

Table S1: Purification procedure of 26S proteasome isoform from *T. bernacchii* red blood cells (RBCs)

Purification step	Total activity (U)	Total protein (mg)	Specific activity (U/mg)	U/ml blood	Purification fold	Yield (%)
Extract	645120	99.4	6490	586473	1	100
DEAE	303206	18.8	16128	-	2.5	47
Phenyl peak 1	30321	1.4	21658	-	3.3	4.7
Phenyl peak 2	23953	2.9	8260	-	1.3	3.7
Superdex 200 peak 1	758	0.02	37900	-	5.8	0.1

The proteasome activity was measured using LLVY as substrate and expressed assuming $\epsilon=1 \text{ mM}^{-1} \text{ cm}^{-1}$

Table S2: Structural analysis of the ten models obtained for the seven proteasome subunits. Analyses have been performed with PROCHECK, PROSA web and Hbplus. Columns concerning the PROCHECK analysis report, as absolute numbers and percentage, the amino acids falling in the Ramachandran plot regions (most favoured, additional favoured, generously allowed, disallowed). PROSA web results report the Z-score obtained, which give a whole measure of the quality of the model in comparison to the value obtained for the template chain (last line for each table). The Hbplus column reports the number of H-bonds observed for each model. This is not a measure of model quality, but it is reported for a comparison among models and to the template chain.

Subunit alpha 4

PROCHECK									PROSA web	Hbplus
	Number of amino acids in regions:				Percentage					
	<i>Most favoured</i>	<i>Generously</i>		<i>Most favoured</i>	<i>Generously</i>		<i>Z-score</i>			
	<i>Additional</i>	<i>Disallowed</i>	<i>Disallowed</i>	<i>Additional</i>	<i>Disallowed</i>	<i>Disallowed</i>		<i>Hbonds</i>		
Model 1	214	10	0	0	95.5	4.5	0	0	-7.12	214
Model 2	215	9	0	0	96	4	0	0	-7.07	208
Model 3	215	9	0	0	96	4	0	0	-7.04	214
Model 4	215	9	0	0	96	4	0	0	-7.24	208
Model 5	214	10	0	0	95.5	4.5	0	0	-7.1	209
Model 6	211	13	0	0	94.2	5.8	0	0	-7.14	201
Model 7	215	9	0	0	96	4	0	0	-7.11	213
Model 8	215	9	0	0	96	4	0	0	-7.12	207
Model 9	215	9	0	0	96	4	0	0	-7.11	208
Model 10	215	9	0	0	96	4	0	0	-7.14	201
Template: 3UNB_B 248aa									-7.12	204

Subunit alpha 5

PROCHECK									PROSA web	Hbplus
	Number of amino acids in regions:				Percentage					
	<i>Most favoured</i>		<i>Generously</i>		<i>Most favoured</i>		<i>Generously</i>		Z-score	Hbonds
	<i>Additional</i>		<i>Disallowed</i>		<i>Additional</i>		<i>Disallowed</i>			
Model 1	199	7	0	0	96.6	3.4	0	0	-7.44	179
Model 2	197	9	0	0	95.6	4.4	0	0	-7.61	178
Model 3	200	5	1	0	97.1	2.4	0.5	0	-7.52	181
Model 4	199	7	0	0	96.6	3.4	0	0	-7.51	168
Model 5	198	7	1	0	96.1	3.4	0.5	0	-7.37	190
Model 6	196	10	0	0	95.1	4.9	0	0	-7.57	183
Model 7	198	7	1	0	96.6	3.4	0.5	0	-7.4	185
Model 8	198	8	0	0	96.6	3.9	0	0	-7.41	180
Model 9	198	8	0	0	96.6	3.9	0	0	-7.58	179
Model 10	198	8	0	0	96.6	3.9	0	0	-7.46	179
Template: 3UNB_D 233aa									-7.24	176

Subunit alpha 7

PROCHECK									PROSA web	Hbplus
Number of amino acids in regions:					Percentage					
	<i>Most favoured</i>	<i>Generously</i>		<i>Most favoured</i>	<i>Generously</i>		<i>Z-score</i>		<i>Hbonds</i>	
	<i>Additional</i>	<i>Disallowed</i>	<i>Additional</i>	<i>Disallowed</i>						
Model 1	207	6	3	0	95.8	2.8	1.4	0	-7.32	173
Model 2	206	7	3	0	95.4	3.2	1.4	0	-7.33	166
Model 3	206	6	3	1	95.4	2.8	1.4	0.5	-7.28	175
Model 4	206	7	3	0	95.4	3.2	1.4	0	-7.4	165
Model 5	206	7	3	0	95.4	3.2	1.4	0	-7.37	168
Model 6	207	5	3	1	95.8	2.3	1.4	0.5	-7.39	168
Model 7	208	5	3	0	96.3	2.3	1.4	0	-7.43	179
Model 8	203	10	3	0	94	4.6	1.4	0	-7.37	183
Model 9	209	4	3	0	96.8	1.9	1.4	0	-7.38	162
Model 10	208	5	3	0	96.3	2.3	1.4	0	-7.27	168
Template: 3UNB_C 239aa									-7.97	157

Subunit beta 1

PROCHECK									PROSA web	Hbplus
	Number of amino acids in regions:				Percentage					
	<i>Most favoured</i>		<i>Generously</i>		<i>Most favoured</i>		<i>Generously</i>		Z-score	Hbonds
	<i>Additional</i>		<i>Disallowed</i>		<i>Additional</i>		<i>Disallowed</i>			
Model 1	175	9	0	1	94.6	4.9	0	0.5	-7.85	159
Model 2	176	8	0	1	95.1	4.3	0	0.5	-7.96	169
Model 3	174	10	0	1	94.1	5.4	0	0.5	-7.98	166
Model 4	174	10	0	1	94.1	5.4	0	0.5	-7.97	159
Model 5	174	10	0	1	94.1	5.4	0	0.5	-7.98	166
Model 6	174	10	0	1	94.1	5.4	0	0.5	-7.92	154
Model 7	173	11	0	1	93.5	5.9	0	0.5	-7.97	161
Model 8	175	9	0	1	94.6	4.9	0	0.5	-7.88	169
Model 9	174	10	0	1	94.1	5.4	0	0.5	-7.89	170
Model 10	173	11	0	1	93.5	5.9	0	0.5	-7.96	158
Template: 3UNB_L 213 aa									-7.78	177

Subunit beta 2

PROCHECK									PROSA web	Hbplus
Number of amino acids in regions:					Percentage					
	<i>Most favoured</i>		<i>Generously</i>		<i>Most favoured</i>		<i>Generously</i>		Z-score	Hbonds
	<i>Additional</i>		<i>Disallowed</i>		<i>Additional</i>		<i>Disallowed</i>			
Model 1	168	10	0	0	94.4	5.6	0	0	-6.41	146
Model 2	166	11	1	0	93.3	6.2	0.6	0	-6.58	154
Model 3	167	10	1	0	93.8	5.6	0.6	0	-6.51	160
Model 4	168	10	0	0	94.4	5.6	0	0	-6.38	152
Model 5	168	10	0	0	94.4	5.6	0	0	-6.44	153
Model 6	170	7	1	0	95.5	3.9	0.6	0	-6.38	158
Model 7	167	11	0	0	93.8	6.2	0	0	-6.50	154
Model 8	167	11	0	0	93.8	6.2	0	0	-6.52	155
Model 9	167	10	1	0	93.8	5.6	0.6	0	-6.42	156
Model 10	168	9	1	0	94,4	5.1	0.6	0	-6.50	155
Template: 3UNB_J 196 aa									-5.98	151

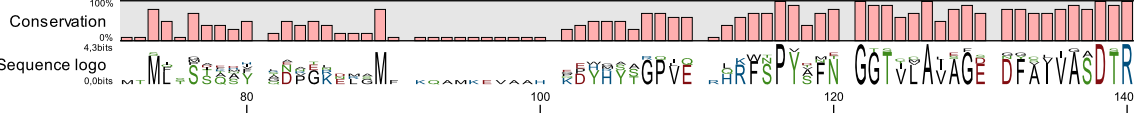
Subunit beta 3

PROCHECK									PROSA web	Hbplus
	Number of amino acids in regions:				Percentage					
	<i>Most favoured</i>		<i>Generously</i>		<i>Most favoured</i>		<i>Generously</i>		Z-score	Hbonds
	<i>Additional</i>		<i>Disallowed</i>		<i>Additional</i>		<i>Disallowed</i>			
Model 1	168	7	1	2	94.4	3.9	0,6	1.1	-8.49	152
Model 2	168	7	1	2	94.4	3.9	0,6	1.1	-8.35	152
Model 3	168	7	1	2	94.4	3.9	0,6	1.1	-8.44	149
Model 4	169	6	1	2	94.9	3.4	0,6	1.1	-8.46	151
Model 5	168	7	1	2	94.4	3.9	0,6	1.1	-8.50	149
Model 6	168	7	1	2	94.4	3.9	0,6	1.1	-8.55	151
Model 7	169	6	1	2	94.9	3.4	0,6	1.1	-8.42	155
Model 8	168	7	1	2	94.4	3.9	0,6	1.1	-8.38	149
Model 9	170	6	1	1	95.5	3.4	0,6	0.6	-8.41	160
Model 10	170	6	1	1	95.5	3.4	0,6	0.6	-8.51	159
Template: 3UNB_I 204 aa									-8.26	153

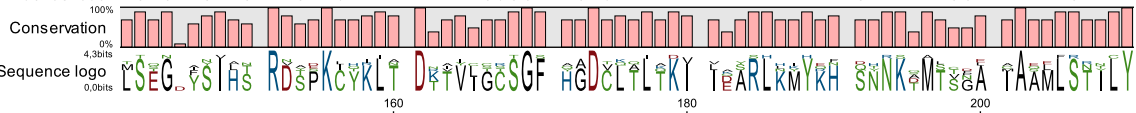
Subunit beta 5

PROCHECK									PROSA web	Hbplus
Number of amino acids in regions:					Percentage					
	<i>Most favoured</i>		<i>Generously</i>		<i>Most favoured</i>		<i>Generously</i>		<i>Z-score</i>	Hbonds
	<i>Additional</i>		<i>Disallowed</i>		<i>Additional</i>		<i>Disallowed</i>			
Model 1	168	10	0	0	94.4	5.6	0	0	-6.18	167
Model 2	169	9	0	0	94.9	5.1	0	0	-6.11	173
Model 3	169	9	0	0	94.9	5.1	0	0	-6.22	169
Model 4	170	8	0	0	95.5	4.5	0	0	-6.23	172
Model 5	170	8	0	0	95.5	4.5	0	0	-6.42	165
Model 6	172	6	0	0	96.6	3.4	0	0	-6.45	176
Model 7	172	6	0	0	96.6	3.4	0	0	-6.21	189
Model 8	172	7	0	0	96.1	3.9	0	0	-6.27	165
Model 9	169	9	0	0	94.9	5.1	0	0	-6.16	174
Model 10	170	8	0	0	95.5	4.5	0	0	-6.22	166
Template: 3UNB_K 205 aa									-6.32	172

