SUPPLEMENTAL MATERIAL

Phylogenetic and Kinetic Characterization of a Suite of Dehydrogenases from a Newly Isolated Bacterium, strain SG61-1L, that Catalyze the Turnover of Guaiacylglycerol-β-guaiacyl Ether Stereoisomers

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Running Head: Characterization of GGE dehydrogenases

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S.P and N.D. contributed equally to this work

Construction of NADH and MPHPV standard curves. The NADH standard curve (shown below) was constructed by adding varying amounts of NADH to wells simulating kinetic assay reaction conditions (50mM Tris pH 8.0 at 28 °C). The MPHPV standard curve was constructed as follows: a GGE dehydrogenase reaction was set up to convert the GGE substrate to MPHPV. The peak corresponding to MPHPV was extracted from the LC-MS and any remaining GGE was quantified. The amount of biosynthetic MPHPV was quantified by subtracting the remaining GGE from the amount of GGE added to the initial reaction. The MPHPV fraction from the LC-MS was then evaporated to dryness and resuspended in 50mM Tris pH 8.0. The standard curve for MPHPV (shown below) was then constructed similarly as for the NADH standard curve.







retention time (min)

FIG. S1. Chiral column separation of GGE stereoisomers. The GGE mixture (top panel) and each individual stereoisomer (bottom four panels) was run separately through the chiral column on the TOF LC-MS.



Fig. S2. Growth of SG61 (panel A) and SYK-6 (panel B) on monoaryl

compounds over time. For each graph, the left y-axis shows the concentration of metabolite and the right y-axis shows the OD600 values for either bacteria. Both bacteria were monitored for growth using vanillin as a sole carbon source. The experiments were monitored for disappearance of vanillin and formation / disappearance of the transient metabolite, vanillic acid.

FIG. S3. Alignment of dehydrogenase genes. Blue blocks are regions of the alignment that were used as input for IQtree.

gi]146275658 Naro/1-269	1 M SGD A I R MDG - KVA I VTGGAG G I GEATARLLTARG - ACVVIA DIA - FERAEALAAD - L A G A I AL PL DL EQEQSVETL VER - 7
gi]334343486 Sphch/1-273	1 M DLR - AEAAEATAAS - IRE - A - G - G - T AEAMAVDVESEAA KSMVDE - 7
gi]146275875 Naro/1-252	1 M A I A I
PP_1946/1-262	1 M T V T V
PP_1817/1-253	1MDLD-PVGGEATVAQ-IHAA-GGEALFIACDVTRDAEVRQLHER-7
gi]87200975[/1-250	1MDID-ER-ADETVAL-ILSE-GGRAAFRKTDVRRAADLDELVAQ-7
SG61_1215/1-250	1MDVD-ER-AEETVAI-IRQA-GGEADFVRTDVADGIQVRALVAA-7
gi]146275951 Naro/1-252	1DRA -GARAEAVAAD - I P G AWGVVVDVVDAAACEAMVEG - 7
SG61_2016/1-248	1M
gi]31615388 Levodione/1-267	1MTATSSPTATATSSP
gi]87200486[/1-256	1DLR-EDWLEAARAT-LPDATRTKL KADVADVAQVEAYVDA - 7
SG61_3730/1-262	1MDID-AAKLEERVKA-LSDA-GHTVFGHHADCADEQQVIGYAEA-7
SLG_20040/1-258	1 M DIA - AS - LEERAAE - LAK I G - E VDF I RADCASET DVRAYVDQ - 7
gi]146275686 Naro/1-245	1MDID-VAGGETLAAQ-IG
gi]334342862 Sphch/1-257	1 M DIN - L DGAQAVAAR - I DA ARG - PG T AYAL RHDVTSEADWIAAVDH - 7
gi]87198897 /1-259	1 M DIN-GEGATATAAA - INA - ELG - AG T AFAMRHDVTSADDWDAAIAF - 7
gi]146275698 Naro/1-254	1 M DRD - L AGAEKVAEG - I RA A - G Q ARALL HDVT NEAQWDEVFAA - 7
gi 334343337 Sphch/1-258	1 M DIS - DEGA - AVARD - I G D AQFLLQDVANEARWAEVVGH - 7
gi]146275892 Naro/1-259	1 M DVL - DEAGEALAAE - L G - D - A ARFFKLDVTSEDNWASVVSE - 7
gi]334342592 Sphch/1-246	1 M DVL - DEEGKALTAE - I G - D - C ARYVHL DVTSEEDWAEAVAL - 7
gi]334342962 Sphch/1-244	1 M D I I - D E E GAGLAAE - L G - P - D - TAYAHL DVADSDAWRAVVDG - 7
gi 334342992 Sphch/1-245	1 M D I D - QERGAALAAA - L G E AAFRTL D VADADDWARAVQ I - 7
gi 334342994 Sphch/1-245	1 M D I D - D V RGAALAEE - L G - P - D - AL FQHL D V SKEGDWTAAI D A - 7
gi]334342590 Sphch/1-248	1 M D I N - T D S G K A L A A E - L G D R L A G - K V A I I T G A G R G M G E S HA R M F V R E G - A K V V L T D I N - T D S G K A L A A E - L G D S A I F V T H D V T R P D Q WS N V E K - 7
gi]87198536 /1-248	1 M DLS - EEAGKALVAE - L G - D N - AVFLKQDVTDPQSWNAVVET - 7
gi]1708836 2,5-DDOL_Sjap/1-250	1 M DL N - EEMAKGVVAE - I RA A A A A L AG - KVAL I TGGAS GLGAAQAKRFAEEG - A KVV I G DL N - EEMAKGVVAE - I RA A - G G D AL F I RL DVT DAASWNNA I AA - 7
gi]62286565 CPNA_COMS9/1-250	1 M DM - ELGHQAVAE - I RR - Q - G K AHFLHLDVTNENHWTGAVDT - 7
gi 33112056 R-specificADH/1-252	1 M GRH - ADVGEKAAKS - I GGTD V I RFVQHDASDEAGWTKLFDT - 7
gi]146275770 Naro/1-271	1 - MELSA DLD - AEA SDTARDVMA RLG Q A ASY I SANVAREEDWERAVAL - 8
gi 334342841 Sphch/1-255	1 M DVA-APE-ALAAE
gi 334343813 Sphch/1-269	1 M
gi 87200879 /1-249	1 M
SG61_3344/1-248	1
SLG_12690/1-249	1 M
gi[146275758]Naro/1-253	1MC
gi[129/13320 SteA_Ctest0Steroni/1-243	A ME AND A A
gi 1402/ 5034 (Naro/1-20/	
rr_1953/1-209 ail30647578lbadH_Roalustris/1_255	
gi[39047070]baur_hpalustris7-200	
gi 334342606 Sphch/1-251	
ai1462757411Naro/1-255	
ail17300321kduD EcoliK12/1-253	
ail334343307 Sphch/1-251	
PP 2794/1-255	
gi]16330475l3-ketoacv/-ACP/1-240	1M
gi]334342640 Sphch/1-240	1M
SLG_38730/1-240	1MAGN-EERAKAFTDAT-GIASYKWDVGDHEACLEGCAQ-6
gi]87201224\/1-240	1MAGN-EEKARTFTAET-GIPAYRWDVGDHEATLEGCAR-6
SG61_907/1-240	1MA-RVAIVTGGTRGIGKAICLALKEQG-RTVVANYAGN-EEKARAFTEET-GIPAYKWDVGDHEATLAGCAK-6
gi]518742570 acetyl-CoA/1-246	1
gi]334343976 Sphch/1-246	1 M
gi]87199449 /1-254	1 M ENR ENR
SG61_1203/1-250	1 M GSN - SAKLRAFRDE - LNA EFG - H - D HVE I TCDLSNTTQVEELVPA - 7
gi 388477173 fabG_Ecoli/1-244	1 ATS - ENGAQA SDY - L G - A N FEG - K ALVTGASR - G GRA AETLAARG - AKV GT ATS - ENGAQA SDY - L G - A N G KGLML NVTDPAS ESVLEK - 7
gi]146318879 gluconate/1-271	1 MNQ QFSLD AHGYVCDVTDEDG QAMVAQ - 8 LKG - KIALVTGASY GIGFA ASAYAKAG - ATIVFN DIN - QELVDRGMAA - YKA A - G I N AHGYVCDVTDEDG QAMVAQ - 8
PP_2783/1-245	1 YVRDEASAAALQAQ - VEGL -GR - DCLAVQCDVKEAPSIQAFFER - 7
gi 334343549 Sphch/1-249	1 DVH - RDEVAEAAQA - IAG A - G G R APFGL DVSDAQMCEALAAR - 7 IGRA I AQGLAEAG - AHVALT DVH - RDEVAEAAQA - IAG A - G R AAPFGL DVSDAQMCEALAAR - 7
gi 334343458 Sphch/1-251	1MTR-QIAIVTGAAA - GFGRAIATRLASDG - TDIVIFDID-APGAHTTAEE - VRA - Q-G - V - T - AEVVIGSVADPDDVRRAFAF - 7
gi(87199578)part2/1-253	1 MP
gi(8/199495)/1-266	1 M
PP_3920/1-255	
gij334343112 Spncn/1-262	
FF_1032/1-249 SC61_1410/1_240	A CONTRACTOR CONT
SIG 12130/1-244	MND DVELVEGSSC GEGAGIVERAGAG ZUVVIT
3L0_12130/1-244 ail640014081/alucose_1_debydrogenese_Bsub/1-261	
gil04301400 /guccse-1-denydrogenase_Dsub/1-201	
ail871995771/1-257	1 MDT GLAKQT GLAKQT
SG61 3726/1-249	1
SLG 20080/1-253	1 MS
gi]334342771 Sphch/1-253	AIAILDD-RVCIITGGAG-SIGLATARLFLSEG-AKVVLVDLH-EDALASAAAE-LAS
gi 512125550 n-pentylphenvlADH Ralstonia/1-251	1 G G G AYR LLN - KTAV I TGGNS G I GLATAKRFVAEG - AYVF I V GR - RKELEQAAAE - I G R N - VTAVKADVTKLEDLDRLYAI - 7
gi 87200895 /1-246	1GIGLAAARLFAAEG-AKLAITGRN-AETLRAVAEELDALCIRSDMGDLNDTERALEE-7
SG61_3191/1-249	1
SLG_07180/1-248	1
gi]87199020[/1-282	1 DID - EAGLAETAAQ S-N G A I RTARCDVTRCEDIKALMDR - 7
gi]334343475 Sphch/1-279	1 M
gi]81821161 PED_AROAE/1-249	1MDLVPAPEAEAA-IRN-L-G-RRVLTVKCDVSQPGDVEAFGKQ-7
SLG_18890/1-249	1 M DIL DCDQTVQS - VKS - A - G - G H - A I AVTGDISSPEAVAQLASR - 7 I GAE I VRTLAHEG - AAVVAT DIL DCDQTVQS - VKS - A - G - G - H - A I AVTGDISSPEAVAQLASR - 7
SLG_18590/1-251	1 DVQ - D AGRTVAA - I EA D - G K ARAYVCDL RDADA I GEL VAG - 7 GL GAAYARRLAADG - FQ I AA I DVQ - D AGRTVAA - I EA D - G K ARAYVCDL RDADA I GEL VAG - 7
gi 167033792 bdh/1-256	1
PP_3073/1-256	1

6	1 M	LQG	- KTALVTGSTC -	- GIGLGIAQALAAQG	- AN I I VN GF F	RADGARQQ - I AA -	- A - GQV I R -	- LGYHGADMSKASE I	EDMMRY - 74
	1 M	LSG	- KTAL I TGSTS -	-GIGLAYAKALAGEG	G - ANVV I N G F G	DADAIEKERVG - LEA -	LS-GGK-	- AL YSGHDL TKADQ I	EAMMQE - 79
	1	MT L KG	- RTAL VTGSTS -	-GIGLAYAKAFAAQG	6 - ANIVIN GF 0	BDAGA I EQERLA - LEA -	AS-GGK-	- AIYSAHDL TRADEI	EAMMAQ - 77
	1	LKD	- KCAL VTGSTS -	-GIGLAYARALAAEG	G - AH I VL N G F G	DPAEIEALCRE - LAD -	AS-GGR-	- A I F A AG DL T R R EG T	EAMMAT - 77
	1	LKG	- KRAVVTGSTS -	-GIGLGIARALAGEG	G-ASVVLNGFO	DAEAISAILHE - LSA -	MS - G A D -	- AMHVPADLMQRSGV	EALMEA - 77
0	1	MQ L KG	- KSAIVTGAAS -	-GIGKAIAELLAKEG	6 - AAVA I A DL N	I-LEAARAAAAG-IEA-	- A - G G K -	- AIAVAMDVTSEASV	NQATDE - 75
	1 M TD	· ARR LTG	- RNAL I TGSVG -	-GLGQAMARKLASAG	G - ANVML H GL E	EPEEAACLTEA - IER -	- EFG V R -	- AFYCRADL RQTAAV	RELVDR - 81
	1 M SD	RRR FEG	- RSVF I TGAGS -	-GIGEATAHAFAEEG	G - AKVT I A EL [) - PAKGEAVRDA - I RA -	- K - G G T -	- AIFVATDATDEASV	KAAIAA - 79
	1 · · · · · · · · · · · · · · · · · · ·	· YD FEG	- KTLLLTGAAG -	-GIGREVARLFAAHG	G - ANL VL A DL [O-AVVLASLADE-LEI-	-P-PER-	- VAVIAFDASSEQDA	QAAVAL - 76
	1 MTF PLPNA	LSG	-QIALVTGATS -	-GLGYRFARILAHAG	G - ARVAVA GRF	R - KDRL DKVVDE - I RA -	- A - G G Q -	- ACAIIL DVGDAGSL	ADAVAQ - 84
	1 · · · M	· AGT FEG	- KVALVTGAAS -	- GIGRAAAIRFAEEG	G - ARVFCA DLN	I-LAGAEAVAAG-I	GKG-	- ASAVQVDVASYASN	IQAMVDA - 74
		FEG	- KNVIVIGAAS -	GIGRATATREAAEG		-VAGLEETAAM-MAS-	-A	- PVIQPFDAVDNASC	KKLVEV - 72
		RFDIKG	- RSAL VIGAAS -			- AEGAEREAAR - LRA -	-E-GTE-	- VRAEKL DVSDWDNV	AAAFDA - 61
			- RSAL VIGAAS -				-A-GYD		TOVEDE 96
	1	VES	- ARVIVIGAAS -				-1-678-		/DDTENA - 81
	1 MI FISGS	T PG HNG	- RVAL VTGAAR -	-GIGIGIAAWI ICEG		- RORGTKVAKA - L		- AWE I TMDVADEAOV	SAGVSE - 80
	1MADD	VAG	- KVAL VTGGTS -	-GIGRMIAEGYAERG	G - VRTYIT GR	- FDRLOGIAAD - LSA -	- STG G T -	- CL PL VADL ADPEGP	ARLVEA - 81
	1MSVSVPPYPTP	LGMLKG	- KTVVVTAAAGT	-GIGFAVAKRAAEEG	G - ARLL I S DF H	- ERRLGEAADR - IAA -	- EVG - CE R -	- PATVVCDVTNEAQV	QDLRDA - 90
	1 M		TAL VTGTAS -	-GIGAASARWLDAQG	GIERLILV DRD	- ADGL NAL EL S	CV-	-VERHAGDVSDPAFW	VQ A 62
	1	IQG	- LAAIVTGGAS -	-GLGAATAELLAARG	- AKVTL F DL N	- ADLGNAKAAE - I	G	-GRFAAVNVTDEDAV	ANAIAE - 70
	1	FRG	- LAAIVTGGAS -	- GLGGATAERLARGG	G - AKVTVF DL N	I-ADLGEAHAKA-I	G	-GHFIKVDVTNEAAV	DAALDE - 70
	1	LEG	- L SAVVTGGAS -	-GLGAATARALSAHG	G-VEVALFDLN	I-EESGEAVARE-I	G	-GIFCKADVSSEESI	EAAFAK - 70
	1	LDN	TVAAVVTGGAS -	-GLGAATARALAAKG	6 - VKVA I F DLO	- KEKGEAVAAE - I	G	-GVFCEVNVTSDESV	DAGFAK - 71
	1	· MK I DN'	TVSAVITGGAS -	-GLGEATARALAARG	6 - AKVAL F DLC	Q-QEKGESVAAE-I	G	-GIFCQVDVTSDESV	DAGFAK - 71
	1	IAN	- KHF I VSGAAS -	-GLGAATAQMLVEAG	6 - AKVML V DL N	I-AQAVEAKARE-L	G D N -	- ARFAVADISDEQAA	QSAVDA - 72
	1	PAG	- KIAIVSGGNS -	-GLGEGGVKCLLAAG	G-AEVVSFDVS	6 - G D A P Q	G	- AEF I RCDVSDEASV	KAAVDQ - 64
	1	MM	- EAVL I TGGAR -	-GLGEVLVRAFHGAG	G - WRVAVS D I [- GDAAHGLAIS - LDA -	- S - G K T -	- ALGLALDVRMQTDF	EAARDV - 72
	1	· M	- KSAL I IGGAS -	- GVGAATARAFAAEG	G - VRVAVA DL A	- VEPAQAL VDE -	-L-GPD-	- HRAYRCDITSETDI	LSLFDK - 68
	1	· MS QNK	- KVALVTGAGS -	-GIGRAVALALLEDN	N-FSLVLAGRH	R-AEPLQAVVEQ-ALA-	-A-GGE-	- ALAVPTDVRDEQSV	AHLFAT - 75
	1	EL LKG	- RVAVIIGAGS -	GIGEACALOXAAAG			-S-PEP-	- ILCVPIDVSDAGSV	AALFUK- 73
	1 M		- HTALITGASS -	-GIGAGIARCEAACG	- ARVVLA ARF				ANLFRQ-70
	1 M T	GNRLDN	- RAAVVTGAAD -	-GIGEGIARREAAEG	- AAVVVA DYI	- DERGPAVARD - L RG -	- G - G A Q -	- AFFIRCDVSRREDV	/ IGAVDL - 78
	1 M	ERPLEG	- KVAL I TGSGS -	-GMGVGIALAVAKAG	G - AAVAL V GR1	- AQTLERTRAQ - LEA -	- A - G G R -	- ALVAPCDITDRAQV	DAAVAR - 77
	1 • • • • • • • • • • • • • • • • • • •	IAG	- KRVIITGGAR -	-GIGADTARYFAHHG	G - AKVVTF DIF	- DEEGDALAKE - ASS -	-Q-G-PGS-	-VVYRRVDITSIPEI	NAGVEF - 77
	1 M		- KRVL VTGGGA -	-GIGLAIAKRFIEDG	G-ARVLTCDVD	- ETAL NAAL EA - VPG -		- LLGLHCDVSREADL	DALFGA - 67
	1 M	TEQ	- RTLLVTGASS -	-GIGAACARRLAAPG	- VRLML HASGRDE	IKRAALEALAAE - LAE -	-G-GAQ-	- TATCFLDLAEPGAG	TALASA - 79
	1 M	SVE	- KVAIITAGGS -	- GMGAAAARRLAADG	6 - F K V G I L S S S	GKGEALAAE-L	G	-GIGVTGSNQSVEDL	. KRLVDA - 68
	1 M		- KTAFVTGASS -	-GFGRAICCTLIGKG	6 - YRV I GG A R F	R-MDKLKALEAE-L	G V N -	- FIPLAL DVTDSVSL	DKAVEQ - 68
	1		-MIVLVTGATA -	-GFGECITRRFIQQG	6 - HKV I AT GRF	R-QERLQELKDE-L	G D N -	- LYIAQLDVRNRAAI	EEMLAS - 67
	1 M A		-GTALITGATA -	- GIGAAAARRFTAAG	G - WK V I V T G R F	R - AERL DAL VAE - L	GAD-	KVHAISFDMRDEAAI	DAALAA - 70
	1 - M		-SIVFIIGAIS-	-GFGEATARRFAEAG	G-WKLVLIGRH	- KERLDALCAE - L	SAKI		IEQAIAN - 71
	1 M		- K I I I VTGASS -	-GIGEATVRELVAAG	- AKLF IG ARF		GEN-	- VAWQEL DVT DGAAF	/FAFVAA - 73
	1 M	FSN	- RVAVVTGGAS -	-GIGFGLAERFLAEG	G - MKVVLG D I E	- AAALDKAVGA - LSE -	- N G E -	- VLGVQTDVSDFRSL	QSLADA - 75
	1 M	VQG	- RTAF I TGGAH -	-GIGLGIARALAADG	G - VKVALA DL	- ANALSLCKAE - LAS -	- I - T E -	- VET VRL DVRDRQGF	VEAIDH - 75
	1 M	FEN	- EIAFITGGAS -	-GAGFGQAQVFGRAG	- AK I VVA DVF	R-AEAVERAVAA-LKA-	- E - G I V -	- AHGL VL DI TDRQAY	AGAADE - 76
	1 M	FQD	-QVAFITGGAS -	-GAGFGQAKVFGQAG	G - AK I VVA DVF	R - AEAVEKAVAE - LEG -	- L - G I T -	- AHGIVLDIMDREAY	ARAADE - 76
	1 M	QD L EG	- KVAFVTGGGS -	-GVALGQAKVLAEEA	QMKVVIA DIF	R-QDHLDEAMGY-FSQ-	- K - N V A -	- VHPVRL DL TDRAAY	AAAVDE - 77
	1 M	· KD FAG	- RTAFVTGGAN -	- G V G I G L V R Q L L N Q G	G - CKVA I A D I F	R-QDSIDKALAT-LEA-	- E - G SGPE -	- VMGVQL DVASREGF	KMAADE - 78
	1 M	KD FAG	- RTAFVTGGAN -	- GVG IG IVRNLLNEG	6 - CKVA I A D I F	R - QDA I DRALAT - L DN -	- R E -	- VMGVQL DVASREGF	KEAADK - 74
	1 M	FAG	- RTAFVTGGAS -	-GIGLGIVKALARRD	D - A F V V I A DM F	R - TDH I SRAL KA - LAS -	- A - GLGE S -	- VAAVEL DVT DRAAY	ASMARR - 80
	1 M P	·	- KVAFVTGGAS -	-GIGLGISKVLIERG	G - AQVVIA DLF	R-QDHIDHALAL - FAG -	-G-GQSNA-	- VSALQLDVTNREKY	REAAER - 80
	1	IAG	- TTAF I TGGAS -	- GIGFGIAQRLLANG	6 - ARL VL A D I F		QQ-GRN-	- VHT I RL DVSDRAQM	IAEAARE - 77
	1		MSFVIGGGS -				-E-GWADR-		AAALDE - 71
	1		- KGAFITGGAS -	-GIGLGMALVEARAG	S-MNVVIADVF		- A - GL AG K -	-VHGLLLDVTDRDAY	(AAAADE - 78
	1	WKEVRG	-KTAFITGGAS	-GMGLGMAKAFAFAG	- MKVVIA DIF	-QQALDEAMAE-FAH-	-T-NFA-	- VHP RL DVTDRDGM	VSKAAEF - 76
	· 1 · · · · · · · · · · · · · · · · · ·	VSG	- KTAF I TGGAS -	- GMGWGMAKAFGEAG	G - MKVIIA DIF	- ODAL DOAMEG - FSK -	- T - NL A -	-VHSILLDVTSRDGW	VARAADE - 76
	1 M TGS	FTG	- KTAF I TGGVN -	-GIGFGIARAFALAG	G-MDLILTYR	- DEDRDDAARW - LAD -	- N - G - L A P -	- ARFVRL DVT DRARF	AQVAAE - 81
	1 M STA	WEG	- RVAF I TGAVT -	-GIGLGVAQAFADAG	G-MRLALSYRN	I-EDDKNRVAEW-FKA-	- K - G - YE Q -	- PLFLKLDVTDRARF	AQVAEE - 81
	1 M	WTG	- KVAF I TGAGT -	-GIGFGIARAFSDAG	G-MRLALSYRN	I-EAQRARCDAW-FAQ-	- R - G - RE A -	- PLWIRL DVT DRPAF	ADAADK - 76
	1 M	LTG	- KVAF I TGGAN -	-GIGFGMVRAFLAEG	6 - MKVVVA DWS	S - TSHIENAKAA - LKG -	- N N A -	- AHF I RT DVADRANL	. KAAVEE - 75
	1 M	RN FAG	- KVAFVTGGAS -	-GIGLGMVRNFLAEG	G - MKVV I A DYN	I-EDHL DQARE I-LRG-	- N N A -	- THL I RVDVADRENL	RAAAQE - 75
	1 · M	RE F RG	- KTAF I TGGGS -	-GIGLGMARAVLDRG	6 - MNVVVA DL L	- DSHLTEAREL - LGS -	- T N R -	- L HCIRLDVSDRAAM	IKEAAEE - 75
	1 M Q		- KRIMITGAGS -	- GLGRE I AQRWAREG	G-WRLALADVN	I-EAGLRETLEQ-VRQ-	- A - G G D -	-GFVQRCDVRDYSQL	. TALAQA - 72
	1	· · · · · M · VER	- KAIFITGGGS -	- GIGRAVARRFAAEG	G-WLVGIADIH	I-PAGMAETAAA-LPP-	GS-	- ASL HQL DVRDREMW	DMKLAEF 73
	1		-KIIFIIGGAS-	- GIGRAVAQREGQGG			GR-	- SSRHKL DVRDRSAW	VDAALADC /1
	1 MMD M		OVALVSCACE	-GEGRALAERI AGEG					DEALKGF /1
	1 M		- FIAIVTGAGP	-GEGRAIAERLAGEG	- AAVALL ARS	- LEQLEEVAGI-IRA-	- A - G G F -	- A LAL CADVIDRASI	DRAVS0 - 76
	1M	SA-RITF	- TVAEVTGGGR	-GLGAGIATAI AFAG	6-ASVVVAART	-LPQVEETVOA-ITR-	-A-GGP-	-ALAVRCDVTDRDSV	/AAAYAD - 77
	1	FAG	-QVVWITGASS -	-GIGAAMARALAAOG	G-AKLVLSGRM	I-EAALAELARNC	GD-	- ALVLPFEATDYAAA	ASAAKK - 71
	1 M	TIALNN	-VVAVVTGAAG -	-GIGRELVKAMKAAN	N-AIVIAT DM4	PSAD-VE	GA-	- DHYLQHDVTSEAGW	VKAVAAL - 68
	1MARET	DNRDRDAFAG	-GVAVITGAGS -	-GIGAGLARRAGELG	G-MTVVVT DIN	-QEGAARTVGE - IEA -	- A - G G K -	- AEAL RVDVSQPEEL	DRLAET - 85
	1 M	TTL	PTVLITGASS -	-GIGATYAERFARRG	G-HDLVLVARD	- KVRL DAL AAR - L RD -	- ESG V A -	- VEALQADL TRPADL	AAVEIR-75
	1 M	TTR	- PTVL I TGASS -	-GIGATYAERFARRG	6 - HDL I L V A R I	- TSRMEALALR - LRE -	- ESH V A -	- VEVL PADL TSSADL	SVLESR - 75
	1 M	VTM	- KKAL VTGSSS -	- G I GAAFAAHL ARQG	6 - SDL VL V ARF	R-QDRLETLAER-LRG-	- ETG V S -	- VEVL KADL ADPT DL	HRIEER - 75
	1	MT	- RYAMITGASS -	-GLGLALAEALARRG	6 - RNL I L V A RG	- RETLEPVAIE - LTQ -	- RFG V E -	- VL F RACDL SQ PL RL	SGFVLE - 73
	1M	G R L AG	- KVAVIMGATRE	GNMGQAIARRFLDEG	G-AHVVVSGRO	- KEGL DVFAAA	- T - G	- ATAMACDIGSRAQI	QSLADA - 73
	1 M		-QTILITGASS -	-GYGLETARHFLERG	G-WNVIATMRS	- PDRS VL P -	- P - S E N -	- L RVL PL DVTSEASI	ATLVEA - 65
	1 M		- KIVLITGCSS -	- GYGLETARHFHANG	🦻 - WN VIAT MRH	1 - P KAD I L P -	- A - U D R -	-MRIVPLDVTRTESI	ALAIEA - 65

gi|84570596|bdh2_Rpickettii/1-256 gi|334345171|Sphch/1-263 SLG_32730/1-261 gi]87199767\/1-261 SG61_1243/1-257 gi]84570594|bdh1_Rpickettii/1-260 gi|334342462|Sphch/1-265 gi|334343092|Sphch/1-255 gi]334343456|Sphch/1-245 gi]334343408|Sphch/1-258 gi|146275993|Naro/1-256 gi|146275997|Naro/1-246 gi]87199890[/1-279 SG61_474/1-283 SLG_24920/1-278 PP_1951/1-275 PP_2002/1-257 SLG_15310/1-259 gi|146275988|Naro/1-261 SG61_609/1-245 gi]146275674|Naro/1-255 gi]334343001|Sphch/1-254 gi]334343319|Sphch/1-259 gi]87199092|/1-261 SG61_354/1-260 PP 2214/1-255 SG61_3175/1-254 gi]146276032|Naro/1-246 gi]334342802|Sphch/1-249 PP_1708/1-252 SLG_05090/1-250 SG61_2863/1-244 SLG_35070/1-243 gi]146275941|Naro/1-266 gi|334343077|Sphch/1-254 gi]334342781|Sphch/1-260 SLG_31530/1-250 SG61_2583/1-255 PP_2175/1-234 PP_0488/1-253 gi|2506152|YDFG_ECOLI/1-248 gi|334345036|Sphch/1-249 PP_4862/1-254 gi]334346119|Sphch/1-241 SLG_33310/1-241 gi|334342779|Sphch/1-273 gi]334342815|Sphch/1-290 gi|87198230|/1-306 SLG_08640/1-305 SLG_35880/1-297 gi]87198815[/1-310 SG61_724/1-305 gi]87199892[/1-280 SG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277 gi]87198816[/1-310 SG61_2705/1-303 SG61_1498/1-309 SLG_35900/1-311 gi|87198727|/1-305 SG61_3329/1-309 SLG_12640/1-304 SG61_2549/1-315 SLG_28340/1-294 SG61_2706/1-296 PP_1745/1-269 gi]334342965|Sphch/1-259 gi|87199139|/1-266 SG61_504/1-269 SG61_782/1-273 SLG_38070/1-265 SLG_27950/1-266 gi]87200928[/1-272 gi|146275769|Naro/1-259 gi]146275845|Naro/1-289 4BMV:A|PDBID|n-pentyl/1-262 PP_2989/1-264 SLG_18780/1-267 PP_0429/1-260 gi]334343146|Sphch/1-268 gi|334343373|Sphch/1-250

