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BLAST® » [blastp suite](#) » results for RID-M2H7NZCC014

Job Title	OAO96815.1 SHD [Arabidopsis thaliana] ...
RID	M2H7NZCC014 Search expires on 08-24 00:16 am
Program	BLASTP
Database	nr
Query ID	lcl Query_34955
Description	OAO96815.1 SHD [Arabidopsis thaliana] ...
Molecule type	amino acid
Query Length	823

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
SHD [Arabidopsis thaliana]	1666	1666	100%	0.0	100.00%	OAO96815.1
SHEPHERD [Arabidopsis thaliana]	1663	1663	100%	0.0	99.88%	BAB86368.1
Chaperone protein htpG family protein [Arabidopsis thaliana]	1660	1660	100%	0.0	99.51%	NP_194150.1
Chaperone protein htpG family protein [Arabidopsis thaliana]	1657	1657	100%	0.0	99.39%	NP_974606.1
PREDICTED: endoplasmin homolog [Camelina sativa]	1633	1633	100%	0.0	97.57%	XP_010433803.1
PREDICTED: endoplasmin homolog isoform X2 [Camelina sativa]	1631	1631	100%	0.0	97.33%	XP_019088210.1
endoplasmin homolog [Arabidopsis lyrata subsp. lyrata]	1630	1630	100%	0.0	97.81%	XP_002867677.1
PREDICTED: endoplasmin homolog isoform X1 [Camelina sativa]	1628	1628	100%	0.0	97.21%	XP_010439073.1
endoplasmin homolog [Capsella rubella]	1627	1627	100%	0.0	97.45%	XP_006283118.1
PREDICTED: endoplasmin homolog [Camelina sativa]	1623	1623	100%	0.0	96.96%	XP_010448597.1
unnamed protein product [Arabis nemorensis]	1452	1452	100%	0.0	92.22%	VVB12715.1
hypothetical protein F2Q68_00030040 [Brassica cretica]	1446	1446	100%	0.0	93.92%	KAF2540583.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein DY000_02027227 [Brassica cretica]	1432	1432	100%	0.0	93.57%	KAF3594314.1
hypothetical protein BRARA_A01424 [Brassica rapa]	1425	1425	100%	0.0	94.17%	RID78617.1
PREDICTED: endoplasmin homolog [Brassica oleracea var. oleracea]	1425	1425	100%	0.0	94.05%	XP_013599404.1
endoplasmin homolog [Brassica napus]	1424	1424	100%	0.0	94.05%	XP_013711046.1
hypothetical protein DY000_02038148 [Brassica cretica]	1423	1423	100%	0.0	93.92%	KAF3531981.1
endoplasmin homolog [Brassica rapa]	1423	1423	100%	0.0	93.92%	XP_009137776.1
endoplasmin homolog [Eutrema salsugineum]	1421	1421	100%	0.0	94.65%	XP_006413464.1
hypothetical protein AALP_AA7G086900 [Arabis alpina]	1421	1421	100%	0.0	92.23%	KFK29085.1
PREDICTED: endoplasmin homolog [Raphanus sativus]	1419	1419	100%	0.0	93.92%	XP_018470582.1
unnamed protein product [Brassica oleracea]	1413	1413	100%	0.0	92.57%	VDD49484.1
LOW QUALITY PROTEIN: endoplasmin homolog [Brassica napus]	1408	1408	100%	0.0	94.05%	XP_013738026.1
unnamed protein product [Microthlaspi erraticum]	1402	1402	100%	0.0	94.05%	CAA7037362.1
PREDICTED: endoplasmin homolog [Brassica oleracea var. oleracea]	1401	1401	100%	0.0	93.69%	XP_013597503.1
PREDICTED: endoplasmin homolog [Raphanus sativus]	1400	1400	100%	0.0	92.01%	XP_018483299.1
BnaA03g46510D [Brassica napus]	1390	1390	99%	0.0	93.39%	CDY10992.1
unnamed protein product [Brassica oleracea]	1390	1390	100%	0.0	92.89%	VDD40276.1
unnamed protein product [Brassica rapa]	1387	1387	100%	0.0	92.96%	VDC83352.1
endoplasmin homolog [Brassica rapa]	1377	1377	100%	0.0	91.98%	XP_033132976.1
