

VisIt - Bug # 1337: PDB Reader segfaults trying to read ProteinDataBank file

Status:	Resolved	Priority:	Normal
Author:	Kathleen Biagas	Category:	
Created:	02/14/2013	Assigned to:	Kathleen Biagas
Updated:	02/14/2013	Due date:	
Likelihood:	3 - Occasional		
Severity:	4 - Crash / Wrong Results		
Found in Version:	trunk		
OS:	All		
Support Group:	Any		
Subject:	PDB Reader segfaults trying to read ProteinDataBank file		
Description:	<p>Our automatic file-type guesser based on extension has the PDB reader being tried before ProteinDataBank files, and it segfaults. This is probably why the ProteinDataBank test is failing.</p> <p>From the mdserver log file:</p> <p>Trying to open the file with the PDB file format, strict mode is on Testing if file contains PF3D data Testing if file contains Flash ST data PP_ZFileReader::Identify() meshDimensionsKnown=false validFile=false Testing if file contains Flash MT data PP_ZFileReader::Identify() meshDimensionsKnown=false validFile=false Testing if file contains LEOS data Testing if file contains JM data JMFileFormat::Identify: The file did not contain cycle JMFileFormat::Identify: false signalhandler_core: SIGSEGV!</p>		

History

02/14/2013 01:39 pm - Kathleen Biagas

- Status changed from New to Resolved
- Assigned to set to Kathleen Biagas
- Target version set to 2.7
- Estimated time set to 1.00

Problem wasn't really in PDB reader, but in some code added to avtDatabaseFactory. 'IsEnsemble' was being set before the return value from the database was checked for NULL.

SVN revision 20291.

M /src/avt/Database/Database/avtDatabaseFactory.C