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 ε=1 mM^{-1} 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					
	Most favoured	*Additional*	*Generously*	*Disallowed*	*Most favoured*	*Additional*	*Generously*	*Disallowed*	Z-score	Hbonds
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					
	Most favoured	*Additional*	*Generously*	*Disallowed*	*Most favoured*	*Additional*	*Generously*	*Disallowed*	Z-score	Hbonds
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					
	Most favoured	*Additional*	*Generously*	*Disallowed*	*Most favoured*	*Additional*	*Generously*	*Disallowed*	Z-score	Hbonds
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					
	Most favoured	*Additional*	*Generously*	*Disallowed*	*Most favoured*	*Additional*	*Generously*	*Disallowed*	Z-score	Hbonds
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

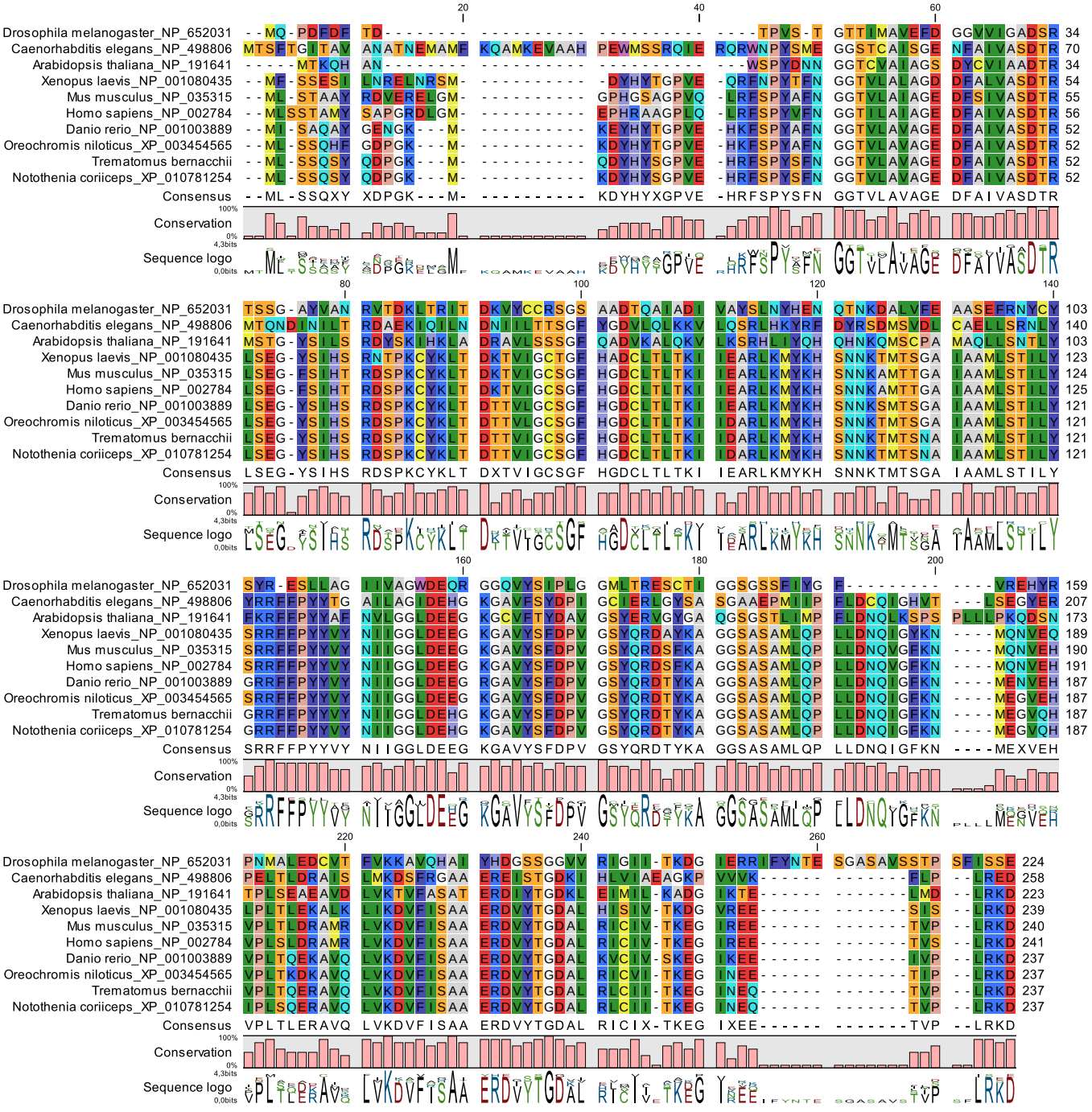
	PROCHECK								PROSA web	Hbplus
	Number of amino acids in regions:				Percentage					
	Most favoured	*Generously*			*Most favoured*	*Generously*			Z-score	
		Additional		*Disallowed*		*Additional*		*Disallowed*		Hbonds
