

Gene: ABL1 - Sequence: NG_012034.1
Transcript: NM_005157.4 - Protein: NP_005148.2
Date : February 23, 2015

1st line: Base numbering. Full stops for intronic +/- 5, 10, 15...
2nd line: Base sequence. lower case Introns, upper case Exons
3rd line: Amino acid sequence. Printed on MIDDLE base of codon
4th line: Amino acid numbering. Numbered on 1st and increments of 10

Exon 2 | Start: 126564 | End: 126645 | Length: 81

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      |1          |11          |21          |31          |41          |51
AAAATGTTGGAGATCTGCCTGAAGCTGGTGGGCTGCAAATCCAAGAAGGGGCTGTCCTCG
      M  L  E  I  C  L  K  L  V  G  C  K  S  K  K  G  L  S  S
      |1                                |11

      |61          |71
TCCTCCAGCTGTTATCTGGAAG
      |21

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Exon 3 | Start: 145184 | End: 145357 | Length: 173

|81 |91 |101 |111 |121 |131
AAGCCCTTCAGCGGCCAGTAGCATCTGACTTTGAGCCTCAGGGTCTGAGTGAAGCCGCTC
 A L Q R P V A S D F E P Q G L S E A A R
 |31 |41

|141 |151 |161 |171 |181 |191
GTTGAACTCCAAGGAAAACCTTCTCGCTGGACCCAGTGAAAATGACCCCAACCTTTTCG
 W N S K E N L L A G P S E N D P N L F V
 |51 |61

|201 |211 |221 |231 |241 |251
TTGCACTGTATGATTTTGTGGCCAGTGAGATAACACTCTAAGCATAACTAAAG
 |71 |81

Exon 4 | Start: 145921 | End: 146216 | Length: 295

|261 |271 |281 |291 |301 |311
 GTGAAAAGCTCCGGGTCTTAGGCTATAATCACAATGGGGAATGGTGTGAAGCCCCAAACCA
 E K L R V L G Y N H N G E W C E A Q T K
 |91 |101

321	331	341	351	361	371
AAAATGGCCAAGGCTGGGTCCCAAGCAACTACATCACGCCAGTCAACAGTCTGGAGAAAC					
N	G	Q	G	W	V
	P	S	N	Y	I
			T	P	V
				N	S
				L	E
				K	H
	111			121	
381	391	401	411	421	431
ACTCCTGGTACCATGGGCCTGTGTCCCGCAATGCCGCTGAGTATCTGCTGAGCAGCGGGA					
S	W	Y	H	G	P
	V	S	R	N	A
		A	A	E	Y
			L	L	S
				S	G
				I	
	131			141	
441	451	461	471	481	491
TCAATGGCAGCTTCTTGGTGCGTGAGAGTGAGAGCAGTCCTGGCCAGAGGTCCATCTCGC					
N	G	S	F	L	V
	R	E	S	E	S
		S	S	P	G
			Q	R	S
				I	S
				L	
	151			161	
501	511	521	531	541	
TGAGATACGAAGGGAGGGTGTACCATTACAGGATCAACACTGCTTCTGATGGCAAG					
	171			181	

Exon 5 | Start: 153883 | End: 154155 | Length: 272

551	561	571	581	591	601
CTCTACGTCTCCTCCGAGAGCCGCTTCAACACCCTGGCCGAGTTGGTTCATCATCTCA					
L	Y	V	S	S	E
		S	R	F	N
			T	L	A
				E	L
				V	H
				H	S
		191		201	
611	621	631	641	651	661
ACGGTGGCCGACGGGCTCATCACACGCTCCATTATCCAGCCCCAAAGCGCAACAAGCCC					
T	V	A	D	G	L
		I	T	T	L
			H	Y	P
			A	P	K
				R	N
				K	P
		211		221	
671	681	691	701	711	721
ACTGTCTATGGTGTGTCCCCCAACTACGACAAGTGGGAGATGGAACGCACGGACATCACC					
T	V	Y	G	V	S
		P	N	Y	D
			K	W	E
			M	E	R
				T	D
				I	T
		231		241	
731	741	751	761	771	781
ATGAAGCACAAGCTGGGCGGGGGCCAGTACGGGGAGGTGTACGAGGGCGTGTGGAAGAAA					
M	K	H	K	L	G
		G	G	Q	Y
			G	E	V
			Y	E	G
				V	W
				K	K
		251		261	
791	801	811	821		
TACAGCCTGACGGTGGCCGTGAAGACCTTGAAG					
	271				

