```
 CLUSTAL 2.1 Multiple Sequence Alignments


Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: epor          115 aa
Sequence 2: ecoli         149 aa
Start of Pairwise alignments
Aligning...




Sequences (1:2) Aligned. Score: 11.3043
Guide tree file created:   [clustalw.dnd]

There are 1 groups
Start of Multiple Alignment

Aligning...
Group 1:                      Delayed
Alignment Score -30

CLUSTAL-Alignment file created  [clustalw.aln]
```

---

clustalw.aln

```
CLUSTAL 2.1 multiple sequence alignment


epor           ---------ASLWP--QVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPE---ELL
ecoli          RGSHHHHHHGSFTPSGTTGTTKLTVTEKCQVRVGDLTVAKTRGQLTDAAPIGPVTVQALG
                        .*: *    .*:  * ::  . .    :*. .* ..:  :  *. **     *

epor           CFTER--LEDLVCFWEEAASAGVGPGN----YSFSYQLEDEPWKLCRLHQAPTARGAVRF
ecoli          CDARQVALKADTDNFEQGKFFLISDNNRDKLYVNIRPTDNSAWTTDNGVFYKNDVGSWGG
               * :.:  *:  .  :*:.    :. .*    *       ::..*.  .     .  *:

epor           WCSLPTADTSSFVPL--------------
ecoli          IIGIYVDGQQTNTPPGNYTLTLTGGYWAK
                 .:  .  . .: .*
```
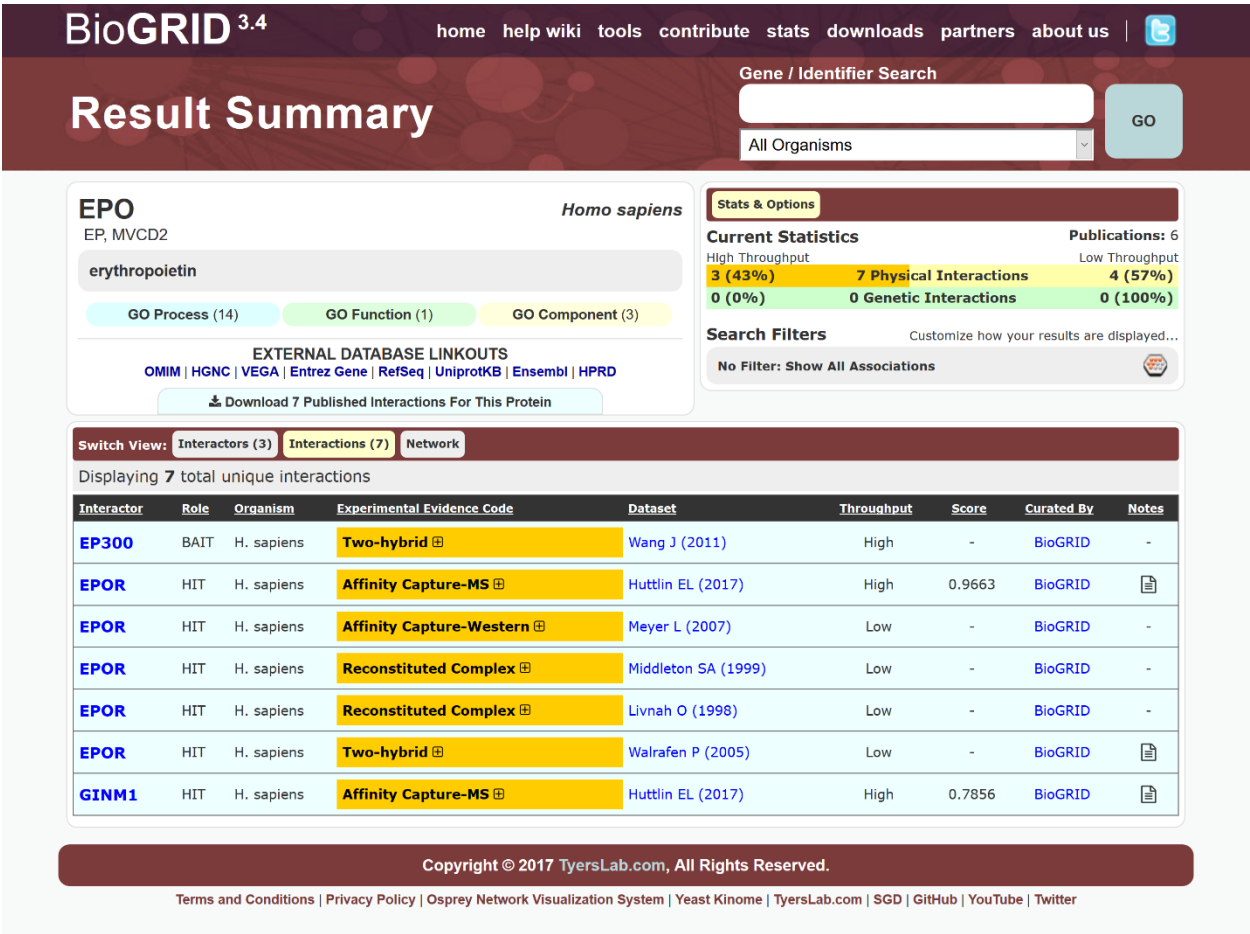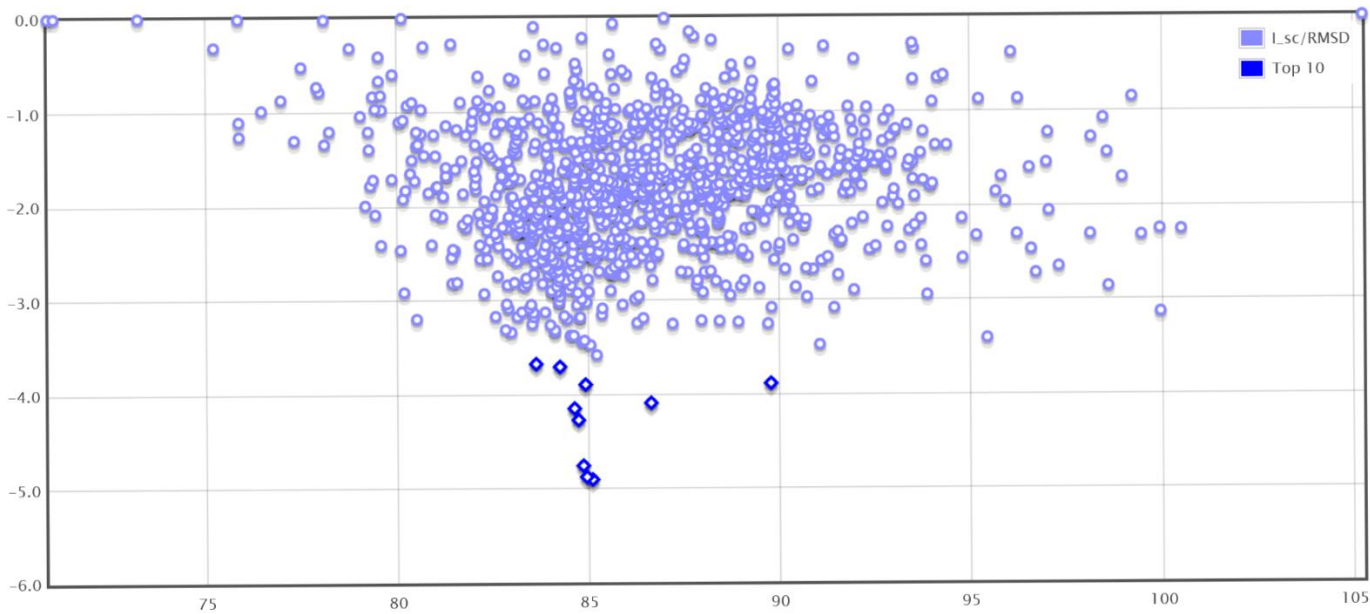
---

clustalw.dnd

```
(epor:0.44348,ecoli:0.44348);
```

Supplementary Fig. 2: EPO interaction (Biogrid 3.4)

