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M1_15999      IDDLKNLGLSYFFQDEIKKILSCIYNEHNF-SQNNKVRDLHFTALGFRLLRHHGFDVSQE 115
ATERS1        IDDLKNLGLSYFFRDEIKTILTSIYNNSFE-NKNNQVGDLYFTSLGFRLLRQHGFNVSD 116
ATERS2        IDDLKNLGLSYFFRDEIKTILTSIYNNSFE-NKNNQVGDLYFTSLGFRLLRQHGFNVSD 116
CINS_LAVAN    IDDLHLKLGISCHFENEILQILKSIYLNQN-----YKRDLYSTSLAFRLLRQNGFILPQE 110
CINS_LAVIN    IDDLHLKLGISCHFENEILQILKSIYLNQN-----YKRDLYSTSLAFRLLRQNGFILPQE 110
CINS_SALOF    IDDLRLRGISCHFDREIVEILNSKYTNN---EIDESDLYSTALRFKLLRQYDFSVSQE 111
CINS_THYAL    IDDLRLGLAISCHFDDEEIERILNHLFHHD----DVEEGDLYSTSLTFKLLRQHGFNISQ 112
Mp_12413      IDDLQRLGISCHFNEEIKQLINSFYNEFNDAIVAERDLYFTALFRLLRQHGFNVSQ 115
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MI_15999      IFDCFKNEEGSDFEKALIGEDMKGILQLYEASFLLRREGEDTLELARKFSTKYLQKRVDGE 175
ATERS1        IFDCFKNEKGSDFDETLLIGEDTKATLQLYEASFHLREGENTLELARQISTKYLQKKVNEG 176
ATERS2        IFDCFKNEKGSDFDETLLIGEDTKATLQLYEVSFHLREGENTLELARQISTKYLQKQVNEG 176
CINS_LAVAN    VFDCFKNEKGT-DFKPSLSHDRKGILLQLYEASFLSRQGEETLQLAREFATKILQKEVDE- 168
CINS_LAVIN    VFDCFKNEKGT-DFKPSLSHDRKGILLQLYEASFLSRQGEETLQLAREFATKILQKEVDE- 168
CINS_SALOF    VFDCFKNDKGT-DFKPSLVDDTRGILLQLYEASFLSAQGEETLHLLARDFATKFLHKKRVLVD 170
CINS_THYAL    LFEHFKCEDGT-DFKPIHVEDTKGILLQLYEASFLSTRGEETLELATQFARKSLQEKLLDH 171
Mp_12413      VFDFYKSEEGIDDFKTIHAEDTKGILLQLYEASFLSTQGEETLELAREYALKFLQKI-LDH 174

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M1_15999      IINDNNNNILSWIRHSLDPLPHWRIQRLEARWFLDAYSTRKDMNPLIFELSILDFNNIQ 235
ATERS1        RISDE---NLSSWIRHSLDPLPHWRIQRLEARWFLDAYAVREDKNPLIFELAKLDFNIIQ 233
ATERS2        RISDE---NLSSLWIRHSLDPLPHWRIQRLEARWFLDAYAAREDKNPLIFKLAKLDFNIIQ 233
CINS_LAVAN    -----RDFETKMGFPSHWRVQMPNARLHIDAYRKRTDMNPVVLELAILDTNIVQ 217
CINS_LAVIN    -----RDFETKMGFPSHWRVQMPNARLHIDAYRKRTDMNPVVLELAILDTNIVQ 217
CINS_SALOF    KDI-----NLLSSIERALELPTHWRVQMPNARSFIDAYKRRPDMNPTVLELAKLDFNMVQ 225
CINS_THYAL    HEID-N-QYILSSIRDALEIPSHWRVRTPYAISFIDAYKKRPLMNPTVLELAILDINI 229
Mp_12413      EIINDE-NLSSSILDAIKIPIHWRVQMPNARSYIDAYERKPRMHPIVLELAKLEITIVQ 233

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Variable Region 1

Ml_15999	ATHILELKEVSRWWNNSCLA EKLPFVRDRVVESFFWAAGLFEGHEYG YQRKMVASII ILI	295
ATERS1	ATQQEELKEVSRGWNDSC LAEKLPFVRDRVVESYFWGVGLFEGHEFGYQRKLTAA NTLLI	293
ATERS2	ATQQEELKEVSRWWNNSCLA EKLPFVRDRVVESYFWGVGLFEGHEFGYQRKLTAAY ILLI	293
CINS_LAVAN	AQFQELKETSRRWWESTSLVQELPFVRDRIVECYLWTTGVIQRREHGYERIMLT KINALV	277
CINS_LAVIN	AQFQELKETSRRWWESTSLVQELPFVRDRIVECYLWTTGVIQRREHGYERIMLT KINALV	277
CINS_SALOF	AQFQELKEASRWWNSTGLVHELPFVRDRIVECYWTTGVVERREHGYERIMLT KINALV	285
CINS_THYAL	AQFQELKEASRWWNGTGLVQQLPFVRDRIVECYFWTTGVLERRQH VYERIMLT KINALV	289
Mp_12413	AQFQELKETSRRWWHSTSLVQQLPFVRDRIVECYWTTGVLERREHGYERIMLT KINALV	293
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      DDxxD Motif
Ml_15999 TAIDDVYDVYGTGLGELQLFTDTIRRWDTESIDQLPYMQLCYLALNYVSNLAYDILKDR 355
ATERS1 SAIDDVYDVYGTLDLRLFTDFVRWDTESIDQLPYMQLCYLALNYVSGVAYDILKD 353
ATERS2 SAIDVDVYGTLEDLRLFTDFRRWDTESIDQLPYMQLCYLALHNVSGVAYDILKD 353
CINS_LAVAN TTIDEVFDIYGTTLEELQLFTTIIQRWDLFSMKQLPYPMLCYLALHKFVIEEAYETLKEK 337
CINS LAVIN TTIDDVFDIYGTTLEELQLFTTIIQRWDLFSMKQLPYPMLCYLALHKFVIEEAYETLKEK 337
CINS_SALOF TTIDDVFDIYGTTLEELQLFTTAIQRWDIESMKQLPYPMQICYLALFNFMAYDTLRDK 345
CINS_THYAL TTIDDIYDVYGTIGELRLFTNAVQRWDIDSINELPPYMQLCYLALNFMNEEAYHTLKDR 349
Mp_12413 TTIDDIYDIYGTFFEEQLFTNAIKRWDIEMNQPLPYPMQOQCYLALQNFMENAYNTLKQK 353
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Variable Region 2

