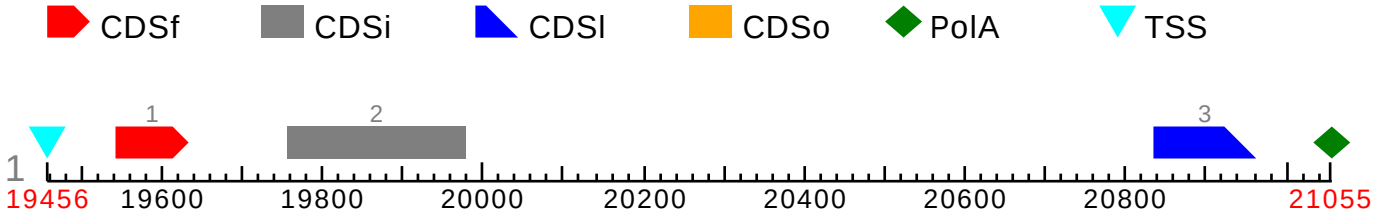
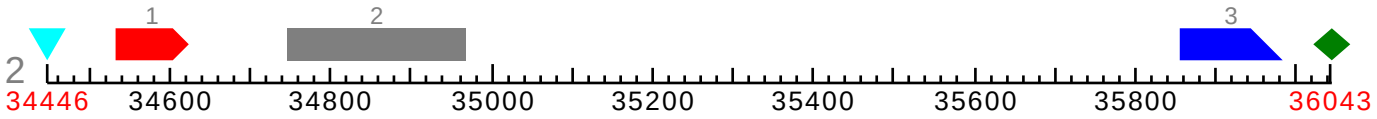
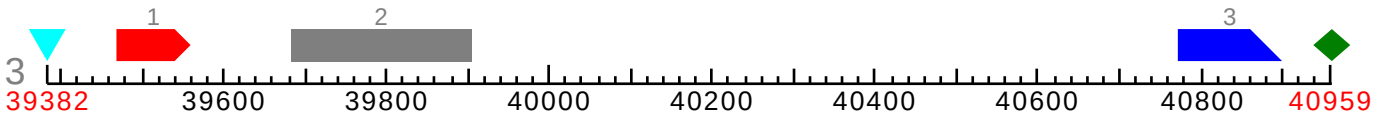
FGENESH 2.6 Prediction of potential genes in Homo_sapiens genomic DNA
Seq name: gi|13907843|ref|NG_000007.1| Homo sapiens genomic beta globin region (HBB@) on
Length of sequence: 73308
Number of predicted genes 10: in +chain 10, in -chain 0.
Number of predicted exons 21: in +chain 21, in -chain 0.
Positions of predicted genes and exons: Variant 1 from 1, Score:180.171887



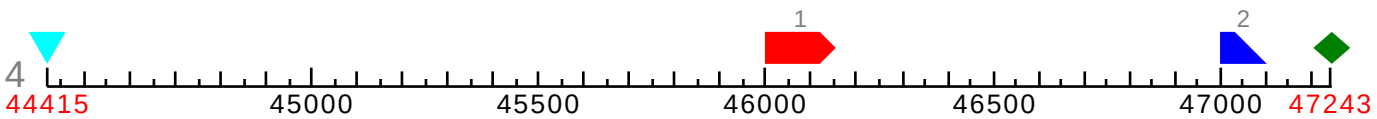
1	+		TSS	19456			-7.09			
1	+	1	CDSf	19541	-	19632	16.13	19541	- 19630	90
1	+	2	CDSi	19755	-	19977	13.37	19756	- 19977	222
1	+	3	CDSl	20833	-	20961	3.34	20833	- 20961	129
1	+		PolA	21055			1.12			



2	+		TSS	34446			-7.09			
2	+	1	CDSf	34531	-	34622	13.42	34531	- 34620	90
2	+	2	CDSi	34745	-	34967	21.52	34746	- 34967	222
2	+	3	CDSl	35854	-	35982	2.92	35854	- 35982	129
2	+		PolA	36043			1.12			

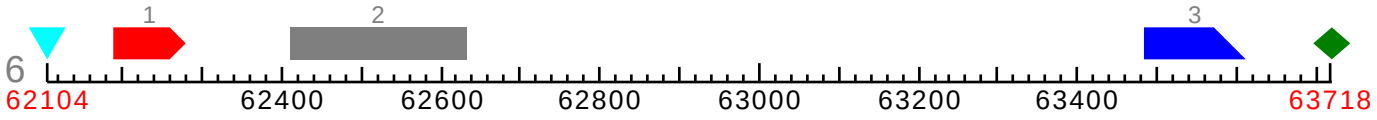


3	+		TSS	39382			-7.09			
3	+	1	CDSf	39467	-	39558	13.42	39467	- 39556	90
3	+	2	CDSi	39681	-	39903	21.52	39682	- 39903	222
3	+	3	CDSl	40770	-	40898	3.66	40770	- 40898	129
3	+		PolA	40959			1.12			



