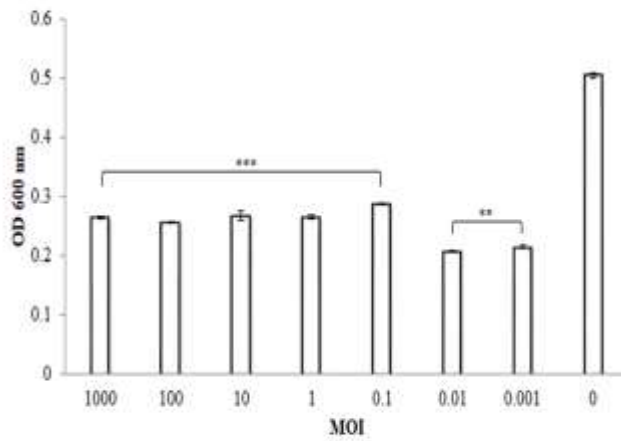
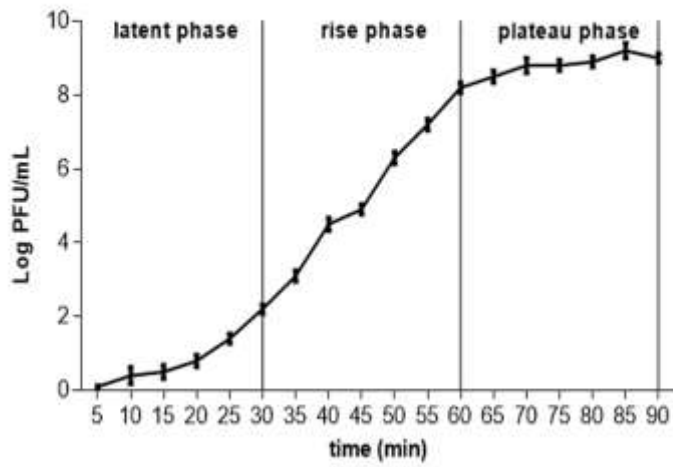


**Figure S1**



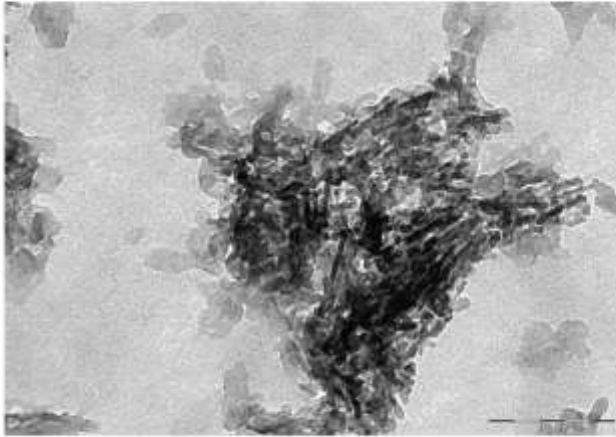
**Figure S1** MOI of SR  $\phi$  1. The absorbance is greatly reduced when MOI is 0.1 compared to control (MOI value of 0). \*\*\*  $p < 0.001$ ; \*\*  $p < 0.01$ . Each value is the mean  $\pm$  DS of 3 independent experiments. Statistical analysis was performed with Student's t test.

**Figure S2**



**Figure S2** One step growth curve of phage SR  $\phi$  1. Each value is the mean  $\pm$  DS of 3 independent experiments with 3 replicates each.

