Supporting Information

Dvir et al. 10.1073/pnas.1114128109



Fig. S1. Representative electron density of the refined structure of the autosomal recessive hypercholesterolemia (ARH)–LDL receptor (LDLR) tail complex. The 2Fo-Fc electron density map (gray mesh) contoured at 1.5 σ around selected ARH residues (green sticks for carbons, red and blue for oxygens and nitrogens, respectively) reveals outstanding atomic resolution.



Fig. S2. Superposition of the structure of ARH (gray) and Dab2 (blue) phosphotyrosine-binding (PTB) structures. The overall fold (*Upper*, ribbon representation) is quite similar despite the low sequence identity (shown in the structure-based alignment, *Lower*). The PTB domains of Dab1 and Dab2 are 57.3% identical, but both are less than 18% identical with ARH. Identical residues are shaded.



Fig. S3. Topology of the conserved PTB domain of ARH. (A) 3D structure of rat ARH (rARH) in complex with LDLR peptide. β -Strands of ARH are represented as green and yellow numbered arrows ($\beta 1-\beta 7$) and α -helices as red ribbons ($\alpha 1$, $\alpha 2$). The LDLR tail is drawn in cyan and the tyrosine (Y_0) of its FxNPxY₀ motif in yellow. (*B*) 2D topology of the PTB domain of ARH shows that it is made of an array of seven anti-parallel β -strands grouped into two β -sheets (yellow and green). Numbers at the top and bottom of each strand and helix indicate the residues that form them, respectively. (*C*) Sequence alignment of PTB domains from various ARH species. The numbering at the top corresponds to the rARH sequence, whereas the percentage identities to the left of each sequence refer to the human sequence. Identical residues are shaded. Amino acids in the proximity (within 5 Å) of the LDLR tail are highlighted in cyan. Residues lining the pocket for Y_0 of the LDLR FXNPX₀ motif are highlighted in yellow.



Fig. S4. Proposed binding area for phosphoinosites. Electrostatic surface representation of the structure of the PTB domain of ARH bound to the LDLR (yellow sticks). The related structure of the Dab1 (1) (PDB id 1NU2) in complex with a inositol-triphosphate (IP3) was overlaid on that of ARH according to the protein positions, and the resulting position of the IP3, the phosphorylated head group of PIP2, is displayed green sticks for carbons and orange for the phosphates. Although the ARH side-chains in corresponding positions to those that bind IP3 in Dab1 are not basic, there are three clusters of lysine residues (labeled in yellow, bottom view) in this vicinity that could bind negatively charged phosphate groups. This indicates that the mechanism of binding phosphoinositides by ARH is not identical but similar to that of Dab2. The electrostatic properties were evaluated using APBS (2) and displayed in PyMol, from –7 kT/e (red) to +7 kT/e (blue).

Stolt PC, et al. (2003) Origins of peptide selectivity and phosphoinositide binding revealed by structures of disabled-1 PTB domain complexes. *Structure* 11:569–579.
Baker NA, Sept D, Joseph S, Holst MJ, McCammon JA (2001) Electrostatics of nanosystems: application to microtubules and the ribosome. *Proc Natl Acad Sci USA* 98:10037–10041.





DNAS

Table S1.	List of protein sequences for	r interaction with ARH	which resulted from	om searching a	sequence database
(motif.gen	ome.jp/MOTIF2.html)				

DLRP01130INFDIPVYQDAB2 interaction proteinQSVWQ8LSFQNPVYQLRP4 (ApoER2)Q14114MINFDNPVYRLRP4 humanQ75096LTYSNPSYRMAP kinase kinase 2 (MAPKK 2)Q07192LLFANPARKRas GTPase-activating protein GAPQ9UIP2LSFQNPVYHVRRas GTPase-activating protein GAPQUIP2LSFQNPVYHRas Grase-activating protein GAPQUIP2LSFQNPVYHRas guanine nucleotide exchange factor KQSAFF3IRITNPVFHRas Grase-activation protein f0APQUIP2LSFQNPVYHRas Grase-activation protein f0APQUIP2LSFNPVFYRase-activation protein f0APQUIP2SGNPARAWFNNPVFRRatrison disease 7 domain-containing protein 1QBFH1MINDRNPVYRCarn1-pending proteinSV isso S09729.1ITFDNPARQCarn1-pending proteinXP_003144122LDLKNPLFRRefor, multiple EGF-like motifs (LRP4/LRP10)GenBank: AB027082.1ITYNPSYRCarn1-pending protein apartokinasehomoserine dehydrogenaseP43096LSINNPLFCRituctional apartokinasehomoserine dehydrogenaseP43096LSINNPLFKProbable cation-transporting ATAset Slubunt 2QS786IKINNPAFRProbable cat	Protein name	Database entry	Sequence
