BLAST ® » blastp suite » RID-9J3VEZXX014

BLAST Results

Job title: Protein Sequence (1228 letters)

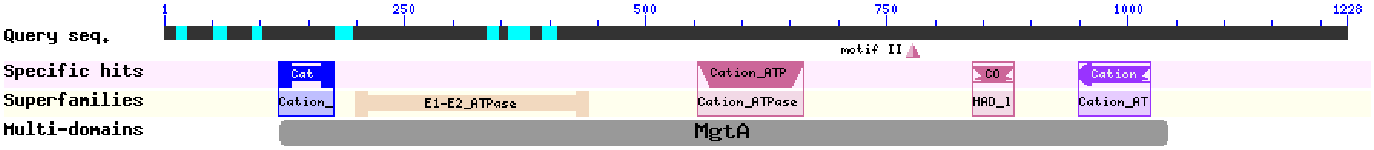
RID 9J3VEZXX014 (Expires on 02-08 07:06 am)

Query ID lcl|Query_96455
Description None
Molecule type amino acid
Query Length 1228

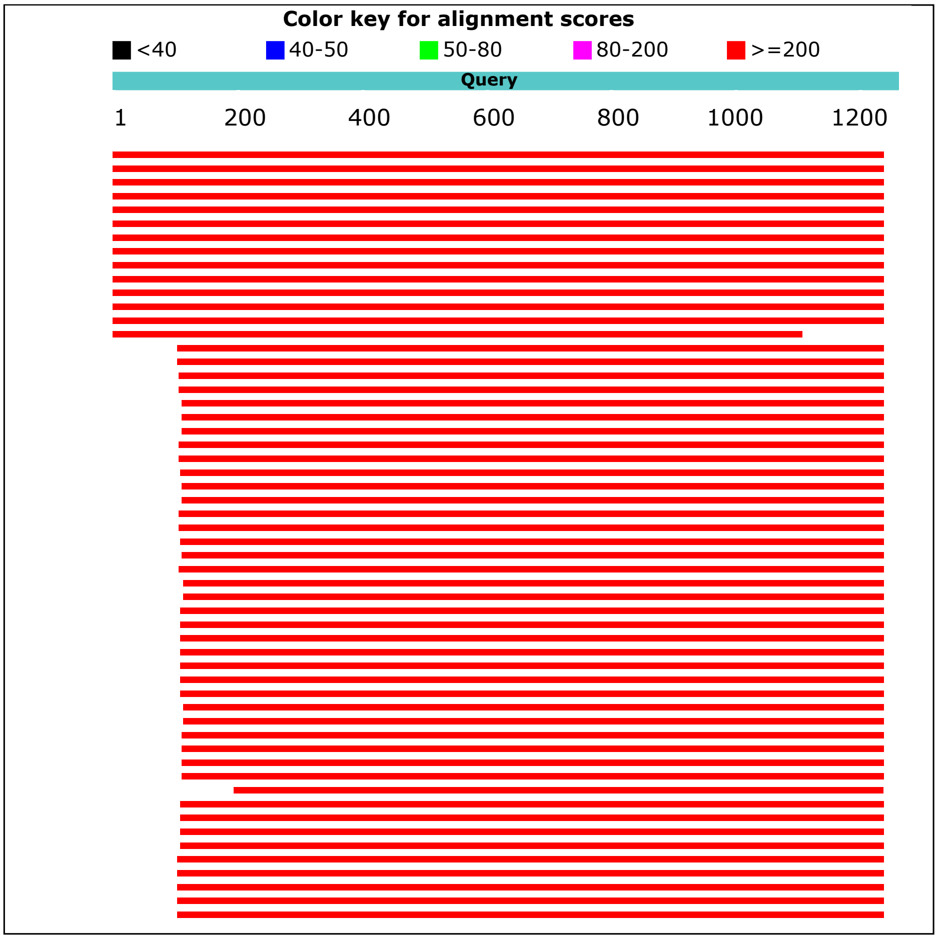
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 114 Blast Hits on 5000 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
P-type ATPase [Plasmodium falciparum]	2280	2280	100%	0.0	100%	AAC47167.1
potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	2248	2248	100%	0.0	99%	ETW17726.1
P-type ATPase4 [Plasmodium falciparum]	2245	2245	100%	0.0	99%	AAF17245.1
potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium falciparum FCH/4]	2245	2245	100%	0.0	99%	ETW30121.1
P-type ATPase4 [Plasmodium falciparum IGH-CR14]	2242	2242	100%	0.0	99%	KNG76774.1
potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium falciparum NF135/5.C10]	2242	2242	100%	0.0	99%	ETW41770.1
potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium falciparum 7G8]	2241	2241	100%	0.0	99%	EUR69264.1
hypothetical protein PFMALIP_03662 [Plasmodium falciparum MaliPS096_E11]	2239	2239	100%	0.0	99%	ETW48289.1
non-SERCA-type Ca2+-transporting P-ATPase [Plasmodium reichenowi]	2206	2206	100%	0.0	98%	XP_012763995.1
non-SERCA-type Ca2+ -transporting P-ATPase [Plasmodium reichenowi]	2206	2206	100%	0.0	97%	KYN95232.1
non-SERCA-type Ca2+ -transporting P-ATPase [Plasmodium gaboni]	2151	2151	100%	0.0	95%	XP_018638931.1
non-SERCA-type Ca2+ -transporting P-ATPase [Plasmodium falciparum 3D7]	2055	2055	100%	0.0	93%	XP_001350527.1
hypothetical protein PFTANZ_03754 [Plasmodium falciparum Tanzania (2000708)]	2052	2052	100%	0.0	93%	ETW35530.1
ATPase [Plasmodium falciparum]	1973	1973	89%	0.0	99%	AAB03496.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium gallinaceum]	1771	1771	91%	0.0	82%	CRG95888.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium relictum]	1739	1739	91%	0.0	82%	CRH03767.1
P-type ATPase [Plasmodium knowlesi strain H]	1737	1737	91%	0.0	80%	XP_002260625.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium vivax]	1734	1734	91%	0.0	80%	SGX79514.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium ovale]	1734	1734	90%	0.0	80%	SBT78701.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium ovale wallikeri]	1734	1734	90%	0.0	80%	SBT45090.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium ovale wallikeri]	1733	1733	90%	0.0	80%	SBT39769.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium vivax]	1732	1732	91%	0.0	80%	SCO69221.1
P-type ATPase4 [Plasmodium vivax Mauritania I]	1732	1732	91%	0.0	80%	KMZ90852.1
P-type ATPase4 [Plasmodium vivax India VII]	1732	1732	91%	0.0	80%	KMZ78465.1
P-type ATPase4, putative [Plasmodium ovale curtisi]	1732	1732	90%	0.0	80%	SBS87150.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium ovale]	1731	1731	90%	0.0	80%	SCP06047.1
P-type ATPase4 [Plasmodium vivax Brazil I]	1731	1731	91%	0.0	80%	KMZ83652.1
P-type ATPase4 [Plasmodium vivax Sal-1]	1729	1729	91%	0.0	80%	XP_001616592.1
potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium fragile]	1729	1729	91%	0.0	81%	XP_012336786.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium ovale curtisi]	1727	1727	90%	0.0	80%	SBS97393.1
P-type ATPase4 [Plasmodium vivax North Korean]	1727	1727	91%	0.0	79%	KMZ97635.1
P-type ATPase [Plasmodium coatneyi]	1724	1724	90%	0.0	81%	XP_019913082.1
hypothetical protein C922_03151 [Plasmodium inui San Antonio 1]	1702	1702	90%	0.0	79%	XP_008816965.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium malariae]	1675	1675	91%	0.0	77%	SBS89310.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium malariae]	1660	1660	91%	0.0	77%	SBT72046.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium chabaudi adami]	1649	1649	91%	0.0	76%	SCM19403.1
ATPase, putative [Plasmodium chabaudi chabaudi]	1648	1648	91%	0.0	76%	XP_731589.2
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium chabaudi adami]	1646	1646	91%	0.0	76%	SCN59014.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium chabaudi chabaudi]	1646	1646	91%	0.0	76%	SCN59015.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium chabaudi chabaudi]	1645	1645	91%	0.0	76%	SCM19772.1
hypothetical protein YYG_03733 [Plasmodium vinckei petteri]	1640	1640	90%	0.0	76%	EUD71100.1
hypothetical protein YYE_03599 [Plasmodium vinckei vinckei]	1638	1638	90%	0.0	76%	XP_008625470.1
P-type ATPase HAD superfamily, subfamily IC [Plasmodium yoelii yoelii 17XNL]	1614	1614	90%	0.0	75%	XP_724204.1
ATPase, putative [Plasmodium yoelii]	1614	1614	90%	0.0	75%	CDZ14792.1
ATPase, putative [Plasmodium yoelii]	1614	1614	90%	0.0	75%	CDU16982.1
potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium yoelii 17X]	1613	1613	90%	0.0	75%	ETB58344.1
P-type ATPase4 [Plasmodium cynomolgi strain B]	1610	1610	84%	0.0	78%	XP_004224278.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium berghei]	1604	1604	91%	0.0	75%	SCM19714.1
ATPase, putative [Plasmodium berghei ANKA]	1601	1601	91%	0.0	75%	CDS45478.1
non-SERCA-type Ca2+-transporting P-ATPase, putative [Plasmodium berghei]	1600	1600	91%	0.0	75%	SCN23457.1
p-type ATPase [Plasmodium berghei strain ANKA] [Plasmodium berghei ANKA]	1422	1422	91%	0.0	70%	XP_678204.1
P-type ATPase4, putative [Toxoplasma gondii ME49]	1152	1152	91%	0.0	55%	XP_018635122.1
putative P-type ATPase4 [Toxoplasma gondii VAND]	1150	1150	91%	0.0	55%	KFH09260.1
putative P-type ATPase4 [Toxoplasma gondii RUB]	1150	1150	91%	0.0	55%	KFG58534.1
putative P-type ATPase4 [Toxoplasma gondii VEG]	1150	1150	91%	0.0	55%	ESS34627.1
putative P-type ATPase4 [Toxoplasma gondii GT1]	1150	1150	91%	0.0	55%	EPR63172.1
PMR1-like calcium ATPase [Toxoplasma gondii]	1150	1150	91%	0.0	55%	ABN55906.1
P-type ATPase4, putative [Hammondia hammondi]	1145	1145	91%	0.0	55%	XP_008887136.1
putative P-type Ca(2+)-ATPase [Neospora caninum Liverpool]	1145	1145	91%	0.0	55%	XP_003886335.1
P-type Ca(2+)-ATPase, putative [Eimeria praecox]	1068	1068	91%	0.0	53%	CDI73850.1
P-type ATPase4 [Babesia bovis T2Bo]	1030	1030	91%	0.0	51%	XP_001610924.1
p-type ATPase family member protein [Theileria equi]	1030	1030	91%	0.0	50%	XP_004833161.1
P-type ATPase4, putative [Babesia bigemina]	1014	1014	91%	0.0	50%	XP_012766644.1
cation ATPase [Theileria orientalis strain Shintoku]	1012	1012	91%	0.0	48%	XP_009689465.1
hypothetical protein cyc_04291 [Cyclospora cayetanensis]	1003	1003	86%	0.0	51%	OEH74329.1
uncharacterized protein [Babesia microti strain RI]	1000	1000	90%	0.0	51%	XP_012648811.1
cation ATPase [Theileria annulata]	988	988	91%	0.0	48%	XP_954058.1
P-type Ca(2+)-ATPase, putative [Eimeria maxima]	988	988	87%	0.0	51%	XP_013334395.1
P-type ATPase [Theileria parva strain Muguga]	979	979	91%	0.0	48%	XP_766241.1
unnamed protein product [Vitrella brassicaformis CCMP3155]	944	944	91%	0.0	50%	CEM38216.1
P-type Ca(2+)-ATPase, putative [Eimeria acervulina]	887	887	76%	0.0	51%	XP_013250937.1
unnamed protein product [Vitrella brassicaformis CCMP3155]	820	820	90%	0.0	44%	CEM23227.1
putative P-type ATPase4 [Toxoplasma gondii ARI]	659	659	59%	0.0	54%	KYF40433.1
putative P-type ATPase4 [Toxoplasma gondii FOU]	657	657	59%	0.0	54%	KFG46191.1
putative P-type ATPase4 [Toxoplasma gondii TgCatPRC2]	630	630	44%	0.0	55%	KYK65310.1
putative P-type ATPase [Gregarina niphandrodes]	568	704	89%	5e-177	39%	XP_011128793.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
potassium sodium efflux p-type fungal-type [Plasmopara halstedii]	552	552	90%	8e-174	37%	CEG37815.1
putative P-type ATPase4 [Toxoplasma gondii TgCatPRC2]	527	527	45%	2e-169	58%	KYK65320.1
ATPase [Cryptosporidium ubiquitum]	544	907	89%	6e-167	45%	OII72100.1
P-ATPase [Cryptosporidium parvum]	543	904	89%	2e-166	45%	AAC47833.1
P-type ATpase involved in cation transport [Cryptosporidium parvum Iowa II]	539	901	89%	3e-165	45%	XP_625857.1
ATPase [Cryptosporidium hominis TU502]	539	904	89%	4e-165	45%	XP_667379.1
E1-E2 ATPase family protein [Cryptosporidium andersoni]	539	892	91%	7e-165	44%	OII77732.1
Sm protein LSm5 [Phytophthora nicotianae]	527	573	80%	9e-164	40%	KUG00010.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica]	528	574	80%	9e-164	39%	ETM48340.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica P1569]	528	574	80%	1e-163	40%	ETI48633.1
E1-E2 ATPase family protein [Cryptosporidium muris RN66]	535	890	90%	1e-163	45%	XP_002140372.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica P1976]	527	573	80%	2e-163	40%	ETO77386.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type, putative [Phytophthora infestans T30-4]	527	573	79%	2e-163	40%	XP_002899328.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica]	527	573	80%	2e-163	40%	ETL41955.1
potassium sodium efflux p-type fungal-type [Plasmopara halstedii]	524	524	72%	2e-163	41%	CEG45014.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica]	527	573	80%	2e-163	40%	ETK88561.1
hypothetical protein PHYSODRAFT_353035 [Phytophthora sojae]	525	525	88%	2e-162	38%	XP_009537795.1
hypothetical protein AM588_10001352 [Phytophthora nicotianae]	518	518	73%	8e-162	41%	KUF87012.1
putative P-type ATPase4 [Toxoplasma gondii MAS]	497	497	32%	1e-161	59%	KFH12419.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica INRA-310]	519	519	73%	1e-160	41%	XP_008896841.1
hypothetical protein PHYSODRAFT_475371 [Phytophthora sojae]	498	498	66%	4e-155	40%	XP_009517681.1
potassium/sodium efflux P-type ATPase, fungal-type [Aphanomyces invadans]	501	501	75%	4e-154	37%	XP_008873575.1
calciumtransporting ATPase 1 putative [Albugo laibachii Nc14]	500	500	72%	5e-154	39%	CCA17472.1
P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	484	484	62%	3e-152	42%	XP_002907306.1
unnamed protein product [Albugo candida]	494	494	75%	6e-152	38%	CCI48557.1
P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	489	489	65%	2e-151	41%	XP_002907304.1
calcium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora infestans T30-4]	488	488	65%	3e-151	41%	XP_002907296.1
calcium-transporting ATPase, putative [Phytophthora infestans T30-4]	488	488	65%	4e-151	41%	XP_002907292.1
P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	487	487	65%	1e-150	40%	XP_002907302.1
putative P-type ATPase4 [Toxoplasma gondii p89]	456	456	29%	8e-147	59%	KFG32006.1
Calcium-transporting ATPase 4, endoplasmic reticulum-type [Symbiodinium microadriaticum]	467	467	88%	1e-140	31%	OLP82742.1
calcium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora infestans T30-4]	448	448	61%	8e-137	40%	XP_002907293.1
P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	447	447	61%	3e-136	40%	XP_002907297.1
Calcium-transporting ATPase 1 [Symbiodinium microadriaticum]	453	453	67%	9e-136	37%	OLQ04979.1
P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	445	445	61%	9e-136	40%	XP_002907301.1
P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	445	445	61%	2e-135	40%	XP_002907298.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
cation-transporting ATPase, putative [Phytophthora infestans T30-4]	441	441	61%	4e-134	40%	XP_002907300.1
p-type ATPase superfamily [Micromonas commoda]	431	431	74%	1e-128	36%	XP_002507786.1
p-type ATPase superfamily [Micromonas pusilla CCMP1545]	424	424	68%	6e-127	35%	XP_003062064.1
putative P-type ATPase4 [Toxoplasma gondii MAS]	405	405	34%	7e-127	49%	KFH12412.1
putative P-type ATPase4 [Toxoplasma gondii p89]	409	409	33%	1e-126	63%	KFG31989.1
hypothetical protein AURANDRAFT_30019 [Aureococcus anophagefferens]	419	419	65%	5e-126	38%	XP_009039254.1
potassium/sodium efflux P-type ATPase, fungal-type [Phytophthora parasitica INRA-310]	416	462	65%	6e-125	39%	XP_008903957.1
hypothetical protein AURANDRAFT_20268 [Aureococcus anophagefferens]	413	413	78%	7e-122	34%	XP_009033039.1
P-type Ca(2+)-ATPase, putative [Eimeria tenella]	395	395	44%	5e-118	47%	XP_013233090.1
cation-transporting E1-E2 ATPase [Trichomonas vaginalis]	390	390	71%	2e-115	33%	AHZ59478.1
cation-transporting E1-E2 ATPase [Trichomonas vaginalis]	388	388	71%	6e-115	33%	AHZ59476.1
cation-transporting E1-E2 ATPase [Trichomonas vaginalis]	388	388	71%	8e-115	33%	AHZ59477.1
hypothetical protein PBRA_004408 [Plasmodiophora brassicae]	389	389	77%	2e-113	34%	CEO95695.1
hypothetical protein V502_09270 [Pseudogymnoascus sp. VKM F-4520 (FW-2644)]	371	371	74%	6e-108	32%	KFZ08586.1
calcium-translocating P-type ATPase, SERCA-type [Pseudogymnoascus sp. 05NY08]	371	371	74%	1e-107	32%	OBT74941.1
hypothetical protein V495_04840 [Pseudogymnoascus sp. VKM F-4514 (FW-929)]	371	371	74%	1e-107	32%	KFY41655.1
calcium-translocating P-type ATPase, SERCA-type [Pseudogymnoascus sp. 23342-1-I1]	370	370	74%	1e-107	32%	OBT61579.1
hypothetical protein O988_01314 [Pseudogymnoascus sp. VKM F-3808]	370	370	74%	2e-107	32%	KFY03675.1
hypothetical protein V500_08745 [Pseudogymnoascus sp. VKM F-4518 (FW-2643)]	369	369	74%	4e-107	33%	KFY85057.1
calcium-translocating P-type ATPase, SERCA-type [Pseudogymnoascus sp. 03VT05]	369	369	74%	5e-107	32%	OBT86580.1
hypothetical protein V490_06839 [Pseudogymnoascus sp. VKM F-3557]	369	369	74%	8e-107	32%	KFX89718.1
hypothetical protein V494_05091 [Pseudogymnoascus sp. VKM F-4513 (FW-928)]	368	368	74%	9e-107	32%	KFY36342.1
calcium-translocating P-type ATPase, SERCA-type [Pseudogymnoascus sp. WSF 3629]	368	368	74%	1e-106	32%	OBT44297.1
calcium-transporting ATPase [Conidiobolus coronatus NRRL 28638]	368	368	74%	1e-106	32%	KXN70998.1
hypothetical protein V499_03236 [Pseudogymnoascus sp. VKM F-103]	368	368	74%	1e-106	32%	KFY77337.1
hypothetical protein V491_03418 [Pseudogymnoascus sp. VKM F-3775]	368	368	74%	2e-106	32%	KFY20797.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Talaromyces islandicus]	368	368	74%	2e-106	33%	CRG87964.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Rhynchosporium secalis]	367	367	74%	2e-106	32%	CZT42798.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Rhynchosporium commune]	367	367	74%	3e-106	33%	CZT09786.1
hypothetical protein V496_08867 [Pseudogymnoascus sp. VKM F-4515 (FW-2607)]	367	367	74%	4e-106	32%	KFY51319.1
potassium/sodium efflux P-type ATPase, fungal-type [Spizellomyces punctatus DAOM BR117]	370	370	74%	4e-106	32%	XP_016609006.1
hypothetical protein V492_03896 [Pseudogymnoascus sp. VKM F-4246]	366	366	74%	5e-106	32%	KFY12400.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Rhynchosporium agropyri]	366	366	74%	6e-106	32%	CZS94368.1
calcium-translocating P-type ATPase, SERCA-type [Pseudogymnoascus verrucosus]	366	366	74%	7e-106	32%	XP_018127093.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
putative endoplasmic reticulum calcium [Phaeomoniella chlamydospora]	367	367	74%	1e-105	33%	KKY19520.1
hypothetical protein V501_09711 [Pseudogymnoascus sp. VKM F-4519 (FW-2642)]	365	365	74%	1e-105	32%	KFZ01936.1
Calcium-transporting ATPase 1 [Choanephora cucurbitarum]	369	369	76%	1e-105	32%	OBZ89528.1
calcium-translocating P-type ATPase, SERCA-type [Pseudogymnoascus destructans 20631-21]	365	365	74%	2e-105	32%	XP_012740443.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Aspergillus lentulus]	365	365	74%	2e-105	32%	GAQ03463.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Coniosporium apollinis CBS 100218]	364	364	75%	4e-105	32%	XP_007784504.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Exophiala aquamarina CBS 119918]	363	363	75%	8e-105	31%	XP_013265640.1
endoplasmic reticulum calcium ATPase, putative [Aspergillus fumigatus Z5]	362	362	74%	2e-104	33%	KMK63003.1
ca2 atpase [Plasmopara halstedii]	363	363	70%	2e-104	33%	CEG39798.1
putative endoplasmic reticulum calcium ATPase [Aspergillus nomius NRRL 13137]	361	361	74%	4e-104	32%	XP_015408171.1
Calcium-transporting ATPase [Rasamsonia emersonii CBS 393.64]	361	361	71%	5e-104	33%	XP_013329418.1
hypothetical protein V498_07051 [Pseudogymnoascus sp. VKM F-4517 (FW-2822)]	361	361	74%	6e-104	31%	KFY87717.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like [Aplysia californica]	360	360	73%	8e-104	32%	XP_012940855.1
hypothetical protein AC578_5807 [Mycosphaerella eumusae]	360	360	73%	1e-103	31%	KXT00076.1
calcium-translocating P-type ATPase, SERCA-type [Blastomyces sp. CAC-2015b]	360	360	73%	1e-103	32%	OJD24233.1
endoplasmic reticulum calcium ATPase, putative [Talaromyces stipitatus ATCC 10500]	363	363	71%	1e-103	33%	XP_002485245.1
calcium-translocating P-type ATPase [Magnaporthe oryzae 70-15]	360	360	74%	1e-103	32%	XP_003710933.1
endoplasmic reticulum calcium ATPase, putative [Aspergillus fischeri NRRL 181]	360	360	74%	1e-103	32%	XP_001257791.1
hypothetical protein V493_08226 [Pseudogymnoascus sp. VKM F-4281 (FW-2241)]	359	359	74%	1e-103	32%	KFY18967.1
hypothetical protein [Parasitella parasitica]	363	363	73%	2e-103	32%	CEP13383.1
calcium-translocating P-type ATPase, SERCA-type [Emmonsia sp. CAC-2015a]	359	359	74%	2e-103	32%	OAX78037.1
Similar to Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type; acc. no. Q7PPA5 [Pyronema omphalodes CBS 100304]	359	359	71%	2e-103	32%	CCX14241.1
putative calcium p-type atpase [Rosellinia necatrix]	359	359	73%	2e-103	33%	GAP83445.1
ATPase, P-type, calcium-transporting [Ascosphaera apis ARSEF 7405]	358	358	70%	4e-103	33%	KZZ93035.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Neurospora crassa OR74A]	358	358	74%	5e-103	32%	XP_964482.3
calcium-translocating P-type ATPase, SERCA-type [Exophiala oligosperma]	358	358	73%	7e-103	32%	XP_016262518.1
sarco/endoplasmic reticulum-type Ca-2+-ATPase [Placopecten magellanicus]	357	357	71%	7e-103	33%	AAC63909.1
putative P-type ATPase4 [Toxoplasma gondii ARI]	332	332	16%	8e-103	75%	KYF40442.1
Calcium-transporting P-type ATPase IIA domain-containing protein [Rozella allomycis CSF55]	357	357	70%	1e-102	33%	EPZ34186.1
calcium-translocating P-type ATPase, SERCA-type [Exophiala xenobiotica]	357	357	74%	1e-102	32%	XP_013322238.1
putative endoplasmic reticulum calcium ATPase [Rhizophagus intraradices]	357	357	73%	1e-102	32%	CCJ31599.1
hypothetical protein SELMODRAFT_102055 [Albugo laibachii Nc14]	358	358	74%	1e-102	31%	CCA24190.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
calcium-translocating P-type ATPase [Blastomyces gilchristii SLH14081]	357	357	74%	1e-102	31%	XP_002627122.1
hypothetical protein AC579_8584 [Pseudocercospora musae]	357	357	74%	1e-102	31%	KXT11922.1
hypothetical protein H072_11171 [Dactylellina haptotyla CBS 200.50]	357	357	71%	1e-102	32%	XP_011116534.1
hypothetical protein NEUTE1DRAFT_72184 [Neurospora tetrasperma FGSC 2508]	357	357	74%	1e-102	32%	XP_009856145.1
calcium-transporting ATPase [Talaromyces cellulolyticus]	356	356	72%	2e-102	32%	GAM40431.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Blastomyces dermatitidis ATCC 18188]	357	357	74%	2e-102	31%	EGE77185.1
hypothetical protein MVEG_08438 [Mortierella verticillata NRRL 6337]	356	356	72%	2e-102	31%	KFH66339.1
hypothetical protein M378DRAFT_158447 [Amanita muscaria Koide BX008]	356	356	74%	2e-102	31%	KIL68618.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Phialocephala subalpina]	356	356	74%	2e-102	31%	CZR51208.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Blastomyces dermatitidis ATCC 26199]	356	356	74%	2e-102	31%	EQL38755.1
calcium-translocating P-type ATPase, SERCA-type [Coccidioides immitis RS]	356	356	73%	3e-102	32%	XP_001243422.2
endoplasmic reticulum calcium ATPase, putative [Aspergillus clavatus NRRL 1]	356	356	73%	3e-102	32%	XP_001272589.1
sarco/endoplasmic reticulum calcium-translocating P-type ATPase [Aspergillus parasiticus SU-1]	356	356	74%	3e-102	32%	KJK64505.1
Na+/K+ P-type ATPase [Mortierella elongata AG-77]	355	355	72%	3e-102	33%	OAQ25202.1
endoplasmic reticulum calcium ATPase, putative [Byssochlamys spectabilis No. 5]	355	355	70%	4e-102	33%	GAD96377.1
endoplasmic reticulum calcium ATPase, putative [Aspergillus flavus NRRL3357]	355	355	74%	4e-102	32%	XP_002375259.1
calcium-transporting ATPase-like protein [Chaetomium thermophilum var. thermophilum DSM 1495]	355	355	73%	5e-102	32%	XP_006695755.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Marssonina brunnea f. sp. 'multigermtubi' MB_m1]	355	355	73%	5e-102	33%	XP_007292711.1
putative calcium P-type ATPase [Neurospora tetrasperma FGSC 2509]	355	355	74%	6e-102	32%	EGZ77326.1
non-SERCA-type Ca2+-transporting P-ATPase, putative (ATP4) [Plasmodium ovale curtisi]	341	341	19%	6e-102	82%	SBS95773.1
hypothetical protein AOL_s00076g244 [Arthrobotrys oligospora ATCC 24927]	355	355	73%	7e-102	32%	XP_011121099.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Exophiala dermatitidis NIH/UT8656]	355	355	73%	7e-102	33%	XP_009152558.1
hypothetical protein THAOC_36093 [Thalassiosira oceanica]	355	355	73%	8e-102	32%	EJK45298.1
calcium P-type ATPase [Sordaria macrospora k-hell]	354	354	74%	9e-102	32%	XP_003345352.1
hypothetical protein SETTUDRAFT_44788 [Setosphaeria turcica Et28A]	354	354	72%	1e-101	31%	XP_008031298.1
sarcoplasmic/endoplasmic reticulum calcium-translocating P-type ATPase, putative [Coccidioides posadasii C735 delta SOWgp]	354	354	73%	1e-101	32%	XP_003066914.1
hypothetical protein HMPREF1544_08119 [Mucor circinelloides f. circinelloides 1006PhL]	358	358	71%	1e-101	32%	EPB85147.1
hypothetical protein ZTR_11064 [Talaromyces verruculosus]	354	354	74%	2e-101	32%	KUL83662.1
hypothetical protein ASPZODRAFT_93900 [Aspergillus zonatus CBS 506.65]	354	354	74%	2e-101	32%	OJJ47460.1
calcium-translocating P-type ATPase [Colletotrichum nymphaeae SA-01]	353	353	73%	2e-101	31%	KXH45539.1
endoplasmic reticulum calcium ATPase, putative [Talaromyces marneffei ATCC 18224]	353	353	72%	2e-101	32%	XP_002148932.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Talaromyces atroroseus]	353	353	71%	2e-101	31%	OKL62345.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein PTT_16365 [Pyrenophora teres f. teres 0-1]	353	353	72%	2e-101	32%	XP_003303962.1
calcium ATPase [Cenococcum geophilum 1.58]	353	353	70%	2e-101	32%	OCK95437.1
calcium ATPase [Paraphaeosphaeria sporulosa]	353	353	72%	3e-101	32%	XP_018029096.1
hypothetical protein TRV_02782 [Trichophyton verrucosum HKI 0517]	353	353	74%	3e-101	31%	XP_003023092.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 1 [Aspergillus oryzae RIB40]	353	353	74%	3e-101	32%	XP_001819290.1
Ca2+ transporting ATPase [Aspergillus oryzae 3.042]	353	353	74%	4e-101	32%	EIT72822.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Colletotrichum chlorophyti]	353	353	70%	4e-101	32%	OLN82035.1
hypothetical protein H257_00743 [Aphanomyces astaci]	354	354	70%	4e-101	32%	XP_009821873.1
calcium-translocating P-type ATPase [Microdochium bolleyi]	352	352	74%	4e-101	32%	KXJ95341.1
hypothetical protein ASPACDRAFT_78508 [Aspergillus aculeatus ATCC 16872]	353	353	73%	4e-101	32%	OJK00553.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 1 [Aspergillus niger CBS 513.88]	352	352	73%	6e-101	32%	XP_001399082.1
hypothetical protein PBRA_006016 [Plasmodiophora brassicae]	352	352	74%	7e-101	32%	CEO97902.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like [Rhagoletis zephyria]	352	352	70%	8e-101	32%	XP_017491630.1
calcium-translocating P-type ATPase [Colletotrichum salicis]	352	352	73%	9e-101	31%	KXH63772.1
Calcium ATPase, transmembrane M [Glarea lozoyensis ATCC 20868]	352	352	74%	1e-100	31%	XP_008076890.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Arthroderma otae CBS 113480]	352	352	74%	1e-100	31%	XP_002843429.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Vicugna pacos]	348	348	70%	1e-100	32%	XP_015095615.1
calcium-translocating P-type ATPase, SERCA-type [Rhinocladiella mackenziei CBS 650.93]	352	352	73%	1e-100	33%	XP_013274686.1
calcium-translocating P-type ATPase, SERCA-type [Exophiala sideris]	352	352	70%	1e-100	33%	KIV77573.1
sarco/endoplasmic reticulum Ca2+-ATPase [Paramecium tetraurelia]	352	352	70%	1e-100	32%	CAB96170.1
calcium ATPase [Coniochaeta ligniaria NRRL 30616]	351	351	74%	1e-100	31%	OIW34549.1
calcium-translocating P-type ATPase, SERCA-type [Exophiala mesophila]	352	352	74%	1e-100	32%	XP_016225853.1
calcium-translocating P-type ATPase, SERCA-type [Uncinocarpus reesii 1704]	351	351	73%	2e-100	31%	XP_002583090.1
hypothetical protein GLOINDRAFT_258058 [Rhizophagus irregularis DAOM 181602]	351	351	70%	2e-100	32%	ESA01669.1
hypothetical protein BC1G_08297 [Botrytis cinerea B05.10]	351	351	74%	2e-100	31%	XP_001553573.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii VGIV IND107]	351	351	73%	2e-100	31%	KIR83964.1
calcium-translocating P-type ATPase [Colletotrichum gloeosporioides Cg-14]	351	351	70%	2e-100	31%	EQB46914.1
hypothetical protein PTRG_08738 [Pyrenophora tritici-repentis Pt-1C-BFP]	351	351	75%	2e-100	31%	XP_001939070.1
calcium-translocating P-type ATPase [Colletotrichum orchidophilum]	351	351	74%	2e-100	31%	OHE97806.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Cladophialophora yegresii CBS 114405]	351	351	74%	2e-100	31%	XP_007754055.1
calcium-translocating P-type ATPase, SERCA-type [Cladophialophora carrionii CBS 160.54]	351	351	74%	2e-100	31%	XP_008724219.1
hypothetical protein RMATCC62417_02661 [Rhizopus microsporus]	355	355	73%	2e-100	32%	CEG66000.1
calcium-transporting atpase sarcoplasmic endoplasmic reticulum type [Stemphylium lycopersici]	350	350	75%	3e-100	30%	KNG49156.1
calcium-translocating P-type ATPase [Colletotrichum simmondsii]	350	350	73%	3e-100	31%	KXH48917.1

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calcium-translocating P-type ATPase, SERCA-type [Capronia semi-immersa]	351	351	74%	3e-100	31%	KIW71875.1
hypothetical protein PHYBLDRAFT_86228 [Phycomyces blakesleeanus NRRL 1555(-)]	345	345	66%	3e-100	33%	XP_018285494.1
calcium ATPase [Lepidopterella palustris CBS 459.81]	350	350	70%	3e-100	32%	OCK83916.1
probable serca-type calcium ATPase [Phaeodactylum tricornutum CCAP 1055/1]	350	350	65%	4e-100	33%	XP_002183209.1
hypothetical protein ARB_01033 [Trichophyton benhamiae CBS 112371]	350	350	71%	5e-100	32%	XP_003012782.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus neoformans var. grubii H99]	350	350	73%	5e-100	31%	XP_012053868.1
calcium-translocating P-type ATPase, SERCA-type [Verruconis gallopava]	350	350	71%	5e-100	33%	XP_016211584.1
calcium-translocating P-type ATPase [Colletotrichum fioriniae PJ7]	349	349	73%	5e-100	31%	XP_007589790.1
hypothetical protein SS1G_12923 [Sclerotinia sclerotiorum 1980]	350	350	74%	5e-100	31%	XP_001586345.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii CA1873]	350	350	73%	6e-100	31%	KIR58116.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Camelus ferus]	347	347	70%	6e-100	32%	XP_014421213.1
calcium-translocating P-type ATPase [Colletotrichum tofieldiae]	349	349	70%	6e-100	32%	KZL76054.1
calcium-translocating P-type ATPase, SERCA-type [Cladophialophora bantiana CBS 173.52]	350	350	70%	6e-100	33%	XP_016621138.1
putative endoplasmic reticulum calcium protein [Neofusicoccum parvum UCRNP2]	349	349	73%	6e-100	32%	XP_007586835.1
calcium ATPase [Pyrenochaeta sp. DS3sAY3a]	350	350	74%	6e-100	30%	OAL49261.1
Calcium-transporting ATPase [Colletotrichum higginsianum IMI 349063]	349	349	71%	7e-100	32%	XP_018164320.1
hypothetical protein CANCADRAFT_25785 [Tortispora caseinolytica NRRL Y-17796]	348	348	71%	7e-100	32%	ODV91001.1
putative P-type ATPase [Gregarina niphandrodes]	356	470	87%	7e-100	34%	XP_011129663.1
isoform B of calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Aspergillus udagawae]	348	348	68%	7e-100	33%	GAO87734.1
putative calcium-translocating P-type ATPase [Colletotrichum sublineola]	349	349	70%	7e-100	32%	KDN63447.1
putative calcium p-type atpase [Erysiphe necator]	349	349	75%	7e-100	31%	KHJ31486.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bos indicus]	345	345	70%	1e-99	32%	XP_019818091.1
hypothetical protein ASPBRDRAFT_128724 [Aspergillus brasiliensis CBS 101740]	349	349	73%	1e-99	32%	OJJ70758.1
hypothetical protein JAAARDRAFT_32974 [Jaapia argillacea MUCL 33604]	348	348	74%	1e-99	31%	KDQ59419.1
calcium-transporting ATPase [Cryptococcus neoformans var. neoformans JEC21]	349	349	73%	1e-99	31%	XP_572412.1
hypothetical protein PFICI_01455 [Pestalotiopsis fici W106-1]	348	348	71%	1e-99	33%	XP_007828227.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Physeter catodon]	347	347	70%	1e-99	32%	XP_007119926.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Cladophialophora carrionii]	349	349	74%	1e-99	31%	OCT46007.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Aspergillus terreus NIH2624]	348	348	71%	1e-99	32%	XP_001212077.1
hypothetical protein BAUCODRAFT_152707 [Baudoinia panamericana UAMH 10762]	348	348	73%	1e-99	31%	XP_007681762.1
calcium-translocating P-type ATPase, SERCA-type [Fonsecaea erecta]	349	349	70%	1e-99	33%	XP_018688428.1
hypothetical protein GALMADRAFT_276480 [Galerina marginata CBS 339.88]	348	348	74%	2e-99	31%	KDR81806.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Taphrina deformans PYCC 5710]	348	348	74%	2e-99	32%	CCG83475.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Vicugna pacos]	347	347	70%	2e-99	32%	XP_006205342.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Vicugna pacos]	346	346	70%	2e-99	32%	XP_006205343.2
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii CA1280]	348	348	73%	2e-99	31%	KIR44186.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 1-like [Octopus bimaculoides]	348	348	71%	2e-99	31%	XP_014786351.1
putative endoplasmic reticulum calcium ATPase [Aspergillus bombycis]	348	348	74%	2e-99	32%	OGM41781.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Physeter catodon]	346	346	70%	2e-99	32%	XP_007119925.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Capra hircus]	346	346	70%	2e-99	32%	XP_017906921.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Ovis aries]	346	346	70%	2e-99	32%	XP_004003394.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Capra hircus]	346	346	70%	2e-99	32%	XP_017906906.1
calcium-translocating P-type ATPase, SERCA-type [Cladophialophora immunda]	348	348	73%	2e-99	32%	XP_016246616.1
hypothetical protein TD95_000482 [Thielaviopsis punctulata]	348	348	71%	2e-99	32%	KKA27395.1
putative calcium p-type atpase protein [Eutypa lata UCREL1]	348	348	74%	2e-99	32%	XP_007798857.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bos taurus]	346	346	70%	2e-99	32%	XP_010799920.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Bubalus bubalis]	347	347	70%	2e-99	32%	XP_006056306.1
hypothetical protein RHOBADRAFT_48315 [Rhodotorula graminis WP1]	348	348	74%	2e-99	31%	XP_018271880.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type (Calcium pump) [Cryptococcus gattii WM276]	348	348	73%	2e-99	31%	XP_003197168.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Nannospalax galili]	345	345	70%	3e-99	32%	XP_008823330.1
calcium-translocating P-type ATPase, SERCA-type [Paracoccidioides brasiliensis]	348	348	74%	3e-99	32%	ODH50939.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like [Tetranychus urticae]	348	348	70%	3e-99	32%	XP_015789622.1
hypothetical protein THITE_127365 [Thielavia terrestris NRRL 8126]	348	348	74%	3e-99	31%	XP_003656676.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Capra hircus]	345	345	70%	3e-99	32%	XP_017906925.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X10 [Cercocebus atys]	348	348	70%	3e-99	32%	XP_011899392.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ovis aries]	346	346	70%	3e-99	32%	XP_011958889.1
calcium-transporting ATPase type 2C member 1 [Bos taurus]	347	347	70%	3e-99	32%	NP_786979.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii Ru294]	348	348	73%	3e-99	31%	KIR52295.1
calcium-translocating P-type ATPase, SERCA-type [Paracoccidioides brasiliensis]	348	348	74%	3e-99	32%	ODH33980.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bos taurus]	345	345	70%	3e-99	32%	XP_010799921.1
calcium-translocating P-type ATPase, SERCA-type [Emmonsia pasteuriana UAMH 9510]	348	348	74%	3e-99	31%	OJD14038.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Miniopterus natalensis]	345	345	70%	3e-99	32%	XP_016079825.1
hypothetical protein ASPFODRAFT_49614 [Aspergillus luchuensis CBS 106.47]	347	347	73%	3e-99	32%	OJZ84103.1
calcium-transporting ATPase type 2C member 1 [Castor canadensis]	345	345	70%	3e-99	32%	JAV44532.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ovis aries]	346	346	70%	3e-99	32%	XP_004003395.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Odobenus rosmarus divergens]	345	345	70%	3e-99	32%	XP_004415494.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Nannospalax galili]	345	345	70%	3e-99	32%	XP_008823329.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Ovis aries]	345	345	70%	3e-99	32%	XP_011958897.1
hypothetical protein COCC4DRAFT_80942 [Bipolaris maydis ATCC 48331]	347	347	75%	3e-99	31%	XP_014079946.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Capra hircus]	346	346	70%	3e-99	32%	XP_017906898.1
hypothetical protein MVEG_04563 [Mortierella verticillata NRRL 6337]	347	347	71%	3e-99	31%	KFH69757.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Cercocebus atys]	348	348	70%	3e-99	32%	XP_011899387.1
calcium-translocating P-type ATPase, SERCA-type [Trichophyton interdigitale H6]	347	347	74%	4e-99	31%	EZF31174.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Rousettus aegyptiacus]	347	347	70%	4e-99	32%	XP_015995755.1
hypothetical protein ASPTUDRAFT_26017 [Aspergillus tubingensis CBS 134.48]	347	347	73%	4e-99	32%	OJI90476.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Equus asinus]	343	343	70%	4e-99	32%	XP_014683964.1
calcium-transporting ATPase 3 [Mortierella elongata AG-77]	347	347	71%	4e-99	31%	OAQ29248.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pan paniscus]	346	346	70%	4e-99	32%	XP_003829496.1
Putative Calcium-translocating P-type ATPase, SERCA-type [Aspergillus calidoustus]	347	347	74%	4e-99	31%	CEN61577.1
calcium-translocating P-type ATPase [Colletotrichum graminicola M1.001]	347	347	70%	4e-99	32%	XP_008093374.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Rousettus aegyptiacus]	345	345	70%	4e-99	32%	XP_015995759.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Orcinus orca]	344	344	70%	4e-99	32%	XP_004283476.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Cercocebus atys]	348	348	70%	4e-99	32%	XP_011899384.1
hypothetical protein MYCFIDRAFT_49900 [Pseudocercospora fijiensis CIRAD86]	347	347	73%	4e-99	31%	XP_007928838.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Pan paniscus]	345	345	70%	4e-99	32%	XP_008953057.1
sarcoplasmic/endoplasmic reticulum calcium ATPase [Trichophyton tonsurans CBS 112818]	347	347	74%	4e-99	31%	EGD96734.1
endoplasmic reticulum calcium ATPase [Aspergillus niger]	348	348	73%	4e-99	32%	GAQ44493.1
PREDICTED: LOW QUALITY PROTEIN: ATPase, Ca++ transporting, type 2C, member 1 [Pantholops hodgsonii]	346	346	70%	4e-99	32%	XP_005985936.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Miniopterus natalensis]	345	345	70%	4e-99	32%	XP_016079826.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Sus scrofa]	345	345	70%	4e-99	32%	XP_013845529.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Nannospalax galili]	345	345	70%	4e-99	32%	XP_017651589.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Camelus ferus]	345	345	70%	4e-99	32%	XP_014421212.1
calcium-translocating P-type ATPase, SERCA-type [Paracoccidioides brasiliensis Pb18]	347	347	74%	5e-99	32%	XP_010759699.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Rousettus aegyptiacus]	346	346	70%	5e-99	32%	XP_015995757.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Nannospalax galili]	346	346	70%	5e-99	32%	XP_008823326.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Miniopterus natalensis]	345	345	70%	5e-99	32%	XP_016079827.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein Z520_06652 [Fonsecaea multimorphosa CBS 102226]	347	347	74%	5e-99	32%	XP_016631997.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Camelus ferus]	346	346	70%	5e-99	32%	XP_014421211.1
endoplasmic reticulum calcium ATPase [Aspergillus kawachii IFO 4308]	347	347	73%	5e-99	32%	GAA90078.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Rousettus aegyptiacus]	346	346	70%	5e-99	32%	XP_015995756.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Rousettus aegyptiacus]	346	346	70%	5e-99	32%	XP_015995754.1
Calcium-transporting ATPase, endoplasmic reticulum-type [Morus notabilis]	348	348	71%	5e-99	33%	XP_010100698.1
calcium-translocating P-type ATPase, SERCA-type [Pneumocystis carinii B80]	347	347	72%	6e-99	32%	XP_018226927.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Sus scrofa]	345	345	70%	6e-99	32%	XP_003358358.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pan paniscus]	345	345	70%	6e-99	32%	XP_008953056.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Pan paniscus]	345	345	70%	6e-99	32%	XP_003829498.1
calcium-translocating P-type ATPase, SERCA-type [Exophiala spinifera]	347	347	73%	6e-99	32%	XP_016232571.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Orcinus orca]	345	345	70%	6e-99	32%	XP_012393571.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Equus przewalskii]	343	343	70%	6e-99	32%	XP_008518083.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Verticillium dahliae VdLs.17]	347	347	71%	6e-99	31%	XP_009655292.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Sus scrofa]	345	345	70%	7e-99	32%	XP_013845528.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Cercocebus atys]	348	348	70%	7e-99	32%	XP_011899380.1
hypothetical protein [Podospora anserina S mat+]	347	347	73%	7e-99	31%	XP_001912923.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bos indicus]	345	345	70%	7e-99	32%	XP_019818082.1
calcium-transporting ATPase [Punctularia strigosozonata HHB-11173 SS5]	346	346	73%	7e-99	32%	XP_007389147.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Camelus dromedarius]	345	345	70%	7e-99	32%	XP_010977993.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bison bison bison]	344	344	70%	8e-99	32%	XP_010833273.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bison bison bison]	344	344	70%	8e-99	32%	XP_010833272.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii E566]	346	346	73%	8e-99	32%	KIY32111.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Odobenus rosmarus divergens]	346	346	70%	8e-99	32%	XP_012423211.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Miniopterus natalensis]	345	345	70%	8e-99	32%	XP_016079824.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Odobenus rosmarus divergens]	345	345	70%	9e-99	32%	XP_012423212.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Odobenus rosmarus divergens]	345	345	70%	9e-99	32%	XP_004415492.1
hypothetical protein ANO11243_072320 [fungal sp. No.11243]	346	346	73%	9e-99	31%	GAM89195.1
calcium-translocating p-type atpase [Colletotrichum incanum]	346	346	70%	9e-99	32%	KZL81025.1
calcium ATPase [Alternaria alternata]	346	346	70%	9e-99	32%	XP_018379263.1
calcium-translocating p-type serca-type [Diplodia corticola]	346	346	73%	1e-98	31%	OJD32786.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Odobenus rosmarus divergens]	345	345	70%	1e-98	32%	XP_004415491.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Fusarium graminearum PH-1]	346	346	71%	1e-98	31%	XP_011317045.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein DCAR_005296 [Daucus carota subsp. sativus]	347	347	73%	1e-98	31%	KZN04459.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Ceratotherium simum simum]	342	342	70%	1e-98	32%	XP_014645134.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Orcinus orca]	345	345	70%	1e-98	32%	XP_012393570.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Tursiops truncatus]	343	343	70%	1e-98	32%	XP_019789945.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Cimex lectularius]	343	343	70%	1e-98	33%	XP_014260302.1
High affinity Ca2+-Mn2+ P-type ATPase [Blumeria graminis f. sp. tritici 96224]	346	346	74%	1e-98	31%	EPQ67475.1
cation-transporting ATPase, putative [Phytophthora infestans T30-4]	343	343	56%	1e-98	37%	XP_002907294.1
Ca2+ transporting ATPase [Nannizzia gypsea CBS 118893]	346	346	73%	1e-98	30%	XP_003172122.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus depauperatus CBS 7855]	345	345	73%	1e-98	31%	ODN87782.1
hypothetical protein BN1708_015482 [Verticillium longisporum]	345	345	70%	1e-98	32%	CRK29132.1
calcium-translocating P-type ATPase, SERCA-type [Capronia coronata CBS 617.96]	346	346	74%	2e-98	32%	XP_007720351.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Sorex araneus]	344	344	70%	2e-98	32%	XP_004603861.1
hypothetical protein FE78DRAFT_33291 [Acidomyces richmondensis]	345	345	73%	2e-98	31%	KXL43692.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Sorex araneus]	343	343	70%	2e-98	32%	XP_004603863.1
Ca2+-transporting ATPase [Saprolegnia diclina VS20]	346	346	70%	2e-98	32%	XP_008609540.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Cladophialophora psammophila CBS 110553]	346	346	71%	2e-98	32%	XP_007751787.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Cimex lectularius]	343	343	70%	2e-98	33%	XP_014260301.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Equus caballus]	345	345	70%	2e-98	32%	XP_005600988.1
putative calcium P-type ATPase [Sclerotinia borealis F-4128]	345	345	72%	2e-98	31%	ESZ95351.1
calcium ATPase [Glonium stellatum]	345	345	70%	2e-98	32%	OCL06258.1
calcium P-type ATPase [Blumeria graminis f. sp. hordei DH14]	345	345	74%	2e-98	32%	CCU78880.1
hypothetical protein [Paramecium tetraurelia strain d4-2]	346	346	70%	3e-98	32%	XP_001453966.1
calcium ATPase [Sphaerulina musiva SO2202]	345	345	74%	3e-98	31%	XP_016758061.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Sorex araneus]	343	343	70%	3e-98	32%	XP_004603862.1
hypothetical protein COCVIDRAFT_110715 [Bipolaris victoriae FI3]	345	345	75%	3e-98	30%	XP_014552292.1
hypothetical protein AOCH_004481 [Aspergillus ochraceoroseus]	342	342	72%	3e-98	32%	KKK16514.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Cimex lectularius]	343	343	70%	3e-98	33%	XP_014260300.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Cebus capucinus imitator]	342	342	70%	3e-98	32%	XP_017365655.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Cercocebus atys]	346	346	70%	3e-98	32%	XP_011899381.1
hypothetical protein MYCTH_2294817 [Thermothelomyces thermophila ATCC 42464]	344	344	74%	3e-98	31%	XP_003658712.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Ailuropoda melanoleuca]	343	343	70%	4e-98	32%	XP_019658743.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ailuropoda melanoleuca]	344	344	70%	4e-98	32%	XP_019658741.1
hypothetical protein cypCar_00019205 [Cyprinus carpio]	341	341	70%	4e-98	32%	KTF90310.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Heterocephalus glaber]	343	343	70%	4e-98	32%	XP_012926034.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein SI65_01121 [Aspergillus cristatus]	344	344	74%	4e-98	31%	ODM23532.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Panthera pardus]	344	344	70%	4e-98	32%	XP_019291784.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Mustela putorius furo]	344	344	70%	4e-98	32%	XP_012916875.1
calcium-translocating P-type ATPase, SERCA-type [Fonsecaea pedrosoi CBS 271.37]	345	345	74%	4e-98	31%	XP_013286705.1
calcium-translocating P-type ATPase [Gaeumannomyces graminis var. tritici R3-111a-1]	344	344	73%	4e-98	31%	XP_009225803.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Equus caballus]	343	343	70%	4e-98	32%	XP_001496877.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Equus caballus]	343	343	70%	4e-98	32%	XP_005600989.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Panthera pardus]	343	343	70%	4e-98	32%	XP_019291792.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Mustela putorius furo]	343	343	70%	4e-98	32%	XP_012916876.1
putative endoplasmic reticulum calcium ATPase [Xylona heveae TC161]	344	344	70%	5e-98	32%	XP_018190173.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Sorex araneus]	343	343	70%	5e-98	32%	XP_004603860.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Heterocephalus glaber]	343	343	70%	5e-98	32%	XP_012926047.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Colobus angolensis palliatus]	342	342	70%	5e-98	32%	XP_011789065.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Heterocephalus glaber]	343	343	70%	5e-98	32%	XP_004834277.1
hypothetical protein FPOA_01305 [Fusarium poae]	344	344	71%	5e-98	31%	OBS27362.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Manis javanica]	343	343	70%	5e-98	32%	XP_017527908.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Ailuropoda melanoleuca]	343	343	70%	5e-98	32%	XP_019658742.1
hypothetical protein PANDA_011698 [Ailuropoda melanoleuca]	342	342	70%	5e-98	32%	EFB26966.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Colobus angolensis palliatus]	342	342	70%	5e-98	32%	XP_011789066.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Mustela putorius furo]	343	343	70%	5e-98	32%	XP_012916874.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Mustela putorius furo]	343	343	70%	5e-98	32%	XP_012916873.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Mustela putorius furo]	342	342	70%	5e-98	32%	XP_012916879.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Mustela putorius furo]	343	343	70%	5e-98	32%	XP_012916877.1
putative endoplasmic reticulum calcium ATPase [Aspergillus rambellii]	344	344	73%	5e-98	32%	KKK23376.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Rhinopithecus roxellana]	342	342	70%	5e-98	32%	XP_010378660.1
calcium transporter ATPase [Zymoseptoria tritici IPO323]	344	344	74%	5e-98	30%	XP_003850768.1
hypothetical protein OIDMADRAFT_159005 [Oidiodendron maius Zn]	344	344	73%	5e-98	32%	KIN03983.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ailuropoda melanoleuca]	343	343	70%	6e-98	32%	XP_011227510.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Octodon degus]	341	341	70%	6e-98	32%	XP_004625083.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X9 [Chlorocebus sabaeus]	341	341	70%	6e-98	32%	XP_008007328.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Heterocephalus glaber]	343	343	70%	6e-98	32%	XP_012926031.1
hypothetical protein ACN42_g11558 [Penicillium freii]	345	345	74%	6e-98	32%	KUM55687.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Capronia epimyces CBS 606.96]	344	344	74%	6e-98	31%	XP_007737115.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Rhinopithecus roxellana]	343	343	70%	6e-98	32%	XP_010378631.1
ATP-dependent Ca2+ pump PMR1 [Homo sapiens]	341	341	70%	6e-98	32%	AAF26296.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Papio anubis]	342	342	70%	6e-98	32%	XP_003895169.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X9 [Pan troglodytes]	341	341	70%	7e-98	32%	XP_001145548.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Rhinopithecus roxellana]	342	342	70%	7e-98	32%	XP_010378653.1
sarcoplasmic/endoplasmic reticulum calcium-translocating P-type ATPase like protein [Zymoseptoria brevis]	344	344	73%	7e-98	30%	KJX94847.1
hypothetical protein COCSADRAFT_38711 [Bipolaris sorokiniana ND90Pr]	344	344	75%	7e-98	30%	XP_007702095.1
hypothetical protein H310_01079 [Aphanomyces invadans]	345	345	71%	7e-98	32%	XP_008862320.1
calcium-transporting ATPase type 2C member 1 isoform 1c [Homo sapiens]	341	341	70%	7e-98	32%	NP_001001485.1
Ca(2+)/Mn(2+)-transporting P-type ATPase PMR1 [Rhizophagus irregularis DAOM 197198w]	347	347	68%	7e-98	32%	EXX59744.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Ceratotherium simum simum]	343	343	70%	7e-98	32%	XP_014645138.1
hypothetical protein PHACADRAFT_256444 [Phanerochaete carnosa HHB-10118-sp]	343	343	71%	7e-98	32%	XP_007395983.1
p-type ATPase superfamily [Micromonas commoda]	344	344	65%	7e-98	32%	XP_002507319.1
hypothetical protein DOTSEDRAFT_75085 [Dothistroma septosporum NZE10]	343	343	74%	7e-98	31%	EME39239.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ceratotherium simum simum]	342	342	70%	7e-98	32%	XP_014645129.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Heterocephalus glaber]	343	343	70%	7e-98	32%	XP_004834278.2
calcium-transporting ATPase type 2C member 1 isoform 1f [Homo sapiens]	341	341	70%	8e-98	32%	NP_001186113.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Loxodonta africana]	341	341	70%	8e-98	32%	XP_010598789.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Ictidomys tridecemlineatus]	342	342	70%	8e-98	32%	XP_013214843.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Loxodonta africana]	342	342	70%	8e-98	32%	XP_010598788.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ceratotherium simum simum]	342	342	70%	8e-98	32%	XP_004419435.1
endoplasmic reticulum calcium ATPase [Aspergillus fumigatus var. RP-2014]	343	343	71%	8e-98	33%	KEY82447.1
Pc14g01690 [Penicillium rubens Wisconsin 54-1255]	343	343	73%	8e-98	32%	XP_002560163.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Rhinopithecus roxellana]	342	342	70%	8e-98	32%	XP_010378646.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Colobus angolensis palliatus]	343	343	70%	8e-98	32%	XP_011789062.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Colobus angolensis palliatus]	342	342	70%	8e-98	32%	XP_011789063.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Rhinopithecus roxellana]	342	342	70%	8e-98	32%	XP_010378639.1
calcium P-type ATPase-1 [Diaporthe helianthi]	343	343	71%	8e-98	32%	OCW31000.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X16 [Cercocebus atys]	341	341	70%	9e-98	32%	XP_011899398.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Pan troglodytes]	342	342	70%	9e-98	32%	XP_001145322.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Rhinopithecus roxellana]	343	343	70%	9e-98	32%	XP_010378621.1
calcium-translocating P-type ATPase, SERCA-type [Fonsecaea nubica]	344	344	74%	9e-98	31%	OAL34446.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Homo sapiens]	342	342	70%	9e-98	32%	XP_005247415.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X8 [Chlorocebus sabaeus]	342	342	70%	9e-98	32%	XP_008007327.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Octodon degus]	342	342	70%	9e-98	32%	XP_004625080.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Rhinolophus sinicus]	341	341	70%	1e-97	32%	XP_019581513.1
calcium-transporting ATPase type 2C member 1 isoform 1e [Homo sapiens]	342	342	70%	1e-97	32%	NP_001186112.1
calcium-translocating P-type ATPase, SERCA-type [Fonsecaea monophora]	344	344	74%	1e-97	31%	OAG39119.1
ATPase, Ca++ transporting, type 2C, member 1, isoform CRA_a [Homo sapiens]	342	342	70%	1e-97	32%	EAW79217.1
endoplasmic reticulum calcium ATPase [Aspergillus fumigatus Af293]	343	343	71%	1e-97	33%	XP_750567.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Rhinolophus sinicus]	341	341	70%	1e-97	32%	XP_019581511.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Rhinolophus sinicus]	342	342	70%	1e-97	32%	XP_019581510.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Pan troglodytes]	342	342	70%	1e-97	32%	XP_009444745.1
calcium ATPase [Stagonospora sp. SRC1lsM3a]	343	343	75%	1e-97	30%	OAL06896.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ictidomys tridecemlineatus]	342	342	70%	1e-97	32%	XP_013214842.1
p-type ATPase family member protein [Theileria equi]	345	345	69%	1e-97	32%	XP_004829101.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Cebus capucinus imitator]	341	341	70%	1e-97	32%	XP_017365654.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X8 [Pan troglodytes]	341	341	70%	1e-97	32%	XP_009444746.1
calcium-transporting ATPase type 2C member 1 isoform 1b [Homo sapiens]	342	342	70%	1e-97	32%	NP_001001487.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Chlorocebus sabaeus]	342	342	70%	1e-97	32%	XP_008007325.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Astyanax mexicanus]	343	343	70%	1e-97	32%	XP_007228659.1
PREDICTED: ATPase, Ca++ transporting, type 2C, member 2 S homeolog isoform X3 [Xenopus laevis]	340	340	68%	1e-97	32%	XP_018115261.1
PREDICTED: ATPase, Ca++ transporting, type 2C, member 2 S homeolog isoform X1 [Xenopus laevis]	343	343	70%	1e-97	32%	XP_018115259.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Pan troglodytes]	342	342	70%	1e-97	32%	XP_009444744.1
hypothetical protein COCCADRAFT_9134 [Bipolaris zeicola 26-R-13]	343	343	74%	1e-97	30%	XP_007717189.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Otolemur garnettii]	340	340	70%	1e-97	32%	XP_003781759.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Pan troglodytes]	342	342	70%	1e-97	32%	XP_001145788.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Macaca fascicularis]	342	342	70%	1e-97	32%	XP_005545816.1
ATP-dependent Ca2+ pump PMR1 [Homo sapiens]	341	341	70%	1e-97	32%	AAF26295.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Harpegnathos saltator]	343	343	73%	1e-97	31%	XP_019697793.1
putative calcium-transporting atpase sarcoplasmic/endoplasmic reticulum type calcium pump isoform 1 [Amblyomma aureolatum]	343	343	71%	1e-97	31%	JAT95028.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ictidomys tridecemlineatus]	342	342	70%	1e-97	32%	XP_005327058.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Cebus capucinus imitator]	341	341	70%	1e-97	32%	XP_017365653.1
hypothetical protein COCMIDRAFT_5099 [Bipolaris oryzae ATCC 44560]	343	343	74%	1e-97	30%	XP_007687714.1
endoplasmic reticulum calcium ATPase, putative [Aspergillus fumigatus A1163]	342	342	71%	1e-97	33%	EDP49241.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Macaca fascicularis]	342	342	70%	1e-97	32%	XP_005545819.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
calcium-transporting ATPase type 2C member 1 [Macaca mulatta]	342	342	70%	1e-97	32%	NP_001252952.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Macaca nemestrina]	341	341	70%	1e-97	32%	XP_011754211.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Chlorocebus sabaeus]	342	342	70%	1e-97	32%	XP_008007320.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Cebus capucinus imitator]	342	342	70%	1e-97	32%	XP_017365648.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X9 [Cercocebus atys]	343	343	70%	1e-97	32%	XP_011899391.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Astyanax mexicanus]	343	343	70%	1e-97	32%	XP_007228660.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Macaca nemestrina]	342	342	70%	1e-97	32%	XP_011754209.1
haloacid dehalogenase [Mucor ambiguus]	347	347	71%	1e-97	31%	GAN02882.1
KIAA1347 protein [Homo sapiens]	341	341	70%	1e-97	32%	BAA92585.1
hypothetical protein PILCRDRAFT_822114 [Piloderma croceum F 1598]	343	343	78%	1e-97	30%	KIM80832.1
calcium-transporting ATPase type 2C member 1 isoform 1d [Homo sapiens]	342	342	70%	1e-97	32%	NP_001001486.1
hypothetical protein EGK_12110 [Macaca mulatta]	342	342	70%	1e-97	32%	EHH16768.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pan troglodytes]	342	342	70%	1e-97	32%	XP_001146246.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X8 [Saimiri boliviensis boliviensis]	341	341	70%	2e-97	32%	XP_003925137.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Cebus capucinus imitator]	341	341	70%	2e-97	32%	XP_017365651.1
calcium transport ATPase ATP2C1 [Homo sapiens]	341	341	70%	2e-97	32%	AAF35375.1
conserved hypothetical protein [Chaetomium globosum CBS 148.51]	343	343	74%	2e-97	32%	XP_001220798.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Saimiri boliviensis boliviensis]	341	341	70%	2e-97	32%	XP_010334118.1
calciumtransporting P-type ATPase, PMR1-type, putative [Acanthamoeba castellanii str. Neff]	341	341	71%	2e-97	32%	XP_004335765.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Purpureocillium lilacinum]	343	343	71%	2e-97	32%	XP_018180309.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Macaca nemestrina]	342	342	70%	2e-97	32%	XP_011754207.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Pongo abelii]	341	341	70%	2e-97	32%	XP_009237588.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Saimiri boliviensis boliviensis]	341	341	70%	2e-97	32%	XP_010334119.1
calcium-transporting ATPase type 2C member 1 isoform 1a [Homo sapiens]	341	341	70%	2e-97	32%	NP_055197.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Octodon degus]	341	341	70%	2e-97	32%	XP_004625082.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Saimiri boliviensis boliviensis]	342	342	70%	2e-97	32%	XP_003925135.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Macaca fascicularis]	342	342	70%	2e-97	32%	XP_005545815.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Cebus capucinus imitator]	342	342	70%	2e-97	32%	XP_017365647.1
calcium-transporting ATPase type 2C member 1 isoform 2a [Homo sapiens]	342	342	70%	2e-97	32%	NP_001186109.1
sarcoplasmic/endoplasmic reticulum calcium ATPase [Histoplasma capsulatum G186AR]	343	343	70%	2e-97	31%	EEH10595.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Chinchilla lanigera]	340	340	70%	2e-97	32%	XP_013361188.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Microcebus murinus]	341	341	70%	2e-97	32%	XP_012622351.1
hypothetical protein ASPSYDRAFT_150596 [Aspergillus sydowii CBS 593.65]	342	342	74%	2e-97	32%	OJJ59346.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 [Galeopterus variegatus]	341	341	70%	2e-97	32%	XP_008570220.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Harpegnathos saltator]	342	342	73%	2e-97	31%	XP_019697794.1
hypothetical protein FPOA_12067 [Fusarium poae]	342	342	71%	2e-97	31%	OBS17418.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Cercocebus atys]	343	343	70%	2e-97	32%	XP_011899389.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Cercocebus atys]	344	344	70%	2e-97	32%	XP_011899383.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Harpegnathos saltator]	343	343	73%	2e-97	31%	XP_011142452.1
sarcoplasmic/endoplasmic reticulum calcium ATPase [Histoplasma capsulatum H88]	343	343	70%	2e-97	31%	EGC42825.1
Ca-transporting ATPase [Calocera viscosa TUFC12733]	342	342	70%	2e-97	32%	KZO95232.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Otolemur garnettii]	340	340	70%	2e-97	32%	XP_003781754.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Balaenoptera acutorostrata scammoni]	340	340	70%	2e-97	32%	XP_007167041.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Saimiri boliviensis boliviensis]	342	342	70%	2e-97	32%	XP_003925134.1
sarco/endoplasmic reticulum Ca2+ -ATPase [Paramecium tetraurelia]	343	343	70%	2e-97	31%	CAA76764.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Octodon degus]	342	342	70%	3e-97	32%	XP_004625079.1
Ca-transporting ATPase [Fomitiporia mediterranea MF3/22]	342	342	74%	3e-97	31%	XP_007264125.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Canis lupus familiaris]	341	341	70%	3e-97	32%	XP_005634475.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like Protein [Tribolium castaneum]	340	340	71%	3e-97	32%	EFA11368.2
PREDICTED: calcium-transporting ATPase type 2C member 1 [Cavia porcellus]	342	342	70%	3e-97	32%	XP_003476770.2
hypothetical protein FPSE_00427 [Fusarium pseudograminearum CS3096]	342	342	71%	3e-97	31%	XP_009251822.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Canis lupus familiaris]	340	340	70%	3e-97	32%	XP_005634477.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Canis lupus familiaris]	341	341	70%	3e-97	32%	XP_851493.2
ATP binding [Ascochyta rabiei]	342	342	70%	3e-97	31%	KZM23080.1
hypothetical protein MVEG_01291 [Mortierella verticillata NRRL 6337]	342	342	74%	3e-97	30%	KFH74078.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Canis lupus familiaris]	342	342	70%	3e-97	32%	XP_005634472.1
calcium-translocating P-type ATPase, SERCA-type [Paracoccidioides brasiliensis Pb03]	340	340	71%	3e-97	33%	KGY15695.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Saimiri boliviensis boliviensis]	342	342	70%	3e-97	32%	XP_010334114.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Hipposideros armiger]	340	340	70%	3e-97	32%	XP_019484462.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Microcebus murinus]	341	341	70%	3e-97	32%	XP_012622348.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Otolemur garnettii]	341	341	70%	3e-97	32%	XP_012661430.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Tribolium castaneum]	340	340	71%	4e-97	32%	XP_015833129.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Canis lupus familiaris]	340	340	70%	4e-97	32%	XP_005634476.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Canis lupus familiaris]	341	341	70%	4e-97	32%	XP_005634474.1
calcium-transporting ATPase [Rhodotorula toruloides NP11]	342	342	74%	4e-97	30%	XP_016276168.1
putative calcium P-type ATPase [Drechmeria coniospora]	342	342	71%	4e-97	32%	KYK55395.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Canis lupus familiaris]	340	340	70%	4e-97	32%	XP_534262.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Panthera tigris altaica]	340	340	70%	4e-97	32%	XP_007087445.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Otolemur garnettii]	340	340	70%	4e-97	32%	XP_012661433.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X12 [Cercocebus atys]	340	340	70%	4e-97	32%	XP_011899394.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Hipposideros armiger]	340	340	70%	4e-97	32%	XP_019484461.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Orycteropus afer afer]	340	340	70%	4e-97	32%	XP_007935045.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Hipposideros armiger]	339	339	70%	4e-97	32%	XP_019484464.1
hypothetical protein SteCoe_13348 [Stentor coeruleus]	341	341	71%	4e-97	31%	OMJ85372.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Trichechus manatus latirostris]	339	339	70%	4e-97	32%	XP_004381453.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Orycteropus afer afer]	340	340	70%	4e-97	32%	XP_007935052.1
calcium-translocating p-type pmca-type [Plasmopara halstedii]	341	341	71%	4e-97	31%	CEG46769.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Lipotes vexillifer]	340	340	70%	4e-97	32%	XP_007462483.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Panthera tigris altaica]	341	341	70%	4e-97	32%	XP_007087443.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Balaenoptera acutorostrata scammoni]	340	340	70%	5e-97	32%	XP_007167040.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Microcebus murinus]	340	340	70%	5e-97	32%	XP_012622350.1
PREDICTED: ATPase, Ca++ transporting, type 2C, member 2 S homeolog isoform X2 [Xenopus laevis]	342	342	70%	5e-97	32%	XP_018115260.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Nomascus leucogenys]	338	338	70%	5e-97	32%	XP_003265453.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Microcebus murinus]	340	340	70%	5e-97	32%	XP_012622349.1
hypothetical protein ASPWEDRAFT_109063 [Aspergillus wentii DTO 134E9]	341	341	74%	5e-97	31%	OJJ36737.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Salmo salar]	341	341	71%	5e-97	31%	XP_014015883.1
calcium ATPase [Phialocephala scopiformis]	341	341	74%	6e-97	31%	XP_018077190.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Aethina tumida]	340	340	71%	6e-97	32%	XP_019878801.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Microbotryum lychnidis-dioicae p1A1 Lamole]	341	341	69%	6e-97	31%	KDE06530.1
hypothetical protein AN5743.2 [Aspergillus nidulans FGSC A4]	340	340	73%	6e-97	31%	XP_663347.1
calcium p-type atpase [Ophiostoma piceae UAMH 11346]	341	341	73%	7e-97	31%	EPE09431.1
ATPase, Ca++ transporting, ubiquitous L homeolog [Xenopus laevis]	342	342	71%	7e-97	32%	NP_001088563.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Nomascus leucogenys]	339	339	70%	7e-97	32%	XP_012363913.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Salmo salar]	342	342	71%	8e-97	31%	XP_014015882.1
unnamed protein product [Homo sapiens]	340	340	70%	8e-97	32%	BAH12365.1
Calcium-transporting ATPase type 2C member 1 [Fukomys damarensis]	340	340	70%	8e-97	32%	KFO32699.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Chinchilla lanigera]	340	340	70%	8e-97	32%	XP_005406901.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium italicum]	341	341	70%	9e-97	32%	KGO76771.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Cercocebus atys]	342	342	70%	9e-97	32%	XP_011899382.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Fukomys damarensis]	339	339	70%	9e-97	32%	XP_019063207.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Panthera tigris altaica]	340	340	70%	9e-97	32%	XP_007087444.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Nomascus leucogenys]	339	339	70%	9e-97	32%	XP_003265454.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Callithrix jacchus]	338	338	70%	9e-97	32%	XP_008982094.1
calcium-transporting ATPase endoplasmic reticulum-type-like protein [Chrysochromulina sp. CCMP291]	342	342	70%	1e-96	31%	KOO23673.1
TPA: Putative calcium ion P-type ATPase (Eurofung) [Aspergillus nidulans FGSC A4]	340	340	73%	1e-96	31%	CBF81294.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Fukomys damarensis]	339	339	70%	1e-96	32%	XP_019063206.1
calcium-transporting atpase sarcoplasmic endoplasmic reticulum type [Colletotrichum orbiculare MAFF 240422]	340	340	70%	1e-96	31%	ENH78159.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Tribolium castaneum]	339	339	71%	1e-96	32%	XP_015833128.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type isoform X1 [Eucalyptus grandis]	343	343	71%	1e-96	33%	XP_010037888.1
ATPase, Ca++ transporting, type 2C, member 2 S homeolog [Xenopus laevis]	338	338	70%	1e-96	32%	NP_001089971.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type [Camelina sativa]	341	341	71%	1e-96	32%	XP_010422743.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Nomascus leucogenys]	340	340	70%	1e-96	32%	XP_003265451.1
unnamed protein product [Homo sapiens]	338	338	70%	1e-96	32%	BAG65057.1
ca2+ transporting sarcoplasmic endoplasmic reticulum [Fusarium avenaceum]	340	340	71%	1e-96	32%	KIL94524.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Bos mutus]	338	338	70%	1e-96	32%	XP_014337999.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Trichechus manatus latirostris]	339	339	70%	1e-96	32%	XP_012412437.1
putative calcium P-type ATPase [Ustilaginoidea virens]	340	340	71%	1e-96	32%	KDB14494.1
hypothetical protein M413DRAFT_407425 [Hebeloma cylindrosporum h7]	340	340	73%	1e-96	30%	KIM49436.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Sinocyclocheilus anshuiensis]	338	338	70%	1e-96	32%	XP_016313778.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Mesocricetus auratus]	338	338	70%	1e-96	32%	XP_005074897.1
hypothetical protein PLICRDRAFT_40683 [Plicaturopsis crispa FD-325 SS-3]	340	340	75%	1e-96	31%	KII89028.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Trichechus manatus latirostris]	338	338	70%	2e-96	32%	XP_012412439.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 1 [Histoplasma capsulatum NAm1]	340	340	70%	2e-96	31%	XP_001540332.1
probable calcium P-type ATPase NCA-1 [Fusarium mangiferae]	340	340	71%	2e-96	32%	CVK83042.1
putative calcium p-type atpase [Diaporthe ampelina]	340	340	71%	2e-96	32%	KKY36814.1
Ca-transporting ATPase [Gloeophyllum trabeum ATCC 11539]	340	340	74%	2e-96	32%	XP_007863602.1
hypothetical protein LIPSTDRAFT_59335 [Lipomyces starkeyi NRRL Y-11557]	339	339	71%	2e-96	32%	ODQ69266.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Trichoderma gamsii]	340	340	70%	2e-96	32%	XP_018660364.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X4 [Sinocyclocheilus rhinocerous]	335	335	69%	2e-96	32%	XP_016379566.1
ATPase P-type K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Macrophomina phaseolina MS6]	338	338	68%	2e-96	32%	EKG14751.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X3 [Sinocyclocheilus rhinocerous]	335	335	69%	2e-96	32%	XP_016379565.1
calcium-translocating P-type ATPase [Magnaporthiopsis poae ATCC 64411]	340	340	73%	2e-96	31%	KLU83652.1

