Supplementary Figure S1:

sp|P00549|KPYK1\_YEAST MSR-----------------------LERLTSLNVVAG-SDLRRTSIIGT 26

sp|P14618|KPYM\_HUMAN MSKPHSEAGTAFIQTQQLHAAMADTFLEHMCRLDIDSPPITARNTGIICT 50

sp|P0AD61|KPYK1\_ECOLI -----------------------------------------MKKTKIVCT 9

tr|Q836R2|Q836R2\_ENTFA -----------------------------------------MKKTKIVCT 9

tr|Q88VY2|Q88VY2\_LACPL -----------------------------------------MKKTKIVST 9

tr|B5XLV5|B5XLV5\_STRPZ ----------------------------------------MNKRVKIVAT 10

tr|Q8DTX7|Q8DTX7\_STRMU ----------------------------------------MNKRVKIVAT 10

sp|Q07637|KPYK\_LACLA ----------------------------------------MNKRVKIVST 10

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sp|P00549|KPYK1\_YEAST IGPKTNN---------------------PETLVALRKAGLNIVRMNFSHG 55

sp|P14618|KPYM\_HUMAN IGPASRS---------------------VETLKEMIKSGMNVARLNFSHG 79

sp|P0AD61|KPYK1\_ECOLI IGPKTES---------------------EEMLAKMLDAGMNVMRLNFSHG 38

tr|Q836R2|Q836R2\_ENTFA IGPASES---------------------VDMLVNLINAGMNVCRLNFSHG 38

tr|Q88VY2|Q88VY2\_LACPL LGPASTD---------------------TDTIVKLIEAGANIFRFNFSHG 38

tr|B5XLV5|B5XLV5\_STRPZ LGPAVEIRGGKKYGEDGYWAGQLDVEESAKKIAELIEAGANVFRFNFSHG 60

tr|Q8DTX7|Q8DTX7\_STRMU LGPAVEIRGGKKFGEDGYWGEKLDVEASAAKIAELITEGANVFRFNFSHG 60

sp|Q07637|KPYK\_LACLA LGPAVEIRGGKKFGESGYWGESLDVEASAKNIAALIEEGANVFRFNFSHG 60

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sp|P00549|KPYK1\_YEAST SYEYHKSVIDNARKSEELYPG-----RPLAIALDTKGPEIRTGTTTN--D 98

sp|P14618|KPYM\_HUMAN THEYHAETIKNVRTATESFASDPILYRPVAVALDTKGPEIRTGLIKGSGT 129

sp|P0AD61|KPYK1\_ECOLI DYAEHGQRIQNLRN-VMSKTG-----KTAAILLDTKGPEIRTMKLEG--G 80

tr|Q836R2|Q836R2\_ENTFA DYEEHGARIKNIREAVKITGK------RVAILLDTKGPEIRT-NDMENGA 81

tr|Q88VY2|Q88VY2\_LACPL DHEEHLDRLNKVHEAEKITGK------TVGIMLDTKGAEIRT-TVQANGK 81

tr|B5XLV5|B5XLV5\_STRPZ DHKEQGDRMATVRLAEEIARQ------KVGFLLDTKGPEMRT-ELFADDA 103

tr|Q8DTX7|Q8DTX7\_STRMU DHAEQGERMATVRRAEELARQ------KVGFLLDTKGPEMRT-ELFADGV 103

sp|Q07637|KPYK\_LACLA DHPEQGARMATVHRAEEIAGH------KVGFLLDTKGPEMRT-ELFADGA 103

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sp|P00549|KPYK1\_YEAST VDYPIPPNHEMIFTTDDKYAKACDDKIMYVD-YKNITKVISAGRIIYVDD 147