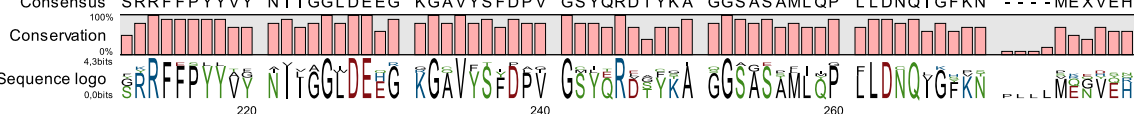
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 Caenorhabditis elegans_NP_498806 MTSFTGITAV ANATNEMAMF KQAMKEVAAH PEWMSSRQIE RQRWNPYSME GGSTCAISGE NFAIVASDTR 70
 Arabidopsis thaliana_NP_191641 ---MTKQH AN----- ---WSPYDNN GGTCVAIAGS DYCVAADTR 34
 Xenopus laevis_NP_001080435 --M-SSESI LNRELNRSY ---DHYHTGPVE -QRFNPTFN GGTVLAVAGE DFAIVASDTR 54
 Mus musculus_NP_035315 --ML-STAA Y RDVERELGM ----- GPHGSAGPVQ -LRFSPYAFN GGTVLAVAGE DFIIVASDTR 55
 Homo sapiens_NP_002784 --MLSSTAMY SAPGRDLGM ----- EPHRAAGPLQ -LRFSPYAFN GGTVLAVAGE DFAIVASDTR 56
 Danio rerio_NP_001003889 --ML-SAQA Y GENK---M ----- -HKFSPYAFN GGTVLAVAGE DFAIVASDTR 52
 Oreochromis niloticus_XP_003454565 --ML-SSQHF GDPGK--M ----- KDYHYTGPVE -HKFSPYAFN GGTVLAVAGE DFAIVASDTR 52
 Trematomus bernacchii --ML-SSQSY QDPGK--M ----- QDYHYSGPVE -HRFSPYSFN GGTVLAVAGE DFAIVASDTR 52
 Notothenia coriiceps_XP_010781254 --ML-SSQSY QDPGK--M ----- KDYHYSGPVE -HRFSPYSFN GGTVLAVAGE DFAIVASDTR 52
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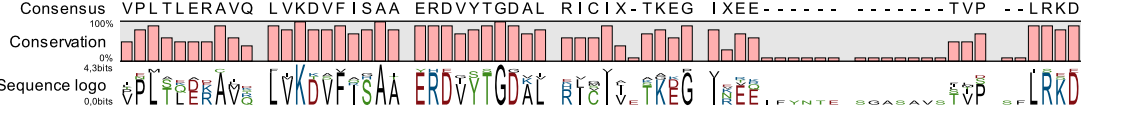
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 Caenorhabditis elegans_NP_498806 MTQNDINILT RDAEKIQILN DNIILTTS GF VGDVLOKKV LQSR LHKYRF DYRSDMSVD CAELSRNLY 140
 Arabidopsis thaliana_NP_191641 MSTG-YSILS RDYSKTHKLA DRAVLSSSGF QADV KALQKV LKSRHLIQH QHNKQMSCPA MAQLLSNTLY 103
 Xenopus laevis_NP_001080435 LSEG-YSIHS RNTPKCYKLT DKTVIGCTGF HADCLLTKI IEARLKMYKH SNNKTMTSGA IAAMLSTILY 123
 Mus musculus_NP_035315 LSEG-FSIIH RDSPKCYKLT DKTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKAMTTGA IAAMLSTILY 124
 Homo sapiens_NP_002784 LSEG-FSIIH RDSPKCYKLT DKTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKAMTTGA IAAMLSTILY 125
 Danio rerio_NP_001003889 LSEG-YSIHS RDSPKCYKLT DTTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKMTSGA IAAMLSTILY 121
 Oreochromis niloticus_XP_003454565 LSEG-YSIHS RDSPKCYKLT DTTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKTMTSGA IAAMLSTILY 121
 Trematomus bernacchii LSEG-YSIHS RDSPKCYKLT DTTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKTMTSNA IAAMLSTILY 121
 Notothenia coriiceps_XP_010781254 LSEG-YSIHS RDSPKCYKLT DTTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKTMTSNA IAAMLSTILY 121
 Consensus LSEG-YSIHS RDSPKCYKLT DXTVIGCSGF HGDCLLTKI IEARLKMYKH SNNKTMTSGA IAAMLSTILY



Drosophila melanogaster_NP_652031 SYR-ESLLAG LIVAGWDEQR GGQVYSIPLG GMLTRESCTI GSGSSSFIY G F-----VREHYR 159
 Caenorhabditis elegans_NP_498806 YRRFFPYTYG AILAGIDEHG KGAVFSYDPI GCITERLGYSA SGAAPMIIIP FLDCQIGHVT ---LSEGYR 207
 Arabidopsis thaliana_NP_191641 FKRFFPYTAF NVLGGDEEG KGCVFYDADF GSYERVYGA QSGSTLIMP FLDNQIKSPS PLLLPKODSN 173
 Xenopus laevis_NP_001080435 SRRFFPYVYV NIIGLDEEG KGAVYSFDPV GSYQRDAYKA GGSASAMLQP FLDNQIGFKN ----MQNVEQ 189
 Mus musculus_NP_035315 SRRFFPYVYV NIIGLDEEG KGAVYSFDPV GSYQRDSFKA GGSASAMLQP LLDNQIGFKN ----MQNVEH 190
 Homo sapiens_NP_002784 SRRFFPYVYV NIIGLDEEG KGAVYSFDPV GSYQRDSFKA GGSASAMLQP LLDNQIGFKN ----MQNVEH 191
 Danio rerio_NP_001003889 GRRFFPYVYV NIIGLDEEG RGAVYSFDPV GSYQRDTYKA GGSASAMLQP LLDNQIGFKN ----MENVEH 187
 Oreochromis niloticus_XP_003454565 SRRFFPYVYV NIIGLDEEG KGAVYSFDPV GSYQRDTYKA GGSASAMLQP LLDNQIGFKN ----MEGVEH 187
 Trematomus bernacchii GRRFFPYVYV NIIGLDEHG KGAVYSFDPV GSYQRDTYKA GGSASAMLQP LLDNQIGFKN ----MEGVQH 187
 Notothenia coriiceps_XP_010781254 GRRFFPYVYV NIIGLDEHG KGAVYSFDPV GSYQRDTYKA GGSASAMLQP LLDNQIGFKN ----MEGVQH 187
 Consensus SRRFFPYVYV NIIGLDEEG KGAVYSFDPV GSYQRDTYKA GGSASAMLQP LLDNQIGFKN ---MEXVEH



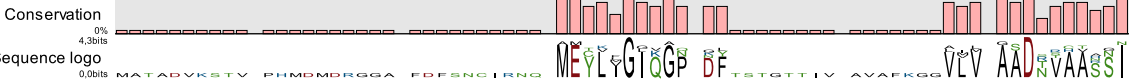
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 Caenorhabditis elegans_NP_498806 PELTDRALIS LMKDSFRGAA EREISTGDKI HLYIAEAGK P VVVK-----FLP --RED 258
 Arabidopsis thaliana_NP_191641 TPSEAEAVD LVKTVFASAT ERDIYTGDKL EIMIL-KADG IKTE-----LMD --LRKD 223
 Xenopus laevis_NP_001080435 LPLTLEKALK LKDVFI SAA ERDVYTGDA L HSIIV-TKD G VREE-----SIS --LRKD 239
 Mus musculus_NP_035315 VPLTDRAMR LVKDVFI SAA ERDVYTGDA L RLCIV-TKE G IREE-----TVP --LRKD 240
 Homo sapiens_NP_002784 VPLSADRMR LVKDVFI SAA ERDVYTGDA L RLCIV-TKE G IREE-----TVP --LRKD 241
 Danio rerio_NP_001003889 VPLTQEKAMQ LVKDVFI SAA ERDVYTGDA L KVICIV-SKE G IREE-----TVP --LRKD 237
 Oreochromis niloticus_XP_003454565 VPLTKDKAMQ LVKDVFI SAA ERDVYTGDA L RLCIV-TKE G INEE-----TVP --LRKD 237
 Trematomus bernacchii VPLTQERAVQ LVKDVFI SAA ERDVYTGDA L RLCIV-TKE G INEQ-----TVP --LRKD 237
 Notothenia coriiceps_XP_010781254 VPLSQRAMQ LVKDVFI SAA ERDVYTGDA L RLCIV-TKE G INEQ-----TVP --LRKD 237
 Consensus VPLTLERAVQ LVKDVFI SAA ERDVYTGDA L RLCIV-TKE G IXEE-----TVP --LRKD



	1	2	3	4	5	6	7	8	9	10
Drosophila melanogaster_NP_652031	1	15,02	21,25	21,26	21,57	21,09	19,84	21,83	21,83	21,83
Caenorhabditis elegans_NP_498806	2	41	35,25	36,82	37,98	36,43	37,21	37,21	38,76	38,37
Arabidopsis thaliana_NP_191641	3	51	92	42,80	43,03	43,27	44,40	44,40	43,15	43,57
Xenopus laevis_NP_001080435	4	54	95	104	78,33	77,18	79,17	80,42	78,75	78,33
Mus musculus_NP_035315	5	55	98	105	188	93,36	81,67	82,50	81,67	80,83
Homo sapiens_NP_002784	6	54	94	106	186	225	79,67	80,91	80,50	80,50
Danio rerio_NP_001003889	7	50	96	107	190	196	192	90,72	88,61	88,19
Oreochromis niloticus_XP_003454565	8	55	96	107	193	198	195	215	91,98	91,56
Trematomus bernacchii	9	55	100	104	189	196	194	210	218	98,73
Notothenia coriiceps_XP_010781254	10	55	99	105	188	194	194	209	217	234

Figure S1. MUSCLE alignment of proteasome subunit beta 1 amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).

Caenorhabditis elegans_NP_493271	MATADVKSTV	PHMDMDRGGG	EDFSNCLRNG	AMCKMGGKAP	KLTSTGTTIV	AVAFKGGLVM	GADSRATAGN	70
Arabidopsis thaliana_NP_193216	-----	-----	-----	MECVFGLVGN	GF-----	-----	ADTSAVHSI	25
Drosophila melanogaster_NP_609804	-----	-----	-----	METLGLKGP	DF-----	-----	AADTTHARS	25
Homo sapiens_NP_002785	-----	-----	-----	MEYLVIGIQGP	DY-----	-----	ASDRVAASNI	25
Mus musculus_NP_036100	-----	-----	-----	MEYLVIGIQGP	DY-----	-----	ASDRVAASNI	25
Xenopus laevis_NP_001084761	-----	-----	-----	MEYLVIGIQGN	DF-----	-----	AADTYCANSI	25
Trematomus bernacchii	-----	-----	-----	MEYLVIGIQGP	NF-----	-----	AADNVAASSI	25
Notothenia coriiceps_XP_010789577	-----	-----	-----	MEYLVIGIQGP	DF-----	-----	AADNVAASSI	25
Danio rerio_NP_001002609	-----	-----	-----	MEYLVIGIQGP	DF-----	-----	AADNVAASSI	25
Oreochromis niloticus_XP_003447226	-----	-----	-----	MEYLVIGIQGP	DF-----	-----	AADNVAASSI	25
Consensus	-----	-----	-----	MEYLVIGIQGP	DF-----	-----	AADNVAASSI	



