

List of the proteins in the alignment:

PAPS reductase (*bona fide* CysH)

WP_012828290_1 Haliangium_ochraceum_DSM_14365
NP_285339_1 Deinococcus_radiodurans_R1
WP_005296954_1 Corynebacterium_jeikeium_K411
WP_010983569_1 Streptomyces_avermitilis_MA-4680_NBRC_14893
WP_023885019_1 Mycobacterium_avium_RCAD0278
WP_041809132_1 Bacillus_cellulosilyticus_DSM_2522
2GOY_A Pseudomonas_aeruginosa
WP_014029954_1 Acidithiobacillus_ferrivorans_SS3
HMI48_11565 A. ferrooxidans_DCM_16786 (In extended type IV-A locus)
WP_012586919_1 Shewanella_baltica_OS223

MGE-associated CysH

WP_011375648_1 Prochlorococcus_marinus_MIT_9312
WP_069868654_1 Pseudomonas_fluorescens_Pt14
WP_003668031_1 Lactobacillus_reuteri_JCM_1112
WP_000391487_1 Acinetobacter_baumannii_AR_0088
WP_011277382_1 Sulfolobus_acidocaldarius_DSM_639
WP_060553423_1 Klebsiella_pneumoniae_KP-1
WP_011950590_1 Sphingomonas_wittichii_RW1
WP_099516204_1 Microvirga_ossetica_V53M
WP_041437462_1 Thermomicrobium_roseum_DSM_5159
ADC73210_1 Thioalkalivibrio_sp._K90mix (In extended type IV-A locus)
ERX94024_1 Pseudomonas_aeruginosa_BL23 (In extended type IV-A locus)
OPY23619_1 Methanobacterium_sp._PtaU1.Bin097

IV-B associated CysH

ALAS01000151.1_4 Bacillus_coagulans_DSM_1 = ATCC_7050
HCZ47720_1 Gammaproteobacteria_bacterium_isolate_UBA10968
WP_069953983_1 Mycobacterium_chimaera_AH16
WP_125053220_1 Rhodococcus_NJ-530
PBA69169_1 Mycobacterium_avium
SKT67694_1 Mycobacteroides_abscessus_subsp._massiliense
ABH00659_1 Rhodococcus_jostii_RHA1

WP_012828290_1 MSTASSQLPPPPAEDEHASGASASAADDTGRGDL SAWFDAERLAAKSAE-----LERATPQEIILAFALASFA
NP_285339_1 -----MMTAEVRTPEQGGGLTTEPRAPRSAPGHADASAPAFGPETDPRDIIRWALAAHP

WP_005296954_1
WP_010983569_1
WP_023885019_1
WP_041809132_1
2GOY_A
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HMI48_11565
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HCZ47720_1
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WP_125053220_1
PBA69169_1
SKT67694_1
ABH00659_1

-----MSLVDATGLLGGNSDDFRDPAESPQGAPTKTTPLSDEERAANEQLVAEWNDKLEGASAEIIMEWVAEHVP
-----MRTVQADTDTGTERATGRDAELKTLAEQAGR-----LEDASALEIILQWAADTFG
-----MSDVATDFTEEQLRELAERGASE-----LEGASAIIDILRWTDEHFG
-----MSNQVLLYENLKDQDYADLNA-----KMKNDALHVIKWAYEQFN
-----MLPFATIPATERNNSAAQHQPSPMSQPFDLPALASSLADKSPQDILKAAFEHFG
-----MSVETRIQDVLLLLFGELHN-----MKPICH-----
-----MVDHQQKTSDTVPTVTVSTAELTALLSAPKAEQAIELKRINQFLAGLSAQERVLWGLTYLP
-----MIENIQKDIQPELINKYNQE-----LRDMTAQEMLTWGYKEFD
-----MSNRI-----
-----MLNERER-----SLNVSLLDQIKTQASITD
-----MEEKIK-----
-----METRVEEAIELIINASE-----
-----MAERH-----
-----MT-----ARGDEGGEPPVRH-----
-----MSAVTKRMEDAALDGK-----
-----MQTGERRVRH-----
MNRSRHPRAADTGPEPVESQMMSHAFDDQMILPGLGDSLGLNLREPPRST-----HEHGVFFSAPSIDLDGYD
-----MHPTISRAHQFDDQVVI PALGQQLTLLGFEPEPPV-----LAEGTYFDAPAVDLDSYD
-----MMPQKDRDFTFMWNRTKEHKQRVKHAEKNVKHTIEYYN
-----MMTEAEKETYMLRATLPGFKRKVSRSLIIRREALAIEG
-----MRPDTVQRALLHART-----RQHRRAVEQAEWLIAHAM
-----MRGPFVDVALRAIRARRRGP-----SAHRHLLDRIAEHLECND
-----MSGTPRADGLDLTTLRALRRPR-----PNLAAIKERIEEHLDNHD
-----MRGPFVDVALRAIRARRRGP-----SAHRHLLDRIAEHLECND
-----MNAQLDMQQLRAIAAHQRGP-----RTYAGLLDRIGEHLDAHD
-----MVNAPDPGLDLAMLRLGRAPSAKADP-----GAVADILTRIEAHLAHD

