Caption:   
Computational models of wild type S1P4 and its E3.29(122)Q mutant with S1P and LPA species. Computational models of the complexes between the wild type S1P4 or its E3.29(122)Q mutant with S1P or various LPA species generated by Autodock 3.0 and minimised using the MMFF94 forcefield in the MOE program. Complexes in each panel are shown from the same viewpoint with the extracellular end of the receptors oriented to the top of the figure. Standard element color codes are used with grey, white red, blue and magenta representing carbon, hydrogen, oxygen, nitrogen and phosphorous. Ribbons are shaded from red at the amino-terminus to blue at the carboxy-terminus. (A) Model of the complex between S1P (spacefilling) and the wild type S1P4 receptor. Residues in the receptor involved in ion pairs with S1P are shown as stick models and labelled. (B) Superimposition of the wild type S1P4 complex with S1P (orange) and the E3.29(122)Q S1P4 mutant complex with 14:0 LPA (green). For clarity, the only position at which the modelled amino acid position is shown for both receptor models is 3.29(122). Other residues had very similar optimised positions in the two model structures. (C) Superimposition of wild type S1P4 complexes with 18:1 LPA (cyan), 16:0 LPA (yellow) and 14:0 LPA (green) on E3.29(122)Q mutant complexes with 18:1 LPA (blue-green), 16:0 LPA (gold) and S1P (orange). For clarity, the only position at which modelled amino acid position is shown for both the wild type and mutant receptor models is 3.29(122). Other residues had very similar optimised positions in all model structures. (D) Space-filling models which represent the minimised extended conformation of each structure were constructed using SYBYL 6.9 software (Tripos Inc., St. Louis, MO., U.S.A.). The distance between phosphorus and terminal carbon atoms was predicted for each structure listed from top to bottom: 18:1 LPA, 27.0 Å; 16:0 LPA, 26.7 Å; 14:0 LPA, 24.2 Å; S1P, 24.0 Å.

Question: What is shown in panel (D) of the figure?   
   
A: The amino acid positions of the wild type and mutant receptors.   
B: Space-filling models of the minimised extended conformation of each structure.   
C: The optimal positions of the wild type and mutant receptors.   
D: The positions of the residues involved in ionic interaction with S1P.

Answer: B: Space-filling models of the minimised extended conformation of each structure.