

## Supplementary material

CLUSTAL O(1.2.4) multiple sequence alignment

|      |        |              |   |     |
|------|--------|--------------|---|-----|
| SP   | P02458 | CO2A1_HUMAN  | MIRLGAPQTLVLL---TLLVAAVLRCQG-QDVQEAGSCVQDQGRYNDKDVWVKPEPCRICV   | 56  |
| SP   | P28481 | CO2A1_MOUSE  | MIRLGAPQSLVLL--TLLIAAVLRCQG-QDAQEAGSCLQNGQRYDKDKDVWKPSSCRICV  | 56  |
| SP   | Q91717 | CO2A1_XENLA  | MFSFVDSRTLVLFAATQVILLAVVRCQDEEDVLDTGSCVQHGRYSDDKDVWKPEPCQICV  | 60  |
| TR   | Q2LDA1 | Q2LDA1_DANRE | MFRL LDSRT LLLL VATHSVLLSLVR CQQEDD QEEFGGCVQD GQQYADRA VWKPEPCRV CV<br>*: : ::*: *: : :*: ** : * : *. *. *. *. * *: ****. *: **: * | 60  |
| <br> |        |              |   |     |
| SP   | P02458 | CO2A1_HUMAN  | CDTGTVLCCDDI ICEDVKDCLSPEIPFGECCPICPTDLAT-ASGQPGPKGQKGEPGD IKDI   | 115 |
| SP   | P28481 | CO2A1_MOUSE  | CDTGNVLCDDI ICED-PDCLNPEIPFGECCPICPADLAT-ASGKLGP KGQKGEPGD I RDI  | 114 |
| SP   | Q91717 | CO2A1_XENLA  | CDTGTVLCCDDI ICEESKD CPNAEIPFGECCPICPTEQSSTSSGQGV LKGQKGEPGD IKDV   | 120 |
| TR   | Q2LDA1 | Q2LDA1_DANRE | CDSGTVLCDEVICEDLNDCANPIISPGECCPICPADTDD-PIGSLGAKGQKGEPGDITDV<br>**:. *. *****.:***: ** . * *****.: : *. ***** **:                   | 119 |
| <br> |        |              |   |     |
| SP   | P02458 | CO2A1_HUMAN  | VGPKGPPPGPQG PAGEQGPRGDRGDKGEKGAPGPRGRDGEPGTPGNPGPPGPPGPPGGL  | 175 |
| SP   | P28481 | CO2A1_MOUSE  | IGPRGPPPGPQG PAGEQGPRGDRGDKGEKGAPGPRGRDGEPGTPGNPGPAGPPGPPGPPGGL   | 174 |
| SP   | Q91717 | CO2A1_XENLA  | LGPRGPPPGPQGPSGEQGSRG ERGDKGEKGAPGPRGRDGEPGTPGNPGPV--GPPGPPGGL  | 177 |
| TR   | Q2LDA1 | Q2LDA1_DANRE | VGPRGPAGPMGPPGEQGT RGERGA KGEKSGPGRGRDGEPGTPGNPGPPGPPGPN GPPGGL<br>: **. ** ** ** ***** **: ** *****:***** ***** ** *****           | 179 |
| <br> |        |              |   |     |
| SP   | P02458 | CO2A1_HUMAN  | G-GNFAAQ MAGGFDEKAGGAQLGVMQGPMGMPGRGPPG PAGAPGPQG FQGNPGEPEGEPG   | 234 |
| SP   | P28481 | CO2A1_MOUSE  | SAGNFAAQ MAGGYDEKAGGAQMGMVMQGPMGMPGRGPPG PAGAPGPQG FQGNPGEPEGEPG  | 234 |
| SP   | Q91717 | CO2A1_XENLA  | G-GNFAAQMTGGFDEKAGGAQMGMVMQGPMGMPGRGPPG PTGAPGPQG FQGNPGEPEGEPG   | 236 |
| TR   | Q2LDA1 | Q2LDA1_DANRE | G-GNFAAQ MAGGFDEKAGGAQMGMVMQGPMGMPGRGPPG PSGAPGPQG FQGNPETGEPEG<br>. *****.: **: *****.:***** *****.:***** ***** *                  | 238 |
| <br> |        |              |   |     |
| SP   | P02458 | CO2A1_HUMAN  | VSGPMGPRGPPGPPGKPGDDGEAGKPGKAGERGPPGPQGARGFP GT PGLPGVKGHRYPG   | 294 |
| SP   | P28481 | CO2A1_MOUSE  | VSGPMGPRGPPG PAGKPGDDGEAGKPGKSGERGLPG PQARGFP GT PGLPGVKGHRYPG  | 294 |
| SP   | Q91717 | CO2A1_XENLA  | AGGPMGPRGPPGPSGKPGDDGEAGKPGKSGERGPPGPQGARGFP GT PGLPGVKGHRYPG   | 296 |
| TR   | Q2LDA1 | Q2LDA1_DANRE | PAGALGPRGPPGPPGKPGSDGEAGKPGKAGERGPPGPQGARGFP GT PGLPGIKGHRHHPG  | 298 |

