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Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	All of SDS-PAGE and blot data were collected with ImageQuant LAS500 (GE). UV-Vis results were collected with Cary Series UV-Vis-NIR Spectrophotometer. FT-IR results were collected with Agilent Resolutions Pro. Fluorescence-measurement data were collected with RF-5301PC v.2.04. Fluorescence images were collected with Leica Application Suite v.4.4. Flow-cytometry data were collected with BD FACSDiva Software v.8.0.2.
Data analysis	All of blot, UV spectra and fluorescence images were analysed with ImageJ v.1.48. Graphs were plotted with originPro 9.0.0. FT-IR results were analysed with Agilent Resolutions Pro. Flow cytometry results were analysed with FlowJo v.10.6.1.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The main data supporting the results in this study are available within the paper and its Supplementary Information. The raw and analysed datasets are too numerous to be readily shared publicly but are available for research purposes from the corresponding author on reasonable request.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We performed all protein purification three times, independently.
Data exclusions	No data were excluded.
Replication	The experimental findings were reliably reproduced.
Randomization	All samples and organisms were randomly allocated into experimental groups.
Blinding	Blinding is not relevant to the study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	anti-6x His tag (ThermoFisher, MA 1-21315), anti-mouse (H+L) Secondary Antibody, HRP (ThermoFisher, A-10677), anti-Human IgG Secondary antibody (H+L) HRP (ThermoFisher, 62-8420), anti-Human IgG (H+L) Secondary Antibody, Alexa Fluor 555 (ThermoFisher, A-21433), Herceptin (Roche, NDC code: 50242-132-01), Human BD Fc Block BD Biosciences, FAB140R), Human B7-1/CD80 Alexa Fluor 647-conjugated antibody (R&D systems, FAB140R), Human CD14 Alexa Fluor 594-conjugated antibody (R&D systems, FAB3832T).
Validation	Validation of each antibody was done under standard information offered by the supplier.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Expi 293 was provided by Prof. SangTaek Jung at Kookmin University. SK-BR-3 were obtained from ATCC. THP-1 cells were provided by Prof. YoungTae Chang.
Authentication	Expi 293 was authenticated by the vendor, ThermoFisher SK-BR-3 was authenticated by the vendor, ATCC THP-1 cell was authenticated by the vendor, ATCC
Mycoplasma contamination	The cell lines were not tested for mycoplasma contamination, but we added anti-mycoplasma agent to each cell-culture media.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	SK-BR-3 cells were cultured in 100 pi dish and trypsinized for transferring to a tube in DMEM media (1 ml) containing 10% (v/v) fetal bovine serum (FBS) and 1% (v/v) penicillin streptomycin. In total, 10,000 cells were counted by flow cytometry using a fluorescence-activated cell sorter. THP-1 cells were differentiated to macrophages in RPMI media (0.5 ml) containing 10% (v/v fetal bovine serum (FBS) and 1% (v/v) penicillin and streptomycin with Phorbol 12-myristate 13-acetate (PMA; 150 nM) at 24 wells plate. In total, 10,000 cells were counted by flow cytometry using a fluorescence-activated cell sorter.
Instrument	Flow cytometry was performed with a LSR Foretessa 5 Laser I (BD Biosciences).
Software	Data were analysed with FlowJo v.10.6.1.
Cell population abundance	No sorting was performed.
Gating strategy	Generally, cells were first gated on FSC/SSC. Singlet cells were usually gated using FSC-H and FSC-A. Surface antigen gating was performed on the live cell population.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.