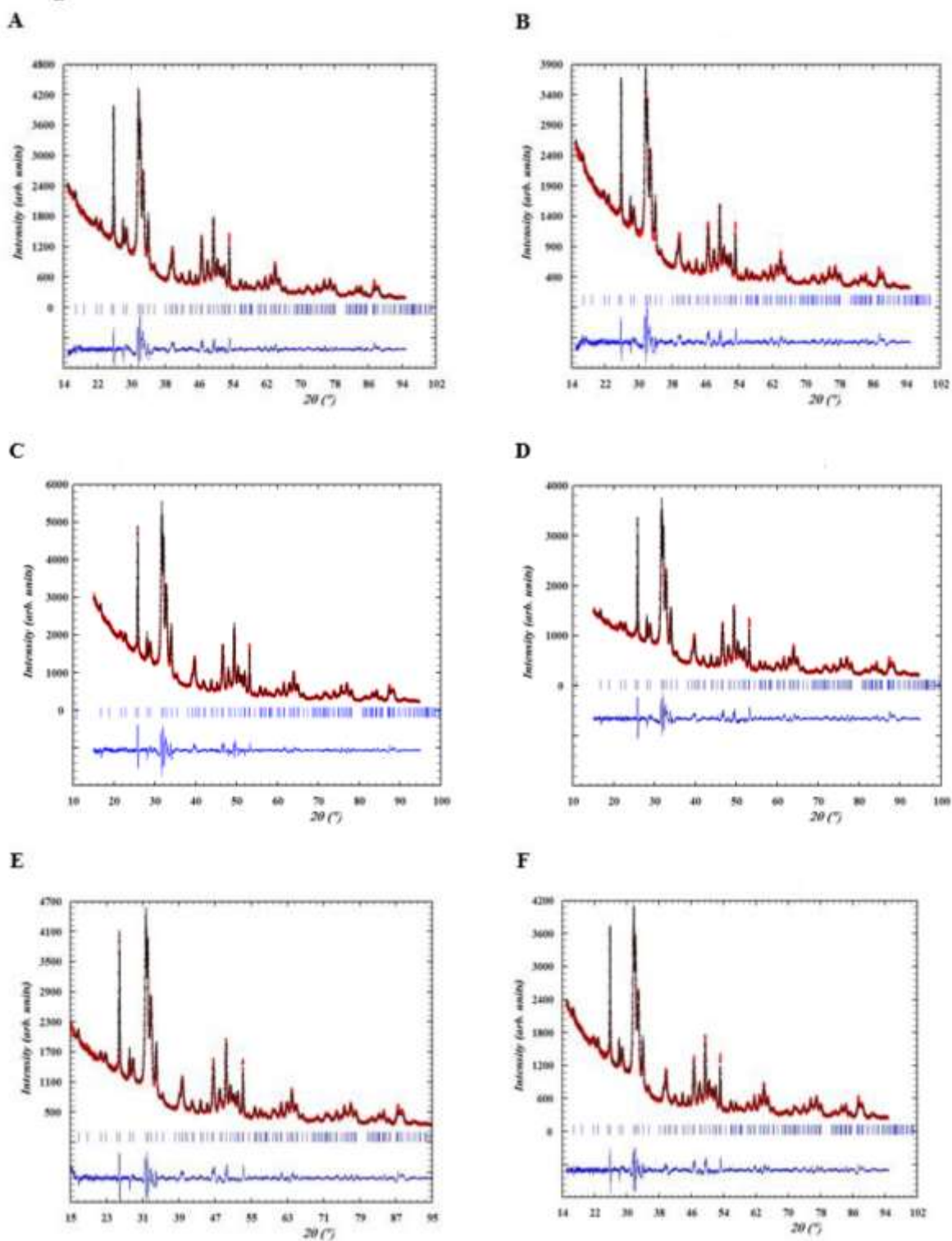
**Figure S3**



**Figure S3** Transmission electron microscope (TEM) analysis of the biomimetic hydroxyapatite.

Note: Scale bars, 100 nm.

