Table S7. Putative transmembrane proteins of the nuclear envelope

Number	Locus	TM tested	chromosome loc	c Dis Locu	Length	pl	SD-extrac				racted NEs		splice variants	Description	annotationannotationannotationannotation
1	gi 8922358 ref NP_060531.1	1	1p13.2		546	10.5	pep 1	spec 2	1.8	рер	spec	seq cov	a	hypothetical protein FLJ10330 [Homo sapiens]	~1/2 of protein is related to splicing PRP38 family
	gi 23621872 ref XP_131120.2 gi 27694972 ref XP_227591.1	1			542 1022	10.5	1	2	1.8				a	RIKEN cDNA 1110021E09 [Mus musculus] norvegicus]	
2		1	1p31		453	11.5	7	26	14.6				b first 250 aa same	RIKEN cDNA 2610019N13 [Mus musculus]	for this splice variant, ~1/4 is annotated as the PRP38 family ~1/6 of protein is RNA recognition motif
3 [NET3]		5 targets to NE, triton resistant	1p32.2	Disease	673 674	8.9	2	5	4	5	5	6.1		RIKEN cDNA 2810475A17 [Mus musculus] hypothetical protein FLJ10407 [Homo sapiens]	no homology to known proteins or functional domains
4 [NET4]		1 targets to NE and ER	1p34.1	Disease	276	8		5	4	1	1	5.1		RIKEN cDNA 1110038M16 [Mus musculus]	no homology to known proteins or functional domains
5	gi 27662674 ref XP_233684.1 gi 28499527 ref XP_149561.2	6	1p36.22	Disease	673 664	9 9.2	3	5	7.9 2	6	11 11	7.9	a	norvegicus] similar to SD10769p [Drosophila melanogaster] [Mus musculus]	no homology to known proteins or functional domains
6	gi 27663154 ref XP_233702.1	1	1p36.23	Disease	676	9.6	1	1	3	1	1	3	b splice product, whole middle different First	norvegicus]	no homology to known proteins or functional domains
		0	1 00 0	B:	671 747	9.4	1	1	3	1	1	3	b0 have diff exons througout	RIKEN cDNA 4632412I24 [Mus musculus]	but this splice variant has a predicted GTP-binding site
7	gi 23956106 ref NP_067278.1 gi 27663586 ref XP_233726.1	1	1p36.3	Disease	752	6.2	2	2 2	2.5 2.5					musculus] AF155546 [Mus musculus] [Rattus norvegicus]	no homology to known proteins or functional domains
	gi 7661606 ref NP_056473.1	2			749	5.5	1	1	1.2					DKFZP564C186 protein [Homo sapiens]	
8 [NET8]	gi 23593471 ref XM_129651.2 gi 20834508 ref XP_129651.1	3 targets to NE, triton resistant 3	1p36.13-q42.3	Disease	370 370	8.8	2	3	6.8				a	gi:26986566 NM_172266 Mus musculus hypothetical protein hypothetical protein LOC226856 [Mus musculus]	~1/4 of protein is acetyltransferase region
	gi 1503993 ref D86960.1	3			370	8.9							a	BC034621 Homo sapiens, similar to KIAA0205 gene product,	
	gi 7661996 ref NP_055688.1 gi 27708562 ref XP_228902.1	1			370 252	8.9 9.5	1	1	3.2 5.2				a b	KIAA0205 gene product [Homo sapiens] similar to Hypothetical protein KIAA0205 [Rattus norvegicus]	all related products also have acetyltransferase region
	gi:27708561 ref XM_228902.1	1			252	9.5							b	KIAA0205 (LOC317456)	
	gi 27680326 ref XP_223077.1 gi:27680325 ref XM_223077.1	3			654 654	9.4	2	3	3.8				c	similar to Hypothetical protein KIAA0205 [Rattus norvegicus] KIAA0205 LOC305074	
9	gi 27370270 ref NP_766431.1	1	1q24.3/1q25.3		502	4.9	2	4	4.8					hypothetical protein A130072J07 [Mus musculus]	this protein is closely related to LAP1 in the last exon, and it
	gi 21450775 ref NP_659471.1 gi 27677474 ref XP_222761.1	1 1			470 567	5 4.7	1 2	1 4	2.1 4.2					AF464140 [Homo sapiens] similar to AF464140 [Homo sapiens] [Rattus norvegicus]	the rat cDNA contains an additional exon close the the begin
