Supplementary Table 2: Sequence alignment of myosin II heavy chains

Entry	Entry name	Myosin HC	Acronym	Protein	Organism	Length	Gene
P35579	MYH9_HUMAN	Nonmuscle A	NMII-A	Myosin-9	*Homo sapiens* (Human)	1,960	*MYH9*
P35580	MYH10_HUMAN	Nonmuscle B	NMII-B	Myosin-10	*Homo sapiens* (Human)	1,976	*MYH10*
P35749	MYH11_HUMAN	Smooth		Myosin-2	*Homo sapiens* (Human)	1,972	*MYH11*
P10587	MYH11_CHICK*	Smooth		Myosin-2	*Gallus gallus* (Chicken)	1,979	*MYH11*
O08638	MYH11_MOUSE	Smooth		Myosin-2	*Mus musculus* (Mouse)	1,972	*MYH11*
Q7Z406	MYH14_HUMAN	Nonmuscle C	NMII-C	Myosin-14	*Homo sapiens* (Human)	1,995	*MYH14*
A0A125S9Y7	A0A125S9Y7_9ARAC	Skeletal		Myosin-2	*Aphonopelma* (Tarantula)	1,953	

The table shows the sequence alignment of the human myosin II heavy chains analyzed in this work. There are three isoforms of nonmuscle myosin: A, B and C, corresponding to genes *MYH9*, *MYH10* and *MYH14*, respectively. These and the smooth muscle gene (*MYH11*) were compared with the chicken smooth muscle sequence, which has close identity to the turkey sequence constituting the 10S structure analyzed in this paper. Sequences were obtained from UniProtKB (https://www.uniprot.org) and the multiple sequence alignment was done using CLUSTAL O(1.2.4). The sequence for the turkey (*Meleagris gallopavo*) gizzard myosin was obtained from GenBank XP_010717783.1, https://www.ncbi.nlm.nih.gov/protein/XP_010717783.1). The turkey sequence differs at only 18 sites from chicken, highlighted in green below: 12 residues with strong similarity [":"] and 4 residues with weak similarity ["."]) to the chicken sequence (P10587). Loops (P-loop, C-loop, CM loop, H-loop, loops 2 and 3), SH3, switches 1 and 2, relay, strut, SH1 and SH2 helices, converter, invariant proline, lever arm, segments 1, 2 and 3, rings 1, 2 and 3, skips, hinges 1 and 2, and tail piece are highlighted in yellow and labelled according to the nomenclature of Ref. 21 for A0A125S9Y7. Symbols in last row: "*" perfect alignment, ":" a site belonging to a group exhibiting strong similarity and "." a site belonging to a group exhibiting weak similarity. The location of disease-causing mutations in smooth and nonmuscle myosin II (Extended Data Table 2) are highlighted in the alignment in blue (deletions: ~~blue~~, duplications: blue) in their equivalent residues in the chicken (MYH11) sequence.