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WP_012586919_1
WP_011375648_1
WP_069868654_1
WP_003668031_1

P---RVAIST---AFGVEGCA--LLHMAVQIDPS--VR---VFTIDTG-----YLFD---ETQQLIERMRERL-G
D---LLMPS---AFNLNGVV--LLDLAAQAGYR--GE---VVFVDTG-----YHFP---ETLATRDRLESRYPE
G---KVAV---TMSMQDTV--LAELAEGRLAEDRAE--LVFLDTG-----YHFA---ETLETRDKVQORY-N
K---KFCV---TSSMEDAV--VAHLASRTFPG--VD---VVFLDTG-----YHFP---ETIGTRDAVEAVM-D
PVDGPRGWATCKYVVACNMQDAV--MVSLACDVRPG--VP---VLFLDTG-----YHFP---ETIGTRDAVEAVY-D
D---DLVYAC---SFGAEGIV--LIDLISKVKKD--AK---VVFLDTN-----VHFD---ETYELIEQMKKKYP
D---ELWISF---S--GAEDVV--LVDMAWKLNRN--VK---VFSLDTG-----RLHP---ETYRFIDQVREHY-G
A-PYAPAAFAT---SFGAEDMV--LTDLIAKHAPW--ME---IFTLDTG-----RLPE---ETYRLMQETRGRHY-R
-----VVSF---SGGKDDTA--TLLLALERVPREQIV---AIFCDTG-----NEIP---VTQRYLDGLERHL-G
G---NHALSS---SFGIQAAV--MLHMVSQAQAN--IP---VILTDTG-----YLFP---ETYQFIDELTQRL-S
N---QFAITT---SFGIQSSV--LLNMVSKLCLQKKIK--IFWIDTG-----YLPP---ETYHYAEKLIVDL-S
-----VCQF---SCGAASAVATKLALAEYGATHDVQ--IINAFLA-----NEHE---DNRRFALNCEAWF-G
S---VLVSF---SMGKDSIA--VMDLCFKYFKH--VQP--FFMYMVP-----LQFQ-----EEALAKYEHYH-N

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HCZ47720_1
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PBA69169_1
SKT67694_1
ABH00659_1

-----VVSF----SGGRTSGYTVNIFKDDPEAH-----FVYMDTG-----AEHP----ATYQFIKDIKVKHW-K
ELSNLPWELGF----SGGKDSSTVLSLTLKAMERGAMIKTLYVVYADTL-----LEHPILRKEALDALESILKVYP-N
-----VLGI----SGGKDSAA-LAIYMRQHHPPELNIE---YFFTDG-----KELP----EVYEFLGKLEGFL-G
-----ILSL----SGGKDSAA-LAIYLRDRVPE--ME---YIFHSD-----KELR----ETYDYLGRLAIL-G
A---RHIVPL----SGGKDSAA-LAIYLSQQYPHLPFE---YVFSDTG-----AELP----ETYEYFERLEHVL-G
-----ILSL----SGGKDSAA-LAIYLRDRIPE--LE---YVFCDTG-----EELP----ETYEYLERLEAFL-G
R----IVVCF----SGGKDSIASLLHLLDEGVDPAATE---LWVHHDVVDGREGSTLMDWP----FMADYNRKLQSF-D
H----VIVC----VSGKDSIACLLTLIEQGVDLRRVE---LWVHHRVDGAEGSTLMDWA----FNDSFIEKFAAAF-N
P-----IILF----SGGKDSLVLHLMVMQNNN--IP---IYSDSG-----YDYG---SQQIKMPKEMTREI--
I----KWSASV----SFGKDSLVMDDLSSQVMDE--IP---VYFMSD-----YKLP----EIYETIELSQERY-K
E--RHTLAVSF----SGGKDSV--IRLLAQQLQPD--VP---VWSDGG-----LQLP----ETLALMEVQPAY-H
G----FVAW----SGGKDSSTVVDLARQVDPN--IP---VVFYDSG-----LQFP----ETLAYMGELAQIW-R
G----YLAF----SGGKDSLVALHLLTAVEPN--IP---VVFYDSG-----LEYP----QTYEYIADLADAW-N
G----FVAW----SGGKDSSTVVDLARQVDPN--IP---VVFYDSG-----LQFP----ETLAYMGELAQIW-R
G----FVSW----SGGKDSSTVVDLARQVDPH--IP---VVFYDSG-----LFFP----ETWHYLEDLADRW-N
G----YVAF----SGGKDSLIVLDLARRIEPD--VP---VVFYDSG-----LDYP----ETYDYLTELTHTW-R