SG61_417/1-252

	77 TVAHF - GRL -	- DVL HN NA	AL - LG	• PEIAQA DGDVE!	R MGTALWDRTFAVNVRGTMIA -	- CRAAL PHL	RE	T R	G	CIVN	ITVSN	148
	77 SVARF - GRL -	DILHNNA	AL-LD	PDITPL DLSVV	TIPADLWDRVMAVNVRSVMLG-	- CKYAIPVM	LE	NG G	G	SIIN	TGST	149
	80 TVDTF-GGL -	DCAFN NA	GI-NR	VT/	D DQYDDA IWERD IA INL SGVMRC -	-MREESAVM	LE	RGG	G	AIVN	TASI	145
	80 VVAHY-GGL -	DIAHN NA	GI-EA	NIVPLAF	E L DSDNWRRV I DVNL SSVFYC -	- LKGEIPLM	LK	RG	· G	AIVN	TASA	147
	78 LMAAY - GRL -	• DYAFN NA	GI-EI	EQHRLAN		-MKYQLPLL	LA	QGG	· G	AIVN	TASV	145
	76 CLURF - GRM		GV-LP	PQRPIH			LK	VG			TASV	143
	72 IRERE-GRI		GI-TE	VTALG							ITTSI	145
	75 AVAOF - GRL -	DLAVN NA	GI-AG	A		-MRYQIPAM	LE		G	SIVN	MASI	142
	86 TTERF-GRI-	DGFFNNA	GI-EG	- K	SFTAAEFDKVVSINLRGVFLG-	-LEKVLKIM	RE	QGS	G	MVVN	TASV	153
	75 TVAQF - GRI -	DGFFNNA	GI-EG	- R	N FGAEEFHRVISINLDGVFYG -	-MAAVLKVM	RE	QG F	G	AIVN	TASV	142
	78 ALKAM-GRV-	DGFFNNA	GI-EG	H LAPTH	E YEVAEFDRVLHVNLRGMFLG -	- L RYVL PDM	VK	RGA	G	AVVN	TASI	145
	75 TVAKH-GRI-	DG F F N NA	GV-EG	· V I T P I H/	E YP I DEYDR I LAVNL RGVFLG -	- L R F V L V Q M	VA	QG S	G	AVVN	TASI	142
	70 APF - ERI -	DVLVNNA	GI-TT	LGSVE	E I T L DQ F R H E L D I D V L G V F M G -	- IQATLPRM	кт	HG	G	SIIN	MSSL	133
	79 ARETM-GGL ·	- SVL VN NA	G I - VV	TGSVE	D L SL DDWHRGMA I NNDSVFLG -	- SKYAL PL L	RE	NQ P	A	SIVN	LSSI	145
	79 AAEKL - GGL -	SVL VN NA	GV-GV	RGNIE	T CTL EEWHRGFAINVDSVFLG -	- CQKALPLL	RD	SQ P	A	SIVN	ISSI	145
	79 IEAED-GKL	DVLVNNA	GI-AV	LRPIA	E MTTADWNLQNSVNLDSVFQG -	- TKRAVVLM	RK		• • • • • G	SIIN	ISSV	146
	73 ALESW-GRL		GI-SM	EVOL					· G	AIVN	ISSM	139
	74 VEAAL-GPV-	- DVL VN NA	GI-CT	MCSIE						SIVN	1000	140
	74 CIDRE-GRL		6V-66	GAFLA		- MRACIPHM	AK			SVIN	1331	140
	74 AAELF-GGV-	DILVNNA	GY - YK	· · · · · · · · · · · · · · · · · · ·	D SHSEEFGRHVEINDKGTFLG -	-MQAVVAPM	RA	AG R	G	AVVN	IIASV	140
	74 AMRAF - GRI -	DILVNDA	GY-YR	ATPLQ	DATVEEFQRHVEVNQLGVFLG-	-MQAVVAPM	RA	AG G	G	AIVN	IISST	140
	74 ALAAF - GKI -	DILVNNA	GI-LG	• P	D L T E E G Y H L V C A I NQ H A V F Y G -	- MQAVL PAM	· VK ·	AN K	G	SIVN	IISSI	141
	74 AVREF-GTI-	DILVNNA	GI-LG	• P	S L DDEGYRKVCAVNQDSVFFG -	-MRAVLPVM	VK	AR R	G	SIVN	ISSI	141
	78 AVDGF - GGL -	TTLSNTA	G I - I H	PGGFE	E ES I EGWNKMVAVNQTA I FLG -	- IKAAIPEL	VK	N	G	SIIN	ISSL	144
	77 ILAES-DRL -	DALVN NA	GI-LT	LKPVQ1	D TSNEEWDRIFEINVRSVFLG -	- TRAVIEPM	RK	АН К	G	CIVN	VSSI	143
	77 TEEAF - GPV -	• T T V V N N A	GI-AV	SKSVEI	D TTTEEWRKLLSVNLDGVFFG -	- TRLGIQRM	KN	KGLG	A	SIIN	MSSI	144
	81 VKERH-GKC-	HVLVNNA	GI-DL	TOPLE		- TKHFVPLM	AE		· S	SIIN	VSSI	152
	70 AQEEA-GGL	- D I L V N NA	GI-LI			- CRYAVPLI	AE		G	AVVN	MSSI	141
	74 AVAAN-GPL	DGI FI NA	61-66		D YGDEAEDAVI AVNI KSVEWA -		KE				TGSI	142
	73 AAAHF - GP I -	EGLFANA	GL - TG	G	SFDPDVFEQTIKVNLTSVFWA-	- IQKVLPAM	IE	AN K	G	AILV	TGSM	140
	74 AADRF - GPA -	YGL FA NA	GL - AG	• N FAPAL	D YPGEL FEDVL RVNL TSVFWA -	-MQAVLPAM	IA	AG E	G	SILV	TGSM	141
	78 TLRLF-GRL-	DTLVNNA	GL - VR	FGTVE	D L SWDDYKLQTDVMAGGTFLG -	- CKAAIPHM	sk	DGS	G	SIIN	MASV	144
	73 IREKL-GTV-	- DVL VN NA	GV-GS	·	D I PDATWERV I GVNL NGAFYC -	- ARAAVKQM	QE	GKG	G	ΑΙ٧Ν	ISST	139
	72 VAARL - GGV -	DILVNNA	GI-GS/	PGDGMAEYYAGQAAQAGGDASA YADQT I !	H CTDDGWSRVLSVTLDGAFRC -	- SRAAVRIM	AE	- QGT G	G	AIVN	IGST	163
	72 VDAKF - GRV -	DVIINAA	GI-NAI	TREANQKMVDANVAALDAMKSGRAPTFDFLA	D TSDQDFRRVMEVNLFSQFYC -	- IREGVPLM	RR	AG G	G	SIVN	ISSV	165
	77 TTTTL-GPV-	DILVNNA	GW-DI	FKPFT	K TEPGEWERLIAINLTGALHM -	- HHAVL PGM	VE		• G	RIVN	IASD	143
	74 MIDWT - GQL -	DTVVNAA	GM - WF	GGTVLI		- ARAAL PRL	KE	TN	· G	SIIN	IASV	139
	77 VI SSL -GGL -	DILVNNA	GI-IR			- SQAAARPM				KIIN	ILASM	144
	79 AVAEF - GHI -	DILVNNA	GL - IR	REDAL	E	- SQAAAKHE	IA		G	KIIN	LIASM	146
	76 VEPLL - AEV -	DILVNNA	GV-AA	DKPFL	DQSEEDWDRVLDTNAKGMFLL-	- SQSAARAM	KA	HGRG	G	SIIN	IASI	143
	84 A G P L -	DVLVNNA	GV-SD		A CDDQTWDHVLDTNLKGAWAV -	- AQESARRM	· VV ·	AG K G	G	SLIN	IVTSI	147
	69 ITDKL-GPV-	YGVVA NA	GI-TK	DNFFP!	<pre>K L T P A D W D A V L N V N L K G V A Y S -</pre>	- IKPFIEGM	YE	RK A	G	SIVA	ISSI	135
	69 VAEAL - GPI -	DVVVN NA	GI-TR	DGVLA	K MSFDDWNEVMRINLGGCFNM -	- AKATFGGM	RE	RGW	G	RFVN	IGSI	135
	69 VAEDL - GPI -	- DVL VN NA	GI-TR	DNVML	K MSFEEWNEVIRINLGGCFNM -	- AKAVFPGM	RE	RGW	G	RIVN	IGSI	135
	69 VAAEV-GPI-	DIVVNNA	GI-TR	DGVL HI	K MSFDDWNEVMRINLGGCFNM -	- AKATFSGM	RE		· G	RIVN	IGSI	135
	69 VEAEV-GPI-	- E I V V N NA	GI-TR		K MSFDDWNEVMRINLGGCFNM -	- AKACFPGM	RE		• • • • • G	RIVN	IGSI	135
	75 VKAEV-GEV-	- D V L V N N A	GI-TR							PIIS	ITSV	141
	82 ALDTL - GKL	DILVNNA	GI-TR		R	-MRAATKPM	MK		G	RIVT	ITSV	148
	78 TVDTL -GKI -	DILVNNA	GI-TR	DNL AM	R MKDEEWDQVIRINLEAAFRL -	-MRASCKPM	MK	AR F	G	RIIT	ITSV	144
	73 IRAEF-GEV-	DILVNNA	GI-TR	DNLLM	R MKDEEWNDIIETNLSSVFRL -	- SKAVMRAM	MK	KRH	G	RIIT	IGSV	139
	85 IESEV-GII-	DILVNNA	GI-IR		E MTAAQFRQVIDIDLNAPFIV -	-SKAVIPSM	I K	KGH	G	KIIN	IICSM	151
	75 VEQRF - ERI -	DLLVNNA	GI-TR	DGLLA	T QSL ND I TEV I QT NL VGT LL C -	- CQQVLPCM	MR	Q R S	G	CIVN	LSSV	141
	76 LEREI-GPV-	SILVNNA	GV - I F	PGRID!	D PGAREKWDRTLAINVGGPFNM -	- CRAFYPQL	RA	T R	G	AVIN	LASI	142
	74 VDDRF - GGV -	DILINNA	GV-TG	NRPTVI	D I T DEEWRRTMS I DL DGVFYC -	- SREAGRAM	IG	RRP	· G	VIVN	IGSI	140
	69 TAGQL - GPV -	- T L L V N N A	GI-VE	PMAKSAI	D QALADFRRTIDVNVKGTIHA -	- SRAAARQM	G	AG	G	AIVN	LSSI	136
	10 IADHF-GGI					- I KTAVPWL	RE		A	SIIN	IVASI	149
	80 I NAEG - PAL	DII VN NG	AL-GG		DSTI GOWENMEDVNVSSMYLL -	- CRDL SKGM				RIIN	FASY	149
	81 TEKAL - GRL -	DILVNNA	GV-LA	VAPVT		- SQAAARYM	GQ	G	G	RIIN	LIGST	145
	81 TADHF - GGL -	DILVNNA	GG - GT	PELIG	EATLANYEHIFAVHVRAAFVA-	-MNEAAKIM	PA		G	RIIT	IGSI	145
	75 VEEA GPL -	- RVL VY NG	GITGA		D ADPETLARVVAVNLTGAMLC -	- ARAAIPLM	STRTGGQ	G	G	AIVF	MSSR	144
ub/1-261	79 AIKEF-GTL -	DIMINNA	GL-EN	· · · · · · · · · · · · · · · · · · ·	E MPL KDWDKV I GTNL TGAFLG -	- SREAIKYF	VE	ND I K	G	NVIN	MSSV	146
	77 VAARH-GRL -	- DML VN NA	MS-VH	YAPIA	K L RL DHWRKDFAVNADAVFVG -	- TKAAMKVM	AA ·	QE QRGRQR	G	AIVN	IAST	148
	83 AAARF - GKI -	DVLVNNA	MW-NS	YDL I AI	D ITPEIFARMTGVGLGGIVWG -	- IQAVLPHM	PE		G	AIVN	IGSM	148
	76 FRYDA - GPL -	• RAVIN NA	SV-LV	· · · · · · · · · · · · · · · · · · ·	D VTEETLELMLSAGLKSVFWG -	- VQAFLAYR	DE	EAS	· G	NILN	YSSP	142
	79 FARAY-GPV-	DILINNA	SY-LV	P COLE	R VIEEILDRMISSGLKSVFWG -	- VQAFLAHR	D-PE	AG K	· G	WIIN	YSSP	146
/1-251	76 VREOR-GSI		GA-IF			- VOKALPII			G	SVII	VSSV	140
-201	71 EDAL - GGL	DVL FV NA	GV-66			- IORALPLL	RD			SIVI	TGSI	135
	72 IGASD-GRI	DVLYINA	GV-GG	FAPLR	DITSEAWDHTHSINLKGCVFA-	- LQKAVRIM	GK	G	G	svvv	TGSI	136
	72 IREAH-GRL	DILFVNA	GI-GT	FAPVA	E VTPAQWDEVHNVNL RGCFFA -	- VQEAL PLM	GK	Ğ	G	AIVI	TGSI	136
	73 AGTET-GGI-	DTVFNNA	GA-GG	D	E I E P E G W D R T M D L L R S V A F G -	- IRYAVPHM	KG	RHG	A	SFVN	ITSSV	140
	103 ALSAF - GRI -	DLLHSNA	G I - I G	E PGP I A(3 ASAANFDRVFSVNVRSAVLM -	- IGAVVPEM	RR	QGG	G	SIVI	TASV	170
	76 VISTF-GRC-	DILVNNA	GI-YP	LIPFD	E L T F E Q W K K T F E I N V D S G F L M -	- AKAF VPGM	KR	NGW	G	RIIN	LTST	142
	75 TAEAF - GPA -	HILVNNA	GL - HP	SPMPFE	ELGFDYWRRTMSVNLDAMFLT-	- IQAFLPQL	KQ	NSW	G	RIVN	FSSA	142
	74 L DKEM - GGV -	DVLVNNA	GV-YD	FTPHE	I VT I DVWRK I MSL NL DGMFLL -	- TQAVL PGM	KA	KGW	• • • • • G	RIIN	VASN	140
	74 AEGQF - GGV -		GI-QH	· · · · · · · · · · · · · · · · · · ·		- TREALPGM	KI		G	RIIN	HASV	140
						- INCALPUM		V	(7			1411

gi|146275658|Naro/1-269 gi|334343486|Sphch/1-273 gi|146275875|Naro/1-252 PP_1946/1-262 PP_1817/1-253 gi]87200975[/1-250 SG61_1215/1-250 gi|146275951|Naro/1-252 SG61_2016/1-248 gi|31615388|Levodione/1-267 gi]87200486|/1-256 SG61_3730/1-262 SLG_20040/1-258 gi]146275686|Naro/1-245 gi]334342862|Sphch/1-257 gi]87198897]/1-259 gi|146275698|Naro/1-254 gi|334343337|Sphch/1-258 gi|146275892|Naro/1-259 gi]334342592|Sphch/1-246 gi|334342962|Sphch/1-244 gi|334342992|Sphch/1-245 gi|334342994|Sphch/1-245 gi|334342590|Sphch/1-248 gi]87198536|/1-248 gi|1708836|2,5-DDOL_Sjap/1-250 gi]62286565|CPNA_COMS9/1-250 gi|33112056|R-specificADH/1-252 gi|146275770|Naro/1-271 gi]334342841|Sphch/1-255 gi]334343813|Sphch/1-269 gi]87200879[/1-249 SG61 3344/1-248 SLG_12690/1-249 gi]146275758|Naro/1-253 gi|729773326|steA_Ctestosteroni/1-243 gi|146275834|Naro/1-267 PP_1953/1-269 gi]39647578|badH_Rpalustris/1-255 gi|334342959|Sphch/1-250 gi]334342606|Sphch/1-251 gi|146275741|Naro/1-255 gi|1730032|kduD_EcoliK12/1-253 gi|334343307|Sphch/1-251 PP_2794/1-255 gi]16330475|3-ketoacyl-ACP/1-240 gi]334342640|Sphch/1-240 gi\87201224\/1-240 gi\87201224\/1-240 SG61_907/1-240 gi|518742570|acetyl-CoA/1-246 gi]334343976|Sphch/1-246 gi]87199449\/1-254 SG61 1203/1-250 gi]388477173|fabG_Ecoli/1-244 gi|146318879|gluconate/1-271 PP_2783/1-245 gi]334343549|Sphch/1-249 gi]334343458|Sphch/1-251 gi]87199578|part2/1-253 gi]87199495|/1-266 PP_3926/1-255 gi]334343112|Sphch/1-262 PP_1852/1-249 SG61 1419/1-249 SLG_12130/1-244 gi]649014081|glucose-1-dehydrogenase_Bs gi|146275833|Naro/1-261 gi]871995771/1-257 SG61_3726/1-249 SLG_20080/1-253 gi]334342771|Sphch/1-253 gi|512125550|n-pentylphenylADH_Ralstonia/ gi|87200895|/1-246 SG61_3191/1-249 SLG_07180/1-248 gi]87199020|/1-282 gi|334343475|Sphch/1-279 gi|81821161|PED_AROAE/1-249 SLG_18890/1-249 SLG_18590/1-251 gi|167033792|bdh/1-256

PP_3073/1-256

75 AEAEF AA - DILVN NAG I - QH	VASIED	FPPERWDAIIAINLTSAFHT TRLALPGM	RQ KN	GRVINIAST 140
80 A A D A F - G G V - D I L I N N A G M - Q H	VAPVEE	FPVDKWNLIIALNLNSAFHT SRLAIPYM	KQ KK	GRIIQTASA 146
78 AAETF - GGV - D I L VN NAGT - QH	VAPVES	FPVDKWNLIIALNLTSAFHT TRLAVPYM	KEKK	• GRIIQTASA 144
78 ALAEF - GAV - DILIN NAGM - QH	VAPVEE	F P V E K W D A I I A L N L T S A F D A C R L A I P G M	KA KG -	GRIIFTASA 144
78 A G P V - D I L V N N A G M - Q H	VSPVDE	FPPEKWDAIIALNLTAAFDT SRLAIPHM	AG	GRIINTASA 140
76 VAQAF - GNI - DILVS NAGI - QI	VNPIQN	YAFSDWKKMQAIHVDGAFLT TKAALKYM		GTVIYMGSV 143
82 TEEAL - GPV - HILIN NAVV - RH	FARIED	FPIEKWTEALAVNVTAAFLA TQMVLPGM	AH	GRVFNMTSV 148
80 ANEAH-GPT-AHAFNNIGM-SR	POSEAD	MSLEDWNWITGISLISIFLAMKYEIPVM	NG	GGIIVNIASM 146
77 CQDRF-GGL-DFLVPSAGT-TV	AOLATE			CRILINVASM 152
				A T G G A V V V T A S A 140
73 GARNGL-DVLCN	WGRSED	FSLEDFDLVMRVNTHSVFTL COAALPHL	S	GNIVNTAGA 146
82 HDKAY - GGL - DICFA NAGI - DTGAGF W		YDHKRWDRSIQINLNGVFYT VSNAVRIM	KKEGRA-NGRT-	GGSIVTTASN 167
82 HAAAY - NGC - D I AFA NAGL - DVGNGF W	TPEGKRNPDGQ DV	YEPERWYKSIGINLNGVFHT VREAARVM	KQNEAL-SGRR-	GGSIVITSSN 167
87 HEAAY - GGL - DIAFA NAGV - GIGPGF W	DPNGHRAPDGQVDS	YNPEYWDRIIAINLTGAYNT MRDAVRLM	KK GGK	GSIIATSSN 167
82 VAAGF-GGL-DIVFANAGI-DPGPGFAAL	NAAGEREPANMLEE	YSDHRWRKVISVSLDAVFYS IRAAARHM	ANR	GSIIVTTSV 163
81 VLGQF - GRL - DAL VC NAA I - AN - PH	NQTLES	L SL AQWNRVLGVNL SGPMLL AKHCAPYL	RA H	GAIVNLTST 148
82 FGERE-GKL-DILVNNAGT-GG	NGP ET	VDIPDWNAAMEVNLRAPFFLVQQALPLL	RA AAAF	°G T Y ASVINLGSI 152
91 ALEKL - GKV - DVL I N NAGL - GG	EVDVVD	MTDDQWSRVIDVTLTSLFRM TRAFLPAM	NK	GVMVNNASV 157
63 LEPQI-GRL-DHAVVNAGI-AA	GAPIAE	ESFEQWRRIMSVNLDGAFLT LATALRLI	GG	NGGGVVLLSSV 130
71 AEAVN-GKA-RILVNCAGI-GP	PAKVLNRDGSP	L PLADFARI ININLLGTENV LSKEASRI	HDAEPLNEDGE-	GVIVNTASV 149
71 AEALN-GKA-RILVNCAGI-GP	ALKTASPSKTTCE	IPLNDFSKIVIINLIGSENVLSKFAARL	HDAEPVGGE-E-	
71 AREAH-GQE-RILINCAGI-GN	A IKTASPSKETGE	KHEPMDAENWI LOINI VGTERC IAKSAAGM		
72 ARAAH-GQE-RILVNCAGI-GN		SHEPLAAFAKTI EVNTVGTERC LAKAAAGM		
73 AVSAF-GSL-HGLVNCAGL-VG	AEKVLGK0GPHG	LASEAKVINVNLIGSENLLRLAAAAM	AEGAADES-GE-	
65 VIERH-GRI-DILLNNAGI-GG	LGPVATPEGPGD	MAAFRAIIGVNLLGATOLVAHVAHRM	MANEPSGPDGF -	RGVIVNTCSI 142
73 ML DRW-GVV - HAL VN NAVV - TR	AQPVLD	I APDDF SAVVEVNL RGTF VG SQVFGRL F	CG-	GRIVNIASL 139
69 VEQDL - GDL - TIL VTAAGTAGFL NGTM - PR	LQD	VPSDHWDQVMNINLRGGFLALREMLRRRMA	KPVP-	ARIVTISSM 142
76 EEVH-GRL-DVMFNNAGI-NA-P	AVPVDE	LPLENWRNVIATNVDGVFLCARAAFGLM	RR QQ	P Q G G R I I NNG S I 145
74 AVARF - GRV - DL L F N NAGL - NG - G		MDVALFREVVDVNLTGAFLC LQAAFRVM	KA QQ	P R G G R I I NNG S I 143
79 AVDRF - GTV - D I L I N NAG I - AD	STPVYE	LSLEMWHRVIETNLTSAFLCSREAFRIM	KD KG -	GRIINVGSI 145
77 A - EAF - SPV - TLL VA NAGM - A I	HRPTVD	VTL EQWRAVIDVNL TAAFL C GREAL RVM	RG	GRIINVGSL 142
79 CVERF-GSV-DILVNNAYR-GE-G	PVRIEK	KTDERFDEALRMCLFATKWA MERALPHM	KAKG	GRVINMASL 146
78 TQAEL-GPV-WLLVNNAVS-TD	NRPIEE	VDDANLDLVLRSSTHGSLYMMQACFPTM	R	GRIVNFGSG 143
68 VDHOL - GGL - DVLVS NVGL - GG - P			KG	GT 1 1 MSSA 134
80 TLAHE-GEL-DGLVSNAGE-AD	RTPFI N	VPRERI DSSESVMTGI FEDIARAAAPAI	SG	GRIVAISSE 146
69 VVEKW-GRI-DVLLNSAGH-GP	RAPILE	ISDEDWHKGMDTYLLNVIRP TRLVTPYM	QRQK	GGVIINISTA 135
69 MREAS - LQ I - DLL VN NAGL - AL - G	VDRAQT	SSAANWQQMIDTNITGLAMV THKILPQM	AD-	GMIINIGSI 136
68 L PAEW-CN I - D I L V N NAGL - AL - G	MEPAHK	ASVEDWETMIDTNNKGLVYM TRAVLPGM	RN-	GHIINIGST 135
71 L PADF - AQ I - DL L I N NAGL - AL - G	TAPAQW	ADL DQWRQM I NTN I TGL VT I TQKLL PRL	I E	RKGAIINLSSV 137
72 L PAGF - EK I - RGL VN NAGL - AL - G	VDAAQN	CSLDDWETMVDTNIKGLMYT TRLLLPRL	I A HG	RGASILNVGSV 140
74 AAERF - GRI - DAL VN NAGI - MP	LSMLAS	L KRDEWKRMIDVNIHGVLNG IAAVLPRF	QE-	GHVINVASV 140
74 AEARF - GRV - DAL VN NAGV - MP	LSPLAA	L KRDEWKKMIDVNIHGVLNG IAAVLPRF	QR	GHVVNVASI 140
76 IVARF-GAV-HLLCNNAGV-GG	HQRFS1	ISLEIWKWILNVDLWGVINGCRIFAPIL	QD	AHILNISSM 142
77 VEOVE-GAAPTILENTAGV-NS		- TSYDDEDWIVGVNIGGVING - MVTEVPRM		BBGHIVTTSSI 145
77 VEAVF-GQAPTLLSNTAGV-NS	FGP1EK	TTYDDFDWIIGVNLNGVING MVTFVPRM	SG	GHIVTVSSL 145
78 AEQVF - GPV - DLLCN TAGV - SQ	FGPIEK	ATFDDWDWQMDVNVNGVING VMTVMPRM	RG	QGGHILITASM 145
79 VEARF - GPV - S I L CN NAGV - NL	FQP EE	SSYDDWDWLLGVNLHGVVNGVTTFVPRM	RVK/	GEQK G GHVVNTASM 151
75 VEAEF - GPV - SLLFN NAG I - NL	FQT ED	SSYDDWDWVLGVDFHGVVNG VMTFAPRM	RAL	GEVK G GH I VNTASM 147
81 MDEEF - GG I - DVL VN NAGV - GV	EGP LQ	ATYPDWDFGLGVNLGGVVNG LQAMLPQM	I A HG	· R G G H V V N T A S L 148
81 MKAEF - GG I - D I L VN NAGV - GL	EGPLLE	ATYADYDFGFGVNVGGVING FTEFLPQM	VA HG -	RGGHIVSTASL 148
78 CEAVM-GGP-DILINNAGI-DP	SGPFKD	ATYQDWDYGLAINLMGPING IMAFTPGM	RA	· R G G H I VNTASL 145
72 AEARL - GPL - RTL VN NAGV - GT	AGPVDE	- ATHEDWDWGVGVNLIGVANG - LVAGLPRI	HG	GGHVVNVASE 139
70 VERLI-GKI-HULONNAGI-GI			HG	GGHIVCTASM 143
77 AEAIF-GHI-HVLALNAGV-GI	AGPMAT	STEKDWDEN I QVN I YGVVNG LVTEL PRM	HG	EECHIVATSST 144
77 AEERF - GNI - HVLAL NAGV - GT	GGSMLT	ATYKDWDFNMGVNVGGVVNG LVTMLPRM	HG	
82 V GKV - HVL VN NAGV - SV	FGPTDE	ASYDDYDWIMGVNFGGVVNG LVSFLPGM	KA HG	
82 VVQHF-GEV-HVLVNNAGV-SV	FGPTDE	ASYDDYDWIMGVNFGGVVNG LVSFLPKI	SH	GRRHVVNIASM 149
77 VIDHF-GKC-HVLVNNAGV-SV	FGPTDE	ASHADYDWIMGVNFGGVANG LVAFLPKI	KA TG	EGGHVVNVASM 144
76 A L D V F - G K I - H V L C N N A G V - NG	GGT A D D	PDFTDFDRVMAVNLGGVING SKIIVPII	KA QG	EGGHVVCTSSM 143
76 ALDVF - GKI - HLLAN NAGV - GG	GGNADD	PDFEDWDRSIGINLGGVVNG TKIIVPII	KA QG -	EGGHIVNTSSM 143
76 TTRIF-GNV-HVLCNNVGV-SQ	RSPIDE	AGYEDWDYVLNVNLGGTIAG IVEFVPGM	HG	EGGHVVNTSSM 143
73 CEAKF-GGV-DVIVNNAGV-AS	GGL F AE	LTLEDWDWQIAVNLMGVVKG CKAFLPLL	ER	GRIINVASM 138
74 VAASG-GRM-DVLFNNAGV-AC	CCALAD	- ARKDEIDSVVDVNVRGMLYG - ANAAHPYL	IE-	
72 ANASG - GRI - DVI AN NAGI - PI				
80 AQEGL-GRI-DULVNNAGV-PG-P		VDPDEWWRAOF I HIRAPMIE MHALLPGM	RGR	GRVVCVSA 147
77 VEAEL - GAP - T I L I N NAGV - PG - P	IGPIWE	L DMDAWWAAQQVH I RAPML F L RRL L PSM	RDR	GRIVIVSAI 144
78 AKAAF - GVP - DLLVN NAGV - QG - P	LGPAGL	VDTQAWWDTQAVHVLGALHC ISTALPDM	RGH	GRILNIASQ 145
72 AWNWQ - G H I - DML VN NAG I - SQ	RSLAVD	TAFEVYERIVAVDLLAPIAL TQALLPRM	RK-	GRIVMVSSI 138
69 AQEKY-GRV-DALVHNAGI-SI	VTKFED	TPLSDFHRVNTVNVDSIIIG TQVLLPLL	KEGGKARAG-	GASVVNFSSV 140
86 VFARH-GEV-RLLINNAGI-ET	VGYTWE	VPAARWEATLNINLHGVIHG VRAFVPRM	I E SG	KEAWIGNLSSV 153
76 L R E D A R I - G I L I N N A G M - A Q	SGG F VQ	QTAEGIERLITLNTTALTRLAAAVAPRF	VQ SG	GAIVNIGSV 141
76 L RDDA N I - GVL I N NAGM - AQ	SGGFLD	QSAEAIERLVTLNTTALTRL AAAIAPRL	SG-	GAIVNVGSV 141
76 I E Q G D - D I - D L L V N NAG I - G D	IAHFVD	QERDTHERMIAVNVLALTRL SHAAIPGM	RG	GTIINVASG 141
74 LEEGE-RRI-DLLVNCAGL-RT	YGPFLA	HEWADEQDLLEVNVLALSRL CHAIGNLM	QG	GOLLNVAGL 140
66 A		EIEEQIDOMLOIIFKUULFF - MUVMVGAM	SG	
66 A GPL - DVL VN NAGL-GL		- TPLAKIRDVFATNTIGTIAM COAVIPOM	RA	