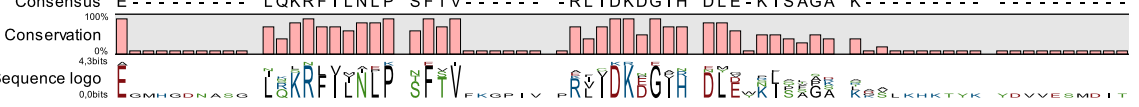
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Arabidopsis thaliana_NP_193216	LHKNKEDKI	MTLDSSHKLV	ASGEPGDRVQ	FTEYVOKNVS	LYQFRNGLP	STAAAANFTR	GELATALR-K	94
Drosophila melanogaster_NP_609804	IVMKEDQNKI	HKVSDSLLIS	TVGEGDTEQQ	FTEFISKNI	LYKMRNGYDL	SPRESAHFTR	KNLAEYLRSS	95
Homo sapiens_NP_002785	VQMKDDHDKM	FKMSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPTAAANFTR	RNLADCLRSS	95
Mus musculus_NP_036100	VQMKDDHDKM	FKMSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPTAAANFTR	RNLADCLRSS	95
Xenopus laevis_NP_001084761	IQMKHDQDKM	FKLSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPTAAANFTR	RNLADYLRSS	95
Trematomus bernacchii	IQMKHDQDKM	FKLSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPSAAANFTR	RNLADYLRSS	95
Notothenia coriiceps_XP_010789577	IQMKHDQDKM	FKLSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPSAAANFTR	RNLADYLRSS	95
Danio rerio_NP_001002609	IQMKHDQDKM	FKLSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPSAAANFTR	RNLADYLRSS	95
Oreochromis niloticus_XP_003447226	IQMKHDQDKM	FKLSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPAAAANFTR	RNLADYLRSS	95
Consensus	IQMKHDQDKM	FKLSEKILL	CVGEGDITVQ	FAEYIQKNVQ	LYKMRNGYEL	SPXAAANFTR	RNLADYLRSS	



Caenorhabditis elegans_NP_493271	GAYV--LILG	GVDPTGPH	YMCANGTMM	AFPFTAQSG	SYAATILER	DFKVDMTKDE	AELVQRALE	206
Arabidopsis thaliana_NP_193216	NPYSVNILLMA	GYDKEAGASL	YYIDYATLH	KVDKGAFIGY	SYFSLSTMDR	HYRSDMSVEE	AIELVQKCL	164
Drosophila melanogaster_NP_609804	TPYQVFVFA	GYDPNAGPEL	TFIDYLANA	PNNYAGHG	AEASSIYDR	YWHPNITQAE	AYDVEKKCIA	165
Homo sapiens_NP_002785	TPYHVNLLA	GYDEHGPAAL	YYMDYAAAL	KAPFAAHGY	AFLLTSLILDR	YYTPTISRER	AVELLRKLE	165
Mus musculus_NP_036100	TPYHVNLLA	GYDEHGPAAL	YYMDYAAAL	KAPFAAHGY	AFLLTSLILDR	YYTPTISRER	AVELLRKLE	165
Xenopus laevis_NP_001084761	TPYHVNLLA	GYDEHAGPSS	YYMDYLSALA	KTFAAAHGY	AYLLTSLILDR	YYKPDLTRED	AVELLRKCL	165
Trematomus bernacchii	TPYHVNLLA	GYDETGGPGL	YYMDYSSLS	KAPFAAHGY	AFLLTSLILDR	HYKPDLTREE	AVDLLKCCIE	165
Notothenia coriiceps_XP_010789577	TPYHVNLLA	GYDETGGPGL	YYMDYSSLS	KAPFAAHGY	AYLLTSLILDR	HYKPDLTREE	AVDLLKCCIE	165
Danio rerio_NP_001002609	TPYHVNLLA	GYDETGGPGL	YYMDYLSALA	KAPFAAHGY	AFLLTSLILDR	YYKPDLTREE	AVDLLKCCLE	165
Oreochromis niloticus_XP_003447226	TPYHVNLLA	GYDDTGGPGL	YYMDHSSLS	KAPFAAHGY	AYLLTSLILDR	YYRPPLSRDE	AVDLLKCCVE	165
Consensus	TPYHVNLLA	GYDETGGPGL	YYMDYLSALA	KAPFAAHGY	AYLLTSLILDR	YYKPDLTREE	AVDLLKCCIE	



Caenorhabditis elegans_NP_493271	AGMHGDNASG	NSLNLVITEP	SETVFKGPIV	PEFCKRPEPN	DLVYKFAQGA	TKVLKHKTYK	YDVVESMDIT	276
Arabidopsis thaliana_NP_193216	E-----	IRSRLVIAPP	NFVI-----	-KLVDKDGAR	EYGWRISTAD	A-----	-----	199
Drosophila melanogaster_NP_609804	E-----	IQKRFVNNLK	NFTV-----	-AMVDKDGVR	DLE-PIISAAS	LAA-----	-----	201
Homo sapiens_NP_002785	E-----	LQKRFILNLP	TFSV-----	-RLIDKNGIH	DLD-NISFPK	QGS-----	-----	201
Mus musculus_NP_036100	E-----	LQKRFILNLP	TFSV-----	-RVIDKDGIH	NLE-NIAFPK	RDS-----	-----	201
Xenopus laevis_NP_001084761	E-----	LQKRFILNLP	SFTV-----	-RVIDKDGIH	DLD-SIPASS	I-----	-----	199
Trematomus bernacchii	E-----	LRKRFILNLP	SFTV-----	-RLIDKEGTH	DLE-KLCSGA	K-----	-----	199
Notothenia coriiceps_XP_010789577	E-----	LRKRFILNLP	SFTV-----	-RLIDKEGTH	DLE-KLSSGA	K-----	-----	199
Danio rerio_NP_001002609	E-----	LNRKFILNLP	SFTV-----	-RLIDKDGTH	DME-KLPYGR	K-----	-----	199
Oreochromis niloticus_XP_003447226	E-----	LKRRFILNLP	SFTV-----	-RLIDKEGTH	DLE-KLTLGA	K-----	-----	199
Consensus	E-----	LQKRFILNLP	SFTV-----	-RLIDKDGTH	DLE-KISAGA	K-----	-----	

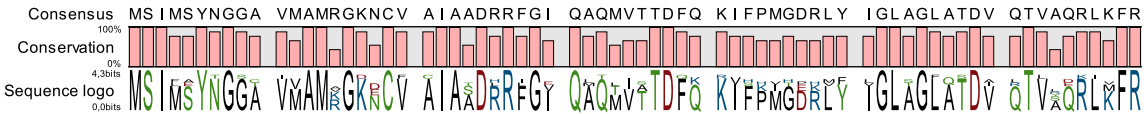


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- Arabidopsis thaliana_NP_193216 - 199
- Drosophila melanogaster_NP_609804 - 201
- Homo sapiens_NP_002785 - 201
- Mus musculus_NP_036100 - 201
- Xenopus laevis_NP_001084761 - 199
- Trematomus bernacchii - 199
- Notothenia coriiceps_XP_010789577 - 199
- Danio rerio_NP_001002609 - 199
- Oreochromis niloticus_XP_003447226 - 199
- Consensus -
- Conservation 100%
- 0%
- 4.3bits
- Sequence logo 0.0bits

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Caenorhabditis elegans_NP_493271	1	14,23	14,95	14,95	14,59	16,73	19,22	19,93	18,86	19,22
Arabidopsis thaliana_NP_193216	2	40	41,09	43,56	43,07	47,00	44,50	45,00	45,50	45,00
Drosophila melanogaster_NP_609804	3	42	83	49,75	50,25	55,72	52,24	53,73	53,23	51,74
Homo sapiens_NP_002785	4	42	88	100	96,52	81,59	77,11	77,11	81,09	78,61
Mus musculus_NP_036100	5	41	87	101	194	81,59	77,11	76,62	81,59	78,61
Xenopus laevis_NP_001084761	6	47	94	112	164	164	81,41	82,41	85,43	82,91
Trematomus bernacchii	7	54	89	105	155	155	162	97,49	90,45	89,45
Notothenia coriiceps_XP_010789577	8	56	90	108	155	154	164	194	90,45	90,45
Danio rerio_NP_001002609	9	53	91	107	163	164	170	180	180	92,96
Oreochromis niloticus_XP_003447226	10	54	90	104	158	158	165	178	180	185

Figure S2. MUSCLE alignment of proteasome subunit beta 2 amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).

Caenorhabditis elegans_NP_494913 MS MSYTG GT VVAMAGDECY CIAASDLRI GE QMTTIA TDQK KVHKVTDK VY VGLAG EQSDA RTVLEKIMFR 70
 Arabidopsis thaliana_NP_565156 MS FEYNGSA VVAMGKNCV AIASDRRLGV QLTIA TD FQ RISK HDH LF IGLSG IATDV QTLYQR LVFR 70
 Drosophila melanogaster_NP_649858 MS LAYNGGC VVAMRGKDCV AIA TDH RFG QAQT I STDFK KV FH IGPRMF IGLTG QTDI LTVRDR LMFR 70
 Homo sapiens_NP_002786 MS MSYNGGA VMAMGKNCV AIAADR RFGI QAQMVT TDFQ KIFPMGDR LY IGLAG IATDV QTVAQR LKFR 70
 Mus musculus_NP_036101 MS MSYNGGA VMAMGKNCV AIAADR RFGI QAQMVT TDFQ KIFPMGDR LY IGLAG IATDV QTVAQR LKFR 70
 Xenopus laevis_NP_001088741 MS MSYNGGA VMAMGKDCV AIAADR RFGI QAQMVT TDFQ KIFPMGER LY IGLAG IATDV QTVAQR LKFR 70
 Danio rerio_NP_001123295 MS MSYNGGA VMAMRGKNCV AIAADR RFGI QAQLVTTDFQ KIFPMGER LY IGLAG IATDV QTVSQR LKFR 70
 Trematodus bernacchii MS MSYNGGA VMAMRGKNCV AIAADR RFGI QAQMVT TDFQ KIFPMGDR LY IGLAG IATDV QTVAQR LKFR 70
 Oreochromis niloticus_XP_003448021 MS MSYNGGA VMAMRGKNCV AIAADR RFGI QAQMVT TDFQ KIFPMGDR LY IGLAG IATDV QTVAQR LKFR 70



Caenorhabditis elegans_NP_494913 KNLYELRENR NIKPQVLSM ISNLAYQHRF GSYFTEP LVA GLD -DTNKPY ICCMDT I GCV SAPRDF VAVG 139
 Arabidopsis thaliana_NP_565156 HKLYQLREER DMKPE T FASL VSAILYKRF GPFLCQPVIA GLG -DDNKPF ICTMBS GAK ELAKDF VVSG 139
 Drosophila melanogaster_NP_649858 KNLYETRENR EMCPK PFSAM MSSFLYEHRF GPYFTEP VVA GLD PKTME PF ICNMDL I GCP NAPDDF VVAG 140
 Homo sapiens_NP_002786 LNLYELKEGR QIKP Y T LMSM VANLLYKRF GPYYTEP VIA GLD PKT FKP F ICSDL I GCP MVTDDF VVSG 140
 Mus musculus_NP_036101 LNLYELKEGR QIKP Y T LMSM VANLLYKRF GPYYTEP VIA GLD PKT FKP F ICSDL I GCP MVTDDF VVSG 140
 Xenopus laevis_NP_001088741 LNLYELKEGR QIKP K T FMSM VANLLYERRF GPYYTEP VIA GLD PKT FQPF ICSDL I GCP METEDF VVSG 140
 Danio rerio_NP_001123295 LNLYELKEGR QIKP R T FMSM VS NLLYERRF GPYYTEP VIA GLD PKT FEP F ICSDL I GCP MVTEDF VVSG 140
 Trematodus bernacchii LNLYELKEGR QIKP K T FMSM VS NLLYKRF GPYYTEP VIA GLD PKTSEPF ICSDL I GCP MVTEDF VVSG 140
 Oreochromis niloticus_XP_003448021 LNLYELKEGR QIKP K T FMSM VS NLLYERRF GPYYTEP VIA GLD PKT FEP F ICSDL I GCP MVTDDF VVSG 140