Model 1	168	10	0	0	94.4	5.6	0	0	-6.41	146
Model 2	166	11	1	0	93.3	6.2	0.6	0	-6.58	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					
	Most favoured	*Additional*	*Generously*	*Disallowed*	*Most favoured*	*Additional*	*Generously*	*Disallowed*	Z-score	Hbonds
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					
	Most favoured	*Additional*	*Generously*	*Disallowed*	*Most favoured*	*Additional*	*Generously*	*Disallowed*	Z-score	Hbonds
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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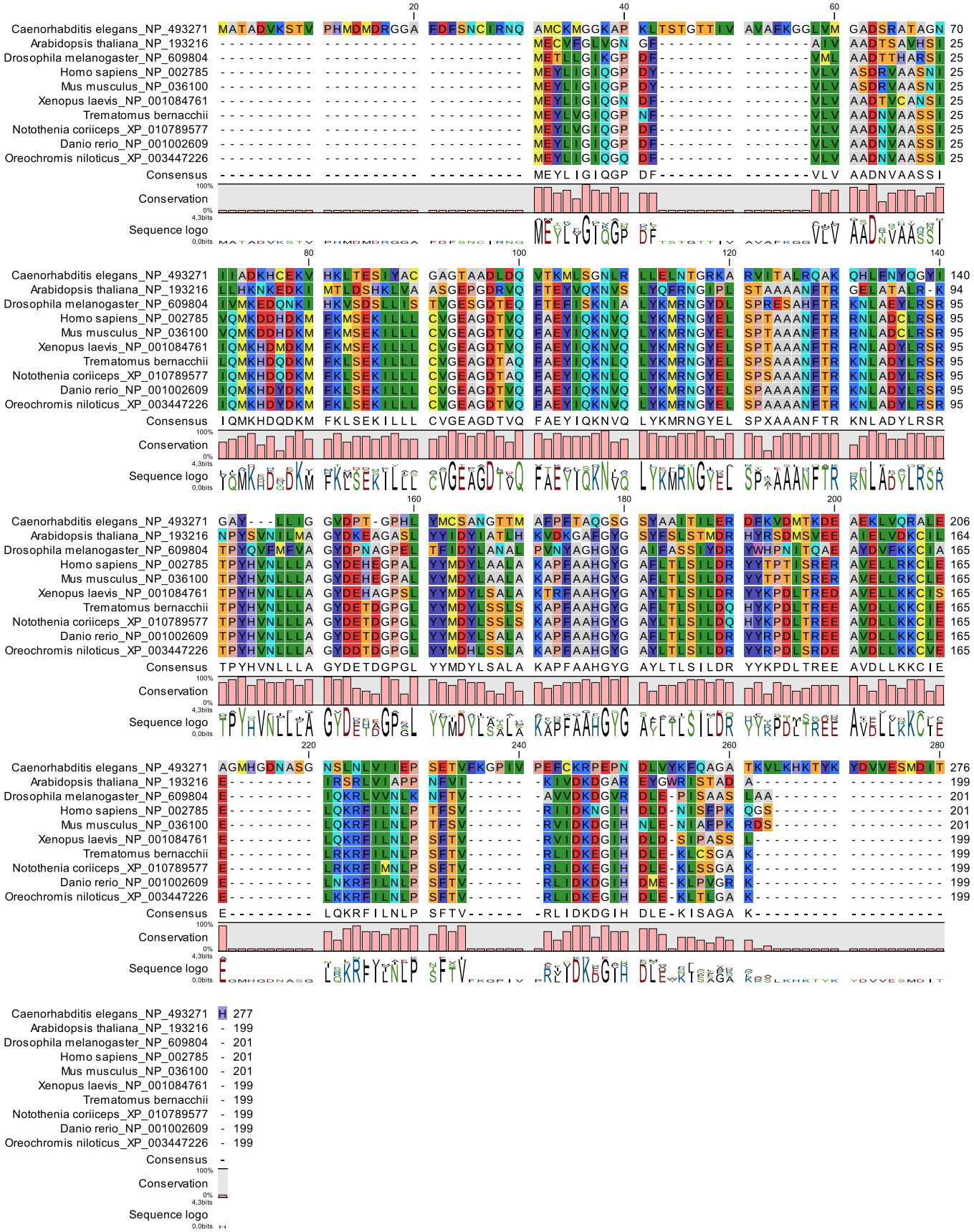
Arabidopsis thaliana_NP_191641
Xenopus laevis_NP_001080435
Mus musculus_NP_035315
Homo sapiens_NP_002784
Danio rerio_NP_001003889
Oreochromis niloticus_XP_003454565
Trematomus bernacchii
Notothenia coriiceps_XP_010781254
Consensus
Conservation
Sequence logo

		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).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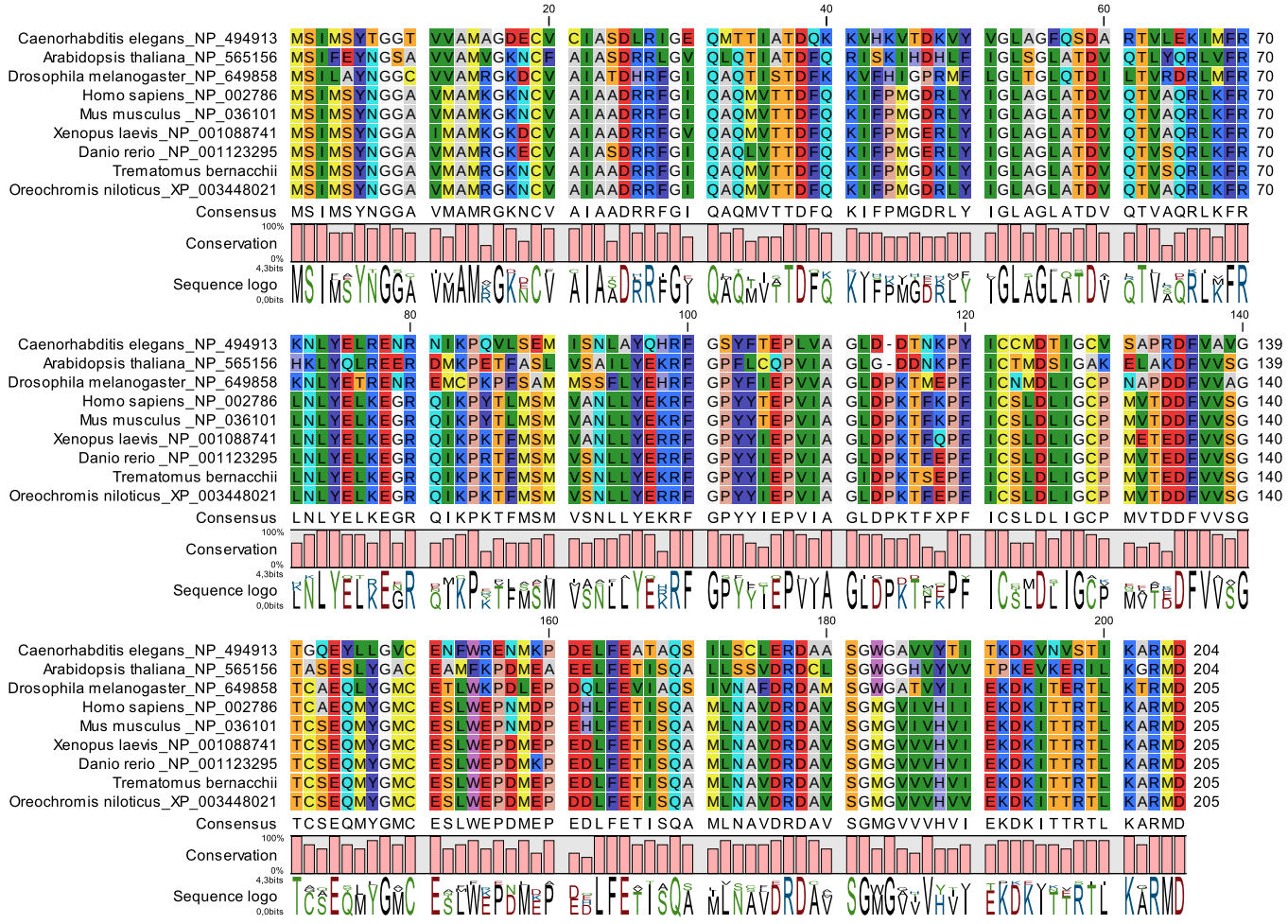
Arabidopsis thaliana_NP_193216
Drosophila melanogaster_NP_609804