PREDICTED: endoplasmin homolog [Tarenaya hassleriana]	1376	1376	100%	0.0	87.00%	XP_010539097.1
endoplasmin homolog [Brassica napus]	1374	1374	100%	0.0	91.86%	XP_013656486.1
BnaA08g14800D [Brassica napus]	1373	1373	100%	0.0	91.74%	CDY24830.1
unnamed protein product [Brassica rapa]	1369	1369	100%	0.0	91.49%	VDD05535.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein BRARA_K00745 [Brassica rapa]	1363	1363	100%	0.0	91.86%	RIA05007.1
unnamed protein product [Brassica oleracea]	1348	1348	100%	0.0	89.19%	VDD55334.1
Endoplasmin-like protein [Morus notabilis]	1326	1326	94%	0.0	84.49%	EXC25010.1
PREDICTED: endoplasmin homolog [Beta vulgaris subsp. vulgaris]	1326	1326	94%	0.0	84.23%	XP_010691883.1
endoplasmin homolog [Morus notabilis]	1323	1323	98%	0.0	82.53%	XP_024030256.1
PREDICTED: endoplasmin homolog [Nicotiana attenuata]	1322	1322	94%	0.0	85.59%	XP_019239585.1
PREDICTED: endoplasmin homolog [Daucus carota subsp. sativus]	1316	1316	94%	0.0	83.78%	XP_017247267.1
hypothetical protein FNV43_RR11973 [Rhamnella rubrinervis]	1315	1315	94%	0.0	83.97%	KAF3446793.1
endoplasmin homolog [Cucurbita maxima]	1307	1307	94%	0.0	82.05%	XP_022996516.1
endoplasmin homolog isoform X3 [Rhodamnia argentea]	1307	1307	94%	0.0	83.51%	XP_030541427.1
endoplasmin homolog [Pistacia vera]	1306	1306	94%	0.0	83.33%	XP_031261550.1
endoplasmin homolog [Ziziphus jujuba]	1305	1305	96%	0.0	81.82%	XP_015884861.1
endoplasmin homolog [Cucurbita pepo subsp. pepo]	1304	1304	94%	0.0	82.90%	XP_023537188.1
endoplasmin homolog isoform X2 [Abrus precatorius]	1303	1303	94%	0.0	83.38%	XP_027368246.1
endoplasmin homolog isoform X1 [Rhodamnia argentea]	1303	1303	94%	0.0	83.35%	XP_030541424.1
endoplasmin homolog isoform X1 [Helianthus annuus]	1303	1303	100%	0.0	82.00%	XP_021999770.1
endoplasmin homolog isoform X3 [Helianthus annuus]	1303	1303	100%	0.0	82.10%	XP_021999772.1
hypothetical protein E3N88_37950 [Mikania micrantha]	1302	1302	100%	0.0	82.18%	KAD2804573.1
PREDICTED: endoplasmin homolog [Nicotiana sylvestris]	1302	1302	94%	0.0	85.86%	XP_009791520.1
endoplasmin homolog [Cynara cardunculus var. scolymus]	1302	1302	94%	0.0	84.92%	XP_024990293.1
hypothetical protein MIMGU_mgv1a001101mg [Erythranthe guttata]	1300	1300	100%	0.0	81.11%	EYU38796.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein F0562_027118 [Nyssa sinensis]	1300	1300	94%	0.0	84.08%	KAA8537510.1
endoplasmin homolog isoform X2 [Rhodamnia argentea]	1300	1300	94%	0.0	83.23%	XP_030541425.1
endoplasmin homolog [Cucurbita moschata]	1300	1300	94%	0.0	82.78%	XP_022951468.1
endoplasmin homolog precursor [Nicotiana tabacum]	1299	1299	94%	0.0	85.81%	NP_001312910.1
endoplasmin homolog [Vigna unguiculata]	1299	1299	94%	0.0	82.03%	XP_027940047.1
PREDICTED: endoplasmin homolog [Erythranthe guttata]	1299	1299	100%	0.0	81.11%	XP_012835715.1
PREDICTED: endoplasmin homolog [Nicotiana tabacum]	1299	1299	94%	0.0	85.60%	XP_016443728.1
PREDICTED: endoplasmin homolog [Daucus carota subsp. sativus]	1298	1298	94%	0.0	81.59%	XP_017258219.1
endoplasmin homolog [Lactuca sativa]	1298	1298	93%	0.0	84.41%	XP_023765821.1