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Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Emmonsia crescens UAMH 3008]	339	339	74%	2e-96	30%	KKZ58593.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Chinchilla lanigera]	340	340	70%	2e-96	32%	XP_013361186.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Mortierella verticillata NRRL 6337]	340	340	73%	2e-96	30%	KFH62632.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Bombus terrestris]	340	340	71%	2e-96	32%	XP_003399858.1
similar to calcium-transporting atpase sarcoplasmic/endoplasmic reticulum type [Leptosphaeria maculans JN3]	340	340	70%	2e-96	31%	XP_003833743.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Ursus maritimus]	339	339	70%	2e-96	32%	XP_008706993.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Sinocyclocheilus rhinocerous]	335	335	69%	2e-96	32%	XP_016379564.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Neonectria ditissima]	339	339	74%	2e-96	31%	KPM37087.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Trichechus manatus latirostris]	338	338	70%	2e-96	32%	XP_012412438.1
calcium-transporting ATPase type 2C member 1 isoform 2b [Homo sapiens]	338	338	70%	2e-96	32%	NP_001186110.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Callithrix jacchus]	339	339	70%	2e-96	32%	XP_008982091.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Chlorocebus sabaeus]	339	339	70%	2e-96	32%	XP_008007319.1
hypothetical protein MUCCIDRAFT_139955 [Mucor circinelloides f. lusitanicus CBS 277.49]	336	336	71%	2e-96	32%	OAD05351.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Loxodonta africana]	338	338	70%	2e-96	32%	XP_010598786.1
hypothetical protein PENARI_c001G08419 [Penicillium arizonense]	340	340	73%	2e-96	32%	OGE58047.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fonticula alba]	339	339	74%	2e-96	30%	XP_009496868.1
hypothetical protein SteCoe_17436 [Stentor coeruleus]	339	339	70%	2e-96	31%	OMJ82001.1
hypothetical protein ACN38_g877 [Penicillium nordicum]	339	339	73%	2e-96	32%	KOS48165.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Sinocyclocheilus rhinocerous]	335	335	69%	3e-96	32%	XP_016379563.1
probable calcium P-type ATPase NCA-1 [Fusarium proliferatum]	339	339	71%	3e-96	32%	CVL10999.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Sinocyclocheilus anshuiensis]	337	337	70%	3e-96	32%	XP_016313777.1
calcium-translocating P-type ATPase, SERCA-type [Cyphellophora europaea CBS 101466]	340	340	74%	3e-96	30%	XP_008719278.1
calcium P-type ATPase-like protein [Trichoderma reesei QM6a]	339	339	70%	3e-96	32%	XP_006963186.1
predicted protein [Hordeum vulgare subsp. vulgare]	340	340	72%	3e-96	31%	BAK00241.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pan troglodytes]	339	339	70%	3e-96	32%	XP_009444739.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum-like protein [Acremonium chrysogenum ATCC 11550]	339	339	73%	3e-96	31%	KFH45786.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Fusarium oxysporum f. sp. cubense race 1]	339	339	71%	3e-96	32%	ENH60601.1
hypothetical protein MVEG_04568 [Mortierella verticillata NRRL 6337]	337	337	74%	3e-96	30%	KFH69762.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Homo sapiens]	339	339	70%	3e-96	32%	XP_005247411.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Cerapachys biroi]	339	339	70%	3e-96	31%	XP_019886931.1
potassium/sodium efflux P-type ATPase, fungal-type [Kwoniella dejecticola CBS 10117]	339	339	73%	3e-96	31%	XP_018264549.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Callithrix jacchus]	338	338	70%	3e-96	32%	XP_008982093.1
putative calcium P-type ATPase NCA-1 [Fusarium fujikuroi]	339	339	71%	3e-96	32%	KLP20869.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Coccidioides posadasii RMSCC 3488]	340	340	69%	3e-96	32%	KMM68348.1
Calcium-transporting ATPase sarcoplasmic reticulum type [Hirsutella minnesotensis 3608]	339	339	71%	3e-96	31%	KJZ77888.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Callithrix jacchus]	338	338	70%	3e-96	32%	XP_008982090.1
probable calcium P-type ATPase NCA-1 [Fusarium fujikuroi IMI 58289]	339	339	71%	3e-96	32%	CCT62028.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Sinocyclocheilus grahami]	337	337	70%	3e-96	32%	XP_016136862.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Callithrix jacchus]	338	338	70%	3e-96	32%	XP_008982092.1
calcium-transporting ATPase [Trichoderma atroviride IMI 206040]	339	339	71%	3e-96	31%	XP_013939123.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Lepisosteus oculatus]	339	339	72%	3e-96	32%	XP_006640894.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Cebus capucinus imitator]	338	338	70%	4e-96	32%	XP_017365646.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Saimiri boliviensis boliviensis]	338	338	70%	4e-96	32%	XP_010334116.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Cerapachys biroi]	339	339	70%	4e-96	31%	XP_019886934.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Sinocyclocheilus grahami]	337	337	70%	4e-96	32%	XP_016136853.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Saimiri boliviensis boliviensis]	338	338	70%	4e-96	32%	XP_010334115.1
smooth endoplasmic reticulum calcium ATPase [Porcellio scaber]	339	339	71%	4e-96	32%	AAN77377.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Eptesicus fuscus]	336	336	70%	4e-96	32%	XP_008151445.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Eptesicus fuscus]	337	337	70%	4e-96	32%	XP_008151437.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Salmo salar]	338	338	71%	4e-96	30%	XP_014027179.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Bombus impatiens]	339	339	71%	4e-96	31%	XP_012236863.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Tupaia chinensis]	337	337	70%	4e-96	32%	XP_014447071.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Bombus terrestris]	339	339	71%	4e-96	32%	XP_012170503.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Hippocampus comes]	338	338	70%	5e-96	31%	XP_019738166.1
RecName: Full=Calcium-transporting ATPase type 2C member 1; Short=ATPase 2C1	337	337	70%	5e-96	32%	Q5R5K5.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Eptesicus fuscus]	338	338	70%	5e-96	32%	XP_008151419.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Sporothrix brasiliensis 5110]	338	338	74%	5e-96	31%	KIH88486.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Eptesicus fuscus]	337	337	70%	5e-96	32%	XP_008151422.1
calcium ATPase [Sistotremastrum niveocremeum HHB9708]	338	338	74%	5e-96	30%	KZS98967.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type [Raphanus sativus]	340	340	71%	5e-96	33%	XP_018457171.1
calcium ATPase [Aureobasidium melanogenum CBS 110374]	338	338	71%	6e-96	31%	KEQ63608.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Valsa mali]	338	338	74%	6e-96	31%	KUI66000.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Cerapachys biroi]	338	338	70%	6e-96	31%	XP_011336454.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Fusarium oxysporum f. sp. cubense race 4]	338	338	71%	6e-96	32%	EMT66676.1
sarco:endoplasmic reticulum calcium ATPase [Echinococcus multilocularis]	338	338	72%	7e-96	31%	CDI98584.1
RecName: Full=Calcium-transporting ATPase type 2C member 1; Short=ATPase 2C1; AltName: Full=ATP-dependent Ca(2+) pump PMR1	336	336	70%	7e-96	31%	Q64566.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium oxysporum f. sp. lycopersici 4287]	338	338	71%	7e-96	32%	XP_018231770.1
calcium-transporting ATPase type 2C member 2 [Xenopus tropicalis]	338	338	71%	7e-96	32%	NP_001072524.1
calcium-transporting ATPase type 2C member 1 [Rattus norvegicus]	336	336	70%	7e-96	31%	NP_571982.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Hippocampus comes]	339	339	70%	7e-96	31%	XP_019738165.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Danio rerio]	336	336	69%	8e-96	33%	XP_005158311.1
endoplasmic reticulum calcium ATPase [Trichophyton rubrum CBS 118892]	338	338	74%	8e-96	30%	XP_003236890.1
putative calcium P-type ATPase NCA-1 [Fusarium fujikuroi]	338	338	71%	8e-96	31%	KLO80635.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Eptesicus fuscus]	337	337	70%	8e-96	32%	XP_008151417.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Salmo salar]	339	339	71%	8e-96	30%	XP_014027177.1
ATPase, Ca++-sequestering, isoform CRA_a [Rattus norvegicus]	337	337	70%	8e-96	31%	EDL77343.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Nelumbo nucifera]	339	339	70%	9e-96	32%	XP_010252600.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X4 [Apis dorsata]	338	338	71%	9e-96	32%	XP_006615687.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Cyphomyrmex costatus]	338	338	71%	9e-96	31%	XP_018394455.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Habropoda laboriosa]	338	338	71%	9e-96	31%	XP_017787617.1
hypothetical protein AUEXF2481DRAFT_69457 [Aureobasidium subglaciale EXF-2481]	338	338	71%	9e-96	31%	XP_013340273.1
putative serca-type calcium atpase [Nannochloropsis gaditana CCMP526]	340	340	65%	1e-95	32%	XP_005853959.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Bombus impatiens]	338	338	71%	1e-95	31%	XP_012236861.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium verticillioides 7600]	338	338	71%	1e-95	31%	XP_018744238.1
calcium-translocating P-type ATPase, SERCA-type [Spizellomyces punctatus DAOM BR117]	338	338	73%	1e-95	29%	XP_016607069.1
PREDICTED: calcium-transporting ATPase type 2C member 2-like [Xenopus laevis]	338	338	70%	1e-95	32%	XP_018113448.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium oxysporum FOSC 3-a]	337	337	71%	1e-95	32%	EWY94606.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Scleropages formosus]	338	338	71%	1e-95	32%	XP_018587207.1
hypothetical protein PDE_02542 [Penicillium oxalicum 114-2]	338	338	73%	1e-95	31%	EPS27599.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Bombus impatiens]	338	338	71%	1e-95	31%	XP_012236862.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium oxysporum f. sp. pisi HDV247]	337	337	71%	1e-95	32%	EXA53788.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Xenopus tropicalis]	335	335	70%	1e-95	31%	XP_017950482.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X4 [Habropoda laboriosa]	337	337	71%	1e-95	31%	XP_017787618.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Myotis lucifugus]	336	336	70%	1e-95	32%	XP_006083754.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Cyphomyrmex costatus]	337	337	71%	1e-95	31%	XP_018394456.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Danio rerio]	335	335	70%	1e-95	32%	XP_003200287.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Ornithorhynchus anatinus]	335	335	70%	1e-95	32%	XP_007664361.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium oxysporum f. sp. raphani 54005]	337	337	71%	1e-95	31%	EXK89256.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pygocentrus nattereri]	335	335	70%	1e-95	32%	XP_017569911.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium camemberti]	337	337	73%	1e-95	32%	CRL27147.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Mesocricetus auratus]	336	336	70%	1e-95	32%	XP_005074894.1
Putative Calcium-translocating P-type ATPase, SERCA-type [Torrubiella hemipterigena]	337	337	73%	1e-95	32%	CEJ81668.1
Putative Calcium P-type ATPase [Rhizopus microsporus]	337	337	74%	1e-95	30%	CEJ01628.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Sporothrix schenckii 1099-18]	337	337	74%	1e-95	31%	XP_016583265.1
hypothetical protein XA68_4445 [Ophiocordyceps unilateralis]	337	337	75%	2e-95	31%	KOM23369.1
calcium-translocating P-type ATPase, SERCA-type [Rhizopus delemar RA 99-880]	337	337	74%	2e-95	30%	EIE82351.1
hypothetical protein g.41366 [Cuerna arida]	336	336	73%	2e-95	32%	JAS41085.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Cyphomyrmex costatus]	337	337	71%	2e-95	31%	XP_018394454.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Xiphophorus maculatus]	338	338	70%	2e-95	32%	XP_005810758.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Myotis lucifugus]	336	336	70%	2e-95	32%	XP_006083751.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Myotis lucifugus]	336	336	70%	2e-95	32%	XP_014306233.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Habropoda laboriosa]	337	337	71%	2e-95	31%	XP_017787614.1
calcium ATPase [Sistotremastrum suecicum HHB10207 ss-3]	337	337	74%	2e-95	30%	KZT44149.1
calcium-transporting ATPase type 2C member 1-like isoform 1 [Cricetulus griseus]	337	337	70%	2e-95	32%	ERE75510.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X1 [Apis dorsata]	337	337	71%	2e-95	32%	XP_006615684.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ornithorhynchus anatinus]	335	335	70%	2e-95	32%	XP_007664360.1
calcium-translocating P-type ATPase, SERCA-type [Sporothrix schenckii ATCC 58251]	337	337	74%	2e-95	31%	ERT02193.1
endoplasmic reticulum calcium ATPase [Trichophyton violaceum]	337	337	74%	2e-95	30%	OAL70186.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Habropoda laboriosa]	337	337	71%	2e-95	31%	XP_017787616.1
hypothetical protein XENTR_v900163821mg, partial [Xenopus tropicalis]	335	335	70%	2e-95	31%	OCA31658.1
Putative Calcium P-type ATPase [Rhizopus microsporus]	337	337	74%	2e-95	30%	CEG70131.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Sinocyclocheilus rhinocerous]	334	334	69%	2e-95	32%	XP_016374960.1
putative endoplasmic reticulum calcium ATPase [Aspergillus ruber CBS 135680]	337	337	74%	2e-95	31%	EYE99482.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Cricetulus griseus]	335	335	70%	2e-95	32%	XP_003497678.1
Calcium-transporting ATPase type 2C member 1 [Nestor notabilis]	333	333	70%	2e-95	32%	KFQ51595.1
endoplasmic reticulum calcium transporter [Moesziomyces aphidis DSM 70725]	337	337	72%	2e-95	31%	ETS59650.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Xenopus tropicalis]	336	336	70%	2e-95	31%	XP_002937789.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Pygocentrus nattereri]	336	336	70%	2e-95	32%	XP_017557218.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Oryctolagus cuniculus]	336	336	70%	2e-95	32%	XP_008264227.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Oryctolagus cuniculus]	335	335	70%	2e-95	32%	XP_017202210.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ornithorhynchus anatinus]	335	335	70%	2e-95	32%	XP_007664359.1
Endoplasmic reticulum calcium ATPase, putative [Penicillium digitatum Pd1]	337	337	70%	2e-95	32%	XP_014531013.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Microtus ochrogaster]	335	335	70%	2e-95	32%	XP_005368527.1
putative serca-type calcium atpase [Nannochloropsis gaditana]	340	340	65%	3e-95	32%	EWM25701.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Scedosporium apiospermum]	336	336	74%	3e-95	32%	XP_016644423.1
sarco:endoplasmic reticulum calcium ATPase [Echinococcus granulosus]	337	337	75%	3e-95	30%	CDS20238.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Pygocentrus nattereri]	337	337	70%	3e-95	32%	XP_017557217.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Takifugu rubripes]	337	337	71%	3e-95	31%	XP_003970855.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium expansum]	337	337	70%	3e-95	32%	XP_016596472.1
predicted protein [Nematostella vectensis]	336	336	71%	3e-95	32%	XP_001639528.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Hippocampus comes]	337	337	71%	3e-95	31%	XP_019740682.1
hypothetical protein HYPSUDRAFT_148432 [Hypholoma sublateritium FD-334 SS-4]	336	336	73%	3e-95	30%	KJA15932.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Apis cerana]	337	337	71%	3e-95	31%	XP_016913985.1
Calcium ATPase at 60A [Schistosoma japonicum]	337	337	72%	3e-95	31%	CAX73007.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pygocentrus nattereri]	334	334	70%	3e-95	32%	XP_017569912.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Copidosoma floridanum]	336	336	71%	3e-95	31%	XP_014204562.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Microtus ochrogaster]	335	335	70%	3e-95	32%	XP_005368526.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X4 [Apis mellifera]	336	336	71%	3e-95	31%	XP_016770982.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Copidosoma floridanum]	337	337	71%	3e-95	31%	XP_014204556.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Apis mellifera]	337	337	71%	3e-95	31%	XP_016770980.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Kryptolebias marmoratus]	336	336	72%	3e-95	32%	XP_017268144.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Myotis lucifugus]	336	336	70%	3e-95	32%	XP_006083749.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Myotis lucifugus]	335	335	70%	3e-95	31%	XP_014306235.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Sinocyclocheilus rhinocerous]	334	334	69%	4e-95	32%	XP_016374959.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Myotis lucifugus]	335	335	70%	4e-95	32%	XP_014306229.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Kryptolebias marmoratus]	336	336	72%	4e-95	32%	XP_017268143.1
probable calcium P-type ATPase NCA-1 [Claviceps purpurea 20.1]	336	336	71%	4e-95	32%	CCE30646.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Oryctolagus cuniculus]	335	335	70%	4e-95	32%	XP_017202208.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium oxysporum Fo47]	336	336	71%	4e-95	31%	EWZ50082.1
Calcium-transporting ATPase 2 family protein [Populus trichocarpa]	337	337	70%	4e-95	32%	XP_002320213.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Nestor notabilis]	333	333	70%	4e-95	32%	XP_010015039.1
hypothetical protein AGABI1DRAFT_69139 [Agaricus bisporus var. burnettii JB137-S8]	336	336	73%	4e-95	31%	XP_007326281.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Sinocyclocheilus grahami]	334	334	70%	4e-95	32%	XP_016147913.1
hypothetical protein TRIVIDRAFT_87963 [Trichoderma virens Gv29-8]	336	336	71%	5e-95	32%	XP_013950785.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Sinocyclocheilus anshuiensis]	333	333	70%	5e-95	32%	XP_016315626.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Nothobranchius furzeri]	336	336	70%	5e-95	32%	XP_015832621.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Apis mellifera]	336	336	71%	5e-95	31%	XP_016770981.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Dasypus novemcinctus]	334	334	70%	5e-95	32%	XP_012383089.1
CRE-SCA-1 protein [Caenorhabditis remanei]	337	337	71%	5e-95	31%	XP_003111065.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Fusarium oxysporum f. sp. vasinfectum 25433]	335	335	71%	6e-95	31%	EXM28604.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus amylolentus CBS 6039]	335	335	73%	6e-95	30%	XP_018995287.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Melopsittacus undulatus]	334	334	70%	6e-95	32%	XP_012983389.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Apis mellifera]	336	336	71%	6e-95	31%	XP_006565281.1
hypothetical protein PFL1_00589 [Anthracocystis flocculosa PF-1]	335	335	69%	7e-95	32%	XP_007876273.1
potassium/sodium efflux P-type ATPase, fungal-type [Tsuchiyaea wingfieldii CBS 7118]	335	335	73%	7e-95	30%	XP_019034430.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Acinonyx jubatus]	335	335	70%	7e-95	31%	XP_014923953.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Penicillium roqueforti FM164]	335	335	73%	8e-95	31%	CDM35017.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Acinonyx jubatus]	334	334	70%	8e-95	31%	XP_014923954.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Erinaceus europaeus]	335	335	73%	8e-95	30%	XP_016043288.1
ATPase, P-type, calcium-transporting [Ophiocordyceps sinensis CO18]	335	335	70%	8e-95	32%	EQL02013.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Oreochromis niloticus]	336	336	71%	8e-95	31%	XP_003448606.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Acinonyx jubatus]	335	335	70%	8e-95	31%	XP_014923952.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Acinonyx jubatus]	333	333	70%	9e-95	31%	XP_014923955.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Ca-transporting ATPase [Agaricus bisporus var. bisporus H97]	335	335	73%	9e-95	31%	XP_006458484.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X4 [Erinaceus europaeus]	335	335	73%	9e-95	30%	XP_007521135.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Trametes pubescens]	335	335	73%	9e-95	32%	OJT08882.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Zootermopsis nevadensis]	335	335	70%	1e-94	31%	KDR21433.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Carlito syrichta]	333	333	70%	1e-94	32%	XP_008071431.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Sinocyclocheilus anshuiensis]	333	333	70%	1e-94	32%	XP_016315625.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Nothobranchius furzeri]	336	336	70%	1e-94	32%	XP_015832609.1
hypothetical protein g.35511 [Graphocephala atropunctata]	333	333	73%	1e-94	31%	JAT35260.1
Calcium-transporting ATPase 1 [[Candida] glabrata]	333	333	72%	1e-94	30%	KTB14664.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Erinaceus europaeus]	335	335	73%	1e-94	30%	XP_016043286.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Polistes canadensis]	335	335	71%	1e-94	32%	XP_014599689.1
calcium transporting ATPase [Thalassiosira pseudonana CCMP1335]	334	334	65%	1e-94	32%	XP_002288284.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Trachymyrmex septentrionalis]	335	335	71%	1e-94	31%	XP_018346803.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Erinaceus europaeus]	335	335	73%	1e-94	30%	XP_007521127.1
Ca-transporting ATPase [Moesziomyces antarcticus]	335	335	72%	1e-94	31%	XP_014656591.1
unnamed protein product [Vitrella brassicaformis CCMP3155]	338	338	70%	1e-94	31%	CEM18264.1
calcium-transporting ATPase [Calocera cornea HHB12733]	334	334	71%	1e-94	31%	KZT54574.1
calcium-transporting ATPase [Trametes versicolor FP-101664 SS1]	334	334	73%	1e-94	31%	XP_008036119.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Apis florea]	335	335	71%	1e-94	31%	XP_003695205.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Oreochromis niloticus]	334	334	71%	1e-94	31%	XP_005473013.1
calcium-transporting ATPase [Rhodotorula sp. JG-1b]	334	334	74%	1e-94	30%	KWU41721.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Orussus abietinus]	334	334	71%	1e-94	31%	XP_012277749.1
predicted protein [Naegleria gruberi]	332	332	76%	1e-94	32%	XP_002677388.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Trachymyrmex cornetzi]	334	334	71%	2e-94	31%	XP_018371159.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Chrysemys picta bellii]	335	335	71%	2e-94	31%	XP_008161767.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Polistes canadensis]	334	334	71%	2e-94	32%	XP_014599694.1
endoplasmic reticulum calcium ATPase [Coccidioides posadasii str. Silveira]	332	332	67%	2e-94	32%	EFW14575.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Polistes dominula]	334	334	71%	2e-94	31%	XP_015173946.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Valsa mali var. pyri]	334	334	74%	2e-94	30%	KUI53930.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Elaeis guineensis]	335	335	70%	2e-94	32%	XP_010933808.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Jaculus jaculus]	332	332	70%	2e-94	31%	XP_004664381.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Trachymyrmex cornetzi]	334	334	71%	2e-94	31%	XP_018371160.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Zonotrichia albicollis]	334	334	71%	2e-94	31%	XP_005491620.2
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Orussus abietinus]	334	334	71%	2e-94	31%	XP_012277750.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Mus musculus]	332	332	70%	2e-94	31%	XP_006511777.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Trachymyrmex septentrionalis]	334	334	71%	2e-94	31%	XP_018346802.1
Ca-transporting ATPase [Tilletiaria anomala UBC 951]	334	334	75%	2e-94	30%	XP_013243079.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Atta colombica]	334	334	71%	2e-94	31%	XP_018058072.1
hypothetical protein g.35519 [Graphocephala atropunctata]	332	332	72%	2e-94	31%	JAT36624.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Agrilus planipennis]	334	334	71%	2e-94	31%	XP_018332136.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Atta colombica]	334	334	71%	2e-94	31%	XP_018058074.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Polistes canadensis]	334	334	71%	2e-94	32%	XP_014599692.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Coturnix japonica]	334	334	71%	2e-94	31%	XP_015733210.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Trachymyrmex septentrionalis]	334	334	71%	2e-94	31%	XP_018346799.1
calcium-transporting ATPase type 2C member 1 isoform 2 [Mus musculus]	332	332	70%	2e-94	31%	NP_778190.3
calcium-transporting ATPase type 2C member 1 isoform X1 [Amazona aestiva]	332	332	70%	2e-94	32%	KQK83817.1
unnamed protein product [Mus musculus]	332	332	70%	2e-94	31%	BAE35481.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Dendroctonus ponderosae]	334	334	71%	3e-94	32%	XP_019754226.1
mKIAA1347 protein [Mus musculus]	332	332	70%	3e-94	31%	BAD32432.1
hypothetical protein BN946_scf184798.g39 [Trametes cinnabarina]	333	333	73%	3e-94	31%	CDO70724.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Pteropus vampyrus]	333	333	70%	3e-94	32%	XP_011376975.1
Calcium-transporting ATPase type 2C member 1 [Chelonia mydas]	331	331	70%	3e-94	33%	EMP31560.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Polistes dominula]	334	334	71%	3e-94	32%	XP_015173943.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Dufourea novaeangliae]	333	333	71%	3e-94	31%	XP_015434673.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Jaculus jaculus]	332	332	70%	3e-94	31%	XP_004664379.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Chelonia mydas]	332	332	70%	3e-94	33%	XP_007064361.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Atta cephalotes]	334	334	71%	3e-94	31%	XP_012063638.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Nicrophorus vespilloides]	333	333	71%	3e-94	31%	XP_017779458.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Trachymyrmex cornetzi]	334	334	71%	3e-94	31%	XP_018371156.1

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sarco/endoplasmic reticulum Ca2+-ATPase [Procambarus clarkii]	334	334	71%	3e-94	32%	AAB82290.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Orussus abietinus]	333	333	71%	4e-94	31%	XP_012277746.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Sturnus vulgaris]	333	333	71%	4e-94	31%	XP_014730413.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Chelonia mydas]	332	332	70%	4e-94	33%	XP_007064362.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Jaculus jaculus]	333	333	70%	4e-94	31%	XP_004664377.1
E1-E2_ATPase domain-containing protein/Cation_ATPase_C domain-containing protein/Cation_ATPase_N domain-containing protein/Hydrolase domain-containing protein [Cephalotus follicularis]	334	334	78%	4e-94	31%	GAV75333.1
putative atpase [Schistosoma mansoni]	333	333	74%	4e-94	30%	XP_018648452.1
hypothetical protein M569_05142 [Genlisea aurea]	330	330	71%	4e-94	30%	EPS69623.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Elephantulus edwardii]	330	330	70%	4e-94	31%	XP_006883383.1
hypothetical protein BRADI_1g09810 [Brachypodium distachyon]	331	331	71%	4e-94	30%	KQK13384.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Gavialis gangeticus]	333	333	71%	4e-94	31%	XP_019362863.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Verticillium alfalfae VaMs.102]	332	332	65%	4e-94	32%	XP_003003530.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Mus musculus]	331	331	70%	4e-94	31%	XP_006511773.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Serinus canaria]	333	333	71%	4e-94	31%	XP_009090706.1
hypothetical protein PHLGIDRAFT_126438 [Phlebiopsis gigantea 11061_1 CR5-6]	333	333	73%	4e-94	31%	KIP09286.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Coturnix japonica]	334	334	71%	4e-94	31%	XP_015733209.1
hypothetical protein S7711_02438 [Stachybotrys chartarum IBT 7711]	333	333	71%	5e-94	31%	KEY67519.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Echinops telfairi]	332	332	70%	5e-94	31%	XP_004704060.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Dufourea novaeangliae]	333	333	71%	5e-94	31%	XP_015434674.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Jaculus jaculus]	332	332	70%	5e-94	31%	XP_004664378.1
calcium-transporting ATPase type 2C member 1 isoform 1 [Mus musculus]	332	332	70%	5e-94	31%	NP_001240760.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Crocodylus porosus]	333	333	71%	5e-94	31%	XP_019394242.1
putative calcium-translocating p-type atpase protein [Phaeoacremonium minimum UCRPA7]	333	333	72%	5e-94	32%	XP_007918272.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X3 [Geospiza fortis]	333	333	71%	6e-94	31%	XP_014163722.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Choanephora cucurbitarum]	333	333	74%	6e-94	31%	OBZ88847.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Xenopus laevis]	330	330	70%	6e-94	31%	XP_018124818.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Phialophora attae]	333	333	70%	6e-94	31%	XP_018005587.1
hypothetical protein MGL_2215 [Malassezia globosa CBS 7966]	330	330	68%	6e-94	32%	XP_001730419.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Capsicum annuum]	333	333	71%	6e-94	32%	XP_016538263.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Austrofundulus limnaeus]	333	333	71%	6e-94	32%	XP_013878552.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Pochonia chlamydosporia 170]	332	332	70%	6e-94	32%	XP_018140958.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Calcium-transporting ATPase 3 [Zancudomyces culisetae]	332	332	70%	7e-94	32%	OMH84339.1
hypothetical protein g.35515 [Graphocephala atropunctata]	330	330	71%	7e-94	31%	JAT22616.1
ATPase, Ca++-sequestering [Mus musculus]	331	331	70%	7e-94	31%	AAH43091.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Sturnus vulgaris]	333	333	71%	7e-94	31%	XP_014730412.1
hypothetical protein S40285_00796 [Stachybotrys chlorohalonata IBT 40285]	332	332	71%	7e-94	31%	KFA64127.1
hypothetical protein EPUS_00644 [Endocarpon pusillum Z07020]	333	333	70%	7e-94	31%	XP_007802864.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Pseudopodoces humilis]	333	333	71%	7e-94	31%	XP_005524316.1
calcium-translocating P-type ATPase, SERCA-type [Puccinia graminis f. sp. tritici CRL 75-36-700-3]	330	330	71%	7e-94	30%	XP_003327868.2
calcium-translocating P-type ATPase, SERCA-type [Pneumocystis murina B123]	332	332	72%	7e-94	32%	XP_007872987.1
calcium-translocating P-type ATPase, SERCA-type [Pneumocystis jirovecii RU7]	332	332	72%	7e-94	32%	XP_018230829.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Austrofundulus limnaeus]	332	332	71%	7e-94	32%	XP_013878551.1
Ca-transporting ATPase [Laccaria bicolor S238N-H82]	332	332	74%	8e-94	30%	XP_001878234.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Pyrus x bretschneideri]	333	333	71%	8e-94	31%	XP_009334375.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium griseofulvum]	340	340	73%	8e-94	31%	KXG45342.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Gavialis gangeticus]	333	333	71%	8e-94	31%	XP_019362862.1
sarco/endoplasmic reticulum calcium transporting ATPase [Capsaspora owczarzaki ATCC 30864]	332	332	70%	8e-94	31%	XP_004344407.2
hypothetical protein K443DRAFT_129791 [Laccaria amethystina LaAM-08-1]	332	332	74%	8e-94	29%	KIK06510.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Chrysochloris asiatica]	331	331	70%	9e-94	31%	XP_006840083.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Microplitis demolitor]	330	330	71%	9e-94	31%	XP_008554717.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Elephantulus edwardii]	331	331	70%	1e-93	31%	XP_006883382.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Microplitis demolitor]	330	330	71%	1e-93	31%	XP_008554716.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Poecilia mexicana]	333	333	70%	1e-93	32%	XP_014866971.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase, putative [Pediculus humanus corporis]	332	332	71%	1e-93	32%	XP_002431870.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Galendromus occidentalis]	332	332	71%	1e-93	31%	XP_003742118.1
hypothetical protein Y1Q_0018779 [Alligator mississippiensis]	332	332	71%	1e-93	31%	KYO39759.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Crocodylus porosus]	333	333	71%	1e-93	31%	XP_019394241.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Xenopus laevis]	331	331	70%	1e-93	31%	XP_018122987.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Chrysochloris asiatica]	330	330	70%	1e-93	31%	XP_006840084.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Nasonia vitripennis]	332	332	70%	1e-93	31%	XP_016837881.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Geospiza fortis]	333	333	71%	1e-93	31%	XP_005424073.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Oryza sativa Japonica Group]	332	332	71%	1e-93	30%	XP_015632272.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Larimichthys crocea]	333	333	71%	1e-93	32%	XP_010752494.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Xenopus laevis]	331	331	70%	1e-93	31%	XP_018124817.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Brachypodium distachyon]	332	332	71%	1e-93	30%	XP_010230478.1
hypothetical protein [Candida glabrata CBS 138]	331	331	72%	1e-93	30%	XP_447786.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Anolis carolinensis]	332	332	71%	1e-93	31%	XP_003222795.1
Ca-transporting ATPase [Sanghuangporus baumii]	332	332	72%	1e-93	31%	OCB91406.1
hypothetical protein Y1Q_0018779 [Alligator mississippiensis]	332	332	71%	1e-93	31%	KYO39760.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Poecilia reticulata]	333	333	70%	1e-93	32%	XP_008417704.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform 1 [Gallus gallus]	332	332	71%	1e-93	31%	NP_001258902.1
ATPase, P-type, calcium-transporting [Aschersonia aleyrodis RCEF 2490]	332	332	74%	1e-93	31%	KZZ94756.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Meleagris gallopavo]	332	332	71%	1e-93	31%	XP_010718409.1
predicted protein [Nectria haematococca mpVI 77-13-4]	332	332	71%	1e-93	32%	XP_003053401.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Poecilia latipinna]	333	333	70%	1e-93	32%	XP_014914349.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Lepidothrix coronata]	332	332	71%	1e-93	31%	XP_017669707.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Eufriesea mexicana]	332	332	70%	1e-93	31%	XP_017762230.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Echinops telfairi]	330	330	70%	1e-93	31%	XP_004704059.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Trichoderma harzianum]	332	332	71%	2e-93	31%	KKP03232.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Calypte anna]	331	331	71%	2e-93	31%	KFO95774.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X14 [Cercocebus atys]	330	330	64%	2e-93	33%	XP_011899396.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Echinops telfairi]	330	330	70%	2e-93	31%	XP_004704061.1
hypothetical protein HMPREF1544_01132 [Mucor circinelloides f. circinelloides 1006PhL]	333	333	74%	2e-93	30%	EPB92068.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Poecilia formosa]	333	333	70%	2e-93	32%	XP_007564712.1
putative atpase [Schistosoma mansoni]	332	332	71%	2e-93	31%	XP_018648453.1
calcium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora infestans T30-4]	332	332	73%	2e-93	31%	XP_002903567.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Falco peregrinus]	332	332	71%	2e-93	31%	XP_005237686.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Taeniopygia guttata]	331	331	71%	2e-93	31%	XP_004176468.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Meleagris gallopavo]	332	332	71%	2e-93	31%	XP_019476563.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Nasonia vitripennis]	331	331	70%	2e-93	31%	XP_016837880.1
hypothetical protein M404DRAFT_952133 [Pisolithus tinctorius Marx 270]	331	331	74%	2e-93	31%	KIO13403.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Leptosomus discolor]	331	331	71%	2e-93	31%	XP_009947772.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Leptosomus discolor]	331	331	71%	2e-93	31%	KFQ09666.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Ceratocystis platani]	331	331	71%	2e-93	32%	KKF94667.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Lipotes vexillifer]	331	331	72%	2e-93	30%	XP_007454235.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
uncharacterized protein MSY001_1947 [Malassezia sympodialis ATCC 42132]	331	331	73%	2e-93	31%	XP_018740502.1
hypothetical protein TREMEDRAFT_62788 [Tremella mesenterica DSM 1558]	332	332	72%	2e-93	31%	XP_007005106.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella britovi]	333	333	73%	2e-93	31%	KRY56388.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Anolis carolinensis]	332	332	71%	2e-93	31%	XP_008111922.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Setaria italica]	331	331	71%	2e-93	30%	XP_004981887.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Rhagoletis zephyria]	329	329	70%	2e-93	32%	XP_017490968.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Cuculus canorus]	331	331	71%	2e-93	31%	XP_009562951.1
RecName: Full=Sarcoplasmic/endoplasmic reticulum calcium ATPase 2; Short=SERCA2; Short=SR Ca(2+)-ATPase 2; AltName: Full=Calcium pump 2; AltName: Full=Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform; AltName: Full=Endoplasmic reticulum class 1/2 Ca(2+) ATPase	332	332	71%	2e-93	31%	Q03669.2
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Aethina tumida]	331	331	70%	2e-93	32%	XP_019869755.1
probable endoplasmic reticulum calcium transporter [Ustilago hordei]	331	331	73%	2e-93	31%	CCF52383.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform 2 [Gallus gallus]	332	332	71%	2e-93	31%	NP_001258903.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Alligator mississippiensis]	332	332	71%	2e-93	31%	XP_006272883.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Callorhinchus milii]	329	329	70%	2e-93	32%	XP_007899892.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Rhagoletis zephyria]	329	329	70%	2e-93	32%	XP_017490961.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Echinococcus granulosus]	335	335	72%	2e-93	31%	EUB59093.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Apteryx australis mantelli]	332	332	71%	3e-93	31%	XP_013814115.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Acyrthosiphon pisum]	331	331	70%	3e-93	32%	XP_016662301.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Nasonia vitripennis]	331	331	70%	3e-93	31%	XP_008209458.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Lipotes vexillifer]	331	331	72%	3e-93	30%	XP_007454236.1
calcium-transporting ATPase [Coprinopsis cinerea okayama7#130]	331	331	73%	3e-93	31%	XP_001833748.2
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Linepithema humile]	331	331	71%	3e-93	31%	XP_012227425.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Balearica regulorum gibbericeps]	331	331	71%	3e-93	31%	XP_010300329.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Chaetura pelagica]	331	331	71%	3e-93	31%	XP_009996702.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Odobenus rosmarus divergens]	330	330	65%	3e-93	32%	XP_012423213.1
hypothetical protein LOTGIDRAFT_211332 [Lottia gigantea]	329	329	71%	3e-93	31%	XP_009066496.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Chaetura pelagica]	331	331	71%	3e-93	31%	KFU90203.1
hypothetical protein SERLADRAFT_357750 [Serpula lacrymans var. lacrymans S7.9]	331	331	73%	3e-93	31%	XP_007321961.1
hypothetical protein KNAG_0E03400 [Kazachstania naganishii CBS 8797]	330	330	71%	3e-93	33%	CCK70598.1
hypothetical protein CY34DRAFT_800504 [Suillus luteus UH-Slu-Lm8-n1]	330	330	74%	3e-93	30%	KIK46336.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Calypte anna]	332	332	71%	3e-93	31%	XP_008491741.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 1-like isoform X2 [Fundulus heteroclitus]	331	331	72%	3e-93	32%	XP_012712315.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Brachypodium distachyon]	331	331	71%	3e-93	30%	XP_003560240.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Aptenodytes forsteri]	331	331	71%	3e-93	31%	XP_009282179.1
calcium-translocating P-type ATPase, SERCA-type [Puccinia sorghi]	330	330	71%	3e-93	30%	KNZ51132.1
hypothetical protein BRADI_1g09810 [Brachypodium distachyon]	331	331	71%	3e-93	30%	KQK13385.1
unnamed protein product [Homo sapiens]	327	327	65%	3e-93	33%	BAC11142.1
MFS general substrate transporter [Aureobasidium pullulans]	330	330	71%	3e-93	31%	OBW69138.1
SERCA [Panulirus argus]	331	331	71%	3e-93	32%	AAW22143.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Dinoponera quadriceps]	331	331	71%	3e-93	31%	XP_014481518.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Aptenodytes forsteri]	330	330	71%	3e-93	31%	KFM10680.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Ceratitis capitata]	328	328	70%	3e-93	32%	XP_012155697.1
hypothetical protein MELLADRAFT_47361 [Melampsora larici-populina 98AG31]	331	331	72%	3e-93	31%	XP_007406821.1
hypothetical protein CAEBREN_30959 [Caenorhabditis brenneri]	332	332	71%	3e-93	31%	EGT34858.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Taeniopygia guttata]	332	332	71%	3e-93	31%	XP_002192568.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Tursiops truncatus]	327	327	65%	3e-93	33%	XP_019789946.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Lepidothrix coronata]	331	331	71%	3e-93	31%	XP_017669705.1
hypothetical protein AZE42_08295 [Rhizopogon vesiculosus]	330	330	75%	3e-93	31%	OJA21123.1
Ca2+ transporting ATPase [Moesziomyces antarcticus T-34]	330	330	72%	3e-93	31%	GAC72184.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Acromyrmex echinatior]	330	330	71%	3e-93	31%	XP_011062570.1
Ca-transporting ATPase [Schizopora paradoxa]	330	330	73%	4e-93	30%	KLO10691.1
unnamed protein product [Coffea canephora]	332	332	70%	4e-93	31%	CDP08644.1
Calcium-transporting ATPase 1 [[Candida] glabrata]	329	329	72%	4e-93	30%	KTA96766.1
related to endoplasmic reticulum calcium transporter [Serendipita indica DSM 11827]	330	330	74%	4e-93	30%	CCA77785.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Linepithema humile]	331	331	71%	4e-93	31%	XP_012227396.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Rhinopithecus bieti]	327	327	65%	4e-93	32%	XP_017717803.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Ceratina calcarata]	331	331	70%	4e-93	32%	XP_017884132.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Polistes dominula]	328	328	70%	4e-93	31%	XP_015186593.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Melopsittacus undulatus]	330	330	71%	4e-93	31%	XP_005145193.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Leptosomus discolor]	331	331	71%	4e-93	31%	XP_009947771.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Balearica regulorum gibbericeps]	331	331	71%	4e-93	31%	XP_010300328.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Monodelphis domestica]	328	328	70%	4e-93	31%	XP_007505174.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Acyrthosiphon pisum]	331	331	70%	4e-93	32%	XP_008185966.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Anas platyrhynchos]	331	331	71%	5e-93	31%	XP_005016370.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Cynoglossus semilaevis]	331	331	70%	5e-93	32%	XP_008314598.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Acromyrmex echinatior]	330	330	71%	5e-93	31%	XP_011062572.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Pelodiscus sinensis]	328	328	70%	5e-93	33%	XP_006117641.1
calcium-transporting ATPase [Coccidioides immitis H538.4]	328	328	73%	5e-93	31%	KMU88778.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Dinoponera quadriceps]	330	330	71%	5e-93	31%	XP_014481520.1
hypothetical protein VOLCADRAFT_105844 [Volvox carteri f. nagariensis]	332	332	70%	5e-93	31%	XP_002953236.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Cuculus canorus]	331	331	71%	5e-93	31%	XP_009562950.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Melopsittacus undulatus]	331	331	71%	5e-93	31%	XP_005145192.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Python bivittatus]	328	328	70%	5e-93	31%	XP_007438592.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Eufriesea mexicana]	328	328	71%	5e-93	31%	XP_017759243.1
hypothetical protein EMIHUDRAFT_522053 [Emiliania huxleyi CCMP1516]	331	331	72%	5e-93	31%	XP_005781031.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Tinamus guttatus]	330	330	72%	6e-93	31%	KGL76810.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Ceratina calcarata]	330	330	70%	6e-93	32%	XP_017884133.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Vitis vinifera]	331	331	69%	6e-93	32%	XP_002277306.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Polistes dominula]	328	328	70%	6e-93	31%	XP_015186592.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Theobroma cacao]	331	331	70%	6e-93	31%	XP_017978465.1
calcium-transporting atpase [Ceraceosorus bombacis]	330	330	70%	6e-93	31%	CEH19504.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Equus asinus]	327	327	65%	6e-93	32%	XP_014683963.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Monodelphis domestica]	328	328	70%	6e-93	31%	XP_016281924.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3-like isoform X1 [Fundulus heteroclitus]	330	330	72%	7e-93	32%	XP_012712313.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Ceratitis capitata]	328	328	70%	7e-93	32%	XP_004522374.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Python bivittatus]	328	328	70%	7e-93	31%	XP_007438591.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Equus caballus]	328	328	65%	7e-93	32%	XP_003363205.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Tolypocladium ophioglossoides CBS 100239]	330	330	70%	7e-93	31%	KND86148.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Dinoponera quadriceps]	330	330	71%	7e-93	31%	XP_014481515.1
hypothetical protein [Absidia glauca]	333	333	67%	7e-93	32%	SAM04578.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Monodelphis domestica]	328	328	70%	7e-93	31%	XP_007505172.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Odobenus rosmarus divergens]	330	330	71%	7e-93	31%	XP_004395917.1
calcium ATPase [Mortierella elongata AG-77]	335	335	73%	7e-93	31%	OAQ30967.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Rhinopithecus bieti]	327	327	65%	7e-93	32%	XP_017717798.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Ceratina calcarata]	330	330	70%	8e-93	32%	XP_017884129.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Aptenodytes forsteri]	330	330	71%	8e-93	31%	XP_009282178.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Populus euphratica]	330	330	70%	8e-93	32%	XP_011038641.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium hirsutum]	330	330	70%	8e-93	32%	XP_016710397.1
calcium ATPase [Aureobasidium pullulans EXF-150]	329	329	71%	8e-93	31%	KEQ84059.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Calidris pugnax]	329	329	71%	8e-93	31%	XP_014817351.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Calidris pugnax]	330	330	71%	8e-93	31%	XP_014817343.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Manis javanica]	326	326	65%	8e-93	32%	XP_017527910.1
Calcium-transporting ATPase 1, endoplasmic reticulum-type -like protein [Gossypium arboreum]	330	330	70%	8e-93	32%	KHG01941.1
Cation-transporting P-type ATPase [Corchorus olitorius]	330	330	78%	9e-93	30%	OMP08650.1
calcium-transporting ATPase [Dacryopinax primogenitus]	329	329	71%	9e-93	31%	EJU05708.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Acromyrmex echinatior]	330	330	71%	9e-93	31%	XP_011062567.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Neodiprion lecontei]	329	329	71%	1e-92	31%	XP_015523873.1
LAMI_0B03400g1_1 [Lachancea mirantina]	328	328	71%	1e-92	32%	SCU80689.1
hypothetical protein E5Q_00045 [Mixia osmundae IAM 14324]	329	329	74%	1e-92	30%	GAA93404.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Athalia rosae]	329	329	71%	1e-92	30%	XP_012258976.1
calcium ATPase [Mortierella elongata AG-77]	334	334	72%	1e-92	31%	OAQ32322.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Neodiprion lecontei]	329	329	72%	1e-92	31%	XP_015523874.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Athalia rosae]	330	330	71%	1e-92	30%	XP_012258971.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Eufriesea mexicana]	328	328	71%	1e-92	31%	XP_017759240.1
hypothetical protein FF38_11991 [Lucilia cuprina]	327	327	70%	1e-92	32%	KNC30576.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X6 [Lingula anatina]	329	329	72%	1e-92	31%	XP_013421506.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Vollenhovia emeryi]	329	329	70%	1e-92	31%	XP_011880448.1
hypothetical protein [Absidia glauca]	330	330	69%	1e-92	31%	SAM09015.1
Calcium-transporting ATPase 1 [[Candida] glabrata]	328	328	72%	1e-92	30%	KTB09933.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Malus domestica]	330	330	71%	1e-92	31%	XP_008376170.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Esox lucius]	329	329	71%	1e-92	31%	XP_010874574.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Egretta garzetta]	329	329	71%	1e-92	31%	KFP19512.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Tinamus guttatus]	330	330	71%	1e-92	31%	XP_010212310.1
hypothetical protein ASPGLDRAFT_115800 [Aspergillus glaucus CBS 516.65]	329	329	74%	1e-92	30%	OJJ89548.1
endoplasmic reticulum calcium P-type ATPase [Grosmannia clavigera kw1407]	328	328	73%	1e-92	31%	XP_014172378.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Athalia rosae]	329	329	71%	1e-92	30%	XP_012258975.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X5 [Lingula anatina]	329	329	72%	1e-92	31%	XP_013421505.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Phoenix dactylifera]	330	330	70%	1e-92	32%	XP_008790538.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium raimondii]	330	330	71%	1e-92	32%	XP_012480875.1
Ca-transporting ATPase [Peniophora sp. CONT]	328	328	74%	1e-92	30%	KZV69679.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Colius striatus]	328	328	71%	2e-92	31%	KFP27739.1
calcium-transporting atpase [Lichtheimia corymbifera JMRC:FSU:9682]	329	329	74%	2e-92	31%	CDH55033.1
hypothetical protein [Absidia glauca]	328	328	74%	2e-92	31%	SAM02208.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X4 [Lingula anatina]	329	329	72%	2e-92	31%	XP_013421503.1
ATPase, P-type, calcium-transporting [Metarhizium rileyi RCEF 4871]	328	328	70%	2e-92	31%	OAA45495.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Bactrocera dorsalis]	326	326	69%	2e-92	32%	XP_011204742.1
RecName: Full=Cation-transporting ATPase CA1	329	329	71%	2e-92	30%	P54209.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Egretta garzetta]	328	328	71%	2e-92	31%	XP_009641408.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium raimondii]	329	329	70%	2e-92	32%	XP_012490146.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Bactrocera cucurbitae]	326	326	69%	2e-92	32%	XP_011195833.1
Calcium-transporting ATPase type 2C member 1 [Zootermopsis nevadensis]	327	327	70%	2e-92	32%	KDR21210.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Lepisosteus oculatus]	326	326	70%	2e-92	32%	XP_015212432.1
Na+/K+ P-type ATPase [Mortierella elongata AG-77]	328	328	72%	2e-92	31%	OAQ32792.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Colius striatus]	328	328	71%	2e-92	31%	XP_010196454.1
PMR1/ATP2C1 protein [Mus musculus]	327	327	70%	2e-92	31%	CAD82864.1
putative calcium P-type ATPase [Metarhizium acridum CQMa 102]	328	328	71%	2e-92	32%	XP_007806868.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Lepisosteus oculatus]	326	326	70%	2e-92	32%	XP_006635593.2
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Cephus cinctus]	328	328	71%	2e-92	31%	XP_015602314.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Bactrocera cucurbitae]	326	326	69%	2e-92	32%	XP_011195825.1
hypothetical protein BN1723_017389 [Verticillium longisporum]	323	323	64%	2e-92	33%	CRK14387.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Daucus carota subsp. sativus]	329	329	71%	2e-92	33%	XP_017245109.1
Ca-transporting ATPase [Stereum hirsutum FP-91666 SS1]	328	328	70%	3e-92	32%	XP_007301369.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X2 [Lingula anatina]	328	328	72%	3e-92	31%	XP_013421499.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Esox lucius]	329	329	71%	3e-92	31%	XP_010874573.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Callithrix jacchus]	327	327	70%	3e-92	31%	XP_017821353.1
hypothetical protein YQE_11064 [Dendroctonus ponderosae]	322	322	68%	3e-92	32%	ENN72282.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Dufourea novaeangliae]	328	328	71%	3e-92	31%	XP_015434670.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Bactrocera latifrons]	326	326	69%	3e-92	32%	XP_018793881.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Kryptolebias marmoratus]	329	329	70%	3e-92	31%	XP_017266122.1
hypothetical protein PAXINDRAFT_168107 [Paxillus involutus ATCC 200175]	328	328	74%	3e-92	30%	KIJ17451.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Bactrocera dorsalis]	326	326	69%	3e-92	32%	XP_011204741.1
calcium ATPase [Cutaneotrichosporon oleaginosus]	328	328	73%	3e-92	31%	XP_018282490.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Chrysemys picta bellii]	326	326	70%	3e-92	32%	XP_008169647.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Egretta garzetta]	328	328	71%	3e-92	31%	XP_009641407.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ceratitis capitata]	328	328	70%	3e-92	32%	XP_004522376.2
ATPase [Salpingoeca rosetta]	328	328	71%	3e-92	31%	XP_004992033.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Vollenhovia emeryi]	327	327	71%	3e-92	31%	XP_011876374.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Dasypus novemcinctus]	327	327	70%	3e-92	32%	XP_004464798.1
uncharacterized protein Dmoj_GI13426, isoform K [Drosophila mojavensis]	325	325	70%	3e-92	32%	XP_015018026.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Oryzias latipes]	328	328	70%	3e-92	31%	XP_004074892.1
ca-transporting atpase [Malassezia pachydermatis]	327	327	72%	3e-92	30%	XP_017993764.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X3 [Lingula anatina]	328	328	72%	4e-92	31%	XP_013421500.1
probable endoplasmic reticulum calcium transporter [Ustilago bromivora]	328	328	73%	4e-92	31%	SAM82917.1
calcium-transporting ATPase [Dichomitus squalens LYAD-421 SS1]	328	328	73%	4e-92	30%	XP_007360939.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Pan troglodytes]	326	326	71%	4e-92	32%	XP_511142.4
calcium-transporting ATPase type 2C member, putative [Pediculus humanus corporis]	325	325	70%	4e-92	32%	XP_002429714.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X4 [Bemisia tabaci]	328	328	71%	4e-92	31%	XP_018914253.1
hypothetical protein g.8370 [Clastoptera arizonana]	326	326	73%	4e-92	30%	JAS26464.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ceratitis capitata]	328	328	70%	4e-92	32%	XP_004522373.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like isoform X1 [Lingula anatina]	328	328	72%	4e-92	31%	XP_013421498.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Fundulus heteroclitus]	328	328	71%	4e-92	31%	XP_012738043.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Bemisia tabaci]	327	327	71%	4e-92	31%	XP_018914252.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Rhagoletis zephyria]	328	328	70%	4e-92	32%	XP_017490953.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Dufourea novaeangliae]	328	328	71%	4e-92	31%	KZC12236.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Cephus cinctus]	328	328	71%	4e-92	31%	XP_015602313.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Pan troglodytes]	326	326	71%	4e-92	32%	XP_016785777.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Cynoglossus semilaevis]	327	327	71%	5e-92	31%	XP_008331025.1
unnamed protein product [Homo sapiens]	326	326	65%	5e-92	32%	BAG61775.1
calcium-transporting ATPase type 2C member 1 isoform 2c [Homo sapiens]	326	326	65%	5e-92	32%	NP_001186111.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Chrysemys picta bellii]	326	326	70%	5e-92	32%	XP_008169646.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Fulmarus glacialis]	327	327	71%	5e-92	31%	KFW08448.1
calcium-transporting ATPase [Metarhizium robertsii ARSEF 23]	327	327	70%	5e-92	32%	XP_007823469.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Cynoglossus semilaevis]	327	327	71%	5e-92	31%	XP_008331026.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Bactrocera latifrons]	325	325	69%	5e-92	32%	XP_018793882.1
Putative Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Penicillium brasilianum]	327	327	75%	5e-92	31%	CEJ54504.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Monomorium pharaonis]	327	327	71%	6e-92	30%	XP_012528436.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Protobothrops mucrosquamatus]	325	325	70%	6e-92	31%	XP_015669844.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Chrysochloris asiatica]	327	327	72%	6e-92	31%	XP_006860350.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Monomorium pharaonis]	327	327	71%	6e-92	30%	XP_012528435.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Protobothrops mucrosquamatus]	325	325	70%	6e-92	31%	XP_015669843.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Puccinia triticina 1-1 BBBD Race 1]	327	327	71%	6e-92	30%	OAV95585.1
ATPase, P-type, calcium-transporting [Metarhizium anisopliae ARSEF 549]	327	327	70%	6e-92	32%	KID63759.1
Na+ P-type ATPase [Mucor ambiguus]	328	328	73%	6e-92	30%	GAN07458.1
Calcium-transporting ATPase [Metarhizium anisopliae BRIP 53293]	327	327	70%	6e-92	32%	KJK77822.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium arboreum]	328	328	70%	6e-92	32%	XP_017631697.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Eptesicus fuscus]	327	327	71%	7e-92	31%	XP_008140925.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Chrysemys picta bellii]	326	326	70%	7e-92	32%	XP_005278716.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Eptesicus fuscus]	328	328	71%	7e-92	31%	XP_008140924.1
ATPase, P-type, calcium-transporting [Metarhizium majus ARSEF 297]	327	327	70%	7e-92	32%	XP_014580814.1
putative calcium-transporting atpase type 2c member 1-like protein [Amblyomma aureolatum]	326	326	70%	7e-92	31%	JAT98814.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Amyelois transitella]	325	325	71%	7e-92	30%	XP_013188612.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Trichogramma pretiosum]	327	327	70%	7e-92	31%	XP_014234331.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Pelecanus crispus]	327	327	71%	7e-92	31%	XP_009487394.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Octodon degus]	327	327	72%	7e-92	31%	XP_004638350.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Octodon degus]	328	328	72%	7e-92	31%	XP_004638349.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Wasmannia auropunctata]	327	327	70%	7e-92	31%	XP_011691312.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Chlamydotis macqueenii]	327	327	71%	8e-92	31%	XP_010118041.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Camelus dromedarius]	327	327	71%	8e-92	31%	XP_010994176.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Vicugna pacos]	327	327	71%	9e-92	31%	XP_006204923.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Wasmannia auropunctata]	327	327	70%	9e-92	31%	XP_011691311.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Pogonomyrmex barbatus]	327	327	71%	9e-92	30%	XP_011631293.1
Calcium-transporting ATPase type 2C member 1 [Picoides pubescens]	323	323	70%	9e-92	32%	KFV69346.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Amyelois transitella]	326	326	71%	9e-92	30%	XP_013188610.1
hypothetical protein g.8372 [Clastoptera arizonana]	324	324	72%	9e-92	31%	JAS15354.1
calcium ATPase [Coccomyxa subellipsoidea C-169]	328	328	71%	1e-91	30%	XP_005646370.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Eufriesea mexicana]	327	327	71%	1e-91	31%	XP_017762222.1
uncharacterized protein Dmoj_GI13426, isoform I [Drosophila mojavensis]	325	325	70%	1e-91	32%	XP_015018024.1
calcium p-type atpase [Colletotrichum gloeosporioides Nara gc5]	326	326	68%	1e-91	31%	XP_007278053.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 1 [Esox lucius]	326	326	70%	1e-91	32%	XP_010892615.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Escovopsis weberi]	326	326	70%	1e-91	31%	KOS20920.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila navojoa]	325	325	70%	1e-91	32%	XP_017957092.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X4 [Wasmannia auropunctata]	326	326	70%	1e-91	31%	XP_011691313.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Trichogramma pretiosum]	327	327	70%	1e-91	31%	XP_014234327.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Agrilus planipennis]	326	326	71%	1e-91	30%	XP_018332137.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Xenopus tropicalis]	325	325	70%	1e-91	31%	XP_017950481.1
hypothetical protein SORBI_001G103300 [Sorghum bicolor]	326	326	71%	1e-91	30%	KXG37640.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Nannospalax galili]	326	326	72%	1e-91	30%	XP_008853850.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Monomorium pharaonis]	327	327	71%	1e-91	30%	XP_012528432.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Austrofundulus limnaeus]	326	326	70%	1e-91	31%	XP_013859363.1
calcium-transporting atpase [Moniliophthora roreri MCA 2997]	326	326	71%	1e-91	32%	XP_007847661.1
Cation transporting ATPase C-terminus [Babesia microti strain RI]	326	326	71%	1e-91	30%	SIO73219.1
uncharacterized protein Dmoj_GI13426, isoform C [Drosophila mojavensis]	325	325	70%	1e-91	32%	XP_015018018.1
endoplasmic reticulum calcium P-type ATPase [Sporothrix insectorum RCEF 264]	326	326	73%	1e-91	30%	OAA64450.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bactrocera dorsalis]	326	326	69%	1e-91	32%	XP_011204740.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Dendroctonus ponderosae]	325	325	71%	1e-91	31%	XP_019768431.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Musca domestica]	324	324	70%	1e-91	32%	XP_011290667.1
Calcium-transporting ATPase 3 [Smittium culicis]	326	326	70%	1e-91	31%	OMJ27947.1
unnamed protein product [Mus musculus]	324	324	72%	1e-91	30%	BAC40903.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Pan paniscus]	324	324	71%	1e-91	32%	XP_014197371.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Apaloderma vittatum]	325	325	65%	1e-91	32%	KFP90725.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Nomascus leucogenys]	325	325	71%	1e-91	32%	XP_003272541.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Amyelois transitella]	325	325	71%	1e-91	30%	XP_013188611.1
SPOSA6832_01395 [Sporidiobolus salmonicolor]	327	327	74%	2e-91	30%	CEQ39834.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Halyomorpha halys]	326	326	70%	2e-91	31%	XP_014283236.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Vicugna pacos]	327	327	71%	2e-91	31%	XP_006204921.1
ATPase, P-type, calcium-transporting [Metarhizium brunneum ARSEF 3297]	326	326	70%	2e-91	32%	XP_014546621.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Chlamydotis macqueenii]	327	327	71%	2e-91	31%	XP_010118040.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Manacus vitellinus]	326	326	71%	2e-91	31%	KFW83269.1
calcium-transporting ATPase 1, endoplasmic reticulum-type [Blastocystis sp. ATCC 50177/Nand II]	327	327	71%	2e-91	30%	OAO17399.1
sarco/endoplasmic reticulum Ca2+-ATPase [Litopenaeus vannamei]	326	326	71%	2e-91	32%	AFC76411.1
calcium-transporting ATPase [Neolentinus lepideus HHB14362 ss-1]	326	326	73%	2e-91	30%	KZT28530.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Rhinopithecus bieti]	325	325	71%	2e-91	32%	XP_017716287.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Heterocephalus glaber]	326	326	72%	2e-91	31%	XP_004857291.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bactrocera latifrons]	326	326	69%	2e-91	32%	XP_018793880.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Eufriesea mexicana]	326	326	70%	2e-91	31%	XP_017762191.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bactrocera cucurbitae]	326	326	69%	2e-91	32%	XP_011195818.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Peromyscus maniculatus bairdii]	325	325	72%	2e-91	30%	XP_006992272.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Cercocebus atys]	324	324	71%	2e-91	32%	XP_011938511.1
TPA: Calcium-transporting ATPase, endoplasmic reticulum-type [Neospora caninum Liverpool]	327	327	70%	2e-91	31%	CEL67293.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Halyomorpha halys]	326	326	70%	2e-91	31%	XP_014283237.1
calcium-transporting ATPase [Auricularia subglabra TFB-10046 SS5]	325	325	73%	2e-91	31%	XP_007338633.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Castor canadensis]	325	325	73%	2e-91	30%	JAV44592.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Rhinopithecus roxellana]	324	324	71%	2e-91	32%	XP_010353932.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Cynoglossus semilaevis]	326	326	71%	2e-91	31%	XP_008333922.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Ceratosolen solmsi marchali]	326	326	70%	2e-91	32%	XP_011503436.1
sarcoplasmic reticulum Ca2+ ATPase Mt-SERCA1a [Molgula tectiformis]	325	325	71%	2e-91	32%	BAG71430.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Heterocephalus glaber]	326	326	72%	2e-91	31%	XP_004857289.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Solenopsis invicta]	325	325	71%	2e-91	30%	XP_011156813.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Ictalurus punctatus]	327	327	71%	2e-91	31%	XP_017318577.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Musca domestica]	324	324	70%	2e-91	32%	XP_011290662.1