Exon 6 | Start: 163249 | End: 163333 | Length: 84

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      |831      |841      |851      |861      |871      |881
GAGGACACCATGGAGGTGGAAGAGTTCTTGAAAGAAGCTGCAGTCATGAAAGAGATCAAA
E D T M E V E E F L K E A A V M K E I K
      |281                      |291

      |891      |901
CACCCCTAACCTGGTGCAGCTCCTTG
      |301
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Exon 7 | Start: 163980 | End: 164157 | Length: 177

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      |911      |921      |931      |941      |951      |961
GGGTCTGCACCCGGGAGCCCCGTTCTATATCATCACTGAGTTCATGACCTACGGGAACC
V C T R E P P F Y I I T E F M T Y G N L
      |311                      |321

      |971      |981      |991      |1001     |1011     |1021
TCCTGGACTACCTGAGGGAGTGCAACCGGCAGGAGGTGAACGCCGTGGTGCTGCTGTACA
L D Y L R E C N R Q E V N A V V L L Y M
      |331                      |341

      |1031     |1041     |1051     |1061     |1071     |1081
TGGCCACTCAGATCTCGTCAGCCATGGAGTACCTGGAGAAGAAAACTTCATCCACAG
      |351                      |361
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Exon 8 | Start: 165988 | End: 166172 | Length: 184

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      |1091     |1101     |1111     |1121     |1131     |1141
AGATCTTGCTGCCCCGAAACTGCCTGGTAGGGGAGAACCACTTGGTGAAGGTAGCTGATTT
D L A A R N C L V G E N H L V K V A D F
      |371                      |381

      |1151     |1161     |1171     |1181     |1191     |1201
TGGCCTGAGCAGGTTGATGACAGGGGACACCTACACAGCCCATGCTGGAGCCAAGTTCCC
G L S R L M T G D T Y T A H A G A K F P
      |391                      |401

      |1211     |1221     |1231     |1241     |1251     |1261
CATCAAATGGACTGCACCCGAGAGCCTGGCCTACAACAAGTTCTCCATCAAGTCCGACGT
I K W T A P E S L A Y N K F S I K S D V
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|411

|421

CTGGG

Exon 9 | Start: 169535 | End: 169687 | Length: 152

|1271 |1281 |1291 |1301 |1311 |1321
CATTGGAGTATTGCTTTGGGAAATTGCTACCTATGGCATGTCCCCTTACCCGGAATTG
F G V L L W E I A T Y G M S P Y P G I D
|431 |441

|1331 |1341 |1351 |1361 |1371 |1381
ACCTGTCCCAGGTGTATGAGCTGCTAGAGAAGGACTACCGCATGGAGCGCCAGAAAGGCT
L S Q V Y E L L E K D Y R M E R P E G C
|451 |461

|1391 |1401 |1411 |1421
GCCCAGAGAAGGTCTATGAACTCATGCGAGCAT
|471

Exon 10 | Start: 171188 | End: 171277 | Length: 89

|1431 |1441 |1451 |1461 |1471 |1481
GTTGGCAGTGAATCCCTCTGACCGGCCCTCCTTTGCTGAAATCCACCAAGCCTTTGAAA
W Q W N P S D R P S F A E I H Q A F E T
|481 |491

