

gi#	COG/KOG#	name	species		motif-1		motif-2		motif-3
18409989	KOG4355		ARATH	206	CLGASTYK(6)---HLGSHYVDSLVEFRVTVSEG---VKEIWLSS---ED(14)LLNA---IVKELPSDQSTML---RIGMTPPF	hhhhhhhhhhhhhhhhhhhhhhhhhh	sssssss	hhhhhhhhhhhhhhhhhhhhhhhhhh	ss--sssss
7299338	KOG2492		DROME	250	CDNMITYI(11)PLASIVAEVKALAEQGVKEVTL(6)YDRRTAQE(6)AT(14)GTPFAAL-LRSVAQAVPDMRI---RFTSPHPKD				
2501533	COG0621	Y019_HAEIN		156	CNKYTFV(11)PVDDVLFELIAQLAEQGVREVNLLG---QNVNAYRG---PT-HDGGQICSPAE-LLRVLVASIDGID---RIRFTTSHP				
20094331	COG1032		METKA	196	CPFRCLFA(5)-GPKWRGKSPDRVVEIISYLVVELG---VERLEFVD---DV-FTAHKRRVRE-ICEKMR---GIDVWPDCG				
15896586	COG4277		CLOAB	63	CIYDQYV(5)-DTPRASFTPRELADLTMNFVRRNY---IEGLFVDS---GV-MKNPDYTCQK-FMEELRILRYEY---NFGYIHDG				
3913815	COG0635	HEMN_AQUAE		60	CEQRQYLG(10)-IEPPLYERVCREMDLVSQYLKDKR-KVILQHWGG---GTPNVLSPQEKW-FBEIKRRFEPGDNAEISIEDLPR				
14520767	COG2100		PYRAB	124	CNMRCIFAS(9)-RKLDFVVDIDYLLKWFDDWVAKK(4)EAHLDAQG---EPLLYPFIVE-LVQALREHPHVS---VISMQSNV				
11499591	COG0535	NirJ2_ARCFU		123	CNLRKHF--(5)-KPLQDELTTDEALEITDK-LDRLG-VTTIIAFSG---GE-PLVRRD---IFELTRYAAEAKGI---YVAIATNGT				
15833984	COG0641	AslB_ECOLI		108	CNLDNYF(9)-EKPVTHMDDTLEAYVRRHYI(4)EVAFTWQG---GEPTLLGLEFVYRAVALQAKYAGRKI---SNSFQT-NG				
549552	COG0820	YFGB_ECOLI		124	CEHGKFS(13)EIEIGQVWRAAKIVGAQKVTGQRP---ITNVMMG-MGE-PLNLNINNVV-AMBIILDDFGFG(4)IRVTLST-SG				
15606957	COG2516		AQUAE	54	CHATCAYG(15)RVEWPTVKTDEIERTKQVGH----AERLCISQ---IT-HPRAIRDTKY-ILEKVRHRELGDKIFISILLNA-TG				
1705463	KOG2900	BIOB_ARATH		93	CSBDQSYSP(8)-VKAQRILMSKDAVIDAAKK-AKEAG---STRFCMGA-AWRDTIGRKTNSQ-ILBYIKERIGMGM---EVCCTL--G				
15606163	COG1060	ThiH_AQUAE		66	CIAGKHF(6)-DEDAYVLDMDTILQVKELVEWGG---TTLMOG---GINPDLPLEFYED-MISQIKKHFPV---QIHCFSAPE				
19705171	COG1509	KamA_FUSNN		126	CSMYKFT(6)---SSDDAMPMDRIDKAIETVAKTPQ---VRDVLLSG---GDALLVSDKKLW-IIQKLRAPHVE---IIRIGSRTP				
18313168	COG1313	PflX_PYRAE		158	CNFRVYQ(6)-FSESGIEVTAALAAIQAKLREEG---ARNINWVG---GE---PTPNIPY-ILESRLILARRGV---NVPQLWNSN				
730103	COG2896	MOAA_BACSU		26	CNFRITYM(11)LKKEELLSFEELERLATLFTVTRFG---VEKIRLTG---GE---PLMRKDMPE-LIKKLARIPGR---DIAMTTNG				
22027536	KOG2876	MOCS1_HUMAN		79	CNLRQY--(8)-TPKANLLTTEILLARL-FVKEG---IDKIRLTG---GE---PLIRPDVVD-IVAQLORLEGLR---TIQVTT-NG				
14521276	COG2108		PYRAB	46	CPRNFYF(11)ANERPVRSKDIIEAKIQDARGA---GITG---GD-PLARLSRIVEYIRLLKEEFGKFF---HHLYT-TG				
