

Gene Name	MATR3
Protein Name	Matrin-3
Synonyms	ALS21, MPD2, VCPDM
Uniprot ID	P43243
Description	May play a role in transcription or may interact with other nuclear matrix proteins to form the internal fibrogranular network. In association with the SFPQ-NONO heteromer may play a role in nuclear retention of defective RNAs. Plays a role in the regulation of DNA virus-mediated innate immune response by assembling into the HDP-RNP complex, a complex that serves as a platform for IRF3 phosphorylation and subsequent innate immune response activation through the cGAS-STING pathway [1]. May bind to specific miRNA hairpins [2, 3].
Antigen Coverage	M389 - R578 of 847
Antigen Sequence (Antigen - <u>C-terminal</u> linker and Avi tag)	SMQKGRVETSRVVHIMDFQRGKNLRYQLLQLVEPFGVISNHLI LNKINEAFIEMATTEDAQAAVDYYTTTPALVFGKPVRVHLSQK YKRIKKPEGKPDQKFDQKQELGRVIHLSNLPHSGYSDSAVLKL AEPYGKIKNYILMRMKSQAFIEMETREDAMAMVDHCLKKALW FQGRCVKVDLSEKYKKLVLR <u>SSKGGYGLNDIFEAQKIEWHE</u>
Z-MATR3-4 scFv Sequence (V _H - <u>linker</u> - V _L)	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSSMYWVRQAP GKGLEWVSSIGSGGSYTGYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARPSHGSYSGVYFDYWGQGTLVTVSS <u>GG</u> <u>GGSGGGGSGGGGS</u> DIQMTQSPSSLSASVGDRVTITCRASQS ISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQGTAPHTFGQGTKLEIK
Antibody Fragment Generation and Production	Z-MATR3-4 was generated by phage display technology from a human synthetic scFv library. The scFv was produced by bacterial expression in <i>E. coli</i> , with secretion to the periplasm, and purified by protein A affinity. The final protein batch of Z-MATR3-4 scFv also carries a C-terminal His ₆ tag and a 3xFLAG tag.
Validated Applications	ELISA, HTRF, Luminex, SPR, and IP-MS.

Enzyme-Linked ImmunoSorbent Assay (ELISA):

Method Description	ELISA screens were performed to assess binding of selected single chain fragment variable (scEv) antibody clones. Each
	clone was tested in duplicate against its target antigen and an unrelated non-target control (Primary ELISA). Positive clones
	were selected and screened against its target antigen and a
	streptavidin control (Secondary ELISA). ELISA screens were
	performed in 384 well plates coated with [1ug/mL] streptavidin.
	Biotinylated antigens were diluted in PBT buffer (0.5% BSA,
	0.05% Tween 20 in PBS) to [1ug/mL] and added prior to the
	addition of scFv bacterial culture supernatants. Bound scFvs,
	which contain a FLAG-tag, were detected using an HRP
	conjugated anti-FLAG M2 antibody (Sigma, [1:10,000]). TMB
	substrate solution (Thermo Scientific) was used as a



chromogenic substrate, before the final addition of 1M H ₂ SO ₄
stop solution. Plates were washed four times in between each
step listed above with PBS-T (0.05% Tween 20 in PBS).
Absorbance was measured at 450nm. Only scFv clones with
high enough absorbance ratios (Target / Non-Target and Target
/ Streptavidin) were selected for further analysis. ELISA results
for Z-MATR3-4 are shown below (blank indicates no scFv was
added).

Z-MATR3-4 binding in Primary ELISA screen:



Z-MATR3-4 binding in Secondary ELISA screen:



Homogenous Time Resolved Fluorescence (HTRF):

Susanne Gräslund, Structural Genomics Consortium Susanne.Gräslund@ki.se



Method Description	HTRF technology was employed to robustly and reliably determine, in solution, the binding of each scFv antibody to its target antigen. Sequence unique clones, that tested positive in ELISA, were evaluated by HTRF. Supernatants from bacterial cultures containing scFvs were diluted in assay buffer (0.1% BSA in PBS), then mixed with biotinylated target antigens to a final concentration of 50nM. Donor anti-FLAG M2 antibody labeled with Terbium (Cisbio) and acceptor Streptavidin labeled with XL665 (Cisbio) were added to each scFv in 384 well plates. Samples were incubated for 2 hours at RT. The binding signal (665nm) and the background/noise signal (615nm) were measured using a EnVision instrument (PerkinElmer). HTRF ratios (ΔR) were determined by subtracting the background from the mean emission fluorescence ratio for each sample. Delta ratios were plotted to compare the energy transfer signal for each
	scFv to its non-target control. Results for Z-MATR3-4 are shown in the graph below (blank indicates no scFv was added).

