SUPPLEMENTARY DATA

Select Summary Report

Format As: Select Summary (protein hits) — Help

Significance threshold p< 0.05 — Max. number of hits AUTO

Standard scoring ○ MudPIT scoring ● Display non-significant matches ☐ Show sub-sets 0

Show pop-ups ● Suppress pop-ups ○ — Require bold red ☐

Preferred taxonomy: All entries

Re-Search — ● All queries ○ Unassigned ○ Below homology threshold ○ Below identity threshold

1. OPTN_HUMAN Mass: 66287 Score: 10798 Matches: 327(327) Sequences: 33(33) emPAI: 11.95

Optineurin OS=Homo sapiens OX=9606 GN=OPTN PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
314	431.2253	860.4361	860.4603	-0.0242	0	35	0.043	1	U	K.TIEELTR.K
605	460.7274	919.4403	919.4684	-0.0281	0	55	0.00035	1	U	K.LSEAELMK.K 604 609 610
684	468.7319	935.4493	935.4633	-0.0141	0	(52)	0.00064	1	U	K.LSEAELMK.K 682 683
801	482.7584	963.5022	963.5237	-0.0215	0	35	0.037	1	U	R.TVSTGTALSK.Y
996	497.7584	993.5022	993.5131	-0.0109	0	52	0.0006	1	U	K.QELVYTNK.K
1312	513.7618	1025.5090	1025.5182	-0.0091	0	38	0.017	1	U	R.QFFEIQSK.E 1292 1298 1306 1307 1310 1311
2548	590.3232	1178.6317	1178.6407	-0.0090	0	35	0.043	1	U	K.LLQEHNNALK.T
2595	396.5168	1186.5286	1186.5652	-0.0366	0	38	0.019	1	U	R.LMALSHENEK.L
2733	601.3069	1200.5993	1200.5986	0.0007	0	77	2.6e-006	1	U	K.NSAIPSELNEK.Q 2723 2724 2725 2727 2730 2734 2736 2737 2738 2740
2748	601.7944	1201.5742	1201.5826	-0.0084	0	(47)	0.0026	1	U	K.NSAIPSELNEK.Q 2750
3025	612.8285	1223.6424	1223.6510	-0.0086	0	44	0.0045	1	U	K.ELLTENHQLK.E 3039 3074
3090	613.3297	1224.6448	1224.6350	0.0099	0	(36)	0.025	1	U	K.ELLTENHQLK.E 3088
3229	620.2950	1238.5755	1238.5819	-0.0064	0	63	5.3e-005	1	U	R.FEELSAWTEK.Q 3225 3226 3227 3231 3242 3246 3247 3249
3796	430.2276	1287.6609	1287.6921	-0.0312	1	(47)	0.0026	1	U	K.ELSEKLELAEK.A 3786 3789 3790 3793 3795 3798 3803
3833	644.8571	1287.6996	1287.6921	0.0075	1	69	1.6e-005	1	U	K.ELSEKLELAEK.A 3812 3814 3815 3827 3830 3834 3838 3841 3850 3851 ;
4054	439.5427	1315.6063	1315.6368	-0.0304	1	49	0.0017	1	U	R.AEAEQEKDQLR.T 398
4181	443.8963	1328.6669	1328.6935	-0.0266	1	(46)	0.0032	1	U	R.KNSAIPSELNEK.Q 4179 4180 4182

Figure S1: **Confirmation of purified Optineurin by peptide mass fingerprinting followed by database search.**