22001767	COG0320	LIPA_YERPE		93	CTRRPFQDV---AHGRPVTPDANEPEKLAQTTQDMG---LRYVVITS---VDRDDLDRGGAQH-FADCSATRANKP---TKIETLVP				
17865692	COG0502	BIOB_SALTY		52	CPEDQKYSP(8)-LEAERLMEVQVLDLSARK-AKNAG---STRFCMGA-AW---RNPHERMEY-LEKIVQGVKAMGL---ETCMLT--G				
14520966	COG1180	PflA_PYRAB		81	CNMHKHQ(6)-ADENFPYLODAPTEAVTLAKHYE-CESIAITY---NE---PTIWFY-VLDTAKLAKKEGL--NNVIL-NG				
13476168	COG1533	SplB_RHILO		74	CEHGQYF(14)DFETKLFAPDARLLDKELSGEYQPTTIAIGT---NT(4)PIEKQYRI-MREILVELEARGH---PVGIVTKSA				
15605904	COG1856		AQUAE	69	CELMDDHASKILWHMIPATTPPELVKVGED-LKKKG---IEGVLSIG---GS-DKNGFVPLWD-FFDAMKYLKEEL---GFLLTCHVG				
15643710	COG5014	THEMA		710	CKFLCAYW(8)-KRAGDLSPEEVAERLLEISKKRK---CDLFRISG---AE-PILGRRSAEH-VRKVIELVNN---TFILET-NG				
15891589	COG0602	NrdG_AGRT5		43	CDYRQSWD(6)-SEYRDTWKPMQVVEIQLQEVLLGSLGGMPLTVSLSG---GN-----PAIQP-LGTLIAKQGEQY---RFALETQGS				

gi#	COG/KOG#	name	species		motif-4		motif-5		motif-6
18409989	KOG4355		ARATH	206	II(5)EIAAV(4)CVYTFELHVPVQSGSD---SVLTAMNREYTASEFRVTVDT---LT---ELVPG---MQIATDIIIC-GFPGETDEDFSQTV(5)-YKFPQVHISQFYPR(208)	hhhhh	sssssss	hh--hhhhhh	hhhhhh-hh---hhhhh
7299338	KOG2492		DROME	250	FI(5)EVIRD-HPNVCKQLHLPAQSGNT---QVLERMMRGYSREAYLELVQH---IR---QFLPN---VGLSSDFIC-GFCGETEEEFQDTVSL---IQQQVYNVAYLFAY(129)				
2501533	COG0621	Y019_HAEIN		156	II(7)DYIRD-TPELVKFLHLPVQAGSD---EVLTKMKRAHTALEYKSIIRK---LR---AVRPD---IQISSDFIV-GFPGETAEDFQTMNL---IAQVNFDMFSFVY(135)				
20094331	COG1032		METKA	196	A(7)ELART(4)GCRTVYVGAESASN---RTLTKRINKGIT---VQDVIACRKVA---KRHG---LIRLLSFIL-GFPWEDREDVFTI(5)-LEPDYQVFTVCTPY(86)				
15896586	COG4277		CLOAB	63	A(5)DTLID(4)LCDRM-SVNIELPSQ---KSLKLLAPNKS(6)PMGYIKN-KIS---ENTT(13)AGQSTQMIIGATPDTD(5)LTESLYSK-YLKRVRFFSAYMPV(181)				
3913815	COG0635	HEMN_AQUAE		60	YLTDQIKA(4)GFNRI-SLGVQDLDP---KVQAVNVRQP(6)KMEKLE---AGFES---INLLDIY-GLPYTKSEFKT(7)-PDRIATYGFYAIYPQ(208)				
14520767	COG2100		PYRAB	124	LLNDKLVVE(4)GLDRV-NLSHSLD---PEKAKMLMGIK(6)VLEMAEA-LV---NAGID---VLIAPVMF-GVNDDE(6)FARRIGV-KRPWALGFQNYIYP(110)				
11499591	COG0535	NirJ2_ARCFU		123	LITEEIAKR(4)GVYV-QISLDGMK---EETHAEFRGIR---GCFDKIVEG---IR---NAVKTG---LNVNMSVTIRRYNHEVPKVVLELCEK---LGVNWFMHYNIPT(177)				
15833984	COG0641	AslB_ECOLI		108	V-LLDDEWC(4)ENHFLVGLSLDGPAAEI-HNQYRVTKGGR-PTHKLVMA---LT---L-LQK---HHVDYNVLV-CVNRTSAQQPLQVYDFLCDAGVEF---IQFIPV(210)				
