate 1,2-dioxygenase (Fragment) OS=Ophiophagus OPPIHA	5
1899	5.05	5.56	32.28	3.465	1.337	tr V8NL75 V8NL75_OPPIHA Threonyl-tRNA synthetase, cytoplasmic OS=Ophiophagus ha OPPIHA	2
1900	5.05	5.42	57.48	5.316	2.907	tr V8PFU7 V8PFU7_OPPIHA Kinesin-like protein (Fragment) OS=Ophiophagus hannah G OPPIHA	3
1901	5.05	5.05	65.59	17.41	17.41	tr V8PEP7 V8PEP7_OPPIHA WD repeat and FYVE domain-containing protein 2 (Fragmen OPPIHA	3
1902	5.05	5.05	30.73	21.95	21.95	tr V8NN53 V8NN53_OPPIHA SPRY domain-containing protein 7 OS=Ophiophagus hannah OPPIHA	3
1903	5.04	5.05	52.17	3.814	3.038	tr V8NZZ4 V8NZZ4_OPPIHA DNA2-like helicase (Fragment) OS=Ophiophagus hannah GN= OPPIHA	4
1904	5.03	5.89	49.73	12.12	9.626	tr V8NGJ1 V8NGJ1_OPPIHA Mitogen-activated protein kinase (Fragment) OS=Ophiopha OPPIHA	4
1905	5.03	5.05	35.01	7.131	7.131	tr V8NTA1 V8NTA1_OPPIHA Katanin p80 WD40-containing subunit B1 (Fragment) OS=Op OPPIHA	3
1906	5.03	5.03	50.99	7.649	7.649	tr V8NW76 V8NW76_OPPIHA 39S ribosomal protein L50, mitochondrial (Fragment) OS= OPPIHA	3
1907	5.03	5.03	73	34	25	tr V8P9K0 V8P9K0_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=L345 O OPPIHA	3
1908	5.02	5.02	54.05	5.263	5.263	tr V8NRX0 V8NRX0_OPPIHA TRMT1-like protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	3

1909	5.01	5.08	64.04	30.34	15.36	tr V8P9P3 V8P9P3_OPHHA Protein mago nashi-like 2 OS=Ophiophagus hannah GN=MAGO OPHHA	3
1910	5.01	5.01	51.3	7.818	4.886	tr V8P3I8 V8P3I8_OPHHA SH3 domain-containing kinase-binding protein 1 OS=Ophiophagus hannah GN=SH3 OPHHA	2
1911	5.01	5.01	70.45	22.16	21.59	tr V8PAK0 V8PAK0_OPHHA Signal recognition particle 19 kDa protein (Fragment) O OPHHA	3
1912	5	5	56.49	22.08	22.08	tr V8PF44 V8PF44_OPHHA 39S ribosomal protein L43, mitochondrial OS=Ophiophagus hannah GN=L43 OPHHA	3
1913	4.99	7.17	54.13	23.39	23.39	tr V8NT43 V8NT43_OPHHA Ras-related protein Rab-4A OS=Ophiophagus hannah GN=RAB OPHHA	4
1914	4.99	4.99	39.4	2.715	1.293	tr V8BP0 V8BP0_OPHHA Vacuolar protein sorting-associated protein 13A (Fragment) OPHHA	3
1915	4.99	4.99	36.06	9.015	9.015	tr V8P2T6 V8P2T6_OPHHA Metalloendopeptidase STEAP4 OS=Ophiophagus hannah GN=STEAP4 OPHHA	3
1916	4.98	4.98	44.27	13.44	13.44	tr V8NB0 V8NB0_OPHHA Endophilin-A2 (Fragment) OS=Ophiophagus hannah GN=SH3GL OPHHA	4
1917	4.97	4.97	49.47	6.823	5.97	tr V8NLY4 V8NLY4_OPHHA COP9 signalosome complex subunit 3 OS=Ophiophagus hannah GN=COP9 OPHHA	4
1918	4.96	5.07	65.9	36.42	31.79	tr V8P757 V8P757_OPHHA Transcription factor BTF3 (Fragment) OS=Ophiophagus hannah GN=BTF3 OPHHA	3
1919	4.95	4.95	71.19	23.73	23.73	tr V8P615 V8P615_OPHHA PEST proteolytic signal-containing nuclear protein OS=Ophiophagus hannah GN=PEST OPHHA	3
1920	4.95	4.95	53.55	29.35	9.355	tr V8NBY7 V8NBY7_OPHHA Retinol dehydrogenase 8 (Fragment) OS=Ophiophagus hannah GN=RDH8 OPHHA	2
1921	4.95	4.95	28.87	12.37	12.37	tr V8NS49 V8NS49_OPHHA Dihydropyrimidine dehydrogenase [NADP+] (Fragment) OS=Ophiophagus hannah GN=NADP+ OPHHA	3
1922	4.95	4.95	54.84	23.39	16.13	tr V8P093 V8P093_OPHHA Thioredoxin domain-containing protein 17 OS=Ophiophagus hannah GN=TRX17 OPHHA	2
1923	4.94	4.95	37.07	3.415	1.951	tr V8PJ58 V8PJ58_OPHHA Tubulin-specific chaperone D (Fragment) OS=Ophiophagus hannah GN=TCPD OPHHA	2
1924	4.94	4.94	51.5	4.954	2.535	tr V8PEY6 V8PEY6_OPHHA Rab5 GDP/GTP exchange factor (Fragment) OS=Ophiophagus hannah GN=RAB5 OPHHA	2
1925	4.93	4.93	39.01	6.656	6.656	tr V8NWF9 V8NWF9_OPHHA Beta-xylosidase/alpha-L-arabinofuranosidase 1 (Fragment) OPHHA	3
1926	4.93	4.93	44.22	15.65	10.54	tr V8NNN1 V8NNN1_OPHHA Dehydrogenase/reductase SDR family member 1 (Fragment) OPHHA	3
1927	4.92	4.92	64.71	16.04	16.04	tr V8NUR5 V8NUR5_OPHHA Actin-related protein 2/3 complex subunit 4 OS=Ophiophagus hannah GN=ARP4 OPHHA	3
1928	4.91	4.91	63.67	16	11	tr V8NYG8 V8NYG8_OPHHA Sorting nexin-30 (Fragment) OS=Ophiophagus hannah GN=SNX30 OPHHA	3
1929	4.91	4.91	36.23	11.83	10.72	tr V8PBJ2 V8PBJ2_OPHHA Protein wntless-like protein (Fragment) OS=Ophiophagus hannah GN=WNTLESS OPHHA	4
1930	4.91	4.91	43.15	8.333	8.333	tr V8NDF4 V8NDF4_OPHHA Apolipoprotein O (Fragment) OS=Ophiophagus hannah GN=AP OPHHA	3
1931	4.9	4.9	49.13	10.26	3.902	tr V8PAX8 V8PAX8_OPHHA 85 kDa calcium-independent phospholipase A2 (Fragment) OPHHA	3
1932	4.9	4.9	41.56	9.494	8.017	tr V8P7Z2 V8P7Z2_OPHHA SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily 1 (Fragment) OPHHA	3
1933	4.9	4.9	70.24	37.5	17.86	tr V8N4Z2 V8N4Z2_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	2
1934	4.89	4.89	35.88	8.779	3.435	tr V8P3J8 V8P3J8_OPHHA E3 ubiquitin-protein ligase CBL (Fragment) OS=Ophiophagus hannah GN=CBL OPHHA	2
1935	4.89	4.89	76.24	37.62	37.62	tr V8NZK2 V8NZK2_OPHHA Thioredoxin (Fragment) OS=Ophiophagus hannah GN=TXN PE= OPHHA	4
1936	4.88	4.88	60.63	24.41	24.41	tr V8NIG8 V8NIG8_OPHHA Regulator complex protein LAMTOR2 (Fragment) OS=Ophiophagus hannah GN=LAMTOR2 OPHHA	3
1937	4.87	4.9	37.66	9.414	8.348	tr V8P3C7 V8P3C7_OPHHA UBX domain-containing protein 4 (Fragment) OS=Ophiophagus hannah GN=UBX OPHHA	3
1938	4.87	4.87	25.94	7.509	7.509	tr V8PG37 V8PG37_OPHHA Putative proline racemase (Fragment) OS=Ophiophagus hannah GN=PRM OPHHA	3
1939	4.87	4.87	20.42	11.11	9.61	tr V8NXM7 V8NXM7_OPHHA BCL2/adenovirus E1B 19 kDa protein-interacting protein OPHHA	3
1940	4.86	4.86	51.98	17.15	12.4	tr V8NF01 V8NF01_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	3
1941	4.85	4.85	62.39	9.057	5.912	tr V8NW99 V8NW99_OPHHA RNA-binding protein 12B (Fragment) OS=Ophiophagus hannah GN=RB12B OPHHA	3
1942	4.85	4.85	55.67	4.418	4.418	tr V8NA09 V8NA09_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	3
1943	4.85	4.85	51.94	14.84	11.31	tr V8NW44 V8NW44_OPHHA Poly(ADP-ribose) glycohydrolase ARH3 (Fragment) OS=Ophiophagus hannah GN=ARH3 OPHHA	3
1944	4.85	4.85	58.71	25.87	25.87	tr V8NTU4 V8NTU4_OPHHA JmC domain-containing protein 7 (Fragment) OS=Ophiophagus hannah GN=JmC OPHHA	3
1945	4.83	4.87	42.71	8.919	3.602	tr V8NQB0 V8NQB0_OPHHA Serine/threonine-protein phosphatase 2A 56 kDa regulator OPHHA	2
1946	4.83	4.83	42.04	9.922	6.789	tr V8NJ14 V8NJ14_OPHHA Mothers against decapentaplegic homolog OS=Ophiophagus hannah GN=SMAD OPHHA	3
1946	0	4.59	16.35	16.35	16.35	tr V8NCH2 V8NCH2_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_1 OPHHA	3
1947	4.83	4.83	74.7	28.31	28.31	tr V8N9P1 V8N9P1_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	3
1948	4.82	4.83	39.9	14.14	14.14	tr V8N4P6 V8N4P6_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	3
1949	4.82	4.82	47.48	26.62	26.62	tr V8NPV9 V8NPV9_OPHHA Mitochondrial import receptor subunit TOM22-like protein OPHHA	4
1950	4.81	4.86	38.63	8.664	8.664	tr V8N5Q6 V8N5Q6_OPHHA Dipeptidyl peptidase 8 (Fragment) OS=Ophiophagus hannah GN=DPPE8 OPHHA	4
1951	4.81	4.81	52.02	6.404	4.532	tr V8NUQ6 V8NUQ6_OPHHA Nuclear receptor coactivator 7 (Fragment) OS=Ophiophagus hannah GN=NR4A OPHHA	3
1952	4.81	4.81	51.33	6.726	6.549	tr V8NHB3 V8NHB3_OPHHA Synembryon-A OS=Ophiophagus hannah GN=RIC8A PE=4 SV=1 OPHHA	3
1953	4.81	4.81	43.82	6.242	4.841	tr V8NPR4 V8NPR4_OPHHA Rho guanine nucleotide exchange factor 6 (Fragment) OS=Ophiophagus hannah GN=GEF6 OPHHA	3
1954	4.81	4.81	52.05	14.38	10.27	tr V8P9J4 V8P9J4_OPHHA CCA tRNA nucleotidyltransferase 1, mitochondrial (Fragment) OPHHA	3
1955	4.81	4.81	59.93	15.6	12.77	tr V8NP32 V8NP32_OPHHA Carnitine O-acetyltransferase (Fragment) OS=Ophiophagus hannah GN=CAAT OPHHA	3
1956	4.8	4.81	58.08	11.98	11.98	tr V8NCL0 V8NCL0_OPHHA G-protein-signaling modulator 1 (Fragment) OS=Ophiophagus hannah GN=GM1 OPHHA	3
1957	4.8	4.8	46.38	18.84	9.42	tr V8PD11 V8PD11_OPHHA Sarcolemmal membrane-associated protein (Fragment) OS=Ophiophagus hannah GN=SMAD OPHHA	2
1958	4.78	4.78	56.06	17.25	7.547	tr V8PFR2 V8PFR2_OPHHA BRCA1-A complex subunit BRE OS=Ophiophagus hannah GN=BR OPHHA	2
1959	4.77	4.77	60	16.67	14.17	tr V8P8D5 V8P8D5_OPHHA F-box-like/WD repeat-containing protein TBL1XR1 (Fragment) OPHHA	3
1960	4.76	4.76	56.53	16.76	9.747	tr V8NHS3 V8NHS3_OPHHA Sister chromatid cohesion protein PDS5-like A-A OS=Ophiophagus hannah GN=PDS5 OPHHA	3
1961	4.76	4.76	57.66	34.23	14.86	tr V8PG36 V8PG36_OPHHA Ras-related protein Rab-32 (Fragment) OS=Ophiophagus hannah GN=RAB32 OPHHA	3
1962	4.74	4.76	24.45	4.679	3.396	tr V8P568 V8P568_OPHHA Cadherin-1 (Fragment) OS=Ophiophagus hannah GN=CDH1 PE= OPHHA	3
1963	4.74	4.74	67.33	42.57	42.57	tr V8N579 V8N579_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	3
1964	4.73	4.73	62	6.4	3.6	tr V8P6Z0 V8P6Z0_OPHHA Lysine-specific histone demethylase 1A OS=Ophiophagus hannah GN=KDM1A OPHHA	2
1965	4.72	4.72	62.22	19.11	19.11	tr V8NNK7 V8NNK7_OPHHA MOB-like protein phocein OS=Ophiophagus hannah GN=MOB4 OPHHA	3
1966	4.71	4.71	58.92	13.13	10.44	tr V8POX7 V8POX7_OPHHA Neural Wiskott-Aldrich syndrome protein OS=Ophiophagus hannah GN=WAS OPHHA	2
1967	4.71	4.71	36.01	10.71	10.71	tr V8N205 V8N205_OPHHA Pigment epithelium-derived factor (Fragment) OS=Ophiophagus hannah GN=PEDF OPHHA	3
1968	4.71	4.71	48.98	14.97	14.97	tr V8NHV6 V8NHV6_OPHHA Ankyrin repeat and SOCS box protein 9 OS=Ophiophagus hannah GN=ANKRD OPHHA	3
1969	4.71	4.71	86.05	26.74	26.74	tr V8NYT5 V8NYT5_OPHHA Cytochrome c oxidase subunit 6B1 OS=Ophiophagus hannah GN=COX6B1 OPHHA	3
1970	4.7	4.7	42.86	12.5	5.893	tr V8NNA5 V8NNA5_OPHHA Pre-mRNA 3'-end-processing factor FIP1 (Fragment) OS=Ophiophagus hannah GN=FIP1 OPHHA	2
1971	4.7	4.7	46.68	13.27	8.85	tr V8P2Q4 V8P2Q4_OPHHA Serine/threonine-protein kinase VRK1 (Fragment) OS=Ophiophagus hannah GN=VRK1 OPHHA	2
1972	4.7	4.7	42.51	15.2	15.2	tr V8NX13 V8NX13_OPHHA Glycoprotein endo-alpha-1,2-mannosidase (Fragment) OS=Ophiophagus hannah GN=MANNA OPHHA	3
1973	4.7	4.7	54	24	24	tr V8N653 V8N653_OPHHA Putative RNA-binding protein EIFIAD OS=Ophiophagus hannah GN=EIFIAD OPHHA	3
1974	4.68	4.69	72.94	19.27	15.14	tr V8PH06 V8PH06_OPHHA Calyculin-binding protein OS=Ophiophagus hannah GN=CAC1 OPHHA	2
1975	4.67	4.67	38.54	7.053	4.786	tr V8NP22 V8NP22_OPHHA D-2-hydroxyglutarate dehydrogenase, mitochondrial (Fragment) OPHHA	3
1976	4.67	4.67	26.74	6.316	4.421	tr V8N717 V8N717_OPHHA N-acetylmuramoyl-L-alanine amidase (Fragment) OS=Ophiophagus hannah GN=NAAM OPHHA	3
1977	4.67	4.67	35.89	10.68	10.68	tr V8NRF9 V8NRF9_OPHHA Protein NDRG2 (Fragment) OS=Ophiophagus hannah GN=NDRG2 OPHHA	4
1978	4.67	4.67	50.91	33.94	20.61	tr V8NQC2 V8NQC2_OPHHA Selenoprotein T (Fragment) OS=Ophiophagus hannah GN=SEL OPHHA	2
1979	4.65	4.65	65.58	20.47	15.81	tr V8NLP3 V8NLP3_OPHHA Serine/threonine-protein phosphatase 2A activator OS=Ophiophagus hannah GN=PPP2R OPHHA	3
1980	4.65	4.65	61.27	27.46	27.46	tr V8N7Q4 V8N7Q4_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=UNCHAR1 OPHHA	4
1981	4.65	4.65	42.86	26.53	19.05	tr V8N722 V8N722_OPHHA Calcium-regulated heat stable protein 1 OS=Ophiophagus hannah GN=HSP1 OPHHA	2
1982	4.64	4.64	43.69	6.99	6.602	tr V8PB77 V8PB77_OPHHA General transcription factor IIF subunit 1 OS=Ophiophagus hannah GN=TFIIF OPHHA	2
1983	4.64	4.64	26.84	5.911	5.911	tr V8PEK3 V8PEK3_OPHHA T-cell immunomodulatory protein (Fragment) OS=Ophiophagus hannah GN=TIMP OPHHA	3
1984	4.64	4.64	41.25	11.27	7.914	tr V8NY35 V8NY35_OPHHA Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Ophiophagus hannah GN=ALG2 OPHHA	2
1985	4.63	4.67	42.19	11.87	8.75	tr V8P8T9 V8P8T9_OPHHA Poly [ADP-ribose] polymerase (Fragment) OS=Ophiophagus hannah GN=PARP OPHHA	3
1986	4.63	4.63	38.38	4.112	1.845	tr V8NWQ3 V8NWQ3_OPHHA Teneurin-3 (Fragment) OS=Ophiophagus hannah GN=ODZ3 PE= OPHHA	2
1987	4.63	4.63	26.01	8.742	6.823	tr V8PHI0 V8PHI0_OPHHA Hyaluronidase (Fragment) OS=Ophiophagus hannah GN=HYAL2 OPHHA	2
1988	4.62	4.62	41.73	4.086	3.405	tr V8NG54 V8NG54_OPHHA Carboxypeptidase D OS=Ophiophagus hannah GN=CPD PE=4 SV= OPHHA	3
1989	4.61	5.09	36.81	11.49	4.178	tr V8NAP3 V8NAP3_OPHHA Dimethylalanine monooxygenase [N-oxide-forming] 5 (Fragment) OPHHA	3
1990	4.61	4.66	46.83	8	5.833	tr V8NPG8 V8NPG8_OPHHA Myosin-XIX (Fragment) OS=Ophiophagus hannah GN=MYO19 PE OPHHA	3
1991	4.61	4.61	33.83	3.58	2.469	tr V8NPF7 V8NPF7_OPHHA Kininogen-1 (Fragment) OS=Ophiophagus hannah GN=KNG1 PE OPHHA	2
1992	4.61	4.61	35.62	13.36	6.849	tr V8PC15 V8PC15_OPHHA Nuclear ubiquitously expressed casein and cyclin-dependent kinases OPHHA	2
1993	4.6	4.61	34.96	5.436	4.311	tr V8PER9 V8PER9_OPHHA Syntaxin-binding protein 5 (Fragment) OS=Ophiophagus hannah GN=STXB OPHHA	3
1994	4.6	4.6	48.07	21.55	12.15	tr V8P805 V8P805_OPHHA Prefoldin subunit 3 (Fragment) OS=Ophiophagus hannah GN=PF3 OPHHA	2
1995	4.59	4.59	41.55	14.61	14.61	tr V8NRL3 V8NRL3_OPHHA C-terminal-binding protein 1 (Fragment) OS=Ophiophagus hannah GN=CTBP1 OPHHA	4
1996	4.58	4.58	40.86	11.11	5.376	tr V8NG22 V8NG22_OPHHA Nicalin (Fragment) OS=Ophiophagus hannah GN=NCLN PE=4 SV= OPHHA	2
1997	4.58	4.58	25.67	10.16	6.15	tr V8P6J2 V8P6J2_OPHHA Cytosolic 5'-nucleotidase 1B OS=Ophiophagus hannah GN=5N1B OPHHA	2
1998	4.57	4.56	34.63	13.42	8.366	tr V8NGP6 V8NGP6_OPHHA Tight junction protein ZO-3 (Fragment) OS=Ophiophagus hannah GN=ZO3 OPHHA	4
1999	4.57	4.57	48.43	8.142	4.175	tr V8PEU4 V8PEU4_OPHHA Cleavage and polyadenylation specificity factor subunit OPHHA	2
2000	4.57	4.57	53.21	9.786	6.728	tr V8NFP3 V8NFP3_OPHHA Far upstream element-binding protein 3 (Fragment) OS=Ophiophagus hannah GN=FUO3 OPHHA	2
2001	4.57	4.57	54.19	25.11	18.06	tr V8NEF7 V8NEF7_OPHHA Cytosolic 5'-nucleotidase III-like protein OS=Ophiophagus hannah GN=5N3 OPHHA	3
2002	4.56	4.97	62.43	29.28	14.36	tr V8NXY5 V8NXY5_OPHHA N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Ophiophagus hannah GN=DDC OPHHA	2
2003	4.56	4.56	31.56	4.734	2.86	tr V8PG14 V8PG14_OPHHA Splicing factor, arginine/serine-rich 15 OS=Ophiophagus hannah GN=SF15 OPHHA	2

2004	4.56	4.56	43.93	7.151	3.746	tr V8PJ81	V8PJ81_OPPIHA Protein FAM59A (Fragment) OS=Ophiophagus hannah GN=FAM5 OPPIHA	3
2005	4.56	4.56	39.31	6.528	3.333	tr V8NU49	V8NU49_OPPIHA Molybdenum cofactor sulfurase (Fragment) OS=Ophiophagus OPPIHA	3
2006	4.56	4.56	49.48	15.81	8.247	tr V8PAK9	V8PAK9_OPPIHA Nitric oxide synthase-interacting protein OS=Ophiophagus OPPIHA	2
2007	4.56	4.56	37.23	17.75	14.29	tr V8P828	V8P828_OPPIHA Transmembrane protein OS=Ophiophagus hannah GN=TMEM111 OPPIHA	2
2008	4.54	4.54	31.09	3.438	1.953	tr V8P1S9	V8P1S9_OPPIHA Nuclear pore complex protein (Fragment) OS=Ophiophagus OPPIHA	2
2009	4.54	4.54	48.58	19.87	13.56	tr V8PBA5	V8PBA5_OPPIHA CD2 antigen cytoplasmic tail-binding protein 2 OS=Ophiophagus OPPIHA	2
2010	4.54	4.54	34.01	15.65	10.88	tr V8P692	V8P692_OPPIHA Galectin OS=Ophiophagus hannah GN=Lgals8 PE=4 SV=1 OPPIHA	3
2011	4.54	4.54	28.4	12.08	3.625	tr V8NH24	V8NH24_OPPIHA Elongation factor Ts OS=Ophiophagus hannah GN=TSFM PE=3 OPPIHA	2
2012	4.54	4.54	35	29.17	20.83	tr V8P6R1	V8P6R1_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPPIHA	4
2013	4.53	4.53	56.29	5.478	4.545	tr V8P6X7	V8P6X7_OPPIHA Zinc finger CCCH domain-containing protein 7B (Fragment OPPIHA	3
2014	4.53	4.53	59.26	12.42	7.407	tr V8NV98	V8NV98_OPPIHA Antithrombin-III (Fragment) OS=Ophiophagus hannah GN=SE OPPIHA	3
2015	4.53	4.53	34.29	6.699	6.699	tr V8NMZ6	V8NMZ6_OPPIHA Mini-chromosome maintenance complex-binding protein OS= OPPIHA	3
2016	4.53	4.53	42.81	15.72	11.04	tr V8PDV0	V8PDV0_OPPIHA Acidic leucine-rich nuclear phosphoprotein 32 family me OPPIHA	2
2017	4.5	4.5	47.36	3.226	3.226	tr V8PIU3	V8PIU3_OPPIHA Signal transducer and activator of transcription 2 OS=O OPPIHA	2
2018	4.5	4.5	42.46	8.101	3.771	tr V8NU08	V8NU08_OPPIHA Conserved oligomeric Golgi complex subunit 2 OS=Ophioph OPPIHA	2
2019	4.5	4.5	42.82	16.8	8.401	tr V8PDD1	V8PDD1_OPPIHA Splicing factor U2AF 35 kDa subunit (Fragment) OS=Ophi OPPIHA	2
2020	4.5	4.5	43.41	8.683	8.683	tr V8P1K8	V8P1K8_OPPIHA 39S ribosomal protein L44, mitochondrial (Fragment) OS= OPPIHA	3
2021	4.5	4.5	78.99	20.29	10.87	tr V8P9M5	V8P9M5_OPPIHA MICOS complex subunit (Fragment) OS=Ophiophagus hannah OPPIHA	2
2022	4.5	4.5	46.46	36.22	30.71	tr V8PF04	V8PF04_OPPIHA Synaptojanin-2-binding protein (Fragment) OS=Ophiophagu OPPIHA	4
2023	4.5	4.5	33.18	12.15	12.15	tr V8PFX7	V8PFX7_OPPIHA Acyl-protein thioesterase 1 (Fragment) OS=Ophiophagus h OPPIHA	3
2024	4.49	4.49	79.23	14.01	9.662	tr V8PIJ7	V8PIJ7_OPPIHA 28S ribosomal protein S34, mitochondrial (Fragment) OS= OPPIHA	2
2025	4.48	4.48	48.81	14.25	10.03	tr V8P926	V8P926_OPPIHA Geranylgeranyl transferase type-1 subunit beta (Fragmen OPPIHA	3
2026	4.48	4.48	33.82	1.984	0.8475	tr V8PGB8	V8PGB8_OPPIHA Putative E3 ubiquitin-protein ligase HERC1 (Fragment) O OPPIHA	3
2027	4.48	4.48	38.99	7.798	3.83	tr V8PJ11	V8PJ11_OPPIHA Translation initiation factor IF-2, mitochondrial OS=Op OPPIHA	2
2028	4.48	4.48	25.63	5.854	5.854	tr V8P2D0	V8P2D0_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_0 OPPIHA	3
2029	4.47	4.59	54.8	2.954	1.352	tr V8P9M1	V8P9M1_OPPIHA Adenomatous polyposis coli protein (Fragment) OS=Ophiop OPPIHA	3
2030	4.47	4.47	51.41	7.699	3.808	tr V8P9U0	V8P9U0_OPPIHA Activity-dependent neuroprotector homeobox protein (Fra OPPIHA	3
2031	4.47	4.47	43.98	6.501	4.011	tr V8P714	V8P714_OPPIHA Phosphatidylinositol 3-kinase regulatory subunit alpha OPPIHA	2
2032	4.47	4.47	34.64	8.776	6.467	tr V8PFK1	V8PFK1_OPPIHA DnaJ-like subfamily B member 6 OS=Ophiophagus hannah GN OPPIHA	2
2033	4.47	4.47	58.28	35.1	27.15	tr V8NM10	V8NM10_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	3
2034	4.46	6.21	67	11.71	6.911	tr V8PBD3	V8PBD3_OPPIHA Guanine nucleotide-binding protein G(Q) subunit alpha O OPPIHA	3
2035	4.46	4.57	58.33	25.52	19.27	tr V8P642	V8P642_OPPIHA COP9 signalosome complex subunit 8 (Fragment) OS=Ophiop OPPIHA	2
2036	4.46	4.46	44.1	10.66	5.574	tr V8NRL0	V8NRL0_OPPIHA Ribosome-releasing factor 2, mitochondrial (Fragment) O OPPIHA	2
2037	4.46	4.46	77.05	11.89	11.89	tr V8NR18	V8NR18_OPPIHA Transcription factor A, mitochondrial OS=Ophiophagus ha OPPIHA	3
2038	4.46	4.46	32.75	9.607	3.712	tr V8NBF7	V8NBF7_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	3
2039	4.46	4.46	56.86	11.37	11.37	tr V8P430	V8P430_OPPIHA Abhydrolase domain-containing protein 10, mitochondrial OPPIHA	3
2040	4.45	4.48	35.63	5.572	5.572	tr V8PBK1	V8PBK1_OPPIHA GA-binding protein alpha chain (Fragment) OS=Ophiophagu OPPIHA	4
2041	4.45	4.45	51.67	23.33	17.22	tr V8PAT4	V8PAT4_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	2
2042	4.44	4.44	43.59	14.1	11.22	tr V8NEB4	V8NEB4_OPPIHA WD repeat-containing protein 18 OS=Ophiophagus hannah G OPPIHA	3
2043	4.44	4.44	53.85	22.56	11.28	tr V8NSV6	V8NSV6_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	2
2044	4.44	4.44	33.74	15.23	11.93	tr V8NU72	V8NU72_OPPIHA Mitochondrial carnitine/acylcarnitine carrier protein (OPPIHA	4
2045	4.43	4.43	50.85	16.72	7.85	tr V8NV82	V8NV82_OPPIHA Tyrosine-protein kinase Vsv (Fragment) OS=Ophiophagus h OPPIHA	2
2046	4.42	5.38	38.78	7.638	5.405	tr V8PEV2	V8PEV2_OPPIHA Integrin beta OS=Ophiophagus hannah GN=ITGB2 PE=3 SV=1 OPPIHA	4
2047	4.42	4.42	36.24	5.529	3.529	tr V8P610	V8P610_OPPIHA Transmembrane and TPR repeat-containing protein 3 (Frag OPPIHA	2
2048	4.41	4.41	59.12	9.343	8.321	tr V8P4Z7	V8P4Z7_OPPIHA Nuclear autoantigenic sperm protein OS=Ophiophagus hann OPPIHA	3
2049	4.41	4.41	48.98	10.24	6.485	tr V8PHJ1	V8PHJ1_OPPIHA Syntaxin-binding protein 2 OS=Ophiophagus hannah GN=STX OPPIHA	3
2050	4.41	4.41	46.5	6.379	4.321	tr V8NMF1	V8NMF1_OPPIHA Regucalcin OS=Ophiophagus hannah GN=RGN PE=4 SV=1 OPPIHA	2
2051	4.41	4.41	20.87	12.46	6.542	tr V8NE60	V8NE60_OPPIHA Wiskott-Aldrich syndrome protein family member 2 (Fragm OPPIHA	3
2052	4.4	4.4	37.94	10.13	7.074	tr V8P9B9	V8P9B9_OPPIHA Guanine nucleotide-binding protein-like 1 (Fragment) OS OPPIHA	3