BioGRID 3.4

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Result Summary

Gene / Identifier Search

[   ] GO

All Organisms

EPO   *Homo sapiens*
EP, MVCD2

erythropoietin

GO Process (14)   GO Function (1)   GO Component (3)

EXTERNAL DATABASE LINKOUTS
OMIM | HGNC | VEGA | Entrez Gene | RefSeq | UniprotKB | Ensembl | HPRD

⬇ Download 7 Published Interactions For This Protein

Stats & Options

Current Statistics   **Publications:** 6
High Throughput   Low Throughput
3 (43%)   **7 Physical Interactions**   4 (57%)
0 (0%)   **0 Genetic Interactions**   0 (100%)

Search Filters   Customize how your results are displayed...
No Filter: Show All Associations

Switch View: Interactors (3)   Interactions (7)   Network

Displaying **7** total unique interactions

Interactor	Role	Organism	Experimental Evidence Code	Dataset	Throughput	Score	Curated By	Notes
EP300	BAIT	H. sapiens	Two-hybrid ⊞	Wang J (2011)	High	-	BioGRID	-
EPOR	HIT	H. sapiens	Affinity Capture-MS ⊞	Huttlin EL (2017)	High	0.9663	BioGRID	📄
EPOR	HIT	H. sapiens	Affinity Capture-Western ⊞	Meyer L (2007)	Low	-	BioGRID	-
EPOR	HIT	H. sapiens	Reconstituted Complex ⊞	Middleton SA (1999)	Low	-	BioGRID	-
EPOR	HIT	H. sapiens	Reconstituted Complex ⊞	Livnah O (1998)	Low	-	BioGRID	-
EPOR	HIT	H. sapiens	Two-hybrid ⊞	Walrafen P (2005)	Low	-	BioGRID	📄
GINM1	HIT	H. sapiens	Affinity Capture-MS ⊞	Huttlin EL (2017)	High	0.7856	BioGRID	📄

Supplementary Fig. 3: Rosetta Docking (EPO-adhesin)

X axis: RMSD score; Y axis: Interface score

Interface score I_sc / RMSD and Top-10 "I_sc score models"

decoy	total_score	rms	Fnat	I_sc	Irms	cen_rms	dslf_ca_dih	dslf_cs_ang	dslf_ss_dih	dslf_ss_dst
proteins_0426	-257.612	86.631	NaN	-4.096	NaN	86.454	0.277	0.502	0.437	-3.582
proteins_0538	-257.049	84.73	NaN	-4.275	NaN	84.816	0.277	0.502	0.437	-3.582
proteins_0892	-256.937	83.507	NaN	-3.048	NaN	83.7	0.277	0.502	0.437	-3.582
proteins_0137	-256.881	84.369	NaN	-3.169	NaN	85.306	0.277	0.502	0.437	-3.582
proteins_0006	-256.846	89.79	NaN	-3.083	NaN	91.459	0.277	0.502	0.437	-3.582
proteins_0032	-256.834	85.283	NaN	-2.698	NaN	87.254	0.277	0.502	0.437	-3.582
proteins_0076	-256.813	84.53	NaN	-3.378	NaN	85.219	0.277	0.502	0.437	-3.582
proteins_0880	-256.779	84.2	NaN	-2.917	NaN	85.56	0.277	0.502	0.437	-3.582
proteins_0933	-256.777	83.626	NaN	-3.678	NaN	84.81	0.277	0.502	0.437	-3.582
proteins_0069	-256.763	93.866	NaN	-2.95	NaN	91.681	0.277	0.502	0.437	-3.582
proteins_0222	-256.756	98.605	NaN	-2.863	NaN	89.604	0.277	0.502	0.437	-3.582
proteins_0133	-256.729	84.131	NaN	-3.32	NaN	84.876	0.277	0.502	0.437	-3.582
proteins_0261	-256.727	85.015	NaN	-2.912	NaN	81.766	0.277	0.502	0.437	-3.582
proteins_0693	-256.722	85.568	NaN	-2.718	NaN	87.492	0.277	0.502	0.437	-3.582
proteins_0455	-256.706	84.256	NaN	-2.963	NaN	86.476	0.277	0.502	0.437	-3.582
proteins_0492	-256.703	84.115	NaN	-3.335	NaN	84.528	0.277	0.502	0.437	-3.582
proteins_0057	-256.697	82.867	NaN	-3.041	NaN	85.652	0.277	0.502	0.437	-3.582
proteins_0044	-256.683	84.895	NaN	-3.431	NaN	85.582	0.277	0.502	0.437	-3.582
proteins_0044	-256.682	88.429	NaN	-3.226	NaN	89.146	0.277	0.502	0.437	-3.582
proteins_0075	-256.678	84.952	NaN	-3.024	NaN	87.394	0.277	0.502	0.437	-3.582