gi]84570596|bdh2_Rpickettii/1-256 gi]334345171|Sphch/1-263 SLG_32730/1-261 gi]87199767[/1-261 SG61 1243/1-257 gi]84570594|bdh1_Rpickettii/1-260 gi]334342462|Sphch/1-265 gi]334343092|Sphch/1-255 gi|334343456|Sphch/1-245 gi]334343408|Sphch/1-258 gi|146275993|Naro/1-256 gi|146275997|Naro/1-246 gi]87199890[/1-279 SG61_474/1-283 SLG_24920/1-278 PP_1951/1-275 PP_2002/1-257 SLG_15310/1-259 gi]146275988|Naro/1-261 SG61_609/1-245 gi]146275674|Naro/1-255 gi]334343001|Sphch/1-254 gi]334343319|Sphch/1-259 gi]87199092|/1-261 SG61_354/1-260 PP_2214/1-255 SG61_3175/1-254 gi]146276032|Naro/1-246 gi]334342802|Sphch/1-249 PP_1708/1-252 SLG_05090/1-250 SG61_2863/1-244 SLG_35070/1-243 gi|146275941|Naro/1-266 gi|334343077|Sphch/1-254 gi]334342781|Sphch/1-260 SLG_31530/1-250 SLG_31530/1-250 SG61_2583/1-255 PP_2175/1-234 PP_0488/1-253 gi]2506152|YDFG_ECOLI/1-248 gi]334345036|Sphch/1-249 PP 4862/1-254 gi|334346119|Sphch/1-241 gi|334342779|Sphch/1-273 gi]334342815|Sphch/1-290 gi]871982301/1-306 SLG_08640/1-305 SLG_35880/1-297 gi]87198815|/1-310 SG61_724/1-305 gi\87199892\/1-280 SG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277 gi]87198816|/1-310 SG61 2705/1-303 SG61_1498/1-309 SLG_35900/1-311 gi|87198727|/1-305 SG61_3329/1-309 SLG_12640/1-304 SLG_12640/1-304 SG61_2549/1-315 SLG_28340/1-294 SG61_2706/1-296 PP_1745/1-269 gi]334342965|Sphch/1-259 gi]87199139|/1-266 SG61_504/1-269 SG61_782/1-273 SLG_38070/1-265 SLG_27950/1-266 gi]87200928[/1-272 gi]146275769|Naro/1-259 gi]146275845|Naro/1-289 4BMV:A|PDBID|n-pentyl/1-262 PP_2989/1-264 SLG_18780/1-267 PP_0429/1-260 gi]334343146|Sphch/1-268 gi|334343373|Sphch/1-250 SG61_417/1-252

gi]146275658 Naro/1-269	149 LALQ-GHLI-QAAYSSSKAAVIQMTRAIAASHGKAGVRCNAVAPGMTMTPA	L - REAF PPAL RQV VE - D - ET L R - DRLGD -	P - RDIAEAIAFLAS D - AAR NVT 241
gi 334343486 Sphch/1-273	150 MGLG-GEAW-QVSYGTSKAAVIQLTKYVATHFGKQGIRCNAIAPALVMTPI	V-ETAM	P-EDIAAAVAFLASD-DARYVT 242
gi]146275875 Naro/1-252	146 NGLV-GNGS-QPAYTAAKHGVVGLARHGALRWAKNGIRVNAVCPGVIETPM	T - APL V QNPE I KAL MD - S - MT PM - GRMGS -	A-MEIAEAVVWLCSP-AASFVT 239
PP_1946/1-262	148 SGLI-GGYR-LSGYTATKHGVVGLTKAAAIDYANQNIRINAVCPGPVDSPF	L-ADMPPI-GRLAT-	A-EEIARSVLWLCSD-DAKYVV 239
ail872009751/1-250	146 AGEG - AAPR - M SATSASKHAVIGET KAAAVEYAQA G I RVNA I APGEVVTPM	T - OHWA	
SG61_1215/1-250	144 GGL I - ADPN - M AAYCAMKHAVIGL TKGAAVEYARH N I RVNA I APGF VVTPM	T - QHWA DSPEFTSA FF - Q - HN VS - GRCAQ -	P-EEIAGTVLHLCSD-AASFVN 237
gi 146275951 Naro/1-252	147 QAHI-SYPR-TAAYTAAKHGVLGLTKAIAKEYGEQGIRCNSVSPGVVDTPL	T-AGVIPL-KRFAT-	P-EDIAKAALWLLSD-ESAYIN 240
SG61_2016/1-248	143 LGSV - GWRG - A AAYVTAKHGVCGMTKSAALEYSAQ G I RVNAVGPAFIETPL	I - ENAM TDEARAA LV - G - MH PI - GRLGQ -	P - EEVAALTNFLLS D - AAS FVT 235
gi 31615388 Levodione/1-267	154 GGIR-GIGN-QSGYAAAKHGVVGLTRNSAVEYGRYGIRINAIAPGAIWTPM	V - ENSMKQL DP ENPRKAAEE FI - Q - VN PS - KRYGE -	A-PEIAAVVAFLLSD-DASYVN 253
SG61 3730/1-262	145 GGER-GUGN-QSGTAAAKHGVVGLTRNSAVEFGQTGVQTNATAPGATMTAM 146 GSER-GLAG-ACAYNAAKHGAVGLTRTAASEVAOKGVRVNCVMPGVTETPL	L - VGML FOMF DDVAAGMRK LG - E - VA TL - NRVGO -	P-EEVAALVAFLLSG-EATFTN 242
SLG_20040/1-258	143 GSER-GLAG-GAAYNAAKHGVVGLTRTAAADLGPKGIRVNCVEPGVIETPL	L - NEVL VQM FD GDL QKGL DT LG - W- VS VM - NRCGK -	P-AEVGHVVSFLLSD-EASFVT 242
gi]146275686 Naro/1-245	134 SGVK - ASAN - L VAYNAAKAAVTLMTKSCAL HFADKGYG I RCNS I HPGA I HTP I	I-DKVLAQSDDPDALYRSFV-D-VHPV-KRLGK-	P - EE I AA I AVYL AS D - ASA FAT 233
gi 334342862 Sphch/1-257	146 AGL I - AAHN - L - ANYNASKAAVWLLSKSIALHCARN GWDIRCNSVHPTFIRTPI	L-DDLIGDRPL-GRLGD	P-EEVAHAVVYLASD-ESRFMT 244
gi 8/19889/ /1-259 ail146275608 Nem/1-254	146 AGLI-ASDI-MPGYNASKAAVWMLIKSVALYCAKRGWDIRCNSVHPIFVDIPI	L - DG I SANAN L EKSVVMGK LA - R - Q I PL - GRVGE -	P-DDTAAGVLYLASD-ESRFMT 246
gi]334343337 Sphch/1-258	140 AGIT - GQRA - L SAYCAAKGGVREFSKAVALECASARDN IRVNSVHPGI I DTPI	F-HATEADERRAPVGPQAMDVGPMA-AFAVPM-GVPGK-	A - ED I AAACL YL AS D - DGR YVT 241
gi 146275892 Naro/1-259	141 DGMK - GANS - L VAYASSKWGVRGLTKVAAMELGHK G I RVNSVHPGGVDTVM	S-NHSGPL-QRIGG-	P-EEVAAASLFLASD-DASYLH 234
gi]334342592 Sphch/1-246	141 QGIE-GIPG-LHGYTASKFAVRGLTRCIAIELAGRGVRANTICPGTIATPM	N-EGLDPM-NRKAD-	P-REVAKLVVFLASD-ESPFIS 226
gi 334342962 Sphch/1-244	141 NGIR-GNRN-RYGYVASKFGVIGLTKTAALDFAPAGVRVNAVLPGMISTPM	T - AGL K V DT - S - L I PL - GRPGN -	M-EEIAQVVAFLASD-EASYIT 227
gi 334342992 Spncn/1-245 ai 334342994 Sphch/1-245	141 AGER-GGPG-MFSYGAAKWAVRGMIRSAAHDLAPFHIRVNAVLPGPIDIQM 141 GGMR-GGPS-LFHYRATKWAVRGMTRSAAHDLASLNIRVNTVLPGPIFTPM	Т - N I G N	P - REVAMATLELAS D - EAS Y VT 233
gi]334342590 Sphch/1-248	142 AGMA - ANYG - FPSL AYVASKFAVRGMTKATAMEYGKY N I RVNSVHPGF I QTPM	M - VEAT DEVGGD AL - A - EI PL - GRIAD -	
gi]87198536 /1-248	142 AGMA - ANYG - FPSLAYVASKFAVRGMTKATAVEFGKH N I RVNSVHPGF I QTPM	M - VEAT PL - GRIAD -	P - SEVSNL VL F L AS D - ESS Y I T 235
gi]1708836 2,5-DDOL_Sjap/1-250	145 IGMF-PTAG-NASYCATKAAVRIMSKAAALEFVDRGVRVNTIVPGGMNTPI	T - ANVP PDVL KQ QT - S - QI PM - GKLGD -	P - I D I ANGAL F L AS D - E A K Y I T 236
gi/62286565/CPNA_COMS9/1-250	144 YGLV - GAPG - A AAYEASKGAVRLFTKACAVDLAPF N IRVNSVHPGVIATPM	T-QQILDAPQSARALL-G-PTLL-GRAAQ	P-MEVSQAVLFLVSD-EASFVH237
gij33112036 R-SpecifiCADH/1-252 ai146275770 Naro/1-271	145 EGFV-GDFT-LGATNASKGAVRIMSKSAALDCALKDTDVRVNTVHPGTTKTPL 153 MGLV-GMNE-VSAYNASKGAVRIFTKGIALEFAOKKTPIRANSLHPGEVETPLIKA	G - FORWVDOG FA	P-NDTAWICVYLASD-ESKFAT 239
gi]334342841 Sphch/1-255	142 AGLR-GTAA-FTAYSASKGAVRLMTKSLAHELAGRRIRVNSVHPGLVETEM	G-RQLVSEIALRDRGDPTCPSDT-A-AVQPL-DSAGA-	P-HDIAHAVVFLASD-KAAFMN 243
gi 334343813 Sphch/1-269	143 SGLR-GDHA-LVGYNAAKGAVVNLTRAMAVDHAPDNVRVNAVCPGLIETPL	T - QAAK DAGL WYA WT - S - T I PM - RRAGT -	A-EEMASVVAFLASE-EASYVS 235
gi\87200879\/1-249	142 ASER-GLPM-NAGYVASKHAVLGLSRAVANEAAEAGVRCNCILPGLIETPM	L-DGLPPQ-GRTGSMA-R-AVPQ-GRTGS-	S-DEVAQVAAFLLSD-AASHVT 233
SG61_3344/1-248	141 GSKR-GMAM-NPAYVASKHGVLGLSBALAVEMARH C. VRCNCVLRGELDTRA	L-DRIPPEQADRIA-A-RVPQ-RRMGS-	P-EELAEVACFLLSD-AASHVT 232
ai1146275758 Naro/1-253	142 ASKR-GMAM-NPATVASKRGVLGLSKATAVEMAPHGVRCNCVTPGPTDTPA	T - AQAL AEL PADNA GL - D - QA HN - HGMGQ -	
gi]729773326 steA_Ctestosteroni/1-243	140 SAVS-GD-G-PAHYCASKAALMGLTRGMAKELASKKIRVNTLVPGPTNTPM	M - QG I P QEWADA I I - A - GV PM - GRMAE -	P-EDIAKVAVFLASD-DSGFVT 230
gi]146275834 Naro/1-267	164 AALA-GN-G-PVPYVTAKAAVLGMTRAMARELAPRGIRVNAVNPGATETPI	Y - APL P DEVKAA VA - A - DS VM - KRL AH -	P - DE I AGAVVFL AG N - DAS FAT 254
PP_1953/1-269	166 AALL - GV - AMP LYYPASKAAVLGLTRAAAAELAPY N I RVNA I APGSVDTPL	M - HEQP PEVVQF LV - S - MQ PI - KRLAQ -	P-EELAQSILFLAGE-HSSFIT 257
gi 39647578 badH_Rpalustris/1-255 ai 334342959 Spbcb/1-250	144 AARV-GSSG-EAVYAACKGGLVAFSKILAREHARHGIIVNVVCPGPIDIAL	L - ADV I SGA ANPEKL I EA F I - K - A I PL - GRLGK - V - DTVI GHE GEAETREA I A - R - RH PL - GRLGK -	P - DDL AGA I AFFGS D - DAG F I I 241
ail334342606 Sphch/1-251	145 L SFQ - GG I R - V PSYAAAKSGVAGVTKAMANEL APQ G VQVNA I APGY I ATNN	T - AALQ ADETRDRQ IR - E - RI PT - GRWGR -	P-EDIAGAAVFLASP-ASDYVT 238
gi 146275741 Naro/1-255	149 L SFQ - GG I R - V PSYTASKSGVAGL TRL LACEWAAR G VNVNA I APGY I AT NN	T - SALQ PE - GRWGD IM - E - R I PE - GRWGD -	P - AD I GGAAV F L AS G - AAD Y VQ 242
gi]1730032 kduD_EcoliK12/1-253	147 LSFQ-GGIR-VPSYTASKSGVMGVTRLMANEWAKHNINVNAIAPGYMATNN	T - QQL R ADEQRSAE IL - D - R I PA - GRWGL -	P-SDLMGPIVFLASS-ASDYVN 240
gi 334343307 Sphch/1-251	144 LGLR-QGSR-VATYAVSKAATIQLTKVAALELARFGVRVNCICPGYIATDI	N-RDFWPQ-RRLGE-	P-RELDGPLLLLAS-D-ASSFMT 236
PP_2/94/1-200 al/16330475l3-ketoacv/-ACP/1-240	146 LASK-VAGA-VGPTLAAKAGLAHLIKAMALELAKHGIKVNALAPGTVMIDL 136 SGER-GNVG-QTNYSATKAGVIGMMKSIAREGARYGVRANAVAPGEIDTEM	N - EAFL ASEAGDK LR - S - RI PS - RRFSV - T - I A I R FD I RFK I T - K - F I PF - RRFGK -	P
gi]334342640 Sphch/1-240	136 NGQA - GQYG - Q VNYAAAKSG I HGFTKAL AQEGAKY G VTVNA I APGY I DTDM	V - AAVP PAVLEK IV - A - KI PV - GRLGH -	A - DE I ARGVAFFCS E - DGG FVT 227
SLG_38730/1-240	136 NGQA - GQYG - Q VNYAAAKSG I HGFTKAL AQEGARA G VTVNA I APGY I DTDM	V - A A V P Q A V L E K I V - A - R I P V - G R L G H ·	A-EEIARGVAFLCSE-DAGFVT 227
gi\87201224\/1-240	136 NGQA - GQYG - Q VNYAAAKSG I HGFT KAL AQEGAKY G VTVNA I APGY I DTDM	V - AAVP PQVLEK IV - A - KI PV - GRLGH -	A-DEIARGVAFLTAD-QGGFVT 227
SG61_907/1-240 all518742570lacetyl-CoA/1-246	136 NGQA - GQYG - Q VNYAAAKSGI HGFTKALAQEGARV G VTVNA I APGYI DTDM	V - AAVP EPVLEK IV - A - KI PV - GRLGH - V - KSI B EVIEK IV - A - KI PV - GRLGH -	A-EETARGVAFLTAE-EAGFVT 227
ail334343976 Sphch/1-246	142 VGVT - GNPG - Q ANYAASKAGI I GMSKSLGQELASR G I TVNCVAPGF I RSAM	T - DAL N DAQKGA I L - A - R I PA - GDLGS -	
gi]87199449 /1-254	149 VGAT - GNPG - Q VNYAAAKAGL VGMSKSLGQELASR G VTVNCVAPGF I RTAM	T - DVL P DGQKDA LN - A - R I PM - GRMGE -	G-SDIGAAVAYLASK-EAGYVT 240
SG61_1203/1-250	145 VGAT - GNPG - Q VNYAAAKAGL VGMSKSLGQEVASR G I TVNCVAPGF I RTAM	T - DVL P DAQKDA L N - A - R I PM - GRMGE -	G - ED I GAAVAYLAS K - EAG YVT 236
gi 388477173 fabG_Ecoli/1-244	140 VGTM - GNGG - Q ANYAAAKAGL IGFSKSLAREVASR - G ITVNVVAPGFIETDM	T - RALS DDQRAG IL - A - QV PA - GRLGG -	A-QEIANAVAFLASD-EAAYIT 231
gi 1463 1667 9 giuconale/ 1-27 1 PP 2783/1-245	142 AAQK - PGKG - Q SNYAAAKGGVFALTRALAVELAPR N I RVNAVAPG I VSTDM	S-OAL V	
gi]334343549 Sphch/1-249	143 RSFV - AAPN - A AAYAASKGAVMQLTRALAVEWGGD G I RVNA I APGF I ETTL	V-PDHE	P-DEIAGTAVYLASD-AACYVS 236
gi]334343458 Sphch/1-251	141 YSLV-AAPE-RASYCASKAGVAMLTRSLAVEWAPHGIRVNCVAPGYADTAM	M - REL A AVGK AL EP LL - R - RT PQ - GRL TQ -	M-EDVAETVAFLCDP-RSVHIT 235
gi\87199578\part2/1-253	137 TASL -GLPG - R NAYCASKSAVTMLTRSLACEWAAH G IRVNAVAPGY ILTPA	V-QALLPV-ARLGQ-	P-DEVADAIAFLASD-AASYVT 231
gi/8/199495/1-266 PP 3026/1-255	150 GSFV-SYPQ-AGAYCAIKGGVLLLIKAIAVDLAKYGIRCNCYCPGAIEIPM	L - QKYLDAA EDKKA I MSV LI - G - AH LI - PRLGK - A - SALV KNFA I I NA AI - O - O I PI - KRVAD -	P-EEVAKLAGFLASD-DSSFIN 247
gi]334343112 Sphch/1-262	147 VSDT - GRPN - L SAYVASKHAVLGLTRS I AADLAPH G VTCNA I APGFFDTDM	A - APTV	P-KEMVGPVQFLASD-ASAYIT 240
PP_1852/1-249	146 NAERMPFAG-GAPYAMSKSALVGLTRGMARDLGPQGITVNNVQPGPVDTDM	N - PA A I - GRYGE L I - P - LM A I - GRYGE -	P-EEIASFVAYLAGP-EAGYIT 237
SG61_1419/1-249	146 NARRL PFTY - G ALYSATKAAL VGLTKGAARDLGPK G ITVNV I EPGP I DTDL	N - PA AL - A - AL AT - GKFGE -	A-SDVAGLAAYLASE-EGRFIT 237
SLG_12130/1-244	145 ATAYGSPNE-WVWYAASKGGIDSLTLGLAREVGIEGIRVNAVSPGPIGTEML	S-PEV-GRIGT-	P-QEAAAAVMFLASD-EASFIT 234
ai1462758331Naro/1-261	147 HEVI-FWFL-FVHTAASKOGTKLMTETLALETAFKGTRVNNTGFGATNTFT	T-OEFA	P-EELAEAIVFMLSE-AAS
gi\87199577\/1-257	149 AGRL - GSAG - A LL YAAVKAGVDGL TRSASVELGPR S I RVNA I APSTVATEG	V-KAIL	I-DDIAQAALWLAGA-RSGFVT 241
SG61_3726/1-249	143 VAYR-GRPN-TGAYTTIKAGIAGLTKVLAGELGPRGIRVNAIAPGSVPTPA	T - DG F V T P E Q Y A Q R A - N - N I P L - R R NG T -	P - EDVARAAAF I L S D - EAD F V N 235
SLG_20080/1-253	147 VAYR-GRPN-TGAYTAIKGAVAALTNVLAGELGPRGIRVNAIAPGSVPTPA	T - AGFV SAEDYER RA - A - G I PL - RRNGR -	P-EDVARAVAFLIGE-DADFIN 239
gij334342771\Spncn/1-253 gij512125550\n-pentylabenylADH_Peletonie/1-251	141 AGLG - GSPG - V YAYUTAKHAQIGLMRSLAKEVAGR G IRVNSLHPGPIDNSF 141 AGVL - GLOA - H DTYSAAKAAVRSLARTWTTELKGP S IRVNAVSPGA - DTPI	Q-TATEDAFSPLIGGGDATAMLN-S-MIPM-GRHGQ- LENOVSTO	
ail872008951/1-246	136 GSMA - AVPG - N VAYAAAKAGL RAMAR I VGKELL PR R I RVNMVSPGPT DT E I	F - KRDASA EE I QGMKDM LS - S - VV PI - GRMGT -	
SG61_3191/1-249	137 GAHA - SLPG - N AVYAAAKGGLYAAMKVFAGELVSE G I RL NMVSPGP I DTPL	L - YRNPGMTD EA I AAL KEK MI - E - NV PM - HRMGQ -	
SLG_07180/1-248	137 GSVA - TVPG - N VIYATAKAGLRAAARTLAAELVGR G IRVNMVSPGPTETPI	I-NRTGGVPAPM-KRMGT-	P-EEIARPVLFLASE-EASFIT 235
gi]87199020[/1-282	141 AAVG - PGYS - P TAYAVAKAGVL HL TKVAAADL AKH Q I RVNAVQPGF I NTN I	F-TSSLEMPEELEAQAKGAIAAMSQ-Q-AQPV-ARGGQ-	P-EDIAQAVLFLASE-AAGFVT 243
gijss4343470jspncn/1-279 nil81821161IPED_&RO&E/1-249	1/1 GOTK-PSPG-LGITAASKLALVALAKTAAVELGVDNTRVNATAPGLTDTPA 143 TYWI-KIFA-YTHYISTKAANIGETRALASDIGKDGITVNATAPSIVPTAT	Г - КАТКЦТРА	
SLG_18890/1-249	143 AANT - APPN - G APYVASKAGVVGLTRAAATEFGKY N ITVNS I APNPVRTPG	A - DDA I NEDMFQA I A - Q - L Q PV - PKVME -	P - RHL TGA I L FL CT D - GAE F I T 235
SLG_18590/1-251	141 SCFI-PPPG-LTAYVASKSASIGYVRSLAGELGQYGITVNAVAPGPTVTEG	T-RGGFPDEASFMDFMNRFV-E-SQSV-KKVSL-	P-EYSAPVVSFFASE-EAGFVT 238
gi]167033792 bdh/1-256	141 HGLV-GSTG-KAAYVAAKHGVVGLTKVVGLETATSKVTCNAICPGWVLTPL	V - QKQ I DDRA - ANGG DPL QAQHDL LA - E - KQ PS - LAFVT -	P - EHLGEL VL FL CS E - AGS QVR 243
PP_3073/1-256	141 HGLV-GSIG-KAAYVAAKHGVIGLTKVVGLETATSHVTCNAICPGWVLTPL	v - u k u i J D R A - A K G G D R L Q A Q H D L L A - E - K Q P S - L A F V T -	P-EHLGELVLFLCSE-AGSQVR 243