DA82 Interaction proteinOSWUQ8LESPQNPVQLRP8 (ApoER2)Q14114MNFDNPVRLRP4 humanQ75096LTYSNPSYRMAP kinase kinase 2 (MAPKK 2)Q07192LIPANPAPKRas guanien culcotide exchange factor KQ3ULP4MTYYNPVFRRas guanien culcotide exchange factor KQ3UF2LSFQNPVYHRNG finger protein nGAPQ2Y23M3VTIDNPVFQRNG finger protein 31Q36EP0VKFNNPVFRRNG finger protein 31Q36EP0VKFNNPVFRRNG finger protein 31Q36EP0VKFNNPVFRZipophorin receptor - Actes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNFDNPVYRParkinson disease 7 domain-containing protein 1Q387H1FNLCMPVFNCell cycle control protein 50C (extracellular domain)Q279H5VKFONPAFQMinor capid protein 12 (LHPV type 67)Swiss 090729.1ITFDNPAFQCarn1-pending protein 50C (extracellular domain)Q279H5VKFONPAFQL2 protein - HPV 97GenBank: AB027082.1ITYSNPSFRReticuline oxidaseP30386LSIONPLFQBifunctional aspartokinase/homoserine dehydrogenaseP43755VDLNNPLYKL3_3'-Cyclic-nucleotide 2:-phosphodisetraseP43755VDLNNPLYKL7_3-GalNA-72Q5M300LUTTYSNPSFRProbable cation-transporting ATPase 13A4Q4VNC1VSSNPVFEL4-ex-glucan glucanohydrolaseP5354PSLSNPLNLP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseP67533FALNPNYKProbable cation-transporting ATPase 13A4	LDLR	P01130	INFDNPVYQ
LRP8 (ApoER2)Q14114MNPDNPVYR LP8 humanQ14114MNPDNPVYR LP8 humanLRP4 humanQ75096LTYSNPSYRMAP kinase kinase 2 (MAPKK 2)Q07192LINFANPAFKRas GTBase-activating protein nGAPQ9U/F2LSFQNPVYHRas GTBase-activating protein nGAPQ9U/F2LSFQNPVYHRas GTBase-activating protein nGAPQ2V7M3VTIDNPVYQDNA-directed RNA polymerase subunit βA15EK1LSFCNPVYFRNG finger protein 31Q96EP0VKFNNPVFRTyrosine-protein phosphatase YVH1Q02256VDFDINPAYKLipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNFDNPVYQCell cycle control protein 50C (extracellular domain)Q219P5VKFQNPAFQMinor capsid protein 12 (HPV type 67)Swiss O90729.1ITFDNPAFQCarm1-pending proteinXP_003144122LDLKNPVFNCarm1-pending proteinXP_003144122LDLKNPVFNReticuline oxidaseP44305VDLNNPTKBifunctional aspartokinase/homoserine dehydrogenaseP44305VDLNNPTKPrizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPitabelial discoidin domain-containing receptor 1Q084953LUSNPAFKPitabelial discoidin domain-containing receptor 1Q08340LUTNPTFKPitabelial discoidin domain-containing receptor 1Q08380LUTNPTFKPitabelial discoidin domain-containing receptor 1Q08345LUSNPAFKPitabelial discoidin domain-containing receptor 1Q08340LUTNPTFKPitabelial discoidi	DAB2 interaction protein	Q5VWQ8	LSFQNPVYQ
LPP4 humanO'75096LTYSNP5YRMAP kinase kinase 2 (MAPKK 2)Q07192LNFANPAFKMAP kinase kinase 2 (MAPKK 2)Q07192LNFANPAFKRas Graine nucleotide exchange factor KQ3ULP4MTYYNPVFRRas guanine nucleotide exchange factor KQ34FF3IRLTNPVFHFusion glycoprotein F0Q2Y2M3VTIONPVYQDNA-directed RNA polymerase subunit βA15EK1LSFENPVFYRNG finger protein 31Q36EP0VKFNNPVFRTyrosine-protein phosphatase YUH1Q02256VDFDNPAYKLipophorin receptor - Acdes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNFDNPVYRParkinson disease 7 domain-containing protein 1Q3B7H1FNLCNPVFNCell cycle control protein 50C (extracellular domain)Q2T9P5VKFQNPAFQCarm1-pending protein 1XP_003144122LDLKNPLFRRefGF7, multiple EGF-like motifs (LRP4LRP10)GenBank: ABA2468.1LTYSNPSYRReticuline oxidaseP43955VDLNNPLYKBfunctional aspartokinase/homoserine dehydrogenaseP47375NIKNPLYNPytatibe ladion initiation factor eIF-28 subunit 2Q57586IKINPAFAY12-yolic-nucleotide 2-phosphodiesteraseP33541EJSNPLFNProbable cation-transporting ATPase 13A4Q4VVC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4VVC1VSYSNPFEIphtabili discidin domain-containing receptor 1Q08345LLISNPAYRProbable cation-transporting ATPase 13A4Q4VVC1VSYSNPFEIphtabili discidin domain-containing receptorQ7M3M8	LRP8 (ApoER2)	Q14114	MNFDNPVYR