2053	4.4	4.4	27.04	7.091	3.966	tr V8NIX5	V8NIX5_OPPIHA Protein lin-54-like protein (Fragment) OS=Ophiophagus h OPPIHA	2
2054	4.4	4.4	51.16	14.85	7.921	tr V8NYL1	V8NYL1_OPPIHA Beta-hexosaminidase subunit alpha (Fragment) OS=Ophioph OPPIHA	2
2055	4.4	4.4	56.25	16.52	16.52	tr V8NGL5	V8NGL5_OPPIHA Lys-63-specific deubiquitinase BRCC36 OS=Ophiophagus ha OPPIHA	3
2056	4.4	4.4	31.18	13.53	9.412	tr V8NQRO	V8NQRO_OPPIHA Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OPPIHA	2
2057	4.39	4.39	28.38	5.135	3.268	tr V8PFV4	V8PFV4_OPPIHA Pumilio-like 2 (Fragment) OS=Ophiophagus hannah GN=PUM2 OPPIHA	3
2058	4.39	4.39	48.77	5.967	5.967	tr V8NVA8	V8NVA8_OPPIHA N-acetylglucosamine-6-sulfatase (Fragment) OS=Ophiophag OPPIHA	3
2059	4.38	4.38	55.43	12	12	tr V8NV66	V8NV66_OPPIHA Polypeptide N-acetylgalactosaminyltransferase OS=Ophiop OPPIHA	3
2060	4.38	4.38	32.04	12.32	9.155	tr V8P2L3	V8P2L3_OPPIHA Dihydroorotate dehydrogenase (quinone), mitochondrial O OPPIHA	2
2061	4.37	8.47	45.31	17.8	15.21	tr V8NXU1	V8NXU1_OPPIHA Serine/threonine-protein phosphatase OS=Ophiophagus han OPPIHA	4
2062	4.36	4.36	36.63	6.79	6.79	tr V8NM42	V8NM42_OPPIHA 26S proteasome non-ATPase regulatory subunit 5 (Fragmen OPPIHA	3
2063	4.35	4.35	36.27	10.48	6.499	tr V8P710	V8P710_OPPIHA Epoxide hydrolase 1 OS=Ophiophagus hannah GN=Ephxl PE=4 OPPIHA	3
2064	4.34	4.34	68.93	7.37	5.058	tr V8P5F3	V8P5F3_OPPIHA MAP/microtubule affinity-regulating kinase 3 OS=Ophioph OPPIHA	2
2065	4.34	4.34	54.91	10.04	6.197	tr V8NG91	V8NG91_OPPIHA Vacuolar protein sorting-associated protein 33A (Fragme OPPIHA	2
2066	4.34	4.34	39.73	21	17.81	tr V8NVM2	V8NVM2_OPPIHA Charged multivesicular body protein 5 OS=Ophiophagus ha OPPIHA	2
2067	4.33	8.67	39.75	8.711	8.711	tr V8PGS5	V8PGS5_OPPIHA Hydroxymethylglutaryl-CoA synthase, cytoplasmic (Fragme OPPIHA	5
2068	4.33	4.7	57.05	15.2	5.507	tr V8NJJ4	V8NJJ4_OPPIHA Beclin-1 (Fragment) OS=Ophiophagus hannah GN=BECL1 PE=4 OPPIHA	2
2069	4.33	4.33	46.15	23.08	14.79	tr V8P079	V8P079_OPPIHA Sideroflexin-1 (Fragment) OS=Ophiophagus hannah GN=SFXX OPPIHA	4
2070	4.32	4.35	42.45	8.955	6.965	tr V8NP51	V8NP51_OPPIHA Fibulin-1 OS=Ophiophagus hannah GN=FBLN1 PE=4 SV=1 OPPIHA	2
2071	4.32	4.32	58.33	12.38	10	tr V8P316	V8P316_OPPIHA Caveolin-1 (Fragment) OS=Ophiophagus hannah GN=CAV1 PE= OPPIHA	3
2072	4.32	4.32	38.42	11.99	10.08	tr V8NQ97	V8NQ97_OPPIHA Ras-related GTP-binding protein D (Fragment) OS=Ophioph OPPIHA	3
2073	4.31	6.36	48.21	22.05	17.95	tr V8N112	V8N112_OPPIHA Ras-related protein Rab-6B (Fragment) OS=Ophiophagus ha OPPIHA	3
2074	4.31	4.82	30.41	24.23	14.43	tr V8NVE1	V8NVE1_OPPIHA Ras-related protein Rap-2a (Fragment) OS=Ophiophagus ha OPPIHA	2
2075	4.3	4.35	38.16	3.223	1.547	tr V8PJ12	V8PJ12_OPPIHA AT-rich interactive domain-containing protein 1A (Fragm OPPIHA	2
2076	4.3	4.3	51.75	5.891	4.628	tr V8PEX9	V8PEX9_OPPIHA Platelet endothelial cell adhesion molecule OS=Ophiopha OPPIHA	3
2077	4.3	4.3	72	15.47	12.8	tr V8NYB4	V8NYB4_OPPIHA Polymerase delta-interacting protein 3 (Fragment) OS=Op OPPIHA	3
2078	4.3	4.3	46.88	8.545	6.467	tr V8NLH6	V8NLH6_OPPIHA Regulator of nonsense transcripts 3B (Fragment) OS=Ophi OPPIHA	2
2079	4.3	4.3	34.07	7.195	3.965	tr V8NR89	V8NR89_OPPIHA TGF-beta-activated kinase 1 and MAP3K7-binding protein OPPIHA	2
2080	4.3	4.3	82.02	38.2	29.21	tr V8PHT9	V8PHT9_OPPIHA Mitochondrial import inner membrane translocase subunit OPPIHA	2
2081	4.29	4.36	46.28	2.212	0.9383	tr V8PHZ8	V8PHZ8_OPPIHA Lysosomal alpha-glucosidase (Fragment) OS=Ophiophagus h OPPIHA	2
2082	4.29	4.29	43.21	12.23	7.065	tr V8ND90	V8ND90_OPPIHA Four and a half LIM domains protein 3 (Fragment) OS=Oph OPPIHA	2
2083	4.29	4.29	69.14	20.37	20.37	tr V8NSN1	V8NSN1_OPPIHA 39S ribosomal protein L13, mitochondrial OS=Ophiophagus OPPIHA	3
2084	4.29	4.29	60	35	22.5	tr V8PFK5	V8PFK5_OPPIHA Enoyl-CoA hydratase domain-containing protein 2, mitoch OPPIHA	2
2085	4.28	7.73	44.21	18.42	11.32	tr V8PAK4	V8PAK4_OPPIHA LIM and hescent cell antigen-like-containing domain p OPPIHA	4
2086	4.28	4.66	39.86	14.99	5.467	tr V8NTT4	V8NTT4_OPPIHA Serine/threonine-protein phosphatase (Fragment) OS=Ophi OPPIHA	2
2087	4.28	4.28	43.07	6.01	4.341	tr V8N842	V8N842_OPPIHA Vacuolar protein sorting-associated protein 33B (Fragme OPPIHA	2
2088	4.28	4.28	44.6	18.56	8.31	tr V8P192	V8P192_OPPIHA Protein TSSC1 (Fragment) OS=Ophiophagus hannah GN=TSSC1 OPPIHA	2
2089	4.27	8.09	56.76	7.206	4.738	tr V8NGR8	V8NGR8_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	5
2090	4.26	4.26	38.7	6.649	3.59	tr V8NU29	V8NU29_OPPIHA Epithelial splicing regulatory protein 2 OS=Ophiophagus OPPIHA	2
2091	4.26	4.26	31.8	11.98	7.834	tr V8NB81	V8NB81_OPPIHA Forkhead box protein K1 (Fragment) OS=Ophiophagus hanna OPPIHA	2
2092	4.26	4.26	32.12	13.87	10.22	tr V8P7H6	V8P7H6_OPPIHA DNA-directed RNA polymerases I and III subunit RPAC1 (F OPPIHA	2
2093	4.26	4.26	40.08	15.87	11.9	tr V8NUG8	V8NUG8_OPPIHA Coiled-coil domain-containing protein 43 OS=Ophiophagus OPPIHA	2
2094	4.26	4.26	70.1	46.39	46.39	tr V8P8K3	V8P8K3_OPPIHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_0 OPPIHA	3
2095	4.25	6.48	68.16	26.53	16.33	tr V8NQ44	V8NQ44_OPPIHA Ras-related protein Rab-30 (Fragment) OS=Ophiophagus ha OPPIHA	4
2096	4.25	4.25	50.69	12.15	6.881	tr V8PHC2	V8PHC2_OPPIHA EF-hand domain-containing family member A2 (Fragment) O OPPIHA	2
2097	4.25	4.25	42.09	11.16	5.349	tr V8PG14	V8PG14_OPPIHA Talin-2 (Fragment) OS=Ophiophagus hannah GN=TLN2 PE=4 S OPPIHA	2
2098	4.24	4.59	42.52	10.63	7.592	tr V8NJ07	V8NJ07_OPPIHA Coronin OS=Ophiophagus hannah GN=CORO1A PE=3 SV=1 OPPIHA	3
2099	4.24	4.39	55.4	15.63	5.966	tr V8NBM9	V8NBM9_OPPIHA Keratin, type II cytoskeletal 5 OS=Ophiophagus hannah G OPPIHA	2

2100	4.24	4.24	33.83	4.505	2.202 tr	V8NHK4	V8NHK4_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2101	4.24	4.24	44.44	11.76	7.19 tr	V8P5W6	V8P5W6_OPHHA	Uncharacterized protein OS=Ophiophagus hanna GN=L345_0 OPHHA	2
2102	4.24	4.24	29.86	16.11	16.11 tr	V8NFZ2	V8NFZ2_OPHHA	Tetraspanin (Fragment) OS=Ophiophagus hanna GN=Tspan2 OPHHA	4
2103	4.23	13.26	64.04	27.45	19.79 tr	V8NIC4	V8NIC4_OPHHA	Sulfotransferase (Fragment) OS=Ophiophagus hanna GN=Su OPHHA	9
2104	4.23	4.25	29.87	6.74	5.464 tr	V8PDE2	V8PDE2_OPHHA	Glycerophosphoinositol inositolphosphodiesterase GDDP2 OPHHA	2
2105	4.23	4.23	51.58	4.246	2.8 tr	V8NS00	V8NS00_OPHHA	Cell division control protein 6-like protein (Fragment) OPHHA	2
2106	4.23	4.23	58.87	11.04	7.359 tr	V8P965	V8P965_OPHHA	E3 ubiquitin-protein ligase RNF14 (Fragment) OS=Ophiophagus hanna OPHHA	2
2107	4.23	4.23	60.14	36.49	20.95 tr	V8N548	V8N548_OPHHA	Eukaryotic translation initiation factor 3 subunit K OS OPHHA	2
2108	4.22	4.24	43.67	8.696	6.616 tr	V8NNZ6	V8NNZ6_OPHHA	Engulfment and cell motility protein 3 OS=Ophiophagus hanna OPHHA	2
2109	4.22	4.22	36.73	12.73	9.818 tr	V8PAS6	V8PAS6_OPHHA	Beta-lactamase-like protein 2 OS=Ophiophagus hanna GN= OPHHA	5
2110	4.22	4.22	57.65	49.41	49.41 tr	V8N7U6	V8N7U6_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	4
2111	4.19	4.24	42.73	11.63	9.302 tr	V8P316	V8P316_OPHHA	54 kDa 2'-5'-oligoadenylate synthase-like protein 2 (Fr OPHHA	3
2112	4.19	4.19	50.8	12.03	12.03 tr	V8NWQ8	V8NWQ8_OPHHA	G-rich sequence factor 1 (Fragment) OS=Ophiophagus hanna OPHHA	4
2113	4.19	4.19	44.26	34.43	22.13 tr	V8N491	V8N491_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2114	4.18	4.22	55.46	4.499	2.812 tr	V8P8Z1	V8P8Z1_OPHHA	Mitogen-activated protein kinase kinase 5 (Fragm OPHHA	2
2115	4.18	4.18	48.6	5.387	5.387 tr	V8PAA6	V8PAA6_OPHHA	Mitogen-activated protein kinase kinase kinase 2 OS=Oph OPHHA	4
2116	4.18	4.18	38.19	6.496	4.331 tr	V8PGH9	V8PGH9_OPHHA	Protein lunapark (Fragment) OS=Ophiophagus hanna GN=LN OPHHA	2
2117	4.18	4.18	27.6	8.2	5.6 tr	V8P7X1	V8P7X1_OPHHA	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Ophiophagus hanna OPHHA	2
2118	4.18	4.18	51.2	7.229	7.229 tr	V8NV71	V8NV71_OPHHA	1-acylglycerol-3-phosphate 0-acyltransferase ABHD5 OS=O OPHHA	2
2119	4.18	4.18	54.76	29.76	19.05 tr	V8PGV1	V8PGV1_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2120	4.17	4.17	47.48	8.14	5.233 tr	V8NGH6	V8NGH6_OPHHA	Uncharacterized protein OS=Ophiophagus hanna GN=L345_1 OPHHA	3
2121	4.17	4.17	75.26	21.13	16.49 tr	V8NED3	V8NED3_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2122	4.17	4.17	69.59	24.74	13.92 tr	V8ND23	V8ND23_OPHHA	Actin-binding LIM protein 1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2123	4.17	4.17	20.28	7.692	6.527 tr	V8P590	V8P590_OPHHA	Cadherin-1 (Fragment) OS=Ophiophagus hanna GN=CDH1 PE= OPHHA	2
2124	4.17	4.17	75.81	33.06	25 tr	V8NVL7	V8NVL7_OPHHA	BAG family molecular chaperone regulator 1 (Fragment) O OPHHA	3
2125	4.17	4.17	32.37	23.12	18.5 tr	V8NB2	V8NB2_OPHHA	Glycerol kinase (Fragment) OS=Ophiophagus hanna GN=GK OPHHA	2
2126	4.16	4.16	65.66	11.31	6.061 tr	V8P005	V8P005_OPHHA	Katanin p60 ATPase-containing subunit A1 OS=Ophiophagus hanna OPHHA	2
2126	0.01	2.83	47.92	5.208	5.208 tr	V8PCW7	V8PCW7_OPHHA	Katanin p60 ATPase-containing subunit A-like 1 (Fragmen OPHHA	2
2127	4.16	4.16	48.76	10.34	3.82 tr	V8NW77	V8NW77_OPHHA	Putative E3 ubiquitin-protein ligase makorin-2 OS=Ophiophagus hanna OPHHA	2
2128	4.16	4.16	51.42	14.2	9.464 tr	V8P813	V8P813_OPHHA	Mitochondrial glutamate carrier 2 (Fragment) OS=Ophiophagus hanna OPHHA	3
2129	4.16	4.16	65.19	20.89	15.19 tr	V8NDV4	V8NDV4_OPHHA	Annexin (Fragment) OS=Ophiophagus hanna GN=Anxa7 PE=3 OPHHA	2
2130	4.15	4.15	51.59	14.65	9.554 tr	V8NVL9	V8NVL9_OPHHA	ATPase family AAA domain-containing protein 1 OS=Ophiophagus hanna OPHHA	2
2131	4.14	4.25	39.02	13.86	8.316 tr	V8N710	V8N710_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2132	4.14	4.14	34.41	1.795	1.01 tr	V8PB32	V8PB32_OPHHA	Ankyrin repeat domain-containing protein 17 (Fragment) OPHHA	2
2133	4.14	4.14	25.74	6.087	4.174 tr	V8PBH5	V8PBH5_OPHHA	Amino acid transporter (Fragment) OS=Ophiophagus hanna OPHHA	2
2134	4.13	4.27	62.96	14.81	9.972 tr	V8NM49	V8NM49_OPHHA	Macrophage erythroblast attacher (Fragment) OS=Ophiophagus hanna OPHHA	2
2135	4.13	4.13	36.61	4.805	2.059 tr	V8P132	V8P132_OPHHA	Desmocollin-2 OS=Ophiophagus hanna GN=DSC2 PE=4 SV=1 OPHHA	2
2136	4.13	4.13	43.21	4.14	3.234 tr	V8PG24	V8PG24_OPHHA	Ubiquitin carboxyl-terminal hydrolase 16 (Fragment) OS= OPHHA	2
2137	4.13	4.13	79.05	15.42	15.42 tr	V8PE10	V8PE10_OPHHA	Eukaryotic translation initiation factor 4H (Fragment) OPHHA	2
2138	4.13	4.13	56.73	15.51	12.65 tr	V8NGH3	V8NGH3_OPHHA	Carboxypeptidase B2 (Fragment) OS=Ophiophagus hanna GN OPHHA	2
2139	4.13	4.13	30.37	10.03	10.03 tr	V8PHN6	V8PHN6_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	3
2140	4.13	4.13	12.35	5.12	4.217 tr	V8P7X5	V8P7X5_OPHHA	Transporter (Fragment) OS=Ophiophagus hanna GN=SLC6A6 OPHHA	2
2141	4.13	4.13	19.89	18.23	14.36 tr	V8NPE1	V8NPE1_OPHHA	Tryptophan-rich protein OS=Ophiophagus hanna GN=Wrb PE OPHHA	2
2142	4.12	4.12	70.95	9.385	3.017 tr	V8P116	V8P116_OPHHA	Pre-mRNA-splicing factor SYF1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2143	4.12	4.12	26.97	11.51	8.224 tr	V8NKB0	V8NKB0_OPHHA	Protein phosphatase 1F (Fragment) OS=Ophiophagus hanna OPHHA	2
2144	4.12	4.12	40.09	18.06	11.01 tr	V8P7K5	V8P7K5_OPHHA	L-xylulose reductase (Fragment) OS=Ophiophagus hanna G OPHHA	2
2145	4.12	4.12	42.31	15.38	15.38 tr	V8NC76	V8NC76_OPHHA	E3 ubiquitin-protein ligase UBR4 (Fragment) OS=Ophiophagus hanna OPHHA	2
2146	4.12	4.12	49.62	20.3	20.3 tr	V8N454	V8N454_OPHHA	Proteasome subunit beta type-6 (Fragment) OS=Ophiophagus hanna OPHHA	2
2147	4.11	5.13	40.19	5.192	4.038 tr	V8NC19	V8NC19_OPHHA	Zinc finger CCH-type antiviral protein 1 OS=Ophiophagus hanna OPHHA	3
2148	4.11	5.06	41.3	5.286	3.965 tr	V8NTC6	V8NTC6_OPHHA	Kn motif and ankyrin repeat domain-containing protein 2 OPHHA	3
2149	4.11	4.82	54.9	2.835	2.255 tr	V8P011	V8P011_OPHHA	Serine/threonine-protein kinase MRCK alpha (Fragment) O OPHHA	3
2150	4.11	4.14	42.6	3.924	3.924 tr	V8P5W3	V8P5W3_OPHHA	Rho-guanine nucleotide exchange factor (Fragment) OS=Op OPHHA	2
2151	4.11	4.11	43.13	5.005	4.26 tr	V8NHJ1	V8NHJ1_OPHHA	DNA mismatch repair protein Msh2 (Fragment) OS=Ophiophagus hanna OPHHA	3
2152	4.11	4.11	73.26	12.09	12.09 tr	V8PC28	V8PC28_OPHHA	Translation initiation factor IF-3, mitochondrial (Frag OPHHA	4
2153	4.11	4.11	58.97	26.5	20.94 tr	V8NLV6	V8NLV6_OPHHA	Ubiquitin fusion degradation protein 1-like protein OS= OPHHA	3
2154	4.11	4.11	56.25	34.9	22.92 tr	V8NQL9	V8NQL9_OPHHA	Death-associated protein 1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2155	4.11	4.11	59.09	41.82	30.91 tr	V8PIY9	V8PIY9_OPHHA	Cytochrome b5 OS=Ophiophagus hanna GN=CYB5A PE=3 SV=1 OPHHA	3
2156	4.1	4.1	78.3	33.02	26.42 tr	V8P3E1	V8P3E1_OPHHA	Serine/threonine-protein kinase 38 (Fragment) OS=Ophiophagus hanna OPHHA	2
2157	4.1	4.1	27.06	17.65	12.94 tr	V8NDX2	V8NDX2_OPHHA	Surfeit locus protein 4 (Fragment) OS=Ophiophagus hanna OPHHA	2
2158	4.09	12.17	62.67	35.48	26.73 tr	V8NJY7	V8NJY7_OPHHA	Glycerol-3-phosphate dehydrogenase [NAD(+)] (Fragment) NAD(+) OPHHA	8
2159	4.09	7.36	47.08	16.99	16.99 tr	V8NZP8	V8NZP8_OPHHA	Putative RNA-binding protein Luc7-like 1 (Fragment) OS= OPHHA	5
2160	4.09	4.15	69.37	15.14	15.14 tr	V8PCH6	V8PCH6_OPHHA	Peptidyl-prolyl cis-trans isomerase OS=Ophiophagus hanna OPHHA	3
2161	4.09	4.11	47.08	17.08	17.08 tr	V8PA39	V8PA39_OPHHA	Nuclear factor 1 C-type (Fragment) OS=Ophiophagus hanna OPHHA	3
2162	4.09	4.09	36.4	4.159	1.863 tr	V8PHQ0	V8PHQ0_OPHHA	GC-rich sequence DNA-binding factor 1 (Fragment) OS=Oph OPHHA	3
2163	4.09	4.09	41.33	6.476	6.476 tr	V8N782	V8N782_OPHHA	Inositol polyphosphate 5-phosphatase OCRL-1 (Fragment) OPHHA	3
2164	4.09	4.09	57.08	29.25	22.17 tr	V8NFE5	V8NFE5_OPHHA	Joergren syndrome/scleroderma autoantigen 1-like protei OPHHA	2
2165	4.09	4.09	23.9	8.353	6.497 tr	V8N760	V8N760_OPHHA	Cytochrome P450 (Fragment) OS=Ophiophagus hanna GN=Cyp OPHHA	3
2166	4.08	4.08	31.07	9.416	4.52 tr	V8NWF6	V8NWF6_OPHHA	Aspartyl-tRNA synthetase, mitochondrial (Fragment) OS=O OPHHA	2
2167	4.08	4.08	38.99	6.193	6.193 tr	V8NLX4	V8NLX4_OPHHA	Striatin-4 (Fragment) OS=Ophiophagus hanna GN=Strn4 PE OPHHA	2
2168	4.08	4.08	76.42	27.51	21.83 tr	V8NHR5	V8NHR5_OPHHA	Heme-binding protein 1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2169	4.07	4.09	62.84	11.06	11.06 tr	V8NCS0	V8NCS0_OPHHA	Colorectal mutant cancer protein (Fragment) OS=Ophiophagus hanna OPHHA	3
2170	4.07	4.08	100	39.8	36.73 tr	V8NII1	V8NII1_OPHHA	Proteasome inhibitor PI31 subunit (Fragment) OS=Ophiophagus hanna OPHHA	2
2171	4.07	4.07	42.99	8.314	8.314 tr	V8P1R8	V8P1R8_OPHHA	DBP1-and CUL4-associated factor 13 (Fragment) OS=Ophiophagus hanna OPHHA	2
2172	4.07	4.07	42.34	17.52	12.41 tr	V8NCF2	V8NCF2_OPHHA	Calcineurin-like phosphoesterase domain-containing prot OPHHA	2
2173	4.06	21.27	55.21	16.06	11.81 tr	V8NKK3	V8NKK3_OPHHA	Clathrin heavy chain 1 (Fragment) OS=Ophiophagus hanna OPHHA	12
2174	4.06	4.86	49.2	12.3	9.091 tr	V8PY8	V8PY8_OPHHA	39S ribosomal protein L12, mitochondrial OS=Ophiophagus hanna OPHHA	3
2175	4.06	4.06	48.04	3.538	3.538 tr	V8NS20	V8NS20_OPHHA	Ubiquitin carboxyl-terminal hydrolase 25 OS=Ophiophagus hanna OPHHA	2
2176	4.06	4.06	33.87	5.376	5.376 tr	V8N9Y9	V8N9Y9_OPHHA	Lipolysis-stimulated lipoprotein receptor (Fragment) OS OPHHA	2
2177	4.06	4.06	51.81	8.29	8.29 tr	V8PBM2	V8PBM2_OPHHA	Nucl domain-containing protein 3 (Fragment) OS=Ophiophagus hanna OPHHA	2
2178	4.06	4.06	37.5	5.388	5.388 tr	V8N5P4	V8N5P4_OPHHA	ATP-dependent RNA helicase DDX1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2179	4.06	4.06	42.25	15.14	10.56 tr	V8N974	V8N974_OPHHA	Starch-binding domain-containing protein 1 (Fragment) O OPHHA	3
2180	4.06	4.06	72.22	34.72	34.72 tr	V8N2A8	V8N2A8_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2181	4.05	4.05	54.18	1.657	1.657 tr	V8NC39	V8NC39_OPHHA	Macrophage mannose receptor 1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2182	4.05	4.05	41.9	2.091	2.091 tr	V8NUE6	V8NUE6_OPHHA	Kinesin-like protein (Fragment) OS=Ophiophagus hanna G OPHHA	2
2183	4.05	4.05	46.66	3.488	3.488 tr	V8P9R8	V8P9R8_OPHHA	Ankyrin repeat and zinc finger domain-containing protei OPHHA	2
2184	4.05	4.05	48.5	6.138	6.138 tr	V8NKL3	V8NKL3_OPHHA	Eukaryotic translation initiation factor 2D (Fragment) OPHHA	2
2185	4.05	4.05	89.19	39.64	25.23 tr	V8NRM2	V8NRM2_OPHHA	Chloride intracellular channel protein 5 (Fragment) OS= OPHHA	2
2186	4.05	4.05	51.25	17.5	13.12 tr	V8NJ82	V8NJ82_OPHHA	Cytochrome b-c1 complex subunit 8 (Fragment) OS=Ophiophagus hanna OPHHA	2
2187	4.05	4.05	75	23.08	23.08 tr	V8NJJ1	V8NJJ1_OPHHA	Exportin-1 (Fragment) OS=Ophiophagus hanna GN=XP01 PE= OPHHA	2
2188	4.04	4.76	84.42	20.1	11.06 tr	V8NVD0	V8NVD0_OPHHA	Protein phosphatase 1 regulatory subunit 12B (Fragment) OPHHA	3
2189	4.04	4.4	55.05	7.423	5.773 tr	V8PJ4	V8PJ4_OPHHA	DnaJ-like subfamily C member 3 OS=Ophiophagus hanna GN OPHHA	2
2190	4.04	4.06	44.44	13.19	6.944 tr	V8NHC2	V8NHC2_OPHHA	Ribosomal protein S6 kinase beta-1 OS=Ophiophagus hanna OPHHA	2
2191	4.04	4.06	79.27	20.73	20.73 tr	V8NSF6	V8NSF6_OPHHA	SH3 domain-binding glutamic acid-rich-like protein 3 OS OPHHA	4
2192	4.04	4.05	44.65	5.68	5.68 tr	V8NFN1	V8NFN1_OPHHA	Double-stranded RNA-specific adenosine deaminase (Fragm OPHHA	2
2193	4.04	4.04	41.18	6.933	3.466 tr	V8NML6	V8NML6_OPHHA	Protein phosphatase 1 regulatory subunit 37 (Fragment) OPHHA	2
2194	4.04	4.04	46.2	3.566	3.566 tr	V8P5A0	V8P5A0_OPHHA	RNA polymerase-associated protein RTF1-like protein (Fr OPHHA	2

2195	4.04	4.04	23.44	1.997	1.997	tr V8POM5 V8POM5_OPPIHA ATP-binding cassette sub-family A member 5 (Fragment) O OPPIHA	2
2196	4.04	4.04	36.9	8.2	5.467	tr V8NYG1 V8NYG1_OPPIHA Chitinase-3-like protein 2 (Fragment) OS=Ophiophagus ha OPPIHA	2
2197	4.04	4.04	37.96	7.082	7.082	tr V8NRE4 V8NRE4_OPPIHA Lanosterol 14-alpha demethylase OS=Ophiophagus hannah G OPPIHA	2
2198	4.04	4.04	33.15	8.625	8.625	tr V8PEW3 V8PEW3_OPPIHA Bifunctional arginine demethylase and lysyl-hydroxylase OPPIHA	2
2199	4.04	4.04	39.51	25.93	25.93	tr V8P4Z9 V8P4Z9_OPPIHA CB1 cannabinoid receptor-interacting protein 1 (Fragment) OPPIHA	2
2200	4.04	4.04	64.41	22.88	22.88	tr V8N2P0 V8N2P0_OPPIHA Talin-1 (Fragment) OS=Ophiophagus hannah GN=TLN1 PE=4 S OPPIHA	2
2201	4.03	4.1	19.44	6.771	5.035	tr V8NWR2 V8NWR2_OPPIHA Sodium-coupled neutral amino acid transporter 3 (Fragment) OPPIHA	2
2202	4.03	4.09	65.1	11.76	11.76	tr V8N7C9 V8N7C9_OPPIHA Acyl-CoA dehydrogenase family member 11 (Fragment) OS=O OPPIHA	3
2203	4.03	4.04	66.49	10.47	10.47	tr V8PFA6 V8PFA6_OPPIHA Calyphosin-like protein OS=Ophiophagus hannah GN=Cap1 OPPIHA	2
2204	4.03	4.03	49.96	1.806	1.806	tr V8PFL0 V8PFL0_OPPIHA DNA mismatch repair protein Msh6 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2205	4.03	4.03	36.67	2.875	2.875	tr V8NZV8 V8NZV8_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2206	4.03	4.03	55.57	7.006	3.822	tr V8PC10 V8PC10_OPPIHA Mitochondrial intermediate peptidase (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2207	4.03	4.03	29.17	5.304	5.304	tr V8PDS8 V8PDS8_OPPIHA Protein unc-93-like B1 OS=Ophiophagus hannah GN=Unc93b1 OPPIHA	2
2208	4.03	4.03	47.18	5.636	3.704	tr V8NQH4 V8NQH4_OPPIHA Complement component C7 OS=Ophiophagus hannah GN=C7 PE= OPPIHA	2
2209	4.03	4.03	48.49	9.799	5.779	tr V8P639 V8P639_OPPIHA Mitochondrial ribonuclease P protein 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2210	4.03	4.03	37.42	3.576	3.576	tr V8NC09 V8NC09_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2211	4.03	4.03	52.04	6.122	6.122	tr V8NGV4 V8NGV4_OPPIHA E3 ubiquitin-protein ligase TRIM11 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2211	0	4.02	36.58	0.5333	0.5333	tr V8NLW4 V8NLW4_OPPIHA E3 ubiquitin-protein ligase TRIM11 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2212	4.03	4.03	43.67	6.667	6.667	tr V8NLQ9 V8NLQ9_OPPIHA Putative phospholipase B-like 2 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2213	4.02	6.37	56.15	13.13	10.34	tr V8NGF0 V8NGF0_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	4
