

BAT1 --MLQRHSLKLGKFSIRT-----LATGAPLDASKLKITRNP 36
 BAT2 -----MTLAPLDASKVKITTTQHA 19
 AFLA_113800 MNSLRQFTRRKALQSLAVPPSQGFSTIRLWQRHFNSTPAVASRLAGIDPSKLTVTKTSSP 60
 AFLA_044190 -----MGSVAHSVAELDASVVKITRSTNL 24
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BAT1 S-KPRPNEELVFGQTF-TDHMLTIPWSAKEGWGTPHIKPYGNLSLDPSACVFHYAFELFE 94
 BAT2 S-KPKPNSELVFGKSF-TDHMLTAEWTAKEGWGTPEIKPYQNLSDPSAVVFHYAFELFE 77
 AFLA_113800 K-ELTPAKDLVFGKTF-TDHMLAIEWSASNGWDAPRIVPYQNLSDPSACVFHYAFECFE 118
 AFLA_044190 RPVPEPGSPEELSHSYCTDHMV TARWTVANGWETPEVKPFENLSIPPTASCLHYATECFE 84
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BAT1 GLKAYRTPQNTITMFRPDKNMARMNKSAARICLPTFESEELIKLTGKLI EQD-KHLVPQG 153
 BAT2 GMKAYRTVDNKITMFRPDMNMKRMNKSAQRICLPTFDPEELITLIGKLIQD-KCLVPEG 136
 AFLA_113800 GMKAYKDNNQIIRLFRPDKNMERLNKSSSRIALPTVDGEALTQLVGELVKLD-SRFIPSA 177
 AFLA_044190 GMKVYRGYDGKLR LFRPDCNGERLLSSAQRASLPSFRYEELKVLIAKLMQIDGPRWLPKD 144
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BAT1 N-GYSLYIRPTMIGTSKGLGVGTPSEALLYVITSPVG-----PYYKTGFKAVRLEATD 205
 BAT2 K-GYSLYIRPTLIGTTAGLVSTPDRALLYVICCPVG-----PYYKTGFKAVRLEATD 188
 AFLA_113800 R-GYSLYLRPTMIGTQSTLGVGPPGSALLFVIASPVG-----PYYPTGFKAISLEATD 229
 AFLA_044190 QPGRFLYLRPTMIGSGPHLGVQTPKEALLFIIAVPWPDP SKLKKPEEGTKPGLKLLASTP 204
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BAT1 YATRAWPGGVGDK K L G A N Y A P C I L P Q L Q A A K R G Y Q Q N L W L F G P E K N I T E V G T M N V F F V F L 265
 BAT2 YATRAWPGGCGDK K L G A N Y A P C V L P Q L Q A A S R G Y Q Q N L W L F G P N N N I T E V G T M N A F F V F K 248
 AFLA_113800 YAVRAWPGGVGDK K L G A N Y A P C I V P Q L S A A S R G F Q Q N L W L F G E E E Y V T E V G T M N L F I A L K 289
 AFLA_044190 DTIRAWPGGFGYAK K L G A N Y G P S L V A H G K A Q A I G F D Q I L W L F G Q D R Q V T E A G A S N F F I V W E 264
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BAT1	NKVTGKKELVTAPLDG-TILEGVTRDSVLTTLARDKLDPEWDIN-----ERYYTITEVAT	319
BAT2	DSKTGKKELVTAPLDG-TILEGVTRDSILNLAKERLEPSEWTIS-----ERYFTIGEVTE	302
AFLA_113800	NKETGQKELVTAPLDG-TILEGVTRDSVLGLARERLAPNGWTVS-----ERKIRMSEVAE	343
AFLA_044190	NKETGKIELVTAPLENQLILPGVTRRSVLQLARTELSKPTGSLAPVEVVERDFTISEVEQ	324
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BAT1	RAKQGELLEAFGSGTAAVVSPIKEIGWNNEDIHVPLLPGEQCGALTKQVAQWIADIQYGR	379
BAT2	RSKNGELLEAFGSGTAAIVSPIKEIGWKGEQINIPLLPGEQTGPLAKEVAQWINGIQYGE	362
AFLA_113800	AADEGRLEIEVFGSGTAAIVSPVRNISYKGMVDCGLKEDEEAGEIASQMKNWIEGIQYGD	403
AFLA_044190	AWKEGRILEAFVCGTAFVTPVKLIRNGDVDMDM-LEAGAARGGYAVQIKSWLEAIMYGK	383
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BAT1	--VNYGNWSKTVADLN--	393
BAT2	--TEHGNWSRVVTDLN--	376
AFLA_113800	--EDH-KWSYVL-----	412
AFLA_044190	DGKENDEWSYIEGESEK	401
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