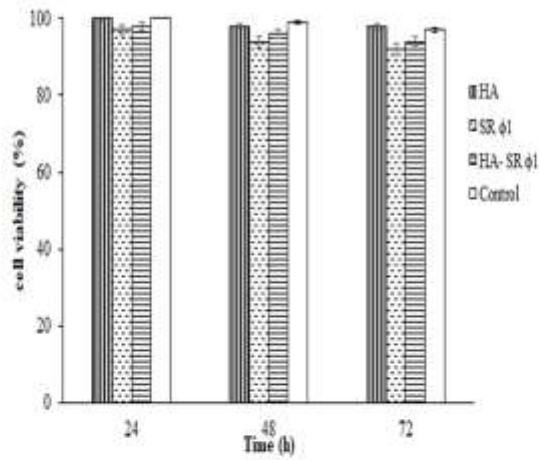
**Figure S4**



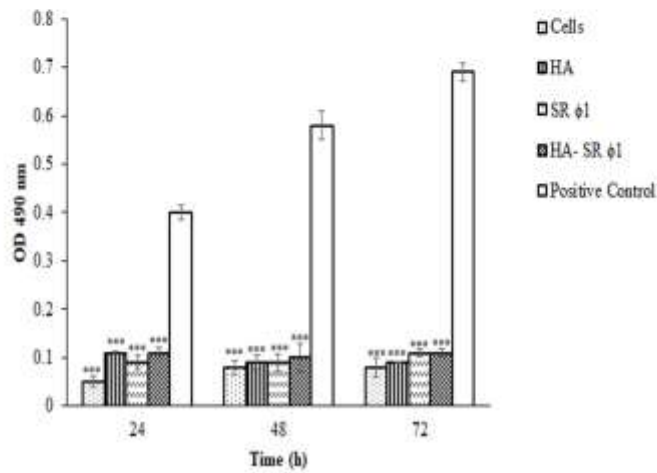
**Figure S4** XPD analysis. Rietveld fits of: (A) the HA\_10 mg sample; (B) Rietveld fits of the HA\_10 mg + SR  $\phi$ 1 sample; (C) Rietveld fits of the HA\_50 mg sample; (D) Rietveld fits of the HA\_50 mg + SR  $\phi$ 1 sample; (E) Rietveld fits of the HA\_100 mg sample; (F) Rietveld fits of the HA\_100 mg + SR  $\phi$ 1 sample.

**Figure S5**

**A**



**B**



**Figure S5** Cytotoxicity trials of SR φ1, HA and HA- SR φ1 complex. **(A)** MTT and **(B)** LDH assays on HepG2 cell-line treated respectively with SR φ1 ( $10^7$  PFU/mL), HA- SR φ1 (100 mg/mL plus  $10^7$  PFU/mL) and HA (100 mg/mL) for 24 h, 48 h, 72 h. Each value is the mean  $\pm$  DS of 3 independent experiments with 3 replicates each. \*\*\*  $p < 0.001$ .

Note: Positive control for LDH assay was provided by the kit.