2214	4.02	4.02	39.76	4.991	4.991	tr V8P6D9 V8P6D9_OPPIHA Protein FAM55C (Fragment) OS=Ophiophagus hannah GN=FAM5 OPPIHA	2
2215	4.02	4.02	40.57	3.872	3.872	tr V8P5Q0 V8P5Q0_OPPIHA Exosome component 10 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2216	4.02	4.02	33.92	5.765	5.765	tr V8PGY9 V8PGY9_OPPIHA Testis-specific Y-encoded-like protein 2 (Fragment) OS=OPPIHA	2
2217	4.02	4.02	49.61	9.819	9.819	tr V8P8K1 V8P8K1_OPPIHA Legumain OS=Ophiophagus hannah GN=Lgm PE=4 SV=1 OPPIHA	2
2218	4.02	4.02	84.31	28.43	28.43	tr V8P3N6 V8P3N6_OPPIHA PHD finger-like domain-containing protein 5A OS=Ophiophagus hannah GN=OPPIHA	2
2219	4.02	4.02	28.3	18.87	18.87	tr V8P983 V8P983_OPPIHA Solute carrier family 2, facilitated glucose transporter 2 OPPIHA	2
2220	4.02	4.02	23.04	10.43	7.391	tr V8NVP4 V8NVP4_OPPIHA Heme-binding protein 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2221	4.01	6.02	30	12.08	12.08	tr V8NGP9 V8NGP9_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	4
2222	4.01	4.01	59.01	6.832	6.832	tr V8NSY8 V8NSY8_OPPIHA Protein arginine N-methyltransferase 5 OS=Ophiophagus hannah GN=OPPIHA	3
2223	4.01	4.01	45.99	7.595	7.595	tr V8N9L3 V8N9L3_OPPIHA Charged multivesicular body protein 2a (Fragment) OS=OPPIHA	2
2224	4.01	4.01	68.67	14	14	tr V8NCT4 V8NCT4_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2225	4.01	4.01	34.71	5.785	5.785	tr V8P824 V8P824_OPPIHA S-phase kinase-associated protein 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2226	4.01	4.01	52.26	10.55	10.55	tr V8N706 V8N706_OPPIHA GDP-fucose protein O-fucosyltransferase 1 (Fragment) OS=OPPIHA	2
2227	4.01	4.01	36	13.33	13.33	tr V8PCV9 V8PCV9_OPPIHA CDGSH iron-sulfur domain-containing protein 2 OS=Ophiophagus hannah GN=OPPIHA	2
2228	4.01	4.01	62.07	34.48	34.48	tr V8NMY6 V8NMY6_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2229	4	45.82	72.68	59.42	59.42	tr V8NV61 V8NV61_OPPIHA Actin, alpha skeletal muscle OS=Ophiophagus hannah GN=OPPIHA	34
2230	4	16.56	93.75	55.56	47.92	tr V8N322 V8N322_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	8
2231	4	7.49	49.12	18.25	18.25	tr V8NFQ3 V8NFQ3_OPPIHA Ras-related protein Ral-A (Fragment) OS=Ophiophagus hannah GN=OPPIHA	4
2232	4	7.08	42.89	7.953	5.606	tr V8PBJ4 V8PBJ4_OPPIHA ATP-dependent 6-phosphofructokinase OS=Ophiophagus hannah GN=OPPIHA	3
2233	4	4.36	41.5	19.39	12.93	tr V8P726 V8P726_OPPIHA Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OPPIHA	3
2234	4	4.01	36.21	3.767	3.767	tr V8PG04 V8PG04_OPPIHA Activating transcription factor 7-interacting protein 1 OPPIHA	2
2235	4	4.01	49.56	11.95	11.95	tr V8PED4 V8PED4_OPPIHA RING finger protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2236	4	4	53.95	5.643	5.643	tr V8P5X9 V8P5X9_OPPIHA Unconventional prefoldin RPB5 interactor (Fragment) OS=OPPIHA	2
2237	4	4	34.8	3.937	3.937	tr V8NVW5 V8NVW5_OPPIHA Receptor-type tyrosine protein phosphatase epsilon (Fragment) OPPIHA	2
2238	4	4	38.68	4.054	4.054	tr V8PJ62 V8PJ62_OPPIHA Kelch-like ECH-associated protein 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2239	4	4	39.51	4.72	4.72	tr V8NU79 V8NU79_OPPIHA Complement factor 1 OS=Ophiophagus hannah GN=CF1 PE=3 S OPPIHA	5
2240	4	4	47.44	9.375	6.534	tr V8P669 V8P669_OPPIHA Leucine carboxyl methyltransferase 1 (Fragment) OS=OPPIHA	2
2241	4	4	55.05	9.121	9.121	tr V8NXF7 V8NXF7_OPPIHA Alpha-(1,3)-fucosyltransferase 11 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2242	4	4	31.41	4.704	4.704	tr V8N5A8 V8N5A8_OPPIHA Alpha-tectorin (Fragment) OS=Ophiophagus hannah GN=Tect OPPIHA	2
2243	4	4	51.97	9.319	9.319	tr V8NRR1 V8NRR1_OPPIHA G protein-coupled receptor kinase 5 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2243	0	2.02	63.3	2.087	2.087	tr V8PEN5 V8PEN5_OPPIHA G protein-coupled receptor kinase 6 OS=Ophiophagus hannah GN=OPPIHA	1
2244	4	4	72.83	14.45	14.45	tr V8NNG0 V8NNG0_OPPIHA Acyl-CoA-binding domain-containing protein 6 (Fragment) OPPIHA	2
2245	4	4	42.24	13.79	9.914	tr V8PG69 V8PG69_OPPIHA Sell repeat-containing protein 1 OS=Ophiophagus hannah GN=OPPIHA	2
2246	4	4	50.69	8.621	8.621	tr V8PB16 V8PB16_OPPIHA Syntaxin-16 (Fragment) OS=Ophiophagus hannah GN=STX16 P OPPIHA	2
2247	4	4	48.28	7.837	7.837	tr V8PJ39 V8PJ39_OPPIHA Proline-rich AKT1 substrate 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2248	4	4	53.26	13.79	13.79	tr V8NPC8 V8NPC8_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2249	4	4	38.91	3.754	3.754	tr V8N913 V8N913_OPPIHA Retinol dehydrogenase 14 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2250	4	4	65.27	21.56	21.56	tr V8NA15 V8NA15_OPPIHA CaiB/baiF CoA-transferase family protein C7orf10 (Fragment) OPPIHA	2
2251	4	4	47.39	7.826	7.826	tr V8N5R0 V8N5R0_OPPIHA Sulfotransferase OS=Ophiophagus hannah GN=Sulf16b1 PE=3 OPPIHA	2
2252	4	4	63.7	18.52	18.52	tr V8NGW7 V8NGW7_OPPIHA COMM domain-containing protein 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2253	4	4	67.39	9.42	9.42	tr V8NZL2 V8NZL2_OPPIHA Emerin OS=Ophiophagus hannah GN=Emd PE=4 SV=1 OPPIHA	2
2254	4	4	50.52	10.1	10.1	tr V8NZ49 V8NZ49_OPPIHA GDP-mannose 4,6 dehydratase (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2255	4	4	37.92	8.257	8.257	tr V8NLQ7 V8NLQ7_OPPIHA Probable cytosolic iron-sulfur protein assembly protein OPPIHA	2
2256	4	4	88.03	16.24	16.24	tr V8N983 V8N983_OPPIHA RNA-binding protein 8A OS=Ophiophagus hannah GN=RBM8A P OPPIHA	3
2257	4	4	86.36	36.36	36.36	tr V8N3J1 V8N3J1_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2258	4	4	28.28	11.48	11.48	tr V8N812 V8N812_OPPIHA 2-acylglycerol O-acyltransferase 2-A (Fragment) OS=OPPIHA	2
2259	4	4	59	23	23	tr V8P5M7 V8P5M7_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2260	4	4	75.49	25.49	25.49	tr V8P2W9 V8P2W9_OPPIHA Ribonuclease OS=Ophiophagus hannah GN=HRSP12 PE=4 SV=1 OPPIHA	4
2261	4	4	14.57	4.933	4.933	tr V8NGJ0 V8NGJ0_OPPIHA Galactose oxidase OS=Ophiophagus hannah GN=galc PE=4 OPPIHA	2
2262	4	4	31.42	13.27	13.27	tr V8PEB6 V8PEB6_OPPIHA Guanylate kinase OS=Ophiophagus hannah GN=GUK1 PE=4 SV= OPPIHA	2
2263	4	4	11.78	6.667	6.667	tr V8P9K9 V8P9K9_OPPIHA Serine incorporator 1 OS=Ophiophagus hannah GN=SERINC1 OPPIHA	2
2264	4	4	19.38	7.752	7.752	tr V8NK08 V8NK08_OPPIHA Ubiquitin-associated protein 1 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2265	4	4	48.35	27.47	27.47	tr V8NGK1 V8NGK1_OPPIHA Leucine-rich repeat-containing protein 16A (Fragment) O OPPIHA	2
2266	4	4	39.67	22.31	22.31	tr V8N8Q1 V8N8Q1_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2267	4	4	53.91	25.22	25.22	tr V8N5B6 V8N5B6_OPPIHA Tax1-binding protein 3 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2268	4	4	26.42	18.87	18.87	tr V8NKM1 V8NKM1_OPPIHA U1 small nuclear ribonucleoprotein C OS=Ophiophagus hannah GN=OPPIHA	2
2269	4	4	44.7	24.24	24.24	tr V8NFR9 V8NFR9_OPPIHA Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=OPPIHA	2
2270	4	4	36.54	21.15	21.15	tr V8N5F2 V8N5F2_OPPIHA Dysferlin OS=Ophiophagus hannah GN=DYSF PE=4 SV=1 OPPIHA	2
2271	4	4	74.36	39.74	39.74	tr V8N346 V8N346_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2272	4	4	13.74	5.852	5.852	tr V8P6G4 V8P6G4_OPPIHA Nuclear factor 1 B-type (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2273	4	4	45.16	34.41	34.41	tr V8P1Q8 V8P1Q8_OPPIHA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit OPPIHA	4
2274	4	4	38.14	38.14	38.14	tr V8NG55 V8NG55_OPPIHA Solute carrier family 25 member 46 (Fragment) OS=OPPIHA	2
2275	3.99	3.99	41.93	2.41	2.41	tr V8NXU8 V8NXU8_OPPIHA Phospholipase A2 (Fragment) OS=Ophiophagus hannah GN=PL OPPIHA	2
2276	3.98	3.98	49.59	4.772	4.772	tr V8P3F8 V8P3F8_OPPIHA Rab11 family-interacting protein 3 (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2277	3.98	3.98	39.72	6.197	6.197	tr V8P1J7 V8P1J7_OPPIHA Sparc (Fragment) OS=Ophiophagus hannah GN=SPARC PE=4 SV OPPIHA	2
2278	3.96	4.18	57.67	7.379	6.214	tr V8NIG0 V8NIG0_OPPIHA Methionyl-tRNA synthetase, mitochondrial (Fragment) OS=OPPIHA	2
2279	3.96	4.03	43.55	9.032	9.032	tr V8NFX4 V8NFX4_OPPIHA Plasma membrane calcium-transporting ATPase 1 (Fragment) OPPIHA	2
2280	3.96	3.96	66.88	6.818	6.818	tr V8P9A6 V8P9A6_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2281	3.96	3.96	43.9	10.84	9.214	tr V8PE19 V8PE19_OPPIHA Myeloid-associated differentiation marker-like protein OPPIHA	2
2282	3.95	8.69	42.46	10.61	8.939	tr V8N763 V8N763_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	4
2283	3.95	3.95	44.45	3.095	1.591	tr V8NH22 V8NH22_OPPIHA Zinc finger protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	4
2284	3.95	3.95	72.91	16.71	8.934	tr V8NUH4 V8NUH4_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2285	3.95	3.95	44.16	8.262	8.262	tr V8P086 V8P086_OPPIHA Tensin (Fragment) OS=Ophiophagus hannah GN=TN PE=4 SV= OPPIHA	2
2286	3.94	3.94	44.33	32.99	32.99	tr V8NQN8 V8NQN8_OPPIHA Acetyl-CoA carboxylase (Fragment) OS=Ophiophagus hannah GN=OPPIHA	3
2287	3.93	3.93	43.85	5.426	2.879	tr V8P3G1 V8P3G1_OPPIHA Protein unc-45-like A (Fragment) OS=Ophiophagus hannah GN=OPPIHA	2
2288	3.93	3.93	45.28	8.399	2.887	tr V8NMZ1 V8NMZ1_OPPIHA High affinity nerve growth factor receptor (Fragment) O OPPIHA	2

2289	3.93	3.93	35.04	7.682	3.908	tr V8NQT5 V8NQT5_OPHHA Zinc finger CCCH domain-containing protein 14 (Fragment OPHHA	2
2290	3.93	3.93	44.26	9.605	4.331	tr V8NJE7 V8NJE7_OPHHA Putative leucyl-tRNA synthetase, mitochondrial (Fragmen OPHHA	2
2291	3.93	3.93	34.44	5.74	5.74	tr V8NWQ7 V8NWQ7_OPHHA Glutathione S-transferase theta-1 OS=Ophiophagus hannah OPHHA	2
2292	3.93	3.93	42.27	10.5	7.58	tr V8NJJ8 V8NJJ8_OPHHA HEAT repeat-containing protein 7A (Fragment) OS=Ophioph	2
2293	3.92	11.53	56.08	17.06	12.15	tr V8NUW6 V8NUW6_OPHHA Septin-8 (Fragment) OS=Ophiophagus hannah GN=SEPT8 PE=3 OPHHA	5
2294	3.92	3.92	64.58	11.6	8.777	tr V8P876 V8P876_OPHHA Abhydrolase domain-containing protein 14A (Fragment) OS OPHHA	2
2295	3.92	3.92	64.65	24.24	24.24	tr V8P6M2 V8P6M2_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2296	3.91	3.91	48.45	2.966	2.401	tr V8NJJ21 V8NJJ21_OPHHA Collagen alpha-3(IV) chain (Fragment) OS=Ophiophagus ha OPHHA	2
2297	3.91	3.91	50.1	6.114	4.536	tr V8NMY7 V8NMY7_OPHHA Scaffold attachment factor B2 (Fragment) OS=Ophiophagus OPHHA	2
2298	3.9	3.97	40.83	2.823	2.823	tr V8NHW6 V8NHW6_OPHHA Coiled-coil domain-containing protein (Fragment) OS=Oph OPHHA	2
2299	3.9	3.9	65.91	18.75	14.2	tr V8NBM7 V8NBM7_OPHHA Tubulin polymerization-promoting protein family member OPHHA	2
2300	3.89	3.89	47.45	6.841	5.677	tr V8P8F1 V8P8F1_OPHHA X-ray repair cross-complementing protein 5 (Fragment) O OPHHA	3
2301	3.88	3.88	39.07	4.055	3.066	tr V8P195 V8P195_OPHHA Alanine-tRNA synthetase, mitochondrial (Fragment) OS=Oph OPHHA	2
2302	3.88	3.88	66.83	7.805	7.805	tr V8N882 V8N882_OPHHA Structural maintenance of chromosomes flexible hinge do OPHHA	2
2303	3.88	3.88	58.05	23.41	20	tr V8N4S1 V8N4S1_OPHHA Basement membrane-specific heparan sulfate proteoglycan OPHHA	3
2304	3.88	3.88	28.07	14.47	11.4	tr V8PG76 V8PG76_OPHHA WASH complex subunit CDC53 (Fragment) OS=Ophiophagus h OPHHA	2
2305	3.88	3.88	56.15	34.62	34.62	tr V8NCJ1 V8NCJ1_OPHHA tRNA methyltransferase-like protein OS=Ophiophagus hann OPHHA	4
2306	3.87	3.87	35.76	21.21	21.21	tr V8N5W7 V8N5W7_OPHHA Complement factor H (Fragment) OS=Ophiophagus hannah GN OPHHA	3
2307	3.86	3.86	33.47	1.902	1.902	tr V8NQD8 V8NQD8_OPHHA DmX-like protein 2 (Fragment) OS=Ophiophagus hannah GN= OPHHA	4
2308	3.86	3.86	28.77	5.936	3.653	tr V8PDR4 V8PDR4_OPHHA Ubiquitin-conjugating enzyme E2 0 (Fragment) OS=Ophioph	2
2309	3.86	3.86	33.12	14.2	8.202	tr V8POC4 V8POC4_OPHHA Protein VAC14-like protein (Fragment) OS=Ophiophagus ha OPHHA	2
2310	3.85	4.11	29.89	4.112	2.307	tr V8NN43 V8NN43_OPHHA Receptor protein-tyrosine kinase (Fragment) OS=Ophioph	3
2311	3.85	3.85	58.53	9.118	9.118	tr V8NP20 V8NP20_OPHHA Serine/threonine-protein kinase 38 (Fragment) OS=Ophioph	2
2312	3.85	3.85	40	12.5	7.5	tr V8PH52 V8PH52_OPHHA UV excision repair protein RAD23-like A (Fragment) OS=O	2
2313	3.85	3.85	64.06	13.82	13.82	tr V8PEQ0 V8PEQ0_OPHHA Guanine nucleotide-binding protein subunit gamma (Fragm OPHHA	2
2314	3.85	3.85	45.45	12	9.455	tr V8P5D1 V8P5D1_OPHHA 28S ribosomal protein S30, mitochondrial (Fragment) OS= OPHHA	2
2315	3.85	3.85	28.19	11.17	7.713	tr V8NRX7 V8NRX7_OPHHA Ubiquitin-conjugating enzyme E2 J1 (Fragment) OS=Ophioph	2
2316	3.85	3.85	31.66	6.533	6.533	tr V8NN17 V8NN17_OPHHA RNA-binding motif, single-stranded-interacting protein OPHHA	2
2317	3.84	3.84	32.86	21.43	21.43	tr V8N980 V8N980_OPHHA Translationally-controlled tumor protein-like protein (OPHHA	4
2318	3.83	8.52	38.56	16.56	11.11	tr V8N158 V8N158_OPHHA Phosphatidylinositol-binding clathrin assembly protein OPHHA	6
2319	3.83	3.83	46.38	26.09	19.32	tr V8NJU7 V8NJU7_OPHHA Exportin-1 (Fragment) OS=Ophiophagus hannah GN=Xpo1 PE= OPHHA	3
2320	3.83	3.83	33.58	17.52	12.41	tr V8PEJ7 V8PEJ7_OPHHA Prefoldin subunit 5 OS=Ophiophagus hannah GN=PFDN5 PE=4 OPHHA	2
2321	3.82	4.15	72.73	31.82	18.18	tr V8N5Z1 V8N5Z1_OPHHA Tropomyosin alpha-3 chain (Fragment) OS=Ophiophagus han OPHHA	2
2322	3.82	3.82	44.84	5.952	5.952	tr V8PHL0 V8PHL0_OPHHA SH3 and PX domain-containing protein 2B (Fragment) OS=O	3
2323	3.82	3.82	15.94	2.772	2.079	tr V8PHC6 V8PHC6_OPHHA Histone deacetylase 5 (Fragment) OS=Ophiophagus hannah OPHHA	2
2324	3.81	3.81	38.45	4.193	2.319	tr V8NEE3 V8NEE3_OPHHA UHRF1-binding protein 1-like protein (Fragment) OS=Ophi	2
2325	3.81	3.81	56.02	13.16	12.78	tr V8PD74 V8PD74_OPHHA Myelin P2 protein OS=Ophiophagus hannah GN=PMP2 PE=3 SV OPHHA	3
2326	3.81	3.81	28.34	5.263	5.263	tr V8P7C8 V8P7C8_OPHHA Gamma-glutamyltransferase 5 (Fragment) OS=Ophiophagus h OPHHA	2
2327	3.81	3.81	66.67	22.22	22.22	tr V8PGE8 V8PGE8_OPHHA Annexin (Fragment) OS=Ophiophagus hannah GN=L345.00743 OPHHA	2
2328	3.81	3.81	20.29	10.27	5.623	tr V8P7Y5 V8P7Y5_OPHHA CAAX prenyl protease 1-like protein OS=Ophiophagus hann OPHHA	2
2329	3.81	3.81	22.7	11.49	8.908	tr V8NEP3 V8NEP3_OPHHA Bifunctional ATP-dependent dihydroxyacetone kinase/FAD- OPHHA	2
2330	3.8	3.81	60.54	15.65	15.65	tr V8PJ80 V8PJ80_OPHHA Glia maturation factor beta (Fragment) OS=Ophiophagus h OPHHA	3
2331	3.8	3.8	49.3	5.578	2.789	tr V8NUX1 V8NUX1_OPHHA Paired amphipathic helix protein Sin3a OS=Ophiophagus h OPHHA	3
2332	3.8	3.8	40	6.024	6.024	tr V8NKZ2 V8NKZ2_OPHHA Protein misato-like 1 (Fragment) OS=Ophiophagus hannah OPHHA	2
2333	3.8	3.8	44.44	12.57	9.064	tr V8PD71 V8PD71_OPHHA Putative transferase CAF17, mitochondrial (Fragment) OS OPHHA	3
2334	3.8	3.8	65.63	21.88	21.88	tr V8NY33 V8NY33_OPHHA Protein transport protein Sec61 subunit beta OS=Ophioph	2
2335	3.77	3.77	56.17	6.168	4.068	tr V8PGB0 V8PGB0_OPHHA Putative RNA-binding protein 15 (Fragment) OS=Ophioph	2
2336	3.77	3.77	33.14	4.551	2.45	tr V8P8P8 V8P8P8_OPHHA Ubiquitin carboxyl-terminal hydrolase 4 (Fragment) OS=O	2
2337	3.77	3.77	49.39	7.085	7.085	tr V8NYS4 V8NYS4_OPHHA 5'-nucleotidase domain-containing protein 2 (Fragment) OPHHA	3
2338	3.77	3.77	34.52	13.1	13.1	tr V8P649 V8P649_OPHHA Eukaryotic translation initiation factor 4E type 3 (Fra OPHHA	3
2339	3.76	3.76	46.44	3.541	1.959	tr V8NAK4 V8NAK4_OPHHA A-kinase anchor protein 12 (Fragment) OS=Ophiophagus ha OPHHA	4
2340	3.76	3.76	57.23	30.82	18.87	tr V8NPK8 V8NPK8_OPHHA Glutathione peroxidase OS=Ophiophagus hannah GN=GPX4 PE OPHHA	3
2341	3.75	4	52.3	7.503	3.024	tr V8NLS6 V8NLS6_OPHHA THO complex subunit 2 (Fragment) OS=Ophiophagus hannah OPHHA	2
2342	3.74	3.77	31.14	2.958	2.958	tr V8PC56 V8PC56_OPHHA Chloride channel protein (Fragment) OS=Ophiophagus hann OPHHA	2
2343	3.74	3.74	37.97	17.11	17.11	tr V8PFC3 V8PFC3_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2344	3.74	3.74	34.2	20.78	20.78	tr V8P5Y0 V8P5Y0_OPHHA Replication protein A 32 kDa subunit OS=Ophiophagus han OPHHA	3
2345	3.74	3.74	22.95	9.426	9.426	tr V8NJB2 V8NJB2_OPHHA 2-oxoisovalerate dehydrogenase subunit beta, mitochondr OPHHA	2
2346	3.73	3.73	39.77	16.37	11.11	tr V8NA97 V8NA97_OPHHA Cleavage and polyadenylation specificity factor subunit OPHHA	2
2347	3.72	3.72	49.38	25	12.5	tr V8PGM6 V8PGM6_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	3
2348	3.72	3.72	29.45	20.25	20.25	tr V8P9D3 V8P9D3_OPHHA Protein tyrosine phosphatase type IVA 2 (Fragment) OS=O	2
2349	3.71	3.71	42.13	6.742	6.742	tr V8PBS6 V8PBS6_OPHHA Synaptic vesicle membrane protein VAT-1-like protein (F OPHHA	2
2350	3.71	3.71	41.32	21.56	21.56	tr V8PGE5 V8PGE5_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345.0 OPHHA	3
2351	3.7	3.74	31.67	20	16.11	tr V8NH05 V8NH05_OPHHA Peripheral plasma membrane protein CASK (Fragment) OS=O	2
2352	3.7	3.7	47.06	9.02	9.02	tr V8NW40 V8NW40_OPHHA Creatine kinase S-type, mitochondrial (Fragment) OS=Oph OPHHA	2
2353	3.7	3.7	32.59	6.685	6.685	tr V8PG84 V8PG84_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345.0 OPHHA	2
2354	3.7	3.7	33.13	22.85	18.13	tr V8NTB7 V8NTB7_OPHHA Coatamer subunit alpha (Fragment) OS=Ophiophagus hannah OPHHA	2
2355	3.7	3.7	32.56	16.86	16.86	tr V8NXZ5 V8NXZ5_OPHHA Ubiquitin-conjugating enzyme E2 D2 OS=Ophiophagus hanna OPHHA	3
2355	0	3.7	26.43	20.71	20.71	tr V8PBB6 V8PBB6_OPHHA Ubiquitin-conjugating enzyme E2 D3 (Fragment) OS=Ophioph	3
2355	0	1.55	19.59	12.16	12.16	tr V8NR52 V8NR52_OPHHA Ubiquitin-conjugating enzyme E2 D1 (Fragment) OS=Ophioph	2
2356	3.7	3.7	13.12	8.597	8.597	tr V8N9Q2 V8N9Q2_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2357	3.69	3.69	38.76	26.36	26.36	tr V8NMT6 V8NMT6_OPHHA AP-2 complex subunit sigma OS=Ophiophagus hannah GN=AP2 OPHHA	3
2358	3.68	3.71	45.4	11.4	2.586	tr V8P5W0 V8P5W0_OPHHA Phosphoinositide phospholipase C OS=Ophiophagus hannah OPHHA	2
2359	3.68	3.7	58.06	29.03	29.03	tr V8P912 V8P912_OPHHA Glycophorin-C OS=Ophiophagus hannah GN=GYPC PE=4 SV=1 OPHHA	2
2360	3.68	3.68	37.83	1.549	1.549	tr V8PFA9 V8PFA9_OPHHA Tyrosine-protein kinase receptor (Fragment) OS=Ophioph	2
2361	3.68	3.68	49.38	7.009	3.427	tr V8P7T9 V8P7T9_OPHHA Sulfhydryl oxidase OS=Ophiophagus hannah GN=QS0X1 PE=4 OPHHA	2
2362	3.68	3.68	19.48	3.177	2.258	tr V8P1N0 V8P1N0_OPHHA Niemann-Pick C1 protein (Fragment) OS=Ophiophagus hanna OPHHA	3
2363	3.68	3.68	73.87	11.71	11.71	tr V8P7G5 V8P7G5_OPHHA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu OPHHA	2
2364	3.68	3.68	88.17	24.73	24.73	tr V8NMJ7 V8NMJ7_OPHHA 28S ribosomal protein S27, mitochondrial (Fragment) OS= OPHHA	2
2365	3.68	3.68	50.47	23.36	23.36	tr V8P736 V8P736_OPHHA 28S ribosomal protein S36, mitochondrial OS=Ophiophagus OPHHA	3
2366	3.67	3.83	19	5.156	4.342	tr V8P3D0 V8P3D0_OPHHA Tenascin (Fragment) OS=Ophiophagus hannah GN=Tnc PE=4 S OPHHA	2
2367	3.67	3.71	43.71	5.222	5.222	tr V8NWX7 V8NWX7_OPHHA 25-hydroxycholesterol 7-alpha-hydroxylase (Fragment) OS OPHHA	2
2368	3.67	3.67	49.17	25.97	15.47	tr V8NXP1 V8NXP1_OPHHA Unc-119-like B protein (Fragment) OS=Ophiophagus hannah OPHHA	2
2369	3.67	3.67	68.46	21.54	16.15	tr V8NPN2 V8NPN2_OPHHA Carnitine O-acetyltransferase (Fragment) OS=Ophiophagus OPHHA	3
2370	3.67	3.67	47.3	17.57	17.57	tr V8N571 V8N571_OPHHA Putative ATP-dependent RNA helicase DDX58 (Fragment) OS OPHHA	2
2371	3.66	3.66	68.24	24.89	20.6	tr V8NX85 V8NX85_OPHHA Lysophospholipase-like protein 1 (Fragment) OS=Ophioph	3