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SP|P02458|CO2A1_HUMAN|LDGAKGEAGAPGVKGESGSPGENSGSPGPMGPRGLPGERGRTGPAGAAGARGNDGQPGPAG|354
SP|P28481|CO2A1_MOUSE|LDGAKGEAGAPGVKGESGSPGENSGSPGPMGPRGLPGERGRTGPAGAAGARGNDGQPGPAG|354
SP|Q91717|CO2A1_XENLA|LDGAKGEAGAAGAKGEGGATGEAGSPGPMGPRGLPGERGRPGSSGAAGARGNDGLPGPAG|356
TR|Q2LDA1|Q2LDA1_DANRE|LDGAKGEAGAAGAKGEAGSNGESGAPGPMGPRGLPGERGRPGATGAAGARGNDGLPGPAG|358
***** * .***. *: ** *:***** * :***** *****

SP|P02458|CO2A1_HUMAN|PPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGGPRGEPGTPGSPGPAGASGNPGTDG|414
SP|P28481|CO2A1_MOUSE|PPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGSRGEPGNPGSPGPAGASGNPGTDG|414
SP|Q91717|CO2A1_XENLA|PPGPVGPAGAPGFPAGPSKGEAGPTGARGPEGAQGPRGESGTPGSPGPAGASGNPGTDG|416
TR|Q2LDA1|Q2LDA1_DANRE|PPGPVGPAGAPGFPSPGSKGEAGPTGARGPEGAQGPRGEAGTPGSPGPAGASGNPGTDG|418
***** .*****:***:***** ***** ** *.*****

SP|P02458|CO2A1_HUMAN|IPGAKGSAGAPGIAGAPGFPGRGPPGPQGATGPLGPKGQTGEPIAGFKGEQGPKEGEPG|474
SP|P28481|CO2A1_MOUSE|IPGAKGSAGAPGIAGAPGFPGRGPPGPQGATGPLGPKGQAGEPIAGFKGDQGPKEGETG|474
SP|Q91717|CO2A1_XENLA|IPGAKGSSGGPIAGAPGFPGRGPPGPQGATGPLGPKGQTGDPGVAGFKGEQGPKEIG|476
TR|Q2LDA1|Q2LDA1_DANRE|IPGAKGSAGASGIAGAPGFPGRGPPGPQGATGPLGPKGQSGDPGIPGFKGEAGPKGERG|478
*****:*. *****:***:*****:****:***** *