MAP kinase kinase 2 (MAPKK 2)Q07192LIFANPAFKTryptophan synthase α chainQ8TLP4MTYYNPVFRRas GTPase-activating protein nGAPQ9U/F2LSFQNPVYHRas GTPase-activating protein nGAPQ9U/F2LSFQNPVYHRas GTPase-activating protein nGAPQ9U/F2LSFQNPVYHRas GTPase-activating protein nGAPQ9U/F2LSFQNPVYHRas GTPase-activating protein nGAPQ92F2WTIDNPVYQDNA-directed RNA polymerase subunit βA15EK1LSFENPVFYRing finger protein nJophatase VVH1Q02256VDFDINPAYKLipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MINFDNPVYRParkinson disease 7 domain-containing protein 1Q3B7H1FNLCNPVFNCell cycle control protein 50C (extraellular domain)Q2T9P5VKFQNPAFCCarn1-pending proteinXP_003144122LDLKNPLFNMGE67, multiple EGF-like motifs (LRP4/LRP10)GenBank: AA027082.1ITYDNPAFNGarn1-pending proteinXP_003144122LDLKNPLFNReticuline oxidaseP30986LSIONPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYKPytative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDPutative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1V5YSNPVFEPitadien initiation factor eIF-2B subunit 1A30R02FKLDNPLYKJ-3-S-MAC-72Q5M900LITINPTFKPitadien indoxipychalseP39578FHIDN	LRP4 human	O75096	LTYSNPSYR
Tryptophan synthase α chainQ8TLP4MTYYNPVFRRas GTPase-activating protein nGAPQ9UJF2L5FQNPVYHRas guarine nucleotide exchange factor KQ54FF3IRILTNVFHFusion glycoprotein F0Q2Y2M3VTIDNPVYGDNA-directed RNA polymerase subunit βA15EK1L5FENPVFFRING finger protein 31Q96EP0VKFNNPVFRTyrosine-protein phosphatase YVH1Q02256VDFDNPAYKLipophorin receptor - Acdes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNPDNPVYRParkinson disease 7 domain-containing protein 1Q387H1FNLCNPVFNCell cycle control protein SOC (extracellular domain)Q2T9P5VKFQNPAFQMinor capsid protein L2 (HPV type 67)Swiss O90729.1ITFDNPAFQCarm1-pending proteinXP_003144122LDLKNPLFRReticuline oxidaseP4003144122LDLKNPLFRReticuline oxidaseP44505VDLNPLYKReticuline oxidaseP44505VDLNPLYKRyclicinucleotida 2-phosphodiesteraseP47376INIKNPLYNP/1.3-GalNAc-T2Q5586KIRNPAFDRhizobactin siderophore biosynthesis protein rhbCQ92780LQTINPLFERhizobactin siderophore biosynthesis protein rhbCQ9178.3FLSNPAYRProbable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFEProtaid polypalaseP3358	MAP kinase kinase 2 (MAPKK 2)	Q07192	LNFANPAFK
Ras GTPase-activating protein nGAPQ9UP2LSFQNPVYHRas guanne nucleotide exchange factor KQ54FF3IRLTNPVFHRusion glycoprotein F0Q2Y2M3VTIDNPVYQDNA-directed RNA polymerase subunit βA15EK1LSFENPVFYRING finger protein 31Q96EP0VKFNNPVFRTyrosine-protein phosphatase YVH1Q02256VDFDNPAYKLipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AGQ16410.1MNFDNPVYRCell cycle control protein 50C (extracellular domain)Q2T9P5VKFQNPAFQMinor capsid protein 12 (HPV type 67)Swiss O90729.1ITFDNPAFQCarn1-pending proteinXP_003144122LDLKNPLFRCarn1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: AB027082.1LTYSNPSYRReticuline oxidaseP30866LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44305VDLNNPLYKEpithelial discoidin domain-containing receptor 1Q08345LLISNPAYRPitabel cation-transporting ATPase 13A4Q4VNC1VSYSPVFEProbable cation-transporting ATPase 13A4Q4VNC1VSYSPVFEProbable cation-transporting ATPase 13A4QMVNC1VSYSPVFEJA-ac-glyglaactosaminyltransferase IIQ5M900LINTNPTFKProbable cation-transporting ATPase VBQ95330FLDNPLYHProbable cation-transporting ATPase VBQ95330YELDNPFQProbable cation-transporting NordinQ57333FALPNPAYKProbable Ras GTPase-activating proteinQ55330 <t< td=""><td>Tryptophan synthase α chain</td><td>Q8TLP4</td><td>MTYYNPVFR</td></t<>	Tryptophan synthase α chain	Q8TLP4	MTYYNPVFR
Ras guanine nucleotide exchange factor KQ54F3IRLTNPVFHFusion glycoprotein F0Q2Y2M3VTIDNPVYQDNA-directed RNA polymerase subunit βA15EK1LSFENPVYYRING finger protein 31Q96EP0VKFNNPVFRTyrosine-protein phosphatase YVH1Q02256VDEDNPAYKLipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNFDNPVYRParkinson disease 7 domain-containing protein 1Q387H1FNLCNPVFNParkinson disease 7 domain-containing protein 1Q387H1FNLCNPVFNCell cycle control protein 50C (extracellular domain)Q2T995VKFQNPAFQL2 protein - HPV 97GenBank: AAQ16410.1ITYDNPAFNCarn1-pending proteinXP_003144122LDLNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: AA22668.1LTYSNPSYRBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2,3'-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNPi-1,3-GalNAc-T2Q57586KIRNPAFDRhizobactin siderophore biosynthesis protein rhbCQ94Z22VEIGNPSYNLAwto-glucanglucanohydrolaseP53354FSLSNPLFNLAwto-glucang glucanohydrolaseP53354FSLSNPLFNLP1-13-Acetylguadtosaminyltransferase IIQ5M900LMITNPTFKProbable cation-transporting ATPase 13A4Q4WC1VYSNPVFGProbable cation-transporting NTPase 13A4Q5M900LMITNPTFKProbable cation-transporting NTPase 13A4Q5M900LMITNPTFKProbable cation sinstransporter (yeast) <td< td=""><td>Ras GTPase-activating protein nGAP</td><td>Q9UJF2</td><td>LSFQNPVYH</td></td<>	Ras GTPase-activating protein nGAP	Q9UJF2	LSFQNPVYH
