

### Supplementary File with protein alignments.

- A. Percent identity matrices for vimentin, S100-A1, glial fibrillary acidic protein (GFAP), desmin.
- B. CLUSTAL O(1.2.4) multiple sequence alignment for vimentin.
- C. CLUSTAL O(1.2.4) multiple sequence alignment for S100 A9.
- D. CLUSTAL O(1.2.4) multiple sequence alignment for S100 A9.
- E. CLUSTAL O(1.2.4) multiple sequence alignment for desmin.

A. Percent identity matrices with the Uniprot Entry of the immunogens provided by the manufacturer.

#### Vimentin Percent Identity Matrix - created by Clustal2.1

1: sp P48674 VIME_ONCMY	100.00	74.34	76.33	75.06	76.40
2: sp P02543 VIME_PIG	74.34	100.00	75.29	71.68	76.40
3: sp P48671 VIM1_CARAU	76.33	75.29	100.00	80.47	74.32
4: tr A0A671V9L3 A0A671V9L3_SPAAU	75.06	71.68	80.47	100.00	95.68
5: tr A0A411KAS9 A0A411KAS9_DICLA	76.40	76.40	74.32	95.68	100.00

#### S100 Percent Identity Matrix - created by Clustal2.1

1: tr A0A6P6R5E7 A0A6P6R5E7_CARAU	100.00	28.26	23.91	33.33	25.27
2: tr A0A671W834 A0A671W834_SPAAU	28.26	100.00	49.49	45.74	46.94
3: tr C1BH93 C1BH93_ONCMY	23.91	49.49	100.00	52.13	52.04
4: sp P02639 S10A1_BOVIN	33.33	45.74	52.13	100.00	62.77
5: tr A0A8C4I043 A0A8C4I043_DICLA	25.27	46.94	52.04	62.77	100.00

#### GFAP Percent Identity Matrix - created by Clustal2.1

1: tr A0A671WZT8 A0A671WZT8_SPAAU	100.00	33.10	32.48	31.49	35.26
2: sp Q28115 GFAP_BOVIN	33.10	100.00	64.37	61.68	72.05
3: tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	32.48	64.37	100.00	76.57	80.39
4: tr A0A8P4G1A2 A0A8P4G1A2_DICLA	31.49	61.68	76.57	100.00	82.19
5: sp P48677 GFAP_CARAU	35.26	72.05	80.39	82.19	100.00

#### Desmin Percent Identity Matrix - created by Clustal2.1

1: tr A0A6P6PJ00 A0A6P6PJ00_CARAU	100.00	37.18	37.66	39.75	37.19
2: sp P17661 DESM_HUMAN	37.18	100.00	74.16	71.95	72.47
3: tr A0A8C4I534 A0A8C4I534_DICLA	37.66	74.16	100.00	77.96	78.24
4: tr Q8UWF1 Q8UWF1_ONCMY	39.75	71.95	77.96	100.00	82.18
5: tr A0A2R2YUL3 A0A2R2YUL3_SPAAU	37.19	72.47	78.24	82.18	100.00

