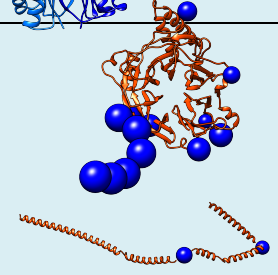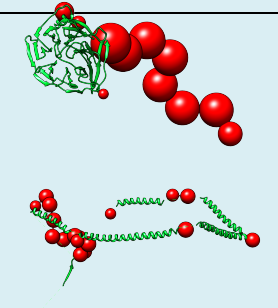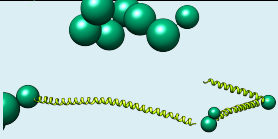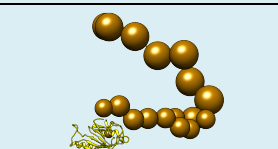**Table S1. Representation of the Nup82 holo-complex components**. Related to Figure 1.

Components	Rigid domains	Segments				
		structured segments with templates		disordered and/or unknown segments without a template		
		begins at	ends at	begins at	ends at	flexible beads
Dyn2	**Dyn2 dimer (7-92)** 7-92: X-ray 4DS1_A / C	7 - 92		1 - 6		1
Nup82	**NTD (7-452), beta-propeller** 7-452: X-ray 3PBP_G (100% seq id)	7 - 16 23 - 120 123 - 452		1 - 6 17 - 22 121 - 122		1 1 1
	Flexible linker region			453 - 521		7
	CTD (522-713), 3 coiled-coils 522-713: Model 5CWS_E (15% seq id, HHpred) Model 5C3L_A (14% seq id, HHpred)	522 - 612 625 - 669 678 - 713		613 - 624 670 - 677		2 1
Nup159	**NTD (1-381), beta-propeller** 2-381: X-ray 1XIP_A (100% seq id)	2 - 347 362 - 381		1 - 1 348 - 361		1 2
	Disordered FG region			382 - 1116		8
	CTD (1117-1460), 3 coiled-coils (1211-1412) 1117-1126: X-ray 4DS1_B / D (bound to Dyn2) 1211-1412: Model 5CWS_D (12% seq id, HHpred) Model 5C3L_B (10% seq id, MUSCLE) 1429-1456: X-ray 3PBP_I (bound to Nup82 NTD)	1117 - 1126 1211 - 1239 1266 - 1321 1332 - 1372 1382 - 1412 1429 - 1456		1127 - 1210 1240 - 1265 1322 - 1331 1373 - 1381 1413 - 1428 1457 - 1460		9 3 1 1 2 1
Nsp1	Disordered FG region			1 - 636		7
	CTD (637-823), 3 coiled-coils 637-823: Model 5CWS_C (32% seq id, HHpred) Model 5C3L_C (26% seq id, HHpred)	637 - 727 742 - 778 788 - 823		728 - 741 779 - 787		2 1
Nup116	Disordered FG region			1 - 750		8
	Flexible linker region			751 - 965		9
	CTD (966-1113) 966-1111: X-ray 3PBP_H (bound to Nup82 NTD) X-ray 3NF5 (59% seq id)	966 - 1111		1112 - 1113		1

Table S3. Unique inter-subunit DSS cross-links identified connecting components of the cytoplasmic mRNA export platform. Related to Figures 3 and 6.