10	gi 27659542 ref XP_226578.1	4	1q42.13	Disease	1504	7.5	2	3	1.5					similar to Hypothetical protein KIAA0133 [Rattus norvegicus]	no homology to known proteins or functional domains
11	gi 7705767 ref NP_057086.1 gi 20832116 ref XP_129627.1	1 1	1q44		428 429	9.1 8.6	1	1 1	5.4 5.4					CGI-49 protein [Homo sapiens] RIKEN cDNA C330023F11 [Mus musculus]	contains a predicted NAD Rossman fold
12	gi 20535866 ref XP_087089.2	1	2p23.3	Disease	677	5.6	2	2	4.4					similar to KIAA0007 [Homo sapiens]	contains FOG:WD40 repeatscontains FOG:WD40 repeats
13	gi 20901019 ref XP_128762.1 gi 12859688 ref BAB31737.1	1	2g21.1		677 823	5.4	2	2	3				2	RIKEN cDNA 2610318G08 [Mus musculus] BAB31737.1 AK019466.1 H [Mus musculus]	contains predicted P-loop, protein was also found in Dreger
13	gi 27229251 ref NP_084221.1	i	_q		823	8	5	6	8.3	3	4	6.6	a	RIKEN cDNA 4122402O22 [Mus musculus]	contains predicted 1 -100p, protein was also found in Dreger
	gi 27665302 ref XP_221266.1 gi 8923277 ref NP_060221.1	1			885 798	7.8	7	8	12.1 1.8	2	2	4.2 2.4	b ident to a to 315	norvegicus] hypothetical protein FLJ20297 [Homo sapiens]	
14	gi 27683629 ref XP_214598.1	2	2q21.1		319	9.6	1	1	9.1			2.4	c distinct from all others except for first 285	norvegicus]	contains FOG:WD40 repeatscontains FOG:WD40 repeats
15	gi 30148844 ref XP_292983.2 gi 27671086 ref XP_234768.1	4	2q21.2 2q32.3		717 754	5.9	2	2	4.8				-	similar to Hypothetical protein DKFZp564C186 [Homo sapiens] norvegicus]	contains predicted ATPase domain: note considerable simila
16	gi 28478908 ref XP_129726.2	1	-		171	6 5.5	1	1	5.3				b has exon internal, but does not align with D	RIKEN cDNA 2410118I19 [Mus musculus]	several proteins were annotated as "weakly similar to vegeta
17		1	3q13.2 4p13-p12	Disease	564 524	9.9	1 1	1	3.7				-	hypothetical protein MGC27931 [Mus musculus] RNA-binding protein [Homo sapiens]	no homology to known proteins or functional domains
19	gi 29728840 ref XP_298567.1	1	4q35.2	Disease	242	10.9	1	1	4.1					hypothetical protein XP_298567 [Homo sapiens]	protein contains RNA recognition motif no homology to known proteins or functional domains
20	gi 9506641 ref NP_061891.1 gi 28482013 ref XP_127968.2	1	5p15.2		356 312	9.3 9.4	1	1	5.3 6.1					hypothetical protein FLJ11127 [Homo sapiens] musculus]	no homology to known proteins or functional domains
	gi 27688689 ref XP_226886.1	1			329	9.4	1	1	5.8					norvegicus]	
21	gi 28526857 ref XP_127498.3 gi 27686925 ref XP_226713.1	1	5q13.3	Disease	528	8.8 9.1	5	5	14.4 14.4					expressed sequence AW544865 [Mus musculus]	protein contains WG repeatsprotein contains WG repeats
22	gi 7706599 ref NP_057688.1	1	5q31	Disease	528 1417		1	1	1.3					norvegicus] [Homo sapiens]	protein function is totally unknown, but was noted as being o
23		3	5q31.3	Disease	378	7.4	0	-	0.0	1	1	6.1		RIKEN cDNA 2610307O08 [Mus musculus]	no homology to known proteins or functional domains
24	gi 13385678 ref NP_080446.1 gi 27668460 ref XP_213272.1	1	5q35.2	Disease	290 145	7.1 9.3	2	5	8.3 16.6				is last half of longer one, they are colinear so	RIKEN cDNA 1200007D18 [Mus musculus] norvegicus]	no homology to known proteins or functional domains
25	gi 22122563 ref NP_666187.1	1	6p21.31		271	6.7				1	2	3.7	this is C-term half of other	hypothetical protein MGC37253 [Mus musculus]	has LEM domain, but does not align with LAP2, emerin or M.