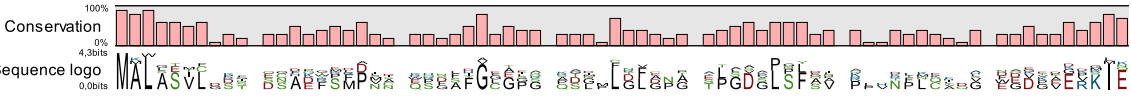
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 Arabidopsis thaliana_NP_565156 TASESLYGAC EAMFKPDMEA EELFETISQA LLSVDRDCL SGWGGHVYV TPKEVKERI KGRMD 204
 Drosophila melanogaster_NP_649858 TC AEQLY GMC ETLWKPDLEP DQLFETISQA IYNAFDRDAM SGWGATVY I EKDK I TERTL KTRMD 205
 Homo sapiens_NP_002786 TC AEQMY GMC ESLWEPNDMP DHLFETISQA MLNAVDRDAV SGMGVVHV I EKDK I TTRTL KARMD 205
 Mus musculus_NP_036101 TCSEQMY GMC ESLWEPNDMP EHLFETISQA MLNAVDRDAV SGMGVVHV I EKDK I TTRTL KARMD 205
 Xenopus laevis_NP_001088741 TCSEQMY GMC ESLWEPDMEP EDLFETISQA MLNAVDRDAV SGMGVVHV I EKDK I TTRTL KARMD 205
 Danio rerio_NP_001123295 TCSEQMY GMC ESLWEPDMP EDLFETISQA MLNAVDRDAV SGMGVVHV I EKDK I TTRTL KARMD 205
 Trematodus bernacchii TCSEQMY GMC ESLWEPDMEP EDLFETISQA MLNAVDRDAV SGMGVVHV I EKDK I TTRTL KARMD 205
 Oreochromis niloticus_XP_003448021 TCSEQMY GMC ESLWEPDMEP EDLFETISQA MLNAVDRDAV SGMGVVHV I EKDK I TTRTL KARMD 205



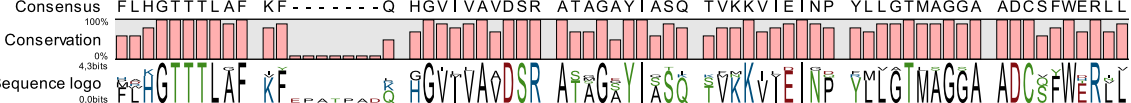
	1	2	3	4	5	6	7	8	9
Caenorhabditis elegans_NP_494913	1	44,61	55,12	51,22	50,73	48,29	50,73	49,76	49,76
Arabidopsis thaliana_NP_565156	2	91	51,22	56,10	57,56	57,07	57,56	58,54	58,54
Drosophila melanogaster_NP_649858	3	113	105	63,90	62,44	63,90	64,88	64,88	66,34
Homo sapiens_NP_002786	4	105	115	131	98,54	91,22	90,24	91,22	93,17
Mus musculus_NP_036101	5	104	118	128	202	92,68	91,71	92,68	93,66
Xenopus laevis_NP_001088741	6	99	117	131	187	190	94,15	93,66	94,63
Danio rerio_NP_001123295	7	104	118	133	185	188	193	95,12	95,12
Trematomus bernacchii	8	102	120	133	187	190	192	195	96,10
Oreochromis niloticus_XP_003448021	9	102	120	136	191	192	194	195	197

Figure S3. MUSCLE alignment of proteasome subunit beta 3 amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).

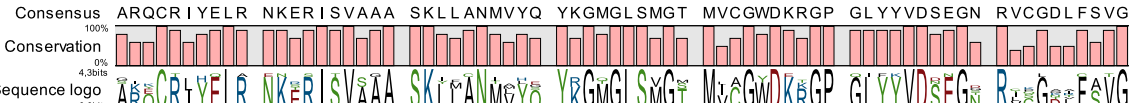
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 Arabidopsis thaliana_NP_172765 M K L - - - - D T S G F E T S M P M I - - - - - G F G S S S D M - D - - - - E L S S Y P S F D P - - - R T K E F D G F Q K K A K D M L K 53
 Xenopus laevis_NP_001084323 M A L L T M C G P T Q S H D W R M P L - - - - - Y G G T I S P T I P F R V C N T E L A M P P G Y Q P A - - K F L Q H - L E E G V D D V K I E 62
 Mus musculus_NP_035316 M A L A S V L - - - - - Q R P M P V N O H G F F G I G G G A D L - D L G P G S P G D G L S L A A P - - - - - S W G V P E E P R I E 55
 Homo sapiens_NP_002788 M A L A S V L - - - - - E R L P L Y N Q R G F F G I G G R A D L - D L G P G S L S D G L S L A A P - - - - - G W G V P E E P G I E 55
 Danio rerio_NP_571226 M A L S S L L - R N E S A D R S D P I D R S F A H G G L N Q T N - G F G - A A L G D S P N F A V K - T - - - - G E D D E P E R K I E 61
 Oreochromis niloticus_XP_003457456 M A L A S V L - S G D S A D F S F D S S Q S F A F G G G P G S G - L G F D - G T P G D G L S F S V K - - N P L C A - G D D D G V E R K I E 64
 Trematomus bernacchii M A L A S V L - S S D C A K F S F D N C E P D S F G C A P G Q S G - L G F D - A T P G D G L S F S V R - - N P L C A - V E E D G V E R K I E 64
 Notothenia coriiceps_XP_010781265 M A L A S V L - S S D C A K F S F D N C E P D S F G C A P G Q S G - L G F D - A T P G D G L S F S V R - - N P L C A - V E E D G V E R K I E 64



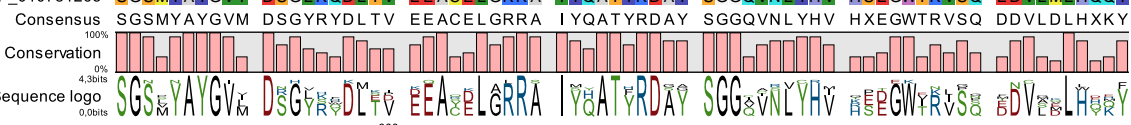
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 Arabidopsis thaliana_NP_172765 HAKGTTLAF LF-----K GGVMVAADSR ASMGGYISSQ SVKVIENP YMLGTMAGGA ADCQVWHRNL 116
 Xenopus laevis_NP_001084323 PWHGTTLAF KF-----Q HGVI VAVDSR ASAGSYSTI KFNKVIENP YLLGTMSSA ADCQYWERLL 125
 Mus musculus_NP_035316 M L H G T T T L A F K F ----- L H G V I V A A D S R A T A G A Y I A S Q T V K K V I E I N P Y L L G T M A G G A A D C S F W E R L L 118
 Homo sapiens_NP_002788 M L H G T T T L A F K F ----- R H G V I V A A D S R A T A G A Y I A S Q T V K K V I E I N P Y L L G T M A G G A A D C S F W E R L L 118
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 Oreochromis niloticus_XP_003457456 F L H G T T T L A F K F ----- Q H G V I V A A D S R A T A G A Y I A S Q T V K K V I E I N P Y L L G T M A G G A A D C S F W E R L L 127
 Trematomus bernacchii F L H G T T T L A F K F ----- Q H G V I V A A D S R A T A G A Y I A S Q T V K K V I E I N P Y L L G T M A G G A A D C S F W E R L L 127
 Notothenia coriiceps_XP_010781265 F L H G T T T L A F K F ----- Q H G V I V A A D S R A T A G A Y I A S Q T V K K V I E I N P Y L L G T M A G G A A D C S F W E R L L 127



Caenorhabditis elegans_NP_493558 AKYCTLYELR E K T S I T V S A A S K Y F A N T L Y G Y R G Q G L S V G S M V A G Y D K K G P Q I F K V D S E G D R C Q L K V C S V G 200
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 Arabidopsis thaliana_NP_172765 G L K R L H E L A N K R R I S V S G A S K L L A N M L Y S Y R G M G L S M G T M I A G W D E T G P G L Y Y D S E G G R L K G D R F S V G 186
 Xenopus laevis_NP_001084323 A K E C R L Y Q L R N N S R I S V S A A S K L M C N M L Q Y R G T G L S V G S M I C G W D K K G P G L Y Y D D N G T R L C G D I F S T G 195
 Mus musculus_NP_035316 A R Q C R I Y E L R N K E R I S V A A A S K L L A N M V Y Q Y K G M G L S M G T M I C G W D K R G P G L Y Y D S E G N R I S G T A F S V G 188
 Homo sapiens_NP_002788 A R Q C R I Y E L R N K E R I S V A A A S K L L A N M V Y Q Y K G M G L S M G T M I C G W D K R G P G L Y Y D S E G N R I S G A T F S V G 188
 Danio rerio_NP_571226 A R Q C R I Y E L R N K E R I S V A A A S K L L A N M V Y Q Y K G M G L S M G T M V C G W D K R G P G L Y Y D S E G N R V C G D L F A V G 194
 Oreochromis niloticus_XP_003457456 A R Q C R I Y E L R N K E R I S V A A A S K L L A N M V Y Q Y K G M G L S M G T M V C G W D K R G P G L Y Y D S E G N R V C G D L F A V G 197
 Trematomus bernacchii A R Q C R I Y E L R N K E R I S V A A A S K L L A N M V Y Q Y K G M G L S M G T M V C G W D K R G P G L Y Y D S E G N R V C G D L F A V G 197
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 Drosophila melanogaster_NP_652014 S G S Y A Y G V L D S G Y H W D L E D K E A Q E L G R R A Y H A T F R D G A S G G I R V Y H I K E D G W N I S N T D C M E L H Y M Y 272
 Arabidopsis thaliana_NP_172765 S G S P Y A Y G V L D S G Y K Y D M S V E E A S E L A R R S Y H A T F R D G A S G G M A S V Y H I G P E G W T K L S G D D V G E L H Y M Y 256
 Xenopus laevis_NP_001084323 S G N S Y A Y G V M D S G Y R F D L T P E E A Y D L G R R A I Y A T H R D A Y S G G C V N L Y H M K E D G W V K I G Q F D V S D L L H K F 265
 Mus musculus_NP_035316 S G S Y A Y G V M D R G Y S Y D L K V E E A Y D L A R R A Y Q A T Y R D A Y S G G A N L Y H V R E D G W I R V S S D N V A D L H D K Y 258
 Homo sapiens_NP_002788 S G S Y A Y G V M D R G Y S Y D L E V E E A Y D L A R R A Y Q A T Y R D A Y S G G A N L Y H V R E D G W I R V S S D N V A D L H E K Y 258
 Danio rerio_NP_571226 S G S M Y A Y G V M D S G L R H D L T I D E A C E L G R R A Y Q A T Y R D A Y S G G Q V N L Y R V H S E G W E R V S Q E D V L Q L H Q Q Y 264
 Oreochromis niloticus_XP_003457456 S G S M Y A Y G V M D S G V R H D L T V E E A C E L G R R A Y Q A T Y R D A Y S G G Q V N L Y H V H S E G W T R I S Q D D V L V L H H Q Y 267
 Trematomus bernacchii S G S M Y A Y G V I D S G L R Q D L T V E E A C E L G R R A Y Q A T Y R D A Y S G G Q V N L Y H V H S E G W T R V S Q E D V L V L H H Q Y 267
 Notothenia coriiceps_XP_010781265 S G S M Y A Y G V I D S G L R Q D L T V E E A C E L G R R A Y Q A T Y R D A Y S G G Q V N L Y H V H S E G W T R V S Q E D V L M L H Q Q Y 267



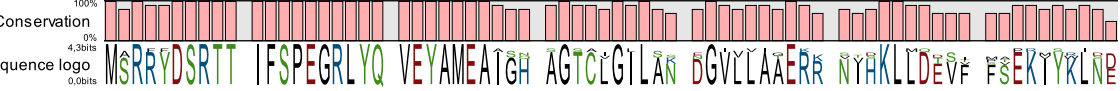
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 Mus musculus_NP_035316 - - - - - S S S V P - - - - - 264
 Homo sapiens_NP_002788 - - - - - S G S T P - - - - - 263
 Danio rerio_NP_571226 - - - - - Q S E K A - - - - - 269
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 Notothenia coriiceps_XP_010781265 - - - - - K S Q A - - - - - 271



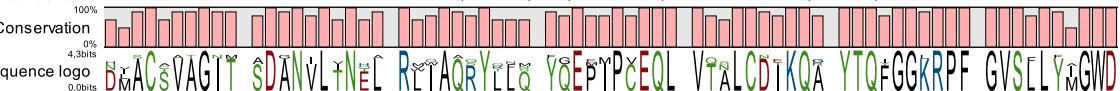
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Arabidopsis thaliana_NP_172765	3	117	138	45,96	50,87	51,92	49,30	50,35	49,30	49,30
Xenopus laevis_NP_001084323	4	104	131	131	52,90	52,54	55,43	55,80	53,62	53,26
Mus musculus_NP_035316	5	103	140	146	146	92,80	69,74	71,17	70,44	70,44
Homo sapiens_NP_002788	6	102	140	149	145	245	69,63	70,33	68,86	68,86
Danio rerio_NP_571226	7	106	145	141	153	189	188	80,51	80,88	80,51
Oreochromis niloticus_XP_003457456	8	106	151	144	154	195	192	219	88,93	89,30
Trematomus bernacchii	9	106	147	141	148	193	188	220	241	99,63
Notothenia coriiceps_XP_010781265	10	106	147	141	147	193	188	219	242	270

Figure S4. MUSCLE alignment of proteasome subunit beta 5 amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).