|1491 |1501 |1511
CAATGTTCCAGGAATCCAGTATCTCAGACG
|501

Exon 11 | Start: 171620 | End: 171784 | Length: 164

|1521 |1531 |1541 |1551 |1561 |1571
AAGTGGAAAAGGAGCTGGGGAAACAAGGCGTCCGTGGGGCTGTGAGTACCTTGCTGCAGG
V E K E L G K Q G V R G A V S T L L Q A
|511 |521

|1581 |1591 |1601 |1611 |1621 |1631
CCCCAGAGCTGCCACCAAGACGAGGACCTCCAGGAGAGCTGCAGAGCACAGAGACACCA
P E L P T K T R T S R R A A E H R D T T

|531 |541
 |1641 |1651 |1661 |1671
 CTGACGTGCCTGAGATGCCTCACTCCAAGGGCCAGGGAGAGAGCG
 |551

Exon 12 | Start: 175089 | End: 178795 | Length: 3706

|1681 |1691 |1701 |1711 |1721 |1731
 ATCCTCTGGACCATGAGCCTGCCGTGTCTCCATTGCTCCCTCGAAAAGAGCGAGGTCCCC
 P L D H E P A V S P L L P R K E R G P P
 |561 |571

|1741 |1751 |1761 |1771 |1781 |1791
 CGGAGGGCGGCCTGAATGAAGATGAGCGCCTTCTCCCCAAAGACAAAAAGACCAACTTGT
 E G G L N E D E R L L P K D K K T N L F
 |581 |591

|1801 |1811 |1821 |1831 |1841 |1851
 TCAGCGCCTTGATCAAGAAGAAGAAGACAGCCCCAACCCCTCCCAAACGCAGCAGCT
 S A L I K K K K T A P T P P K R S S S
 |601 |611

|1861 |1871 |1881 |1891 |1901 |1911
 CCTTCCGGGAGATGGACGGCCAGCCGGAGCGCAGAGGGGCCGCGAGGAAGAGGGCCGAG
 F R E M D G Q P E R R G A G E E E G R D
 |621 |631

|1921 |1931 |1941 |1951 |1961 |1971
 ACATCAGCAACGGGGCACTGGCTTTCACCCCCTTGGACACAGCTGACCCAGCCAAGTCCC
 I S N G A L A F T P L D T A D P A K S P
 |641 |651

|1981 |1991 |2001 |2011 |2021 |2031
 CAAAGCCCAGCAATGGGGCTGGGGTCCCCAATGGAGCCCTCCGGGAGTCCGGGGGCTCAG
 K P S N G A G V P N G A L R E S G G S G
 |661 |671

|2041 |2051 |2061 |2071 |2081 |2091
 GCTTCCGGTCTCCCCACCTGTGGAAGAAGTCCAGCACGCTGACCAGCAGCCGCCTAGCCA
 F R S P H L W K K S S T L T S S R L A T
 |681 |691

|2101 |2111 |2121 |2131 |2141 |2151
 CCGGCGAGGAGAGGGCGGTGGCAGCTCCAGCAAGCGCTTCCTGCGCTCTTGCTCCGCCT

G E E E G G G S S S K R F L R S C S A S
 |701 |711

 |2161 |2171 |2181 |2191 |2201 |2211
 CCTGCGTTCCCATGGGGCCAAGGACACGGAGTGGAGGTCAGTCACGCTGCCTCGGGACT
 C V P H G A K D T E W R S V T L P R D L
 |721 |731

 |2221 |2231 |2241 |2251 |2261 |2271
 TGCAGTCCACGGGAAGACAGTTTGACTCGTCCACATTTGGAGGGCACAAAAGTGAGAAGC
 Q S T G R Q F D S S T F G G H K S E K P
 |741 |751

 |2281 |2291 |2301 |2311 |2321 |2331
 CGGCTCTGCCTCGGAAGAGGGCAGGGGAGAACAGGTCTGACCAGGTGACCCGAGGCACAG
 A L P R K R A G E N R S D Q V T R G T V
 |761 |771