26* INFT261	gi 27498518 ref XP_166338.3 gi 13384766 ref NP_079663.1	4 targets to NE and ER	6p24.1		503 112	9.8				1	3	5.6 10.5		[Homo sapiens] RIKEN cDNA 1110021D01 [Mus musculus]	has UPF0136 uncharacterized protein family region
27	gi 25071721 ref XP_125972.3	1	7p13	Disease	920	7.1	1	1	1.6					RIKEN cDNA 2410117E06 [Mus musculus] similar to KIAA1440 protein [Homo sapiens]	no homology to known proteins or functional domains
28		5	7p22.3 7q11.23		1882 343	6.1 8.9		-	0.8	1	1	5		RIKEN cDNA 2010310D06 [Mus musculus]	no homology to known proteins or functional domains no homology to known proteins or functional domains
30		2	7q22		235 235	8.5 8.5	1	1	9.4 9.4					RIKEN cDNA 5133401H10 [Mus musculus]	~1/2 of protein is annotated as major sperm protein domain
31 [NET31]	gi 27663614 ref XP_213738.1 gi 14249558 ref NP_116231.1	2 targets to NE and ER	7q32.3		561	8.5	6	16	9.4				a	norvegicus] hypothetical protein FLJ14803 [Homo sapiens]	no homology to known proteins or functional domains
	gi 28522840 ref XP_194313.2 gi 27709446 ref XP_231568.1	note diff between COS7 and HeLa cells			561 377	8.7 9.2	14 12	45 33	22.6 35.5				a	RIKEN cDNA 2700094F01 [Mus musculus] norvegicus]	
32	gi 23956396 ref NP_705820.1		8p11.2		340	5.5	1	1	3.2				b0 colinear, but lacks TM exon. Alignment inc	hypothetical protein MGC27952 [Mus musculus]	no homology to known proteins or functional domains
33	gi 22296589 ref NP_083179.1 gi 27701294 ref XP_224299.1	1	8p21.1		491 470	6.8	1	1	3.1 3.2					RIKEN cDNA 4933425F03 [Mus musculus] [Rattus norvegicus]	~1/4 of protein is similar to scavenger receptor region
34	gi 27701964 ref XP_224332.1	7	8p21.2		721	6.4	1	2	2.6					MGC38539; hypothetical protein, BC021530; cDNA sequence,	protein has homology to a zinc transporter from arabidopsis
35	3-lam - man - e l'en l'en = e e e · e · e · e ·	1	8p22	Disease	181 305	7.9 4.7	11	1	9.9	- 1	1	0.5	b has longer splice variant known that lacks T	hypothetical protein MGC7730 [Mus musculus]	two splice variants which are > 4 times larger (gi 24432106 a
37		2 2	8q23.2 9	Disease	716	8.3				1	1	2.1		norvegicus] similar to KIAA1161 protein [Homo sapiens] [Mus musculus]	no homology to known proteins or functional domains ~2/3 of protein has homology to sugar hydrolases
38	gi 9910440 ref NP_064382.1 gi 27714517 ref XP_232987.1	1	9q22.33		415 415	8	2	2	5.8 5.8					hypothetical protein MNCb-5081 [Mus musculus]	~1/2 of protein is likely glycosyltransferase region
36 [NET39]	gi 14349303 ref NP_116117.1	3 targets to NE, triton resistant			201	9.6				1	1	10		[Rattus norvegicus] hypothetical protein MGC12921 [Homo sapiens]	~1/2 of protein has phosphatase region similarity
40	gi 27735125 ref NP_775961.1 gi 28485292 ref XP_130243.2	2	9q34.11		629 606	8.5 8.6	1	1	3.3 3.5					hypothetical protein FLJ36664 [Homo sapiens] RIKEN cDNA A930041I02 gene [Mus musculus]	no homology to known proteins or functional domains
	gi 27707228 ref XP_231194.1	1			471	6	1	1	4.5					norvegicus]	
41	gi 20860640 ref XP_125636.1		10q22.2		568	7.2	1	1	4.4					RIKEN cDNA 1300019N10 [Mus musculus]	no homology to known proteins or functional domains
43	gi 23346561 ref NP_694766.1	1	10q25.1 11p13		721 1024	8.5 8.3	1	1	3.1 1.5				a	hypothetical protein 4832416E03 [Mus musculus] hypothetical protein MGC25461 [Mus musculus]	contains von Willebrand factor type A/ EGF-like domains contains predicted ATPase and acetyltransferase regions