SP|P02458|CO2A1_HUMAN|PAGPQAGAPGAGEEGKRGARGEPPGVPIGPPGERGAPGNRGFPQGDLGAPKGPAGERG|534
SP|P28481|CO2A1_MOUSE|PAGPQAGAPGAGEEGKRGARGEPPGAGPIGPPGERGAPGNRGFPQGDLGAPKGPAGERG|534
SP|Q91717|CO2A1_XENLA|SAGPQAGAPGAGEEGKRGARGEPPGAAGPNPGERGAPGNRGFPQGDLGAPKGPAGERG|536
TR|Q2LDA1|Q2LDA1_DANRE|VLGPQGPSPGSGEEGKRGRGEPGSAGPLGPPGERGAPGNRGFPQGDLGAPKGPAGDRG|538
**** ***:***** *****. ** ***** *****:***

SP|P02458|CO2A1_HUMAN|PSGLAGPKGANGDPGRPGEPGLPGARGLTGPRPDAGPQGVGSPGAPGEDGRPGPPGPQG|594
SP|P28481|CO2A1_MOUSE|PSGLTGPKGANGDPGRPGEPGLPGARGLTGPRPDAGPQGVGSPGAPGEDGRPGPPGPQG|594
SP|Q91717|CO2A1_XENLA|VPGLGGPKGNGDPGRPGEPGLPGARGLTGPRPDAGPQGVGSPGASGEDGRPGPPGPQG|596
TR|Q2LDA1|Q2LDA1_DANRE|VPGLSGPKGGTGDPGRPGEPGLPGARGLTGPRPDAGAQQGVGATGAPGEDGRPGPPGPLG|598
** ****.***** *****:*** ***** *

SP|P02458|CO2A1_HUMAN|ARGQPGVMGFPGPKGANGEPGKAGEKGLPGAPGLRGLPGKDGETGAAGPPGPAGPAGERG|654
SP|P28481|CO2A1_MOUSE|ARGQPGVMGFPGPKGANGEPGKAGEKGLAGAPGLRGLPGKDGETGAAGPPGPSGPAGERG|654
SP|Q91717|CO2A1_XENLA|ARGQPGVMGFPGPKGANGEPGKAGEKGLVGAPGLRGLPGKDGETGSQGPNGPAGPAGERG|656
TR|Q2LDA1|Q2LDA1_DANRE|ARGQPGVMGFPGPKGANGEPGKPEKGLVGRGTGLRGLPGKDGETGPSGPPGPVAVGERG|658
***** ***** * ***** ** ** * .****

SP|P02458|CO2A1_HUMAN|EQGAPGPSGFQGLPGPPGPPGEGGKPGDQGVPEAGAPGLVGPRGERGFPGERGSPGAQG|714
SP|P28481|CO2A1_MOUSE|EQGAPGPSGFQGLPGPPGPPGEGGKQGDQGIPEAGAPGLVGPRGERGFPGERGSPGAQG|714
SP|Q91717|CO2A1_XENLA|EQGPPGPSGFQGLPGPPGSPGEGGKPGDQGVPEAGAPGLVGPRGERGFPGERGSSGPQG|716