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ALAS01000151.1_4
HCZ47720_1

TEI-----ET----FHP-----ELSVAEQDER--Y-GE----ALYTRDSDA----CC-
LTF-----VTLNAGASP-----DDG-----QTPPDLYASDPDACC-
LPL-----EN----ITP-----VLNREEQDKV--Y-GP----RLYSRDNTA----CC-
VNV-----IT----LTP-----RRTVAEQDAE--Y-GP----KLHDRD-PDL---CC-
IHL-----LN----VTP-----EHTVAEQDEL--L-GK----DLFARDPNE---CC-
LRI-----EL----KQP-----EITLEEQADQ--Y-GN----ELWIKN-PDL---CC-
IAI-----DV--LSPDP-----RLLEPLVKEKG--L-----FSFYRDGHGE---CC-
LPI-----QV----YFP-----EHGTVERYVRE--H-GP----NAFYES-QELRKTCC-
VRI-----HRLKADFSAEIAAKRRFIARDQRTKREYQRV--PVLVDVYGNPVPSPRSNSQGRIRYRTV
LNV-----KV----YQA-----PMTAAWQEAR--F-G----KLWEQGLDGLLEQYN--
LEI-----EVLQSELSP-----ARMETIHG-----KLWETNKASDLDKYH-
RPV-----TVLRDEKYGA-----DILQVFHRRERF--MKGRN---GAP-----CT-
THI-----IR----VP-----HFETADFYRYGSF-----RDPDYSVPRV-----
INL-----VCLRVVVPKMNKGVGYKIIPIDELKQDLEP--WKEMLKKYGSPYDMPF---CT-
VKP-----IR----LTP-----IEDFISMMVERGY-----PAP----SHRFRWCM-
KKI-----EY----LNP-----DRDFDFWLKE--Y-NH----FLP----SPQTRWCT-
KPI-----IR----TSP-----VDTFDHWLAV--F-GG----MLP----SNHRRWCT-
KKV-----TR----ITA-----LDLLGVSEKHGRSPF--DVVLYEHFSGFLPSRSPRWCT-
KPI-----VR----LNP-----ERPFSHYLDL--YRG----VLP----DARTRWCT-
LPLYFSWLEGGFEGEMCKENAHGRPHKVETP-----EGLITLERDTR--RSKPGTRLKFPQVSASLQTRWCS-
LPVYFSWLQGGIEGEMLKMDAYSKPHMVETP-----GGVICLDRDTS--RTLTPATRRRFPQQSASLTTRWCS-
LKI-----GR-----KAGAKHLYSC----GH----RDPN-----
INI-----SR--AYFA-----DRRPIQEVWEK--F-----GIPGINRTTNMQNKAL
VQS-----VT-----W-WH----RFPAAGRSPE-----

WP_069953983_1
WP_125053220_1
PBA69169_1
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LNF-----EV--IPAEP-----DLLTVFIAAGG--F-DH----RAPDRDLAGTLA-----
LNL-----EV--HRADP-----PLLTVLADSGE--W-DH----HLPTRATTRALR-----
LNF-----EV--IPAEP-----DLLTVFIAAGG--F-DH----RAPDRDLAGTLA-----
LNF-----HT--VNAEP-----DLLTLLIAGGG--F-DH----NAPDRRLPVQLA-----
LDL-----HR--IPTDP-----PLLQVLADSGH--W-DH----SAPVGTPLDLH-----