Homo sapiens_NP_002785
Mus musculus_NP_036100
Xenopus laevis_NP_001084761
Trematomus bernacchii
Notothenia coriiceps_XP_010789577
Danio rerio_NP_001002609
Oreochromis niloticus_XP_003447226
Consensus
Conservation
Sequence logo

		1	2	3	4	5	6	7	8	9	10
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).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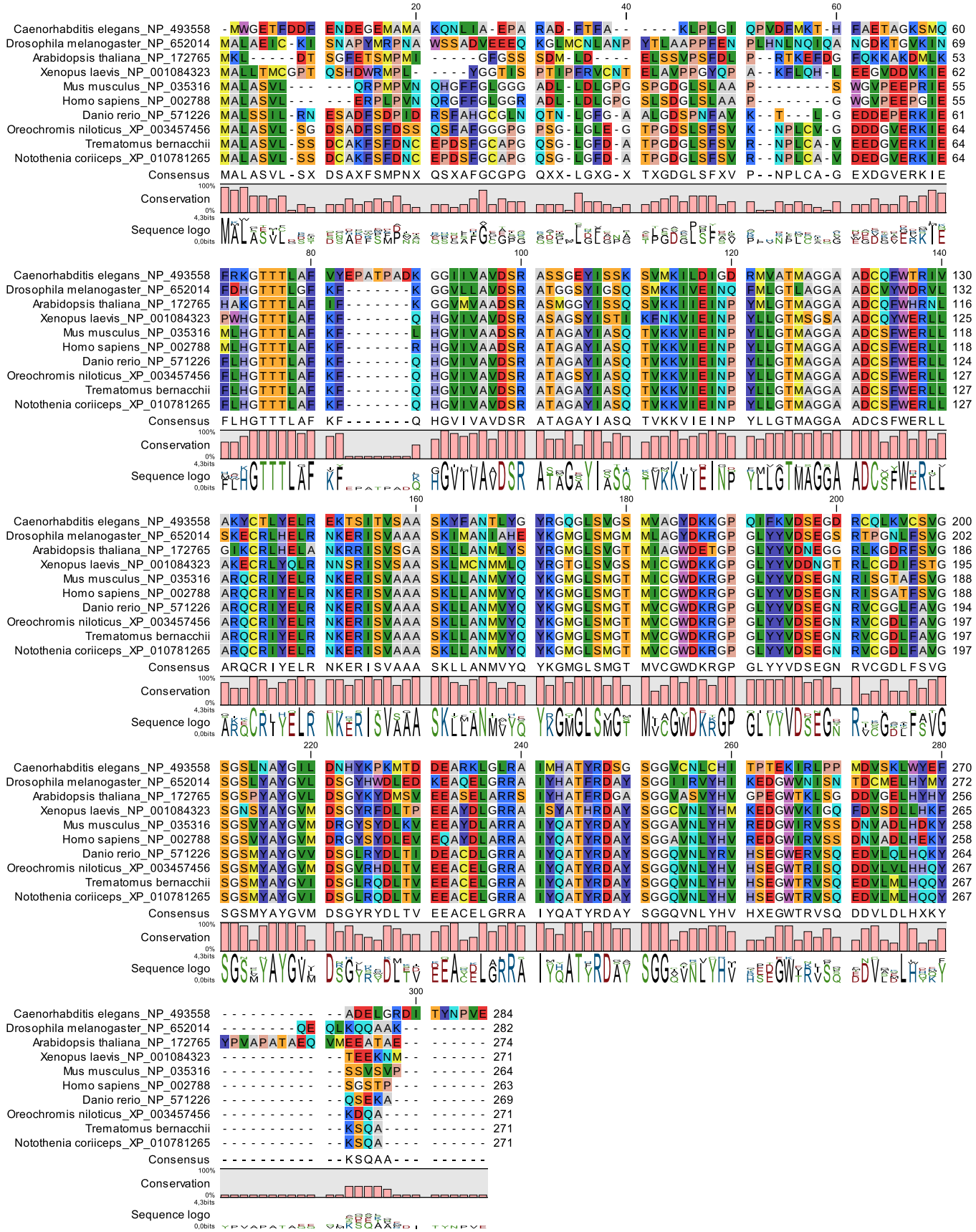
Drosophila melanogaster_NP_649858
Homo sapiens_NP_002786
Mus musculus _NP_036101
Xenopus laevis_NP_001088741
Danio rerio _NP_001123295
Trematomus bernacchii
Oreochromis niloticus_XP_003448021
Consensus
Conservation
Sequence logo
100%
0%
4,3bits
0,0bits

		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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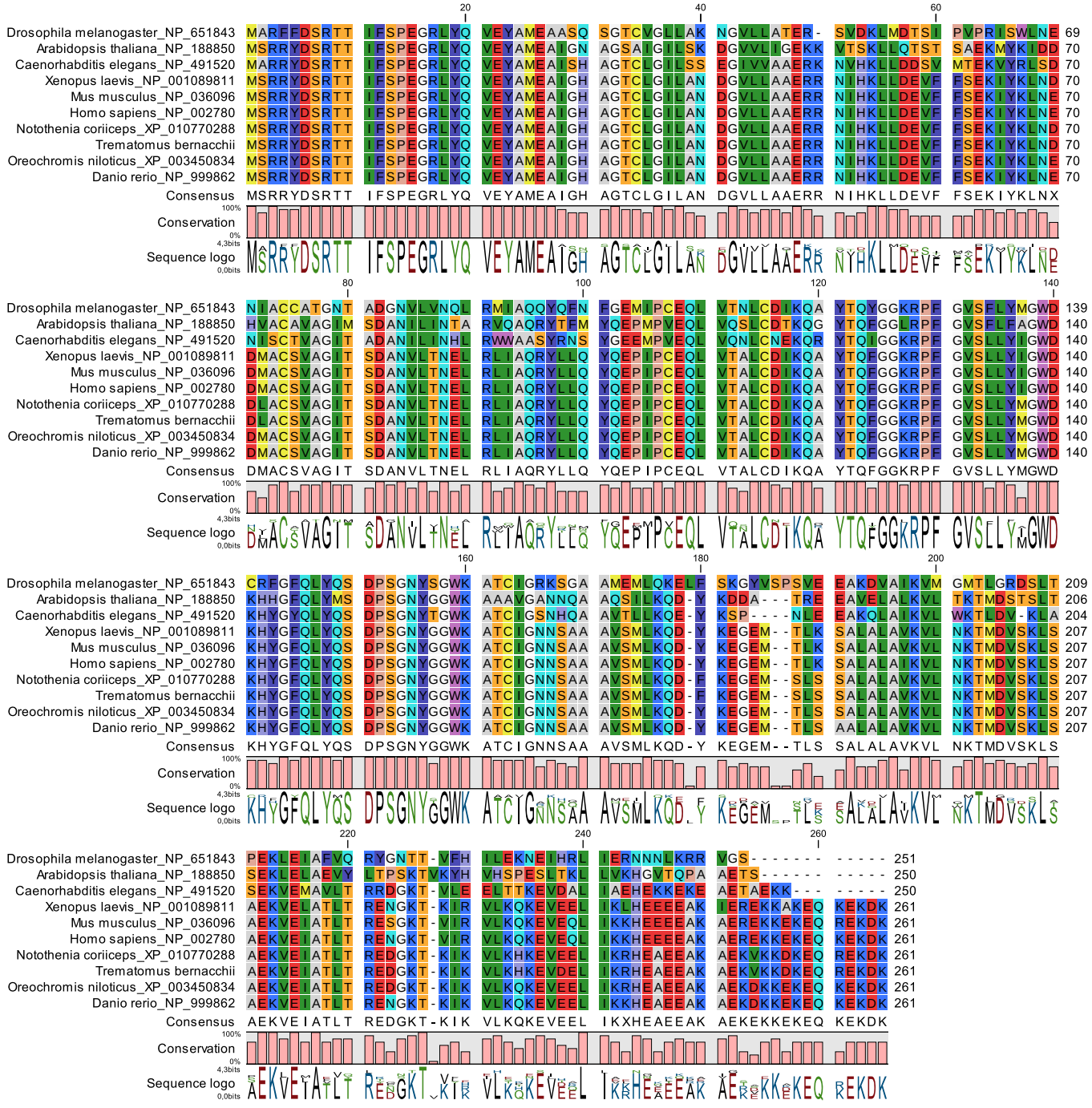
Arabidopsis thaliana_NP_172765
Xenopus laevis_NP_001084323
Mus musculus_NP_035316
Homo sapiens_NP_002788
Danio rerio_NP_571226
Oreochromis niloticus_XP_003457456
Trematomus bernacchii
Notothenia coriiceps_XP_010781265
Consensus
Conservation
Sequence logo