Score data [Download original score file]

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X axis: RMSD score; Y axis: Interface score

Interface score I_sc / RMSD and Top-10 "I_sc score models"
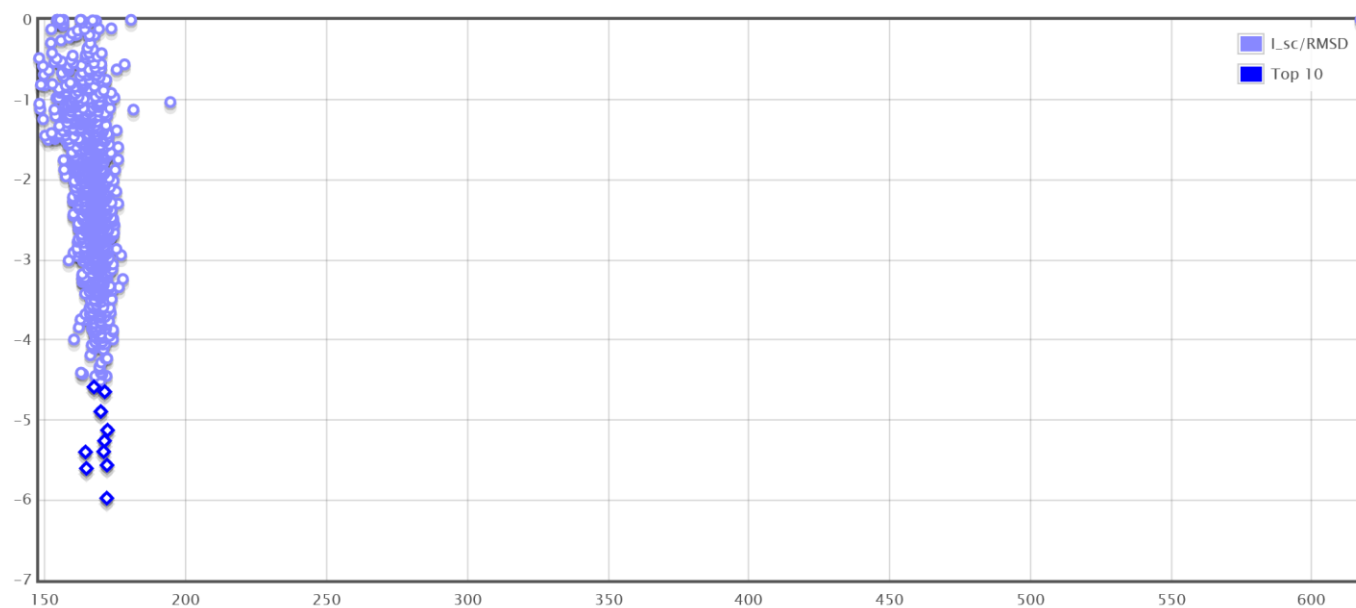
Score data [Download original score file]