Fusion glycoprotein F0Q2Y2M3VTIDNPVYQDNA-directed RNA polymerase subunit βA15EK1LSFENPVFYRING finger protein 31Q96EP0VKFNNPVFXIlyophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNEDNPVYQDarkinson disease 7 domain-containing protein 1Q3B7H1FNLCNPVFNCell cycle control protein 50C (extracellular domain)Q2T9P5VKFQNPAFQDihor capsid protein 12 (HPV type 67)Swiss O90729.1ITFDNPAFQL2 protein - HPV 97GenBank: AB027082.1ITYDNPAFNCarm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2,3 - Cyclic-nucleotide 2-phosphodiesteraseP443736INIKNPLYNPitheilal discoidin domain-containing receptor 1Q05M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFE1,4-α-σ-glucan glucanohydrolaseP53354FSLSNPLFNLPHBQ9XR2VEGINPSYNDiadenosine tetraphosphataseA3N0C2Probable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFEAnaceglugalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M308FOLNPLFYCrovi-lipotizinosis neuronal protein 5 homologQ533W9YNISNPYYQCrovi-lipotizinosis neuronal protein 5 homologQ533W9YNISNPYYQCr	Ras guanine nucleotide exchange factor K	Q54FF3	IRLTNPVFH
DNA-directed RNA polymerase subunit βA1SEK1LSFENPVFYRING finger protein 31Q96EP0VKFNNPVFRTyrosine-protein phosphatase YVH1Q02256VDFDNPAYKLipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNFDNPVYRParkinson disease 7 domain-containing protein 1Q3B7H1FNLCNPVFNCell cycle control protein 50C (extracellular domain)Q2T9P5VKFQNPAFQMinor capsid protein 12 (HPV type 67)Sviss 090729.1ITFDNPAFQ12 protein - HPV 97GenBank: AB027082.1ITFDNPAFQCarm1-pending proteinXP_003144122LDKNPLFRReticuline oxidaseP39986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYKX_2,Cyclic-nucleotide 2'-phosphodiesteraseP437376INIKNPLYNEpitheliad discolidin domain-containing receptor 1Q08345LLISNPAYRProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFEPi-Ja-GaundydrolaseP33534FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHPi-Ja-Acettylgalactosaminytransferase IIQ1M388FQLQNPLFYCreid-ipofuscinosis neuronal protein 5 homologQ533W9YNISNPYQCCR4-NT transcription complex subunit 1A01985YELDNPFFQProbable RS Trase-activating protein 5 homologQ513W9YNISNPYQCR4-NT transcription complex subunit 1A01985YELDNPFFX<	Fusion glycoprotein F0	Q2Y2M3	VTIDNPVYQ
RING finger protein 31Q96EP0VKFNNPVFRTyrosine-protein phosphatase YVH1Q02256VDFDNPAYKLipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNFDNPVYRParkinson disease 7 domain-containing protein 1Q3279F5VKFQNPAFQMinor capid protein 12 (HPV type 67)Swiss 090729.1ITFDNPAFQ2arm1-pending proteinXP 003144122LDLKNPLFRCarm1-pending proteinXP 003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: AAQ2468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2,3-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNPj-13-GalNA-T2QSM900LUTINPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LOTINPLFEPutative translation initiation factor elF-2B subunit 2Q57866IKIRNPAFDProbable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFELRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseFSLSNPLFNProbable cation-transporting 5 homologQ533W9YNISNPVYQCRvi-AH transcription catorQ7M3M8FQLQNPLFYProbable cativiang protein 5 homologQ533W9YNISNPYYQDNA polymeraseP87503FALPNPAYKProtein dIDP39578FHIDNPYKYKProbable RAS GTAse-activating proteinNonga aminivirus)Q5UQN6MGFNPSYNDiadenosine tetraphosphataseP87503FALPNPAYK	DNA-directed RNA polymerase subunit β	A1SEK1	LSFENPVFY