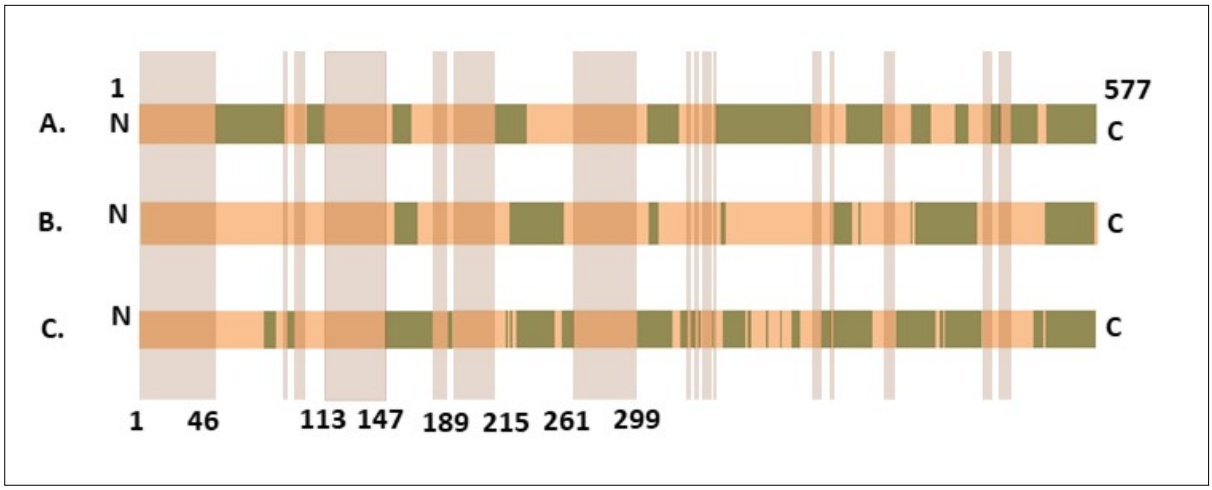


Figure S2: **Schematic diagram of intrinsically disordered regions of OPTN;** Disordered regions (peach) and ordered regions (olive) were predicted by online software A.PONDR, B.PONDR-FIT and C.IUPred2A. The shaded portions show the overlapping stretches of disordered regions by all three softwares.

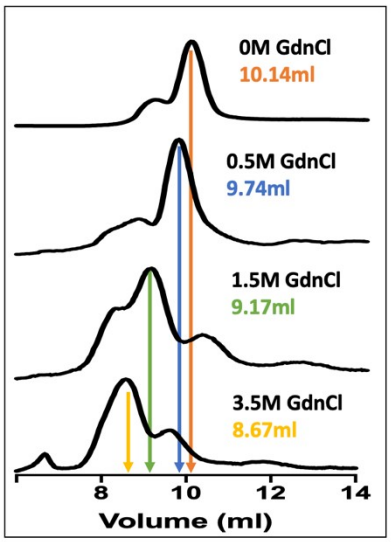


Figure S3: **Size exclusion chromatography of Ni-NTA purified OPTN in presence of various concentrations of Guanidine hydrochloride**