549552	COG0820	YFGB_ECOLI		124	V(4)DKLGD---MIDVALAISLHAPND---EIRDEIVPINKKYNIETFLAA---VR---RYLE(7)-RVTIYVMLDHVNDGT(5)LAELLK---DTPCKINLIPNMPF(70)				
15606957	COG2516		AQUAE	54	H-TYEDLED(4)GAETL-TVALDAAT---PELFEKLRGR(6)WETYVQV---LEWACINDG---GHVGAHLV-GLGETEE-MVRTIQRVRLDGGRTLHFSWPE(130)				
1705463	KOG2900	BIOB_ARATH		93	MIEKQQALE(4)GLTAY-NHNLDSR---EYYPNVITTR---YDRLET---LS---H-VR(3)-INVCSGGII-GLGEAE(5)LLHTLATLPSHPSPVINALLVA(107)				
15606163	COG1060	ThiH_AQUAE		66	II(13)VIRR(4)GLMSIPGGGAELISQ---EVRDKISPGKC(4)WEVVRT---AH---R-LG---MTTATMMF-GHVESI(5)HLERVRKIQDETGGF---TAFIPW(109)				
19705171	COG1509	KamA_FUSNN		126	V---VLPQ(4)ELCNM---LKKYH---PIWLNTRHPN(6)AKKACEM---LA---DAGVP---LGNQTVLLR-GINDSPVP-MKRLV---HDLVMMVRVYIY(132)				
18313168	COG1313	PflX_PYRAE		158	M-YLTPEGL(4)HVIDWLDPFKYGN---DAHALRYSVAP-RCWETVTRNFVSI---CKRE---DIIVRHLVLPGHVECTKPLRWL---AENCNHALVNIIMDQ(44)				
730103	COG2896	MOAA_BACSU		26	L-LPVYAKR(4)GLKRV-TISLDSLE---DERFKKINGRG(6)LEGIEAA-KQ---AGLG---KIVNMVQK-GVNEKD---ILPMARYFKEGHILRFIEFMDV(137)				
22027536	KOG2876	MOCS1_HUMAN		79	II(6)PQLQK---AGLSAI-NISLDTLVPKAFEFIVRRKGFH-KVMEGIHKA---IE---LGYNP---KVCNVVMR-GLNEDELDFAAALTEGL-PLDVRF---IEYMP(133)				
14521276	COG2108		PYRAB	46	II(4)EALEK(4)GLDEI-RFHDPDLQPNKSKFEREIEIN(6)WDVGGEV-PAV---PGFE(8)-LLDKLGAKFLNINELE(5)LRALL(13)IKGSLEMGLKVLWEW(122)				
22001767	COG0320	LIPA_YERPE		93	D(5)DRALD(4)TPPDVFNHLENVP---RVYRQVRPGAN-YDWSLKLE-RFK---EAHPD---IPTKSGLMV-GLGETN(5)VMHDLR---HGVTMITLQGLVQ(53)				
17865692	COG0502	BIOB_SALTY		52	MLNESQAQR(4)GLDYV-NHNLDTSP---EFYGNIIITRT---YQERLDT---LE---K-VR(3)-IKVCSGGIV-GLGETV(5)LLQLANLPTGSPSPVINMLQV(118)				
14520966	COG1180	PflA_PYRAB		81	Y-INEEPFR(4)YIDAM-NIDKAFDD---RFYMKIASVNP-GEPSRRIAK-IAK---KEFGI---HVELYLIIPTLNDKE(5)FARVWDELGGPTPVHFSRFFPH(90)				
13476168	COG1533	SplB_RHILO		74	II(5)DILSR(4)GLAKV-ALSVTLD---RMLARTMEPRA-STPTKRLEA---IR---Q-LS(5)-TSVMVAPIIPGLTDOE---MERILDSAYAAGARE------(99)				
15605904	COG1856		AQUAE	69	L(6)EKLE---ANVDV-LLDIIGDN---ETIAQVYKLPH-KSVEDYDRS---LR---L-LK(3)-LRIVPHVI-GLHYGK(6)AIDMIAK---YEPDALVLVVMYPY(99)				
15643710	COG5014	THEMA		710	L-----MFGFDPSL-----VD---L-FVN---LNVLIRVSVIKGWDEES---FEKITGASGEYFRY(50)				
15891589	COG0602	NrdG_AGRT5		43	II-----AK(4)DLDDL-VLSPKPPS-----SGME-TDWAQFEDC---LA-----AAGDG---PQVALKVVII---FDDADYA-YAKAA(5)-HLPVYLQPGNHTPP(49)				