Multiple sequence alignment of bZIP family consensus sequences, showing the Basic region and Leucine zipper.

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                   1         10        20        30        40        50        60
Canonical bZIP sequence  XXXXKRRRREKNREAAQXCRKKKKEYXXXLEXXVXXLXXXNXXLXXEVXXLXXEXXXLK

ATF2 consensus (18)      DPDE..XKFL....A..XR..Q.R.XWV....KKA.........Q.........VAQ..
CREB consensus (19)      EA.R..EX.LM......RE..R.....VKC..NR.AV..NQ.KT.IE.LK...E.YC..X
ATF6 consensus (16)      .K....QQ.MI...S.CLS......L.....L..............N...........X
OASIS consensus (36)     E..L.KV..KI..KIS..ES.R....D......R.........KK......N.S.X
PAR consensus (50)       .KDD.YWE..R..N...KRS.DARRXKENZ..IRAAF..K..AK.RA...A.K.....R
CEBP consensus (34)      K.SDEY.XX..NX.VRKS.X.A.XR..ET..R..E.....E....Z.X......K.L...
FOS-ATF3 consensus (29)  .EEER..X.....KX..AK..XRRX.XT....EXE..........I...Z..ZZ.X
JUN consensus (21)       QE...XE.K.X....X.SK..R.L.R...DK.K...........XA....Z.V.Z..
NFE2 consensus (20)      L.LIRDI...G..KV...N...R.LDXI...DE.........K.....X.........
MAF consensus (37)       V.RL.Q..TL..GY.X...X.RXXQK....EX.....X.......X....RD...
XBP1 consensus (16)      S.EE.XL..KL...V...TA.DR..AXM.E.............K....N...K.....X
ATF4 consensus (14)      ...D.KX.KKZQ.KX..RY.X....XE......EX.........E.K.KX.....I.Y..
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Basic region   Leucine zipper