		1	2	3	4	5	6	7	8	9	10
Caenorhabditis elegans_NP_493558	1		37,25	38,61	35,49	35,27	34,93	36,43	36,43	36,43	36,43
Drosophila melanogaster_NP_652014	2	111		47,59	46,29	49,65	49,65	51,42	53,55	52,13	52,13
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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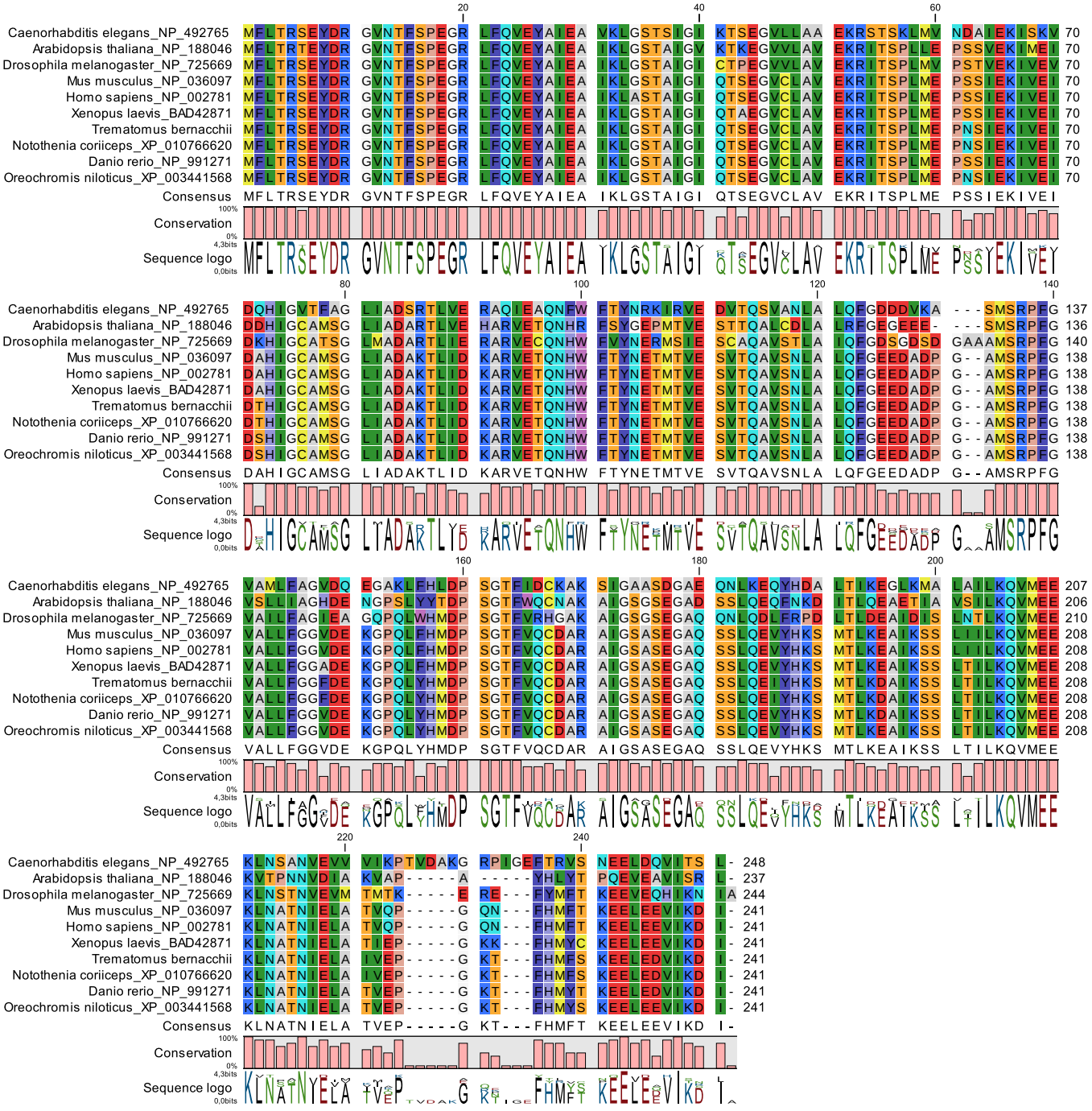
Caenorhabditis elegans_NP_491520
Xenopus laevis_NP_001089811
Mus musculus_NP_036096
Homo sapiens_NP_002780
Notothenia coriiceps_XP_010770288
Trematomus bernacchii
Oreochromis niloticus_XP_003450834
Danio rerio_NP_999862
Consensus
Conservation
Sequence logo

		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).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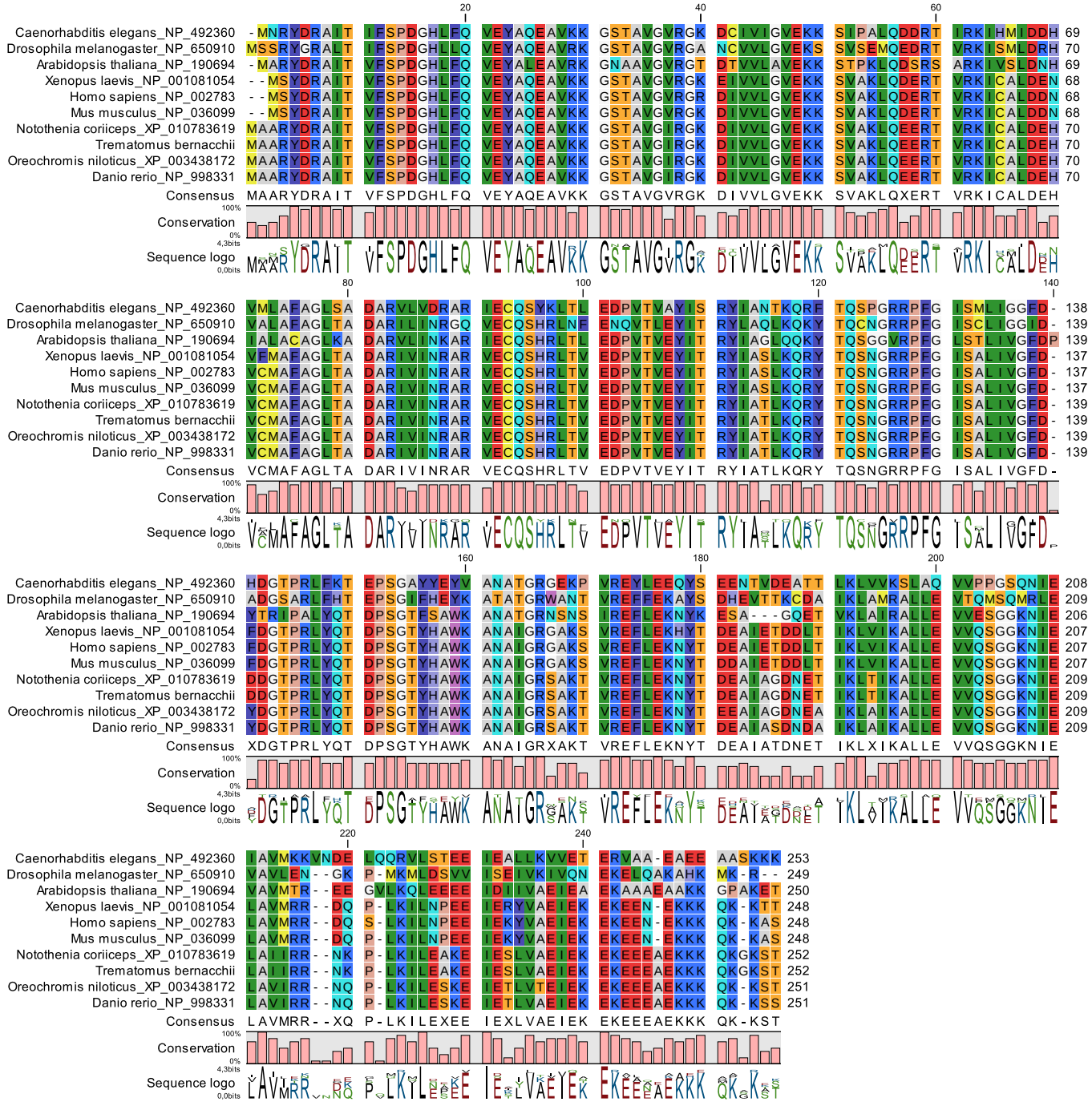
Arabidopsis thaliana_NP_188046
Drosophila melanogaster_NP_725669
Mus musculus_NP_036097
Homo sapiens_NP_002781
Xenopus laevis_BAD42871
Trematomus bernacchii
Notothenia coriiceps_XP_010766620
Danio rerio_NP_991271
Oreochromis niloticus_XP_003441568
Consensus
Conservation
Sequence logo