CLUSTAL O(1.2.4) multiple sequence alignment

```
                                                 ←-----------------------SH3-------------------
SP|P35579|MYH9HUMAN            ------------------M-AQQAADKYLYVDKNF------INNPLAQADWAAKKLVWVPS 36
SP|P35580|MYH10_HUMAN           -------------MAQRT-GLEDPERYLFVDRAV------IYNPATQADWTAKKLVWIPS 40
SP|P35749|MYH11_HUMAN           -------------MAQKG-QLSDDEKFLFVDKNF------INSPVAQADWAAKRLVWVPS 40
SP|P10587|MYH11_CHICK           --------------MSQK-PLSDDEKFLFVDKNF------VNNPLAQADWSAKKLVWVPS 39
SP|O08638|MYH11_MOUSE           -------------MAQKG-QLSDDEKFLFVDKNF------MNSPMAQADWVAKKLVWVPS 40
SP|Q7Z406|MYH14_HUMAN           MAAVTMSVPGRKAPPRPGPVPEAAQPFLFTPRGPSAGGGPGSGTSPQVEWTARRLVWVPS 60
TR|A0A125S9Y7|A0A125S9Y7_9ARAC -----------------MAEDPDPTEYLYISMEQ-------KRKDQTKPYDGKKMVWVAD 36
                                                          :*:                    : .:::**: .
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                               -------------SH3----------------------->
SP|P35579|MYH9_HUMAN           DKSGFEPASLKEEVGEEAIVELVENGKKVKVNKDDIQKMNPPKFSKVEDMAELTCLNEAS 96
SP|P35580|MYH10_HUMAN          ERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQKMNPPKFSKVEDMAELTCLNEAS 100
SP|P35749|MYH11_HUMAN          EKQGFEAASIKEEKGDEVVVELVENGKKVTVGKDDIQKMNPPKFSKVEDMAELTCLNEAS 100
SP|P10587|MYH11_CHICK          EKHGFEAASIKEEKGDEVTVELQENGKKVTLSKDDIQKMNPPKFSKVEDMAELTCLNEAS 99
SP|O08638|MYH11_MOUSE          EKQGFEAASIKEEKGDEVVVELVENGKKVTVGKDDIQKMNPPKFSKVEDMAELTCLNEAS 100
SP|Q7Z406|MYH14_HUMAN          ELHGFEAAALRDEGEEEAEVELAESGRRLRLPRDQIQRMNPPKFSKAEDMAELTCLNEAS 120
TR|A0A125S9Y7|A0A125S9Y7_9ARAC EKEGYLLGLIKSTQGDICTVDIEGQ-ESRQVKKDLLQQVNPPKYEKCEDMSNLTYLNDAS 95
                               :  *:  . ::.   :   *::  . .   : :* :*::****:.* ***::** **:**

SP|P35579|MYH9_HUMAN           VLHNLKERYYSGLIYTYSGLFCVVINPYKNLPIYSEEIVEMYKGKKRHEMPPHIYAITDT 156
SP|P35580|MYH10_HUMAN          VLHNLKDRYYSGLIYTYSGLFCVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISES 160
SP|P35749|MYH11_HUMAN          VLHNLRERYFSGLIYTYSGLFCVVVNPYKHLPIYSEKIVDMYKGKKRHEMPPHIYAIADT 160
SP|P10587|MYH11_CHICK          VLHNLRERYFSGLIYTYSGLFCVVINPYKQLPIYSEKIIDMYKGKKRHEMPPHIYAIADT 159
SP|O08638|MYH11_MOUSE          VLHNLRERYFSGLIYTYSGLFCVVVNPYKYLPIYSEKIVDMYKGKKRHEMPPHIYAIADT 160
SP|Q7Z406|MYH14_HUMAN          VLHNLRERYYSGLIYTYSGLFCVVINPYKQLPIYTEAIVEMYRGKKRHEVPPHVYAVTEG 180
TR|A0A125S9Y7|A0A125S9Y7_9ARAC VLHNLKQRYYANLIYTYSGLFCVAINPYKRFPIYTNRTVQIYKGRRRTEVPPHLFAISDG 155
                               *****::**::.***********.:**** :***::  :::*:*::* *:***::*:::

                                                                    <---25-50 kDa loop--->
SP|P35579|MYH9_HUMAN           AYRSMMQDREDQSILCTGESGAGKTENTKKVIQYLAYVASSHKSKKD---Q--------GE 206
SP|P35580|MYH10_HUMAN          AYRCMLQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHNIP--------GE 213
SP|P35749|MYH11_HUMAN          AYRSMLQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKKDTSIT--------GE 213
SP|P10587|MYH11_CHICK          AYRSMLQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKKDTSITQGPSFSYGE 219
SP|O08638|MYH11_MOUSE          AYRSMLQDREDQSILCTGESGAGKTENTQKVIQYLAVVASSHKGKKDSSIT--------GE 213
SP|Q7Z406|MYH14_HUMAN          AYRSMLQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSPKGRKEPGVP--------GE 233
TR|A0A125S9Y7|A0A125S9Y7_9ARAC AYSAMLANRENQSMLITGESGAGKTENTKKVIAYYANVGAATPKPGK---EAPTKEKKAT 212
                               ** .*: :**:**:* ************:*** * * *.::     .           .
                                                                         <-----Loop 1--->
                                                                           25/50 Junction
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                                                   ←Switch 1→
SP|P35579|MYH9_HUMAN           LERQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVNGYIVGANIETYLLEKSRAIR 266
SP|P35580|MYH10_HUMAN          LERQLLQANPILESFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEKSRAVR 273
SP|P35749|MYH11_HUMAN          LEKQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEKSRAIR 273
SP|P10587|MYH11_CHICK          LEKQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEKSRAIR 279
SP|O08638|MYH11_MOUSE          LEKQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEKSRAIR 273
SP|Q7Z406|MYH14_HUMAN          LERQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVAGYIVGANIETYLLEKSRAIR 293
TR|A0A125S9Y7|A0A125S9Y7_9ARAC LEDQVVQTNPVLEAFGNAKTVRNDNSSRFGKFIRIHFGPMGKLAGADIETYLLEKARVIS 272
                               ** *::*:**:**:*******:*************:*.  * :.**:********:*.:

                                                    ←-----------I-loop------------→
SP|P35579|MYH9_HUMAN           QAKEERTFHIFYYLLSGAGEHLKTDLLLE-PYNKYRFLSNGHVTIPGQQDKDMFQETMEA 325
SP|P35580|MYH10_HUMAN          QAKDERTFHIFYQLLSGAGEHLKSDLLLE-GFNNYRFLSNGYIPIPGQQDKDNFQETMEA 332
SP|P35749|MYH11_HUMAN          QARDERTFHIFYYMIAGAKEKMRSDLLLE-GFNNYTFLSNGFVPIPAAQDDEMFQETVEA 332
SP|P10587|MYH11_CHICK          QAKDERTFHIFYYLIAGASEQMRNDLLLE-GFNNYTFLSNGHVPIPAQQDDEMFQETLEA 338
SP|O08638|MYH11_MOUSE          QARDERTFHIFYYLLAGAKEKMKSDLLLE-SFNSYTFLSNGFVPIPAAQDDEMFQETLEA 332
SP|Q7Z406|MYH14_HUMAN          QAKDECSFHIFYQLLGGAGEQLKADLLLE-PCSHYRFLTNGPSSSPGQ-ERELFQETLES 351
TR|A0A125S9Y7|A0A125S9Y7_9ARAC QQTLERSYHIFYQLMSGGIENLKADLLLSDDIYDYHFVSQGKIEIPGVDDAEELRLTDTA 332
                               *   * ::**** ::.*. *::: ****.     * *:::*    *.  : : :: *  :

                                                       ←------C-loop------→
SP|P35579|MYH9_HUMAN           MRIMGIPEEEQMGLLRVISGVLQLGNIVFKKERNTDQASMPDNTAAQKVSHLLGINVTDF 385
SP|P35580|MYH10_HUMAN          MHIMGFSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKLCHLLGMNVMEF 392
SP|P35749|MYH11_HUMAN          MAIMGFSEEEQLSILKVVSSVLQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDF 392
SP|P10587|MYH11_CHICK          MTIMGFTEEEQTSILRVVSSVLQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDF 398
SP|O08638|MYH11_MOUSE          MSIMGFNEEEQLAILKVVSSVLQLGNIVFKKERNTDQASMPDNTAAQKVCHLVGINVTDF 392
SP|Q7Z406|MYH14_HUMAN          LRVLGFSHEEIISMLRMVSAVLQFGNIALKRERNTDQATMPDNTAAQKLCRLLGLGVTDF 411
TR|A0A125S9Y7|A0A125S9Y7_9ARAC FDILGFSHEYKTDVYKITASCMHLGEMKFKQRPREEQAEADGTEEGERVAHLLGVNAADL 392
                               : ::*: .*    : :: :. :::*:: :*:. . :**    .  .:::.:*:*:.. ::
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                                    ←---CM-loop---→
SP|P35579|MYH9_HUMAN           TRGILTPRIKVGRDYVQKAQTKEQADFAIEALAKATYERMFRWLVLRINKALDKTKRQGA 445
SP|P35580|MYH10_HUMAN          TRAILTPRIKVGRDYVQKAQTKEQADFAVEALAKATYERLFRWLVHRINKALDRTKRQGA 452
SP|P35749|MYH11_HUMAN          TRSILTPRIKVGRDVVQKAQTKEQADFAVEALAKATYERLFRWILTRVNKALDKTHRQGA 452
SP|P10587|MYH11_CHICK          TRSILTPRIKVGRDVVQKAQTKEQADFAIEALAKAKFERLFRWILTRVNKALDKTKRQGA 458
SP|O08638|MYH11_MOUSE          TRAILTPRIKVGRDVVQKAQTKEQADFAIEALAKATYERLFRWILSRVNKALDKTHRQGA 452
SP|Q7Z406|MYH14_HUMAN          SRALLTPRIKVGRDYVQKAQTKEQADFALEALAKATYERLFRWLVLRLNRALDRSPRQGA 471
TR|A0A125S9Y7|A0A125S9Y7_9ARAC YKNLVKPKIKVGNEMVTQGRNATQVSYSVGGLAKAMFDRTFKWLVKRLNETLDTK-QKRQ 451
                                : ::.*:****.: * :.:.  *..::: .**** ::* *:*:: *:*.:** . ::

                                     ←switch 2→                   ←----------Relay-------------
SP|P35579|MYH9_HUMAN           SFIGILDIAGFEIFDLNSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG 505
SP|P35580|MYH10_HUMAN          SFIGILDIAGFEIFELNSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG 512
SP|P35749|MYH11_HUMAN          SFLGILDIAGFEIFEVNSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG 512
SP|P10587|MYH11_CHICK          SFLGILDIAGFEIFEINSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG 518
SP|O08638|MYH11_MOUSE          SFLGILDIAGFEIFEVNSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG 512
SP|Q7Z406|MYH14_HUMAN          SFLGILDIAGFEIFQLNSFEQLCINYTNEKLQQLFNHTMFVLEQEEYQREGIPWTFLDFG 531
TR|A0A125S9Y7|A0A125S9Y7_9ARAC YFIGVLDIAGFEIFDYNGFEQLCINFTNEKLQQFFNHHMFVLEQEEYKREGIDWVFIDFG 511
                                *:*:*********: *.*******:*******:*** **:******:**** * *:***

                               ->         ←-----------H-loop---------------→       <-Loop 3 ---
SP|P35579|MYH9_HUMAN           LDLQPCIDLIEKPAGPPGILALLDEECWFPKATDKSFVEKVMQE-QGTHPKFQKPKQL-- 562
SP|P35580|MYH10_HUMAN          LDLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQE-QGSHSKFQKPRQL-- 569
SP|P35749|MYH11_HUMAN          LDLQPCIELIERPNNPPGVLALLDEECWFPKATDKSFVEKLCTE-QGSHPKFQKPKQL-- 569
SP|P10587|MYH11_CHICK          LDLQPCIELIERPTNPPGVLALLDEECWFPKATDTSFVEKLIQE-QGNHAKFQKSKQL-- 575
SP|O08638|MYH11_MOUSE          LDLQPSIELIERPNNPPGVLALLDEECWFPKATDKSFVEKLCSE-QGNHPKFQKPKQL-- 569
SP|Q7Z406|MYH14_HUMAN          LDLQPCIDLIERPANPPGLLALLDEECWFPKATDKSFVEKVAQE-QGGHPKFQRPRHL-- 588
TR|A0A125S9Y7|A0A125S9Y7_9ARAC LDLAACIELIEKP---MGILSILEEESMFPKATDKSFQDKLNANHLGKSPNFVKPKPPKP 568
                               ***  .*:***:*    *:*::*:**. ******.:* :*:  :  *   :* : :
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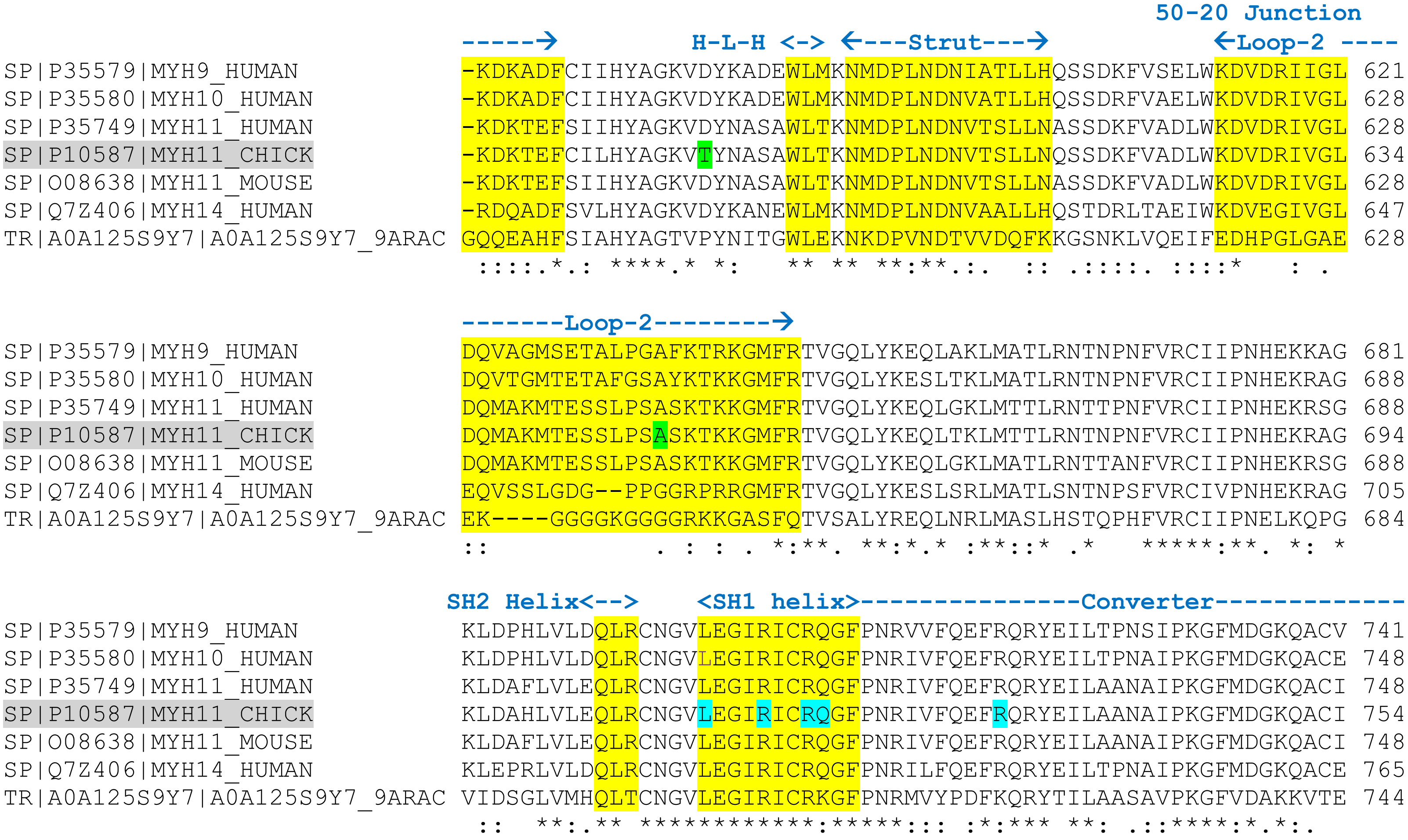

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                                                                                              50-20 Junction
                               -----→          H-L-H <-> ←---Strut---→            ←Loop-2 ----
SP|P35579|MYH9_HUMAN           -KDKADFCIIHYAGKVDYKADEWLMKNMDPLNDNIATLLHQSSDKFVSELWKDVDRIIGL 621
SP|P35580|MYH10_HUMAN          -KDKADFCIIHYAGKVDYKADEWLMKNMDPLNDNVATLLHQSSDRFVAELWKDVDRIVGL 628
SP|P35749|MYH11_HUMAN          -KDKTEFSIIHYAGKVDYNASAWLTKNMDPLNDNVTSLLNASSDKFVADLWKDVDRIVGL 628
SP|P10587|MYH11_CHICK          -KDKTEFCILHYAGKVTYNASAWLTKNMDPLNDNVTSLLNQSSDKFVADLWKDVDRIVGL 634
SP|O08638|MYH11_MOUSE          -KDKTEFSIIHYAGKVDYNASAWLTKNMDPLNDNVTSLLNASSDKFVADLWKDVDRIVGL 628
SP|Q7Z406|MYH14_HUMAN          -RDQADFSVLHYAGKVDYKANEWLMKNMDPLNDNVAALLHQSTDRLTAEIWKDVEGIVGL 647
TR|A0A125S9Y7|A0A125S9Y7_9ARAC GQQEAHFSIAHYAGTVPYNITGWLEKNKDPVNDTVVDQFKKGSNKLVQEIFEDHPGLGAE 628
                                ::::.*.: ****.* *:   ** ** **:**.:.  :: .::::. ::::*   : .

                               -------Loop-2--------→
SP|P35579|MYH9_HUMAN           DQVAGMSETALPGAFKTRKGMFRTVGQLYKEQLAKLMATLRNTNPNFVRCIIPNHEKKAG 681
SP|P35580|MYH10_HUMAN          DQVTGMTETAFGSAYKTKKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAG 688
SP|P35749|MYH11_HUMAN          DQMAKMTESSLPSASKTKKGMFRTVGQLYKEQLGKLMTTLRNTTPNFVRCIIPNHEKRSG 688
SP|P10587|MYH11_CHICK          DQMAKMTESSLPSASKTKKGMFRTVGQLYKEQLTKLMTTLRNTNPNFVRCIIPNHEKRAG 694
SP|O08638|MYH11_MOUSE          DQMAKMTESSLPSASKTKKGMFRTVGQLYKEQLGKLMATLRNTTANFVRCIIPNHEKRSG 688
SP|Q7Z406|MYH14_HUMAN          EQVSSLGDG--PPGGRPRRGMFRTVGQLYKESLSRLMATLSNTNPSFVRCIVPNHEKRAG 705
TR|A0A125S9Y7|A0A125S9Y7_9ARAC EK----GGGGKGGGGRKKGASFQTVSALYREQLNRLMASLHSTQPHFVRCIIPNELKQPG 684
                               ::           . : : . *:**. **:*.* :**::* .*   *****:**. *: *

                              SH2 Helix<-->    <SH1 helix>---------------Converter-------------
SP|P35579|MYH9_HUMAN           KLDPHLVLDQLRCNGVLEGIRICRQGFPNRVVFQEFRQRYEILTPNSIPKGFMDGKQACV 741
SP|P35580|MYH10_HUMAN          KLDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTPNAIPKGFMDGKQACE 748
SP|P35749|MYH11_HUMAN          KLDAFLVLEQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILAANAIPKGFMDGKQACI 748
SP|P10587|MYH11_CHICK          KLDAHLVLEQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILAANAIPKGFMDGKQACI 754
SP|O08638|MYH11_MOUSE          KLDAFLVLEQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILAANAIPKGFMDGKQACI 748
SP|Q7Z406|MYH14_HUMAN          KLEPRLVLDQLRCNGVLEGIRICRQGFPNRILFQEFRQRYEILTPNAIPKGFMDGKQACE 765
TR|A0A125S9Y7|A0A125S9Y7_9ARAC VIDSGLVMHQLTCNGVLEGIRICRKGFPNRMVYPDFKQRYTILAASAVPKGFVDAKKVTE 744
                                ::  **:.** ************:*****::: :*:*** **: .::****:*.*:.
```