1	gi 27703111 ref XP_230334.1	2		Di-	530	8.6	2	3	7.2				b start is at 530 in the long one, but only 21	[Rattus norvegicus]	
44		3 2	11p15.5	Disease	323 291	9.1 8.5	2	3	14.9 8.9					RIKEN cDNA 1300006L01 [Mus musculus] norvegicus]	~2/3 of protein has mitochondrial carrier protein region similar
45	gi 20149621 ref NP_056348.2	1	11q12.2		575	7.5	1	1	3.7					DKFZP586B1621 protein [Homo sapiens]	~1/2 of protein is DAG kinase-like and 1/2 is similar to phosp
46	gi 21703976 ref NP_663471.1 gi 27734797 ref NP_775857.1	6	11q12.3	1	578 322	6.9 5.7	1	1	3.6	1	1	2.2		similar to DKFZP586B1621 protein [Mus musculus] hypothetical protein MGC34821 [Homo sapiens]	protein is annotated as being similar to a sugar transporter, I
47	gi 20884659 ref XP_129087.1	7	11q13	<u> </u>	399	8.6				3	3	2.2 5.3		RIKEN cDNA 3110041O18 [Mus musculus]	this protein is similar to C14 sterol reductase which is a func
48	gi 11024686 ref NP_060634.1 gi 20270295 ref NP_620096.1	1 1	12p11.23	Disease	706 732	6.8	1	1	1.6 1.5				a b note Align program finds no match	hypothetical protein FLJ10637 [Homo sapiens] hypothetical protein MGC28965 [Mus musculus]	no homology to known proteins or functional domains
49	gi 23956360 ref NP_705798.1	1	12q24.33		516	6.7	1	1	2.1				and the state of t	hypothetical protein MGC28606 [Mus musculus]	~1/5 of protein is CBF/Mak21 family region
50 51 [NET51]	gi 27665688 ref XP_234304.1 gi 10946822 ref NP_067421.1	2 3 targets to NE, triton resistant	14q23.1 14q24.3	Disease Disease	462 140	7.2 9.9	1	1	5.2	2	2	11.4		similar to CGI-86 protein [Homo sapiens] [Rattus norvegicus] open reading frame 11 [Mus musculus]	~1/2 of protein is annotated as short chain dehydrogenases protein is related to an uncharacterized protein family
5. [HE151]	gi 27667056 ref XP_216756.1	3	'		140	9.9				2	2	11.4		norvegicus]	
52	gi 6005719 ref NP_009107.1 gi 29736045 ref XP_027330.4	3	14q24.3	Disease	140 706	9.8	11	23	15.2	1	1	5 2.1	2	chromosome 14 open reading frame 1 [Homo sapiens]	no homology to known proteins or functional domains
	gi 23956206 ref NP_081625.1	0			240	8.8	10	21	32.1				b0, lacks TM exon	RIKEN cDNA 2610015J01 [Mus musculus]	
53	gi 27369682 ref NP_766088.1 gi 27717295 ref XP_234559.1	1	14q32.2 14q32.33	Disease Disease	895 1546		1	2	0.7	1 2	1	1.5		musculus] norvegicus]	protein contains spectrin repeats and SMC regions (which ke
55	gi 21492616 ref NP_080950.1	6	15q21.3	Disonati	258	8			0.7	1	1	6.6		RIKEN cDNA 0610008A10 [Mus musculus]	~1/3 has homology to RNA methylases and ~2/3 to helicase annotated as likely ortholog of pharynx defective (celegans);
56** [NET56]	gi 23956160 ref NP_080293.1 gi 27672973 ref XP_213339.1	1 targets to NE, triton resistant	17p13		244 111	9.8 8.2	1	5	9 19.8				shorter one is C term	Dullard homolog [Mus musculus] similar to Dullard homolog [Mus musculus] [Rattus norvegicus]	***************************************
	gi 7661722 ref NP_056158.1	1			244	9.8	1	5	9				shorter one is C-term part, are colinear	likely ortholog of Xenopus dullard [Homo sapiens]	
57	gi 27690880 ref XP_221193.1 gi 29743162 ref XP_292696.1		17q25.3			8.4	1	1	0.9	4	4	2.4		similar to FLJ00039 protein [Homo sapiens] [Rattus norvegicus] similar to KIAA1689 protein [Homo sapiens]	protein contains predicted Zn finger RING, ubiquitin ligase, a
