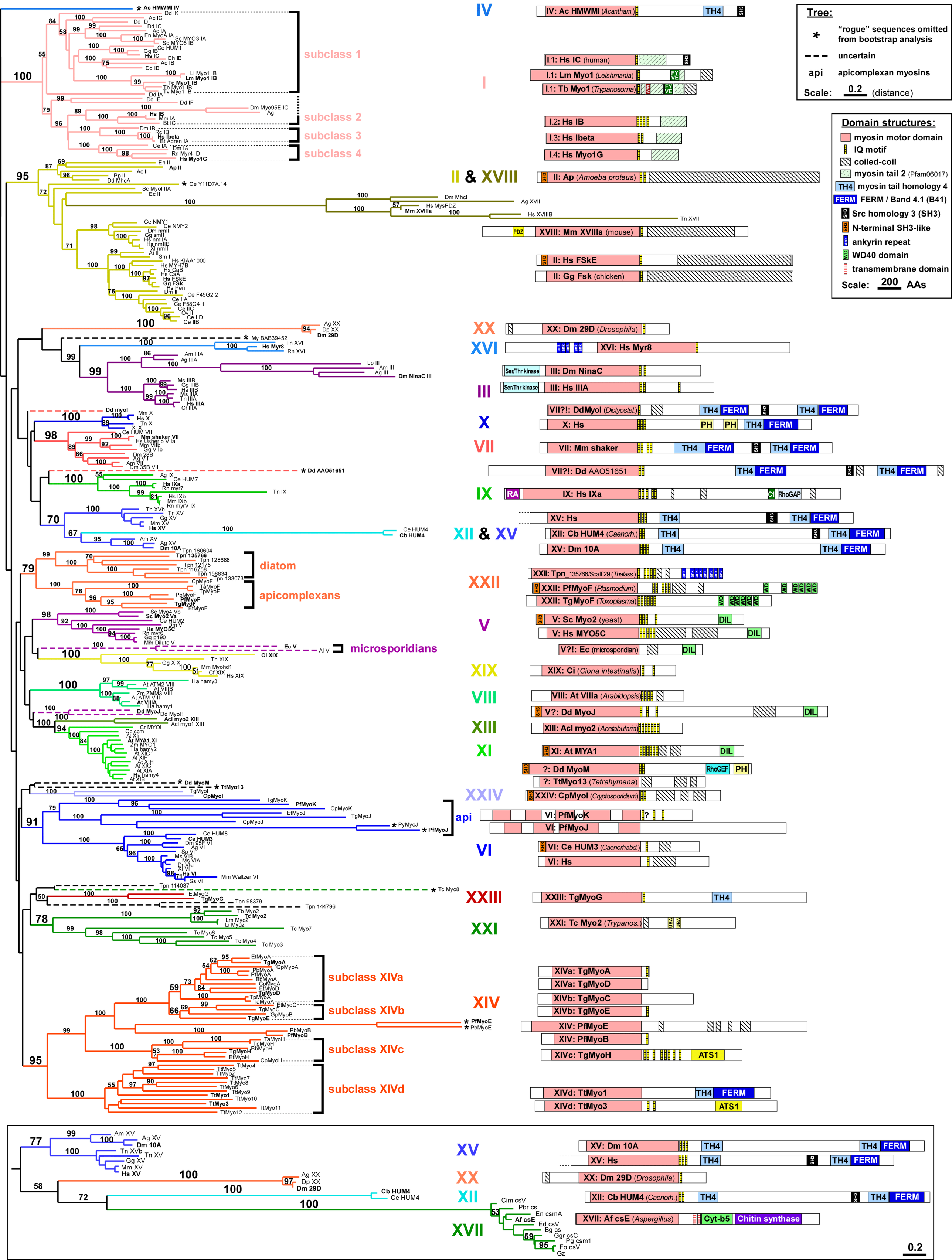
Tree:
* "rogue" sequences omitted from bootstrap analysis
– – – uncertain
api apicomplexan myosins
Scale: 0.2 (distance)
Domain structures:
myosin motor domain
IQ motif
coiled-coil
myosin tail 2 (Pfam06017)
TH4 myosin tail homology 4
FERM FERM / Band 4.1 (B41)
SH3 Src homology 3 (SH3)
SH3 N-terminal SH3-like
ank ankyrin repeat
WD WD40 domain
transmembrane domain
Scale: 200 AAs
subclass 1
subclass 2
subclass 3
subclass 4
IV
I
II & XVIII
XX
XVI
III
X
VII
IX
XII & XV
XXII
V
XIX
VIII
XIII
XI
XXIV
VI
XXIII
XXI
XIV
XV
XII
XVII
diatom
apicomplexans
microsporidians
subclass XIVa
subclass XIVb
subclass XIVc
subclass XIVd
api
IV: Ac HMWMI (Acantham.)
I.1: Hs IC (human)
I.1: Lm Myo1 (Leishmania)
I.1: Tb Myo1 (Trypanosoma)
I.2: Hs IB
I.3: Hs Ibeta
I.4: Hs Myo1G
II: Ap (Amoeba proteus)
XVIII: Mm XVIIIa (mouse)
II: Hs FSkE
II: Gg Fsk (chicken)
XX: Dm 29D (Drosophila)
XVI: Hs Myr8
III: Dm NinaC
III: Hs IIIA
VII?!: DdMyoI (Dictyostel.)
X: Hs
VII: Mm shaker
VII?!: Dd AAO51651
IX: Hs IXa
XV: Hs
XII: Cb HUM4 (Caenorh.)
XV: Dm 10A
XXII: Tpn_135766/Scaff.29 (Thalass.)
XXII: PfMyoF (Plasmodium)
XXII: TgMyoF (Toxoplasma)
V: Sc Myo2 (yeast)
V: Hs MYO5C
V?!: Ec (microsporidian)
XIX: Ci (Ciona intestinalis)
VIII: At VIIIa (Arabidopsis)
V?: Dd MyoJ
XIII: Acl myo2 (Acetabularia)
XI: At MYA1
?: Dd MyoM
?: TtMyo13 (Tetrahymena)
XXIV: CpMyoI (Cryptosporidium)
VI: PfMyoK
VI: PfMyoJ
VI: Ce HUM3 (Caenorhabd.)
VI: Hs
XXIII: TgMyoG
XXI: Tc Myo2 (Trypanos.)
XIVa: TgMyoA
XIVa: TgMyoD
XIVb: TgMyoC
XIVb: TgMyoE
XIV: PfMyoE
XIV: PfMyoB
XIVc: TgMyoH
XIVd: TtMyo1
XIVd: TtMyo3
XV: Dm 10A
XV: Hs
XX: Dm 29D (Drosophila)
XII: Cb HUM4 (Caenorh.)
XVII: Af csE (Aspergillus)
0.2