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                               ------------------------Converter--→  <--------Lever arm-------
                                                           Pliant |
SP|P35579|MYH9_HUMAN           LMIKALELDSNLYRIGQSKVFFRAGVLAHLEEERDLKITDVIIGFQACCRGYLARKAFAK 801
SP|P35580|MYH10_HUMAN          RMIRALELDPNLYRIGQSKIFFRAGVLAHLEEERDLKITDIIIFFQAVCRGYLARKAFAK 808
SP|P35749|MYH11_HUMAN          LMIKALELDPNLYRIGQSKIFFRTGVLAHLEEERDLKITDVIMAFQAMCRGYLARKAFAK 808
SP|P10587|MYH11_CHICK          LMIKALELDPNLYRIGQSKIFFRTGVLAHLEEERDLKITDVIIAFQAQCRGYLARKAFAK 814
SP|O08638|MYH11_MOUSE          LMIKALELDPNLYRIGQSKIFFRTGVLAHLEEERDLKITDVIMAFQAMCRGYLARKAFTK 808
SP|Q7Z406|MYH14_HUMAN          KMIQALELDPNLYRVGQSKIFFRAGVLAQLEEERDLKVTDIIVSFQAAARGYLARRAFQK 825
TR|A0A125S9Y7|A0A125S9Y7_9ARAC AVLGAIQLDANDYRLGNTKVFFRAGVLGRLEEMRDDRLGKIVTWLQAWIRWYLSKKEFKK 804
                                :: *::** * **:*::*:***:***.:*** ** :: .::  :**  * **::: * *