B. CLUSTAL O(1.2.4) multiple sequence alignment for vimentin.

sp P48674 VIME_ONCMY	MNRTTSRQTTSSSSYKRMFGGEGRPVSGMARSTLSSRQYSSPVR-----SSRMS	49
sp P02543 VIME_PIG	----MSTRIVSSSSYRRMFGGPGTASR---PSSRSYVTTSTRTYSLGSALRPSTSRSL	52
sp P48671 VIM1_CARAU	-----MSHRATPSSSYKRMFGGERSAR---SSYTSRQFSIPVR-----SSRAT	0
tr A0A671V9L3 A0A671V9L3_SPAAU	-----MSHRATPSSSYKRMFGGERSAR---SSYTSRQFSIPVR-----SSRAT	41
tr A0A411KAS9 A0A411KAS9_DICLA	-----MSHRATPSSSYKRMFGGERSAR---SSYTSRQFSIPVR-----SSRAT	0
sp P48674 VIME_ONCMY	YVSAPPSIYASKN--VRLRSSAPMPRLSSDVTDFALSDAINSEFKANRTNEKAEMQHLN	107
sp P02543 VIME_PIG	YT-SSPGGVYATRSSAVRLRSSVPGVRLQLQDAVDFSLADAINTEFKNTRTNEKVELQELN	111
sp P48671 VIM1_CARAU	-----YVSAPPSIYASKN--VRLRSSAPMPRLSSDVTDFALSDAINSEFKANRTNEKAEMQHLN	0
tr A0A671V9L3 A0A671V9L3_SPAAU	YGVSLAPTIVYAAKT--QRLRSTAAMPRLASENLDFSLSDAINSEFMTNRTNEKVQMQLSLN	99
tr A0A411KAS9 A0A411KAS9_DICLA	-----YGVSLAPTIVYAAKT--QRLRSTAAMPRLASENLDFSLSDAINSEFMTNRTNEKVQMQLSLN	0
sp P48674 VIME_ONCMY	DRFASYIDKVRFLQEQNKILLAELEQLKGKGASRIGDLYEDEMRLRRQVDQLTNEKAHV	167
sp P02543 VIME_PIG	DRFANYIDKVRFLQEQNKILLAELEQLKGKGASRIGDLYEDEMRLRRQVDQLTNDKARV	171
sp P48671 VIM1_CARAU	-----DRFASYIDKVRFLQEQNKILLAELEQLKGKGASRIGDLYEDEMRLRRQVDQLTNEKAHV	0
tr A0A671V9L3 A0A671V9L3_SPAAU	DRFASYIEKVRFLQEQNKILLAELEQLKGKGASRIGDLYEDEMRLRRQVDQLTNEKARV	159
tr A0A411KAS9 A0A411KAS9_DICLA	-----DRFASYIEKVRFLQEQNKILLAELEQLKGKGASRIGDLYEDEMRLRRQVDQLTNEKARV	0
sp P48674 VIME_ONCMY	EVDRDNMGEDIERLREKLQDEMIQKEEAHNLQSFQDQVDNASLARLDLERKVESIQEEI	227
sp P02543 VIME_PIG	EVERDNLAEDIMRLREKLQEETLQREEAESTLQSFQDQVDNASLARLDLERKVESIQEEI	231
sp P48671 VIM1_CARAU	-----EVDRDNMGEDIERLREKLQDEMIQKEEAHNLQSFQDQVDNASLARLDLERKVESIQEEI	0
tr A0A671V9L3 A0A671V9L3_SPAAU	EVYRDNLAEIDIRLREKLQDEIAQREDAESNMQSFQDQVDNAALARLDLERKVESIQDEI	219
tr A0A411KAS9 A0A411KAS9_DICLA	-----EVYRDNLAEIDIRLREKLQDEIAQREDAESNMQSFQDQVDNAALARLDLERKVESIQDEI	22
sp P48674 VIME_ONCMY	IFLRKLHDEEVAELQAQIQ-DQHVQIDMDVAKPDLTAALRDVVRVQYETLASRNLQDSEDW	286