141 HOLV-ASAO-K-SAYVAAKHOLVOLTKVTALETAON-I	R VTANA I CPGWVI TPI	V - OKOVOARP - AHGI -	SVEOAKREL	V I . E . KO PS . G		- DELGALAVELAS	E - AGR OVR 243
			TREGVILLE			E CONTRACTOR CONTRACTOR	
147 HSLI-ASPY-KSAYVIAKHGLAGLIKILALELAIFG	G ITANCISPGYVWIPL	V-ENQIPDIMKARGM-	I REQVMNDV	LL - A - GQ PT - K	QFVIV	- EQVASMALYLCS	D - AAA N I I 250
145 HSLV-ASPF-KSAYVTAKHGLAGFTKTIALELATF(G VTANCISPGYVWTPL	V - ENQ I PDTMKARNM -	T REQ V I ND V	L L - A - G Q P T - K	Q F V T A	- EQVAEIALFLGS	D - AAS N I T 248
145 HSLT-ASPE-KAAYVSAKHGIAGLTKTLALELATHC	G VTANCISPGYVWTPL	V-ENQIPDTMKARGM-	TREQVINDV	L L - T - RQ P T - K	Q F V Q F	- EDVAALALELCR	H - EAR N I T 248
			TREQUINDY				
141 HSLV-ASPF-KAAYVAAKHGTAGLIKILALELAQFC	G I I VNCI SPG I VWI PL	V - ENQIPDIMKARGM -	I REQVMHDV	L L - A - KQ P I - K	KF VQ V	- EEVAALALFLOR	D - E AQ N I N 244
144 HSHE - ASPL - K SAYVAAKHALLGLARVLAKEGAEF I	N VRSHVICPGFVRTPL	V-DKQIPEQAKELGI-	SEEEVVRRV	ML - G - G T V D - G	VFTT V	- DDVARTALFLCA	F - PSA AL T 247
149 YGYR-GTVN-RVDYVTTKTA LOGL TRATAL ETAGGI	P ITCHALMPGSVLTPL	W-SDRLERMMIEEGL-	TRPEAEIRE	L D - G - KQ PS - G	RFVD A	- DSVAEVLLLLCG	P - AGT DMN 252
			TAFFOAFI			DELANAVIELOO	
147 AARL - YIPS - AP - CSYAAAKAGVIHLSHHASCAYADD I	N IRVNAVLPGLIAIPQ	I-ASMF	IAEEQAEI	AG - E - NQ V I - R	RAVD F	-RETANAVLELSS	D-DASMIT 241
142 AAHR-GSAQ-HAHYAATKGAINSLVRSLAKEIGPD	I RVNAVAPGL I AT PM	T-VALL	QGRGVT	DL - E - ST PL - K	RHGQ F	- AEVASVIGFLCS	S - SAS YVT 232
153 AAEHYPGKG - A SI YAITKSAVVRMTEVI AVEWATA I	N INVNCIAPGAESSEM	M-DGMR	SRIGDG	F . F . K F P R . K	RI G D F	- AOL DSTLL YLAS	P - A S F A V T 245
						AGEDOTEETERO	
141 AGIV-GHPA-NPAYSAAKHGVVGLVKSCVDAFAARC	G ARINAL CPGGVETPL	I-GAPD	VAI VPAA	DL - P - RV PA - R	GMG R A	-QHVAEVALWLSS	P - AAG F I T 233
137 AALQ-GIAY-TVAYVASKHAVAGMTKSLAVEFASRC	G VRVNA I CPGDVKTPM	T - QQ T A	VPENVDWA	LVMR - NAP - KLL - D	GSCE F	- EDIAELFAFLAS	E - RAR K I T 233
168 AGLV-TEPL-VG-L PYMPAKAGVI HMVRALGI ELAEE	G IRINALAPGREVINI				SVAF	- DO LKPLALLIAS	D - A S D VMT 263
						-DQTRFEALLEAG	
168 AAEV - NEAI - VG - VPYMAAKAGVKHFMRHAAFELAAY 0	G IRVNA IAPGPFVTNI	G - DGWV	KKNPAAKKA	WD - E - L C P L - G	RMAE T	- YQIKPLALLLAS	D - AGS YMT 263
168 AAVI-CEAI-VP-LPYMPAKAGVSHMVKHLAFELAEYI	H IRVNAILPGPFVTNI	A - DGSL	KDPVVREA	WD - K - ST PM - G	R I A E F	- YQIKPLALYLAS	D - AAS YVT 262
164 SALE BAVE LC AAVAAAKACAAOLVBATALELASD		C CCEM		MA A GV BM G		EELKBLALVLAS	
104 SALK-FAVI-LO-AATAAAKAGAAQLVKATALELASDC	GVRVNATAFGFFEIDT				KIAE V	- EEIKPLALILAS	K-A33FVI 230
149 RARQ - SEPD - T EAYAASKGGL VAL THALAMSLGPE	I RVNAVSPGWI DARD	P - SQRR	AEPLSEA	DH - A - QH PT - G	RVGT V	- EDVAAMVAWLLS	R - Q A A F V T 240
153 GGL HVPNWE - A HAYGASKAAL HHL TRSLAKRLGRD (G IRVNA IAPGPFHSRM	T-DTTS	EAVKAS	VA - A - H I PL - G	RPGE A	- DDVKGLCLFLAS	R - AGA YVH 245
							DISS VMT 250
136 LOWK - AQKG - Q AHTAAAKAG VMAFTIKCAAL EAADH Q	G VRINAVAF SLAWINFF			LV-K-IE AI-G	KFAE V	- WEVANVINEFLAS	D-L33 HWT 250
131 TGVK - PMAG - T GAYGSSKAALAHLAK I AALENAGA 0	G IRVNA IAPGGVDTPI	W-DSDANFRAMAAD	MGRDAA I AG	F A - S - G T P L - K	RFAT F	- DEIAATIGFLLS	A - Q A A N I T 233
150 AAFE-GQIG-QPAYAASKGGVVGMALPIAREFARYC	G I RVNT I APG I FWT RL	L - G S L P	QEAQDS	LG - R - QVP FP - S	RLGK F	- AEYAKMVEAIV -	
140 AAED COLC O AAYAAEKCOVVCMTL DLABEEABY			054006			DEVALMIZED IV	AND MUN 220
149 AAFD-GQTG-QAATAASKGGVVGMTLPTAREFARTC	GIRVMITAPGLFLIPL	L-ASLP	QEAQDS	LG-R-QVPFP-3	KLGHP	-DETALMVEQTV-	ANP ML N 238
154 AAED-GQMG-QAAYAASKSGVVGLTLPVARDLMSEC	G IRVNTILPGIFNTPL	M-NRAP	EEVKAA	L A - A - S V P F P - K	RLGN F	- EEYASLAVEMC -	RNS YFN 244
156 AAED-GOMG-OAAYSASKGGVVGMTLPLARDLMSE(G IRVNTIL PGIENTPL	L-0GAP	DNVKAA	L A - A - SVP FP - K	RL GQ F	- FEYANLALCMI -	YEN 246
			544050				
155 AAVD-GQMG-QAAYSASKGGIVGMILPIARDLMSEG	G IRVNI ILPGIFRIPL	L - AGL P	EAAQES	L A - A - Q V P F P - K	RLGH F	- EEYAALVMIMI -	E I G Y F N 245
150 AAYD-GQIG-QAAYAASKGAIASLTLPAARELARFC	G IRVMTIAPGIFETPM	M - AGMS	DEVRAS	LA - A - GVP FP - P	RLGR P	-QEYAALARHII-	ENS MLN 240
143 ASEE GOEG - M GAYTASKSALAALTI VWARDI SHH		V-AMI P	PDEVAE		RAGR	- FEYGOVAFEL L -	RTPI IN 233
			DI CI VAL				
140 AGQN-GGTA-TG-AHYAASKGGIITLTKVFARDLAPFC	G VAVSATAPGPLDLPS	V - REL V	PAEALTA	LT - E - T I PV - R	QLGD P	-GFIARTAVHLAG	R - DAA FAN 233
143 APQK - I PSV - AG - AAYVVSKGALLTLTKVAAGEAAPF 0	G MTVNTVAPGA I DTPM	L-RERT	PVEQFEQ	LF - G - PT LA - G	RPAR F	- DE I ASAVL YL AS	E - QAA F V N 236
146 SAHT - PRPE - T ARYTASKHAVI GI TKALAL DORRY I			POVPOANG				I PL - DAN VI N 238
140 SART-FRFF-TAFTTASKRAVLGLTKALALDGRFTT	HIVCSQVDIGNALIEL					- KHVADAVKI IAA	
144 SAYS - PRPD - T VAYCASKHGVLGLTKAASLEGRRH I	D IAVGQ IDIGNAASAF	S - EAFA	RGVPQADG	RL V - P E	PVMD A	- SVVGETVAYMDS	LPP - DAN AQF 236
146 SARV - PRAD - S PAYAASKWGL DGL TRSLA I DGREF I	N IAASMFNPGIVATEI	A - PGAV	KLDKDF		- A A M F	- EDIADAIIHMTA	L P D - H L N F Y E 230
112 SAON DRAD T LANTASKED ED TRALAL SORDH						BHWAEL VATMAA	VDD ELN VI 8 220
143 SAQM-PRAD-1TATTASKFGLEGLIRALALEGRPHC	GTTASTTHPGATTSEL			L RAS-ASP		- KHVAEL VAIMAA	VPD-EINVL 3 228
147 NGVN-AHMG-SADYNVAKEAVRAYSRTAAREWAPYC	G I CVNV I CPAAVSAAY	R - RFAE	MAPQVAAA	TA - A - AN PM - G	RMG D F	ESDIGGVAAFLAS	E - DAR YLT 241
144 GATM - GLPE - V GAYA LAKEGVRGLTKTAATGWGRY (G ITVNTVCP - MVATPL	F-DTWWQ	SL SEAEREH	QL - S - M I PM - R	RMGD	EQDVGGLIVFLGS	E - GAG Y T 239
			EEOOOEBAK		KMCE T		
145 AGIL - DUPI - HS - CATSASKGAVHSTSKILAKEWAKT I	N IRVNSVNPIMAINAE	I-DILAKMIP	EEQQQFRAK	PLGG	KMGE I	TRDLAPVLAFLAS	D-DSRF11 246
135 AGRY - GYPN - R I AYATSKWGLVGFAKTLA I ELGPH I	D ISVNAILPGAVGGER	F - DRV I EGRARASG	RSFEEEVAL	GL -G - SQSL - K	R I V A F	- AHVADLALFLTT	P - AGR S S 237
147 VAHR - FAPDGI F - AVTAAAKAGI FALARSI AVELGPO (G VTVNCVAPGYTRKEA		IPFAMI AF	MA.S.RAPT.G	R I A F F	- DDIAAAVAFIMG	P - DAR O I T 242
			11 27002772				
136 WAFE-PSEL-FPISAVFRSGLAAFIKIFADQFAGDI	N VRINNVLPGWIDSLP	A I - EQRR		D - SV PL - K	RYGI C	- EETAATTAFLAS	E - GAA Y I I 220
137 AGTY - PYPG - G NVYGASKAFVRQFSLNLRADLAGT I	R VRVSNIEPGLCSGTD	F-SVVRL	NGDMDAVQA	L Y R D V	EALL F	- EDIAATVAWVAE	Q P A H V N 228
136 AGSW- RYAG-G- NVYGATKAEVROESI NI RTDI HGT.	A VRVTDIEPGI VGGTE		KGDDGKAEK	TYON		- EDVSEAVWWVST	
			KODDOKAEK			- EDVOEXVMIVOT	
138 AATY - PYAG - G NVYGGTKAFVSQFSLGLRSDLHGT (G VRVTSIEPGMV - ETE	F-TLVR	TGSQTASDA	L Y HA A	NPMT A	- EDIAETLFWVAT	Q P A H L N 227
AN AGNIN BY BO O NUVYOOTY A FUGOEOL OL BODI DOT	G VRVSNIEPGI C . ESE		CODOAKVDA		F P I Q F		
141 AGNY - PYPG - S NVYGGIKAFVGQFSLSLRCDLRGI 0	G V K V S N I E F G L C - E G L	F-SLVRF		T Y AG A			QPA H I N 231
141 AGNY - PYPG - S NVYGGI KAFVGQFSLSLRCDLRGI (TYAGA	AAO 8 5		QPAHIN 231
141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRGT (141 AARI - VTPA - S SVYSATKHAVRV I TDGLRQEHN I	N IRATLISPGPTTSEL		DPNIAAW	T Y AG AG AG	AAQS F	- FAIAQAIRYALE	QPD NVD 228
141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRGT (141 AARI - VTPA - S SVYSATKHAVRV I TDGLRQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWA I TDGLRQEHD I	N I RATL I SPGPTTSEL D I RATVI SPGVVATEL		DPNIAAW	T Y AG A I K - Q GL - T LQ - E WR - R	AAQS F KSLT F	- FAIAQAIRYALE - DAIARAIRFALE	QPD NVD 228 QPE GVD 228
141 AGNY - PYPG - S NVYGG I KAFVGQ F SLSL RCDL RG F (141 AARI - VTPA - S SVYSATKHAVRV I TDGL RQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWA I TDGL RQEHD 1 143 AAIM - HPPF - L OPYNVAKTAVVAL SSGL ROEFOFF (N I RATL I SPGPTTSEL D I RATVI SPGVVATEL GAPIGVSVLYPEETOTRI			T Y AG A I K - Q GL - T LQ - E WR - R LR - E - E VR - AGL - A	AAQSF KSLTF	- FAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR	QPA HTN 231 QPD NVD 228 QPE GVD 228 A - DRL HTF 250
141 AGNY - PYPG - S NVYGGT KAFVGQF SLSLRCDLRGT (141 AARI - VTPA - S SVYSATKHAVRV I TDGLRQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWA I TDGLRQEHO 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (N I RATL I SPGPTTSEL D I RATVI SPGVVATEL GAPIGVSVL YPFFTQTRI				AAQS F KSLT F TGQT F	- FAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR	QPA H N 231 QPD NVD 228 QPE GVD 228 A - DRL H I F 250
141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWAITDGLRQEHD 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTR I G IGVSVL CPGPVATS I			T Y AG A I K - Q GL - T L Q - E WR - R L R - E - E V R - AGL - A RD - A - QMS - NVL - E	AAQS F KSL T F TGQT F KA I Q F	- FAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR	QPA HTN 23 QPD NVD 228 QPE GVD 228 - A - DRL HTF 250 - A - NQF YTH 248
141 AGNY - PYPG - S NVYGGT KAFVGQF SLSLRCDLRCHRGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWAITDGLRQEHD 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (N IRATLISPGPTTSEL D IRATVISPGVVATEL GAPIGVSVLYPFFTQTRI G IGVSVLCPGPVATSI G IGVSVLCPANIKSNI	G - HDVS		A 	AAQS F KSLT F TGQT F KAIQ F HGMD F	- FAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - VELAEHVKAGIV	QPD NVD 228 QPD NVD 228 QPE GVD 228 - A - DRL HIF 250 - A - NQF YIH 248 A - NQL YII 248
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRGF (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN 1 141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A GPYSAAKAASINI MEGYRQGLDKH (N IRATLISPGPTTSEL D IRATVISPGVVATEL GAPIGVSVLYPFFTQTRI G IGVSVLCPGPVATSI G IGVSVLCPANIKSNI G IGVSVCTPANIKSNI				A A Q S F K S L T F T G Q T F K A I Q F HGMD F HGI F F	- GDTAETTFWTEN - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - FKLAFATKKGVF	QPA HIN 23 QPD NVD 228 QPE GVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YIH 248
141 AARI - VTPA - S SVYSATKHAVRVITDGLRCELRCDL	N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTR I G IGVSVL CPGPVATS I G IGVSVL CPAN I KSN I G IGVSVL CPAN I KSN I	G - HDVS			AAQS F KSLT F TGQT F HGMD F HGLE F	- FAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - VELAEHVKAGIV - EKLAEAIKKGVE	QPD NVD 228 QPE GVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YIH 248 - D - NAL YIH 248
141 AGNY - PYPG - S NVYGGT KAFVGQF SLSLRCDLRC HRGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWAITDGLRQEHD 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 1	N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPANIKSNI G IGVSVCTPANIKSNI N IGVSLL CPGGVNTNI	F - SL VRF G - HDVS A - DDERNL PASMKGR L - THSAENL ASVSV A - EASRL RPAQFGK A - EASRL RPAQFGK A - EASRL RPAKYGT			AAQS F KSLT F TGQT F KAIQ F HGMD F HGLE F HGFD F	- GATAGATRYALE - DATAGATRYALE - DATAGATRATE - DEVGRRVLAATR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR	QPA H I N 23 QPD NVD 228 A - DRL H I F 250 - A - NQF Y I H 248 - A - NQL Y I I 248 - D - NAL Y I I 248 - N - DRF WVL 250
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCF (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN 1 141 AAHF - VMPT - A AVYCATKHAVWAITDGLRQEHD 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY (N IRATL ISPGPTTSEL D IRATVISPGVVATEL GAPIGVSVLYPFFTQTRI G IGVSVLCPGPVATSI G IGVSVLCPANIKSNI G IGVSVLCPANIKSNI N IGVSLLCPGGVNTNI E IGVSVLCPGLVKSYI	F - SL VRF G - HDVS			A A Q S F K S L T F K A I Q F H G M D F H G L E F H G F D F F G M E F	- GATAGATRYALE - DATAGATRYALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK	QPA H I N 23 QPD NVD 228 QPE GVD 228 - A - DRL H I F 250 - A - NQF Y I H 248 - A - NQL Y I I 248 - D - NAL Y I I 248 - N - DRF WVL 250 - A - NRL H I F 258
141 AGNY - PYPG - S NVYGGT KAFVGQF SLSLRCDLRCGT (141 AARI - VTPA - S SVYSATKHAVRVI TDGLRQEHN (141 AAHF - VMPT - A AVYCATKHAVWAI TDGLRQEHD (143 AAIM - HPPF - L QPYNVAKTAVVAL SSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGL SESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVI NLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAASI NLMEGYRQGLEKY (146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P GIYNTTKFAVRGLSESLHYSLLKY 1 148 ASFL - AGGA - P GIYNTKFAVRGLSESLHYSLKY 1	N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPAN I KSN I G IGVSVL CPGGVNTN I E IGVSVL CPGLVKSY I	F - SL VKF G - HDVS			AAQS F KSLT F TGQT F HGMD F HGLE F HGFD F FGME F FGME F	- GATAGATRYALE - DATAGATRYALE - DATAGATRYALE - DEVGRRVLAATR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK	QPA H I N 23 QPE NVD 228 - A - DRL H I F 256 - A - NQF Y I H 248 - A - NQL Y I I 248 - D - NAL Y I I 248 - N - DRF WVL 256 - A - NRL H I F 258 - F - NRL H I F 258
141 AARI - VTPA - S SVYSATKHAVRVITDGLRCEHRCH (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD (143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P GIYNTTKFAVRGLSESLHYSLLKY (148 ASFI - AGGA - P GIYNTAKFAVRGMSYSLRHSMYKY (N IRATLISPGPTTSEL D IRATVISPGVVATEL GAPIGVSVLVPFFTQTRI G IGVSVLCPGPVATSI G IGVSVLCPANIKSNI G IGVSVCTPANIKSNI N IGVSLLCPGGVNTNI E IGVSVLCPGLVKSYI G IGVSVVHPGLVKSYI	F - SL VRF G - HDVS			AAQS F KSLT F TGQT F HGMD F HGLE F HGFD F FGME F FGME F	- GATAGATRYALE - DATAGATRYALE - DATAGATRYALE - DEVAEAVMAGTR - DEVAEAVMAGTR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK - DTTGARTLDGVR	QPA HTN 23 QPD NVD 228 QPE GVD 228 - A - DRL HTF 250 - A - NQF Y H 248 - A - NQL Y H 248 - D - NAL Y H 248 - N - DRF WVL 250 - A - NRL HTF 255 - E - NRA N TF 251
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCF (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN 1 141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD 1 143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P GIYNTTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P GIYNTAKFAVRGMSYSLRHSMYKY (149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR (G IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPANIKSNI G IGVSVCTPANIKSNI N IGVSVL CPGGVNTNI E IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI	F - SL VRF G - HDVS			A A Q S F K S L T F T G Q T F H G M D F H G L E F H G F D F F G M E F F G M E F E WM D F	- GATAGATRYALE - DATARATRYALE - DATARATRYALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DYTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL	QPA HIN 23 QPE RVD 228 - A - DRL GVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 249 - N - DRF WVL 250 - A - NRF HIF 258 - A - NRA NIF 251 - A - DQL YVI 253
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 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - (146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY - 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY - 1 148 ASFI - AGGA - P - GIYNTTKFAVRGLSESLHYSLLKY - 1 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR - (149 AAEV - VMPP - QM - AIYAASKAAVCHFCEAAKGELAQH - 1 140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK - (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - (147 AGVL - QY - S - QA - GMYVATKFAVVGLSEALRAELAPQ - (145 GGFS - AV - G - T A - GLYCTAKFAISGMMEALATELEGT - 1 	 N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGGVNTNI E IGVSVL CPGL VKSYI G IGVSVL CPGL VKSYI G IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSVC CPGFVRSNI G IGVSVC CPGFVRSNI G IGVSVC CPGFVATNI G IGVSVL CPGFVRSNI G IGVSVC CPGFVATNI G VI CSAF CPGAVQSNI G IGVSAF CPGGVRSNI P IGVSCFYPGPVQTNL 	F - SL VKF G - HDVS			AAQS F KSLT F HGQT F HGLE F HGLE F FGME F FGME F SGME F NWME F NWME F NWME F NWME F NWME F NFMHLYQTK LTAS F	- GATAGET IF WILN - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DUTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EUVGNTVDATV - LDVGHMTLHATR - EQVGERVLEGT - EEVGKRVLRGTR	QPA HTN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF HTF 256 - A - NQL YTT 248 - D - NAL YTT 248 - N - DRF WVL 250 - A - NRL HTF 255 - E - NRA - NTF 251 - A - DQL YVT 253 - N - NTT YVT 253 - H - NKL YT 253 - H - NK YT 253 - H - NK YT 253 - H - NK YT 253 - H
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 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A AVYCATKHAVWAITDGLRQEHD (143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A APYSAAKAASINLMEGYRQGLEKY (146 AGFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P GIYNTKFAVRGLSESLHYSLLKY (148 ASFI - AGGA - P GIYNTAKFAVRGMSYSLRHSMYKY (149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR (144 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 147 AGVL - QY - S - QA - GMYVATKFAVVGLSEALRAELAPQ (145 GGFS - AV - G - TA - GLYCTAKFAYGGI TECLARYNLAPH (146 AGYL - SGPQ - A GLYTAKFAYGGI TECLARYNLAPH (147 AGVL - QY - S - QA - GLYCAAKYCVAGMFESLATDLRGT	N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVNTNI E IGVSLL CPGGVNTNI E IGVSUL CPGFVRSVI G IGVSVL CPGFVRSVI D IGVSUL LPGPVKSVI D IGVSILL PGPVKSVI SLA IGASVVCPGPVATNI G IGVSAF CPGGVQSNI G IGVSAF CPGGVQSNI G IGVSAF CPGGVQTVL A LGASVFFPGPVQTQL G IGVSIMCPGI TNTA	F - SL VKF G - HDVS	DQNVAAA DQNVAAA		AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F SWMD F NWME F NWME F NWME F NWME F NFMHLYQTK LTAS F VFMS F VFMS S LGMD S	- GATAGET IN WILN - FATAQATRYALE - DATAGET ALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - TEVGDMTVDATV - LDVGHMTLHATR - EQVGERVLEGTL - EEVGQRVLRGTR - EEVGQRVLRGTR	QPA HIN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL YVI 253 - N - DRT YVI 253 - N - NTT YVI 253 - H - NKL YVI 253 - H - NKL YVI 250 - A - NKL YVI 250 - R - GDL FIM 252 - R - RDL FIM 256
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - (146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY - 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY - (148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMKY - (149 AATV - VMPG - HL - AIYAAGKAAVINLTENMRADLAGR - (146 AGLT - PMPS - FM - AIYAASKAAVCHFCEAAKGELAQH - 1 146 AGLT - PMPS - FM - AIYAASKAAVTAMMECMRPELEGR - (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - (145 GGFS - AV - G - TA - GLYCTAKFA ISGMMEALATELEGT - 1 145 GGFS - AV - G - GA - GLYCAAKYCVAGMFESLATDLRGT - (N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGNIKSNI S IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSVL CPGFVRSNI G IGVSVC CPGAVQSNI G VICSAFCPGAVQSNI G IGVSAFCPGGVRSNI P IGVSCFYPGPVQTNL A LGASVFFPGPVQTQL G IGVSLKCPGLTTTAA 		GG DUAKTDA- DPNIAAW- EEADPTLAA- SGYVENEES- SGYVENEES- TGYYGRDEA- EMKPVDKTA- SGFAASEQA- SGFAASEQA- SGFKASEKK- SGLAETEQQ- TGYAEADK- TGYAEADK- DEAPKGPPP- PQPEVGP- PQPEVGAQQ- 		AAQS F KSLT F HGQT F HGMD F HGE F FGME F FGME F FGME F NWME F NWME F NWME F NWME F VFML F VFMS F VFMS F VFMS F	- GATAGATRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DTTGARTLDGVR - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - TEVGDMTVDATV - LDVGHMTLHAT - EQVGERVLEGT - EEVGQRVLRGTR - EEVGQRVLRGTR	QPA HTN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF HTF 255 - A - NQL YTT 248 - D - NAL YTT 248 - N - DRF WVL 250 - A - NRL HTF 255 - E - NRA - NTF 251 - A - DQL YVT 253 - N - NTT YVT 253 - N - NTT YVT 253 - N - NKL YVT 253 - R - NKL YTT 253 - N - NKL
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD (143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGFM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 GGFM - GSAL - A GIYNTTKFAVRGLSESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P GIYNTTKFAVRGLSESLHYSLKY (149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR (140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR (145 GGFS - AV - G - GA - GIYTASKFAVRGLTESLATDLRGT 1 146 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH (N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVXTNI SUL CPGGVNTNI SUL CPGGVNTNI G IGVSVL CPGFVRSVI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSVI G IGVSILL PGPVKSNI N IGVTVLMPGPIKSRI GLA IGASVVCPGPVATNI G IGVSAF CPGGVRSNI P IGVSCFYPGPVQTNL A LGASVFFPGPVQTQL G IGVSLMCPGLTRTNA K IGCSL CCPALTRTNA 	F - SL VKF G - HDVS			AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F FGME F NWME F NWME F NWME F NVME F VFMS F VFMS F LGMD F EGMD F	- GATAGATRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DTTGARTLDGVR - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - TEVGDMTVDATV - LDVGHMTLHATR - EQVGERVLEGTL - EEVGQRVLRGTR - EEVGQRTLAGMT - YEVGTKTLAGMT	QPA HIN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - D - NAL YII 248 - D - NAL YII 248 - A - NRL HIF 258 - E - NRA NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NKL YVI 253 - N - DEL YIL 247 - D - NAL YIE 256 - R - GDL FIM 255 - R - RDL FIM 255 - R - RMG - LIL 254
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVWAITDGLRQEHD (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLEKY (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 ASFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLKY 1 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY (149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR (144 GAUT - PMPS - FM - AIYAATKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYAATKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYATKAAVISLTEHLRLELEAK (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR (145 GGFS - AV - G - GA - GLYCAKFA VGGLTESLRYNLAPH (146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH (N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGGVNTNI E IGVSVL CPGFVKSVI G IGVSVL CPGFVKSVI D IGVSVL CPGFVKSVI G IGVSVL CPGFVKSVI G IGVSVL CPGFVKSVI G IGVSVL CPGFVKSVI G IGVSTCPGFVATNI G IGVSAF CPGGVRSNI G IGVSAF CPGGVRSNI P IGVSAF CPGGVRSNI P IGVSCFYPGPVQTNL A LGASVFFPGPVQTQL G IGVSL CCPALTRTNA G IGVSL VCPALVATDA	F - SL VKF G - HDVS			AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F EWMD F NWME F NWME F NWME F NWME F NFMHLYQTK LTAS F VFMS F SLGMD F EGMD F	- GATAGATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL - EVGONTVDATV - LDVGHMTLHATR - EQVGERVLEGTL - EEVGGRVLRGTR - EEVGQRVLRGTR - FEVGQKTLAGMT - YEVGTKTLAGMT - YEVGTKTLAGMS	QPA HIN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL YVI 253 - N - DRT YVI 253 - N - NKL YVI 253 - N - NKL YVI 253 - N - NKL YVI 253 - N - DEL YVI 253 - N - DEL YVI 253 - N - DEL YVI 253 - R - RDL FIM 253 - R - RDL FIM 255 - R - RDL FIM 255 - E - NRG - LIL 254 - E - NRG - LIL 254
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCGT (141 AARI - VTPA - S SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN (143 AAIM - HPPF - L QPYNVAKTAVVALSSGLRQEFQEE (144 SGLV - GGTA - T MAYCTAKAGVVGLSESLRTELKGS (146 GGFM - GSAL - A APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH (146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P GIYNTTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P GIYNTAKFAVRGMSYSLRHSMYKY (149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR (149 AAEV - VMPP - QM - AIYAASKAAVCHFCEAAKGELAQH 1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 147 AGVL - QY - S - QA - GMYVATKFAVRGLSEALRAELAPQ (145 GGFS - AV - G - T A - GIYCAKFA SOMMEALATELEGT 1 145 GGFS - AV - G - A - GIYTASKFAVRGLTESLRYNLAPH (146 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 147 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 144 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 144 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 	 N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI N IGVSILL PGPVKSNI G IGVSVC CPGAVQSNI G IGVSAFCPGAVQSNI G IGVSCFYPGPVQTQL G IGVSLMCPGLTRTNA K IGCSL CCPALTATNA G IGVSVL CPGATATNA 	F - SL VKF G - HDVS			A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F N W M E F N W M E F N W M E F N F M H L Y Q T K L T A S F V F M S K L G M D F R G M D F A M D F	- GATAGATRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EUVGNLVADATL - EEVGGRVLEGT - EEVGGRVLEGTR - FEVGQKTLAGMT - YEVGTKTLAGMT - LAGEAVVDATK	QPA HIN 23 QPE RVD 228 - A - DRL GVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - D - NAL YII 248 - D - NAL YII 248 - A - NRL HIF 250 - A - NRL HIF 250 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTL YVI 253 - N - NKL YVI 253 - N - NKL YVI 253 - N - DEL YIL 247 - D - NAL YIL 247 - D - NAL YIL 247 - D - NAL FIM 256 - R - RDL FIM 256 - E - NRG - LIL 250 - E - NRG - LIL 250 - E - NRG - LIL 250 - E - NRG - LIL 247
 141 AGNY - PYPG - S NVYGGTKAFVGQFSLSLRCDLRCGT	A - IRATL ISPGPTTSEL D - IRATVISPGVVATEL GAPIGVSVL YPFFTQTRI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGFVRSNI D - IGVSUL CPGFVRSVI G - IGVSVL CPGFVRSVI G - IGVSVL CPGFVRSNI D - IGVSVL CPGFVRSNI D - IGVSILL PGPVKSNI N - IGVSILL PGPVKSNI G - IGVSILL PGPVKSNI G - IGVSAF CPGGVRSNI G - IGVSAF CPGGVRSNI G - IGVSCFYPGPVQTNL A - LGASVFFPGPVQTQL G - IGVSL MCPGL TRTNA K - IGCSL CCPAL TRTAG G - IGVSL VCPAL VATDA G - IGVSL FPGATRTGM				AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F FGME F NWME F NWME F NWME F NVME F SWLD F LGMD F LGMD F NGMD F	- GATAGENTRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DTGARTLDGVR - DTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - TEVGDMTVDATV - LDVGHMTLHATR - EEVGGRVLEGTL - EEVGQRVLEGTR - EEVGQRVLEGTR - EEVGQRVLEGTR - EEVGQRVLEGTR - EEVGQRTLAGMT - EEVGQRTTAGEN - EAGEKTLEGNS - LEAGEKTLEGNS	QPA HTN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQF YIH 248 - A - NQL YII 248 - D - NAL YII 248 - A - NRL HIF 258 - E - NRA NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NKL YVI 253 - N - DEL YIL 247 - D - NAL YIE 256 - R - GDL FIM 256 - R - GDL FIM 256 - R - RDL FIM 254 - R - RNG - LIL 254 - E - NRG - LIL 254 - E - NRG - LIF 248 - E - NRG - LIF 248
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - (146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 ASFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLKY 1 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY - (149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR - (144 GALT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYATKAAVISLTEHLRLELEAK - (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - (145 GGFS - AV - G - GA - GLYCAKFA VGGLTESLRYNLAPH - (146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH (147 AGVL - QY - S - QA - GIYTASKFAVRGLTESLRYNLAPH (148 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH (144 AGIV - PLPG - F AAYSTSKYAVRGYAESLRMQLAPL - (N - I RATL I SPGPTTSEL D - I RATV I SPGVATEL GAP I GVSVL YPFFTQTRI G - I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGFVATSI G - I GVSVL CPGFVKSVI G - I GVSVL CPGFVKSVI G - I GVSVL CPGFVKSVI D - I GVSVL CPGFVKSVI D - I GVSVL CPGFVKSVI G - I GVSVL CPGFVKSVI G - I GVSVL CPGFVKSVI G - I GVSVL CPGFVKSVI G - I GVSFC CPGAVQSVI G - I GVSAF CPGGVRSVI G - I GVSAF CPGGVRSVI C - I GVSFF PGPVQTNL A - LGASVFF PGPVQTNL A - LGASVFFPGPVQTNL G - I GVSL CCPALTRTNA G - I GVSL VCPALVATDA G - I GVSL VCPALVATDA				A A Q S F K S L T F H G M D F H G L E F F G M E F F G M E F F G M E F N W M E F N M M E F N M M E F N G M D F A A I D F	- GATA A CALL A	QPA HIN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF HIF 258 - A - NQL YII 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 256 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL YVI 253 - N - DRT YVI 253 - N - NKL YVI 253 - N - NKL YVI 253 - N - NKL YVI 253 - N - DEL - YVI 253 - N - DEL - YVI 253 - R - RDL FIM 252 - R - RDL FIM 255 - E - NRG - LIL 254 - E - NRG - LIL 254 - E - NRF HIF 245
