

Gene: ABL1 - Sequence: NG_012034.1
Transcript: NM_005157.4 - Protein: NP_005148.2
Date : February 20, 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

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

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

    |201         |211         |221         |231         |241         |251
TTGCACTGTATGATTTTGTGGCCAGTGGAGATAACACTCTAAGCATAACTAAAG
          |71                      |81
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Exon 4 | Start: 145921 | End: 146216 | Length: 295

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|261         |271         |281         |291         |301         |311
GTGAAAAGCTCCGGGTCTTAGGCTATAATCACAATGGGGAATGGTGTGAAGCCCAAACCA
G  E  K  L  R  V  L  G  Y  N  H  N  G  E  W  C  E  A  Q  T
          |91                      |101
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321	331	341	351	361	371
AAAATGGCCAAGGCTGGGTCCCAAGCAACTACATCACGCCAGTCAACAGTCTGGAGAAAC					
K	N	G	Q	G	W
		V	P	S	N
		Y	I	T	P
			V	N	S
				L	E
				K	
	111			121	
381	391	401	411	421	431
ACTCCTGGTACCATGGGCCTGTGTCCCGCAATGCCGCTGAGTATCTGCTGAGCAGCGGGA					
H	S	W	Y	H	G
		P	V	S	R
		N	A	A	E
		Y	L	L	S
				S	G
	131			141	
441	451	461	471	481	491
TCAATGGCAGCTTCTTGGTGCGTGAGAGTGAGAGCAGTCCTGGCCAGAGGTCCATCTCGC					
I	N	G	S	F	L
		V	R	E	S
		E	S	S	P
			G	Q	R
				S	I
				S	
	151			161	
501	511	521	531	541	
TGAGATACGAAGGGAGGGTGTACCATTACAGGATCAACACTGCTTCTGATGGCAAG					
	171			181	

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

551	561	571	581	591	601
CTCTACGTCTCCTCCGAGAGCCGCTTCAACACCCTGGCCGAGTTGGTTCATCATCATTCA					
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
ACGGTGGCCGACGGGCTCATCACGCTCCATTATCCAGCCCCAAAGCGCAACAAGCCC					
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	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
G V C T R E P P F Y I I T E F M T Y G N
      |311                        |321

      |971      |981      |991      |1001     |1011     |1021
TCCTGGACTACCTGAGGGAGTGCAACCGGCAGGAGGTGAACGCCGTGGTGCTGCTGTACA
L L D Y L R E C N R Q E V N A V V L L Y
      |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
CATTGGAGTATTGCTTTGGGAAATTGCTACCTATGGCATGTCCCCTTACCCGGGAATTG
A F G V L L W E I A T Y G M S P Y P G I
|431 |441