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|    |        |              |                        |                           |                           |                                |                |
|----|--------|--------------|------------------------|---------------------------|---------------------------|--------------------------------|----------------|
| TR | Q2LDA1 | Q2LDA1_DANRE | EQGQPGPSGFQGLPGPTGAPGE | PGKPGDQGV                 | PEGGAAGPTGPRGERGF         | PGERGGAGPQG                    | 718            |
|    |        |              | ***                    | *****                     | * **                      | ***:***.* *                    | *****.* **     |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | LQGPRGLPGT             | PGTDGPKGASG               | PAGPPGAQGPPGLQ            | GMPGERGAAGIAGPKGDRGDVGEKG      | 774            |
| SP | P28481 | CO2A1_MOUSE  | LQGPRGLPGT             | PGTDGPKGAAGPDGPPGAQGPPGLQ | GMPGERGAAGIAGPKGDRGDVGEKG |                                | 774            |
| SP | Q91717 | CO2A1_XENLA  | LQGPRGLPGT             | PGTDGPKGASGPSGPNQAQGPPGLQ | GMPGERGAAGISGPKGDRGDTGEKG |                                | 776            |
| TR | Q2LDA1 | Q2LDA1_DANRE | LQGPRGLPGT             | PGTDGPKGAI                | GPAGAAGQGPPGLQ            | GMPGERGAVGISGAKGDRGDSGEKG      | 778            |
|    |        |              | *****                  | *****                     | ** *                      | *****.**:*                     | ***** ****     |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | PEGAPGKDGG             | RGLTGPIGPPG               | PAGANGEKGEV               | GPPGPAGSAGARGAPGERGETGPPGPAG   | 834            |
| SP | P28481 | CO2A1_MOUSE  | PEGAPGKDGG             | RGLTGPIGPPG               | PAGANGEKGEV               | GPPGPSGTGARGAPGERGETGPPGPAG    | 834            |
| SP | Q91717 | CO2A1_XENLA  | PEGASGKDG              | SRGLTGPIGPPG              | PAGPNGEKGESG              | PSGPPGIVGARGAPGDRGENGPPGPAG    | 836            |
| TR | Q2LDA1 | Q2LDA1_DANRE | PEGAPGKDG              | SRGLTGPIGPPG              | PSGPNKAKGETGPI            | GSIGAPGARGAPGDRGEIGAPGPAG      | 838            |
|    |        |              | ****                   | ****                      | *****.*                   | ** *** ** *                    | * *****.* ** * |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | FAGPPGADGQ             | PGAKGEQGEAGQ              | KGDAGAPGPQG               | PSGAPGPQGPTGVTGPKGARGAQGPPG    | 894            |
| SP | P28481 | CO2A1_MOUSE  | FAGPPGADGQ             | PGAKGDQGEAGQ              | KGDAGAPGPQG               | PSGAPGPQGPTGVTGPKGARGAQGPPG    | 894            |
| SP | Q91717 | CO2A1_XENLA  | FAGPPGADGQ             | SGLKGDQGESGQ              | KGDAGAPGPQG               | PSGAPGPQGPTGVFGPKGARGAQGPAG    | 896            |
| TR | Q2LDA1 | Q2LDA1_DANRE | FAGPPGADGQ             | PGNKGEQGESGQ              | KDGSAGGPQG                | PSGAPGPVGPTGVTGPKGARGAQGAPG    | 898            |