2372	3.66	3.66	84.55	18.7	18.7	tr V8N1E1 V8N1E1_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2373	3.66	3.66	40.2	37.25	29.41	tr V8NC66 V8NC66_OPHHA AP-3 complex subunit sigma-1 (Fragment) OS=Ophiophagus OPHHA	3
2374	3.65	3.65	63.43	7.025	7.025	tr V8PH18 V8PH18_OPHHA Zinc finger protein OS=Ophiophagus hannah GN=ZNF622 PE= OPHHA	2
2375	3.65	3.65	36.93	11.85	11.85	tr V8P1K7 V8P1K7_OPHHA Phosphoinositide 3-kinase adapter protein 1 (Fragment) OPHHA	2
2376	3.64	3.64	70.79	31.46	31.46	tr V8NZE2 V8NZE2_OPHHA WD repeat-containing protein 70 (Fragment) OS=Ophioph	2
2377	3.63	3.63	46.47	13.46	7.372	tr V8P1A1 V8P1A1_OPHHA Beta-1,4-galactosyltransferase 4 (Fragment) OS=Ophioph	2
2378	3.63	3.63	47.41	21.48	21.48	tr V8NG83 V8NG83_OPHHA Lipoma-preferred partner-like protein (Fragment) OS=Oph OPHHA	2
2379	3.63	3.63	69.72	48.62	23.85	tr V8NX51 V8NX51_OPHHA Dihydrofolate reductase (Fragment) OS=Ophiophagus hanna OPHHA	2
2380	3.62	3.62	42.88	6.47	4.806	tr V8PHW1 V8PHW1_OPHHA Ecotropic viral integration site 5 protein-like protein OPHHA	2
2381	3.61	3.61	33.43	2.798	1.833	tr V8NWU0 V8NWU0_OPHHA Protein ELYS (Fragment) OS=Ophiophagus hannah GN=AHCTF1 OPHHA	3
2382	3.61	3.61	37.28	5.013	3.856	tr V8P7Q6 V8P7Q6_OPHHA Rho GTPase-activating protein 26 (Fragment) OS=Ophioph	2

2383	3.6	3.6	34.42	3.323	2.696	tr V8N7W1 V8N7W1_OPHHA	WD repeat-containing protein 81 (Fragment) OS=Ophiophag	OPHHA	3
2384	3.6	3.6	49.49	5.102	5.102	tr V8NVR8 V8NVR8_OPHHA	Phosphatidate phosphatase LPIN1 (Fragment) OS=Ophiophag	OPHHA	4
2385	3.6	3.6	35.41	5.253	5.253	tr V8P684 V8P684_OPHHA	Leucine-rich repeat protein SHOC-2 (Fragment) OS=Ophiop	OPHHA	2
2386	3.59	3.59	47.72	6.14	4.211	tr V8NZ15 V8NZ15_OPHHA	CCR4-NOT transcription complex subunit 10 (Fragment) OS	OPHHA	2
2387	3.59	3.59	37.24	13.51	8.408	tr V8NKJ5 V8NKJ5_OPHHA	NAD-dependent deacetylase sirtuin-2 (Fragment) OS=Ophi	OPHHA	2
2388	3.59	3.59	81.05	29.47	21.05	tr V8NY00 V8NY00_OPHHA	U6 snRNA-associated Sm-like protein LSM2 OS=Ophiophag	OPHHA	2
2389	3.59	3.59	57.69	23.85	23.85	tr V8N786 V8N786_OPHHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345_1	OPHHA	2
2390	3.58	3.58	74.21	25.79	20.81	tr V8NW75 V8NW75_OPHHA	Ras-related protein Rab-20 (Fragment) OS=Ophiophagus h	OPHHA	3
2391	3.57	3.57	36.3	7.942	4.7	tr V8PDK2 V8PDK2_OPHHA	Drebrin (Fragment) OS=Ophiophagus hannah GN=DBN1 PE=4	S OPHHA	2
2392	3.57	3.57	63.04	14.4	8.56	tr V8NZ48 V8NZ48_OPHHA	Syntaxin-6 (Fragment) OS=Ophiophagus hannah GN=STX6	PE= OPHHA	2
2393	3.57	3.57	31.14	4.878	4.878	tr V8P472 V8P472_OPHHA	Phosphatidylserine synthase 1 (Fragment) OS=Ophiophag	OPHHA	2
2394	3.57	3.57	45.51	6.667	6.667	tr V8NXM8 V8NXM8_OPHHA	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxyla	OPHHA	2
2395	3.57	3.57	64.79	12.68	12.68	tr V8PGD7 V8PGD7_OPHHA	Ecotropic viral integration site 5 protein-like protein	OPHHA	2
2396	3.57	3.57	55.32	15.43	10.11	tr V8NZQ3 V8NZQ3_OPHHA	Trafficking protein particle complex subunit 5 (Fragmen	OPHHA	2
2397	3.57	3.57	48.37	26.8	15.69	tr V8NX71 V8NX71_OPHHA	Retinol-binding protein 4 (Fragment) OS=Ophiophagus han	OPHHA	2
2398	3.56	3.56	40.5	6.387	6.218	tr V8PF92 V8PF92_OPHHA	Phosphatidylinositol-glycan-specific phospholipase D (F	OPHHA	3
2399	3.56	3.56	66.91	21.58	12.95	tr V8PF32 V8PF32_OPHHA	Cytoglobin (Fragment) OS=Ophiophagus hannah GN=Cygb	PE= OPHHA	2
2400	3.55	3.55	55.44	12.73	4.928	tr V8PJ6 V8PJ6_OPHHA	Phosphatidylinositol 4-kinase type 2-alpha (Fragment) 0	OPHHA	2
2401	3.55	3.55	51.37	10.27	10.27	tr V8N9P4 V8N9P4_OPHHA	Queuine tRNA-ribosyltransferase (Fragment) OS=Ophiophag	OPHHA	2
2402	3.55	3.55	84.13	36.51	36.51	tr V8N2T4 V8N2T4_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	2
2403	3.54	4.77	43.47	6.999	6.999	tr V8NLL1 V8NLL1_OPHHA	Lysophosphatidylcholine acyltransferase 2 (Fragment) OS	OPHHA	4
2404	3.54	3.58	33.33	2.715	1.377	tr V8NDM8 V8NDM8_OPHHA	Peroxisomal proliferator-activated receptor A-interacti	OPHHA	3
2405	3.54	3.54	38.29	11.6	9.409	tr V8N7Y1 V8N7Y1_OPHHA	Beta-galactosidase-1-like protein 2 (Fragment) OS=Ophi	OPHHA	3
2406	3.54	3.54	51.3	36.52	18.26	tr V8P6Y5 V8P6Y5_OPHHA	Protein LBH (Fragment) OS=Ophiophagus hannah GN=LBH	PE= OPHHA	2
2407	3.52	3.52	53.35	4.345	1.296	tr V8POL6 V8POL6_OPHHA	Intersectin-2 (Fragment) OS=Ophiophagus hannah GN=Itsn2	OPHHA	2
2408	3.51	5.7	44.14	9.742	8.151	tr V8PIC2 V8PIC2_OPHHA	TATA-binding protein-associated factor 2N OS=Ophiophagu	OPHHA	3
2409	3.51	5.22	45.77	15.16	12.83	tr V8NJY6 V8NJY6_OPHHA	Long-chain fatty acid transport protein 4 (Fragment) OS	OPHHA	3
2410	3.51	3.51	12.17	12.17	12.17	tr V8NMC1 V8NMC1_OPHHA	Translocon-associated protein subunit alpha (Fragment)	OPHHA	3
2411	3.5	3.51	35.6	2.785	2.785	tr V8PH57 V8PH57_OPHHA	Neurabin-2 (Fragment) OS=Ophiophagus hannah GN=Ppplr9b	OPHHA	2
2412	3.5	3.5	34.65	3.477	2.398	tr V8NLF8 V8NLF8_OPHHA	E3 ubiquitin-protein ligase (Fragment) OS=Ophiophagus h	OPHHA	2
2413	3.5	3.5	45.02	4.739	4.739	tr V8PDZ7 V8PDZ7_OPHHA	GRAM domain-containing protein 4 (Fragment) OS=Ophiopha	OPHHA	2
2414	3.5	3.5	52.7	12.33	5.236	tr V8N7J5 V8N7J5_OPHHA	Neuropilin-2 (Fragment) OS=Ophiophagus hannah GN=NRP2	P OPHHA	2
2415	3.49	3.49	41.84	3.567	2.126	tr V8NN78 V8NN78_OPHHA	Gem-associated protein 5 (Fragment) OS=Ophiophagus hann	OPHHA	2
2416	3.49	3.49	30.05	6.39	6.39	tr V8PEZ4 V8PEZ4_OPHHA	Beta-glucuronidase OS=Ophiophagus hannah GN=GUSB	PE=3 S OPHHA	3
2417	3.49	3.49	77.03	25	19.59	tr V8NEZ6 V8NEZ6_OPHHA	Transmembrane and coiled-coil domain-containing protein	OPHHA	2
2418	3.48	3.48	62.16	24.32	24.32	tr V8PEV3 V8PEV3_OPHHA	Cytoglobin (Fragment) OS=Ophiophagus hannah GN=Cygb	PE= OPHHA	2
2419	3.47	5.53	45.15	14.56	5.696	tr V8N680 V8N680_OPHHA	Plectin (Fragment) OS=Ophiophagus hannah GN=PLEC	PE=4 S OPHHA	2
2420	3.47	3.47	55.08	6.581	2.861	tr V8NMV3 V8NMV3_OPHHA	tRNA (Cytosine(34)-(C(5))-methyltransferase OS=Ophiophag	OPHHA	2
2421	3.47	3.47	35.62	5.961	3.428	tr V8P2F9 V8P2F9_OPHHA	Cartilage acidic protein 1 (Fragment) OS=Ophiophagus ha	OPHHA	2
2422	3.47	3.47	33.67	27.55	26.53	tr V8NUK8 V8NUK8_OPHHA	Laminin subunit alpha-5 (Fragment) OS=Ophiophagus hanna	OPHHA	3
2423	3.46	5.87	30.57	11.06	7.805	tr V8PES6 V8PES6_OPHHA	Epsin-2 OS=Ophiophagus hannah GN=Epn2	PE=4 SV=1 OPHHA	4
2424	3.44	4.1	30.18	6.852	1.631	tr V8PA58 V8PA58_OPHHA	E3 ubiquitin-protein ligase (Fragment) OS=Ophiophagus h	OPHHA	1
2425	3.44	3.44	27.12	3.211	2.1	tr V8NNO6 V8NNO6_OPHHA	Baculoviral IAP repeat-containing protein 6 (Fragment)	OPHHA	5
2426	3.44	3.44	80	32.67	32.67	tr V8NU37 V8NU37_OPHHA	U5 small nuclear ribonucleoprotein 40 kDa protein OS=Op	OPHHA	3
2427	3.44	3.44	51.61	31.18	31.18	tr V8N1U1 V8N1U1_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	2
2428	3.42	3.42	56.88	17.43	12.84	tr V8PHN4 V8PHN4_OPHHA	Autophagy-related protein OS=Ophiophagus hannah GN=ATG1	OPHHA	2
2429	3.42	3.42	61.49	17.39	13.04	tr V8NXW6 V8NXW6_OPHHA	MOB kinase activator 2 (Fragment) OS=Ophiophagus hanna	OPHHA	3
2430	3.42	3.42	34.82	5.292	5.292	tr V8NPW8 V8NPW8_OPHHA	Protein OSCP1 (Fragment) OS=Ophiophagus hannah GN=OSCP1	OPHHA	2
2431	3.42	3.42	40.31	23.26	17.05	tr V8NY43 V8NY43_OPHHA	Brain protein 44 OS=Ophiophagus hannah GN=BRP44	PE=4 SV OPHHA	2
2432	3.41	3.43	42.35	3.128	2.198	tr V8NU99 V8NU99_OPHHA	PDZ domain-containing protein 8 (Fragment) OS=Ophiophag	OPHHA	2
2433	3.41	3.41	35.96	5.512	4.462	tr V8NBD3 V8NBD3_OPHHA	Contactin-1 (Fragment) OS=Ophiophagus hannah GN=CNTN1	P OPHHA	2
2434	3.4	3.4	16.76	4.655	4.655	tr V8PC35 V8PC35_OPHHA	Nucleoporin p58/p45 (Fragment) OS=Ophiophagus hannah	GN OPHHA	2
2435	3.39	3.39	25.81	16.77	10.32	tr V8P3R6 V8P3R6_OPHHA	Tumor protein p53-inducible protein 11 OS=Ophiophagus	h OPHHA	2
2436	3.37	8.73	32.62	13.98	11.26	tr V8P5N0 V8P5N0_OPHHA	Importin subunit alpha OS=Ophiophagus hannah GN=KPN1	P OPHHA	5
2437	3.36	3.49	41.69	14.42	10.66	tr V8P2U9 V8P2U9_OPHHA	Protein FAM84A (Fragment) OS=Ophiophagus hannah GN=FAM8	OPHHA	2
2438	3.36	3.37	37.91	2.662	2.662	tr V8NNH2 V8NNH2_OPHHA	Importin-8 (Fragment) OS=Ophiophagus hannah GN=IPO8	PE= OPHHA	4
2439	3.36	3.36	53.87	11.45	9.091	tr V8NE76 V8NE76_OPHHA	Surfeit locus protein 1 (Fragment) OS=Ophiophagus hanna	OPHHA	2
2440	3.36	3.36	37.5	15.13	13.82	tr V8NNS4 V8NNS4_OPHHA	1-acyl-sn-glycerol-3-phosphate acyltransferase beta OS=	OPHHA	2
2441	3.35	3.36	54.61	29.08	29.08	tr V8NOK4 V8NOK4_OPHHA	EH domain-containing protein 1 (Fragment) OS=Ophiophagu	OPHHA	2
2442	3.35	3.35	34.04	12.12	9.038	tr V8PHA5 V8PHA5_OPHHA	Spondin-1 (Fragment) OS=Ophiophagus hannah GN=SPON1	PE= OPHHA	2
2443	3.35	3.35	31.36	6.684	6.684	tr V8PH48 V8PH48_OPHHA	RNA-binding motif, single-stranded-interacting protein	OPHHA	2
2444	3.34	3.34	55.91	8.861	8.861	tr V8NJ65 V8NJ65_OPHHA	Tetratricopeptide repeat protein 27 (Fragment) OS=Ophi	OPHHA	3
2445	3.34	3.34	43.36	20.31	4.297	tr V8P5S4 V8P5S4_OPHHA	Guanylate cyclase soluble subunit alpha-2 (Fragment) OS	OPHHA	1
2446	3.33	3.34	41.22	7.379	1.908	tr V8NRN9 V8NRN9_OPHHA	Cleavage and polyadenylation specificity factor subunit	OPHHA	1
2447	3.33	3.33	57.42	7.742	7.742	tr V8PAN5 V8PAN5_OPHHA	CDKN2A-interacting protein OS=Ophiophagus hannah GN=Cdk	OPHHA	2
2448	3.32	3.46	42.15	3.927	1.813	tr V8P8K9 V8P8K9_OPHHA	UDP-glucose:glycoprotein glucosyltransferase 1 (Fragmen	OPHHA	2
2449	3.32	3.33	64.41	7.415	7.415	tr V8PAH2 V8PAH2_OPHHA	DNA methyltransferase 1-associated protein 1 (Fragment)	OPHHA	2
2450	3.32	3.33	68.66	20.15	20.15	tr V8N8C4 V8N8C4_OPHHA	Phosphatidylinositol 3-kinase catalytic subunit type 3	OPHHA	2
2451	3.32	3.32	31.15	5.533	5.533	tr V8NR93 V8NR93_OPHHA	Clusterin (Fragment) OS=Ophiophagus hannah GN=CLU	PE=3 OPHHA	3
2452	3.31	3.31	41.21	2.633	1.531	tr V8NZR7 V8NZR7_OPHHA	Serine/threonine-protein kinase TAO2 (Fragment) OS=Ophi	OPHHA	2
2453	3.31	3.31	53.44	3.077	2.429	tr V8NU12 V8NU12_OPHHA	Protein Shroom1 (Fragment) OS=Ophiophagus hannah GN=shr	OPHHA	2
2454	3.31	3.31	35.67	1.619	1.619	tr V8NQA0 V8NQA0_OPHHA	Rho GTPase-activating protein 32 (Fragment) OS=Ophiopha	OPHHA	2
2455	3.31	3.31	28.39	4.816	2.251	tr V8P468 V8P468_OPHHA	Zinc finger SWIM domain-containing protein (Fragment) 0	OPHHA	2
2456	3.31	3.31	37.9	4.338	4.338	tr V8N8V2 V8N8V2_OPHHA	Rhomoid-like protein (Fragment) OS=Ophiophagus hannah	OPHHA	3
2457	3.31	3.31	41.81	7.345	7.345	tr V8NA44 V8NA44_OPHHA	Protein jagunal-like 1 (Fragment) OS=Ophiophagus hannah	OPHHA	2
2458	3.3	4.32	52.17	2.879	1.952	tr V8PIZ1 V8PIZ1_OPHHA	Myosin-3 (Fragment) OS=Ophiophagus hannah GN=Myh3	PE=4 OPHHA	4
2459	3.3	3.31	49.59	10.33	10.33	tr V8PIY6 V8PIY6_OPHHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345	0 OPHHA	2
2460	3.3	3.3	59.18	7.823	3.912	tr V8P9Q8 V8P9Q8_OPHHA	La-related protein 7 OS=Ophiophagus hannah GN=LARP7	PE= OPHHA	2
2461	3.3	3.3	33.68	11.34	11.34	tr V8PF00 V8PF00_OPHHA	RNA binding protein fox-1-like 2 OS=Ophiophagus hannah	OPHHA	2
2462	3.3	3.3	32.35	10.13	10.13	tr V8NBQ5 V8NBQ5_OPHHA	5-oxoprolinase (Fragment) OS=Ophiophagus hannah GN=Opla	OPHHA	2
2463	3.29	6.18	40.95	9.524	8.19	tr V8NW43 V8NW43_OPHHA	STE20/SPS1-related proline-alanine-rich protein kinase	OPHHA	4
2464	3.29	3.31	28.77	3.774	3.774	tr V8P1M3 V8P1M3_OPHHA	RNA-binding protein 26 OS=Ophiophagus hannah GN=RBM26	P OPHHA	2
2465	3.29	3.3	61.27	15.85	15.85	tr V8NIZ8 V8NIZ8_OPHHA	RING finger protein OS=Ophiophagus hannah GN=RNFI41	PE= OPHHA	3
2466	3.29	3.29	51.9	1.62	1.62	tr V8N7J9 V8N7J9_OPHHA	Rho GTPase-activating protein 21 OS=Ophiophagus hannah	OPHHA	2
2467	3.29	3.29	44.36	2.159	1.542	tr V8PCE0 V8PCE0_OPHHA	Ankyrin repeat and SAM domain-containing protein 6 (Fra	OPHHA	2
2468	3.29	3.29	50.72	4.337	3.614	tr V8NE10 V8NE10_OPHHA	Protein CIP2A-like protein (Fragment) OS=Ophiophagus ha	OPHHA	2
2469	3.29	3.29	40.14	4.577	4.577	tr V8NKB1 V8NKB1_OPHHA	Oxidoreductase NAD-binding domain-containing protein 1	OPHHA	2
2470	3.28	3.32	33.67	12.24	7.823	tr V8NLY5 V8NLY5_OPHHA	Golgi pH regulator OS=Ophiophagus hannah GN=GPR89	PE=4 OPHHA	2
2471	3.28	3.28	32.47	19.48	14.94	tr V8N771 V8N771_OPHHA	Galectin (Fragment) OS=Ophiophagus hannah GN=LGAL59C	PE OPHHA	4
2472	3.27	3.27	54.35	10.25	5.609	tr V8NS41 V8NS41_OPHHA	Cell cycle regulator Mat89Bb-like protein (Fragment) OS	OPHHA	2
2473	3.27	3.27	46.13	9.369	5.766	tr V8NIW5 V8NIW5_OPHHA	Cytochrome protein (Fragment) OS=Ophiophagus hannah GN=	OPHHA	3
2474	3.27	3.27	79.49	20	12.31	tr V8P295 V8P295_OPHHA	Prothrombin (Fragment) OS=Ophiophagus hannah GN=F2	PE=3 OPHHA	2
2475	3.27	3.27	49.07	8.696	8.696	tr V8N2L3 V8N2L3_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	2
2476	3.25	3.25	40.16	2.561	2.561	tr V8NFK4 V8NFK4_OPHHA	Phospholipid-transporting ATPase (Fragment) OS=Ophiopha	OPHHA	2
2477	3.25	3.25	44.36	4.246	4.246	tr V8NKV9 V8NKV9_OPHHA	DEP domain-containing protein 5 (Fragment) OS=Ophiophag	OPHHA	2
2478	3.25	3.25	41.48	7.615	5.411	tr V8NEL7 V8NEL7_OPHHA	Disks large-associated protein 4 (Fragment) OS=Ophiopha	OPHHA	2

2479	3.25	3.25	25.42	4.583	2.396	tr V8P217 V8P217_OPHHA Importin-13 (Fragment) OS=Ophiophagus hannah GN=IP013 P OPHHA	2
2480	3.25	3.25	45.11	7.16	7.16	tr V8NPP8 V8NPP8_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_1 OPHHA	2
2481	3.25	3.25	63.95	13.73	8.155	tr V8PCQ3 V8PCQ3_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2482	3.25	3.25	23.77	5.85	4.753	tr V8NA18 V8NA18_OPHHA TBC domain-containing protein kinase-like protein (Frag OPHHA	2
2483	3.24	3.28	15.64	5.545	5.545	tr V8NKR5 V8NKR5_OPHHA Sodium-coupled neutral amino acid transporter 3 OS=Ophi OPHHA	2
2484	3.24	3.25	39	2.259	1.784	tr V8P9P2 V8P9P2_OPHHA Rapamycin-insensitive companion of mTOR (Fragment) OS=O OPHHA	2
2485	3.24	3.24	49.18	8.197	8.197	tr V8P022 V8P022_OPHHA Rho-related GTP-binding protein RhoE OS=Ophiophagus han OPHHA	2
2486	3.24	3.24	45.08	10.25	10.25	tr V8NR32 V8NR32_OPHHA GEM-associated protein 2 OS=Ophiophagus hannah GN=GEMIN OPHHA	2
2487	3.23	3.23	33	2.242	2.242	tr V8NRY6 V8NRY6_OPHHA WD repeat-containing protein 24 (Fragment) OS=Ophiophag OPHHA	2
2488	3.23	3.23	43.21	9.239	6.522	tr V8N9F8 V8N9F8_OPHHA Ribosomal L1 domain-containing protein 1 OS=Ophiophagus OPHHA	2
2489	3.22	3.53	52.25	10.11	6.742	tr V8P7Y7 V8P7Y7_OPHHA Replication factor C subunit 3 OS=Ophiophagus hannah GN OPHHA	2
2490	3.22	3.26	47.94	3.196	3.196	tr V8NVW3 V8NVW3_OPHHA Myosin-1A OS=Ophiophagus hannah GN=Myo31DF PE=4 SV=1 OPHHA	2
2491	3.22	3.22	58.04	6.309	6.309	tr V8NRE8 V8NRE8_OPHHA Ankyrin repeat and MYND domain-containing protein 2 OS= OPHHA	2
2492	3.22	3.22	54.42	10.7	10.7	tr V8P111 V8P111_OPHHA DBP1-and CUL4-associated factor 11 (Fragment) OS=Ophiop OPHHA	2
2493	3.21	3.21	41.77	5.17	3.946	tr V8P621 V8P621_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah GN=O OPHHA	2
2494	3.21	3.21	55.17	12.93	12.93	tr V8N5D6 V8N5D6_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2495	3.2	3.2	43.72	1.826	1.826	tr V8NAM7 V8NAM7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2496	3.2	3.2	47.5	14.5	9.25	tr V8NPH7 V8NPH7_OPHHA Zinc finger FYVE domain-containing protein 19 (Fragment OPHHA	2
2497	3.2	3.2	13.21	9.286	8.929	tr V8NRF5 V8NRF5_OPHHA Transmembrane protein (Fragment) OS=Ophiophagus hannah OPHHA	2
2498	3.19	3.22	47.15	4.863	4.863	tr V8NQA3 V8NQA3_OPHHA Chitotriosidase-1 (Fragment) OS=Ophiophagus hannah GN=C OPHHA	2
2499	3.19	3.19	57.39	7.536	3.333	tr V8P4V0 V8P4V0_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2500	3.19	3.19	30.01	3.547	3.547	tr V8PB58 V8PB58_OPHHA NEDD4-binding protein 1 (Fragment) OS=Ophiophagus hanna OPHHA	2
2501	3.18	3.2	25.25	1.69	1.69	tr V8PG89 V8PG89_OPHHA Ral GTPase-activating protein subunit alpha-1 (Fragment OPHHA	3
2502	3.18	3.2	48.15	33.33	21.3	tr V8NER7 V8NER7_OPHHA Leucine-rich repeat-containing protein 16A (Fragment) O OPHHA	2
2503	3.18	3.18	44.6	5.755	5.755	tr V8NEN8 V8NEN8_OPHHA Tripartite motif-containing protein 39 (Fragment) OS=Op OPHHA	2
2504	3.18	3.18	49.14	18.97	18.97	tr V8NHA7 V8NHA7_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345_1 OPHHA	2
2505	3.16	3.16	42.82	3.457	3.457	tr V8P4A1 V8P4A1_OPHHA Dedicator of cytokinesis protein 1 OS=Ophiophagus hanna OPHHA	2
2506	3.15	3.15	56.43	8.233	6.024	tr V8NG59 V8NG59_OPHHA Pre-B-cell leukemia transcription factor-interacting pr OPHHA	2
2507	3.15	3.15	64.4	15.6	9.6	tr V8PF23 V8PF23_OPHHA Vesicle transport protein USE1 (Fragment) OS=Ophiophagu OPHHA	2
2508	3.15	3.15	54.58	8.765	8.765	tr V8P3Q6 V8P3Q6_OPHHA ELMO domain-containing protein 2 OS=Ophiophagus hannah OPHHA	2
2509	3.15	3.15	36.49	8.635	8.635	tr V8PAB2 V8PAB2_OPHHA Ubiquitin carboxyl-terminal hydrolase 12 (Fragment) OS= OPHHA	2
2509	0	2	28.99	4.423	4.423	tr V8N5M7 V8N5M7_OPHHA Ubiquitin carboxyl-terminal hydrolase 46 (Fragment) OS= OPHHA	1
2510	3.14	3.22	54.81	7.115	5	tr V8NHL1 V8NHL1_OPHHA Pyruvate kinase muscle isozyme (Fragment) OS=Ophiophagu OPHHA	2
2511	3.14	3.14	66.23	7.456	5.044	tr V8NK82 V8NK82_OPHHA Golgin subfamily A member 2 OS=Ophiophagus hannah GN=GO OPHHA	2
2512	3.14	3.14	27.45	9.586	7.843	tr V8PFY5 V8PFY5_OPHHA Sorting nexin-18 (Fragment) OS=Ophiophagus hannah GN=S OPHHA	3
2513	3.14	3.14	69.35	16.94	16.94	tr V8P3Z8 V8P3Z8_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2514	3.12	3.17	32.16	14.04	14.04	tr V8N8Z4 V8N8Z4_OPHHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPHHA	3
2515	3.12	3.12	50.7	16.2	4.93	tr V8NUC4 V8NUC4_OPHHA GDP-fucose protein O-fucosyltransferase 2 (Fragment) OS OPHHA	2
2516	3.12	3.12	45.15	12.42	9.697	tr V8NH44 V8NH44_OPHHA 55 kDa erythrocyte membrane protein (Fragment) OS=Ophi OPHHA	2
2517	3.11	3.11	45.41	6.118	6.118	tr V8NPS2 V8NPS2_OPHHA Protein AATF (Fragment) OS=Ophiophagus hannah GN=AATF P OPHHA	2
2518	3.11	3.11	93.75	37.5	37.5	tr V8N6J0 V8N6J0_OPHHA Fragile X mental retardation syndrome-related protein 2 OPHHA	2
2519	3.1	3.1	48.18	11.94	4.656	tr V8PFT7 V8PFT7_OPHHA Ganglioside-induced differentiation-associated protein OPHHA	2
2520	3.1	3.1	48.45	8.031	5.699	tr V8PHA3 V8PHA3_OPHHA PCI domain-containing protein 2 (Fragment) OS=Ophiophag OPHHA	2
2521	3.1	3.1	33.85	21.54	12.31	tr V8PEM2 V8PEM2_OPHHA Dynactin subunit 6 (Fragment) OS=Ophiophagus hannah GN= OPHHA	2
2522	3.1	3.1	63.11	23.77	17.21	tr V8N3W1 V8N3W1_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2523	3.1	3.1	83.33	45	45	tr V8N1M8 V8N1M8_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2524	3.09	3.11	22.59	9.917	5.51	tr V8N9Y0 V8N9Y0_OPHHA Aminoglycoside phosphotransferase domain-containing pro OPHHA	2
2525	3.09	3.09	40.73	2.909	2.909	tr V8BPB8 V8BPB8_OPHHA Transmembrane protein 68 (Fragment) OS=Ophiophagus hann OPHHA	2
2526	3.08	3.09	44.3	8.725	6.711	tr V8P655 V8P655_OPHHA Calcium signal-modulating cyclophilin ligand (Fragment) OPHHA	2
2527	3.08	3.08	72.41	13.79	13.79	tr V8N8X9 V8N8X9_OPHHA Allograft inflammatory factor 1-like protein (Fragment) OPHHA	2
2528	3.08	3.08	21.4	8.696	6.355	tr V8NTK6 V8NTK6_OPHHA Derlin-1 (Fragment) OS=Ophiophagus hannah GN=DERL1 PE=4 OPHHA	2
2529	3.07	3.07	29.96	1.673	1.673	tr V8P311 V8P311_OPHHA Protein-associating with the carboxyl-terminal domain o OPHHA	2
2530	3.07	3.07	31.96	6.545	3.957	tr V8NVB0 V8NVB0_OPHHA GTP-binding protein 1 OS=Ophiophagus hannah GN=GTPBP1 P OPHHA	2
2531	3.07	3.07	44.98	3.903	3.903	tr V8P8R1 V8P8R1_OPHHA Tether containing UBX domain for GLUT4 (Fragment) OS=Op OPHHA	2
2532	3.07	3.07	35.2	12.01	4.555	tr V8NNC0 V8NNC0_OPHHA Regulator of microtubule dynamics protein 3 (Fragment) OPHHA	2
2533	3.06	5.15	58.28	8.284	8.284	tr V8N155 V8N155_OPHHA Fibroblast growth factor receptor 2 (Fragment) OS=Ophi OPHHA	3
2533	0.01	4.02	30.12	2.143	2.143	tr V8PHB3 V8PHB3_OPHHA Fibroblast growth factor receptor 4 (Fragment) OS=Ophi OPHHA	2
2533	0	2.01	20.09	1.129	1.129	tr V8NKM6 V8NKM6_OPHHA Receptor protein-tyrosine kinase (Fragment) OS=Ophiophagu OPHHA	1
2534	3.06	3.06	55.31	13.08	10.08	tr V8NLS4 V8NLS4_OPHHA Cytohesin-2 OS=Ophiophagus hannah GN=CYT2 PE=4 SV=1 OPHHA	2