sp P02543 VIME_PIG	AFLKKLHDEEIQELQAQIQ-EQHVQIDMDVSKPDLTAALRDVRQQYESVAAKNLQEAEEW	290
sp P48671 VIM1_CARAU	-----IFLRKLHDEEVAELQAQIQ-DQHVQIDMDVAKPDLTAALRDVVRVQYETLASRNLQDSEDW	0
tr A0A671V9L3 A0A671V9L3_SPAAU	NFLKKLHDEEMLELQSQMQQQQHVQVDMEMAKPDLTAALRDVRLQYENLASKNIHESSEW	279
tr A0A411KAS9 A0A411KAS9_DICLA	NFLKKLHDEEMLELQSQMQQQQHVQVDMEMAKPDLTAALRDVRLQYENLASKNIHESSEW	82
sp P48674 VIME_ONCMY	YKSKFADLSEAANRNTDAIRQAKQEANEYRRQVQALTCEVDLSKGTNESMERQMLEEES	346
sp P02543 VIME_PIG	YKSKFADLSEAANRNDALRQAKQESNEYRRQVQSLTCEVDALKGTNESLERQMRMEEN	350
sp P48671 VIM1_CARAU	-----DLTEAANKSNEALRLAKQESNDYRRQVQALTCEVDALKGTNESLERQMRMEEN	54
tr A0A671V9L3 A0A671V9L3_SPAAU	YKSKFADLTEAAARNNDALRVAKQEANDYRRQVQALTCEVDALKGTNESLDRQMRMEEN	339
tr A0A411KAS9 A0A411KAS9_DICLA	YKSKFADLTEAAARNNDALRVAKQEANDYRRQVQALTCEVDALKGTNESMERQIRELEEN	142
	***:*** :..*: * *****:*****:*****:*****:*****:***:***:***	
sp P48674 VIME_ONCMY	FGCEANNFQDTISRLEDDIRNMKDEMARHLREYQDLLNVKMALDIEIATYRKLLGEESR	406
sp P02543 VIME_PIG	FAVEAANYQDTIGRLQDEIQNMKEEMARHLREYQDLLNVKMALDIEIATYRKLLGEESR	410
sp P48671 VIM1_CARAU	FAMESSSSQDKIVQLEEDTQNMKDEMAKHLHEYQDLLNVKMALDIEIATYRKLLGEESR	114
tr A0A671V9L3 A0A671V9L3_SPAAU	FSLETGGYQDTIGRLEEDIHNMKDEMARHLREYQDLLNVKMALDIEIATYRKLLGEESR	399
tr A0A411KAS9 A0A411KAS9_DICLA	FSLETGSYQDTIGHLEEDIH-----FSLETGSYQDTIGHLEEDIH-----	162
	*. *. . *. * :*: : :	
sp P48674 VIME_ONCMY	ITTPMPNFSSFNLRRESMLEA-----RPMID-NLSKKVVIKTIETRD	446
sp P02543 VIME_PIG	ISLPLPNFSSNLNRETNLDES-----LPLVDTHSKRTLLIKTVETRD	451
sp P48671 VIM1_CARAU	ISTPLPNFSSFNLRRETMLLEL-----KPNIESTFTKKVLIKTIETRD	155
tr A0A671V9L3 A0A671V9L3_SPAAU	ITTPLASFSSNLNLRGRITSLHVDITNKLFLSFLETMMDSKPHIE-TTTKKVLIKTIETRD	458
tr A0A411KAS9 A0A411KAS9_DICLA	-----ITTPMPNFSSFNLRRESMLEA-----RPMID-NLSKKVVIKTIETRD	162
sp P48674 VIME_ONCMY	GHVINESTQNHHDDLE	461
sp P02543 VIME_PIG	GQVINETSQHHDHDDLE	466
sp P48671 VIM1_CARAU	GQVLNQUESTQNHHDDLE	170
tr A0A671V9L3 A0A671V9L3_SPAAU	GQVINESTQNHHDDME	473
tr A0A411KAS9 A0A411KAS9_DICLA	-----GHVINESTQNHHDDLE	162