|    |        |              | *****                  | *                         | **.***.*                  | *****.*                        | ***** *        |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | ATGFPGAAGR             | VGPPGPNPGPP               | PGPSGKDGPKG               | ARGDSGPPGRAGEPGLQGPAGPPG       | 954            |
| SP | P28481 | CO2A1_MOUSE  | ATGFPGAAGR             | VGPPGANGNPG               | PAGPPGPAGKDG              | PKGVRGDSGPPGRAGDPGLQGPAGAPG    | 954            |
| SP | Q91717 | CO2A1_XENLA  | ATGFPGAAGR             | VGTPGPNNGPP               | PGPSAGKEGPKG              | VRGDAGPPGRAGDPGLQGAAGAPG       | 956            |
| TR | Q2LDA1 | Q2LDA1_DANRE | ATGFPGAAGR             | VGPPGPNNGPA               | AGPAGPSGKDG               | PKGVRGDAGPPGRAGDAGLRGPPGAPG    | 958            |
|    |        |              | *****                  | **                        | *****                     | ** *                           | :**.***.***.*  |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | EKGEPGDDG              | PSGAEGPPGPQ               | GLAGQRGIVGLP              | QRGGERGFPLPGPSGEPGKQGAPGASG    | 1014           |
| SP | P28481 | CO2A1_MOUSE  | EKGEPGDDG              | PSGLDGPPGPQ               | GLAGQRGIVGLP              | QRGGERGFPLPGPSGEPGKQGAPGASG    | 1014           |
| SP | Q91717 | CO2A1_XENLA  | EKGEPGEDG              | PSGPDGPPGPQ               | GLSGQRGIVGLP              | QRGGERGFPLPGPSGEPGKQGGPGSSG    | 1016           |
| TR | Q2LDA1 | Q2LDA1_DANRE | EKGEAGEDG              | PPGPDGPSGPA               | GLAGQRGIVGLP              | QRGGERGFPLPGPSGEPGKQAGPGSSG    | 1018           |
|    |        |              | ****                   | *                         | :*** *                    | :** ** *                       | :*****.***.*   |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | DRGPPGPVG              | PPGLTGPA                  | GEFGREGSPGADG             | PPGRDGAAGVKGDRGETGAVGAPGAPGPPG | 1074           |
| SP | P28481 | CO2A1_MOUSE  | DRGPPGPVG              | PPGLTGPA                  | GEFGREGSPGADG             | PPGRDGAAGVKGDRGETGALGAPGAPGPPG | 1074           |
| SP | Q91717 | CO2A1_XENLA  | DRGPPGPVG              | PPGLTGPSG                 | EPGREGNPGSDG              | PPGRDGATGIKGDRTGTGPLGAPGAPGAPG | 1076           |
| TR | Q2LDA1 | Q2LDA1_DANRE | DRGPPGPVG              | PPGLTGPA                  | GETGREGNPGSDG             | PPGRDGAAGVKGERGNTGPIGAPGAPGAPG | 1078           |
|    |        |              | *****                  | :**                       | ****.*                    | :*****.*                       | :**.***.*      |
|    |        |              |                        |                           |                           |                                |                |
| SP | P02458 | CO2A1_HUMAN  | SPGPAGPTG              | KQGDREAGAQ                | QPMGPSGPAGARGI            | QGPQGPGRGDKGEAGEPGERGLKGHRG    | 1134           |
| SP | P28481 | CO2A1_MOUSE  | SPGPAGPTG              | KQGDREAGAQ                | QPMGPSGPAGARGI            | AGPQGPGRGDKGESGEQGERGLKGHRG    | 1134           |