2535	3.06	3.06	45.81	10.97	10.97	tr V8P8C0 V8P8C0_OPHHA 28S ribosomal protein S31, mitochondrial OS=Ophiophagus OPHHA	2
2536	3.06	3.06	75.76	21.21	21.21	tr V8NU98 V8NU98_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2537	3.05	5.19	38.76	30.23	30.23	tr V8NSM1 V8NSM1_OPHHA Histone H2A (Fragment) OS=Ophiophagus hannah GN=L345_09 OPHHA	3
2537	0	6	33.33	30.95	30.95	tr V8NTL3 V8NTL3_OPHHA Histone H2A (Fragment) OS=Ophiophagus hannah GN=H1ST2H2 OPHHA	3
2538	3.05	3.05	42.25	2.89	1.147	tr V8NQ19 V8NQ19_OPHHA Cation-independent mannose-6-phosphate receptor OS=Ophi OPHHA	2
2539	3.05	3.05	36.39	2.128	2.128	tr V8NX67 V8NX67_OPHHA C-type mannose receptor 2 (Fragment) OS=Ophiophagus han OPHHA	2
2540	3.05	3.05	30.26	8.216	2.605	tr V8NGF6 V8NGF6_OPHHA Aminopeptidase N (Fragment) OS=Ophiophagus hannah GN=AN OPHHA	2
2541	3.05	3.05	13.58	3.88	3.88	tr V8PJH3 V8PJH3_OPHHA Protein arginine N-methyltransferase 3 (Fragment) OS=Op OPHHA	2
2542	3.05	3.05	24.43	15.27	10.69	tr V8NFJ8 V8NFJ8_OPHHA Maspardin (Fragment) OS=Ophiophagus hannah GN=Spg21 PE= OPHHA	2
2543	3.05	3.05	24.32	10.81	10.81	tr V8NUJ5 V8NUJ5_OPHHA Alkylglycerol monooxygenase OS=Ophiophagus hannah GN=ag OPHHA	2
2544	3.04	3.24	54.18	8.696	3.846	tr V8NDU6 V8NDU6_OPHHA TBC1 domain family member 4 (Fragment) OS=Ophiophagus h OPHHA	2
2545	3.04	3.04	34.95	8.981	4.854	tr V8P519 V8P519_OPHHA Muscblind-like protein 1 (Fragment) OS=Ophiophagus h OPHHA	2
2545	0	3.04	33.33	13.86	7.491	tr V8PD64 V8PD64_OPHHA Muscblind-like protein 3 OS=Ophiophagus hannah GN=mbn OPHHA	2
2545	0	1.68	21.6	7.467	2.933	tr V8P8K4 V8P8K4_OPHHA Muscblind-like protein 2 (Fragment) OS=Ophiophagus ha OPHHA	1
2546	3.04	3.04	40.37	19.72	8.257	tr V8NVZ4 V8NVZ4_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2547	3.04	3.04	24.21	9.474	6.842	tr V8NUC1 V8NUC1_OPHHA Endonuclease domain-containing 1 protein (Fragment) OS= OPHHA	2
2548	3.03	3.05	47.07	8.511	8.511	tr V8P7W8 V8P7W8_OPHHA Guanine nucleotide-binding protein G(Z) subunit alpha (OPHHA	2
2549	3.03	3.03	61.85	5.749	4.181	tr V8PB37 V8PB37_OPHHA Myotubularin-related protein 6 (Fragment) OS=Ophiophagu OPHHA	2
2550	3.03	3.03	58.17	6.422	3.67	tr V8NNY7 V8NNY7_OPHHA Lamin-B receptor (Fragment) OS=Ophiophagus hannah GN=LB OPHHA	2
2551	3.02	3.02	32.17	4.755	4.755	tr V8P4R8 V8P4R8_OPHHA Mannan-binding lectin serine protease 2 OS=Ophiophagus OPHHA	2
2552	3.02	3.02	49.15	7.458	7.458	tr V8NRP3 V8NRP3_OPHHA Mitochondrial carnitine/acylcarnitine carrier protein C OPHHA	2
2553	3.01	3.01	62.79	6.977	4.651	tr V8NW42 V8NW42_OPHHA Phosphorylase b kinase gamma catalytic chain, testis/li OPHHA	2
2554	3.01	3.01	29.06	3.973	2.838	tr V8P682 V8P682_OPHHA Ectonucleotide pyrophosphatase/phosphodiesterase family OPHHA	2
2555	3	8.51	51.03	19.01	11.36	tr V8NRY8 V8NRY8_OPHHA Vacuolar protein sorting-associated protein 4B (Fragmen OPHHA	4
2556	3	3	32.71	4.122	2.793	tr V8PD03 V8PD03_OPHHA Aftiphilin (Fragment) OS=Ophiophagus hannah GN=AFTPH PE OPHHA	2
2557	3	3	45.07	17.25	13.73	tr V8P5R4 V8P5R4_OPHHA Phosphatase and actin regulator OS=Ophiophagus hannah G OPHHA	2
2558	3	3	38.42	11.82	11.82	tr V8N7B6 V8N7B6_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2559	2.99	2.99	50	5.263	5.263	tr V8N799 V8N799_OPHHA Sterile alpha and TIR motif-containing protein 1 (Fragm OPHHA	2
2560	2.99	2.99	43.8	12.79	8.915	tr V8PFQ7 V8PFQ7_OPHHA Carbonic anhydrase 13 OS=Ophiophagus hannah GN=Ca13 PE= OPHHA	2
2561	2.99	2.99	49.68	20	20	tr V8NEW7 V8NEW7_OPHHA Endothelial differentiation-related factor 1-like prote OPHHA	2
2562	2.99	2.99	15.82	6.646	6.646	tr V8PAR7 V8PAR7_OPHHA Cyclic AMP-responsive element-binding protein 1 (Fragme OPHHA	2
2563	2.98	10.28	67.57	21.13	15.72	tr V8N7F6 V8N7F6_OPHHA Polyadenylate-binding protein 4 (Fragment) OS=Ophiophag OPHHA	6
2564	2.98	3.01	51.08	4.574	3.685	tr V8NJ85 V8NJ85_OPHHA Semaphorin-4C OS=Ophiophagus hannah GN=Sema4c PE=4 SV=1 OPHHA	2
2565	2.98	2.98	49.71	22.54	17.92	tr V8NX15 V8NX15_OPHHA Vesicle-associated membrane protein 7 (Fragment) OS=Oph OPHHA	2
2566	2.98	2.98	53.65	10.73	10.73	tr V8P9E3 V8P9E3_OPHHA Acyl-coenzyme A thioesterase 10, mitochondrial (Fragmen OPHHA	2
2567	2.97	2.97	63.47	3.276	1.556	tr V8N9V0 V8N9V0_OPHHA Synemin (Fragment) OS=Ophiophagus hannah GN=Synm PE=4 S OPHHA	3
2568	2.97	2.97	30.54	3.829	2.917	tr V8P0Z7 V8P0Z7_OPHHA Phospholipid-transporting ATPase (Fragment) OS=Ophioph OPHHA	3

2569	2.97	2.97	79.62	15.29	15.29	tr	V8NY99	V8NY99_OPHHA	Endonuclease 8-like 1 (Fragment) OS=Ophiophagus hannah OPHHA	2
2570	2.97	2.97	49.59	9.016	9.016	tr	V8P2Z4	V8P2Z4_OPHHA	Ubiquitin domain-containing protein UBFD1 (Fragment) OS OPHHA	2
2571	2.97	2.97	74.42	19.53	11.63	tr	V8NCF9	V8NCF9_OPHHA	Caspase-3 (Fragment) OS=Ophiophagus hannah GN=CASP3 PE= OPHHA	2
2572	2.97	2.97	35.41	14.79	8.171	tr	V8P9G8	V8P9G8_OPHHA	KH domain-containing, RNA-binding, signal transduction- OPHHA	2
2573	2.97	2.97	47.42	13.92	13.92	tr	V8NBE2	V8NBE2_OPHHA	MAGUK p55 subfamily member 7 (Fragment) OS=Ophiophagus OPHHA	2
2574	2.96	3.87	35.73	7.625	5.447	tr	V8NU81	V8NU81_OPHHA	Tumor suppressor candidate 3 OS=Ophiophagus hannah GN=T OPHHA	3
2575	2.96	2.96	39.24	1.549	1.549	tr	V8PHV3	V8PHV3_OPHHA	Putative helicase with zinc finger domain protein (Fragr OPHHA	2
2576	2.96	2.96	49.14	2.058	2.058	tr	V8N8A7	V8N8A7_OPHHA	NACHT, LRR and PYD domains-containing protein 12 (Fragm OPHHA	2
2577	2.96	2.96	50.97	7.799	3.621	tr	V8PDQ5	V8PDQ5_OPHHA	Adseverin OS=Ophiophagus hannah GN=SCIN PE=4 SV=1 OPHHA	2
2578	2.96	2.96	50	7.831	7.831	tr	V8NH53	V8NH53_OPHHA	Histone acetyltransferase (Fragment) OS=Ophiophagus han OPHHA	2
2579	2.96	2.96	50.3	7.298	4.931	tr	V8NK97	V8NK97_OPHHA	Rab-3A-interacting protein (Fragment) OS=Ophiophagus ha OPHHA	2
2580	2.96	2.96	43.48	13.66	9.317	tr	V8P4Y7	V8P4Y7_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2581	2.95	2.95	73.78	19.85	13.86	tr	V8NDB9	V8NDB9_OPHHA	Syntaxin-18 OS=Ophiophagus hannah GN=STX18 PE=4 SV=1 OPHHA	2
2582	2.95	2.95	59.46	34.23	19.82	tr	V8NE38	V8NE38_OPHHA	Agrin (Fragment) OS=Ophiophagus hannah GN=AGRN PE=4 SV= OPHHA	2
2583	2.94	3.19	52.98	5.614	3.392	tr	V8NP87	V8NP87_OPHHA	Pre-mRNA-processing factor 40-like B (Fragment) OS=Ophi OPHHA	2
2584	2.94	2.94	39.55	4.264	2.665	tr	V8NJL5	V8NJL5_OPHHA	Cyclin-T2 (Fragment) OS=Ophiophagus hannah GN=CCNT2 PE= OPHHA	2
2585	2.94	2.94	51.02	25.17	25.17	tr	V8P306	V8P306_OPHHA	cAMP-regulated phosphoprotein 19 (Fragment) OS=Ophiophag OPHHA	2
2586	2.94	2.94	46.03	9.205	9.205	tr	V8PII2	V8PII2_OPHHA	39S ribosomal protein L45, mitochondrial OS=Ophiophagus OPHHA	2
2587	2.94	2.94	26.19	8.036	8.036	tr	V8NDT9	V8NDT9_OPHHA	Steryl-sulfatase (Fragment) OS=Ophiophagus hannah GN=ST OPHHA	2
2588	2.93	9.04	29.81	12.78	11.67	tr	V8NNB7	V8NNB7_OPHHA	Importin subunit alpha-6 (Fragment) OS=Ophiophagus hann OPHHA	6
2589	2.93	4.3	71.24	23.45	16.37	tr	V8NKK6	V8NKK6_OPHHA	Chloride intracellular channel protein 2 OS=Ophiophagus OPHHA	3
2590	2.92	2.97	59.69	5.581	1.473	tr	V8NRE0	V8NRE0_OPHHA	A-kinase anchor protein 9 (Fragment) OS=Ophiophagus han OPHHA	1
2591	2.92	2.92	54.16	4.836	4.836	tr	V8PGK5	V8PGK5_OPHHA	Poly [ADP-ribose] polymerase 12 (Fragment) OS=Ophiophag ADP-ribo:	2
2592	2.92	2.92	49.24	9.15	9.15	tr	V8NKK2	V8NKK2_OPHHA	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondria OPHHA	3
2593	2.92	2.92	40.07	17.73	4.255	tr	V8NXW0	V8NXW0_OPHHA	Cathepsin D (Fragment) OS=Ophiophagus hannah GN=CTSD PE OPHHA	1
2594	2.92	2.92	39.38	13.72	13.72	tr	V8PGY5	V8PGY5_OPHHA	U2 small nuclear ribonucleoprotein B OS=Ophiophagus han OPHHA	2
2595	2.92	2.92	42.04	16.56	16.56	tr	V8NVF8	V8NVF8_OPHHA	39S ribosomal protein L30, mitochondrial OS=Ophiophagus OPHHA	2
2596	2.92	2.92	46.91	27.16	27.16	tr	V8PB96	V8PB96_OPHHA	Uncharacterized protein OS=Ophiophagus hannah GN=L345 O OPHHA	2
2597	2.91	5.18	52.31	20.51	15.9	tr	V8NYM4	V8NYM4_OPHHA	Serine/arginine-rich splicing factor 7 OS=Ophiophagus h OPHHA	3
2598	2.91	2.91	89.25	17.76	5.14	tr	V8NFT7	V8NFT7_OPHHA	39S ribosomal protein L47, mitochondrial (Fragment) OS= OPHHA	1
2599	2.91	2.91	67.98	10.34	10.34	tr	V8NY19	V8NY19_OPHHA	Cholesterol 24-hydroxylase OS=Ophiophagus hannah GN=Cyp OPHHA	2
2600	2.91	2.91	71.33	22	16.67	tr	V8NOW2	V8NOW2_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2601	2.9	2.9	22.97	3.596	3.596	tr	V8NGE6	V8NGE6_OPHHA	Integrator complex subunit 2 (Fragment) OS=Ophiophagus OPHHA	2
2602	2.9	2.9	57.48	10.28	10.28	tr	V8NUT4	V8NUT4_OPHHA	Charged multivesicular body protein 2b OS=Ophiophagus h OPHHA	2
2603	2.9	2.9	52.82	11.79	11.79	tr	V8P7G3	V8P7G3_OPHHA	NF-kappa-B inhibitor-interacting Ras-like protein 2 OS= OPHHA	2
2604	2.9	2.9	51.64	20.49	20.49	tr	V8N5W3	V8N5W3_OPHHA	Phosphomannomutase (Fragment) OS=Ophiophagus hannah GN OPHHA	3
2605	2.89	2.94	36.92	8.462	6.923	tr	V8P8E2	V8P8E2_OPHHA	Secernin-3 (Fragment) OS=Ophiophagus hannah GN=SCRN3 PE OPHHA	2
2606	2.89	2.89	55.14	3.618	3.618	tr	V8NQH9	V8NQH9_OPHHA	2-5A-dependent ribonuclease (Fragment) OS=Ophiophagus h OPHHA	2
2607	2.89	2.89	39.07	9.091	6.143	tr	V8PG65	V8PG65_OPHHA	Neutral cholesterol ester hydrolase 1 OS=Ophiophagus ha OPHHA	2
2608	2.89	2.89	28.82	5.222	5.222	tr	V8PHN9	V8PHN9_OPHHA	Apolipoprotein F (Fragment) OS=Ophiophagus hannah GN=AP OPHHA	2
2609	2.89	2.89	63.71	9.677	9.677	tr	V8P543	V8P543_OPHHA	60S ribosomal protein L24 (Fragment) OS=Ophiophagus han OPHHA	2
2610	2.88	9.19	53.05	14.93	14.73	tr	V8NMQ1	V8NMQ1_OPHHA	Serine/threonine-protein phosphatase 2A 55 kDa regulato OPHHA	5
2611	2.88	7.43	50	29.17	21.76	tr	V8PG32	V8PG32_OPHHA	ADP-ribosylation factor-like protein 8B (Fragment) OS=O OPHHA	5
2612	2.88	2.88	37.95	7.78	3.795	tr	V8P8E8	V8P8E8_OPHHA	Tubby-like protein OS=Ophiophagus hannah GN=Tub PE=3 SV OPHHA	2
2613	2.88	2.88	33.5	19.9	11.17	tr	V8N5Y5	V8N5Y5_OPHHA	26S proteasome non-ATPase regulatory subunit 4 (Fragmen OPHHA	2
2614	2.87	2.88	34.93	3.425	3.425	tr	V8P061	V8P061_OPHHA	Anoctamin (Fragment) OS=Ophiophagus hannah GN=ANO1 PE=3 OPHHA	2
2615	2.87	2.87	43.8	3.17	3.17	tr	V8NP26	V8NP26_OPHHA	Leucine-rich repeat-containing protein 8A (Fragment) OS OPHHA	2
2616	2.87	2.87	33.89	7.778	5.278	tr	V8P9X0	V8P9X0_OPHHA	Ketosamine-3-kinase (Fragment) OS=Ophiophagus hannah GN OPHHA	2
2617	2.87	2.87	16.1	3.121	3.121	tr	V8NKU7	V8NKU7_OPHHA	TSC22 domain family protein 2 (Fragment) OS=Ophiophagus OPHHA	2
2618	2.87	2.87	58.51	39.36	25.53	tr	V8PGX1	V8PGX1_OPHHA	Bridging integrator 3 (Fragment) OS=Ophiophagus hannah OPHHA	2
2619	2.86	2.86	47.35	5.291	3.571	tr	V8PFF3	V8PFF3_OPHHA	Cytotubularin-related protein 10 (Fragment) OS=Ophiophag OPHHA	2
2620	2.86	2.86	49.56	8.211	8.211	tr	V8P382	V8P382_OPHHA	Cdc42 effector protein 4 (Fragment) OS=Ophiophagus hann OPHHA	2
2621	2.86	2.86	57.55	18.87	5.66	tr	V8P2H9	V8P2H9_OPHHA	Programmed cell death protein 10 OS=Ophiophagus hannah OPHHA	1
2622	2.86	2.86	35.32	5.319	3.83	tr	V8NP75	V8NP75_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2623	2.85	2.85	40.21	15.38	12.94	tr	V8NWF2	V8NWF2_OPHHA	Putative hydroxyypyruvate isomerase (Fragment) OS=Ophiop OPHHA	2
2624	2.85	2.85	48.24	14.12	14.12	tr	V8NVK1	V8NVK1_OPHHA	Polyadenylate-binding protein 2 OS=Ophiophagus hannah G OPHHA	2
2625	2.84	2.84	37.73	3.83	2.837	tr	V8P9K1	V8P9K1_OPHHA	CCR4-NOT transcription complex subunit 3 (Fragment) OS= OPHHA	2
2626	2.84	2.84	51.72	10.34	7.958	tr	V8PH26	V8PH26_OPHHA	Endoplasmic reticulum-Golgi intermediate compartment pr OPHHA	3
2627	2.84	2.84	39.1	10.53	10.53	tr	V8P499	V8P499_OPHHA	Sulfotransferase (Fragment) OS=Ophiophagus hannah GN=SU OPHHA	2
2628	2.84	2.84	29.19	11.8	7.143	tr	V8NZL8	V8NZL8_OPHHA	Phenazine biosynthesis-like domain-containing protein (OPHHA	2
2629	2.83	2.83	41.94	6.183	3.763	tr	V8PFH8	V8PFH8_OPHHA	Protein farnesyltransferase subunit beta OS=Ophiophagus OPHHA	1
2630	2.83	2.83	58.79	13.57	13.57	tr	V8NLV1	V8NLV1_OPHHA	39S ribosomal protein L40, mitochondrial (Fragment) OS= OPHHA	2
2631	2.82	4	43.24	9.459	9.459	tr	V8NXH0	V8NXH0_OPHHA	Glyceraldehyde 3-phosphate dehydrogenase, testis-specif OPHHA	3
2632	2.82	2.83	39.43	2.71	2.71	tr	V8PON9	V8PON9_OPHHA	Long-chain-fatty-acid--CoA ligase 6 (Fragment) OS=Ophiop OPHHA	2
2633	2.82	2.83	74.14	13.79	5.747	tr	V8NG17	V8NG17_OPHHA	Calpain small subunit 1 (Fragment) OS=Ophiophagus hanna OPHHA	1
2634	2.82	2.82	45.68	3.602	3.602	tr	V8NV87	V8NV87_OPHHA	ATP-dependent RNA helicase DDX51 (Fragment) OS=Ophiophag OPHHA	2
2635	2.82	2.82	68.92	25	15.54	tr	V8NQF6	V8NQF6_OPHHA	Vacuolar protein sorting-associated protein 29 (Fragmen OPHHA	2
2635	0	2	28.5	3.14	3.14	tr	V8NHQ7	V8NHQ7_OPHHA	Vacuolar protein sorting-associated protein 29 (Fragmen OPHHA	1
2636	2.82	2.82	49.04	19.11	19.11	tr	V8ND40	V8ND40_OPHHA	Stromal cell-derived factor 2-like protein 1 (Fragment) OPHHA	3
2637	2.82	2.82	36.55	18.07	7.229	tr	V8NXP5	V8NXP5_OPHHA	Copper homeostasis protein cutC-like protein OS=Ophioph OPHHA	1
2638	2.8	2.8	54.15	6.829	6.829	tr	V8NM91	V8NM91_OPHHA	tRNA-dihydrouridine(47) synthase [NAD(P)(+)] (Fragment) NAD(P)(+)	2
2639	2.8	2.8	23.77	4.277	4.277	tr	V8NX04	V8NX04_OPHHA	cGMP-inhibited 3',5'-cyclic phosphodiesterase A (Fragme OPHHA	2
2640	2.8	2.8	40.4	6.623	6.623	tr	V8P714	V8P714_OPHHA	Protein DPCD (Fragment) OS=Ophiophagus hannah GN=dpcd P OPHHA	2
2641	2.8	2.8	54.44	11.83	11.83	tr	V8P9P6	V8P9P6_OPHHA	Heme-binding protein 2 (Fragment) OS=Ophiophagus hannah OPHHA	2
2642	2.8	2.8	48.72	14.36	10.26	tr	V8NMF4	V8NMF4_OPHHA	Methionine-R-sulfoxide reductase B1 (Fragment) OS=Ophiop OPHHA	2
2643	2.8	2.8	64.46	35.54	26.45	tr	V8N403	V8N403_OPHHA	N-alpha-acetyltransferase 20 (Fragment) OS=Ophiophagus OPHHA	2
2644	2.79	7.05	61.94	11.55	6.824	tr	V8PHA4	V8PHA4_OPHHA	Reticulocalbin-1 (Fragment) OS=Ophiophagus hannah GN=RC OPHHA	3
2645	2.79	2.79	37.99	4.951	4.464	tr	V8PHG1	V8PHG1_OPHHA	Coagulation factor X isoform 1 (Fragment) OS=Ophiophagu OPHHA	2
2646	2.79	2.79	35.52	7.825	3.912	tr	V8PAB6	V8PAB6_OPHHA	Hermansky-Pudlak syndrome 1 protein-like protein OS=Oph OPHHA	2
2647	2.79	2.79	24.35	6.087	6.087	tr	V8NKY3	V8NKY3_OPHHA	Cation-dependent mannose-6-phosphate receptor OS=Ophiop OPHHA	2
2648	2.78	4.88	37.7	18.32	18.32	tr	V8N7Z8	V8N7Z8_OPHHA	Rho-related GTP-binding protein RhoG (Fragment) OS=Ophi OPHHA	3
2649	2.78	2.79	68.09	27.66	27.66	tr	V8N4E4	V8N4E4_OPHHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2650	2.77	2.77	32.91	5.087	3.339	tr	V8NT82	V8NT82_OPHHA	Protein-glutamine gamma-glutamyltransferase K (Fragment OPHHA	2
2651	2.76	2.76	29.22	4.174	1.336	tr	V8PI65	V8PI65_OPHHA	Exportin-4 OS=Ophiophagus hannah GN=XPO4 PE=3 SV=1 OPHHA	1
2652	2.76	2.76	62.64	6.32	2.416	tr	V8NRF6	V8NRF6_OPHHA	Rap1 GTPase-GDP dissociation stimulator 1 (Fragment) OS OPHHA	1
2653	2.76	2.76	49.03	9.749	3.064	tr	V8P8P7	V8P8P7_OPHHA	Nuclear pore complex protein Nup50 (Fragment) OS=Ophiop OPHHA	1
2654	2.76	2.76	33.33	11.7	11.7	tr	V8NQCO	V8NQCO_OPHHA	Ectonucleoside triphosphate diphosphohydrolase 5 (Fragm OPHHA	2
2655	2.75	2.76	51.71	18	5.143	tr	V8NTD5	V8NTD5_OPHHA	ATP-dependent RNA helicase DHX8 (Fragment) OS=Ophiophag OPHHA	1
2656	2.75	2.75	42.08	7.415	5.411	tr	V8P255	V8P255_OPHHA	Rap1 GTPase-activating protein 2 (Fragment) OS=Ophiophag OPHHA	2
2657	2.75	2.75	39.75	15.57	6.557	tr	V8PJ61	V8PJ61_OPHHA	Ypr1 (Fragment) OS=Ophiophagus hannah GN=YPR1 PE=4 SV=1 OPHHA	1
2658	2.74	2.74	23.7	3.179	1.156	tr	V8NVE7	V8NVE7_OPHHA	Histone deacetylase complex subunit OS=Ophiophagus hann OPHHA	1
2659	2.74	2.74	44.31	7.927	6.098	tr	V8PCT8	V8PCT8_OPHHA	Protein mab-21-like 3 (Fragment) OS=Ophiophagus hannah OPHHA	2
2660	2.74	2.74	62.63	10.32	5.694	tr	V8N537	V8N537_OPHHA	Glyoxalase domain-containing protein 4 (Fragment) OS=Op OPHHA	2
2661	2.74	2.74	31.28	4.112	4.112	tr	V8P8NO	V8P8NO_OPHHA	Gigaxonin (Fragment) OS=Ophiophagus hannah GN=GAN PE=4 OPHHA	2
2662	2.74	2.74	27.53	7.532	2.857	tr	V8NKJ3	V8NKJ3_OPHHA	Phosphatidylserine synthase 2 (Fragment) OS=Ophiophagus OPHHA	1
2663	2.74	2.74	37.09	15.89	15.89	tr	V8P3Z4	V8P3Z4_OPHHA	NRP2-like protein 1 (Fragment) OS=Ophiophagus hannah GN OPHHA	2

2664	2.73	2.73	58.33	12.08	12.08	tr V8NNY3 V8NNY3_OPHHA Phosducin-like protein 3 (Fragment) OS=Ophiophagus hann	OPHHA	2		
2665	2.72	2.72	46.3	6.921	6.921	tr V8PCJ3 V8PCJ3_OPHHA BRCA1-associated protein OS=Ophiophagus hannah GN=BRAP	OPHHA	2		
2666	2.72	2.72	63.79	16.67	8.046	tr V8NXD5 V8NXD5_OPHHA LDLR chaperone MESD (Fragment) OS=Ophiophagus hannah GN	OPHHA	1		
2667	2.71	2.71	71.82	13.39	3.002	tr V8NIE4 V8NIE4_OPHHA UDP-glucose 6-dehydrogenase OS=Ophiophagus hannah GN=UG	OPHHA	1		
2668	2.71	2.71	34.95	15.22	11.07	tr V8NSW9 V8NSW9_OPHHA Syntaxin-3 (Fragment) OS=Ophiophagus hannah GN=Stx3 PE=	OPHHA	3		
2669	2.71	2.71	40	19.17	8.75	tr V8NEP9 V8NEP9_OPHHA COP9 signalosome complex subunit 6 (Fragment) OS=Ophiop	OPHHA	1		
2670	2.7	2.7	53.16	20.25	20.25	tr V8ND61 V8ND61_OPHHA MACRO domain-containing protein 2 (Fragment) OS=Ophiophag	OPHHA	2		
2671	2.69	2.69	66.9	23.45	7.586	tr V8NX77 V8NX77_OPHHA Ras-related protein Rab-12 (Fragment) OS=Ophiophagus ha	OPHHA	1		
2672	2.69	2.69	48.94	22.34	9.574	tr V8NT30 V8NT30_OPHHA Receptor-binding cancer antigen expressed on SiSo cells	OPHHA	1		
2673	2.68	2.68	47.82	2.909	2.364	tr V8NIT4 V8NIT4_OPHHA Membrane-associated guanylate kinase, WW and PDZ domain	OPHHA	2		
2674	2.68	2.68	32.82	12.27	12.27	tr V8NWX1 V8NWX1_OPHHA Endothelial cell-selective adhesion molecule (Fragment) OPHHA		2		
2675	2.68	2.68	57.46	23.13	15.67	tr V8NQN3 V8NQN3_OPHHA Apolipoprotein O-like protein (Fragment) OS=Ophiophagus	OPHHA	1		
2676	2.68	2.68	46.67	14.76	14.76	tr V8PDJ3 V8PDJ3_OPHHA Ras-related protein Rab-24 (Fragment) OS=Ophiophagus ha	OPHHA	2		
2677	2.67	2.67	31.21	6.667	6.667	tr V8NY94 V8NY94_OPHHA F-box only protein 22 (Fragment) OS=Ophiophagus hannah	OPHHA	2		
2678	2.67	2.67	42.02	10.92	10.92	tr V8PC68 V8PC68_OPHHA Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitoc	OPHHA	2		
2679	2.66	2.71	48.86	5.314	3.037	tr V8P166 V8P166_OPHHA Tyrosine-protein kinase BAZ1B (Fragment) OS=Ophiophagus	OPHHA	2		
2680	2.66	2.66	57.85	3.723	3.723	tr V8NSX1 V8NSX1_OPHHA Zinc finger CCCH domain-containing protein 11A OS=Ophio	OPHHA	2		
2681	2.66	2.66	34.3	4.042	1.963	tr V8PE14 V8PE14_OPHHA Myb-binding protein 1A OS=Ophiophagus hannah GN=MYBBP1A	OPHHA	2		
2682	2.66	2.66	51.68	5.12	4	tr V8NZN8 V8NZN8_OPHHA Cleavage stimulation factor subunit 3 OS=Ophiophagus ha	OPHHA	2		
2683	2.66	2.66	26.04	11.83	11.83	tr V8NR59 V8NR59_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	2		
2684	2.65	2.65	34.07	16.3	9.63	tr V8PBC8 V8PBC8_OPHHA Fatty acid-binding protein, epidermal OS=Ophiophagus ha	OPHHA	1		
2685	2.65	2.65	78.46	60	60	tr V8P4L3 V8P4L3_OPHHA Homogentisate 1,2-dioxygenase (Fragment) OS=Ophiophagus	OPHHA	2		
2686	2.65	2.65	21.8	10.03	10.03	tr V8ND07 V8ND07_OPHHA Hydroxysteroid 11-beta-dehydrogenase l-like protein B O	OPHHA	3		
2687	2.64	2.64	44.8	4.461	4.461	tr V8N9E8 V8N9E8_OPHHA Histone-lysine N-methyltransferase, H3 lysine-79 specif	OPHHA	2		
2688	2.64	2.64	34.69	11.73	9.949	tr V8PFB7 V8PFB7_OPHHA Golgi reassembly-stacking protein 1 (Fragment) OS=Ophio	OPHHA	3		
2689	2.64	2.64	48.1	19.62	6.962	tr V8PEU6 V8PEU6_OPHHA Putative 7,8-dihydro-8-oxoguanine triphosphatase NUDT15	OPHHA	1		
2690	2.63	2.93	40.32	3.402	1.379	tr V8P9V8 V8P9V8_OPHHA Plexin-D1 (Fragment) OS=Ophiophagus hannah GN=PLXND1	PE	OPHHA	2	
2691	2.63	2.63	33.88	3.297	1.374	tr V8P2G6 V8P2G6_OPHHA Tetratricopeptide repeat protein 17 OS=Ophiophagus hann	OPHHA	1		
2692	2.63	2.63	37.68	4.674	1.841	tr V8P9X3 V8P9X3_OPHHA FYN-binding protein (Fragment) OS=Ophiophagus hannah GN	OPHHA	1		
2693	2.63	2.63	62.05	13.39	8.036	tr V8PCP7 V8PCP7_OPHHA 60S ribosomal protein L37a (Fragment) OS=Ophiophagus ha	OPHHA	1		