Tyrosine-protein phosphatase YVH1Q02256VDFDNPAYKLipophorin receptor - Aedes aegypti (yellow feve mosquito)GenBank: AAQ16410.1MNFDNPVYRParkinson disease 7 domain-containing protein 1Q387H1FNLCNPVFNCell cycle control protein 50C (extracellular domain)Q279P5VKFQNPAFQMinor capsid protein L2 (HPV type 67)Swiss 090729.1ITFDNPAFQZ protein - HPV 97GenBank: ABQ27082.1ITYDNPAFNCarm1-pending proteinXP_003144122LDKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTSVSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2,3-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLISNPARRβ-1,3-GalNAc-T2Q5M9000LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEProtable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-glucan glucanohydrolaseP33534FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseQ3300LNITNPTFKPranscription factor castorQ7M3M8FQL0NPLFYCR4+1/T transcription complex subunit 1A0JP85YELDNPSFQProbable Ras GTase-activating protein 5 homologQ553W9YNISNPVYQCR4+1/T transcription complex subunit 1P33578FHIDNPVYKProbable Ras GTase-activating protein 5 homologQ553W9 <td>RING finger protein 31</td> <td>Q96EP0</td> <td>VKFNNPVFR</td>	RING finger protein 31	Q96EP0	VKFNNPVFR
Lipophorin receptor - Aedes aegypti (yellow fever mosquito)GenBank: AAQ16410.1MNEDNPVYRParkinson disease 7 domain-containing protein 1Q3B7H1FNLCNPVFNCell cycle control protein 50C (extracellular domain)QZT9P5VKFQNPAFQMinor capsid protein L2 (HPV type 67)Swiss 090729.1ITFDNPAFQL2 protein - HPV 97GenBank: ABO27082.1ITYDNPAFNCarm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRReticuline oxidaseP44505VDLNNPLYK2,3-Cyclic-nucleotide 2'-phosphodiesteraseP44505VDLNNPLYK2,3-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLISNPAYRPh.1.3-GaINAc-T2QSM900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4WNC1VSYSNPVFE1.4-ac-glucan glucanohydrolaseP53354FSLSNPLFNLRP18Q9MZR2VEIGNPSYNDiadenosine tetraphosphataseQ53090LNITNPTFKFranscription factor castorQ7M3M8FQLQNPLFYCredi-ipofuscinosis neuronal protein 5 homologQ533W9YNISNPVYQProtein dItDP39578FHIDNPYKNDNA polymeraseQ5505IQANPSFNProbable Ras GTPase-activating protein SynGAPQ96FV0LSFQNPLFHProbable	Tyrosine-protein phosphatase YVH1	Q02256	VDFDNPAYK
Parkinson disease 7 domain-containing protein 1Q387H1FNLCNPVFNCell cycle control protein SOC (extracellular domain)Q279P5VKFQNPAFQMinor capsid protein L2 (HPV type 67)Swiss O90729.1ITFDNPAFQL2 protein - HPV 97GenBank: A8027082.1ITYDNPAFNCarm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: AA32468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYKCy3Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRβ-1,3-GaINAc-T2Q5M900LNITNPTFKPutative translation initiation factor elf-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFELRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseP53534FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseQ503289YNISNPVYCProbable Ras GTPase-activating protein 5 homologQ51498LAFKNPSYQCR4+NT transcription complex subunit 1A0IP85YELDNPFSQProbable Ras GTPase-activating protein 5 homologQ50228YGIKNPVFQProbable Ras GTPase-activating protein 5 homologQ50228YGIKNPVFQProbable Ras GTPase-activating protein 5 homologQ50228YGIKNPVFQ<	Lipophorin receptor - Aedes aegypti (yellow fever mosquito)	GenBank: AAQ16410.1	MNFDNPVYR
Cell cycle control protein 50C (extracellular domain)Q2T9P5VKFC0NPAFQMinor capsid protein L2 (HPV type 67)Swiss O90729.1ITFDNPAFQCarm1-pending proteinXP_003144122LDLKNPLFRCarm1-pending proteinXP_003144122LDLKNPLFRCarm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2,3-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLISNPAYRP.1.3-GallNAc-T2QSM900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-p-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3NOC2FKLDNPFRQProtoin factor castorQ7M3M8FQLQNPLFYCR4-NT transcription complex subunit 1A0JP85YEIDNPFRQDNA polymeraseP39578FHIDNPVYKProbable cas GTPase-activating protein 5 homologQ553W9YNISNPVYQCR4-NT transcription complex subunit 1A0JP8578FALPNPAYKDNA polymeraseP39578FHIDNPYFKProbable Ras GTPase-activating proteinQ51208 <t< td=""><td>Parkinson disease 7 domain-containing protein 1</td><td>Q3B7H1</td><td>FNLCNPVFN</td></t<>	Parkinson disease 7 domain-containing protein 1	Q3B7H1	FNLCNPVFN