                                                                  ←------Segment 1------------
                               -----Lever arm--------------------→
                                               Invariant proline |
SP|P35579|MYH9_HUMAN           RQQQLTAMKVLQRNCAAYLKLRNWQWWRLFTKVKPLLQVSRQEEEMMAKEEELVKVREKQ 861
SP|P35580|MYH10_HUMAN          KQQQLSALKVLQRNCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVKEKQ 868
SP|P35749|MYH11_HUMAN          RQQQLTAMKVIQRNCAAYLKLRNWQWWRLFTKVKPLLQVTRQEEEMQAKEDELQKTKERQ 868
SP|P10587|MYH11_CHICK          RQQQLTAMKVIQRNCAAYLKLRNWQWWRLFTKVKPLLQVTRQEEEMQAKDEELQRTKERQ 874
SP|O08638|MYH11_MOUSE          RQQQLTAMKVIQRNCAAYLKLRNWQWWRLFTKVKPLLQVTRQEEEMQAKEEEMQKITERQ 868
SP|Q7Z406|MYH14_HUMAN          RQQQQSALRVMQRNCAAYLKLRHWQWWRLFTKVKPLLQVTRQDEVLQARAQELQKVQELQ 885
TR|A0A125S9Y7|A0A125S9Y7_9ARAC LQEQRVALLVIQRNLRKFLTLRNWLWYKLYIKVKPLLTMAKVEDELKALEEKLKKALESL 864
                                *:*  *: *:***   :*.**:* *:::: ****** ::: :: : *  ::: :  *