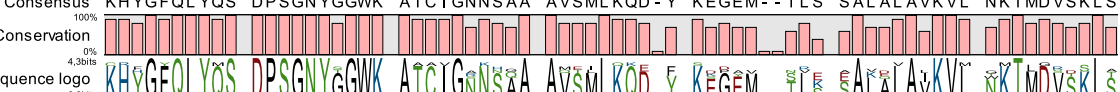
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 Xenopus laevis_NP_001089811
 Mus musculus_NP_036096
 Homo sapiens_NP_002780
 Notothenia coriiceps_XP_010770288
 Trematomus bernacchii
 Oreochromis niloticus_XP_003450834
 Danio rerio_NP_999862



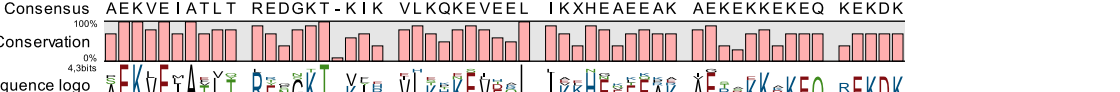
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 Arabidopsis thaliana_NP_188850
 Caenorhabditis elegans_NP_491520
 Xenopus laevis_NP_001089811
 Mus musculus_NP_036096
 Homo sapiens_NP_002780
 Notothenia coriiceps_XP_010770288
 Trematomus bernacchii
 Oreochromis niloticus_XP_003450834
 Danio rerio_NP_999862



Drosophila melanogaster_NP_651843
 Arabidopsis thaliana_NP_188850
 Caenorhabditis elegans_NP_491520
 Xenopus laevis_NP_001089811
 Mus musculus_NP_036096
 Homo sapiens_NP_002780
 Notothenia coriiceps_XP_010770288
 Trematomus bernacchii
 Oreochromis niloticus_XP_003450834
 Danio rerio_NP_999862



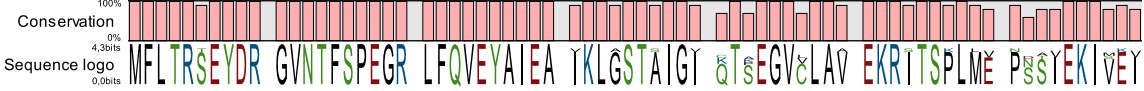
Drosophila melanogaster_NP_651843
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 Caenorhabditis elegans_NP_491520
 Xenopus laevis_NP_001089811
 Mus musculus_NP_036096
 Homo sapiens_NP_002780
 Notothenia coriiceps_XP_010770288
 Trematomus bernacchii
 Oreochromis niloticus_XP_003450834
 Danio rerio_NP_999862



	1	2	3	4	5	6	7	8	9	10
Drosophila melanogaster_NP_651843	1	44,88	50,78	50,76	51,89	52,27	52,65	52,65	52,27	51,89
Arabidopsis thaliana_NP_188850	2	114	55,34	56,49	56,11	56,11	55,73	55,73	56,11	56,49
Caenorhabditis elegans_NP_491520	3	130	140	62,84	63,22	63,60	62,84	63,22	62,84	62,45
Xenopus laevis_NP_001089811	4	134	148	164	96,55	96,93	93,87	93,49	95,40	95,40
Mus musculus_NP_036096	5	137	147	165	252	98,85	93,87	93,49	95,79	95,79
Homo sapiens_NP_002780	6	138	147	166	253	258	93,10	92,72	95,79	96,17
Notothenia coriiceps_XP_010770288	7	139	146	164	245	245	243	99,62	96,93	95,79
Trematomus bernacchii	8	139	146	165	244	244	242	260	96,55	95,40
Oreochromis niloticus_XP_003450834	9	138	147	164	249	250	250	253	252	98,85
Danio rerio_NP_999862	10	137	148	163	249	250	251	250	249	258

Figure S5. MUSCLE alignment of proteasome subunit alpha 4 amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).

Caenorhabditis elegans_NP_492765 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA VKLGSTSGI KTSEGVLLAA EKRSTSKLMV NDAIEKISKV 70
 Arabidopsis thaliana_NP_188046 MFLTRTEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV KTKEGVVLA EKRITSPLE PSSVEKIMEI 70
 Drosophila melanogaster_NP_725669 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV CTPGVLAV EKRITSPLMV PSTVEKIVEI 70
 Mus musculus_NP_036097 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PSSIEKIVEI 70
 Homo sapiens_NP_002781 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PSSIEKIVEI 70
 Xenopus laevis_BAD42871 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PSSIEKIVEI 70
 Trematodus bernacchii MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PMSIEKIVEI 70
 Notothenia coriiceps_XP_01076620 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PMSIEKIVEI 70
 Danio rerio_NP_991271 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PSSIEKIVEI 70
 Oreochromis niloticus_XP_003441568 MFLTRSEYDR GVNTFSPEGR LFQVEYAIEA KLGSTAGV QTSEGVCLAV EKRITSPLME PSSIEKIVEI 70



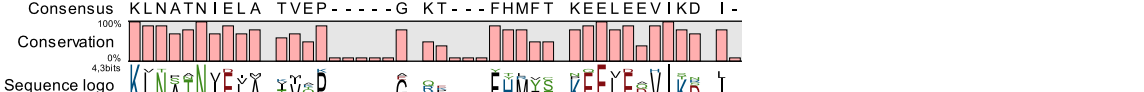
Caenorhabditis elegans_NP_492765 DQHIGVTFAG LIADARTLVE RAQIEAQNFW FTYNRKIRVE DYTQSVANLA LQFGDDVKA ---SMSRPF 137
 Arabidopsis thaliana_NP_188046 DDHIGCAMS G LIADARTLVE HARVEQNHW FSYGEPMTVE STTQALCDLA LRFGEFEE - ---SMSRPF 136
 Drosophila melanogaster_NP_725669 DKHIGCATSG LMADARTLIE RARVEQNHW FYNERMSIE SCQAVSTEA LQFGSDSD GAAAMS RPF 140
 Mus musculus_NP_036097 DAHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138
 Homo sapiens_NP_002781 DAHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138
 Xenopus laevis_BAD42871 DAHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138
 Trematodus bernacchii DAHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138
 Notothenia coriiceps_XP_01076620 DTHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138
 Danio rerio_NP_991271 DSHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138
 Oreochromis niloticus_XP_003441568 DSHIGCAMS G LIADAKTLID KARVETQNHW FTYNETMTVE SVTQAVSNLA LQFG EEDADP G - AMSRPF 138



Caenorhabditis elegans_NP_492765 VAMLFAGVDQ EGAKLFLHDP SGTFLDCKAK SIIGASDGA E QNLKEQYHDA LTIKELKMA LAILKQVME 207
 Arabidopsis thaliana_NP_188046 VSLILAGHDE NGPSLYYTD P SGTFWQCNAK AIGSGSEGAD SSLQEQFNKD ITLQEAETIA VSILKQVME 206
 Drosophila melanogaster_NP_725669 VAILFAGIEA GQPQLWHMDDP SGTFRHGAK AIGSGSEGAQ QNLQDLFRPD LTLDEAIDIS LTLKQVME 210
 Mus musculus_NP_036097 VALLFGGVDE KGPQLFHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKEAIKSS LTLKQVME 208
 Homo sapiens_NP_002781 VALLFGGVDE KGPQLFHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKEAIKSS LTLKQVME 208
 Xenopus laevis_BAD42871 VALLFGGAE KGPQLFHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKEAIKSS LTLKQVME 208
 Trematodus bernacchii VALLFGGVDE KGPQLYHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKDAIKSS LTLKQVME 208
 Notothenia coriiceps_XP_01076620 VALLFGGVDE KGPQLYHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKDAIKSS LTLKQVME 208
 Danio rerio_NP_991271 VALLFGGVDE KGPQLYHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKDAIKSS LTLKQVME 208
 Oreochromis niloticus_XP_003441568 VALLFGGVDE KGPQLYHMDP SGTFLVQCDAR AIGSASEGAQ SSLQEVYHKS MTLKDAIKSS LTLKQVME 208



Caenorhabditis elegans_NP_492765 KLNANVEVYVIKPTVDKGRPIGEFTRVSN EELDQVITS L - 248
 Arabidopsis thaliana_NP_188046 KVTNNVDIAKVAP - - - - A - - - - YHLYT PQEEAVISR L - 237
 Drosophila melanogaster_NP_725669 KLNSTNVEVM TMTK - - - - E RE - - - FYMFT KEVEEQH IKN IA 244
 Mus musculus_NP_036097 KLNATNIEA TVQP - - - - G QN - - - FHMFT KEEL EEV I KD I - 241
 Homo sapiens_NP_002781 KLNATNIEA TVQP - - - - G QN - - - FHMFT KEEL EEV I KD I - 241
 Xenopus laevis_BAD42871 KLNATNIEA TVEP - - - - G KK - - - FHYMC KEEL EEV I KD I - 241
 Trematodus bernacchii KLNATNIEA TVEP - - - - G KT - - - FHMFS KEEL EDV I KD I - 241
 Notothenia coriiceps_XP_01076620 KLNATNIEA TVEP - - - - G KT - - - FHMFS KEEL EDV I KD I - 241
 Danio rerio_NP_991271 KLNATNIEA TVEP - - - - G KT - - - FHMYS KEEL EDV I KD I - 241
 Oreochromis niloticus_XP_003441568 KLNATNIEA TVEP - - - - G KT - - - FHMYS KEEL EEV I KD I - 241



	1	2	3	4	5	6	7	8	9	10
Caenorhabditis elegans_NP_492765	1	52,82	55,95	60,64	60,24	60,24	59,84	59,84	59,84	60,64
Arabidopsis thaliana_NP_188046	2	131	61,07	68,05	67,63	67,63	67,22	67,22	68,46	68,05
Drosophila melanogaster_NP_725669	3	141	149	70,08	69,67	69,26	68,44	68,44	69,26	68,85
Mus musculus_NP_036097	4	151	164	171	99,59	96,27	94,61	94,61	96,27	96,27
Homo sapiens_NP_002781	5	150	163	170	240	95,85	94,19	94,19	95,85	95,85
Xenopus laevis_BAD42871	6	150	163	169	232	231	94,61	94,61	96,27	96,68
Trematomus bernacchii	7	149	162	167	228	227	228	100,00	97,10	97,10
Notothenia coriiceps_XP_010766620	8	149	162	167	228	227	228	241	97,10	97,10
Danio rerio_NP_991271	9	149	165	169	232	231	232	234	234	98,34
Oreochromis niloticus_XP_003441568	10	151	164	168	232	231	233	234	234	237

Figure S6. MUSCLE alignment of proteasome subunit alpha 5 amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).