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - TMAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 147 AAFL - AAGS - P GIYNTTKFAVRGLSESLHYSLLKY 148 ASFI - AGGA - P GIYNTAKFAVRGMSYSLRHSMYKY 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR 146 AGLT - PMPS - FM - AIYAASKAAVCHFCEAAKGELAQH 146 AGLT - PMPS - FM - AIYATAKAAVISLTEHLRLELEAK 147 AGVL - QY - S - QA - GMYVATKFAVRGLSEALRAELAPQ 145 GGFS - AV - G - T - TIYSAGKAAVTAMMECMRPELEGR 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 147 AGVL - QY - S - GA - GIYTASKFAVRGLTESLRYNLAPH 144 AGIV - PLPG - M GAYSAGKYAVRGFTQALRLDLAPH 144 AGVV - PLPG - M GAYSAGKYAVRGFTQALRLDLAPH 144 AGNI - PVPP - FA - GVYAASKFAVRGLTESLRMQLAPL 	 N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGLVKSVI E IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSVI G IGVSVFPGLVKSNI S IGVSVFPGLVKSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSILCPGFVRSNI G IGVSAFCPGAVQSNI G IGVSCFPGPVQTQL G IGVSLMCPGLTRTNA K IGCSL CCPALTRTNA G IGVSCL FPGATRTGM G IGVSCL PGATKTAG G IGVSCL VPGAVKTAL N IGVSVL CPGMVKTAL 				A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F S M M D F N M M E F N M M E F N M M E F L G M D F L G M D F S L G M D F A A I D F G G M D F	- GATAGENTRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EDVGNLVADATL - EQVGERVLEGT - EEVGGRVLEGTR - FEVGQKTLAGMT - FEVGQKTLAGMT - FEVGGKTLAGMT - LEAGEKTLRGMS - LDTGRAVVDATR - MDMGRLVVDATR	QPA HIN 23 QPE NVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - D - NAL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - A - NQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NKL YVI 253 - R - RDL FIM 256 - E - NRG - LIL 256 - E - NRG - LIL 256 - E - NRG - LIL 254 - E - NRF HIF 248 - E - NRF HIF 248 - E - NRF HIL 243 - N - NRP YIF 241
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - (146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTKFAVRGLSESLHYSLLKY - (148 ASFI - AGGA - P - GIYNTKFAVRGLSESLHYSLKY - (149 AATV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR - (149 AAEV - VMPP - QM - AIYAASKAAVCHF CEAAKGELAQH 1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED - 1 140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK - (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - (145 GGFS - AV - G - GA - GLYCTAKFAISGMMEALATELEGT - 1 145 GGFS - AV - G - GA - GLYCTAKFAISGMEALATELEGT - 1 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH - (144 AGYU - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL - (144 AGVV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL - (144 AGVV - PLPG - F - AAYSTSKYAVRGISDSLRLALAPH - (144 AGWI - PVP - FA - GVYAASKFAVRGLSDSLRLALAPH - (N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGFVRSVI F IGVSVL CPGFVRSVI G IGVSVL CPGFVRSVI G IGVSVL CPGFVRSVI D IGVSILL PGPVKSVI D IGVSILL PGPVKSVI G IGVSILL PGPVKSVI G IGVSFCPGFVRSVI G IGVSFCPGFVRSVI P IGVSFCPGFVRSVI P IGVSL CPGFVRSVI G IGVSL CPALTRINA G IGVSL VCPALVATDA G IGVSL VCPALVATDA G IGVSL VCPALVATA G IGVSL VCPALVATA M IGVSL VCPALVATA C - IGVSL CPALVATA C - IGVSL CPALVATA				AAQS F KSLT F KSLT F HGMD F HGFD F HGFD F FGME F FGME F SGME F NWME F NWME F NWME F NWME F SGMD F EGMD F AAID F GGMD F	- GATAGENTRYLE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DTGARVTEAMK - DTGARVTEAMK - DTGARVTEAMK - DTGARVTEAMK - DTGARVTEAMK - EDVGNLVADATL - EVGDMTVDATV - LOVGHMTLHATR - EEVGQRVLEGT - EEVGQRVVE - EEVGQRVVE - EEVGQRVVE - EEVGQRVVE - EEVG - EEVGQRVVE - EEVG -	QPA HTN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - E - NRA NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - H - NKL YVI 253 - H - NKL YVI 253 - H - NKL YVI 253 - A - NRL YVI 253 - N - DEL YVI 253 - A - NKL YVI 253 - N - DEL YVI 253 - R - GDL FIM 256 - R - GDL FIM 256 - E - NRG - LIL 254 - E - NRG - LIL 254 - E - NRF - HIF 248 - E - NRF - HIF 248 - N - NRP - YIF 241 - A - NRP - YIF 241
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT- (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AARF - VMPT - A - AVYCATKHAVWAITDGLRQEHN	A - IRATL ISPGPTTSEL D - IRATVISPGVATEL GAPIGVSVL YPFFTQTRI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGVATSI G - IGVSVL CPGLVKSVI G - IGVSVL CPGLVKSYI G - IGVSVL CPGFVRSNI D - IGVSILL PGPVKSVI G - IGVSILL PGPVKSNI D - IGVSILL PGPVKSNI G - IGVSILL PGPVKSNI G - IGVSILCPGAVQSNI G - IGVSAFCPGQVQSNI G - IGVSAFCPGQVATNI A - LGASVFFPGPVQTQL G - IGVSLMCPGLTRTNA K - IGVSLMCPGLTRTNA G - IGVSLVCPALVATDA G - IGVSLVCPALVATDA G - IGVSLVCPAVKTAL N - IGVSVLCPGMVKTRA E - VAVHVVCPSFFQTNL				A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F S M M D F NWM E F NWM E F W L D F S K L F M T S L G M D F S G M D F S G M D F G G M D F G G M D F	- GATAGATRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DTTGARTLDGVR - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EDVGNLVADATL - EQVGERVLEGTL - EEVGQRVLRGTR - EEVGQRVLRGTR - FEVGQKTLAGMT - LEAGEKTLRGMS - DTGRAVVDATR - FDLGNEVVDATR - ADTADYTHQQVA	QPA HIN 23 QPE RVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 249 - D - NAL YII 249 - N - DRF WVL 250 - A - NRF WVL 250 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - H - NKL YVS 250 - A - NKL YVI 253 - H - NKL YVI 253 - R - RDL YIL 247 - D - NAL YIL 247 - D - NAL YIL 255 - R - RDL FIM 252 - R - RDL FIM 254 - E - NRG - LIL 254 - E - NRG - LIL 243 - E - NRF HIF 244 - E - NRF HIF 244 - N - NRP - YIF 241 - A - GEF - LIL 232
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT. 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 141 AARI - VMPT - A - AVYCATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVAL SSGLRQEFQEE (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS (146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH (146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLEKY (146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY (146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P - GIYNTTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY (149 AAEV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR (144 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 1 146 AGU - 9VAG - T - TIYSAGKAAVTAMMECMRPELEGR (147 AGVL - QY - S - QA - GMYVATKFAVVGLSEALRAELAPQ (145 GGFS - AV - G - T A - GLYCTAKFAISGMMEALATELEGT 1 145 AGYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH (144 AGYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 145 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 144 AGVV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL (144 AGVV - PLPG - M GAYSAGKYAVRGFTQALRLDLAPH 1 145 AAHL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 1 144 AGNI - PVPP - FA - GVYAASKFAVRGLTESLLVELRQV 1 145 ALM - QGPG - M SNYNVAKAGVLALSESLLVELRQV 1 	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSUL CPGFVRSNI D IGVSUL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSIL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSIL CPGFVRSNI G IGVSIL CPGFVRSNI G IGVSAF CPGAVQSNI G IGVSCF YPGPVQTQL G IGVSL CCPAL TRTNA G IGVSL VCPAL VATDA G IGVSL CPGATRTGM G IGVSL CPGAVKTAL M IGVSVL CPGMVKTAA C VKVRCL FPTFVDTPM 				A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F N W M E F N W M E F N W M E F N W M E F N F M H L Y Q T K L T A S F V F M S F N G M D F A A I D F S G M D F S G M D F S G A T L T S - V	- GATA A CALL A	QPA HIN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - D - NAL YII 248 - A - NRL HIF 258 - E - NRA - NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTL YVI 253 - N - NLL YVI 253 - N - DLL YIL 247 - D - NAL YIL 247 - D - NAL YIL 247 - R - GDL FIM 256 - R - GDL FIM 256 - R - GDL FIM 256 - R - RDL Y
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 147 AAGS - P - GIYNTKFAVRGLSESLHYSLLKY 148 ASFI - AGGS - P - GIYNTAKFAVRGLSESLHYSLLKY 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR 144 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 145 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 146 AGLT - PMPS - FM - AIYATKFAVRGLSELRAKELAPQ 147 AGVL - QY - S - QA - GMYVATKFAVVGLSEALRAELAPQ 145 GGFS - AV - G - TA - GLYCTAKFAISGMMEALATELEGT 146 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 147 AGVL - QY - S - QA - GIYTASKFAVRGLTESLRYNLAPH 148 AAFL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 144 AGIV - PLPG - F AAYSTSKYAVRGYAESLRMQLAPL 144 AGV - PLPG - M GAYSAGKYAVRGFTQALRLDLAPH 144 AGNI - PVPP - FA - GVYAASKFAVRGLSDSLRLALAPY1 139 AALM - QGPG - M SNYNVAKAGVALSESLVELRYNLAPH 141 SALY - GSPG - L - AVYSATKYAIRGLSEALDVEWRSS 	N - I RATL I SPGPTTSEL D - I RATV I SPGVATEL GAP I GVSVL YPFFTQTRI G - I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGFVTSI E - I GVSVL CPGFVTSI C - I GVSVL CPGFVKSVI D - I GVSVL CPGFVKSVI D - I GVSVL CPGFVKSVI D - I GVSVL CPGFVKSVI G - I GVSVL CPGFVKSNI F - I GVSFCPGFVATNI G - I GVSAFCPGGVQSNI G - I GVSAFCPGGVQSNI G - I GVSAFCPGGVQSNI G - I GVSAFCPGGVQSNI G - I GVSL CCPALTRTNA G - I GVSL CCPALTRTNA G - I GVSL VCPALVATDA G - I GVSL VCPALVATDA G - I GVSL VCPALVATDA G - I GVSL VCPALVATDA G - I GVSL CPGMVKTAL N - I GVSVL CPGMVKTAL N - I GVSVL CPGMVKTAL C - V VVVCPSFFQTNL G - V VVVCPSFFQTNL G - I VKVRCL FPTFVDTPM G - I RVRDL MPGFIFTPI				AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F FGME F SGMD F NWME F NWME F NWME F NWME F SGMD F C GGMD F AAID F SGMD F SGMD F SGMD F AAID F SGMD F SGATLTS - A SGATLTS - V	- GATA A CALL A	QPA HIN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL YVI 253 - H - NKL YVI 253 - A - NQL YVI 253 - A - NQL YVI 253 - A - NKL YVI 253 - N - NKR YI 253 - N - NRG LIL 254 - E - NRG LIL 254 - E - NRF HIL 243 - N - NRP - YIF 241 - A - GEF - LIL 234 - D - DRL HVL 234 - D - DRL HVL 234
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH 146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY 149 AATV - VMPG - HL - AIYAAGKAAVINL TENMRADLAGR 149 AAEV - VMPP - QM - AIYAASKAAVCHFCEAAKGELAQH 146 AGLT - PMPS - FM - AIYATAKAAVITL TETIRDSMAED 147 AGVL - QY - S - QA - GMYVATKFAVRGLSEALRAELAPQ 145 GGFS - AV - G - T - TIYSAGKAAVTAMMECMRPELEGR 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 147 AGVL - QY - S - GA - GIYTASKFAVRGLTESLRYNLAPH 148 ASFL - PGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 144 AGIV - PLPG - M - GAYSAGKYAVRGFTQALRLDLAPH 144 AGVL - PLPG - M - GAYSAGKYAVRGFTQALRLDLAPH 144 AGVL - PLPG - M 144 AGVL - PLPG - M - SAYSKYAVRGLASLLATELESL 144 AGIV - PLPG - M - SAYSKYAVRGLASLESLVELRQV 144 AGVL - PLPG - M - SAYSKYAVRGLASLESLVELRQV 144 AGVL - SPG - M - SAYSKYAVRGLASLESLVELRQV 144 AGVL - PLPG - M - SAYSKYAVRGLASLESLVELRQV 144 AGVL - PLPG - M - SAYSAKFAVRGLASLESLVELRQV 	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI M IGVSVL CPGFVRSNI G IGVSVC PGFVRSNI G IGVSVC PGFVRSNI G IGVSFCPGAVQSNI G IGVSAFCPGAVQSNI G IGVSL CPGFVRSNI P IGVSCFYPGPVQTNL A LGASVFFPGPVQTQL G IGVSL CPALTATNA G IGVSL CPGATRTGM G IGVSL CPGATRTGM G IGVSCL PGATRTGM G IGVSL CPGMVKTAL N IGVSVL CPGMVKTAL N IGVSVL CPGMVKTAL S. VAVHVVCPSFFQTNL G IRVRCL FPTFVDTPM G IRVRCL PTFVDTPM 		GG DUAKTDA- DPNIAAW- DQNVAAA SRPVPSAER - SGYVENEES - SGYVENEES - TGYYGRDEA - EMKPVDKTA - SGFAASEQA - SGFAASEQA - SGFAASEQA - SGFKASEKK - SGLAETEQQ - TGYAEADK - DEAPKGPPP - - PQPEVGP - - PQPEVGP - - PQPEVGP - - SGFKPADAT - - SGFAPVDEA - - SGFAPVDEA - - EAAGTFQKA - - EAGTFQKA - AGADEKRD - VGKLLEGSP -		A A Q S F K S L T F K S L T F H G M D F H G F D F H G F D F F G M E F F G M E F N W M E F N W M E F N W M E F N W M E F N F M H L Y Q T K L T A S F V F M S F S G M D F G G M D F G G M D F G G M D F G G M D F S G A T L T S - V A G L E I T P - V	- GATAGENTRYALE - FATAQATRYALE - DATARATRFALE - AEVAEAVMAGTR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DVTGARVTEAMK - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EDVGNLVADATL - EUVGRNLVADATL - EEVGGRVLEGT - EEVGGRVLEGTR - FEVGQRVLRGTR - FEVGQKTLAGMT - FEVGQKTLAGMT - FEVGQKTLAGMT - FDLGREVVDATR - ADTADYTHQQVA - EEVADHAWKAVH - SEVAEAAWAAVH	QPA HIN 23 QPE NVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTL YVI 253 - N - NTL YVI 253 - N - NLL YVI 253 - R - RDL FIM 256 - R - RDL FIM 256 - R - RDL FIM 256 - E - NRG - LIL 256 - E - NRG HIL 248
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 148 ASFI - AGGA - P - GIYNTTKFAVRGLSESLHYSLLKY 148 ASFI - AGGA - P - GIYNTTKFAVRGLSESLHYSLLKY 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY 149 AAEV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 140 GAVM - SARL - TR - GIYAPTKAAVISL TEHLRLELEAK 144 AGL - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 145 GGFS - AV - G - TA - GIYTASKFAVRGL SELATDLRGT 146 AGLL - SGPQ - A GIYTASKFAVRGL TESLRYNLAPH 147 AGVL - QY - S - GA - GIYTASKFAVRGL TESLRYNLAPH 148 AAYL - SGPQ - A GIYTASKFAVRGL TESLRYNLAPH 144 AGVV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL 144 AGVV - PLPG - M - GAYSAGKYAVRGFTQALRLDLAPH 144 AGVV - PLPG - M - SNYNVAKAGVLALSESLLVELRQV 144 AGNI - PVP - FA - GVYAASKFAVRGL TESLRWLAPH 144 AGVV - PLPG - M - SNYNVAKAGVLALSESLLVELRQV 144 AGVY - GSPG - L - AVYSATKYA I RGLSEALDVEWRSS 140 AALY - GSPG - L - AVYSATKYA I TESLDGEWAED 	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI G IGVSILL PGPVKSNI G IGVSL CPGFVRSNI G IGVSCF CPGAVQSNI G IGVSL CCPALTRTNA G IGVSL VCPALVATDA G IGVSL VCPALVATDA G IGVSL VCPALVATDA G IGVSL VCPALVATDA G IGVSCL FPGAVKTAL N IGVSVL CPGMVKTRA E VAVHVVCPSFFQTNL G IRVRSLMPSFIDTPL 				AAQS F KSLT F KSLT F HGMD F HGFD F HGFD F FGME F FGME F SGMD F NVME F NVME F NVME F NVME F NFMHLYQTK LTAS F VFMS K LGMD F AAID F GGMD F SGMD F SGATLTS - V AGLETTP - V	- GAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - VELAEHVKAGIV - EKLAEAIKKGVE - VDLGRVVLDAVR - DVIGARVIEAMK - DIIGARILDGVR - DAVGEMVADAIL - EDVGNLVADAIL - EUVGNLVADAIL - EUVGHMTLHAIR - EQVGERVLEGIL - EEVGGRVLRGIR - FEVGQKTLAGMI - YEVGTKILAGMT - LEAGEKILRGMS - LDTGRAVVDAIK - DDGRAVVDAIR - FDLGNEVVDAIE - ADIADYIHQQVA - EEVADHAWKAVH - SEVAEAAWAAVH	QPA HTN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 249 - D - NAL YII 249 - A - NRL HTF 259 - A - NRL HTF 259 - A - NRL YVI 253 - A - NRL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NKL YVI 255 - N - DEL YVI 255 - R - RDL FIM 256 - R - GDL FIM 256 - R - GDL FIM 256 - R - RDL R - RDL R - R - R - R - R - R - R - R - R
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHD (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - (146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P - GIYNTAKFAVRGNSYSLRHSMYKY - (149 AATV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR - (144 AGV - VMPP - QM - AIYAASKAAVCHF CEAAKGELAQH 1 146 AGLT - PMPS - FM - AIYATAKAAVITL TETIRDSMAED - 1 140 GAVM - SARL - TR - GIYAPTKAAVISL TEHLRLELEAK - (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - (145 GGFS - AV - G - GA - GIYTASKFAVRGL TESLRYNLAPH - (146 AAYL - SGPQ - A - GIYTASKFAVRGL TESLRYNLAPH - (147 AGVL - QY - S - QA - GIYTASKFAVRGL TESLRYNLAPH - (148 AAFL - SGPQ - A - GIYTASKFAVRGL TESLRYNLAPH - (144 AGVV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL - (144 AGVV - PLPG - F - AAYSTSKYAVRGL SDSLRLALAPY - 1 145 AAYL - SGPQ - A - GIYTASKFAVRGL TESLRYNLAPH - (144 AGV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL - (144 AGV - PLPG - M - GAYSAGKYAVRGFTQALRLDLAPH - (144 AGV - PLPG - M - SAYSTSKYAVRGL SDSLRLALAPY - 1 139 AALM - QGPG - M - SNYNVAKAGVALSESLLVELRQV - 1 141 SALY - GSPG - L - AVYSATKFAVRGL TESLDGEWAED - (144 AGNI - PVPP - FA - SVYSATKFAVRGL ALSESLLVELRQV - 1 144 AGNI - PVPP - FA - SVYSATKFAVRGL ALSESLLVELRQV - 1 145 AAYL - SGPG - L - AVYSATKAGVRALTESLDGEWAED - (144 AGN - APNS - L - SYYSATKFAVRALTESLDGEWAED - (144 ASRM - VAPN - L - SAYCTGKIAQNRVVAEAAAELAGT - (N IRATL ISPGPTTSEL D IRATV ISPGVVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGNIKSNI N IGVSLL CPGGVNTNI E IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSLL LPGPVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI S IGVSVL CPGFVRSNI G VICSAFCPGAVQSNI G VICSAFCPGGVRSNI G IGVSL CPGFVRSNI G IGVSCF YPGPVQTNL A LGASVFFPGPVQTQL G IGVSL CPALTRTNA G IGVSL CPALTRTNA G IGVSL CPGAVATDA G IGVSL VPGAVKTAL N IGVSVL CPGMVKTRA E VAVHVVCPSFFQTNL G VKVRCL FPTFVDTPM G IRVRSLMPSFIDTPL G VSVFAI DPGFVFTQL 				AAQS F KSLT F KSLT F HGMD F HGLE F FGME F FGME F FGME F NWME F NWME F NWME F NWME F NWME F NGMD F SGMD F GGMD F GGMD F GGMD F SGATLTS A SGATLTS A AGLE TP - V PAAQ - TDL	- GATA A CALL A	QPA HIN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL YVI 253 - H - NKL YVI 253 - A - DQL YVI 253 - H - NKL YVI 253 - A - NKL YVI 253 - A - NKL YVI 253 - R - RDL FIM 255 - R - GDL FIM 255 - R - RDL FIM 255 - E - NRG - LIL 256 - E -
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH	G - I RATL I SPGPTTSEL D - I RATV I SPGVATEL GAP I GVSVL CPGPVATEL GAP I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGLVKSVI G - I GVSVL CPGLVKSYI G - I GVSVL CPGLVKSYI G - I GVSVL CPGFVRSNI D - I GVSVL CPGFVRSNI D - I GVSILL PGPVKSNI N - I GVSILL PGPVKSNI G - I GVSL CPGFVRSNI G - I GVSL CPGFVATNI G - I GVSL CPGAVATNA G - I GVSL CPGAVATNA G - I GVSL CPGAVATNA G - I GVSL CPGAVATNA G - I GVSL CPGAVKTAL N - I GVSVL CPGMVKTAL N - I GVSVL CPGMVKTAL C - VAVHVVCPSFFQTNL G - I RVRSLMPGFI ETPL G - I RVRSLMPSFI DTPL G - VSVFAI DPGFVFTSI			- TYAG	A A Q S F K S L T F K S L T F H G M D F H G F D F H G F D F F G M E F F G M E F S M M E F N W M E F N W M E F N W M E F N W M E F S W M D F V F M S F V F M S F S G M D F G G M D F S G A T L T S - V A G L E I T P - V A G L E F T P - V P A A Q T D S E T A A Q	- GATA A CALL A	QPA HTN 23 QPE NVD 228 - A - DRL HTF 250 - A - NQF Y H 248 - A - NQL Y H 248 - A - NQL Y H 248 - D - NAL Y H 248 - D - NAL Y H 250 - A - NRL HTF 250 - A - NRL YVI 253 - N - NTT - YVI 253 - N - NTL - YVI 253 - N - NL YIL 247 - D - NAL YIL 247 - D - NAL FIM 256 - E - NRG - L IL 254 - E - NRG - L IL 254 - E - NRF - HIL 243 - N - NRP - YIF 241 - A - GEF - L IL 232 - D - DRL - HVL 234 - G - ERV - HYL 234 - G - RY 245
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN AVYCATKHAVRVITDGLRQEHN	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVKSVI G IGVSVL CPGFVKSVI G IGVSVL CPGFVKSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSL CPGFVRSNI G IGVSCF PGPVQTNL G IGVSL CPGFVATNIA G IGVSL CPALTATNA G IGVSL CPALTATNA G IGVSL CPALVATDA G IGVSL CPALVATDA G IGVSCL FPGAVKTAL N IGVSL CPGMVKTAL S IGVSCL PPGAVKTAL G IGVSCL PPGAVKTAL G IGVSCL PPGAVKTAL G IGVSCL PPFVDTPM G IRVRDLMPGFIETPL G IRVRSLMPSFIDTPL G VKIFAI DPGFVFTQL G VKIFAI DPGFVFTQL 				AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F FGME F EWMD F NWME F NWME F NWME F NWME F NFML J F SWLD F SWLD F SWLD F SWLD F SGMD F GGMD F GGMD F SGATLT A SGATLT S - V AGLE IT P - V AGLE FT P - V PAAQ - T DL SETA - AGL	- GATA A CALL A	QPA HTN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF - WVL 250 - A - NRL HIF 255 - E - NRA - NIF 251 - A - DQL - YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NKL - YVI 253 - R - RDL FIM 256 - R - GDL FIM 256 - R - GDL FIM 256 - R - RDL FIM 254 - R - NRF - HIL 243 - R - NRF - HIL 243 - N - NRP - YIF 241 - A - GEF - LIL 232 - N - NRP - YIF 241 - A - GEF - LIL 234 - G - RY 246 - G - RY 246 - C - RY
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH 146 SAFV - ALPT - T GIYCTTKYAVRGLAESLRVEMPKY 148 ASFI - AGGA - P GIYNTAKFAVRGLSESLHYSLLKY 148 ASFI - AGGA - P GIYNTAKFAVRGMSYSLRHSMYKY 149 AATV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 149 AATV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 146 AGLT - PMPS - FM - AIYAASKAAVCHFCEAAKGELAQH 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED 147 AGVL - QY - S - QA - GMYVATKFAVRGLSEALRAELAPG 145 GGFS - AV - G - T A - GIYTASKFAVRGLTESLRYNLAPH 146 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 147 AGVL - QP - A GIYTASKFAVRGLTESLRYNLAPH 148 ASFL - PGPQ - A GIYTASKFAVRGLTESLRYNLAPH 144 AGNU - PLPG - M GIYTASKFAVRGLTESLRYNLAPH 145 AAYL - SGPQ - A GIYTASKFAVRGLTESLRYNLAPH 144 AGNU - PLPG - M GAYSAGKYAVRGTALALELGT 144 AGNU - PLPG - M SAYSTSKYAVRGTALALELAPY 144 AGNI - PVPP - FA - GVYAASKFAVRGLTESLRYNLAPH 144 AGNI - PVPP - FA - GVYAASKFAVRGLTESLRYNLAPH 144 AGNI - PVPP - FA - SYYSATKYA IRGLSEALDVEWRSS 144 AGNI - PVPP - FA - SYYSATKYA IRGLSEALDVEWRSS 144 AGNI - PVPP - FA - SYYSATKYA IRGLSEALDVEWRSS 144 AGNY - PLPG - M SAYCTGKIAQNRIVEEAAAELAGT 144 AGNY - PVP - L SAYCTGKIAQNRIVEEAAAELAGT 146 AARK - VAPN - L SAYAVAKASLIRLTEHLDFEQKAA 	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGVANIKSNI D IGVSLL CPGGVNTNI G IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSVL CPGFVRSNI G IGVSVC CPGAVQSNI G VI CSAFCPGAVQSNI G IGVSL CPGFVRSNI G IGVSAFCPGQVATNI G IGVSL CPGFVRSNI D IGVSL CPGFVRSNI G IGVSL CPGAVQSNI G IGVSL CPGAVATNA G IGVSL CPGAVATNA G IGVSL CPGAVATNA G IGVSL CPGAVKTAL N IGVSVL CPGMVKTRA E VAVHVVCPSFFQTNL G VKVRCL FPTFVDTPM G IRVRSLMPGFI ETPL G VKVFAI DPGFVFTQL G VKIFAI DPGFVFTSL G VKIFAI DPGFVFTSL G VKAFAI QPGT IMTAM 				A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F F G M E F NWM E F NWM E F NWM E F NWM E F S G M D F G G M D F G G M D F S G A T L T S - V A G L E I T P - V A G L E F T P - V P A A Q T D L S E T A A G L E S A Q G M	- GATA A CALL A A CALL A CALL A CALL A CALL A CALL A CALL A A CALL A CALL A A CALL A CALL A A A A	QPA HTN 23 QPE RVD 228 - A - DRL HTF 250 - A - NQF Y H 248 - A - NQF Y H 248 - A - NQL Y H 248 - A - NQL Y H 248 - N - DRF WVL 250 - A - NRF WVL 250 - A - NRL HTF 255 - A - DQL YVI 253 - A - NKL YVI 253 - R - RDL FIM 252 - R - RDL FIM 254 - E - NRG - L I L 254 - E - NRG - L I L 254 - E - NRF HIF 248 - E - NRF HIF 248 - E - NRF HIF 244 - A - GEF - L I L 232 - D - DRL HVL 234 - G - RY 244 - G - RY
 141 AGNY - PYPG - S - NVYGG TKAFVGQ FSLSLRCDLRCG F. (141 AARI - VTPA - S - SVYSATKHAVRVI TDGLRQEHN	G - IRATLISPGPTTSEL D - IRATVISPGVATEL GAPIGVSVLYPFFTQTRI G - IGVSVLCPGPVATSI G - IGVSVLCPGPVATSI G - IGVSVLCPGPVATSI G - IGVSVLCPGLVKSVI G - IGVSVLCPGLVKSYI G - IGVSVLCPGFVRSNI D - IGVSVLCPGFVRSNI D - IGVSILLPGPVKSNI N - IGVSILLPGPVKSNI G - IGVSILLPGPVKSNI G - IGVSILCPGFVRSNI G - IGVSILCPGFVRSNI G - IGVSILCPGFVRSNI G - IGVSLCPGFVRSNI G - IGVSCFYPGPVQTQL G - IGVSLCCPALTRTNA K - IGCSLCCPALTRTNA G - IGVSLLPGATRTGM G - IGVSLLCPGAVKTAL M - IGVSLLCPGAVKTAL G - IGVSLLCPGAVKTAL G - IGVSLCPGAVKTAL G - IGVSLCPGAVKTAL G - IRVRSLMPGFIETPL G - IRVRSLMPSFIDTPL G - VKIFAIDPGFVFTSL G - VKIFAIDPGFVFTSL G - VKVRCLFPTSLTDV			- TYAG	A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F F W M D F N W M E F N G M D F S G A T L T S - V A G L E F T P - V P A A Q T D L S E T A A G L E S A Q G N G L D F	- GATA A CALLA A A A	QPA HIN 23 QPE NVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - D - NAL YII 248 - D - NAL YII 248 - A - NRL HIF 250 - A - NRL HIF 250 - A - NRL YVI 253 - F - NRA - NIF 251 - A - DQL - YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NKL - YVS 250 - A - NKL - YVS 250 - A - NKL - YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NKL YVI 253 - R - RDL FIM 256 - R - RDL R - RDL R - R
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT - (141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN (141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHD (143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - (146 GGFM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY - (146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY1 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLKY - (148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY - (149 AAFV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR - (149 AAEV - VMPG - HL - AIYAASKAAVCHF CEAAKGELAQH1 146 AGLT - PMPS - FM - AIYATAKAAVITLTETIRDSMAED - 1 140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK - (144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - (145 GGFS - AV - G - GA - GLYCTAKFAISGMMEALATELEGT - 1 145 GGFS - AV - G - GA - GLYCTAKFAISGMMEALATELEGT - 1 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH - (147 AGVL - QP - F - AAYSTSKYAVRGTAELRALLAPQ - (144 AGIV - PLPG - F - AAYSTSKYAVRGTALRLLALPH - (144 AGV - PLPG - M - GAYSAGKYAVRGTALSLRMQLAPL - (144 AGV - PLPG - M - SAYSTSKYAVRGTALLESLLVELRQV - 1 145 AAYL - SGPQ - A - SIYNAKAGVLALSESLLVELRQV - 1 144 AGIV - PLPG - M - SAYSTSKYAVRGTALSLMQLAPL - (144 AGIV - PLPG - M - SAYCTGKIAQNRVVAEAAAELAGT - (144 AGYV - PLPG - M - SAYCTGKIAQNRVAEAAAELAGT - (145 AARK - VAPY - L - SAYCTGKIAQNRIVEEAAAELAGT - (146 AGTF - VAPF - A - SAYAVAKASLIRLTEHLDFEQKAA - (147 AGKY - SPN - L - SAYCTGKIAQNRIVEEAAAELAGT - (148 ASRM - VAPN - L - SAYCTGKIAQNRIVEEAAAELAGT - (144 AGTF - VAPF - A - SAYAVAKASLIRLTEHLDFEQKAAE - (N - IRATL ISPGPTTSEL D - IRATVISPGVATEL GAPIGVSVL YPFFTQTRI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGFVRSNI D - IGVSLL CPGGVNTNI C - IGVSVL CPGFVRSNI D - IGVSUL CPGFVRSNI D - IGVSUL CPGFVRSNI D - IGVSILL PGPVKSNI N - IGVSILL PGPVKSNI G - IGVSL CPGFVRSNI G - IGVSCFYPGPVQTNL A - LGASVFFPGPVQTQL G - IGVSL CCPAL TRTNA G - IGVSL VCPAL VATDA G - IGVSL CPGMVKTRA C - IGVSL CPGMVKTRA C - IGVSL CPGMVKTRA C - IRVRDL MPGF I ETPL G - IRVRSL MPSF I DTPL G - VKIFAI DPGFVFTSL G - VKIFAI DPGFVFTSL G - VKAFAI QPGT IMTAM G - IKVNU APGS I RTDV GYN I RVNSVHPGC I DTPM			- TYAG	A A Q S F K S L T F K S L T F K A I Q F H G F D F H G F D F F G M E F F W M D F N W M E F N W M E F N W M E F N W M E F S G M D F G G M D F S G A T D	- GATA A CARATRYALE - DATARATRYALE - DATARATRYALE - DEVGRRVLAATR - DEVGRRVLAATR - DEVGRRVLAATR - VELAEHVKAGTV - EKLAEATKKGVE - VDLGRVVLDAVR - DTTGARTLDGVR - DTTGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EDVGNLVADATL - TEVGDMTVDATV - LDVGHMTLHATR - EEVGGRVLEGTL - EEVGQRVLEGTR - EEVGQRVLRGTR - EEVGQRVLAGTR - EEVADAWDATR - ADTANAWDAVH - ARCAQRVLDLAS - ARLRRFVVALAA ADAVDQMLSATAA	QPA HTN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HTF 255 - E - NRA - NTT 253 - N - DRF YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NKL YVI 253 - R - RDL FIM 256 - R - GDL FIM 256 - R - RDL FIM 256 - R - RDL FIM 256 - R - RRF HTL 248 - E - NRF HTL 248 - E - NRF HTL 248 - E - NRF HTL 248 - C - DRL - HTL 244 - G - CRY 244 - G - RY 244 - D - C - C - C - 244 - D - C - C - C - C - 244 - C - C - C - C - C - C - 244 - C - C - C - C - C - C - 244 - C - C - C - C - C - C - C - C - C - C