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hypothetical protein SCHCODRAFT_65798 [Schizophyllum commune H4-8]	325	325	73%	2e-91	31%	XP_003035126.1
uncharacterized protein [Babesia microti strain RI]	325	325	71%	2e-91	30%	XP_012647248.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Oryza brachyantha]	325	325	71%	2e-91	30%	XP_006651781.1
calcium-transporting ATPase [Fibulorhizoctonia sp. CBS 109695]	325	325	74%	2e-91	30%	KZP20856.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bactrocera dorsalis]	326	326	69%	2e-91	32%	XP_019846211.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Ceratosolen solmsi marchali]	326	326	70%	2e-91	32%	XP_011503432.1
uncharacterized protein Dmoj_GI13426, isoform L [Drosophila mojavensis]	325	325	70%	2e-91	32%	XP_015018027.1
Calcium-transporting ATPase 3 [Smittium culicis]	325	325	70%	2e-91	32%	OMJ28236.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Hypsizygus marmoreus]	325	325	74%	2e-91	30%	KYQ39727.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Colobus angolensis palliatus]	324	324	71%	2e-91	32%	XP_011797592.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Cariama cristata]	326	326	71%	2e-91	31%	XP_009704316.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Agrilus planipennis]	325	325	71%	3e-91	30%	XP_018332133.1
hypothetical protein, variant [Mortierella verticillata NRRL 6337]	328	328	74%	3e-91	30%	KFH73316.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Ochotona princeps]	326	326	71%	3e-91	31%	XP_004594122.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Nanorana parkeri]	324	324	70%	3e-91	31%	XP_018422615.1
E1-E2 ATPase, putative [Ixodes scapularis]	325	325	65%	3e-91	32%	XP_002401874.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Halyomorpha halys]	325	325	70%	3e-91	31%	XP_014283233.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila kikkawai]	323	323	70%	3e-91	32%	XP_017032599.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Cerapachys biroi]	324	324	71%	3e-91	32%	XP_019888204.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Chlorocebus sabaeus]	324	324	71%	3e-91	32%	XP_007992416.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella zimbabwensis]	325	325	71%	3e-91	32%	KRZ14285.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Rhizoctonia solani]	325	325	74%	3e-91	31%	CUA72335.1
uncharacterized protein Dvir_GJ11786, isoform C [Drosophila virilis]	323	323	70%	3e-91	32%	XP_015030615.1
uncharacterized protein Dvir_GJ11786, isoform H [Drosophila virilis]	323	323	70%	3e-91	32%	XP_015030620.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Papilio xuthus]	324	324	68%	3e-91	31%	XP_013172448.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila suzukii]	325	325	71%	3e-91	30%	XP_016940874.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Ictalurus punctatus]	327	327	72%	3e-91	31%	XP_017318576.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Merops nubicus]	325	325	71%	3e-91	31%	XP_008944576.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila kikkawai]	323	323	70%	3e-91	32%	XP_017032598.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Picoides pubescens]	323	323	70%	3e-91	32%	XP_009901432.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Gorilla gorilla gorilla]	324	324	71%	3e-91	32%	XP_004058123.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Peromyscus maniculatus bairdii]	325	325	72%	3e-91	30%	XP_015841327.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Linepithema humile]	324	324	71%	3e-91	31%	XP_012226172.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Colobus angolensis palliatus]	323	323	65%	3e-91	32%	XP_011789064.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Macaca nemestrina]	324	324	71%	3e-91	32%	XP_011765672.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Linepithema humile]	323	323	71%	3e-91	31%	XP_012226173.1
hypothetical protein BOTBODRAFT_104155 [Botryobasidium botryosum FD-172 SS1]	325	325	74%	4e-91	30%	KDQ18481.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Papilio xuthus]	324	324	68%	4e-91	31%	XP_013172447.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Ictidomys tridecemlineatus]	325	325	65%	4e-91	32%	XP_005334975.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Stomoxys calcitrans]	323	323	70%	4e-91	32%	XP_013104506.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Wasmannia auropunctata]	325	325	70%	4e-91	31%	XP_011691306.1
Ca-transporting ATPase [Cylindrobasidium torrendii FP15055 ss-10]	325	325	71%	4e-91	31%	KIY64129.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Papilio xuthus]	323	323	68%	4e-91	31%	XP_013172450.1
sarcoendoplasmic reticulum Ca2+ ATPase SERCA3a [Mus musculus]	325	325	72%	4e-91	30%	AAB04099.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Cebus capucinus imitator]	323	323	71%	4e-91	32%	XP_017399110.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Bactrocera oleae]	325	325	69%	4e-91	32%	XP_014086330.1
hypothetical protein ASPVEDRAFT_131443 [Aspergillus versicolor CBS 583.65]	324	324	74%	4e-91	31%	OJJ02928.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila suzukii]	325	325	71%	4e-91	30%	XP_016940873.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Sinocyclocheilus grahami]	323	323	71%	4e-91	31%	XP_016141671.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Fulmarus glacialis]	325	325	71%	4e-91	31%	XP_009580006.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Chlorocebus sabaeus]	324	324	71%	4e-91	32%	XP_007992415.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bactrocera cucurbitae]	325	325	69%	4e-91	32%	XP_011195811.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Xiphophorus maculatus]	324	324	72%	4e-91	32%	XP_005800846.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bactrocera latifrons]	325	325	69%	4e-91	32%	XP_018793878.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Peromyscus maniculatus bairdii]	325	325	72%	5e-91	30%	XP_006992271.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Sesamum indicum]	325	325	72%	5e-91	30%	XP_011074341.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila bipectinata]	322	322	71%	5e-91	31%	XP_017093226.1
uncharacterized protein Dvir_GJ11786, isoform E [Drosophila virilis]	323	323	70%	5e-91	32%	XP_015030617.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila kikkawai]	323	323	70%	5e-91	32%	XP_017032600.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella patagoniensis]	324	324	70%	5e-91	32%	KRY13462.1
Ca-transporting ATPase [Gelatoporia subvermispora B]	324	324	73%	5e-91	31%	EMD38572.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila bipectinata]	323	323	71%	5e-91	31%	XP_017093225.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila suzukii]	325	325	71%	5e-91	30%	XP_016940869.1
sarcoendoplasmic reticulum Ca2+ ATPase SERCA3b [Mus musculus]	325	325	72%	5e-91	30%	AAB04098.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 2 [Carlito syrichta]	323	323	71%	5e-91	32%	XP_008056007.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Melopsittacus undulatus]	321	321	65%	5e-91	33%	XP_005144842.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform a [Mus musculus]	324	324	72%	5e-91	30%	NP_001156808.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Macaca fascicularis]	323	323	71%	5e-91	32%	XP_005592730.1
Ca2+ transporting ATPase [Kalmanozyma brasiliensis GHG001]	324	324	73%	5e-91	30%	XP_016289697.1
uncharacterized protein Dwil_GK20534, isoform C [Drosophila willistoni]	322	322	70%	5e-91	32%	XP_015033236.1
uncharacterized protein Dvir_GJ11786, isoform B [Drosophila virilis]	323	323	70%	5e-91	32%	XP_015030614.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Mandrillus leucophaeus]	323	323	65%	6e-91	32%	XP_011833362.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella pseudospiralis]	325	325	71%	6e-91	32%	KRZ41316.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Merops nubicus]	325	325	71%	6e-91	31%	XP_008944575.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Musa acuminata subsp. malaccensis]	325	325	70%	6e-91	31%	XP_009388640.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Panthera tigris altaica]	324	324	65%	6e-91	32%	XP_007073518.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Neolamprologus brichardi]	324	324	71%	6e-91	31%	XP_006797570.1
uncharacterized protein Dmoj_GI13426, isoform A [Drosophila mojavensis]	325	325	70%	6e-91	32%	XP_002008331.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella pseudospiralis]	325	325	71%	6e-91	32%	KRY01755.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella spiralis]	325	325	70%	6e-91	32%	KRY42010.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Nasonia vitripennis]	322	322	70%	6e-91	31%	XP_003426720.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Stomoxys calcitrans]	322	322	70%	6e-91	32%	XP_013104502.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Leucoagaricus sp. SymC.cos]	324	324	73%	6e-91	30%	KXN82561.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform b [Mus musculus]	325	325	72%	6e-91	30%	NP_058025.2
PREDICTED: calcium-transporting ATPase type 2C member 1 [Orussus abietinus]	322	322	73%	6e-91	31%	XP_012273075.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Octodon degus]	323	323	65%	7e-91	33%	XP_004625081.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Tupaia chinensis]	324	324	73%	7e-91	30%	XP_006167661.2
endomembrane Ca2+ ATPase 2 [Arabidopsis thaliana]	322	322	71%	7e-91	32%	ABJ90445.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila navojoa]	325	325	70%	7e-91	32%	XP_017957089.1
uncharacterized protein Dana_GF10997, isoform B [Drosophila ananassae]	322	322	71%	7e-91	31%	XP_014764580.1
hypothetical protein MVEG_00534 [Mortierella verticillata NRRL 6337]	329	329	73%	7e-91	30%	KFH73317.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Vollenhovia emeryi]	323	323	71%	7e-91	31%	XP_011876375.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Hydra vulgaris]	322	322	70%	7e-91	32%	XP_012561295.1
hypothetical protein HMPREF1544_09483 [Mucor circinelloides f. circinelloides 1006PhL]	325	325	75%	7e-91	29%	EPB83742.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Papio anubis]	323	323	71%	7e-91	32%	XP_003917301.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila miranda]	322	322	70%	8e-91	32%	XP_017137586.1
unnamed protein product [Mus musculus]	324	324	72%	8e-91	30%	BAE33495.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella zimbabwensis]	325	325	71%	8e-91	32%	KRZ14283.1
endoplasmic reticulum calcium transporter [Ustilago maydis 521]	324	324	74%	8e-91	30%	XP_011388455.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T8]	325	325	70%	8e-91	32%	KRZ94729.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Nestor notabilis]	321	321	65%	8e-91	32%	XP_010015040.1
hypothetical protein PAXRUDRAFT_822015 [Paxillus rubicundulus Ve08.2h10]	324	324	74%	8e-91	31%	KIL00139.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella murrelli]	325	325	70%	8e-91	32%	KRX51128.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella spiralis]	325	325	70%	8e-91	32%	KRY42008.1
hypothetical protein Ecym_6112 [Eremothecium cymbalariae DBVPG#7215]	323	323	71%	9e-91	30%	XP_003647323.1
uncharacterized protein Dvir_GJ11786, isoform D [Drosophila virilis]	323	323	70%	9e-91	32%	XP_015030616.1
hypothetical protein [Sporisorium scitamineum]	324	324	72%	9e-91	30%	CDW96255.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X3 [Latimeria chalumnae]	323	323	70%	9e-91	31%	XP_014344105.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Felis catus]	324	324	65%	9e-91	32%	XP_011283388.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like isoform X1 [Musa acuminata subsp. malaccensis]	325	325	70%	9e-91	31%	XP_009389358.1
hypothetical protein [Parasitella parasitica]	328	328	74%	9e-91	31%	CEP17873.1
uncharacterized protein Dana_GF10997, isoform D [Drosophila ananassae]	322	322	71%	9e-91	31%	XP_014764581.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Vollenhovia emeryi]	323	323	70%	1e-90	31%	XP_011880451.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Tupaia chinensis]	324	324	73%	1e-90	30%	XP_006167662.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Haplochromis burtoni]	325	325	71%	1e-90	31%	XP_005949727.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Vollenhovia emeryi]	323	323	70%	1e-90	31%	XP_011880450.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Neolamprologus brichardi]	324	324	71%	1e-90	31%	XP_006797569.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Musa acuminata subsp. malaccensis]	323	323	71%	1e-90	31%	XP_018683308.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Dinoponera quadriceps]	322	322	71%	1e-90	31%	XP_014472684.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Miniopterus natalensis]	324	324	65%	1e-90	32%	XP_016078893.1
endoplasmic reticulum calcium transporter [Ustilago maydis]	323	323	74%	1e-90	30%	CAE11789.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Diuraphis noxia]	323	323	70%	1e-90	31%	XP_015376120.1
Ca2+ transporting ATPase [Klebsormidium flaccidum]	323	323	71%	1e-90	30%	GAQ88260.1
Calcium-transporting ATPase type 2C member 1 [Heterocephalus glaber]	324	324	70%	1e-90	31%	EHA98127.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Diuraphis noxia]	324	324	70%	1e-90	31%	XP_015376112.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella papuae]	324	324	71%	1e-90	32%	KRZ79309.1
Na+/K+-ATPase alpha subunit [Pagrus major]	324	324	65%	1e-90	32%	ALA65287.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Marmota marmota marmota]	323	323	65%	1e-90	32%	XP_015357714.1
ATPase, P-type, calcium-transporting [Metarhizium album ARSEF 1941]	323	323	71%	1e-90	31%	KHN94144.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Latimeria chalumnae]	323	323	70%	1e-90	31%	XP_005996488.2
hypothetical protein CAPTEDRAFT_176941 [Capitella teleta]	321	321	70%	1e-90	31%	ELU14696.1
calcium-translocating P-type ATPase [Leptomonas seymouri]	323	323	73%	1e-90	29%	KPI84659.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform c [Mus musculus]	323	323	72%	1e-90	30%	NP_001156809.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Diuraphis noxia]	323	323	70%	1e-90	31%	XP_015376119.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Dinoponera quadriceps]	321	321	71%	1e-90	31%	XP_014472687.1
calcium-translocating P-type ATPase, SERCA-type [Batrachochytrium dendrobatidis JEL423]	323	323	73%	1e-90	31%	OAJ44148.1
calcium-transporting atpase type 2c member 1 [Lasius niger]	321	321	71%	1e-90	31%	KMQ87515.1
LAFE_0B07646g1_1 [Lachancea fermentati]	322	322	69%	1e-90	32%	SCW00018.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Condylura cristata]	323	323	65%	1e-90	32%	XP_012585536.1
AaceriAEL301Wp [Saccharomycetaceae sp. 'Ashbya aceri']	322	322	71%	1e-90	31%	AGO10199.1
uncharacterized protein Dwil_GK15853, isoform A [Drosophila willistoni]	323	323	71%	1e-90	31%	XP_002063787.1
sarcoplasmic reticulum Ca2+ ATPase Mt-SERCA2 [Molgula tectiformis]	323	323	70%	1e-90	32%	BAG71432.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila miranda]	321	321	70%	1e-90	32%	XP_017137585.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T9]	324	324	70%	1e-90	31%	KRX62296.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Cariama cristata]	323	323	65%	2e-90	32%	KFP67232.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Myotis brandtii]	322	322	70%	2e-90	31%	XP_005863654.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Eptesicus fuscus]	322	322	65%	2e-90	32%	XP_008151430.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Struthio camelus australis]	323	323	71%	2e-90	31%	KFV76784.1
uncharacterized protein Dana_GF10997, isoform C [Drosophila ananassae]	323	323	71%	2e-90	31%	XP_014764579.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Nannospalax galili]	323	323	72%	2e-90	30%	XP_008853849.1
calcium-transporting ATPase, endoplasimc reticulum type [Cyanidioschyzon merolae strain 10D]	323	323	73%	2e-90	30%	XP_005539258.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Phalacrocorax carbo]	322	322	65%	2e-90	32%	KFW92441.1
E1-E2_ATPase domain-containing protein/Cation_ATPase_C domain-containing protein/Cation_ATPase_N domain-containing protein/Hydrolase domain-containing protein [Cephalotus follicularis]	324	324	69%	2e-90	33%	GAV64988.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella murrelli]	324	324	70%	2e-90	32%	KRX51130.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X6 [Homo sapiens]	323	323	75%	2e-90	29%	XP_011522190.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T8]	324	324	70%	2e-90	32%	KRZ94730.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Myotis brandtii]	322	322	70%	2e-90	31%	XP_014393022.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila miranda]	321	321	70%	2e-90	32%	XP_017137584.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform d [Homo sapiens]	324	324	75%	2e-90	29%	NP_777614.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform c [Homo sapiens]	323	323	75%	2e-90	29%	NP_777616.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella nativa]	323	323	70%	2e-90	32%	KRZ59415.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Falco cherrug]	323	323	71%	2e-90	31%	XP_005434633.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Larimichthys crocea]	327	327	71%	2e-90	32%	KKF20309.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T6]	324	324	65%	2e-90	33%	KRX76969.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Apis mellifera]	321	321	71%	2e-90	32%	XP_006561736.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X5 [Homo sapiens]	323	323	75%	2e-90	29%	XP_011522187.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Cariama cristata]	323	323	65%	2e-90	32%	XP_009702956.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Mucor circinelloides f. circinelloides 1006PhL]	323	323	74%	2e-90	30%	EPB84536.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform b [Homo sapiens]	323	323	75%	2e-90	29%	NP_777615.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X6 [Pan troglodytes]	323	323	75%	2e-90	29%	XP_016786721.1
hypothetical protein g.43715 [Homalodisca liturata]	318	318	66%	2e-90	32%	JAS84009.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Acinonyx jubatus]	323	323	65%	2e-90	32%	XP_014921647.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X7 [Pan troglodytes]	323	323	75%	2e-90	29%	XP_016786722.1
hypothetical protein HELRODRAFT_156619 [Helobdella robusta]	323	323	70%	2e-90	31%	XP_009013683.1
sarco-/endoplasmic reticulum Ca-ATPase 3 [Homo sapiens]	323	323	75%	2e-90	29%	AAC24525.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform a [Homo sapiens]	323	323	75%	2e-90	29%	NP_005164.2
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Juglans regia]	323	323	70%	2e-90	31%	XP_018814821.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Cathartes aura]	322	322	65%	2e-90	32%	KFP55085.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform f [Homo sapiens]	323	323	75%	2e-90	29%	NP_777617.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella nativa]	323	323	70%	2e-90	32%	KRZ59418.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Dinoponera quadriceps]	321	321	71%	2e-90	31%	XP_014472686.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila kikkawai]	323	323	70%	2e-90	32%	XP_017032597.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Amazona aestiva]	322	322	71%	2e-90	31%	KQK83706.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Camponotus floridanus]	320	320	71%	2e-90	31%	XP_011264679.1
hypothetical protein SELMODRAFT_122175 [Selaginella moellendorffii]	323	323	70%	2e-90	31%	XP_002985331.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Haliaeetus albicilla]	323	323	71%	3e-90	31%	XP_009925628.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Maylandia zebra]	323	323	71%	3e-90	31%	XP_014262770.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella spiralis]	323	323	70%	3e-90	32%	KRY42009.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X7 [Homo sapiens]	323	323	75%	3e-90	29%	XP_011522191.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
calcium-transporting atpase [Mucor ambiguus]	322	322	74%	3e-90	30%	GAN04733.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Apis dorsata]	321	321	71%	3e-90	31%	XP_006607922.1
hypothetical protein PHYSODRAFT_247933 [Phytophthora sojae]	321	321	71%	3e-90	30%	XP_009525761.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Gekko japonicus]	322	322	71%	3e-90	31%	XP_015273175.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella patagoniensis]	323	323	70%	3e-90	32%	KRY13461.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Grifola frondosa]	322	322	73%	3e-90	31%	OBZ75070.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila bipectinata]	323	323	71%	3e-90	31%	XP_017093224.1
hypothetical protein LRAMOSA06169 [Lichtheimia ramosa]	322	322	74%	3e-90	31%	CDS13998.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Bemisia tabaci]	323	323	71%	3e-90	30%	XP_018914247.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Microtus ochrogaster]	322	322	73%	3e-90	30%	XP_005349673.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Trachymyrmex zeteki]	322	322	71%	3e-90	30%	XP_018302361.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Trachymyrmex zeteki]	322	322	71%	3e-90	30%	XP_018302360.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Cimex lectularius]	322	322	71%	3e-90	31%	XP_014240087.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X7 [Pongo abelii]	322	322	75%	3e-90	30%	XP_009249417.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Apis mellifera]	321	321	71%	3e-90	31%	XP_001120297.2
sarco/endoplasmic reticulum Ca2+ -ATPase [Homo sapiens]	323	323	75%	3e-90	29%	CAA75739.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Tetranychus urticae]	320	320	70%	3e-90	31%	XP_015787398.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella britovi]	323	323	73%	3e-90	31%	KRY56387.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X6 [Pongo abelii]	322	322	75%	3e-90	30%	XP_002826902.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Cimex lectularius]	322	322	71%	3e-90	31%	XP_014240091.1
sarco/endoplasmic reticulum calcium transporting ATPase, variant [Capsaspora owczarzaki ATCC 30864]	321	321	65%	3e-90	32%	KJE96463.1
unnamed protein product [Homo sapiens]	322	322	74%	3e-90	29%	BAF85405.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Homo sapiens]	324	324	75%	3e-90	29%	XP_011522184.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Myotis brandtii]	322	322	70%	3e-90	31%	XP_005863652.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X4 [Homo sapiens]	323	323	75%	3e-90	29%	XP_016880181.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Polistes canadensis]	321	321	70%	3e-90	31%	XP_014607375.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Mesocricetus auratus]	322	322	74%	3e-90	30%	XP_005067493.1
calcium-translocating P-type ATPase, PMCA-type [Phytophthora parasitica INRA-310]	322	322	71%	3e-90	30%	XP_008912490.1
endoplasmic reticulum-type calcium-transporting ATPase [Blastocystis sp. ATCC 50177/Nand II]	326	326	69%	3e-90	30%	OAO15716.1
Calcium-transporting ATPase type 2C member 1 [Phytophthora nicotianae]	322	322	71%	3e-90	30%	KUF83591.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Oreochromis niloticus]	323	323	71%	4e-90	31%	XP_005461382.2
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella nelsoni]	323	323	70%	4e-90	32%	KRX19625.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Homo sapiens]	323	323	75%	4e-90	29%	XP_011522186.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X5 [Pan troglodytes]	322	322	75%	4e-90	29%	XP_016786720.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Halyomorpha halys]	320	320	70%	4e-90	31%	XP_014271202.1
uncharacterized protein Dana_GF10997, isoform A [Drosophila ananassae]	323	323	71%	4e-90	31%	XP_001958581.2
uncharacterized protein Dwil_GK20534, isoform B [Drosophila willistoni]	323	323	70%	4e-90	32%	XP_002068552.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Myotis brandtii]	322	322	70%	4e-90	31%	XP_014393019.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Bemisia tabaci]	322	322	71%	4e-90	30%	XP_018914251.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Camponotus floridanus]	321	321	71%	4e-90	31%	XP_011264678.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Coccidioides immitis RMSCC 2394]	321	321	64%	4e-90	32%	KMP02435.1
uncharacterized protein Dvir_GJ11786, isoform A [Drosophila virilis]	323	323	70%	4e-90	32%	XP_002047680.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2, partial [Chlamydotis macqueenii]	322	322	71%	4e-90	31%	KFP41628.1
Ca2+ transporting ATPase sarcoplasmic/endoplasmic reticulum [Clonorchis sinensis]	322	322	71%	4e-90	31%	GAA36484.2
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Camponotus floridanus]	322	322	71%	4e-90	31%	XP_011261310.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Penicillium subrubescens]	322	322	75%	4e-90	31%	OKO93954.1
Calcium-transporting ATPase type 2C member 1 [Camponotus floridanus]	320	320	71%	4e-90	31%	EFN62566.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Apis florea]	320	320	71%	4e-90	31%	XP_012347702.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Falco peregrinus]	322	322	65%	4e-90	33%	XP_005231152.1
calcium ATPase [Aureobasidium namibiae CBS 147.97]	322	322	71%	4e-90	30%	XP_013425005.1
potassium/sodium efflux P-type ATPase, fungal-type [Spizellomyces punctatus DAOM BR117]	321	321	76%	4e-90	29%	XP_016603943.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Nomascus leucogenys]	321	321	65%	4e-90	32%	XP_003265455.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform e [Homo sapiens]	323	323	75%	4e-90	29%	NP_777613.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Halyomorpha halys]	320	320	70%	4e-90	31%	XP_014271201.1
sarco/endoplasmic reticulum calcium transporting ATPase [Capsaspora owczarzaki ATCC 30864]	321	321	65%	4e-90	32%	KJE96462.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Carlito syrichta]	322	322	65%	4e-90	31%	XP_008071711.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Phaethon lepturus]	322	322	71%	4e-90	31%	KFQ69606.1
hypothetical protein HYDPIDRAFT_105948 [Hydnomerulius pinastri MD-312]	322	322	74%	4e-90	30%	KIJ69348.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X4 [Mesocricetus auratus]	322	322	74%	4e-90	30%	XP_005067492.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Gekko japonicus]	322	322	71%	4e-90	31%	XP_015273174.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Ceratotherium simum simum]	322	322	65%	4e-90	31%	XP_004420673.1

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Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella patagoniensis]	319	319	64%	5e-90	33%	KRY13465.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Halyomorpha halys]	321	321	70%	5e-90	31%	XP_014271197.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Halyomorpha halys]	319	319	70%	5e-90	31%	XP_014271203.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Apis florea]	320	320	71%	5e-90	31%	XP_012347708.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Trachymyrmex zeteki]	322	322	71%	5e-90	30%	XP_018302356.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Camponotus floridanus]	322	322	71%	5e-90	31%	XP_011261309.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Cimex lectularius]	322	322	71%	5e-90	31%	XP_014240090.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Halyomorpha halys]	320	320	70%	5e-90	31%	XP_014271199.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Homo sapiens]	323	323	75%	5e-90	29%	XP_011522183.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Nipponia nippon]	322	322	71%	5e-90	31%	XP_009471083.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T8]	322	322	70%	5e-90	32%	KRZ94728.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Mesocricetus auratus]	322	322	74%	5e-90	30%	XP_012967208.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Microtus ochrogaster]	322	322	73%	5e-90	30%	XP_005349672.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Gavia stellata]	321	321	71%	5e-90	31%	KFV57800.1
unnamed protein product [Albugo candida]	322	322	71%	5e-90	31%	CCI44411.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella murrelli]	322	322	70%	5e-90	32%	KRX51129.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X12 [Pan troglodytes]	322	322	75%	5e-90	29%	XP_016786728.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella nativa]	322	322	70%	6e-90	32%	KRZ59416.1
calcium-translocating P-type ATPase, PMCA-type [Phytophthora parasitica]	321	321	71%	6e-90	30%	ETK77012.1
PREDICTED: sarco/endoplasmic reticulum calcium transporting ATPase isoform X1 [Strongylocentrotus purpuratus]	322	322	72%	6e-90	31%	XP_011663710.1
hypothetical protein cypCar_00027973 [Cyprinus carpio]	322	322	71%	6e-90	31%	KTG46027.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Phaethon lepturus]	321	321	71%	6e-90	31%	XP_010287786.1
calcium-translocating P-type ATPase, SERCA-type [Allomyces macrogynus ATCC 38327]	323	323	71%	6e-90	30%	KNE68426.1
Calcium-transporting ATPase type 2C member 1 [Harpegnathos saltator]	319	319	71%	6e-90	31%	EFN86535.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Camponotus floridanus]	322	322	71%	6e-90	31%	XP_011261306.1
P-type ATPase superfamily protein [Toxoplasma gondii FOU]	296	296	14%	6e-90	76%	KFG46174.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Lates calcarifer]	322	322	70%	6e-90	32%	XP_018539949.1
calcium-translocating P-type ATPase [Trypanosoma grayi]	321	321	70%	7e-90	30%	XP_009312974.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Halyomorpha halys]	320	320	70%	7e-90	31%	XP_014271200.1
Calcium-transporting ATPase type 2C member 1 [Eufriesea mexicana]	320	320	70%	7e-90	31%	OAD55788.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Galeopterus variegatus]	323	323	65%	7e-90	32%	XP_008581763.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Pongo abelii]	322	322	75%	7e-90	30%	XP_002826901.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Phoenix dactylifera]	318	318	72%	7e-90	30%	XP_008790244.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Sinocyclocheilus rhinocerous]	322	322	70%	7e-90	31%	XP_016368025.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X5 [Pongo abelii]	322	322	75%	7e-90	30%	XP_002826903.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Cucumis melo]	319	319	71%	7e-90	30%	XP_016900030.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Apis florea]	320	320	71%	7e-90	31%	XP_012347683.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Gavia stellata]	321	321	71%	7e-90	31%	XP_009815288.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Musa acuminata subsp. malaccensis]	321	321	71%	7e-90	31%	XP_009405782.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Brassica napus]	321	321	72%	8e-90	29%	XP_013716478.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Halyomorpha halys]	320	320	70%	8e-90	31%	XP_014271198.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T9]	322	322	70%	8e-90	32%	KRX62299.1
HFL052Wp [Eremothecium sinecaudum]	320	320	71%	8e-90	31%	XP_017988800.1
Calcium-transporting ATPase type 2C member 1 [Habropoda laboriosa]	319	319	71%	8e-90	31%	KOC61582.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X11 [Pan troglodytes]	322	322	75%	8e-90	29%	XP_016786727.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X4 [Pongo abelii]	322	322	75%	8e-90	30%	XP_009249416.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Lates calcarifer]	321	321	71%	8e-90	31%	XP_018524020.1
calcium ATPase [Rhizopogon vinicolor AM-OR11-026]	321	321	75%	9e-90	30%	OAX36610.1
adenosine triphosphatase, calcium [Homo sapiens]	321	321	75%	9e-90	29%	CAA93737.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Callithrix jacchus]	320	320	71%	9e-90	32%	XP_002761269.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella patagoniensis]	322	322	70%	9e-90	32%	KRY13464.1
RecName: Full=Calcium-transporting ATPase type 2C member 2; Short=ATPase 2C2; AltName: Full=Secretory pathway Ca(2+)-ATPase 2	320	320	71%	9e-90	32%	O75185.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Phaethon lepturus]	322	322	71%	9e-90	31%	XP_010287778.1
uncharacterized protein Dpse_GA16915, isoform C [Drosophila pseudoobscura pseudoobscura]	322	322	70%	9e-90	32%	XP_001353367.3
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Latimeria chalumnae]	320	320	70%	9e-90	31%	XP_014344104.1
calcium-transporting ATPase type 2C member 2 [Rattus norvegicus]	320	320	71%	9e-90	31%	NP_604457.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila miranda]	322	322	70%	9e-90	32%	XP_017137582.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Harpegnathos saltator]	320	320	71%	9e-90	31%	XP_011136384.1
hypothetical protein PBRA_008483 [Plasmodiophora brassicae]	322	322	65%	9e-90	31%	CEP01171.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Apis cerana]	319	319	72%	9e-90	31%	XP_016922338.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Nelumbo nucifera]	322	322	70%	1e-89	31%	XP_010267484.1
unnamed protein product [Phytomonas sp. isolate Hart1]	321	321	71%	1e-89	30%	CCW66645.1

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Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella britovi]	322	322	73%	1e-89	31%	KRY56386.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Sinocyclocheilus grahami]	322	322	71%	1e-89	31%	XP_016095698.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella nativa]	321	321	70%	1e-89	32%	KRZ59417.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Eurypyga helias]	321	321	65%	1e-89	32%	KFW03259.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Diachasma alloeum]	318	318	69%	1e-89	32%	XP_015110444.1
ER-type Ca2+-ATPase 2 [Arabidopsis thaliana]	322	322	70%	1e-89	32%	NP_191999.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T6]	322	322	70%	1e-89	32%	KRX76972.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Cercocebus atys]	319	319	71%	1e-89	32%	XP_011938420.1
hypothetical protein g.35981 [Homalodisca liturata]	320	320	71%	1e-89	30%	JAT05569.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Rattus norvegicus]	320	320	71%	1e-89	30%	NP_037046.1
RE31249p [Drosophila melanogaster]	319	319	70%	1e-89	31%	ADD01316.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Merops nubicus]	320	320	71%	1e-89	31%	KFQ35390.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila elegans]	320	320	71%	1e-89	30%	XP_017124911.1
hypothetical protein A6R68_02299 [Neotoma lepida]	318	318	70%	1e-89	30%	OBS69190.1
putative calcium-translocating P-type ATPase [Trypanosoma vivax Y486]	321	321	70%	1e-89	30%	CCC48085.1
calcium-translocating P-type ATPase, SERCA-type family protein [Cryptosporidium muris RN66]	323	323	69%	1e-89	29%	XP_002141105.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Drosophila ficusphila]	318	318	70%	1e-89	31%	XP_017042232.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Cricetulus griseus]	321	321	74%	1e-89	30%	XP_007615305.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Eurypyga helias]	320	320	65%	1e-89	32%	XP_010147794.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Diachasma alloeum]	318	318	69%	1e-89	32%	XP_015110442.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Equus caballus]	320	320	65%	1e-89	32%	XP_014595480.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Maylandia zebra]	321	321	71%	1e-89	31%	XP_004567378.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Maylandia zebra]	320	320	71%	1e-89	31%	XP_004567379.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Saimiri boliviensis boliviensis]	319	319	71%	2e-89	32%	XP_003922855.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Echinops telfairi]	318	318	65%	2e-89	31%	XP_004704062.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Crassostrea gigas]	318	318	70%	2e-89	31%	XP_019923242.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila takahashii]	318	318	70%	2e-89	31%	XP_016997923.1
hypothetical protein SELMODRAFT_158488 [Selaginella moellendorffii]	320	320	72%	2e-89	31%	XP_002987187.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Diachasma alloeum]	318	318	69%	2e-89	32%	XP_015110441.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila busckii]	318	318	70%	2e-89	32%	XP_017843479.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila busckii]	318	318	70%	2e-89	32%	XP_017843480.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Diachasma alloeum]	318	318	69%	2e-89	32%	XP_015110443.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Nicotiana attenuata]	321	321	71%	2e-89	32%	XP_019239024.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Crassostrea gigas]	318	318	70%	2e-89	31%	XP_011428934.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Lates calcarifer]	321	321	71%	2e-89	31%	XP_018524019.1
hypothetical protein B456_009G220900 [Gossypium raimondii]	319	319	71%	2e-89	30%	KJB58671.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Saimiri boliviensis boliviensis]	317	317	70%	2e-89	32%	XP_010331963.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Gossypium arboreum]	320	320	71%	2e-89	30%	XP_017606052.1
ATPase, Ca++ transporting, ubiquitous, isoform CRA_b [Rattus norvegicus]	320	320	71%	2e-89	30%	EDM05127.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Esox lucius]	321	321	71%	2e-89	30%	XP_010889916.1
calcium-transporting P-type ATPase, PMR1-type [Trichuris suis]	318	318	70%	2e-89	31%	KHJ44387.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Lepisosteus oculatus]	320	320	70%	2e-89	31%	XP_006640332.2
PREDICTED: calcium-transporting ATPase type 2C member 2 [Mesocricetus auratus]	318	318	71%	2e-89	31%	XP_005073146.1
secretory pathway calcium atpase, isoform A [Drosophila melanogaster]	318	318	70%	2e-89	31%	NP_730745.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Habropoda laboriosa]	318	318	71%	2e-89	31%	XP_017794138.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Equus przewalskii]	320	320	65%	2e-89	32%	XP_008513358.1
uncharacterized protein Dyak_GE22637, isoform D [Drosophila yakuba]	318	318	70%	2e-89	31%	XP_015051077.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella sp. T9]	321	321	70%	2e-89	32%	KRX62297.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Macaca mulatta]	318	318	71%	2e-89	32%	XP_014982205.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Clupea harengus]	320	320	70%	2e-89	31%	XP_012670372.1
secretory pathway calcium atpase, isoform E [Drosophila melanogaster]	318	318	70%	2e-89	31%	NP_001163496.1
hypothetical protein MVEG_03384 [Mortierella verticillata NRRL 6337]	323	323	73%	2e-89	31%	KFH70534.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Chelonia mydas]	317	317	65%	2e-89	33%	XP_007064363.1
calcium-translocating P-type ATPase, PMCA-type [Phytophthora parasitica]	319	319	71%	2e-89	30%	ETM36875.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Kryptolebias marmoratus]	320	320	71%	3e-89	31%	XP_017270160.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella pseudospiralis]	321	321	71%	3e-89	31%	KRY01756.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila takahashii]	318	318	70%	3e-89	31%	XP_016997921.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila elegans]	320	320	71%	3e-89	30%	XP_017124910.1
calcium-transporting ATPase [Fistulina hepatica ATCC 64428]	319	319	73%	3e-89	30%	KIY51059.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Podiceps cristatus]	318	318	65%	3e-89	31%	KFZ65267.1
uncharacterized protein Dana_GF12053, isoform B [Drosophila ananassae]	319	319	71%	3e-89	30%	XP_014763068.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Echinops telfairi]	319	319	71%	3e-89	32%	XP_004704818.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila ficusphila]	318	318	70%	3e-89	31%	XP_017042231.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila busckii]	319	319	70%	3e-89	32%	XP_017843478.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
uncharacterized protein Dyak_GE22637, isoform B [Drosophila yakuba]	318	318	70%	3e-89	31%	XP_015051075.1
hypothetical protein [Parasitella parasitica]	321	321	65%	3e-89	30%	CEP09449.1
hypothetical protein B456_009G220900 [Gossypium raimondii]	318	318	71%	3e-89	30%	KJB58670.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Saimiri boliviensis boliviensis]	318	318	71%	3e-89	32%	XP_010331962.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Pongo abelii]	323	323	75%	3e-89	30%	XP_009249415.1
uncharacterized protein Dere_GG16277, isoform E [Drosophila erecta]	317	317	70%	3e-89	31%	XP_015014186.1
calcium-transporting ATPase type 2C member 2 isoform 2 [Homo sapiens]	318	318	71%	3e-89	32%	NP_055676.3
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila ficusphila]	318	318	70%	3e-89	31%	XP_017042230.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Galeopterus variegatus]	317	317	65%	3e-89	32%	XP_008565452.1
calcium-transporting ATPase [Cordyceps confragosa RCEF 1005]	319	319	73%	3e-89	30%	OAA80023.1
uncharacterized protein Dana_GF12053, isoform A [Drosophila ananassae]	319	319	71%	3e-89	30%	XP_001959439.1
GH20185 [Drosophila grimshawi]	320	320	70%	3e-89	30%	XP_001987043.1
sodium/potassium-transporting ATPase subunit alpha-1 [Equus caballus]	320	320	65%	3e-89	32%	AEP26351.1
hypothetical protein g.33962 [Clastoptera arizonana]	319	319	71%	3e-89	31%	JAS16065.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Bombus impatiens]	318	318	71%	4e-89	31%	XP_003484455.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila eugracilis]	319	319	71%	4e-89	30%	XP_017070169.1
calcium-translocating P-type ATPase, SERCA-type [Trichophyton rubrum MR850]	319	319	68%	4e-89	30%	EZF13387.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Gossypium raimondii]	319	319	71%	4e-89	30%	XP_012445385.1
secretory pathway calcium atpase, isoform C [Drosophila melanogaster]	317	317	70%	4e-89	31%	NP_730744.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila busckii]	319	319	71%	4e-89	30%	XP_017837630.1
hypothetical protein B456_009G220900 [Gossypium raimondii]	320	320	71%	4e-89	30%	KJB58672.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Mesitornis unicolor]	319	319	71%	4e-89	31%	XP_010191019.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Pongo abelii]	323	323	75%	4e-89	30%	XP_009249414.1
Ca-transporting ATPase [Coniophora puteana RWD-64-598 SS2]	319	319	73%	4e-89	30%	XP_007764616.1
GH16765 [Drosophila grimshawi]	320	320	70%	4e-89	32%	XP_001984939.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Astyanax mexicanus]	320	320	71%	4e-89	31%	XP_007256169.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Equus przewalskii]	319	319	65%	4e-89	32%	XP_008513356.1
unnamed protein product [Homo sapiens]	318	318	71%	4e-89	32%	BAG62238.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Equus caballus]	319	319	65%	4e-89	32%	NP_001108004.2
hypothetical protein CICLE_v10000142mg [Citrus clementina]	319	319	72%	4e-89	30%	XP_006433652.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Bombus impatiens]	317	317	71%	4e-89	31%	XP_012241472.1
RecName: Full=Sarcoplasmic/endoplasmic reticulum calcium ATPase 3; Short=SERCA3; Short=SR Ca(2+)-ATPase 3; AltName: Full=Calcium pump 3	320	320	71%	4e-89	30%	P18596.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bombus impatiens]	318	318	71%	4e-89	31%	XP_012241361.1
calcium-transporting ATPase, putative [Eimeria maxima]	320	320	71%	4e-89	31%	XP_013338093.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Cucumis melo]	319	319	71%	4e-89	30%	XP_008444533.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Nicotiana tabacum]	320	320	71%	4e-89	32%	XP_016480053.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Kryptolebias marmoratus]	320	320	71%	5e-89	31%	XP_017270159.1
Calcium-transporting ATPase type 2C member 1 [Exaiptasia pallida]	317	317	72%	5e-89	29%	KXJ17852.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Fopius arisanus]	317	317	71%	5e-89	31%	XP_011311172.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila eugracilis]	317	317	70%	5e-89	31%	XP_017084293.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 1 [Bathycoccus prasinos]	321	321	67%	5e-89	30%	XP_007512204.1
ATPase, Ca++ transporting, ubiquitous, isoform CRA_a [Rattus norvegicus]	319	319	71%	5e-89	30%	EDM05126.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Mesitornis unicolor]	320	320	71%	5e-89	31%	XP_010191018.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X3 [Glycine max]	315	315	71%	5e-89	29%	XP_006578061.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Nothobranchius furzeri]	320	320	72%	5e-89	30%	XP_015809968.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Haplochromis burtoni]	320	320	71%	5e-89	31%	XP_005940609.1
hypothetical protein GYMLUDRAFT_244928 [Gymnopus luxurians FD-317 M1]	318	318	74%	5e-89	29%	KIK59711.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-1; Short=Sodium pump subunit alpha-1; AltName: Full=Na(+)/K(+) ATPase alpha-1 subunit; Flags: Precursor	319	319	65%	5e-89	32%	P18907.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Nicotiana tomentosiformis]	320	320	71%	5e-89	32%	XP_009600380.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Drosophila rhopaloa]	317	317	70%	5e-89	31%	XP_016977911.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Fopius arisanus]	317	317	71%	5e-89	31%	XP_011311174.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Juglans regia]	315	315	70%	5e-89	30%	XP_018843310.1
hypothetical protein LLEC1_03707 [Cordyceps confragosa]	318	318	73%	6e-89	30%	OAQ96613.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Rhinopithecus roxellana]	320	320	75%	6e-89	30%	XP_010380533.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bombus impatiens]	317	317	71%	6e-89	31%	XP_012241235.1
ECA2 [Arabidopsis thaliana]	320	320	70%	6e-89	32%	OAO97862.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Beta vulgaris subsp. vulgaris]	318	318	70%	6e-89	30%	XP_010687183.1
calcium-translocating P-type ATPase, PMCA-type [Phytophthora parasitica CJ01A1]	318	318	71%	6e-89	30%	ETP06626.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Drosophila elegans]	316	316	70%	6e-89	31%	XP_017116028.1
hypothetical protein MUCCIDRAFT_42770 [Mucor circinelloides f. lusitanicus CBS 277.49]	315	315	68%	6e-89	30%	OAD01022.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Phoenicopterus ruber ruber]	318	318	71%	6e-89	31%	KFQ87589.1
uncharacterized protein Dere_GG16277, isoform D [Drosophila erecta]	317	317	70%	6e-89	31%	XP_015014185.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Phoenix dactylifera]	318	318	72%	6e-89	30%	XP_008790243.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Galeopterus variegatus]	318	318	65%	6e-89	32%	XP_008565451.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Erinaceus europaeus]	316	316	70%	7e-89	31%	XP_007529952.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Eufriesea mexicana]	320	320	65%	7e-89	32%	OAD62001.1
hypothetical protein g.33974 [Clastoptera arizonana]	318	318	71%	7e-89	31%	JAS34645.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Melipona quadrifasciata]	321	321	65%	7e-89	32%	KOX76050.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Nothobranchius furzeri]	320	320	71%	7e-89	31%	XP_015809969.1
calcium-translocating P-type ATPase, PMCA-type [Phytophthora parasitica P1569]	318	318	71%	7e-89	30%	ETI36803.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Tribolium castaneum]	318	318	70%	7e-89	31%	XP_015839082.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila eugracilis]	317	317	70%	7e-89	31%	XP_017084291.1
RH03344p [Drosophila melanogaster]	319	319	70%	7e-89	31%	AAX51640.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila eugracilis]	318	318	71%	8e-89	30%	XP_017070168.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila eugracilis]	318	318	71%	8e-89	30%	XP_017070164.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Myotis lucifugus]	318	318	65%	8e-89	32%	XP_006099078.2
uncharacterized protein Dyak_GE11511, isoform B [Drosophila yakuba]	318	318	71%	8e-89	30%	XP_015051618.1
Calcium-transporting ATPase 3 [Smittium mucronatum]	318	318	74%	8e-89	31%	OLY81433.1
probable PMR1-Ca++-transporting P-type ATPase located in Golgi [Zygosaccharomyces bailii ISA1307]	317	317	69%	8e-89	31%	CDH11577.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila biarmipes]	316	316	70%	8e-89	31%	XP_016959428.1
uncharacterized protein Dere_GG19978, isoform C [Drosophila erecta]	318	318	71%	8e-89	30%	XP_015011535.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Tribolium castaneum]	318	318	70%	9e-89	31%	XP_966783.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila bipectinata]	318	318	71%	9e-89	30%	XP_017090277.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Otolemur garnettii]	318	318	64%	9e-89	32%	XP_003795244.1
ATPase, Ca++ transporting, ubiquitous, isoform CRA_e [Homo sapiens]	318	318	75%	9e-89	29%	EAW90464.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Musca domestica]	318	318	71%	9e-89	30%	XP_019892864.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Bombus terrestris]	317	317	71%	9e-89	31%	XP_003398033.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Fopius arisanus]	318	318	71%	1e-88	30%	XP_011306358.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Tribolium castaneum]	318	318	70%	1e-88	31%	XP_015839084.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Drosophila elegans]	316	316	70%	1e-88	31%	XP_017116027.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Bombus terrestris]	317	317	71%	1e-88	31%	XP_012167633.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Rhizoctonia solani AG-1 IB]	318	318	74%	1e-88	31%	CEL52335.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Gossypium raimondii]	314	314	70%	1e-88	30%	XP_012445387.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila suzukii]	316	316	70%	1e-88	31%	XP_016926936.1

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hypothetical protein g.33978 [Clastoptera arizonana]	318	318	71%	1e-88	31%	JAS10819.1
hypothetical protein A3Q56_06285 [Intoshia linei]	318	318	64%	1e-88	33%	OAF65999.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Jaculus jaculus]	317	317	65%	1e-88	31%	XP_004664380.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Fopius arisanus]	316	316	71%	1e-88	31%	XP_011311173.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Elaeis guineensis]	318	318	72%	1e-88	30%	XP_010936144.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Manis javanica]	317	317	71%	1e-88	31%	XP_017499884.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Raphanus sativus]	318	318	73%	1e-88	29%	XP_018486123.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila busckii]	318	318	70%	1e-88	32%	XP_017843477.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila elegans]	318	318	71%	1e-88	30%	XP_017124907.1
hypothetical protein MUCCIDRAFT_153802 [Mucor circinelloides f. lusitanicus CBS 277.49]	317	317	70%	1e-88	31%	OAC99834.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Brassica oleracea var. oleracea]	318	318	72%	1e-88	29%	XP_013601936.1
Calcium-transporting ATPase type 2C member 1 [Myotis davidii]	317	317	70%	1e-88	31%	ELK25330.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Orycteropus afer afer]	316	316	65%	1e-88	32%	XP_007941139.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Latimeria chalumnae]	316	316	73%	1e-88	30%	XP_014350574.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Fopius arisanus]	318	318	71%	1e-88	30%	XP_011306353.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella spiralis]	319	319	65%	1e-88	31%	KRY31167.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila elegans]	316	316	70%	1e-88	31%	XP_017116026.1
GD15051 [Drosophila simulans]	318	318	70%	1e-88	31%	EDX11522.1
Cation-transporting P-type ATPase [Cynara cardunculus var. scolymus]	319	319	69%	2e-88	33%	KVH94581.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Drosophila biarmipes]	315	315	70%	2e-88	31%	XP_016959427.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Columba livia]	317	317	71%	2e-88	31%	XP_013227443.1
calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type-like protein [Sarcoptes scabiei]	319	319	70%	2e-88	31%	KPM02996.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella spiralis]	319	319	65%	2e-88	31%	KRY31170.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Ceratotherium simum simum]	318	318	65%	2e-88	32%	XP_004442834.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Xiphophorus maculatus]	318	318	70%	2e-88	31%	XP_005802178.1
uncharacterized protein Dyak_GE22637, isoform C [Drosophila yakuba]	317	317	70%	2e-88	31%	XP_015051076.1
uncharacterized protein Dere_GG19978, isoform B [Drosophila erecta]	318	318	71%	2e-88	30%	XP_015011534.1
uncharacterized protein Dsimw501_GD15051, isoform F [Drosophila simulans]	317	317	70%	2e-88	31%	XP_016032999.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila bipectinata]	317	317	71%	2e-88	30%	XP_017090276.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Crassostrea gigas]	317	317	72%	2e-88	31%	XP_019922302.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like [Raphanus sativus]	317	317	73%	2e-88	29%	XP_018491481.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Erinaceus europaeus]	316	316	65%	2e-88	32%	XP_016047969.1
uncharacterized protein Dyak_GE11511, isoform A [Drosophila yakuba]	317	317	71%	2e-88	30%	XP_002092715.1
uncharacterized protein Dyak_GE11511, isoform C [Drosophila yakuba]	317	317	71%	2e-88	30%	XP_015051619.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Sarcophilus harrisii]	315	315	71%	2e-88	32%	XP_012396184.1
calcium-translocating P-type ATPase [Trypanosoma cruzi strain CL Brener]	317	317	70%	2e-88	30%	XP_814228.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Oryzias latipes]	317	317	71%	2e-88	31%	XP_004072815.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Trichechus manatus latirostris]	317	317	65%	2e-88	32%	XP_004388806.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Bos mutus]	318	318	64%	2e-88	32%	XP_005903938.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Manis javanica]	317	317	65%	2e-88	32%	XP_017510102.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Myotis davidii]	317	317	70%	2e-88	31%	XP_006770255.2
uncharacterized protein Dsimw501_GD15051, isoform G [Drosophila simulans]	318	318	70%	2e-88	31%	XP_016033000.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Alligator sinensis]	314	314	62%	2e-88	32%	XP_006015272.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila busckii]	317	317	71%	2e-88	30%	XP_017837629.1
uncharacterized protein Dere_GG19978, isoform A [Drosophila erecta]	317	317	71%	2e-88	30%	XP_001976498.1
secretory pathway calcium atpase, isoform D [Drosophila melanogaster]	317	317	70%	2e-88	31%	NP_001097666.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Citrus sinensis]	317	317	72%	2e-88	30%	XP_006472318.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila kikkawai]	317	317	71%	2e-88	30%	XP_017018614.1
hypothetical protein TDEL_0B05460 [Torulaspora delbrueckii]	316	316	69%	2e-88	32%	XP_003679886.1
calcium-translocating P-type ATPase, putative [Trypanosoma cruzi marinkellei]	317	317	70%	2e-88	30%	EKF27364.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Latimeria chalumnae]	315	315	69%	2e-88	31%	XP_006004265.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like [Brassica rapa]	317	317	72%	2e-88	29%	XP_009118267.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Erinaceus europaeus]	315	315	70%	2e-88	31%	XP_016046649.1
uncharacterized protein Dsimw501_GD24994, isoform H [Drosophila simulans]	317	317	71%	2e-88	29%	XP_016029333.1
hypothetical protein L969DRAFT_96071 [Mixia osmundae IAM 14324]	317	317	74%	2e-88	30%	XP_014566126.1
unnamed protein product [Oncorhynchus mykiss]	318	318	71%	2e-88	31%	CDQ68192.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Oryzias latipes]	317	317	71%	2e-88	31%	XP_011477858.1
unnamed protein product [Homo sapiens]	317	317	65%	2e-88	32%	BAH12194.1
uncharacterized protein Dyak_GE22637, isoform A [Drosophila yakuba]	317	317	70%	2e-88	31%	XP_002095847.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila takahashii]	317	317	70%	2e-88	31%	XP_016997920.1
sarco/endoplasmic reticulum calcium transporting ATPase [Strongylocentrotus purpuratus]	317	317	72%	3e-88	31%	NP_001032719.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila ficusphila]	317	317	70%	3e-88	31%	XP_017042229.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila busckii]	317	317	71%	3e-88	30%	XP_017837628.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Mustela putorius furo]	316	316	65%	3e-88	32%	XP_012919582.1
Ca-transporting ATPase [Mycena chlorophos]	317	317	74%	3e-88	29%	GAT43961.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila ficusphila]	317	317	70%	3e-88	31%	XP_017042227.1
SPoCk [Drosophila busckii]	318	318	70%	3e-88	32%	ALC44544.1
secretory pathway calcium atpase, isoform B [Drosophila melanogaster]	317	317	70%	3e-88	31%	NP_730742.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like isoform X1 [Gossypium hirsutum]	317	317	71%	3e-88	30%	XP_016687217.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X3 [Musa acuminata subsp. malaccensis]	316	316	70%	3e-88	31%	XP_018683309.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Nicotiana sylvestris]	317	317	71%	3e-88	32%	XP_009770829.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Camelus bactrianus]	316	316	70%	3e-88	31%	XP_010959545.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila takahashii]	317	317	70%	3e-88	31%	XP_016997919.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Cucumis sativus]	317	317	71%	3e-88	30%	XP_011649561.1
uncharacterized protein [Blastocystis hominis]	317	317	71%	3e-88	30%	XP_012895489.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Manis javanica]	316	316	65%	3e-88	32%	XP_017510095.1
BnaC08g42380D [Brassica napus]	317	317	72%	3e-88	29%	CDY22604.1
Na(+)/K(+)-ATPase alpha 3 [Cavia porcellus]	316	316	65%	3e-88	32%	ADD82419.1
putative calcium-transporting atpase type 2c member 1-like isoform x1 [Nyssomyia neivai]	315	315	70%	3e-88	30%	JAV04986.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Erinaceus europaeus]	315	315	70%	3e-88	31%	XP_016046644.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Myotis brandtii]	317	317	65%	3e-88	32%	XP_005876319.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Pygoscelis adeliae]	316	316	71%	3e-88	31%	KFW65144.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Camelus ferus]	316	316	65%	3e-88	32%	XP_006175113.1
unnamed protein product [Rattus norvegicus]	311	311	62%	3e-88	32%	AAA73342.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila kikkawai]	317	317	71%	3e-88	30%	XP_017018613.1
GM22470 [Drosophila sechellia]	317	317	70%	3e-88	31%	XP_002040951.1
calcium-translocating P-type ATPase, putative [Trypanosoma cruzi]	317	317	70%	3e-88	30%	EKF98558.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Salmo salar]	317	317	71%	3e-88	31%	XP_013983891.1
calcium-translocating P-type ATPase [Trypanosoma cruzi Dm28c]	317	317	70%	4e-88	30%	ESS65423.1
uncharacterized protein Dere_GG16277, isoform C [Drosophila erecta]	316	316	70%	4e-88	31%	XP_015014184.1
uncharacterized protein Dsimw501_GD24994, isoform B [Drosophila simulans]	317	317	71%	4e-88	29%	XP_016029327.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Ipomoea nil]	316	316	71%	4e-88	29%	XP_019156301.1
GM15491 [Drosophila sechellia]	316	316	71%	4e-88	29%	XP_002040177.1
ZYBA0S06-03004g1_1 [Zygosaccharomyces bailii CLIB 213]	315	315	69%	4e-88	31%	CDF90199.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Fukomys damarensis]	316	316	65%	4e-88	32%	KFO33633.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Ovis aries musimon]	315	315	65%	4e-88	32%	XP_012017947.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Ipomoea nil]	316	316	71%	4e-88	29%	XP_019156300.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X4 [Erinaceus europaeus]	316	316	65%	4e-88	32%	XP_007532980.1
KIAA0703 gene product, isoform CRA_a [Homo sapiens]	315	315	70%	4e-88	32%	EAW95483.1
hypothetical protein MUCCIDRAFT_186097 [Mucor circinelloides f. lusitanicus CBS 277.49]	316	316	74%	4e-88	30%	OAD07576.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Stegodyphus mimosarum]	316	316	70%	4e-88	31%	KFM58607.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Sarcophilus harrisii]	316	316	65%	4e-88	32%	XP_012402172.1
putative calcium-transporting atpase type 2c member 1-like isoform x1 [Nyssomyia neivai]	315	315	70%	4e-88	30%	JAV04985.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Orycteropus afer afer]	315	315	65%	4e-88	32%	XP_007941137.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Hipposideros armiger]	316	316	65%	4e-88	32%	XP_019484611.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Microplitis demolitor]	316	316	70%	4e-88	31%	XP_014300760.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Camelina sativa]	316	316	72%	5e-88	29%	XP_010475872.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Carlito syrichta]	316	316	65%	5e-88	32%	XP_008065591.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Ailuropoda melanoleuca]	316	316	65%	5e-88	32%	XP_019660115.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Hipposideros armiger]	316	316	65%	5e-88	32%	XP_019484612.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Rattus norvegicus]	319	319	71%	5e-88	30%	XP_006246659.1
cation transport ATPase [Thalassiosira pseudonana CCMP1335]	316	316	73%	5e-88	30%	XP_002286890.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Myotis brandtii]	315	315	70%	5e-88	31%	XP_014393020.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Acyrthosiphon pisum]	315	315	69%	5e-88	31%	XP_001950200.2
calcium-transporting ATPase, putative [Eimeria acervulina]	317	317	71%	5e-88	30%	XP_013247929.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Mesitornis unicolor]	316	316	71%	5e-88	31%	KFQ40862.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X4 [Sorex araneus]	314	314	65%	5e-88	32%	XP_004616286.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3 [Nomascus leucogenys]	315	315	65%	5e-88	32%	XP_012352153.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Miniopterus natalensis]	316	316	65%	5e-88	32%	XP_016064663.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila eugracilis]	317	317	70%	5e-88	31%	XP_017084290.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Diachasma alloeum]	316	316	71%	5e-88	31%	XP_015111451.1
hypothetical protein PHSY_000679 [Pseudozyma hubeiensis SY62]	316	316	72%	5e-88	30%	XP_012186704.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Lipotes vexillifer]	315	315	65%	5e-88	32%	XP_007458654.1
unnamed protein product [Homo sapiens]	315	315	71%	5e-88	32%	BAH14499.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Pelodiscus sinensis]	316	316	71%	5e-88	31%	XP_014435047.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Charadrius vociferus]	317	317	65%	5e-88	31%	XP_009878582.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Propithecus coquereli]	316	316	65%	5e-88	32%	XP_012508801.1

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uncharacterized protein Dere_GG16277, isoform B [Drosophila erecta]	317	317	70%	5e-88	31%	XP_001973765.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Microcebus murinus]	316	316	65%	5e-88	32%	XP_012613923.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Chlorocebus sabaeus]	316	316	65%	5e-88	32%	XP_007995139.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila biarmipes]	316	316	70%	5e-88	31%	XP_016959426.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Cercocebus atys]	317	317	65%	6e-88	32%	XP_011942295.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Parasteatoda tepidariorum]	314	314	70%	6e-88	30%	XP_015927389.1
cation transporting ATPase [Thalassiosira pseudonana CCMP1335]	316	316	70%	6e-88	30%	XP_002294029.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Rousettus aegyptiacus]	316	316	65%	6e-88	32%	XP_015979826.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Apaloderma vittatum]	313	313	62%	6e-88	32%	XP_009871507.1
sodium/potassium-transporting ATPase subunit alpha-3 isoform 2 [Homo sapiens]	316	316	65%	6e-88	32%	NP_001243142.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Nicotiana tabacum]	317	317	71%	6e-88	32%	XP_016498836.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Odobenus rosmarus divergens]	316	316	65%	6e-88	32%	XP_004408220.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Picoides pubescens]	315	315	71%	6e-88	31%	XP_009907887.1
putative Na(+)-exporting P-type ATPase ENA5 [Rhizophagus irregularis DAOM 197198w]	315	315	69%	6e-88	32%	EXX53770.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Alligator sinensis]	314	314	62%	6e-88	32%	XP_006015273.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Callithrix jacchus]	316	316	65%	6e-88	32%	XP_002762227.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Pygoscelis adeliae]	316	316	71%	6e-88	31%	XP_009319494.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Erinaceus europaeus]	316	316	65%	6e-88	32%	XP_007532978.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Erinaceus europaeus]	316	316	65%	6e-88	32%	XP_007532979.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Acyrthosiphon pisum]	313	313	69%	6e-88	31%	XP_008180469.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Crassostrea gigas]	316	316	72%	6e-88	31%	EKC33522.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Sinocyclocheilus rhinocerous]	316	316	70%	6e-88	31%	XP_016366534.1
ATPase, P-type, calcium-transporting [Metarhizium guizhouense ARSEF 977]	317	317	65%	6e-88	33%	KID87054.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Sorex araneus]	315	315	65%	6e-88	32%	XP_004620761.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Chinchilla lanigera]	316	316	65%	6e-88	32%	XP_005412458.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Ictidomys tridecemlineatus]	316	316	65%	6e-88	32%	XP_013219625.1
ATPase, Ca++ transporting, ubiquitous, isoform CRA_c [Mus musculus]	315	315	68%	6e-88	30%	EDL12703.1
Calcium-transporting ATPase type 2C member 1 [Dufourea novaeangliae]	313	313	71%	6e-88	30%	KZC11673.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Balaenoptera acutorostrata scammoni]	315	315	65%	6e-88	32%	XP_007168107.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Sinocyclocheilus grahami]	317	317	71%	7e-88	31%	XP_016088537.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Ovis aries musimon]	315	315	65%	7e-88	32%	XP_012017946.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Myotis lucifugus]	316	316	65%	7e-88	32%	XP_014301482.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Na+/K+ -ATPase alpha 3 subunit variant [Homo sapiens]	316	316	65%	7e-88	32%	BAD97289.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Colobus angolensis palliatus]	316	316	65%	7e-88	32%	XP_011791957.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Stomoxys calcitrans]	315	315	71%	7e-88	30%	XP_013101847.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Miniopterus natalensis]	316	316	65%	7e-88	32%	XP_016064662.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Myotis brandtii]	315	315	70%	7e-88	31%	XP_014393021.1
calcium-transporting ATPase 2, endoplasmic reticulum-type [Arabidopsis lyrata subsp. lyrata]	317	317	70%	7e-88	32%	XP_002872919.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like isoform X1 [Ziziphus jujuba]	315	315	71%	7e-88	30%	XP_015884878.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila biarmipes]	316	316	70%	7e-88	31%	XP_016959425.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X4 [Hipposideros armiger]	316	316	65%	7e-88	32%	XP_019484613.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Odobenus rosmarus divergens]	316	316	65%	7e-88	32%	XP_004408219.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Struthio camelus australis]	316	316	71%	7e-88	31%	XP_009665081.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Camelus bactrianus]	316	316	65%	7e-88	32%	XP_010945046.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Picoides pubescens]	316	316	71%	7e-88	31%	XP_009907886.1
sodium/potassium-transporting ATPase subunit alpha-3 isoform 1 [Homo sapiens]	316	316	65%	7e-88	32%	NP_689509.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Otolemur garnettii]	316	316	65%	7e-88	32%	XP_003799509.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Camelina sativa]	315	315	72%	7e-88	29%	XP_010458348.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Heterocephalus glaber]	316	316	65%	7e-88	32%	EHB02517.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Orycteropus afer afer]	315	315	65%	7e-88	32%	XP_007941138.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Panthera pardus]	316	316	65%	8e-88	32%	XP_019289950.1
sodium/potassium-transporting ATPase subunit alpha-3 [Sus scrofa]	316	316	65%	8e-88	32%	NP_001165224.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Equus asinus]	316	316	65%	8e-88	32%	XP_014723001.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Otolemur garnettii]	316	316	65%	8e-88	32%	XP_003799510.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Callithrix jacchus]	316	316	65%	8e-88	32%	XP_002762226.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Gorilla gorilla gorilla]	316	316	70%	8e-88	30%	XP_018869117.1
calcium-transporting ATPase [Obba rivulosa]	315	315	73%	8e-88	32%	OCH95585.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Bos taurus]	315	315	65%	8e-88	32%	XP_010813416.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Camelus dromedarius]	315	315	65%	8e-88	32%	XP_010979756.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Camelus dromedarius]	316	316	65%	8e-88	32%	XP_010979755.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Eucalyptus grandis]	313	313	70%	8e-88	30%	XP_018731690.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Camelus dromedarius]	316	316	65%	8e-88	32%	XP_010979754.1
KIAA0703 protein [Homo sapiens]	316	316	70%	8e-88	32%	BAA31678.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Octodon degus]	316	316	65%	8e-88	32%	XP_004644410.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sarco/endoplasmic reticulum Ca2+-ATPase [Toxoplasma gondii ME49]	317	317	69%	8e-88	30%	XP_002367953.1
Ca2+ transporting ATPase,sarcoplasmic/endoplasmic reticulum [Rhizoctonia solani AG-1 IB]	319	319	74%	8e-88	31%	CCO26138.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Bos mutus]	315	315	65%	8e-88	32%	XP_005909047.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Capra hircus]	315	315	65%	8e-88	32%	XP_017917960.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Galeopterus variegatus]	315	315	65%	8e-88	32%	XP_008581762.1
hypothetical protein TBLA_0C00190 [Tetrapisispora blattae CBS 6284]	314	314	71%	8e-88	30%	XP_004179359.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Drosophila elegans]	315	315	70%	8e-88	31%	XP_017116025.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Elephantulus edwardii]	316	316	65%	9e-88	32%	XP_006900990.1
hypothetical protein PANDA_013230 [Ailuropoda melanoleuca]	315	315	65%	9e-88	32%	EFB28107.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Bos taurus]	316	316	65%	9e-88	32%	XP_015323036.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Leptonychotes weddellii]	316	316	65%	9e-88	32%	XP_006732052.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Camelus bactrianus]	315	315	65%	9e-88	32%	XP_010945047.1
putative P-type ATPase [Phytophthora infestans T30-4]	315	315	71%	9e-88	29%	XP_002899894.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Chlorocebus sabaeus]	316	316	65%	9e-88	32%	XP_007995138.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Anthurium amnicola]	316	316	71%	9e-88	30%	JAT47916.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Parasteatoda tepidariorum]	313	313	70%	9e-88	30%	XP_015927388.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Cercocebus atys]	315	315	65%	9e-88	32%	XP_011942294.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Orcinus orca]	315	315	65%	9e-88	32%	XP_004271274.1
unnamed protein product [Homo sapiens]	315	315	65%	9e-88	32%	BAH14440.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Myotis brandtii]	316	316	65%	9e-88	32%	XP_005883948.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-A; Short=Na(+)/K(+) ATPase alpha-A subunit; AltName: Full=Sodium pump subunit alpha-A	315	315	71%	9e-88	30%	P17326.1
sodium/potassium-transporting ATPase subunit alpha-3 isoform 3 [Homo sapiens]	315	315	65%	9e-88	32%	NP_001243143.1
ATPase, Ca++ transporting, ubiquitous, isoform CRA_b [Mus musculus]	315	315	68%	1e-87	30%	EDL12702.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Dufourea novaeangliae]	314	314	71%	1e-87	30%	XP_015433890.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Elephantulus edwardii]	315	315	65%	1e-87	32%	XP_006900991.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila suzukii]	315	315	70%	1e-87	31%	XP_016926935.1
sodium/potassium-transporting ATPase subunit alpha-3 [Mus musculus]	315	315	65%	1e-87	32%	NP_001277398.1
sodium/potassium-transporting ATPase subunit alpha-3 [Rattus norvegicus]	315	315	65%	1e-87	32%	NP_036638.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Bison bison bison]	315	315	65%	1e-87	32%	XP_010861314.1
Calcium-transporting ATPase type 2C member 1 [Crassostrea gigas]	313	313	70%	1e-87	31%	EKC29072.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Condylura cristata]	315	315	65%	1e-87	32%	XP_004694211.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Fukomys damarensis]	315	315	65%	1e-87	32%	XP_010621596.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Stomoxys calcitrans]	315	315	71%	1e-87	30%	XP_013101849.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Mus musculus]	315	315	65%	1e-87	32%	XP_011248822.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Bos taurus]	315	315	65%	1e-87	32%	XP_002695120.2
calcium-transporting ATPase, putative [Eimeria necatrix]	316	316	71%	1e-87	31%	XP_013436484.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Fukomys damarensis]	313	313	67%	1e-87	30%	XP_019061158.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Brassica oleracea var. oleracea]	315	315	72%	1e-87	29%	XP_013587663.1
ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_a [Rattus norvegicus]	315	315	65%	1e-87	32%	EDM08049.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Bos mutus]	315	315	65%	1e-87	32%	ELR46673.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Microtus ochrogaster]	315	315	65%	1e-87	32%	XP_005361184.1
uncharacterized protein Dvir_GJ21881, isoform C [Drosophila virilis]	315	315	71%	1e-87	30%	XP_015029872.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Hipposideros armiger]	315	315	65%	1e-87	32%	XP_019484610.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Heterocephalus glaber]	315	315	65%	1e-87	32%	XP_004873108.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Fukomys damarensis]	314	314	68%	1e-87	31%	KFO20364.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Eptesicus fuscus]	315	315	65%	1e-87	32%	XP_008158464.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Heterocephalus glaber]	313	313	67%	1e-87	31%	XP_012932354.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Galeopterus variegatus]	313	313	62%	1e-87	32%	XP_008568671.1
ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_a [Mus musculus]	315	315	65%	1e-87	32%	EDL24296.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Smittium mucronatum]	315	315	74%	1e-87	31%	OLY82235.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Pteropus alecto]	315	315	65%	1e-87	32%	XP_006903931.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Microtus ochrogaster]	315	315	65%	1e-87	32%	XP_005361183.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Myotis brandtii]	316	316	65%	1e-87	32%	EPQ18710.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Panthera pardus]	315	315	65%	1e-87	32%	XP_019289949.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Ochotona princeps]	315	315	65%	1e-87	31%	XP_004598028.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Microplitis demolitor]	315	315	70%	1e-87	31%	XP_008548678.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X3 [Parasteatoda tepidariorum]	313	313	70%	1e-87	30%	XP_015927390.1
hypothetical protein B456_009G220900 [Gossypium raimondii]	314	314	71%	1e-87	30%	KJB58673.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Heterocephalus glaber]	315	315	68%	1e-87	31%	EHB05789.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Equus caballus]	316	316	65%	1e-87	32%	XP_014587374.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Pan paniscus]	314	314	71%	1e-87	29%	XP_008960836.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Glycine max]	315	315	71%	1e-87	29%	XP_003524018.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Noccaea caerulescens]	315	315	72%	1e-87	29%	JAU57860.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Pan paniscus]	314	314	71%	1e-87	29%	XP_008960835.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Brassica napus]	315	315	72%	1e-87	29%	XP_013645928.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Drosophila elegans]	315	315	70%	1e-87	31%	XP_017116024.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X3 [Branchiostoma belcheri]	313	313	72%	1e-87	30%	XP_019629131.1
hypothetical protein XELAEV_18036444mg [Xenopus laevis]	315	315	69%	1e-87	29%	OCT73467.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Ictalurus punctatus]	315	315	70%	1e-87	31%	XP_017347928.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Sinocyclocheilus anshuiensis]	316	316	71%	1e-87	31%	XP_016310655.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Bos mutus]	315	315	65%	1e-87	32%	XP_005909046.1
probable calcium ATPase [Phaeodactylum tricornutum CCAP 1055/1]	315	315	71%	1e-87	31%	XP_002177149.1
putative calcium P-type ATPase [Metarhizium anisopliae]	315	315	65%	1e-87	32%	KFG86816.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Branchiostoma belcheri]	314	314	72%	1e-87	30%	XP_019629129.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Capra hircus]	315	315	65%	1e-87	32%	XP_017917959.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Myotis brandtii]	314	314	65%	2e-87	32%	XP_014390018.1
sarcoplasmic/endoplasmic reticulum calcium ATPase [Rhizoctonia solani 123E]	315	315	71%	2e-87	31%	KEP55558.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Dipodomys ordii]	315	315	65%	2e-87	32%	XP_012888115.1
hypothetical protein EUTSA_v10006682mg [Eutrema salsugineum]	314	314	72%	2e-87	30%	XP_006417493.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pteropus alecto]	314	314	65%	2e-87	32%	XP_006919736.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Orcinus orca]	315	315	65%	2e-87	32%	XP_004271273.1
uncharacterized protein Dana_GF12053, isoform C [Drosophila ananassae]	315	315	71%	2e-87	30%	XP_014763069.1
ATPase, Na+/K+ transporting, alpha 3 polypeptide, isoform CRA_b [Rattus norvegicus]	314	314	65%	2e-87	32%	EDM08050.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Nicotiana attenuata]	313	313	71%	2e-87	29%	XP_019263578.1
uncharacterized protein Dvir_GJ21881, isoform D [Drosophila virilis]	314	314	71%	2e-87	30%	XP_002049966.2
sodium/potassium ATPase alpha subunit [Acanthopagrus schlegelii]	315	315	65%	2e-87	32%	ABR10300.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Nannospalax galili]	315	315	65%	2e-87	32%	XP_008844659.1
calcium-translocating P-type ATPase [Trypanosoma rangeli]	314	314	70%	2e-87	30%	AGN32970.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Erinaceus europaeus]	315	315	65%	2e-87	32%	XP_007525565.1
hypothetical protein Kpol_541p36 [Vanderwaltozyma polyspora DSM 70294]	313	313	69%	2e-87	33%	XP_001645651.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Rousettus aegyptiacus]	314	314	65%	2e-87	32%	XP_015985445.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Galeopterus variegatus]	313	313	69%	2e-87	30%	XP_008566976.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Tarenaya hassleriana]	314	314	72%	2e-87	29%	XP_010544013.1
endoplasmic reticulum calcium transporter [Sporisorium reilianum SRZ2]	314	314	73%	2e-87	30%	CBQ72623.1
hypothetical protein [Absidia glauca]	315	315	68%	2e-87	30%	SAM05739.1