Caenorhabditis elegans_NP_492360 - MNR Y DRA I T I F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K D C I V I G V E K K S I P A L Q D D R T I R K I H M I D D H 69
Drosophila melanogaster_NP_650910 M S S R Y G R A L T I F S P D G H L L Q V E Y A Q E A V R K G S T A V G V R G A N C V V L G V E K S S V S E M Q E D R T V R K I S M L D R H 70
Arabidopsis thaliana_NP_190694 - M A R Y D R A I T V F S P D G H L F Q V E Y A L E A V R K G N A A V G V R G T D T V V L A V E K K S T P K L Q D S R S A R K I V S E D N H 69
Xenopus laevis_NP_001081054 - - M S Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K E I V V L G V E K K S V A K L Q D E R T V R K I C A L D E N 68
Homo sapiens_NP_002783 - - M S Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G R D I V V L G V E K K S V A K L Q D E R T V R K I C A L D D N 68
Mus musculus_NP_036099 - - M S Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K D I V V L G V E K K S V A K L Q D E R T V R K I C A L D D N 68
Notothenia coriiceps_XP_010783619 M A A R Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K D I V V L G V E K K S V A K L Q E E R T V R K I C A L D E H 70
Trematomus bernacchii M A A R Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K D I V V L G V E K K S V A K L Q E E R T V R K I C A L D E H 70
Oreochromis niloticus_XP_003438172 M A A R Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K D I V V L G V E K K S V A K L Q E E R T V R K I C A L D E H 70
Danio rerio_NP_998331 M A A R Y D R A I T V F S P D G H L F Q V E Y A Q E A V K K G S T A V G V R G K D I V V L G V E K K S V A K L Q E E R T V R K I C A L D E H 70



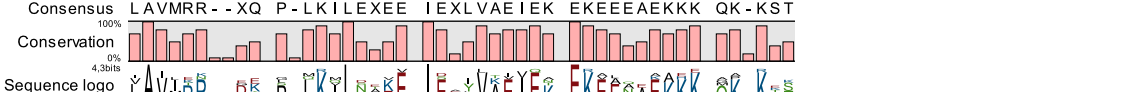
Caenorhabditis elegans_NP_492360 V M L A F A G L S A D A R V L V D R A R I E C Q S Y K L T E D P V T V A Y I S R Y I A N T K Q R F T Q S P G R R P F G I S M L I G G F D 138
Drosophila melanogaster_NP_650910 V A L A F A G L T A D A R I L I N R G Q V E C Q S H R L N F E N Q V T L E Y I T R Y L A Q L K Q K Y T Q C N G R R P F G I S C L I G G I D 139
Arabidopsis thaliana_NP_190694 I A L A C A G L K A D A R V L I N K A R I E C Q S H R L T V E D P V T V E Y I T R Y I A G L Q Q K Y T Q S G G V R P F G L S T L I V G F D P 139
Xenopus laevis_NP_001081054 V F M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A S L K Q R Y T Q S N G R R P F G I S A L I V G F D 137
Homo sapiens_NP_002783 V C M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A S L K Q R Y T Q S N G R R P F G I S A L I V G F D 137
Mus musculus_NP_036099 V C M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A S L K Q R Y T Q S N G R R P F G I S A L I V G F D 137
Notothenia coriiceps_XP_010783619 V C M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A T L K Q R Y T Q S N G R R P F G I S A L I V G F D 139
Trematomus bernacchii V C M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A T L K Q R Y T Q S N G R R P F G I S A L I V G F D 139
Oreochromis niloticus_XP_003438172 V C M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A T L K Q R Y T Q S N G R R P F G I S A L I V G F D 139
Danio rerio_NP_998331 V C M A F A G L T A D A R I V I N R A R V E C Q S H R L T V E D P V T V E Y I T R Y I A T L K Q R Y T Q S N G R R P F G I S A L I V G F D 139



Caenorhabditis elegans_NP_492360 H D G T P R L F K T E P S G A Y E Y E V A N A T G R G E K P V R E Y L E E Q Y S E E N T V D E A T T L K L V I K S L A Q V V P P G S Q N I E 208
Drosophila melanogaster_NP_650910 A D G S A R L F H T E P S G T F H E Y K A T A T G R W A N T V R E F F E K A Y S D H E V T T K C D A I K L A M R A L L E V T Q M S Q M R L E 209
Arabidopsis thaliana_NP_190694 Y T R I P A L Y Q T D P S G T F S A W K A N A T G R N S N S A N A T G R N S N S V R E F L E K N Y T E S A - - - G Q E T V K L A I R A L L E V V E S G G K N I E 206
Xenopus laevis_NP_001081054 F D G T P R L Y Q T D P S G T Y H A W K A N A I G R G A K S V R E F L E K H Y T D E A I E T D D T I K L V I K A L L E V V Q S G G K N I E 207
Homo sapiens_NP_002783 F D G T P R L Y Q T D P S G T Y H A W K A N A I G R G A K S V R E F L E K N Y T D E A I E T D D T I K L V I K A L L E V V Q S G G K N I E 207
Mus musculus_NP_036099 F D G T P R L Y Q T D P S G T Y H A W K A N A I G R G A K S V R E F L E K N Y T D D A I E T D D T I K L V I K A L L E V V Q S G G K N I E 207
Notothenia coriiceps_XP_010783619 D D G T P R L Y Q T D P S G T Y H A W K A N A I G R S A K T V R E F L E K N Y T D E A I A G D N E T I K L T I K A L L E V V Q S G G K N I E 209
Trematomus bernacchii D D G T P R L Y Q T D P S G T Y H A W K A N A I G R S A K T V R E F L E K N Y T D E A I A G D N E T I K L T I K A L L E V V Q S G G K N I E 209
Oreochromis niloticus_XP_003438172 Y D G T P R L Y Q T D P S G T Y H A W K A N A I G R S A K T V R E F L E K N Y T E E A I A G D N E A I K L A I K A L L E V V Q S G G K N I E 209
Danio rerio_NP_998331 Y D G T P R L Y Q T D P S G T Y H A W K A N A I G R S A K T V R E F L E K N Y T D E A I A S D N D A I K L A I K A L L E V V Q S G G K N I E 209

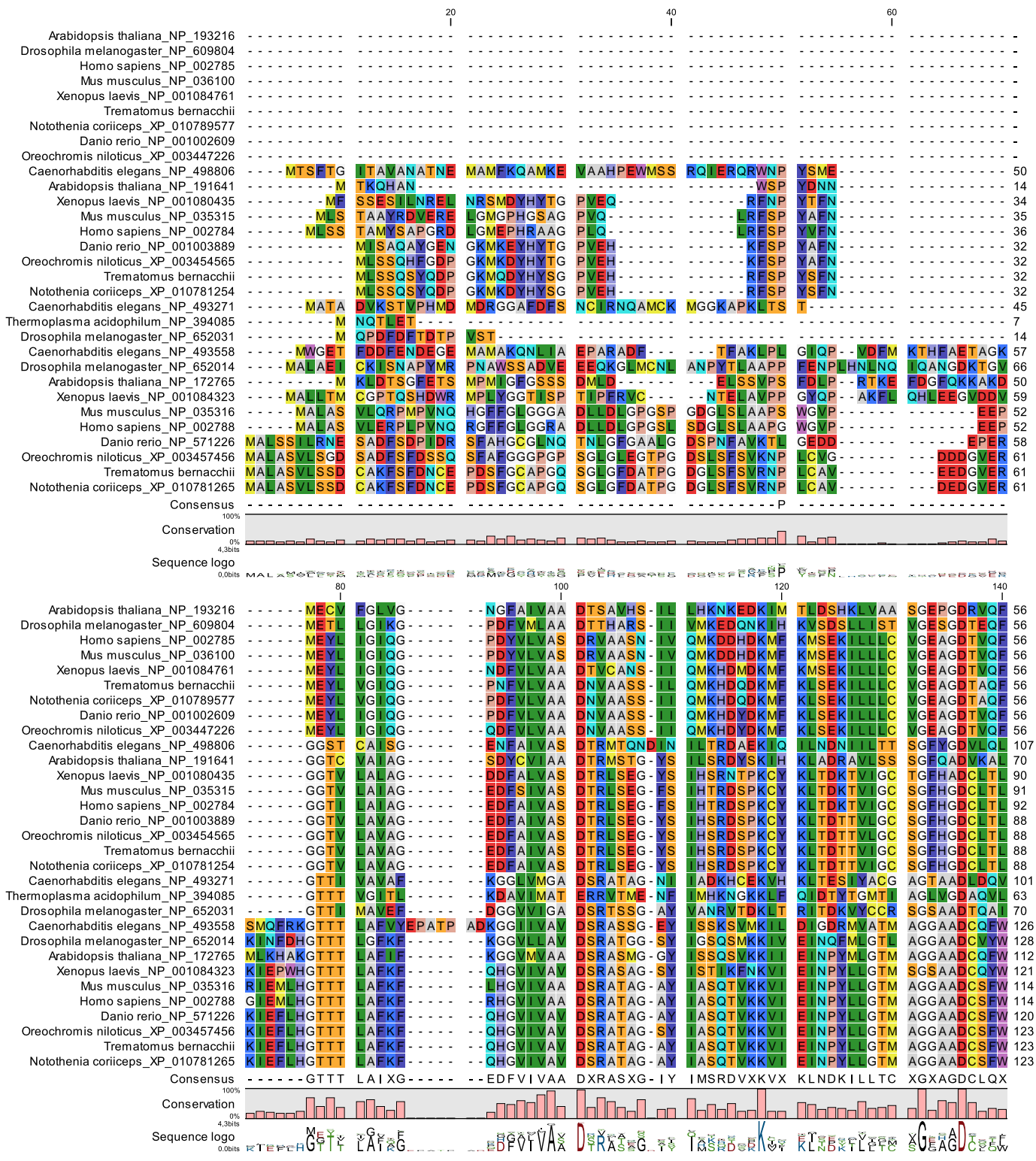


Caenorhabditis elegans_NP_492360 I A V M K K Y N D E L Q Q R V L S T E E I E A L L K V V E T E R V A A - E A E E A A S K K K 253
Drosophila melanogaster_NP_650910 V A V L E N - - G K P - M K M D S V Y S E I V K L V Q N E K E L Q A K A H K M K - R - - 249
Arabidopsis thaliana_NP_190694 V A V M T R - - E E G V L K Q E E E E I D I I V A E I E A E K A A A E A A K K G P A K E T 250
Xenopus laevis_NP_001081054 L A V M R R - - D Q P - L K T L N P E E I E R Y V A E I E K E K E E N - E K K K Q K - K T T 248
Homo sapiens_NP_002783 L A V M R R - - D Q S - L K I L N P E E I E K Y V A E I E K E K E E N - E K K K Q K - K A S 248
Mus musculus_NP_036099 L A V M R R - - D Q P - L K I L N P E E I E K Y V A E I E K E K E E N - E K K K Q K - K A S 248
Notothenia coriiceps_XP_010783619 L A I T R R - - N K P - L K I L E A K E I E S L V A E I E K E K E E E A E K K K Q K G K S T 252
Trematomus bernacchii L A I T R R - - N K P - L K I L E A K E I E S L V A E I E K E K E E E A E K K K Q K G K S T 252
Oreochromis niloticus_XP_003438172 L A V R R - - N Q P - L K I L E S K E I E T L V T E I E K E K E E E A E K K K Q K - K S T 251
Danio rerio_NP_998331 L A V R R - - N Q P - L K I L E S K E I E T L V A E I E K E K E E E A E K K K Q K - K S S 251

