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## BLAST® » [blastp suite](#) » results for RID-M2GXXZUD01R

Job Title	<a href="#">NP_178487.1 Chaperone protein htpG family... ..</a>
RID	<a href="#">M2GXXZUD01R</a> Search expires on 08-24 00:11 am
Program	BLASTP
Database	nr
Query ID	lcl Query_68330
Description	<a href="#">NP_178487.1 Chaperone protein htpG family protein [Arabidopsis thaliana] ...</a>
Molecule type	amino acid
Query Length	780

### Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Chaperone protein htpG family protein [Arabidopsis thaliana]	1599	1599	100%	0.0	100.00%	<a href="#">NP_178487.1</a>
At2g04030/F3C11.14 [Arabidopsis thaliana]	1595	1595	100%	0.0	99.87%	<a href="#">AAM19795.1</a>
Chaperone protein htpG family protein [Arabidopsis thaliana]	1587	1587	100%	0.0	99.62%	<a href="#">NP_849932.1</a>
heat shock protein 90-5, chloroplastic [Arabidopsis lyrata subsp. lyrata]	1580	1580	100%	0.0	98.59%	<a href="#">XP_020880857.1</a>
heat shock protein 90-5, chloroplastic [Capsella rubella]	1561	1561	100%	0.0	97.06%	<a href="#">XP_006292451.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic [Camelina sativa]	1559	1559	100%	0.0	96.81%	<a href="#">XP_010425190.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic-like [Camelina sativa]	1556	1556	100%	0.0	96.55%	<a href="#">XP_010514162.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic [Camelina sativa]	1547	1547	100%	0.0	96.17%	<a href="#">XP_010502419.1</a>
unnamed protein product [Arabis nemorensis]	1489	1489	100%	0.0	94.30%	<a href="#">VVB04038.1</a>
unnamed protein product [Brassica oleracea]	1475	1475	100%	0.0	93.65%	<a href="#">VDD38399.1</a>
BnaC09g22180D [Brassica napus]	1474	1474	100%	0.0	92.27%	<a href="#">CDY33122.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
heat shock protein 90-5, chloroplastic [Eutrema salsugineum]	1470	1470	100%	0.0	94.04%	<a href="#">XP_006395659.1</a>
PREDICTED: heat shock protein 83-like [Brassica oleracea var. oleracea]	1465	1465	100%	0.0	94.39%	<a href="#">XP_013598451.1</a>
heat shock protein 90-5, chloroplastic [Brassica rapa]	1464	1464	100%	0.0	93.91%	<a href="#">XP_009152136.1</a>
unnamed protein product [Microthlaspi erraticum]	1462	1462	100%	0.0	94.55%	<a href="#">CAA7049849.1</a>
hypothetical protein BRARA_I02117 [Brassica rapa]	1460	1460	100%	0.0	92.63%	<a href="#">RID45386.1</a>
hypothetical protein DY000_02025202 [Brassica cretica]	1459	1459	100%	0.0	93.91%	<a href="#">KAF3596266.1</a>
heat shock protein 90-5, chloroplastic-like [Brassica napus]	1458	1458	100%	0.0	93.53%	<a href="#">XP_013644800.1</a>
PREDICTED: heat shock protein 83-like [Brassica oleracea var. oleracea]	1457	1457	100%	0.0	93.26%	<a href="#">XP_013612297.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic [Raphanus sativus]	1451	1451	100%	0.0	92.71%	<a href="#">XP_018458385.1</a>
heat shock protein 90-5, chloroplastic-like [Brassica napus]	1449	1449	100%	0.0	92.87%	<a href="#">XP_013714527.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic-like [Raphanus sativus]	1448	1448	100%	0.0	92.46%	<a href="#">XP_018484585.1</a>
hypothetical protein AALP_AA5G025000 [Arabis alpina]	1437	1437	100%	0.0	93.02%	<a href="#">KFK33530.1</a>