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ATPase, Ca++ transporting, ubiquitous, isoform CRA_f [Homo sapiens]	312	312	70%	2e-87	29%	EAW90465.1
calcium ATPase SERCA-like [Toxoplasma gondii]	316	316	69%	2e-87	30%	AAU93917.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Ochotona princeps]	314	314	65%	2e-87	31%	XP_004598029.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Mus musculus]	315	315	65%	2e-87	32%	XP_011248821.1
hypothetical protein CISIN_1g0018772mg [Citrus sinensis]	312	312	65%	2e-87	31%	KDO81475.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Mus musculus]	315	315	65%	2e-87	32%	XP_011248820.1
unnamed protein product [Homo sapiens]	315	315	65%	2e-87	32%	BAH12387.1
hypothetical protein CISIN_1g0018772mg [Citrus sinensis]	312	312	65%	2e-87	31%	KDO81476.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Chrysochloris asiatica]	314	314	65%	2e-87	32%	XP_006871444.1
calcium-transporting ATPase, putative [Eimeria tenella]	315	315	70%	2e-87	31%	XP_013228780.1
calcium-transporting P-type ATPase [Capsaspora owczarzaki ATCC 30864]	313	313	76%	2e-87	30%	KJE91439.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Erinaceus europaeus]	314	314	65%	2e-87	32%	XP_007525566.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Myotis davidii]	314	314	65%	2e-87	32%	XP_006761137.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Peromyscus maniculatus bairdii]	313	313	71%	3e-87	31%	XP_015863963.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X3 [Ricinus communis]	310	310	71%	3e-87	29%	XP_015575063.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Pteropus vampyrus]	314	314	65%	3e-87	32%	XP_011381111.1
sarco/endoplasmic reticulum Ca2+-ATPase [Toxoplasma gondii VAND]	315	315	69%	3e-87	30%	KFH03163.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Tupaia chinensis]	314	314	68%	3e-87	30%	ELV11186.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Fukomys damarensis]	312	312	67%	3e-87	30%	XP_010609666.2
sarco:endoplasmic reticulum calcium ATPase [Hymenolepis microstoma]	314	314	64%	3e-87	32%	CDS27558.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Columba livia]	315	315	71%	3e-87	31%	EMC86924.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Pteropus vampyrus]	314	314	65%	3e-87	32%	XP_011381110.1
uncharacterized protein Dvir_GJ21881, isoform B [Drosophila virilis]	314	314	71%	3e-87	30%	XP_015029871.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Callithrix jacchus]	316	316	65%	3e-87	32%	XP_008986344.1
AGAP012115-PA-like protein [Anopheles sinensis]	311	311	70%	3e-87	30%	KFB51291.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Sorex araneus]	313	313	65%	3e-87	32%	XP_004616285.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Clupea harengus]	314	314	71%	3e-87	31%	XP_012673224.1
hypothetical protein CISIN_1g0018772mg [Citrus sinensis]	311	311	65%	3e-87	31%	KDO81477.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Marmota marmota marmota]	316	316	65%	3e-87	32%	XP_015352507.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Corvus brachyrhynchos]	311	311	62%	3e-87	32%	XP_017590279.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Camelina sativa]	313	313	72%	3e-87	29%	XP_010490720.1
unnamed protein product [Oncorhynchus mykiss]	314	314	70%	3e-87	31%	CDQ83085.1
hypothetical protein LRAMOSA05783 [Lichtheimia ramosa]	315	315	71%	3e-87	31%	CDS13607.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Sinocyclocheilus rhinocerous]	313	313	71%	3e-87	31%	XP_016430228.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Solanum tuberosum]	311	311	70%	4e-87	30%	XP_006347866.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Esox lucius]	313	313	70%	4e-87	32%	XP_010875761.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Carlito syrichta]	311	311	67%	4e-87	30%	XP_008058929.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Noccaea caerulescens]	315	315	73%	4e-87	29%	JAU06414.1
hypothetical protein g.36009 [Homalodisca liturata]	313	313	71%	4e-87	30%	JAS96327.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Carlito syrichta]	311	311	67%	4e-87	30%	XP_008058928.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Myotis davidii]	313	313	65%	4e-87	32%	ELK32312.1
hypothetical protein XELAEV_18038010mg [Xenopus laevis]	314	314	69%	4e-87	29%	OCT71101.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Tupaia chinensis]	315	315	65%	4e-87	32%	XP_014438012.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Amborella trichopoda]	313	313	71%	4e-87	30%	XP_006857120.1
BnaCnng01680D [Brassica napus]	314	314	70%	4e-87	31%	CDY07153.1
uncharacterized protein LOC733327 [Xenopus laevis]	314	314	69%	4e-87	29%	NP_001135833.1
Calcium-transporting ATPase [Rhodotorula toruloides ATCC 204091]	313	313	74%	4e-87	29%	EGU12502.1
sarco/endoplasmic reticulum calcium ATPase [Medicago truncatula]	314	314	71%	4e-87	29%	XP_013461797.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Noccaea caerulescens]	313	313	72%	4e-87	29%	JAU42214.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-1 [Esox lucius]	313	313	66%	5e-87	32%	XP_012995352.2
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Theobroma cacao]	313	313	71%	5e-87	30%	XP_007018465.2
plasma membrane calcium-transporting ATPase 2 [Culex quinquefasciatus]	312	312	70%	5e-87	31%	XP_001844593.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Salmo salar]	314	314	70%	5e-87	31%	XP_014064426.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Bos indicus]	313	313	64%	5e-87	32%	XP_019843721.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Sorex araneus]	313	313	65%	5e-87	32%	XP_012789881.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Dasypus novemcinctus]	313	313	71%	5e-87	31%	XP_004448484.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Fukomys damarensis]	313	313	65%	5e-87	31%	XP_010629504.1
sarco/endoplasmic reticulum Ca2+-ATPase [Hammondia hammondi]	315	315	69%	5e-87	30%	XP_008889593.1
hypothetical protein TPHA_0D00630 [Tetrapisispora phaffii CBS 4417]	312	312	69%	5e-87	31%	XP_003685141.1
hypothetical protein TRIADDRAFT_19369 [Trichoplax adhaerens]	311	311	72%	5e-87	31%	XP_002109012.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila biarmipes]	313	313	71%	5e-87	29%	XP_016953290.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Carlito syrichta]	312	312	67%	6e-87	30%	XP_008058930.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Sinocyclocheilus anshuiensis]	313	313	70%	6e-87	31%	XP_016311182.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Eucalyptus grandis]	313	313	70%	6e-87	30%	XP_010061643.1
sarcoplasmic/endoplasmic reticulum calcium ATPase [Rhizoctonia solani AG-3 Rhs1AP]	313	313	71%	6e-87	31%	EUC67146.1
calcium-transporting ATPase [Cordyceps militaris CM01]	313	313	73%	6e-87	31%	XP_006672168.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Nannospalax galili]	311	311	67%	6e-87	30%	XP_017650482.1
hypothetical protein [Parasitella parasitica]	313	313	72%	6e-87	30%	CEP18689.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like isoform X2 [Ziziphus jujuba]	309	309	70%	6e-87	30%	XP_015884879.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like isoform X2 [Raphanus sativus]	313	313	72%	6e-87	29%	XP_018440003.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila bipectinata]	313	313	71%	6e-87	29%	XP_017090272.1
sodium/potassium-transporting ATPase subunit alpha-4 [Bos taurus]	313	313	64%	7e-87	32%	NP_001137575.2
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nativa]	314	314	65%	7e-87	30%	KRZ52541.1
Na+, K+ -ATPase catalytic subunit [Homo sapiens]	313	313	65%	7e-87	31%	AAA51798.1
uncharacterized protein [Blastocystis hominis]	313	313	72%	7e-87	30%	XP_012895122.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 [Drosophila takahashii]	312	312	71%	7e-87	29%	XP_017013448.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Esox lucius]	313	313	70%	8e-87	32%	XP_010875759.1
hypothetical protein OsJ_12452 [Oryza sativa Japonica Group]	314	314	71%	8e-87	29%	EEE59867.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Corvus brachyrhynchos]	311	311	62%	8e-87	32%	XP_017590278.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Jaculus jaculus]	311	311	67%	8e-87	30%	XP_004672472.2
Calcium-transporting ATPase 3 [Choanephora cucurbitarum]	313	313	75%	8e-87	29%	OBZ87856.1
Calcium-transporting ATPase type 2C member 1 [Tinamus guttatus]	309	309	70%	8e-87	31%	KGL77785.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Pan troglodytes]	312	312	71%	8e-87	31%	XP_003315263.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X8 [Homo sapiens]	313	313	70%	8e-87	30%	XP_016880182.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Sinocyclocheilus rhinocerous]	313	313	71%	8e-87	31%	XP_016430226.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Octopus bimaculoides]	311	311	71%	9e-87	32%	XP_014783176.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Xenopus laevis]	313	313	69%	9e-87	29%	XP_018082052.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Termitomyces sp. J132]	312	312	74%	1e-86	30%	KNZ75442.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Phalacrocorax carbo]	310	310	62%	1e-86	32%	XP_009505602.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type-like isoform X2 [Camelina sativa]	313	313	70%	1e-86	31%	XP_010456182.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila kikkawai]	313	313	71%	1e-86	29%	XP_017018608.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Ananas comosus]	312	312	72%	1e-86	30%	OAY62961.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila biarmipes]	313	313	71%	1e-86	29%	XP_016953286.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Fukomys damarensis]	313	313	65%	1e-86	31%	KFO30324.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Mesocricetus auratus]	310	310	69%	1e-86	30%	XP_012967207.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Erinaceus europaeus]	311	311	71%	1e-86	31%	XP_007528427.1
predicted protein [Physcomitrella patens]	312	312	70%	1e-86	31%	XP_001778460.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like [Brassica napus]	312	312	72%	1e-86	29%	XP_013640937.1
hypothetical protein AALP_AA1G107600 [Arabis alpina]	312	312	72%	1e-86	29%	KFK43308.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type [Brassica oleracea var. oleracea]	313	313	70%	1e-86	30%	XP_013612644.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Nicotiana attenuata]	312	312	71%	1e-86	29%	XP_019263577.1
hypothetical protein TRIADDRAFT_28963 [Trichoplax adhaerens]	312	312	75%	1e-86	29%	XP_002115035.1
Calcium-transporting P-type ATPase, subfamily IIA, SERCA-type [Cynara cardunculus var. scolymus]	313	313	70%	1e-86	32%	KVH88471.1
H+-exporting ATPase (EC 3.6.3.6) - Trypanosoma brucei	312	312	75%	1e-86	30%	A45598
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Noccaea caerulescens]	312	312	72%	1e-86	29%	JAU91034.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like isoform X2 [Gossypium hirsutum]	311	311	71%	1e-86	30%	XP_016687218.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Nannospalax galili]	311	311	71%	1e-86	31%	XP_008826133.1
hypothetical protein PLEOSDRAFT_1061214 [Pleurotus ostreatus PC15]	311	311	74%	1e-86	30%	KDQ33561.1
Sarco/endoplasmic reticulum Ca(2+)-ATPase, isoform I [Drosophila melanogaster]	312	312	71%	1e-86	29%	NP_001286796.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Octopus bimaculoides]	311	311	71%	1e-86	32%	XP_014783175.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Smittium culicis]	312	312	69%	1e-86	32%	OMJ19670.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Nelumbo nucifera]	310	310	71%	1e-86	29%	XP_010273148.1
hypothetical protein OCBIM_22038129mg [Octopus bimaculoides]	310	310	71%	1e-86	32%	KOF73284.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X1 [Drosophila takahashii]	312	312	71%	1e-86	29%	XP_017013442.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Egretta garzetta]	310	310	70%	1e-86	31%	XP_009638471.1
Endoplasmic reticulum-type calcium-transporting ATPase 3 isoform 1 [Theobroma cacao]	311	311	71%	1e-86	30%	EOY15690.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Calidris pugnax]	312	312	65%	1e-86	32%	XP_014812640.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X3 [Eucalyptus grandis]	308	308	69%	1e-86	30%	XP_010061645.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila biarmipes]	311	311	71%	2e-86	29%	XP_016953289.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Fragaria vesca subsp. vesca]	311	311	72%	2e-86	29%	XP_004290983.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Egretta garzetta]	310	310	70%	2e-86	31%	XP_009638470.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Acromyrmex echinatior]	311	311	65%	2e-86	32%	EGI60476.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Xiphophorus maculatus]	312	312	70%	2e-86	31%	XP_014325405.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Pteropus alecto]	310	310	71%	2e-86	31%	XP_006926784.1
probable PMR1-Ca++-transporting P-type ATPase located in Golgi [Zygosaccharomyces bailii ISA1307]	310	310	69%	2e-86	31%	CDH16581.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Lupinus angustifolius]	311	311	71%	2e-86	29%	XP_019437891.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Myotis davidii]	312	312	65%	2e-86	32%	XP_006768969.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Rhinolophus sinicus]	313	313	65%	2e-86	32%	XP_019569313.1
Calcium-transporting ATPase 2, endoplasmic reticulum-type [Noccaea caerulescens]	313	313	70%	2e-86	32%	JAU23132.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Microcebus murinus]	311	311	68%	2e-86	30%	XP_012634758.1
calcium-transporting P-type ATPase [Capsaspora owczarzaki ATCC 30864]	311	311	76%	2e-86	30%	XP_004349323.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
Calcium-transporting ATPase type 2C member 1 [Trichinella papuae]	310	310	71%	2e-86	30%	KRZ72217.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Microcebus murinus]	311	311	68%	2e-86	30%	XP_012634755.1
potassium-transporting ATPase alpha chain 1 [Xenopus laevis]	312	312	70%	2e-86	29%	NP_001084343.1
unnamed protein product [Tetraodon nigroviridis]	313	313	71%	2e-86	30%	CAG02473.1
Calcium-transporting ATPase type 2C member 2 [Pteropus alecto]	312	312	71%	2e-86	31%	ELK00457.1
H/K ATPase:SUBUNIT=alpha	312	312	70%	2e-86	29%	2112199A
calcium-transporting ATPase [Daedalea quercina L-15889]	311	311	73%	2e-86	31%	KZT65495.1
calcium-transporting atpase sarcoplasmic endoplasmic reticulum type isoform x1 [Lasius niger]	310	310	65%	2e-86	31%	KMQ90734.1
potassium/sodium efflux P-type ATPase [Rhizopus delemar RA 99-880]	312	312	67%	2e-86	30%	EIE86803.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type-like [Camelina sativa]	312	312	70%	2e-86	31%	XP_010428048.1
Calcium-transporting ATPase 2, endoplasmic reticulum-type [Noccaea caerulescens]	312	312	70%	2e-86	32%	JAU87477.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila takahashii]	311	311	71%	2e-86	29%	XP_017013447.1
Na+,K+ ATPase [Homo sapiens]	311	311	65%	2e-86	31%	CAA31390.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Rattus norvegicus]	311	311	66%	2e-86	30%	XP_017452527.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type-like isoform X1 [Camelina sativa]	312	312	70%	2e-86	31%	XP_010456183.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Equus przewalskii]	312	312	65%	2e-86	32%	XP_008518698.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Buceros rhinoceros silvestris]	309	309	62%	2e-86	32%	XP_010129918.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Egretta garzetta]	310	310	70%	2e-86	31%	XP_009638469.1
sarco/endoplasmic reticulum-type Ca-2+-ATPase [Drosophila melanogaster]	311	311	71%	2e-86	29%	AAB00735.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Pygocentrus nattereri]	312	312	71%	2e-86	30%	XP_017571608.1
Calcium-transporting ATPase type 2C member 1 [Trichinella sp. T6]	309	309	71%	2e-86	31%	KRX77915.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Equus caballus]	311	311	65%	3e-86	32%	XP_001491371.3
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Anolis carolinensis]	311	311	65%	3e-86	30%	XP_008115492.1
RecName: Full=Probable calcium-transporting ATPase; AltName: Full=Calcium pump	311	311	75%	3e-86	30%	P35315.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Chrysochloris asiatica]	311	311	65%	3e-86	31%	XP_006871445.1
Sarco/endoplasmic reticulum Ca(2+)-ATPase, isoform B [Drosophila melanogaster]	311	311	71%	3e-86	29%	NP_726381.1
Sarco/endoplasmic reticulum Ca(2+)-ATPase, isoform A [Drosophila melanogaster]	311	311	71%	3e-86	29%	NP_476832.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Equus przewalskii]	311	311	65%	3e-86	32%	XP_008518699.1
hypothetical protein MANES_18G047600 [Manihot esculenta]	311	311	72%	3e-86	29%	OAY23047.1
hypothetical protein EGK_10669 [Macaca mulatta]	314	314	65%	3e-86	32%	EHH30082.1
uncharacterized protein Dwil_GK15853, isoform D [Drosophila willistoni]	311	311	71%	3e-86	29%	XP_015034154.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Anolis carolinensis]	311	311	65%	3e-86	30%	XP_016851584.1
calcium-translocating P-type ATPase [Trypanosoma equiperdum]	311	311	75%	3e-86	30%	SCU65125.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Nestor notabilis]	310	310	65%	3e-86	32%	XP_010017710.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Microcebus murinus]	311	311	68%	3e-86	30%	XP_012634754.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Gossypium arboreum]	310	310	71%	3e-86	30%	XP_017606053.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Equus asinus]	311	311	65%	3e-86	32%	XP_014703823.1
hypothetical protein BATDEDRAFT_33634 [Batrachochytrium dendrobatidis JAM81]	310	310	73%	3e-86	31%	XP_006681447.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Nestor notabilis]	310	310	65%	4e-86	32%	KFQ44608.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Panthera pardus]	310	310	71%	4e-86	32%	XP_019268578.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Brassica rapa]	310	310	72%	4e-86	29%	XP_009148335.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Picoides pubescens]	310	310	71%	4e-86	31%	KFV77293.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Solanum tuberosum]	310	310	71%	4e-86	29%	XP_006347865.1
ATPase alpha2,Na/K	311	311	65%	4e-86	32%	1309271B
GH26644p [Drosophila melanogaster]	311	311	71%	4e-86	29%	AAL13694.1
hypothetical protein EGM_09782 [Macaca fascicularis]	314	314	65%	4e-86	32%	EHH59627.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X2 [Otolemur garnettii]	308	308	68%	4e-86	30%	XP_012666402.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Solanum tuberosum]	311	311	71%	4e-86	30%	XP_006339743.1
predicted protein [Nematostella vectensis]	311	311	70%	4e-86	29%	XP_001628518.1
uncharacterized protein Dwil_GK15853, isoform B [Drosophila willistoni]	311	311	71%	4e-86	29%	XP_015034152.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Solanum pennellii]	311	311	71%	5e-86	30%	XP_015057690.1
unnamed protein product [Coffea canephora]	310	310	71%	5e-86	29%	CDP01269.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Phlebia centrifuga]	310	310	68%	5e-86	31%	OKY65072.1
KIAA0703 gene product, isoform CRA_b [Homo sapiens]	310	310	70%	5e-86	32%	EAW95484.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X2 [Drosophila ficusphila]	310	310	71%	5e-86	29%	XP_017045024.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Equus asinus]	311	311	65%	5e-86	32%	XP_014703822.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Ochotona princeps]	311	311	65%	5e-86	31%	XP_004581930.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Ochotona princeps]	311	311	65%	5e-86	31%	XP_004581929.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Tinamus guttatus]	308	308	70%	5e-86	31%	XP_010213724.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Brassica oleracea var. oleracea]	310	310	72%	5e-86	30%	XP_013587664.1
AAEL003518-PA [Aedes aegypti]	306	306	70%	5e-86	31%	XP_001656907.1
endoplasmic reticulum-type calcium-transporting ATPase 3 [Arabidopsis thaliana]	310	310	72%	5e-86	29%	NP_563860.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Python bivittatus]	311	311	65%	5e-86	30%	XP_007429514.1
hypothetical protein cypCar_00032097 [Cyprinus carpio]	307	307	72%	6e-86	31%	KTF82329.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X1 [Otolemur garnettii]	308	308	68%	6e-86	30%	XP_012666401.1
Calcium-transporting ATPase 1 [Smittium culicis]	316	316	74%	6e-86	31%	OMJ17362.1
Ca2+-ATPase [Arabidopsis thaliana]	310	310	72%	6e-86	29%	CAA10660.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Ornithorhynchus anatinus]	309	309	71%	6e-86	32%	XP_007669837.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Loxodonta africana]	309	309	65%	6e-86	31%	XP_010593170.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Pteropus alecto]	308	308	70%	7e-86	31%	XP_015441252.1
predicted protein [Nematostella vectensis]	308	308	71%	7e-86	30%	XP_001627716.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X3 [Otolemur garnettii]	309	309	68%	7e-86	30%	XP_012666403.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Condylura cristata]	309	309	64%	7e-86	31%	XP_004690325.1
hypothetical protein PANDA_020289 [Ailuropoda melanoleuca]	309	309	65%	8e-86	31%	EFB23739.1
putative plasma membrane calcium-transporting atpase 2 [Culex tarsalis]	308	308	70%	8e-86	31%	JAV23761.1
putative plasma membrane calcium-transporting atpase 2 [Culex tarsalis]	306	306	63%	8e-86	31%	JAV23631.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Octodon degus]	308	308	71%	8e-86	31%	XP_004645065.1
hypothetical protein BN1708_000538 [Verticillium longisporum]	311	311	63%	8e-86	32%	CRK19901.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Eurypyga helias]	309	309	65%	8e-86	31%	KFV98038.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Acanthisitta chloris]	308	308	62%	8e-86	32%	XP_009069802.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Solanum pennellii]	310	310	71%	8e-86	29%	XP_015082139.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Vigna angularis]	310	310	71%	8e-86	28%	XP_017421978.1
Na+ P-type-ATPase [Mucor ambiguus]	309	309	75%	9e-86	30%	GAN01532.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X4 [Otolemur garnettii]	308	308	68%	9e-86	30%	XP_012666404.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Solanum lycopersicum]	309	309	71%	9e-86	29%	XP_004242949.1
hypothetical protein NCAS_0C04250 [Naumovozyma castellii CBS 4309]	308	308	70%	9e-86	31%	XP_003675779.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Miniopterus natalensis]	308	308	62%	9e-86	32%	XP_016058547.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like [Gossypium hirsutum]	310	310	71%	9e-86	30%	XP_016749012.1
calcium pump, putative [Trypanosoma brucei gambiense DAL972]	310	310	75%	9e-86	30%	XP_011773626.1
Ca2+ ATPase [Blastocystis sp. subtype 4]	310	310	70%	1e-85	30%	XP_014526596.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Vigna radiata var. radiata]	309	309	71%	1e-85	28%	XP_014500933.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X4 [Ricinus communis]	305	305	70%	1e-85	30%	XP_015575065.1
BnaA09g52060D [Brassica napus]	310	310	70%	1e-85	31%	CDY51719.1
Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [Mucor circinelloides f. circinelloides 1006PhL]	310	310	71%	1e-85	30%	EPB85748.1
calcium ATPase [Exidia glandulosa HHB12029]	309	309	71%	1e-85	30%	KZV91087.1
sodium/potassium-transporting ATPase subunit alpha [Trichinella spiralis]	311	311	65%	1e-85	31%	XP_003369418.1
hypothetical protein BC1G_02758 [Botrytis cinerea B05.10]	308	308	63%	1e-85	32%	XP_001558687.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Loxodonta africana]	307	307	64%	1e-85	32%	XP_010593171.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Ricinus communis]	309	309	71%	1e-85	29%	XP_015575058.1
Calcium-transporting ATPase 2, endoplasmic reticulum-type [Noccaea caerulescens]	310	310	70%	1e-85	32%	JAU62676.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X1 [Camelus ferus]	306	306	62%	1e-85	32%	XP_006178126.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Monodelphis domestica]	308	308	71%	1e-85	31%	XP_007477304.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
putative plasma membrane calcium-transporting atpase 2 [Culex tarsalis]	308	308	70%	1e-85	31%	JAV23545.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Pyrus x bretschneideri]	305	305	71%	1e-85	29%	XP_018507095.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Nelumbo nucifera]	309	309	71%	1e-85	29%	XP_010273141.1
Calcium-transporting ATPase 1 [Hanseniaspora osmophila]	308	308	64%	1e-85	32%	OEJ85107.1
putative plasma membrane calcium-transporting atpase 2 [Culex tarsalis]	308	308	70%	1e-85	31%	JAV23663.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type [Brassica rapa]	310	310	70%	1e-85	31%	XP_009111394.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Camelus ferus]	310	310	65%	1e-85	32%	XP_006173996.1
hypothetical protein SOVF_010410 [Spinacia oleracea]	309	309	72%	1e-85	29%	KNA24986.1
sarcoplasmic/endoplasmic calcium-ATPase1 [Trypanosoma evansi]	309	309	75%	1e-85	30%	AIB10160.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Melopsittacus undulatus]	308	308	65%	1e-85	32%	XP_005146712.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Cricetulus griseus]	308	308	71%	2e-85	31%	XP_003495163.1
sodium/potassium-transporting ATPase subunit alpha-1 [Oryctolagus cuniculus]	309	309	65%	2e-85	31%	NP_001156546.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Tupaia chinensis]	316	316	65%	2e-85	32%	ELW71044.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Ailuropoda melanoleuca]	308	308	65%	2e-85	31%	XP_019648316.1
calcium-translocating P-type ATPase [Leishmania major strain Friedlin]	309	309	72%	2e-85	29%	XP_888512.1
Calcium-transporting ATPase 1 [Symbiodinium microadriaticum]	316	316	65%	2e-85	33%	OLP86454.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 isoform X1 [Camelus dromedarius]	309	309	65%	2e-85	31%	XP_010991407.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Felis catus]	309	309	71%	2e-85	32%	XP_019674520.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Solanum pennellii]	305	305	69%	2e-85	30%	XP_015082140.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Capsicum annuum]	308	308	71%	2e-85	29%	XP_016547347.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Camelus bactrianus]	309	309	65%	2e-85	32%	XP_010953937.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X4 [Vitis vinifera]	306	306	70%	2e-85	29%	XP_019072112.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Melopsittacus undulatus]	309	309	65%	2e-85	32%	XP_005146711.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Propithecus coquereli]	307	307	72%	2e-85	32%	XP_012503674.1
uncharacterized protein [Blastocystis hominis]	308	308	70%	2e-85	31%	XP_012895050.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Myotis brandtii]	304	304	62%	2e-85	32%	XP_014393023.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Odobenus rosmarus divergens]	308	308	65%	2e-85	31%	XP_004416566.1
hypothetical protein RvY_18537 [Ramazzottius varieornatus]	306	306	70%	2e-85	31%	GAV08918.1
Calcium-transporting ATPase 2, endoplasmic reticulum-type [Noccaea caerulescens]	309	309	70%	2e-85	32%	JAU37285.1
calcium-translocating P-type ATPase [Trypanosoma brucei brucei TREU927]	308	308	75%	2e-85	30%	XP_845010.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella pseudospiralis]	308	308	71%	2e-85	31%	KRY01757.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Nestor notabilis]	307	307	65%	2e-85	31%	KFQ54091.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Theobroma cacao]	308	308	71%	3e-85	30%	XP_017981280.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Anser cygnoides domesticus]	306	306	70%	3e-85	31%	XP_013053206.1
unnamed protein product [Pneumocystis jirovecii]	306	306	72%	3e-85	31%	CCJ29465.1
unnamed protein product [Oikopleura dioica]	308	308	69%	3e-85	31%	CBY21930.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Pteropus alecto]	315	315	65%	3e-85	32%	ELK19627.1
hypothetical protein SORBIDRAFT_01g009225 [Sorghum bicolor]	304	304	65%	3e-85	30%	XP_002463936.1
putative endoplasmic reticulum-type calcium-transporting ATPase 3 [Arabidopsis thaliana]	308	308	72%	3e-85	29%	AAD29961.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Daucus carota subsp. sativus]	308	308	72%	3e-85	29%	XP_017222851.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Rousettus aegyptiacus]	308	308	65%	4e-85	31%	XP_015979827.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Anser cygnoides domesticus]	306	306	70%	4e-85	31%	XP_013053205.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-1 [Sarcophilus harrisii]	308	308	65%	4e-85	31%	XP_003769870.2
Calcium-transporting ATPase type 2C member 1 [Nipponia nippon]	305	305	70%	4e-85	31%	KFR04428.1
hypothetical protein TSUD_315880 [Trifolium subterraneum]	308	308	71%	4e-85	29%	GAU31163.1
sodium/potassium-transporting ATPase subunit alpha-1 [Pongo abelii]	307	307	65%	4e-85	31%	NP_001127327.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Gallus gallus]	306	306	70%	4e-85	31%	XP_015137242.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Alligator mississippiensis]	306	306	70%	4e-85	32%	XP_014458035.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Camelus ferus]	306	306	62%	4e-85	31%	XP_014409111.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Gavialis gangeticus]	306	306	70%	4e-85	32%	XP_019364384.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Picoides pubescens]	307	307	65%	4e-85	31%	XP_009897052.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Octodon degus]	308	308	65%	4e-85	31%	XP_004641716.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Odobenus rosmarus divergens]	308	308	65%	4e-85	31%	XP_004416565.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X3 [Brassica oleracea var. oleracea]	307	307	72%	4e-85	30%	XP_013587665.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Anolis carolinensis]	306	306	70%	4e-85	31%	XP_008110972.1
calcium-transporting ATPase, endoplasimc reticulum type [Chondrus crispus]	308	308	70%	4e-85	31%	XP_005715614.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Opisthocomus hoazin]	305	305	70%	4e-85	31%	XP_009936367.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Jatropha curcas]	308	308	78%	4e-85	30%	XP_012083146.1
Sodium/potassium-transporting ATPase subunit alpha-2 [Exaiptasia pallida]	304	304	65%	5e-85	31%	KXJ20388.1
Calcium-transporting ATPase type 2C member 1 [Struthio camelus australis]	304	304	70%	5e-85	31%	KFV87984.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X5 [Aedes albopictus]	305	305	70%	5e-85	31%	XP_019555184.1
Calcium-transporting ATPase type 2C member 1 [Leptosomus discolor]	304	304	70%	5e-85	31%	KFQ15377.1
hypothetical protein Y1Q_0017635 [Alligator mississippiensis]	306	306	70%	5e-85	32%	KYO43359.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Anolis carolinensis]	305	305	70%	5e-85	31%	XP_008110974.1
PMR1-like protein [Saccharomyces eubayanus]	306	306	73%	5e-85	31%	XP_018222076.1
hypothetical protein B456_009G220900 [Gossypium raimondii]	306	306	65%	5e-85	31%	KJB58674.1

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endoplasmic reticulum-type calcium-transporting ATPase [Medicago truncatula]	305	305	72%	5e-85	30%	XP_013444582.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Fulmarus glacialis]	306	306	70%	5e-85	31%	XP_009572961.1
Calcium-transporting ATPase type 2C member 1 [Pygoscelis adeliae]	304	304	70%	6e-85	31%	KFW72206.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Aedes albopictus]	305	305	70%	6e-85	31%	XP_019552702.1
Calcium-transporting ATPase type 2C member 1 [Trichinella sp. T9]	305	305	71%	6e-85	31%	KRX59059.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Alligator sinensis]	305	305	70%	6e-85	32%	XP_014374000.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella nelsoni]	307	307	70%	6e-85	31%	KRX19622.1
Calcium-transporting ATPase type 2C member 1 [Trichinella papuae]	305	305	71%	6e-85	30%	KRZ72216.1
Calcium-transporting ATPase sarcoplasmic/endoplasmi c reticulum type [Beauveria bassiana D1-5]	307	307	73%	6e-85	30%	KGQ05024.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Hipposideros armiger]	307	307	65%	6e-85	31%	XP_019517006.1
putative calcium P-type ATPase [Beauveria bassiana ARSEF 2860]	307	307	73%	6e-85	30%	XP_008601355.1
Calcium-transporting ATPase type 2C member 1 [Pteropus alecto]	307	307	70%	6e-85	31%	ELK16746.1
Calcium-transporting ATPase 3 [Smittium culicis]	306	306	70%	6e-85	31%	OMJ29548.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Picoides pubescens]	307	307	65%	6e-85	31%	KFV66013.1
Putative Potassium/sodium efflux P-type ATPase [Rhizopus microsporus]	306	306	65%	7e-85	31%	CEI94814.1
hypothetical protein PHAVU_009G072800g [Phaseolus vulgaris]	307	307	71%	7e-85	29%	XP_007136772.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Tyto alba]	305	305	70%	7e-85	31%	XP_009964208.1
P-type ATPase [Schizosaccharomyces japonicus yFS275]	305	305	73%	7e-85	30%	XP_002174978.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Eptesicus fuscus]	307	307	65%	7e-85	31%	XP_008145440.1
sodium/potassium-transporting ATPase subunit alpha-1 [Cavia porcellus]	306	306	65%	7e-85	31%	NP_001166519.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Jatropha curcas]	307	307	71%	7e-85	29%	XP_012068199.1
Pmr1p [Saccharomyces cerevisiae YJM326]	306	306	67%	7e-85	33%	AJR79940.1
calcium transporting ATPase [Chlamydomonas reinhardtii]	307	307	67%	7e-85	30%	XP_001696782.1
Calcium-transporting ATPase 3 [Choanephora cucurbitarum]	306	306	75%	7e-85	29%	OBZ82559.1
calcium-transporting ATPase, endoplasmic reticulum-type [Dorcoceras hygrometricum]	308	308	71%	7e-85	31%	KZV48564.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Camelus bactrianus]	305	305	65%	7e-85	31%	XP_010966518.1
calcium-transporting ATPase type 2C member 2 [Mus musculus]	306	306	71%	8e-85	31%	NP_081198.1
potassium/sodium eff [Peniophora sp. CONT]	308	308	69%	8e-85	29%	KZV67109.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Gallus gallus]	305	305	70%	9e-85	31%	XP_015137243.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Nipponia nippon]	305	305	70%	9e-85	31%	XP_009469895.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Tyto alba]	305	305	70%	9e-85	31%	XP_009964207.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Microcebus murinus]	307	307	65%	9e-85	31%	XP_012617266.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Tyto alba]	305	305	62%	1e-84	31%	XP_009966102.1
Pmr1p [Saccharomyces cerevisiae YJM451]	305	305	67%	1e-84	33%	AJR81407.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Dendroctonus ponderosae]	306	306	66%	1e-84	30%	XP_019765940.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Smittium culicis]	306	306	74%	1e-84	31%	OMJ29198.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia mexicana]	307	307	65%	1e-84	32%	XP_014846019.1
Pmr1p [Saccharomyces cerevisiae YJM428]	305	305	67%	1e-84	33%	AJR80400.1
calcium-transporting ATPase [Isaria fumosorosea ARSEF 2679]	306	306	73%	1e-84	31%	XP_018704591.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pseudopodoces humilis]	304	304	70%	1e-84	31%	XP_014104026.1
hypothetical protein QG37_02759 [[Candida] auris]	305	305	71%	1e-84	31%	XP_018169942.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Erythranthe guttata]	306	306	66%	1e-84	30%	XP_012838793.1
similar to calcium-transporting P-type ATPase [Botrytis cinerea T4]	308	308	63%	1e-84	32%	CCD46288.1
Pmr1p [Saccharomyces cerevisiae YJM693]	305	305	67%	1e-84	33%	AJR87378.1
sodium/potassium-ATPase alpha-subunit isoform 1 splice-variant a [Cavia porcellus]	306	306	65%	1e-84	31%	ACB20771.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Tupaia chinensis]	306	306	65%	1e-84	31%	XP_006161452.1
calcium-transporting ATPase [Cordyceps brongniartii RCEF 3172]	306	306	73%	1e-84	30%	OAA42991.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Struthio camelus australis]	304	304	70%	1e-84	31%	XP_009686157.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Nipponia nippon]	305	305	70%	1e-84	31%	XP_009469894.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Lipotes vexillifer]	305	305	67%	1e-84	30%	XP_007466405.1
AGAP012115-PA [Anopheles gambiae str. PEST]	304	304	63%	1e-84	30%	XP_320413.3
Pmr1p [Saccharomyces cerevisiae YJM1479]	305	305	67%	1e-84	33%	AJS05549.1
Pmr1p [Saccharomyces cerevisiae YJM541]	305	305	67%	1e-84	33%	AJR83389.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Chinchilla lanigera]	306	306	65%	1e-84	31%	XP_005389097.1
Pmr1p [Saccharomyces cerevisiae YJM1248]	305	305	67%	1e-84	33%	AJR96684.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Otolemur garnettii]	306	306	65%	1e-84	31%	XP_012663099.1
hypothetical protein PRUPE_1G421100 [Prunus persica]	304	304	71%	1e-84	29%	ONI33388.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Tupaia chinensis]	306	306	65%	1e-84	31%	ELV14143.1
Pmr1p [Saccharomyces cerevisiae YJM1419]	305	305	67%	1e-84	33%	AJR99672.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Orycteropus afer afer]	304	304	65%	1e-84	30%	XP_007946886.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X3 [Aedes albopictus]	305	305	70%	1e-84	31%	XP_019552703.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Pyrus x bretschneideri]	306	306	71%	2e-84	29%	XP_009375144.1
Na+/K+ transporting ATPase alpha 1 [Sousa chinensis]	304	304	65%	2e-84	31%	AGV55495.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pseudopodoces humilis]	304	304	70%	2e-84	31%	XP_005519055.1
hypothetical protein PRUPE_1G421100 [Prunus persica]	304	304	71%	2e-84	29%	ONI33387.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X3 [Aedes albopictus]	304	304	70%	2e-84	31%	XP_019555182.1
Calcium-transporting ATPase 1 [Neolecta irregularis DAH-3]	301	301	72%	2e-84	30%	OLL24667.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Aedes albopictus]	305	305	70%	2e-84	31%	XP_019555180.1
putative calcium-transporting ATPase 3 [Moniliophthora roreri]	304	304	67%	2e-84	29%	KTB43661.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pygoscelis adeliae]	305	305	70%	2e-84	31%	XP_009329531.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Ca2+-translocating ATPase [Saccharomyces cerevisiae YJM789]	305	305	67%	2e-84	33%	EDN61957.1
Pmr1p [Saccharomyces cerevisiae YJM1443]	305	305	67%	2e-84	33%	AJS01650.1
Pmr1p [Saccharomyces cerevisiae YJM1434]	305	305	67%	2e-84	33%	AJS00665.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X4 [Aedes albopictus]	304	304	70%	2e-84	31%	XP_019555183.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X4 [Aedes albopictus]	304	304	70%	2e-84	31%	XP_019552704.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Nipponia nippon]	304	304	70%	2e-84	31%	XP_009469893.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Balaenoptera acutorostrata scammoni]	304	304	67%	2e-84	30%	XP_007164312.1
Pmr1p [Saccharomyces cerevisiae YJM1399]	305	305	67%	2e-84	33%	AJS28135.1
hypothetical protein HMPREF1544_06249 [Mucor circinelloides f. circinelloides 1006PhL]	306	306	75%	2e-84	30%	EPB86926.1
predicted protein [Lichtheimia corymbifera JMRC:FSU:9682]	307	307	73%	2e-84	30%	CDH50327.1
calcium-translocating P-type ATPase [Leishmania mexicana MHOM/GT/2001/U1103]	306	306	72%	2e-84	29%	XP_003871768.1
Pmr1p [Saccharomyces cerevisiae YJM195]	305	305	67%	2e-84	33%	AJR76956.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Dipodomys ordii]	305	305	65%	2e-84	31%	XP_012880133.1
Pmr1p [Saccharomyces cerevisiae YJM1190]	305	305	67%	2e-84	33%	AJR93785.1
Ca(2+)/Mn(2+)-transporting P-type ATPase PMR1 [Saccharomyces cerevisiae S288c]	305	305	67%	2e-84	33%	NP_011348.1
putative calcium-transporting p-type atpase protein [Botrytis cinerea BcDW1]	307	307	63%	2e-84	32%	EMR87948.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Geospiza fortis]	306	306	71%	2e-84	31%	XP_005424074.1
Pmr1p [Saccharomyces cerevisiae YJM1478]	305	305	67%	2e-84	33%	AJS05049.1
Na+/K+ transporting ATPase alpha 1 [Kogia sima]	304	304	65%	2e-84	31%	AGV55499.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Castor canadensis]	306	306	65%	2e-84	31%	JAV44600.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Bubalus bubalis]	306	306	65%	2e-84	31%	XP_006058746.1
Pmr1p [Saccharomyces cerevisiae YJM1078]	305	305	67%	2e-84	33%	AJP38638.1
Pmr1p [Saccharomyces cerevisiae YJM244]	305	305	67%	2e-84	33%	AJR77456.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Parus major]	303	303	70%	2e-84	31%	XP_015473439.1
Na+/K+ transporting ATPase alpha 1 [Mesoplodon densirostris]	304	304	65%	2e-84	31%	AGV55496.1
Calcium-transporting ATPase type 2C member 1 [Trichinella sp. T8]	303	303	71%	2e-84	31%	KRZ84705.1
Calcium-transporting ATPase type 2C member 1 [Trichinella zimbabwensis]	303	303	71%	2e-84	30%	KRZ03670.1
hypothetical protein AC578_3138 [Mycosphaerella eumusae]	306	306	72%	2e-84	30%	KXT00585.1
hypothetical protein CARUB_v10008220mg [Capsella rubella]	305	305	66%	2e-84	30%	XP_006306697.1
unnamed protein product [Oikopleura dioica]	305	305	69%	2e-84	31%	CBY43764.1
ECA3 [Arabidopsis thaliana]	305	305	72%	2e-84	29%	AAT68271.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Pan troglodytes]	306	306	65%	2e-84	31%	XP_513679.3
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Camelus ferus]	305	305	65%	2e-84	31%	XP_014423165.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Elaeis guineensis]	303	303	65%	2e-84	31%	XP_019710044.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Ursus maritimus]	306	306	65%	2e-84	31%	XP_008695957.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Nomascus leucogenys]	306	306	65%	2e-84	31%	XP_004090024.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Gorilla gorilla gorilla]	305	305	65%	2e-84	31%	XP_018876320.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Nomascus leucogenys]	305	305	65%	3e-84	31%	XP_004090025.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Ovis aries]	306	306	65%	3e-84	31%	NP_001009360.1
unnamed protein product [Ovis aries]	305	305	65%	3e-84	31%	CAA26582.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Coturnix japonica]	303	303	70%	3e-84	31%	XP_015709533.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pan paniscus]	305	305	65%	3e-84	31%	XP_008971666.1
hypothetical protein g.15271 [Homalodisca liturata]	305	305	66%	3e-84	30%	JAS77286.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Parus major]	303	303	70%	3e-84	31%	XP_015473435.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Cavia porcellus]	304	304	67%	3e-84	30%	XP_013007707.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Chrysochloris asiatica]	303	303	65%	3e-84	31%	XP_006874863.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ciona intestinalis]	305	305	69%	3e-84	31%	XP_009860106.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Gorilla gorilla gorilla]	305	305	65%	3e-84	31%	XP_004026461.1
PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Anoplophora glabripennis]	307	307	65%	3e-84	32%	XP_018575654.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Parus major]	304	304	70%	3e-84	31%	XP_015473434.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Bos indicus]	305	305	65%	3e-84	31%	XP_019812297.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Meleagris gallopavo]	304	304	70%	3e-84	31%	XP_003207275.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Cicer arietinum]	305	305	71%	3e-84	29%	XP_012571631.1
Na+/K+ transporting ATPase alpha 1 [Lipotes vexillifer]	303	303	65%	3e-84	31%	AGV55497.1
TPA: sodium/potassium-transporting ATPase subunit alpha-1 precursor [Bos taurus]	305	305	65%	3e-84	31%	DAA31562.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Canis lupus familiaris]	305	305	65%	3e-84	31%	NP_001003306.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Lipotes vexillifer]	303	303	65%	3e-84	31%	XP_007452698.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ciona intestinalis]	305	305	69%	3e-84	31%	XP_018669558.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X4 [Cercocebus atys]	304	304	65%	3e-84	31%	XP_011938628.1
Pmr1p [Saccharomyces cerevisiae YJM1527]	304	304	67%	3e-84	33%	AJS06536.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Neolamprologus brichardi]	305	305	65%	4e-84	31%	XP_006802880.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Pan troglodytes]	305	305	65%	4e-84	31%	XP_016780478.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Camelus dromedarius]	305	305	65%	4e-84	31%	XP_010979001.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Mustela putorius furo]	305	305	65%	4e-84	31%	XP_012900503.1
putative serca-type calcium ATPase [Chrysochromulina sp. CCMP291]	306	306	70%	4e-84	30%	KOO33828.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Ailuropoda melanoleuca]	305	305	65%	4e-84	31%	XP_002923630.1
sodium/potassium-transporting ATPase subunit alpha-1 [Bos taurus]	305	305	65%	4e-84	31%	NP_001070266.1
sodium/potassium-transporting ATPase subunit alpha-1 [Sus scrofa]	305	305	65%	4e-84	31%	BAM28740.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X1 [Vitis vinifera]	305	305	70%	4e-84	29%	XP_010664492.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
predicted protein [Nematostella vectensis]	306	306	69%	4e-84	30%	XP_001632743.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Nomascus leucogenys]	305	305	65%	4e-84	31%	XP_003268083.1
Na+/K+ transporting ATPase alpha 1 [Tursiops aduncus]	303	303	65%	4e-84	31%	AGV55493.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha; Short=Na(+)/K(+) ATPase alpha subunit; AltName: Full=Sodium pump subunit alpha; Flags: Precursor	305	305	65%	4e-84	31%	P05025.1
unnamed protein product [Homo sapiens]	305	305	65%	4e-84	31%	BAG37313.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Bison bison bison]	305	305	65%	4e-84	31%	XP_010829032.1
hypothetical protein AC579_4191 [Pseudocercospora musae]	306	306	72%	4e-84	30%	KXT13965.1
Na+/K+ transporting alpha 1 polypeptide [Sus scrofa]	305	305	65%	4e-84	31%	ADB19852.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Aedes albopictus]	305	305	70%	4e-84	31%	XP_019555178.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Ailuropoda melanoleuca]	305	305	65%	4e-84	31%	XP_019659721.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Meleagris gallopavo]	303	303	70%	4e-84	31%	XP_010711225.1
hypothetical protein H696_05252 [Fonticula alba]	308	308	72%	4e-84	29%	XP_009497389.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Pyrus x bretschneideri]	305	305	71%	4e-84	29%	XP_009360936.1
Pmr1p [Saccharomyces cerevisiae YJM681]	303	303	67%	4e-84	32%	AJR85389.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Orycteropus afer afer]	305	305	65%	5e-84	31%	XP_007946870.1
Chain A, Crystal Structure Of A Na+-bound Na+,k+-atpase Preceding The E1p State Without Oligomycin	305	305	65%	5e-84	31%	3WGU_A
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Propithecus coquereli]	305	305	65%	5e-84	31%	XP_012513925.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Pantholops hodgsonii]	305	305	65%	5e-84	31%	XP_005971434.1
Ca-transporting ATPase [Gloeophyllum trabeum ATCC 11539]	306	306	72%	5e-84	30%	XP_007866524.1
potassium/sodium eff [Wallemia mellicola CBS 633.66]	305	305	70%	5e-84	30%	XP_006956013.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Mustela putorius furo]	305	305	65%	5e-84	31%	XP_004771136.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X4 [Rhinopithecus bieti]	301	301	62%	5e-84	32%	XP_017705298.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Meleagris gallopavo]	303	303	70%	5e-84	31%	XP_019472095.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pelecanus crispus]	304	304	65%	5e-84	31%	XP_009478386.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Aedes albopictus]	304	304	70%	5e-84	31%	XP_019552700.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Mustela putorius furo]	305	305	65%	5e-84	31%	XP_004771137.1
calcium-transporting P [Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993]	303	303	71%	5e-84	32%	XP_018711690.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Macaca fascicularis]	305	305	65%	6e-84	31%	XP_005542266.1
hypothetical protein PANDA_012807 [Ailuropoda melanoleuca]	305	305	65%	6e-84	31%	EFB13576.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-1; Short=Na(+)/K(+) ATPase alpha-1 subunit; AltName: Full=Sodium pump subunit alpha-1; Flags: Precursor	305	305	65%	6e-84	31%	Q5RDR3.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Echinops telfairi]	304	304	65%	6e-84	31%	XP_004714919.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Orycteropus afer afer]	305	305	65%	6e-84	31%	XP_007946879.1
hypothetical protein Csa_2G354610 [Cucumis sativus]	302	302	65%	6e-84	30%	KGN62435.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sodium/potassium-transporting ATPase subunit alpha-1 [Heterocephalus glaber]	304	304	65%	6e-84	31%	EHB08058.1
Calcium-transporting ATPase type 2C member 1 [Papilio xuthus]	307	360	60%	6e-84	32%	KPI97197.1
hypothetical protein [Homo sapiens]	304	304	71%	6e-84	31%	CAI46049.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Oryctolagus cuniculus]	300	300	62%	6e-84	32%	XP_017195687.1
potassium-transporting ATPase alpha chain 1 [Canis lupus familiaris]	305	305	64%	6e-84	31%	NP_001003342.1
Ca2+-ATPase [Arabidopsis lyrata subsp. lyrata]	304	304	72%	6e-84	29%	XP_002889791.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Pelecanus crispus]	304	304	65%	6e-84	31%	KFQ59921.1
Pmr1 ATPase [Candida orthopsilosis Co 90-125]	302	302	71%	7e-84	31%	XP_003871374.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Haliaeetus albicilla]	304	304	65%	7e-84	31%	XP_009920638.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Chrysemys picta bellii]	303	303	71%	7e-84	33%	XP_008166866.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type isoform X1 [Brassica napus]	305	305	70%	7e-84	31%	XP_013722817.1
hypothetical protein XELAEV_18037278mg [Xenopus laevis]	305	305	64%	7e-84	31%	OCT70360.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Saimiri boliviensis boliviensis]	304	304	65%	7e-84	31%	XP_010342366.1
Calcium transporting ATPase [Trichuris trichiura]	302	302	60%	7e-84	33%	CDW58226.1
K7_Pmr1p [Saccharomyces cerevisiae Kyokai no. 7]	303	303	67%	7e-84	33%	GAA23231.1
Na+/K+ transporting ATPase alpha 1 [Neophocaena phocaenoides]	302	302	65%	7e-84	31%	AGV55494.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Larimichthys crocea]	304	304	65%	7e-84	31%	XP_019128761.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X2 [Cynoglossus semilaevis]	302	302	62%	7e-84	32%	XP_016898635.1
Calcium-transporting ATPase type 2C member 1 [Trichinella nelsoni]	302	302	71%	7e-84	30%	KRX16823.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Leptonychotes weddellii]	303	303	71%	7e-84	32%	XP_006739859.1
cation-transporting atpase, putative [Ricinus communis]	304	304	71%	7e-84	30%	EEF52265.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Chrysemys picta bellii]	303	303	66%	7e-84	29%	XP_008174837.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Elephantulus edwardii]	301	301	62%	7e-84	32%	XP_006900992.1
Chain A, Crystal Structure Of The Na,k-atpase From Bovine	304	304	65%	7e-84	31%	4XE5_A
hypothetical protein PRUPE_ppa000801mg [Prunus persica]	304	304	71%	7e-84	29%	XP_007227661.1
hypothetical protein EGK_01137 [Macaca mulatta]	304	304	65%	8e-84	31%	EHH15093.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Loxodonta africana]	300	300	65%	8e-84	32%	XP_010596126.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Orcinus orca]	304	304	65%	8e-84	31%	XP_004263287.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Aotus nancymaae]	304	304	65%	8e-84	31%	XP_012314297.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Heterocephalus glaber]	304	304	65%	8e-84	31%	XP_004853865.1
hydrogen/potassium-exchanging ATPase 12A [Xenopus laevis]	305	305	64%	8e-84	31%	NP_001080818.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Rhinopithecus roxellana]	303	303	65%	8e-84	31%	XP_010366208.1
Putative Potassium/sodium efflux P-type ATPase [Rhizopus microsporus]	304	304	72%	8e-84	31%	CEG63080.1
hypothetical protein CPAR2_301360 [Candida parapsilosis]	302	302	71%	9e-84	31%	CCE41147.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Chlamydotis macqueenii]	303	303	65%	9e-84	31%	XP_010119967.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein SERLA73DRAFT_162342 [Serpula lacrymans var. lacrymans S7.3]	303	303	73%	9e-84	30%	EGN95477.1
hypothetical protein TanjilG_30635 [Lupinus angustifolius]	303	303	71%	9e-84	29%	OIW14916.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Microcebus murinus]	304	304	65%	9e-84	32%	XP_012604632.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Exaiptasia pallida]	300	300	72%	9e-84	31%	KXJ11278.1
type IIA calcium ATPase [Medicago truncatula]	305	305	71%	9e-84	30%	AAL35972.1
sodium/potassium-transporting ATPase subunit alpha-1 isoform d [Homo sapiens]	303	303	65%	9e-84	31%	NP_001153706.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Jaculus jaculus]	304	304	65%	1e-83	31%	XP_004667579.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Physeter catodon]	304	304	65%	1e-83	31%	XP_007115837.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Haliaeetus albicilla]	304	304	65%	1e-83	31%	KFQ06840.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Ficedula albicollis]	301	301	70%	1e-83	31%	XP_016151961.1
hypothetical protein PRUPE_1G421100 [Prunus persica]	303	303	71%	1e-83	29%	ONI33385.1
P-ATPase family transporter: calcium ion [Ostreococcus lucimarinus CCE9901]	304	304	66%	1e-83	31%	XP_001417061.1
Calcium-transporting ATPase type 2C member 1 [Trichinella nativa]	302	302	71%	1e-83	30%	KRZ51197.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Caprimulgus carolinensis]	303	303	65%	1e-83	31%	XP_010164234.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Tyto alba]	303	303	65%	1e-83	31%	XP_009964342.1
hypothetical protein A4X09_g7140 [Tilletia walkeri]	304	304	70%	1e-83	31%	OAJ11219.1
hypothetical protein MUCCIDRAFT_71674 [Mucor circinelloides f. lusitanicus CBS 277.49]	302	302	71%	1e-83	31%	OAD08254.1
sodium/potassium-transporting ATPase subunit alpha-1 isoform c [Homo sapiens]	304	304	65%	1e-83	31%	NP_001153705.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Caprimulgus carolinensis]	304	304	65%	1e-83	31%	KFZ56292.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Aquila chrysaetos canadensis]	304	304	65%	1e-83	31%	XP_011584390.1
sodium/potassium-transporting ATPase subunit alpha-1 isoform 2 [Camelus ferus]	305	305	65%	1e-83	31%	EPY73283.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Aotus nancymaae]	304	304	65%	1e-83	31%	XP_012314296.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Orcinus orca]	301	301	62%	1e-83	32%	XP_004271275.1
endoplasmic reticulum-type calcium-transporting ATPase [Medicago truncatula]	304	304	71%	1e-83	30%	XP_013444583.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Jaculus jaculus]	303	303	65%	1e-83	31%	XP_004667580.1
unnamed protein product [Homo sapiens]	304	304	65%	1e-83	31%	BAH11971.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pygoscelis adeliae]	303	303	65%	1e-83	31%	XP_009327625.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha [Tribolium castaneum]	303	303	66%	1e-83	29%	XP_972369.1
Pmr1p [Saccharomyces cerevisiae YJM1311]	302	302	67%	1e-83	33%	AJS20183.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Pygoscelis adeliae]	303	303	65%	1e-83	31%	KFW61640.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Chaetura pelagica]	301	301	70%	1e-83	31%	XP_010005787.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Callithrix jacchus]	304	304	65%	1e-83	31%	XP_002751328.1
sodium/potassium-transporting ATPase subunit alpha-1 [Macaca mulatta]	304	304	65%	1e-83	31%	NP_001253602.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Neolamprologus brichardi]	304	304	65%	1e-83	31%	XP_006802879.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Calcium-transporting ATPase type 2C member 1 [Chaetura pelagica]	301	301	70%	1e-83	31%	KFU85061.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Haliaeetus leucocephalus]	303	303	65%	1e-83	31%	XP_010565753.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Sorex araneus]	303	303	64%	1e-83	30%	XP_012787841.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Opisthocomus hoazin]	303	303	65%	1e-83	31%	XP_009939920.1
Calcium-transporting ATPase type 2C member 1 [Podiceps cristatus]	300	300	70%	1e-83	31%	KFZ64806.1
Calcium-transporting ATPase type 2C member 1 [Trichinella sp. T6]	301	301	71%	1e-83	30%	KRX77914.1
Calcium-transporting ATPase type 2C member 1 [Phalacrocorax carbo]	300	300	70%	1e-83	31%	KFW89923.1
hypothetical protein EGM_00988 [Macaca fascicularis]	303	303	65%	1e-83	31%	EHH50200.1
sodium/potassium-transporting ATPase subunit alpha-1 isoform a [Homo sapiens]	303	303	65%	1e-83	31%	NP_000692.2
hypothetical protein KGM_11072 [Danaus plexippus]	303	303	68%	1e-83	30%	EHJ65189.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Stegastes partitus]	301	301	72%	2e-83	29%	XP_008296187.1
Calcium-transporting ATPase type 2C member 1 [Aptenodytes forsteri]	300	300	70%	2e-83	31%	KFM01131.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Tauraco erythrolophus]	303	303	65%	2e-83	32%	XP_009990636.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Chrysochloris asiatica]	301	301	62%	2e-83	32%	XP_006871446.1
pmr1p [Saccharomyces arboricola H-6]	302	302	71%	2e-83	31%	EJS43816.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Ficedula albicollis]	301	301	70%	2e-83	31%	XP_005041290.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Sorex araneus]	301	301	62%	2e-83	32%	XP_012790977.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Tinamus guttatus]	303	303	65%	2e-83	31%	XP_010212050.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X3 [Stegastes partitus]	301	301	72%	2e-83	29%	XP_008296188.1
cation transporting ATPase [Thalassiosira pseudonana CCMP1335]	301	301	66%	2e-83	31%	XP_002290036.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Balearica regulorum gibbericeps]	303	303	65%	2e-83	31%	XP_010310738.1
ATPase alpha,Na/K	303	303	65%	2e-83	31%	1210234A
hypothetical protein GUITHDRAFT_80735 [Guillardia theta CCMP2712]	303	303	74%	2e-83	30%	XP_005821222.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pantholops hodgsonii]	303	303	65%	2e-83	31%	XP_005974488.1
Pmr1p [Saccharomyces cerevisiae YJM1463]	302	302	67%	2e-83	33%	AJS04073.1
Calcium-transporting ATPase type 2C member 1 [Corvus brachyrhynchos]	300	300	70%	2e-83	31%	KFO59349.1
unnamed protein product [Homo sapiens]	303	303	65%	2e-83	31%	BAH12337.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Struthio camelus australis]	303	303	65%	2e-83	32%	KFV81512.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X4 [Cynoglossus semilaevis]	303	303	65%	2e-83	31%	XP_008322799.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Loxodonta africana]	303	303	65%	2e-83	31%	XP_010587900.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Leptosomus discolor]	303	303	65%	2e-83	31%	XP_009948199.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Struthio camelus australis]	303	303	65%	2e-83	31%	XP_009673576.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Tauraco erythrolophus]	303	303	65%	2e-83	31%	KFV07044.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Alligator sinensis]	301	301	70%	2e-83	32%	XP_006020679.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sodium/potassium-transporting ATPase subunit alpha-1 [Tinamus guttatus]	303	303	65%	2e-83	31%	KGL76630.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Papio anubis]	300	300	62%	2e-83	32%	XP_003915656.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Nipponia nippon]	302	302	65%	2e-83	31%	XP_009458805.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Stegastes partitus]	301	301	72%	2e-83	29%	XP_008296186.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Tyto alba]	303	303	65%	2e-83	31%	KFV49868.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Stegastes partitus]	304	304	71%	2e-83	31%	XP_008278480.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Propithecus coquereli]	303	303	73%	2e-83	29%	XP_012508083.1
Calcium-transporting ATPase type 2C member 1 [Trichinella spiralis]	301	301	71%	2e-83	30%	KRY29038.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Cuculus canorus]	302	302	65%	2e-83	31%	XP_009555289.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Gavialis gangeticus]	301	301	70%	2e-83	32%	XP_019364383.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Alligator mississippiensis]	301	301	70%	2e-83	32%	XP_019339101.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Phalacrocorax carbo]	303	303	65%	2e-83	31%	KFW91568.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Eurypyga helias]	301	301	62%	2e-83	31%	XP_010153588.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Phalacrocorax carbo]	302	302	65%	2e-83	31%	XP_009503973.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Cuculus canorus]	303	303	65%	2e-83	31%	XP_009555288.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Phalacrocorax carbo]	303	303	65%	2e-83	31%	XP_009503972.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Cathartes aura]	303	303	65%	2e-83	31%	KFP56596.1
Sodium/potassium-transporting ATPase subunit alpha-1, partial [Chlamydotis macqueenii]	303	303	65%	2e-83	31%	KFP42565.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Chrysochloris asiatica]	303	303	65%	2e-83	31%	XP_006874862.1
Calcium-transporting ATPase type 2C member 1 [Trichinella nativa]	300	300	71%	3e-83	30%	KRZ51196.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Nipponia nippon]	303	303	65%	3e-83	31%	KFQ93491.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Mesitornis unicolor]	303	303	65%	3e-83	31%	KFQ40708.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Mesitornis unicolor]	302	302	65%	3e-83	31%	XP_010190740.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Cebus capucinus imitator]	303	303	65%	3e-83	31%	XP_017379685.1
Na+, K+-ATPase alpha-subunit precursor [Sus scrofa]	303	303	65%	3e-83	31%	AAA31002.1
ECA3 [Arabidopsis thaliana]	302	302	72%	3e-83	29%	OAP15177.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Balaenoptera acutorostrata scammoni]	303	303	65%	3e-83	31%	XP_007169389.1
Sodium/potassium-transporting ATPase subunit alpha-1, partial [Balearica regulorum gibbericeps]	303	303	65%	3e-83	31%	KFO07855.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Cuculus canorus]	302	302	65%	3e-83	31%	KFO73311.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Nicrophorus vespilloides]	302	302	70%	3e-83	29%	XP_017783269.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Colius striatus]	302	302	65%	3e-83	31%	XP_010196409.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Leptosomus discolor]	302	302	65%	3e-83	31%	KFQ10064.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Apteryx australis mantelli]	302	302	65%	3e-83	31%	XP_013805557.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Colius striatus]	302	302	65%	3e-83	31%	KFP30213.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Gavialis gangeticus]	302	302	65%	4e-83	30%	XP_019382319.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Rhinolophus sinicus]	303	303	63%	4e-83	30%	XP_019566166.1
hypothetical protein GLYMA_04G046700 [Glycine max]	300	300	65%	4e-83	30%	KRH61433.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Camelus dromedarius]	301	301	71%	4e-83	31%	XP_010978810.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Aptenodytes forsteri]	301	301	65%	4e-83	31%	XP_009272832.1
sodium/potassium-transporting ATPase subunit alpha-2 precursor [Camelus ferus]	308	650	65%	4e-83	31%	EPY88987.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Aptenodytes forsteri]	302	302	65%	4e-83	31%	KFM00740.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Physeter catodon]	300	300	71%	4e-83	31%	XP_007122663.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Fulmarus glacialis]	301	301	65%	4e-83	31%	XP_009585011.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Python bivittatus]	301	301	65%	5e-83	31%	XP_007435355.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Chaetura pelagica]	301	301	65%	5e-83	31%	XP_009996516.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Meleagris gallopavo]	302	302	65%	5e-83	32%	XP_010717402.1
Calcium-transporting ATPase 1 [Symbiodinium microadriaticum]	293	293	37%	5e-83	38%	OLQ08420.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Prunus mume]	301	301	70%	5e-83	29%	XP_008220383.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Charadrius vociferus]	301	301	65%	5e-83	31%	XP_009878202.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Ictalurus punctatus]	302	302	65%	5e-83	30%	XP_017308505.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Charadrius vociferus]	301	301	65%	5e-83	31%	KGL89091.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Fulmarus glacialis]	302	302	65%	5e-83	31%	KFV98186.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X2 [Cyprinodon variegatus]	299	299	62%	6e-83	31%	XP_015259942.1
hypothetical protein VIGAN_02054100 [Vigna angularis var. angularis]	300	300	65%	6e-83	29%	BAT77926.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Monodelphis domestica]	302	302	64%	6e-83	31%	XP_001363624.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Cynoglossus semilaevis]	302	302	65%	6e-83	31%	XP_008322794.1
mKIAA0703 protein [Mus musculus]	297	297	68%	6e-83	31%	BAD90414.1
Calcium-transporting ATPase type 2C member 1 [Acanthisitta chloris]	298	298	70%	6e-83	31%	KFP74023.1
hypothetical protein BRAFLDRAFT_127845 [Branchiostoma floridae]	300	300	64%	6e-83	31%	XP_002612126.1
hypothetical protein OsI_13389 [Oryza sativa Indica Group]	303	303	71%	6e-83	29%	EEC76121.1
hypothetical protein FOMPIDRAFT_102065 [Fomitopsis pinicola FP-58527 SS1]	301	301	70%	7e-83	31%	EPS93054.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Phaethon lepturus]	301	301	65%	7e-83	31%	XP_010281107.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Coturnix japonica]	301	301	65%	7e-83	31%	XP_015730415.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X3 [Ovis aries musimon]	301	301	63%	7e-83	32%	XP_014944818.1
secretory pathway calcium atpase-like protein [Daphnia pulex]	300	300	71%	7e-83	29%	EFX81621.1