C. CLUSTAL O(1.2.4) multiple sequence alignment for S100-A1

tr A0A6P6R5E7 A0A6P6R5E7_CARAU	-----	0
tr A0A671W834 A0A671W834_SPAAU	MAFSTLFALSLSLPLCAWVSLPLPLPSIFLGVAWLHYKYNNKLLGEPLHSSQITTKPQLL	60
tr C1BH93 C1BH93_ONCMY	-----	0
sp P02639 S10A1_BOVIN	-----	0
tr A0A8C4I043 A0A8C4I043_DICLA	-----	0
tr A0A6P6R5E7 A0A6P6R5E7_CARAU	-----MEGAIKTVVTQFL---SSARGKESLGGKNFQKLVSQSLGNILSDTD	43
tr A0A671W834 A0A671W834_SPAAU	PLYVLHLLSAAMSELEVCMKELILLFHKYADEDGDKKHLKKEFKKLVE TELPTFLKTQK	120
tr C1BH93 C1BH93_ONCMY	-----MPSDLERAMESMITVFHKYAAKEGSGNTLSRRELKDL MENELSGFLKSQK	50
sp P02639 S10A1_BOVIN	-----MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQK	50
tr A0A8C4I043 A0A8C4I043_DICLA	-----MPSQLEGAMDALITVFYNYSGNDGDKYKLNKGELKELLNSELTDFLT SQK	50
	: * . : . : : * . . * . : : . * : * .	
tr A0A6P6R5E7 A0A6P6R5E7_CARAU	SSSAVKDMMKGLDDNQDGKVGFEYLMVLVGYLANSLSEQKAQSSAAGGP	92
tr A0A671W834 A0A671W834_SPAAU	NPKAVECIMKDLDTNKKDKLSFEEFLPLVAGLSMACDKCYNLQQKHCKK	169
tr C1BH93 C1BH93_ONCMY	DPATVDKIMKDLSNGGGEVNFEEFVSLVVGLSIACEQCYQMHHKKMKMGK	99
sp P02639 S10A1_BOVIN	DADAVDKVMKELDENGDEVDFFEYVVLVAALTVACNFFWENS-----	94
tr A0A8C4I043 A0A8C4I043_DICLA	DPMLVEKIMNDLDSNKNDFNEFVVLVAALTVACNDFFEQKKKKNK-	98
	. * . : * : * * * . : : . * : : * * * : : . .	

