

Result of Blast

Summary

| Number of all alignments | Number of predicted | Number of normal alignments | Number of syntetic | Number of weird | Number of species | Number of species in predicted |
|--------------------------|---------------------|-----------------------------|--------------------|-----------------|-------------------|--------------------------------|
| 116 | 76 | 37 | 3 | 0 | 18 | 10 |

Means for all data

| Mean length | Mean identities | Mean score | Mean percent |
|---------------|-----------------|---------------|---------------|
| 6209.62068966 | 1330.84482759 | 2325.20811638 | 97.4052586207 |

Normal alignments

Means for normal alignments

| Mean length | Mean identities | Mean score | Mean percent |
|---------------|-----------------|---------------|---------------|
| 5898.99346405 | 1333.66013072 | 2345.93068758 | 97.7069281046 |

Details

Homo sapiens

| Gap | Percent | Title |
|-----|---------|---|
| 0 | 100.00 | Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 1, mRNA |
| 0 | 100.00 | Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 2, mRNA |
| 0 | 100.00 | Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:4804551), partial cds |
| 0 | 100.00 | Homo sapiens cDNA, FLJ98032 |
| 0 | 100.00 | Homo sapiens breast and ovarian cancer susceptibility protein 1 (BRCA1) mRNA, complete cds |
| 0 | 100.00 | Homo sapiens breast and ovarian cancer susceptibility protein (BRCA1) mRNA, BRCA1-2201T/2430C/2731T/3232G/3667G/4427C/4956G allele, partial cds |
| 0 | 100.00 | Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:40017569), partial cds |
| 0 | 100.00 | Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 3, mRNA |
| 0 | 100.00 | Homo sapiens cDNA clone IMAGE:7961445 >gi 146147644 gb BC115038.1 Homo sapiens cDNA clone IMAGE:7961448 |
| 0 | 100.00 | Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:40017573) |
| 0 | 100.00 | Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:40017573) |
| 0 | 99.94 | Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone MGC:131629 IMAGE:7961446), complete cds |
| 0 | 99.94 | Homo sapiens breast cancer 1, early onset, mRNA (cDNA clone IMAGE:3996658), with apparent retained intron |
| 0 | 99.93 | Homo sapiens cDNA, FLJ98032 |
| 1 | 99.69 | Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA, complete cds |
| 7 | 99.52 | Homo sapiens cDNA clone IMAGE:40017575, containing frame-shift errors |
| 0 | 99.42 | Homo sapiens IRIS mRNA, complete cds; alternatively spliced |
| 6 | 97.52 | Homo sapiens BRCA1, DNA repair associated (BRCA1), transcript variant 3, mRNA |
| 6 | 97.03 | Homo sapiens cDNA clone IMAGE:7961445 >gi 146147644 gb BC115038.1 Homo sapiens cDNA clone IMAGE:7961448 |

Nomascus gabriellae

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 98.59 | Nomascus gabriellae breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Hylobates agilis

| Gap | Percent | Title |
|-----|---------|---|
| 6 | 98.13 | Hylobates agilis breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Macaca fascicularis

| Gap | Percent | Title |
|-----|---------|--|
| 3 | 96.45 | Macaca fascicularis BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713702 gb KM017624.1 Macaca fascicularis breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Pongo pygmaeus

| Gap | Percent | Title |
|-----|---------|---|
| 0 | 98.39 | Pongo pygmaeus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Pan paniscus

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 99.4 | Pan paniscus BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713686 gb KM017616.1 Pan paniscus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Lophocebus albigena

| Gap | Percent | Title |
|-----|---------|--|
| 6 | 96.06 | Lophocebus albigena breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Nomascus leucogenys

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 98.59 | Nomascus leucogenys BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713708 gb KM017627.1 Nomascus leucogenys breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Colobus guereza

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 96.45 | Colobus guereza breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Papio anubis

| Gap | Percent | Title |
|-----|---------|--|
| 3 | 96.39 | Papio anubis BRCA1, DNA repair associated (BRCA1), mRNA >gi 667713712 gb KM017629.1 Papio anubis breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Miopithecus talapoin

| Gap | Percent | Title |
|-----|---------|---|
| 3 | 96.45 | Miopithecus talapoin breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Pan troglodytes

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 99.4 | Pan troglodytes BRCA1 (BRCA1) mRNA, partial cds |
| 0 | 99.2 | Pan troglodytes BRCA1, DNA repair associated (BRCA1), mRNA |

Macaca mulatta

| Gap | Percent | Title |
|-----|---------|---|
| 3 | 96.45 | Macaca mulatta BRCA1, DNA repair associated (BRCA1), mRNA |

Hylobates lar

| Gap | Percent | Title |
|-----|---------|--|
| 6 | 98.06 | Hylobates lar breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Cercopithecus wolfi

| Gap | Percent | Title |
|-----|---------|--|
| 3 | 96.32 | Cercopithecus wolfi breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Hylobates pileatus

| Gap | Percent | Title |
|-----|---------|---|
| 6 | 98.19 | Hylobates pileatus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Trachypithecus francoisi

| Gap | Percent | Title |
|-----|---------|---|
| 2 | 96.25 | Trachypithecus francoisi breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Symphalangus syndactylus

| Gap | Percent | Title |
|-----|---------|---|
| 6 | 98.39 | Symphalangus syndactylus breast cancer type 1 susceptibility protein (BRCA1) mRNA, complete cds |