sp|P14618|KPYM\_HUMAN AEVELKKGATLKITLDNAYMEKCDENILWLD-YKNICKVVEVGSKIYVDD 178

sp|P0AD61|KPYK1\_ECOLI NDVSLKAGQTFTFTTDKSVIG--NSEMVAVT-YEGFTTDLSVGNTVLVDD 127

tr|Q836R2|Q836R2\_ENTFA --ITMKIGDSVRISMTEVLG-TNEKFSITYP---ELINDVNVGSHILLDD 125

tr|Q88VY2|Q88VY2\_LACPL --SEYKIGDKVRITMDDSLDTTHDKIAVTYK---NLYDDVHVGGHVLFDD 126

tr|B5XLV5|B5XLV5\_STRPZ KEFSYVTGEKIRVATTQGIQSTRDVIALNVAGSLDIYDEVEVGHTILIDD 153

tr|Q8DTX7|Q8DTX7\_STRMU KEYEYKTGDKLRIATKQGIESTKDVIALNVAGGLDIYDDVAVGQTILIDD 153

sp|Q07637|KPYK\_LACLA DAISVVTGDKFRVATKQGLKSTPELIALNVAGGLDIFDDVEIGQTILIDD 153

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sp|P00549|KPYK1\_YEAST GVLSFQVLEVVDDK-TLKVKALNAGKICSHKGVNLPGTDVDLPALSEKDK 196

sp|P14618|KPYM\_HUMAN GLISLQVKQKGAD--FLVTEVENGGSLGSKKGVNLPGAAVDLPAVSEKDI 226

sp|P0AD61|KPYK1\_ECOLI GLIGMEVTAIEGN--KVICKVLNNGDLGENKGVNLPGVSIALPALAEKDK 175

tr|Q836R2|Q836R2\_ENTFA GLIDLEVTDIDRDANEIVTVVKNEGVLKNKKGVNVPGVSVNLPGITEKDA 175

tr|Q88VY2|Q88VY2\_LACPL GLLDMKIDEKDEANRELVTTVQNAGVLGSRKGVNAPGVSINLPGITEKDS 176

tr|B5XLV5|B5XLV5\_STRPZ GKLGLKVIDKDIATRQFIVEVENDGIIAKQKGVNIPNTKIPFPALAERDN 203

tr|Q8DTX7|Q8DTX7\_STRMU GKLGLTVTAKDITTREFEVTVENDGIIAKQKGVNIPNTKIPFPALAERDN 203

sp|Q07637|KPYK\_LACLA GKLGLSLTGKDAATREFEVEAQNDGVIGKQKGVNIPNTKIPFPALAERDD 203

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sp|P00549|KPYK1\_YEAST EDLRFGVKN--GVHMVFASFIRTANDVLTIREVLGEQG-KDVKIIVKIEN 243

sp|P14618|KPYM\_HUMAN QDLKFGVEQ--DVDMVFASFIRKASDVHEVRKVLGEKG-KNIKIISKIEN 273

sp|P0AD61|KPYK1\_ECOLI QDLIFGCEQ--GVDFVAASFIRKRSDVIEIREHLKAHGGENIHIISKIEN 223

tr|Q836R2|Q836R2\_ENTFA NDIRFGIGQ--GIDFIAASFVRRASDVLEITKILEEENATHIQIIPKIEN 223

tr|Q88VY2|Q88VY2\_LACPL SDIRFGLDH--EINYIAASFVRKPQDVLDIRELLEEKHMEHVQIFPKIES 224

tr|B5XLV5|B5XLV5\_STRPZ ADIRFGLEQ--GLNFIAISFVRTAKDVEEVREICRETGNDHVQLFAKIEN 251

tr|Q8DTX7|Q8DTX7\_STRMU ADIRFGLEQ--GLNFIAISFVRTAKDVNEVRQICKETGNEHVKLFAKIEN 251

sp|Q07637|KPYK\_LACLA ADIRFGLSQPGGINFIAISFVRTANDVKEVRRICEETGNPHVQLLAKIEN 253

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sp|P00549|KPYK1\_YEAST QQGVNNFDEILKVTDGVMVARGDLGIEIPAPEVLAVQKKLIAKSNLAGKP 293

