

Protein Family 1 : PS00571 - Amdiasse Enzyme (631 sequences) 3,07,691 chars

G-[GAV]-S-[GS](2)-G-x-[GSAE]-[GSAVYCT]-x-[LIVMT]-[GSA]-x(6)-[GSAT]-x-[GA]-x-[DE]-x-[GA]-x-S-[LIVM]-R-x-P-[GSACTL].

Protein Family 2 : PS01199 - Ribosomal L1 Protein (867 sequences) 2,00,193 chars

[IMGV]-x(2)-[LIVA]-x(2,3)-[LIVMY]-[GAS]-x(2)-[LMSF]-[GSNH]-[PTKR]-[KRAVG]-[GN]-x-[LIMF]-P-[DENSTKQPRAGVI].

Segments in MDL output common to both families :

A 8146	G 3723	TVT 19	QVR 7	SVDV 4
L 6283	R 3336	IGK 18	GIDP 6	AKGE 4
V 5273	N 2804	VKN 15	FDATV 6	ALSS 4
S 5144	Q 2642	ENF 13	KIKE 6	KAKE 4
K 4861	P 2211	RIL 11	VIAS 6	ATAV 4
E 4820	F 1823	GKT 11	QQV 6	DATV 4
I 4446	M 1755	EALK 10	LPH 6	KEC 3
T 4208	Y 1389	VNL 9	EAGA 6	TIGK 3
D 4194	H 1069	KEN 8	EKVD 5	EEAIK 3
	C 680	GRV 7	VSLP 5	TNLT 2
	W 253	YLK 7	DVII 4	AVKN 2
		YFK 7		IVGM 2
				RIAV 2

Segments of Family 1

A 5680	EEV 20
L 4434	SSL 20
S 3597	DGV 18
E 3548	PW 18
V 3303	IKD 18
D 3035	EVKRRIMIGTYVLSAGYYDAYY 18
G 2928	PGGSSGGSAAAVAA 18
K 2874	RVPGGSSGGSAAAVA 18
I 2840	VKD 17
T 2768	GLP 17
R 2443	DLLDMYKKSRAEGFGPEVKRRILVG 17
N 1874	MYLNDIFTVTVNMAGLPGIAPVAG 17
Q 1797	YEALGATLVPVSLPKTELSIPVYYVI 16
P 1745	SKYGVAVYYIIASSEASSNLQRFDGI 16
F 1420	SLP 15
M 1238	AAF 15
Y 1070	RVPGGSSGGSAAAVAA 15
H 906	EQA 15
C 577	EVQRRILIGTYALSAGY 15
W 240	VPGGSSGGSAAAVA 14
EKL 27	TYVLSHGYDAYYLQAQKIRRIIA 14
YY 26	LDQ 14
NM 24	LAGVPLALKDVFTT 14
KPTYGRVSRYGMIASFSSLDQGGPMA 24	VPGGSSGGSAAAVAA 14
RVPGGSSGGSAAAVAAG 24	YDA 14
LAR 24	GVR 14

SLD 22	KLN 14
LSR 21	VKE 12
LDE 21	SNL 12
LAPAAATGTDGTGGSIRQPASFAGVTGI 14	EVS 12
DMY 13	NPWD 12
VGL 13	VSR 12
GLR 13	MYLADLLTIPVNLAGLPGISIPAGF 12
GSD 13	EGF 12
LNA 13	NLS 12
CG 13	EVKRRIMLGTFSLSSGYDAYFKKAG 12
DNI 13	EVKRRIMLGTFALSSGYDAYYKKAQ 12
WD 13	AFE 12
NPW 13	VPGGSSGGSAAAVAAG 12
DIKGMKIALPKEYLGEGIDPE 13	ELT 12
AAAV 12	EFF 12

Segments of Family 2

A 2466	EAA 16
K 1987	VESVDVAVNLGIDARKSDQNVRGATV 16
V 1970	EDL 15
L 1849	ILGPRGLMPNPK 15
I 1606	FDRCIATPDMMPPLVGRLGKVLGPRG 15
S 1547	ALKKAKPTQAKGVYIKKVSISTTMGA 15
T 1440	RLGVDPRKADQMVRGTVNLPHGTGK 15
E 1272	GVAVDQAGLSASVNMALTKRMRVIR 15
D 1159	KADQQIRGAMVLPNGTGKTQRVLVF 14
N 930	LGPRGLMPSPKGGTVT 13
R 893	RKSDQNVRGATVLPHTGR 13
Q 845	VYIKKVSISTTMGAGVAVDQAGLSAS 13
G 795	LGVDPRHADQMVRG 13
M 517	DADKLKENLEALLVALKKAKPSQAKG 13
P 466	W 13
F 403	VGRLGRVLGPRNLMPNPKTGTVTMDV 13
Y 319	IGK 13
H 163	LPNGTGKT 12
C 103	EEI 12
PN 30	DLA 12
NP 29	AVALLKELATAKFVESVDVAVNLGID 12
SF 27	LGPRGLMPNPKVGTVTPDVA 12
NAKAGQVRYRNDKNGIHTTIGKVDF 24	PR 12
ARGAKAEAAKAAGADFVGEDDLVAKI 24	IQQGWFDVDFVVPATPDMMGEGVGLGR 12
DQ 22	GPRGLMPNPKVGTVTPNVAEAVKNAK 12
FD 21	KAY 11
QIKKGEMNFDVVIASPDAMRVVGQLG 21	KKVSISTTMGAGVAVDQ 11
MP 19	IKKGEMNFDVVIASPDAMRVVGQLGQ 11
NF 19	ETV 11
EAL 19	KPAAAKG 11
LPHGTGK 18	AKKSKQLRAALEKIDSTKAYSVEEAV 11
QVLGPRGLMPNPKVGTVTPNVAEAVK 17	LPHG 11
MPKHGKKY 17	ALAKETNFAKFDATVEVAYNLNIDVK 11
AEA 17	LGQVLGPRGLMPNPKVGTVT 11
TM 17	VRVAVFTQGANAEEAAKAAGAEVGM 11
EKVDATKQYDINEAIALKELATAKF 17	ENF 11
LGPRNLMPNPKTGTVTMDVAKAVEES 17	ARKSDQNVRGATVLPHTGRSVRVAV 11