		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).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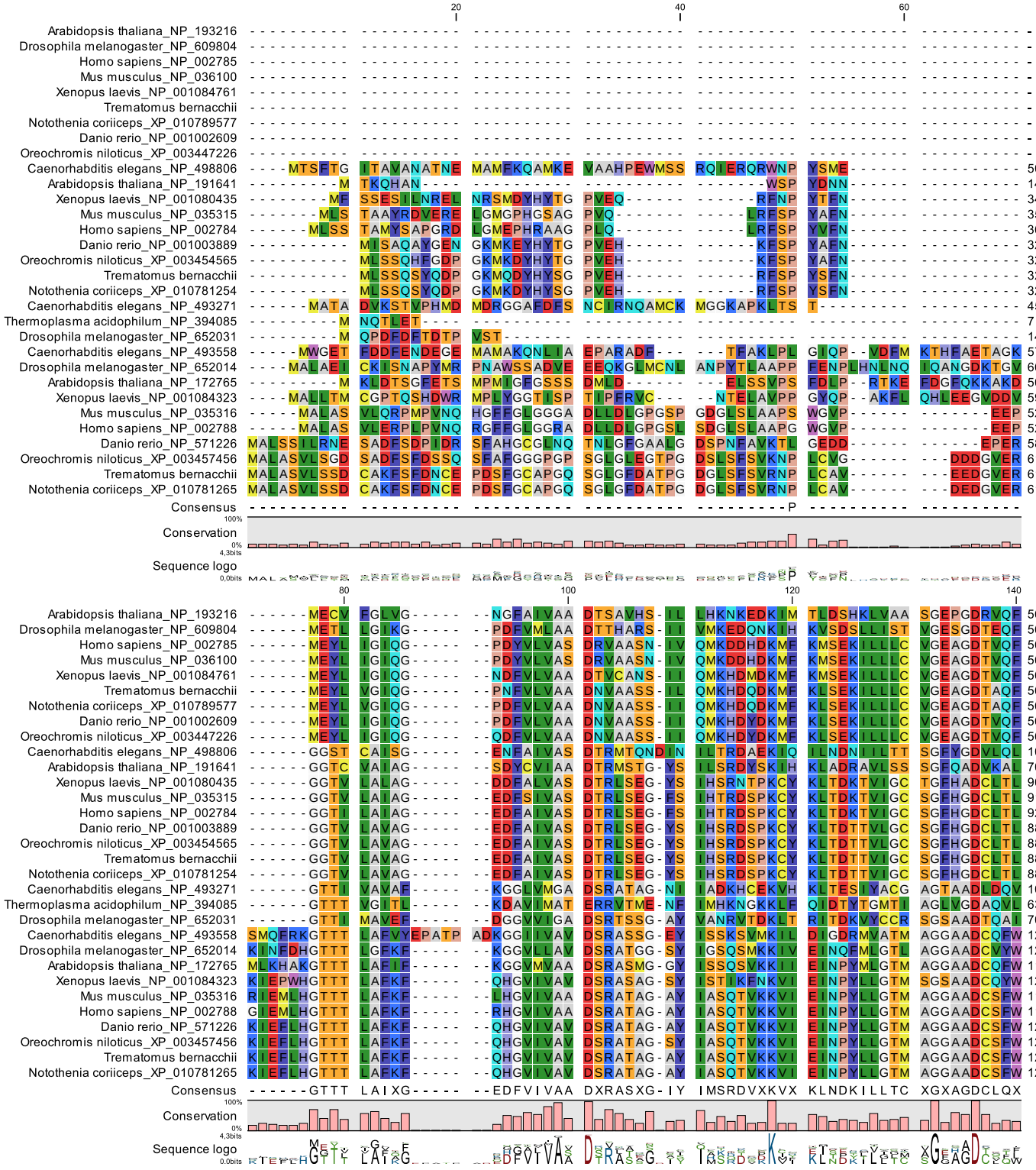
Drosophila melanogaster_NP_650910
Arabidopsis thaliana_NP_190694
Xenopus laevis_NP_001081054
Homo sapiens_NP_002783
Mus musculus_NP_036099
Notothenia coriiceps_XP_010783619
Trematomus bernacchii
Oreochromis niloticus_XP_003438172
Danio rerio_NP_998331
Consensus
Conservation
Sequence logo

		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).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Drosophila melanogaster_NP_609804
Homo sapiens_NP_002785
Mus musculus_NP_036100
Xenopus laevis_NP_001084761
Trematomus bernacchii
Notothenia coriiceps_XP_010789577
Danio rerio_NP_001002609
Oreochromis niloticus_XP_003447226
Caenorhabditis elegans_NP_498806
Arabidopsis thaliana_NP_191641
Xenopus laevis_NP_001080435
Mus musculus_NP_035315
Homo sapiens_NP_002784
Danio rerio_NP_001003889
Oreochromis niloticus_XP_003454565
Trematomus bernacchii
Notothenia coriiceps_XP_010781254
Caenorhabditis elegans_NP_493271
Thermoplasma acidophilum_NP_394085
Drosophila melanogaster_NP_652031