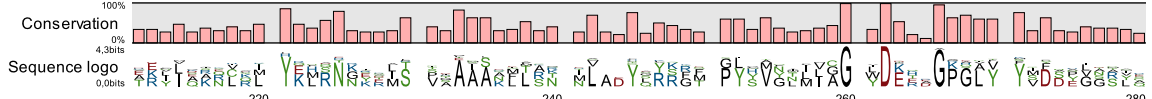


	1	2	3	4	5	6	7	8	9	10
Caenorhabditis elegans_NP_492360	1	50,20	54,51	59,68	60,08	60,08	57,65	57,65	58,04	57,65
Drosophila melanogaster_NP_650910	2	128	51,57	58,17	57,77	58,17	59,52	59,52	60,56	61,35
Arabidopsis thaliana_NP_190694	3	139	131	65,61	66,01	66,01	65,75	65,75	66,54	65,75
Xenopus laevis_NP_001081054	4	151	146	166	96,37	96,77	87,30	87,30	87,25	87,65
Homo sapiens_NP_002783	5	152	145	167	239	98,79	86,90	86,90	86,85	88,05
Mus musculus_NP_036099	6	152	146	167	240	245	87,30	87,30	87,25	88,45
Notothenia coriiceps_XP_010783619	7	147	150	167	220	219	220	100,00	96,03	95,63
Trematomus bernacchii	8	147	150	167	220	219	220	252	96,03	95,63
Oreochromis niloticus_XP_003438172	9	148	152	169	219	218	219	242	242	98,01
Danio rerio_NP_998331	10	147	154	167	220	221	222	241	241	246

Figure S7. MUSCLE alignment of proteasome alpha 7 subunit amino acid sequences, with species names and accession numbers. The consensus sequence, the conservation histogram and the sequence logo are shown at the bottom of the alignment. The Table in the last page contains the pairwise comparison of the sequences, with the number of identities (below the diagonal) and percent identity (above the diagonal).



			160		180		200	
Arabidopsis thaliana_NP_193216	TEYVQKNVSL	YQFRNGTPLS	TAAAAANFTRG	ELA-TALRKN	PYSVNLMLAG	YDKEAGASLY	YID-YIATLH	124
Drosophila melanogaster_NP_609804	TEFVSKNIAL	YKMRNGYDLS	PRESAHFTRK	NLAELYLRST	PYQVFMFVAG	YDPNAGPELT	FID-YLANAL	125
Homo sapiens_NP_002785	AEYVQKNVQL	YKMRNGYELS	PTAAANFTRR	NLADCLRSRT	PYHVNLLIAG	YDEHEGPALY	YMD-YLAAAL	125
Mus musculus_NP_036100	AEYVQKNVQL	YKMRNGYELS	PTAAANFTRR	NLADCLRSRT	PYHVNLLIAG	YDEHEGPALY	YMD-YLAAAL	125
Xenopus laevis_NP_001084761	AEYVQKNVQL	YKMRNGYELS	PTAAANFTRR	NLADYLRST	PYHVNLLIAG	YDEHAGPSLY	YMD-YLSALA	125
Trematomus bernacchii	AEYVQKNLQL	YKMRNGYELS	PSAAANFTRK	NLADYLRST	PYHVNLLIAG	YDETDGPGLY	YMD-YLSSIS	125
Notothenia coriiceps_XP_010789577	AEYVQKNLQL	YKMRNGYELS	PSAAANFTRK	NLADYLRST	PYHVNLLIAG	YDETDGPGLY	YMD-YLSSIS	125
Danio rerio_NP_001002609	AEYVQKNVQL	YKMRNGYELS	PAAAAANFTRK	NLADYLRST	PYHVNLLIAG	YDETDGPGLY	YMD-YLSALA	125
Oreochromis niloticus_XP_003447226	AEYVQKNVQL	YKMRNGYELS	PAAAAANFTRK	NLADYLRST	PYHVNLLIAG	YDDTDGPGLY	YMD-HLSSLA	125
Caenorhabditis elegans_NP_498806	KKVLSRSLHK	YRFDRSDMS	VDLCAELLSR	NL--YRFRFF	PYYTGALLAG	LDEH-GKGA	YSYDPLGLE	174
Arabidopsis thaliana_NP_191641	QKVLKSRHLI	YQHGHKQMS	CPAMAQLLSN	TL--YFKRFF	PYYAFNLVGG	LDEE-GKGV	FTYDAVGSYE	137
Xenopus laevis_NP_001080435	TKILTEARLKM	YKHSNNKTMT	SGAIAAMLST	TL--YSRRFF	PYYVYNIIGG	LDEE-GKGA	YSFDPVGSYQ	157
Mus musculus_NP_035315	TKILTEARLKM	YKHSNNKAMT	TGAIAAMLST	TL--YSRRFF	PYYVYNIIGG	LDEE-GKGA	YSFDPVGSYQ	158
Homo sapiens_NP_002784	TKILTEARLKM	YKHSNNKAMT	TGAIAAMLST	TL--YSRRFF	PYYVYNIIGG	LDEE-GKGA	YSFDPVGSYQ	159
Danio rerio_NP_001003889	TKILTEARLKM	YKHSNNKAMT	TGAIAAMLST	TL--YSRRFF	PYYVYNIIGG	LDEE-GKGA	YSFDPVGSYQ	155
Oreochromis niloticus_XP_003454565	TKILTEARLKM	YKHSNNKTMT	SGAIAAMLST	TL--YSRRFF	PYYVYNIIGG	LDEE-GKGA	YSFDPVGSYQ	155
Trematomus bernacchii	TKILTEARLKM	YKHSNNKTMT	SNAIAAMLST	TL--YGRFF	PYYVYNIIGG	LDEH-GKGA	YSFDPVGSYQ	155
Notothenia coriiceps_XP_010781254	TKILTEARLKM	YKHSNNKTMT	SNAIAAMLST	TL--YGRFF	PYYVYNIIGG	LDEH-GKGA	YSFDPVGSYQ	155
Caenorhabditis elegans_NP_493271	TKMLSGNRLI	LELNTGRKAR	VITALRQAKQ	HL--FNYQGY	-GAYLLVGG	YDPT-GPHLY	MCSANGTITMA	167
Thermoplasma acidophilum_NP_394085	VRVMKAELE	YRLQRRVMP	TEAVATLSN	ML--NQVKYM	PYMVQLVGG	IDT--APHVF	SIDAAGGSVE	129
Drosophila melanogaster_NP_652031	ADIVAYSINLY	HENQTNKDAL	VEFAASEERN	YC--YSYR-E	SLLAGTIVAG	WDEQRGGQVY	SIP-LGGMLT	136
Caenorhabditis elegans_NP_493558	TRIVAKYCTL	YELREKTSIT	VAASKYFAN	TL--HEYRGG	GLSFGSMVAG	YDKK-GPFI	KVDSEGRQC	193
Drosophila melanogaster_NP_652014	DRVLSKECRL	HELNRKERTS	VAAASKIMAN	IA--HGKGM	GLSMGMMLAG	YDKR-GPGLY	YVDSEGRTP	195
Arabidopsis thaliana_NP_172765	HRNLGKCRLL	HELANKRRIS	VGASKLLAN	ML--YSYRGM	GLSFGTMVAG	WDET-GPGLY	YVDNEGRLLK	179
Xenopus laevis_NP_001084323	ERLLAKECRL	YQLRNNSTRS	VAAASKMCN	MM--LQYRGT	GLSFGSMVAG	WDKK-GPGLY	YVDNNGTRLC	188
Mus musculus_NP_035316	ERLLARQCCRJ	YELRNKERIS	VAAASKLLAN	MV--YQYKGM	GLSMGTMVCG	WDKR-GPGLY	YVDSEGNRIS	181
Homo sapiens_NP_002788	ERLLARQCCRJ	YELRNKERIS	VAAASKLLAN	MV--YQYKGM	GLSMGTMVCG	WDKR-GPGLY	YVDSEGNRIS	181
Danio rerio_NP_571226	ERLLARQCCRJ	YELRNKERIS	VAAASKLLAN	MV--YQYKGM	GLSMGTMVCG	WDKR-GPGLY	YVDSEGNRVC	187
Oreochromis niloticus_XP_003457456	ERLLARQCCRJ	YELRNKERIS	VAAASKLLAN	MV--YQYKGM	GLSMGTMVCG	WDKR-GPGLY	YVDSEGNRVC	190
Trematomus bernacchii	ERLLARQCCRJ	YELRNKERIS	VAAASKLLAN	MV--YQYKGM	GLSMGTMVCG	WDKR-GPGLY	YVDSEGNRVC	190
Notothenia coriiceps_XP_010781265	ERLLARQCCRJ	YELRNKERIS	VAAASKLLAN	MV--YQYKGM	GLSMGTMVCG	WDKR-GPGLY	YVDSEGNRVC	190
Consensus	TRXIXKNLRL	YKLRNXKRXS	VAAAAKLLXN	XL--YXRRGX	PYSVGLXIAG	YDEX-GPGLY	YVDDEGGSLLQ	