Protein1 (residue1)	Protein2 (residue2)	Cross-linked peptides (residue)	Modification	P-value	mass	ppm
Nup159(1384)	Seh1(198)	RLDDNPLVAKLAK(10)-GKDGK(2)		1.E-03	2093.184	0.5
Nup159(1367)	Seh1(244)	INHTEELLNILKLFTVK(12)-IFKITEK(3)		5.E-06	3039.762	2.4
Nup159(1387)	Seh1(198)	LAKESLAR(3)-GKDGK(2)		4.E-02	1527.862	1.5
Seh1(244)	Nup159(1372)	IFKITEK(3)-LFTVKNK(5)		6.E-04	1864.107	-1.3
Nup82(649)	Nup85(2)	NQILQFNSFVHSQKSLQQDLSYLK(14)-TIDDSNR(1)		7.E-07	3821.922	2.6
Nup82(659)	Nup85(2)	SLQQDLSYLKSELTR(10)-TIDDSNR(1)		2.E-09	2737.377	5.3
Nup85(231)	Nup82(622)	SDGEPDEEYIEQVFSVKDSTAGK(17)-KISHGEMK(1)		2.E-04	3595.687	0.7
Nup82(671)	Nup145(773)	IEAETIKVDKK(7)-DIVGKSGVSIK(5)		4.E-03	2512.436	1.7
Nup145(696)	Nup159(1397)	LDVSKDWVEQLILAGSSLR(5)-DGLLKEIK(5)		4.9E-02	3192.839	2.5
Nup82(251)	Gle1(48)	NVIKQLQFVSK(4)-LPSFTKVGTK(6)		2.E-05	2517.457	3.8
Nup116(1070)/(1067)	Gle1(48)	KPIKDPNHQLVK(4)-LPSFTKVGTK(6)		4.E-06	2630.516	-2.7
Gle1(53)	Nup82(251)	KLVNESVVILDPALENALR(1)-NVIKQLQFVSK(4)		3.E-02	3533.023	1.9
Gle1(115)	Nsp1(613)	ASHSSLLDNAKNSNATAPLLEAIEESFQR(11)-STADVKSSDSLK(6)		9.E-07	4487.230	-3.7
Nup159(1198)	Gle1(134)	EYYTSAKVSNIPFVSQNSTLR(7)-KMQNLVLANQK(1)		8.E-17	3826.993	0.9
Gle1(144)	Nsp1(613)	MQNLVLANQKEIQSIR(10)-STADVKSSDSLK(6)		5.E-07	3258.713	0.9
Gle1(144)	Nsp1(607)	KMQNLVLANQKEIQSIR(11)-TEESSTGKSTADVK(8)		1.E-09	3588.867	-1.2
Gle1(144)	Nsp1(599)	KMQNLVLANQKEIQSIR(11)-KTEESSTGK(1)		2.E-08	3115.655	1.8
Gle1(144)	Nsp1(574)	MQNLVLANQKEIQSIR(10)-AAISFGAKPEEQK(8)		7.E-02	3396.807	4.1
Gle1(144)	Nsp1(585)	MQNLVLANQKEIQSIR(10)-SSDTSKPAFTFGAQK(6)		1.E-06	3592.856	0.6
Nup42(407)	Gle1(231)	FVQGLSSEKDGILELADLAEETLKIFR(24)-EHEAKLLQQK(5)		4.E-04	4381.342	2.3
Nup42(392)	Gle1(259)	FVQGLSSEKDGILELADLAEETLK(9)-DKIAQIK(2)		5.E-06	3556.913	0.5
Nup116(952)	Nsp1(370)/(465)	QEYSEDDKKAVFADVAEK(9)-KDGDASKPAFSFGAK(1)		4.E-04	3733.800	-5.3
Nup116(1067)	Nup159(1460)	KPIKDPNHQLVK(1)-NLN**M**AK(6)	Oxi	1.E-05	2259.241	3.7
Nup116(935)	Nup82(587)	HHSRNMDEENKENVADLQK(11)-KWDAQLSR(1)		2.E-02	3433.643	9.6

Table S4. Summary of SAXS experiments. Related to Figure 2.

Data collection

Beamline	SSRL Beam Line BL4-2, SLAC National Accelerator Laboratory
Defining Slits size (mm)	0.3 (H) × 0.3 (V)
Beam energy (keV)	11
Sample-Detector Distance (m)	1.7
Detector	Rayonix MX225-HE
Pixel binning	8 × 8
Pixel size (μm)	292
Exposure time (sec)	1
Images	Images taken for duration of run = ~20 images per concentration
Type of sample Cell	Quartz capillary (Diameter = 1.5mm)
Temperature (K)	288
Calibrant	AgBe
Final q range (Å^{-1})	0.01 up to 0.45

Data analysis

Programs	SASTOOL (SasTool, 2013), PRIMUS (Konarev et al., 2003)
Buffer	10mM HEPES, 150mM NaCl, 10% (v/v) glycerol, 5mM DTT, pH 7.5
Concentration range (mg/mL)	0.5 - 5.0 (SAXS profiles at 1 mg/mL were shown in Figure S4)
Guiner R_g (Å)	23.0 (Nup82$^{4-220}$), 26.6 (Nup82$^{4-452}$), and 38.7 (Nup82$^{572-690}$)
Guiner qR_g limits	1.236, 1.032, and 1.293 (in the same order as above)
D_{max} (Å)	72.2, 89.7, and 110.3 (in the same order as above)

Modeling

Programs	FoXS, DAMMIF, DAMMIN, DAMAVER
NSD* of the *ab initio* shapes	0.540 (± 0.012), 0.597 (± 0.027), and 0.853 (± 0.027)
Data plotting	GNUPLOT, OPTIMUS, SAXS MOW, UCSF Chimera 1.10

*Normalized spatial discrepancy