58	91/20140102 181 AP_292090.1	1-1	18q23		669	8.2		1				2.1		Johnna to Alex roos protein [morito sapiens]	no homology to known proteins or functional domains

59	gi 27717667 ref XP_234929.1 3	19p13.3	709	6.7	1	3	2					norvegicus]	~1/15 of protein has predicted aminopeptidase region	
60	gi 11034845 ref NP_067038.1 0	20q11.21-q12	326	6	1	2	4.6					chromosome 20 open reading frame 77 [Homo sapiens] chror	mosome 20 open reading frame 77 [Homo sapiens]	
	gi 28488213 ref XP_130605.4 0		326	6	1	2	4.6					RIKEN cDNA 2610304G08 [Mus musculus] RIKEN cDNA 2610304G08 [Mus musculus]		
	gi 27704394 ref XP_230798.1 1		414	6.2	1	2	3.6					similar to Protein C20orf77 homolog [Rattus norvegicus]	~1/4 of protein is domain of proteins involved in regulation of	
	gi 21450083 ref NP_659110.1 0		312	7.6	1	2	4.8					hypothetical protein MGC36325 [Mus musculus] hypothetical protein MGC36325 [Mus musculus]		
	gi 21361709 ref NP_060640.2 0		312	7.5	1	2	4.8					hypothetical protein FLJ10656; cyclin-dependent kinase inhibi	itor-related protein [Homo sapiens]	
61	gi 27670274 ref XP_221669.1 2	21q22.11	2282	6.9	5	9	3				a	similar to Hypothetical protein KIAA0539 [Rattus norvegicus]	no homology to known proteins or functional domains	
	gi 28496556 ref XP_128377.3 0		992	8.1	1	1	1.2				b0 lacks TM exon	similar to Hypothetical protein KIAA0539 [Mus musculus]		
62	gi 27663300 ref XP_235527.1 1	22q13.31	380	8.1	1	1	9.2					norvegicus]	protein contains similarity to both S-malonyl and acyl transfe	
63	gi 27721269 ref XP_243957.1 1	no hum homolog	699	9.3				1	1	3		hypothetical protein XP_243957 [Rattus norvegicus]	no homology to known proteins or functional domains	
64	gi 20886081 ref XP_150109.1 2	no hum homolog	157	9.8	1	1	15.9					RIKEN cDNA A330008L17 gene [Mus musculus]	no homology to known proteins or functional domains	
65	gi 20844230 ref XP_163618.1 1	no hum homolog	120	9.6				1	1	16.7		hypothetical protein XP_163618 [Mus musculus]	contains RNA recognition motif	
66	gi 20866411 ref XP_137321.1 1	no hum homolog	257	8	1	1	5.8				· · · · · · · · · · · · · · · · · · ·	similar to Inner nuclear membrane protein Man1 [Mus muscul	us] has LEM domain, but does not align with LAP2, emerin or M	
67	gi 28522903 ref XP_285910.1 1	no hum homolog	602	5.9	1	1	3					hypothetical protein XP_285910 [Mus musculus]	no homology to known proteins or functional domains	

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note: this protein initially passed all selection criteria; however when the dataset was reanalyzed after cloning and testing for targeting to the NE, one peptide was also detected in the MM fraction during the course of our study a paper was published (27) showing a function for this protein, now called dullard, in eneral development in C. elegans. However, the intracellular localization of the protein was not investigated.

The number of transmembrane segments predicted using TMPred with a minimum sociol enfound in one individual to both. These sociol emilitations were based on an average to match those of the previously characterized NE proteins.

pep spec seq cov

the number of peptides detected in NaOH-extrated and salt- and detergent-extracted NEs spectrum matches the percentage of the total protein sequence covered by peptide matches the peptide/ spectrum matches passed all the SEQUEST and PEP_PROBE criteria defined in Table 1.