			220		240		260		280
Arabidopsis thaliana_NP_193216	KVDKGAFGYG	SYFSSTMDR	HY-----	-----	RSDMS	VEEALELDV	CILELRSLV	IAPPNFVKI	181
Drosophila melanogaster_NP_609804	PVNYAGHYG	AIFASSYDR	YV-----	-----	HPNIT	QAEAMDVFKK	CIAEQKRLV	VNLKNFTAV	182
Homo sapiens_NP_002785	KAPFAAHGYG	AFLTSLDR	YY-----	-----	TPTIS	RERAEELLRK	CLEELQKRFI	NLPTFSVRI	182
Mus musculus_NP_036100	KAPFAAHGYG	AFLTSLDR	YY-----	-----	TPTIS	RERAEELLRK	CLEELQKRFI	NLPTFSVRI	182
Xenopus laevis_NP_001084761	KTRFAAHGYG	AYTSLDR	YY-----	-----	KPDLT	REDAVELKK	CISEQKRFI	NLPSFTVRV	182
Trematomus bernacchii	KAPFAAHGYG	AFLTSLDQ	HY-----	-----	KPDLT	REEAVDLKK	CIEELRKRFI	NLPSFTVRL	182
Notothenia coriiceps_XP_010789577	KAPFAAHGYG	AFLTSLDQ	HY-----	-----	KPDLT	REEAVDLKK	CIEELRKRFI	NLPSFTVRL	182
Danio rerio_NP_001002609	KAPFAAHGYG	AFLTSLDR	YY-----	-----	RPDLT	REEAVDLKK	CLEELNKRFI	NLPSFTVRL	182
Oreochromis niloticus_XP_003447226	KAPFAAHGYG	AYTSLDR	YY-----	-----	RPDLT	RDEAVDLKK	CVEEKRFI	NLPSFTVRL	182
Caenorhabditis elegans_NP_498806	RIGYSASGAA	EPMTIPLDC	QIHVTS--	-EGVERPEIT	LDRAISLMKD	SFRGAAEREI	STGDKIHLVI	241	
Arabidopsis thaliana_NP_191641	RVGCAQSSG	STLIMPLDN	QLKSPSLLL	PKQDSNTPLS	EAEAMDVFKT	VFASATERDI	YTGDKLEIM	207	
Xenopus laevis_NP_001080435	RDAFKAGGSA	SAMLQPLDN	QIGYKNM--	-QNVNQLPLT	LEKALKIKD	VFISAAERDV	YTGDKALRCI	223	
Mus musculus_NP_035315	RDSFKAGGSA	SAMLQPLDN	QIGYKNM--	-QNVNQLPLT	LEKALKIKD	VFISAAERDV	YTGDKALRCI	224	
Homo sapiens_NP_002784	RDSFKAGGSA	SAMLQPLDN	QIGYKNM--	-QNVNQLPLT	LEKALKIKD	VFISAAERDV	YTGDKALRCI	225	
Danio rerio_NP_001003889	RDTYKAGGSA	SAMLQPLDN	QIGYKNM--	-ENVEHVPLT	QEKAVQLVKD	VFISAAERDV	YTGDKALRCI	221	
Oreochromis niloticus_XP_003454565	RDTYKAGGSA	SAMLQPLDN	QIGYKNM--	-ENVEHVPLT	QEKAVQLVKD	VFISAAERDV	YTGDKALRCI	221	
Trematomus bernacchii	RDTYKAGGSA	SAMLQPLDN	QIGYKNM--	-EGVHVPLT	KDKAVQLVKD	VFISAAERDV	YTGDKALRCI	221	
Notothenia coriiceps_XP_010781254	RDTYKAGGSA	SAMLQPLDN	QIGYKNM--	-EGVHVPLT	QERAVQLVKD	VFISAAERDV	YTGDKALRCI	221	
Caenorhabditis elegans_NP_493271	-FPFTAQSSG	SYAAITLER	DF-----	-----	KVDMT	KDEAEKLVQR	ALVAGMHGDN	ASGNSLNLI	223
Thermoplasma acidophilum_NP_394085	-DJYASTGSS	SPFYGVLES	QY-----	-----	SEKMT	VDEGVDLVR	AISAAKQSDS	ASGGMDLAV	185
Drosophila melanogaster_NP_652031	RESCITGSSG	SSFIYGFRE	HY-----	-----	RPNMA	VEDCMTFVKK	AVQHAIVHDG	SSGGVVRIG	193
Caenorhabditis elegans_NP_493558	KVCSV-GSS	SLNAYGLDN	HY-----	-----	KPKMT	DDEARKLGLR	AIMHATYRDS	GSGGVCNLCH	249
Drosophila melanogaster_NP_652014	GNLFSV-GSS	SLYAYGLDS	GY-----	-----	HWDLT	DKEAQELGRR	AIYHATERDA	YSGGITRYVH	251
Arabidopsis thaliana_NP_172765	GDRFSV-GSS	SPYAYGLDS	GY-----	-----	KYDMS	VEEASELARR	SIYHATERDG	ASGGVASYVH	235
Xenopus laevis_NP_001084323	GDLFST-GSS	NSYAYGVMS	GY-----	-----	RFDLT	PEEAVDGLRR	AIYATHRDA	YSGGCVNLVH	244
Mus musculus_NP_035316	GTAFSV-GSS	SVYAYGVMDR	GY-----	-----	SYDLK	VEEAYDLARR	AIYQATYRDA	YSGGAVNLVH	237
Homo sapiens_NP_002788	GATFSV-GSS	SVYAYGVMDR	GY-----	-----	SYDLE	VEQAVDLARR	AIYQATYRDA	YSGGAVNLVH	237
Danio rerio_NP_571226	GDLFAM-GSS	SMYAYGVMS	GY-----	-----	RYDLT	IDEACDLGRR	AIYQATYRDA	YSGGQVNLVH	243
Oreochromis niloticus_XP_003457456	GDLFAM-GSS	SMYAYGVMS	GY-----	-----	RHDLT	VEEACEGLRR	AIYQATYRDA	YSGGQVNLVH	246
Trematomus bernacchii	GDLFAM-GSS	SMYAYGVMS	GY-----	-----	RQDLT	VEEACEGLRR	AIYQATYRDA	YSGGQVNLVH	246
Notothenia coriiceps_XP_010781265	GDLFAM-GSS	SMYAYGVMS	GY-----	-----	RQDLT	VEEACEGLRR	AIYQATYRDA	YSGGQVNLVH	246
Consensus	RDPFAA-GSS	SAYAYGXLDL	QY-----	-----	RPDLT	VEEAVDLVCR	AIYEATERDX	YSGGAXNXYI	



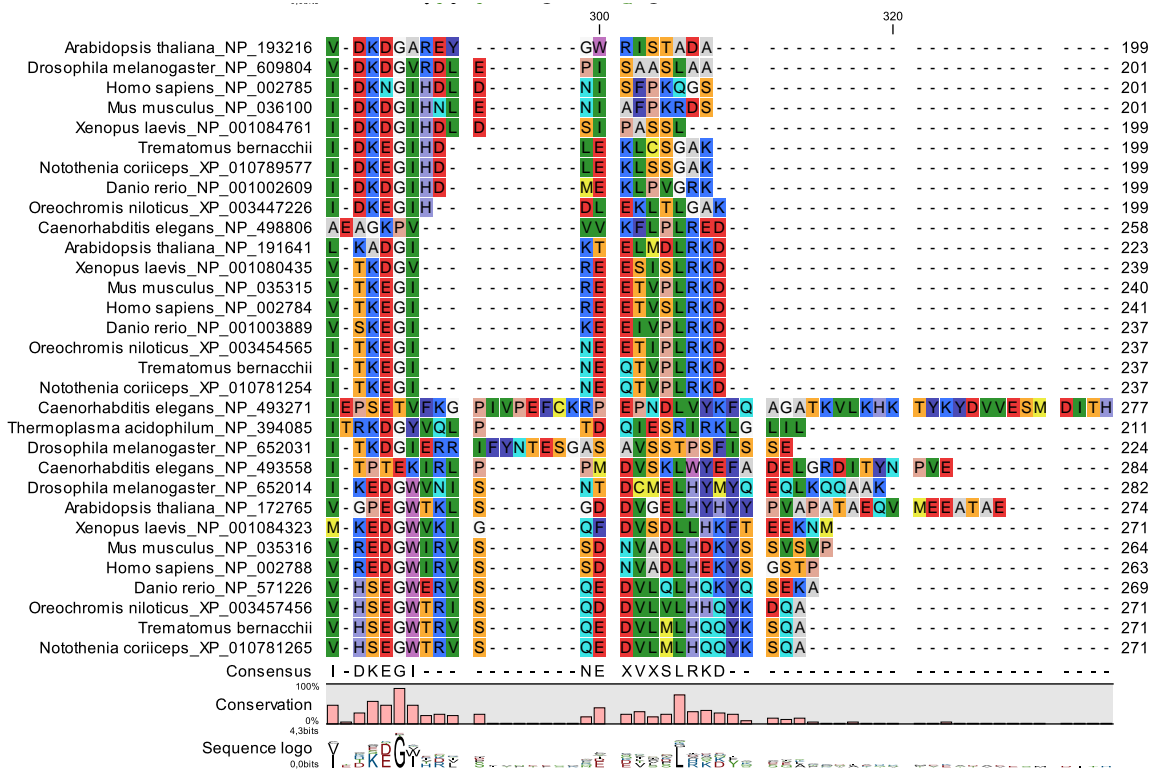


Figure S8. MUSCLE alignment of the catalytic proteasome subunits, with species names and accession numbers, utilized for the phylogenetic analysis.

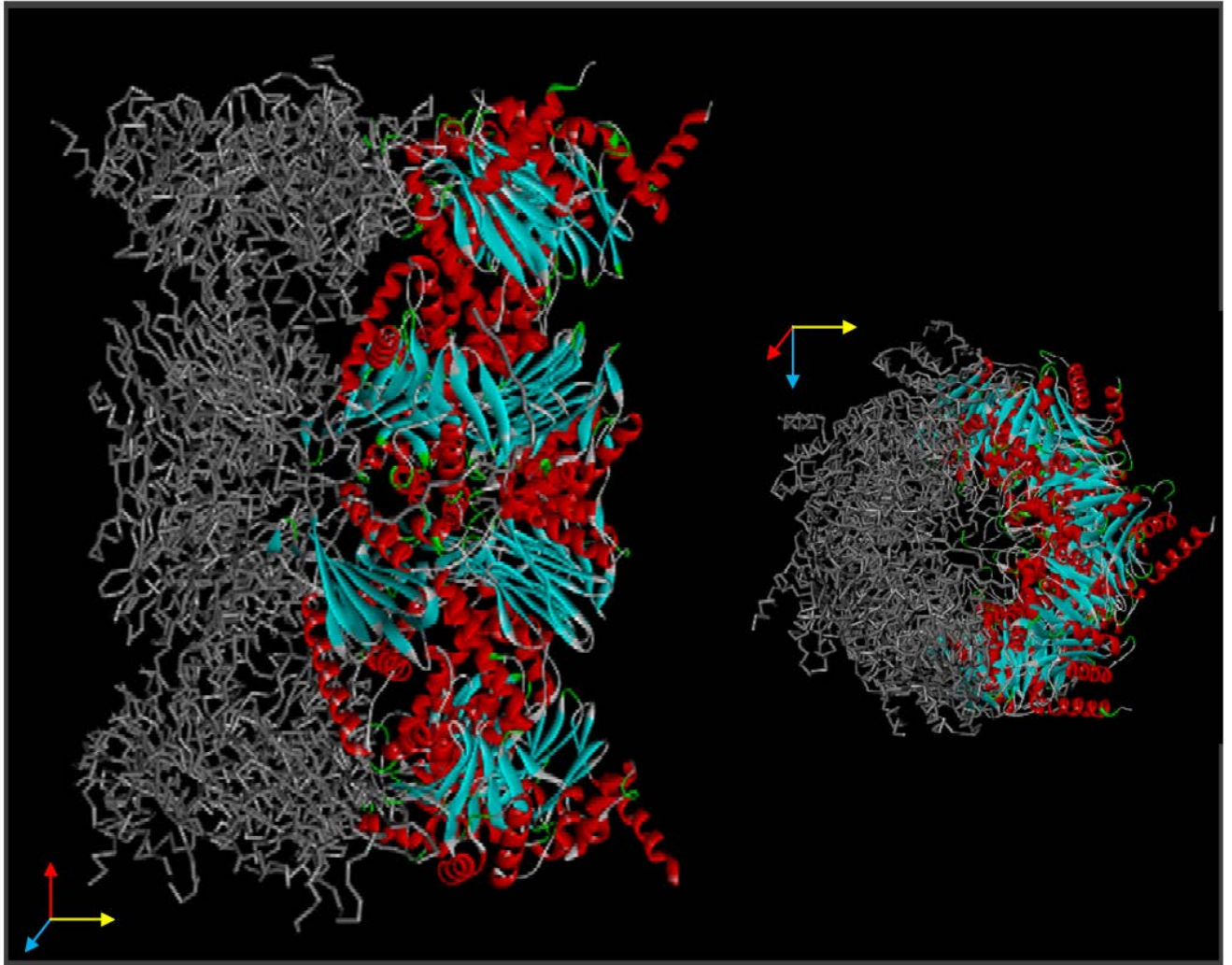


Figure S9. Theoretical assembly of the seven modelled chains of *T. bernacchii* proteasome (in red, alpha helices; in cyan, beta strands). The assembly is based on the reference structure of mouse whole proteasome (PDB code: 3UNB). The simple backbone (in grey) of the corresponding mouse chains is shown for the remaining chains (not modelled).