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hypothetical protein NCLIV_030940 [Neospora caninum Liverpool]	302	302	70%	7e-83	30%	XP_003883339.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Corvus brachyrhynchos]	299	299	70%	7e-83	31%	XP_008632135.1
Na,K-ATPase alpha-2-subunit [Rattus norvegicus]	300	300	65%	7e-83	31%	AAA41672.1
Calcium-transporting ATPase type 2C member 1 [Orchesella cincta]	300	300	70%	7e-83	29%	ODM95806.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Apteryx australis mantelli]	298	298	70%	8e-83	31%	XP_013806204.1
mCG129284 [Mus musculus]	300	300	71%	8e-83	31%	EDL11614.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Myotis brandtii]	302	302	65%	8e-83	31%	EPQ03777.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Phaethon lepturus]	301	301	65%	8e-83	31%	KFQ69222.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Corvus brachyrhynchos]	299	299	70%	8e-83	31%	XP_008632134.1
unnamed protein product [Homo sapiens]	299	299	62%	8e-83	32%	BAH11595.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Haliaeetus albicilla]	298	298	70%	8e-83	31%	XP_009925293.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Fulmarus glacialis]	299	299	70%	8e-83	31%	XP_009572963.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Anser cygnoides domesticus]	301	301	65%	9e-83	31%	XP_013038857.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Sorex araneus]	298	298	62%	9e-83	32%	XP_004616287.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Zonotrichia albicollis]	299	299	70%	9e-83	31%	XP_005481057.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Python bivittatus]	300	300	71%	1e-82	32%	XP_007435287.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Manis javanica]	301	301	65%	1e-82	30%	XP_017505811.1
Calcium-transporting ATPase type 2C member 1, partial [Balearica regulorum gibbericeps]	298	298	70%	1e-82	31%	KFO06752.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Pterocles gutturalis]	299	299	62%	1e-82	31%	XP_010071170.1
Chain A, Crystal Structure Of The Sodium-Potassium Pump	300	300	65%	1e-82	30%	3B8E_A
Sodium/potassium-transporting ATPase subunit alpha-1 [Chaetura pelagica]	301	301	65%	1e-82	31%	KFU90062.1
calcium transporting ATPase [Ogataea polymorpha]	298	298	73%	1e-82	29%	XP_018208597.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Merops nubicus]	300	300	65%	1e-82	31%	XP_008943893.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Zonotrichia albicollis]	299	299	70%	1e-82	31%	XP_014129349.1
Na+/K+ transporting ATPase alpha 1 [Balaenoptera acutorostrata]	299	299	65%	1e-82	30%	AGV55498.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Opisthocomus hoazin]	298	298	64%	1e-82	31%	KFR12837.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Zonotrichia albicollis]	300	300	70%	1e-82	31%	XP_005481055.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Cyprinodon variegatus]	299	299	62%	1e-82	31%	XP_015259941.1
hypothetical protein MANES_01G243100 [Manihot esculenta]	301	301	71%	1e-82	30%	OAY62121.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Sturnus vulgaris]	299	299	70%	1e-82	31%	XP_014733869.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Sturnus vulgaris]	298	298	70%	1e-82	31%	XP_014733870.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Columba livia]	300	300	65%	1e-82	31%	XP_005511501.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Ovis aries]	301	301	63%	1e-82	32%	XP_012039716.1
hypothetical protein A4X03_g8740 [Tilletia caries]	301	301	70%	1e-82	30%	OAJ02045.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Zonotrichia albicollis]	299	299	70%	1e-82	31%	XP_005481056.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Geospiza fortis]	298	298	70%	1e-82	31%	XP_014163665.1
sodium/potassium-transporting ATPase subunit alpha-1a [Oncorhynchus masou]	301	301	68%	1e-82	30%	BAJ13363.1
Calcium-transporting ATPase type 2C member 1 [Haliaeetus albicilla]	298	298	70%	1e-82	31%	KFQ10457.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Sus scrofa]	301	301	65%	1e-82	30%	NP_999414.1
Calcium-transporting ATPase type 2C member 1 [Manacus vitellinus]	297	297	70%	1e-82	31%	KFW75986.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Serinus canaria]	298	298	70%	1e-82	31%	XP_009084419.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Fulmarus glacialis]	299	299	70%	1e-82	31%	XP_009572962.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Columba livia]	300	300	65%	1e-82	31%	EMC90480.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Corvus cornix cornix]	299	299	70%	1e-82	31%	XP_010397162.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Acanthisitta chloris]	298	298	70%	1e-82	31%	XP_009082894.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Falco peregrinus]	298	298	70%	1e-82	31%	XP_005242304.2
Chain A, Crystal Structure Of The High Affinity Complex Between Ouabain And The E2p Form Of The Sodium-potassium Pump	300	300	65%	1e-82	30%	3N23_A
Calcium-transporting ATPase type 2C member 1 [Phoenicopterus ruber ruber]	298	298	70%	1e-82	31%	KFQ83421.1
sodium/potassium-transporting ATPase subunit alpha-1 [Anas platyrhynchos]	300	300	65%	2e-82	31%	NP_001297314.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Scleropages formosus]	302	302	72%	2e-82	31%	XP_018593738.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Salmo salar]	301	301	71%	2e-82	31%	XP_013989686.1
Putative Potassium/sodium efflux P-type ATPase [Rhizopus microsporus]	298	298	64%	2e-82	30%	CEG63081.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Merops nubicus]	300	300	65%	2e-82	31%	KFQ34748.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Ovis aries musimon]	300	300	63%	2e-82	32%	XP_014944817.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Lepidothrix coronata]	297	297	70%	2e-82	31%	XP_017673462.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Serinus canaria]	298	298	70%	2e-82	31%	XP_009084418.1
calcium-transporting P [Sphaerulina musiva SO2202]	301	301	71%	2e-82	30%	XP_016760995.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Sturnus vulgaris]	299	299	70%	2e-82	31%	XP_014733868.1
hypothetical protein PFL1_00514 [Anthracocystis flocculosa PF-1]	303	303	70%	2e-82	28%	XP_007876199.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Malus domestica]	300	300	71%	2e-82	29%	XP_008393711.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Acanthisitta chloris]	298	298	70%	2e-82	31%	XP_009082893.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Geospiza fortis]	298	298	70%	2e-82	31%	XP_005424009.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Charadrius vociferus]	298	298	70%	2e-82	31%	XP_009877898.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Crocodylus porosus]	300	300	65%	2e-82	30%	XP_019404281.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Apaloderma vittatum]	300	300	65%	2e-82	31%	XP_009863609.1

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PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Gavia stellata]	298	298	70%	2e-82	31%	XP_009807636.1
Calcium-transporting ATPase type 2C member 1 [Egretta garzetta]	295	295	64%	2e-82	32%	KFP17143.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Myotis lucifugus]	298	298	68%	2e-82	29%	XP_006110099.2
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Nestor notabilis]	298	298	62%	2e-82	31%	XP_010017770.1
Chain A, Na,k-atpase In The E2p State With Bound Ouabain And Mg2+ In The Cation-binding Site	300	300	65%	3e-82	30%	4HYT_A
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Bemisia tabaci]	298	298	69%	3e-82	30%	XP_018908195.1
hypothetical protein [Monosiga brevicollis MX1]	297	297	72%	3e-82	29%	XP_001745967.1
unnamed protein product [Oncorhynchus mykiss]	301	301	64%	3e-82	31%	CDQ58897.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Falco peregrinus]	298	298	70%	3e-82	31%	XP_013158557.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Balearica regulorum gibbericeps]	298	298	70%	3e-82	31%	XP_010310377.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Apaloderma vittatum]	300	300	65%	3e-82	31%	KFP84941.1
Ca2+-transporting ATPase [Coniosporium apollinis CBS 100218]	300	300	70%	3e-82	30%	XP_007779142.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Papio anubis]	298	298	64%	3e-82	30%	XP_009192433.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Calypte anna]	300	300	65%	3e-82	31%	KFP04595.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Taeniopygia guttata]	298	298	70%	3e-82	31%	XP_002196418.3
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Calidris pugnax]	298	298	70%	3e-82	31%	XP_014793253.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Gavia stellata]	298	298	70%	3e-82	31%	XP_009807620.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Orcinus orca]	300	300	64%	3e-82	30%	XP_004284206.1
hypothetical protein A4X06_g4072 [Tilletia controversa]	300	300	70%	3e-82	30%	OAJ28659.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Calidris pugnax]	297	297	70%	3e-82	31%	XP_014793255.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Corvus brachyrhynchos]	298	298	65%	3e-82	31%	KFO59417.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Haliaeetus albicilla]	297	297	70%	3e-82	31%	XP_009925285.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Vitis vinifera]	298	298	65%	3e-82	30%	XP_010664493.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Egretta garzetta]	300	300	65%	3e-82	31%	KFP16212.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Leptosomus discolor]	297	297	70%	3e-82	31%	XP_009956095.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Falco cherrug]	298	298	70%	3e-82	31%	XP_005445929.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Apteryx australis mantelli]	298	298	70%	3e-82	31%	XP_013806202.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Gavia stellata]	298	298	70%	3e-82	31%	XP_009807628.1
Potassium-transporting ATPase alpha chain 1 [Chelonia mydas]	300	300	65%	4e-82	29%	EMP24795.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Pelecanus crispus]	297	297	70%	4e-82	31%	XP_009486437.1
Na+/K+-ATPase alpha-subunit 1 [Protopterus annectens]	300	300	65%	4e-82	31%	AGR45921.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Charadrius vociferus]	298	298	70%	4e-82	31%	XP_009877897.1
Calcium-transporting ATPase 3 [Madurella mycetomatis]	301	301	72%	4e-82	29%	KXX81602.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Calypte anna]	299	299	65%	4e-82	31%	XP_008496844.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Haliaeetus albicilla]	297	297	70%	4e-82	31%	XP_009925283.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Manacus vitellinus]	297	297	70%	4e-82	31%	XP_017931023.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Leptosomus discolor]	298	298	70%	4e-82	31%	XP_009956093.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Pygoscelis adeliae]	297	297	70%	4e-82	31%	XP_009329533.1
hypothetical protein TREMEDRAFT_43224 [Tremella mesenterica DSM 1558]	298	298	72%	4e-82	30%	XP_007003348.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Lepidothrix coronata]	297	297	70%	4e-82	31%	XP_017673460.1
Calcium-transporting ATPase 1 [Ogataea parapolymorpha DL-1]	297	297	73%	4e-82	30%	XP_013937332.1
calcium-translocating P-type ATPase, putative [Bodo saltans]	299	299	69%	4e-82	29%	CUI14093.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X3 [Vitis vinifera]	297	297	65%	4e-82	30%	XP_010664494.1
Calcium-transporting ATPase type 2C member 1 [Charadrius vociferus]	297	297	70%	4e-82	31%	KGL88797.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Chelonia mydas]	300	300	64%	4e-82	30%	XP_007071467.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X3 [Saimiri boliviensis boliviensis]	297	297	64%	4e-82	30%	XP_010346234.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Mesitornis unicolor]	297	297	70%	4e-82	31%	XP_010193113.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Cuculus canorus]	297	297	70%	4e-82	31%	XP_009568702.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Calidris pugnax]	298	298	70%	5e-82	31%	XP_014793252.1
Calcium-transporting ATPase type 2C member 1 [Trichinella murrelli]	297	297	71%	5e-82	30%	KRX50586.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pygoscelis adeliae]	297	297	70%	5e-82	31%	XP_009329532.1
Calcium-transporting ATPase type 2C member 1 [Cathartes aura]	297	297	70%	5e-82	31%	KFP51012.1
Calcium-transporting ATPase type 2C member 1 [Apaloderma vittatum]	296	296	70%	5e-82	31%	KFP74784.1
calcium-translocating P-type ATPase [Leishmania infantum JPCM5]	299	299	73%	5e-82	29%	XP_001462838.2
PREDICTED: calcium-transporting ATPase type 2C member 1 [Aptenodytes forsteri]	298	298	70%	5e-82	31%	XP_009278753.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Leptosomus discolor]	297	297	70%	5e-82	31%	XP_009956094.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Protobothrops mucrosquamatus]	299	299	65%	5e-82	31%	XP_015673566.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Egretta garzetta]	298	298	65%	5e-82	31%	XP_009637386.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-1 [Rhinolophus sinicus]	299	299	65%	5e-82	31%	XP_019585894.1
calcium-translocating P-type ATPase [Leishmania donovani]	299	299	73%	5e-82	29%	XP_003858064.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 1 [Columba livia]	298	298	70%	5e-82	31%	XP_005505641.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Propithecus coquereli]	299	299	64%	6e-82	32%	XP_012517341.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Struthio camelus australis]	297	297	70%	6e-82	31%	XP_009686155.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Manacus vitellinus]	298	298	70%	6e-82	31%	XP_017931017.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Rattus norvegicus]	294	294	62%	6e-82	33%	XP_008770817.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Lepidothrix coronata]	298	298	70%	6e-82	31%	XP_017673456.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Lepidothrix coronata]	298	298	70%	6e-82	31%	XP_017673454.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pelecanus crispus]	297	297	70%	6e-82	31%	XP_009486436.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Ophiophagus hannah]	299	299	65%	6e-82	31%	ETE67008.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pelecanus crispus]	297	297	70%	6e-82	31%	XP_009486435.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Canis lupus familiaris]	297	297	71%	6e-82	31%	XP_536762.3
hypothetical protein OIDMADRAFT_177085 [Oidiodendron maius Zn]	300	300	70%	6e-82	29%	KIN04707.1
hypothetical protein PISMIDRAFT_269070 [Pisolithus microcarpus 441]	300	300	74%	6e-82	29%	KIK16331.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Manacus vitellinus]	298	298	70%	6e-82	31%	XP_017931013.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Manacus vitellinus]	299	299	70%	6e-82	31%	XP_017931015.1
Calcium-transporting ATPase type 2C member 1 [Cuculus canorus]	297	297	70%	6e-82	31%	KFO70810.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Aquila chrysaetos canadensis]	296	296	70%	6e-82	31%	XP_011598290.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pongo abelii]	298	298	64%	7e-82	30%	XP_002829117.1
ATP1A1 [Bos indicus]	298	298	65%	7e-82	30%	AGY54951.1
PREDICTED: LOW QUALITY PROTEIN: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Opisthocomus hoazin]	297	297	62%	7e-82	31%	XP_009935508.1
Calcium-transporting ATPase type 2C member 1 [Mesitornis unicolor]	296	296	70%	7e-82	31%	KFQ29624.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Manacus vitellinus]	298	298	65%	7e-82	30%	XP_008920776.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Falco cherrug]	297	297	70%	7e-82	31%	XP_014141012.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Panthera pardus]	297	297	71%	7e-82	31%	XP_019268579.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Neodiprion lecontei]	296	296	69%	7e-82	30%	XP_015514321.1
Calcium-transporting ATPase type 2C member 1 [Pelecanus crispus]	296	296	70%	7e-82	31%	KFQ63878.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Takifugu rubripes]	296	296	72%	8e-82	29%	XP_003965848.1
calcium-translocating P-type ATPase [Trypanosoma congolense IL3000]	298	298	71%	8e-82	29%	CCC90639.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Manacus vitellinus]	298	298	70%	8e-82	31%	XP_017931016.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Lepidothrix coronata]	298	298	70%	8e-82	31%	XP_017673453.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pterocles gutturalis]	298	298	65%	9e-82	31%	XP_010079616.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Thelohanellus kitauei]	295	295	61%	9e-82	31%	KII70370.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Neodiprion lecontei]	296	296	69%	9e-82	30%	XP_015514320.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Lepidothrix coronata]	298	298	65%	9e-82	31%	XP_017670216.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Aquila chrysaetos canadensis]	296	296	70%	9e-82	31%	XP_011598286.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Chelonia mydas]	296	296	64%	9e-82	30%	XP_007062134.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Austrofundulus limnaeus]	297	297	70%	9e-82	30%	XP_013884860.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sodium/potassium-transporting ATPase subunit alpha-1 [Manacus vitellinus]	298	298	65%	1e-81	30%	KFW79823.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Takifugu rubripes]	296	296	72%	1e-81	29%	XP_011603518.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Pterocles gutturalis]	298	298	65%	1e-81	31%	KFV13486.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Gorilla gorilla gorilla]	296	296	64%	1e-81	30%	XP_018871820.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Zonotrichia albicollis]	298	298	65%	1e-81	31%	XP_005486168.1
calcium-transporting ATPase type 2C member 2 [Cricetulus griseus]	301	301	74%	1e-81	30%	ERE80590.1
Na+/K+ transporting ATPase alpha 1 [Tursiops truncatus]	296	296	65%	1e-81	31%	AGV55492.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Acanthisitta chloris]	298	298	65%	1e-81	31%	XP_009069874.1
Calcium-transporting ATPase 1 [Smittium culicis]	303	303	75%	1e-81	30%	OMJ21408.1
Na+/K+-ATPase alpha-subunit 1c [Anabas testudineus]	298	298	65%	1e-81	31%	AFK29494.1
Na+/K+-ATPase alpha 1a1b subunit [Solea senegalensis]	298	298	65%	1e-81	31%	BAN17691.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Neodiprion lecontei]	296	296	69%	1e-81	30%	XP_015514319.1
Calcium-transporting ATPase type 2C member 1 [Trichinella murrelli]	296	296	71%	1e-81	30%	KRX50587.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Plutella xylostella]	297	297	71%	1e-81	29%	XP_011561324.1
AGL097Cp [Eremothecium gossypii ATCC 10895]	299	299	71%	1e-81	29%	NP_986570.2
PREDICTED: potassium-transporting ATPase alpha chain 1 [Chlorocebus sabaeus]	298	298	64%	1e-81	30%	XP_007994570.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Bubalus bubalis]	298	298	64%	1e-81	30%	XP_006068866.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Acanthisitta chloris]	298	298	65%	1e-81	31%	KFP77270.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3 [Aotus nancymaae]	297	297	65%	1e-81	31%	XP_012316962.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Plutella xylostella]	296	296	71%	1e-81	29%	XP_011561323.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Rhinopithecus roxellana]	298	298	64%	1e-81	30%	XP_010367589.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Colobus angolensis palliatus]	298	298	64%	1e-81	30%	XP_011803558.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X1 [Hippocampus comes]	297	297	71%	1e-81	29%	XP_019748417.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Bos mutus]	298	298	65%	1e-81	30%	ELR51856.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Plutella xylostella]	296	296	71%	1e-81	30%	XP_011564815.1
ATP binding [Ascochyta rabiei]	299	299	69%	2e-81	30%	KZM22298.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Aquila chrysaetos canadensis]	296	296	70%	2e-81	31%	XP_011598296.1
Na+/K+ ATPase alpha 1a subunit isoform [Dicentrarchus labrax]	298	298	65%	2e-81	31%	AKQ12834.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 3 [Clonorchis sinensis]	291	291	59%	2e-81	32%	GAA52521.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Mandrillus leucophaeus]	298	298	64%	2e-81	30%	XP_011837630.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Dipodomys ordii]	298	298	64%	2e-81	30%	XP_012881665.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Corvus cornix cornix]	297	297	65%	2e-81	31%	XP_010394259.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Callithrix jacchus]	298	298	64%	2e-81	30%	XP_008985996.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Cricetulus griseus]	298	298	64%	2e-81	30%	XP_007622535.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Oreochromis niloticus]	297	297	65%	2e-81	31%	XP_005455572.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Chelonia mydas]	297	297	64%	2e-81	30%	XP_007062133.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Corvus brachyrhynchos]	297	297	65%	2e-81	31%	XP_008629963.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Gavia stellata]	297	297	65%	2e-81	31%	XP_009811967.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Saimiri boliviensis boliviensis]	298	298	64%	2e-81	30%	XP_003937412.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Bison bison bison]	298	298	64%	2e-81	30%	XP_010847314.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Serinus canaria]	297	297	65%	2e-81	31%	XP_009100827.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Saimiri boliviensis boliviensis]	297	297	64%	2e-81	30%	XP_010346233.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Chelonia mydas]	296	296	64%	2e-81	30%	EMP33651.1
potassium-transporting ATPase alpha chain 1 [Oryctolagus cuniculus]	298	298	64%	2e-81	30%	NP_001095171.1
putative Calcium-transporting ATPase 1 [Glarea lozoyensis 74030]	300	300	60%	2e-81	31%	EHL02839.1
p-type had subfamily ic [Nannochloropsis gaditana CCMP526]	301	301	72%	2e-81	31%	XP_005854105.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Geospiza fortis]	296	296	65%	2e-81	31%	XP_005420628.1
hypothetical protein MYCFIDRAFT_38601 [Pseudocercospora fijiensis CIRAD86]	297	297	72%	2e-81	30%	XP_007927961.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pan paniscus]	297	297	64%	2e-81	30%	XP_003816138.1
sarcoplasmic-endoplasmic reticulum calcium ATPase [Leishmania donovani]	297	297	73%	2e-81	29%	AAV65111.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Chrysemys picta bellii]	297	297	65%	2e-81	30%	XP_005292736.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Dipodomys ordii]	297	297	64%	2e-81	30%	XP_012881664.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Microtus ochrogaster]	297	297	64%	2e-81	30%	XP_005361277.1
Calcium-transporting ATPase type 2C member 2 [Picoides pubescens]	295	295	71%	2e-81	32%	KFV70397.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Clupea harengus]	297	297	68%	2e-81	29%	XP_012673538.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Bison bison bison]	297	297	64%	2e-81	31%	XP_010845177.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Alligator sinensis]	296	296	65%	2e-81	30%	XP_006030232.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Nanorana parkeri]	295	295	65%	2e-81	30%	XP_018429721.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Papio anubis]	297	297	64%	2e-81	30%	XP_003915402.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Amphimedon queenslandica]	297	297	64%	3e-81	30%	XP_019852321.1
hypothetical protein [Homo sapiens]	296	296	64%	3e-81	30%	CAH56338.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Alligator mississippiensis]	297	297	65%	3e-81	30%	XP_006261532.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Aotus nancymaae]	297	297	64%	3e-81	30%	XP_012293414.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Chinchilla lanigera]	297	297	64%	3e-81	30%	XP_013377837.1
calcium-transporting ATPase type 2C member 2 [Cricetulus griseus]	301	301	74%	3e-81	30%	ERE80589.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like [Kryptolebias marmoratus]	297	297	65%	3e-81	31%	XP_017266450.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pan troglodytes]	298	298	64%	3e-81	30%	XP_016791181.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Heterocephalus glaber]	297	297	64%	3e-81	30%	XP_004858871.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Neodiprion lecontei]	295	295	69%	3e-81	30%	XP_015514318.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Cephus cinctus]	295	295	69%	3e-81	30%	XP_015593942.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Chrysemys picta bellii]	297	297	65%	3e-81	30%	XP_008172109.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like [Austrofundulus limnaeus]	296	296	65%	3e-81	30%	XP_013868506.1
predicted protein [Naegleria gruberi]	297	297	67%	3e-81	30%	XP_002681456.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Microtus ochrogaster]	295	295	70%	3e-81	30%	XP_005345812.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Oreochromis niloticus]	297	297	65%	3e-81	31%	XP_003450710.1
H,K-ATPase catalytic subunit [Homo sapiens]	297	297	64%	3e-81	30%	AAA35988.1
Calcium-transporting ATPase type 2C member [Daphnia magna]	295	295	71%	3e-81	29%	JAN52735.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pantholops hodgsonii]	297	297	64%	3e-81	30%	XP_005958254.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Geospiza fortis]	297	297	65%	3e-81	31%	XP_014162323.1
Putative calcium-translocating P-type ATPase,organelle-type calcium ATPase [Leishmania guyanensis]	296	296	72%	3e-81	29%	CCM12693.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Marmota marmota marmota]	297	297	64%	3e-81	30%	XP_015352607.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Peromyscus maniculatus bairdii]	297	297	64%	3e-81	30%	XP_006982122.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Manis javanica]	296	296	64%	4e-81	30%	XP_017518852.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Corvus brachyrhynchos]	296	296	65%	4e-81	31%	KFO57681.1
unnamed protein product [Oncorhynchus mykiss]	293	293	60%	4e-81	31%	CDQ67109.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Camelus ferus]	296	296	64%	4e-81	30%	XP_014414474.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Stegastes partitus]	296	296	65%	4e-81	31%	XP_008282351.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Gallus gallus]	296	296	65%	4e-81	31%	NP_990852.1
hypothetical protein CRE_10215 [Caenorhabditis remanei]	296	296	67%	4e-81	30%	XP_003108295.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nelsoni]	297	297	65%	5e-81	30%	KRX24045.1
potassium-transporting ATPase alpha chain 1 [Rattus norvegicus]	296	296	64%	5e-81	30%	NP_036641.1
Calcium-transporting ATPase type 2C member 1 [Tyto alba]	292	292	65%	5e-81	32%	KFV49694.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Ochotona princeps]	296	296	64%	5e-81	30%	XP_004595108.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Ceratina calcarata]	295	295	70%	5e-81	30%	XP_017882714.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Ursus maritimus]	296	296	64%	5e-81	30%	XP_008710330.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Solenopsis invicta]	295	295	71%	5e-81	30%	XP_011166238.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Dasypus novemcinctus]	296	296	64%	5e-81	30%	XP_004483351.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Ochotona princeps]	296	296	64%	5e-81	30%	XP_012785244.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Fukomys damarensis]	296	296	64%	5e-81	30%	XP_010624654.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Tauraco erythrolophus]	295	295	62%	6e-81	31%	XP_009980230.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like [Aethina tumida]	296	296	70%	6e-81	29%	XP_019878226.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Amphimedon queenslandica]	296	296	64%	6e-81	30%	XP_019852322.1
ATPase, H+/K+ exchanging, alpha polypeptide [Rattus norvegicus]	296	296	64%	6e-81	30%	EDM07724.1
RecName: Full=Potassium-transporting ATPase alpha chain 1; AltName: Full=Gastric H(+)/K(+) ATPase subunit alpha; AltName: Full=Proton pump	296	296	64%	7e-81	30%	P09626.3
PREDICTED: potassium-transporting ATPase alpha chain 1 [Odobenus rosmarus divergens]	296	296	64%	7e-81	30%	XP_004417145.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Ficedula albicollis]	295	295	65%	7e-81	30%	XP_005038681.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X4 [Pan troglodytes]	291	291	61%	7e-81	32%	XP_009429605.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pseudopodoces humilis]	296	296	65%	7e-81	30%	XP_005523946.1
Potassium-transporting ATPase alpha chain 1 [Heterocephalus glaber]	296	296	64%	7e-81	30%	EHB13993.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Octodon degus]	296	296	64%	7e-81	30%	XP_004636754.1
unnamed protein product [Homo sapiens]	291	291	61%	7e-81	32%	BAG52269.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Opisthocomus hoazin]	296	296	65%	8e-81	31%	KFR00853.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Panthera pardus]	294	294	65%	8e-81	32%	XP_019268580.1
Potassium-transporting ATPase alpha chain 1 [Cricetulus griseus]	295	295	64%	8e-81	30%	EGW03707.1
potassium-transporting ATPase alpha chain 1 [Homo sapiens]	296	296	64%	8e-81	30%	NP_000695.2
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Cricetulus griseus]	296	296	64%	8e-81	30%	XP_003505605.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Erinaceus europaeus]	296	296	64%	8e-81	30%	XP_007538738.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Chinchilla lanigera]	296	296	64%	9e-81	30%	XP_013377836.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Lepisosteus oculatus]	295	295	70%	9e-81	28%	XP_015191976.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Diaphorina citri]	295	295	67%	9e-81	30%	XP_008471186.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Nothobranchius furzeri]	294	294	70%	9e-81	30%	XP_015805066.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Nothobranchius furzeri]	293	293	70%	1e-80	30%	XP_015805067.1
Na+,K+ ATPase alpha-subunit 2 [Tetraopes tetrophthalmus]	294	294	74%	1e-80	28%	AFU25696.1
calcium-transporting P [Nadsonia fulvescens var. elongata DSM 6958]	293	293	71%	1e-80	31%	ODQ66871.1
calcium-transporting ATPase [Laetiporus sulphureus 93-53]	295	295	70%	1e-80	30%	KZT11543.1
hypothetical protein g.57469 [Auxenochlorella protothecoides]	295	295	71%	1e-80	31%	JAT72461.1
putative calcium-transporting atpase type 2c member 1 [Rosellinia necatrix]	296	296	70%	1e-80	29%	GAP83400.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Lepisosteus oculatus]	295	295	64%	1e-80	31%	XP_006639435.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Sturnus vulgaris]	295	295	65%	1e-80	30%	XP_014745774.1
hypothetical protein g.40724 [Clastoptera arizonana]	295	295	69%	1e-80	29%	JAS09278.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Leptonychotes weddellii]	295	295	64%	1e-80	30%	XP_006742891.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Sorex araneus]	293	293	70%	1e-80	30%	XP_004600893.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Cebus capucinus imitator]	290	290	61%	1e-80	32%	XP_017399112.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
p-type had subfamily ic [Nannochloropsis gaditana]	299	299	70%	1e-80	31%	EWM23830.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Pogonomyrmex barbatus]	292	292	71%	2e-80	30%	XP_011643376.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Phalacrocorax carbo]	292	292	70%	2e-80	31%	XP_009500933.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 2 [Balaenoptera acutorostrata scammoni]	293	293	71%	2e-80	31%	XP_007182626.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Branchiostoma belcheri]	293	293	72%	2e-80	30%	XP_019629130.1
Calcium ATPase, transmembrane M [Glarea lozoyensis ATCC 20868]	295	295	70%	2e-80	29%	XP_008087659.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Saimiri boliviensis boliviensis]	293	293	65%	2e-80	31%	XP_010329412.1
sodium potassium ATPase alpha 1 subunit a1a [Coregonus clupeaformis]	291	291	68%	2e-80	30%	AIB08905.1
hypothetical protein LR48_Vigan04g241200 [Vigna angularis]	294	294	65%	2e-80	30%	KOM42214.1
calcium-translocating P-type ATPase [Leishmania braziliensis MHOM/BR/75/M2904]	294	294	72%	2e-80	29%	XP_001561691.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Pogonomyrmex barbatus]	293	293	71%	2e-80	30%	XP_011643374.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Caprimulgus carolinensis]	290	290	60%	3e-80	31%	KFZ62896.1
sodium potassium ATPase alpha 1 subunit a1a [Salvelinus alpinus]	291	291	68%	3e-80	30%	AIB08899.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Pan paniscus]	289	289	61%	3e-80	32%	XP_014197372.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Nomascus leucogenys]	289	289	61%	3e-80	32%	XP_012360692.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X4 [Orycteropus afer afer]	291	291	63%	4e-80	30%	XP_007946893.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Salmo salar]	294	294	68%	4e-80	31%	XP_014065332.1
calcium-transporting ATPase type 2C member 2 isoform 3 [Homo sapiens]	289	289	61%	4e-80	32%	NP_001278383.1
KIAA0703 gene product, isoform CRA_c [Homo sapiens]	289	289	61%	4e-80	32%	EAW95485.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T6]	295	295	65%	4e-80	30%	KRX84807.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Trachymyrmex septentrionalis]	292	292	71%	4e-80	30%	XP_018357152.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Jaculus jaculus]	293	293	64%	4e-80	30%	XP_004659981.1
Calcium-transporting ATPase type 2C member 1 [Trachymyrmex septentrionalis]	291	291	71%	4e-80	30%	KYN43199.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Trachymyrmex septentrionalis]	291	291	71%	4e-80	30%	XP_018357158.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella murrelli]	295	295	65%	5e-80	30%	KRX38989.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Orycteropus afer afer]	293	293	64%	5e-80	30%	XP_007953037.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Pantholops hodgsonii]	293	293	63%	5e-80	31%	XP_005981760.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Populus euphratica]	293	293	71%	5e-80	29%	XP_010999893.1
sodium/potassium-transporting ATPase subunit alpha-3 [Gallus gallus]	293	293	65%	5e-80	30%	NP_990806.1
sodium potassium ATPase alpha 1 subunit a1b [Esox lucius]	290	290	63%	5e-80	32%	AIB08909.1
calcium-transporting P [Pyrenochaeta sp. DS3sAY3a]	293	293	72%	5e-80	30%	OAL52100.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Cebus capucinus imitator]	288	288	61%	6e-80	32%	XP_017399111.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T8]	295	295	65%	6e-80	30%	KRZ90291.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Cercocebus atys]	288	288	61%	6e-80	32%	XP_011938597.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Colobus angolensis palliatus]	288	288	61%	6e-80	32%	XP_011797593.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nativa]	294	294	65%	6e-80	30%	KRZ50957.1
probable calcium P-type ATPase [Rhynchosporium secalis]	294	294	70%	6e-80	29%	CZT47897.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Trachymyrmex zeteki]	291	291	71%	7e-80	30%	XP_018317960.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Geospiza fortis]	291	291	70%	7e-80	31%	XP_014163664.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Nannospalax galili]	293	293	71%	7e-80	29%	XP_008822627.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Tupaia chinensis]	293	293	64%	7e-80	30%	XP_006171692.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Alligator sinensis]	293	293	65%	7e-80	30%	XP_006037826.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X1 [Myotis davidii]	293	293	67%	8e-80	30%	XP_006765128.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Salmo salar]	293	293	68%	8e-80	31%	XP_014050103.1
probable calcium P-type ATPase [Phialocephala subalpina]	294	294	70%	8e-80	29%	CZR50365.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Atta colombica]	290	290	71%	8e-80	30%	XP_018059384.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Atta cephalotes]	291	291	71%	8e-80	30%	XP_012057428.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Atta colombica]	291	291	71%	9e-80	30%	XP_018059312.1
potassium-transporting ATPase alpha chain 2 b [Rattus norvegicus]	291	291	71%	9e-80	29%	NP_001288593.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Atta colombica]	291	291	71%	9e-80	30%	XP_018059374.1
Potassium-transporting ATPase alpha chain 1 [Myotis brandtii]	295	295	64%	9e-80	30%	EPQ05353.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Esox lucius]	293	293	63%	9e-80	32%	XP_012995326.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Trachymyrmex zeteki]	291	291	71%	9e-80	30%	XP_018317957.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Cavia porcellus]	293	293	64%	9e-80	30%	XP_003466692.1
H-K-ATPase alpha 2b subunit [Rattus norvegicus]	291	291	71%	1e-79	29%	AAB93902.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-2 [Equus caballus]	292	292	64%	1e-79	31%	XP_001915271.2
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X3 [Myotis davidii]	292	292	67%	1e-79	30%	XP_015420327.1
ATPase, Na+/K+ transporting, alpha 2a polypeptide [Danio rerio]	292	292	65%	1e-79	30%	AAI63629.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Gorilla gorilla gorilla]	288	288	61%	1e-79	32%	XP_018868381.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X3 [Myotis brandtii]	292	292	67%	1e-79	30%	XP_014383656.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Dichanthelium oligosanthes]	291	291	65%	1e-79	30%	OEL38425.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Anser cygnoides domesticus]	290	290	59%	1e-79	32%	XP_013029241.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Apteryx australis mantelli]	290	290	70%	1e-79	31%	XP_013806203.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X2 [Myotis davidii]	292	292	67%	1e-79	30%	XP_015420326.1
sodium potassium transporting ATPase alpha subunit [Schistosoma mansoni]	292	292	69%	1e-79	29%	XP_018651572.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Na+/K+ ATPase alpha2 subunit [Danio rerio]	292	292	65%	1e-79	30%	AAK33032.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Echinops telfairi]	290	290	62%	1e-79	31%	XP_004714920.1
hypothetical protein A3Q56_04371 [Intoshia linei]	292	292	65%	1e-79	31%	OAF67883.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Trachymyrmex zeteki]	291	291	71%	1e-79	30%	XP_018317956.1
Sodium/potassium-transporting ATPase subunit alpha [Caenorhabditis elegans]	292	292	67%	1e-79	29%	NP_497034.2
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Diuraphis noxia]	290	290	70%	1e-79	30%	XP_015380443.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X1 [Myotis brandtii]	292	292	67%	1e-79	30%	XP_005880078.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Tupaia chinensis]	292	292	64%	1e-79	31%	XP_006168897.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 [Sinocyclocheilus anshuiensis]	292	292	65%	1e-79	31%	XP_016347567.1
hypothetical protein sscle_01g002310 [Sclerotinia sclerotiorum 1980 UF-70]	293	293	63%	1e-79	31%	APA05461.1
Sodium/potassium-transporting ATPase subunit alpha-2 [Cricetulus griseus]	294	294	64%	1e-79	31%	EGV93401.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X4 [Papio anubis]	287	287	61%	2e-79	32%	XP_009195226.1
unnamed protein product [Kluyveromyces dobzhanskii CBS 2104]	290	290	71%	2e-79	31%	CDO94423.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X4 [Rhinopithecus bieti]	287	287	61%	2e-79	32%	XP_017716310.1
E1-E2_ATPase domain-containing protein/Cation_ATPase_C domain-containing protein/Cation_ATPase_N domain-containing protein/Hydrolase domain-containing protein [Cephalotus follicularis]	291	291	65%	2e-79	30%	GAV56597.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Diuraphis noxia]	290	290	70%	2e-79	30%	XP_015380441.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Gekko japonicus]	290	290	61%	2e-79	30%	XP_015273570.1
hypothetical protein g.33837 [Graphocephala atropunctata]	291	291	71%	2e-79	29%	JAT35421.1
sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Amazona aestiva]	292	292	65%	2e-79	31%	KQK85052.1
calcium-translocating P-type ATPase [Leishmania panamensis]	291	291	70%	2e-79	29%	XP_010703651.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X2 [Myotis brandtii]	292	292	67%	2e-79	30%	XP_014383655.1
calcium-transporting ATPase 1 [Nannizzia gypsea CBS 118893]	292	292	74%	2e-79	30%	XP_003174478.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Python bivittatus]	291	291	65%	2e-79	30%	XP_007437634.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Trachymyrmex cornetzi]	290	290	71%	2e-79	30%	XP_018363238.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 3 isoform X9 [Pan troglodytes]	290	290	75%	2e-79	28%	XP_016786725.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Trachymyrmex cornetzi]	289	289	71%	2e-79	30%	XP_018363240.1
sodium potassium ATPase alpha 1 subunit a1a [Salmo salar]	288	288	68%	3e-79	30%	AIB08901.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Trachymyrmex cornetzi]	290	290	71%	3e-79	30%	XP_018363239.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Capra hircus]	291	291	63%	3e-79	31%	XP_013831391.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X3 [Chrysochloris asiatica]	288	288	62%	3e-79	31%	XP_006874864.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Capra hircus]	291	291	63%	3e-79	31%	XP_005677289.2
PREDICTED: potassium-transporting ATPase alpha chain 2 [Elephantulus edwardii]	289	289	67%	3e-79	29%	XP_006879616.1

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hypothetical protein GLOINDRAFT_32681 [Rhizophagus irregularis DAOM 181602]	285	285	51%	3e-79	33%	ESA07591.1
Calcium-transporting ATPase type 2C member 1 [Trachymyrmex cornetzi]	290	290	71%	3e-79	30%	KYN19729.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X3 [Pygocentrus nattereri]	288	288	62%	3e-79	31%	XP_017571610.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Balaenoptera acutorostrata scammoni]	287	287	61%	4e-79	32%	XP_007168106.1
probable calcium P-type ATPase [Rhynchosporium agropyri]	292	292	70%	4e-79	29%	CZT11236.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Acromyrmex echinatior]	288	288	71%	4e-79	30%	XP_011050747.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Acromyrmex echinatior]	289	289	71%	4e-79	30%	XP_011050741.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X4 [Myotis brandtii]	289	289	66%	4e-79	30%	XP_014383657.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nelsoni]	292	292	65%	4e-79	30%	KRX24043.1
DEHA2F13464p [Debaryomyces hansenii CBS767]	289	289	70%	4e-79	32%	XP_460949.1
Calcium-transporting ATPase type 2C member 1 [Trichinella sp. T8]	288	288	71%	4e-79	30%	KRZ84704.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Equus przewalskii]	290	290	64%	4e-79	30%	XP_008532152.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Leptonychotes weddellii]	291	291	65%	4e-79	31%	XP_006743492.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X1 [Nothobranchius furzeri]	290	290	64%	4e-79	29%	XP_015811570.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Bubalus bubalis]	291	291	63%	5e-79	31%	XP_006060547.1
putative H+/K+-ATPase isoform alpha 1 [Dasyatis sabina]	290	290	65%	5e-79	29%	AAP35241.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Monomorium pharaonis]	289	289	71%	5e-79	29%	XP_012522996.1
sodium/potassium-transporting ATPase subunit alpha-2 [Danio rerio]	290	290	65%	5e-79	30%	NP_571758.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Aotus nancymaae]	286	286	58%	5e-79	32%	XP_012322222.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X3 [Pelodiscus sinensis]	288	288	71%	5e-79	31%	XP_014434867.1
P-type ATPase [Schizosaccharomyces octosporus yFS286]	288	288	73%	5e-79	30%	XP_013016506.1
Na/K ATPase alpha subunit isoform 1a [Oncorhynchus mykiss]	290	290	68%	5e-79	30%	NP_001117933.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Pelodiscus sinensis]	289	289	71%	5e-79	31%	XP_006134934.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Tupaia chinensis]	288	288	60%	5e-79	31%	XP_014443554.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Hipposideros armiger]	290	290	64%	5e-79	30%	XP_019480352.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Pterocles gutturalis]	288	288	67%	5e-79	29%	XP_010071478.1
Potassium-transporting ATPase alpha chain 1 [Macaca mulatta]	290	290	64%	5e-79	30%	EHH29928.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Aotus nancymaae]	285	285	58%	6e-79	32%	XP_012322223.1
hypothetical protein COCMIDRAFT_79763 [Bipolaris oryzae ATCC 44560]	290	290	72%	6e-79	31%	XP_007682258.1
hypothetical protein T265_12551 [Opisthorchis viverrini]	290	290	71%	6e-79	28%	XP_009162539.1
non-gastric H+,K+-ATPase alpha subunit [Schmidtea mediterranea]	290	290	69%	6e-79	30%	AGF90974.1
PREDICTED: potassium-transporting ATPase alpha chain 2-like [Xenopus laevis]	290	290	65%	6e-79	31%	XP_018118012.1
sodium/potassium-transporting ATPase subunit alpha-4 [Cricetulus griseus]	296	580	65%	6e-79	31%	ERE72878.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 [Anolis carolinensis]	290	290	70%	6e-79	30%	XP_008117666.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Anolis carolinensis]	288	288	71%	8e-79	32%	XP_008121417.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Esox lucius]	290	290	72%	8e-79	30%	XP_010892776.1
P-type calcium transporting ATPase [Bathycoccus prasinos]	291	382	67%	8e-79	34%	XP_007515588.1
hypothetical protein TD95_004549 [Thielaviopsis punctulata]	290	290	70%	8e-79	28%	KKA28666.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Sus scrofa]	290	290	65%	8e-79	31%	XP_001929014.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Podiceps cristatus]	289	289	65%	8e-79	30%	KFZ67533.1
P-type ATPase, cytoplasmic domain N [Pseudocohnilembus persalinus]	293	293	74%	9e-79	28%	KRX06972.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Cyphomyrmex costatus]	287	287	71%	9e-79	30%	XP_018401172.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Cyphomyrmex costatus]	288	288	71%	9e-79	29%	XP_018401169.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Bemisia tabaci]	289	289	71%	1e-78	29%	XP_018896615.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Bemisia tabaci]	289	289	71%	1e-78	29%	XP_018896616.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Lipotes vexillifer]	290	290	64%	1e-78	29%	XP_007471057.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Bemisia tabaci]	290	290	71%	1e-78	29%	XP_018896611.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 2 [Myotis lucifugus]	290	290	67%	1e-78	30%	XP_006110162.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Camelus bactrianus]	290	290	60%	1e-78	31%	XP_010968061.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 1 [Physeter catodon]	290	290	64%	1e-78	29%	XP_007106608.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Bemisia tabaci]	290	290	71%	1e-78	29%	XP_018896607.1
sodium potassium ATPase alpha 1 subunit a1a-y [Esox lucius]	286	286	67%	1e-78	30%	AIB08908.1
calcium-transporting ATPase 2 protein [Trichinella spiralis]	286	286	60%	1e-78	32%	XP_003376005.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Bemisia tabaci]	289	289	71%	1e-78	29%	XP_018896612.1
potassium/sodium eff [Cutaneotrichosporon oleaginosus]	290	290	72%	2e-78	30%	XP_018278279.1
potassium-transporting ATPase alpha chain 1 isoform 1 [Mus musculus]	289	289	63%	2e-78	30%	NP_001277556.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Mustela putorius furo]	289	289	67%	2e-78	29%	XP_004778280.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X4 [Ictalurus punctatus]	286	286	64%	2e-78	29%	XP_017317367.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Rousettus aegyptiacus]	290	290	64%	2e-78	29%	XP_015975229.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X4 [Myotis davidii]	287	287	66%	2e-78	30%	XP_015420328.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 1 [Balaenoptera acutorostrata scammoni]	289	289	64%	2e-78	29%	XP_007165196.1
Potassium-transporting ATPase alpha chain 1 [Pteropus alecto]	288	288	64%	2e-78	29%	ELK05780.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Wasmannia auropunctata]	287	287	71%	2e-78	30%	XP_011706652.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Manis javanica]	289	289	67%	2e-78	29%	XP_017512427.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	286	286	65%	2e-78	29%	KRX93493.1

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PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X4 [Cercocebus atys]	286	286	64%	2e-78	29%	XP_011898997.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3 [Bos indicus]	290	290	65%	2e-78	32%	XP_019833818.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Ceratotherium simum simum]	287	287	71%	2e-78	30%	XP_004437114.1
unnamed protein product [Tetraodon nigroviridis]	290	290	64%	2e-78	31%	CAF98515.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Rousettus aegyptiacus]	289	289	64%	2e-78	29%	XP_015975230.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	289	289	65%	2e-78	29%	KRY93306.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T8]	289	289	65%	2e-78	29%	KRZ85828.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X2 [Salmo salar]	288	288	65%	2e-78	30%	XP_014047345.1
Potassium-transporting ATPase alpha chain 2 [Myotis davidii]	288	288	67%	2e-78	30%	ELK29258.1
Calcium-transporting ATPase 3 family protein [Populus trichocarpa]	288	288	71%	3e-78	29%	XP_002320682.1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Tupaia chinensis]	288	288	71%	3e-78	29%	ELW65524.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella zimbabwensis]	289	289	65%	3e-78	29%	KRZ11380.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella murrelli]	289	289	65%	3e-78	29%	KRX35740.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Protobothrops mucrosquamatus]	288	288	69%	3e-78	30%	XP_015670344.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Acanthisitta chloris]	285	285	65%	3e-78	31%	XP_009082895.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nativa]	289	289	65%	3e-78	29%	KRZ52540.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pteropus alecto]	288	288	64%	3e-78	29%	XP_006919940.1
hypothetical protein BAUCODRAFT_34659 [Baudoinia panamericana UAMH 10762]	289	289	63%	3e-78	30%	XP_007676823.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Agrilus planipennis]	287	287	65%	3e-78	29%	XP_018321825.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T6]	289	289	65%	3e-78	29%	KRX71322.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	288	288	65%	3e-78	29%	KRZ12533.1
calcium/mangenease P-type ATPase-like protein [Chaetomium thermophilum var. thermophilum DSM 1495]	290	290	62%	3e-78	30%	XP_006695986.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella britovi]	289	289	65%	3e-78	29%	KRY49844.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella patagoniensis]	288	288	65%	3e-78	29%	KRY08382.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Rhagoletis zephyria]	287	287	65%	3e-78	30%	XP_017486499.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Propithecus coquereli]	288	288	64%	3e-78	29%	XP_012507070.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	289	289	65%	3e-78	29%	KRY76684.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T9]	289	289	65%	3e-78	29%	KRX56878.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Capra hircus]	287	287	64%	4e-78	29%	XP_017918782.1
Potassium-transporting ATPase alpha chain 1 [Bos mutus]	288	288	64%	4e-78	29%	ELR47229.1
Sodium/potassium-transporting ATPase subunit alpha-B [Orchesella cincta]	288	288	74%	4e-78	29%	ODM99113.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Capra hircus]	288	288	64%	4e-78	29%	XP_005692361.2
gastric proton pump [Scyliorhinus canicula]	288	288	64%	4e-78	29%	AOJ00399.1

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Sodium/potassium-transporting ATPase subunit alpha [Trichinella spiralis]	289	289	65%	4e-78	29%	KRY31169.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X2 [Ictalurus punctatus]	288	288	64%	4e-78	29%	XP_017317365.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Ceratotherium simum simum]	286	286	64%	4e-78	29%	XP_014650284.1
putative ca2+ transporting atpase [Culex tarsalis]	286	286	65%	5e-78	31%	JAV31380.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Bos mutus]	288	288	64%	5e-78	29%	XP_005908254.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X1 [Ictalurus punctatus]	287	287	64%	6e-78	29%	XP_017317364.1
hypothetical protein ANO11243_045600 [fungal sp. No.11243]	288	288	71%	6e-78	29%	GAM86546.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type, putative, expressed [Oryza sativa Japonica Group]	288	288	65%	6e-78	29%	ABF98693.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X1 [Oryctolagus cuniculus]	287	287	68%	6e-78	29%	XP_008257860.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Neolamprologus brichardi]	282	282	62%	6e-78	31%	XP_006809657.1
calcium-transporting P-type ATPase [Galdieria sulphuraria]	288	288	69%	6e-78	30%	XP_005707399.1
ATPase, H+/K+ exchanging, alpha polypeptide variant [Homo sapiens]	287	287	64%	6e-78	30%	BAD96979.1
potassium-transporting ATPase alpha chain 1 [Bos taurus]	287	287	64%	6e-78	29%	NP_001137561.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3 [Loxodonta africana]	286	286	65%	7e-78	30%	XP_010584705.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Odobenus rosmarus divergens]	287	287	65%	7e-78	31%	XP_004407919.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Cercocebus atys]	286	286	64%	7e-78	29%	XP_011898995.1
Calcium-transporting ATPase 3 [Wallemia ichthyophaga EXF-994]	287	287	69%	7e-78	28%	XP_009266295.1
Calcium-transporting ATPase type 2C member 1 [Opisthocomus hoazin]	282	282	64%	7e-78	31%	KFR13537.1
P-type ATPase, A domain-containing protein [Rozella allomycis CSF55]	289	289	72%	8e-78	30%	EPZ33470.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Chaetura pelagica]	286	286	67%	8e-78	30%	XP_010001183.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pelodiscus sinensis]	287	287	64%	8e-78	30%	XP_014428115.1
Na+/K+-ATPase alpha-subunit [Dugesia japonica]	287	287	65%	8e-78	31%	BAA32798.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X3 [Salmo salar]	283	283	56%	8e-78	31%	XP_014015884.1
Potassium-transporting ATPase alpha chain 2 [Chaetura pelagica]	286	286	67%	9e-78	30%	KFU93564.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Bemisia tabaci]	288	288	70%	9e-78	29%	XP_018896610.1
hypothetical protein H072_10975 [Dactylellina haptotyla CBS 200.50]	286	286	63%	9e-78	30%	XP_011116364.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Athalia rosae]	285	285	70%	9e-78	29%	XP_012269213.1
H,K-ATPase alpha2 subunit [Oryctolagus cuniculus]	287	287	68%	9e-78	29%	AAD11800.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Athalia rosae]	285	285	70%	1e-77	29%	XP_012269211.1
C. briggsae CBR-PMR-1 protein [Caenorhabditis briggsae]	285	285	70%	1e-77	29%	XP_002646059.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Ovis aries musimon]	287	287	64%	1e-77	29%	XP_011975860.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Haliaeetus albicilla]	283	283	65%	1e-77	31%	XP_009925291.1
Na-ATPase [Heterosigma akashiwo]	290	290	73%	1e-77	28%	BAA82752.2
putative ca2+ transporting atpase [Culex tarsalis]	285	285	64%	1e-77	31%	JAV34717.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 isoform X2 [Callorhinchus milii]	286	286	65%	1e-77	29%	XP_007910396.1

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PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X7 [Manacus vitellinus]	285	285	65%	1e-77	31%	XP_017931024.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Myotis davidii]	284	284	64%	1e-77	29%	XP_015420259.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Camelus bactrianus]	286	286	64%	1e-77	29%	XP_010948397.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Ovis aries]	286	286	64%	1e-77	29%	XP_014955441.1
Sodium/potassium-transporting ATPase subunit alpha-2 [Tupaia chinensis]	291	577	64%	1e-77	31%	ELV10586.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like isoform X1 [Sinocyclocheilus rhinocerous]	283	283	62%	1e-77	31%	XP_016390005.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Physeter catodon]	285	285	67%	1e-77	29%	XP_007114254.1
calcium-transporting ATPase 2C1 isoform 1d variant [Homo sapiens]	277	277	47%	1e-77	34%	BAD92502.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Ceratotherium simum simum]	286	286	64%	1e-77	29%	XP_014650283.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Miniopterus natalensis]	285	285	64%	2e-77	29%	XP_016076379.1
Potassium-transporting ATPase alpha chain 1 [Larimichthys crocea]	285	285	65%	2e-77	29%	KKF32592.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Manacus vitellinus]	285	285	65%	2e-77	31%	XP_017931019.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Orcinus orca]	285	285	71%	2e-77	31%	XP_004280137.1
sodium potassium ATPase alpha 1 subunit a1a [Thymallus arcticus]	283	283	68%	2e-77	30%	AIB08903.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Nannospalax galili]	286	286	64%	2e-77	29%	XP_008826246.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X3 [Lepidothrix coronata]	285	285	65%	2e-77	31%	XP_017673455.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X6 [Lepidothrix coronata]	285	285	65%	2e-77	31%	XP_017673461.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 isoform X1 [Callorhinchus milii]	286	286	64%	2e-77	29%	XP_007910395.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Miniopterus natalensis]	286	286	64%	2e-77	29%	XP_016076378.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Nannospalax galili]	286	286	64%	2e-77	29%	XP_008826245.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Chrysemys picta bellii]	279	279	62%	2e-77	31%	XP_005312559.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Aquila chrysaetos canadensis]	283	283	65%	2e-77	31%	XP_011598295.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Otolemur garnettii]	286	286	64%	2e-77	29%	XP_003796133.1
Calcium-transporting ATPase type 2C member [Daphnia magna]	285	285	71%	2e-77	28%	JAN78137.1
hypothetical protein AMSG_11881 [Thecamonas trahens ATCC 50062]	290	290	67%	2e-77	29%	XP_013757922.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X17 [Cercocebus atys]	281	281	47%	2e-77	34%	XP_011899399.1
hypothetical protein g.17423 [Homalodisca liturata]	285	285	70%	2e-77	29%	JAS95163.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Vicugna pacos]	284	284	66%	2e-77	31%	XP_015097433.1
potassium/sodium efflux P-type ATPase, fungal-type [Batrachochytrium dendrobatidis JEL423]	288	378	68%	2e-77	33%	OAJ36565.1
Potassium-transporting ATPase alpha chain 2 [Myotis brandtii]	289	289	67%	2e-77	30%	EPQ16271.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Vicugna pacos]	285	285	64%	2e-77	29%	XP_015105681.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 1 [Myotis lucifugus]	286	286	64%	2e-77	29%	XP_014319699.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Pteropus vampyrus]	285	285	65%	2e-77	31%	XP_011371380.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Pundamilia nyererei]	283	283	60%	2e-77	32%	XP_005753450.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Cricetulus griseus]	285	285	64%	2e-77	30%	XP_007622536.1
ATPase, H+/K+ transporting, nongastric, alpha polypeptide, locus 1 [Xenopus tropicalis]	285	285	65%	3e-77	30%	CAJ83065.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella papuae]	286	286	65%	3e-77	29%	KRZ73739.1
calcium-transporting P-type ATPase, PMR1-type [Rhizopus delemar RA 99-880]	282	282	71%	3e-77	29%	EIE79996.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Salmo salar]	285	285	69%	3e-77	28%	XP_014011545.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Felis catus]	285	285	64%	3e-77	29%	XP_003997950.2
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X3 [Dipodomys ordii]	285	285	64%	3e-77	30%	XP_012881666.1
Potassium-transporting ATPase alpha chain 1 [Myotis davidii]	285	285	64%	4e-77	29%	ELK29278.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Orcinus orca]	284	284	71%	4e-77	31%	XP_012392278.1
hypothetical protein AC631_05266 [Debaryomyces fabryi]	283	283	70%	4e-77	32%	XP_015465071.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Panthera tigris altaica]	285	285	64%	4e-77	29%	XP_007097013.1
sodium potassium ATPase alpha 1 subunit a1a-x [Esox lucius]	282	282	64%	4e-77	30%	AIB08907.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Scleropages formosus]	284	284	60%	4e-77	31%	KPP69092.1
Calcium-transporting ATPase 3, endoplasmic reticulum-type [Aegilops tauschii]	285	285	62%	4e-77	30%	EMT13895.1
Na+/K+-ATPase alpha-subunit [Brachionus sp. 'koreanus']	285	285	65%	4e-77	30%	ALJ53300.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Microcebus murinus]	285	285	64%	4e-77	29%	XP_012630489.1
hypothetical protein IMG5_002750 [Ichthyophthirius multifiliis]	285	285	48%	4e-77	35%	XP_004040046.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Felis catus]	285	285	64%	5e-77	29%	XP_019674241.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Esox lucius]	285	285	69%	5e-77	27%	XP_010883375.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Myotis brandtii]	285	285	64%	5e-77	29%	XP_014392262.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X5 [Homo sapiens]	277	277	47%	5e-77	34%	XP_011510988.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Panthera tigris altaica]	285	285	65%	5e-77	30%	XP_015395000.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Bemisia tabaci]	285	285	70%	5e-77	29%	XP_018896609.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Crocodylus porosus]	282	282	65%	5e-77	30%	XP_019397242.1
Protein CBR-PMR-1 [Caenorhabditis briggsae]	284	284	70%	5e-77	29%	CAP27845.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Microtus ochrogaster]	285	285	71%	5e-77	29%	XP_005368631.2
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Marmota marmota marmota]	285	285	64%	5e-77	30%	XP_015352608.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Vicugna pacos]	285	285	65%	5e-77	30%	XP_006215708.1
PREDICTED: calcium-transporting ATPase-like [Drosophila kikkawai]	283	283	71%	5e-77	30%	XP_017032429.1
hypothetical protein Y032_0343g3054 [Ancylostoma ceylanicum]	283	283	71%	6e-77	29%	EYB83076.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4-like [Orycteropus afer afer]	284	284	64%	6e-77	30%	XP_007945980.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
H+,K+-ATPase alpha 2a subunit [Oryctolagus cuniculus]	285	285	68%	6e-77	29%	AAB80941.1
hypothetical protein TRV_01438 [Trichophyton verrucosum HKI 0517]	285	285	73%	6e-77	29%	XP_003024372.1
H+,K+-ATPase alpha 2 subunit [Oryctolagus cuniculus]	284	284	68%	7e-77	29%	AAS76541.1
Potassium-transporting ATPase alpha chain 1 [Fukomys damarensis]	285	285	64%	7e-77	29%	KFO32385.1
sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Rhizoctonia solani AG-1 IA]	284	284	70%	7e-77	31%	ELU44621.1
calcium-transporting atpase [Lentinula edodes]	284	284	74%	7e-77	29%	GAW08457.1
potassium-transporting ATPase alpha chain 2 [Oryctolagus cuniculus]	285	285	68%	7e-77	29%	NP_001075496.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Cricetulus griseus]	284	284	64%	7e-77	31%	XP_003500331.1
hypothetical protein SETTUDRAFT_117351 [Setosphaeria turcica Et28A]	284	284	72%	7e-77	30%	XP_008027444.1
hypothetical protein COCC4DRAFT_171229 [Bipolaris maydis ATCC 48331]	284	284	60%	7e-77	32%	XP_014078362.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Larimichthys crocea]	282	282	66%	7e-77	29%	XP_019125850.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Arachis ipaensis]	283	283	71%	7e-77	28%	XP_016165337.1
potassium-transporting ATPase alpha chain 2 [Xenopus tropicalis]	284	284	65%	8e-77	30%	NP_001025550.1
hypothetical protein Y032_0343g3054 [Ancylostoma ceylanicum]	283	283	71%	8e-77	29%	EYB83075.1
potassium-transporting ATPase alpha chain 1 [Sus scrofa]	284	284	64%	8e-77	29%	NP_999456.1
hypothetical protein HELRODRAFT_94922 [Helobdella robusta]	283	283	64%	8e-77	30%	XP_009022592.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 [Caprimulgus carolinensis]	279	279	56%	8e-77	32%	XP_010171001.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X3 [Ochotona princeps]	284	284	64%	9e-77	30%	XP_004595109.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Elephantulus edwardii]	284	284	64%	9e-77	29%	XP_006899738.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Fukomys damarensis]	284	284	64%	9e-77	30%	XP_010624655.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Octodon degus]	284	284	64%	9e-77	30%	XP_004636755.1
hypothetical protein XENTR_v90018286mg [Xenopus tropicalis]	284	284	71%	1e-76	29%	OCA28627.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 1 [Equus asinus]	284	284	64%	1e-76	29%	XP_014693737.1
PREDICTED: potassium-transporting ATPase alpha chain 1-like [Salmo salar]	284	284	69%	1e-76	28%	XP_014056965.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Panthera pardus]	284	284	67%	1e-76	29%	XP_019292030.1
calcium-transporting P [Alternaria alternata]	284	284	70%	1e-76	30%	XP_018382445.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Cricetulus griseus]	283	283	64%	1e-76	29%	XP_003505606.1
hypothetical protein COCCADRAFT_36849 [Bipolaris zeicola 26-R-13]	284	284	72%	1e-76	30%	XP_007712387.1
sodium transport atpase [Melanopsichium pennsylvanicum 4]	285	285	70%	1e-76	28%	CDI51148.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella britovi]	284	284	65%	1e-76	30%	KRY48184.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Esox lucius]	283	283	64%	1e-76	30%	XP_010886547.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Ursus maritimus]	285	285	67%	1e-76	29%	XP_008690492.1
hypothetical protein UMAG_00204 [Ustilago maydis 521]	285	285	70%	1e-76	28%	XP_011386140.1
Na+/K+ ATPase 1 [Valsa mali var. pyri]	284	284	72%	1e-76	30%	AMR06580.1
putative ca2+ transporting atpase [Culex tarsalis]	281	281	64%	1e-76	30%	JAV34762.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ATP4A [Botia histrionica]	278	278	65%	1e-76	29%	AEQ38528.1
putative ca2+ transporting atpase [Culex tarsalis]	281	281	64%	2e-76	30%	JAV34851.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X7 [Panthera pardus]	282	282	65%	2e-76	30%	XP_019288732.1
TPA: Calcium-transporting ATPase [Trichophyton benhamiae CBS 112371]	283	283	72%	2e-76	29%	DAA78933.1
potassium/sodium efflux P-type ATPase, fungal-type [Tsuchiyaea wingfieldii CBS 7118]	284	284	73%	2e-76	28%	XP_019028838.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Chrysochloris asiatica]	283	283	64%	2e-76	29%	XP_006867422.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Ailuropoda melanoleuca]	285	285	67%	2e-76	29%	XP_011215834.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Picoides pubescens]	281	281	71%	2e-76	31%	XP_009902839.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella britovi]	284	284	65%	2e-76	30%	KRY48185.1
Calcium-transporting ATPase 1 [Valsa mali]	283	283	72%	2e-76	29%	KUI66363.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Galeopterus variegatus]	283	283	64%	2e-76	29%	XP_008584087.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Canis lupus familiaris]	283	283	67%	2e-76	29%	XP_848278.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X5 [Panthera pardus]	283	283	65%	2e-76	30%	XP_019288729.1
calcium-transporting ATPase 1 (Golgi Ca(2+)-ATPase) [Trichophyton tonsurans CBS 112818]	283	283	73%	2e-76	29%	EGD95316.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Pteropus alecto]	283	283	65%	2e-76	31%	XP_006922963.1
potassium-transporting ATPase alpha chain 1 [Camelus ferus]	285	285	64%	2e-76	29%	EPY81295.1
calcium-transporting atpase 1 [Lichtheimia corymbifera JMRC:FSU:9682]	280	280	71%	2e-76	29%	CDH60754.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Odobenus rosmarus divergens]	283	283	67%	3e-76	29%	XP_012418160.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 1 [Camelus dromedarius]	283	283	64%	3e-76	29%	XP_010977190.1
Calcium-transporting ATPase 1 [Valsa mali var. pyri]	283	283	60%	3e-76	31%	KUI61630.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Thamnophis sirtalis]	280	280	67%	3e-76	30%	XP_013912440.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Cricetulus griseus]	282	282	64%	3e-76	31%	XP_007637428.1
sodium/potassium-transporting ATPase alpha chain, putative [Pediculus humanus corporis]	282	282	64%	3e-76	30%	XP_002429419.1
H/K ATPase:SUBUNIT=alpha	282	282	63%	4e-76	29%	2112199B
PREDICTED: potassium-transporting ATPase alpha chain 1 [Trichechus manatus latirostris]	282	282	64%	4e-76	29%	XP_004388170.1
calcium-transporting P-type ATPase [Gaeumannomyces graminis var. tritici R3-111a-1]	283	283	60%	4e-76	30%	XP_009222447.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Chrysochloris asiatica]	281	281	65%	4e-76	30%	XP_006861704.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Panthera pardus]	283	283	65%	4e-76	30%	XP_019288725.1
hypothetical protein AOL_s00080g344 [Arthrobotrys oligospora ATCC 24927]	281	281	72%	4e-76	30%	XP_011123021.1
hypothetical protein BRAFLDRAFT_222013 [Branchiostoma floridae]	280	280	72%	4e-76	29%	XP_002612354.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X3 [Panthera pardus]	282	282	65%	5e-76	30%	XP_019288727.1
p-type calcium ATPase [Grosmannia clavigera kw1407]	282	282	62%	5e-76	31%	XP_014169446.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Echinops telfairi]	281	281	64%	5e-76	29%	XP_012863513.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T9]	282	282	65%	5e-76	29%	KRX56880.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	282	282	65%	5e-76	29%	KRY76685.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Larimichthys crocea]	279	279	65%	5e-76	30%	XP_019129610.1
potassium/sodium efflux P-type ATPase, fungal-type [Allomyces macrogynus ATCC 38327]	281	281	69%	6e-76	29%	KNE72470.1
calcium-transporting ATPase 1 [Trichophyton rubrum CBS 118892]	282	282	73%	6e-76	29%	XP_003236225.1
PREDICTED: potassium-transporting ATPase alpha chain 2-like [Nanorana parkeri]	282	282	68%	6e-76	30%	XP_018416828.1
sodium potassium-transporting atpase subunit alpha [Ascaris suum]	281	281	64%	6e-76	30%	ERG81932.1
calcium-transporting P [Coniophora puteana RWD-64-598 SS2]	282	282	74%	6e-76	29%	XP_007769062.1
hypothetical protein COCSADRAFT_35014 [Bipolaris sorokiniana ND90Pr]	281	281	61%	6e-76	32%	XP_007697558.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X2 [Lingula anatina]	280	280	73%	6e-76	28%	XP_013393466.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Ceratosolen solmsi marchali]	281	281	65%	6e-76	30%	XP_011503992.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 2 [Coturnix japonica]	281	281	67%	6e-76	29%	XP_015739441.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like isoform X1 [Lingula anatina]	280	280	73%	6e-76	28%	XP_013393465.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Notothenia coriiceps]	281	281	64%	7e-76	29%	XP_010783654.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Ceratosolen solmsi marchali]	281	281	65%	7e-76	30%	XP_011504000.1
proton pump alpha subunit [Siniperca scherzeri]	281	281	69%	7e-76	28%	ACQ90249.1
gastric H+/K+ ATPase alpha subunit [Siniperca chuatsi]	281	281	69%	7e-76	28%	ADK25708.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Camelus ferus]	278	278	68%	7e-76	31%	XP_014414081.1
hypothetical protein g.33834 [Graphocephala atropunctata]	279	279	64%	8e-76	30%	JAT38157.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Tupaia chinensis]	281	281	64%	8e-76	29%	XP_014440898.1
calcium-transporting P-type ATPase, PMR1-type [Trichophyton interdigitale H6]	281	281	73%	8e-76	29%	EZF35012.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Macaca fascicularis]	279	279	64%	8e-76	31%	XP_015310368.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Ceratosolen solmsi marchali]	281	281	65%	8e-76	30%	XP_011503985.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Rhagoletis zephyria]	283	283	70%	9e-76	29%	XP_017483653.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Ceratosolen solmsi marchali]	281	281	65%	9e-76	30%	XP_011503977.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Felis catus]	282	282	67%	9e-76	29%	XP_019681413.1
hypothetical protein B456_004G024800 [Gossypium raimondii]	280	280	64%	9e-76	30%	KJB21987.1
hypothetical protein PTT_02780 [Pyrenophora teres f. teres 0-1]	280	280	72%	1e-75	29%	XP_003295773.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Ceratosolen solmsi marchali]	281	281	65%	1e-75	30%	XP_011503970.1
ATPase, H+/K+ exchanging, gastric, alpha polypeptide, isoform CRA_b [Mus musculus]	281	281	63%	1e-75	29%	EDL23995.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Jaculus jaculus]	281	281	64%	1e-75	29%	XP_004659982.1
RecName: Full=Potassium-transporting ATPase alpha chain 1; AltName: Full=Gastric H(+)/K(+) ATPase subunit alpha; AltName: Full=Proton pump	281	281	63%	1e-75	29%	Q64436.3
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Chlorocebus sabaeus]	281	281	64%	1e-75	31%	XP_007974711.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
calcium-transporting P-type ATPase [Magnaporthiopsis poae ATCC 64411]	281	281	70%	1e-75	29%	KLU85304.1
Na,H/K antiporter P-type ATPase, alpha subunit [Ancylostoma ceylanicum]	281	281	65%	1e-75	30%	EPB68404.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Eptesicus fuscus]	281	281	63%	1e-75	30%	XP_008138041.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Rattus norvegicus]	280	280	71%	1e-75	29%	XP_017454251.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Thamnophis sirtalis]	278	278	64%	1e-75	30%	XP_013927230.1
ATPase and Haloacid dehalogenase hydrolase domain containing protein [Haemonchus contortus]	280	280	65%	1e-75	30%	CDJ90668.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Papio anubis]	280	280	64%	1e-75	31%	XP_003892961.1
calcium-transporting P-type ATPase-like protein [Phialocephala scopiformis]	281	281	70%	1e-75	29%	XP_018073049.1
hypothetical protein B456_004G024800 [Gossypium raimondii]	280	280	64%	1e-75	30%	KJB21991.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Colobus angolensis palliatus]	280	280	64%	1e-75	31%	XP_011813047.1
uncharacterized protein Dyak_GE14534 [Drosophila yakuba]	280	280	71%	1e-75	28%	XP_002099569.2
SNaK1 [Schistosoma mansoni]	280	280	69%	1e-75	29%	AAL09322.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Chlorocebus sabaeus]	280	280	64%	2e-75	31%	XP_007974710.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Papio anubis]	280	280	64%	2e-75	31%	XP_009182958.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Zea mays]	277	277	60%	2e-75	30%	XP_008665351.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Macaca mulatta]	280	280	64%	2e-75	31%	XP_014968437.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase type 2C member 2 [Miniopterus natalensis]	276	276	61%	2e-75	32%	XP_016052563.1
P-type ATPase, cytoplasmic domain N [Pseudocohnilembus persalinus]	280	388	65%	2e-75	33%	KRW99833.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Cavia porcellus]	280	280	64%	2e-75	29%	XP_013004586.1
ATPase, Na+/K+ transporting, alpha 4 polypeptide [Rattus norvegicus]	280	280	71%	2e-75	29%	AAH87015.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Galeopterus variegatus]	280	280	64%	2e-75	29%	XP_008584088.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Ceratosolen solmsi marchali]	280	280	65%	2e-75	30%	XP_011503956.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Macaca nemestrina]	280	280	64%	2e-75	31%	XP_011768359.1
hypothetical protein SPRG_00285 [Saprolegnia parasitica CBS 223.65]	283	283	74%	2e-75	28%	XP_012193777.1
Na P-type ATPase [Marchantia polymorpha]	279	279	70%	2e-75	28%	CAX27437.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Myotis brandtii]	280	280	65%	2e-75	30%	XP_005857831.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X3 [Hippocampus comes]	276	276	56%	2e-75	31%	XP_019738167.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Macaca fascicularis]	280	280	64%	2e-75	31%	XP_015310366.1
hypothetical protein g.17427 [Homalodisca liturata]	277	277	64%	2e-75	30%	JAS81760.1
hypothetical protein SNOG_02911 [Parastagonospora nodorum SN15]	280	280	72%	2e-75	29%	XP_001793504.1
H+/K+-transporting nongastric ATPase alpha polypeptide [Scotophilus kuhlii]	273	273	64%	2e-75	30%	ADI40575.1
sodium/potassium-transporting ATPase subunit alpha-4 [Rattus norvegicus]	280	280	71%	2e-75	29%	NP_074039.1
Na+/K+ ATPase alpha subunit [Halocaridina rubra]	280	280	64%	2e-75	30%	AIM43570.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein O988_00643 [Pseudogymnoascus sp. VKM F-3808]	280	280	70%	2e-75	28%	KFY04651.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Mus musculus]	275	275	61%	2e-75	32%	XP_006531407.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Cebus capucinus imitator]	280	280	64%	2e-75	30%	XP_017359129.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-1 [Dasypus novemcinctus]	279	279	65%	2e-75	30%	XP_012375036.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium hirsutum]	277	277	63%	3e-75	31%	XP_016745492.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2 isoform X3 [Eptesicus fuscus]	277	277	62%	3e-75	31%	XP_008140926.1
sarcoplasmic/endoplasmic reticulum calcium ATPase [Paramecium tetraurelia]	275	275	50%	3e-75	32%	AAC05375.1
hypothetical protein AXG93_1881s1000 [Marchantia polymorpha subsp. polymorpha]	280	280	73%	3e-75	28%	OAE27810.1
hypothetical protein XELAEV_18035220mg [Xenopus laevis]	280	280	68%	3e-75	29%	OCT72250.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Rhinopithecus roxellana]	280	280	64%	3e-75	31%	XP_010359069.1
potassium/sodium eff [Auricularia subglabra TFB-10046 SS5]	280	280	65%	3e-75	29%	XP_007336566.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Corvus brachyrhynchos]	278	278	71%	3e-75	29%	XP_017596221.1
hydrogen/potassium-exchanging ATPase 12A b [Xenopus laevis]	280	280	68%	3e-75	29%	NP_001079596.1
Hypothetical protein CBG01656 [Caenorhabditis briggsae]	279	279	67%	3e-75	29%	XP_002634104.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X2 [Gossypium raimondii]	280	280	64%	3e-75	30%	XP_012473061.1
Na+/K+ ATPase alpha subunit isoform 1 [Halocaridina rubra]	279	279	64%	4e-75	30%	AIM43571.1
ATPase, Na+/K+ transporting, alpha 1 polypeptide [Strongyloides ratti]	278	278	65%	4e-75	30%	CEF63551.1
Calcium-transporting ATPase 3 [Wallemia ichthyophaga EXF-994]	280	280	71%	4e-75	29%	XP_009268654.1
hypothetical protein A3Q56_03462 [Intoshia linei]	280	280	65%	4e-75	30%	OAF68794.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Rhinopithecus bieti]	279	279	64%	4e-75	31%	XP_017720344.1
P-type ATPase [Dictyostelium lacteum]	281	281	70%	4e-75	29%	KYQ89383.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X1 [Gossypium raimondii]	280	280	64%	4e-75	30%	XP_012473060.1
hypothetical protein B456_004G024800 [Gossypium raimondii]	280	280	64%	4e-75	30%	KJB21993.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Cercocebus atys]	279	279	64%	4e-75	31%	XP_011923048.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Mandrillus leucophaeus]	279	279	64%	4e-75	31%	XP_011825784.1
Putative Calcium ATPase [Rhizopus microsporus]	273	273	51%	4e-75	32%	CEG75031.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii E566]	280	280	72%	5e-75	28%	KIY37106.1
Potassium-transporting ATPase alpha chain 1 [Tupaia chinensis]	279	279	64%	5e-75	29%	ELV09366.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii NT-10]	280	280	72%	5e-75	28%	KJE00815.1
calcium-transporting P-type ATPase [Microdochium bolleyi]	279	279	69%	5e-75	28%	KXJ85988.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Carlito syrichta]	279	279	64%	6e-75	29%	XP_008069182.1
unnamed protein product [Oikopleura dioica]	278	278	70%	6e-75	29%	CBY23627.1
secretory pathway Ca2+-ATPase [Xylona heveae TC161]	279	279	70%	6e-75	29%	XP_018187906.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Cercocebus atys]	279	279	64%	6e-75	31%	XP_011923047.1