Minor capsid protein L2 (HPV type 67)Swiss O90729.1ITFDNPAFQL2 protein - HPV 97GenBank: ABO27082.1ITFDNPAFNCarm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2,3-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRp-1,3-GalNAc-T2Q5M900LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586KIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-o-glucan glucanohydrolaseP53354FSLSNPLFNLRP18Q9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHp-1,3-N-acetylgalactosaminyltransferase IIQ553W9YNISNPVYCCrexi-NT transcription complex subunit 1A0JP85YELDNPFSFQProtain dItDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ51498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061YTINPSFNGTPase-activating protein kinase erb8-1)P00533GSVQNPYYHLRP18Q9NZR2VEIGNPSYNLRP14LAFKNPSYQHigh	Cell cycle control protein 50C (extracellular domain)	Q2T9P5	VKFQNPAFQ
L2 protein - HPV 97GenBank: ABO27082.1ITYDNPAFNCarm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2/3 - Cyclic-nucleotide 2 - phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLISNPAYRβ-1,3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586IKINPAPDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-~o-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFYp-1,3-Nacetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ5533V9YNISNPYVQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dItDP39578FHIDINPVYKDNA polymeraseR97503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPYGPProbable Ras GTPase-activating proteinQ50505IQIANPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q502N <td>Minor capsid protein L2 (HPV type 67)</td> <td>Swiss O90729.1</td> <td>ITFDNPAFQ</td>	Minor capsid protein L2 (HPV type 67)	Swiss O90729.1	ITFDNPAFQ
Carm1-pending proteinXP_003144122LDLKNPLFRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRMEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2',3'-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRP.1.3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-car-glucan glucanohydrolaseP53354FSLSNPLFNLRP18Q9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFF\$\phi.3-MA-cetylgalactosaminyltransferase IIQ5M900LNITNPTFKCranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0IP85YELDNPSFQProbable Ras GTPase-activating proteinP87503FALPNPAYKFormide amidohydrolaseP87503FALPNPAYKProbable Ras GTPase-activating proteinP00533GSVQNPVYHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNSpheroidin (viral)P23061YTINPSFNGFR(Receptor tyrosine-protein kinase erbB-1)P00533<	L2 protein - HPV 97	GenBank: ABO27082.1	ITYDNPAFN
MEGF7, multiple EGF-like motifs (LRP4/LRP10)GenBank: BAA32468.1LTYSNPSYRReticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYKSj.3'-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYR\p-1,3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor elf-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-p-glucan glucanohydrolaseP53354FSLSNPLFNLRP18Q9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFH\p-1,3-N-acetylgalactosaminyltransferase IIQ533W9YNISNPVFQCeroid-ipofuscinosis neuronal protein 5 homologQ533W9YNISNPVFQCroid-ipofuscinosis neuronal protein 5 homologQ50228YGIKNPVFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseP50505IQIANPSFNSpheroidin (viral)P23061VYITNPFSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein SynGAPQ96PV0LSFQNPLFNUncharacterized protein SynGAPQ902028YGIKNPSFNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q902282VEIGNPSYNLRP18	Carm1-pending protein	XP_003144122	LDLKNPLFR
Reticuline oxidaseP30986LSIQNPLFQBifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2',3'-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRβ-1,3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative transporting factor elF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-D-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3NOC2FKLDNPLFHP-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCercid-ipofuscinosis neuronal protein 5 homologQ533V9YNISNPVYCDNA polymeraseP87503FALPNPAYKProbable Ras GTPase-activating proteinP39578FHIDNPVYKDNA polymeraseP50505IQIANPSFNSpheroidin (viral)P23061YTINPSFNSpheroidin (viral)P23061YTINPSFNGTPase-activating protein singer polyphaga mimivirus)Q5UQN6MGFHNPSYNLRP18Q9NZR2VEIGNPSYNLRP18Q9NZR2VEIGNPSYNLRP14Q9NZR2VEIGNPSYNLRP14Q9NZR2VEIGNPSYNLRP18Q9NZR2VEIGNPSYNLRP18Q9NZR2VEIGNPSYNLRP18Q9NZR2	MEGF7, multiple EGF-like motifs (LRP4/LRP10)	GenBank: BAA32468.1	LTYSNPSYR