heat shock protein [Arabidopsis thaliana]	1433	1433	100%	0.0	92.78%	<a href="#">CAA72515.1</a>
hypothetical protein DY000_02013960 [Brassica cretica]	1414	1414	97%	0.0	92.85%	<a href="#">KAF3568670.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic-like [Raphanus sativus]	1406	1406	100%	0.0	90.76%	<a href="#">XP_018457251.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic isoform X2 [Tarenaya hassleriana]	1378	1378	100%	0.0	86.75%	<a href="#">XP_010528014.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic isoform X1 [Tarenaya hassleriana]	1373	1373	100%	0.0	86.64%	<a href="#">XP_010528013.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PREDICTED: heat shock protein 90-5, chloroplastic [Tarenaya hassleriana]	1345	1345	100%	0.0	87.10%	<a href="#">XP_010554255.1</a>
PREDICTED: heat shock protein 83-like isoform X1 [Gossypium raimondii]	1340	1340	100%	0.0	85.25%	<a href="#">XP_012478818.1</a>
hypothetical protein F2Q68_00020435 [Brassica cretica]	1335	1335	92%	0.0	92.11%	<a href="#">KAF2538767.1</a>
hypothetical protein E1A91_D02G156600v1 [Gossypium mustelinum]	1335	1335	100%	0.0	84.99%	<a href="#">TYI93752.1</a>
hypothetical protein E1A91_A03G122300v1 [Gossypium mustelinum]	1335	1335	100%	0.0	85.62%	<a href="#">TYJ42969.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic [Gossypium arboreum]	1334	1334	100%	0.0	84.99%	<a href="#">XP_017645753.1</a>
heat shock protein 90-5, chloroplastic [Carica papaya]	1333	1333	100%	0.0	84.34%	<a href="#">XP_021897609.1</a>
hypothetical protein ES319_D02G151000v1 [Gossypium barbadense]	1333	1333	100%	0.0	84.87%	<a href="#">KAB2041484.1</a>
hypothetical protein ES332_A03G131500v1 [Gossypium tomentosum]	1331	1331	100%	0.0	84.87%	<a href="#">TYI36299.1</a>
heat shock protein 90-5, chloroplastic [Herrania umbratica]	1326	1326	100%	0.0	83.71%	<a href="#">XP_021292957.1</a>
Heat shock protein Hsp90 [Corchorus olitorius]	1324	1324	100%	0.0	83.61%	<a href="#">OMO72217.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic [Vitis vinifera]	1324	1324	100%	0.0	83.88%	<a href="#">XP_002267463.2</a>
hypothetical protein GOBAR_AA19168 [Gossypium barbadense]	1324	1324	100%	0.0	83.52%	<a href="#">PPS01499.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic-like isoform X1 [Gossypium hirsutum]	1323	1323	100%	0.0	84.49%	<a href="#">XP_016724686.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic isoform X1 [Gossypium hirsutum]	1323	1323	100%	0.0	84.36%	<a href="#">XP_016667099.1</a>
heat shock protein 90-5, chloroplastic [Gossypium australe]	1317	1317	100%	0.0	83.98%	<a href="#">KAA3483849.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein FNV43_RR26382 [Rhamnella rubrinervis]	1314	1314	100%	0.0	83.10%	<a href="#">KAF3431651.1</a>
heat shock protein 90-5, chloroplastic [Manihot esculenta]	1313	1313	100%	0.0	82.94%	<a href="#">XP_021615743.1</a>
heat shock protein 90-5, chloroplastic [Ziziphus jujuba]	1312	1312	100%	0.0	83.02%	<a href="#">XP_015895264.1</a>
DNA-directed RNA polymerase 1B [Hibiscus syriacus]	1308	1308	98%	0.0	83.72%	<a href="#">KAE8730024.1</a>