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hypothetical protein KAFR_0B01960 [Kazachstania africana CBS 2517]	277	277	49%	6e-75	34%	XP_003955629.1
calcium-transporting ATPase 3 [Cryptococcus gattii WM276]	279	279	72%	6e-75	28%	XP_003191525.1
sodium/potassium-transporting ATPase subunit alpha-4 [Cricetulus griseus]	283	628	65%	7e-75	31%	ERE72877.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X4 [Pelodiscus sinensis]	275	275	70%	8e-75	31%	XP_014434868.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii Ru294]	279	279	72%	8e-75	28%	KIR53769.1
hypothetical protein B456_004G024800 [Gossypium raimondii]	279	279	64%	8e-75	30%	KJB21984.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Scleropages formosus]	278	278	69%	8e-75	28%	XP_018582433.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 2 [Ochotona princeps]	280	280	66%	8e-75	29%	XP_012782237.1
proton pump alpha subunit-like [Scleropages formosus]	278	278	69%	8e-75	28%	KPP74416.1
hypothetical protein SCHCODRAFT_75697 [Schizophyllum commune H4-8]	279	279	73%	8e-75	29%	XP_003033035.1
hypothetical protein B456_004G024800 [Gossypium raimondii]	279	279	64%	8e-75	30%	KJB21983.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Gorilla gorilla gorilla]	278	278	64%	8e-75	31%	XP_018880750.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Camelina sativa]	278	370	72%	9e-75	32%	XP_010487820.1
Na,H/K antiporter P-type ATPase alpha subunit family protein [Tetrahymena thermophila SB210]	280	280	65%	9e-75	29%	XP_001015374.1
Calcium-transporting ATPase type 2C member 1 [Larimichthys crocea]	281	281	71%	9e-75	29%	KKF32356.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Stegastes partitus]	278	278	69%	1e-74	28%	XP_008275275.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X1 [Propithecus coquereli]	272	272	47%	1e-74	34%	XP_012519717.1
Calcium-transporting ATPase 4, endoplasmic reticulum-type [Anthurium amnicola]	279	364	65%	1e-74	34%	JAT50309.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Nanorana parkeri]	277	277	63%	1e-74	29%	XP_018424265.1
hypothetical protein [Paramecium tetraurelia strain d4-2]	278	376	64%	1e-74	34%	XP_001447148.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Acinonyx jubatus]	278	278	65%	1e-74	30%	XP_014931688.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella patagoniensis]	271	271	48%	1e-74	34%	KRY13466.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X2 [Propithecus coquereli]	271	271	47%	1e-74	34%	XP_012519722.1
P-type II D ATPase [Mortierella elongata AG-77]	273	273	59%	1e-74	31%	OAQ33185.1
Pmr1p [Saccharomyces cerevisiae FostersB]	273	273	62%	1e-74	33%	EGA58724.1
Protein CBG01656 [Caenorhabditis briggsae]	277	277	67%	1e-74	29%	CAP22963.2
hypothetical protein B456_004G024800 [Gossypium raimondii]	278	278	64%	2e-74	30%	KJB21990.1
unnamed protein product [Oikopleura dioica]	277	277	70%	2e-74	29%	CBY30656.1
hypothetical protein PRUPE_ppa000629mg [Prunus persica]	278	278	47%	2e-74	35%	XP_007208423.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Ochotona princeps]	277	277	65%	2e-74	30%	XP_004589131.1
Na+/K+_ATPase [Palaemon carinicauda]	276	276	64%	2e-74	30%	AFM54541.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X3 [Salmo salar]	274	274	62%	2e-74	30%	XP_014047346.1
putative Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Glarea lozoyensis 74030]	270	270	50%	2e-74	34%	EHK98091.1
hypothetical protein Y032_0027g1554 [Ancylostoma ceylanicum]	276	276	69%	3e-74	29%	EYC18506.1

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PREDICTED: potassium-transporting ATPase alpha chain 1 [Lates calcarifer]	276	276	69%	3e-74	28%	XP_018545168.1
Ca2+-translocating ATPase, putative; high affinity Ca2+/Mn2+ P-type ATPase, putative [Candida dubliniensis CD36]	275	275	71%	3e-74	30%	XP_002421273.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii VGIV IND107]	277	277	72%	3e-74	28%	KIR86671.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-4 [Balaenoptera acutorostrata scammoni]	276	276	65%	3e-74	30%	XP_007171840.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Pan paniscus]	276	276	64%	3e-74	30%	XP_003811939.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Pan troglodytes]	276	276	64%	3e-74	30%	XP_016785786.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Camelina sativa]	277	277	64%	4e-74	30%	XP_010443383.1
hypothetical protein PANDA_021268 [Ailuropoda melanoleuca]	276	276	67%	4e-74	29%	EFB23830.1
calcium-transporting P-type ATPase [Diaporthe helianthi]	277	277	70%	4e-74	29%	OCW40171.1
hypothetical protein PV08_10083 [Exophiala spinifera]	276	276	65%	4e-74	30%	XP_016231000.1
sarcoplasmic-endoplasmic reticulum calcium ATPase [Tritrichomonas foetus]	275	275	64%	4e-74	31%	OHT02611.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Condylura cristata]	276	276	64%	4e-74	29%	XP_004688430.1
hypothetical protein ARB_05061 [Trichophyton benhamiae CBS 112371]	276	276	72%	4e-74	29%	XP_003016768.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Ceratosolen solmsi marchali]	276	276	64%	5e-74	30%	XP_011503963.1
unnamed protein product [Albugo candida]	279	279	64%	5e-74	29%	CCI45657.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like [Jatropha curcas]	276	276	65%	5e-74	30%	XP_012080805.1
Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type [Trichinella patagoniensis]	270	270	48%	5e-74	34%	KRY13463.1
hypothetical protein JCGZ_16227 [Jatropha curcas]	276	276	65%	6e-74	30%	KDP30671.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Condylura cristata]	275	275	64%	6e-74	29%	XP_004688431.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like isoform X2 [Brassica napus]	276	367	67%	6e-74	34%	XP_013695901.1
Sodium/potassium-transporting ATPase subunit alpha-3 [Corvus brachyrhynchos]	273	273	71%	7e-74	29%	KFO62953.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Erythranthe guttata]	276	368	64%	7e-74	35%	XP_012827834.1
calcium-transporting atpase type 2c member 1 [Colletotrichum orbiculare MAFF 240422]	276	276	70%	7e-74	28%	ENH78248.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Tetranychus urticae]	275	275	71%	7e-74	30%	XP_015784858.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Felis catus]	277	277	65%	7e-74	30%	XP_019676928.1
putative P-type ATPase4 [Toxoplasma gondii MAS]	261	261	23%	7e-74	59%	KFH12402.1
uncharacterized protein Dsimw501_GD19691, isoform B [Drosophila simulans]	272	272	70%	7e-74	28%	XP_016033146.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X2 [Microtus ochrogaster]	275	275	64%	7e-74	29%	XP_005361278.1
sodium/potassiumtransporting ATPase subunit alpha2 precursor putative [Albugo laibachii Nc14]	278	278	64%	7e-74	29%	CCA16430.1
endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis thaliana]	271	271	47%	7e-74	34%	AAD29957.1
PREDICTED: calcium-transporting ATPase type 2C member 1 isoform X4 [Amyelois transitella]	269	269	57%	8e-74	30%	XP_013188613.1
putative P-type ATPase4 [Toxoplasma gondii p89]	256	256	25%	8e-74	44%	KFG32002.1
Ca2+ transporting ATPase [Klebsormidium flaccidum]	276	362	66%	8e-74	35%	GAQ82464.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Daucus carota subsp. sativus]	275	375	69%	9e-74	33%	XP_017233217.1

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hypothetical protein M569_13311 [Genlisea aurea]	275	372	71%	1e-73	33%	EPS61486.1
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus gattii VGII R265]	276	276	72%	1e-73	28%	KGB75548.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Thamnophis sirtalis]	271	271	61%	1e-73	30%	XP_013921119.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type isoform X2 [Brassica oleracea var. oleracea]	275	368	67%	1e-73	34%	XP_013604458.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Pantholops hodgsonii]	274	274	71%	1e-73	29%	XP_005980427.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Musa acuminata subsp. malaccensis]	275	275	47%	1e-73	35%	XP_009392704.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Miniopterus natalensis]	275	275	65%	1e-73	30%	XP_016070203.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Maylandia zebra]	275	275	64%	1e-73	29%	XP_004541463.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Pundamilia nyererei]	275	275	64%	1e-73	29%	XP_005738678.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Hydra vulgaris]	275	275	65%	1e-73	30%	XP_012560801.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Haplochromis burtoni]	275	275	64%	1e-73	29%	XP_005937605.1
ECA4 [Arabidopsis thaliana]	275	367	67%	1e-73	34%	OAP15076.1
sodium/potassium-transporting ATPase subunit alpha [Saprolegnia diclina VS20]	278	278	72%	1e-73	27%	XP_008607481.1
PREDICTED: potassium-transporting ATPase alpha chain 1 [Oreochromis niloticus]	274	274	64%	1e-73	29%	XP_003450965.1
calcium-transporting ATPase [Verticillium alfalfae VaMs.102]	275	275	72%	1e-73	27%	XP_003004940.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Vigna angularis]	275	275	64%	1e-73	31%	XP_017410398.1
calcium-transporting ATPase 1 [Coccidioides immitis H538.4]	275	275	71%	2e-73	28%	KMU83425.1
PREDICTED: potassium-transporting ATPase alpha chain 1-like [Neolamprologus brichardi]	274	274	64%	2e-73	29%	XP_006801541.1
calcium-transporting ATPase type 2C member 1 [Cordyceps militaris CM01]	275	275	71%	2e-73	28%	XP_006671426.1
hypothetical protein PISMIDRAFT_121226 [Pisolithus microcarpus 441]	275	275	74%	2e-73	30%	KIK12236.1
potassium/sodium efflux P-type ATPase, fungal-type [Kwoniella heveanensis BCC8398]	275	275	70%	2e-73	28%	OCF34901.1
calcium/mangenease P-type ATPase [Scheffersomyces stipitis CBS 6054]	272	272	71%	2e-73	30%	XP_001386754.2
Na+/K+-ATPase alpha subunit [Carcinus maenas]	271	271	64%	2e-73	29%	AAK62046.1
hypothetical protein B456_009G220900 [Gossypium raimondii]	271	271	60%	2e-73	30%	KJB58675.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Amborella trichopoda]	275	358	65%	2e-73	35%	XP_006850677.1
GM10716 [Drosophila sechellia]	272	272	69%	2e-73	28%	XP_002038269.1
endomembrane-type CA-ATPase 4 [Arabidopsis thaliana]	274	366	72%	2e-73	32%	NP_172246.3
Sodium/potassium-transporting ATPase subunit alpha [Toxocara canis]	273	273	64%	3e-73	29%	KHN82508.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Brassica oleracea var. oleracea]	274	367	67%	3e-73	34%	XP_013585383.1
calcium-transporting ATPase 3, endoplasmic reticulum-type-like [Dorcoceras hygrometricum]	274	274	66%	3e-73	28%	KZV54526.1
hypothetical protein UVI_02035570 [Ustilaginoidea virens]	273	273	70%	3e-73	29%	GAO14004.1
calcium-transporting ATPase type 2C member 1 [Ustilaginoidea virens]	274	274	70%	3e-73	29%	KDB14784.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X3 [Nannospalax galili]	273	273	64%	3e-73	29%	XP_008826247.1
hypothetical protein B456_002G252900 [Gossypium raimondii]	271	367	68%	3e-73	34%	KJB16884.1
Na+,K+ ATPase alpha-subunit 2 [Cyrtepistomus castaneus]	273	273	64%	3e-73	28%	AFU25672.1

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uncharacterized protein Dsimw501_GD19691, isoform A [Drosophila simulans]	273	273	74%	3e-73	27%	XP_002102073.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T9]	273	273	65%	4e-73	29%	KRX56876.1
Sodium/potassium-transporting ATPase subunit alpha [Orchesella cincta]	273	273	71%	4e-73	27%	ODM98837.1
ECA1 [Arabidopsis thaliana]	273	368	67%	4e-73	34%	OAP12923.1
Na,H/K antiporter P-type ATPase alpha subunit family protein [Tetrahymena thermophila SB210]	275	275	69%	4e-73	29%	XP_001014798.2
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Vigna radiata var. radiata]	274	274	64%	5e-73	30%	XP_014508576.1
Calcium-transporting ATPase 1 [Phialophora attae]	272	272	64%	5e-73	31%	XP_018000141.1
predicted protein [Physcomitrella patens]	273	374	72%	5e-73	32%	XP_001778955.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Camelina sativa]	273	273	64%	5e-73	29%	XP_010451807.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4-like [Dipodomys ordii]	272	272	65%	5e-73	30%	XP_012885947.1
Sodium/potassium-transporting ATPase subunit alpha [Schistosoma haematobium]	270	270	61%	6e-73	31%	XP_012796364.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X5 [Myotis brandtii]	270	270	63%	6e-73	30%	XP_014383658.1
hypothetical protein SERLADRAFT_447402 [Serpula lacrymans var. lacrymans S7.9]	273	273	68%	7e-73	29%	XP_007316319.1
potassium/sodium efflux P-type ATPase, fungal-type [Kwoniella dejecticola CBS 10117]	273	273	70%	7e-73	29%	XP_018266144.1
PREDICTED: potassium-transporting ATPase alpha chain 2 isoform X5 [Myotis davidii]	270	270	63%	7e-73	30%	XP_015420329.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like isoform X3 [Ictalurus punctatus]	272	272	61%	7e-73	29%	XP_017317366.1
Na+/K+ ATPase alpha subunit [Callinectes sapidus]	273	273	64%	7e-73	29%	AAG47843.1
Calcium-transporting ATPase 1 [Choanephora cucurbitarum]	270	270	73%	7e-73	29%	OBZ90941.1
ER-type Ca2+-ATPase 1 [Arabidopsis thaliana]	273	367	67%	8e-73	34%	NP_172259.1
Sodium/potassium-transporting ATPase subunit alpha-4 [Myotis davidii]	271	271	65%	8e-73	29%	ELK38498.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X4 [Brassica oleracea var. oleracea]	269	269	60%	8e-73	30%	XP_013587666.1
sarco/endoplasmic reticulum calcium-translocating P-type ATPase [Tetrahymena thermophila SB210]	272	272	48%	8e-73	33%	XP_001030432.2
hypothetical protein CICLE_v10027724mg [Citrus clementina]	273	369	70%	9e-73	33%	XP_006424716.1
hypothetical protein CARUB_v10008142mg [Capsella rubella]	273	365	72%	9e-73	32%	XP_006306624.1
sodium-potassium-activated adenosine triphosphatase alpha subunit C isoform [Pachygrapsus marmoratus]	272	272	64%	9e-73	30%	ABA02167.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella spiralis]	272	272	65%	9e-73	29%	KRY31168.1
calcium-transporting P [Stagonospora sp. SRC1lsM3a]	272	272	72%	1e-72	29%	OAL01404.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type [Arachis duranensis]	271	271	71%	1e-72	28%	XP_015935073.1
calcium transporter ATPase [Aureobasidium melanogenum CBS 110374]	272	272	72%	1e-72	28%	KEQ58957.1
alpha subunit of putative Na+/K+ ATPase [Daphnia pulex]	271	271	69%	1e-72	29%	EFX71105.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Camelina sativa]	272	363	72%	1e-72	32%	XP_010457963.1
putative calcium-transporting p-type atpase [Diplodia seriata]	272	272	72%	1e-72	28%	KKY24222.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Myotis davidii]	271	271	65%	1e-72	29%	XP_006752901.1
Ca2+-transporting ATPase [Exophiala aquamarina CBS 119918]	271	271	63%	2e-72	30%	XP_013257018.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
P-ATPase family transporter: calcium ion [Ostreococcus lucimarinus CCE9901]	271	271	48%	2e-72	33%	XP_001415608.1
Calcium-transporting ATPase 4, endoplasmic reticulum-type [Anthurium amnicola]	271	362	67%	2e-72	34%	JAT56907.1
endomembrane Ca2+ ATPase 4 [Arabidopsis thaliana]	271	363	72%	2e-72	32%	ABJ90443.1
putative Calcium-transporting ATPase [Zostera marina]	271	374	67%	2e-72	34%	KMZ63623.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Amborella trichopoda]	271	361	66%	2e-72	34%	XP_006851877.2
calcium-transporting ATPase [Coprinopsis cinerea okayama7#130]	271	271	73%	2e-72	29%	XP_001830557.2
hypothetical protein NDAI_0G03610 [Naumovozyma dairenensis CBS 421]	270	346	66%	2e-72	34%	XP_003671381.2
hypothetical protein LRAMOSA00615 [Lichtheimia ramosa]	269	269	71%	2e-72	29%	CDS03213.1
hypothetical protein [Absidia glauca]	270	270	60%	2e-72	30%	SAL96127.1
hypothetical protein AMTR_s00041p00115630 [Amborella trichopoda]	271	361	66%	2e-72	34%	ERN13344.1
potassium/sodium efflux P-type ATPase, fungal-type [Kwoniella bestiolae CBS 10118]	272	272	70%	2e-72	28%	XP_019048189.1
hypothetical protein CNA05130 [Cryptococcus neoformans var. neoformans JEC21]	271	271	72%	2e-72	28%	XP_566813.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Tarenaya hassleriana]	271	363	67%	3e-72	34%	XP_010557282.1
P-type ATPase [Dictyostelium discoideum AX4]	271	271	65%	3e-72	30%	XP_647420.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X4 [Panthera pardus]	271	271	63%	3e-72	30%	XP_019288728.1
hypothetical protein MYCTH_2294253 [Thermothelomyces thermophila ATCC 42464]	271	271	70%	3e-72	27%	XP_003658462.1
Pc22g08540 [Penicillium rubens Wisconsin 54-1255]	271	271	72%	3e-72	29%	XP_002564866.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Colobus angolensis palliatus]	268	268	62%	4e-72	31%	XP_011813048.1
P-type ATPase [Dictyostelium fasciculatum]	272	272	69%	4e-72	29%	XP_004352438.1
calcium-transporting P-type ATPase [Colletotrichum gloeosporioides Cg-14]	271	271	70%	4e-72	28%	EQB48772.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Myotis lucifugus]	270	270	65%	4e-72	29%	XP_006096963.1
calcium-transporting ATPase type 2C member 1 [Aschersonia aleyrodis RCEF 2490]	270	270	63%	6e-72	29%	OAA33026.1
hypothetical protein Y032_0027g1554 [Ancylostoma ceylanicum]	270	270	69%	6e-72	29%	EYC18507.1
hypothetical transcript [Hymenolepis microstoma]	265	265	56%	9e-72	31%	CUU99269.1
CBN-EAT-6 protein [Caenorhabditis brenneri]	268	268	65%	9e-72	28%	EGT55546.1
calcium-transporting P-type ATPase, putative [Coccidioides posadasii C735 delta SOWgp]	270	270	71%	1e-71	29%	XP_003066127.1
potassium sodium efflux p-type fungal-type [Fusarium langsethiae]	270	270	73%	1e-71	26%	KPA38203.1
alpha subunit of putative Na+/K+ ATPase [Daphnia pulex]	268	268	71%	1e-71	28%	EFX88361.1
calcium-transporting ATPase 1 [Coccidioides posadasii RMSCC 3488]	270	270	71%	1e-71	29%	KMM65524.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Sesamum indicum]	269	269	47%	1e-71	34%	XP_011089395.1
potassium/sodium eff [Cylindrobasidium torrendii FP15055 ss-10]	269	269	73%	1e-71	27%	KIY72345.1
Na,H/K antiporter P-type ATPase alpha subunit family protein [Tetrahymena thermophila SB210]	270	270	64%	1e-71	29%	XP_001023740.1
hypothetical protein SORBIDRAFT_01g038990 [Sorghum bicolor]	269	269	53%	1e-71	32%	XP_002465447.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Glycine max]	265	265	60%	1e-71	29%	XP_014629950.1
calcium-transporting P-type ATPase-like protein [Cenococcum geophilum 1.58]	269	269	70%	2e-71	28%	OCK94358.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Tarenaya hassleriana]	269	269	62%	2e-71	30%	XP_010536881.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
predicted protein [Physcomitrella patens]	269	365	72%	2e-71	32%	XP_001765945.1
Hypothetical protein CBG19651 [Caenorhabditis briggsae]	268	268	68%	2e-71	28%	XP_002634668.1
Sodium/potassium-transporting ATPase subunit alpha [Caenorhabditis elegans]	268	268	65%	2e-71	29%	NP_506269.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Brassica napus]	268	363	67%	2e-71	34%	XP_013750567.1
ATPase, H+/K+ exchanging, gastric, alpha polypeptide, isoform CRA_a [Mus musculus]	268	268	63%	2e-71	29%	EDL23994.1
predicted protein [Fibroporia radiculosa]	267	267	73%	2e-71	29%	XP_012178229.1
Calcium-transporting ATPase [Giardia intestinalis]	269	269	70%	2e-71	29%	ESU39117.1
Plasma membrane calcium-transporting ATPase 2 [Giardia intestinalis assemblage B]	269	269	73%	2e-71	29%	KWX14404.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Solanum lycopersicum]	265	265	60%	2e-71	30%	XP_019070375.1
calcium-transporting P-type ATPase, PMR1-type [Pseudogymnoascus sp. 23342-1-I1]	268	268	70%	3e-71	28%	OBT61699.1
HAD ATPase, P-type, family IC [Coccidioides immitis RS]	268	268	71%	3e-71	29%	XP_001247232.1
hypothetical protein CICLE_v10003326mg [Citrus clementina]	268	268	64%	3e-71	29%	XP_006432655.1
calcium mangenease p-type [Diplodia corticola]	268	268	72%	3e-71	28%	OJD32586.1
calcium-transporting atpase type 2c member 1 [Colletotrichum gloeosporioides Nara gc5]	268	268	60%	3e-71	29%	XP_007278587.1
Calcium-transporting ATPase [Giardia intestinalis]	268	268	73%	3e-71	29%	ESU43533.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Beta vulgaris subsp. vulgaris]	268	365	65%	3e-71	34%	XP_010685850.1
hypothetical protein THITE_2121031 [Thielavia terrestris NRRL 8126]	268	268	70%	3e-71	28%	XP_003656427.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Oryza brachyantha]	265	265	47%	3e-71	34%	XP_006651260.2
putative Calcium-transporting ATPase [Zostera marina]	268	354	65%	3e-71	34%	KMZ75146.1
hypothetical protein PANDA_009759 [Ailuropoda melanoleuca]	266	266	64%	4e-71	29%	EFB29866.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type-like [Citrus sinensis]	267	267	64%	4e-71	30%	XP_006471461.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like isoform X1 [Brassica napus]	268	359	67%	4e-71	33%	XP_013695900.1
hypothetical protein PV06_06524 [Exophiala oligosperma]	267	267	72%	4e-71	29%	XP_016261133.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium hirsutum]	267	366	67%	5e-71	34%	XP_016743674.1
sodium potassium ATPase subunit A isoform 1 [Pachycara brachycephalum]	261	261	48%	5e-71	33%	ACF33473.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X8 [Oreochromis niloticus]	265	352	59%	5e-71	33%	XP_019206977.1
hypothetical protein AXG93_4492s1310 [Marchantia polymorpha subsp. polymorpha]	268	268	65%	5e-71	30%	OAE28240.1
hypothetical protein V498_05473 [Pseudogymnoascus sp. VKM F-4517 (FW-2822)]	271	271	70%	5e-71	28%	KFY91389.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Maylandia zebra]	266	348	65%	6e-71	33%	XP_004571310.1
potassium-transporting ATPase alpha chain 1 isoform 2 [Mus musculus]	266	266	63%	6e-71	29%	NP_061201.2
hypothetical protein V496_06518 [Pseudogymnoascus sp. VKM F-4515 (FW-2607)]	271	271	70%	6e-71	28%	KFY57244.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X7 [Oreochromis niloticus]	265	350	59%	6e-71	33%	XP_019206976.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Brassica napus]	267	361	67%	6e-71	33%	XP_013696365.1
hypothetical protein VOLCADRAFT_84661 [Volvox carteri f. nagariensis]	267	267	48%	6e-71	32%	XP_002958852.1
hypothetical protein g.41369 [Cuerna arida]	260	260	49%	6e-71	32%	JAS66005.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X5 [Haplochromis burtoni]	266	348	59%	7e-71	33%	XP_014193912.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type isoform X1 [Brassica oleracea var. oleracea]	267	360	67%	7e-71	34%	XP_013604455.1
hypothetical protein AYO20_08076 [Fonsecaea nubica]	266	266	70%	8e-71	30%	OAL31683.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Gossypium arboreum]	266	364	67%	8e-71	34%	XP_017606090.1
Calcium-transporting ATPase, endoplasmic reticulum-type [Gossypium arboreum]	266	364	67%	8e-71	34%	KHG03262.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Brassica rapa]	266	358	67%	9e-71	33%	XP_009147075.1
sodium/potassium-transporting ATPase subunit alpha-1 [Fundulus heteroclitus]	266	347	59%	1e-70	34%	NP_001296942.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Haplochromis burtoni]	266	348	59%	1e-70	33%	XP_005937374.1
hypothetical protein Z517_06942 [Fonsecaea pedrosoi CBS 271.37]	266	266	70%	1e-70	30%	XP_013284135.1
putative calcium-transporting atpase type 2c member 1 protein [Phaeoacremonium minimum UCRPA7]	270	270	63%	1e-70	29%	XP_007910917.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-3; Short=Na(+)/K(+) ATPase alpha-3 subunit; AltName: Full=Na(+)/K(+) ATPase alpha(III) subunit; AltName: Full=Sodium pump subunit alpha-3	265	265	65%	1e-70	29%	P58312.1
hypothetical protein TanjilG_16163 [Lupinus angustifolius]	266	266	64%	1e-70	30%	OIV97402.1
Calcium-transporting ATPase 1 [Diplodia seriata]	264	264	64%	1e-70	30%	OMP84984.1
calcium-transporting ATPase 3 [Trichosporon asahii var. asahii CBS 2479]	265	265	63%	1e-70	29%	XP_014179098.1
hypothetical protein PISMIDRAFT_96153 [Pisolithus microcarpus 441]	266	266	73%	1e-70	29%	KIK25798.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Gossypium raimondii]	266	362	66%	1e-70	34%	XP_012468366.1
Na,K-ATPase alpha subunit [Caenorhabditis elegans]	265	265	65%	1e-70	29%	AAB02615.1
hypothetical protein CISIN_1g001751mg [Citrus sinensis]	265	265	47%	2e-70	33%	KDO73014.1
PREDICTED: LOW QUALITY PROTEIN: potassium-transporting ATPase alpha chain 1 [Ailuropoda melanoleuca]	266	266	64%	2e-70	29%	XP_019657036.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella zimbabwensis]	266	266	65%	2e-70	28%	KRZ11378.1
calcium-transporting ATPase 8, plasma membrane-type protein [Medicago truncatula]	266	266	64%	2e-70	30%	XP_013454581.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Sesamum indicum]	266	356	66%	2e-70	35%	XP_011089397.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Malus domestica]	266	375	65%	2e-70	34%	XP_008369823.1
hypothetical protein A6R68_12667 [Neotoma lepida]	265	265	64%	2e-70	28%	OBS72796.1
hypothetical protein V495_07613 [Pseudogymnoascus sp. VKM F-4514 (FW-929)]	265	265	70%	2e-70	28%	KFY36777.1
hypothetical protein ASPVEDRAFT_136200 [Aspergillus versicolor CBS 583.65]	266	266	72%	2e-70	29%	OJJ04547.1
calcium pump1 [Zea mays]	265	265	57%	2e-70	31%	NP_001104922.2
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Lupinus angustifolius]	266	266	64%	2e-70	30%	XP_019417350.1
calcium transporting ATPase type 2C member [Echinococcus multilocularis]	265	332	69%	2e-70	32%	CUT98796.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Brassica napus]	265	355	67%	2e-70	33%	XP_013716271.1
hypothetical protein GPECTOR_46g261 [Gonium pectorale]	265	265	48%	2e-70	33%	KXZ46192.1
calcium pump1 [Zea mays]	262	262	48%	2e-70	34%	AFW82813.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 [Ursus maritimus]	264	264	65%	2e-70	31%	XP_008698923.1
hypothetical protein SBOR_4979 [Sclerotinia borealis F-4128]	266	266	63%	3e-70	30%	ESZ94632.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Scleropages formosus]	265	347	59%	3e-70	32%	XP_018603204.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X3 [Condylura cristata]	262	262	61%	3e-70	30%	XP_004688432.1
calcium-transporting P-type ATPase, PMR1-type [Pseudogymnoascus destructans 20631-21]	265	265	70%	3e-70	28%	XP_012744561.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Cucumis sativus]	265	265	65%	3e-70	29%	XP_004150387.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Oreochromis niloticus]	265	348	59%	3e-70	33%	XP_003446597.2
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Cucumis melo]	265	265	65%	3e-70	29%	XP_008450934.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-1; Short=Na(+)/K(+) ATPase alpha-1 subunit; AltName: Full=Sodium pump subunit alpha-1; Flags: Precursor	264	342	59%	4e-70	33%	Q9YH26.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Oryctolagus cuniculus]	264	264	62%	4e-70	31%	XP_008262461.1
Na+/K+ ATPase alpha-1a [Galaxias maculatus]	257	257	47%	4e-70	34%	AFM73918.1
Na+/K+ ATPase [Amphiprion melanopus]	259	259	48%	4e-70	33%	ADO60023.1
putative calcium-transporting atpase type 2c member 1-like isoform x1 [Nyssomyia neivai]	257	257	47%	4e-70	31%	JAV04936.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Gossypium hirsutum]	265	361	66%	4e-70	34%	XP_016687351.1
calcium transporting ATPase type 2C member [Echinococcus granulosus]	263	329	69%	4e-70	32%	CDS18096.1
unnamed protein product [Homo sapiens]	257	257	48%	4e-70	32%	BAG53671.1
sodium/potassium-transporting ATPase alpha-1 subunit [Oreochromis urolepis hornorum]	264	347	59%	5e-70	33%	AGO02179.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X1 [Carlito syrichta]	261	261	62%	5e-70	30%	XP_008056912.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Raphanus sativus]	264	360	68%	5e-70	34%	XP_018438349.1
calcium-transporting P-type ATPase-like protein [Glonium stellatum]	264	264	70%	6e-70	28%	OCL08573.1
putative calcium-transporting atpase type 2c member 1-like isoform x1 [Nyssomyia neivai]	256	256	47%	6e-70	31%	JAV04937.1
hypothetical protein A1Q2_02466 [Trichosporon asahii var. asahii CBS 8904]	264	264	69%	7e-70	29%	EKD03245.1
hypothetical protein M408DRAFT_240164 [Serendipita vermifera MAFF 305830]	265	265	65%	7e-70	28%	KIM31882.1
Na+ K+ ATPase alpha subunit [Homo sapiens]	258	258	59%	7e-70	30%	AAA51803.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Arachis ipaensis]	264	264	47%	8e-70	33%	XP_016208007.1
sodium/potassium-transporting ATPase subunit alpha-1 [Trichuris suis]	261	261	65%	8e-70	29%	KHJ49479.1
hypothetical protein A6R68_04597 [Neotoma lepida]	261	261	65%	8e-70	29%	OBS66873.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type isoform X2 [Vigna radiata var. radiata]	263	370	66%	9e-70	34%	XP_014524131.1
hypothetical protein PFL1_04558 [Anthracocystis flocculosa PF-1]	265	377	66%	9e-70	31%	XP_007880275.1
hypothetical protein AYO21_01229 [Fonsecaea monophora]	263	263	70%	1e-69	30%	OAG44739.1
Na+/K+-ATPase alpha-subunit 1 [Periophthalmodon schlosseri]	263	349	59%	1e-69	33%	AGR87393.1
Calcium-transporting ATPase 4, endoplasmic reticulum-type [Ananas comosus]	263	353	72%	1e-69	32%	OAY72139.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type isoform X2 [Ricinus communis]	260	260	60%	1e-69	30%	XP_015575061.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-1-like [Acropora digitifera]	263	263	63%	1e-69	30%	XP_015764548.1
Calcium-transporting ATPase 4, endoplasmic reticulum-type [Ananas comosus]	263	353	65%	1e-69	34%	OAY71267.1
hypothetical protein SORBIDRAFT_09g001850 [Sorghum bicolor]	263	263	54%	1e-69	31%	XP_002440489.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Sinocyclocheilus grahami]	262	348	59%	1e-69	32%	XP_016110639.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type isoform X1 [Vigna radiata var. radiata]	263	370	66%	1e-69	34%	XP_014524129.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala mesophila]	264	391	69%	1e-69	30%	XP_016227148.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Arachis ipaensis]	263	367	66%	1e-69	33%	XP_016181699.1
calcium-transporting ATPase 1 [Saitoella complicata NRRL Y-17804]	261	261	73%	2e-69	28%	XP_019021221.1
endoplasmic reticulum-type calcium-transporting ATPase [Coccomyxa subellipsoidea C-169]	263	263	48%	2e-69	34%	XP_005652084.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-4 isoform X2 [Carlito syrichta]	260	260	62%	2e-69	30%	XP_008056913.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Hippocampus comes]	262	346	59%	2e-69	33%	XP_019712111.1
Ca2+-transporting ATPase [Exophiala dermatitidis NIH/UT8656]	263	263	72%	2e-69	27%	XP_009160341.1
BnaC05g07470D [Brassica napus]	259	259	57%	2e-69	30%	CDX94924.1
Atp1a3 protein [Mus musculus]	257	257	48%	2e-69	32%	AAH27000.1
Na+/K+-ATPase alpha-subunit 1c1 [Electrophorus electricus]	262	349	65%	2e-69	33%	AJR20270.1
Cation transporting ATPase [Caenorhabditis elegans]	262	262	66%	2e-69	28%	NP_504328.1
ATPase [Loa loa]	261	261	64%	2e-69	28%	EJD75689.1
sodium/potassium-transporting ATPase alpha-1 subunit [Oreochromis mossambicus x niloticus]	262	345	59%	2e-69	33%	AGZ87948.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Vigna angularis]	262	370	66%	2e-69	34%	XP_017405823.1
probable calcium P-type ATPase [Claviceps purpurea 20.1]	262	262	60%	3e-69	30%	CCE31343.1
sodium transport atpase [Moniliophthora roreri MCA 2997]	259	259	57%	3e-69	30%	XP_007856566.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Gossypium arboreum]	262	358	66%	3e-69	34%	XP_017622826.1
Plasma membrane calcium-transporting ATPase [Spironucleus salmonicida]	262	262	72%	3e-69	28%	EST46418.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Arachis duranensis]	262	262	47%	3e-69	33%	XP_015969915.1
Plasma membrane calcium-transporting ATPase 2 [Giardia lamblia ATCC 50803]	262	262	67%	3e-69	29%	XP_001708564.1
probable Calcium-transporting ATPase 1 [Hanseniaspora guilliermondii]	260	260	49%	3e-69	32%	SGZ37944.1
hypothetical protein V494_01643 [Pseudogymnoascus sp. VKM F-4513 (FW-928)]	265	265	70%	3e-69	28%	KFY44068.1
hypothetical protein cypCar_00042003 [Cyprinus carpio]	260	345	59%	3e-69	33%	KTF83352.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Maylandia zebra]	261	345	59%	4e-69	33%	XP_004571308.1
Cation-transporting P-type ATPase [Cynara cardunculus var. scolymus]	261	349	59%	4e-69	36%	KVI12001.1
Cation transporting ATPase [Caenorhabditis elegans]	261	261	66%	4e-69	28%	NP_001309616.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pundamilia nyererei]	261	345	59%	4e-69	33%	XP_005749507.1
hypothetical protein ZTR_06701 [Talaromyces verruculosus]	262	383	64%	4e-69	31%	KUL84631.1
sodium potassium enzyme subunit alpha 1b [Scatophagus argus]	261	346	59%	4e-69	32%	AHB86584.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X2 [Lupinus angustifolius]	262	262	64%	4e-69	29%	XP_019417352.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-1; Short=Na(+)/K(+) ATPase alpha-1 subunit; AltName: Full=Sodium pump subunit alpha-1; Flags: Precursor	261	346	59%	4e-69	33%	P25489.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Sinocyclocheilus rhinocerous]	261	347	59%	5e-69	32%	XP_016429447.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein HMPREF1541_05382 [Cyphellophora europaea CBS 101466]	261	261	72%	5e-69	29%	XP_008717944.1
putative P-type ATPase [Oryza sativa Japonica Group]	256	256	48%	5e-69	32%	AAO38471.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Vollenhovia emeryi]	260	260	67%	5e-69	28%	XP_011883537.1
hypothetical protein [Paramecium tetraurelia strain d4-2]	263	263	66%	6e-69	29%	XP_001423444.1
Sodium/potassium-transporting ATPase subunit alpha [Papilio xuthus]	259	259	66%	6e-69	28%	KPI97351.1
hypothetical protein V492_01767 [Pseudogymnoascus sp. VKM F-4246]	265	265	70%	7e-69	27%	KFY15768.1
P-type ATPase [Talaromyces cellulolyticus]	261	381	64%	8e-69	31%	GAM41775.1
sodium/potassium-transporting ATPase subunit alpha-1 [Danio rerio]	260	345	59%	8e-69	33%	NP_571765.1
hypothetical protein Z520_05467 [Fonsecaea multimorphosa CBS 102226]	261	387	66%	8e-69	31%	XP_016633129.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Sinocyclocheilus anshuiensis]	260	345	59%	1e-68	33%	XP_016300217.1
Sodium/potassium-transporting ATPase alpha-3 chain protein [Daphnia magna]	260	260	70%	1e-68	27%	JAN65680.1
hypothetical protein MANES_18G047600 [Manihot esculenta]	256	256	60%	1e-68	30%	OAY23049.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Scleropages formosus]	260	347	59%	1e-68	32%	XP_018613803.1
hypothetical protein PHSY_003817 [Pseudozyma hubeiensis SY62]	263	387	68%	1e-68	31%	XP_012189824.1
hypothetical protein GUITHDRAFT_158817 [Guillardia theta CCMP2712]	259	352	63%	1e-68	33%	XP_005821433.1
TPA: hypothetical protein ZEAMMB73_784521 [Zea mays]	258	258	48%	1e-68	32%	DAA51163.1
p-type calcium ATPase [Sporothrix insectorum RCEF 264]	261	261	60%	1e-68	29%	OAA60991.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like isoform X2 [Musa acuminata subsp. malaccensis]	258	258	48%	1e-68	32%	XP_018678780.1
hypothetical protein G7K_4025-t1 [Saitoella complicata NRRL Y-17804]	260	260	71%	1e-68	28%	GAO49888.1
hypothetical protein PABG_01233 [Paracoccidioides brasiliensis Pb03]	260	260	72%	2e-68	28%	EEH18914.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Lepisosteus oculatus]	259	345	59%	2e-68	33%	XP_006639434.1
Calcium-transporting ATPase 12, plasma membrane-type [Morus notabilis]	259	259	64%	2e-68	30%	XP_010102299.1
hypothetical protein PADG_03808 [Paracoccidioides brasiliensis Pb18]	260	260	72%	2e-68	28%	XP_010759609.1
hypothetical protein GX48_06455 [Paracoccidioides brasiliensis]	260	260	72%	2e-68	28%	ODH47419.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Scleropages formosus]	259	344	58%	2e-68	33%	XP_018603205.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Salmo salar]	259	339	58%	2e-68	33%	XP_014007631.1
hypothetical protein PaG_02734 [Moesziomyces aphidis DSM 70725]	260	382	66%	2e-68	32%	ETS62965.1
hypothetical protein ACO22_01876 [Paracoccidioides brasiliensis]	259	259	72%	2e-68	28%	ODH39419.1
GL24999 [Drosophila persimilis]	252	252	47%	2e-68	33%	XP_002021118.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Thamnophis sirtalis]	256	256	60%	3e-68	31%	XP_013927231.1
hypothetical protein TSUD_350500 [Trifolium subterraneum]	259	359	67%	3e-68	33%	GAU47185.1
probable ENA2-Plasma membrane P-type ATPase [Melanopsichium pennsylvanicum 4]	260	371	66%	3e-68	32%	CDI52611.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Salmo salar]	259	339	58%	3e-68	33%	XP_014007630.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Sinocyclocheilus grahami]	258	344	59%	3e-68	32%	XP_016110637.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like [Glycine max]	259	358	73%	4e-68	32%	XP_003554341.1
hypothetical protein M514_01462 [Trichuris suis]	261	261	65%	4e-68	29%	KFD65483.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala sideris]	258	258	65%	4e-68	29%	KIV82167.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Eucalyptus grandis]	259	357	64%	4e-68	34%	XP_010043634.1
hypothetical protein AYO22_05152 [Fonsecaea multimorphosa]	261	387	66%	4e-68	31%	OAL25275.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like isoform X2 [Papilio xuthus]	257	257	66%	5e-68	28%	XP_013172407.1
putative P-type ATPase [Leishmania braziliensis MHOM/BR/75/M2904]	259	259	66%	6e-68	29%	XP_001563826.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Rattus norvegicus]	251	251	55%	6e-68	32%	XP_008770818.1
sodium potassium ATPase subunit alpha 1 short isoform [Amphibalanus improvisus]	258	350	65%	6e-68	31%	AGZ13695.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Prunus mume]	258	319	59%	6e-68	30%	XP_008223854.1
hypothetical protein ASPSYDRAFT_45789 [Aspergillus sydowii CBS 593.65]	258	258	72%	6e-68	29%	OJJ57845.1
Ca2+ transporting ATPase [Moesziomyces antarcticus T-34]	258	379	66%	7e-68	31%	GAC76706.1
P-type ATPase, putative [Leishmania guyanensis]	258	258	66%	7e-68	29%	CCM14304.1
hypothetical protein MANES_11G137000 [Manihot esculenta]	258	355	66%	7e-68	34%	OAY37891.1
hypothetical protein g.675 [Cuerna arida]	248	248	47%	7e-68	32%	JAS48016.1
hypothetical protein Ccrd_009747 [Cynara cardunculus var. scolymus]	259	304	55%	7e-68	32%	KVI11821.1
P-type ATPase, putative [Leishmania panamensis]	257	257	66%	7e-68	29%	XP_010697747.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Lupinus angustifolius]	258	353	68%	8e-68	33%	XP_019444380.1
unnamed protein product [Oikopleura dioica]	253	253	48%	8e-68	30%	CBY14695.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Vitis vinifera]	258	354	67%	8e-68	33%	XP_002284552.1
sodium potassium ATPase alpha subunit [Rhabdosargus sarba]	257	346	59%	9e-68	32%	AAT48993.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X2 [Populus euphratica]	258	258	64%	9e-68	30%	XP_011020086.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X1 [Populus euphratica]	258	258	64%	9e-68	30%	XP_011020078.1
hypothetical protein VITISV_034639 [Vitis vinifera]	257	354	67%	1e-67	33%	CAN79679.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus anshuiensis]	257	343	59%	1e-67	32%	XP_016355526.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pygocentrus nattereri]	257	340	59%	1e-67	32%	XP_017550811.1
Na+-exporting ATPase [Exophiala aquamarina CBS 119918]	258	377	69%	1e-67	29%	XP_013266376.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Tursiops truncatus]	253	253	65%	1e-67	29%	XP_019795800.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type [Cicer arietinum]	258	258	64%	1e-67	30%	XP_012573108.1
BnaA06g05910D [Brassica napus]	258	258	62%	1e-67	30%	CDX93457.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Scleropages formosus]	256	350	64%	1e-67	32%	XP_018613812.1
hypothetical protein AXG93_1998s1100 [Marchantia polymorpha subsp. polymorpha]	258	354	68%	1e-67	34%	OAE21873.1
hypothetical protein T265_13488 [Opisthorchis viverrini]	258	336	73%	1e-67	28%	XP_009167367.1
hypothetical protein FPOA_00511 [Fusarium poae]	257	257	70%	1e-67	28%	OBS26568.1
Na+/K+-ATPase alpha 1a3b subunit [Solea senegalensis]	256	340	59%	2e-67	32%	BAN17692.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Scleropages formosus]	256	339	59%	2e-67	32%	XP_018594835.1

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calcium-transporting P-type ATPase-like protein [Lepidopterella palustris CBS 459.81]	257	257	70%	2e-67	28%	OCK79935.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Cynoglossus semilaevis]	256	337	59%	2e-67	32%	XP_008321044.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Cynoglossus semilaevis]	255	337	59%	2e-67	32%	XP_008321045.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like [Juglans regia]	257	257	64%	2e-67	29%	XP_018847260.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Clupea harengus]	255	342	59%	2e-67	33%	XP_012673740.1
potassium/sodium efflux P-type ATPase, fungal-type [Rhinocladiella mackenziei CBS 650.93]	256	256	65%	2e-67	29%	XP_013270721.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Pongo abelii]	250	250	47%	2e-67	33%	XP_002826752.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Cynoglossus semilaevis]	256	338	59%	2e-67	32%	XP_008321046.1
Calcium-transporting ATPase 1 [Zancudomyces culisetae]	259	346	71%	2e-67	30%	OMH79210.1
calcium-transporting P-type ATPase, PMR1-type [Pseudogymnoascus sp. WSF 3629]	256	256	72%	3e-67	27%	OBT45019.1
P-Type II D ATPase [Rhizophagus intraradices]	252	252	55%	3e-67	32%	CAJ42021.1
Calcium-transporting ATPase type 2C member 1 [Cariama cristata]	250	250	58%	3e-67	31%	KFP64796.1
hypothetical protein Z520_05584 [Fonsecaea multimorphosa CBS 102226]	256	256	70%	3e-67	29%	XP_016632406.1
sodium potassium ATPase subunit alpha 1 long isoform [Amphibalanus improvisus]	256	350	65%	3e-67	31%	AGZ13694.1
calcium-translocating P-type ATPase [Mitosporidium daphniae]	255	255	48%	3e-67	33%	XP_013236565.1
predicted protein [Arabidopsis lyrata subsp. lyrata]	256	256	64%	3e-67	28%	XP_002866184.1
Na+-exporting ATPase [Xylona heveae TC161]	256	382	66%	4e-67	30%	XP_018190425.1
Calcium-transporting ATPase, endoplasmic reticulum-type [Cajanus cajan]	256	360	72%	4e-67	31%	KYP54666.1
calcium-transporting ATPase 1 [Fusarium graminearum PH-1]	256	256	70%	4e-67	27%	XP_011316182.1
hypothetical protein CTHT_0049790 [Chaetomium thermophilum var. thermophilum DSM 1495]	256	368	66%	4e-67	32%	XP_006695331.1
hypothetical protein PENARI_c011G04556 [Penicillium arizonense]	255	255	72%	5e-67	28%	OGE52221.1
hypothetical protein PHAVU_003G140200g [Phaseolus vulgaris]	256	256	64%	5e-67	30%	XP_007154697.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Cariama cristata]	250	250	58%	5e-67	31%	XP_009698027.1
calcium-transporting P-type ATPase [Colletotrichum tofieldiae]	258	258	70%	5e-67	27%	KZL73920.1
calcium-transporting ATPase 1 (Golgi Ca(2+)-ATPase) [Pyrenophora tritici-repentis Pt-1C-BFP]	253	253	47%	5e-67	32%	XP_001942035.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type isoform X2 [Beta vulgaris subsp. vulgaris]	255	255	64%	5e-67	29%	XP_010687434.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type isoform X1 [Beta vulgaris subsp. vulgaris]	255	255	64%	6e-67	29%	XP_010687432.1
Calcium-transporting ATPase 10, plasma membrane-type [Morus notabilis]	256	256	64%	6e-67	29%	XP_010094240.1
secretory pathway Ca2+-ATPase [Histoplasma capsulatum H88]	255	255	72%	6e-67	27%	EGC46392.1
hypothetical protein A1O7_07186 [Cladophialophora yegresii CBS 114405]	256	380	66%	6e-67	30%	XP_007759376.1
P-type II D ATPase [Rhizophagus intraradices]	251	251	55%	7e-67	32%	CAJ42022.1
calcium-transporting P-type ATPase, PMR1-type [Pseudogymnoascus sp. 03VT05]	255	255	70%	7e-67	27%	OBT85699.1
calcium-transporting ATPase type 2C member 1 [Metarhizium rileyi RCEF 4871]	255	255	70%	7e-67	28%	OAA48668.1
hypothetical protein BN946_scf184940.g30 [Trametes cinnabarina]	256	256	64%	7e-67	29%	CDO71883.1

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Calcium-transporting ATPase 1, endoplasmic reticulum-type [Dichanthelium oligosanthes]	254	254	48%	7e-67	33%	OEL26074.1
PREDICTED: calcium-transporting ATPase type 2C member 1-like [Bemisia tabaci]	250	250	59%	8e-67	30%	XP_018897640.1
hypothetical protein EUTSA_v10012523mg [Eutrema salsugineum]	254	254	64%	9e-67	29%	XP_006401243.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-1-like [Notothenia coriiceps]	254	341	59%	9e-67	32%	XP_010794637.1
Ca2+-transporting ATPase [Capronia coronata CBS 617.96]	254	254	72%	9e-67	28%	XP_007723616.1
potassium/sodium efflux P-type ATPase, fungal-type [Capronia semi-immersa]	255	379	66%	1e-66	31%	KIW65341.1
Na/K ATPase alpha subunit isoform 1b [Oncorhynchus mykiss]	254	334	58%	1e-66	33%	NP_001117932.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X1 [Ipomoea nil]	254	254	64%	1e-66	29%	XP_019177913.1
hypothetical protein MANES_06G017700 [Manihot esculenta]	254	254	64%	1e-66	29%	OAY46668.1
Ca2+-transporting ATPase [Angomonas deanei]	246	246	48%	1e-66	31%	EPY32060.1
Calcium-transporting ATPase 8, plasma membrane-type [Noccaea caerulescens]	254	254	65%	1e-66	28%	JAU19103.1
similar to P-type ATPase [Botrytis cinerea T4]	255	370	66%	1e-66	31%	CCD34821.1
hypothetical protein SELMODRAFT_451600 [Selaginella moellendorffii]	254	254	64%	1e-66	30%	XP_002973134.1
Plasma membrane calcium-transporting ATPase [Spironucleus salmonicida]	254	254	67%	1e-66	30%	EST45438.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Brachypodium distachyon]	254	308	59%	1e-66	31%	XP_003580413.1
calcium-transporting P-type ATPase, PMR1-type [Pseudogymnoascus sp. 24MN13]	254	254	70%	1e-66	27%	OBT54644.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type [Populus euphratica]	254	347	67%	1e-66	33%	XP_011041968.1
hypothetical protein EUTSA_v10012523mg [Eutrema salsugineum]	254	254	64%	2e-66	29%	XP_006401244.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like isoform X1 [Tarenaya hassleriana]	254	350	67%	2e-66	33%	XP_010521805.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Xiphophorus maculatus]	253	337	59%	2e-66	32%	XP_005798792.1
putative sodium/potassium-transporting ATPase subunit alpha-1 [Dictyocaulus viviparus]	249	249	58%	2e-66	30%	KJH48096.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Prunus mume]	253	253	47%	2e-66	34%	XP_016651383.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Saccoglossus kowalevskii]	253	347	59%	2e-66	34%	XP_006819726.1
Na+/K+ transporting ATPase subunit alpha K01539 sodium/potassium-transporting ATPase subunit alpha [Clonorchis sinensis]	253	352	64%	2e-66	33%	GAA27822.2
hypothetical protein BC1G_15342 [Botrytis cinerea B05.10]	254	369	66%	2e-66	31%	XP_001546156.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like isoform X1 [Raphanus sativus]	249	249	49%	2e-66	31%	XP_018439995.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Poecilia latipinna]	253	337	59%	2e-66	32%	XP_014891522.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Poecilia mexicana]	253	337	59%	2e-66	32%	XP_014842623.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Poecilia latipinna]	253	337	59%	2e-66	32%	XP_014891520.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Poecilia mexicana]	253	337	59%	2e-66	32%	XP_014842624.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Anoplophora glabripennis]	253	336	59%	2e-66	31%	XP_018565491.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Papilio machaon]	252	252	70%	2e-66	27%	XP_014368845.1

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Sodium/potassium-transporting ATPase subunit alpha [Papilio machaon]	251	251	66%	3e-66	28%	KPJ07193.1
hypothetical protein AOL_s00080g160 [Arthrobotrys oligospora ATCC 24927]	253	373	67%	3e-66	30%	XP_011122837.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X2 [Ipomoea nil]	253	253	64%	3e-66	29%	XP_019177916.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X1 [Gossypium arboreum]	253	253	64%	3e-66	29%	XP_017626008.1
Endoplasmic reticulum [ER]-type calcium ATPase isoform 2 [Theobroma cacao]	250	346	66%	3e-66	33%	EOY34194.1
Na/K ATPase alpha subunit isoform 1c [Oncorhynchus mykiss]	253	337	58%	3e-66	32%	NP_001117931.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X2 [Gossypium arboreum]	253	253	64%	3e-66	29%	XP_017626009.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Oryza brachyantha]	253	253	64%	3e-66	29%	XP_015695930.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Poecilia formosa]	252	337	59%	3e-66	32%	XP_007550277.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Poecilia formosa]	252	337	59%	3e-66	32%	XP_007550278.1
hypothetical protein g.28854 [Cuerna arida]	250	332	61%	3e-66	31%	JAS51304.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Glycine max]	253	253	64%	3e-66	30%	XP_003533744.1
hypothetical protein SS1G_10477 [Sclerotinia sclerotiorum 1980]	253	370	66%	4e-66	31%	XP_001588929.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Ictalurus punctatus]	252	334	59%	4e-66	32%	XP_017336848.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T6]	252	340	64%	4e-66	32%	KRX84808.1
calcium-transporting P-type ATPase [Colletotrichum fioriniae PJ7]	252	252	70%	4e-66	27%	XP_007593664.1
calcium-transporting ATPase 1 [Arthroderma otae CBS 113480]	252	252	72%	4e-66	28%	XP_002846925.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nelsoni]	252	321	64%	4e-66	32%	KRX24044.1
p-type atpase sodium involved in na+ and li+ efflux to allow salt tolerance [Brettanomyces bruxellensis AWRI1499]	251	359	66%	5e-66	31%	EIF45506.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala spinifera]	253	374	69%	5e-66	29%	XP_016239862.1
hypothetical protein AYO22_05269 [Fonsecaea multimorphosa]	254	254	70%	5e-66	29%	OAL24933.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Oryzias latipes]	252	336	59%	5e-66	32%	XP_011483791.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Salmo salar]	252	332	58%	5e-66	33%	XP_014006213.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T6]	252	339	59%	5e-66	32%	KRX84806.1
Na,H/K antiporter P-type ATPase alpha subunit family protein [Tetrahymena thermophila SB210]	253	253	64%	5e-66	29%	XP_001033343.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella nelsoni]	252	339	59%	5e-66	32%	KRX24042.1
Na,H/K antiporter P-type ATPase alpha subunit family protein [Tetrahymena thermophila SB210]	253	253	67%	5e-66	29%	XP_001007458.3
calcium-transporting P-type ATPase [Colletotrichum higginsianum]	252	252	72%	5e-66	26%	CCF35042.1
hypothetical transcript [Hymenolepis microstoma]	249	249	48%	5e-66	32%	CUU99633.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Oryzias latipes]	251	336	59%	6e-66	32%	XP_004078051.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Aethina tumida]	251	340	64%	6e-66	31%	XP_019873687.1
putative calcium-transporting P-type ATPase [Colletotrichum sublineola]	252	252	70%	7e-66	26%	KDN61809.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
potassium/sodium efflux P-type ATPase, fungal-type [Allomyces macrogynus ATCC 38327]	251	340	63%	7e-66	32%	KNE56773.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X1 [Gossypium hirsutum]	252	252	64%	7e-66	29%	XP_016712524.1
calcium-transporting P-type ATPase [Colletotrichum orchidophilum]	252	252	72%	7e-66	25%	OHE95811.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X2 [Gossypium hirsutum]	252	252	64%	7e-66	29%	XP_016712525.1
Calcium-transporting ATPase 1 [Penicillium subrubescens]	251	251	72%	8e-66	28%	OKO95731.1
sodium/potassium-transporting ATPase subunit alpha-1 [Salpingoeca rosetta]	253	358	67%	8e-66	31%	XP_004990317.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Glycine max]	252	252	64%	8e-66	30%	XP_014623401.1
ATPase, P-type, calcium-transporting, PMCA-type [Metarhizium majus ARSEF 297]	253	253	63%	8e-66	29%	XP_014572309.1
sodium/potassium-transporting ATPase subunit alpha-1b [Oncorhynchus masou]	251	331	58%	9e-66	33%	BAJ13362.1
calcium-transporting p-type atpase [Ophiostoma piceae UAMH 11346]	252	252	47%	9e-66	32%	EPE06807.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Brassica rapa]	251	251	64%	9e-66	29%	XP_009126900.1
calcium-translocating P-type ATPase, PMCA-type [Pneumocystis murina B123]	253	253	64%	9e-66	30%	XP_019613300.1
hypothetical protein PV07_05785 [Cladophialophora immunda]	251	251	70%	1e-65	29%	XP_016250220.1
calcium-transporting P-type ATPase [Colletotrichum salicis]	251	251	70%	1e-65	26%	KXH67419.1
sodium transport ATPase 5 [Aspergillus udagawae]	251	360	66%	1e-65	31%	GAO83598.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Saccoglossus kowalevskii]	251	344	59%	1e-65	33%	XP_002737354.1
hypothetical protein POPTR_0006s07240g [Populus trichocarpa]	251	251	64%	1e-65	29%	XP_002309001.2
hypothetical protein FPSE_04413 [Fusarium pseudograminearum CS3096]	251	251	70%	1e-65	27%	XP_009255806.1
calcium-transporting P-type ATPase [Colletotrichum nymphaeae SA-01]	251	251	70%	1e-65	26%	KXH45442.1
ATPase, P-type, calcium-transporting, PMCA-type [Metarhizium brunneum ARSEF 3297]	253	253	63%	1e-65	30%	XP_014541422.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Pygocentrus nattereri]	251	338	59%	1e-65	32%	XP_017557418.1
calcium-translocating P-type ATPase, PMCA-type [Pneumocystis carinii B80]	253	253	67%	1e-65	28%	XP_018225174.1
Calcium-transporting ATPase 12, plasma membrane-type [Glycine soja]	251	251	65%	1e-65	29%	KHN02549.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Maylandia zebra]	250	333	59%	1e-65	32%	XP_004550930.1
secretory pathway Ca2+-ATPase [Histoplasma capsulatum G186AR]	251	251	72%	1e-65	27%	EEH11405.1
Calcium-transporting ATPase 3 [Cladophialophora carrionii]	251	377	66%	1e-65	30%	OCT48990.1
calcium-transporting ATPase 1 [Purpureocillium lilacinum]	251	251	60%	2e-65	28%	XP_018179609.1
hypothetical protein CHLNCDRAFT_6358 [Chlorella variabilis]	247	247	65%	2e-65	28%	XP_005849646.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Pundamilia nyererei]	250	338	64%	2e-65	33%	XP_005749512.1
CLUMA_CG008418, isoform A [Clunio marinus]	250	333	58%	2e-65	32%	CRK94927.1
Na+/K+ ATPase alpha-1c [Galaxias maculatus]	248	332	59%	2e-65	33%	AFM73917.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Brassica napus]	251	251	64%	2e-65	28%	XP_013673252.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type-like [Gossypium hirsutum]	251	347	66%	2e-65	33%	XP_016749099.1
hypothetical protein SELMODRAFT_451372 [Selaginella moellendorffii]	251	251	64%	2e-65	30%	XP_002976723.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia reticulata]	250	332	59%	2e-65	32%	XP_008421606.1
calcium-transporting P-type ATPase [Colletotrichum simmondsii]	250	250	70%	2e-65	26%	KXH39434.1
hypothetical protein CARUB_v10027891mg [Capsella rubella]	251	305	59%	2e-65	31%	XP_006281735.1
hypothetical protein H634G_07620 [Metarhizium anisopliae BRIP 53293]	252	252	63%	2e-65	29%	KJK77044.1
hypothetical protein EPUS_03768 [Endocarpon pusillum Z07020]	251	360	67%	2e-65	30%	XP_007805942.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Pundamilia nyererei]	249	333	59%	2e-65	32%	XP_005731899.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Arachis duranensis]	250	355	66%	2e-65	32%	XP_015947938.1
Calcium-transporting ATPase type 2C member 1 [Trichinella sp. T6]	248	334	65%	2e-65	31%	KRX77912.1
BnaC02g11860D [Brassica napus]	251	251	64%	2e-65	28%	CDY32902.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-4 [Tursiops truncatus]	249	249	65%	2e-65	30%	XP_019788037.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Brassica oleracea var. oleracea]	250	250	64%	3e-65	28%	XP_013620571.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Maylandia zebra]	249	333	59%	3e-65	32%	XP_004550929.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type-like [Glycine max]	250	250	65%	3e-65	29%	XP_006604467.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Dasypus novemcinctus]	243	243	46%	3e-65	32%	XP_004455984.1
Calcium-transporting ATPase type 2C member 1 [Schistosoma haematobium]	250	336	67%	3e-65	31%	XP_012792432.1
Putative Ca2-transporting ATPase [Aspergillus calidoustus]	250	250	71%	3e-65	28%	CEL04404.1
cation-transporting ATPase [Mucor ambiguus]	250	333	60%	3e-65	31%	GAN01257.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Fundulus heteroclitus]	245	245	48%	3e-65	32%	XP_012725726.1
probable ENA2-Plasma membrane P-type ATPase [Ustilago bromivora]	250	372	66%	3e-65	31%	SAM80842.1
BnaA02g08330D [Brassica napus]	250	250	64%	3e-65	28%	CDY20693.1
hypothetical protein PHAVU_010G116200g [Phaseolus vulgaris]	249	353	67%	3e-65	32%	XP_007135282.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia reticulata]	249	338	59%	3e-65	32%	XP_008421596.1
potassium/sodium efflux P-type ATPase, fungal-type [Cladophialophora carrionii CBS 160.54]	250	371	66%	3e-65	29%	XP_008725489.1
hypothetical protein g.11977 [Graphocephala atropunctata]	249	327	71%	3e-65	30%	JAT14413.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Clupea harengus]	249	335	59%	4e-65	32%	XP_012670902.1
hypothetical protein H072_1627 [Dactylellina haptotyla CBS 200.50]	249	367	67%	4e-65	30%	XP_011107619.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X2 [Ricinus communis]	249	249	64%	4e-65	29%	XP_015571849.1
hypothetical protein ACJ73_07304 [Blastomyces sp. CAC-2015b]	250	250	71%	4e-65	27%	OJD21355.1
hypothetical protein ASPFODRAFT_306828 [Aspergillus luchuensis CBS 106.47]	248	351	63%	4e-65	30%	OJZ83086.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia formosa]	249	338	59%	4e-65	32%	XP_016534895.1
calcium-transporting p-type atpase [Colletotrichum incanum]	252	252	70%	4e-65	27%	KZL82291.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X1 [Ricinus communis]	249	249	64%	4e-65	29%	XP_015571847.1
hypothetical protein PMKS-002959 [Pichia membranifaciens]	248	355	59%	4e-65	31%	GAV29459.1
hypothetical protein [Sporisorium scitamineum]	249	374	66%	5e-65	30%	CDS00015.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Poecilia mexicana]	249	330	59%	5e-65	32%	XP_014856541.1
Na+ or K+ P-type ATPase [Ustilago maydis]	249	371	66%	5e-65	31%	CAQ86600.1
hypothetical protein H310_07028 [Aphanomyces invadans]	251	330	60%	5e-65	30%	XP_008870525.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Pundamilia nyererei]	249	332	59%	5e-65	32%	XP_005731898.1
secretory pathway Ca2+-ATPase [Histoplasma capsulatum H143]	249	249	72%	5e-65	27%	EER39222.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea nubica]	249	370	66%	5e-65	30%	OAL35198.1
hypothetical protein MANES_18G047600 [Manihot esculenta]	244	244	50%	5e-65	31%	OAY23048.1
PREDICTED: calcium-transporting ATPase 4, endoplasmic reticulum-type-like isoform X2 [Tarenaya hassleriana]	249	346	67%	6e-65	33%	XP_010521806.1
sodium potassium ATPase alpha 1 subunit a1c [Esox lucius]	246	332	58%	6e-65	32%	AIB08910.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea pedrosoi CBS 271.37]	249	374	66%	6e-65	30%	XP_013287117.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha; Short=Na(+)/K(+) ATPase alpha subunit; AltName: Full=Sodium pump subunit alpha; AltName: Full=TNaK1-alpha	248	343	65%	6e-65	32%	Q6RWA9.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea monophora]	249	374	66%	6e-65	30%	OAG45631.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Poecilia formosa]	248	330	59%	6e-65	32%	XP_007560045.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Astyanax mexicanus]	248	332	59%	6e-65	31%	XP_007253156.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala oligosperma]	249	369	69%	7e-65	29%	XP_016268946.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala xenobiotica]	249	368	66%	7e-65	30%	XP_013316995.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Camelina sativa]	249	304	59%	7e-65	31%	XP_010483208.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia latipinna]	248	337	59%	7e-65	32%	XP_014907081.1
uncharacterized protein LOC100383276 [Zea mays]	241	241	48%	8e-65	30%	NP_001169407.1
E1-E2_ATPase domain-containing protein/Cation_ATPase_C domain-containing protein/Cation_ATPase_N domain-containing protein/Hydrolase domain-containing protein [Cephalotus follicularis]	248	248	64%	8e-65	29%	GAV71418.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Fragaria vesca subsp. vesca]	248	342	65%	8e-65	32%	XP_004306639.1
unnamed protein product [Aspergillus niger]	248	363	68%	8e-65	29%	CAL00329.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella sp. T9]	249	325	59%	8e-65	32%	KRX62116.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus rhinocerous]	248	334	59%	8e-65	32%	XP_016380304.1
sodium transport ATPase 5 [Aspergillus niger CBS 513.88]	248	368	68%	8e-65	29%	XP_001393393.2
potassium/sodium efflux P-type ATPase, fungal-type [Cladophialophora immunda]	249	361	66%	8e-65	30%	XP_016243125.1
unknown [Zea mays]	242	242	55%	1e-64	31%	ACR34999.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella patagoniensis]	249	323	59%	1e-64	32%	KRY10799.1
Ca2+-transporting ATPase [Sporothrix brasiliensis 5110]	248	248	47%	1e-64	31%	KIH91795.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Trichechus manatus latirostris]	246	333	59%	1e-64	31%	XP_004380412.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus anshuiensis]	248	333	59%	1e-64	32%	XP_016295959.1
hypothetical protein PICMEDRAFT_18434 [Pichia membranifaciens NRRL Y-2026]	248	354	59%	1e-64	31%	XP_019015284.1
hypothetical protein SBOR_10057 [Sclerotinia borealis F-4128]	249	348	69%	1e-64	30%	ESZ89557.1
sodium P-type ATPase [Aspergillus kawachii IFO 4308]	248	369	68%	1e-64	30%	GAA90254.1