Caenorhabditis elegans_NP_493558
Drosophila melanogaster_NP_652014
Arabidopsis thaliana_NP_172765
Xenopus laevis_NP_001084323
Mus musculus_NP_035316
Homo sapiens_NP_002788
Danio rerio_NP_571226
Oreochromis niloticus_XP_003457456
Trematomus bernacchii
Notothenia coriiceps_XP_010781265
Consensus
Conservation
Sequence logo
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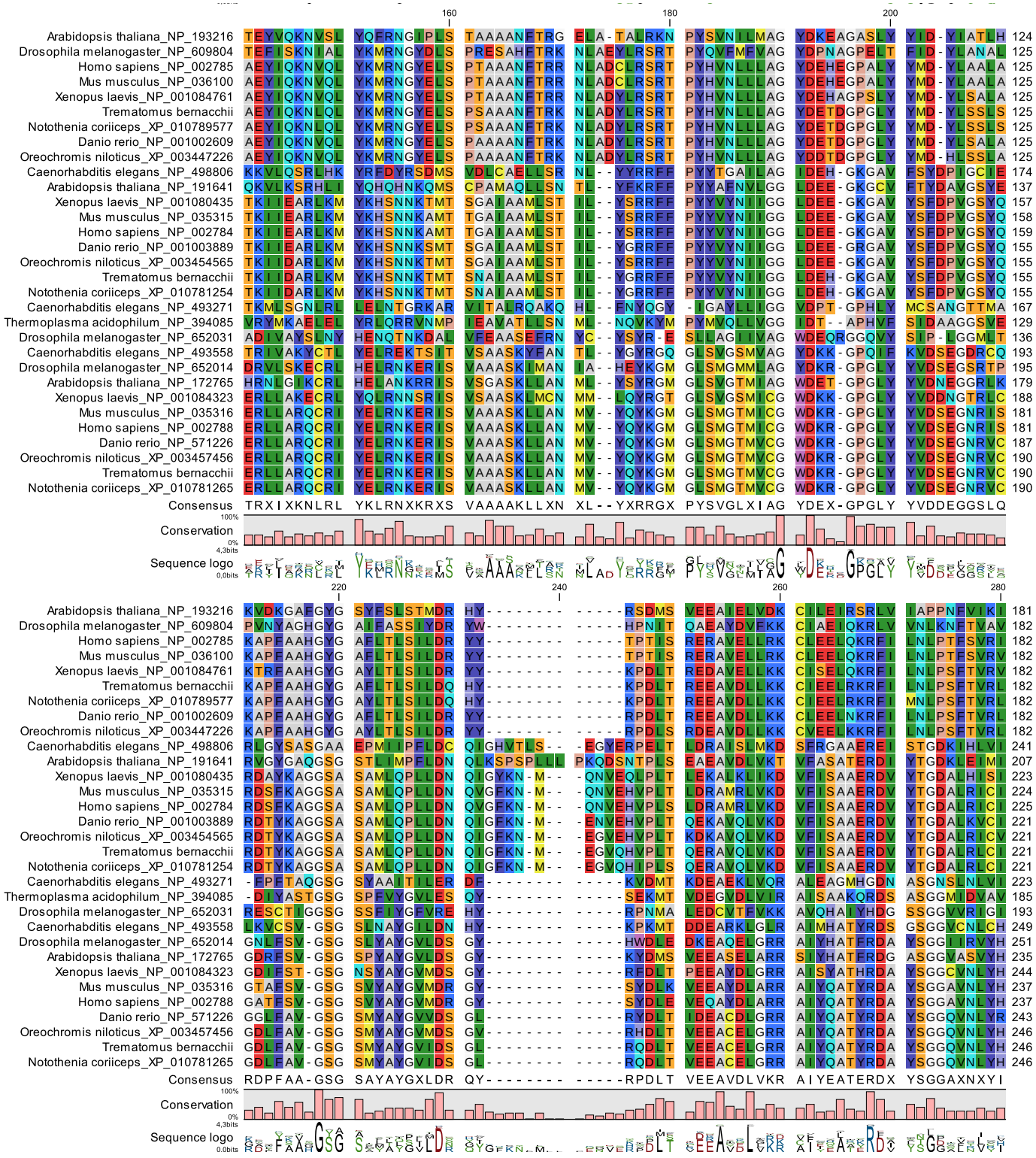
40
60
80
100
120
140


160
180
200
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Mus musculus_NP_036100 125
Xenopus laevis_NP_001084761 125
Trematomus bernacchii 125
Notothenia coriiceps_XP_010789577 125
Danio rerio_NP_001002609 125
Oreochromis niloticus_XP_003447226 125
Caenorhabditis elegans_NP_498806 174
Arabidopsis thaliana_NP_191641 137
Xenopus laevis_NP_001080435 157
Mus musculus_NP_035315 158
Homo sapiens_NP_002784 159
Danio rerio_NP_001003889 155
Oreochromis niloticus_XP_003454565 155
Trematomus bernacchii 155
Notothenia coriiceps_XP_010781254 155
Caenorhabditis elegans_NP_493271 167
Thermoplasma acidophilum_NP_394085 129
Drosophila melanogaster_NP_652031 136