**Table S1** Predicted genes and gene products of pSs-1.

Gene name	Range		Bps size	Direction
	Minimum	Maximum		
conserved hypothetical protein CDS	34,417	34,770	354	<i>reverse</i>
FIG00637995: hypothetical protein CDS	13,871	14,041	171	<i>forward</i>
FIG00638922: hypothetical protein CDS	4,795	5,064	270	<i>reverse</i>
FIG00642795: hypothetical protein CDS	8,776	8,937	162	<i>reverse</i>
FIG01045771: hypothetical protein CDS	167	853	687	<i>reverse</i>
FIG01045895: hypothetical protein CDS	40,075	41,151	1,077	<i>reverse</i>
FIG01046357: hypothetical protein CDS	38,252	38,689	438	<i>reverse</i>
FIG01047095: hypothetical protein CDS	42,899	43,825	927	<i>reverse</i>
FIG01047205: hypothetical protein CDS	15,361	15,654	294	<i>forward</i>
FIG01047296: hypothetical protein CDS	38,777	39,139	363	<i>reverse</i>
FIG01047895: hypothetical protein CDS	37,869	38,255	387	<i>reverse</i>
FIG01047943: hypothetical protein CDS	47,650	48,147	498	<i>reverse</i>
FIG01048207: hypothetical protein CDS	35,712	36,242	531	<i>reverse</i>
FIG01049728: hypothetical protein CDS	24,102	25,076	975	<i>reverse</i>
generated by GeneMarkS CDS	47,396	47,653	258	<i>reverse</i>
gp5 CDS	43,785	45,134	1,350	<i>reverse</i>
gp7 CDS	41,631	42,896	1,266	<i>reverse</i>
gp8 CDS	41,169	41,618	450	<i>reverse</i>
HNH homing endonuclease CDS	49,814	50,332	519	<i>reverse</i>
Holliday junction resolvase / Crossover junction endodeoxyribonuclease rusA (EC 3.1.22.-) CDS	4,113	4,508	396	<i>reverse</i>
hypothetical protein CDS	50,611	51,222	612	<i>reverse</i>
hypothetical protein CDS	34,853	35,230	378	<i>reverse</i>
hypothetical protein CDS	35,223	35,597	375	<i>reverse</i>
hypothetical protein CDS	34,028	34,315	288	<i>reverse</i>
hypothetical protein CDS	20,068	20,346	279	<i>forward</i>
hypothetical protein CDS	49,318	49,590	273	<i>reverse</i>
hypothetical protein CDS	15,829	16,083	255	<i>forward</i>
hypothetical protein CDS	51,380	51,622	243	<i>reverse</i>
hypothetical protein CDS	9,382	9,591	210	<i>reverse</i>
hypothetical protein CDS	11,605	11,808	204	<i>reverse</i>
hypothetical protein CDS	840	1,031	192	<i>reverse</i>
hypothetical protein CDS	19,764	19,949	186	<i>forward</i>
hypothetical protein CDS	14,038	14,220	183	<i>forward</i>
hypothetical protein CDS	28,586	28,750	165	<i>forward</i>
hypothetical protein CDS	10,338	10,469	132	<i>forward</i>
hypothetical protein CDS	20,478	20,603	126	<i>forward</i>
hypothetical protein CDS	2,453	2,566	114	<i>forward</i>
Lysozyme (EC 3.2.1.17) CDS	48,821	49,318	498	<i>reverse</i>
Mobile element protein CDS	21,489	22,340	852	<i>forward</i>
ORF23 CDS	10,523	11,566	1,044	<i>forward</i>
Origin specific replication initiation factor CDS	7,968	8,789	822	<i>reverse</i>
Phage anti-RecBCD 1 CDS	15,030	15,314	285	<i>forward</i>
Phage antitermination protein N CDS	12,140	12,523	384	<i>forward</i>