 |2341 |2351 |2361 |2371 |2381 |2391
 TAACGCCTCCCCCAGGCTGGTGAAAAAGAATGAGGAAGCTGCTGATGAGGTCTTCAAAG
 T P P P R L V K K N E E A A D E V F K D
 |781 |791

 |2401 |2411 |2421 |2431 |2441 |2451
 ACATCATGGAGTCCAGCCCGGGCTCCAGCCCGCCCAACCTGACTCCAAAACCCCTCCGGC
 I M E S S P G S S P P N L T P K P L R R
 |801 |811

 |2461 |2471 |2481 |2491 |2501 |2511
 GGCAGGTACCGTGGCCCTGCCTCGGGCCTCCCCACAAGGAAGAAGCTGGAAGGGCA
 Q V T V A P A S G L P H K E E A G K G S
 |821 |831

 |2521 |2531 |2541 |2551 |2561 |2571
 GTGCCTTAGGGACCCCTGCTGCAGCTGAGCCAGTGACCCCAACAGCAAAGCAGGCTCAG
 A L G T P A A A E P V T P T S K A G S G
 |841 |851

 |2581 |2591 |2601 |2611 |2621 |2631
 GTGCACCAGGGGGCACCAGCAAGGGCCCCGCGAGGAGTCCAGAGTGAGGAGGCACAAGC
 A P G G T S K G P A E E S R V R R H K H
 |861 |871

 |2641 |2651 |2661 |2671 |2681 |2691
 ACTCCTCTGAGTCGCCAGGGAGGGACAAGGGGAAATTGTCCAGGCTCAAACCTGCCCCGC
 S S E S P G R D K G K L S R L K P A P P

|881 |891
 |2701 |2711 |2721 |2731 |2741 |2751
 CGCCCCACCAGCAGCCTCTGCAGGGAAGGCTGGAGGAAAGCCCTCGCAGAGCCCGAGCC
 P P P A A S A G K A G G K P S Q S P S Q
 |901 |911
 |2761 |2771 |2781 |2791 |2801 |2811
 AGGAGGCGCGGGGAGGCAGTCCTGGGCGCAAAGACAAAAGCCACGAGTCTGGTTGATG
 E A A G E A V L G A K T K A T S L V D A
 |921 |931
 |2821 |2831 |2841 |2851 |2861 |2871
 CTGTGAACAGTGACGCTGCCAAGCCAGCCAGCCGGGAGAGGGCCTCAAAAAGCCCGTGC
 V N S D A A K P S Q P G E G L K K P V L
 |941 |951
 |2881 |2891 |2901 |2911 |2921 |2931
 TCCGCGCCACTCCAAAGCCACAGTCCGCCAAGCCGTCGGGGACCCCATCAGCCAGCCC
 P A T P K P Q S A K P S G T P I S P A P
 |961 |971
 |2941 |2951 |2961 |2971 |2981 |2991
 CCGTTCCCTCCACGTTGCCATCAGCATCCTCGGCCCTGGCAGGGGACCAGCCGTCTTCCA
 V P S T L P S A S S A L A G D Q P S S T
 |981 |991
 |3001 |3011 |3021 |3031 |3041 |3051
 CGGCCTTCATCCCTCTCATATCAACCCGAGTGTCTTTCGAAAAACCCGCCAGCCTCCAG
 A F I P L I S T R V S L R K T R Q P P E
 |1001 |1011
 |3061 |3071 |3081 |3091 |3101 |3111
 AGCGGATCGCCAGCGGCGCCATCACCAAGGGCGTGGTCCTGGACAGCACCGAGGCGCTGT
 R I A S G A I T K G V V L D S T E A L C
 |1021 |1031
 |3121 |3131 |3141 |3151 |3161 |3171
 GCCTCGCCATCTCTAGGAACTCCGAGCAGATGGCCAGCCACAGCGCAGTGCTGGAGGCCG
 L A I S R N S E Q M A S H S A V L E A G
 |1041 |1051
 |3181 |3191 |3201 |3211 |3221 |3231
 GCAAAAACCTCTACACGTTCTGCGTGAGCTATGTGGATTCCATCCAGCAAATGAGGAACA
 K N L Y T F C V S Y V D S I Q Q M R N K
 |1061 |1071