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2GOY_A

---AMRKVEPTQRAL---R--GLDAWIA-----
---AARKVDPLQRYL---KEQGPSALLN-----
---RMRKVEPLARML---NPFNAWIT-----
---KLRKVQPLEQGL---T--AYDAWAT-----
---RLRKVEPLRRAL---RGYAAWVS-----
---KLRKNTPLKSVL---S--GSKAWLS-----
---GIRKIEPLKRKL---AGVRAWAT-----
---HMRKVEPLRRAL---RGKGAWVT-----

WP_014029954_1
HMI48_11565

VRNGIEQQEVI PKTR---KAHGKVRWSNKA KRRLAVLYPTGNPFLDLCLWKGRFPSRMAQFCTEELKRNI AVTFQLD

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WP_041437462_1

---RLNKVEPMQRAL---AELDVGTWFA-----
---DLRKIKPLENGL---EKYKINCWAS-----
---KLLKRRLLD AWK---Q--PGDVMVF-----
---KIRGIYAYLRKQ---TGIAWIAG-----
---ARMKTEPF EKYCNDVFGKNNYERWI-----
---ERLKL RPKRFRM---EQLGK FVQLS-----
---RQLKL RPFELWVRPMLASGDTVTSYV-----
---KMLKLKPFENYV-----GDSPVIN YV-----
---RMLKIHPFENHI-----GGDKAYS YI-----
---RMLKIRPFERYV---GDDPTIHYI-----

ADC73210_1
ERX94024_1
OPY23619_1

---SALKIDVGRRALNNQSRFDGKRVLFVT-----
---SAAKIDVGRRAITNQDRFLGTKTLFVT-----
---SKRFFGNLFRVM---KKHNCNLELL-----
---KVLKKDVSDKWA---KEHGYNGIFW-----

ALAS01000151.1_4
HCZ47720_1

---AVSKAALCRRE---GWDGYIL-----
---NILISGPAAQAH---ARHGRGSLW-----
---DILIGAPSRAAH---KAHGPGEIW-----
---NILISGPAAQAH---ARHGRGSLW-----

WP_069953983_1
WP_125053220_1
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---DLMIAAPAALAH---ERFGSGSLW-----
---EVLITEPARRAH---QLLGP GELW-----

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WP_010983569_1
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-----GLRRDQGG-----ATRAQLAILERYQRGDAE--PLIKVH-----PLAN--WNR
-----ARSRDQAS-----TRADIPFVEEGGARRRVN-----PLAH--WTR
-----GVRRVDNA-----LRANTPVLDVDRGTGRL-----KIN-----PIVA--WSD
-----GLRRDESP-----TRANTPVVSWDEKRRKV-----KIS-----PIAR--WTQ
-----GLRRVEAP-----TRADAPLISFDESFKVV-----KVN-----PIAA--WTD

WP_041809132_1
2GOY_A
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-----GLRREQSP-----TRANTQFVNKDDKFQSI-----KIC-----PLIH--WTW
-----GQRDQSP-----GTRSQVAVLEIDGAFSTPEKPLYKFN-----PLSS--MTS
-----GMRREQAL-----SRQDLAVREWDAAHEMP-----KFN-----PLAD--WHG
LIDQGFPPVSWQGIRREDESP-----NRRNAKRLERIGPKLWAFR-----PLVD--WTA
-----GLRRSQAS-----TREALPILAIHGTRFKLL-----PIIE--WSN
-----GVRSSQTE-----NRKEMKFLDLIRQLSLR-----PLLN--WTN
-----GYTAEVE-----RLEDFRDRNPDRPVA-----PLIDAGLGK
-----GEKINDSI-----VRRAMLKHSIDTQRGRFY-----PVMY--WTD
-----GIRSDEPK-----RLPIEVLEKLSLPIHKDAKNQKAG--FRYLAEISD--FTK
-----GVRMTESS-----ERAKQTAYNGKHEKIIRLGNPIIM-----PILD--WTT
-----AIRADEEY-----REGYASKHKNLKIAL-----PFRENGIDK
-----GLRADEKR-----VGYISTKANITAVY-----PFIEDGLVR
-----GIRADENR-----SGYIGKGQVMLSEEPNIIPVY-----PFKDDGITI
-----AIRADEAH-----RKGYSKKNITPRY-----PFIEAGITK
-----GERREESS-----NRAKYNQMEPHACDRRAGRKARHVDRAWR-----PVLH--WPE
-----GERRAESS-----NRSKYNQLEPHAVDRRKGRGRHVDRAWR-----PVLH--YSE
-----GIRAGEST-----GRKNRTKGPLVRIEGSRRIAF-----PIRD--FDW
-----GIRKQESA-----QRKWMVTSFGVTFENKQGFYRCA-----PIAY--WDA
-----GLRAEESR-----VRAINTAQRGLLYRVQTEGYAGAWHCQ-----PIAR--WSV
-----GVRSQESS---GRRHLY--RTQLARQARAHDFVFDRAGARQRFGGTVHRVDGTITYG-PIWD--WQT
-----GVRADESAKGTGRWSMYNALNVRVTEDECTDCCTTAAQQRQTHGGALDRADGTHVFG-PVWN--WSS
-----GVRSQESS---GRRHLY--RTQLARQARAHDFVFDRAGARQRFGGTVHRVDGTITYG-PIWD--WQT
-----GVRAEESH---DRALLY--RARLAAQTQAHDPMT-RAQVRAHFGGVVARKNGTITYG-PIWD--WQR
-----GVRADESA-----ARRHLYTRGGRRDGI---VTRADGTTAYG-PIWN--WTI

