

Conservation: 5 5 6 6999795 9997996 6 76 7 7 9

4kxq_chainA_SIRT1 1 -----HMRKK-RKDINTIEDAVKLLQ--ECKKIIVLTGAGVSVSCGIPDFRSRD-GIYARLAVDFPDLDPQAMFDIEYFRKDRP 77

4l3o_chainA_SIRT2 1 -----KER-LLDELTLLEGVARYMQSERCRRVICLVGAGISTASGIPDFRS-----YDNLKLEK--YHLPYPEAIFPEISYFKKHPEP 71

4fvt_chainA_SIRT3 1 -----KLSLQDVAELIRARACQRVVMVVGAGISTSPGIPDFRSPGSGLYSNLQQ--YDLPYPEAIFELPFFHNP 70

4bvg_chainA_SIRT3 1 -----KLSLQDVAELIRARACQRVVMVVGAGISTSPGIPDFRSPGSGLYSNLQQ--YDLPYPEAIFELPFFHNP 70

lszc_chainA_yHST2 1 -----MASMSVST-ASTEMSVRKIAAHMKSNNPNAKVIFMVGAGISTSCGIPDFRSPGTGLYHNLAR--LKLPEAFAVDFVDFQSDPLP 81

3zg6_chainA_SIRT6 1 MNYYAAGLSPYADKGCGLPEIFDPPEELERKVVWELARLVW--QSSSVVFHTGAGISTASGIPDFRGPV--MEE-----RGLAP-- 78

2h4f_chainA_Sir2T 1 -----MKMKEFLDLLN--ESRLTVTLTGAGISTSPGIPDFRGPY-----SQNVFDIDFFYSHPEE 53

lyc2_chainB_Sir2A 1 -----MEDEIRKAAEILA--KSKHAVVFTGAGISAESGIPDFRGPV--GLWR-----KYDPEEVASISGFKRNPRA 62

Consensus aa:c.pIpc.tppGAGISGIPDFRt.@p.h.PpsI@F-Is@F.ppPcs

Consensus ss: hhhhhhhhhhhh h eeeee hhh hh hhh hhhhhh hhh

Conservation: 9 67 5 9 9 5 7 5 79979 96 69 7 99 9 9 5 5 9

4kxq_chainA_SIRT1 78 FFFAK-ELY-PGQFQPSLCHKFIASDKEGKLLRNYTQNIIDTLEQVAGIQ--RIIQCHGSFATASCL--ICKYKVDCEAVRGDIFN---QVPRCP--- 165

4l3o_chainA_SIRT2 72 FFLAK-ELY-PGQFKPTICHYFMRLLDKGLLRRCYTQNIIDTLERIALGLEQEDLVEAHGTFFYTSCHVSASCRHEYP LSWMKKEKIFS---EVTPKCE--- 163

4fvt_chainA_SIRT3 71 FFTLAK-ELY-PGNYKPNVTHYFLRLLHDKGLLRRLRYTQNIIDGLERVSGIPASKLVEAHGTFFASATC--TVCQRFPPGEDIRADVMA---DRVPRCP--- 160

4bvg_chainA_SIRT3 71 FFTLAK-ELY-PGNYKPNVTHYFLRLLHDKGLLRRLRYTQNIIDGLERVSGIPASKLVEAHGTFFASATC--TVCQRFPPGEDIRADVMA---DRVPRCP--- 160

lszc_chainA_yHST2 82 FYTLAK-ELY-PGNFRPSPKFHYLLKLFQDKDVLKRVYVQNIIDTLERQAGVKKDDLIIEAHGSAFHCHCI--GCGKVPYPPQVFKSKLAEHPIKDFVKCD--- 174

3zg6_chainA_SIRT6 79 -----KFDTTFESARPTQTHMALVQLERVGLLRFLVSNQVNDGLHVRSGFPRDKLAEHLGNMFVEECA--KCKTQYVVDTVVGTMLG--KATGRLCTVKA 168

2h4f_chainA_Sir2T 54 FYRFAKEGIFPMLQAKPNLAHVLLAKLEEKGLIEAVITQNIIDRLHQRAGSK--KVIELHGNVVEEYCYV--RCEKKYTVEDVIKKLES---SDVPLCD--- 143

lyc2_chainB_Sir2A 63 FWFES-MEMKDKLFAEPNPAHYATAELERMGIVKAVITQNIIDMLHQRAGSR--RVLELHGSMKLDLCL--DCHETYDWESEFVEDFNK---GEIPRCR--- 151

Consensus aa: F@phhhl. bhccbGllb. hhtQNIID. Lcp. tG.cIleHGsh. p. pC.Cp. @. s. p. h.hs. C.