2694	2.63	2.63	67.19	18.75	18.75	tr V8P4Z2 V8P4Z2_OPHHA 40S ribosomal protein S26 (Fragment) OS=Ophiophagus han	OPHHA	2		
2695	2.63	2.63	14.55	7.121	7.121	tr V8NQJ5 V8NQJ5_OPHHA Ataxin-3 (Fragment) OS=Ophiophagus hannah GN=ATXN3	PE=4	OPHHA	2	
2696	2.62	2.7	62.77	20	8.615	tr V8N910 V8N910_OPHHA Alpha-2-macroglobulin (Fragment) OS=Ophiophagus hannah	OPHHA	2		
2697	2.62	2.65	52.83	4.357	1.307	tr V8PHP8 V8PHP8_OPHHA WD repeat-containing protein 3 (Fragment) OS=Ophiophagu	OPHHA	1		
2698	2.62	2.62	54.33	6.557	2.81	tr V8NK93 V8NK93_OPHHA Putative arginyl-tRNA synthetase, mitochondrial (Fragme	OPHHA	1		
2699	2.62	2.62	40.65	18.7	10.57	tr V8NCA0 V8NCA0_OPHHA 60S ribosomal protein L35 OS=Ophiophagus hannah GN=RPL3	OPHHA	3		
2700	2.61	2.62	63.74	6.977	1.903	tr V8NPU9 V8NPU9_OPHHA CAP-Gly domain-containing linker protein 1 (Fragment) O	OPHHA	1		
2701	2.61	2.62	60	8.364	4.727	tr V8P1Y9 V8P1Y9_OPHHA 39S ribosomal protein L19, mitochondrial OS=Ophiophagus	OPHHA	2		
2702	2.61	2.61	55.81	6.058	4.866	tr V8NHT3 V8NHT3_OPHHA Insulin receptor substrate 2-A (Fragment) OS=Ophiophagu	OPHHA	3		
2703	2.6	2.61	39.56	2.719	1.903	tr V8P5V8 V8P5V8_OPHHA Protein LAP2 (Fragment) OS=Ophiophagus hannah GN=ERBB2I	OPHHA	2		
2704	2.6	2.6	79.62	10.03	10.03	tr V8NVW0 V8NVW0_OPHHA Pre-mRNA-splicing factor ISY1-like protein (Fragment) O	OPHHA	2		
2705	2.6	2.6	58.95	5.234	5.234	tr V8NPF2 V8NPF2_OPHHA Replication factor C subunit 4 OS=Ophiophagus hannah GN	OPHHA	2		
2706	2.6	2.6	61.9	19.73	6.803	tr V8NRC7 V8NRC7_OPHHA Transmembrane protein OS=Ophiophagus hannah GN=L345_101	OPHHA	1		
2707	2.6	2.6	17.47	5.677	5.677	tr V8PAS2 V8PAS2_OPHHA Transcription factor Sp3 (Fragment) OS=Ophiophagus hann	OPHHA	3		
2708	2.6	2.6	50.47	19.81	5.66	tr V8N9K1 V8N9K1_OPHHA Phospholysine phosphohistidine inorganic pyrophosphate	OPHHA	1		
2709	2.6	2.6	54.42	11.95	11.95	tr V8POY2 V8POY2_OPHHA Proteasome assembly chaperone 1 OS=Ophiophagus hannah G	OPHHA	2		
2710	2.6	2.6	62.73	40.91	25.45	tr V8P3Q9 V8P3Q9_OPHHA Leucyl-cystinyl aminopeptidase OS=Ophiophagus hannah GN	OPHHA	2		
2711	2.59	2.59	23.34	2.087	1.661	tr V8P8U8 V8P8U8_OPHHA Neurogenic locus notch-like protein 3 (Fragment) OS=Oph	OPHHA	2		
2712	2.59	2.59	46.8	10.42	2.011	tr V8P356 V8P356_OPHHA Vacuolar fusion protein MON1-like A (Fragment) OS=Ophio	OPHHA	1		
2713	2.59	2.59	62.77	30.66	9.489	tr V8NXV9 V8NXV9_OPHHA ADP-ribosylation factor-like protein 6 OS=Ophiophagus h	OPHHA	1		
2714	2.59	2.59	18.29	5.556	5.556	tr V8P182 V8P182_OPHHA Transmembrane protein 62 (Fragment) OS=Ophiophagus hann	OPHHA	2		
2715	2.58	2.59	57.05	18.12	12.75	tr V8PAJ1 V8PAJ1_OPHHA Tubulin-specific chaperone A (Fragment) OS=Ophiophagus	OPHHA	1		
2716	2.58	2.58	54.3	6.143	6.143	tr V8PCE4 V8PCE4_OPHHA Mothers against decapentaplegic homolog (Fragment) OS=O	OPHHA	2		
2717	2.58	2.58	36	9.333	6	tr V8NH41 V8NH41_OPHHA Putative gamma-glutamyltransferase ywD (Fragment) OS=O	OPHHA	1		
2718	2.57	2.57	47.66	11.21	2.804	tr V8P1S3 V8P1S3_OPHHA Glutamine-dependent NAD(+) synthetase OS=Ophiophagus ha	OPHHA	1		
2719	2.57	2.57	39.26	11.85	11.85	tr V8PFI3 V8PFI3_OPHHA Interferon regulatory factor 2-binding protein 2 (Fragm	OPHHA	2		
2720	2.56	13.83	60.23	30.41	30.41	tr V8N7N4 V8N7N4_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPHHA	8		
2721	2.56	2.57	27.66	12.77	9.362	tr V8NCO1 V8NCO1_OPHHA Exocyst complex component 4 (Fragment) OS=Ophiophagus h	OPHHA	2		
2722	2.56	2.56	44.27	1.723	0.5942	tr V8PD99 V8PD99_OPHHA Dedicator of cytokinesis protein 9 OS=Ophiophagus hanna	OPHHA	1		
2723	2.56	2.56	50.87	9.884	6.686	tr V8PC49 V8PC49_OPHHA Protein FAM49A (Fragment) OS=Ophiophagus hannah GN=FAM4	OPHHA	2		
2724	2.56	2.56	27.11	3.815	2.41	tr V8NTH9 V8NTH9_OPHHA Monocarboxylate transporter 1 OS=Ophiophagus hannah GN=	OPHHA	2		
2725	2.56	2.56	44.55	15.17	10.9	tr V8PGP1 V8PGP1_OPHHA 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (F	OPHHA	2		
2726	2.55	6.76	40.75	11.2	6.532	tr V8PO28 V8PO28_OPHHA CTP synthase OS=Ophiophagus hannah GN=CTPS2	PE=3	SV=1	OPHHA	3
2727	2.55	3.77	54.33	4.329	3.226	tr V8NYM2 V8NYM2_OPHHA Formin-like protein 1 (Fragment) OS=Ophiophagus hannah	OPHHA	3		
2728	2.55	2.55	47.17	5.031	3.145	tr V8P886 V8P886_OPHHA Polypeptide N-acetylglucosaminyltransferase (Fragment	OPHHA	1		
2729	2.55	2.55	56.63	10.75	3.943	tr V8ND35 V8ND35_OPHHA Alpha-taxilin OS=Ophiophagus hannah GN=Txlna	PE=4	SV=1	OPHHA	1
2730	2.55	2.55	27.08	10.42	5.729	tr V8NIF9 V8NIF9_OPHHA Mature T-cell proliferation 1 neighbor protein (Fragmen	OPHHA	1		
2731	2.55	2.55	70.79	31.46	20.22	tr V8NVU4 V8NVU4_OPHHA G-protein-signaling modulator 1 (Fragment) OS=Ophiophag	OPHHA	1		
2732	2.54	4.63	52.56	11.59	8.086	tr V8NCN9 V8NCN9_OPHHA Cytoplasmic dynein 1 light intermediate chain 1 (Fragme	OPHHA	2		
2733	2.54	3.36	40.53	2.82	1.289	tr V8NWX0 V8NWX0_OPHHA Nesprin-2 (Fragment) OS=Ophiophagus hannah GN=SYNE2	PE=	OPHHA	2	
2734	2.54	2.56	41.84	12.24	2.245	tr V8NQG1 V8NQG1_OPHHA Putative prolyl-tRNA synthetase, mitochondrial (Fragmen	OPHHA	1		
2735	2.54	2.55	44.96	4.435	2.419	tr V8NDG0 V8NDG0_OPHHA Tensin-3 OS=Ophiophagus hannah GN=Tns3	PE=4	SV=1	OPHHA	1
2736	2.54	2.55	32.51	11.52	7.819	tr V8PEC3 V8PEC3_OPHHA Ectonucleoside triphosphate diphosphohydrolase 5 (Fragm	OPHHA	1		
2737	2.54	2.54	42.02	4.141	2.761	tr V8NPE8 V8NPE8_OPHHA NCK-interacting protein with SH3 domain protein (Fragme	OPHHA	1		
2738	2.54	2.54	46.84	14.35	5.485	tr V8NDI6 V8NDI6_OPHHA Leucine-rich repeat and calponin-like domain-containin	OPHHA	1		
2739	2.53	2.53	53.24	2.854	1.713	tr V8PHM5 V8PHM5_OPHHA DCN1-like protein (Fragment) OS=Ophiophagus hannah GN=a	OPHHA	2		
2740	2.53	2.53	56.33	9.177	5.38	tr V8P6V5 V8P6V5_OPHHA Heparan sulfate 2-O-sulfotransferase 1 (Fragment) OS=Op	OPHHA	1		
2741	2.52	2.9	21.73	2.817	1.408	tr V8NPV2 V8NPV2_OPHHA Phospholipid scramblase 1 (Fragment) OS=Ophiophagus han	OPHHA	1		
2742	2.52	2.53	33.99	4.89	2.445	tr V8PAA7 V8PAA7_OPHHA Interferon regulatory factor 3 (Fragment) OS=Ophiophagu	OPHHA	1		
2743	2.52	2.52	55.41	2.212	1.164	tr V8PBD0 V8PBD0_OPHHA Squamous cell carcinoma antigen recognized by T-cells 3	OPHHA	1		
2744	2.52	2.52	35.93	2.464	1.351	tr V8NU15 V8NU15_OPHHA Period circadian protein-like 2 (Fragment) OS=Ophiophag	OPHHA	2		
2745	2.52	2.52	28.61	3.399	1.841	tr V8NBB9 V8NBB9_OPHHA Olfactory receptor (Fragment) OS=Ophiophagus hannah GN=	OPHHA	2		
2746	2.52	2.52	37.79	12.21	8.721	tr V8NL85 V8NL85_OPHHA HD domain-containing protein 2 OS=Ophiophagus hannah GN	OPHHA	1		
2747	2.51	3.06	31.93	8.635	5.02	tr V8PEX3 V8PEX3_OPHHA Ribosomal protein S6 kinase beta-2 (Fragment) OS=Ophiop	OPHHA	2		
2748	2.51	2.51	38.35	7.965	3.54	tr V8NC24 V8NC24_OPHHA E3 ubiquitin-protein ligase UBR4 (Fragment) OS=Ophioph	OPHHA	1		
2749	2.51	2.51	51.64	7.377	4.372	tr V8NEQ0 V8NEQ0_OPHHA Inositol polyphosphate 5-phosphatase K OS=Ophiophagus h	OPHHA	1		
2750	2.51	2.51	32.29	11.11	7.128	tr V8PDH8 V8PDH8_OPHHA Non-syndromic hearing impairment protein 5-like protein	OPHHA	2		
2751	2.5	2.5	43.1	2.132	0.8167	tr V8NKF0 V8NKF0_OPHHA Microtubule-associated protein 1B (Fragment) OS=Ophioph	OPHHA	1		
2752	2.5	2.5	45.83	8.333	5.903	tr V8P3Q5 V8P3Q5_OPHHA 39S ribosomal protein L4, mitochondrial (Fragment) OS=O	OPHHA	1		
2753	2.5	2.5	53.62	12.56	7.729	tr V8P1I9 V8P1I9_OPHHA Dual specificity mitogen-activated protein kinase kinas	OPHHA	1		
2754	2.5	2.5	29.11	10.8	5.634	tr V8NEP1 V8NEP1_OPHHA Upstream stimulatory factor 2 (Fragment) OS=Ophiophagus	OPHHA	1		
2755	2.49	2.49	59.22	11.69	7.273	tr V8PFY8 V8PFY8_OPHHA Choline kinase alpha OS=Ophiophagus hannah GN=CHKA	PE=4	OPHHA	2	
2756	2.49	2.49	55.06	11.9	6.25	tr V8PCZ6 V8PCZ6_OPHHA Casein kinase I isoform alpha OS=Ophiophagus hannah GN=	OPHHA	1		
2757	2.49	2.49	70.15	14.03	5.373	tr V8NGG4 V8NGG4_OPHHA Plexin-A1 (Fragment) OS=Ophiophagus hannah GN=PLXNA1	PE	OPHHA	1	
2758	2.49	2.49	50.73	10.24	6.341	tr V8NJT9 V8NJT9_OPHHA Retinol dehydrogenase 11 (Fragment) OS=Ophiophagus hann	OPHHA	1		
2759	2.49	2.49	36.28	19.47	11.5	tr V8NCQ0 V8NCQ0_OPHHA Long-chain-fatty-acid-CoA ligase 5 (Fragment) OS=Ophio	OPHHA	1		

2760	2.49	2.49	22.22	22.22	11.9	tr V8PC24 V8PC24_OPHHA Protein C10 (Fragment) OS=Ophiophagus hannah GN=L345_02 OPHHA	1
2761	2.48	2.48	40.83	6.846	3.912	tr V8NX89 V8NX89_OPHHA Glycosaminoglycan xylosylkinase OS=Ophiophagus hannah G OPHHA	1
2762	2.48	2.48	54.96	30.53	15.27	tr V8NCY5 V8NCY5_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2763	2.47	2.52	26.15	5.827	1.626	tr V8PH29 V8PH29_OPHHA Semaphorin-4G (Fragment) OS=Ophiophagus hannah GN=SEMA4 OPHHA	1
2764	2.47	2.48	34.52	7.565	2.6	tr V8P7T2 V8P7T2_OPHHA WD repeat domain phosphoinositide-interacting protein 4 OPHHA	1
2765	2.47	2.47	27.09	3.206	1.138	tr V8PA96 V8PA96_OPHHA MHC class II regulatory factor RFX1 (Fragment) OS=Ophiophagus hannah OPHHA	1
2766	2.47	2.47	67.23	25.99	6.215	tr V8PIN2 V8PIN2_OPHHA Four and a half LIM domains protein 2 OS=Ophiophagus hannah OPHHA	1
2767	2.47	2.47	29.47	10.14	5.797	tr V8N1D2 V8N1D2_OPHHA Putative asparaginyl-tRNA synthetase, mitochondrial (Fr OPHHA	1
2768	2.47	2.47	48.68	27.63	27.63	tr V8N6C0 V8N6C0_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	2
2769	2.46	4.89	54.13	11.65	7.282	tr V8PBK4 V8PBK4_OPHHA SWI/SNF-related matrix-associated actin-dependent regul OPHHA	2
2770	2.46	2.47	44.61	7.353	3.922	tr V8P4Y3 V8P4Y3_OPHHA Histone acetyltransferase type B catalytic subunit (Fra OPHHA	1
2771	2.46	2.46	47.32	7.229	1.533	tr V8PHZ0 V8PHZ0_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2772	2.46	2.46	32.37	7.629	3.918	tr V8NTL7 V8NTL7_OPHHA Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS= OPHHA	2
2773	2.45	2.45	37.54	10.92	10.92	tr V8P155 V8P155_OPHHA Serine/threonine-protein kinase N2 (Fragment) OS=Ophiophagus hannah OPHHA	3
2774	2.45	2.45	52.33	26.74	15.12	tr V8N9K2 V8N9K2_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2775	2.44	9.52	44.94	12.43	9.947	tr V8N563 V8N563_OPHHA Receptor-type tyrosine-protein phosphatase S (Fragment) OPHHA	6
2776	2.44	2.5	47.8	4.545	2.893	tr V8NF12 V8NF12_OPHHA Kinesin-like protein (Fragment) OS=Ophiophagus hannah G OPHHA	2
2776	0.02	1.21	56.83	4.781	1.503	tr V8P1F2 V8P1F2_OPHHA Kinesin-like protein (Fragment) OS=Ophiophagus hannah G OPHHA	1
2777	2.44	2.44	67.17	10.1	7.071	tr V8NDR7 V8NDR7_OPHHA SEC14-like protein 2 (Fragment) OS=Ophiophagus hannah G OPHHA	2
2778	2.44	2.44	36.98	16.67	6.771	tr V8PA09 V8PA09_OPHHA Histone H1.0 (Fragment) OS=Ophiophagus hannah GN=H1f0 P OPHHA	1
2779	2.43	13.02	34.35	21.12	12.21	tr V8N8S7 V8N8S7_OPHHA Cytochrome protein OS=Ophiophagus hannah GN=cyp2k1 PE=3 OPHHA	7
2780	2.43	8.7	42.28	5.541	3.751	tr V8NRS5 V8NRS5_OPHHA von Willebrand factor A domain-containing protein 5A (F OPHHA	4
2781	2.43	2.91	37.83	11.98	3.232	tr V8NMB2 V8NMB2_OPHHA Serine/threonine-protein phosphatase 2B catalytic subun OPHHA	1
2782	2.43	2.43	51.34	3.476	1.896	tr V8PD79 V8PD79_OPHHA Neutral and basic amino acid transport protein rBAT (Fr OPHHA	1
2783	2.43	2.43	47.06	7.294	3.059	tr V8NY68 V8NY68_OPHHA Cytosolic Fe-S cluster assembly factor NARFL (Fragment) OPHHA	1
2784	2.43	2.43	35.21	4.475	2.529	tr V8PBW3 V8PBW3_OPHHA Periodic tryptophan protein l-like protein (Fragment) O OPHHA	1
2785	2.43	2.43	27.6	16.15	12.5	tr V8NDG7 V8NDG7_OPHHA Biogenesis of lysosome-related organelles complex 1 sub OPHHA	1
2786	2.42	2.42	53.73	5.422	1.807	tr V8NLR5 V8NLR5_OPHHA Serine/arginine repetitive matrix protein 1 OS=Ophiophagus hannah OPHHA	1
2787	2.42	2.42	36.14	4.028	1.185	tr V8N8I1 V8N8I1_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2788	2.42	2.42	38.64	11.74	4.924	tr V8NJ05 V8NJ05_OPHHA Translational activator of cytochrome c oxidase 1 (Fra OPHHA	1
2789	2.42	2.42	29.34	9.266	5.019	tr V8P183 V8P183_OPHHA Metaxin-2 OS=Ophiophagus hannah GN=MTX2 PE=4 SV=1 OPHHA	1
2790	2.42	2.42	50	19.01	19.01	tr V8PDG6 V8PDG6_OPHHA Dermatopectin (Fragment) OS=Ophiophagus hannah GN=DPT P OPHHA	2
2791	2.41	2.43	52.16	4.795	2.69	tr V8PIQ8 V8PIQ8_OPHHA Serine/threonine-protein kinase 10 (Fragment) OS=Ophiophagus hannah OPHHA	2
2792	2.41	2.41	52.96	9.259	6.667	tr V8N9F9 V8N9F9_OPHHA Protein canopy-like 3 OS=Ophiophagus hannah GN=CNYP3 PE OPHHA	2
2793	2.41	2.41	36.86	11.26	7.85	tr V8P5Z5 V8P5Z5_OPHHA Geranylgeranyl pyrophosphate synthase (Fragment) OS=Ophiophagus hannah OPHHA	2
2794	2.41	2.41	63.56	22.88	11.02	tr V8N5J3 V8N5J3_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2795	2.41	2.41	79.03	18.55	18.55	tr V8N687 V8N687_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	2
2796	2.4	2.48	37.51	2.376	0.7707	tr V8P1R6 V8P1R6_OPHHA NLR family member X1 OS=Ophiophagus hannah GN=NlrX1 PE= OPHHA	1
2797	2.4	2.46	35.45	4.108	1.761	tr V8NX25 V8NX25_OPHHA Reversion-inducing cysteine-rich protein with Kazal mot OPHHA	1
2798	2.4	2.4	35.4	4.416	0.9972	tr V8NV66 V8NV66_OPHHA Zinc finger FYVE domain-containing protein 16 (Fragment OPHHA	1
2799	2.4	2.4	33.69	7.082	3.004	tr V8NW18 V8NW18_OPHHA Nucleotide exchange factor SIL1 OS=Ophiophagus hannah G OPHHA	1
2800	2.4	2.4	57.78	33.33	33.33	tr V8PC12 V8PC12_OPHHA Small VCP/p97-interacting protein OS=Ophiophagus hannah OPHHA	1
2801	2.39	2.98	74.58	20.83	7.917	tr V8PFC7 V8PFC7_OPHHA Phosphatidylinositol transfer protein beta isoform OS=O OPHHA	2
2802	2.39	2.39	32.62	8.156	4.61	tr V8P197 V8P197_OPHHA Collectin-11 (Fragment) OS=Ophiophagus hannah GN=COL1C1 OPHHA	1
2803	2.39	2.39	67.92	16.98	11.95	tr V8NGS1 V8NGS1_OPHHA Sortilin-related receptor (Fragment) OS=Ophiophagus hannah OPHHA	1
2804	2.39	2.39	61.86	13.4	11.34	tr V8PEH2 V8PEH2_OPHHA Cytochrome c oxidase assembly protein COX16-like, mitoc OPHHA	1
2805	2.38	2.38	40.95	4.095	4.095	tr V8PJ28 V8PJ28_OPHHA Regulatory-associated protein of mTOR (Fragment) OS=Ophiophagus hannah OPHHA	2
2806	2.38	2.38	70.81	18.32	4.969	tr V8P503 V8P503_OPHHA WD repeat-containing protein 92 (Fragment) OS=Ophiophagus hannah OPHHA	1
2807	2.38	2.38	69.29	15.77	6.224	tr V8N8D7 V8N8D7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2808	2.38	2.38	79.25	33.02	13.21	tr V8PGA7 V8PGA7_OPHHA Argininosuccinate lyase (Fragment) OS=Ophiophagus hannah OPHHA	2
2809	2.38	2.38	64.24	17.22	12.58	tr V8N316 V8N316_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2810	2.38	2.38	9.504	9.504	5.372	tr V8PJM6 V8PJM6_OPHHA Bax inhibitor 1 (Fragment) OS=Ophiophagus hannah GN=TM6 OPHHA	1
2811	2.37	2.41	79.08	21.43	12.76	tr V8P304 V8P304_OPHHA Calcium/calmodulin-dependent protein kinase type II sub OPHHA	1
2812	2.37	2.38	32.26	4.274	2.137	tr V8NRP1 V8NRP1_OPHHA Plasma alpha-L-fucosidase OS=Ophiophagus hannah GN=FUCA OPHHA	1
2813	2.37	2.37	34.3	2.463	0.9675	tr V8PCM9 V8PCM9_OPHHA Stonin-2 (Fragment) OS=Ophiophagus hannah GN=Ston2 PE=4 OPHHA	1
2814	2.37	2.37	26.19	1.777	1.029	tr V8PDL3 V8PDL3_OPHHA Tyrosine-protein kinase receptor Tie-1 (Fragment) OS=Ophiophagus hannah OPHHA	1
2815	2.37	2.37	62.43	15.03	10.4	tr V8PHZ6 V8PHZ6_OPHHA Adrenodoxin OS=Ophiophagus hannah GN=FDX1 PE=4 SV=1 OPHHA	2
2816	2.37	2.37	38.86	11.4	5.699	tr V8NN33 V8NN33_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2817	2.36	4.7	50.81	28.11	21.62	tr V8NNT8 V8NNT8_OPHHA Chromobox protein-like 1 OS=Ophiophagus hannah GN=CBX1 OPHHA	3
2818	2.36	2.38	38.49	3.152	0.7331	tr V8P6N0 V8P6N0_OPHHA Baculoviral IAP repeat-containing protein 1 (Fragment) OPHHA	1
2819	2.36	2.37	55.81	43.02	32.56	tr V8NT56 V8NT56_OPHHA Splicing factor 3B subunit 5 (Fragment) OS=Ophiophagus hannah OPHHA	2
2820	2.36	2.36	37.33	21.33	8.667	tr V8P375 V8P375_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2821	2.36	2.36	28.86	11.41	5.369	tr V8NLQ4 V8NLQ4_OPHHA Bis(5'-nucleosyl)-tetrakisphosphate (Fragment) OS=Ophiophagus hannah OPHHA	1
2822	2.35	2.36	55.56	25.56	14.44	tr V8N0U1 V8N0U1_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2823	2.35	2.35	32.26	7.4	3.226	tr V8NBT8 V8NBT8_OPHHA PX domain-containing protein kinase-like protein OS=Ophiophagus hannah OPHHA	1
2824	2.35	2.35	58.2	22.95	11.48	tr V8PEQ7 V8PEQ7_OPHHA Pre-mRNA branch site protein p14 (Fragment) OS=Ophiophagus hannah OPHHA	1
2825	2.35	2.35	43.68	11.58	6.316	tr V8NZM0 V8NZM0_OPHHA Integrin alpha-5 (Fragment) OS=Ophiophagus hannah GN=it OPHHA	1
2826	2.35	2.35	68.09	55.32	25.53	tr V8N327 V8N327_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2827	2.35	2.35	71.43	46.75	36.36	tr V8N9V2 V8N9V2_OPHHA Cysteine-rich protein 1 OS=Ophiophagus hannah GN=CRIP1 OPHHA	1
2828	2.34	2.34	52.59	30.37	14.81	tr V8P5Z9 V8P5Z9_OPHHA Transmembrane protein OS=Ophiophagus hannah GN=TM6222 OPHHA	1
2829	2.33	2.34	61.65	12.09	4.425	tr V8PIG0 V8PIG0_OPHHA Exocyst complex component 6 (Fragment) OS=Ophiophagus hannah OPHHA	3
2830	2.33	2.35	22.95	4.825	2.339	tr V8NN63 V8NN63_OPHHA Protein angel-like 1 (Fragment) OS=Ophiophagus hannah G OPHHA	1
2831	2.33	2.33	70.35	14.07	8.04	tr V8NUW1 V8NUW1_OPHHA Sulfhydryl oxidase (Fragment) OS=Ophiophagus hannah GN= OPHHA	1
2832	2.33	2.33	84.68	19.82	19.82	tr V8NHU7 V8NHU7_OPHHA Mitochondrial import inner membrane translocase subunit OPHHA	2
2833	2.33	2.33	40.99	8.14	8.14	tr V8PDW5 V8PDW5_OPHHA FGFR1 oncogene partner (Fragment) OS=Ophiophagus hannah OPHHA	2
2834	2.32	2.33	49.71	5.882	3.824	tr V8NHX5 V8NHX5_OPHHA Apoptosis regulator BAX (Fragment) OS=Ophiophagus hannah OPHHA	1
2835	2.32	2.32	31.67	1.663	0.998	tr V8P4B6 V8P4B6_OPHHA HEAT repeat-containing protein 1 (Fragment) OS=Ophiophagus hannah OPHHA	1
2836	2.32	2.32	73.79	9.972	4.558	tr V8NTW7 V8NTW7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2837	2.32	2.32	39.79	4.844	2.768	tr V8P3W9 V8P3W9_OPHHA Fucose-1-phosphate guanylyltransferase (Fragment) OS=Ophiophagus hannah OPHHA	1
2838	2.32	2.32	26.81	5.094	3.217	tr V8PG55 V8PG55_OPHHA Polyadenylate-binding protein-interacting protein 1 (Fr OPHHA	1
2839	2.32	2.32	15.95	5.063	5.063	tr V8N6Y9 V8N6Y9_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	2
2840	2.31	2.32	19.35	8.602	5.018	tr V8NBV8 V8NBV8_OPHHA Exocyst complex component 6B OS=Ophiophagus hannah GN=E OPHHA	1
2841	2.3	2.3	71.1	5.255	2.299	tr V8PI57 V8PI57_OPHHA Putative sodium-coupled neutral amino acid transporter OPHHA	1
2842	2.3	2.3	24.96	0.7849	0.7849	tr V8NGE7 V8NGE7_OPHHA Fibrillin-2 (Fragment) OS=Ophiophagus hannah GN=FBN2 PE OPHHA	2
2843	2.3	2.3	41.54	3.532	1.208	tr V8NTM3 V8NTM3_OPHHA Dentin matrix protein 4 (Fragment) OS=Ophiophagus hannah OPHHA	1
2844	2.3	2.3	63.52	12.38	12.38	tr V8NDW7 V8NDW7_OPHHA Protein BUD31-like protein (Fragment) OS=Ophiophagus hannah OPHHA	3
2845	2.3	2.3	62.5	26.04	15.63	tr V8N5T7 V8N5T7_OPHHA Rab GDP dissociation inhibitor beta (Fragment) OS=Ophiophagus hannah OPHHA	1
2846	2.29	12.54	51.4	18.92	17.63	tr V8PG33 V8PG33_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hannah OPHHA	6
2847	2.29	2.31	46.68	6.463	2.693	tr V8NVN4 V8NVN4_OPHHA TBC1 domain family member 24 (Fragment) OS=Ophiophagus hannah OPHHA	1
2848	2.29	2.29	39.31	2.659	1.734	tr V8NWW8 V8NWW8_OPHHA Oxyesterol-binding protein (Fragment) OS=Ophiophagus hannah OPHHA	1
2849	2.29	2.29	40.68	3.215	2.251	tr V8PHL9 V8PHL9_OPHHA Growth arrest-specific protein 6 (Fragment) OS=Ophiophagus hannah OPHHA	1
2850	2.29	2.29	28.18	5.925	2.312	tr V8P5Y2 V8P5Y2_OPHHA Sodium/hydrogen exchanger (Fragment) OS=Ophiophagus hannah OPHHA	1
2851	2.29	2.29	60.91	17.77	9.645	tr V8PIL8 V8PIL8_OPHHA Vesicle transport protein SEC20 OS=Ophiophagus hannah G OPHHA	1
2852	2.29	2.29	36.34	11.34	2.835	tr V8NM69 V8NM69_OPHHA Forkhead box protein A2 (Fragment) OS=Ophiophagus hannah OPHHA	1
2853	2.29	2.29	96.43	36.9	36.9	tr V8NJY5 V8NJY5_OPHHA Phosphatidylinositol 3-kinase catalytic subunit type 3 OPHHA	2
2854	2.29	2.29	22.36	7.595	7.595	tr V8P850 V8P850_OPHHA Uroporphyrinogen-III synthase (Fragment) OS=Ophiophagus hannah OPHHA	2

