**Figure S1.** The ten regular patterns that define the hfAIM motif. Each pattern contains at least two acidic amino acids. X represents any amino acid.

**Figure S2.** Additional controls for PEX10 and Atg8 interaction assays. No YFP fluorescence was observed following transient coexpression of the unfused YC with YN-Atg8 (**A**), the unfused YN with PEX10-YC (**B**), PEX10Y96A-YC with YN (**C**), PEX10F253A-YC with YN (**D**) or PEX1G93E-YC with YN-Atg8 (**E**). Bar: 20 µm.

**Figure S3.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX10. The AtPEX10 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX10 proteins from various species. The location of the AIMs identified in AtPEX10 by either hfAIM or iLIR is indicated on the top. The PEX10 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.

**Figure S4.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX1. The AtPEX1 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX1 proteins from various species. The location of the AIMs identified in AtPEX1 by either hfAIM or iLIR is indicated on the top. The PEX1 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.

**Figure S5.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX6. The AtPEX6 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX6 proteins from various species. The location of the AIMs identified in AtPEX6 by either hfAIM or iLIR is indicated on the top. The PEX6 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.

**Figure S6.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX3-2. The AtPEX3-2 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX3-2 proteins from various species. The location of the AIMs identified in AtPEX3-2 by either hfAIM or iLIR is indicated on the top. The PEX3-2 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.

**Figure S7.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX5. The AtPEX5 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX5 proteins from various species. The location of the AIMs identified in AtPEX5 by either hfAIM or iLIR is indicated on the top. The PEX5 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.

**Figure S8.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX7. The AtPEX7 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX7 proteins from various species. The location of the AIMs identified in AtPEX7 by either hfAIM or iLIR is indicated on the top. The PEX7 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW

**Figure S9.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX14. The AtPEX14 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX14 proteins from various species. The location of the AIMs identified in AtPEX14 by either hfAIM or iLIR is indicated on the top. The PEX14 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW

**Figure S10.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX17. The AtPEX17 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX17 proteins from various species. The location of the AIMs identified in AtPEX17 by either hfAIM or iLIR is indicated on the top. The PEX17 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.

**Figure S11.** Multiple sequence alignment of the predicted AIM containing regions of AtPEX19-2. The AtPEX19-2 regions containing either hfAIM or iLIR predicted AIMs were aligned with the corresponding regions from PEX14 proteins from various species. The location of the AIMs identified in AtPEX19-2 by either hfAIM or iLIR is indicated on the top. The PEX19-2 protein sequences derived from the PeroxisomeDB (<http://www.peroxisomedb.org/home.jsp>) were aligned using ClustalW.