4	+		TSS	44415			-8.69			
4	+	1	CDSf	45995	-	46151	16.58	45995	- 46150	156
4	+	2	CDSl	46997	-	47100	-1.94	46999	- 47100	102
4	+		PolA	47243			1.12			

5	+		TSS	54707			-4.39			
5	+	1	CDSf	54790	-	54881	13.44	54790	-	54879	90
5	+	2	CDSi	55010	-	55232	17.01	55011	-	55232	222
5	+	3	CDSl	56425	-	56535	2.53	56425	-	56535	111
5	+		PolA	56931			1.12			



6	+		TSS	62104			-6.59			
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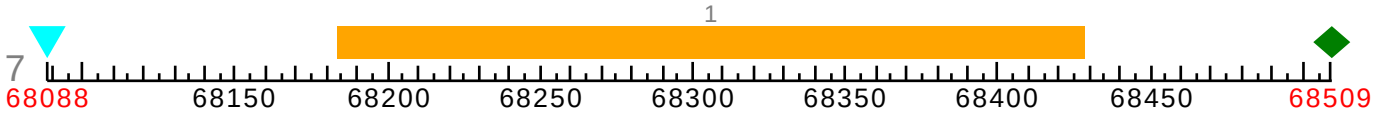
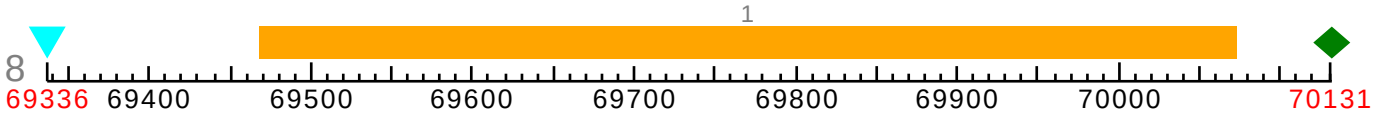
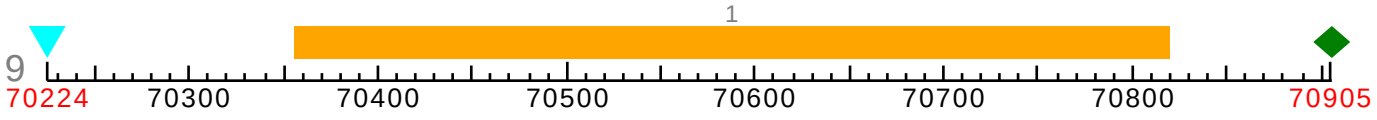
6	+	2	CDSi	62409	-	62631	20.06	62410	-	62631	222
6	+	3	CDSl	63482	-	63610	9.54	63482	-	63610	129
6	+		PolA	63718			1.12			



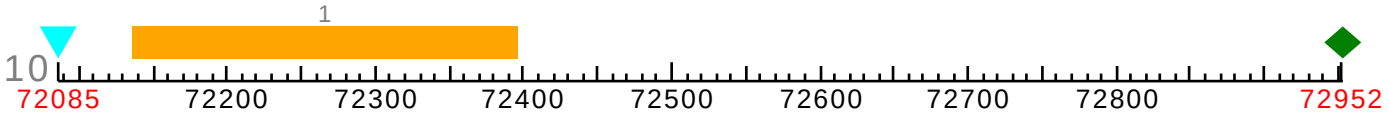
7	+		TSS	68088			-9.39			
7	+	1	CDSo	68183	-	68428	19.52	68183	-	68428	246
7	+		PolA	68509			1.12			



8	+		TSS	69336			-10.29			
8	+	1	CDSo	69467	-	70072	16.45	69467	-	70072	606
8	+		PolA	70131			-1.07			



9	+		TSS	70224			-12.49			
9	+	1	CDSo	70355	-	70819	17.10	70355	-	70819	465
9	+		PolA	70905			1.12			



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10 +      TSS      72085                -6.39
10 +    1 CDSo     72135 -     72395     7.31     72135 -     72395    261
10 +      PolA     72952                 1.12
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Predicted protein(s):