Caenorhabditis elegans_NP_493558 193
Drosophila melanogaster_NP_652014 195
Arabidopsis thaliana_NP_172765 179
Xenopus laevis_NP_001084323 188
Mus musculus_NP_035316 181
Homo sapiens_NP_002788 181
Danio rerio_NP_571226 187
Oreochromis niloticus_XP_003457456 190
Trematomus bernacchii 190
Notothenia coriiceps_XP_010781265 190
Consensus
100%
Conservation
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4,3bits
Sequence logo
0,0bits
220
240
260
280
Arabidopsis thaliana_NP_193216 181
Drosophila melanogaster_NP_609804 182
Homo sapiens_NP_002785 182
Mus musculus_NP_036100 182
Xenopus laevis_NP_001084761 182
Trematomus bernacchii 182
Notothenia coriiceps_XP_010789577 182
Danio rerio_NP_001002609 182
Oreochromis niloticus_XP_003447226 182
Caenorhabditis elegans_NP_498806 241
Arabidopsis thaliana_NP_191641 207
Xenopus laevis_NP_001080435 223
Mus musculus_NP_035315 224
Homo sapiens_NP_002784 225
Danio rerio_NP_001003889 221
Oreochromis niloticus_XP_003454565 221
Trematomus bernacchii 221
Notothenia coriiceps_XP_010781254 221
Caenorhabditis elegans_NP_493271 223