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Na+/K+-ATPase alpha-subunit 3 [Electrophorus electricus]	248	331	59%	1e-64	31%	AJR20273.1
sodium potassium ATPase alpha 1 subunit a1-1 [Osmerus mordax]	245	331	59%	1e-64	32%	AIB08911.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like [Arachis duranensis]	248	248	64%	1e-64	29%	XP_015938019.1
PREDICTED: calcium-transporting ATPase type 2C member 1 [Phaethon lepturus]	243	243	58%	1e-64	31%	XP_010294588.1
hypothetical protein UA08_04800 [Talaromyces atroroseus]	248	350	59%	1e-64	30%	OKL59981.1
hypothetical protein PBRA_008806 [Plasmodiophora brassicae]	249	327	64%	1e-64	29%	CEP01863.1
CIC11C00000005842 [[Candida] intermedia]	248	353	67%	1e-64	31%	SGZ49448.1
hypothetical protein ASPBRDRAFT_138041 [Aspergillus brasiliensis CBS 101740]	248	370	68%	1e-64	29%	OJJ66388.1
hypothetical protein ASPSYDRAFT_49587 [Aspergillus sydowii CBS 593.65]	246	340	60%	1e-64	30%	OJJ54461.1
potassium/sodium efflux P-type ATPase, fungal-type [Rhinocladiella mackenziei CBS 650.93]	248	373	66%	1e-64	30%	XP_013268742.1
Na:K ATPase alpha subunit [Echinococcus granulosus]	247	342	65%	1e-64	32%	CDS22215.1
Sodium/potassium-transporting ATPase subunit alpha [Echinococcus granulosus]	247	342	65%	1e-64	32%	EUB57119.1
potassium/sodium efflux P-type ATPase, fungal-type [Spizellomyces punctatus DAOM BR117]	248	377	67%	2e-64	31%	XP_016606375.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Pygocentrus nattereri]	247	331	59%	2e-64	32%	XP_017563988.1
sodium transport ATPase 5 [Coccidioides immitis H538.4]	242	242	51%	2e-64	30%	KMU82353.1
CIC11C00000005421 [[Candida] intermedia]	248	352	67%	2e-64	30%	SGZ53135.1
ATPase, P-type, calcium-transporting, PMCA-type [Metarhizium guizhouense ARSEF 977]	249	249	63%	2e-64	29%	KID85861.1
Na:K ATPase alpha subunit [Echinococcus multilocularis]	247	342	65%	2e-64	32%	CDS36343.1
Calcium-transporting ATPase type 2C member 1 [Phaethon lepturus]	243	243	58%	2e-64	31%	KFQ70207.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea erecta]	248	369	66%	2e-64	31%	XP_018697150.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Notothenia coriiceps]	241	241	46%	2e-64	32%	XP_010782432.1
potassium/sodium efflux P-type ATPase, fungal-type [Capronia coronata CBS 617.96]	248	369	66%	2e-64	30%	XP_007724484.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Poecilia reticulata]	247	329	59%	2e-64	32%	XP_008421059.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Elaeis guineensis]	248	248	64%	2e-64	28%	XP_010928700.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X9 [Oreochromis niloticus]	246	330	59%	2e-64	32%	XP_019206978.1
Na+/K+ ATPase alpha 1b subunit isoform [Dicentrarchus labrax]	247	336	59%	2e-64	32%	AKQ12835.1
Putative Secretory pathway Ca2-ATPase [Penicillium brasilianum]	247	247	70%	2e-64	28%	CEJ59454.1
putative ENA2-plasma membrane P-type ATPase [Tilletiaria anomala UBC 951]	248	370	69%	2e-64	31%	XP_013243622.1
hypothetical protein EUGRSUZ_H04353 [Eucalyptus grandis]	246	246	67%	2e-64	29%	KCW61616.1
ATP4A [Beaufortia kweichowensis]	242	242	64%	2e-64	27%	AEQ38526.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus grahami]	246	333	59%	3e-64	32%	XP_016110238.1
hypothetical protein H257_15606 [Aphanomyces astaci]	249	328	60%	3e-64	31%	XP_009842069.1
sodium P-type ATPase [Aspergillus fumigatus Z5]	247	349	63%	3e-64	31%	KMK54685.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus rhinocerous]	246	332	59%	3e-64	32%	XP_016380412.1
hypothetical protein cypCar_00028622 [Cyprinus carpio]	246	332	59%	3e-64	32%	KTF75833.1
cation-transporting atpase plant, putative [Ricinus communis]	246	246	64%	3e-64	29%	EEF47971.1

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Calcium-transporting ATPase-like protein [Acremonium chrysogenum ATCC 11550]	247	247	70%	3e-64	26%	KFH43004.1
Calcium-transporting ATPase 1 [Hanseniaspora uvarum]	246	246	49%	3e-64	31%	OEJ84738.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Hippocampus comes]	246	334	59%	3e-64	32%	XP_019712110.1
PREDICTED: calcium-transporting ATPase 1, endoplasmic reticulum-type [Theobroma cacao]	247	343	66%	3e-64	34%	XP_007027146.2
PREDICTED: potassium-transporting ATPase alpha chain 1 [Rhinopithecus bieti]	241	241	47%	3e-64	31%	XP_017703077.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Trichechus manatus latirostris]	246	334	59%	3e-64	31%	XP_004380410.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase, endoplasmic reticulum-type [Erythranthe guttata]	246	341	67%	3e-64	32%	XP_012843886.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type [Eucalyptus grandis]	246	246	67%	3e-64	29%	XP_010025026.1
Protein CBG19651 [Caenorhabditis briggsae]	248	248	65%	4e-64	28%	CAP36858.2
Sodium/potassium-transporting ATPase subunit alpha [Trichinella spiralis]	246	333	59%	4e-64	32%	KRY33278.1
calcium-transporting ATPase 1 [Coccidioides immitis RMSCC 2394]	246	246	71%	4e-64	28%	KMP00916.1
sodium P-type ATPase [Aspergillus fumigatus Af293]	246	349	64%	4e-64	32%	XP_751881.1
sodium potassium ATPase alpha 1 subunit a1c [Salmo salar]	244	330	58%	4e-64	32%	AIB08902.1
Na+/K+ ATPase alpha subunit [Doryteuthis opalescens]	246	324	58%	4e-64	33%	ABO61333.1
P-type ATPase [Schizosaccharomyces cryophilus OY26]	244	326	67%	4e-64	32%	XP_013025584.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Trichechus manatus latirostris]	246	334	59%	4e-64	31%	XP_004380411.1
CLUMA_CG009717, isoform A [Clunio marinus]	246	324	58%	4e-64	32%	CRK96297.1
Calcium-transporting ATPase 3 [Talaromyces marneffei PM1]	246	350	59%	4e-64	31%	KFX48436.1
Atp1a1 protein [Mus musculus]	241	241	48%	4e-64	31%	AAH25037.1
sodium P-type ATPase, putative [Talaromyces islandicus]	246	356	65%	4e-64	31%	CRG87726.1
hypothetical protein cypCar_00026023 [Cyprinus carpio]	246	332	59%	4e-64	32%	KTF75784.1
hypothetical protein EUTSA_v10028380mg [Eutrema salsugineum]	246	348	67%	4e-64	33%	XP_006396324.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X2 [Tursiops truncatus]	242	242	62%	4e-64	30%	XP_019795808.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3-like [Lates calcarifer]	246	327	59%	5e-64	32%	XP_018529643.1
Na+/K+ ATPase alpha subunit [Doryteuthis pealeii]	246	323	58%	5e-64	33%	ABO61332.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Tursiops truncatus]	242	242	50%	5e-64	30%	XP_019791986.1
calcium-transporting P-type ATPase [Magnaporthe oryzae 70-15]	246	246	70%	5e-64	27%	XP_003709985.1
P-type ATPase 1 [Schwanniomyces occidentalis]	246	352	64%	5e-64	31%	AAB86426.1
endomembrane Ca2+ ATPase 2 [Arabidopsis thaliana]	242	242	47%	5e-64	33%	ABJ90444.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Apteryx australis mantelli]	241	241	48%	5e-64	31%	XP_013805558.1
putative Ca/Mn-transporting ATPase [Trichoderma virens Gv29-8]	246	246	71%	5e-64	27%	XP_013958976.1
Na+-exporting ATPase [Exophiala dermatitidis NIH/UT8656]	247	368	68%	5e-64	30%	XP_009160060.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium camemberti]	246	360	68%	5e-64	30%	CRL30688.1
sodium P-type ATPase, putative [Talaromyces marneffei ATCC 18224]	246	363	64%	5e-64	31%	XP_002151171.1
Calcium transporting ATPase [Klebsormidium flaccidum]	246	246	62%	5e-64	30%	GAQ91595.1
hypothetical protein ASPVEDRAFT_43703 [Aspergillus versicolor CBS 583.65]	244	244	66%	6e-64	28%	OJJ04243.1
ATP binding [Ascochyta rabiei]	246	246	71%	6e-64	28%	KZM19906.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X6 [Oreochromis niloticus]	245	329	65%	6e-64	32%	XP_005452413.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
Calcium-transporting ATPase 1 [Hanseniaspora uvarum DSM 2768]	245	245	49%	6e-64	31%	KKA03249.1
sodium/potassium-transporting ATPase alpha-1 subunit [Sarotherodon melanotheron]	245	329	59%	6e-64	32%	ADB03120.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus grahami]	245	331	59%	6e-64	32%	XP_016093485.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Scleropages formosus]	246	332	59%	6e-64	31%	XP_018613796.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Kryptolebias marmoratus]	245	329	59%	7e-64	32%	XP_017282391.1
Calcium-transporting ATPase 3 [Phialophora attae]	246	352	68%	7e-64	31%	XP_017998725.1
sodium transport atpase [Aspergillus fischeri NRRL 181]	245	357	67%	7e-64	30%	XP_001267067.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Ipomoea nil]	246	343	67%	7e-64	32%	XP_019184599.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Pundamilia nyererei]	245	327	59%	7e-64	32%	XP_005749511.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella britovi]	245	333	64%	7e-64	31%	KRY48181.1
potassium/sodium efflux P-type ATPase, fungal-type [Emmonsia sp. CAC-2015a]	244	244	53%	7e-64	29%	OAX80157.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Alligator mississippiensis]	242	242	58%	8e-64	30%	XP_019339701.1
potassium/sodium efflux P-type ATPase, fungal-type [Cladophialophora bantiana CBS 173.52]	246	370	66%	8e-64	30%	XP_016624095.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X5 [Oreochromis niloticus]	245	329	65%	8e-64	32%	XP_019206975.1
sodium transport ATPase 5 [Sphaerulina musiva SO2202]	246	342	64%	8e-64	30%	XP_016765699.1
Na+ or K+ P-type ATPase [Kalmanozyma brasiliensis GHG001]	246	373	68%	8e-64	30%	XP_016292687.1
unnamed protein product [Mus musculus]	241	241	48%	8e-64	31%	BAE29635.1
P-type Na+-ATPase [Ophiocordyceps sinensis CO18]	246	352	66%	8e-64	30%	EQK99186.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Oreochromis niloticus]	245	329	65%	9e-64	32%	XP_003446598.2
Na+/K+-ATPase alpha subunit [Litopenaeus stylirostris]	245	322	58%	9e-64	32%	AEX07319.1
hypothetical protein A4X13_g2619 [Tilletia indica]	246	342	64%	9e-64	30%	OAJ05162.1
Similar to Sodium transport ATPase 2; acc. no. Q01896 [Pyronema omphalodes CBS 100304]	246	359	67%	9e-64	29%	CCX08193.1
hypothetical protein ASPWEDRAFT_62805 [Aspergillus wentii DTO 134E9]	245	353	69%	1e-63	30%	OJJ30141.1
sodium/potassium-transporting ATPase alpha-1 subunit [Chanos chanos]	245	327	59%	1e-63	32%	ABF58911.1
sodium potassium ATPase alpha 1 subunit a1b [Salvelinus alpinus]	243	319	58%	1e-63	32%	AIB08900.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Xiphophorus maculatus]	244	327	59%	1e-63	31%	XP_005802906.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Brassica napus]	245	245	64%	1e-63	28%	XP_013684992.1
calcium-transporting P-type ATPase [Galdieria sulphuraria]	244	335	64%	1e-63	33%	XP_005704597.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X4 [Neolamprologus brichardi]	244	326	59%	1e-63	32%	XP_006792877.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X3 [Neolamprologus brichardi]	244	325	59%	1e-63	32%	XP_006792876.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Neolamprologus brichardi]	244	325	65%	1e-63	32%	XP_006792874.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Parasteatoda tepidariorum]	244	311	59%	1e-63	32%	XP_015930974.1
Calcium-transporting ATPase 3 [Smittium culicis]	244	355	65%	1e-63	33%	OMJ26537.1
hypothetical protein MIMGU_mgv1a000743mg [Erythranthe guttata]	244	302	60%	1e-63	31%	EYU18198.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Diachasma alloeum]	245	245	64%	1e-63	28%	XP_015113630.1
unnamed protein product [Coffea canephora]	242	242	64%	1e-63	28%	CDP12667.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
potassium/sodium efflux P-type ATPase [Diaporthe helianthi]	245	342	66%	2e-63	31%	OCW34286.1
sodium transport ATPase 5 [Aspergillus lentulus]	245	357	67%	2e-63	31%	GAQ08109.1
putative sodium P-type ATPase [Aspergillus bombycis]	244	358	64%	2e-63	31%	OGM42799.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Neolamprologus brichardi]	244	325	65%	2e-63	32%	XP_006792875.1
hypothetical protein A1O3_09259 [Capronia epimyces CBS 606.96]	245	368	66%	2e-63	31%	XP_007737543.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia formosa]	244	327	59%	2e-63	32%	XP_007567656.1
sodium potassium ATPase alpha 1 subunit a1b [Thymallus arcticus]	242	321	58%	2e-63	32%	AIB08904.1
hypothetical protein UA08_04996 [Talaromyces atroroseus]	244	343	59%	2e-63	31%	OKL59539.1
potassium/sodium efflux P-type ATPase, fungal-type [Cladophialophora immunda]	244	347	66%	2e-63	31%	XP_016252856.1
hypothetical protein ARAM_003675 [Aspergillus rambellii]	244	244	63%	2e-63	29%	KKK25632.1
sarcoplasmic/endoplasmic reticulum calcium ATPase, putative [Talaromyces stipitatus ATCC 10500]	244	358	64%	2e-63	30%	XP_002341868.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Callorhinchus milii]	244	327	59%	2e-63	31%	XP_007889793.1
Sodium-exporting ATPase [Rasamsonia emersonii CBS 393.64]	245	363	66%	2e-63	30%	XP_013326066.1
unnamed protein product [Oncorhynchus mykiss]	243	330	58%	2e-63	32%	CDQ89554.1
hypothetical protein AOCH_000562 [Aspergillus ochraceoroseus]	244	244	63%	2e-63	29%	KKK19866.1
type IIB Ca2+ATPase [Oryza sativa]	244	299	59%	2e-63	31%	AGW24530.1
Na+-exporting ATPase [Glonium stellatum]	244	363	65%	2e-63	29%	OCL02738.1
hypothetical protein A4X09_g2778 [Tilletia walkeri]	245	342	65%	2e-63	29%	OAJ18858.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium expansum]	244	355	69%	2e-63	30%	XP_016596764.1
Sodium/potassium-transporting ATPase subunit alpha [Stegodyphus mimosarum]	243	330	59%	2e-63	32%	KFM66853.1
KLTH0G17138p [Lachancea thermotolerans]	243	332	67%	2e-63	32%	XP_002555776.1
Na+,K+ ATPase alpha-subunit 2 [Aphis nerii]	244	244	54%	2e-63	29%	AFU25666.1
calcium ATPase [Gonapodya prolifera JEL478]	239	239	56%	2e-63	31%	KXS09138.1
hydrolase [Pristionchus pacificus]	236	236	50%	2e-63	30%	KKA79819.1
hypothetical protein Y1Q_0020807 [Alligator mississippiensis]	243	243	58%	2e-63	30%	KYO42508.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Salmo salar]	244	331	58%	2e-63	32%	XP_014006214.1
hypothetical protein ASPTUDRAFT_51510 [Aspergillus tubingensis CBS 134.48]	243	346	63%	2e-63	29%	OJI87858.1
putative sodium P-type ATPase [Aspergillus nomius NRRL 13137]	244	360	68%	2e-63	30%	XP_015403409.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Salmo salar]	244	331	58%	2e-63	32%	XP_014007633.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Erythranthe guttata]	244	302	60%	2e-63	31%	XP_012828723.1
sodium transport ATPase 5 [Kluyveromyces marxianus DMKU3-1042]	244	244	71%	2e-63	28%	BAO40226.1
hypothetical protein CANARDRAFT_26732 [Candida arabinofermentans NRRL YB-2248]	244	358	67%	2e-63	30%	ODV87324.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Chelonia mydas]	239	239	47%	2e-63	31%	XP_007062135.1
hypothetical protein DRE_01460 [Drechslerella stenobrocha 248]	244	355	63%	3e-63	31%	EWC43573.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Stegastes partitus]	243	327	59%	3e-63	31%	XP_008298212.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type-like [Populus euphratica]	243	243	64%	3e-63	30%	XP_011004262.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sodium potassium ATPase alpha 1 subunit a1b [Coregonus clupeaformis]	241	321	58%	3e-63	32%	AIB08906.1
calcium-transporting ATPase 1 [Magnaporthe oryzae Y34]	246	246	70%	3e-63	27%	ELQ36667.1
Na+/K+ -ATPase alpha 1 subunit [Danio rerio]	243	328	59%	3e-63	31%	NP_571761.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Cricetulus griseus]	239	298	55%	3e-63	31%	EGW05797.1
sodium P-type ATPase [Aspergillus niger]	244	358	68%	3e-63	30%	GAQ45806.1
TPA: hypothetical protein ZEAMMB73_748084 [Zea mays]	243	300	59%	3e-63	30%	DAA36132.1
probable ENA2-Plasma membrane P-type ATPase [Ustilago hordei]	244	365	66%	3e-63	30%	CCF53452.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Nothobranchius furzeri]	243	328	59%	3e-63	32%	XP_015802160.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Acyrthosiphon pisum]	243	243	54%	3e-63	29%	XP_008186677.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Oryza sativa Japonica Group]	244	298	59%	3e-63	30%	XP_015636669.1
ATPase, Na+/K+ transporting, alpha 1 polypeptide [Danio rerio]	243	327	59%	3e-63	31%	AAH45283.1
hypothetical protein Y1Q_0020807 [Alligator mississippiensis]	242	242	58%	3e-63	30%	KYO42509.1
hypothetical protein EUGRSUZ_F04017 [Eucalyptus grandis]	243	243	64%	3e-63	28%	KCW70887.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Latimeria chalumnae]	243	330	59%	3e-63	31%	XP_014347449.1
TPA: hypothetical protein ZEAMMB73_748084 [Zea mays]	243	299	59%	4e-63	30%	DAA36133.1
E1-E2_ATPase domain-containing protein/Cation_ATPase_C domain-containing protein/Cation_ATPase_N domain-containing protein/Hydrolase domain-containing protein/CaATP_NAI domain-containing protein [Cephalotus follicularis]	244	244	64%	4e-63	29%	GAV59710.1
PREDICTED: putative calcium-transporting ATPase 13, plasma membrane-type [Nicotiana tomentosiformis]	243	243	64%	4e-63	30%	XP_009613944.1
hypothetical protein AC578_4194 [Mycosphaerella eumusae]	243	345	67%	4e-63	30%	KXT02510.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Austrofundulus limnaeus]	243	327	59%	4e-63	32%	XP_013868866.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Austrofundulus limnaeus]	241	327	59%	4e-63	31%	XP_013874893.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Stegastes partitus]	243	327	59%	4e-63	31%	XP_008298215.1
hypothetical protein ACJ72_00130 [Emmonsia sp. CAC-2015a]	243	243	70%	4e-63	28%	OAX85498.1
hypothetical protein BN1723_000285 [Verticillium longisporum]	246	246	56%	4e-63	29%	CRK20433.1
sodium P-type ATPase-like protein [Cenococcum geophilum 1.58]	243	357	66%	4e-63	30%	OCK90761.1
calcium-transporting P-type ATPase, PMR1-type [Necator americanus]	239	239	56%	4e-63	31%	XP_013303535.1
P-type ATPase 2 [Schwanniomyces occidentalis]	243	363	67%	5e-63	30%	AAB86427.1
LADA_0F06678g1_1 [Lachancea dasiensis CBS 10888]	240	330	67%	5e-63	31%	SCU90837.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia latipinna]	243	325	59%	5e-63	32%	XP_014907082.1
hypothetical protein MYCFIDRAFT_149581 [Pseudocercospora fijiensis CIRAD86]	243	342	66%	5e-63	30%	XP_007921802.1
PREDICTED: potassium-transporting ATPase alpha chain 2 [Orcinus orca]	239	239	50%	5e-63	30%	XP_012392875.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Oryzias latipes]	243	326	65%	5e-63	32%	XP_004066575.1
Autoinhibited Ca(2+)-ATPase 9 isoform 3 [Theobroma cacao]	243	243	64%	5e-63	29%	EOY26434.1
Atp1a1 protein [Mus musculus]	242	330	59%	5e-63	31%	AAH10319.1
unnamed protein product [Mus musculus]	243	330	59%	5e-63	31%	BAE34957.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Ictalurus punctatus]	241	322	58%	5e-63	31%	XP_017312769.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Maylandia zebra]	243	330	59%	5e-63	31%	XP_004571307.1
ena2-plasma membrane p-type atpase [Malassezia pachydermatis]	243	349	66%	6e-63	29%	XP_017992933.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Diuraphis noxia]	242	242	54%	6e-63	30%	XP_015364998.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Cynoglossus semilaevis]	243	331	59%	6e-63	31%	XP_008322795.1
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Mus musculus]	243	330	59%	6e-63	31%	NP_659149.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Takifugu rubripes]	243	329	59%	6e-63	32%	XP_003966638.1
putative calcium-transporting atpase 3 [Diaporthe ampelina]	243	353	66%	6e-63	30%	KKY35508.1
Sodium transport ATPase 2 [Talaromyces islandicus]	245	352	72%	6e-63	29%	CRG92287.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Lates calcarifer]	242	326	59%	6e-63	31%	XP_018527804.1
Calcium-transporting ATPase 3 [Smittium mucronatum]	242	347	66%	6e-63	30%	OLY78124.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X2 [Zea mays]	243	298	59%	6e-63	30%	XP_008663568.1
hypothetical protein A6R68_14717 [Neotoma lepida]	242	329	59%	6e-63	31%	OBS74747.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Eucalyptus grandis]	243	302	59%	6e-63	31%	XP_010046915.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Eucalyptus grandis]	243	243	64%	6e-63	28%	XP_010048692.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X4 [Oryza brachyantha]	243	294	59%	6e-63	30%	XP_015696711.1
hypothetical protein ASPVEDRAFT_141936 [Aspergillus versicolor CBS 583.65]	243	358	69%	6e-63	30%	OJJ07708.1
Putative Cation transporting ATPase [Torrubiella hemipterigena]	241	286	55%	7e-63	31%	CEJ80042.1
hypothetical protein HMPREF1624_03171 [Sporothrix schenckii ATCC 58251]	243	243	47%	7e-63	31%	ERS99806.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Scleropages formosus]	242	321	59%	7e-63	32%	XP_018587532.1
ATPase, Na+/K+ transporting, alpha 1 polypeptide, isoform CRA_a [Rattus norvegicus]	242	330	59%	7e-63	31%	EDL85522.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Haplochromis burtoni]	242	329	59%	7e-63	32%	XP_014193913.1
Na,K-ATPase alpha subunit [Litopenaeus vannamei]	242	317	58%	7e-63	32%	AIR93635.1
Na+/K+-ATPase alpha 1 [Monopterus albus]	242	330	59%	7e-63	31%	AGV06212.1
Na+/K+-ATPase alpha-1a subunit [Solea senegalensis]	242	330	59%	7e-63	31%	AFS60173.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Protobothrops mucrosquamatus]	239	309	56%	7e-63	31%	XP_015683861.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pygocentrus nattereri]	242	330	58%	7e-63	31%	XP_017557414.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Larimichthys crocea]	242	330	59%	8e-63	32%	KKF17285.1
PREDICTED: putative calcium-transporting ATPase 13, plasma membrane-type isoform X1 [Nicotiana tabacum]	242	242	64%	8e-63	30%	XP_016458324.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Oreochromis niloticus]	242	331	59%	8e-63	31%	XP_005452414.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X2 [Nicotiana tabacum]	241	241	62%	8e-63	29%	XP_016482462.1
putative potassium sodium efflux p-type atpase [Phaeomoniella chlamydospora]	244	356	68%	8e-63	28%	KKY28880.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Kryptolebias marmoratus]	242	331	59%	9e-63	32%	XP_017282369.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Peromyscus maniculatus bairdii]	242	329	59%	9e-63	31%	XP_006989155.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sodium/potassium-transporting ATPase subunit alpha-1 precursor [Rattus norvegicus]	242	329	59%	9e-63	31%	NP_036636.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Zea mays]	243	299	59%	9e-63	30%	XP_008668924.1
hypothetical protein HELRODRAFT_157527 [Helobdella robusta]	238	238	47%	9e-63	31%	XP_009024103.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type-like [Glycine max]	242	344	67%	9e-63	32%	XP_003548255.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Neolamprologus brichardi]	241	328	59%	9e-63	31%	XP_006792878.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Larimichthys crocea]	242	330	59%	9e-63	32%	XP_010740896.2
ATPase alpha1,Na/K	242	330	59%	9e-63	31%	1309271A
Na+-exporting ATPase [Blastomyces dermatitidis ATCC 26199]	242	353	68%	9e-63	30%	EQL34682.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Cricetulus griseus]	241	329	59%	9e-63	31%	XP_007639555.1
Putative Calcium ion P-type ATPase (Eurofung) [Aspergillus calidoustus]	243	243	64%	9e-63	28%	CEL11039.1
potassium/sodium efflux P-type ATPase, fungal-type [Blastomyces dermatitidis ATCC 18188]	242	353	68%	9e-63	30%	EGE80645.1
P-type Na+-ATPase, putative [Coccidioides posadasii C735 delta SOWgp]	242	357	70%	9e-63	30%	XP_003069007.1
sodium/potassium-transporting ATPase subunit alpha [Salpingoeca rosetta]	243	342	65%	9e-63	31%	XP_004993806.1
putative potassium sodium efflux p-type atpase [Diplodia seriata]	243	361	67%	9e-63	30%	KKY14838.1
potassium/sodium efflux P-type ATPase, fungal-type [Coccidioides immitis RS]	242	357	70%	1e-62	30%	XP_001243667.2
LAQU0S06e03576g1_1 [Lachancea quebecensis]	241	333	67%	1e-62	32%	CUS22681.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Zea mays]	243	297	59%	1e-62	30%	XP_008663567.1
hypothetical protein VIGAN_03117800 [Vigna angularis var. angularis]	243	243	64%	1e-62	29%	BAT81454.1
sodium transport ATPase 5 [Coccidioides posadasii str. Silveira]	241	355	69%	1e-62	30%	EFW18777.1
Atp1a1a.1 protein [Xenopus laevis]	242	328	59%	1e-62	31%	AAH72077.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Cynoglossus semilaevis]	242	330	59%	1e-62	32%	XP_008322797.1
Plasma membrane calcium-transporting ATPase 2 [Giardia intestinalis ATCC 50581]	240	240	61%	1e-62	30%	EES98239.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Kryptolebias marmoratus]	241	331	59%	1e-62	32%	XP_017282368.1
calcium-transporting ATPase 3 [Nannizzia gypsea CBS 118893]	242	365	67%	1e-62	31%	XP_003171173.1
hypothetical protein W97_06215 [Coniosporium apollinis CBS 100218]	243	357	65%	1e-62	30%	XP_007782130.1
potassium/sodium efflux P-type ATPase [Blastomyces gilchristii SLH14081]	242	348	68%	1e-62	30%	XP_002622113.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala xenobiotica]	242	345	66%	1e-62	31%	XP_013319238.1
potassium/sodium efflux P-type ATPase, fungal-type [Blastomyces gilchristii SLH14081]	242	353	68%	1e-62	30%	OAT12127.1
P-type Na+-ATPase [Ustilaginoidea virens]	242	347	67%	1e-62	31%	KDB14293.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X2 [Daucus carota subsp. sativus]	239	294	59%	1e-62	30%	XP_017247687.1
p-type ATPase superfamily [Micromonas pusilla CCMP1545]	242	242	47%	1e-62	32%	XP_003062749.1
potassium sodium efflux p-type atpase [Colletotrichum incanum]	242	341	66%	1e-62	30%	KZL81776.1
Calcium-transporting ATPase 3 [Diplodia seriata]	242	358	66%	1e-62	30%	OMP86542.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein [Theobroma cacao]	241	241	67%	1e-62	30%	EOY11090.1
Sodium/potassium-transporting ATPase alpha-3 chain protein [Daphnia magna]	241	241	64%	2e-62	28%	JAN65684.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Takifugu rubripes]	241	328	59%	2e-62	32%	XP_003966636.1
sodium/potassium-transporting ATPase subunit alpha-1 [Cricetulus griseus]	241	329	59%	2e-62	31%	ERE90023.1
sodium p-type atpase [Colletotrichum orbiculare MAFF 240422]	242	345	67%	2e-62	30%	ENH79152.1
probable ENA2-Plasma membrane P-type ATPase [Sporisorium reilianum SRZ2]	242	365	66%	2e-62	30%	CBQ71963.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase 9, plasma membrane-type [Arachis ipaensis]	242	242	64%	2e-62	29%	XP_016174767.1
hypothetical protein SETIT_009222mg [Setaria italica]	240	296	58%	2e-62	30%	KQK98798.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Clupea harengus]	241	328	59%	2e-62	31%	XP_012681980.1
Sodium/potassium-transporting ATPase subunit alpha [Daphnia magna]	242	242	64%	2e-62	28%	KZS20243.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type isoform X2 [Setaria italica]	241	298	59%	2e-62	30%	XP_004976722.1
Autoinhibited Ca(2+)-ATPase 9 isoform 1 [Theobroma cacao]	241	241	64%	2e-62	29%	EOY26432.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Austrofundulus limnaeus]	241	328	59%	2e-62	31%	XP_013874892.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Microtus ochrogaster]	241	328	59%	2e-62	31%	XP_005357163.1
putative plasma membrane P-type ATPase [Ustilago maydis 521]	242	363	66%	2e-62	31%	XP_011388144.1
sodium/potassium-transporting ATPase subunit alpha-1 [Cricetulus griseus]	241	328	59%	2e-62	31%	ERE90024.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X1 [Oryza brachyantha]	241	293	59%	2e-62	30%	XP_015696708.1
Cation-transporting P-type ATPase, C-terminal [Ostreococcus tauri]	241	241	48%	2e-62	31%	CEF97299.1
Calcium-transporting ATPase 1 [Neonectria ditissima]	244	244	60%	2e-62	28%	KPM34861.1
Sodium transport ATPase 5 [Pichia kudriavzevii]	241	348	63%	2e-62	30%	ONH74313.1
Ca2+-ATPase (ISS) [Ostreococcus tauri]	241	241	48%	2e-62	31%	XP_003078384.1
Autoinhibited Ca(2+)-ATPase 9 isoform 4 [Theobroma cacao]	241	241	64%	2e-62	29%	EOY26435.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X5 [Oryza brachyantha]	241	293	59%	2e-62	30%	XP_006660797.2
P-type Na+-ATPase [Blastomyces dermatitidis ATCC 18188]	242	357	69%	2e-62	30%	EGE85553.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Fundulus heteroclitus]	241	330	59%	2e-62	31%	XP_012714443.1
Sodium transport ATPase 5 [Pichia kudriavzevii]	241	352	65%	2e-62	30%	ONH71408.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Nothobranchius furzeri]	241	330	59%	2e-62	32%	XP_015802159.1
potassium/sodium efflux P-type ATPase, fungal-type [Blastomyces sp. CAC-2015b]	240	336	62%	2e-62	30%	OJD20333.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type [Theobroma cacao]	241	241	64%	2e-62	29%	XP_007023810.2
hypothetical protein LIPSTDRAFT_63905 [Lipomyces starkeyi NRRL Y-11557]	241	341	66%	2e-62	29%	ODQ72644.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Ictalurus punctatus]	241	328	59%	2e-62	31%	XP_017312768.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Leptonychotes weddellii]	234	285	34%	2e-62	37%	XP_006748508.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Austrofundulus limnaeus]	241	325	59%	2e-62	31%	XP_013889304.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type isoform X1 [Setaria italica]	241	298	59%	2e-62	30%	XP_014661052.1

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putative potassium sodium efflux p-type atpase protein [Neofusicoccum parvum UCRNP2]	241	367	66%	3e-62	30%	XP_007585942.1
potassium/sodium efflux P-type ATPase [Blastomyces dermatitidis ER-3]	241	356	69%	3e-62	30%	EEQ88153.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Stegastes partitus]	241	322	59%	3e-62	31%	XP_008287595.1
hypothetical protein GLOINDRAFT_29393 [Rhizophagus irregularis DAOM 181602]	233	233	47%	3e-62	32%	ESA10494.1
hypothetical protein BDFG_05643 [Blastomyces dermatitidis ATCC 26199]	241	357	69%	3e-62	30%	EQL32162.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X4 [Macaca nemestrina]	240	308	57%	3e-62	31%	XP_011763473.1
Na+:K+ ATPase alpha subunit protein [Trichuris trichiura]	240	327	58%	3e-62	31%	CDW54807.1
Potassium/sodium efflux P-type ATPase [Colletotrichum higginsianum IMI 349063]	241	343	68%	3e-62	30%	XP_018163471.1
hypothetical protein BDBG_16537 [Blastomyces gilchristii SLH14081]	241	357	66%	3e-62	30%	OAT05995.1
PREDICTED: calcium-transporting ATPase type 2C member 2 isoform X1 [Pongo abelii]	236	236	47%	3e-62	32%	XP_009249275.1
sodium transport ATPase 5 [Aspergillus oryzae RIB40]	241	349	64%	3e-62	30%	XP_001821124.2
sodium P-type ATPase, putative [Aspergillus flavus NRRL3357]	241	354	64%	3e-62	30%	XP_002376874.1
Na+/K+-ATPase alpha subunit [Litopenaeus vannamei]	234	234	45%	3e-62	31%	ADM87522.1
adenosine triphosphatase, sodium-potassium pump alpha1 subunit [Xenopus laevis]	240	326	59%	3e-62	31%	AAC59759.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Clupea harengus]	240	323	59%	3e-62	32%	XP_012670904.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X2 [Nicotiana attenuata]	239	239	62%	3e-62	29%	XP_019229870.1
sodium/potassium-transporting ATPase subunit alpha-1 [Xenopus laevis]	240	326	59%	3e-62	31%	NP_001084064.1
Putative Calcium-translocating P-type ATPase, PMCA-type [Rhizopus microsporus]	241	241	49%	3e-62	29%	CEG70029.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Mesocricetus auratus]	240	328	59%	3e-62	31%	XP_005076578.1
hypothetical protein RSOLAG1IB_04729 [Rhizoctonia solani AG-1 IB]	241	348	64%	3e-62	30%	CEL61978.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	240	326	59%	3e-62	32%	KRZ20156.1
Ena2 sodium transporter [Candida orthopsilosis Co 90-125]	241	354	64%	4e-62	31%	XP_003867841.1
Na/K ATPase alpha	240	326	59%	4e-62	31%	1513185A
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like isoform X2 [Octopus bimaculoides]	239	304	58%	4e-62	32%	XP_014785623.1
Sodium transport ATPase 2 [Pichia kudriavzevii]	239	345	59%	4e-62	30%	ONH70378.1
potassium/sodium efflux P-type ATPase, fungal-type [Paracoccidioides brasiliensis Pb18]	240	334	67%	4e-62	30%	XP_010762190.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	240	326	59%	4e-62	32%	KRY70032.1
calcium ATPase [Zea mays]	240	240	50%	4e-62	31%	AAF73985.1
potassium/sodium efflux P-type ATPase [Uncinocarpus reesii 1704]	239	339	62%	4e-62	30%	XP_002543333.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Xenopus laevis]	240	326	59%	4e-62	31%	XP_018100421.1
putative sodium/potassium-transporting ATPase subunit alpha-1 [Trichuris suis]	241	241	47%	4e-62	31%	KHJ40873.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Nannospalax galili]	240	328	59%	4e-62	31%	XP_008832248.1
putative sodium P-type ATPase [Aspergillus flavus AF70]	240	345	64%	4e-62	30%	KOC09199.1
Sodium/potassium-transporting ATPase alpha chain-like protein [Sarcoptes scabiei]	239	330	58%	4e-62	32%	KPM05683.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type-like [Citrus sinensis]	239	239	64%	4e-62	29%	XP_006471663.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Austrofundulus limnaeus]	240	325	58%	4e-62	31%	XP_013874891.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Poecilia mexicana]	240	329	59%	4e-62	31%	XP_014846020.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Nannospalax galili]	240	328	59%	4e-62	31%	XP_008832247.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Biomphalaria glabrata]	240	328	71%	4e-62	31%	XP_013071167.1
hypothetical protein SORBIDRAFT_06g027770 [Sorghum bicolor]	240	296	59%	4e-62	30%	XP_002448481.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like isoform X1 [Daucus carota subsp. sativus]	240	295	59%	5e-62	30%	XP_017247685.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Branchiostoma belcheri]	240	318	58%	5e-62	31%	XP_019642761.1
unnamed protein product [Aspergillus oryzae RIB40]	240	341	64%	5e-62	30%	BAE59122.1
potassium/sodium efflux P-type ATPase, fungal-type [Paracoccidioides brasiliensis Pb03]	240	334	67%	5e-62	30%	EEH15954.2
putative Na+/K+-ATPase alpha subunit [Bathypolypus bairdii]	239	319	58%	5e-62	31%	AEH68839.1
potassium/sodium efflux P-type ATPase, fungal-type [Paracoccidioides brasiliensis]	240	326	67%	5e-62	30%	ODH13380.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Branchiostoma belcheri]	240	318	58%	5e-62	31%	XP_019642760.1
RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-1; Short=Na(+)/K(+) ATPase alpha-1 subunit; AltName: Full=Sodium pump subunit alpha-1; Flags: Precursor	239	323	59%	5e-62	31%	Q92030.1
hypothetical protein ACN42_g845 [Penicillium freii]	240	352	67%	5e-62	30%	KUM66211.1
potassium/sodium efflux P-type ATPase, fungal-type [Emmonsia pasteuriana UAMH 9510]	241	351	67%	5e-62	29%	OJD13943.1
Na+,K+ ATPase alpha-subunit 1 [Tetraopes tetrophthalmus]	239	321	59%	5e-62	32%	AFU25695.1
potassium/sodium efflux P-type ATPase, fungal-type [Cyphellophora europaea CBS 101466]	240	338	68%	5e-62	31%	XP_008710932.1
calcium-transporting ATPase [Paracoccidioides lutzii Pb01]	240	240	72%	6e-62	27%	XP_002797161.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Neolamprologus brichardi]	239	321	59%	6e-62	32%	XP_006794509.1
calcium-translocating P-type ATPase [Conidiobolus coronatus NRRL 28638]	241	241	67%	6e-62	28%	KXN66752.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea pedrosoi CBS 271.37]	240	345	67%	6e-62	29%	XP_013288933.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-B-like [Diachasma alloeum]	239	239	69%	6e-62	27%	XP_015125098.1
hypothetical protein MANES_14G162600 [Manihot esculenta]	240	301	60%	6e-62	29%	OAY32051.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Beta vulgaris subsp. vulgaris]	240	335	69%	6e-62	31%	XP_010693884.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type [Ricinus communis]	239	301	60%	6e-62	30%	XP_002512214.1
LANO_0G07514g1_1 [Lachancea nothofagi CBS 11611]	240	366	66%	6e-62	30%	SCV03996.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium camemberti]	239	353	68%	7e-62	31%	CRL24776.1
hypothetical protein DCAR_014677 [Daucus carota subsp. sativus]	240	296	59%	7e-62	30%	KZM97961.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X2 [Citrus sinensis]	238	238	64%	7e-62	29%	XP_015390011.1
PREDICTED: potassium-transporting ATPase alpha chain 1 isoform X1 [Macaca nemestrina]	240	308	57%	7e-62	31%	XP_011763470.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3-like [Sinocyclocheilus anshuiensis]	239	321	59%	7e-62	31%	XP_016357224.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X3 [Oryza brachyantha]	239	291	58%	7e-62	30%	XP_015696710.1

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putative sodium P-type ATPase [Aspergillus flavus AF70]	239	356	64%	8e-62	30%	KOC08937.1
potassium/sodium efflux P-type ATPase, fungal-type [Emmonsia sp. CAC-2015a]	238	337	61%	8e-62	29%	OAX77833.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	239	325	59%	8e-62	31%	KRZ20155.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Tupaia chinensis]	230	230	31%	8e-62	36%	XP_006161451.1
Na+/K+ ATPase alpha subunit [Takifugu obscurus]	239	324	59%	8e-62	31%	ADD60471.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	239	325	59%	8e-62	31%	KRY82140.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Athalia rosae]	239	329	68%	8e-62	30%	XP_012257126.1
hydrolase [Oryctes borbonicus]	237	309	55%	8e-62	31%	KRT85602.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella papuae]	239	326	59%	8e-62	31%	KRZ74907.1
hypothetical protein AJ78_05623 [Emmonsia pasteuriana UAMH 9510]	239	239	70%	9e-62	28%	OJD13986.1
hypothetical protein A1O5_09588 [Cladophialophora psammophila CBS 110553]	240	362	66%	9e-62	30%	XP_007748357.1
Ca-transporting ATPase [Reticulomyxa filosa]	235	235	33%	9e-62	35%	ETO09386.1
hypothetical protein ASPSYDRAFT_144235 [Aspergillus sydowii CBS 593.65]	239	339	65%	9e-62	31%	OJJ62925.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Acyrthosiphon pisum]	238	315	58%	9e-62	31%	XP_016658328.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella pseudospiralis]	239	325	59%	1e-61	31%	KRY70033.1
putative Na+/K+-ATPase alpha subunit [Octopus bimaculatus]	239	305	58%	1e-61	32%	AEH68837.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella zimbabwensis]	239	326	59%	1e-61	31%	KRZ04306.1
hypothetical protein CISIN_1g047874mg [Citrus sinensis]	238	238	64%	1e-61	29%	KDO48938.1
ATPase, Na+/K+ transporting, alpha 1 polypeptide S homeolog [Xenopus laevis]	239	324	59%	1e-61	31%	NP_001082580.1
Sodium/potassium-transporting ATPase subunit alpha-like Protein [Tribolium castaneum]	237	318	59%	1e-61	31%	KYB26515.1
Pc16g14380 [Penicillium rubens Wisconsin 54-1255]	239	345	68%	1e-61	30%	XP_002561735.1
P-type ATPase [Schizosaccharomyces octosporus yFS286]	239	350	67%	1e-61	31%	XP_013017663.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Astyanax mexicanus]	238	323	59%	1e-61	31%	XP_007227954.1
Na(+)-exporting P-type ATPase ENA2 [Rhizophagus irregularis DAOM 197198w]	238	347	65%	1e-61	33%	EXX62354.1
Na+,K+ ATPase alpha-subunit 1A [Rhyssomatus lineaticollis]	238	321	59%	1e-61	32%	AFU25693.1
hypothetical protein CICLE_v10000126mg [Citrus clementina]	238	238	64%	1e-61	29%	XP_006432948.1
sodium P-type ATPase, putative [Trichophyton benhamiae CBS 112371]	238	345	62%	1e-61	30%	XP_003011584.1
Na+,K+ ATPase alpha-subunit 1B [Rhyssomatus lineaticollis]	239	322	59%	1e-61	32%	AFU25692.1
hypothetical protein XELAEV_18014489mg [Xenopus laevis]	239	324	59%	1e-61	31%	OCT91435.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Oreochromis niloticus]	238	320	59%	1e-61	31%	XP_005459144.1
Sodium transport ATPase [Penicillium chrysogenum]	239	350	68%	1e-61	30%	KZN93359.1
hypothetical protein CICLE_v10024770mg [Citrus clementina]	238	238	64%	1e-61	29%	XP_006427751.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X11 [Nicrophorus vespilloides]	238	320	59%	1e-61	31%	XP_017784206.1
Na(+)/Li(+)-exporting P-type ATPase [Zymoseptoria tritici IPO323]	239	331	66%	1e-61	30%	XP_003852150.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Oryzias latipes]	238	322	64%	1e-61	31%	XP_011491492.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein UVI_02014090 [Ustilaginoidea virens]	235	235	49%	1e-61	30%	GAO13402.1
Calcium-transporting ATPase 8, plasma membrane-type [Aegilops tauschii]	239	293	59%	1e-61	29%	EMT10847.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Sinocyclocheilus grahami]	238	321	58%	1e-61	31%	XP_016093487.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Diuraphis noxia]	238	321	65%	1e-61	31%	XP_015370436.1
Sodium/potassium-transporting ATPase alpha chain [Brugia malayi]	234	234	47%	2e-61	30%	XP_001900031.1
Na,K-ATPase alpha-1 subunit [Rattus norvegicus]	238	306	59%	2e-61	31%	AAA41671.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Lates calcarifer]	238	327	59%	2e-61	31%	XP_018516522.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X1 [Oryzias latipes]	238	322	64%	2e-61	31%	XP_004084912.1
Na+/K+-ATPase alpha-subunit 1c2 [Electrophorus electricus]	238	327	58%	2e-61	31%	AJR20271.1
putative sodium P-type ATPase [Saitoella complicata NRRL Y-17804]	238	354	64%	2e-61	30%	XP_019023864.1
TPA: putative Sodium P-type ATPase [Trichophyton benhamiae CBS 112371]	238	359	67%	2e-61	30%	DAA74136.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella britovi]	238	325	59%	2e-61	31%	KRY48183.1
LADA_0C00474g1_1 [Lachancea dasiensis CBS 10888]	239	349	63%	2e-61	30%	SCU81688.1
hypothetical protein ACN38_g3809 [Penicillium nordicum]	237	340	63%	2e-61	30%	KOS45311.1
PREDICTED: calcium-transporting ATPase 2, endoplasmic reticulum-type [Brassica napus]	238	308	62%	2e-61	32%	XP_013732726.1
TPA: sodium ion P-type ATPase (Eurofung) [Aspergillus nidulans FGSC A4]	238	346	67%	2e-61	30%	CBF85251.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Lates calcarifer]	238	324	59%	2e-61	30%	XP_018516524.1
ATPase P-type K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Macrophomina phaseolina MS6]	239	356	73%	2e-61	28%	EKG13112.1
Atp2c2 protein [Mus musculus]	232	232	47%	2e-61	32%	AAH42772.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Nicrophorus vespilloides]	238	320	59%	2e-61	31%	XP_017784198.1
predicted protein [Physcomitrella patens]	238	238	64%	2e-61	29%	XP_001767354.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Diuraphis noxia]	238	319	65%	2e-61	31%	XP_015370434.1
Na+,K+ ATPase alpha-subunit 1 [Cyrtepistomus castaneus]	238	321	59%	2e-61	32%	AFU25671.1
LAME_0H02102g1_1 [Lachancea meyersii CBS 8951]	238	350	66%	2e-61	30%	SCV02508.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Dendroctonus ponderosae]	238	320	59%	2e-61	31%	XP_019769257.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Ictalurus punctatus]	238	325	64%	2e-61	31%	XP_017312766.1
hypothetical protein BRAFLDRAFT_57104 [Branchiostoma floridae]	237	315	58%	2e-61	31%	XP_002610679.1
hypothetical protein ASPVEDRAFT_143566 [Aspergillus versicolor CBS 583.65]	238	238	67%	2e-61	28%	OJJ08409.1
hypothetical protein YQE_11557 [Dendroctonus ponderosae]	238	320	59%	2e-61	31%	ENN71823.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Maylandia zebra]	238	328	65%	2e-61	31%	XP_004571309.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type-like [Daucus carota subsp. sativus]	238	238	64%	2e-61	28%	XP_017252240.1
potassium/sodium efflux P-type ATPase, fungal-type [Emmonsia crescens UAMH 3008]	238	341	68%	2e-61	31%	KKZ66997.1
hypothetical protein AN1628.2 [Aspergillus nidulans FGSC A4]	238	339	67%	2e-61	30%	XP_659232.1
hypothetical protein SCHCODRAFT_53464 [Schizophyllum commune H4-8]	238	363	65%	2e-61	29%	XP_003034044.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella britovi]	238	325	64%	2e-61	31%	KRY48182.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sodium P-type ATPase, putative [Trichophyton verrucosum HKI 0517]	237	344	62%	3e-61	30%	XP_003024364.1
p-type na+-atpase [Colletotrichum orbiculare MAFF 240422]	238	360	65%	3e-61	30%	ENH82292.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Acyrthosiphon pisum]	238	320	65%	3e-61	31%	XP_003243206.1
putative P-type II calcium ATPase [Physcomitrella patens]	238	238	64%	3e-61	29%	CAD67615.1
Sodium transport ATPase 5-like protein 3 [Colletotrichum chlorophyti]	238	339	66%	3e-61	30%	OLN89647.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Thamnophis sirtalis]	230	230	31%	3e-61	37%	XP_013925536.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Pelodiscus sinensis]	237	324	59%	3e-61	30%	XP_006132947.1
potassium/sodium efflux P-type ATPase, fungal-type [Cyphellophora europaea CBS 101466]	238	363	66%	3e-61	30%	XP_008713507.1
predicted protein [Nectria haematococca mpVI 77-13-4]	238	347	67%	3e-61	30%	XP_003053962.1
PREDICTED: calcium-transporting ATPase type 2C member 2 [Marmota marmota marmota]	236	236	47%	3e-61	32%	XP_015351765.1
calcium-transporting ATPase, putative [Phytophthora infestans T30-4]	238	238	65%	3e-61	28%	XP_002999157.1
ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem duplicate 4 [Danio rerio]	237	322	58%	3e-61	31%	NP_571764.1
hypothetical protein D910_10271 [Dendroctonus ponderosae]	238	319	59%	3e-61	31%	ERL92967.1
hypothetical protein RvY_01321 [Ramazzottius varieornatus]	237	325	66%	3e-61	30%	GAU88671.1
Na+/K+ ATPase alpha subunit isoform 8 [Danio rerio]	237	322	58%	3e-61	31%	AAG27060.1
calcium-transporting ATPase 8, plasma membrane-type protein [Medicago truncatula]	238	292	60%	3e-61	31%	XP_013454580.1
hypothetical protein EUGRSUZ_H04351 [Eucalyptus grandis]	236	236	67%	3e-61	29%	KCW61614.1
hypothetical protein XENTR_v90029850mg [Xenopus tropicalis]	237	322	59%	3e-61	31%	OCA15477.1
hypothetical protein SELMODRAFT_78895 [Selaginella moellendorffii]	237	332	68%	3e-61	32%	XP_002962638.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X1 [Citrus sinensis]	238	238	64%	3e-61	29%	XP_006492040.1
hypothetical protein EMPG_14099 [Emmonsia parva UAMH 139]	238	349	64%	3e-61	29%	KLJ10521.1
uncharacterized protein MSY001_0060 [Malassezia sympodialis ATCC 42132]	238	347	66%	3e-61	29%	XP_018738709.1
hypothetical protein [Paramecium tetraurelia strain d4-2]	229	229	29%	3e-61	38%	XP_001457711.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Acyrthosiphon pisum]	237	320	65%	3e-61	31%	XP_008181088.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Esox lucius]	237	316	58%	3e-61	31%	XP_010883994.1
hypothetical protein CICLE_v10024770mg [Citrus clementina]	238	238	64%	3e-61	29%	XP_006427752.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Acyrthosiphon pisum]	238	315	58%	4e-61	31%	XP_016658325.1
LAFA_0G07536g1_1 [Lachancea sp. CBS 6924]	238	358	64%	4e-61	30%	SCU96681.1
hypothetical protein HELRODRAFT_94925 [Helobdella robusta]	236	319	58%	4e-61	32%	XP_009022593.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Acyrthosiphon pisum]	238	320	65%	4e-61	31%	XP_016658327.1
predicted protein [Physcomitrella patens]	238	238	64%	4e-61	29%	XP_001780927.1
hypothetical protein AC631_04986 [Debaryomyces fabryi]	238	353	64%	4e-61	31%	XP_015465344.1
hypothetical protein [Monosiga brevicollis MX1]	237	327	58%	4e-61	30%	XP_001742517.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Acyrthosiphon pisum]	237	320	65%	4e-61	31%	XP_016658326.1
Similar to Sodium transport ATPase 2; acc. no. Q01896 [Pyronema omphalodes CBS 100304]	238	338	65%	4e-61	30%	CCX34699.1
putative Ptype ATPase [Albugo laibachii Nc14]	240	350	67%	4e-61	30%	CCA25933.1

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hypothetical protein CANTEDRAFT_119074 [[Candida] tenuis ATCC 10573]	237	341	64%	4e-61	30%	XP_006684585.1
sodium/potassium-transporting ATPase subunit alpha-4 [Castor canadensis]	231	281	34%	4e-61	37%	JAV44179.1
similar to sodium P-type ATPase [Leptosphaeria maculans JN3]	237	349	66%	4e-61	29%	XP_003837611.1
calcium-translocating P-type ATPase, PMCA-type protein [Tetrahymena thermophila SB210]	237	237	68%	4e-61	27%	XP_001031770.2
potassium/sodium efflux P-type ATPase, fungal-type [Cryptococcus depauperatus CBS 7841]	236	376	59%	4e-61	35%	ODN87343.1
potassium sodium efflux p-type fungal-type [Fusarium avenaceum]	237	353	67%	4e-61	29%	KIL84873.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Acyrthosiphon pisum]	238	315	58%	4e-61	31%	XP_016658323.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Pundamilia nyererei]	237	327	65%	5e-61	31%	XP_005749513.1
sodium transport ATPase [Histoplasma capsulatum H88]	237	334	67%	5e-61	31%	EGC44177.1
potassium/sodium efflux P-type ATPase [Colletotrichum graminicola M1.001]	237	349	68%	5e-61	29%	XP_008100270.1
hypothetical protein g.17429 [Homalodisca liturata]	234	320	65%	5e-61	31%	JAS73390.1
P-type Na+-ATPase [Metarhizium majus ARSEF 297]	238	339	66%	5e-61	30%	XP_014578834.1
hypothetical protein S7711_04111 [Stachybotrys chartarum IBT 7711]	238	352	67%	5e-61	29%	KEY67798.1
hypothetical protein CHGG_00089 [Chaetomium globosum CBS 148.51]	237	349	67%	5e-61	30%	XP_001219310.1
Calcium-transporting ATPase 3 [Neonectria ditissima]	238	349	68%	5e-61	31%	KPM38274.1
hypothetical protein HELRODRAFT_185638 [Helobdella robusta]	236	328	69%	5e-61	29%	XP_009018416.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala aquamarina CBS 119918]	237	342	68%	5e-61	31%	XP_013263956.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X12 [Nicrophorus vespilloides]	236	318	58%	5e-61	32%	XP_017784207.1
Sodium transport ATPase 1 [Candida maltosa Xu316]	237	349	64%	5e-61	31%	EMG45982.1
sodium transport ATPase 5 [Histoplasma capsulatum NAm1]	237	335	67%	5e-61	31%	XP_001542093.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X10 [Tribolium castaneum]	236	318	59%	5e-61	31%	XP_008196425.1
putative Ptype ATPase [Albugo laibachii Nc14]	240	350	67%	5e-61	30%	CCA25936.1
sodium/potassium-transporting ATPase subunit alpha-1 [Xenopus tropicalis]	236	322	59%	5e-61	31%	NP_989407.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X1 [Vitis vinifera]	237	237	64%	5e-61	29%	XP_002275074.2
sodium P-type ATPase-like protein [Microdochium bolleyi]	237	342	67%	5e-61	31%	KXJ96324.1
Na+/K+-ATPase alpha-subunit 1b [Anabas testudineus]	236	328	64%	6e-61	30%	AFK29493.1
putative Ptype ATPase [Albugo laibachii Nc14]	240	350	67%	6e-61	30%	CCA25931.1
Na+ ATPase [Scheffersomyces stipitis CBS 6054]	236	339	58%	6e-61	31%	XP_001385604.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Nicrophorus vespilloides]	236	319	58%	6e-61	32%	XP_017784200.1
Na+/K+-ATPase alpha-subunit 3 [Protopterus annectens]	236	322	59%	6e-61	30%	AGR45923.1
Calcium-transporting ATPase 3 [Smittium culicis]	236	336	66%	6e-61	30%	OMJ16621.1
potassium/sodium efflux P-type ATPase, fungal-type [Emmonsia crescens UAMH 3008]	237	347	69%	6e-61	29%	KKZ63462.1
Calcium-transporting ATPase 3 [Tolypocladium ophioglossoides CBS 100239]	237	346	65%	6e-61	30%	KND87068.1
Putative Calcium-transporting ATPase [Aspergillus calidoustus]	236	347	68%	6e-61	30%	CEL08567.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Nicrophorus vespilloides]	236	318	58%	6e-61	32%	XP_017784201.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Nicrophorus vespilloides]	236	318	58%	6e-61	32%	XP_017784204.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Tribolium castaneum]	236	318	59%	7e-61	31%	XP_008196419.1
hypothetical protein PFICI_15126 [Pestalotiopsis fici W106-1]	236	329	67%	7e-61	30%	XP_007841898.1
Calcium-transporting ATPase 3 [Smittium culicis]	236	337	66%	7e-61	30%	OMJ08674.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X2 [Oryza brachyantha]	236	288	59%	7e-61	29%	XP_015696709.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X10 [Nicrophorus vespilloides]	236	318	58%	7e-61	32%	XP_017784205.1
sodium transport ATPase [Histoplasma capsulatum G186AR]	236	333	68%	7e-61	30%	EEH09703.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Nicrophorus vespilloides]	236	318	58%	7e-61	32%	XP_017784203.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Poecilia reticulata]	236	320	59%	7e-61	31%	XP_008429550.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea monophora]	236	341	67%	7e-61	29%	OAG41192.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P57055]	236	347	64%	7e-61	30%	KGU37262.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Nicrophorus vespilloides]	236	318	58%	7e-61	32%	XP_017784202.1
Na+,K+ ATPase alpha-subunit 1A [Chrysochus auratus]	236	320	58%	7e-61	32%	AFU25669.1
sodium transport atpase [Moniliophthora roreri MCA 2997]	237	358	66%	8e-61	31%	XP_007854873.1
Na(+)-exporting P-type ATPase [Candida albicans SC5314]	236	346	64%	8e-61	30%	XP_719032.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Poecilia reticulata]	236	320	59%	8e-61	31%	XP_008429551.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X3 [Vitis vinifera]	236	236	64%	8e-61	29%	XP_010655162.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type isoform X2 [Vitis vinifera]	236	236	64%	8e-61	29%	XP_010655160.1
potassium/sodium efflux P-type ATPase [Trichophyton rubrum CBS 118892]	237	353	70%	8e-61	29%	XP_003232295.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like [Bemisia tabaci]	236	316	59%	8e-61	31%	XP_018906490.1
sodium potassium-transporting atpase subunit alpha [Ascaris suum]	236	319	58%	8e-61	30%	ERG79961.1
hypothetical protein CPAR2_105760 [Candida parapsilosis]	236	350	64%	8e-61	31%	CCE40540.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Nicrophorus vespilloides]	236	318	58%	8e-61	32%	XP_017784199.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P94015]	236	347	64%	8e-61	30%	KGQ99171.1
Calcium ATPase, transmembrane M [Glarea lozoyensis ATCC 20868]	237	358	65%	9e-61	31%	XP_008084582.1
hypothetical protein Z043_104545 [Scleropages formosus]	226	226	31%	9e-61	36%	KPP76140.1
DEHA2G09108p [Debaryomyces hansenii CBS767]	236	347	64%	9e-61	32%	XP_461943.2
Na+,K+ ATPase alpha-subunit 1 [Aphis nerii]	236	318	65%	9e-61	31%	AFU25665.1
sodium transport ATPase [Trichophyton tonsurans CBS 112818]	236	357	67%	9e-61	30%	EGD95726.1
potassium/sodium efflux P-type ATPase [Colletotrichum orchidophilum]	236	352	67%	9e-61	30%	OHE95069.1
putative Na(+)/Li(+)-exporting P-type ATPase isoform 2A [Hortaea werneckii]	235	327	67%	9e-61	30%	AGT96031.1
hypothetical protein g.17416 [Homalodisca liturata]	234	320	65%	9e-61	31%	JAS75529.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Nicrophorus vespilloides]	236	318	58%	9e-61	32%	XP_017784196.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P57072]	236	346	64%	9e-61	30%	KGR15184.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Apis florea]	234	313	59%	1e-60	31%	XP_012345707.1
hypothetical protein PGUG_02728 [Meyerozyma guilliermondii ATCC 6260]	236	334	58%	1e-60	31%	XP_001484999.1
sodium transport ATPase 2 [Candida albicans WO-1]	236	346	64%	1e-60	30%	EEQ43097.1