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>FGENESH:[mRNA] 1 3 exon (s) 19541 - 20961 444 bp, chain +
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AGATTTTTTGACAGCTTTGGAAACCTGTCGTCTCCCTCTGCCATCCTGGGCAACCCCAAG
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AACCTCAAGCCCGCCTTTGCTAAGCTGAGTGAGCTGCACTGTGACAAGCTGCATGTGGAT
CCTGAGAACTTCAAGCTCCTGGGTAACGTGATGGTGATTATTCTGGCTACTCACTTTGGC
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GCCCTGGCCCATAAGTACCACTGA
>FGENESH: 1 3 exon (s) 19541 - 20961 147 aa, chain +
MVHFTAEEKAAVTSLWSKMNVEEAGGEALGRLLVVYPWTQRFFDSFGNLSSPSAILGNPK
VKAHGKKVLTSFGDAIKNMDNLKPAFAKLSELHCDKLHVDPENFKLLGNVMVIILATHFG
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>FGENESH:[mRNA] 2 3 exon (s) 34531 - 35982 444 bp, chain +
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AGGTTCTTTGACAGCTTTGGCAACCTGTCCTCTGCCTCTGCCATCATGGGCAACCCCAAA
GTCAAGGCACATGGCAAGAAGGTGCTGACTTCCTTGGGAGATGCCATAAAGCACCTGGAT
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CCTGAGAACTTCAAGCTCCTGGGAAATGTGCTGGTGACCGTTTTGGCAATCCATTTCGGC
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GCCCTGTCCTCCAGATACCACTGA
>FGENESH: 2 3 exon (s) 34531 - 35982 147 aa, chain +
MGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSSASAIMGNPK
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>FGENESH:[mRNA] 3 3 exon (s) 39467 - 40898 444 bp, chain +
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GTCAAGGCACATGGCAAGAAGGTGCTGACTTCCTTGGGAGATGCCATAAAGCACCTGGAT
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CCTGAGAACTTCAAGCTCCTGGGAAATGTGCTGGTGACCGTTTTGGCAATCCATTTCGGC
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>FGENESH: 3 3 exon (s) 39467 - 40898 147 aa, chain +
MGHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSSASAIMGNPK
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>FGENESH:[mRNA] 4 2 exon (s) 45995 - 47100 261 bp, chain +
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TGTTTTGGCAACCCACTTCAGCGAGGATTTTACCCTACAGATACAGGCTTCTTGGCAGTA
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>FGENESH:[mRNA] 5 3 exon (s) 54790 - 56535 426 bp, chain +
ATGGTGCATCTGACTCCTGAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAAC
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>FGENESH: 5 3 exon (s) 54790 - 56535 141 aa, chain +
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LFYKEYMGKEKSKGTVQGING
>FGENESH:[mRNA] 6 3 exon (s) 62187 - 63610 444 bp, chain +
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>FGENESH: 6 3 exon (s) 62187 - 63610 147 aa, chain +
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK
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>FGENESH:[mRNA] 7 1 exon (s) 68183 - 68428 246 bp, chain +
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GAAAAAAAATTAGATGAATGGATAACTAGAATAACCAATGCACAGAAGTCCTTAAAGGAC
CTGATGGAGCTGAAAACCAAGGCAGGAGAACTACGTGACAAATACACAAGCCTCAGTAAC
CGATGA
>FGENESH: 7 1 exon (s) 68183 - 68428 81 aa, chain +
MEQSWAENDFDELREEGFRRSNYSKLKEEVRTNGKEVKNFEKKLDEWITRITNAQKSLKD
LMELKTKAGELRDKYTSLSNR
>FGENESH:[mRNA] 8 1 exon (s) 69467 - 70072 606 bp, chain +
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CACACAATAATAATGGGAGACTTTAACACCCCACTGTCAACATTAGACAGATCAACGAGA
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TTATAG
>FGENESH: 8 1 exon (s) 69467 - 70072 201 aa, chain +
MAKGSIQEEELTILNIYAPNTGAPRFIKQVLSDLQRDLDAHTIIMGDFNTPLSTLDRSTR
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>FGENESH:[mRNA] 9 1 exon (s) 70355 - 70819 465 bp, chain +
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>FGENESH: 9 1 exon (s) 70355 - 70819 154 aa, chain +
MTRGITTDPTEIQTTVREYYKHLYANKLENLEEMDKFLDTYTLPRLNQEEVVSLNRPITG
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>FGENESH:[mRNA] 10 1 exon (s) 72135 - 72395 261 bp, chain +
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>FGENESH: 10 1 exon (s) 72135 - 72395 86 aa, chain +
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