Bifunctional aspartokinase/homoserine dehydrogenaseP44505VDLNNPLYK2',3'-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRP-1,3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor elF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-ac-pglucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFH -1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCercid-ipofuscinosis neuronal protein 5 homologQ553V9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProbable Ras GTPase-activating proteinP87503FALPNPAYKPorbable Ras GTPase-activating proteinQ87498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP14Q9NZR2VEIGNPSYNProbable Ras GTPAse-protein kinase erbB-1)P00533GSVQNPVYHLRP14LAptNPSFNVFIGNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLR	Reticuline oxidase	P30986	LSIQNPLFQ
2',3'-Cyclic-nucleotide 2'-phosphodiesteraseP47376INIKNPLYNEpithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRp-1,3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor elF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFH-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ45498LAFKNPSYQHigh-afflinity potassium transporter (yeast)P50505IQIANP5FNSpheroidin (viral)P23061VYITNP5FNGTPase-activating protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9MZR2VEIGNPSYNLRP14Q9MZR2VEIGNPSYNLRP16Q90754VEIGNPSYNProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Bifunctional aspartokinase/homoserine dehydrogenase	P44505	VDLNNPLYK
Epithelial discoidin domain-containing receptor 1Q08345LLLSNPAYRβ-1,3-GalNAc-T2QSM900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor elF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-D-glucan glucanohydrolaseP53354FSLSNPLFNLRP18Q9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ367498LAFKNPSYQHigh-affinity potassium transporter (yeast)P23061YYTTNPFNSpheroidin (viral)P23061YYTTNPFNGTPase-activating protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9MZR2VEIGNPSYNLRP14Q07954VEIGNPSYNLRP18Q9MZR2VEIGNPSYNProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	2',3'-Cyclic-nucleotide 2'-phosphodiesterase	P47376	INIKNPLYN
β-1,3-GalNAc-T2Q5M900LNITNPTFKRhizobactin siderophore biosynthesis protein rhbCQ9Z3R0LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586IKIRPPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFEProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-D-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ53W9YNISNPVYQCCR4-NT transcription complex subunit 1A0IP85YELDNPSFQProtein dItDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein kinase erbB-1)P00533GSVQNPVFHLRP18Q9NZR2VEIGNPSYNLRP18Q9NZR2VEIGNPSYNProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Epithelial discoidin domain-containing receptor 1	Q08345	LLLSNPAYR
Rhizobactin siderophore biosynthesis protein rhbCQ923R0LQITNPLFEPutative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-D-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dHDP39578FHIDNPYYKDNA polymeraseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ3601VYITNPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein kinase erbB-1)P0533GSVQNPYHLRP1(ApoER)Q07954VEIGNPSYNLRP18Q9NZR2VEIGNPSYNLRP14Q07954VEIGNPSYNLRP14Q07954VEIGNPSYNLRP14Q07954VEIGNPSYNProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	β-1,3-GalNAc-T2	Q5M900	LNITNPTFK
Putative translation initiation factor eIF-2B subunit 2Q57586IKIRNPAFDProbable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4~p-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHP.1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseQ50228YGIKNPVFQForbmide amidohydrolaseQ50228YGIKNPVFQHigh-affinity potasium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP1Q07954VEIGNPSYNLRP14Q07954VEIGNPSYNProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Rhizobactin siderophore biosynthesis protein rhbC	Q9Z3R0	LQITNPLFE
Probable cation-transporting ATPase 13A4Q4VNC1VSYSNPVFE1,4-α-D-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)Q250206MGFHNPSFNGTPase-activating protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSFNLRP1 (ApoER)Q9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPSYNProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Putative translation initiation factor eIF-2B subunit 2	Q57586	IKIRNPAFD