2855	2.29	2.29	18.64	18.64	13.56	tr V8N6X3 V8N6X3_OPHHA Ectonucleotide pyrophosphatase/phosphodiesterase family OPHHA	1
2856	2.28	8.66	46.41	8.146	6.324	tr V8ND84 V8ND84_OPHHA Plasma membrane calcium-transporting ATPase 2 (Fragment) OPHHA	4
2856	0.04	8.33	35.76	8.565	6.829	tr V8NFL1 V8NFL1_OPHHA calcium-transporting ATPase OS=Ophiophagus hannah GN=AT OPHHA	4
2857	2.28	2.28	60.95	12.7	9.206	tr V8NRV6 V8NRV6_OPHHA MAP kinase-activated protein kinase 2 (Fragment) OS=Oph OPHHA	2
2858	2.28	2.28	62.14	12.62	6.796	tr V8NJD7 V8NJD7_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345.1 OPHHA	1
2859	2.28	2.28	90	13.53	7.647	tr V8NH14 V8NH14_OPHHA Protein rogdi-like protein (Fragment) OS=Ophiophagus ha OPHHA	1
2860	2.28	2.28	38.75	10.75	3.75	tr V8NDN1 V8NDN1_OPHHA Dystrophin (Fragment) OS=Ophiophagus hannah GN=DMD PE=4 OPHHA	1
2861	2.27	4.46	68.11	18.94	11.63	tr V8N59 V8N59_OPHHA Calcium/calmodulin-dependent protein kinase type 1D OS=OPHHA	3
2862	2.27	2.56	38.31	10.14	3.662	tr V8P366 V8P366_OPHHA [Protein ADP-ribosylarginine] hydrolase OS=Ophiophagus Protein /	1
2863	2.27	2.31	59.34	24.48	7.054	tr V8PC40 V8PC40_OPHHA DnaJ-like subfamily A member 3, mitochondrial OS=Ophiophagus OPHHA	1
2864	2.26	2.26	39.62	10.38	5.896	tr V8PA73 V8PA73_OPHHA F-box/LRR-repeat protein 20 (Fragment) OS=Ophiophagus h OPHHA	2
2865	2.26	2.26	62.58	29.45	8.589	tr V8NDK1 V8NDK1_OPHHA 39S ribosomal protein L49, mitochondrial (Fragment) OS=OPHHA	1
2866	2.26	2.26	37.41	12.22	5.185	tr V8N9W2 V8N9W2_OPHHA Myotubularin-related protein 1 (Fragment) OS=Ophiophagu OPHHA	1
2867	2.26	2.26	43.4	8.805	8.805	tr V8P185 V8P185_OPHHA Exostosin-like 2 OS=Ophiophagus hannah GN=Ext12 PE=4 SV OPHHA	2
2868	2.26	2.26	48.31	13.53	9.662	tr V8NC57 V8NC57_OPHHA Multiple inositol polyphosphate phosphatase 1 (Fragment) OPHHA	1
2869	2.25	3.32	33.8	5.429	2.102	tr V8NSX5 V8NSX5_OPHHA Pumilio-like 1 OS=Ophiophagus hannah GN=PUM1 PE=4 SV=1 OPHHA	2
2870	2.25	2.25	50.65	4.748	1.727	tr V8NZ00 V8NZ00_OPHHA Protein Hook-like 1 OS=Ophiophagus hannah GN=HOOK1 PE=4 OPHHA	1
2871	2.25	2.25	54.55	10.91	6.818	tr V8NCQ8 V8NCQ8_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
2872	2.25	2.25	32.56	4.157	2.54	tr V8NB83 V8NB83_OPHHA Phosphofurin acidic cluster sorting protein 1 (Fragment) OPHHA	1
2873	2.25	2.25	89.81	22.22	14.81	tr V8NR91 V8NR91_OPHHA Coatomer subunit alpha (Fragment) OS=Ophiophagus hannah OPHHA	1
2874	2.24	3	42.16	5.882	3.922	tr V8P380 V8P380_OPHHA Calpain-5 (Fragment) OS=Ophiophagus hannah GN=CAPN5 PE=OPHHA	2
2875	2.24	2.24	41.8	3.88	1.627	tr V8NZF8 V8NZF8_OPHHA Mitogen-activated protein kinase kinase kinase 5 OPHHA	1
2876	2.24	2.24	37.08	7.295	3.343	tr V8NXV2 V8NXV2_OPHHA Prostaglandin reductase 1 OS=Ophiophagus hannah GN=Ptgr OPHHA	1
2877	2.24	2.24	35.06	4.329	3.03	tr V8PDU5 V8PDU5_OPHHA Splicing factor 3B subunit 4 OS=Ophiophagus hannah GN=S OPHHA	1
2878	2.24	2.24	25.54	10.22	2.957	tr V8NPJ6 V8NPJ6_OPHHA Peroxisomal biogenesis factor 3 (Fragment) OS=Ophiophag OPHHA	1
2879	2.23	4.08	58.17	7.692	5.048	tr V8NZM9 V8NZM9_OPHHA Keratin, type II cytoskeletal 8 OS=Ophiophagus hannah G OPHHA	2
2880	2.23	2.23	49.92	2.276	1.22	tr V8P3D6 V8P3D6_OPHHA Pleckstrin-like-like domain family B member 2 (Fragmen OPHHA	1
2881	2.23	2.23	33.6	2.4	1.3	tr V8P2E2 V8P2E2_OPHHA Carboxypeptidase B (Fragment) OS=Ophiophagus hannah GN=OPHHA	1
2882	2.22	2.43	61.64	6.347	3.103	tr V8NUL4 V8NUL4_OPHHA Kinesin-like protein (Fragment) OS=Ophiophagus hannah G OPHHA	2
2883	2.22	2.27	29.23	5.275	3.516	tr V8NU97 V8NU97_OPHHA Ubiquitin-associated domain-containing protein 2 (Fragm OPHHA	1
2884	2.22	2.24	43.46	11.21	3.738	tr V8PAR6 V8PAR6_OPHHA Sulfotransferase (Fragment) OS=Ophiophagus hannah GN=Su OPHHA	1
2884	0.01	0.15	38.36	5.479	0	tr V8N5K4 V8N5K4_OPHHA Sulfotransferase (Fragment) OS=Ophiophagus hannah GN=Su OPHHA	0
2885	2.22	2.22	69.34	3.416	1.025	tr V8NDD7 V8NDD7_OPHHA Rootletin (Fragment) OS=Ophiophagus hannah GN=CROCC PE=OPHHA	2
2886	2.22	2.22	36.59	3.02	3.02	tr V8PEK2 V8PEK2_OPHHA Rho GTPase-activating protein 12 OS=Ophiophagus hannah OPHHA	2
2887	2.22	2.22	45.42	8.779	4.198	tr V8N5Q1 V8N5Q1_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
2888	2.22	2.22	43.9	14.15	8.293	tr V8NNW3 V8NNW3_OPHHA 39S ribosomal protein L9, mitochondrial (Fragment) OS=O OPHHA	1
2889	2.22	2.22	42.56	11.79	7.179	tr V8NMH8 V8NMH8_OPHHA Septin-5 (Fragment) OS=Ophiophagus hannah GN=Sept5 PE=4 OPHHA	1
2889	0	2	34.1	2.682	2.682	tr V8PH90 V8PH90_OPHHA Septin-4 (Fragment) OS=Ophiophagus hannah GN=Sept4 PE=3 OPHHA	1
2890	2.22	2.22	31.03	22.41	18.97	tr V8NZT8 V8NZT8_OPHHA Signal peptidase complex subunit 3 OS=Ophiophagus hanna OPHHA	2
2891	2.21	2.21	35.74	1.755	0.6849	tr V8NJW2 V8NJW2_OPHHA Death-inducer obliterator 1 (Fragment) OS=Ophiophagus h OPHHA	1
2892	2.21	2.21	43.95	5.185	2.716	tr V8P7I1 V8P7I1_OPHHA Plexin-A1 (Fragment) OS=Ophiophagus hannah GN=PLXNA1 PE OPHHA	1
2893	2.21	2.21	39.18	7.602	7.602	tr V8NU15 V8NU15_OPHHA Mitochondrial carnitine/acylcarnitine carrier protein (OPHHA	1
2894	2.2	3.01	61.89	9.221	3.484	tr V8NEB0 V8NEB0_OPHHA Merlin (Fragment) OS=Ophiophagus hannah GN=NF2 PE=4 SV= OPHHA	2
2895	2.2	2.31	38.82	3.522	1.149	tr V8P018 V8P018_OPHHA RRP12-like protein OS=Ophiophagus hannah GN=RRp12 PE=4 OPHHA	1
2896	2.2	2.2	40.55	1.651	0.6116	tr V8PCC0 V8PCC0_OPHHA Spermatogenesis-associated protein 13 (Fragment) OS=Oph OPHHA	1
2896	0.03	2.07	36.3	1.65	1.65	tr V8P0Q2 V8P0Q2_OPHHA Rho guanine nucleotide exchange factor 9 (Fragment) OS=OPHHA	1
2896	0	2.01	55.03	1.972	1.972	tr V8PBZ0 V8PBZ0_OPHHA Rho guanine nucleotide exchange factor 4 (Fragment) OS=OPHHA	1
2897	2.2	2.2	60.23	4.509	2.899	tr V8NRP7 V8NRP7_OPHHA Tudor domain-containing protein 3 (Fragment) OS=Ophioph OPHHA	1
2898	2.2	2.2	59.86	5.735	2.33	tr V8P4L4 V8P4L4_OPHHA Elongator complex protein 3 (Fragment) OS=Ophiophagus h OPHHA	1
2899	2.2	2.2	57.87	6.43	2.882	tr V8NRW0 V8NRW0_OPHHA BAG family molecular chaperone regulator 5 (Fragment) O OPHHA	1
2900	2.2	2.2	51.74	9.13	5.217	tr V8PBN7 V8PBN7_OPHHA Ectonucleotide pyrophosphatase/phosphodiesterase family OPHHA	1
2901	2.19	2.19	48.5	3.645	1.682	tr V8NXG3 V8NXG3_OPHHA S phase cyclin A-associated protein in the endoplasmic OPHHA	1
2902	2.19	2.19	18.53	1.796	1.04	tr V8N7U9 V8N7U9_OPHHA Gem-associated protein 4 (Fragment) OS=Ophiophagus hann OPHHA	1
2903	2.19	2.19	25.92	4.11	1.686	tr V8N8Z9 V8N8Z9_OPHHA Tenascin (Fragment) OS=Ophiophagus hannah GN=TNC PE=4 S OPHHA	1
2904	2.19	2.19	33.33	5.975	5.975	tr V8P5T2 V8P5T2_OPHHA Ras-related GTP-binding protein B OS=Ophiophagus hannah OPHHA	2
2905	2.18	2.18	42.73	5.954	2.102	tr V8P6E4 V8P6E4_OPHHA Pre-mRNA-processing factor 17 (Fragment) OS=Ophiophagus OPHHA	1
2906	2.18	2.18	54.5	2.725	2.725	tr V8N7R3 V8N7R3_OPHHA Phospholipase D3 (Fragment) OS=Ophiophagus hannah GN=P1 OPHHA	1
2907	2.18	2.18	29.88	5.102	2.915	tr V8NV00 V8NV00_OPHHA Choline transporter-like protein 5 (Fragment) OS=Ophiop OPHHA	3
2908	2.18	2.18	49.68	7.419	5.161	tr V8NPY2 V8NPY2_OPHHA 60S ribosomal protein L8 (Fragment) OS=Ophiophagus hann OPHHA	1
2909	2.18	2.18	46.1	5.29	3.526	tr V8NL15 V8NL15_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345.1 OPHHA	1
2910	2.18	2.18	77.94	29.41	16.18	tr V8NHT1 V8NHT1_OPHHA BoA-like protein 2 OS=Ophiophagus hannah GN=BoLA2 PE=4 OPHHA	1
2911	2.17	4.33	38.02	9.505	6.139	tr V8NQA1 V8NQA1_OPHHA NAD(P) transhydrogenase, mitochondrial (Fragment) OS=Op OPHHA	4
2912	2.17	2.17	38.3	3.254	2.003	tr V8NKF3 V8NKF3_OPHHA Gamma-tubulin complex component 2 (Fragment) OS=Ophioph OPHHA	1
2913	2.17	2.17	42.75	4.51	3.137	tr V8PH47 V8PH47_OPHHA Phenylalanyl-tRNA synthetase alpha chain OS=Ophiophagus OPHHA	1
2914	2.17	2.17	34.5	2.805	1.543	tr V8POA6 V8POA6_OPHHA Suppressor of tumorigenicity 14 protein-like protein (F OPHHA	1
2915	2.17	2.17	53.13	8.854	5.208	tr V8P4X7 V8P4X7_OPHHA Cytochrome b-c1 complex subunit Rieske, mitochondrial (OPHHA	1
2916	2.17	2.17	38.46	5.594	3.73	tr V8NZH4 V8NZH4_OPHHA Translation initiation factor eIF-2B subunit beta (Frag OPHHA	1
2917	2.17	2.17	14.74	4.851	3.172	tr V8NV11 V8NV11_OPHHA Solute carrier family 40 member 1 OS=Ophiophagus hannah OPHHA	1
2918	2.16	4.24	49.34	18.94	14.54	tr V8N4Z8 V8N4Z8_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	2
2919	2.16	2.2	33.56	9.885	3.678	tr V8NZS8 V8NZS8_OPHHA Nucleoporin Nup43 (Fragment) OS=Ophiophagus hannah GN=N OPHHA	1
2920	2.16	2.16	62.64	2.983	2.041	tr V8NV68 V8NV68_OPHHA Adenylate kinase isoenzyme 6 (Fragment) OS=Ophiophagus OPHHA	1
2921	2.16	2.16	45.74	3.369	3.369	tr V8NDK2 V8NDK2_OPHHA Focal adhesion kinase 1 (Fragment) OS=Ophiophagus hanna OPHHA	1
2922	2.16	2.16	46.54	4.615	4.615	tr V8NJN6 V8NJN6_OPHHA CCR4-NOT transcription complex subunit 2 OS=Ophiophagus OPHHA	2
2923	2.16	2.16	74.68	10.3	6.438	tr V8N5T2 V8N5T2_OPHHA Mitotic spindle assembly checkpoint protein MAD1 (Fragm OPHHA	1
2924	2.16	2.16	60.38	12.26	6.604	tr V8NMQ6 V8NMQ6_OPHHA Thymidylate kinase OS=Ophiophagus hannah GN=DTYMK PE=3 OPHHA	1
2925	2.16	2.16	47.46	9.746	5.932	tr V8NR48 V8NR48_OPHHA Exosome complex component RRP40 (Fragment) OS=Ophiophag OPHHA	1
2926	2.16	2.16	33.51	13.83	6.915	tr V8NQ70 V8NQ70_OPHHA PCTP-like protein (Fragment) OS=Ophiophagus hannah GN=S OPHHA	1
2927	2.16	2.16	54.03	35.48	12.9	tr V8P5A8 V8P5A8_OPHHA Regulator complex protein LAMTOR3 OS=Ophiophagus hannah OPHHA	1
2928	2.15	2.18	35.38	6.388	4.423	tr V8NUP1 V8NUP1_OPHHA TBC1 domain family member 22A OS=Ophiophagus hannah GN= OPHHA	1
2929	2.15	2.16	34.88	33.72	24.42	tr V8N7T3 V8N7T3_OPHHA NEDD8-conjugating enzyme Ubc12 OS=Ophiophagus hannah GN OPHHA	2
2930	2.15	2.15	30.25	5.158	1.29	tr V8POR2 V8POR2_OPHHA RNA-binding protein 27 (Fragment) OS=Ophiophagus hannah OPHHA	1
2931	2.15	2.15	40.49	3.766	2.072	tr V8PA62 V8PA62_OPHHA N6-adenosine-methyltransferase 70 kDa subunit (Fragment OPHHA	1
2932	2.15	2.15	34.59	3.903	2.153	tr V8NYD9 V8NYD9_OPHHA Cadherin-5 OS=Ophiophagus hannah GN=Cdh5 PE=4 SV=1 OPHHA	1
2933	2.14	2.14	66.67	8.889	4.167	tr V8NLB6 V8NLB6_OPHHA Matrix metalloproteinase-14 (Fragment) OS=Ophiophagus h OPHHA	1
2934	2.14	2.14	58.09	16.6	4.979	tr V8PFZ3 V8PFZ3_OPHHA Sulfatase-modifying factor 2 (Fragment) OS=Ophiophagus OPHHA	1
2935	2.14	2.14	65.65	10.88	5.102	tr V8NHN3 V8NHN3_OPHHA UBX domain-containing protein 6 OS=Ophiophagus hannah G OPHHA	1
2936	2.14	2.14	59.89	18.08	6.78	tr V8NSW4 V8NSW4_OPHHA A-kinase anchor protein 9 (Fragment) OS=Ophiophagus han OPHHA	1
2937	2.14	2.14	34.75	7.958	5.57	tr V8P514 V8P514_OPHHA Uncharacterized protein OS=Ophiophagus hannah GN=L345.0 OPHHA	1
2938	2.14	2.14	55.56	21.69	11.64	tr V8P268 V8P268_OPHHA X-ray repair cross-complementing protein 5 (Fragment) O OPHHA	2
2939	2.13	6.61	39.31	3.817	3.817	tr V8NBM3 V8NBM3_OPHHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPHHA	5
2940	2.13	2.16	41.72	5.317	3.067	tr V8P1W0 V8P1W0_OPHHA Conserved oligomeric Golgi complex subunit 8 OS=Ophioph OPHHA	1
2941	2.13	2.13	26.68	3.236	1.189	tr V8NHE3 V8NHE3_OPHHA Huntingtin (Fragment) OS=Ophiophagus hannah GN=HTT PE=4 OPHHA	2
2942	2.13	2.13	44.4	6.422	6.422	tr V8PEQ4 V8PEQ4_OPHHA Mitochondrial ribonuclease P protein 3 (Fragment) OS=Op OPHHA	2
2943	2.13	2.13	50	6.561	4.525	tr V8P4B3 V8P4B3_OPHHA Dipeptidase (Fragment) OS=Ophiophagus hannah GN=DPEP1 P OPHHA	1
2944	2.13	2.13	45.77	10.92	10.92	tr V8NPN7 V8NPN7_OPHHA Isopentenyl-diphosphate Delta-isomerase 1 (Fragment) OS OPHHA	2
2945	2.13	2.13	49.85	7.077	4	tr V8N3U5 V8N3U5_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1

2946	2.13	2.13	33.45	7.117	4.982	tr V8N3S6 V8N3S6_OPPIHA COUP transcription factor 2 (Fragment) OS=Ophiophagus h OPPIHA	1
2947	2.13	2.13	77.02	15.53	6.832	tr V8NVV0 V8NVV0_OPPIHA Peptidyl-prolyl cis-trans isomerase OS=Ophiophagus hann OPPIHA	1
2948	2.13	2.13	33.5	15	5.5	tr V8NJ9 V8NJ9_OPPIHA GliA maturation factor gamma (Fragment) OS=Ophiophagus OPPIHA	1
2949	2.12	2.21	67.57	16.89	11.49	tr V8P7Q4 V8P7Q4_OPPIHA Putative tRNA threonylcarbamoyladenine biosynthesis p OPPIHA	1
2950	2.12	2.13	27.82	8.815	6.061	tr V8NRB5 V8NRB5_OPPIHA Nucleolysin TIAR OS=Ophiophagus hannah GN=TIAR1 PE=4 SV OPPIHA	2
2951	2.12	2.12	35.48	3.337	1.446	tr V8NRR7 V8NRR7_OPPIHA 39S ribosomal protein L16, mitochondrial (Fragment) OS= OPPIHA	1
2952	2.12	2.12	42.23	8.495	3.641	tr V8PET3 V8PET3_OPPIHA Interferon-inducible GTPase 5 (Fragment) OS=Ophiophagus OPPIHA	2
2953	2.12	2.12	26.69	8.185	4.982	tr V8PC87 V8PC87_OPPIHA D-amino-acid oxidase OS=Ophiophagus hannah GN=DAO PE=4 OPPIHA	1
2954	2.12	2.12	21.47	11.14	3.533	tr V8NLJ2 V8NLJ2_OPPIHA Secl family domain-containing protein 2 (Fragment) OS=O OPPIHA	1
2955	2.11	2.12	39.44	2.394	1.197	tr V8NQT3 V8NQT3_OPPIHA Nucleoporin-like protein (Fragment) OS=Ophiophagus hann OPPIHA	1
2956	2.11	2.11	48.09	1.911	1.911	tr V8NCQ9 V8NCQ9_OPPIHA YLP motif-containing protein 1 (Fragment) OS=Ophiophagu OPPIHA	2
2957	2.11	2.11	55.31	4.81	3.206	tr V8NLHO V8NLHO_OPPIHA GTPase SLIP-GC (Fragment) OS=Ophiophagus hannah GN=L345 OPPIHA	1
2958	2.11	2.11	51.01	4.212	3.12	tr V8P329 V8P329_OPPIHA Influenza virus NS1A-binding protein-like protein OS=Op OPPIHA	1
2959	2.11	2.11	43.13	5.213	2.844	tr V8NJO1 V8NJO1_OPPIHA Putative ATP-dependent RNA helicase DDX47 (Fragment) OS OPPIHA	1
2960	2.11	2.11	27.37	3.888	3.888	tr V8NSV6 V8NSV6_OPPIHA Lipase maturation factor (Fragment) OS=Ophiophagus hann OPPIHA	2
2961	2.11	2.11	41.68	7.559	7.559	tr V8PDA8 V8PDA8_OPPIHA Glypican-4 (Fragment) OS=Ophiophagus hannah GN=Gpc4 PE= OPPIHA	2
2962	2.11	2.11	47.34	10.64	6.383	tr V8PBE9 V8PBE9_OPPIHA Gamma-glutamylaminocyclotransferase (Fragment) OS=Ophi OPPIHA	1
2963	2.11	2.11	63.85	16.92	11.54	tr V8NVK3 V8NVK3_OPPIHA Rho guanine nucleotide exchange factor 2 (Fragment) OS= OPPIHA	1
2964	2.1	2.69	52.58	15.46	6.701	tr V8PAD1 V8PAD1_OPPIHA Protein lin-7-like B (Fragment) OS=Ophiophagus hannah G OPPIHA	1
2965	2.1	2.16	33.64	12.62	5.607	tr V8PJB5 V8PJB5_OPPIHA Prolyl-tRNA synthetase associated domain-containing pro OPPIHA	1
2966	2.1	2.1	58.44	4.174	2.541	tr V8P614 V8P614_OPPIHA WD and tetratricopeptide repeats protein 1 (Fragment) O OPPIHA	1
2967	2.1	2.1	37.61	3.058	3.058	tr V8P9L7 V8P9L7_OPPIHA Mitogen-activated protein kinase kinase kinase 7 (Fragm OPPIHA	1
2968	2.1	2.1	35.48	5.53	3.456	tr V8NYJ5 V8NYJ5_OPPIHA Protein FAN OS=Ophiophagus hannah GN=Nmaf PE=4 SV=1 OPPIHA	1
2969	2.1	2.1	37.6	8.696	3.581	tr V8NPL8 V8NPL8_OPPIHA Protein-lysine 6-oxidase (Fragment) OS=Ophiophagus hann OPPIHA	1
2970	2.1	2.1	27.61	4.565	3.261	tr V8NS56 V8NS56_OPPIHA Nuclear pore complex protein Nup98-Nup96 (Fragment) OS= OPPIHA	1
2971	2.1	2.1	65.57	14.75	9.836	tr V8P6B8 V8P6B8_OPPIHA Chloride intracellular channel protein 5 (Fragment) OS= OPPIHA	1
2972	2.09	2.09	37.63	5.376	2.688	tr V8NUS3 V8NUS3_OPPIHA Mitochondrial enolase superfamily member 1 (Fragment) O OPPIHA	1
2973	2.09	2.09	46.08	6.536	6.536	tr V8N819 V8N819_OPPIHA Pentatricopeptide repeat-containing protein 3, mitochon OPPIHA	2
2974	2.09	2.09	70.4	11.21	8.072	tr V8PIA3 V8PIA3_OPPIHA Sodium/potassium-transporting ATPase subunit beta OS=Op OPPIHA	1
2975	2.09	2.09	40.07	4.255	4.255	tr V8NYT6 V8NYT6_OPPIHA Mitogen-activated protein kinase kinase kinase 7 (Fragm OPPIHA	1
2976	2.09	2.09	38.24	6.723	3.782	tr V8P3F4 V8P3F4_OPPIHA CMP-N-acetylneuraminate-beta-1,4-galactoside alpha-2,3- OPPIHA	1
2977	2.09	2.09	39.72	8.333	3.889	tr V8P786 V8P786_OPPIHA Protein kinase C iota type OS=Ophiophagus hannah GN=Prk OPPIHA	1
2978	2.09	2.09	67.24	20.69	17.24	tr V8N2L8 V8N2L8_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	1
2979	2.09	2.09	24.11	12.05	8.036	tr V8P5Z6 V8P5Z6_OPPIHA Collagen alpha-1(XVII) chain (Fragment) OS=Ophiophagus OPPIHA	1
2980	2.08	2.1	57.08	1.606	1.606	tr V8PH86 V8PH86_OPPIHA Differentially expressed in FDCP 6-like protein (Fragme OPPIHA	1
2981	2.08	2.08	41.2	3.052	2.035	tr V8NL77 V8NL77_OPPIHA 5'-3' exoribonuclease 2 (Fragment) OS=Ophiophagus hanna OPPIHA	1
2982	2.08	2.08	47.73	5.481	3.342	tr V8P7N6 V8P7N6_OPPIHA Serine/threonine-protein phosphatase 1 regulatory subun OPPIHA	1
2983	2.08	2.08	34.64	5.866	3.073	tr V8PGW2 V8PGW2_OPPIHA Protein HEXIM1 (Fragment) OS=Ophiophagus hannah GN=Hexi OPPIHA	1
2984	2.08	2.08	46.01	4.255	4.255	tr V8NKP8 V8NKP8_OPPIHA L-threonine 3-dehydrogenase, mitochondrial OS=Ophiophag OPPIHA	1
2985	2.08	2.08	44.65	13.21	13.21	tr V8N5G8 V8N5G8_OPPIHA Tyrosine-protein kinase transforming protein erbB (Frag OPPIHA	1
2986	2.07	2.85	47.94	2.578	2.026	tr V8P2A0 V8P2A0_OPPIHA Chromodomain-helicase-DNA-binding protein 3 (Fragment) OPPIHA	2
2987	2.07	2.09	50.26	3.665	2.356	tr V8P6X4 V8P6X4_OPPIHA Gamma-tubulin complex component 5 (Fragment) OS=Ophioph OPPIHA	1
2988	2.07	2.08	32.93	1.208	1.208	tr V8NDT1 V8NDT1_OPPIHA Cytochrome protein (Fragment) OS=Ophiophagus hannah GN= OPPIHA	1
2989	2.07	2.07	37.64	1.741	1.072	tr V8P230 V8P230_OPPIHA Laminin subunit gamma-3 (Fragment) OS=Ophiophagus hanna OPPIHA	1
2990	2.07	2.07	43.71	2.746	2.746	tr V8NKB5 V8NKB5_OPPIHA Protein LSM14-like A OS=Ophiophagus hannah GN=LSM14A PE OPPIHA	1
2991	2.07	2.07	45.32	2.709	2.709	tr V8NH72 V8NH72_OPPIHA 28S ribosomal protein S5, mitochondrial (Fragment) OS=O OPPIHA	1
2992	2.07	2.07	42.67	6.015	3.947	tr V8NB88 V8NB88_OPPIHA Eukaryotic elongation factor 2 kinase (Fragment) OS=Oph OPPIHA	1
2993	2.07	2.07	58.08	13.64	7.576	tr V8NNM1 V8NNM1_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	1
2994	2.07	2.07	43.11	9.439	5.357	tr V8P8S5 V8P8S5_OPPIHA Exosome complex component RRP45 (Fragment) OS=Ophiophag OPPIHA	1
2995	2.07	2.07	36.81	5.521	3.374	tr V8NY39 V8NY39_OPPIHA Acyl-CoA-binding domain-containing protein 5 (Fragment) OPPIHA	1
2996	2.07	2.07	62.83	9.735	9.735	tr V8P2W5 V8P2W5_OPPIHA CDGSH iron-sulfur domain-containing protein 3, mitochon OPPIHA	1
2997	2.07	2.07	27.41	2.998	2.998	tr V8P6V8 V8P6V8_OPPIHA Protein SAAL1 (Fragment) OS=Ophiophagus hannah GN=SAAL1 OPPIHA	1
2998	2.07	2.07	83.72	13.95	13.95	tr V8NR14 V8NR14_OPPIHA STIPI1-likey and U box-containing protein 1 (Fragment) O OPPIHA	1
2999	2.07	2.07	38.89	11.11	7.143	tr V8NQ90 V8NQ90_OPPIHA 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase OPPIHA	1
3000	2.07	2.07	29.62	7.331	3.519	tr V8NMM3 V8NMM3_OPPIHA Protein YIPF (Fragment) OS=Ophiophagus hannah GN=YIPF4 OPPIHA	1
3001	2.07	2.07	19.65	10.48	6.987	tr V8N439 V8N439_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	1
3002	2.07	2.07	58.33	25.93	17.59	tr V8NIE0 V8NIE0_OPPIHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPPIHA	1
3003	2.06	2.06	42.11	0.6309	0.6309	tr V8NTL8 V8NTL8_OPPIHA Endoribonuclease Dicer (Fragment) OS=Ophiophagus hannah OPPIHA	1
3004	2.06	2.06	26.84	1.176	1.176	tr V8P1N8 V8P1N8_OPPIHA RNA polymerase II-associated protein 1 (Fragment) OS=Op OPPIHA	1
3005	2.06	2.06	26.87	1.264	1.264	tr V8NIY0 V8NIY0_OPPIHA Non-structural maintenance of chromosomes element 4-lik OPPIHA	1
3006	2.06	2.06	27.62	1.48	1.48	tr V8P197 V8P197_OPPIHA Integrator complex subunit 7 (Fragment) OS=Ophiophagus OPPIHA	1
3007	2.06	2.06	47.27	5.191	3.552	tr V8NFW8 V8NFW8_OPPIHA Elongation factor Tu GTP-binding domain-containing prot OPPIHA	1
3008	2.06	2.06	37.28	5.357	2.902	tr V8PFE21 V8PFE21_OPPIHA Lactation elevated protein 1 (Fragment) OS=Ophiophagus OPPIHA	1
3009	2.06	2.06	28.75	3.834	3.834	tr V8NNE5 V8NNE5_OPPIHA Protein phosphatase 1K, mitochondrial (Fragment) OS=Oph OPPIHA	1
3010	2.06	2.06	38.31	3.571	3.571	tr V8P272 V8P272_OPPIHA rRNA adenine N(6)-methyltransferase (Fragment) OS=Ophi OPPIHA	1
3011	2.06	2.06	27.57	4.399	4.399	tr V8PG79 V8PG79_OPPIHA Kynurenine 3-monooxygenase OS=Ophiophagus hannah GN=KMO OPPIHA	1
3012	2.06	2.06	23.64	12.73	9.091	tr V8NRX5 V8NRX5_OPPIHA Ribonuclease P protein subunit p30 (Fragment) OS=Ophiop OPPIHA	1