tr A0A671WZT8 A0A671WZT8_SPAAU	MSSSPERMSSSYRRHFEGNLAASSTYQLRVSSPSPARRESRPRSVSYYTRGGGTMVRRASSK	60
sp Q28115 GFAP_BOVIN	-MERRRVTSATR-----SYVSS---SEMVGGR-----R-----LGPG	30
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	-----RERGERKKARRHLYL--SGRAQTIPGTGPHRMTH-----SSTI	36
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	-MEGQRYSYRKRYGPQGSSSTGVRIGSHSSSRSLSWHGTPRNLT-----SSPI	49
sp P48677 GFAP_CARAU	-----	0
tr A0A671WZT8 A0A671WZT8_SPAAU	AGLTSSSVSGT-LCLGLETKLDLDAAAAENRAFMTVTRSSSERQEMVVLNDRLAVYIEKVRS	119
sp Q28115 GFAP_BOVIN	TRLSLAR----MPPLPARVDVSLAGALNSGFKETRASERAEMMELNDRFASYIEKVRF	85
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	SRLSLGSAGGALLLTGPNRLDFSADSLKAQYRETRTNEKVEMMGLNDRFAFASIEKVRF	96
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	SRLSLGSTNTALLGSPGDRLDFSADTLMAKYKETRTNEKMEMMGLNDRFASYIEKVRL	10
sp P48677 GFAP_CARAU	-----REVDRVMLGNDRFASYIEKVRF *   .:  ****:*  *****	22
tr A0A671WZT8 A0A671WZT8_SPAAU	LESKNKLLEAEIEALRSRYARPSGLRQLYESQLKDLHRVAEQMRVQRDTSLAAKEAMFGQ	179
sp Q28115 GFAP_BOVIN	LEQQNKALAAEINQLRAK--EPTKLDAPVQAELRELRLRLDQLTANSARLEVERDNLAQD	143
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	LEQQNTVLVTETLQLRGK--EPSRLGDIQEELRELRLRQVDLSAGAKARLEIERDNMAAD	154
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	LEQQNMKLVAELNLQKGK--EPSRLGDIQEELRELRLRQVDGLTAGAKARLEIERDNLASD	167
sp P48677 GFAP_CARAU	LEQQNKMLVAELNLQRGK--EPSRLGDIQEELRELRLRQVDGLNAGAKARLEIERDNLASD **.*.  *  *:  *:.  *.  *  ::  *:*:*  :  .        :  :  :	80
tr A0A671WZT8 A0A671WZT8_SPAAU	LDSLKAKYEAAVVARKETEQDIEALRPQDVDRATSARIHLEKREHLEVELAFLRQHVKEE	239
sp Q28115 GFAP_BOVIN	LGTLRQKLQDEANTQRLAEANNLAAAYRPQDEATLARLDLERKIESLEEIRFLRKIHEEE	203
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	VATLKQRLQDEMVLRLQDAESNLNAFRQDVDEASLNVRVQLERKIDALQDEIAFLKKIHEEE	214
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	VATLKQRLQEEMGLRQDAEGNLNAFRQDVDEASLNVRVQLERKIDALQDEINFLKKTTHDEE	227
sp P48677 GFAP_CARAU	LATLKQRLQEENALRQEAENNLTFRQDVDEAALNRVQLERKIDALQDESIFLRKHHEEE :  *:  :  :      *  *:  :  :  *  :.*.*:  *:.***::  *:  *:  *:  *.*	140
tr A0A671WZT8 A0A671WZT8_SPAAU	IEELMQQIYAAASKVDLTFLGPLDTALKQIQISQYDSIAAKNLKEMDAWYASKFQDLSSA	299
sp Q28115 GFAP_BOVIN	VRELQEQLAQQQVHVEMDVAKPDLTAAALREIRTQYEAASSNNMHEAEWEYRSKFADLNDA	263
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	LRELQEQLMAQQVHVDDVSKPDLTAALRDILRVQYEVSASSNIQETEWEYRSKFADLTDA	274
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	LREFQEQLIMAAQQVHVDDLVS KPDLTAALRDILRVQYETMATSNMQETEWEYRSKFADLTDA	287
sp P48677 GFAP_CARAU	MRQLQEQLIAQQVHVDDLVS KPDLTTALKEIRAQFEAMATSNMQETEWEYRSKFADLTDA :  :  :  *:          *:  :  ..  ***:***:*:  *::::*.*:*:  *  *  *  *.*	200
tr A0A671WZT8 A0A671WZT8_SPAAU	STKHAQSVRTLREEIAGYRKNILDKERELDAVKTRNEYLVNQIRDTEVHKHKEEEDLQER	359
sp Q28115 GFAP_BOVIN	AARNAELLRQAKHEANDYRRQLQALTCDLES LRGTNESLERQMREQEERHAREAASYQEA	323
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	ATRNADALRLAKQEGNEYRRQLQAMTCDVLEARGTNESLEQQLRMEDRFVSBTAGYQDM	334
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	ASRNAEALRQAKQANEYRRQIQVVTCDLEALRGTNESLERQLREMEDRFSDMTTG YQDT	347
sp P48677 GFAP_CARAU	AGRNAEALRQAKQANEYRRQIQGLTCDLES LRGSNESLERQLREMEERFAIETAGYQDT :  *:  *:  *  *.*  *.*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *	260
tr A0A671WZT8 A0A671WZT8_SPAAU	MEANKLDLKVTEKIALLLREHQDLLNVKMALEIEITTYRKLIEGEDSRLSTTVQNLSLT	419
sp Q28115 GFAP_BOVIN	LARLEEEGQSLLKEDIAMRHLEQYQDLLNVKLALDIEIATYRKLLEGESNRITVPVQTFNSL	383
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	VGHLEEEIQLKEGMARHLQEYQDLLNVKLALDIEIATYRKLLEGESNRITVPVMSQFSNL	394
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	VSHLEEEIQLKEGMARHLQEYQDLLNVKLALDIEIATYRKLLEGESNRITVETECFPLS	407
sp P48677 GFAP_CARAU	VARLEDEIQMLKEEMARHLQEYQDLLNVKLALDIEIATYRKLLEGESNRITVPVNFTNL :  :  :  :  *:  *  *.*:*****.*.*.*.*.*.*.*.*.*.*:  :  :	320
tr A0A671WZT8 A0A671WZT8_SPAAU	GGLQLTTSVSLCAASASDSSATAALKLNEARDESTISRAEAASEEQSIEMSEKTVLIIR	479
sp Q28115 GFAP_BOVIN	QIRET-SLD-TKSVS-----EG-----HLKRNIIVK	407
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	QIRET-SMD-TKFS-----EA-----HVKRSIIVR	418
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	PSTHPSETNL-DTKTP-----EA-----HVKRSILVR	433
sp P48677 GFAP_CARAU	QPRDT-SLD-TKLT-----EA-----HVKRSIIVR .  :                              .	344
tr A0A671WZT8 A0A671WZT8_SPAAU	TVKTDDEDKYES--DTQTRTIISGAADDTTEE	509
sp Q28115 GFAP_BOVIN	TVEMRDGEVIKESKQEHKDVD-	428
tr A0A8C7NQ31 A0A8C7NQ31_ONCMY	TVETRDGEVCRTS-----	431
tr A0A8P4G1A2 A0A8P4G1A2_DICLA	TVETRDGEIIKESTTEHKDLP-----	454
sp P48677 GFAP_CARAU	TVETRDGEIIKESTTERKDLP-----	365