|    |        |              |   |      |
|----|--------|--------------|---|------|
| SP | Q91717 | CO2A1_XENLA  | APGSVGPTGKQGDRGESGPQGGLPGSPGAGARGLAGPQGPRGDKGEAGEAGERGQKGHRG  | 1136 |
| TR | Q2LDA1 | Q2LDA1_DANRE | APGSVGPIGKQGDRGENGPQGAGPPGPAGARGMVGPQGPRGDKGEAGEAGERGQKGHRG<br>: ** . ** ***** * *** ** *****: *****: ** *****  | 1138 |
|    |        |              |   |      |
| SP | P02458 | CO2A1_HUMAN  | FTGLQGLPGPPGPSGDQGASGPAGPSGPRGPPGPVGP   | 1194 |
| SP | P28481 | CO2A1_MOUSE  | FTGLQGLPGPPGPSGDQGASGPAGPSGPRGPPGPVGP   | 1194 |
| SP | Q91717 | CO2A1_XENLA  | FTGLQGLPGPPGSAGDQGATGPAGPAGPRGPPGPVGP   | 1196 |
| TR | Q2LDA1 | Q2LDA1_DANRE | FTGLQGLPGPPGPSGDQGAAGPAGPSGAKGPSGPVGP<br>***** *****:*****: * : ** *****:*****: ** *****                        | 1198 |
|    |        |              |   |      |
| SP | P02458 | CO2A1_HUMAN  | ETGPAGPPGNPGPPGPPGPGIDMSAFAGLGPREKGPDP  | 1254 |
| SP | P28481 | CO2A1_MOUSE  | ETGPVGGPGSPGPPGPPGPGIDMSAFAGLGPREKGPDP  | 1254 |
| SP | Q91717 | CO2A1_XENLA  | ETGPSGPPGQPPGPPGPPGPGIDMSAFAGLSQPEKGPDP   | 1253 |
| TR | Q2LDA1 | Q2LDA1_DANRE | ESGPVGGPNPGPPGPPGPPGPGIDMSAFAGLSQPEKGPDP<br>*: ** *****:*****:*****: * . * . :                                  | 1258 |
|    |        |              |   |      |
| SP | P02458 | CO2A1_HUMAN  | VDTLKSNNQIESIRSPESGRKNPARTCRDLKLCHPEWKS   | 1314 |
| SP | P28481 | CO2A1_MOUSE  | VDTLKSNNQIESIRSPDGRKNPARTCQDLKLCHPEWKS  | 1314 |
| SP | Q91717 | CO2A1_XENLA  | VEATLKSNNQIENIRSPDGTKKNPARTCRDLKLCHPEWKS  | 1313 |
| TR | Q2LDA1 | Q2LDA1_DANRE | VDTLKSINGQIEDIRSPDGRKNPARSCRDLKLCHPEWKS<br>*:*****:*.***.*****:*.*****:*****:*****:****.*: **:                  | 1318 |
|    |        |              |   |      |
| SP | P02458 | CO2A1_HUMAN  | CNMETGETCVYPNPANVPKKNWSSKSKEKKHIWFGETING  | 1374 |
| SP | P28481 | CO2A1_MOUSE  | CNMETGETCVYPNPATVPRKNWSSKSKEKKHIWFGETING  | 1374 |
| SP | Q91717 | CO2A1_XENLA  | CDMETGETCVYPNPSPKIPKKNWWSAKGKEKKHIWFGETING  | 1373 |
| TR | Q2LDA1 | Q2LDA1_DANRE | CNMETGETCVKPSSTPKIPRKNWWSKSKAQKHVWFGESMNGG<br>*:***** * . . :*:*****:*. * :*:*****:*****:***. * . . :*. * . : * | 1378 |
|    |        |              |   |      |
| SP | P02458 | CO2A1_HUMAN  | MTFLRLLSTEGSQNITYHCKNSIAYLDEAAGNLKKALLIQ  | 1434 |
| SP | P28481 | CO2A1_MOUSE  | MTFLRLLSTEGSQNITYHCKNSIAYLDEAAGNLKKALLIQ  | 1434 |
| SP | Q91717 | CO2A1_XENLA  | MTFLRLLSTDASQNITYHCKNSIAFMDEASGNLKKAVLLQ  | 1433 |
| TR | Q2LDA1 | Q2LDA1_DANRE | LNFLRLLSTEATQTITYHCKNSVAYMDQATGNLKKAILLQ<br>: . *****: . : *. *****:*. :*. :*. *****:*. :*****:***** * . *      | 1438 |
|    |        |              |   |      |
| SP | P02458 | CO2A1_HUMAN  | KDGCTKHTGKWGKTVIEWRSQKTSRLPIIDIAPMDIGGPE  | 1487 |
| SP | P28481 | CO2A1_MOUSE  | KDGCTKHTGKWGKTVIEWRSQKTSRLPIIDIAPMDIGGAE  | 1487 |
| SP | Q91717 | CO2A1_XENLA  | EDGCKKHTGKWSKTVIEWRTQKTSRLPIVDIAPMDIGGAD  | 1486 |
| TR | Q2LDA1 | Q2LDA1_DANRE | EDGCKKHTGQWAKTVIEYKTQKTSRLPIMDIAPMDIGGAD<br>:***.*****:*. *****:*****:***** :***** *****                        | 1491 |

Protein sequence alignment of COL2A1 protein. COL2A1 proteins show high conservation of the primary structure among distant species. The figure shows CLUSTAL OMEGA (1.2.4) multiple sequence alignment of the regions of COL2A1 protein of different organisms: Human, Mus musculus, Xenopus laevis, and Danio rerio [Uniprot identifiers: P02458, P28481, Q91717, Q2LDA, respectively]. Highlighted amino acids show the mutations found in Perthes patients. c.638 G > A (p.Gly213Asp) (exon 9); c.2014 G > T (p.Gly672Cys) (exon 31) (NM\_001844.5) [50]; c.1888 G > A (p.Gly630Ser) (exon 29) (NM\_033150.3) [51]; c.3665 G > A (p.Gly1170Ser) (exon 50) (NM\_033150.3) [48,49].

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