Phage antitermination protein Q CDS	2,672	3,190	519	<i>reverse</i>
Phage EaA protein CDS	18,640	19,764	1,125	<i>forward</i>
Phage EaD protein CDS	17,483	18,643	1,161	<i>forward</i>
Phage EaD protein CDS	16,070	16,936	867	<i>forward</i>
Phage endopeptidase CDS	48,357	48,824	468	<i>reverse</i>
Phage excisionase # Lambda family excisionase CDS	21,074	21,292	219	<i>forward</i>
Phage head completion protein CDS	39,772	40,065	294	<i>reverse</i>
Phage holin, class II CDS	2,005	2,208	204	<i>reverse</i>
Phage lysin (EC 3.2.1.17) # Phage lysozyme or muramidase (EC 3.2.1.17) CDS	1,530	2,033	504	<i>reverse</i>
Phage minor tail protein CDS	22,793	24,091	1,299	<i>,reverse</i>
Phage minor tail protein CDS	29,439	30,143	705	<i>reverse</i>
Phage minor tail protein CDS	30,872	31,219	348	<i>reverse</i>
Phage Nin protein CDS	3,187	3,366	180	<i>reverse</i>
Phage NinB DNA recombination CDS	5,883	6,320	438	<i>reverse</i>
Phage NinE CDS	5,570	5,746	177	<i>reverse</i>
Phage NinF CDS	5,057	5,233	177	<i>reverse</i>
Phage NinH CDS	3,347	3,550	204	<i>reverse</i>
Phage NinX CDS	5,226	5,567	342	<i>reverse</i>
Phage outer membrane lytic protein Rz; Endopeptidase (EC 3.4.-.-) CDS	1,066	1,533	468	<i>reverse</i>
Phage protein CDS	37,119	37,853	735	<i>reverse</i>
Phage protein CDS	36,426	37,079	654	<i>reverse</i>
Phage protein CDS	3,547	4,116	570	<i>reverse</i>
Phage protein CDS	39,311	39,712	402	<i>reverse</i>
Phage protein CDS	31,312	31,710	399	<i>forward</i>
Phage protein CDS	20,590	20,964	375	<i>forward</i>
Phage protein CDS	13,266	13,631	366	<i>forward</i>
Phage protein CDS	17,193	17,486	294	<i>forward</i>
Phage protein CDS	4,505	4,795	291	<i>reverse</i>
Phage protein CDS	30,308	30,595	288	<i>forward</i>
Phage protein CDS	30,600	30,860	261	<i>reverse</i>
Phage protein CDS	6,301	6,513	213	<i>reverse</i>
Phage protein CDS	39,123	39,311	189	<i>reverse</i>
Phage protein CDS	15,665	15,832	168	<i>forward</i>
Phage replicative DNA helicase (EC 3.6.1.-) CDS	6,595	7,971	1,377	<i>reverse</i>
Phage repressor CDS	9,701	10,354	654	<i>forward</i>
Phage repressor CDS	8,958	9,248	291	<i>reverse</i>
Phage tail assembly protein CDS	28,720	29,439	720	<i>reverse</i>
Phage tail assembly protein CDS	28,250	28,597	348	<i>reverse</i>
Phage tail fiber protein CDS	25,070	28,240	3,171	<i>reverse</i>
Phage tail length tape-measure protein 1 CDS	31,711	33,966	2,256	<i>reverse</i>
Phage terminase, large subunit CDS	45,267	46,586	1,320	<i>reverse</i>
Phage terminase, small subunit CDS	46,570	47,001	432	<i>reverse</i>
Putative DNA-binding protein Erf CDS	14,323	15,030	708	<i>forward</i>
superinfection exclusion CDS	12,544	13,122	579	<i>reverse</i>

**Abbreviation:** CDS, coding DNA sequences.

**Table S2** Cell parameters and space group of the hexagonal hydroxyapatite structure (ICSD code # 56306).

HA			
<b>a (Å)</b>	<b>b (Å)</b>	<b>c (Å)</b>	<b>Space group</b>
9.410	9.410	6.879	P63/m
<b><math>\alpha</math> (°)</b>	<b><math>\beta</math> (°)</b>	<b><math>\gamma</math> (°)</b>	
90	90	120	



**Table S3** Cell parameters and domain size for HA, HA + SR  $\phi$ 1

	<b>a (Å)</b>	<b>b (Å)</b>	<b>c (Å)</b>	<b>App Size (nm) [002]</b>	<b>App Size (nm) [110]</b>
<b>HA_10 mg</b>	9.434	9.434	6.885	42.4±0.5	14.3±0.5
<b>HA_10 mg + SR <math>\phi</math>1</b>	9.434	9.434	6.885	46.0±0.5	14.8±0.5
<b>HA_50 mg</b>	9.434	9.434	6.885	42.9±0.5	14.7±0.5
<b>HA_50 mg + SR <math>\phi</math>1</b>	9.434	9.434	6.885	41.7±0.5	14.0±0.5
<b>HA_100 mg</b>	9.434	9.434	6.885	42.9±0.5	14.2±0.5
<b>HA_100 mg + SR <math>\phi</math>1</b>	9.434	9.434	6.885	40.4±0.5	13.7±0.5