sp|P14618|KPYM\_HUMAN HEGVRRFDEILEASDGIMVARGDLGIEIPAEKVFLAQKMMIGRCNRAGKP 323

sp|P0AD61|KPYK1\_ECOLI QEGLNNFDEILEASDGIMVARGDLGVEIPVEEVIFAQKMMIEKCIRARKV 273

tr|Q836R2|Q836R2\_ENTFA QEGIDNIDEILKVSDGLMVARGDMGVEIPTEDVPVVQKALIKKCNALGKP 273

tr|Q88VY2|Q88VY2\_LACPL QEGIDNADEILKVCDGLMVARGDMGVEIPAENVPLVQKSLIKKCNALGMP 274

tr|B5XLV5|B5XLV5\_STRPZ QQGIDNLDEIIEAADGIMIARGDMGIEVPFEMVPVFQKMIITKVNAAGKA 301

tr|Q8DTX7|Q8DTX7\_STRMU QQGIDNIDEIIDAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKS 301

sp|Q07637|KPYK\_LACLA QQGIENLDEIIEAADGIMIARGDMGIEVPFEMVPVYQKLIISKVNKAGKI 303

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sp|P00549|KPYK1\_YEAST VICATQMLESMTYNPRPTRAEVSDVGNAILDGADCVMLSGETAKGNYPIN 343

sp|P14618|KPYM\_HUMAN VICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLE 373

sp|P0AD61|KPYK1\_ECOLI VITATQMLDSMIKNPRPTRAEAGDVANAILDGTDAVMLSGESAKGKYPLE 323

tr|Q836R2|Q836R2\_ENTFA VITATQMLDSMQRNPRPTRAEANDVANAIYDGTDAVMLSGETAAGDYPLE 323

tr|Q88VY2|Q88VY2\_LACPL VITATQMLDSMQENPRPTRAEASDVANAVFDGTDATMLSGESANGLYPVE 324

tr|B5XLV5|B5XLV5\_STRPZ VITATNMLETMTEKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVE 351

tr|Q8DTX7|Q8DTX7\_STRMU AITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVE 351

sp|Q07637|KPYK\_LACLA VVTATNMLESMTYNPRATRSEISDVFNAVIDGTDATMLSGESANGKYPRE 353

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sp|P00549|KPYK1\_YEAST AVTTMAETAVIAEQAIAY-LPNYDDMRNCTPKPTSTTETVAASAVAAVFE 392

sp|P14618|KPYM\_HUMAN AVRMQHLIAREAEAAIYH-LQLFEELRRLAPITSDPTEATAVGAVEASFK 422

sp|P0AD61|KPYK1\_ECOLI AVSIMATICERTDRVMNSRLEFNNDNRKLR-----ITEAVCRGAVETAEK 368

tr|Q836R2|Q836R2\_ENTFA AVQTMARIAVRTEETLVN----QDSFALKLYSKTDMTEAIGQSVGHTARN 369

tr|Q88VY2|Q88VY2\_LACPL SVAMMAKIDEKAENTLAE----NGTLQLNRFDKTSVTETIGIAIARAAKN 370

tr|B5XLV5|B5XLV5\_STRPZ SVRTMATIDRNAQTLLNE----YGRLDSSAFPRTNKTDVIASAVKDATHS 397

tr|Q8DTX7|Q8DTX7\_STRMU AVRTMATIDKNAQTLLNE----YGRLNSDNLPRTNKTEVVASAVKDATKS 397

sp|Q07637|KPYK\_LACLA SVRTMATVNKNAQTMLKE----YGRLHPERYDKSTVTEVVAASVKNAAEA 399

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sp|P00549|KPYK1\_YEAST QKAKAIIVLSTSGTTPRLVSKYRPNCPIILVTRCPRAARFSHLYRGVFPF 442

sp|P14618|KPYM\_HUMAN CCSGAIIVLTKSGRSAHQVARYRPRAPIIAVTRNPQTARQAHLYRGIFPV 472

sp|P0AD61|KPYK1\_ECOLI LDAPLIVVATQGGKSARAVRKYFPDATILALTTNEKTAHQLVLSKGVVPQ 418

tr|Q836R2|Q836R2\_ENTFA LGIQTIVAATESGHTARMISKYRPKAHIVAITFSEQKARSLSLSWGVYAT 419

tr|Q88VY2|Q88VY2\_LACPL LNIKTIVAATESGYTAKMISKYRPNADILAITFDERTQRGLMVNWGVQPI 420

tr|B5XLV5|B5XLV5\_STRPZ MDIKLVVTITETGNTARAISKFRPDADILAVTFDEKVQRALMINWGVIPV 447

tr|Q8DTX7|Q8DTX7\_STRMU MDIKLVVTITESGNTARLISKYRPDADILALTFDEKVQKSLMINWGVIPI 447

sp|Q07637|KPYK\_LACLA MDIKLIVALTESGNTARLISKHRPNADILAITFDEKVERGLMINWGVIPT 449

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sp|P00549|KPYK1\_YEAST VFEKEPVSDWTDDVEARINFGIEKAKEFGILKKGDTYVSIQGFKAGA-GH 491