                               ----------------------------Segment 1---------------------------
                               ------------------S1------------→←---------------S2--------------
                                                             ←-Ring 1 -→               ←------
SP|P35579|MYH9_HUMAN           LAAENRLTEMETLQSQLMAEKLQLQEQLQAETELCAEAEELRARLTAKKQELEEICHDLE 921
SP|P35580|MYH10_HUMAN          TKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEMRARLAAKKQELEEILHDLE 928
SP|P35749|MYH11_HUMAN          QKAENELKELEQKHSQLTEEKNLLQEQLQAETELYAEAEEMRVRLAAKKQELEEILHEME 928
SP|P10587|MYH11_CHICK          QKAEAELKELEQKHTQLCEEKNLLQEKLQAETELYAEAEEMRVRLAAKKQELEEILHEME 934
SP|O08638|MYH11_MOUSE          QKAETELKELEQKHTQLAEEKTLLQEQLQAETELYAESEEMRVRLAAKKQELEEILHEME 928
SP|Q7Z406|MYH14_HUMAN          QQSAREVGELQGRVAQLEEERARLAEQLRAEAELCAEAEETRGRLAARKQELELVVSELE 945
TR|A0A125S9Y7|A0A125S9Y7_9ARAC EKEEKVRKDIEVQNVKLLQEKNDLFLQLESERSGAGDVEERLTKAISMKNDLEGQVQELQ 924
                                       :::    :*  *:  *  :*.:* .  .: **   :  : *::**    :::
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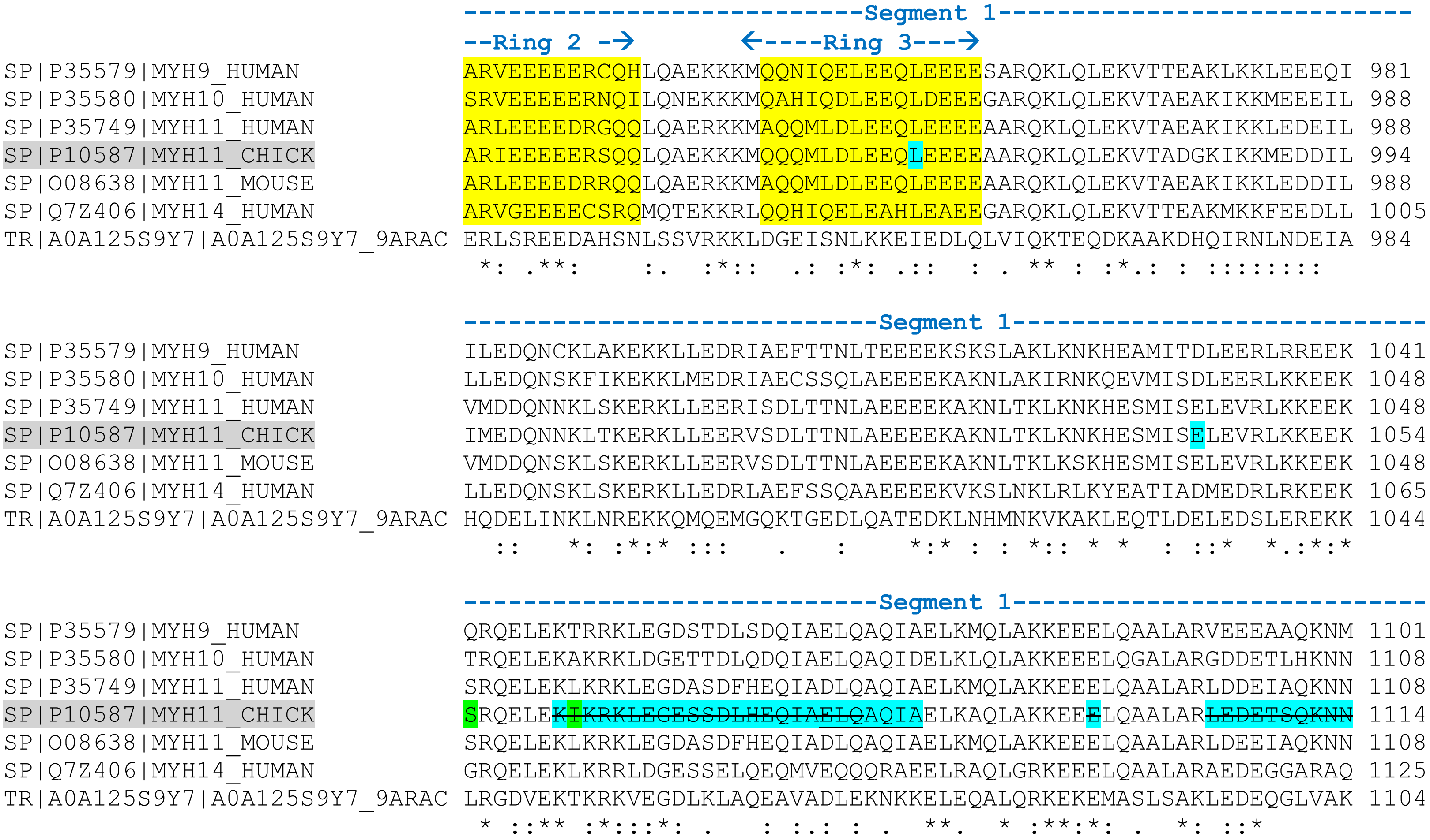

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                               ----------------------------Segment 1----------------------------
                               --Ring 2 -→        ←----Ring 3---→
SP|P35579|MYH9_HUMAN           ARVEEEEERCQHLQAEKKKMQQNIQELEEQLEEEESARQKLQLEKVTTEAKLKKLEEEQI 981
SP|P35580|MYH10_HUMAN          SRVEEEEERNQILQNEKKKMQAHIQDLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEIL 988
SP|P35749|MYH11_HUMAN          ARLEEEEDRGQQLQAERKKMAQQMLDLEEQLEEEEAARQKLQLEKVTAEAKIKKLEDEIL 988
SP|P10587|MYH11_CHICK          ARIEEEEERSQQLQAEKKKMQQQMLDLEEQLEEEEAARQKLQLEKVTADGKIKKMEDDIL 994
SP|O08638|MYH11_MOUSE          ARLEEEEDRRQQLQAERKKMAQQMLDLEEQLEEEEAARQKLQLEKVTAEAKIKKLEDDIL 988
SP|Q7Z406|MYH14_HUMAN          ARVGEEEECSRQMQTEKKRLQQHIQELEAHLEAEEGARQKLQLEKVTTEAKMKKFEEDLL 1005
TR|A0A125S9Y7|A0A125S9Y7_9ARAC ERLSREEDAHSNLSSVRKKLDGEISNLKKEIEDLQLVIQKTEQDKAAKDHQIRNLNDEIA 984
                                *: .**:    :.  :*::  .: :*: .::  : . ** : :*.: : ::::::::

                               ----------------------------Segment 1----------------------------
SP|P35579|MYH9_HUMAN           ILEDQNCKLAKEKKLLEDRIAEFTTNLTEEEEKSKSLAKLKNKHEAMITDLEERLRREEK 1041
SP|P35580|MYH10_HUMAN          LLEDQNSKFIKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEERLKKEEK 1048
SP|P35749|MYH11_HUMAN          VMDDQNNKLSKERKLLEERISDLTTNLAEEEEKAKNLTKLKNKHESMISELEVRLKKEEK 1048
SP|P10587|MYH11_CHICK          IMEDQNNKLTKERKLLEERVSDLTTNLAEEEEKAKNLTKLKNKHESMISELEVRLKKEEK 1054
SP|O08638|MYH11_MOUSE          VMDDQNSKLSKERKLLEERVSDLTTNLAEEEEKAKNLTKLKSKHESMISELEVRLKKEEK 1048
SP|Q7Z406|MYH14_HUMAN          LLEDQNSKLSKERKLLEDRLAEFSSQAAEEEEKVKSLNKLRLKYEATIADMEDRLRKEEK 1065
TR|A0A125S9Y7|A0A125S9Y7_9ARAC HQDELINKLNREKKQMQEMGQKTGEDLQATEDKLNHMNKVKAKLEQTLDELEDSLEREKK 1044
                                 ::   *: :*:* :::   .   :    *:* : : *:: * *  : ::*  *.:*:*