Consensus ss: hhhhhh hhhhhh hhhhhhhhhh eeeee hhhh hhhheeeeeeeeeee hhhhhhhh

Conservation: 9 67 775777 99 57 5 9699 7 9 7 75 6 9

4kxq_chainA_SIRT1 166 ----RCPADEPLAIMKPEIVVFGENLPEQFHRAMKYDKDEV-----DLLIVIGSSLVKVRPVALIPSSIP-HEVPQILINREPL----- 238

4l3o_chainA_SIRT2 164 ----DCQ----SLVKPDIVFFGESLPARFFSCMQSDFLKV-----DLLLLVMGTSLQVQPFASLISKAP-LSTPRLINKEKAGQSDPFLGMIMGLG 245

4fvt_chainA_SIRT3 161 ----VCT----GVVQPDIVVFGPELPLQRFLLHVVDFPMA-----DLLLLILGTSLEVEPFASLTEAVR-SSVPRLLINRD-----LV 227

4bvg_chainA_SIRT3 161 ----VCT----GVVQPDIVVFGPELPLQRFLLHVVDFPMA-----DLLLLILGTSLEVEPFASLTEAVR-SSVPRLLINRD-----LV 227

lszc_chainA_yHST2 175 ----VCG----ELVKPAIVVFGEDLPSDFSETWLNDSWLRKITTQQPLVIVVGTSLAVYFASLPEEIP-RKVKRVLCNLETV----- 250

3zg6_chainA_SIRT6 169 RGLRACR----GELRDTILDWEDSLPDRDLALADEASRNA-----DLSITLGTSLQIRPSGNLPLATKRGGRLVIVNLQPT----- 241

2h4f_chainA_Sir2T 144 ----DCN----SLIRPNIVVFGENLPQDALREAIGLSSRA-----SLMIVLGSLLVYPAEALPLITVRSKKLVIVNLGET----- 212

lyc2_chainB_Sir2A 152 ----KCG----SYVVKPRVLFGEPLPQRTLFEAIEEAKHC-----DAFMVVGSSLVVYPAEALPYIAKAGAKMIIVNAEPT----- 221

Consensus aa:C.hI+PpIV

Consensus ss: e hhhhhhhhhhhh eeeee hhhhhhhhhhhh eeee

Conservation: 76 5 5 5 57

4kxq_chainA_SIRT1 239 PHL-----HFDVELLGDINELCHRLGGEYAKLCCNPV---KLSEI----- 279

4l3o_chainA_SIRT2 246 GGMDFDSKAYRVDVAWLGCLALAE-WKKELEDLVRREHASIDAQS----- 297

4fvt_chainA_SIRT3 228 GPLAWHPRS--RDVAQLGDVVHGVESLVLELLG-WTEEMRDVLRQRETGKLD----- 274

4bvg_chainA_SIRT3 228 GPLAWHPRS--RDVAQLGDVVHGVESLVLELLG-WTEEMRDVLRQRETGKLD----- 273

lszc_chainA_yHST2 251 GDFKAN--KRPTDLIVHQYSDEFQLVEELG-WQEDFEKILTA----- 291

3zg6_chainA_SIRT6 242 KHDR-----HADLRHIGYVDEVMTRLMKHLG---LEIPAW-----DGPRVLERALPPLPRPPTPK 293

2h4f_chainA_Sir2T 213 PFDD-----IATLKYNMDVVEFARRVMEEGG-IS----- 240

lyc2_chainB_Sir2A 222 MADP-----IFDVKIIGKAGEVLPKIVEEVK-R-----LRSE 252

Consensus aa:Dl. hh.hsp. h. plhc. lG. b.

Consensus ss: eeeee hhhhhhhhhhhh h