HTRF results for Z-MATR3-4:



Luminex Assay:

Method Description	The specificity of the anti-MATR3 scFv antibodies were evaluated against 48 different antigens (including MATR3) using a bead based multiplex Luminex assay. Color-coded magnetic beads (Magplex Luminex Corp.) were activated with [5mg/mL] NHS and EDC in activation buffer (0.1M NaH ₂ PO ₄ , pH 6.2), then added to 96 well plates and incubated with shake at RT for 20min. Beads were washed twice with MES buffer (0.05M 2-(N-morpholino) ethane sulfonic acid, pH 5.0) before adding neutravidin and incubating for 2 hours at RT with shake. Beads were then washed
	twice with PBS-T before storage buffer (Blocking Reagent for
	ELISA (Roche) with 0.1% ProClin300 (Sigma) was added and



Luminex results for Z-MATR3-4:





Surface Plasmon Resonance (SPR) Affinity Measurements:

Method Description	Kinetic measurements were performed using SPR on a Biacore T200 (GE Healthcare). The anti-FLAG M2 antibody (Sigma) was used to capture the FLAG-tagged scFv before antigen injection.
	Single Cycle Kinetics was performed. Accordingly, five
	order within the same cycle before regeneration with Glycine-HCl, pH 2.5. Antigen concentrations tested against Z-MATR3-4
	include: 0.16, 0.8, 4, 20, and 100nM with a flowrate of 30μ L/min.
	Evaluation Software 3.1 and the 1:1 Langmuir binding model,
	after removal of the reference cycle (running buffer instead of antigen) and the reference channel. Transient spikes from <i>e.g.</i> air
	bubbles were also removed from the obtained sensorgrams. The Single Cycle Kinetic sensorgram for Z-MATR3-4 is shown below.



Single Cycle Kinetics curve for Z-MATR3-4:



Preliminary data - optimization on-going

Immunoprecipitation – Mass Spectrometry (IP-MS):

Method Description	Immunoprecipitation followed by mass spectrometry was
	employed to verify the interaction specificity of each solv
	antibody with its intended target. Immunoprecipitation was
	performed on HEK293 cell lysates expressing endogenous
	MATR3 protein as previously described [4]. Obtained samples
	were loaded onto a Dionex Ultimate 3000 HPLC system (Thermo
	Fisher Scientific) coupled to an o-QTOF impact II [™] (Bruker
	Daltonics) mass spectrometer with a Captive Spray ion source
	(Bruker Daltonics). Data was analyzed with Protein Scape
	software (Bruker Daltonics) using Mascot search engine (Matrix
	Science Ltd.). Normalized spectral abundance factor (NSAF)
	values were calculated as previously described [4].

Z-MATR3-4 was able to capture endogenous MATR3 from HEK293 cell lysates. The target protein was at the top of the list of immunoprecipitated proteins with an NSAF value of 459 and 26 unique peptides detected. No other specific interactors were found. More detailed data can be shared upon request.

Comments and Contact:

Two additional scFv antibodies against MATR3, from the same selection campaign, passed all validation criteria, but with slightly lower values. Sequences for those can be provided upon request. For all inquiries, please contact Dr. Susanne Gräslund (<u>susanne.graslund@ki.se</u>) at SGC Karolinska.

References:

- 1. Morchikh, M., et al., *HEXIM1 and NEAT1 Long Non-coding RNA Form a Multi-subunit Complex that Regulates DNA-Mediated Innate Immune Response.* Mol Cell, 2017. **67**(3): p. 387-399 e5.
- Zhang, Z., et al., The Fate of dsRNA in the Nucleus: Ap54nrb Containing Complex Mediates the Nuclear Retention of Promiscuously A-to-I Edited RNA. Cell, 2001. 106(4): p. 465–475.
- 3. Treiber, T., et al., A Compendium of RNA-Binding Proteins that Regulate MicroRNA Biogenesis. Mol Cell, 2017. 66(2): p. 270-284 e13.
- Persson, H., et al., Antibody Validation by Immunoprecipitation Followed by Mass Spectrometry Analysis, in Synthetic Antibodies: Methods and Protocols, T. Tiller, Editor. 2017, Springer New York: New York, NY. p. 175-187.

Susanne Gräslund, Structural Genomics Consortium Susanne.Gräslund@ki.se