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M1_15999      RFNTIPYLHKSWLCLVETYLKEAEWYESGYTPTLEEYLSNAKISIGSLTILLQVELSLQK 415
ATERS1        RRNTIPYLQETWVELVEAYMKEAEWYKSGYTPSLEEYLTIAKISIASLTILLSVELSLPD 413
ATERS2        RRNTIPYLQETWVELVEAYMKEAEWYQSGYTPSLEEYLTIAKISIGSLPILLSVELSLPD 413
CINS_LAVAN    GFNSIPYVTKWVNLVESYMKEATWYNYNGYKPSMQEYINNAWISIGGLPILSHLFFRFTD 397
CINS_LAVIN    GFNSIPYVTKWVNLVESYMKEATWYNYNGYKPSMQEYINNAWISIGGLPILSHLFFRFTD 397
CINS_SALOF    GFNSTPYLRKAWVDLVESYLIEAKWYMGHKPSLEEYMKNSWISIGGIPILSHLFFRLTD 405
CINS_THYAL    GFNSIPFLRKTWIDLVEYTMREAWEYHNGHNP SLGEYMENAWISIGGVPILSHLFFRLTD 409
Mp_12413      GFNSIPYLHKTWVDLVEAYMREAWEYHNGHKPSLEEYMNAWISIGGVPILSHIFFCVD 413
               *: *: : *: **:*: ** ** *:.: : *: : **:.: ** : : .

M1_15999      STLDRT--AFDLRHKILYLSALVSRLADDLGTAPSELKRGDVPNAIQCYMKD-KNCSEEE 472
ATERS1        STIDRA--TFDRRHKMFYLSATVSRLADDLGTAPSELERGDVPKAIQCYMKD-TNASEEE 470
ATERS2        STIDRA--TFDRRHKMFYLSATVSRLADDLGTAPSELERGDVPKAIQCYMKD-TNASEEE 470
CINS_LAVAN    SIE-----SMDKYRDMRASCTILRLADDMGTS LVEVERGDVPKAIQCYMNE-TNASEEE 451
CINS_LAVIN    SIE-----SMDKYRDMRASCTILRLADDMGTS LVEVERGDVPKAIQCYMNE-TNASEEE 451
CINS_SALOF    SIEEEDAESMHKYHDIVRASCTILRLADDMGTS LDEVERGDVPKSVQCYMNE-KNASEEE 464
CINS_THYAL    SIDDETVERMHEYHNIVRGSC TILRLADDLGTSLDEVKRGDVPKSVQCYMNE-KNASEEE 468
Mp_12413      SIDEVTVERVHEYHDIVRASCTILRLADDLGTSLDEVKRGDVPKSVCEYMNDEKNASEQE 473
               *      ..  :.:  *. :  *****: ** : **:*****: : **:.: *.**:*

M1_15999      ARAHVRGMIGE VWKEMNTAMAVSD--DDCPFTEQVVEAAANLGRAAQFIYME---GDGHG 527
ATERS1        ARGHVRFMIGETWKELNTAMAK-P--DDCPFTEQVVEATANLGRAAQFIYRE---GDGHG 524
ATERS2        AQGHVRFMIREAWKELNTAMAE-P--DDCPFTEQVVEATANIGRAAQYIYRE---GDGHG 524
CINS_LAVAN    AREYVRRLIEKEWEKMNTETMWDDDDDDFTLSKHYCEVVANLARMAQFIYQDGLDGFQMK 511
CINS_LAVIN    AREYVRRLIEKEWEKMNTETMWDDDDDDFTLSKYCEVVANLARMAQFIYQDGLDGFQMK 511
CINS_SALOF    AREHVRSLIDQTWKMMNKEMMTS-----SFSKYFVQVSANLARMAQWIYQHESDGFQMK 518
CINS_THYAL    AREYVRSLIEETWRTMNTELMASAD---SPFSKYFVEAAANLGRMAQCVYQHESDGFQMK 525
Mp_12413      ARAHVRSIIKNTWKT MNEEMMTSTN---SQFSKYFVEAAANLGRMSLCIYQDECDFGFMQ 530
               *: **: *: : *. : *      :.:  :. **:.* : : * .  * *

M1_15999      HSQIHEQMRSLLFHPYI----- 544
ATERS1        HFQIHQHMGNLFFHPYV----- 541
ATERS2        HFQIRQHVRNLFFHPYV----- 541
CINS_LAVAN    DSKVNKLLKELLFERYE----- 528
CINS_LAVIN    DSKVNKLLKELLFERYE----- 528
CINS_SALOF    HSLVNKMLRGLLFD RYE----- 535
CINS_THYAL    HSRVNTMLRSLLFD PYA----- 542
Mp_12413      HSRVNKMLRGLLFD PCI----- 547
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