                               ----------------------------Segment 1----------------------------
SP|P35579|MYH9_HUMAN           QRQELEKTRRKLEGDSTDLSDQIAELQAQIAELKMQLAKKEEELQAALARVEEEAAQKNM 1101
SP|P35580|MYH10_HUMAN          TRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQLAKKEEELQGALARGDDETLHKNN 1108
SP|P35749|MYH11_HUMAN          SRQELEKLKRKLEGDASDFHEQIADLQAQIAELKMQLAKKEEELQAALARLDDEIAQKNN 1108
SP|P10587|MYH11_CHICK          SRQELEKIKRKLEGESSDLHEQIAELQAQIAELKAQLAKKEEELQAALARLEDETSQKNN 1114
SP|O08638|MYH11_MOUSE          SRQELEKLKRKLEGDASDFHEQIADLQAQIAELKMQLAKKEEELQAALARLDEEIAQKNN 1108
SP|Q7Z406|MYH14_HUMAN          GRQELEKLKRRLDGESSELQEQMVEQQQRAEELRAQLGRKEEELQAALARAEDEGGARAQ 1125
TR|A0A125S9Y7|A0A125S9Y7_9ARAC LRGDVEKTKRKVEGDLKLAQEAVADLEKNKKELEQALQRKEKEMASLSAKLEDEQGLVAK 1104
                                * ::** :*:::*: .   : :.: : .  **.  * :**:*: .  *: ::*
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                               -----------------------------Segment 1-----------------------------
SP|P35579|MYH9_HUMAN           ALKKIRELESQISELQEDLESERASRNKAEKQKRDLGEELEALKTELEDTLDSTAAQQEL 1161
SP|P35580|MYH10_HUMAN          ALKVVRELQAQIAELQEDFESEKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQEL 1168
SP|P35749|MYH11_HUMAN          ALKKIRELEGHISDLQEDLDSERAARNKAEKQKRDLGEELEALKTELEDTLDSTATQQEL 1168
SP|P10587|MYH11_CHICK          ~~ALKKIRELESHISDLQEDLESEKAARNKAEKQKRDLSEELEALKTELEDTLDTTATQQEL~~ 1174
SP|O08638|MYH11_MOUSE          ALKKIRELEGHISDLQEDLDSERAARNKAEKQKRDLGEELEALKTELEDTLDSTATQQEL 1168
SP|Q7Z406|MYH14_HUMAN          LLKSLREAQAALAEAQEDLESERVARTKAEKQRRDLGEELEALRGELEDTLDSTNAQQEL 1185
TR|A0A125S9Y7|A0A125S9Y7_9ARAC LQKQIKELQARIEELEEELEAERQARAKAEKQRADLAREIEELSERLEEAGGATSAQVEL 1164
                                 * ::* :. : : :*::::*: :* *****: **..*:* *  .**:: .:* :* **

                              →←--------------Segment 2--------------------------------------
                       Hinge 1 |                      Skip 1 |
SP|P35579|MYH9_HUMAN           RSKREQEVNILKKTLEEEAKTHEAQIQEMRQKHSQAVEELAEQLEQTKRVKANLEKAKQT 1221
SP|P35580|MYH10_HUMAN          RTKREQEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKRFKANLEKNKQG 1228
SP|P35749|MYH11_HUMAN          RAKREQEVTVLKKALDEETRSHEAQVQEMRQKHAQAVEELTEQLEQFKRAKANLDKNKQT 1228
SP|P10587|MYH11_CHICK          ~~R~~AKREQEVTVLKRALEEETRTHEAQVQEMRQKHTQAVEELTEQ~~LEQ~~FKRAKANLDKTKQT 1234
SP|O08638|MYH11_MOUSE          RAKREQEVTVLKKALDEETRSHEAQVQEMRQKHTQAVEELTEQLEQFKRAKANLDKSKQT 1228
SP|Q7Z406|MYH14_HUMAN          RSKREQEVTELKKTLEEETRIHEAAVQELRQRHGQALGELAEQLEQARRGKGAWEKTRLA 1245
TR|A0A125S9Y7|A0A125S9Y7_9ARAC NKRREAEMAKLRRDLEESNIQHEQTLANLRKKHNDVVAELSEQIDQLNKHKARLEKEKAQ 1224
                               . :** *:  *:: *:*.   **  : ::*::*  .: **:**::* .: *.  :* :

                                -----------------------------Segment 2--------------------------
SP|P35579|MYH9_HUMAN           LENERGELANEVKVLLQGKGDSEHKRKKVEAQLQELQVKFNEGERVRTELADKVTKLQVE 1281
SP|P35580|MYH10_HUMAN          LETDNKELACEVKVLQQVKAESEHKRKKLDAQVQELHAKVSEGDRLRVELAEKASKLQNE 1288
SP|P35749|MYH11_HUMAN          LEKENADLAGELRVLGQAKQEVEHKKKKLEAQVQELQSKCSDGERARAELNDKVHKLQNE 1288
SP|P10587|MYH11_CHICK          LEKDNADLANEIRSLSQAKQDVEHKKKKLEVQLQDLQSKYSDGERVRTELNEKVHKLQIE 1294
SP|O08638|MYH11_MOUSE          LEKENADLAGELRVLGQAKQEVEHKKKKLEVQLQDLQSKCSDGERARAELSDKVHKLQNE 1288
SP|Q7Z406|MYH14_HUMAN          LEAEVSELRAELSSLQTARQEGEQRRRRLELQLQEVQGRAGDGERARAEAAEKLQRAQAE 1305
TR|A0A125S9Y7|A0A125S9Y7_9ARAC MKGELDDVRSSVDHVNKEKANAEKQAKQLEMQLTELQGKMDEAHRSLGDFDAAKKRLTVE 1284
                               :: :  ::  .:  :   : : *:: :::: *: ::: : .:..*   :      :   *
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                               ----------------------------Segment 2---------------------------
SP|P35579|MYH9_HUMAN           LDNVTGLLSQSDSKSSKLTKDFSALESQLQDTQELLQEENRQKLSLSTKLKQVEDEKNSF 1341
SP|P35580|MYH10_HUMAN          LDNVSTLLEEAEKKGIKFAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSL 1348
SP|P35749|MYH11_HUMAN          VESVTGMLNEAEGKAIKLAKDVASLSSQLQDTQELLQEETRQKLNVSTKLRQLEEERNSL 1348
SP|P10587|MYH11_CHICK          VENVTSLLNEAESKNIKLTKDVATLGSQLQDTQELLQEETRQKLNVTTKLRQLEDDKNSL 1354
SP|O08638|MYH11_MOUSE          VESVTGMLNEAEGKAIKLAKDVASLGSQLQDTQELLQEETRQKLNVSTKLRQLEDERNSL 1348
SP|Q7Z406|MYH14_HUMAN          LENVSGALNEAESKTIRLSKELSSTEAQLHDAQELLQEETRAKLALGSRVRAMEAEAAGL 1365
TR|A0A125S9Y7|A0A125S9Y7_9ARAC NTELTRQLEDAESQVSQLSKLKTSLQTQLEDTKRMADEESRERATAMGKFRSVEHDLDSL 1344
                                 .::  *.::: :  :::*  ::  :**.*::.: :**.* :     :.: :* :  .:

                               ----------------------------Segment 2----------------------------
SP|P35579|MYH9_HUMAN           REQLEEEEEAKHNLEKQIATLHAQVADMKKKMED-SVGCLETAEEVKRKLQKDLEGLSQR 1400
SP|P35580|MYH10_HUMAN          QEQQEEEEEARKNLEKQVLALQSQLADTKKKVDD-DLGTIESLEEAKKKLLKDAEALSQR 1407
SP|P35749|MYH11_HUMAN          QDQLDEEMEAKQNLERHISTLNIQLSDSKKKLQD-FASTVEALEEGKKRFQKEIENLTQQ 1407
SP|P10587|MYH11_CHICK          QEQLDEEVEAKQNLERHISTLTIQLSDSKKKLQE-FTATVETMEEGKKKLQREIESLTQQ 1413
SP|O08638|MYH11_MOUSE          QDQLDEEMEAKQNLERHVSTLNIQLSDSKKKLQD-FASTIEVMEEGKKRLQKEMEGLSQQ 1407
SP|Q7Z406|MYH14_HUMAN          REQLEEEAAARERAGRELQTAQAQLSEWRRRQEE-EAGALEAGEEARRRAAREAEALTQR 1424
TR|A0A125S9Y7|A0A125S9Y7_9ARAC REQIDEEQEGKADLQRQLSKANAEVQLWRSKYESEGLARLEELEESKRKLDAKLQEAMET 1404
                               ::* :**  .:    :.:     ::   : : :.   . :*  ** :::   . :   :