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARF - VMPT - A - AVYCATKHAVRVITDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGLM - GSAL - A APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAAVINLMESYRQGLDKH 146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 147 AAGS - P - GIYNTAKFAVRGLSESLHYSLLKY 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY 149 AATV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 149 AATV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 146 AGLT - PMPS - FM - AIYATAKAAVITL TETIRDSMAED 146 AGLT - PMPS - FM - AIYATAKAAVITL TETIRDSMAED 147 AGVL - QY - S - QA - GMYVATKFAVVGLSEALRAELAPQ 145 GGFS - AV - G - T A - GIYTASKFAVRGLTESLRYNLAPH 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 147 AGVL - QY - S - QA - GIYTASKFAVRGLTESLRYNLAPH 148 ASFL - PGPQ - A GIYTASKFAVRGLTESLRYNLAPH 144 AGIV - PLPG - M GAYSAGKYAVRGTALALELGT 144 AGIV - PLPG - M SAYSTSKYAVRGTALALELDLAPH 144 AGIV - PLPG - M SAYSTSKYAVRGTALALELAPY 145 AAYL - SGPG - L - AVYSATKYA IRGLSEALDVEWRSS 144 AGIV - PLPG - M - SAYCTGKIAQNRIVEAAAALAPY 145 AARK - VAPN - L - SAYCTGKIAQNRIVEAAAALAAELAAPY 146 ASRM - VAPN - L - SAYCTGKIAQNRIVEAAAALAAELAAPT 147 AGVL - GSPG - L - AVYSATKYA IRGLSEALDVEWRSS 148 ASRM - VAPN - L - SAYCTGKIAQNRIVEAAAAELAAFLAAT 149 AGRF - VAPF - A - SAYAVAKASLIRLTEHLDFEQKAA 140 AGIY - GSPM - R - TGYSAAKFGLFGYSDALRAEVAGL 141 GGLR - GAAF - N - AAYCTSKAAVKMLSKCLGAEFAAL 	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGVANIKSNI N IGVSLL CPGGVNTNI E IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSVC CPGAVQSNI G IGVSAFCPGAVQSNI G IGVSAFCPGQVATNI G IGVSL CPGFVRSNI D IGVSAFCPGQVATNI G IGVSAFCPGQVATNI G IGVSL CPGFVATNI G IGVSL CPGAVATNA G IGVSL CPGAVATNA G IGVSL CPGAVKTAL N IGVSU CPGAVKTAL N IGVSU CPGMVKTRA E VAVHVVCPSFFQTNL G IRVRSLMPGFI ETPL G IRVRSLMPSFI DTPL G VKIFAI DPGFVFTQL G VKVFAL DPGFVFTQL G VKIFAI DPGFVFTQL 		GG DUARTDA DPNIAAW EEADPTLAA SRPVPSAER SGYVENEES SGYVENEES TGYYGRDEA EMKPVDKTA EMKPVDKTA SGFAASEQA SGFAASEQA SGFKASEKK SGLAETEQQ SGFKASEKK DEAPKGPPP TGYAEADK PQPEVGP - PQPEVGP - PQPEVGP - PQPEVGP SGFKPADAT - SGFFDVAKG - SGFFDVAKG SGFFDVAKG EAGTFQKA - EAGTFQKA EAGTFQKA 		A A Q S F K S L T F H G M D F H G M D F H G F D F F G M E F F G M E F F W M D F NWME F NWME F NWME F N G M D F V F M S F V F M S F U T A S F S G M D F G G M D F G G M D F G G M D F S G A T L T S - V A G L E I T P - V A G L E I T P - V A G L E F T P - V A C	- GATA A CALL A A A A	QPA HTN 23 QPE NVD 226 - A - DRL HTF 250 - A - NQF Y H 246 - A - NQF Y H 246 - A - NQF Y H 246 - A - NQF WVL 250 - A - NRF WVL 250 - A - NRL HTF 255 - A - DQL YVI 253 - A - DQL YVI 253 - A - DQL YVI 253 - A - NKL YVI 253 - R - RDL FIM 252 - R - RDL FIM 252 - R - RDL FIM 253 - E - NRG - L L 254 - E - NRG - L L 254 - E - NRG - L I 254 - E
 141 AGNY - PYPG - S - NVYGG TKAFVGQ FSLSLRCDLRG F - (141 AARI - VTPA - S - SVYSATKHAVRVI TDGLRQEHN 141 AARI - VMPT - A - AVYCATKHAVRVI TDGLRQEHN 143 AAIM - HPPF - L - QPYNVAKTAVVAL SSGLRQEFQEE - (144 SGLV - GGTA - T - MAYCTAKAGVVGL SESLRTELKGS - (146 GGFM - GSAL - A - APYSAAKAAVI NLMESYRQGLDKH - (146 GGFM - GSAL - A - APYSAAKAAVI NLMESYRQGL EKY (146 GGFM - GSAL - A - GPYSAAKAASI NLMEGYRQGLEKY (146 AGFV - ALPT - T - GI YCTTKYAVRGL AESLRVEMPKY 1 152 AAFL - AAGS - P - GI YNTTKFAVRGL SESLHYSLLKY 1 148 ASFI - AGGA - P - GI YNTTKFAVRGL SESLHYSLLKY 1 148 ASFI - AGGA - P - GI YNTAKFAVRGMSYSLRHSMYKY - (149 AAEV - VMPG - HL - AI YAAGKAAVLNL TENMRADLAGR - (149 AAEV - VMPP - QM - AI YAASKAAVCHF CEAAKGELAQH 1 146 AGLT - PMPS - FM - AI YATAKAAVI TL TETI RDSMAED 1 146 AGLT - PMPS - FM - AI YATAKAAVI SL TEHLRLELEAK - (147 AGVL - QY - S - QA - GMYVATKFAVVGL SEALRAELAPQ - (145 GGFS - AV - G - TA - GL YCTAKFA I SGMMEALATELEGT 1 145 AGYL - SGPQ - A - GI YTASKFAVRGL TESLRYNLAPH - (146 AAYL - SGPQ - A - GI YTASKFAVRGL TESLRYNLAPH (147 AGVL - QP - M - GAYSAGKYAVRG TESLRYNLAPH (144 AGI V - PLPG - M - GAYSAGKYAVRG TAALR LDLAPH (144 AGI V - PLPG - M - GAYSAGKYAVRG TAALR LDLAPH (144 AGI V - PLPG - M - SAYSTSKYAVRG YAESLRMQLAPL (144 AGI V - PLPG - M - SAYSTSKYAVRG TAALR LDLAPH (144 AGI V - PLPG - M - SAYSTSKYAVRG TAALR LDLAPH (144 AGI V - PLPG - M - SAYCTGK AQNRVAEAAAELADT (144 AGI V - PLPG - M - SAYCTGK AQNRVAEAAAELADT (145 AARK - VAPY - L - SAYCTGK AQNRVAEAAAELADT (146 AGT - VAPF - A - SAYAVAKASL IRL TEHLDFEQKAA (147 AGKV - GSPM - R - TGYSAAKFGLFGYSDALRAELADT (148 ASRM - VAPF - L - SAYCTGKAAVKMLSKCLGAEFAAL (149 AGKV - GAF -	G - VKVSKLEPGPTTSEL D - IRATLISPGPTTSEL GAPIGVSVLYPFFTQTRI G - IGVSVLCPGPVATSI G - IGVSVLCPGPVATSI G - IGVSVLCPGPVATSI G - IGVSVLCPGVKSVI G - IGVSVLCPGLVKSYI G - IGVSVLCPGFVKSVI G - IGVSVLCPGFVRSNI D - IGVSILLPGPVKSVI G - IGVSILLPGPVKSNI N - IGVTVLMPGPIKSRI GLAIGASVVCPGPVATNI G - VICSAFCPGAVQSNI G - IGVSCFYPGPVQTQL G - IGVSCFYPGPVQTQL G - IGVSLCCPALTRTNA K - IGCSLCCPALTRTNA G - IGVSLVCPALVATDA G - IGVSLVCPALVATDA G - IGVSLFPGATRTGM G - IGVSLFPGATRTGM G - IGVSLFPGAVKTAL N - IGVSLFPGAVKTAL G - VKVRCLFPTFVDTPM G - IRVRSLMPSFIDTPL G - VKIFAIDPGFVFTQL G - VKAFAIQPGTIMTAM G - IKVNVAPGGIDTPM GLPIHVSAIVPGMIRTNI			- TYAG A 	AAQS F KSLT F KSLT F HGMD F HGFD F FGME F FGME F FGME F SWMD F NWME F NWME F NWME F NWME F NFMHL YQTK LTAS F VFMS K LGMD F SGMD F SGMD F SGMD F SGMD F SGMD F SGMD F SGATLTS - V AGLE FTP - V SETA - AGL SETA - AGL SETA AGL	- GATA A CALL A A CAL	QPA HIN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - D - NAL YII 248 - A - NRL HIF 258 - E - NRA - NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTL YVI 253 - N - NLL YVI 255 - A - NKL YVI 255 - A - NKL YVI 255 - R - RQL FIM 256 - R - GDL FIM 256 - R - RDL RE
 141 AGNY - PYPG - S - NVYGGTKAFVGQFSLSLRCDLRCGT 141 AARI - VTPA - S - SVYSATKHAVRVITDGLRQEHN 141 AAHF - VMPT - A - AVYCATKHAVRVITDGLRQEHD 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS 146 GGFM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 GGFM - GSAL - A GPYSAAKAASINLMEGYRQGLEKY 146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 152 AAFL - AAGS - P - GIYNTKFAVRGLSESLHYSLKY 148 ASFI - AGGA - P - GIYNTKFAVRGLSESLHYSLKY 149 AAFV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 149 AAEV - VMPG - HL - AIYAAGKAAVLNL TENMRADLAGR 140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK 144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR 145 GGFS - AV - G - GA - GLYCTAKFA VGL SEALRAELAPQ 145 GGFS - AV - G - GA - GLYCTAKFA ISGMMEALATELEGT 146 AAYL - SGPQ - A GIYTASKFAVRGL TESLRYNLAPH 147 AGVL - QP - F AAYSTSKYAVRGTELCLRYNLAPH 148 AGI - PLPG - F AAYSTSKYAVRGL TESLRYNLAPH 144 AGIV - PLPG - F AAYSTSKYAVRGL SDSLRLALAPU 144 AGV - PLPG - M GAYSAGKYAVRGFTQALRLDLAPH 145 AAYL - SGPQ - A GIYTASKFAVRGL SDSLRLALAPU 144 AGV - PLPG - M - SAYCTGKIAQNRVVAEAAAELAGT 145 AAYL - SGPG - L - AVYSATKYAIRGLSBALLVELRQV 144 AGY - PLPG - M - SAYCTGKIAQNRVVAEAAAELAGT 145 AARK - VAPY - L - SAYCTGKIAQNRIVEEAAAELAGT 146 AGTF - VAPF - A - SAYAVAKASLIRLTEHLDFEQKAA 147 AGKV - GPF - A - SAYAVAKASLIRLTEHLDFEQKAA 148 ASRM - VAPN - L - SAYCTGKIAQNRIVEEAAAELAGT 149 AGKY - GPF - M GIYTASKFAVRGLFGYSDALRAEVAGL 144 AGTF - VAPF - A - SAYAVAKASLIRLTEHLDFEQKAA 145 AARK - VAPY - L - SAYCTGKIAQNRIVEEAAAELAGT 146 AGTF - VAPF - A - SAYAVAKAS	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGNIKSNI N IGVSLL CPGGVNTNI E IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSLL LPGPVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI S IGVSVL CPGFVRSNI G IGVSILL PGPVKSNI G IGVSL CPGGVRSNI G IGVSCF CPGGVRSNI G IGVSL CPGAVATNA G IGVSL CPGAVATNA G IGVSL CPGAVATAL A IGVSVL CPGMVKTRA G IGVSVL CPGMVKTRA E VAVHVVCPSFFQTNL G IRVRSLMPSFIDTPL G IKVRVL PATTSL G VKIFAI DPGFVFTSL G IKVHVIAPGSI RTDV GYNIRVNSVHPGG IDTPM GLPIHVSAI VPGMIRTNI G IVVQAVLPAATRTE 			- TYAG A 	A A Q S F K S L T F H G M D F H G M D F H G M D F F G M E F F G M E F F G M E F N W M E F S G M D F G G M D F G G M D F G G M D F G G M D F S G A T L T S A S C A T L	- GATA A CALL A CALL - FATA A CALL - FATA A CALL - FATA A CALL - AEVAEAVMAGIR - DEVGRRVLAATR - DEVGRRVLAATR - VELAEHVKAGIV - EKLAEATKKGVE - VDLGRVVLDAVR - DTIGARTLDGVR - DTIGARTLDGVR - DAVGEMVADATL - EDVGNLVADATL - EDVGNLVADATL - TEVGDMTVDATV - LDVGHMTLHATR - EEVGGRVLEGIL - EEVGGRVLEGIL - EEVGQRVLEGIR - ADTADY INQUA - EEVADHAWKAVH - EEVADHAWKAVH - ARCAQRVLDLAS - ARCAQRCLDLVS - ARLRFVVALAA ADAVDQMLSATAA - AEMGGGVVYLCS - EQMAEKKFWAHS	QPA HTN 23 QPD NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HTF 255 - E - NRA - NTT 255 - N - DRF YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NKL YVI 253 - R - RKL YTL 247 - D - NAL YTL 247 - D - NAL YTL 247 - R - GDL FIM 256 - R - GDL FIM 256 - R - RKG - L L 254 - E - NRG - L I L 254 - E - NRF - HTL 244 - E - NRF - HTL 244 - E - NRF - HTL 244 - A - GEF - L I L 232 - D - DRL - HTL 234 - G - RY 244 - D - AAS - FVT 246 QP DQ SEQ - I I A 265 RRE - L VT 225
 141 AGNY - PYPG - S - NVYGG TKAFVGQ FSLSLRCDLRG F - (141 AARI - VTPA - S - SVYSATKHAVRVI TDGLRQEHN	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGVATSI G IGVSVL CPGVATSI G IGVSVL CPGL VKSYI G IGVSVL CPGL VKSYI G IGVSVL CPGFVRSNI D IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI N IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSVL CPGFVRSNI G IGVSILL PGPVKSNI S IGVSVL CPGFVRSNI G IGVSILL PGPVKSNI G IGVSIL CPGFVRSNI G IGVSL CPGAVQSNI G IGVSAF CPGAVQSNI G IGVSL CPGPVQTUL G IGVSL MCPGL TRTNA G IGVSL VCPAL VATDA G IGVSL CPGAVKTAL N IGVSVL CPGMVKTAL G IGVSL CPGAVKTAL G VKVRCL FPTFVDTPM G IRVRSLMPSFIDTPL G VKVFAI DPGFVFTSL G VKVFAI QPGT IMTAM G IKVHVI APGSI RTDV GYNI RVNSVHPGGI DTPM GL PIHVSAI VPGMIRTNI G IYVQAVL PAATRTEI G VYVA VU PAATRTEI 		GG DUARTDA DRNIAAW DQNVAAA EEADPTLAA SRPVPSAER SGYVENEES SGYVENEES TGYYGRDEA EMKPVDKTA SGFAASEQA SGFAASEQA SGFAASEQA SGFKASEKK SGLAETEQQ TGYAEADK DEAPKGPPP TGYAEADK DEAPKGPPP PQPEVGP - PQPEVGP - PQPEVGP SGFKPADAT - SGFPDVAKG SGFAPVDEA EAAGTFQKA EAGTFQKA 	- TYAG	A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F F G M E F N W M E F N W M E F N W M E F N W M E F S G M D F V F M S K L F M T S L G M D F S G M D F S G M D F S G M D F G G M D F S G A T L T S - V A G L E I T P - V A G L E I T P - V A G L E F T P -	- G J A A A I RYALE - DA I A RA I RYALE - DA I A RA I RFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - VELAEHVKAGIV - EKLAEAIKKGVE - VDLGRVVLDAVR - DVIGARVIEAMK - DIIGARILDGVR - DVGGRVLDAIL - EDVGNLVADAIL - EDVGNLVADAIL - EUVGRVLEGIR - EEVGGRVLEGIR - EEVGGRVLEGIR - FEVGQRVLRGIR - FEVGQKTLAGMI - YEVGTKILAGMI - YEVGTKILAGMI - YEVGTKILAGMI - FDLGNEVVDAIE - ADIADYIHQQVA - EUVADHAWKAVH - SEVAEAAWAAVH - ARCAQRVLDLAS - ARLRRFVVALAA ADAVDQMLSAIAA - AEMGGGVVYLCS - GELVDAALVGF	QPA HIN 23 QPE NVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NTL YVI 253 - N - NL YIL 247 - D - NAL FIM 256 - E - NRG - L IL 254 - E - NRF - HIL 243 - G - RY YIF 241 - A - GEF - L IL 232 - D - DRL - HIL 234 - G - RY 244 - D - ERE - IIM 232 - D - AAS - FVT 246 QPDQSEQ - IIA 265 RRE - LVT 225 RRE - LVT 225
 141 AGNY - PYPG - S - NVYGG TKAFVGQ FSLSLRCDLRG T - (141 AARF - VMPT - A - AVYCATKHAVRVI TDGLRQEHN	 N. VINIERSE N IRATLISPGPTTSEL D IRATVISPGVVATEL GAPIGVSVLYPFFTQTRI G IGVSVLCPGPVATSI G IGVSVLCPGPVATSI G IGVSVLCPGVATSI G IGVSVLCPGVATSI G IGVSVLCPGVXSYI G IGVSVLCPGLVKSYI G IGVSVLCPGFVRSNI D IGVSILLPGPVKSNI N IGVTVLMPGPIKSRI GLAIGASVVCPGPVATNI G VICSAFCPGAVQSNI G IGVSLCPGFVRSNI G IGVSCFPGPVQTNL A LGASVFFPGPVQTNL G IGVSLCPGAVASNI G IGVSLCPGAVASNI G IGVSLCPGAVASNI G IGVSLCPGAVATNA G IGVSLCPGAVATNA G IGVSLCPGAVKTAL M IGVSLCPGAVKTAL G IGVSLLPGAVKTAL G IGVSLLPGAVKTAL G VKVRCLFPTFVDTPM G IRVRSLMPSFIDTPL G VKVFAIDPGFVFTQL G VKVSIPGGIDTPM GLPIHVSAIVPGMIRTNI G IYVQAVLPAATRTEI G VYVQAVLPAATRTEI G VYVQAVLPAATRTEI 		GG DUARTDA DPNIAAW DQNVAAA EEADPTLAA SRPVPSAER SGYVENEES SGYVENEES TGYYGRDEA EMKPVDKTA AMKPVDTEA SGFAASEQA SGFAASEQA SGFAASEQA SGFAASEQA SGFAASEQA SGFAASEQA SGFAASEQA SGFAASEQA SGFAASEQA 		A A Q S F K S L T F K S L T F H G M D F H G F D F H G F D F F G M E F F G M E F N W M E F N W M E F N W M E F N W M E F V M M E F S G M D F S G A T L T S - V A G L E T T P - V A G L E F T P	- GATA A CALL A A CALL A A CALL A A A A A A A	QPA HTN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YIH 248 - A - NQL YII 249 - D - NAL YII 249 - D - NAL YII 253 - A - NRL HIF 255 - A - DQL YVI 253 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NKL YVI 253 - N - NKL YVI 255 - A - DQL YVI 255 - A - DQL YVI 255 - A - NKL YVI 255 - N - DEL - YVI 255 - R - RDL FIM 256 - R - GDL FIM 256 - R - RDL FIM 254 - R - GDL FIM 254 - R - RDL FIM 254 - R - RDL HIL 243 - G - RKF HIL 243 - G - DRV HYL 234 - G - BRV HYL 234 - G - RY 242 - D - AAS FVT 246 QPDQSEQ 1 IA 265 RRE - LVT 225 RRE LVT 225 RRE LVT 225 RRE LVT 225 RRE LVT 225
 141 AGNY - PYPG - S - NVYGG TKAFVGQ FSLSLRCDLRG F- (141 AARI - VTPA - S - SVYSATKHAVRVI TDGLRQEHN	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGNIKSNI N IGVSLL CPGGVNTNI E IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSLL LPGPVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI S IGVSVL CPGFVRSNI G IGVSVC CPGAVQSNI G VICSAFCPGAVQSNI G VICSAFCPGQVATNI G VICSAFCPGQVQSNI G IGVSL CPGFVRSNI D IGVSAFCPGQVQSNI G IGVSL CPGPVQTNL A LGASVFFPGPVQTQL G IGVSL CPALTRTNA G IGVSL CPALTRTNA G IGVSL CPGAVKTAL N IGVSVL CPGMVKTRA E VAVHVVCPSFFQTNL G IRVRSLMPSFIDTPL G VKVRCL FPTFVDTPM G IRVRSLMPSFIDTPL G VKIFAI DPGFVFTQL G VKIFAI DPGFVFTQL G VKIFAI DPGFVFTQL G VKVRVLPAATRTEI G IKVNSVHPGGI DTPM GLPI HVSAI VPGMIRTNI G IVVQAVLPAATRTEI G WRFQAL VPGL TRTE 		GG DUAKTDA DPNIAAW EEADPTLAA SRPVPSAER SGYVENEES SGYVENEES TGYYGRDEA EMKPVDKTA AMKPVDTEA SGFAASEQA SGFAASEQA SGFKASEKK SGLAETEQQ SGFKASEKK DEAPKGPPP TGYAEADK PQPEVGP - PQPEVGP - PQPEVGP - PQPEVGP - PQPEVGP SGFKPADAT - SGFAPVDEA SGFKPADAT - SGFAPVDEA SGFKPADAT SGFFDVAKG SGFKPADAT SGFFDVAKG SGFKPADAT SGFFDVAKG SGFKPADAT SGFFDVAKG 		A A Q S F K S L T F H G M D F H G M D F H G F D F F G M E F F G M E F F G M E F NWM E F NWM E F NWM E F NWM E F N G M D F C M C F S G M D F S M D	- GAIAQAIRYALE - FAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - VELAEHVKAGIV - EKLAEAIKKGVE - VDLGRVVLDAVR - DVIGARVIEAMK - DIIGARILDGVR - DVGGRVLDAIL - EDVGNLVADAIL - EDVGNLVADAIL - EUVGRVLEGIL - EEVGRVLEGIL - EEVGRVLEGIR - EEVGQRVLRGIR - FEVGQKTLAGMI - EEVGQRVLRGIR - FEVGQKTLAGMI - EEVGQKVLRGIR - FEVGQKTLAGMI - EEVGQKVLRGIR - FEVGQKTLAGMI - EEVGQRVLRGIR - FEVGQKTLAGMI - EEVGQRVLRGIR - FEVGQKTLAGMI - EEVGQRVLRGIR - FEVGQKTLAGMI - EEVADHAWKAVH - SEVAEAAWAAVH - SEVAEAAWAAVH - ARCAQRVLDLAS - ARLRFVVALAA ADAVDQMLSAIAA - AEMGGGVVYLCS - GELVDAALVGFD - EVLVEVSLASLE	QPA HIN 23 QPE RVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQF YIH 248 - A - NQL YII 249 - N - DRF WVL 250 - A - NRF WVL 250 - A - NRL HIF 258 - A - DQL YVI 253 - A - NKL YVS 250 - R - RDL FIM 252 - R - RDF LIL 243 - G - RRF HIL 243 - G - RRF HIL 243 - G - DRV HVL 234 - G - CRV 244 - G - CRY 244 - G - CRY 244 - G - RY 244 - G - RRE LY Y 225 RRE LY Y 225 LGE RV C 226
 141 AGNY - PYPG - S - NVYGGTKAF VGGFSLSLRCDLRGT - C 141 AARI - VTPA - S - SVYSATKHAVRVIT DGLRQEHN 1 141 AAHF - VMPT - A - AVYCATKHAVWA I TDGLRQEHD 1 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE C 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - C 146 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH C 146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY C 146 SAFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTKFAVRGLSESLHYSLLKY 1 148 ASFI - AGGA - P - GIYNTKFAVRGMSYSLRHSMYKY C 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR - C 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR - C 140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK C 144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR C 145 GGFS - AV - G - TA - GLYCTAKFA I SGMMEALATELEGT 1 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH C 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH C 144 AGV - PLPG - F - AAYSTSKYAVRGYAESLRYNLAPH C 144 AGV - PLPG - M - GAYSAGKYAVRGFTQALRLDLAPH C 144 AGYU - PLPG - M - SAYSTKYAVRGLALSESLVELRQV 1 145 AAYL - SGPG - L - AVYSATKFAVRGLTESLRYNLAPH C 144 AGY - PLPG - M - SAYSTSKYAVRGYAESLRMQLAPL C 144 AGY - PLPG - M - SAYSTKYAIRGVRAITESLDGEWAED C 144 AGY - PLPG - M - SAYSTKYAIRGVRAITESLDGEWAED C 145 AARK - VAPY - L - SAYCTGKIAQNRIVAEAAAELAGT - C 146 AAYL - SGPG - L - AVYSATKYAIRGVRAITESLDGEWAED C 147 AGKY - PLPG - M - SAYAYAKASLIRLTEHLDFEQKAA - C 148 ASR - VAPF - A - SAYAYAKASLIRLTEHLDFEQKAA - C 140 AALY - GMPS - Q - SIYGATKAFVLFLSQGLSQELARAELAGT - C 141 AGVA - PEFG - M - SIYGATKAFVLFLSQGLSQLSPK - C 142 VGFA - PEFG - M - SIYGATKAFVLFLSQGLNELESS - C 144 AGYA - PEFG - M - SIYGATKAFVLFLSQGLNELESS - C 144 AGVA - PEFG W SAYAYAKASLIRTELAGUNGLARELARE - C <!--</td--><td> N. VINIERSE VINIERSE <</td><td></td><td></td><td>- TYAG - K - Q GL - T - LQ - E WR - R RD - A - QMS - NVL - E </td><td>A A Q S F K S L T F K S L T F H G M D F H G M D F H G F D F F G M E F F G M E F S M M D F N W M E F N W M E F N W M E F N W M E F S G M D F U F M S F S G M D F S G M D F G G M D F G G M D F G G M D F S G A T L T S - V A G L E F T P - V S G A T L T S - V A G L E F T P - V S E T A - A G L E S A Q F R M G R F - V M E V V M E V H V M S F - C L S F</td><td>- GATA A CALLA A A CALLA</td><td> QPA HIN 23 QPE NVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - A - NRL HIF 255 - A - NRL YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NTL - YVI 253 - N - NTL - YVI 253 - N - NTL - YVI 253 - N - NLL - YVI 253 - R - RDL - FIM 256 - E - NRG - LIL 256 - R - RDL - FIM 256 R - RDL FIM 256 </td>	 N. VINIERSE VINIERSE <			- TYAG - K - Q GL - T - LQ - E WR - R LQ - E WR - R LQ - E WR - R LQ - E WR - R RD - A - QMS - NVL - E 	A A Q S F K S L T F K S L T F H G M D F H G M D F H G F D F F G M E F F G M E F S M M D F N W M E F N W M E F N W M E F N W M E F S G M D F U F M S F S G M D F S G M D F G G M D F G G M D F G G M D F S G A T L T S - V A G L E F T P - V S G A T L T S - V A G L E F T P - V S E T A - A G L E S A Q F R M G R F - V M E V V M E V H V M S F - C L S F	- GATA A CALLA A A CALLA	QPA HIN 23 QPE NVD 228 - A - DRL HIF 250 - A - NQF YIH 248 - A - NQL YII 248 - A - NQL YII 248 - D - NAL YII 248 - N - DRF WVL 250 - A - NRL HIF 255 - A - NRL HIF 255 - A - NRL YVI 253 - N - NTT - YVI 253 - N - NTT - YVI 253 - N - NTL - YVI 253 - N - NTL - YVI 253 - N - NTL - YVI 253 - N - NLL - YVI 253 - R - RDL - FIM 256 - E - NRG - LIL 256 - R - RDL - FIM 256 R - RDL FIM 256
 141 AGNY - PYPG - S - NVYGGTKAF VGGTSLSLRCDLRGT - C 141 AARI - VTPA - S - SVYSATKHAVRVIT DGLRQEHN 1 141 AAHF - VMPT - A - AVYCATKHAVWA I TDGLRQEHD 1 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE	N - IRATL ISPGPTTSEL D - IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGPVATSI G - IGVSVL CPGVKSVI C - IGVSVL CPGLVKSYI G - IGVSVL CPGLVKSYI G - IGVSVL CPGFVRSNI D - IGVSILL PGPVKSNI N - IGVSILL PGPVKSNI N - IGVSILL PGPVKSNI G - IGVSL CPGFVRSNI G - IGVSCFYPGPVQTNL A - LGASVFFPGPVQTQL G - IGVSL CCPALTRTNA G - IGVSLL CPGAVKTAL G - IGVSL VCPALVATDA G - IGVSCL FPGATRTGM G - IGVSCL FPGAVTTAL G - VKVRCL FPTFVDTPM G - IRVRDL MPGFIETPL G - VKVRCL FPTFVDTPM G - IRVRSL MPSFIDTPL G - VKVFAI DPGFVFTSL G - VKIFAI DPGFVFTSL G - VKIFAI DPGFVFTSL G - VKIFAI DPGFVFTSL G - VKVRSL PAATRTEI G - IKVNVL PAATRTEI G - VYVQAVL PAATRTEI G - VKVRCL CPGPVRSAR C - IKVSVL CPGPVRSAR			- TYAG - K - Q GL - T - LQ - E WR - R LR - E - EVR - AGL - A RD - A - QMS - NVL - E IA SL H - SI H - Q IA SL H - SI H - Q VF - A - GL K - RVI - E VE RLA - GVH - E VE RLA - GVH - E VE RLA - GVH - E LS - M - RE TG - S - LA - K - RV VA - D 	A A Q S F K S L T F K S L T F H G M D F H G F D F H G F D F F G M E F F W M D F N W M E F S G M D F C M C F S G M D F S G A T L T S - V A G L E T P - V S E T A - A G L S E T A	- GAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - UELAEHVKAGIV - EKLAEAIKKGVE - VDLGRVVLDAVR - DVIGARVIEAMK - DIIGARILDGVR - DVGEMVADAIL - EDVGNLVADAIL - EDVGNLVADAIL - TEVGDMIVDAIV - LDVGHMTLHAIR - EQVGERVLEGIL - EEVGKRVLRGIR - FEVGQKTLAGMI - YEVGTKILAGMT - LEAGEKILRGMS - LDTGRAVVDAIK - FDLGNEVVDAIE - FDLGNEVVDAIE - FDLGNEVVDAIE - ADIADYIHQQVA - EEVADHAWKAVH - SEVAEAAWAAVH - SEVAAWAAVH - SEVAEAAWAAVH - SEVAEAAWAAVH - SEVAEAAWAAVH - SEVAEAAWAAVH - SEVAEAAWAAVH - SEVAEAAWAAVH - SEVAEAWAAVH - SEV	QPA HTN 23 QPE NVD 228 - A - QPE GVD 228 - A - NQF YIH 248 - A - NQL YII 248 - A - NQL YII 248 - D - NAL YII 248 - D - NAL YII 248 - A - NRL HIF 258 - E - NRA - NIF 251 - A - DQL YVI 253 - N - NTT YVI 253 - N - NTT YVI 253 - N - NKL YVI 253 - R - RDL FIM 255 - R - RDL FIM 255 - R - RDL FIM 255 - R - RDL FIM 254 - E - NRF HIL 254 - E - NRF HIL 243 - E - NRF HIL 243 - N - NRP - YIF 241 - A - GEF - LIL 234 - G - RY 244 - G - RY
 141 AGNY - PYPG - S - NVYGG TKAF VGG FSLSLRODLRG I - C 141 AARI - VTPA - S - SVYSATKHAVRV I TDGLRQEHN I 141 AAHF - VMPT - A - AVYCATKHAVWA I TDGLRQEHD I 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - C 144 GGLM - GSAL - A - APYSAAKAAVINLMESYRQGLDKH - C 146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY C 146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY C 146 ASFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY I 152 AAFL - AAGS - P - GIYNTTKFAVRGLSESLHYSLLKY I 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY - C 149 AATV - VMPG - HL - AIYAAKAAVUNLTENMRADLAGR - C 144 AGVT - PMPS - FM - AIYATAKAAVISLTEHLRLELEAK - C 145 GGFS - AV - G - T - TIYSAGKAAVTAMMECMRPELEGR - C 146 AGLT - PMPS - FM - GLYCTAKFA I SGMMEALATELEGT I 145 GGFS - AV - G - T - GIYTASKFAVRGLTESLRYNLAPH C 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH C 146 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH C 147 AGVL - QY - S - QA GMYVATKFAVRGLTESLRYNLAPH C 148 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH C 144 AGVV - PLPG - F - AAYSTSKYAVRGYAESLRULAPH C 144 AGVU - PLPG - F - AAYSTSKYAVRGYAESLRULAPH C 144 AGWI - PVPP - FA - GVYAASKFAVRGLAESLVELRQU C 144 AGMI - PVPP - FA - GYYAASKFAVRGLAESLVELRQU C 144 AGMI - PVPP - FA - GYYAASKFAVRGLAESLVELRQU C 144 AGMI - PVPP - FA - GYYAASKFAVRGLAESLVELRQU C 144 AGMT - PVPP - FA - SAYCTGKIAQNRVVAEAAAELAGT - C 145 AARK - VAPY - L - SAYCTGKIAQNRVVAEAAAELAGT - C 146 AART - GAFF - N - AAYCTSKAAVKMLSKCLGAEFAAL - C 147 GAFF - PEFG - M - SIYGATKAFVLFLSQGLNELSPS - C 144 AGVA - PEFG - M - SIYGATKAFVLFLSQGLNELSPS - C 145 AARK - VAPF - L - SAYCTGKIAQNRVVAEAAAELAGT - C 146 AGTF - VAPF - A - SAYAVAKASLIRT TEHLDFEQKAA - C 147 GAFF - PEFG - M - SIYGATKAFVLFLSQGLNELSPS - C 148	 N IRATL ISPGPTTSEL D IRATV ISPGVATEL GAP IGVSVL YPFFTQTRI G IGVSVL CPGPVATSI G IGVSVL CPGPVATSI G IGVSVL CPGNIKSNI N IGVSLL CPGGVNTNI E IGVSVL CPGLVKSYI G IGVSVL CPGFVRSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI D IGVSILL PGPVKSNI G IGVSVCPGFVRSNI G IGVSVCPGFVRSNI G IGVSVCPGFVRSNI G IGVSAFCPGAVQSNI G VICSAFCPGAVQSNI G VICSAFCPGAVQSNI G IGVSLCPGFVRSNI P IGVSCFYPGPVQTNL A LGASVFFPGPVQTQL G IGVSLMCPGLTRTNA G IGVSLVCPALVATDA G IGVSLVCPALVATDA G IGVSLCPGAVKTAL N IGVSVLCPGMVKTRA EVXVHVVCPSFFQTNL G IRVRDLMPGFIETPL G IKVRDLPGFVFTQL G VKIFAIDPGFVFTQL G VKIFAIDPGFVFTSL G VKVFAIDPGFVFTSL G VKVAQAVLPAATRTEI G MRFQALVPGLTRTEL G IRVRLAPGSTRTE 			- TYAG - K - Q GL - T - LQ - E WR - R LQ - E WR - R LQ - E WR - R LR - E - E VR - AGL - A RD - A - QMS - NVL - E VK RL - SL H - SI H - Q VK RL - SL H - SI H - Q VK RL - GLK - RVI - E VK RL - GLK - RVI - E VK RL - GLK - RVI - E VK RL - GLK - RVI - E LA - R - RI VG - D LA - K - RV VA - D 	A A Q S F K S L T F H G M D F H G M D F H G F D F F G M E F F G M E F F G M E F NWME F NWME F NWME F NWME F S G M D F C M C F S G M D F S M D	- GAIAQAIRYALE - DAIARAIRFALE - AEVAEAVMAGIR - DEVGRRVLAAIR - DEVGRRVLAAIR - VELAEHVKAGIV - EKLAEAIKKGVE - VDLGRVVLDAVR - DVIGARVIEAMK - DIIGARILDGVR - DAVGEMVADAIL - EDVGNLVADAIL - EDVGNLVADAIL - EUGGRVLEGIL - EEVGRVLEGIR - EEVGQRVLEGIR - EEVGQRVLRGIR - FEVGQKTLAGMI - YEVGTKILAGMI - YEVGTKILAGMI - FDLGRAVVDAIR - FDLGREVVDAIE - ADIADYIHQQVA - EEVADHAWKAVH - SEVAEAAWAAVH - EEVADNAWDAVH - ARCAQRVLDLAS - ARCAQRCLDLVS - ARLRFVVALAA ADAVDQMLSAIAA - AEMGGGVVYLCS - DIVAALVGFD - EVLVEVSLASLE - EEVALYTVRALD - EUANALFMAS	QPA HTN 23 QPE NVD 226 - A - DRL HTF 250 - A - NQF Y H 246 - A - NQF Y H 246 - A - NQF Y H 246 - A - NQF WVL 250 - A - NRF WVL 250 - A - NRL HTF 255 - A - DQL YVI 253 - A - NRL Y V 253 - A - NRL YVI 253 - A - DQL YVI 253 - A - NRL YVI 253 - R - RDL YIL 247 - D - NAL YIL 255 - R - RDL - F IM 255 - R - RDL - F IM 255 - R - RDL - F IM 255 - E - NRG - L IL 254 - D - DRL - HVL 234 - D - DRL - HVL 234 - G - BRV Y IF 241 - A - GEF - L IL 232 - D - DRL - HVL 234 - G - BRV L VT 225 RRE - L VT 225 LGE - RWC 226 KNR - AL I 222 DEC - FMT 236 DEC - FMT 236 CEC - FMT 236 CEC - FMT 236 CEC - FMT 236 CEC - FMT 236
 141 AGNY - PYPG - S - NVYGG TKAF VGG FSLSLRCDLRGT - C 141 AARI - VTPA - S - SVYSATKHAVRV I TDGLRQEHN 1 141 AAHF - VMPT - A - AVYCATKHAVWA I TDGLRQEHD 1 143 AAIM - HPPF - L - QPYNVAKTAVVALSSGLRQEFQEE - C 144 SGLV - GGTA - T - MAYCTAKAGVVGLSESLRTELKGS - C 146 GGFM - GSAL - A - APYSAAKAAVINLMESYRQGLEKY C 146 GGFM - GSAL - A - GPYSAAKAASINLMEGYRQGLEKY C 146 AGFV - ALPT - T - GIYCTTKYAVRGLAESLRVEMPKY 1 152 AAFL - AAGS - P - GIYNTAKFAVRGMSYSLRHSMYKY - C 148 ASFI - AGGA - P - GIYNTAKFAVRGMSYSLRHSMYKY - C 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR - C 149 AATV - VMPG - HL - AIYAAGKAAVLNLTENMRADLAGR - C 140 GAVM - SARL - TR - GIYAPTKAAVISLTEHLRLELEAK - C 144 SALV - PVAG - T - TIYSAGKAAVTAMMECMRPELEGR - C 145 GGFS - AV - G - TA - GLYCTAKFAISGMMEALATELEGT 146 AGLL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 147 AGVL - QY - S - QA - GNYTASKFAVRGLTESLRYNLAPH 148 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 144 AGIV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL - C 144 AGIV - PLPG - M - GAYSAGKYAVRGLAESLRWLAPH 145 AAYL - SGPQ - A - GIYTASKFAVRGLTESLRYNLAPH 144 AGIV - PLPG - F - AAYSTSKYAVRGYAESLRMQLAPL - C 144 AGNV - PLPG - M - SNYNVAKAGVLALSESLLVELRQV - 1 145 AAYL - SGPG - A - SVYSATKFAVRGLSDSLRLALAPY 146 AAYL - SGPG - A - SVYSATKAGVRSLTETLDGEWQAD 147 AGK - VAPN - L - SAYCTGKIAQNRIVAEAAAELAGT - C 148 ASRM - VAPN - L - SAYCTGKIAQNRIVAEAAAELAGT - C 149 AGRY - GPFG - M - SIYGATKAGVRSLTETLDGEWQAD 144 AGTF - VAPF - A - SAYAVKASL RLTEHLDFEQKAA - C 145 AARK - VAPY - L - SAYCTGKIAQNRIVAEAAAELAGT - C 146 AGTF - VAPF - A - SYYAAKSULRFLYRLAPH - 1 147 AGVA - PEFG - M - SIYGATKAFVLFLSQGLNELSPS - C 142 VGFA - PEFG - M - SIYGATKAFVLFLSQGLNELSPS - C 142 VGFA - PEFG - M - SIYGATKAFVLFLSQGLNEL	G - I RATL I SPGPTTSEL D - I RATV I SPGVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGPVATSI G - I GVSVL CPGVATSI G - I GVSVL CPGVKSVI G - I GVSVL CPGL VKSYI G - I GVSVL CPGL VKSYI G - I GVSVL CPGFVRSNI D - I GVSVL CPGFVRSNI D - I GVSILL PGPVKSNI N - I GVSVL CPGFVRSNI G - I GVSILL PGPVKSNI G - I GVSL CPGAVQSNI G - I GVSL CPGAVQSNI G - I GVSL CPGAVTNA A - LGASVF FPGPVQTQL G - I GVSL CPGAVTNA G - I GVSL CPGAVTNA G - I GVSL CPGAVKTAL M - I GVSL CPGAVKTAL G - VKVRCL FPTFVDTPM G - I RVRSLMPGFI ETPL G - VKVFAL DPGFVFTQL G - VKVFAL DPGFVFTSL G - VKVFAL DPGFVFTSL G - VKVFAL VPGMIRTNI G - I KVNVL PAATRTEI G - NKFQAL VPGLTRTEL G - I RANIL APGLT I TPM G - I RANIL APGLT I TPM G - I RANIL APGLT I TPM G - VRAKL VEPGYAPTTR		GG DU AK T DA D N I AAW E E AD PT L AA S R P V PS A E R - S G Y V E N E E S - S G Y V E N E E S - T G Y Y G R DE A - 	- TYAG - K - Q GL - T - LQ - E WR - R LQ - E WR - R LQ - E WR - R LQ - E WR - R 	A A Q S F K S L T F K S L T F H G M D F H G F D F F G M E F F G M E F F G M E F N W M E F S G M D F C M G L D F S G A T L T S - V A G L E F T P - V A G	- GATA A CALLA A A A	QPA HTN 23 QPE NVD 228 - A - DRL HTF 250 - A - NQF Y H 248 - A - NQL Y H 248 - A - NQL Y H 248 - D - NAL Y H 248 - D - NAL Y H 253 - A - NRL HTF 255 - A - NRL HTF 255 - A - NRL YVI 253 - N - NTT - YVI 253 - N - NTL - YVI 255 - A - DQL YVI 255 - A - DQL YVI 255 - A - NKL YVI 255 - R - RDL FTM 255 - R - RDL FTM 255 - R - RDL FTM 256 - R - RTF L 242 - D - DRL HTL 234 - G - RY 242 - G - RY 242 - D - RRE L VT 225 RRE - L VT 225 RRE L VT 225