heat shock protein 90-5, chloroplastic isoform X2 [Durio zibethinus]	1306	1306	100%	0.0	83.42%	<a href="#">XP_022776680.1</a>
heat shock protein 90-5, chloroplastic-like [Manihot esculenta]	1306	1306	100%	0.0	81.42%	<a href="#">XP_021591904.1</a>
hypothetical protein GOBAR_DD14545 [Gossypium barbadense]	1306	1306	98%	0.0	84.80%	<a href="#">PPD88516.1</a>
PREDICTED: heat shock protein 83 [Fragaria vesca subsp. vesca]	1306	1306	100%	0.0	82.12%	<a href="#">XP_004297188.1</a>
hypothetical protein B456_005G148100 [Gossypium raimondii]	1305	1305	95%	0.0	87.97%	<a href="#">KJB30530.1</a>
PREDICTED: heat shock protein 83-like [Populus euphratica]	1305	1305	100%	0.0	83.46%	<a href="#">XP_011021135.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic [Eucalyptus grandis]	1305	1305	100%	0.0	83.40%	<a href="#">XP_010044352.1</a>
heat shock protein 90-5, chloroplastic [Prosopis alba]	1303	1303	99%	0.0	81.44%	<a href="#">XP_028761874.1</a>
heat shock family protein [Populus tomentosa]	1303	1303	100%	0.0	83.33%	<a href="#">APR63800.1</a>
heat shock protein 90-5, chloroplastic [Cannabis sativa]	1303	1303	100%	0.0	82.21%	<a href="#">XP_030484972.1</a>
HSP90 domain-containing protein/HATPase_c_3 domain-containing protein [Cephalotus follicularis]	1301	1301	100%	0.0	82.21%	<a href="#">GAV59072.1</a>
heat shock protein 90-5, chloroplastic isoform X1 [Durio zibethinus]	1301	1301	100%	0.0	84.11%	<a href="#">XP_022776679.1</a>
heat shock protein 90-5, chloroplastic [Populus trichocarpa]	1301	1301	100%	0.0	83.21%	<a href="#">XP_002311417.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PREDICTED: heat shock protein 90-5, chloroplastic-like [Lupinus angustifolius]	1301	1301	99%	0.0	82.28%	<a href="#">XP_019460635.1</a>
heat shock protein 90-5, chloroplastic [Citrus sinensis]	1301	1301	100%	0.0	82.01%	<a href="#">XP_006484274.1</a>
heat shock protein 90-5, chloroplastic [Citrus clementina]	1301	1301	100%	0.0	82.01%	<a href="#">XP_006437833.1</a>
heat shock protein 90-5, chloroplastic-like [Populus alba]	1300	1300	100%	0.0	83.21%	<a href="#">XP_034902744.1</a>
hypothetical protein F2Q69_00055710 [Brassica cretica]	1300	1887	89%	0.0	91.45%	<a href="#">KAF3488590.1</a>
heat shock protein 90-5, chloroplastic-like [Hevea brasiliensis]	1299	1299	100%	0.0	82.04%	<a href="#">XP_021657274.1</a>
heat shock protein 90-5, chloroplastic [Camellia sinensis]	1299	1299	100%	0.0	82.12%	<a href="#">XP_028122433.1</a>
heat shock protein 90-5, chloroplastic isoform X1 [Pistacia vera]	1297	1297	100%	0.0	84.17%	<a href="#">XP_031278977.1</a>
heat shock protein 90-5, chloroplastic isoform X3 [Abrus precatorius]	1297	1297	99%	0.0	83.84%	<a href="#">XP_027359634.1</a>
heat shock protein 90-5, chloroplastic [Rosa chinensis]	1297	1297	100%	0.0	82.14%	<a href="#">XP_024195154.1</a>
heat shock protein 90-5, chloroplastic [Momordica charantia]	1296	1296	100%	0.0	82.60%	<a href="#">XP_022146433.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic isoform X1 [Vigna angularis]	1296	1296	99%	0.0	83.23%	<a href="#">XP_017427485.1</a>
heat shock protein 90-5, chloroplastic-like isoform X1 [Durio zibethinus]	1295	1295	100%	0.0	82.37%	<a href="#">XP_022725780.1</a>