Thermoplasma acidophilum_NP_394085 185
Drosophila melanogaster_NP_652031 193
Caenorhabditis elegans_NP_493558 249
Drosophila melanogaster_NP_652014 251
Arabidopsis thaliana_NP_172765 235
Xenopus laevis_NP_001084323 244
Mus musculus_NP_035316 237
Homo sapiens_NP_002788 237
Danio rerio_NP_571226 243
Oreochromis niloticus_XP_003457456 246
Trematomus bernacchii 246
Notothenia coriiceps_XP_010781265 246
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Conservation
0%
4,3bits
Sequence logo
0,0bits

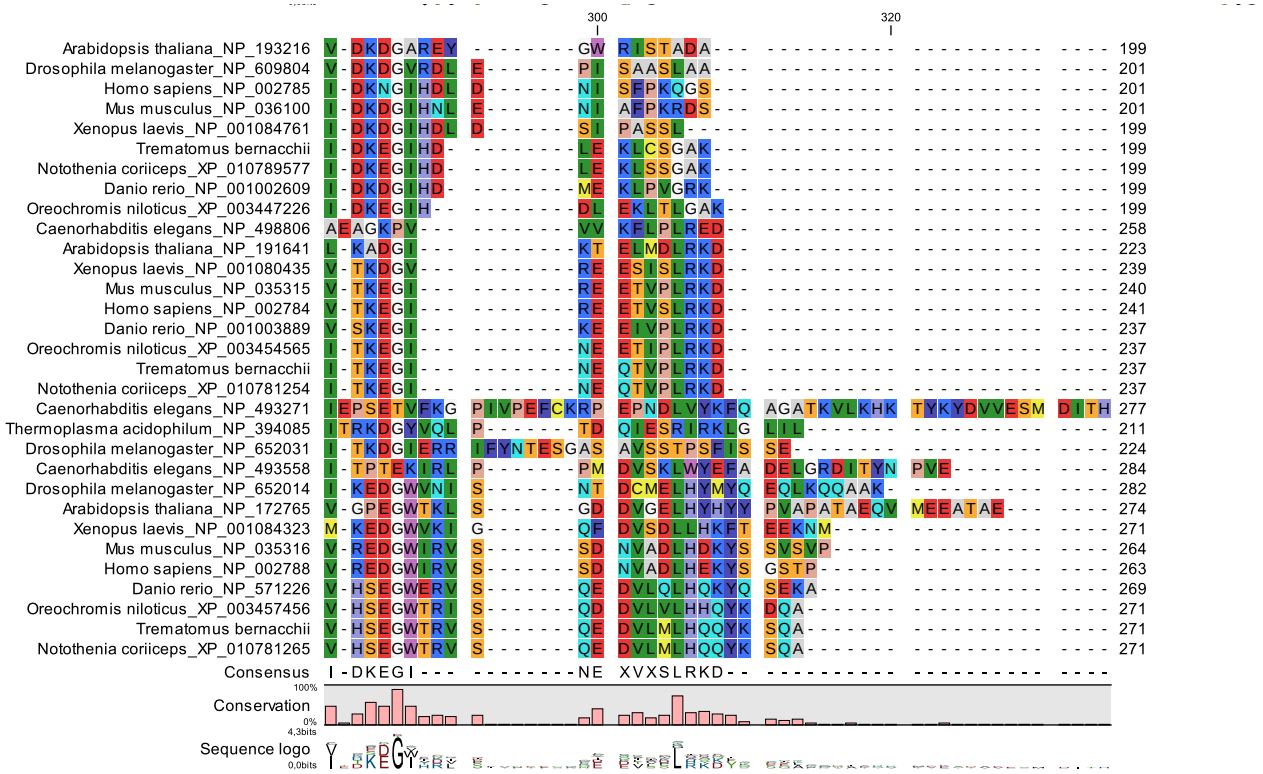

Figure S8. MUSCLE alignment of the catalytic proteasome subunits, with species names and accession numbers, utilized for the phylogenetic analysis.

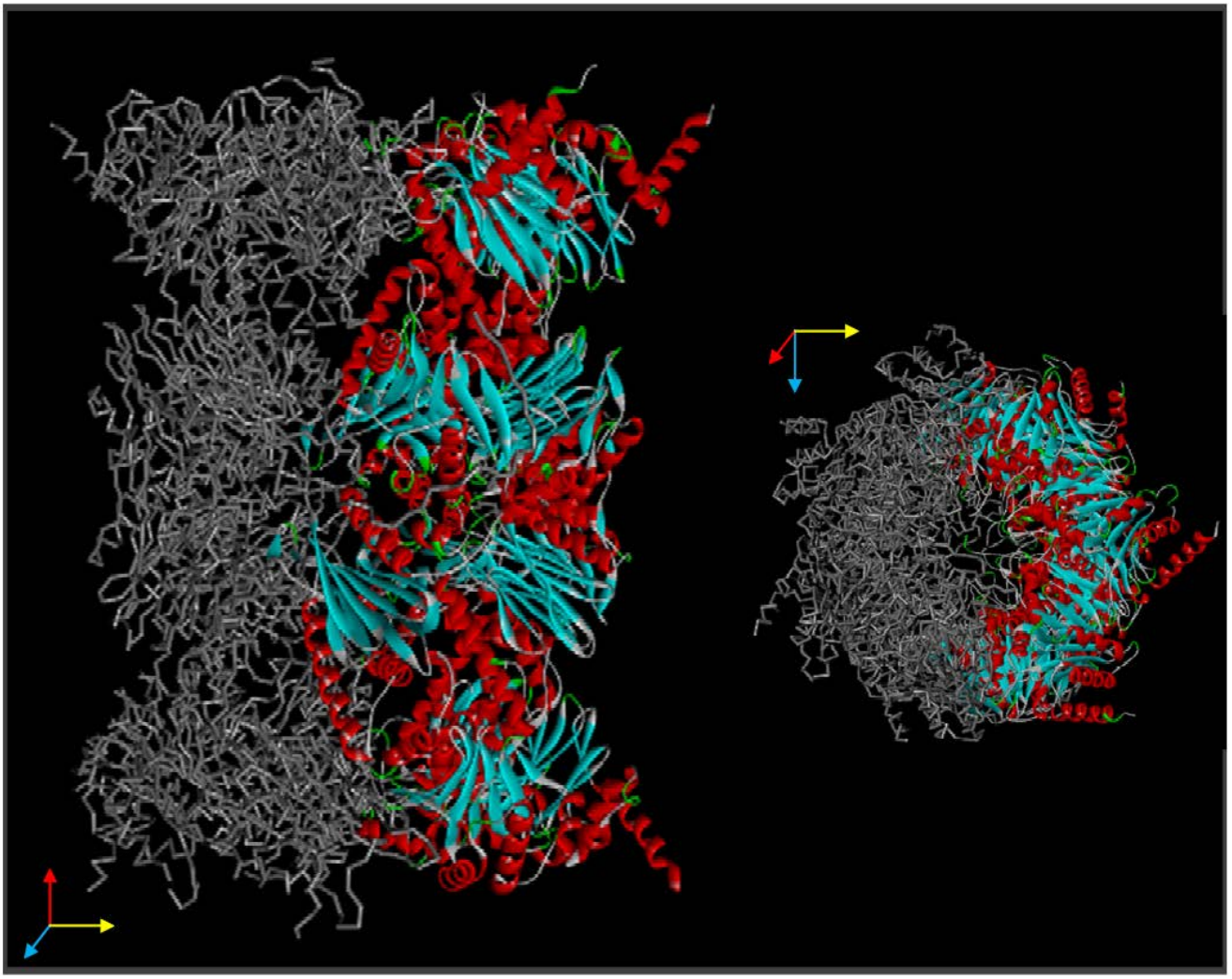

Figure S9. Theoretical assembly of the seven modelled chains of *T. bernacchii* proteasome (in red, alpha helices; in cyan, beta strands). The assembly is based on the reference structure of mouse whole proteasome (PDB code: 3UNB). The simple backbone (in grey) of the corresponding mouse chains is shown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