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

|1391 |1401 |1411 |1421
GCCCAGAGAAGGTCTATGAACTCATGCGAGCAT
|471

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

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

|1491 |1501 |1511
CAATGTTCCAGGAATCCAGTATCTCAGACG
|501

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

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

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

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

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

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

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

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

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

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

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

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

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

T G E E E G G G S S S K R F L R S C S A
|701 |711
|2161 |2171 |2181 |2191 |2201 |2211
CCTGCGTTCCCATGGGGCCAAGGACACGGAGTGGAGGTCAGTCACGCTGCCTCGGGACT
S C V P H G A K D T E W R S V T L P R D
|721 |731
|2221 |2231 |2241 |2251 |2261 |2271
TGCAGTCCACGGGAAGACAGTTTGACTCGTCCACATTTGGAGGGCACAAAAGTGAGAAGC
L Q S T G R Q F D S S T F G G H K S E K
|741 |751
|2281 |2291 |2301 |2311 |2321 |2331
CGGCTCTGCCTCGGAAGAGGGCAGGGGAGAACAGGTCTGACCAGGTGACCCGAGGCACAG
P A L P R K R A G E N R S D Q V T R G T
|761 |771
|2341 |2351 |2361 |2371 |2381 |2391
TAACGCCTCCCCCAGGCTGGTGAAGAAGAATGAGGAAGCTGCTGATGAGGTCTTCAAAG
V T P P P R L V K K N E E A A D E V F K
|781 |791
|2401 |2411 |2421 |2431 |2441 |2451
ACATCATGGAGTCCAGCCCGGGCTCCAGCCCGCCCAACCTGACTCCAAAACCCCTCCGGC
D I M E S S P G S S P P N L T P K P L R
|801 |811
|2461 |2471 |2481 |2491 |2501 |2511
GGCAGGTACCGTGGCCCTGCCTCGGGCCTCCCCACAAGGAAGAAGCTGGAAAGGGCA
R Q V T V A P A S G L P H K E E A G K G
|821 |831
|2521 |2531 |2541 |2551 |2561 |2571
GTGCCTTAGGGACCCCTGCTGCAGCTGAGCCAGTGACCCCAACAGCAAAGCAGGCTCAG
S A L G T P A A A E P V T P T S K A G S
|841 |851
|2581 |2591 |2601 |2611 |2621 |2631
GTGCACCAGGGGGCACCAGCAAGGGCCCGGAGGAGTCCAGAGTGAGGAGGCACAAGC
G A P G G T S K G P A E E S R V R R H K
|861 |871
|2641 |2651 |2661 |2671 |2681 |2691
ACTCCTCTGAGTCGCCAGGGAGGGACAAGGGGAAATTGTCCAGGCTCAAACCTGCCCCGC
H S S E S P G R D K G K L S R L K P A P

881		891
2701	2711	2721
CGCCCCACCAGCAGCCTCTGCAGGGAAGGCTGGAGGAAAGCCCTCGCAGAGCCCAGGCC		
P P P P A A S A G K A G G K P S Q S P S		
901		911
2761	2771	2781
AGGAGGCGCGCGGGGAGGCAGTCCTGGGCGCAAAGACAAAAGCCACGAGTCTGGTTGATG		
Q E A A G E A V L G A K T K A T S L V D		
921		931
2821	2831	2841
CTGTGAACAGTGACGCTGCCAAGCCAGCCAGCCGGGAGAGGGCCTCAAAAAGCCCGTGC		
A V N S D A A K P S Q P G E G L K K P V		
941		951
2881	2891	2901
TCCCGGCCACTCCAAAGCCACAGTCCGCCAAGCCGTCGGGGACCCCATCAGCCAGCCC		
L P A T P K P Q S A K P S G T P I S P A		
961		971
2941	2951	2961
CCGTTCCCTCCACGTTGCCATCAGCATCCTCGGCCCTGGCAGGGGACCAGCCGTCTTCCA		
P V P S T L P S A S S A L A G D Q P S S		
981		991
3001	3011	3021
CGGCCTTTCATCCCTCTCATATCAACCCGAGTGCTCTTTCGAAAAACCCGCCAGCCTCCAG		
T A F I P L I S T R V S L R K T R Q P P		
1001		1011
3061	3071	3081
AGCGGATCGCCAGCGGCGCCATCACCAAGGGCGTGGTCCTGGACAGCACCGAGGCGCTGT		
E R I A S G A I T K G V V L D S T E A L		
1021		1031
3121	3131	3141
GCCTCGCCATCTCTAGGAACTCCGAGCAGATGGCCAGCCACAGCGCAGTGCTGGAGGCCG		
C L A I S R N S E Q M A S H S A V L E A		
1041		1051
3181	3191	3201
GCAAAAACCTCTACACGTTCTGCGTGAGCTATGTGGATTCCATCCAGCAAATGAGGAACA		
G K N L Y T F C V S Y V D S I Q Q M R N		
1061		1071