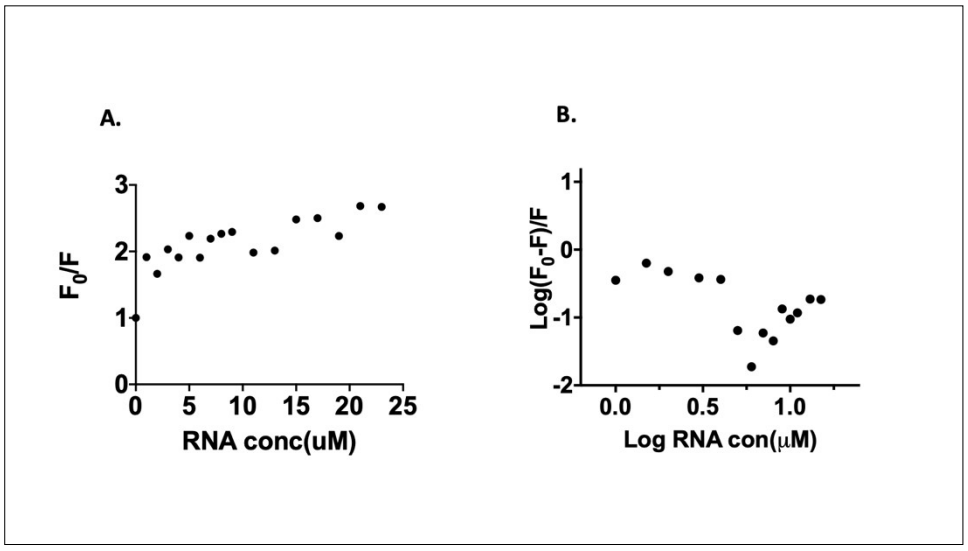
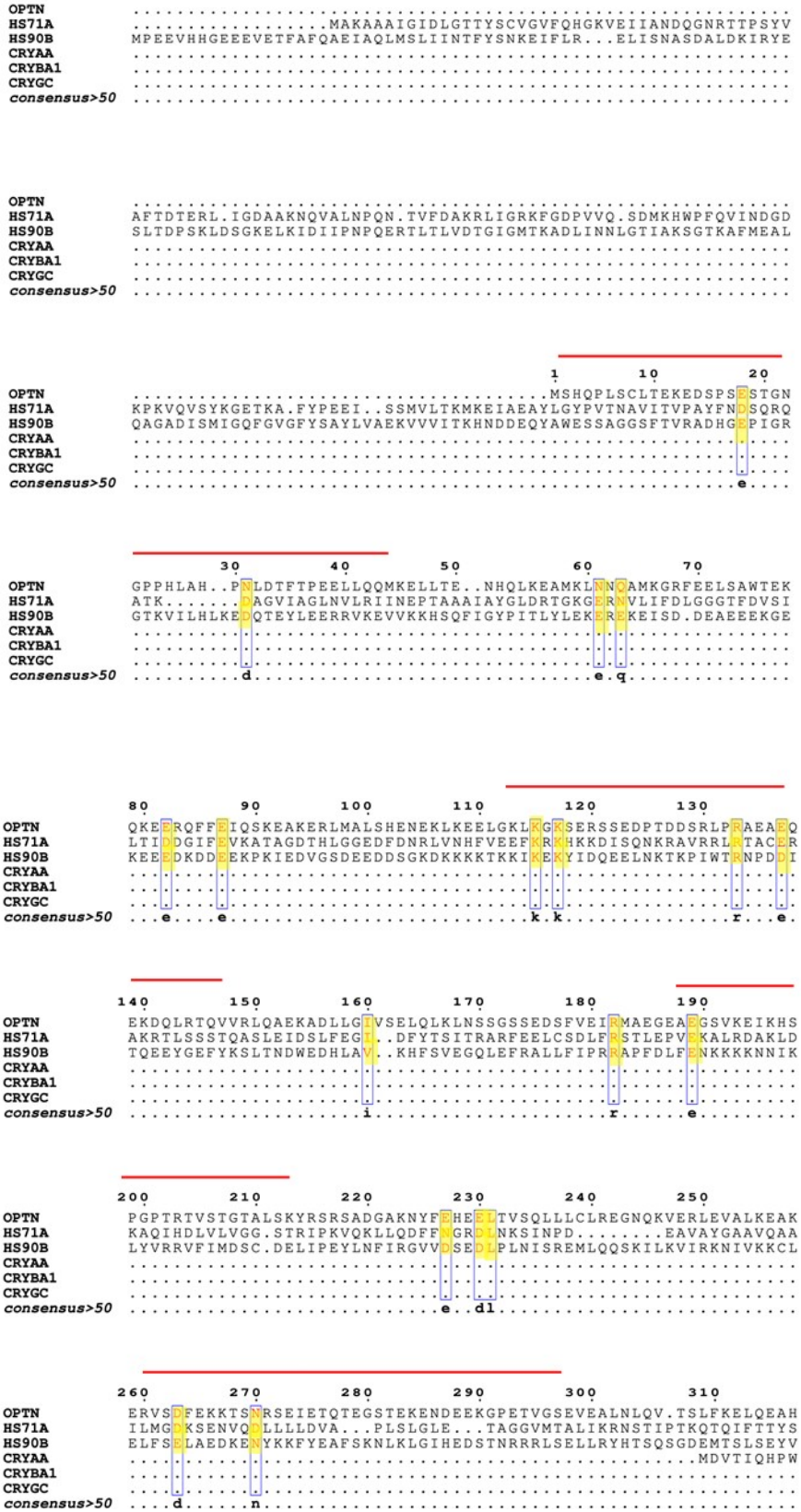


Figure S4: **Fluorescence quenching of OPTN at 60 °C in the presence RNA;** (A) Stern-Volmer plot of OPTN in the presence of various concentrations of RNA at 60 °C. (B) The plot of $\log(F_0 - F)/F$ vs log[Q] of OPTN at 60 °C as a function of RNA concentration.