gi]84570596|bdh2_Rpickettii/1-256 gi|334345171|Sphch/1-263 SLG_32730/1-261 gi]87199767\/1-261 SG61 1243/1-257 gi]84570594|bdh1_Rpickettii/1-260 gi]334342462|Sphch/1-265 gi]334343092|Sphch/1-255 gi]334343456|Sphch/1-245 gi|334343408|Sphch/1-258 gi|146275993|Naro/1-256 gi|146275997|Naro/1-246 gi]87199890[/1-279 SG61_474/1-283 SLG_24920/1-278 PP_1951/1-275 PP_2002/1-257 SLG_15310/1-259 gi]146275988|Naro/1-261 SG61_609/1-245 gi|146275674|Naro/1-255 gi|334343001|Sphch/1-259 gi|334343319|Sphch/1-259 gi]87199092|/1-261 SG61_354/1-260 PP_2214/1-255 SG61_3175/1-254 gi]146276032|Naro/1-246 gi|334342802|Sphch/1-249 PP_1708/1-252 SG61_2863/1-244 SLG_35070/1-243 gi]146275941|Naro/1-266 gi]334343077|Sphch/1-254 gi|334342781|Sphch/1-260 SLG_31530/1-250 SG61_2583/1-255 PP_2175/1-234 PP_0488/1-253 gi]2506152|YDFG_ECOLI/1-248 gi]334345036|Sphch/1-249 PP_4862/1-254 gi|334346119|Sphch/1-241 SLG_33310/1-241 gi]334342779|Sphch/1-273 gi]334342815|Sphch/1-290 gi|87198230|/1-306 SLG_08640/1-305 SLG_35880/1-297 gi\87198815\/1-310 SG61_724/1-305 gi]87199892[/1-280 SG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277 gi]87198816[/1-310 SG61_2705/1-303 SG61_1498/1-309 SLG_35900/1-311 gi|87198727|/1-305 SG61_3329/1-309 SLG_12640/1-304 SG61_2549/1-315 SLG_28340/1-294 SG61_2706/1-296 PP_1745/1-269 gi]334342965|Sphch/1-259 gi|87199139|/1-266 SG61_504/1-269 SG61_782/1-273 SLG_38070/1-265 SLG_27950/1-266 gi]87200928[/1-272 gi|146275769|Naro/1-259 gi|146275845|Naro/1-289 4BMV:A|PDBID|n-pentyl/1-262 PP_2989/1-264 SLG_18780/1-267 PP_0429/1-260 gi|334343146|Sphch/1-268 gi]334343373|Sphch/1-250