                               ----------------------------Segment 2----------------------------
SP|P35579|MYH9_HUMAN           HEEKVAAYDKLEKTKTRLQQELDDLLVDLDHQRQSACNLEKKQKKFDQLLAEEKTISAKY 1460
SP|P35580|MYH10_HUMAN          LEEKALAYDKLEKTKNRLQQELDDLTVDLDHQRQVASNLEKKQKKFDQLLAEEKSISARY 1467
SP|P35749|MYH11_HUMAN          YEEKAAAYDKLEKTKNRLQQELDDLVVDLDNQRQLVSNLEKKQRKFDQLLAEEKNISSKY 1467
SP|P10587|MYH11_CHICK          FEEKAASYDKLEKTKNRLQQELDDLVVDLDNQRQLVSNLEKKQKKFDQMLAEEKNISSKY 1473
SP|O08638|MYH11_MOUSE          YEEKAAAYDKLEKTKNRLQQELDDLVVDLDNQRQLVSNLEKKQKKFDQLLAEEKNISSKY 1467
SP|Q7Z406|MYH14_HUMAN          LAEKTETVDRLERGRRRLQQELDDATMDLEQQRQLVSTLEKKQRKFDQLLAEEKAAVLRA 1484
TR|A0A125S9Y7|A0A125S9Y7_9ARAC IDQLNSKTSGLEKTKSRLQGELEDMTIEVEKANALASAMEKKQKSFDRIISEWKQKVDDL 1464
                                 :     . **: : *** **:*  ::::: .  .. :****:.**::::* *
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                               ----------------------------Segment 2----------------------------
SP|P35579|MYH9_HUMAN           AEERDRAEAEAREKETKALSLARALEEAMEQKAELERLNKQFRTEMEDLMSSKDDVGKSV 1520
SP|P35580|MYH10_HUMAN          AEERDRAEAEAREKETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVGKNV 1527
SP|P35749|MYH11_HUMAN          ADERDRAEAEAREKETKALSLARALEEALEAKEELERTNKMLKAEMEDLVSSKDDVGKNV 1527
SP|P10587|MYH11_CHICK          ADERDRAEAEAREKETKALSLARALEEALEAKEELERTNKMLKAEMEDLVSSKDDVGKNV 1533
SP|O08638|MYH11_MOUSE          ADERDRAEAEAREKETKALSLARALEEALEAKEELERTNKMLKAEMEDLVSSKDDVGKNV 1527
SP|Q7Z406|MYH14_HUMAN          VEERERAEAEGREREARALSLTRALEEEQEAREELERQNRALRAELEALLSSKDDVGKSV 1544
TR|A0A125S9Y7|A0A125S9Y7_9ARAC ALELDASQKECRNYSTEVFKLRSQYEESQEHYESVKRENKNLQDEIKDLVDQLGEGGRSV 1524
                               . * : :: * *: .:..:.*    **   *   ..:* *: :: ::: *:.. .: *:.*

                               →←--------------------------segment 3 --------------------------
                       Hinge 2 |                                                    Skip 2 |
SP|P35579|MYH9_HUMAN           HELEKSKRALEQQVEEMKTQLEELEDELQATEDAKLRLEVNLQAMKAQFERDLQGRDEQS 1580
SP|P35580|MYH10_HUMAN          HELEKSKRALEQQVEEMRTQLEELEDELQATEDAKLRLEVNMQAMKAQFERDLQTRDEQN 1587
SP|P35749|MYH11_HUMAN          HELEKSKRALETQMEEMKTQLEELEDELQATEDAKLRLEVNMQALKGQFERDLQARDEQN 1587
SP|P10587|MYH11_CHICK          HELEKSKRTLEQQVEEMKTQLEELEDELQAAEDAKLRLEVNMQAMKSQFERDLQARDEQN 1593
SP|O08638|MYH11_MOUSE          HELEKSKRALETQMEEMKTQLEESEDDVQATEDAKLRLEVNMQALKGQFERDLQARDEQN 1587
SP|Q7Z406|MYH14_HUMAN          HELERACRVAEQAANDLRAQVTELEDELTAAEDAKLRLEVTVQALKTQHERDLQGRDEAG 1604
TR|A0A125S9Y7|A0A125S9Y7_9ARAC HELEKARKRLELEKEELQAALEEAEAALEQEENKVLRAQLELSQVRQEIDRRLQEKEEEF 1584
                               ****:: :  *   ::::: : * *  :   *:  ** :: :. :: : :* ** ::*

                               ----------------------------Segment 3----------------------------
SP|P35579|MYH9_HUMAN           EEKKKQLVRQVREMEAELEDERKQRSMAVAARKKLEMDLKDLEAHIDSANKNRDEAIKQL 1640
SP|P35580|MYH10_HUMAN          EEKKRLLIKQVRELEAELEDERKQRALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQL 1647
SP|P35749|MYH11_HUMAN          EEKRRQLQRQLHEYETELEDERKQRALAAAAKKKLEGDLKDLELQADSAIKGREEAIKQL 1647
SP|P10587|MYH11_CHICK          EEKRRQLLKQLHEHETELEDERKQRALAAAAKKKLEVDVKDLESQVDSANKAREEAIKQL 1653
SP|O08638|MYH11_MOUSE          EEKRRQLQRQLHEYETELEDERKQRALAAAAKKKLEGDLKDLELQADSAIKGREEAIKQL 1647
SP|Q7Z406|MYH14_HUMAN          EERRRQLAKQLRDAEVERDEERKQRTLAVAARKKLEGELEELKAQMASAGQGKEEAVKQL 1664
TR|A0A125S9Y7|A0A125S9Y7_9ARAC ENTRKNHQRAIDSMQASLEAEAKGKAEALRMKKKLESDINELEIALDHSNKANAEAQKNI 1644
                               *: ::   : : . :.. : * * :: *   :**:* ::::*:     : : . *. *::
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                               ----------------------------Segment 3----------------------------
SP|P35579|MYH9_HUMAN           RKLQAQMKDCMRELDDTRASREEILAQAKENEKKLKSMEAEMIQLQEELAAAERAKRQAQ 1700
SP|P35580|MYH10_HUMAN          RKLQAQMKDYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASSERARRHAE 1707
SP|P35749|MYH11_HUMAN          RKLQAQMKDFQRELEDARASRDEIFATAKENEKKAKSLEADLMQLQEDLAAAERARKQAD 1707
SP|P10587|MYH11_CHICK          RKLQAQMKDYQRDLDDARAAREEIFATARENEKKAKNLEAELIQLQEDLAAAERARKQAD 1713
SP|O08638|MYH11_MOUSE          RKLQAQMKDFQRELDDARASRDEIFATSKENEKKAKSLEADLMQLQEDLAAAERARKQAD 1707
SP|Q7Z406|MYH14_HUMAN          RKMQAQMKELWREVEETRTSREEIFSQNRESEKRLKGLEAEVLRLQEELAASDRARRQAQ 1724
TR|A0A125S9Y7|A0A125S9Y7_9ARAC KKYQIQLKETQQALEEEQRARDEVREQYAMSERRCNAMHGELEESRQLLEQADRARRAAD 1704
                               :* * *:*:  : ::: : :*:*:      .*:: : :..:: . :: *  ::**:: *:

                               ----------------------------Segment 3----------------------------
SP|P35579|MYH9_HUMAN           QERDELADEIANSSGKGALALEEKRRLEARIAQLEEELEEEQGNTELINDRLKKANLQID 1760
SP|P35580|MYH10_HUMAN          QERDELADEITNSASGKSALLDEKRRLEARIAQLEEELEEEQSNMELLNDRFRKTTLQVD 1767
SP|P35749|MYH11_HUMAN          LEKEELAEELASSLSGRNALQDEKRRLEARIAQLEEELEEEQGNMEAMSDRVRKATQQAE 1767
SP|P10587|MYH11_CHICK          LEKEEMAEELASANSGRTSLQDEKRRLEARIAQLEEELDEEHSNIETMSDRMRKAVQQAE 1773
SP|O08638|MYH11_MOUSE          LEKEELAEELASSLSGRNTLQDEKRRLEARIAQLEEELEEEQGNMEAMSDRVRKATLQAE 1767
SP|Q7Z406|MYH14_HUMAN          QDRDEMADEVANGNLSKAAILEEKRQLEGRLGQLEEELEEEQSNSELLNDRYRKLLLQVE 1784
TR|A0A125S9Y7|A0A125S9Y7_9ARAC SELAELHENVNELSAQNSSLSMAKRKLEGEMQALHADLDEMLNEAKSSEEKAKKAMVDAA 1764
                                :  *: ::: .           **:**..:  *. :*:*  .: :  .:: :*   :

                               ----------------------------Segment 3----------------------------
                                                                   Skip 3 |
SP|P35579|MYH9_HUMAN           QINTDLNLERSHAQKNENARQQLERQNKELKVKLQEMEGTVKSKYKASITALEAKIAQLE 1820
SP|P35580|MYH10_HUMAN          TLNAELAAERSAAQKSDNARQQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLE 1827
SP|P35749|MYH11_HUMAN          QLSNELATERSTAQKNESARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLE 1827
SP|P10587|MYH11_CHICK          QLNNELATERATAQKNENARQQLERQNKELRSKLQEMEGAVKSKFKSTIAALEAKIASLE 1833
SP|O08638|MYH11_MOUSE          QLSNELATERSTAQKNESARQQLERQNKELRSKLQEVEGAVKAKLKSTVAALEAKIAQLE 1827
SP|Q7Z406|MYH14_HUMAN          SLTTELSAERSFSAKAESGRQQLERQIQELRGRLGEEDAGARARHKMTIAALESKLAQAE 1844
TR|A0A125S9Y7|A0A125S9Y7_9ARAC RLADELRAEQEHAQQQEKMRKAMEGQIKELQVRLDEAEAAALKGGKKIIQKLEQKVRELE 1824
                                :  :*  *:  : : :. *: :* * :**: :* * :.  .    *  :  ** *: . *
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                               ----------------------------Segment 3----------------------------
SP|P35579|MYH9_HUMAN           EQLDNETKERQAACKQVRRTEKKLKDVLLQVDDERRNAEQYKDQADKASTRLKQLKRQLE 1880
SP|P35580|MYH10_HUMAN          EQLEQEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKANARMKQLKRQLE 1887
SP|P35749|MYH11_HUMAN          EQVEQEAREKQAATKSLKQKDKKLKEILLQVEDERKMAEQYKEQAEKGNARVKQLKRQLE 1887
SP|P10587|MYH11_CHICK          EQLEQEAREKQAAAKTLRQKDKKLKDALLQVEDERKQAEQYKDQAEKGNLRLKQLKRQLE 1893
SP|O08638|MYH11_MOUSE          EQVEQEAREKQAATKSLKQKDKKLKEVLLQVEDERKMAEQYKEQAEKGNTKVKQLKRQLE 1887
SP|Q7Z406|MYH14_HUMAN          EQLEQETRERILSGKLVRRAEKRLKEVVLQVEEERRVADQLRDQLEKGNLRVKQLKRQLE 1904
TR|A0A125S9Y7|A0A125S9Y7_9ARAC TELDNEQRRHSEAAKNVRRSERRVKELQFQAEEDRKNQERMQDLVDKLQQKIKTYKRQIE 1884
                                ::::* :.:  : * ::: ::::*:  :*.:::*:  :: ::  :* . ::*  ***:*

                               ----------------------------Segment 3----------------------------
SP|P35579|MYH9_HUMAN           EAEEEAQRANASRRKLQRELEDATETADAMNREVSSLKNKLRRGDLP-FVVP-RRMARKG 1938
SP|P35580|MYH10_HUMAN          EAEEEATRANASRRKLQRELDDATEANEGLSREVSTLKNRLRRGGPI-SFSS-SRSGRRQ 1945
SP|P35749|MYH11_HUMAN          EAEEESQRINANRRKLQRELDEATESNEAMGREVNALKSKLRRGNE-TSFVPSRRSGGRR 1946
SP|P10587|MYH11_CHICK          EAEEESQRINANRRKLQRELDEATESNDALGREVAALKSKLRRGNEPVSFAPPRRSGGRR 1953
SP|O08638|MYH11_MOUSE          EAEEESQCINANRRKLQRELDEATESNEAMGREVNALKSKLRRGNE-ASFVPSRRAGGRR 1946
SP|Q7Z406|MYH14_HUMAN          EAEEEASRAQAGRRRLQRELEDVTESAESMNREVTTLRNRLRRGPLTFTTRTVRQVF--R 1962
TR|A0A125S9Y7|A0A125S9Y7_9ARAC EAEEIAALNLAKFRKVQQELEDAEERADMAENVAAKLRAKNRSSASVGRAMSPIPMGKPG 1944
                               **** :    *  *::*:**::. *  :   . .  *: : * .

                               ----------------------(Tail piece)----→
SP|P35579|MYH9_HUMAN           -A---GDGSDEEV-D-----GK-ADGAEAKPAE-- 1960
SP|P35580|MYH10_HUMAN          LH---LEGASLEL-SDDDTESKTSDVNETQPPQSE 1976
SP|P35749|MYH11_HUMAN          VIENA-DGSEEET-DTRDA-----DFNGTKASE-- 1972
SP|P10587|MYH11_CHICK          VIENATDGGEEEI-DGRDG-----DFNGKASE--- 1979
SP|O08638|MYH11_MOUSE          VIENT-DGSEEEM-DARDS-----DFNGTKASE-- 1972
SP|Q7Z406|MYH14_HUMAN          LEE--GVASDEEAEEAQPGSGPSPEPEGSPPAHPQ 1995
TR|A0A125S9Y7|A0A125S9Y7_9ARAC RPKS---KIDEE----------------------- 1953
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