decoy	total_score ▲	rms	Fnat	I_sc	Irms	cen_rms	dslf_ca_dih	dslf_cs_ang	dslf_ss_dih	dslf_ss_dst
proteins_0753	-313.739	167.341	NaN	-4.587	NaN	167.798	0.592	0.62	3.101	-7.149
proteins_0057	-313.729	166.567	NaN	-4.062	NaN	165.967	0.592	0.62	3.101	-7.149
proteins_0574	-313.676	169.694	NaN	-4.509	NaN	169.815	0.592	0.62	3.101	-7.149
proteins_0084	-313.596	164.649	NaN	-5.605	NaN	166.77	0.592	0.62	3.101	-7.149
proteins_0111	-313.582	171.083	NaN	-5.261	NaN	172.455	0.592	0.62	3.101	-7.149
proteins_0677	-313.568	160.25	NaN	-3.994	NaN	162.246	0.592	0.62	3.101	-7.149
proteins_0242	-313.442	171.97	NaN	-5.564	NaN	171.597	0.592	0.62	3.101	-7.149
proteins_0016	-313.441	164.109	NaN	-3.75	NaN	166.264	0.592	0.62	3.101	-7.149
proteins_0603	-313.4	164.322	NaN	-5.4	NaN	166.749	0.592	0.62	3.101	-7.149
proteins_0112	-313.382	171.883	NaN	-5.977	NaN	172.884	0.592	0.62	3.101	-7.149
proteins_0144	-313.36	165.876	NaN	-3.675	NaN	167.824	0.592	0.62	3.101	-7.149
proteins_0028	-313.35	163.413	NaN	-4.425	NaN	166.082	0.592	0.62	3.101	-7.149
proteins_0319	-313.315	170.506	NaN	-3.797	NaN	171.308	0.592	0.62	3.101	-7.149
proteins_0244	-313.314	167.975	NaN	-4.56	NaN	168.546	0.592	0.62	3.101	-7.149
proteins_0522	-313.27	162.746	NaN	-4.409	NaN	165.699	0.592	0.62	3.101	-7.149
proteins_0412	-313.125	167.234	NaN	-3.207	NaN	168.792	0.592	0.62	3.101	-7.149
proteins_0133	-313.074	167.285	NaN	-3.671	NaN	167.103	0.592	0.62	3.101	-7.149
proteins_0004	-313.025	172.64	NaN	-3.358	NaN	171.083	0.592	0.62	3.101	-7.149
proteins_0517	-313.009	167.458	NaN	-3.839	NaN	169.141	0.592	0.62	3.101	-7.149
proteins_0905	-312.991	166.077	NaN	-4.191	NaN	167.079	0.592	0.62	3.101	-7.149

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Supplementary Fig. 5: Molecular Dynamics simulation between EPO and *E. coli* Adhesin
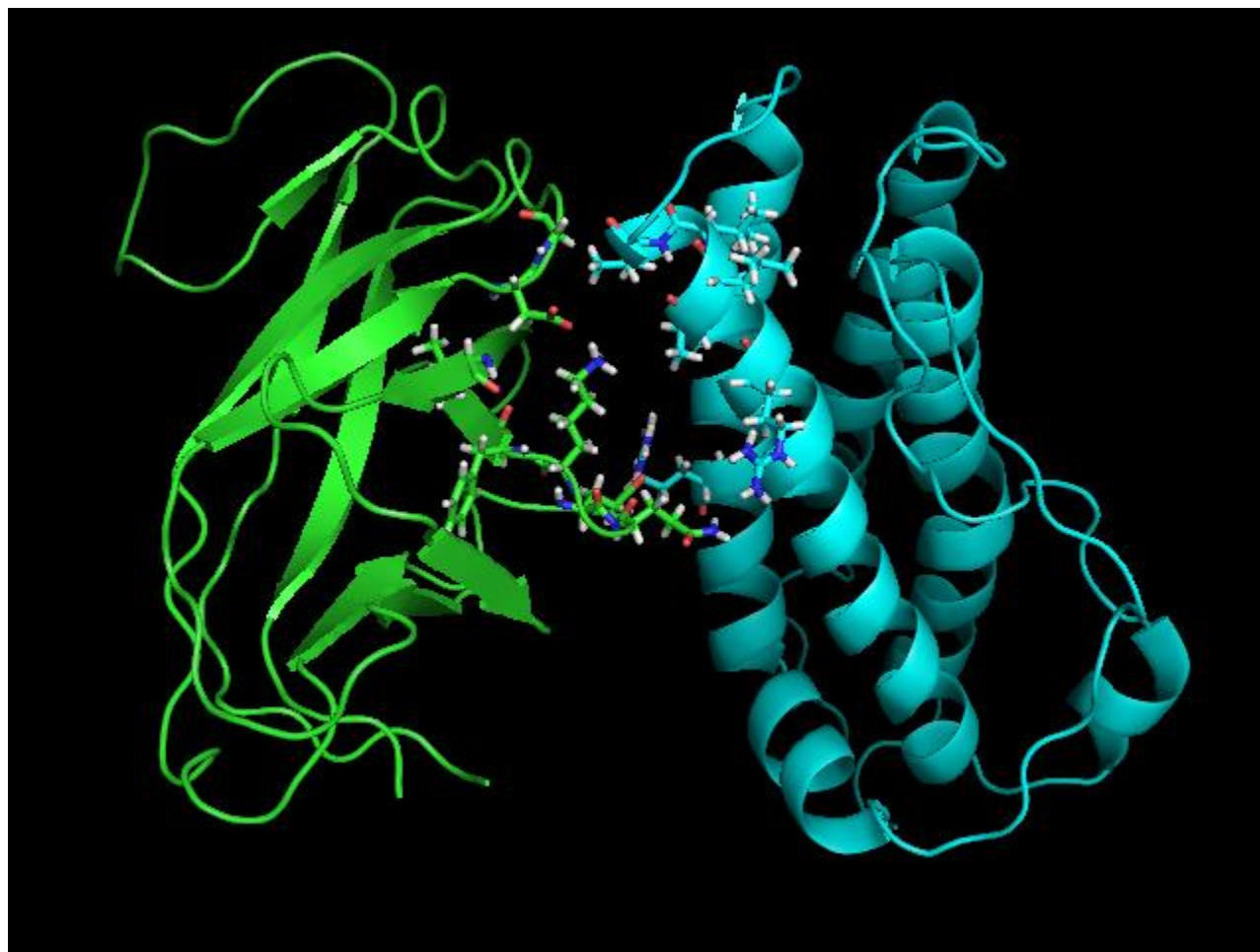
The png file of the complex structure after dynamics is attached. The green and cyan cartoons represent the EPO and adhesin, respectively. The interface residues in between the complex are represented in stick.