OPTN
HS71A
HS90B
CRYAA
CRYBA1
CRYGC
consensus>50
1 10 20
30 40 50 60 70
80 90 100 110 120 130
140 150 160 170 180 190
200 210 220 230 240 250
260 270 280 290 300 310

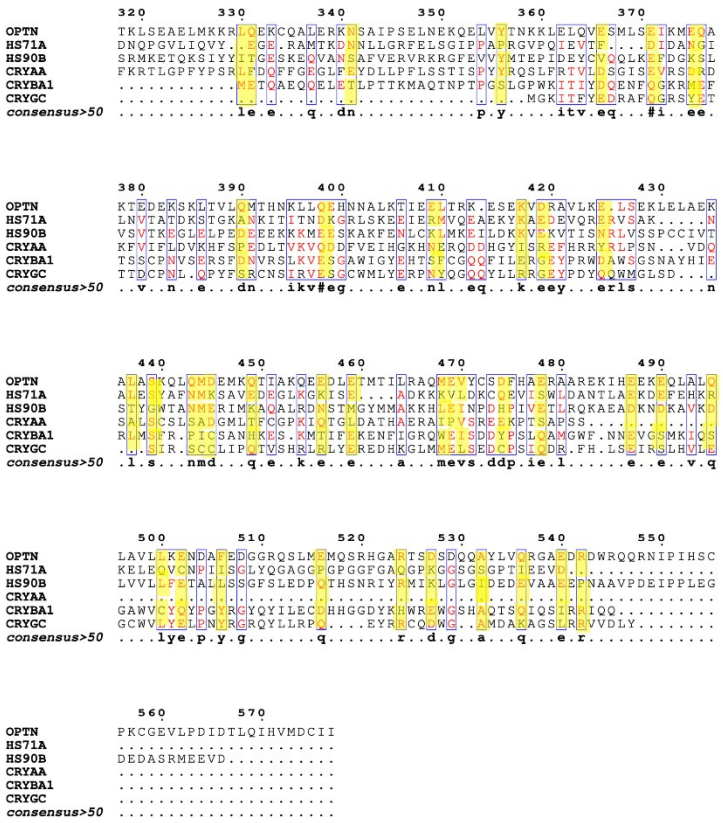


Figure S5: **Multiple sequence alignment of human OPTN with HSPs** (A) Optineurin (OPTN), (B) heat shock protein 70 (HS71A), (C) heat shock protein 90 (HS90B), (D) α-crystallin (CRYAA), (E) β-crystallin (CRYBA1) and (F) γ-crystallin (CRYGC). The red-coloured letters depict the similar amino acid residues at the aligned position, while the yellow highlighted portion shows OPTN-specific similarity. The red line spanning the N terminal of OPTN represents the IDR residues in OPTN sequence.

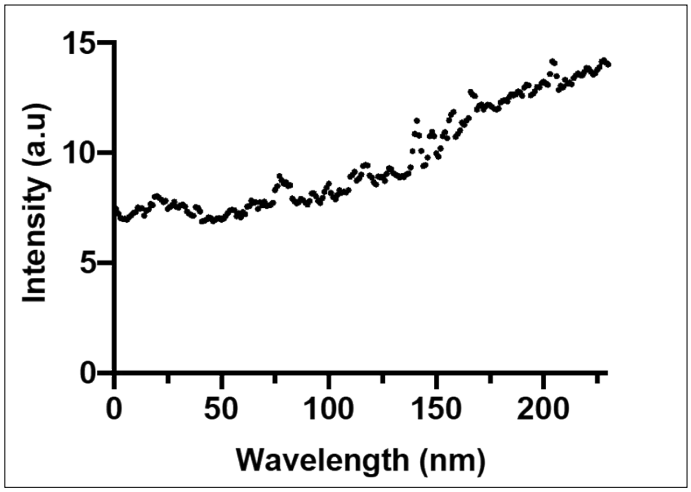


Figure S6: **Light scattering profile of only OPTN (3mM) heated at 65 °C.**