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SDTWRYVLD---NEVPYNPLLDQ-GYK-----SIGCWPCTR-----AVG
EQLEAYAAE---HDLPVNPLYFD-GFL-----SIGCWPCTR-----AVK
EDVEAYIND---HDLIINPLTKQ-GYP-----SIGCETCTL-----PVA
DDVDAYVAE---HGVLTNPLLLMD-GYP-----SVGCAPCTR-----RVL
EQVDEYIER---NRVLVNPLVQE-GYP-----SIGCAPCTA-----KPA
DEIWEYIHL---FNLPYNKLHDQ-GYP-----SIGSKCTF-----PVE
EEVWGYIRM---LELPYNLSHER-GYI-----SIGCEPCTR-----PVL
EEVWDYIRR---FEVPYNRLHDQ-GYP-----SIGCAPCTRA-----VSP
QQTVDVFRS---QDCPLNPLYSQ-GQS-----RVGCV-CINTNKQGLAQTAARYPEEIDRIEDWEWL
KDVHLYLTQ---FDLPYHPLWDQ-GYV-----SVGDTHSSK-----PLE
KDIFFYMKE---NNLPAHPLFSK-GYS-----TVGDWHSSTPDG-----NKT
EDCEAMVLR---AGIKLPLMYRL-GYD-----NANCIGCVKGGEGYFRAIRQDFPEQFEA----LCR
KEVKHYIKM---NKL LYPKFNRELGFS-----F-----HSL
EDILDWW-----EQQPFDLAITE--HL-----G-NCVFCIKKHLNKVALAAKDEPEQAVKW--IEVT
EDVFRYLRSERRWDGREFDYLLNL--YEVKEDNDGCGCALTTDVRFCGWVCTVVKND-----KMP
AAVGEILEA---SGVWPEYYKW--RS-----RSGCTFCFFQKIEWARLKEYHPDAFEEA---KAY

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KDIMQILED----SGLGLPPYMEW-GRS-----RSGCYFCFYQQKIEWVRLYEMHPDLY-----ALA
GDVQRLDD----TGLGLPEYYQW--RS-----RSGCYFCFYQQIGEWQGLKERHPELY-----EKA
HDVIRILQE----SSIGLPSYYTW--RS-----RSGCYFCFFQKIEWIGLLQHHPDLYEKA---MSY
EQVWDALER----YGV TAPVPYRL-GWG-----RSSCMKCI FNDPTIWATLRHHFPGSL-----DAI
EQVWELLAR----HRVEAPVPYRL-GWG-----RFSCMTCIYNSPKVWATIRKYFPERV-----TPI
KDVWAYIIS----NNIEYLSYYDQ--YA-----AIEGYDKVRLSS-----RFS
KDVWAYIVS----RNLDPKLYDYQKY-----QTRDWIRNT-----GWA
LDVWAYLLT----RGATYNAAYDR--MD-----ELGIPLERQVRG-----PPL
SHVFEYLAG----RGI PPNPLYRK--LA-----HLGAPPSLIRVD-----SII
EDIWTHIAA----HDL PVNPIYDK--LR-----RLGTPEQHLRVS-----HIL
SHVFEYLAG----RGI PPNPLYRK--LA-----HLGAPPSLIRVD-----SII
GQVFSYLAG----RGI EPNPLYEK--LA-----RLGAPPAHLIRVD-----SMI
IDVWAHIAAR----HQLPINPVYAK--LR-----ELGVPEQQHRLS-----HLI