$$\begin{array}{ccccccc} \star & \star & : & & : & & : \\ & & : & & : & . & : \\ & & & & & & \end{array}$$

E. CLUSTAL O(1.2.4) multiple sequence alignment for desmin.

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tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      ----- 0
sp|P17661|DESM_HUMAN                MSQAY-SSSQRVSSYRRTFGGAPGFPLGSPVFPFRAGFGSKGSSSVTSRVYQVSRT 59
tr|A0A8C4I534|A0A8C4I534_DICLA      -MASYSSSAQSASSYRRHFGHGTYS---PSLN-----RSLVYEVTRS 39
tr|Q8UWF1|Q8UWF1_ONCMY              -----ISSYRRTFGSGIGST---PGMSSMFSGHGGSS-GSAHMSRVYEMTKS 45
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      MSKSYSSSAQSASSYRRTFGSGVGST---PMSSYYSSGAGGRSS-SSASMSRVYEVKS- 55

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      MRAHWQCGN-----ATAGSRDKAHY-----SHF-CERT-DRAHDAH 35
sp|P17661|DESM_HUMAN                SGGAGG-LGSLRAS----RLGTTTRTPSSYGAGELLDFSLADAVNQEFLLTRTNEKVELQE 114
tr|A0A8C4I534|A0A8C4I534_DICLA      SATPTYRVSSGGYKGPLAASRASVGRSYAGMGETLDFSLADALNQEFLLTRTNEKVELQH 99
tr|Q8UWF1|Q8UWF1_ONCMY              SARPSYSSGSIRSSS-GGAM-----RSYAGMGKELDFNLADATNRDFLDTRTNEKAELOH 99
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      SSLPSYSSYRVSSGA-GGAGYGASTAIRTYSGEKLDNFLADAMNQDFLNTRTNEKAELOH 114
                                     :  .:      . *  ** :... .

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      TVFSYSPVATKVRSLQKNKLEIEALKNRYLKPTGLRLLYEEQLQELKRLAEQMRIQ 95
sp|P17661|DESM_HUMAN                LNDRFANYIEKVRFLQQAALAAEVNRLKGRE--PTRVAELYEEELRELRRQVEVLTNQ 172
tr|A0A8C4I534|A0A8C4I534_DICLA      LNDRFASYIEKVRFLQQNQVLAVEVERLRGRE--PTRIADLYEEEMSELRRQVEILTNQ 157
tr|Q8UWF1|Q8UWF1_ONCMY              LNDRFASYIEKVRFLQQNATLVVEIERLRGHE--PTRVAEMYEEEMRELRRQVQDMSND 157
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      LNDRFASYIEKVRFLQQAALTVEIEKLRGRE-GPGRVAEMYEEEMRELRRQIESHSNQ 173
                                     : :  *** ***** * .*: *: :  * :  :****: **: * :

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      RDLAIAAKDAMAGQLEMIVKYEEAVEMRKKAEIDIEAFRPDVAATAARIALAKQLENL 155
sp|P17661|DESM_HUMAN                RARVDVERDNLDDDLQRLKAKLQEEIQLKEEAENNLAAFRADVDAATLARIDLERRIESL 232
tr|A0A8C4I534|A0A8C4I534_DICLA      RSRVEVERDNLADDLQKLRLQEEILQKEDAENNLAAFRADVDAATLARLDLERRIETL 217
tr|Q8UWF1|Q8UWF1_ONCMY              RARMEVERDNLADDLQKLRLQEVHQRREEAENNLAFRADVDSATLARLDLERRIESL 217
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      RARVEVERDNLADDLQKLRLQEEIHQKEEAENNLAFRADVDNATLARLDLERRIESL 233
*      . *: : .*: : * : * : : :.* : : *** ** * *: * : :.*