SG61_417/1-252

gi 146275658 Naro/1-269	242 GQVLVCDGGGASHVPGLAGFRSFFAGEQ
gi]334343486 Sphch/1-273	243 GHCL PVDGGTMAHL P T SPAAHG W L RRNMG I D
gi]146275875 Naro/1-252	240 GHAMVVDGGATAF
PP_1946/1-262	240 GHSMSVDGGVAVTAVGTRMDDLF
PP_1817/1-253	241 GHCLTVDGGATAI
gi]87200975 /1-250	238 GATFTIDGGQTAH
SG61_1215/1-250	238 GATEVIDGGQTAH
gi]146275951 Naro/1-252	241 GATLAADGGYLA
SG61_2016/1-248	236 GAYYPVDGAYLAQ
gi 31615388 Levoaione/1-267	
gij87200480µ1-200	
SIG 20040/1-258	243 GAAWPVDGGALATTK H
al146275686INaro/1-245	234 GAFFRVDGGASI
ail334342862 Sphch/1-257	245 GAELKL DGG I SAM
gil871988971/1-259	247 GAELKLDGGISAM
gi]146275698 Naro/1-254	242 GTELVVDGGMTAL
gi]334343337 Sphch/1-258	246 GTEV I VDGGF CAA
gi]146275892 Naro/1-259	235 GAEIVVDGGMTVGTYYMGFPGSPGM
gi]334342592 Sphch/1-246	227 GTDILIDGAELAGHGPLAAL
gi 334342962 Sphch/1-244	228 GAEFLVDGGVVQRVIGQ
gi 334342992 Sphch/1-245	234 GTEIIVDGGYSA
gi 334342994 Sphch/1-245	234 GIDLPVDGGTMA
gi]334342590 Sphch/1-248	236 ASEHL VDAGMLAH
gi 87198536 /1-248	236 GSEHLVDAGMLAH
gi 1708836 2,5-DDOL_Sjap/1-250	
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gi 33112056 R-specificADH/1-252	
gi 1402/3//000000000000000000000000000000000	
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gil872008791/1-249	
SG61 3344/1-248	
SLG 12690/1-249	234 AQGWAVDGGVLETLEV
gi]146275758 Naro/1-253	241 GTN I V I DNG ETMA
gi]729773326 steA_Ctestosteroni/1-243	231 GQNVAVNGGSAFL
gi]146275834 Naro/1-267	255 G S T V N V NGG AWF S
PP_1953/1-269	258 GQTLSPNGGMHM
gi 39647578 badH_Rpalustris/1-255	242 GQVLSVSGGLTMNG
gi]334342959 Sphch/1-250	237 GTSLVVDGGTMAGA
gi 334342606 Sphch/1-251	239 GQ I L VVDGGWL AR
gi]146275741 Naro/1-255	243 GHVLAVDGGWLAR
gi 1/30032 kduD_EcoliK12/1-253	241 GYIIAVDGGWLAR
gij334343307 Sprich/1-251	
rr_2/94/1-200 all 1633047513-ketopov/-0CP/1-240	
ail3343426401Sphch/1-240	228 GEVENVNGAMM
SI G 38730/1-240	228 G STMS I NGGQHMY
ail872012241/1-240	228 GSTMSL NGGQHMY
SG61 907/1-240	228 GSTMSLNGGQHMY
gi]518742570 acetyl-CoA/1-246	234 GADFSLNGGLHMG
gi]334343976 Sphch/1-246	234 GQTLHVNGGMAMI
gi 87199449 /1-254	241 GQTLHVNGGMAMIS
SG61_1203/1-250	237 GQTLHVNGGMAMMS
gi]388477173 fabG_Ecoli/1-244	232 GETLHVNGGMYMV
gi]146318879 gluconate/1-271	252 GHILYVDGGILAYIGKQPEA
PP_2783/1-245	233 GEVL SVNGGL KMP
gi 334343549 Sphch/1-249	237 GATTPVDGAYLAG
gi 334343458 Spncn/1-257 #187100579 port2/1_252	
gijor 1995/ ojpanz/ 1-253 ni]87199495]/1_266	232 GATLEVIDGTLA300 PRUSEWE
PP .3926/1-255	246 GASTINDGGELS
ail334343112 Sphch/1-262	241 G HML PVDGGVAN I L S L PVVVET
PP 1852/1-249	238 GASLTVDGGFAA
SG61 1419/1-249	238 GAELAIDGGYSI
SLG_12130/1-244	235 GANLAVSGGR
gi]649014081 glucose-1-dehydrogenase_Bsub/1-261	241 GITLFADGGMTQYPSFQAGRG
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gi]87199577 /1-257	242 GQSLAVDGGLGHTLRR
SG61_3726/1-249	236 GAMLA I DGG I I AAG
SLG_20080/1-253	240 GAMLAIDGGIIAAG
gi 334342771 Sphch/1-253	242 GSTLVADGGFTA
gito12125550/n-pentyiphenyiADH_Raistonia/1-251	
910720009077-240 SC61 3101/1-240	200 GVDLGVDGGGTELG
SIG 07180/1-248	
all871990201/1-282	244 GTSL I VDGG I TVGPRHSWDPNMPGL FDAI
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gi]81821161 PED_AROAE/1-249	237 GQTLAVDGGMVRH
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SLG_18590/1-251	239 GQTLVVDGGDAKH
gi 167033792 bdh/1-256	244 GAAWNVDGGWLAQ
PP_3073/1-256	244 GAAWNVDGGWLAQ

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ail334345171 Sphch/1-263	251 GANMS DGGWTAQ
SLG 32730/1-261	249 GAN I SVDGGWT AG
ail871997671/1-261	249 GANYNMDGGWVAE
SG61 1243/1-257	245 GANYS I DGGWTAE
gi]84570594\bdh1 Rpickettii/1-260	248 GQSF I VSHGWYMQ
gi]334342462 Sphch/1-265	253 GAILPIEGGWLAR
gi]334343092 Sphch/1-255	242 GRG I EVSGGRRHAS
gi]334343456 Sphch/1-245	233 GEIIHVNGGLFMA
gi 334343408 Sphch/1-258	246 GTVIKIDDGQSPR
gi 146275993 Naro/1-256	234 GQAQVLDAGLLSTFAPVMLPVGP
gi 146275997 Naro/1-246	234 GALFSIDGGQLAG
gi 87199890 /1-279	264 GSHVVIDGGMMLGKY
SG61_474/1-283	264 GSHVMIDGGMQLGPIKPLND
SLG_24920/1-278	263 GAQML I DGGMALGKF H
PP_1951/1-275	259 GQQFVIDGGLSLSAARARA
PP_2002/1-257	241 GQEF VVDGGMTRKM
SLG_15310/1-259	246 GST I AL DGGY I AAL
gi 146275988 Naro/1-261	
SG61_609/1-245	
gi 140213014 [Nato/1-200	
ai 234343310 Sphch/1-250	
a1871990921/1-261	
SG61_354/1-260	
PP 2214/1-255	241 GEV I RL DGAL RMAAK
SG61 3175/1-254	234 GEVIRLDAGARPPARTKWAAG
	234 GATWDANGGLFMR
gi]334342802 Sphch/1-249	237 GACLDINGGMLMR
PP_1708/1-252	239 MT VMA S NMP F VG RG
SLG_05090/1-250	237 L T VM P T KM P F I G R G
SG61_2863/1-244	231 AM I VQNKL PFLGRG
SLG_35070/1-243	230 TTILPIAQPYLGRG
gi]146275941 Naro/1-266	242 GNTLFVDGGGHINGVPWVPDFGPED
gi 334343077 Sphch/1-254	240 SRTLHVDGGRAFYDR
gi 334342781 Sphch/1-260	247 SQMIPVNGGLAYTR
SLG_31530/1-250	238 GAALPIDCDLQHG
SG61_2583/1-255	243 GQTLFVDGGLCLT
PP_2175/1-234	
77_0400/1-200 a125061521VDEG_ECOL//1-248	229 INTIEIMFVAQSSAA - LINVINNL - FRA- 228 INTIEMPVTOSVAG - INVINDO
-122/2/2/50200-b-b// 2/0	
01.3.34.345(1.30).50000/1=249	778 NR FI MPV SUSFAG FUVARFA
gij334345030 Sprcn/1-249 PP 4862/1-254	228 L NR I ELMPV SQSFAG FQVAREA
g 334345030 5pncn/1-249 PP_4862/1-254 gi 334346119 Sphch/1-241	228 L NR TELMPVSQSFAGFQVAREA
g 334345030 Sprich/1-249 PP_4862/1-254 g 334346119 Sprich/1-241 SLG_33310/1-241	228 LNRTELMPVSQSFAGFQVAREA 232 INSLELMPVSQDWAGFSIDRSKG- 229 VSEMVVRPTASPF
g 334345030 Sphch/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273	228 L NR I ELMP VSQSFAG
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290	228 L NR TELMP VSQSFAGFQVAREA 232 INSLELMP VSQDWAG
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230//1-306	228 LNRTELMPVSQSFAG
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230/1-306 SLG_08640/1-305 SLG_08640/1-307	228 LNRTELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 239 VSEMVVRPTASPF
g 334345030 Sphch/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230 /1-306 SLG_08640/1-305 SLG_35880/1-297 a 87198845 1/1-310	228 LNRTELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF
g 334345036 Sphch/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230 /1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815 /1-310 SG61_724/1-305	228 LNRTELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF
g 334345036 Sphch/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230 /1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815 /1-310 SG61_724/1-305 a 87199882 /1-280	228 LNRTELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230 /1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815 /1-310 SG61_724/1-305 g 87199892 /1-280 SG61_2550/1-291	228 LNRTELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230 /1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815 /1-310 SG61_724/1-305 g 87199892 /1-280 SG61_2550/1-291 SLG_33660/1-289	228 LNRTELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 871988230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815/1-310 SG61_724/1-305 g 87199892/1-280 SG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277	228 LNR1ELMPVSQSFAG FQVAREA 232 INSLELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF 229 INEIVVRPTAAGM 229 INEIVVRPTAAGM 251 PHPQSIALVEEAANR 249 TDRVMLQALEDRHRE 1VDAVLPLEADPEGARARTE 250 PYPEAKDGLRQHFDA 1VDAVLPLEADPEGARARTE 250 PYPEVREGLEKHFQA 251 PYPEVREGLEKHFQA 2520 PYPEVREGLEKHFQA 251 PYPEFAEGQKARDQE 251 PYPEFAEGQKARDQE 252 VIDAMMSYADHPDYARRMK 253 PYPEVREGLEKHFQA 254 PYPEFAEGQKARDQE 255 SHPDHKEELKELFDE 1LADYRDYPQDPGFEQRVG 255 THPDHKEELKELFDE 256 SHPDHKEELKELFDE 257 THPDHKELKELFDE 258 CHPDHKEELKELFDE 259 THPDHKEELKELFDE 250 PYPEVRGA 251 THOMKEAAA 252 THPDHKEELKELFDE 253 THPDHKEELKELFDE 254 THGEFANRMRERAEA 255 THPOHKEELAAA 251 THGNWRETCEARFQA 251 THGNWRETCEARFQA 251 THGNWRETCEARFQA 251 THPQFIDSVKARHAA
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g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 871988230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815/1-310 SG61_724/1-305 g 87199892/1-280 SLG_33660/1-289 SLG_07240/1-277 g 87198816/1-310 SG61_2705/1-303	228 LNRTELMPVSQDWAG - FGIDRSK 232 INSLELMPVSQDWAG - FSIDRSK 229 VSEMVVRPTASPF - 229 INEIVVRPTAAGM - 229 INEIVVRPTAAGM - 249 TDRVMLQALEDRHRE - 250 PYPEAKDGLRQHFDA - 10D VVLPLEADPEGARARTE - 250 PYPEAKDGLRQHFDA - 11DSVAPMESDPEGARQRVE - 250 PYPEVREGLEKHFQA - 251 PYPEFAEGQKARDQE - 252 PYPEVREGLEKHFQA - 253 PYPEVREGLEKHFQA - 254 PYPEFAEGQKARDQE - 255 PYPEVREGLEKELFDE - 256 SHPDHKEELREIFDE - 257 PYPEFAEQQKARDQE - 258 SHPDHKEELREIFDE - 259 THPDHKEELKELFDE - 250 THPDHKEELKELFDE - 251 PYPEFAEQQKARDQE - 252 THPDHKEELKELFDE - 254 THGEFANRMRERAEA - 254 THGEYANMRERAEA - 254 THGNYKDAMRARAQA - 254 THGNYKDAMRARAQA - 254 THGNYKDAMRARAQA - 255 THGNYKDAMR
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g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 SphCh/1-241 SLG_33310/1-241 g 334342779 SphCh/1-273 g 334342815 SphCh/1-290 g 87198230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 871998815 /1-310 SG61_724/1-305 g 87199892 /1-280 SG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277 g 871998816 /1-310 SG61_2705/1-303 SG61_1498/1-309 SLG_35900/1-311	222 LNR IELMPVSQ5PAG -FQVAREA 223 INSLELMPVSQDWAG -FSIDRSK 229 VSEMVVRPTASPF - 229 INE IVVRPTASGM - 229 INE IVVRPTASGM - 229 INE IVVRPTASPF - 229 INE IVVRPTASGM - 251 PHPQSIAL VEEAANR - 249 TDRVMLQALEDRHRE - 250 PYPEAKDGLRQHFDA - 10 DSVAPMESDPEGARQRVE - 250 PYPEVREGLEKHFQA - 11 DSVAPMESDPEGARQRVE - 250 PYPEVREGLEKHFQA - 10 DSVAPMESDPEGARQRVE - 250 PYPEVREGLEKHFQA - 11 DSVAPMESDPEGARQRVE - 250 PYPEVREGLEKHFQA - 251 PYPEFAEGQKARDQE - 252 THPDHKEELKELFDE - 253 THPDHKEELKELFDE - 254 THGGFANRMERAEA - 255 THPDHKEELKELFDE - 256 SHDMWRRAQA - 257 THPOHKEELKELFDE - 258 THPDHKEELKELFDE - 259 THPDHKEELKELFDE - 250 THPDHKEELKELFDE - 251 THPGFTORFAA
g 33434503(5)phCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 37198230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 87199845 J/1-310 SG61_724/1-305 g 87199892 J1-280 SG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277 g 87198816 J'1-310 SG61_2705/1-303 SG61_1498/1-309 SLG_35900/1-311 g 87198727 J-305	222 LNR I ELMP VSQS FAG FQ VAREA 223 LNS LELMP VSQDWAG FS I DRSK 229 VSEMVVRPTASPF 229 INE I VVRPTAAGM 229 INE I VVRPTAAGM 249 TDRVMLQALEDRHRE I VDAMPDEEM - SLFTAELSA 250 PYPEAKDGLRQHFDA I VDAVLPLEADPEGARARTE 250 PYPEAKDGLRQHFDA I VDAVLPLEADPEGARARTE 250 PYPEKRGLEKHFQA I DSVAPMESDPEGARQRVE 251 PYPEFAEGQKARDQE V I DAMMS YADHPD YARRMK 256 SHPOHKEEL RE I FDE I LADYRDYPOPGYDQRVA 256 SHPOHKEELKEL FDE I LADYRDYPOPGYDQRVA 252 THPDHKEELKELFDE I LADYRDYPOPGYDQRVA 254 THGEFANRMRERAEA LLAATPVCEM 254 THGEFANRMRERAEA LLAATPVCEM 251 THPQFI DSVKARHAA I EAAMAPDYL - PR 251 THPQFI SVKARHAA I EAAMAPDYL - PR 264 THAEFLTGVEERGLA TTAAVQTHLP 255 THPP FROG IT DRFEA MLRA IGHDEEREKTALDL I PGLVGS - P IYREAP 256 THPEFAPG I KARNNA LLRAIPVEAPNEARANLVAQFGTLL 257 THPEFTKG I EARNNA LLRAIPVEAPNEARANLVAQFGTLL 251 THOGY MLRAIGHDEEREKTALDL I PGLVGS - P IYREAP 253 THPEFAPG I KARNAA LLRAIPVEAPNEARANLVAQFGTLL 254 THPEFTYOT SLAARDA LLRAIPVEAPNEA
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g 334345030 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_3310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815/1-310 SG61_724/1-305 GG61_2705/1-303 SG61_2705/1-303 SG61_1498/1-309 SLG_35900/1-311 g 87198727/1-305 SG61_3329/1-309 SLG_12640/1-304 SG61_2649/1-315 SIG6_2840/1-304	222 INFLELMPVSQSFAG FQUAREA 222 INSELMPVSQDWAG FSIDRSK 229 VSEMVVRPTASPF 229 INEIVVRPTAAGM 251 PHPQSIALVEEAANR LVTDAKAS 249 TDRVMLQALEDRHRE IVDAVLPLEADPEGARQRTE ALN 250 PYPEAKDGLRQHFDA IVDAVLPLEADPEGARQRYE ALN 250 PYPEYREGLEKHFQA IIDSVAPMESDPEGARQRYE ALN 251 PHPEYREGLEKHFQA IIDSVAPMESDPEGARQRYE ALN 250 PYPETAEGQKARDQE VIDAMMSYADHPDYARRMK MEKNAAQKA 251 PYPEFAEGQKARDQE VIDAMMSYADHPDYARRMK AEGDKKGA 252 THPDHKELLFDE IIAEYQDYPKDPGYDQRVA FEKFRADSF AEARROSRA 252 THPDHKELKELFDE ILADYRDYPQDPGFQRVG FEKMRRDNF EETRRAADA VQ 254 THGEFANRMRERAEA LLAATPVCEM
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g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_3310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 87198230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815/1-310 SG61_724/1-305 GG61_2705/1-303 SG61_2705/1-303 SG61_1498/1-309 SLG_35900/1-311 g 87198727 /1-305 SG61_3329/1-309 SLG_12640/1-304 SG61_2705/1-303 SG61_2705/1-309 SLG_12640/1-304 SG61_2706/1-294 SG61_2706/1-294 SG61_2706/1-296 PP 1745/1-269	222 INK IELMPVSQSPAG FQUAREA 223 INS IELMPVSQDWAG FSI DRSK 229 INE IVVRPTASPF 220 INE IVVRPTASPF 250 PYPEVREGLEKHFQA I DSVAPMESDPEGARQRVE ALM AWGRDRTRVF 250 PYPEVREGLEKHFQA 1 DSVAPMESDPEGARQRVE ALM AWGRDRTRVF 250 PYPEVREGLEKHFQA 251 PHPETASUKARQA 252 PHPERAEQGKARDQE 253 HPDHKEELKEL FDE 254 HGMYKDAMRARAQA 254 HGMYKDAMRARAQA 254 HGMYKDAMRARAQA 254 HGMYKDAMRARAQA 254 HGM
g 334345036 SphCh/1-249 PP_4862/1-254 g 334346119 Sphch/1-241 SLG_33310/1-241 g 334342779 Sphch/1-273 g 334342815 Sphch/1-290 g 37198230/1-306 SLG_08640/1-305 SLG_35880/1-297 g 87198815/1-310 SG61_724/1-305 GG61_2550/1-291 SLG_33660/1-289 SLG_07240/1-277 g 87198816/1-310 SG61_2705/1-303 SG61_1498/1-309 SLG_15500/1-311 g 87198727/1-305 SG61_3329/1-309 SLG_12640/1-304 SG61_2705/1-305 SG61_2705/1-305 SG61_2705/1-296 PP_1745/1-269 g 334342965 Sphch/1-259	222 INK IELMPYSQDWAG FGVAKEA 223 INK IELMPYSQDWAG FSIDRK 229 INE IVVRPTASPF 229 INE IVVRPTASOF 250 PYPEXAGUE CANROL 250 PYPEVREGLEKHFQA 10 NDAMSYADHPDGARART 250 PYPEVREGLEKHFQA 251 PYPEVREGLEKHFQA 252 TYDPKKEIRER IFDE 253 HYDPKEELKELFDE 254 THODHKEELKELFDE 252 THPDHKEELKELFDE 254 THGMYKDAMRARAQA 255 THPORMKEAAA 254 THGMYKDAMRARAQA 254 THGMYKDAMRARAQA 254 THGMYKDAMRARAQA 254 THGMYKDAMRARAQA 254 THGMYKDAMRARAQA 255 THPERERGELA
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Fig. S4. SDS-PAGE Gel of purified GGE dehydrogenase enzymes. lane 1. Precision Plus Protein[™] Prestained Standards; lane 2. SG61-1L 474; lane 3. SG61-1L 724; lane 4. SG61-1L 1498; lane 5. SG61-1L 2705; lane 6. SG61-1L 2550; lane 7. SG61-1L 3175; lane 8. SG61-1L 3329; lane 9. SG61-1L 3344; lane 10. SG61-1L 3726; lane 11. SG61-1L 3730.

Table S1. Retention times and m/z values for metabolites observed during GGE degradation

Common and	Molecular	Authentic standard			SYK-6	SG61-1L		
Compound	weight	Rt (min)	m/z [molecular ion]	Rt (min)	m/z [molecular ion]	Rt (min)	m/z [molecular ion]	
GGE	320.34	5.10	303.12 [M-H₂O+H]⁺	5.12	303.12 [M-H ₂ O+H]+	5.10	303.13 [M-H ₂ O+H] ⁺	
MPHPV	318.32	-	-	6.78	319.10 [M+H]+	6.77	319.12 [M+H]+	
HPV	196.20	-	-	3.78	197.06 [M+H]+	3.79	197.03 [M+H] +	
Vanillin	152.15	5.52	153.05 [M+H]+	5.53	153.05 [M+H] +	5.52	153.05 [M+H] +	
Vanillic acid	168.15	4.16	169.05 [M+H]+	4.16	169.08 [M+H]+	4.16	169.04 [M+H]+	
Guaiacol	124.14	7.50	n/a	7.54	n/a	7.52	n/a	

Table S2. Protein names and corresponding accession numbers for genes encoding proteins included in the phylogenetic analysis.

Gene name	gene identification (GI)	Reference		
	number or accession ID			
ADH_Syanoikuyae	4BMV (pdb ID)	(1)		
Ga5DH_Ssuis	146318879	(2)		
phaB_Synechocystis	16330475	(3)		
bdh_Pputida	167033792	(4, 5)		
2,5-DDOL_Spaucimobilis	1708836	(6)		
kduD_Ecoli	1730032	(7)		
ydfG_Ecoli	2506152	(8)		
LVR_Caquaticum	31615388	(9)		
(R)-ADH_Lkefiri	33112056	(10)		
fabG_Ecoli	388477173	(11)		
badH_Rpalustris	39647578	(12)		
ADH_Ralstonia	512125550	(1)		
phaB_Burkholderia	518742570	(13)		
CPNA_Comamonas	62286565	(14)		
Gluc-DH_Bsubtilis	649014081	(15)		
steA_Ctestosteroni	729773326	(16)		
(S)-PED_Aaro	81821161	(17)		
bdh1_Rpickettii	84570594	(18)		
bdh2_Rpickettii	84570596	(18)		
SG61_1203	SZ64_06710			
SG61_1215	SZ64_06655			
SG61_1243	SZ64_06525			
SG61_1419	SZ64_05615			
SG61_1498	SZ64_05225	this work		
SG61_2016	SZ64_08220			
SG61_2549	SZ64_00035	this work		
SG61_2550	SZ64_00030	this work		
SG61_2583	SZ64_09815			
SG61_2705	SZ64_01645	this work		
SG61_2706	SZ64_01650	this work		
SG61_2863	SZ64_11380			
SG61_3175	SZ64_16025	this work		
SG61_3191	SZ64_15940	this work		
SG61_3329	SZ64_12360	this work		
SG61_3344	SZ64_12435	this work		
SG61_354	SZ64_16980			
SG61_3726	SZ64_14315	this work		
SG61_3730	SZ64_14335	this work		
SG61_417	SZ64_16655	this work		
SG61_474	SZ64_16365			
SG61_504	SZ64_17190			
SG61_609	SZ64_02580			
SG61_724	SZ64_15290	this work		
SG61_782	SZ64_15575			
SG61_907	SZ64_14565			

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