

Sequences producing significant alignments:		Score (Bits)	E Value
refINM_001541.21	Homo sapiens heat shock 27kDa protein 2 (HSPB2)	700	0.0
refINT_033899.71Hs11_34054	Homo sapiens chromosome 11 genomic co	577	7e-162
refINW_925173.1HsCraAADB02_444	Homo sapiens chromosome 11 ge...	577	7e-162
refINT_011525.71Hs22_11682	Homo sapiens chromosome 22 genomic co	42.1	0.98
refINT_022517.171Hs3_22673	Homo sapiens chromosome 3 genomic con	42.1	0.98
refINW_927650.11HsCraAADB02_667	Homo sapiens chromosome 22 ge...	42.1	0.98
refINW_921651.11HsCraAADB02_127	Homo sapiens chromosome 3 gen...	42.1	0.98
refINM_207454.11	Homo sapiens FLJ44815 protein (FLJ44815), mRNA	40.1	3.9
refINT_011903.121HsY_12060	Homo sapiens chromosome Y genomic con	40.1	3.9
refINT_011109.151Hs19_11266	Homo sapiens chromosome 19 genomic c	40.1	3.9
refINT_010799.141Hs17_10956	Homo sapiens chromosome 17 genomic c	40.1	3.9
refINT_010498.151Hs16_10655	Homo sapiens chromosome 16 genomic c	40.1	3.9
refINT_008583.161Hs10_8740	Homo sapiens chromosome 10 genomic co	40.1	3.9
refINT_008413.171Hs9_8570	Homo sapiens chromosome 9 genomic cont	40.1	3.9

Alignment Summary and Scores

Score = 577 bits (291), Expect = 7e-162 Identities = 420/463 (90%), Gaps = 0/463 (0%) Strand=Plus/Plus			
Query	116	AGGCCCTCTGCCAGAAGAGATCCTGACCCCCACCTCTATCACGGCTACTATGTTCGGCC	175
Sbjct	15346579	AGGCCCTCTGCCAGAAGAGATCCTGACCCCCACACTCTACCATGGCTACTATGTCCGGCC	15346638
Query	176	TCGGGGCCGCCAGAGCTGGCGAGGGGCCAGGGCAGGGGCTCAGAGCTCAGGCTCAGTGA	235
Sbjct	15346639	TCGGGGCCGGCCAGCTGGGAGGGCAGCAGGGCAGGGGCTCCGAGCTTAGGCTCAGTGA	15346698
Query	236	AGGCAAGTTCCAGGCGTTTCTGGATGTGAGCCACTTTACCCAGATGAGGTGACGGTGAG	295
Sbjct	15346699	GGGCAAGTTCCAGGCATTCTGGATGTGAGCCACTTTACCCAGACGAGGTGACTGTGAG	15346758
Query	296	GACTGTGGATAACCTGCTGGAGGTGTCTGCCCCGACACCCGACGCTCTGGATCGCCACGG	355
Sbjct	15346759	GACTGTGGATAACCTGCTGGAGGTGTCTGCCCCGACACCCGACGCTGGAACGCCACGG	15346818
Query	356	CTTCGTGTCCCGAGAGTTCTGTGCGACCATATGTCTCTGCATGATGAGCCCTGGCG	415
Sbjct	15346819	CTTCGTGTCCCGAGAGTTCTGCGCACCATATGTCTCTGCTGATGTGACCCCTGGCG	15346878
Query	416	GGTTCGAGCTGCTCTATCCCATGATGGCATCTTAACCTGGAGGCGCCGCGGGTGCCG	475
Sbjct	15346879	AGTCCGAGCTGCTCTCTCCCATGATGGCATCTTAAACCTGGAAGCACTCGGGTGCCG	15346938
Query	476	GCATTTGGACACGGAAGTCAATGAAGTCTACATCTCCCTGCTTCTGCTCCTCTGACCC	535
Sbjct	15346939	ACATTTGGACACAGAGTCAATGAGGTCTACATCTCCCTGCTCCTGCGCCTCTGATCC	15346998
Query	536	CGAGGAAGAGGAAGAGATAGCCAGAGTTGAGCCCTGACTGCCA	578
Sbjct	15346999	AGAGGAAGAGGAGGAGGCCATAGTTGAGCCCTGATTGCCA	15347041

Individual Alignment Details

Database: human build 36 RNA, alternate and reference assemblies.		
Posted date: Nov 6, 2006 9:33 AM		
Number of letters in database: 1,663,010,206		
Number of sequences in database: 46,285		
Lambda	K	H
1.37	0.711	1.31
Gapped		
Lambda	K	H
1.37	0.711	1.31
Matrix: blastn matrix:1 -3		
Gap Penalties: Existence: 5, Extension: 2		
Number of Sequences: 46285		
Number of Hits to DB: 4164965		
Number of extensions: 246350		
Number of successful extensions: 324		
Number of sequences better than 10: 3		
Number of HSP's better than 10 without gapping: 0		
Number of HSP's gapped: 324		
Number of HSP's successfully gapped: 4		
Length of query: 811		
Length of database: 5957977502		
Length adjustment: 22		
Effective length of query: 789		
Effective length of database: 5956959232		
Effective search space: 4700040834048		
Effective search space used: 4700040834048		

Database and Query Statistics