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      EVELEFLRRVHKEIEBELMKQIYAAHATAADAYSLPDLSSAIKQIQLYDDIAAKNLQEM 215
sp|P17661|DESM_HUMAN                NEEIAFLKKVHEEEIRELQAQLQEQQVQVEMDMSPDLTAALRDIRAQYETIAAKNISEA 292
tr|A0A8C4I534|A0A8C4I534_DICLA      QEEIAFLKKIHEEEIRELQSQMQETQVQIQMDMSKPDLTAAALRDIRAQYEGIAAKNIAEA 277
tr|Q8UWF1|Q8UWF1_ONCMY              QEEITFLKKIHEEEIHELTSQMQETSQVQVQMDMSKPDLTVALRDIRMQYEGIAAKNISEA 277
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      QEEIGFLKKIHEEEIRELQSQMQESQVQIQMDMSKPDLTAAALRDIRMQYEGIAAKNISEA 293
: *: *: : : :*.** *:      .      * *: : *: : :*: *: *: *: *

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      DSWYKSKFDDLNKSSKHVDKVRSVREEIVTAKKDIQNKERDLDLSLKTNEALEAQIRET 275
sp|P17661|DESM_HUMAN                EEWYKSKVSDLTQAANKNDALRQAKQEMMEYRHQIQSYTCEIDALKGTNDSLMRQMREL 352
tr|A0A8C4I534|A0A8C4I534_DICLA      EDWYKSKVSDLNQAVSKNNEALKQARQETMEFRHQIQSYTCEIDSLKGTNESLMRQMMDM 337
tr|Q8UWF1|Q8UWF1_ONCMY              EDWYKSKVSDLNQAVNKNNDALRQAKQESMEFRHQIQSYTCEIDSLKGTNESLLRQMREM 337
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      EEWYKSKVSDLNQAVNKNNDALRQAKQESMEYRHQIQSYTCEIDSLKGTNESLLRQMREM 353
:.*****.:.*: : : : :*: : : :*.** :*:** .*: * *: :

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      QEKYRKELEELQARIEALQLELKSSKQRTAMLLREYQDLLNVKMALEIEITTYRKLIEGE 335
sp|P17661|DESM_HUMAN                EDRFASEASGYQDNARLEEEIRHLKDEMARHLREYQDLLNVKMALEDVEIATYRKLIEGE 412
tr|A0A8C4I534|A0A8C4I534_DICLA      EDRHGVEAGRFQDNARLEAEIANMKDEMARHLREYQDLLNVKMALEDVEIATYRKLIEGE 397
tr|Q8UWF1|Q8UWF1_ONCMY              EDRLGNEAGGYQDSVTRLEAEIAKMKDEMARHLREYQDLLNVKMALEDIEIATYRKLIEGE 397
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      EDRMGREASGFQDTIARLEADIAMKDDMARHLREYQDLLNVKMALEDIEIATYRKLIEGE 413
: :  *      * :  * : : :  * :  * *****: :*:*****:***

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      DSRITSVMQSMQTMSLMSGISVHSAGAAGVAGIVDKVGGGPDGGAASGLGGNGGGLLN 395
sp|P17661|DESM_HUMAN                ESRINLP-----I----- 420
tr|A0A8C4I534|A0A8C4I534_DICLA      ESRITLP-----V----- 405
tr|Q8UWF1|Q8UWF1_ONCMY              ESRITVSGSKSSH---SGSHSA-----A----- 417
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      ESRITTTAP-----V-----Q----- 424
:***.

tr|A0A6P6PJ00|A0A6P6PJ00_CARAU      GITSGVGPGTTVDYTQEQAVEKTERKTVLIRTVKTEDDTLESNTQESYSISGAADDEE 455
sp|P17661|DESM_HUMAN                QTYNALNFRETSP---QRGSEVHTKKTVMIKTIETRDGEVVSEATQQQHEVL----- 470
tr|A0A8C4I534|A0A8C4I534_DICLA      QSYSTLSFRETSPEHQ-QRASEMHSKKTVLIKTIETRDGEVVSESTQHQQDIM----- 457
tr|Q8UWF1|Q8UWF1_ONCMY              SLYSTVGFRETSQPDV--GRSAEVHKKTVLIKTIETRDGEVVSE----- 459
tr|A0A2R2YUL3|A0A2R2YUL3_SPAAU      SAYSSIGFRETSPEHQRSSEVHKKTVLIKTIETRDGEVVSESTQHQQDIM----- 477
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