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

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

3361	3371	3381	3391	+11	+21
CGGTGAAGGAAATCAGTGACATAGTGCAGAGGTAGCAGCAGTCAGGGGTCAGGTGTCAGG					
S	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
GCATGCCAGGACCCGCCAGCCCCGCTCCCACCTAGTGCCCAGACTGAGCTCTCCAGGCC					

+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
AAGAACCGCATTTTCGGGAAGGGCATGCACGGGCATGCACACGGCTGGTCACTCTGCCCTC					

+571	+581	+591	+601	+611	+621
TGCTGCTGCCCCGGGTGGGGTGACTCGCCATTCCTCACGTGCAGGACAGCTCTTGATT					

+631	+641	+651	+661	+671	+681
TGGGTGAAAAACAGGGTGCTAAAGCCAACCAGCCTTTGGGTCCTGGGCAGGTGGGAGCTG					
+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
CAGTGGCTAGTGGGGTGAACAGCTGGTGCCAAATAGCCCCAGACTGGGCCCAGGCAGGTC					
+931	+941	+951	+961	+971	+981
TGCAAGGGCCCAGAGTGAACCGTCCTTTCACACATCTGGGTGCCCTGAAAGGGCCCTTCC					
+991	+1001	+1011	+1021	+1031	+1041
CCTCCCCCACTCCTCTAAGACAAAGTAGATTCTTACAAGGCCCTTTCCTTTGGAACAAGA					
+1051	+1061	+1071	+1081	+1091	+1101
CAGCCTTCACTTTTCTGAGTTCTTGAAGCATTTCAAAGCCCTGCCTCTGTGTAGCCGCC					
+1111	+1121	+1131	+1141	+1151	+1161
TGAGAGAGAATAGAGCTGCCACTGGGCACCTGCGCACAGGTGGGAGGAAAGGGCCTGGCC					
+1171	+1181	+1191	+1201	+1211	+1221
AGTCCTGGTCCTGGCTGCACTCTTGAAGTGGGCGAATGTCTTATTTAATTACCGTGAGTG					
+1231	+1241	+1251	+1261	+1271	+1281
ACATAGCCTCATGTTCTGTGGGGTTCATCAGGGAGGGTTAGGAAAACCACAAACGGAGCC					
+1291	+1301	+1311	+1321	+1331	+1341
CCTGAAAGCCTCACGTATTTACAGAGCACGCCTGCCATCTTCTCCCCGAGGCTGCCCCA					
+1351	+1361	+1371	+1381	+1391	+1401
GGCCGGAGCCCAGATACGGGGGCTGTGACTCTGGGCAGGGACCCGGGGTCTCCTGGACCT					
+1411	+1421	+1431	+1441	+1451	+1461
TGACAGAGCAGCTAACTCCGAGAGCAGTGGGCAGGTGGCCGCCCCTGAGGCTTCACGCCG					
+1471	+1481	+1491	+1501	+1511	+1521
GGAGAAGCCACCTTCCCACCCCTTCATACCGCCTCGTGCCAGCAGCCTCGCACAGGCCCT					
+1531	+1541	+1551	+1561	+1571	+1581

AGCTTTACGCTCATCACCTAACTTGTA CTTTATTTTCTGATAGAAATGGTTTCCTCTG

+1591	+1601	+1611	+1621	+1631	+1641
GATCGTTTTATGCGGTTCTTACAGCACATCACCTCTTTGCCCCGACGGCTGTGACGCAG					
+1651	+1661	+1671	+1681	+1691	+1701
CCGGAGGGAGGCACTAGTCACCGACAGCGGCCTTGAAGACAGAGCAAAGCGCCCACCCAG					
+1711	+1721	+1731	+1741	+1751	+1761
GTCCCCGACTGCCTGTCTCCATGAGGTACTGGTCCCTTCCCTTTGTTAACGTGATGTGC					
+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	
TCTGTCCTCTGTAGTATTTTTTAAATAAATCAGTGTTTACATTAGAA					

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