heat shock protein 90-5, chloroplastic-like [Cucurbita pepo subsp. pepo]	1294	1294	100%	0.0	82.16%	<a href="#">XP_023528296.1</a>
heat shock protein 90-5, chloroplastic [Rhodamnia argentea]	1294	1294	100%	0.0	83.19%	<a href="#">XP_030512157.1</a>
hypothetical protein GOBAR_AA12609 [Gossypium barbadense]	1293	1293	100%	0.0	82.58%	<a href="#">PPS08036.1</a>
heat shock protein 90-5, chloroplastic [Elaeis guineensis]	1293	1293	100%	0.0	81.62%	<a href="#">XP_010943343.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
heat shock protein 90-5, chloroplastic [Morus notabilis]	1292	1292	99%	0.0	83.10%	<a href="#">XP_024018236.1</a>
heat shock protein 90-5, chloroplastic [Prunus persica]	1292	1292	100%	0.0	82.10%	<a href="#">XP_007225664.1</a>
hypothetical protein FH972_008834 [Carpinus fangiana]	1291	1291	100%	0.0	81.30%	<a href="#">KAE8023089.1</a>
heat shock protein 90-5, chloroplastic [Prunus avium]	1291	1291	100%	0.0	83.08%	<a href="#">XP_021815098.1</a>
Heat shock protein Hsp90 family [Macleaya cordata]	1291	1291	100%	0.0	81.15%	<a href="#">OVA15421.1</a>
PREDICTED: heat shock protein 90-5, chloroplastic-like [Gossypium arboreum]	1290	1290	100%	0.0	82.52%	<a href="#">XP_017620025.1</a>
hypothetical protein ES332_A13G113400v1 [Gossypium tomentosum]	1290	1290	100%	0.0	82.64%	<a href="#">TYH91406.1</a>
heat shock protein 90-5, chloroplastic-like [Cucurbita moschata]	1289	1289	100%	0.0	82.17%	<a href="#">XP_022939001.1</a>
heat shock protein 90-5, chloroplastic [Jatropha curcas]	1289	1289	100%	0.0	81.34%	<a href="#">XP_012080479.1</a>
heat shock protein 90-5, chloroplastic-like [Cucurbita moschata]	1289	1289	100%	0.0	82.29%	<a href="#">XP_022922458.1</a>
heat shock protein 90-5, chloroplastic-like [Gossypium australe]	1289	1289	100%	0.0	82.62%	<a href="#">KAA3487920.1</a>
hypothetical protein ES319_A13G105600v1 [Gossypium barbadense]	1288	1288	100%	0.0	82.64%	<a href="#">KAB2048314.1</a>
heat shock protein 90-5, chloroplastic [Syzygium oleosum]	1288	1288	100%	0.0	82.54%	<a href="#">XP_030449476.1</a>
heat shock protein 90-5, chloroplastic [Cucumis sativus]	1288	1288	100%	0.0	82.70%	<a href="#">XP_011654561.1</a>
heat shock protein 90-5, chloroplastic-like [Cucurbita maxima]	1288	1288	100%	0.0	82.17%	<a href="#">XP_022992781.1</a>
heat shock protein 90-5, chloroplastic isoform X2 [Abrus precatorius]	1288	1288	99%	0.0	83.21%	<a href="#">XP_027359633.1</a>
heat shock protein 90-5, chloroplastic [Punica granatum]	1288	1288	100%	0.0	82.83%	<a href="#">XP_031386915.1</a>
putative Heat shock protein Hsp90 family [Lupinus albus]	1288	1288	99%	0.0	81.42%	<a href="#">KAE9605622.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
heat shock protein 90-5 [Cucumis melo var. makuwa]	1288	1288	100%	0.0	81.89%	<a href="#">TYJ98158.1</a>
hypothetical protein GH714_040979 [Hevea brasiliensis]	1287	1287	100%	0.0	82.01%	<a href="#">KAF2321390.1</a>
heat shock protein 90-5, chloroplastic-like [Cucurbita maxima]	1287	1287	100%	0.0	82.12%	<a href="#">XP_022990630.1</a>
heat shock protein 90-5, chloroplastic-like [Hevea brasiliensis]	1287	1287	100%	0.0	82.43%	<a href="#">XP_021674820.1</a>

Graphic Summary

Alignments

Taxonomy