3241	3251	3261	3271	3281	3291
AGTTTGCCTTCCGAGAGGCCATCAACAACTGGAGAATAATCTCCGGGAGCTTCAGATCT					
F	A	F	R	E	A
I	N	K	L	E	N
N	L	R	E	L	Q
I	C				
1081			1091		

3301	3311	3321	3331	3341	3351
GCCCCGGCAGCAGGCAGTGGTCCAGCGGCCACTCAGGACTTCAGCAAGCTCCTCAGTT					
P	A	T	A	G	S
G	P	A	A	T	Q
D	F	S	K	L	L
S	S				
1101			1111		

3361	3371	3381	3391	*11	*21
CGGTGAAGGAAATCAGTGACATAGTGCAGAGGTAGCAGCAGTCAGGGGTCAGGTGTCAGG					
V	K	E	I	S	D
I	V	Q	R	*	
1121			1131		

*31	*41	*51	*61	*71	*81
CCCGTCGGAGCTGCCTGCAGCACATGCGGGCTCGCCCATACCCGTGACAGTGGCTGACAA					

*91	*101	*111	*121	*131	*141
GGGACTAGTGAGTCAGCACCTTGGCCCAGGAGCTCTGCGCCAGGCAGAGCTGAGGGCCCT					

*151	*161	*171	*181	*191	*201
GTGGAGTCCAGCTCTACTACCTACGTTTGCACCGCCTGCCCTCCCGCACCTTCCTCCTCC					

*211	*221	*231	*241	*251	*261
CCGCTCCGTCTCTGTCTCGAATTTTATCTGTGGAGTTCCTGCTCCGTGGACTGCAGTCG					

*271	*281	*291	*301	*311	*321
GCATGCCAGGACCCGCCAGCCCCGCTCCACCTAGTGCCCCAGACTGAGCTCTCCAGGCC					

*331	*341	*351	*361	*371	*381
AGGTGGGAACGGCTGATGTGGACTGTCTTTTTCATTTTTTCTCTCTGGAGCCCCCTCCTC					

*391	*401	*411	*421	*431	*441
CCCCGGCTGGGCCTCCTTCTTCCACTTCTCCAAGAATGGAAGCCTGAACTGAGGCCTTGT					

*451	*461	*471	*481	*491	*501
GTGTCAGGCCCTCTGCCTGCACTCCCTGGCCTTGCCCGTCGTGTGCTGAAGACATGTTTC					

*511	*521	*531	*541	*551	*561
AAGAACCGCATTTTCGGAAGGGCATGCACGGGCATGCACACGGCTGGTCACTCTGCCCTC					

*571	*581	*591	*601	*611	*621
TGCTGCTGCCCCGGGTGGGGTGACTCGCCATTTCTCACGTGCAGGACAGCTCTTGATT					

*631	*641	*651	*661	*671	*681
TGGGTGAAAAACAGGTGCTAAAGCCAACCAGCCTTTGGGTCTGGGCAGGTGGGAGCTG					
*691	*701	*711	*721	*731	*741
AAAAGGATCGAGGCATGGGGCATGTCCTTTCCATCTGTCCACATCCCCAGAGCCCAGCTC					
*751	*761	*771	*781	*791	*801
TTGCTCTCTTGTGACGTGCACTGTGAATCCTGGCAAGAAAGCTTGAGTCTCAAGGGTGGC					
*811	*821	*831	*841	*851	*861
AGGTCACTGTCACTGCCGACATCCCTCCCCAGCAGAATGGAGGCAGGGGACAAGGGAGG					
*871	*881	*891	*901	*911	*921
CAGTGGCTAGTGGGTGAACAGCTGGTGCCAAATAGCCCCAGACTGGGCCCAGGCAGGTC					
*931	*941	*951	*961	*971	*981
TGCAAGGGCCCAGAGTGAACCGTCCTTTCACACATCTGGGTGCCCTGAAAGGGCCCTTC					
*991	*1001	*1011	*1021	*1031	*1041
CCTCCCCACTCCTCTAAGACAAAGTAGATTCTTACAAGGCCCTTTCCTTTGGAACAAGA					
*1051	*1061	*1071	*1081	*1091	*1101