3013	2.06	2.06	11.48	7.778	7.778	tr V8NRM7 V8NRM7_OPPIHA TLD domain-containing protein (Fragment) OS=Ophiophagus OPPIHA	2
3014	2.05	12.84	46.45	11.09	9.705	tr V8P9R3 V8P9R3_OPPIHA Transforming protein RhoA (Fragment) OS=Ophiophagus han OPPIHA	8
3015	2.05	2.34	33.07	3.467	2.667	tr V8NUH8 V8NUH8_OPPIHA Transducin beta-like protein 3 OS=Ophiophagus hannah GN OPPIHA	1
3016	2.05	2.22	51.75	21.93	14.04	tr V8PC70 V8PC70_OPPIHA Ras-related protein Rap-2C (Fragment) OS=Ophiophagus ha OPPIHA	1
3017	2.05	2.07	49.3	1.729	1.28	tr V8P8Z9 V8P8Z9_OPPIHA Traf2 and NCK-interacting protein kinase OS=Ophiophagus OPPIHA	1
3018	2.05	2.07	39.31	2.41	2.41	tr V8NZY6 V8NZY6_OPPIHA Constitutive coactivator of peroxisome proliferator-act OPPIHA	1
3019	2.05	2.06	40.76	1.895	0.5363	tr V8P200 V8P200_OPPIHA Zinc finger protein (Fragment) OS=Ophiophagus hannah GN OPPIHA	1
3020	2.05	2.05	32.96	0.9818	0.9818	tr V8P1D3 V8P1D3_OPPIHA Glutamine and serine-rich protein 1 (Fragment) OS=Ophi OPPIHA	1
3021	2.05	2.05	43.65	1.336	1.336	tr V8P6D6 V8P6D6_OPPIHA ZZ-type zinc finger-containing protein 3 (Fragment) OS= OPPIHA	1
3022	2.05	2.05	46.26	2.424	2.424	tr V8NET0 V8NET0_OPPIHA Something about silencing protein 10 (Fragment) OS=Ophi OPPIHA	1
3023	2.05	2.05	37.41	3.922	1.961	tr V8NAG7 V8NAG7_OPPIHA Paxillin (Fragment) OS=Ophiophagus hannah GN=Pxn PE=4 S OPPIHA	1
3024	2.05	2.05	37.11	2.787	2.787	tr V8PFW2 V8PFW2_OPPIHA Dual specificity tyrosine-phosphorylation-regulated kin OPPIHA	1
3025	2.05	2.05	41.53	4.237	4.237	tr V8PF06 V8PF06_OPPIHA Transmembrane protein (Fragment) OS=Ophiophagus hannah OPPIHA	1
3026	2.05	2.05	65.19	3.481	3.481	tr V8PH75 V8PH75_OPPIHA Ribonucleoside-diphosphate reductase subunit M2 B (Frag OPPIHA	1
3027	2.05	2.05	44.66	3.053	3.053	tr V8N9U5 V8N9U5_OPPIHA Coagulation factor IX (Fragment) OS=Ophiophagus hannah OPPIHA	2
3028	2.05	2.05	44.03	3.704	3.704	tr V8P2N7 V8P2N7_OPPIHA Serine/threonine-protein kinase RIO3 (Fragment) OS=Ophi OPPIHA	1
3029	2.05	2.05	59.11	5.112	5.112	tr V8NWX2 V8NWX2_OPPIHA Integrin alpha-L (Fragment) OS=Ophiophagus hannah GN=IT OPPIHA	1
3030	2.05	2.05	31.37	2.526	2.526	tr V8P654 V8P654_OPPIHA Methyltransferase-like protein 16 OS=Ophiophagus hannah OPPIHA	1
3031	2.05	2.05	48.56	5.048	5.048	tr V8PC64 V8PC64_OPPIHA Negative elongation factor A (Fragment) OS=Ophiophagus OPPIHA	1
3032	2.05	2.05	54.23	4.389	4.389	tr V8P3B2 V8P3B2_OPPIHA Complex I intermediate-associated protein 30, mitochond OPPIHA	1
3033	2.05	2.05	28.54	3.474	3.474	tr V8NX02 V8NX02_OPPIHA Leucine-rich repeat-containing protein 1 OS=Ophiophagus OPPIHA	1
3034	2.05	2.05	80.15	7.634	7.634	tr V8NJG5 V8NJG5_OPPIHA U6 snRNA-associated Sm-like protein LSM4 (Fragment) OS= OPPIHA	1
3035	2.05	2.05	70.34	7.586	7.586	tr V8N183 V8N183_OPPIHA Nuclear pore complex protein Nup98-Nup96 (Fragment) OS= OPPIHA	1
3036	2.05	2.05	49.17	17.13	17.13	tr V8PHK1 V8PHK1_OPPIHA Charged multivesicular body protein 6 OS=Ophiophagus ha OPPIHA	2
3037	2.05	2.05	29.75	4.545	4.545	tr V8P138 V8P138_OPPIHA Major prion protein (Fragment) OS=Ophiophagus hannah GN OPPIHA	1
3038	2.05	2.05	36.48	5.579	5.579	tr V8N6X8 V8N6X8_OPPIHA Glutathione S-transferase kappa 1 (Fragment) OS=Ophioph OPPIHA	1
3039	2.05	2.05	39.16	9.639	9.639	tr V8PEC1 V8PEC1_OPPIHA Methylmalonyl-CoA epimerase, mitochondrial (Fragment) O OPPIHA	1
3040	2.05	2.05	28.04	9.346	5.607	tr V8NIZ1 V8NIZ1_OPPIHA Microfibrillar-associated protein 5 (Fragment) OS=Ophi OPPIHA	1
3041	2.05	2.05	30	17.14	17.14	tr V8P178 V8P178_OPPIHA U6 snRNA-associated Sm-like protein LSM3 OS=Ophiophagus OPPIHA	1

3042	2.04	6.99	60.55	24.46	22.02	tr	V8PA25	V8PA25_OPPIHA	Calcium/calmodulin-dependent protein kinase type II sub	OPPIHA	4	
3043	2.04	2.22	51.05	1.905	1.333	tr	V8PCF9	V8PCF9_OPPIHA	CAP-Gly domain-containing linker protein 2 (Fragment)	OPPIHA	1	
3044	2.04	2.06	57.33	7.556	7.556	tr	V8NH4	V8NH4_OPPIHA	cAMP-dependent protein kinase type II-beta regulatory s	OPPIHA	1	
3045	2.04	2.05	45.48	2.934	2.934	tr	V8NTP7	V8NTP7_OPPIHA	Oxysterol-binding protein OS=Ophiophagus hannah GN=OSBP	OPPIHA	1	
3046	2.04	2.04	31.79	0.9444	0.9444	tr	V8PAR9	V8PAR9_OPPIHA	Nuclear receptor coactivator 2 (Fragment) OS=Ophiophagu	OPPIHA	1	
3047	2.04	2.04	43.37	1.827	1.058	tr	V8NZD3	V8NZD3_OPPIHA	Hexokinase (Fragment) OS=Ophiophagus hannah GN=HKDC1	PE	OPPIHA	1
3048	2.04	2.04	41.62	0.8902	0.8902	tr	V8P7Z0	V8P7Z0_OPPIHA	Neural cell adhesion molecule L1 (Fragment) OS=Ophiophag	OPPIHA	1	
3049	2.04	2.04	66.97	5.963	5.963	tr	V8PFS7	V8PFS7_OPPIHA	Growth arrest and DNA damage-inducible proteins-interac	OPPIHA	1	
3050	2.04	2.04	53.16	2.299	2.299	tr	V8NRG9	V8NRG9_OPPIHA	Acetyl-CoA carboxylase (Fragment) OS=Ophiophagus hannah	OPPIHA	1	
3051	2.04	2.04	46.13	2.933	2.933	tr	V8PBH3	V8PBH3_OPPIHA	Prolyl 4-hydroxylase subunit alpha-2 OS=Ophiophagus han	OPPIHA	1	
3052	2.04	2.04	47.33	4.545	4.545	tr	V8NMG3	V8NMG3_OPPIHA	Interleukin-1 receptor-associated kinase 4 OS=Ophiophag	OPPIHA	1	
3053	2.04	2.04	46.77	6.183	6.183	tr	V8NMO1	V8NMO1_OPPIHA	Wiskott-Aldrich syndrome protein (Fragment) OS=Ophiophag	OPPIHA	1	
3054	2.04	2.04	54.19	7.742	7.742	tr	V8NXY6	V8NXY6_OPPIHA	Centrin-2 (Fragment) OS=Ophiophagus hannah GN=Cetn2	PE=	OPPIHA	1
3055	2.04	2.04	67.86	12.95	12.95	tr	V8P5Y5	V8P5Y5_OPPIHA	DnaJ-like subfamily C member 8 (Fragment) OS=Ophiophagu	OPPIHA	1	
3056	2.04	2.04	55.83	5.521	5.521	tr	V8NNQ2	V8NNQ2_OPPIHA	LYR motif-containing protein 5 (Fragment) OS=Ophiophagu	LYR	OPPIHA	1
3057	2.04	2.04	39.9	5.419	5.419	tr	V8NMI2	V8NMI2_OPPIHA	Serine/threonine-protein kinase TBK1 (Fragment) OS=Ophi	OPPIHA	1	
3058	2.04	2.04	26.65	3.166	3.166	tr	V8PFM8	V8PFM8_OPPIHA	Syndecan (Fragment) OS=Ophiophagus hannah GN=Sdc1	PE=3	OPPIHA	1
3059	2.04	2.04	87.88	17.17	17.17	tr	V8N8N6	V8N8N6_OPPIHA	Inositol 1,4,5-trisphosphate receptor type 2 (Fragment)	OPPIHA	1	
3060	2.04	2.04	20.16	4.032	4.032	tr	V8PGA3	V8PGA3_OPPIHA	Monocarboxylate transporter 5 OS=Ophiophagus hannah GN=	OPPIHA	1	
3061	2.04	2.04	46.72	9.489	9.489	tr	V8N1I6	V8N1I6_OPPIHA	Endoplasmic reticulum-Golgi intermediate compartment pr	OPPIHA	1	
3062	2.04	2.04	27.53	5.668	5.668	tr	V8P376	V8P376_OPPIHA	RING finger protein (Fragment) OS=Ophiophagus hannah GN	OPPIHA	1	
3063	2.04	2.04	52.17	34.78	34.78	tr	V8N5N7	V8N5N7_OPPIHA	Barrier-to-autointegration factor (Fragment) OS=Ophioph	OPPIHA	1	
3064	2.03	6.04	54.5	16.4	16.4	tr	V8PH17	V8PH17_OPPIHA	Myosin light chain 4 OS=Ophiophagus hannah GN=MYL4	PE=4	OPPIHA	5
3065	2.03	2.3	43.18	1.651	1.129	tr	V8N4Q2	V8N4Q2_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3066	2.03	2.04	26.11	7.188	1.163	tr	V8NJK5	V8NJK5_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3067	2.03	2.04	32.26	9.677	6.912	tr	V8NGC6	V8NGC6_OPPIHA	Small glutamine-rich tetratricopeptide repeat-containin	OPPIHA	1	
3068	2.03	2.03	40.26	0.9167	0.9167	tr	V8PFZ4	V8PFZ4_OPPIHA	ATP-dependent RNA helicase DHX29 (Fragment) OS=Ophiophag	OPPIHA	1	
3069	2.03	2.03	40.67	3.197	1.776	tr	V8P839	V8P839_OPPIHA	Protein kinase C-binding protein 1 (Fragment) OS=Ophioph	OPPIHA	1	
3070	2.03	2.03	44.13	2.462	2.462	tr	V8P054	V8P054_OPPIHA	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitoc	OPPIHA	1	
3071	2.03	2.03	39.32	2.794	2.794	tr	V8NUC3	V8NUC3_OPPIHA	RAS guanyl-releasing protein 2-A OS=Ophiophagus hannah	OPPIHA	1	
3072	2.03	2.03	27.79	3.301	1.651	tr	V8P2B2	V8P2B2_OPPIHA	alpha-1,2-Mannosidase OS=Ophiophagus hannah GN=MAN1C1	P	OPPIHA	1
3073	2.03	2.03	39.49	1.989	1.989	tr	V8NLB9	V8NLB9_OPPIHA	Spermine synthase (Fragment) OS=Ophiophagus hannah GN=S	OPPIHA	1	
3074	2.03	2.03	65.28	6.038	6.038	tr	V8NKR9	V8NKR9_OPPIHA	Regulation of nuclear pre-mRNA domain-containing protei	OPPIHA	1	
3075	2.03	2.03	24.32	2.725	2.725	tr	V8N7U1	V8N7U1_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3076	2.03	2.03	43.43	4	4	tr	V8P7X3	V8P7X3_OPPIHA	Partitioning defective 6-like beta (Fragment) OS=Ophioph	OPPIHA	1	
3077	2.03	2.03	36.54	5.382	3.116	tr	V8P516	V8P516_OPPIHA	E3 ubiquitin-protein ligase (Fragment) OS=Ophiophagus h	OPPIHA	1	
3078	2.03	2.03	58.12	7.692	7.692	tr	V8NCU0	V8NCU0_OPPIHA	Cleavage and polyadenylation specificity factor subunit	OPPIHA	1	
3079	2.03	2.03	48.78	8.78	8.78	tr	V8P8T1	V8P8T1_OPPIHA	Polyglutamine-binding protein 1 OS=Ophiophagus hannah G	OPPIHA	1	
3080	2.03	2.03	30.09	5.45	4.028	tr	V8NX87	V8NX87_OPPIHA	F-box/WD repeat-containing protein 2 (Fragment) OS=Ophi	OPPIHA	1	
3081	2.03	2.03	26.28	3.413	3.413	tr	V8NP64	V8NP64_OPPIHA	Putative methyltransferase C20orf7, mitochondrial OS=Op	OPPIHA	1	
3082	2.03	2.03	43.35	5.78	5.78	tr	V8NLZ3	V8NLZ3_OPPIHA	Golgi-specific brefeldin A-resistance guanine nucleotid	OPPIHA	1	
3083	2.03	2.03	24.57	4.046	4.046	tr	V8NG00	V8NG00_OPPIHA	Tetratricopeptide repeat protein 27 (Fragment) OS=Ophi	OPPIHA	1	
3084	2.03	2.03	48.13	7.487	7.487	tr	V8P1R8	V8P1R8_OPPIHA	COB domain-containing protein 2 (Fragment) OS=Ophiophag	OPPIHA	1	
3085	2.03	2.03	13.8	3.906	3.906	tr	V8PHN2	V8PHN2_OPPIHA	Zinc transporter 7 OS=Ophiophagus hannah GN=SLC30A7	PE=	OPPIHA	1
3086	2.03	2.03	43.57	5	5	tr	V8P453	V8P453_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3087	2.03	2.03	43.21	16.05	16.05	tr	V8NT13	V8NT13_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3088	2.02	9.53	59.3	13.75	13.75	tr	V8N5T9	V8N5T9_OPPIHA	Cytochrome protein OS=Ophiophagus hannah GN=CYP2C41	PE=	OPPIHA	6
3089	2.02	8.3	52.86	31.43	25.71	tr	V8NH17	V8NH17_OPPIHA	ADP/ATP translocase 2 (Fragment) OS=Ophiophagus hanna	OPPIHA	4	
3090	2.02	7.51	51.32	6.444	5.524	tr	V8P0D3	V8P0D3_OPPIHA	Protein argonaute-4 (Fragment) OS=Ophiophagus hannah GN	OPPIHA	4	
3091	2.02	2.05	46.55	6.897	6.897	tr	V8N3M8	V8N3M8_OPPIHA	Elongation factor 2 (Fragment) OS=Ophiophagus hannah GN	OPPIHA	1	
3092	2.02	2.03	51.03	0.9164	0.9164	tr	V8NFX9	V8NFX9_OPPIHA	E3 ubiquitin-protein ligase RBBP6 (Fragment) OS=Ophioph	OPPIHA	1	
3093	2.02	2.03	56.38	2.029	2.029	tr	V8NL68	V8NL68_OPPIHA	Tripartite motif-containing protein 15 (Fragment) OS=Op	OPPIHA	1	
3094	2.02	2.02	52.71	1.961	1.961	tr	V8NND5	V8NND5_OPPIHA	Ankyrin repeat and LEM domain-containing protein 2 OS=O	OPPIHA	1	
3095	2.02	2.02	40.72	1.485	1.485	tr	V8NHX7	V8NHX7_OPPIHA	Ecto-NOX disulfide-thiol exchanger 2 (Fragment) OS=Ophi	OPPIHA	2	
3096	2.02	2.02	50.59	2.207	2.207	tr	V8PFN2	V8PFN2_OPPIHA	Glucocorticoid-induced transcript 1 protein (Fragment)	OPPIHA	1	
3097	2.02	2.02	49.04	2.443	2.443	tr	V8NQJ9	V8NQJ9_OPPIHA	Insulin-like growth factor 2 mRNA-binding protein 3 (Fr	OPPIHA	1	
3098	2.02	2.02	49.04	2.299	2.299	tr	V8PCZ8	V8PCZ8_OPPIHA	Adenylosuccinate synthetase (Fragment) OS=Ophiophagus h	OPPIHA	1	
3099	2.02	2.02	73.36	6.542	6.542	tr	V8NRJ2	V8NRJ2_OPPIHA	FGFR1 oncogene partner 2-like protein OS=Ophiophagus ha	OPPIHA	1	
3100	2.02	2.02	57.34	5.245	5.245	tr	V8P509	V8P509_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3101	2.02	2.02	43.26	3.09	3.09	tr	V8PBG1	V8PBG1_OPPIHA	Beta-soluble NSF attachment protein (Fragment) OS=Ophi	OPPIHA	2	
3102	2.02	2.02	38.11	8.108	3.514	tr	V8N892	V8N892_OPPIHA	Abhydrolase domain-containing protein 16A (Fragment)	OS	OPPIHA	1
3103	2.02	2.02	37.5	2.926	2.926	tr	V8PGC8	V8PGC8_OPPIHA	Lysosome-associated membrane glycoprotein 1 OS=Ophiophag	OPPIHA	1	
3104	2.02	2.02	66.83	6.931	6.931	tr	V8NGX5	V8NGX5_OPPIHA	Fumarylacetoacetate hydrolase domain-containing protein	OPPIHA	1	
3105	2.02	2.02	62.12	7.071	7.071	tr	V8NIH9	V8NIH9_OPPIHA	Tumor necrosis factor alpha-induced protein 8 (Fragment	OPPIHA	1	
3106	2.02	2.02	29.52	3.492	3.492	tr	V8NIF4	V8NIF4_OPPIHA	Acidic leucine-rich nuclear phosphoprotein 32 family me	OPPIHA	1	
3107	2.02	2.02	27.95	4.969	4.969	tr	V8PED2	V8PED2_OPPIHA	Mitochondrial translocator assembly and maintenance pro	OPPIHA	1	
3108	2.02	2.02	33.64	4.673	4.673	tr	V8PHF7	V8PHF7_OPPIHA	Transcription factor Dp-1 (Fragment) OS=Ophiophagus han	OPPIHA	1	
3109	2.02	2.02	33.45	6.05	6.05	tr	V8PED9	V8PED9_OPPIHA	Cell cycle checkpoint protein RAD1 (Fragment) OS=Ophioph	OPPIHA	1	
3110	2.02	2.02	41.76	2.784	2.784	tr	V8P9T0	V8P9T0_OPPIHA	Lysophospholipid acyltransferase 7 (Fragment) OS=Ophioph	OPPIHA	1	
3111	2.02	2.02	49.28	6.699	6.699	tr	V8N411	V8N411_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	2	
3112	2.02	2.02	49.11	16.07	16.07	tr	V8PEE3	V8PEE3_OPPIHA	Protein Churchill OS=Ophiophagus hannah GN=churc1	PE=4	OPPIHA	1
3113	2.02	2.02	29.41	9.412	9.412	tr	V8PANO	V8PANO_OPPIHA	Uridine diphosphate glucose pyrophosphatase (Fragment)	OPPIHA	1	
3114	2.02	2.02	72.34	18.09	18.09	tr	V8NIY2	V8NIY2_OPPIHA	Hepatocyte growth factor activator (Fragment) OS=Ophioph	OPPIHA	1	
3115	2.02	2.02	16.9	4.225	4.225	tr	V8NDF8	V8NDF8_OPPIHA	Protein YIF1B (Fragment) OS=Ophiophagus hannah GN=yif1b	OPPIHA	1	
3116	2.02	2.02	78.41	18.18	18.18	tr	V8NCE2	V8NCE2_OPPIHA	28 kDa heat-and acid-stable phosphoprotein (Fragment)	OPPIHA	1	
3117	2.02	2.02	47.5	20	20	tr	V8NBV5	V8NBV5_OPPIHA	ATP synthase subunit f, mitochondrial (Fragment) OS=Oph	OPPIHA	1	
3118	2.02	2.02	72.73	29.55	29.55	tr	V8N485	V8N485_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3119	2.01	10.07	48.69	14.8	14.8	tr	V8PHU8	V8PHU8_OPPIHA	Cyclin-dependent kinase 2 (Fragment) OS=Ophiophagus han	OPPIHA	5	
3120	2.01	4.01	46.76	8.633	8.633	tr	V8NLE2	V8NLE2_OPPIHA	Intersectin-2 (Fragment) OS=Ophiophagus hannah GN=ITSN2	OPPIHA	2	
3121	2.01	3.17	36.82	3.738	3.738	tr	V8NBD7	V8NBD7_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	2	
3122	2.01	2.04	35.86	2.664	2.664	tr	V8P8F4	V8P8F4_OPPIHA	Methyltransferase-like protein 14 (Fragment) OS=Ophioph	OPPIHA	1	
3123	2.01	2.02	30.92	6.763	6.763	tr	V8NCW9	V8NCW9_OPPIHA	Uncharacterized protein (Fragment) OS=Ophiophagus hanna	OPPIHA	1	
3124	2.01	2.01	36.45	0.9036								

3137	2.01	2.01	50	3.441	3.441	tr V8NX78 V8NX78_OPHHA 60 kDa lysophospholipase (Fragment) OS=Ophiophagus hann OPHHA	1
3138	2.01	2.01	36.76	3.784	3.784	tr V8NYS6 V8NYS6_OPHHA 3 beta-hydroxysteroid dehydrogenase type 7 (Fragment) O OPHHA	1
3139	2.01	2.01	58.3	6.273	6.273	tr V8NWJ7 V8NWJ7_OPHHA DCN1-like protein (Fragment) OS=Ophiophagus hannah GN=D OPHHA	1
3140	2.01	2.01	52.83	3.774	3.774	tr V8NSR8 V8NSR8_OPHHA Methyl-CpG-binding domain protein 2 (Fragment) OS=Ophiophagus hann OPHHA	1
3141	2.01	2.01	42.35	7.492	7.492	tr V8N947 V8N947_OPHHA Alkaline phosphatase (Fragment) OS=Ophiophagus hannah G OPHHA	1
3142	2.01	2.01	38.94	2.885	2.885	tr V8PB51 V8PB51_OPHHA Protein cereblon (Fragment) OS=Ophiophagus hannah GN=CR OPHHA	1
3143	2.01	2.01	57.14	6.897	6.897	tr V8NY65 V8NY65_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3144	2.01	2.01	40.72	4.072	4.072	tr V8NH44 V8NH44_OPHHA Suppressor of cytokine signaling 7 (Fragment) OS=Ophiophagus hann OPHHA	1
3145	2.01	2.01	48.81	3.754	3.754	tr V8PCE5 V8PCE5_OPHHA SAGA-associated factor 29-like protein OS=Ophiophagus h OPHHA	1
3146	2.01	2.01	51.92	4.487	4.487	tr V8P2S7 V8P2S7_OPHHA Nucleoside diphosphate kinase 7 (Fragment) OS=Ophiophagus hann OPHHA	1
3147	2.01	2.01	56.02	6.019	6.019	tr V8NDW3 V8NDW3_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3148	2.01	2.01	46.15	4.808	4.808	tr V8N709 V8N709_OPHHA O-phosphoserine-tRNA(Sec) selenium transferase (Fragment) OPHHA	1
3149	2.01	2.01	43.57	6.224	6.224	tr V8N6N0 V8N6N0_OPHHA Pantothenate kinase 2, mitochondrial (Fragment) OS=Ophiophagus hann OPHHA	1
3150	2.01	2.01	32.77	5.068	5.068	tr V8NAJ1 V8NAJ1_OPHHA RNA-binding protein with serine-rich domain 1 OS=Ophiophagus hann OPHHA	1
3151	2.01	2.01	78.23	9.524	9.524	tr V8N3K8 V8N3K8_OPHHA Poly [ADP-ribose] polymerase OS=Ophiophagus hannah GN=P ADP-ribo:	1
3152	2.01	2.01	35.79	4.682	4.682	tr V8PC93 V8PC93_OPHHA Transmembrane protein (Fragment) OS=Ophiophagus hannah OPHHA	1
3153	2.01	2.01	66.16	6.566	6.566	tr V8NEM8 V8NEM8_OPHHA Partitioning defective 3-like B (Fragment) OS=Ophiophagus hann OPHHA	1
3154	2.01	2.01	42.59	4.074	4.074	tr V8N906 V8N906_OPHHA Solute carrier family 2, facilitated glucose transport OPHHA	1
3155	2.01	2.01	61.38	8.466	8.466	tr V8P9E7 V8P9E7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3156	2.01	2.01	44.64	7.296	7.296	tr V8PHM9 V8PHM9_OPHHA Ashwin OS=Ophiophagus hannah GN=L345_00293 PE=4 SV=1 OPHHA	1
3157	2.01	2.01	15.31	2.153	2.153	tr V8P8X8 V8P8X8_OPHHA GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransf OPHHA	1
3158	2.01	2.01	26.65	3.872	3.872	tr V8P006 V8P006_OPHHA Alpha-N-acetylgalactosaminidase OS=Ophiophagus hannah G OPHHA	1
3159	2.01	2.01	11.96	1.669	1.669	tr V8NU11 V8NU11_OPHHA Glutamine-rich protein 1 (Fragment) OS=Ophiophagus hann OPHHA	1
3160	2.01	2.01	56.71	10.98	10.98	tr V8NLM8 V8NLM8_OPHHA SH3 domain-binding glutamic acid-rich-like protein (Fra OPHHA	3
3161	2.01	2.01	28.33	5	5	tr V8P9J3 V8P9J3_OPHHA Eukaryotic translation elongation factor 1 epsilon-1 (F OPHHA	1
3162	2.01	2.01	39.04	8.219	8.219	tr V8P5J8 V8P5J8_OPHHA Mitochondrial fission 1 protein OS=Ophiophagus hannah G OPHHA	1
3163	2.01	2.01	22.51	3.081	3.081	tr V8NXX5 V8NXX5_OPHHA Tubulointerstitial nephritis antigen (Fragment) OS=Ophiophagus hann OPHHA	1
3164	2.01	2.01	63.45	13.1	13.1	tr V8NRC4 V8NRC4_OPHHA Pallidin (Fragment) OS=Ophiophagus hannah GN=PLDN PE=4 SV=1 OPHHA	1
3165	2.01	2.01	32.31	2.857	2.857	tr V8NPM5 V8NPM5_OPHHA Signal peptide peptidase-like 2A (Fragment) OS=Ophiophagus hann OPHHA	1
3166	2.01	2.01	46.59	6.25	6.25	tr V8NM16 V8NM16_OPHHA Ubiquitin-conjugating enzyme E2 N OS=Ophiophagus hannah OPHHA	1
3167	2.01	2.01	35.78	7.328	7.328	tr V8NG30 V8NG30_OPHHA Ribosylidihydronicotinamide dehydrogenase [quinone] (Fra OPHHA	1
3168	2.01	2.01	54.61	7.895	7.895	tr V8NA63 V8NA63_OPHHA Glycerophosphodiester phosphodiesterase domain-containi OPHHA	1
3169	2.01	2.01	45.05	10.99	10.99	tr V8P245 V8P245_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3170	2.01	2.01	36	5.333	5.333	tr V8NY17 V8NY17_OPHHA Transmembrane protein OS=Ophiophagus hannah GN=tmem147 OPHHA	1
3171	2.01	2.01	37.04	6.349	6.349	tr V8N777 V8N777_OPHHA Vacuolar protein sorting-associated protein 52-like pro OPHHA	1
3172	2.01	2.01	46.15	7.692	7.692	tr V8NW78 V8NW78_OPHHA Sulfatase-modifying factor 1 (Fragment) OS=Ophiophagus hann OPHHA	1
3173	2.01	2.01	15.66	2.41	2.41	tr V8NKP5 V8NKP5_OPHHA Membrane-bound transcription factor site-2 protease (Fr OPHHA	1
3174	2.01	2.01	36.84	7.895	7.895	tr V8NH42 V8NH42_OPHHA Sortilin-related receptor OS=Ophiophagus hannah GN=SORL OPHHA	1
3175	2.01	2.01	60.15	11.28	11.28	tr V8NG64 V8NG64_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3176	2.01	2.01	42	15	15	tr V8N8N9 V8N8N9_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3177	2.01	2.01	96.97	21.21	21.21	tr V8N3Q5 V8N3Q5_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3177	0	2	64.47	18.42	18.42	tr V8N501 V8N501_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3178	2.01	2.01	28.81	6.215	6.215	tr V8NIT2 V8NIT2_OPHHA CCAAT/enhancer-binding protein beta (Fragment) OS=Ophiophagus hann OPHHA	1
3179	2.01	2.01	22.8	5.699	5.699	tr V8NC12 V8NC12_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3180	2.01	2.01	26.15	6.538	6.538	tr V8NAT7 V8NAT7_OPHHA Target of rapamycin complex 2 subunit MAPKAP1 (Fragment OPHHA	1
3181	2.01	2.01	30	8.571	8.571	tr V8NR88 V8NR88_OPHHA Vacuolar ATPase assembly integral membrane protein VMA2 OPHHA	1
3182	2.01	2.01	31.96	14.43	14.43	tr V8N2V4 V8N2V4_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3183	2.01	2.01	21.5	12.15	12.15	tr V8PA46 V8PA46_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3184	2.01	2.01	16.89	8.108	8.108	tr V8NM09 V8NM09_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3185	2.01	2.01	27.95	11.8	11.8	tr V8NJT7 V8NJT7_OPHHA Uncharacterized protein (Fragment) OS=Ophiophagus hanna OPHHA	1
3186	2.01	2.01	26.23	22.95	22.95	tr V8NQ13 V8NQ13_OPHHA Short-chain specific acyl-CoA dehydrogenase, mitochondr OPHHA	1