endoplasmin homolog [Populus trichocarpa]	1298	1298	97%	0.0	81.60%	XP_002307732.1
PREDICTED: endoplasmin homolog [Nicotiana attenuata]	1298	1298	94%	0.0	85.48%	XP_019253531.1
unnamed protein product [Lactuca saligna]	1297	1297	93%	0.0	84.54%	CAB4108344.1
endoplasmin homolog [Cucurbita maxima]	1296	1296	94%	0.0	83.16%	XP_023002234.1
endoplasmin homolog [Nicotiana tomentosiformis]	1296	1296	94%	0.0	85.04%	XP_009606988.1
chaperon protein [Coffea canephora]	1296	1296	100%	0.0	80.97%	AMA33774.1
PREDICTED: endoplasmin homolog [Nicotiana tabacum]	1294	1294	94%	0.0	84.91%	XP_016497895.1
endoplasmin homolog [Hevea brasiliensis]	1294	1294	97%	0.0	82.13%	XP_021692667.1
chaperone protein htpG family protein [Artemisia annua]	1294	1294	100%	0.0	81.60%	PWA71326.1
endoplasmin homolog [Tanacetum cinerariifolium]	1294	1294	94%	0.0	83.76%	GEU31214.1
PREDICTED: endoplasmin homolog [Fragaria vesca subsp. vesca]	1294	1294	96%	0.0	81.51%	XP_004291352.1
endoplasmin homolog [Prosopis alba]	1293	1293	94%	0.0	82.61%	XP_028784634.1
endoplasmin homolog [Rosa chinensis]	1293	1293	94%	0.0	82.80%	XP_024164985.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
endoplasmin homolog [Populus alba]	1292	1292	94%	0.0	83.87%	XP_034931576.1
Heat shock protein Hsp90 [Cynara cardunculus var. scolymus]	1292	1292	94%	0.0	84.66%	KVI05215.1
endoplasmin homolog isoform X4 [Helianthus annuus]	1292	1292	100%	0.0	82.20%	XP_021999773.1
endoplasmin homolog [Coffea eugenoides]	1291	1291	100%	0.0	80.97%	XP_027148437.1
endoplasmin homolog isoform X2 [Helianthus annuus]	1291	1291	100%	0.0	82.10%	XP_021999771.1
hypothetical protein CISIN_1g003458mg [Citrus sinensis]	1291	1291	94%	0.0	83.06%	KDO84884.1
putative Heat shock protein Hsp90 family [Helianthus annuus]	1291	1291	100%	0.0	82.30%	KAF5771519.1
PREDICTED: endoplasmin homolog [Cucumis melo]	1291	1291	94%	0.0	83.29%	XP_008444821.1
endoplasmin homolog [Chenopodium quinoa]	1291	1291	92%	0.0	84.74%	XP_021755954.1
endoplasmin homolog [Hevea brasiliensis]	1290	1290	94%	0.0	83.95%	XP_021668062.1
endoplasmin homolog [Prosopis alba]	1290	1290	94%	0.0	82.48%	XP_028788281.1
hypothetical protein DKX38_008602 [Salix brachista]	1290	1290	94%	0.0	83.61%	KAB5557693.1
endoplasmin homolog [Ricinus communis]	1290	1290	94%	0.0	83.85%	XP_002510550.1
endoplasmin homolog [Jatropha curcas]	1289	1289	94%	0.0	83.46%	XP_012073780.1
endoplasmin homolog isoform X1 [Abrus precatorius]	1289	1289	94%	0.0	83.27%	XP_027368245.1
endoplasmin homolog [Vigna radiata var. radiata]	1289	1289	94%	0.0	82.59%	XP_014504844.1
endoplasmin homolog [Citrus sinensis]	1289	1289	94%	0.0	82.63%	XP_006473673.1
endoplasmin homolog [Citrus clementina]	1288	1288	94%	0.0	82.59%	XP_006435195.1
endoplasmin homolog [Chenopodium quinoa]	1288	1288	92%	0.0	84.74%	XP_021755293.1
HSP90 [Populus alba x Populus glandulosa]	1288	1288	94%	0.0	83.61%	AMM72795.1
endoplasmin homolog [Arachis ipaensis]	1288	1288	94%	0.0	83.51%	XP_016167432.1
endoplasmin homolog [Vitis riparia]	1288	1288	94%	0.0	83.63%	XP_034675729.1
PREDICTED: endoplasmin homolog [Vitis vinifera]	1288	1288	94%	0.0	83.63%	XP_002273785.1

Graphic Summary

Alignments

Taxonomy