1,4-α-p-glucan glucanohydrolaseP53354FSLSNPLFNLRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPYYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP1 (ApoER)VEIGNPSYNHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Probable cation-transporting ATPase 13A4	Q4VNC1	VSYSNPVFE
LRP1BQ9NZR2VEIGNPSYNDiadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNLRP1Q9NZR2VEIGNPSYNLRP1Q07954VEIGNPSYNLRP1Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	1,4-α-D-glucan glucanohydrolase	P53354	FSLSNPLFN
Diadenosine tetraphosphataseA3N0C2FKLDNPLFHβ-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ81498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein kinase erbB-1)Q0533GSVQNPVYHLRP1Q9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	LRP1B	Q9NZR2	VEIGNPSYN
β-1,3-N-acetylgalactosaminyltransferase IIQ5M900LNITNPTFKTranscription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Diadenosine tetraphosphatase	A3N0C2	FKLDNPLFH
Transcription factor castorQ7M3M8FQLQNPLFYCeroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP14Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	β-1,3-N-acetylgalactosaminyltransferase II	Q5M900	LNITNPTFK
Ceroid-ipofuscinosis neuronal protein 5 homologQ553W9YNISNPVYQCCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP18Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Transcription factor castor	Q7M3M8	FQLQNPLFY
CCR4-NT transcription complex subunit 1A0JP85YELDNPSFQProtein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Ceroid-ipofuscinosis neuronal protein 5 homolog	Q553W9	YNISNPVYQ
Protein dltDP39578FHIDNPVYKDNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	CCR4-NT transcription complex subunit 1	A0JP85	YELDNPSFQ
DNA polymeraseP87503FALPNPAYKFormmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP18Q9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Protein dltD	P39578	FHIDNPVYK
Formmide amidohydrolaseQ50228YGIKNPVFQProbable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	DNA polymerase	P87503	FALPNPAYK
Probable Ras GTPase-activating proteinQ8T498LAFKNPSYQHigh-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Formmide amidohydrolase	Q50228	YGIKNPVFQ
High-affinity potassium transporter (yeast)P50505IQIANPSFNSpheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Probable Ras GTPase-activating protein	Q8T498	LAFKNPSYQ
Spheroidin (viral)P23061VYITNPSFNGTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	High-affinity potassium transporter (yeast)	P50505	IQIANPSFN
GTPase-activating protein SynGAPQ96PV0LSFQNPLFHUncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Spheroidin (viral)	P23061	VYITNPSFN
Uncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)Q5UQN6MGFHNPSYNEGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	GTPase-activating protein SynGAP	Q96PV0	LSFQNPLFH
EGFR(Receptor tyrosine-protein kinase erbB-1)P00533GSVQNPVYHLRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	Uncharacterized protein L442 (Acanthamoeba polyphaga mimivirus)	Q5UQN6	MGFHNPSYN
LRP1BQ9NZR2VEIGNPSYNLRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	EGFR(Receptor tyrosine-protein kinase erbB-1)	P00533	GSVQNPVYH
LRP1 (ApoER)Q07954VEIGNPTYKHepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	LRP1B	Q9NZR2	VEIGNPSYN
Hepatocyte growth factor receptorP08581IYVHNPVFKProbable phospholipid-transporting ATPase VBO94823GQLSNPTFY	LRP1 (ApoER)	Q07954	VEIGNPTYK
Probable phospholipid-transporting ATPase VB O94823 GQLSNPTFY	Hepatocyte growth factor receptor	P08581	IYVHNPVFK
	Probable phospholipid-transporting ATPase VB	O94823	GQLSNPTFY

The structure-based ARH specificity formula $\Phi_{-7}x\Phi_{-5}xNP\psi[F/Y]_{0}\Omega_{+1}$ was used. Φ stands for a bulky aliphatic or aromatic residue such as lle, Met, or Phe; x for mostly polar (these are the noncontacting residues that contribute least to the binding); ψ for small aliphatic residues such as Val, Ala, or possibly Thr; and Ω for long polar residues with hydrogen-donating group such as Gln, Asn, His, Tyr, Lys, or Arg. To keep all of the possible sequences resulting from this search, the whole raw list is presented and no filtering for specific organisms was applied. Only sequences of cytoplasmic domains are shown. Uniprot database entries are listed unless otherwise indicated.

PNAS PNAS