Predicted alignments

Means for predicted alignments

| Mean length | Mean identities | Mean score | Mean percent |
|---------------|-----------------|---------------|---------------|
| 6217.65065502 | 1328.70742358 | 2319.51202183 | 97.3712663755 |

Details

Piliocolobus tephrosceles

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 98.00 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA |
| 0 | 96.17 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X5, mRNA |
| 0 | 96.17 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA |
| 0 | 96.17 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA |
| 0 | 96.14 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA |
| 3 | 95.97 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X6, mRNA |
| 4 | 95.60 | PREDICTED: Piliocolobus tephrosceles BRCA1, DNA repair associated (BRCA1), transcript variant X2, mRNA |

Pan troglodytes

| Gap | Percent | Title |
|-----|---------|---|
| 0 | 99.41 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X12, misc_RNA |
| 0 | 99.41 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X8, mRNA |
| 0 | 99.41 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA |
| 0 | 99.41 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA |
| 0 | 99.40 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X2, mRNA |
| 0 | 99.30 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X12, misc_RNA |
| 0 | 99.30 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X8, mRNA |
| 0 | 99.30 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA |
| 0 | 99.30 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA |
| 0 | 99.30 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X5, mRNA |
| 3 | 99.21 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X6, mRNA |
| 3 | 99.21 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X5, mRNA |
| 6 | 99.03 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA |

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 98.85 | PREDICTED: Pan troglodytes BRCA1, DNA repair associated (BRCA1), transcript variant X7, mRNA |

Macaca mulatta

| Gap | Percent | Title |
|-----|---------|--|
| 3 | 96.26 | PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X3, mRNA |
| 3 | 96.26 | PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X1, mRNA |
| 6 | 96.07 | PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X4, mRNA |
| 9 | 95.89 | PREDICTED: Macaca mulatta breast cancer 1 (BRCA1), transcript variant X2, mRNA |

Macaca fascicularis

| Gap | Percent | Title |
|-----|---------|---|
| 3 | 96.50 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X3, mRNA |
| 3 | 96.50 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X4, mRNA |
| 3 | 96.26 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X2, mRNA |
| 9 | 95.89 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X6, mRNA |
| 9 | 95.89 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X1, mRNA |
| 12 | 95.71 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X7, mRNA |
| 16 | 95.47 | PREDICTED: Macaca fascicularis breast cancer 1 (BRCA1), transcript variant X5, mRNA |

Nomascus leucogenys

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 98.38 | PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA |
| 0 | 98.21 | PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA |
| 0 | 98.10 | PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA |
| 0 | 98.07 | PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA |
| 0 | 98.07 | PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA |
| 6 | 93.39 | PREDICTED: Nomascus leucogenys breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA |

Macaca nemestrina

| Gap | Percent | Title |
|-----|---------|--|
| 3 | 96.37 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA |
| 3 | 96.36 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA |
| 3 | 96.14 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA |
| 3 | 96.14 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA |
| 3 | 96.14 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA |
| 6 | 95.95 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X6, mRNA |
| 9 | 95.77 | PREDICTED: Macaca nemestrina breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA |

Cebus capucinus

| Gap | Percent | Title |
|-----|---------|--|
| 13 | 92.80 | PREDICTED: Cebus capucinus initiator BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA |
| 13 | 92.80 | PREDICTED: Cebus capucinus initiator BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA |
| 16 | 92.62 | PREDICTED: Cebus capucinus initiator BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA |

Callithrix jacchus

| Gap | Percent | Title |
|-----|---------|---|
| 13 | 92.62 | PREDICTED: Callithrix jacchus BRCA1, DNA repair associated (BRCA1), transcript variant X4, mRNA |
| 13 | 92.62 | PREDICTED: Callithrix jacchus BRCA1, DNA repair associated (BRCA1), transcript variant X3, mRNA |
| 13 | 92.62 | PREDICTED: Callithrix jacchus BRCA1, DNA repair associated (BRCA1), transcript variant X1, mRNA |

| Gap | Percent | Title |
|--------------|---------|-------|
| Pongo abelii | | |

| Gap | Percent | Title |
|-----|---------|--|
| 0 | 98.55 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA |
| 0 | 98.55 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA |
| 0 | 98.52 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X10, mRNA |
| 0 | 98.46 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X12, mRNA |
| 0 | 98.46 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X13, mRNA |
| 1 | 98.45 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X11, mRNA |
| 0 | 98.31 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA |
| 0 | 98.29 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X15, mRNA |
| 0 | 98.29 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X14, mRNA |
| 0 | 98.29 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA |
| 6 | 97.95 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA |
| 13 | 97.45 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X6, mRNA |
| 19 | 97.05 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X7, mRNA |
| 6 | 94.63 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X13, mRNA |
| 6 | 94.37 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X12, mRNA |
| 0 | 93.33 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X10, mRNA |
| 0 | 93.26 | PREDICTED: Pongo abelii breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA |

Cercocebus atys

| Gap | Percent | Title |
|-----|---------|---|
| 6 | 96.17 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA |
| 6 | 96.17 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X6, mRNA |
| 6 | 95.83 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X4, mRNA |
| 13 | 95.65 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X11, mRNA |
| 13 | 95.65 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X2, mRNA |
| 12 | 95.47 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X3, mRNA |
| 16 | 95.47 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X5, mRNA |
| 0 | 92.31 | PREDICTED: Cercocebus atys breast cancer 1, early onset (BRCA1), transcript variant X1, mRNA |