Supplementary Fig. 6: Growth curves of different bacteria in presence and absence of rhuEPO repeated 6 times.
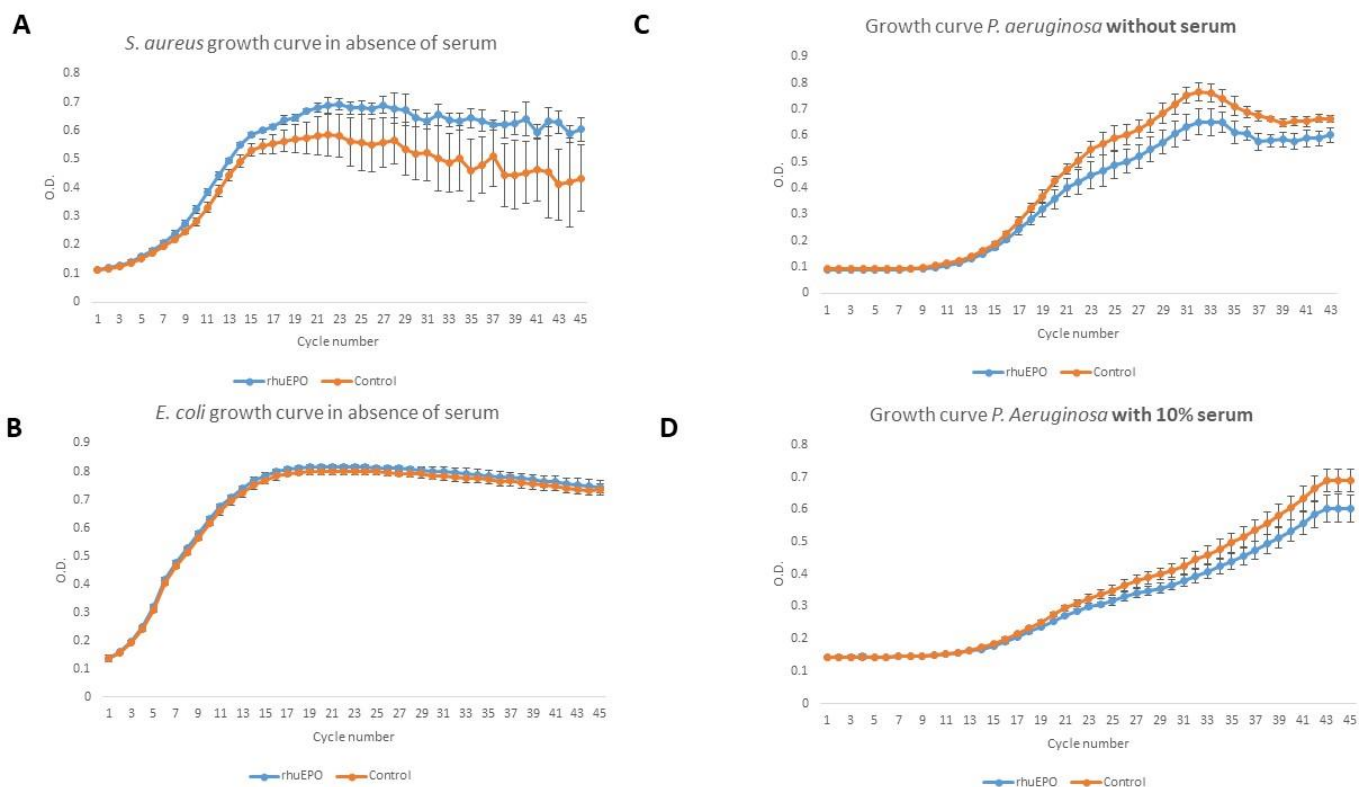
Growth curve of bacteria repeated 6 times are shown. The growth curve of P. aeruginosa in presence of 10% serum is also shown. Experiments of S. aureus and E. coli in presence of 10% serum in our experimental conditions did not yield any growth (data not shown).