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HCZ47720_1
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WP_125053220_1
PBA69169_1

ADADERAG-----R-----WGGKKA-E-----CGIHTFLPRAPESGSADGDDSDA-
PGEDARAG-----R-----WAGKGKTE-----CGLWQGENKL-----
PGQDPRSG-----R-----WAGSNKTE-----CGLHT-----
EGEDARAG-----R-----WAGSTKTE-----CGLHG-----
PGEDPRSG-----R-----WRGRNKVE-----CGLHAS-----
EGEDLRAG-----R-----WSGSNKTE-----CGLHTK-----
PNQHEREG-----RWWWEEATHKE-----CGLHAGNLI SKALEHHHHHH-----
GGQDIRAG-----RWWWENPD TRE-----CGLHVVDGKVIRARSATPQKT PGQ
VGQVSKRGFSTFMCDADDRKDRRAIFADLNIRARVEWAKGDNGTMDLFDHLELPA CASSFGLCE-----
LGMTEET-----RFNGL--KRE-----CGLHYDI-----
KGRATRF-----GI--KQE-----CGIHTNN-----
VQDDL GEG-----SYLFRNRTTNVRFSLRELGDGPVRRNEKIPSCSFFCEMAEADLAAA
AGKELSAI-----KKIYPQDYERILK---FFPEAQAGVLOYEAYKKGDE-----
EGPRVRSE-----GRKYNHHRMYRSRLHLSDVIEAFKDHNRDELFSALRSSKRYGSGSCSESC
VSDTLKEA----RKMIMDISRDLRYRIIDKNGKPRSLNEEGRKEVAKVF-----IGVLEKEPEAFGYDTKELREKLEK
EKNAMDHG-----SPFTWTQGESLSEL---EKPERIIQIFKDYDERKARASAKTLNPLR
QGYEEKAV-----EYGEQFYWCQNETLADLAKPERRAQ- IKRNWEI SEARKKAKRKNVALVET
KGYEQGKN-----GRRYT WVDGRSLNDV-----ENMPRRDIKQKSDE-----
EKLDPVTG-----QRFTWNPEESLQEL---ARPERVEDILT KAGQYKRDKDSTNLLSIL
AAAYEQRFGTTIHRKKIPIKDL SRQA EPM-----EIQDAEAELEQAMRTEYTL PVRSKPGAWGLPKGAYSRS GCGPS-----
AGYEEFGCTISRQKINVV DLSATAEAFDIID-LDALAQARQREYVLP IFTP---EGKAWQLPAGAFVTEGCGSV-----
RGLLHKG-----SLYLDGVLMP-----YRNERPDDWNKLNK-----
TTDGAERG-----RIIWLREFYPNYY-----DEL RWMLPKIDAYV-----
DERAVAAG-----SMEVLRVGWPEQY-----AAWISAIPEGAAAAVAEEG-----
DAAKLSNG-----HITWLQKGWPDF-----DRLSAALPRLREWA-----
DGAFLERG-----RITRLRRGWPA LF-----EELARVLPRIREFV-----
DAAKLSNG-----HITWLQKGWPDF-----DRLSAALPRLREWA-----

SKT67694_1
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DASQLANG-----HITWLAAGWPDQF-----ARLASSLPRLHEFT-----
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WP_012828290_1	-----	285
NP_285339_1	-----	255
WP_005296954_1	-----	266
WP_010983569_1	-----	245
WP_023885019_1	-----	247
WP_041809132_1	-----	238
2GOY_A	-----	275
WP_014029954_1	I-----	246
HMI48_11565	-----	359
WP_012586919_1	-----	260
WP_011375648_1	-----	241
WP_069868654_1	P-----	254
WP_003668031_1	-----	232
WP_000391487_1	IV-----	291
WP_011277382_1	VIEE-----	308
WP_060553423_1	PVEIEDIDDIYGDDEGNCSNICCHK	278
WP_011950590_1	LGGLEPEDDPGLRD----GCLICSL	278
WP_099516204_1	-----DGCVICHL	271
WP_041437462_1	FDDDW-----DACLICHL	264
ADC73210_1	-----	387
ERX94024_1	-----	372
OPY23619_1	-----	239
ALAS01000151.1_4	-----	258
HCZ47720_1	-----	244
WP_069953983_1	-----	277
WP_125053220_1	-----	284
PBA69169_1	-----	277
SKT67694_1	-----	276
ABH00659_1	-----	264