CAGCCTTCACTTTTCTGAGTTCTTGAAGCATTTCAAAGCCCTGCCTCTGTGTAGCCGCC					
*1111	*1121	*1131	*1141	*1151	*1161
TGAGAGAGAATAGAGCTGCCACTGGGCACCTGCGCACAGGTGGGAGGAAAGGGCCTGGCC					
*1171	*1181	*1191	*1201	*1211	*1221
AGTCCTGGTCTCTGGCTGCACTCTTGAAGTGGGCGAATGTCTTATTTAATTACCGTGAGTG					
*1231	*1241	*1251	*1261	*1271	*1281
ACATAGCCTCATGTTCTGTGGGGTTCATCAGGGAGGGTTAGGAAAACCACAAACGGAGCC					
*1291	*1301	*1311	*1321	*1331	*1341
CCTGAAAGCCTCACGTATTTACAGAGCACGCCTGCCATCTTCTCCCCGAGGCTGCCCA					
*1351	*1361	*1371	*1381	*1391	*1401
GGCCGAGCCCAGATACGGGGGCTGTGACTCTGGGCAGGGACCCGGGGTCTCCTGGACCT					
*1411	*1421	*1431	*1441	*1451	*1461
TGACAGAGCAGCTAACTCCGAGAGCAGTGGGCAGGTGGCCGCCCTGAGGCTTCACGCCG					
*1471	*1481	*1491	*1501	*1511	*1521
GGAGAAGCCACCTTCCACCCCTTCATACCGCCTCGTGCCAGCAGCCTCGCACAGGCCCT					
*1531	*1541	*1551	*1561	*1571	*1581

AGCTTTACGCTCATCACCTAACTTGTA CTTTATTTTCTGATAGAAATGGTTTCCTCTG

*1591	*1601	*1611	*1621	*1631	*1641
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GATCGTTTTATGCGGTTCTTACAGCACATCACCTCTTTGCCCCGACGGCTGTGACGCAG

*1651	*1661	*1671	*1681	*1691	*1701
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CCGGAGGGAGGCACTAGTCACCGACAGCGGCCTTGAAGACAGAGCAAAGCGCCCACCCAG

*1711	*1721	*1731	*1741	*1751	*1761
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GTCCCCGACTGCCTGTCTCCATGAGGTACTGGTCCCTTCCTTTTGTTAACGTGATGTGC

*1771	*1781	*1791	*1801	*1811	*1821
-------	-------	-------	-------	-------	-------

CACTATATTTTACAGTATCTCTTGGTATGCATCTTTTATAGACGCTCTTTTCTAAGTGG

*1831	*1841	*1851	*1861	*1871	*1881
-------	-------	-------	-------	-------	-------

CGTGTGCATAGCGTCCTGCCCTGCCCCCTCGGGGGCCTGTGGTGGCTCCCCCTCTGCTTC

*1891	*1901	*1911	*1921	*1931	*1941
-------	-------	-------	-------	-------	-------

TCGGGGTCCAGTGCATTTTGTCTGTATATGATTCTCTGTGGTTTTTTTTGAATCCAAA

*1951	*1961	*1971	*1981	*1991
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TCTGTCCTCTGTAGTATTTTTTAAATAAATCAGTGTTTACATTAGAA

LRG Parser: Version: 1.1, Version Date: 11/02/2015
 Reader: Version: 1, Version Date: 11/02/2015
 Writer: Version: 1, Version Date: 11/02/2015
 Control: Version: 1, Version Date: 11/02/2015