Supplementary Fig. 7: Absorbance spectra of membrane protein at 280nm

Supplementary Fig. 8: Fluorescence emission spectra of phosphate buffer (3ml) when excited at 240nm.
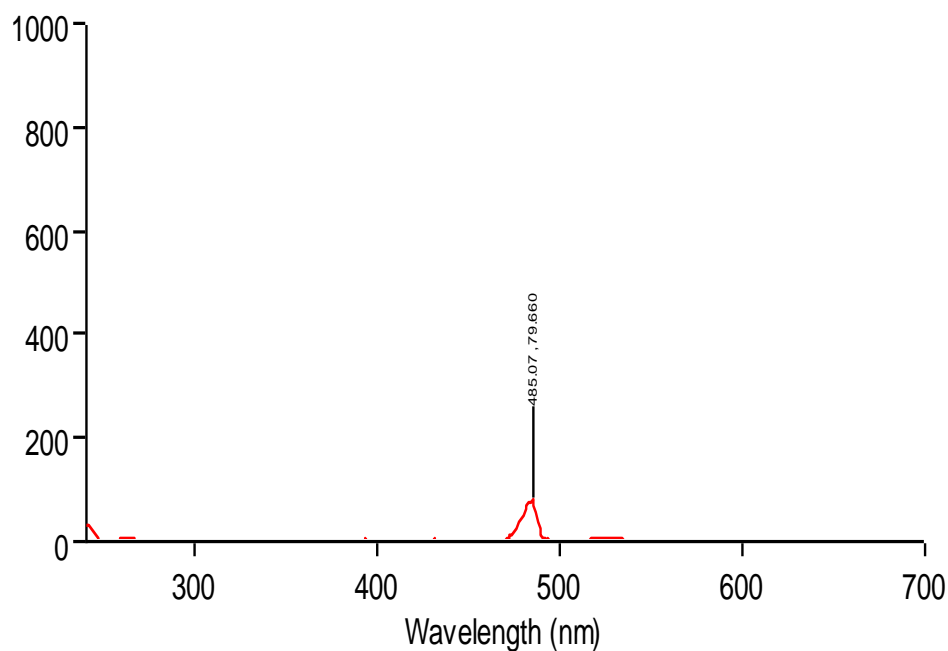
Supplementary Fig. 9: Fluorescence emission spectra of phosphate buffer after addition of membrane protein (0.025mg/3ml)