

R. ruber	229	DIAPGRSLAEWAVQHGRTVFMISYRNPDESMRHITMDDYYVDGIATALDVVEEITGSPKI	288
phaC3	236	DIAPGRSLIEYLLQOGQOVFTISWRNPLARHRSDADT-YGQAIIDALDAVEQITGADRT	294
phaC2	236	DIAPGRSLVEYLLQOGQOVFAISWRNPHARHRDWGADT-YGAAIVEALDAVQCIAGTDSA	294
phaC1	239	DISPGRSMVEYELGOGQOVFTISWRNPKARHRTWGLDT-YGQAIVDALDAVEKITGSTRT	297

R. ruber	289	EVIISICLGAMAAMAAARAFVGD-KRVSAFTMLNTLLDYSQVGELGLLTDPATLDLVEF	347
phaC3	295	HLIATCSGHLAAMTAAHLTEIGEGDRIAGLALAVTVLDQNRAGEASAALSERAAASAAIR	354
phaC2	295	HLIGTCSGHLAAMVAAHLTQVGEGRVAGLTAVTVLDQTQAGIAAAVMSERAAAAAIR	354
phaC1	298	HLFGSCSGMLAAMTAAHLTHIGQGDRLAGLTAVTVLDQSRAGEAAAALDPTTAQAAIQ	357

R. ruber	348	RMROQGELSGKEMAGSFDMIRAKDLVENYWVSRWMKGEKPAAFDILAWNEDSTSMFAEMH	407
phaC3	355	ASSAQGYLDGRTLAEVFAWLRPTDLVWRYWVNYYVQGRRPAAFDVLFWNSDTTRMTAALH	414
phaC2	355	ASAAKGYLDGRTLAEMFAWLRPTDLVWRYWVNYYVQGRAPAAFDVLFWNSDTTRMTAALH	414
phaC1	358	VSAARGYLDGRSLAEVFAWLRPTDLVWRYWVNYYIQGRTPPFDFVLFWNADTTRMTATLH	417

R. ruber	408	SHYLRSLYGRNELAEGLYVLDGQPLNLHDIACDTYVVGAINDHIVPWTSSYQAVNLLGG-	466
phaC3	415	RDLVMMALRNALTTPGAVSMLGTPVDLSTVTADAYVIGGIADHISPWQSAYRSARLLGSK	474
phaC2	415	RDLVLLGLRNALTTPGAATMLGTPVDLATVTADAYVVGGSADHLCPWQSTYRSARLLGSK	474
phaC1	418	KDMVQIGLSNALTTPGAVSMLGTPVDLSKVIVDSYVIAGIADHISPWQACYRSARLLGSE	477

R. ruber	467	DVRYVLTNGGHVAGAVNPPGKRVWFKAVGAPDAESGTPLPADPQVWDEAATRYEHSWWED	526
phaC3	475	DNREFVLSSSGHIASMVNPPNN-----PRASFRFAQADHETPEQWLDTAQTATDSWWPD	527
phaC2	475	DSREFVLSSNGHIASLVNPPGN-----PRASFRFGCPAETPDEWLTAETAPDSWWPD	527
phaC1	478	SSREFVLSTSGHIAAMVNPPGN-----PRASYRMASPSTEHPAEWLETSSQQQDSWWPD	530