sp|P14618|KPYM\_HUMAN LCKDPVQEAWAEDVDLRVNFAMNVGKARGFFKKGDVVIVLTGWRPGS-GF 521

sp|P0AD61|KPYK1\_ECOLI LVKEITS---TDDFYR---LGKELALQSGLAHKGDVVVMVSGALVPS-GT 461

tr|Q836R2|Q836R2\_ENTFA VADKPSS---TDEMFN---LASKVSQEEGYASEGDLIIITAGVPVGEKGT 463

tr|Q88VY2|Q88VY2\_LACPL VAEKPET---TDDMFD---LAASKAVELGFAKEGDLILITAGVPVGERGT 464

tr|B5XLV5|B5XLV5\_STRPZ LAEKPAS---TDDMFE---VAERVAVEAGLVQSGDNIVIVAGVPVGT-GG 490

tr|Q8DTX7|Q8DTX7\_STRMU LTEKPAS---TDDMFE---IAEKAALKSGLVESGDNIVIVAGVPVGS-GG 490

sp|Q07637|KPYK\_LACLA MTEKPSS---TDDMFE---VAEKVALASGLVESGDNIIIVAGVPVGT-GR 492

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sp|P00549|KPYK1\_YEAST SNTLQVSTV----------------------------------------- 500

sp|P14618|KPYM\_HUMAN TNTMRVVPVP---------------------------------------- 531

sp|P0AD61|KPYK1\_ECOLI TNTASVHVL----------------------------------------- 470

tr|Q836R2|Q836R2\_ENTFA TNLMKIQMIGSKLVQGQGVGEEAIIAKAVVAATAEEAVAKATEGAILVTK 513

tr|Q88VY2|Q88VY2\_LACPL TNIMKIQLIGSKLADGQGVGDETVIGKAVIATSAQEAIDKAVEGGVLVTK 514

tr|B5XLV5|B5XLV5\_STRPZ TNTMRVRTVK---------------------------------------- 500

tr|Q8DTX7|Q8DTX7\_STRMU TNTMRVRTVQ---------------------------------------- 500

sp|Q07637|KPYK\_LACLA TNTMRIRTVK---------------------------------------- 502

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sp|P00549|KPYK1\_YEAST --------------------------------------------------

sp|P14618|KPYM\_HUMAN --------------------------------------------------

sp|P0AD61|KPYK1\_ECOLI --------------------------------------------------

tr|Q836R2|Q836R2\_ENTFA TTDKEYMPAIEKASALVVEEGGLTSHAAVVAIAQNIPVIVGAADATSLIN 563

tr|Q88VY2|Q88VY2\_LACPL TTDKDYLPAIEKSSALVVENGGLTSHAAVVGISMGIPVIVGVKDATSVIA 564

tr|B5XLV5|B5XLV5\_STRPZ --------------------------------------------------

tr|Q8DTX7|Q8DTX7\_STRMU --------------------------------------------------

sp|Q07637|KPYK\_LACLA --------------------------------------------------

sp|P00549|KPYK1\_YEAST ----------------------

sp|P14618|KPYM\_HUMAN ----------------------

sp|P0AD61|KPYK1\_ECOLI ----------------------

tr|Q836R2|Q836R2\_ENTFA NDEVITVDPRRGIVYRGATTAI 585

tr|Q88VY2|Q88VY2\_LACPL DGQLITVDSRRGLVYRGASNAL 586

tr|B5XLV5|B5XLV5\_STRPZ ----------------------

tr|Q8DTX7|Q8DTX7\_STRMU ----------------------

sp|Q07637|KPYK\_LACLA ----------------------