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potassium/sodium efflux P-type ATPase, fungal-type [Emmonsia pasteuriana UAMH 9510]	236	348	68%	1e-60	31%	OJD18482.1
unnamed protein product [Oncorhynchus mykiss]	234	317	59%	1e-60	30%	CDQ90178.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Kryptolebias marmoratus]	236	318	59%	1e-60	31%	XP_017270842.1
hypothetical protein S40285_06042 [Stachybotrys chlorohalonata IBT 40285]	236	350	67%	1e-60	29%	KFA60340.1
potassium/sodium efflux P-type ATPase, fungal-type [Fusarium verticillioides 7600]	236	350	63%	1e-60	29%	XP_018747639.1
hypothetical protein SMAC_08578 [Sordaria macrospora k-hell]	236	368	66%	1e-60	30%	XP_003349732.1
Sodium/potassium-transporting ATPase subunit alpha-2 [Fukomys damarensis]	239	681	65%	1e-60	31%	KFO18152.1
P-type Na+-ATPase [Aschersonia aleyrodis RCEF 2490]	236	347	71%	1e-60	29%	KZZ98991.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Haplochromis burtoni]	236	325	65%	1e-60	31%	XP_005937371.1
hypothetical protein PENARI_c018G06740 [Penicillium arizonense]	236	343	67%	1e-60	31%	OGE50077.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Kryptolebias marmoratus]	235	318	59%	1e-60	31%	XP_017270843.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Cyprinodon variegatus]	236	324	59%	1e-60	31%	XP_015229450.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha [Apis cerana]	235	316	59%	1e-60	31%	XP_016911763.1
hypothetical protein PGUG_02728 [Meyerozyma guilliermondii ATCC 6260]	236	335	63%	1e-60	31%	EDK38630.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Tribolium castaneum]	235	317	59%	1e-60	31%	XP_015837164.1
probable ENA5-Plasma membrane P-type ATPase involved in Na+ and Li+ efflux [Rhynchosporium secalis]	236	349	65%	1e-60	30%	CZT45766.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Sinocyclocheilus grahami]	235	320	58%	1e-60	31%	XP_016093494.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Vollenhovia emeryi]	236	318	59%	1e-60	31%	XP_011876340.1
P-type Na+-ATPase [Metarhizium brunneum ARSEF 3297]	236	338	66%	1e-60	30%	XP_014549441.1
Calcium-transporting ATPase 3 [Phialophora attae]	236	350	66%	1e-60	30%	XP_017996332.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Tribolium castaneum]	235	317	59%	1e-60	31%	XP_008196423.1
hypothetical protein ASPFODRAFT_83998 [Aspergillus luchuensis CBS 106.47]	238	238	64%	1e-60	30%	OJZ82554.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Apis mellifera]	235	316	59%	1e-60	31%	XP_016767657.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Apis florea]	235	315	59%	1e-60	31%	XP_012345706.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X15 [Agrilus planipennis]	235	319	59%	1e-60	31%	XP_018327787.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Ictalurus punctatus]	235	323	59%	1e-60	31%	XP_017312771.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Tribolium castaneum]	235	317	59%	1e-60	31%	XP_008196420.1
ATP binding [Ascochyta rabiei]	236	347	67%	1e-60	29%	KZM18926.1
plasma membrane Na+ ATPase [Debaryomyces hansenii]	236	344	64%	1e-60	32%	AAK52600.2
potassium/sodium efflux P-type ATPase, fungal-type [Blastomyces sp. CAC-2015b]	236	353	69%	1e-60	29%	OJD23654.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Apis mellifera]	235	316	59%	1e-60	31%	XP_016767654.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Tribolium castaneum]	235	317	59%	1e-60	31%	XP_008196422.1
P-type ATPase 2 [Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993]	236	352	66%	1e-60	29%	XP_018712538.1
hypothetical protein IMG5_164760 [Ichthyophthirius multifiliis]	236	236	67%	1e-60	29%	XP_004030253.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Apis florea]	235	315	59%	1e-60	31%	XP_012345703.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Tribolium castaneum]	235	317	59%	1e-60	31%	XP_008196417.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Ictalurus punctatus]	235	323	59%	1e-60	31%	XP_017312770.1
Na+/K+-ATPase alpha-subunit 1a [Anabas testudineus]	235	326	64%	1e-60	31%	AFK29492.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Apis mellifera]	235	316	59%	1e-60	31%	XP_016767653.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Apis florea]	235	314	59%	1e-60	31%	XP_012345705.1
hypothetical protein M413DRAFT_441360 [Hebeloma cylindrosporum h7]	236	361	65%	1e-60	30%	KIM46275.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P60002]	234	344	58%	2e-60	30%	KHC45529.1
PREDICTED: calcium-transporting ATPase 9, plasma membrane-type [Capsicum annuum]	236	236	64%	2e-60	29%	XP_016562376.1
hypothetical protein [Kluyveromyces lactis NRRL Y-1140]	236	359	67%	2e-60	30%	XP_454607.1
ATPase, Na+/K+ transporting, alpha 3a polypeptide [Danio rerio]	235	317	59%	2e-60	31%	NP_571759.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Apis mellifera]	235	316	59%	2e-60	31%	XP_016767656.1
hypothetical protein SELMODRAFT_112465 [Selaginella moellendorffii]	235	330	68%	2e-60	31%	XP_002980453.1
hypothetical protein ASPVEDRAFT_49889 [Aspergillus versicolor CBS 583.65]	235	342	68%	2e-60	31%	OJI98064.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Agrilus planipennis]	235	319	59%	2e-60	31%	XP_018327708.1
Atp1a1a.2 protein [Danio rerio]	235	343	70%	2e-60	31%	AAH95306.1
Calcium-transporting ATPase 10, plasma membrane-type [Noccaea caerulescens]	235	235	64%	2e-60	28%	JAU52829.1
hypothetical protein ARB_03734 [Trichophyton benhamiae CBS 112371]	236	354	70%	2e-60	29%	XP_003010032.1
Calcium-transporting ATPase 10, plasma membrane-type [Noccaea caerulescens]	235	235	64%	2e-60	28%	JAU61339.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Apis florea]	235	315	59%	2e-60	31%	XP_012345701.1
sodium/potassium-transporting ATPase alpha-1 chain, putative [Pediculus humanus corporis]	235	324	58%	2e-60	31%	XP_002427714.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Anoplophora glabripennis]	234	319	65%	2e-60	32%	XP_018562057.1
TPA: hypothetical protein ZEAMMB73_416489 [Zea mays]	236	288	58%	2e-60	30%	DAA48121.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Apis florea]	235	314	59%	2e-60	31%	XP_012345704.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Anoplophora glabripennis]	235	319	65%	2e-60	32%	XP_018562051.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Athalia rosae]	235	318	59%	2e-60	31%	XP_012269652.1
potassium/sodium efflux P-type ATPase, fungal-type [Trichophyton interdigitale H6]	228	228	47%	2e-60	29%	EZF29730.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Apis mellifera]	235	316	59%	2e-60	31%	XP_006564223.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Apis mellifera]	234	315	59%	2e-60	31%	XP_016767655.1
Calcium-transporting ATPase 1 [Zostera marina]	232	232	64%	2e-60	28%	KMZ70473.1
hypothetical protein DICPUDRAFT_47441 [Dictyostelium purpureum]	236	314	69%	2e-60	31%	XP_003287590.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X3 [Oreochromis niloticus]	234	324	64%	2e-60	32%	XP_019206973.1
hypothetical protein ASPSYDRAFT_160407 [Aspergillus sydowii CBS 593.65]	235	347	63%	2e-60	30%	OJJ54551.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Nothobranchius furzeri]	234	318	59%	2e-60	31%	XP_015805770.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sodium/potassium-transporting ATPase alpha-1 chain, putative [Pediculus humanus corporis]	234	321	64%	2e-60	31%	XP_002428077.1
LALA0S12e02476g1_1 [Lachancea lanzarotensis]	235	360	66%	2e-60	30%	CEP64592.1
hypothetical protein NEUTE1DRAFT_144929 [Neurospora tetrasperma FGSC 2508]	235	359	66%	2e-60	29%	XP_009849096.1
predicted protein [Naegleria gruberi]	234	310	61%	2e-60	30%	XP_002683336.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Bombus terrestris]	235	318	59%	2e-60	31%	XP_012163874.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Arachis duranensis]	235	293	59%	2e-60	29%	XP_015954407.1
calcium-transporting ATPase 3 [Trichophyton tonsurans CBS 112818]	236	353	70%	2e-60	29%	EGD97988.1
potassium/sodium efflux P-type ATPase, fungal-type [Rhinocladiella mackenziei CBS 650.93]	235	235	50%	2e-60	30%	XP_013270472.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Arachis ipaensis]	235	293	59%	2e-60	30%	XP_016188939.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 isoform X1 [Latimeria chalumnae]	231	231	56%	2e-60	30%	XP_006001914.1
Na+/K+-ATPase alpha-subunit 3 [Himantura signifer]	234	320	59%	2e-60	31%	AHD24598.1
P-type Na+-ATPase [Metarhizium guizhouense ARSEF 977]	235	337	66%	2e-60	30%	KID90417.1
P-type Na+-ATPase [Metarhizium acridum CQMa 102]	235	339	64%	2e-60	30%	XP_007807518.1
sodium/potassium-transporting ATPase subunit alpha [Saprolegnia diclina VS20]	236	310	59%	2e-60	30%	XP_008604114.1
hypothetical protein V501_08847 [Pseudogymnoascus sp. VKM F-4519 (FW-2642)]	235	345	65%	2e-60	30%	KFZ04906.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Nothobranchius furzeri]	234	318	59%	2e-60	31%	XP_015805769.1
potassium/sodium efflux P-type ATPase [Metarhizium robertsii ARSEF 23]	235	337	66%	2e-60	30%	XP_007821745.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Hippocampus comes]	234	318	59%	2e-60	31%	XP_019751669.1
putative sodium p-type atpase protein [Botrytis cinerea BcDW1]	235	353	67%	2e-60	29%	EMR80692.1
hypothetical protein g.33845 [Graphocephala atropunctata]	234	321	65%	3e-60	31%	JAT18092.1
Sodium/potassium-transporting ATPase subunit alpha [Exaiptasia pallida]	235	316	67%	3e-60	30%	KXJ20422.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P37039]	234	343	58%	3e-60	30%	KHC47467.1
P-type Na+-ATPase [Histoplasma capsulatum G186AR]	235	348	69%	3e-60	28%	EEH07235.1
P-type Na+-ATPase [Metarhizium anisopliae]	235	337	66%	3e-60	30%	KFG84401.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Anoplophora glabripennis]	234	318	65%	3e-60	32%	XP_018562054.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Hippocampus comes]	234	318	59%	3e-60	31%	XP_019751672.1
putative ca2+ transporting atpase [Culex tarsalis]	234	316	59%	3e-60	31%	JAV34693.1
calcium-transporting ATPase 3 [Neurospora crassa OR74A]	235	359	66%	3e-60	29%	XP_962099.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Cephus cinctus]	234	316	59%	3e-60	31%	XP_015585115.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Aethina tumida]	234	317	59%	3e-60	31%	XP_019873769.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Megachile rotundata]	234	317	59%	3e-60	31%	XP_003705422.2
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans 19F]	234	345	64%	3e-60	30%	KGU19783.1
potassium/sodium efflux P-type ATPase, fungal-type [Trichophyton interdigitale H6]	235	353	70%	3e-60	29%	EZF30294.1
sodium P-type ATPase [Trichophyton equinum CBS 127.97]	234	342	64%	3e-60	29%	EGE04988.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Cerapachys biroi]	234	316	59%	3e-60	31%	XP_011343659.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium griseofulvum]	234	344	68%	3e-60	30%	KXG46330.1

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potassium/sodium efflux P-type ATPase, fungal-type [Cladophialophora bantiana CBS 173.52]	235	333	66%	3e-60	29%	XP_016618287.1
calcium-transporting ATPase 3 [Aspergillus terreus NIH2624]	235	340	62%	3e-60	31%	XP_001214443.1
BN860_08328g1_1 [Zygosaccharomyces bailii CLIB 213]	235	235	64%	3e-60	27%	CDF87523.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X10 [Aethina tumida]	234	316	58%	3e-60	31%	XP_019873774.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Anoplophora glabripennis]	234	318	65%	3e-60	32%	XP_018562055.1
hypothetical protein BC1G_11540 [Botrytis cinerea B05.10]	233	278	55%	3e-60	29%	XP_001549707.1
hypothetical protein METBIDRAFT_31192 [Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993]	234	344	68%	3e-60	29%	XP_018712762.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Neodiprion lecontei]	234	316	59%	3e-60	31%	XP_015514137.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like isoform X2 [Sinocyclocheilus grahami]	234	316	58%	3e-60	31%	XP_016093488.1
Na+/K+ ATPase alpha subunit [Danaus plexippus]	231	310	58%	3e-60	31%	CCW28388.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Linepithema humile]	234	316	59%	3e-60	31%	XP_012228926.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like isoform X1 [Oryza brachyantha]	234	288	59%	3e-60	30%	XP_006652779.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Aethina tumida]	234	317	59%	4e-60	31%	XP_019873765.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Aethina tumida]	234	317	58%	4e-60	31%	XP_019873768.1
potassium/sodium efflux P-type ATPase [Rhizoctonia solani 123E]	235	338	64%	4e-60	30%	KEP49966.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Copidosoma floridanum]	234	320	59%	4e-60	31%	XP_014205894.1
hypothetical protein CAPTEDRAFT_182016 [Capitella teleta]	234	313	58%	4e-60	32%	ELU16373.1
putative Na+/K+-ATPase alpha subunit [Octopus defilippi]	234	301	58%	4e-60	32%	AEH68840.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Aethina tumida]	234	316	58%	4e-60	31%	XP_019873772.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Gekko japonicus]	233	356	53%	4e-60	38%	XP_015265330.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Aethina tumida]	234	317	58%	4e-60	31%	XP_019873764.1
potassium/sodium efflux P-type ATPase [Trichophyton violaceum]	235	351	70%	4e-60	29%	OAL72022.1
Chain A, Crystal Structure Of The Sodium - Potassium Pump In The E2.2k+.Pi State	234	314	59%	4e-60	29%	2ZXE_A
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Atta cephalotes]	234	316	59%	4e-60	31%	XP_012057440.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Ictalurus punctatus]	233	320	59%	4e-60	30%	XP_017325785.1
Calcium-transporting ATPase 10, plasma membrane-type [Noccaea caerulescens]	234	234	64%	4e-60	28%	JAU83488.1
hypothetical protein cypCar_00011416 [Cyprinus carpio]	234	316	59%	4e-60	30%	KTG36082.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Lates calcarifer]	234	317	59%	4e-60	30%	XP_018527801.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Sinocyclocheilus rhinocerous]	234	318	58%	4e-60	30%	XP_016380413.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala sideris]	234	356	67%	4e-60	29%	KIV84966.1
potassium/sodium efflux P-type ATPase, fungal-type [Fusarium oxysporum FOSC 3-a]	234	349	66%	4e-60	29%	EWY95019.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Cyprinodon variegatus]	234	318	59%	4e-60	31%	XP_015226252.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Esox lucius]	234	315	64%	4e-60	32%	XP_010878503.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-like [Nasonia vitripennis]	234	317	59%	4e-60	31%	XP_016840422.1

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PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Aethina tumida]	234	316	58%	4e-60	31%	XP_019873773.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Cerapachys biroi]	234	316	59%	4e-60	31%	XP_011343653.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Anoplophora glabripennis]	234	318	65%	4e-60	32%	XP_018562052.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Anoplophora glabripennis]	234	318	65%	4e-60	32%	XP_018562049.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Cyprinodon variegatus]	234	318	59%	4e-60	31%	XP_015226253.1
putative sodium/potassium-transporting atpase subunit alpha isoform x3 [Culex tarsalis]	233	314	59%	4e-60	31%	JAV31383.1
ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem duplicate 2 [Danio rerio]	234	339	64%	4e-60	31%	NP_571762.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Cerapachys biroi]	233	316	59%	4e-60	31%	XP_011343658.1
Na,H/K antiporter P-type ATPase, alpha subunit [Necator americanus]	233	233	48%	4e-60	31%	XP_013309313.1
KLTH0F08030p [Lachancea thermotolerans]	234	342	66%	4e-60	29%	XP_002554551.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P78048]	234	344	64%	4e-60	30%	KGR21811.1
potassium/sodium efflux P-type ATPase [Rhizoctonia solani AG-3 Rhs1AP]	234	338	64%	4e-60	30%	EUC59099.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Cerapachys biroi]	233	316	59%	4e-60	31%	XP_011343657.1
Piso0_000862 [Millerozyma farinosa CBS 7064]	234	336	64%	5e-60	32%	XP_004203841.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Tribolium castaneum]	233	305	60%	5e-60	30%	XP_015840522.1
potassium/sodium efflux P-type ATPase [Trichoderma reesei RUT C-30]	234	355	69%	5e-60	29%	ETR98034.1
potassium/sodium efflux P-type ATPase, fungal-type [Pseudogymnoascus destructans]	232	333	60%	5e-60	30%	OAF56264.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Dendroctonus ponderosae]	234	315	59%	5e-60	31%	XP_019769258.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Cerapachys biroi]	234	316	59%	5e-60	31%	XP_011343655.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Tribolium castaneum]	233	318	60%	5e-60	30%	XP_008190275.2
putative sodium/potassium-transporting atpase subunit alpha isoform x3 [Culex tarsalis]	234	316	59%	5e-60	31%	JAV31381.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Eufriesea mexicana]	234	313	59%	5e-60	31%	XP_017767678.1
hypothetical protein SPRG_13744 [Saprolegnia parasitica CBS 223.65]	235	309	59%	5e-60	30%	XP_012208076.1
Na+,K+ ATPase alpha-subunit 1C [Oncopeltus fasciatus]	233	321	65%	5e-60	31%	AFU25687.1
potassium/sodium eff [Coniochaeta ligniaria NRRL 30616]	233	335	61%	5e-60	30%	OIW33055.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Eucalyptus grandis]	234	292	59%	5e-60	31%	XP_010046912.1
calcium-transporting atpase [Colletotrichum gloeosporioides Nara gc5]	235	235	66%	5e-60	28%	XP_007279249.1
Pc21g21610 [Penicillium rubens Wisconsin 54-1255]	234	350	64%	5e-60	30%	XP_002569134.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X1 [Ictalurus punctatus]	233	320	59%	5e-60	30%	XP_017325784.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Habropoda laboriosa]	234	316	59%	5e-60	31%	XP_017796075.1
hypothetical protein AUEXF2481DRAFT_30887 [Aureobasidium subglaciale EXF-2481]	234	331	66%	5e-60	30%	XP_013342274.1
hypothetical protein TRV_06589 [Trichophyton verrucosum HKI 0517]	234	352	70%	5e-60	29%	XP_003019386.1
potassium/sodium efflux P-type ATPase, fungal-type [Fonsecaea nubica]	234	337	65%	5e-60	29%	OAL38404.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Cerapachys biroi]	233	316	59%	6e-60	31%	XP_011343656.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Orussus abietinus]	233	316	59%	6e-60	31%	XP_012272095.1
cation transporting ATPase [Trichoderma atroviride IMI 206040]	234	351	66%	6e-60	30%	XP_013943684.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P78042]	233	341	58%	6e-60	30%	KHC67888.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Acromyrmex echinatior]	233	315	59%	6e-60	31%	XP_011050717.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Atta colombica]	233	315	59%	6e-60	31%	XP_018058956.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella papuae]	233	320	59%	6e-60	31%	KRZ74909.1
sodium/potassium-transporting ATPase subunit alpha-1 [Wuchereria bancrofti]	228	228	46%	6e-60	29%	EJW83812.1
Ena21p [Candida albicans SC5314]	233	342	58%	6e-60	30%	XP_716992.1
Na+/K+ ATPase alpha subunit isoform 5 [Danio rerio]	233	314	59%	6e-60	30%	AAG30275.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella zimbabwensis]	233	320	59%	6e-60	31%	KRZ04307.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Kryptolebias marmoratus]	233	315	59%	6e-60	31%	XP_017283128.1
calcium-transporting ATPase 2 [Aspergillus lentulus]	234	234	64%	6e-60	29%	GAQ05475.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P57072]	233	342	58%	6e-60	30%	KGR02366.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Dendroctonus ponderosae]	233	315	59%	6e-60	31%	XP_019769261.1
hypothetical protein CARUB_v10006503mg [Capsella rubella]	234	234	64%	6e-60	28%	XP_006285159.1
putative sodium/potassium-transporting atpase subunit alpha isoform x4 [Culex tarsalis]	232	314	59%	6e-60	31%	JAV31376.1
potassium/sodium eff [Stagonospora sp. SRC1lsM3a]	234	351	67%	6e-60	29%	OAK95120.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3 [Esox lucius]	233	315	59%	6e-60	31%	XP_012994941.1
Sodium transport ATPase 5 [Fusarium oxysporum f. sp. cubense race 1]	234	348	66%	6e-60	29%	ENH69362.1
hypothetical protein FOXB_10443 [Fusarium oxysporum Fo5176]	234	348	66%	6e-60	29%	EGU79014.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X10 [Agrilus planipennis]	233	316	58%	6e-60	31%	XP_018327744.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Ceratina calcarata]	233	313	59%	6e-60	31%	XP_017891321.1
Na+/K+-ATPase alpha 3b [Monopterus albus]	234	318	66%	6e-60	30%	AGV06214.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Salmo salar]	233	311	59%	7e-60	31%	XP_014022853.1
hypothetical protein g.33841 [Graphocephala atropunctata]	229	229	47%	7e-60	31%	JAT17765.1
Ca++-ATPase [Oxytricha trifallax]	234	234	68%	7e-60	29%	EJY84863.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Agrilus planipennis]	233	317	58%	7e-60	31%	XP_018327715.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Apis mellifera]	231	311	59%	7e-60	31%	XP_016767658.1
potassium/sodium efflux P-type ATPase, fungal-type [Fusarium oxysporum f. sp. lycopersici 4287]	234	347	66%	7e-60	29%	XP_018241151.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Agrilus planipennis]	233	316	58%	7e-60	31%	XP_018327738.1
Na+,K+ ATPase alpha-subunit 1 [Lycorea halia]	233	315	59%	7e-60	31%	AFU25681.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Dendroctonus ponderosae]	233	314	58%	7e-60	31%	XP_019769264.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Ceratina calcarata]	233	313	59%	7e-60	31%	XP_017891318.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Ceratina calcarata]	233	314	59%	7e-60	31%	XP_017891317.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Dendroctonus ponderosae]	233	314	58%	7e-60	31%	XP_019769265.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Agrilus planipennis]	233	317	58%	7e-60	31%	XP_018327684.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Vitis vinifera]	233	290	59%	7e-60	31%	XP_002262829.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Ceratina calcarata]	233	313	59%	7e-60	31%	XP_017891320.1
unnamed protein product [Vitis vinifera]	233	290	59%	8e-60	31%	CBI17890.3
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Pogonomyrmex barbatus]	233	315	59%	8e-60	31%	XP_011643348.1
Piso0_000862 [Millerozyma farinosa CBS 7064]	233	340	64%	8e-60	32%	XP_004203259.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X11 [Agrilus planipennis]	233	316	58%	8e-60	31%	XP_018327751.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Trachymyrmex septentrionalis]	233	315	59%	8e-60	30%	XP_018343333.1
Na+,K+ ATPase alpha-subunit 1 [Megacyllene robiniae]	233	316	59%	8e-60	31%	AFU25686.1
PREDICTED: putative calcium-transporting ATPase 13, plasma membrane-type [Tarenaya hassleriana]	233	233	64%	8e-60	28%	XP_010532587.1
potassium/sodium efflux P-type ATPase, fungal-type [Fusarium oxysporum f. sp. melonis 26406]	233	348	66%	8e-60	29%	EXK32677.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Dendroctonus ponderosae]	233	315	58%	8e-60	31%	XP_019769256.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Dendroctonus ponderosae]	233	315	58%	8e-60	31%	XP_019769263.1
PREDICTED: calcium-transporting ATPase 12, plasma membrane-type [Theobroma cacao]	233	233	67%	8e-60	29%	XP_007030588.2
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Buceros rhinoceros silvestris]	224	224	31%	8e-60	36%	XP_010139819.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Dinoponera quadriceps]	233	313	59%	8e-60	31%	XP_014476228.1
potassium/sodium efflux P-type ATPase, fungal-type [Pseudogymnoascus destructans 20631-21]	233	340	65%	8e-60	30%	XP_012743353.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X10 [Dendroctonus ponderosae]	233	314	58%	8e-60	31%	XP_019769266.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Dinoponera quadriceps]	233	313	59%	8e-60	31%	XP_014476230.1
Na+,K+ ATPase alpha-subunit 1 [Plagiodera versicolora]	233	318	58%	8e-60	31%	AFU25691.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Ceratina calcarata]	233	314	59%	8e-60	31%	XP_017891315.1
BMA-CATP-4 [Brugia malayi]	234	315	64%	8e-60	30%	CDP98168.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Pygocentrus nattereri]	233	315	59%	8e-60	30%	XP_017561561.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Dendroctonus ponderosae]	233	315	58%	9e-60	31%	XP_019769259.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Agrilus planipennis]	233	316	58%	9e-60	31%	XP_018327723.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Dendroctonus ponderosae]	233	315	58%	9e-60	31%	XP_019769260.1
plasma membrane calcium-transporting ATPase [Aspergillus kawachii IFO 4308]	235	235	64%	9e-60	30%	GAA92859.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Sinocyclocheilus anshuiensis]	233	315	65%	9e-60	30%	XP_016319537.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Megachile rotundata]	231	312	59%	9e-60	31%	XP_012145650.1
potassium sodium efflux p-type fungal-type [Diplodia corticola]	234	352	67%	9e-60	29%	OJD36706.1
sodium transport ATPase [Trichophyton rubrum CBS 118892]	233	352	67%	9e-60	30%	XP_003231319.1
sodium transport atpase 5 [[Candida] auris]	233	332	64%	9e-60	31%	XP_018172361.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Salmo salar]	233	311	59%	9e-60	31%	XP_014022846.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Cimex lectularius]	233	322	65%	9e-60	31%	XP_014250369.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P34048]	233	343	64%	9e-60	30%	KGU33431.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Austrofundulus limnaeus]	233	313	59%	9e-60	31%	XP_013866735.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X13 [Nicrophorus vespilloides]	233	315	58%	9e-60	32%	XP_017784208.1
calcium-translocating P-type ATPase, SERCA-type [Kwoniella heveanensis BCC8398]	233	377	61%	1e-59	34%	OCF34697.1
Ca2+ ATPase [Plasmodium vivax]	211	211	14%	1e-59	89%	CAA67110.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Halyomorpha halys]	233	324	65%	1e-59	31%	XP_014271920.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-like isoform X1 [Octopus bimaculoides]	231	296	58%	1e-59	32%	XP_014785615.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X3 [Sinocyclocheilus anshuiensis]	233	315	65%	1e-59	30%	XP_016319539.1
potassium/sodium efflux P-type ATPase, fungal-type [Trichophyton interdigitale MR816]	233	354	67%	1e-59	30%	KDB27940.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Xiphophorus maculatus]	231	314	42%	1e-59	37%	XP_005815459.1
ATPase P-type K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Macrophomina phaseolina MS6]	233	338	66%	1e-59	31%	EKG20739.1
potassium/sodium efflux P-type ATPase, fungal-type [Pseudogymnoascus sp. 05NY08]	233	344	65%	1e-59	30%	OBT77491.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Sinocyclocheilus anshuiensis]	233	315	65%	1e-59	30%	XP_016319538.1
P-type ATPase involved in Na+ efflux [Scheffersomyces stipitis CBS 6054]	233	340	66%	1e-59	30%	XP_001387351.1
putative sodium/potassium-transporting atpase subunit alpha [Culex tarsalis]	233	315	58%	1e-59	31%	JAV31385.1
Na+/K+-ATPase alpha1 [Locusta migratoria]	233	319	59%	1e-59	31%	AHH35009.1
sodium/potassium-transporting ATPase subunit alpha-3-like [Scleropages formosus]	232	313	58%	1e-59	31%	KPP65694.1
LAMI_0H19196g1_1 [Lachancea mirantina]	233	337	66%	1e-59	29%	SCV04793.1
LAFE_0H05776g1_1 [Lachancea fermentati]	233	341	65%	1e-59	30%	SCW04093.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Nicrophorus vespilloides]	233	315	58%	1e-59	32%	XP_017784197.1
hypothetical protein S40293_05182 [Stachybotrys chartarum IBT 40293]	233	337	66%	1e-59	31%	KFA47878.1
LAFE_0D02960g1_1 [Lachancea fermentati]	234	234	65%	1e-59	29%	SCW01004.1
hypothetical protein CAPTEDRAFT_168025 [Capitella teleta]	233	312	58%	1e-59	31%	ELU12040.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Larimichthys crocea]	232	315	59%	1e-59	30%	XP_019116783.1
hypothetical protein S7711_09189 [Stachybotrys chartarum IBT 7711]	233	338	66%	1e-59	31%	KEY66263.1
Sodium/potassium-transporting ATPase subunit alpha-1 [Buceros rhinoceros silvestris]	224	224	31%	1e-59	37%	KFO85081.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Dinoponera quadriceps]	233	313	59%	1e-59	31%	XP_014476226.1
potassium/sodium efflux P-type ATPase, fungal-type [Exophiala oligosperma]	233	330	66%	1e-59	29%	XP_016256486.1
hypothetical protein VE01_08331 [Pseudogymnoascus verrucosus]	233	233	63%	1e-59	28%	XP_018127306.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Larimichthys crocea]	232	315	59%	1e-59	30%	XP_019116781.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Dinoponera quadriceps]	232	313	59%	1e-59	31%	XP_014476229.1
Na/K-ATPase isoform a [Ixodes scapularis]	232	320	59%	1e-59	32%	AMK38059.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Pygocentrus nattereri]	232	313	65%	1e-59	31%	XP_017557415.1
P-type Na+-ATPase [Fusarium oxysporum f. sp. lycopersici]	233	346	66%	1e-59	29%	AAR01872.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Sinocyclocheilus rhinocerous]	233	315	65%	1e-59	30%	XP_016387520.1
potassium/sodium efflux P-type ATPase [Colletotrichum salicis]	233	349	69%	1e-59	30%	KXH26827.1
probable ENA5-Plasma membrane P-type ATPase involved in Na+ and Li+ efflux [Rhynchosporium agropyri]	233	346	65%	1e-59	30%	CZT07220.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type [Musa acuminata subsp. malaccensis]	233	286	59%	1e-59	30%	XP_009414910.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Neolamprologus brichardi]	232	321	65%	1e-59	31%	XP_006792879.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X3 [Sinocyclocheilus rhinocerous]	232	314	65%	1e-59	30%	XP_016387522.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Sinocyclocheilus rhinocerous]	232	314	65%	1e-59	30%	XP_016387521.1
calcium-transporting ATPase 3 [Nannizzia gypsea CBS 118893]	232	339	68%	1e-59	29%	XP_003170830.1
potassium/sodium efflux P-type ATPase, fungal-type [Trichophyton soudanense CBS 452.61]	232	351	67%	2e-59	30%	EZF78570.1
Sodium/potassium-transporting ATPase subunit alpha [Melipona quadrifasciata]	233	315	59%	2e-59	31%	KOX77067.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha [Drosophila miranda]	232	307	64%	2e-59	29%	XP_017156381.1
hypothetical protein TSUD_333860 [Trifolium subterraneum]	231	231	64%	2e-59	29%	GAU50647.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Sinocyclocheilus grahami]	232	314	65%	2e-59	30%	XP_016123222.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Hippocampus comes]	232	313	59%	2e-59	31%	XP_019729762.1
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter [Penicillium camemberti]	231	337	58%	2e-59	30%	CRL30702.1
predicted protein [Physcomitrella patens]	232	411	59%	2e-59	37%	XP_001765694.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Sinocyclocheilus grahami]	232	314	65%	2e-59	30%	XP_016123223.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Hippocampus comes]	232	313	59%	2e-59	31%	XP_019729760.1
potassium/sodium efflux P-type ATPase, fungal-type, variant [Capronia semi-immersa]	231	331	67%	2e-59	30%	KIW62606.1
Na/K-ATPase alpha-subunit [Eurythoe complanata]	231	319	65%	2e-59	31%	AOG19177.1
Calcium-transporting ATPase 3-like protein 1 [Colletotrichum chlorophyti]	233	350	65%	2e-59	30%	OLN89013.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Notothenia coriiceps]	229	229	48%	2e-59	30%	XP_010768502.1
unnamed protein product [Tetraodon nigroviridis]	232	320	59%	2e-59	31%	CAF95488.1
Sodium/potassium-transporting ATPase subunit alpha [Stegodyphus mimosarum]	230	310	56%	2e-59	31%	KFM80606.1
hypothetical protein GGTG_08053 [Gaeumannomyces graminis var. tritici R3-111a-1]	233	354	66%	2e-59	29%	XP_009224153.1
unnamed protein product [Oncorhynchus mykiss]	223	223	28%	2e-59	38%	CDQ89555.1
hypothetical protein SOVF_172410 [Spinacia oleracea]	232	330	67%	2e-59	30%	KNA07381.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Amyelois transitella]	232	313	59%	2e-59	31%	XP_013192142.1
potassium/sodium eff [Alternaria alternata]	232	347	68%	2e-59	29%	XP_018391769.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Papilio machaon]	232	313	59%	2e-59	31%	XP_014372069.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Myotis davidii]	231	332	54%	2e-59	36%	XP_015419023.1
predicted protein [Nectria haematococca mpVI 77-13-4]	233	347	69%	2e-59	30%	XP_003044649.1
BA75_01103T0 [Komagataella pastoris]	232	352	66%	2e-59	29%	ANZ73913.1
PREDICTED: calcium-transporting ATPase, endoplasmic reticulum-type [Cicer arietinum]	232	333	66%	2e-59	32%	XP_004510638.1
Na+,K+ ATPase alpha-subunit 1 [Danaus eresimus]	231	312	58%	2e-59	32%	AFU25674.1
calcium-transporting ATPase PMC1 [Sugiyamaella lignohabitans]	233	233	64%	2e-59	29%	XP_018733565.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sodium/potassium-transporting ATPase alpha-3 chain protein [Daphnia magna]	231	303	58%	2e-59	31%	JAN65681.1
potassium/sodium efflux P-type ATPase [Colletotrichum tofieldiae]	232	336	66%	2e-59	30%	KZL63814.1
BnaC05g44550D [Brassica napus]	232	327	67%	2e-59	31%	CDY28053.1
Sodium/potassium-transporting ATPase subunit alpha [Trichinella zimbabwensis]	232	319	59%	2e-59	30%	KRZ04305.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Equus przewalskii]	225	225	31%	2e-59	37%	XP_008508825.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Papilio machaon]	231	312	58%	2e-59	32%	XP_014372070.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Papilio machaon]	232	313	59%	2e-59	31%	XP_014372062.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Amyelois transitella]	232	313	58%	2e-59	31%	XP_013192138.1
putative Na+/K+-ATPase alpha subunit [Pareledone sp. GG-2011]	232	289	57%	2e-59	32%	AEH68836.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Astyanax mexicanus]	231	314	59%	2e-59	31%	XP_015461719.1
Ca2+-transporting ATPase [Talaromyces islandicus]	234	234	67%	2e-59	28%	CRG85033.1
Sodium/potassium-transporting ATPase alpha-3 chain protein [Daphnia magna]	231	303	58%	2e-59	31%	JAN65682.1
na+/k+ atpase alpha subunit [Anopheles darlingi]	229	310	59%	2e-59	31%	ETN62539.1
putative Na+/K+-ATPase alpha subunit [Paroctopus digueti]	231	298	58%	2e-59	32%	AEH68841.1
PREDICTED: LOW QUALITY PROTEIN: calcium-transporting ATPase 9, plasma membrane-type [Eucalyptus grandis]	232	232	64%	2e-59	28%	XP_018719958.1
sodium transport ATPase [Trichophyton violaceum]	232	350	67%	2e-59	30%	OAL71834.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like [Poecilia latipinna]	224	224	31%	2e-59	36%	XP_014912148.1
sodium P-type ATPase-like protein [Glonium stellatum]	232	334	66%	2e-59	30%	OCL11911.1
Sodium transport ATPase 5 [Fusarium oxysporum f. sp. cubense race 4]	234	645	66%	2e-59	29%	EMT71871.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Papilio machaon]	231	313	58%	2e-59	32%	XP_014372066.1
TPA: Na,K-ATPase [Drosophila mojavensis]	231	310	65%	2e-59	28%	DAA64534.1
Na+/K+ ATPase alpha subunit isoform 6 [Danio rerio]	231	314	59%	2e-59	30%	AAG27058.1
Na+/K+-ATPase alpha2 [Locusta migratoria]	231	314	58%	2e-59	31%	AHH35010.1
PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 2-like [Notothenia coriiceps]	217	217	28%	2e-59	36%	XP_010777871.1
potassium/sodium eff [Exidia glandulosa HHB12029]	231	231	46%	2e-59	29%	KZV86414.1
unnamed protein product [Vitis vinifera]	232	232	64%	2e-59	28%	CBI25301.3
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Aethina tumida]	231	315	59%	2e-59	31%	XP_019873766.1
Sodium/potassium-transporting ATPase subunit alpha [Orchesella cincta]	232	309	70%	2e-59	29%	ODN05419.1
Sodium/potassium-transporting ATPase subunit alpha [Stegodyphus mimosarum]	231	318	59%	2e-59	31%	KFM68400.1
PREDICTED: LOW QUALITY PROTEIN: sodium/potassium-transporting ATPase subunit alpha-3 [Pongo abelii]	231	287	51%	3e-59	32%	XP_009230932.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Tribolium castaneum]	231	313	59%	3e-59	31%	XP_015837163.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Bombyx mori]	231	313	58%	3e-59	32%	XP_012544719.1
Calcium-transporting ATPase 9, plasma membrane-type [Morus notabilis]	232	232	64%	3e-59	28%	XP_010109302.1
potassium/sodium efflux P-type ATPase, fungal-type [Capronia semi-immersa]	231	331	67%	3e-59	30%	KIW62605.1
hypothetical protein AURANDRAFT_70232 [Aureococcus anophagefferens]	233	321	64%	3e-59	30%	XP_009038618.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Bombyx mori]	231	313	59%	3e-59	31%	XP_004921830.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Na,K-ATPase alpha subunit 3 [Carassius auratus]	231	314	59%	3e-59	30%	BAB60722.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Papilio machaon]	231	312	58%	3e-59	32%	XP_014372063.1
potassium/sodium efflux P-type ATPase, fungal-type [Pneumocystis carinii B80]	231	343	64%	3e-59	29%	XP_018226890.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Oryzias latipes]	231	312	59%	3e-59	31%	XP_004074116.1
probable putative calcium P-type ATPase NCA-2 [Rhynchosporium secalis]	233	233	64%	3e-59	29%	CZT43099.1
calcium-translocating P-type ATPase [Colletotrichum gloeosporioides Cg-14]	233	233	64%	3e-59	28%	EQB45553.1
potassium sodium efflux p-type fungal-type [Stemphylium lycopersici]	232	343	66%	3e-59	30%	KNG47397.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2-like [Poecilia mexicana]	224	224	31%	3e-59	36%	XP_014868011.1
unnamed protein product [Kluyveromyces dobzhanskii CBS 2104]	232	357	67%	3e-59	29%	CDO96311.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Amyelois transitella]	231	311	58%	3e-59	31%	XP_013192141.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 [Xiphophorus maculatus]	223	223	31%	3e-59	36%	XP_005815773.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Haplochromis burtoni]	231	313	59%	3e-59	31%	XP_005941265.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Tribolium castaneum]	231	313	58%	3e-59	32%	XP_008196418.1
Calcium ATPase, transmembrane M [Glarea lozoyensis ATCC 20868]	231	329	64%	3e-59	31%	XP_008077566.1
potassium sodium efflux p-type fungal-type ATPase [Colletotrichum incanum]	232	345	67%	3e-59	30%	KZL73567.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X11 [Tribolium castaneum]	231	313	58%	3e-59	32%	XP_008196424.1
hypothetical protein ACN38_g11383 [Penicillium nordicum]	230	337	58%	3e-59	30%	KOS37810.1
hypothetical protein SPRG_17035 [Saprolegnia parasitica CBS 223.65]	233	306	59%	3e-59	30%	XP_012211712.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Bombyx mori]	231	313	58%	3e-59	32%	XP_004921831.1
putative Na(+)/Li(+)-exporting P-type ATPase isoform 2B [Hortaea werneckii]	230	323	66%	3e-59	30%	AGT96032.1
potassium/sodium efflux P-type ATPase [Magnaporthe oryzae 70-15]	232	356	69%	3e-59	29%	XP_003712598.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Bombyx mori]	231	313	58%	3e-59	32%	XP_004921833.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Tribolium castaneum]	231	313	58%	3e-59	32%	XP_008196421.1
potassium/sodium efflux P-type ATPase [Colletotrichum nymphaeae SA-01]	231	348	67%	3e-59	30%	KXH61616.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Papilio polytes]	231	312	59%	3e-59	31%	XP_013139198.1
unnamed protein product [Tetraodon nigroviridis]	231	316	59%	3e-59	30%	CAF93092.1
Na+/K+-ATPase alpha-subunit 3 [Periophthalmodon schlosseri]	231	314	59%	3e-59	30%	AGR87394.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Bombyx mori]	231	312	59%	3e-59	31%	XP_004921834.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X4 [Oreochromis niloticus]	231	320	65%	3e-59	31%	XP_005452412.1
Na+,K+ ATPase alpha-subunit 1 [Euchaetes egle]	231	313	58%	3e-59	31%	AFU25677.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Papilio xuthus]	231	312	58%	3e-59	32%	XP_013170719.1
sodium transport ATPase [Trichophyton rubrum]	233	352	67%	3e-59	30%	OAL68401.1
Calcium-transporting ATPase 3 [Ceratocystis platani]	232	335	65%	3e-59	30%	KKF93809.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Papilio xuthus]	231	313	59%	3e-59	31%	XP_013170711.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
potassium/sodium efflux P-type ATPase [Isaria fumosorosea ARSEF 2679]	232	338	66%	3e-59	29%	XP_018706381.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X2 [Salmo salar]	231	309	59%	3e-59	31%	XP_014055887.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans P87]	230	340	58%	3e-59	30%	KGU02756.1
calcium-transporting ATPase 3 [Magnaporthe oryzae P131]	231	355	69%	4e-59	29%	ELQ58159.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X6 [Papilio xuthus]	231	313	58%	4e-59	32%	XP_013170716.1
Na+,K+ ATPase alpha-subunit 1 [Danaus plexippus]	231	312	58%	4e-59	32%	AFU25676.1
Sodium/potassium-transporting ATPase alpha-3 chain protein [Daphnia magna]	231	286	58%	4e-59	31%	JAN47235.1
cation-transporting atpase fungi [Aspergillus fischeri NRRL 181]	231	231	64%	4e-59	28%	XP_001262739.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Sinocyclocheilus anshuiensis]	231	313	59%	4e-59	30%	XP_016311404.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Papilio xuthus]	231	312	59%	4e-59	31%	XP_013170718.1
putative potassium/sodium efflux P-type ATPase [Colletotrichum sublineola]	232	348	68%	4e-59	29%	KDN71213.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X4 [Haplochromis burtoni]	231	320	64%	4e-59	31%	XP_014193911.1
potassium/sodium efflux P-type ATPase, fungal-type [Candida albicans Ca6]	230	340	58%	4e-59	30%	KHC31448.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Vollenhovia emeryi]	231	313	58%	4e-59	31%	XP_011876341.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Dufourea novaeangliae]	231	314	59%	4e-59	31%	XP_015440152.1
AaceriAGL097Cp [Saccharomycetaceae sp. 'Ashbya aceri']	231	347	65%	4e-59	30%	AGO13772.1
Na,K-ATPase alpha-subunit [Bombyx mori]	231	312	59%	4e-59	31%	BAS22117.1
putative sodium pump alpha subunit [Danaus plexippus]	232	314	61%	4e-59	31%	EHJ73788.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Vollenhovia emeryi]	231	313	58%	4e-59	31%	XP_011876338.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X3 [Sinocyclocheilus grahami]	231	313	59%	4e-59	30%	XP_016088879.1
calcium transporting ATPase (Pmc1) [Aspergillus fumigatus Z5]	231	231	64%	4e-59	29%	KMK55816.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Fopius arisanus]	231	312	59%	4e-59	30%	XP_011305856.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Vollenhovia emeryi]	231	313	58%	4e-59	31%	XP_011876343.1
calcium-transporting ATPase 3 [Purpureocillium lilacinum]	231	339	69%	4e-59	29%	OAQ75266.1
PREDICTED: calcium-transporting ATPase 10, plasma membrane-type [Ziziphus jujuba]	229	229	60%	4e-59	29%	XP_015895714.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Papilio polytes]	231	311	59%	4e-59	31%	XP_013139201.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Papilio xuthus]	231	312	58%	4e-59	32%	XP_013170712.1
alpha subunit of putative Na+/K+ ATPase [Daphnia pulex]	231	296	59%	4e-59	30%	EFX69525.1
potassium/sodium efflux P-type ATPase [Colletotrichum simmondsii]	231	350	67%	4e-59	30%	KXH52018.1
P-type ATPase [Histoplasma capsulatum H88]	231	340	64%	4e-59	27%	EGC41320.1
potassium/sodium efflux P-type ATPase like protein [Zymoseptoria brevis]	231	323	64%	4e-59	29%	KJY00439.1
hypothetical protein cypCar_00027006 [Cyprinus carpio]	230	294	57%	4e-59	30%	KTF94441.1
hypothetical protein DOTSEDRAFT_57843 [Dothistroma septosporum NZE10]	231	333	68%	4e-59	29%	EME48512.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Salmo salar]	231	308	59%	4e-59	31%	XP_014055886.1
ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem duplicate 3 [Danio rerio]	231	315	58%	4e-59	30%	NP_571763.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein Kpol_1052p20 [Vanderwaltozyma polyspora DSM 70294]	231	337	66%	4e-59	29%	XP_001644531.1
probable Na+-transporting ATPase ENA-1 (sodium P-type ATPase ENA-1) [Fusarium fujikuroi IMI 58289]	231	343	63%	4e-59	29%	CCT64892.1
Na+/K+ ATPase, alpha subunit, putative [Ixodes scapularis]	231	318	58%	4e-59	32%	XP_002404061.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Fundulus heteroclitus]	229	298	56%	4e-59	30%	XP_012711044.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X2 [Takifugu rubripes]	230	313	59%	5e-59	30%	XP_011604274.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 [Esox lucius]	231	313	59%	5e-59	30%	XP_010899757.1
sodium pump alpha subunit [Ctenocephalides felis]	231	310	58%	5e-59	31%	AAB28239.1
probable Na+-transporting ATPase ENA-1 (sodium P-type ATPase ENA-1) [Fusarium proliferatum]	231	343	63%	5e-59	29%	CVL12071.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1 isoform X2 [Haplochromis burtoni]	230	320	64%	5e-59	31%	XP_014193910.1
hypothetical protein PPTG_03625 [Phytophthora parasitica INRA-310]	231	392	57%	5e-59	38%	XP_008894556.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Aethina tumida]	231	313	58%	5e-59	31%	XP_019873770.1
hypothetical protein L917_13045 [Phytophthora parasitica]	231	392	57%	5e-59	38%	ETL87808.1
probable ENA5-Plasma membrane P-type ATPase involved in Na+ and Li+ efflux [Rhynchosporium commune]	231	344	65%	5e-59	29%	CZS89197.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha [Galendromus occidentalis]	231	313	58%	5e-59	32%	XP_018494795.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Vollenhovia emeryi]	230	312	58%	5e-59	31%	XP_011876342.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Trichogramma pretiosum]	231	312	59%	5e-59	31%	XP_014232355.1
Atp1a1a.3 protein [Danio rerio]	230	313	58%	5e-59	30%	AAH54591.1
hypothetical protein L916_13221 [Phytophthora parasitica]	231	391	57%	5e-59	38%	ETL34547.1
putative sarcoplasmic/endoplasmic reticulum calcium ATPase [Auricularia subglabra TFB-10046 SS5]	230	337	63%	5e-59	30%	XP_007355930.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Plutella xylostella]	230	310	58%	5e-59	31%	XP_011548240.1
unnamed protein product [Albugo candida]	231	395	60%	5e-59	35%	CCI41983.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like [Maylandia zebra]	230	312	59%	5e-59	31%	XP_004572707.1
hypothetical protein M407DRAFT_211793 [Tulasnella calospora MUT 4182]	231	315	63%	5e-59	28%	KIO24876.1
sodium transport ATPase 5 [Arthroderma otae CBS 113480]	230	316	58%	5e-59	30%	XP_002849940.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3 isoform X1 [Takifugu rubripes]	230	314	59%	5e-59	30%	XP_011604273.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-1-like [Ictalurus punctatus]	230	321	65%	5e-59	31%	XP_017312773.1
PREDICTED: calcium-transporting ATPase 8, plasma membrane-type-like [Raphanus sativus]	231	283	59%	5e-59	30%	XP_018471112.1
potassium/sodium efflux P-type ATPase [Magnaporthiopsis poae ATCC 64411]	231	350	69%	5e-59	28%	KLU88879.1
Na+/K+ ATPase alpha subunit [Euchaetes egle]	227	306	58%	5e-59	31%	CCJ05447.1
Na,K-ATPase alpha subunit [Brugia malayi]	230	313	59%	6e-59	31%	XP_001901816.1
hypothetical protein ASPNIDRAFT_48676 [Aspergillus niger ATCC 1015]	231	340	63%	6e-59	29%	EHA24550.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Orussus abietinus]	229	311	59%	6e-59	30%	XP_012272101.1
potassium/sodium efflux P-type ATPase, fungal-type [Trichoderma harzianum]	231	347	66%	6e-59	30%	KKO98809.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X8 [Anoplophora glabripennis]	230	314	64%	6e-59	32%	XP_018562056.1
Na+/K+ ATPase alpha subunit [Danaus genutia]	227	306	58%	6e-59	31%	CCW28387.1
hypothetical protein g.33849 [Graphocephala atropunctata]	230	317	64%	6e-59	31%	JAT36939.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
calcium-transporting ATPase 3 [Purpureocillium lilacinum]	231	339	69%	6e-59	29%	XP_018174742.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-3-like isoform X1 [Sinocyclocheilus rhinocerous]	230	311	59%	6e-59	29%	XP_016425513.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X9 [Plutella xylostella]	230	310	59%	6e-59	31%	XP_011548242.1
Ca2+ transporting ATPase [Klebsormidium flaccidum]	231	340	63%	6e-59	30%	GAQ85006.1
hypothetical protein ASPTUDRAFT_131144 [Aspergillus tubingensis CBS 134.48]	231	341	63%	6e-59	29%	OJI79860.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Apis florea]	230	310	58%	6e-59	31%	XP_012345702.1
predicted protein [Physcomitrella patens]	229	229	64%	6e-59	29%	XP_001758854.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X4 [Agrilus planipennis]	230	314	58%	6e-59	31%	XP_018327700.1
P-type ATPase, calcium transporting Cta3 [Schizosaccharomyces pombe 972h-]	230	342	67%	6e-59	30%	NP_595246.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Plutella xylostella]	230	310	58%	6e-59	31%	XP_011548233.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X7 [Linepithema humile]	230	311	58%	6e-59	31%	XP_012228931.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Copidosoma floridanum]	230	316	59%	6e-59	31%	XP_014205893.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha-2 [Gekko japonicus]	224	275	33%	6e-59	36%	XP_015285056.1
Sodium transport ATPase 5 [Scedosporium apiospermum]	231	340	66%	6e-59	29%	XP_016638874.1
Sodium/potassium-transporting ATPase alpha-3 chain protein [Daphnia magna]	230	303	65%	6e-59	31%	JAN30194.1
PREDICTED: calcium-transporting ATPase 3, endoplasmic reticulum-type-like [Nicotiana tabacum]	224	224	47%	7e-59	30%	XP_016495335.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Diachasma alloeum]	230	311	59%	7e-59	30%	XP_015120701.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Plutella xylostella]	230	310	58%	7e-59	31%	XP_011548237.1
Na+/K+ ATPase alpha subunit [Idea leuconoe]	227	306	58%	7e-59	31%	CCW28391.1
BMA-EAT-6, isoform a [Brugia malayi]	230	313	59%	7e-59	31%	CRZ24266.1
uncharacterized protein Dpse_GA23078 [Drosophila pseudoobscura pseudoobscura]	230	304	64%	7e-59	28%	XP_002133780.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Bombus terrestris]	230	313	59%	7e-59	31%	XP_012163875.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Apis mellifera]	230	311	58%	7e-59	31%	XP_006564222.1
hypothetical protein V499_04145 [Pseudogymnoascus sp. VKM F-103]	230	341	65%	7e-59	30%	KFY75993.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X5 [Athalia rosae]	230	313	58%	7e-59	31%	XP_012269655.1
unnamed protein product [Homo sapiens]	224	224	31%	7e-59	36%	BAG52899.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Diuraphis noxia]	230	311	70%	7e-59	30%	XP_015370437.1
sodium/potassium-transporting ATPase subunit alpha-B [Salpingoeca rosetta]	231	317	68%	7e-59	29%	XP_004991633.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X2 [Athalia rosae]	230	313	58%	7e-59	31%	XP_012269651.1
hypothetical protein ASPVEDRAFT_137456 [Aspergillus versicolor CBS 583.65]	230	332	67%	7e-59	29%	OJJ04785.1
Na+/K+-ATPase alpha 3a [Monopterus albus]	230	311	65%	7e-59	31%	AGV06213.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X13 [Agrilus planipennis]	230	313	58%	7e-59	31%	XP_018327769.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X1 [Athalia rosae]	230	313	58%	7e-59	31%	XP_012269650.1
PREDICTED: sodium/potassium-transporting ATPase subunit alpha isoform X3 [Plutella xylostella]	230	310	59%	7e-59	31%	XP_011548234.1
P-type Na+-ATPase [Metarhizium rileyi RCEF 4871]	231	333	66%	7e-59	29%	OAA45654.1

Alignments

P-type ATPase [Plasmodium falciparum]

Sequence ID: **AAC47167.1** Length: 1228 Number of Matches: 1

Range 1: 1 to 1228

Score	Expect	Method	Identities	Positives	Gaps	Frame
2280 bits(5908)	0.0()	Compositional matrix adjust.	1228/1228(100%)	1228/1228(100%)	0/1228(0%)	

Features:

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Query  1     MSSQNNNKQGGQdinnkkdsddikPSVSKEDLINSLKNDELNKNTTMDQNDmkknenmni  60
             MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI
Sbjct  1     MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI  60

Query  61    kkneVLNNSNNVEDGDNENSKFMNKSKEGLnningeknddnnSIVKVEESPKSIGYNYYA  120
             KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA
Sbjct  61    KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA  120

Query  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPvvll  180
             SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL
Sbjct  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL  180

Query  181   llvaavaslalnevvEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240
             LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ
Sbjct  181   LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240

Query  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300
             KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST
Sbjct  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300

Query  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIAsqlkksskgsklTPLQVALNKlggl  360
             PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL
Sbjct  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL  360

Query  361   igliaiivlvviislaviiKYRDPAHADKDPTfviiiigvgfavssiPEGLPMVVTITLS  420
             IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS
Sbjct  361   IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS  420

Query  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480
             AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN
Sbjct  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480

Query  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540
             KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI
Sbjct  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540

Query  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600
             VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY
Sbjct  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600

Query  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD  660
             LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD
Sbjct  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD  660

Query  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720
             RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL
Sbjct  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720

Query  721   KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  780
             KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ
Sbjct  721   KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  780

Query  781   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  840
             KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY
Sbjct  781   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  840

Query  841   SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  900
             SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL
Sbjct  841   SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  900

Query  901   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  960
             IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL
Sbjct  901   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  960

Query  961   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1020
             NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF
Sbjct  961   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1020

Query  1021  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1080
             SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW
Sbjct  1021  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1080

Query  1081  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1140
             DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS
Sbjct  1081  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1140

Query  1141  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW  1200
             DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW
Sbjct  1141  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW  1200

Query  1201  MHLACSISATLTFLSTCIPGITSILNTT  1228
             MHLACSISATLTFLSTCIPGITSILNTT
Sbjct  1201  MHLACSISATLTFLSTCIPGITSILNTT  1228
```

potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]

Sequence ID: **ETW17726.1** Length: 1264 Number of Matches: 1

See 1 more title(s)

Range 1: 1 to 1226

Score	Expect	Method	Identities	Positives	Gaps	Frame

2248 bits(5826)	0.0()	Compositional matrix adjust.	1220/1228(99%)	1221/1228(99%)	2/1228(0%)

Features:

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Query  1     MSSQNNNKQGGQdinnkkdsddikPSVSKEDLINSLKNDELNKNTTMDQNDmkknenmni  60
             MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI
Sbjct  1     MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI  60

Query  61    kkneVLNNSNNVEDGDNENSKFMNKSKEGLnningeknddnnSIVKVEESPKSIGYNYYA  120
             KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA
Sbjct  61    KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA  120

Query  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPvvll  180
             SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL
Sbjct  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL  180

Query  181   llvaavaslalnevvEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240
             LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ
Sbjct  181   LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240

Query  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300
             KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST
Sbjct  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300

Query  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIAsqlkksskgsklTPLQVALNKlggl  360
             PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL
Sbjct  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL  360

Query  361   igliaiivlvviislaviiKYRDPAHADKDPTfviiiigvgfavssiPEGLPMVVTITLS  420
             IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS
Sbjct  361   IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS  420

Query  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480
             AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN
Sbjct  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480

Query  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540
             KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI
Sbjct  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540

Query  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600
             VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY
Sbjct  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600

Query  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD  660
             LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKP K YTH+ALIKGAPDRLLD
Sbjct  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPGKVYTHVALIKGAPDRLLD  660

Query  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720
             RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL
Sbjct  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720

Query  721   KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  780
             KKLEDAD  ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ
Sbjct  721   KKLEDAD--ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  778

Query  781   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  840
             KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY
Sbjct  779   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  838

Query  841   SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  900
             SRAQ EDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL
Sbjct  839   SRAQPEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  898

Query  901   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  960
             IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL
Sbjct  899   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  958

Query  961   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1020
             NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF
Sbjct  959   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1018

Query  1021  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1080
             SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW
Sbjct  1019  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1078

Query  1081  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1140
             DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS
Sbjct  1079  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1138

Query  1141  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW  1200
             DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVR  EPFYKVFNRNMW
Sbjct  1139  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRSWEPFYKVFNRNMW  1198

Query  1201  MHLACSISATLTFLSTCIPGITSILNTT  1228
             MHLACSISATLTFLSTCIPGITSILNTT
Sbjct  1199  MHLACSISATLTFLSTCIPGITSILNTT  1226
```

P-type ATPase4 [Plasmodium falciparum]

Sequence ID: **AAF17245.1** Length: 1264 Number of Matches: 1

See 3 more title(s)

Range 1: 1 to 1226

Score	Expect	Method	Identities	Positives	Gaps	Frame
2245 bits(5818)	0.0()	Compositional matrix adjust.	1219/1228(99%)	1220/1228(99%)	2/1228(0%)	

Features:

```
Query  1     MSSQNNNKQGGQdinnkkdsddikPSVSKEDLINSLKNDELNKNTTMDQNDmkknenmni  60
             MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI
Sbjct  1     MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI  60

Query  61    kkneVLNNSNNVEDGDNENSKFMNKSKEGLnningeknddnnSIVKVEESPKSIGYNYYA  120
             KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA
```

```
Sbjct  61    KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA  120

Query  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPvvll  180
             SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL
Sbjct  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL  180

Query  181   llvaavaslalnevvEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240
             LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ
Sbjct  181   LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240

Query  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300
             KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST
Sbjct  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300

Query  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIAsqlkksskgsklTPLQVALNKlggl  360
             PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL
Sbjct  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL  360

Query  361   igliaiivlvviislaviiKYRDPAHADKDPTfviiiigvgfavssiPEGLPMVVTITLS  420
             IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS
Sbjct  361   IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS  420

Query  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480
             AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN
Sbjct  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480

Query  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540
             KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI
Sbjct  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540

Query  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600
             VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY
Sbjct  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600

Query  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD  660
             LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKP K YTH+ALIKGAPDRLLD
Sbjct  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPGKVYTHVALIKGAPDRLLD  660

Query  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720
             RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL
Sbjct  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720

Query  721   KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  780
             KKLEDAD  ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ
Sbjct  721   KKLEDAD--ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  778

Query  781   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  840
             KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY
Sbjct  779   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  838

Query  841   SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  900
             SRAQ EDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL
Sbjct  839   SRAQPEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  898

Query  901   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  960
             IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL
Sbjct  899   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  958

Query  961   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1020
             NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF
Sbjct  959   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1018

Query  1021  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1080
             SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW
Sbjct  1019  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1078

Query  1081  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1140
             DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDEN WCRPKDNKTS
Sbjct  1079  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENGWCRPKDNKTS  1138

Query  1141  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW  1200
             DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVR  EPFYKVFNRNMW
Sbjct  1139  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRSWEPFYKVFNRNMW  1198

Query  1201  MHLACSISATLTFLSTCIPGITSILNTT  1228
             MHLACSISATLTFLSTCIPGITSILNTT
Sbjct  1199  MHLACSISATLTFLSTCIPGITSILNTT  1226
```

potassium/sodium efflux P-type ATPase, fungal-type [Plasmodium falciparum FCH/4]

Sequence ID: **ETW30121.1** Length: 1264 Number of Matches: 1

See 3 more title(s)

Range 1: 1 to 1226

Score	Expect	Method	Identities	Positives	Gaps	Frame
2245 bits(5818)	0.0()	Compositional matrix adjust.	1219/1228(99%)	1221/1228(99%)	2/1228(0%)	

Features:

```
Query  1     MSSQNNNKQGGQdinnkkdsddikPSVSKEDLINSLKNDELNKNTTMDQNDmkknenmni  60
             MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI
Sbjct  1     MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI  60

Query  61    kkneVLNNSNNVEDGDNENSKFMNKSKEGLnningeknddnnSIVKVEESPKSIGYNYYA  120
             KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA
Sbjct  61    KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA  120

Query  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPvvll  180
             SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL
Sbjct  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL  180

Query  181   llvaavaslalnevvEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240
             LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ
Sbjct  181   LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240

Query  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300
             KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST
```

```
Sbjct  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300

Query  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIAsqlkksskgskltPLQVALNKlggl  360
             PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL
Sbjct  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL  360

Query  361   igliaiivlvviislaviiKYRDPAHADKDPTfviiiigvgfavssiPEGLPMVVTITLS  420
             IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS
Sbjct  361   IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS  420

Query  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480
             AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN
Sbjct  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480

Query  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540
             KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI
Sbjct  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540

Query  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600
             VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY
Sbjct  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600

Query  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD  660
             LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKP K YTH+ALIKGAPDRLLD
Sbjct  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPGKVYTHVALIKGAPDRLLD  660

Query  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720
             RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL
Sbjct  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720

Query  721   KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  780
             KKLEDAD  ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ
Sbjct  721   KKLEDAD--ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  778

Query  781   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  840
             KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY
Sbjct  779   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  838

Query  841   SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  900
             SRAQ EDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL
Sbjct  839   SRAQPEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  898

Query  901   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  960
             IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL
Sbjct  899   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  958

Query  961   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1020
             NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF
Sbjct  959   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1018

Query  1021  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1080
             SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW
Sbjct  1019  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1078

Query  1081  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1140
             DP+NNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS
Sbjct  1079  DPKNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1138

Query  1141  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW  1200
             DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVR  EPFYKVFNRNMW
Sbjct  1139  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRSWEPFYKVFNRNMW  1198

Query  1201  MHLACSISATLTFLSTCIPGITSILNTT  1228
             MHLACSISATLTFLSTCIPGITSILNTT
Sbjct  1199  MHLACSISATLTFLSTCIPGITSILNTT  1226
```

P-type ATPase4 [Plasmodium falciparum IGH-CR14]

Sequence ID: **KNG76774.1** Length: 1264 Number of Matches: 1

Range 1: 1 to 1226

Score	Expect	Method	Identities	Positives	Gaps	Frame
2242 bits(5810)	0.0()	Compositional matrix adjust.	1218/1228(99%)	1220/1228(99%)	2/1228(0%)	

Features:

```
Query  1     MSSQNNNKQGGQdinnkkdsddikPSVSKEDLINSLKNDELNKNTTMDQNDmkknenmni  60
             MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI
Sbjct  1     MSSQNNNKQGGQDINNKKDSDDIKPSVSKEDLINSLKNDELNKNTTMDQNDMKKNENMNI  60

Query  61    kkneVLNNSNNVEDGDNENSKFMNKSKEGLnningeknddnnSIVKVEESPKSIGYNYYA  120
             KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA
Sbjct  61    KKNEVLNNSNNVEDGDNENSKFMNKSKEGLNNINGEKNDDNNSIVKVEESPKSIGYNYYA  120

Query  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPvvll  180
             SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL
Sbjct  121   SESIENLCKEFGLESINTGLNSEQVKINRDKYGENFIEKDEVVPVWLIFLSQYCSPVVLL  180

Query  181   llvaavaslalnevvEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240
             LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ
Sbjct  181   LLVAAVASLALNEVVEGVAIISIVTLNACLATYMEKSSGDAIGKLAEMASPQCTVLRNGQ  240

Query  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300
             KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST
Sbjct  241   KVVIPSREVVVGDVVLINTGDSISADLRLFDVIELKTNESLLTGESEDIKKTIVADNLST  300

Query  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIAsqlkksskgskltPLQVALNKlggl  360
             PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL
Sbjct  301   PFATNLCFATTSVTSGSGKGIVISTGLDTQVGKIASQLKKSSKGSKLTPLQVALNKLGGL  360

Query  361   igliaiivlvviislaviiKYRDPAHADKDPTfviiiigvgfavssiPEGLPMVVTITLS  420
             IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS
Sbjct  361   IGLIAIIVLVVIISLAVIIKYRDPAHADKDPTFVIIIIGVGFAVSSIPEGLPMVVTITLS  420

Query  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480
             AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN
Sbjct  421   AGAKDMVKKNANVRKLPAVETLGCCSVICSDKTGTLTEGKMTAINAVTICKNSSLSDENN  480
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Query  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540
             KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI
Sbjct  481   KLTKTFDFYPTKGFEPCGGLFDSNELTSEKKKEIVIAKNQNTSYDKVLYNYGNPSNKSVI  540

Query  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600
             VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY
Sbjct  541   VDKTRSLMFAAYLNSYDTTLSRDPKTLKWGIHGNMSEGPIVVAAAKVGYSFINNPNHKSY  600

Query  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPRKEYTHIALIKGAPDRLLD  660
             LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKP K YTH+ALIKGAPDRLLD
Sbjct  601   LDNFQRLDDLEVTFNSSRKMKITFYKLKTVNVFENVYLDKPGKVYTHVALIKGAPDRLLD  660

Query  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720
             RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL
Sbjct  661   RSTHLLEETSMKKVQVSWNSTITQEERNVLIKKNLELSQKALRVLSICIKPLTDQNIEEL  720

Query  721   KKLEDADADERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  780
             KKLEDAD  ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ
Sbjct  721   KKLEDAD--ERLKYVNYDENGGFIPMGYVASFDPPRPGVKEAIQTCREAQVKVIMITGDQ  778

Query  781   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  840
             KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY
Sbjct  779   KPTAVAIGKLIGLIEEKSEQVEDINSLAIECSELHINKNPNEPILPNDQLDEFTDKILIY  838

Query  841   SRAQQEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  900
             SRAQ EDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL
Sbjct  839   SRAQPEDKITIVQSLKRKGYLVAMTGDGVNDAPALKAADIGVAMGINGTEVAKGASEMIL  898

Query  901   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  960
             IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL
Sbjct  899   IDDNFCTVVSAIDVGRTIFSNIQKFVCFLLGTNIGEIIYLSVAIVAQMPFPLEALQILFL  958

Query  961   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1020
             NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF
Sbjct  959   NLMTDGCPAVALSREPPNDDNMKTPPRPKKQPIMTKRWWFYGILPHTIFEALCVLLSLAF  1018

Query  1021  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1080
             SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW
Sbjct  1019  SLYICTGFYNLNGIHNLCKTVNLVDVNDANVYHEYKYFCSSYEYRISTDYVGWVTNVSFW  1078

Query  1081  DPQNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENRWCRPKDNKTS  1140
             DP+NNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDEN WCRPKDNKTS
Sbjct  1079  DPKNNEAVNFWGAAKGKVENINPLSDIVHPELRLRMQDGCSGDLTLDENGWCRPKDNKTS  1138

Query  1141  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRRREPFYKVFNRNMW  1200
             DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVR  EPFYKVFNRNMW
Sbjct  1139  DGYNDELEGILKKGFEDVTAKGSKRGRTMAFISAVWCEMLRAYTVRSWEPFYKVFNRNMW  1198

Query  1201  MHLACSISATLTFLSTCIPGITSILNTT  1228
             MHLACSISATLTFLSTCIPGITSILNTT
Sbjct  1199  MHLACSISATLTFLSTCIPGITSILNTT  1226
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