

Fig. 1

Peptide	Mean Viability (PI)	Mean PI Delivery Score	Mean % cell PI+	Mean Viability (GFP)	Mean GFP Delivery Score	Mean % cell GFP+	Overall Delivery Factor	Sequence [SEQ ID NO]	AA	pH	Helical Wheel Projection	Positively Charged Angle (Position)/% Positively Charged Residues (K and/or R)	Hydrophobic Angle (Position)/% Strong Hydrophobic Residues (F, I, W, and/or L)
NT	100%	0.2	2%	100%	0.0	0%	0.1	-	-	-	-	-	-
GFP/PI only	84%	0.3	5%	101%	0.0	0%	0.1	-	-	-	-	-	-
C(LLKK) ₃ C	7%	0.8	7%	5%	0.0	1%	0.0	CLLKLLKKLLK KC [SEQ ID NO: 347]	14	4.99		140 degrees K4-K9 83.3% 180 degrees L11-L2 75%	
His-PTD4	130%	0.2	3%	104%	0.0	0%	0.1	HHHHHHYARAA ARQARA [SEQ ID NO: 345]	17	3.51		60 degrees R7-R10 100% 220 degrees A11-A6 0%	
FSD10-12- 1	102%	0.2	3%	132%	0.0	1%	0.1	LARAFARAIKKL [SEQ ID NO: 350]	12	4.99		100 degrees K11-K10 100% 200 degrees A4-A6 50%	
FSD10-12- 2	91%	0.2	3%	127%	0.0	2%	0.1	KWKLARAFARAI [SEQ ID NO: 351]	12	2.74		80 degrees K3-R6 100% 220 degrees A7-W2 44.4%	

Fig. 1 (cont'd)

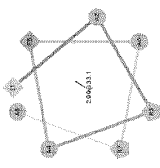
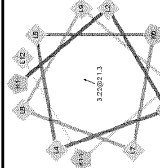
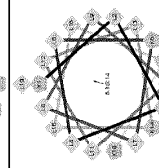
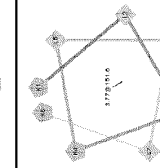
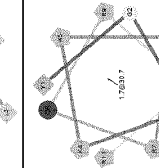
FSD10-8	100%	0.1	2%	128%	0.0	1%	0.1	LARAFARA [SEQ ID NO: 349]	8	2.99		40 degrees R7-R3 100%	200 degrees A4-A6 33.3%
FSD418-12-1	100%	0.1	2%	123%	0.0	2%	0.1	KLKLLKLLKLL [SEQ ID NO: 354]	12	3.22		60 degrees K3-K6 100%	220 degrees L7-L2 77.8%
FSD418-19	110%	0.1	2%	126%	0.0	2%	0.1	KLKLLKLLKLL LKLLKLL [SEQ ID NO: 357]	19	6.3		80 degrees K14-K6 100%	240 degrees 85.7%
FSD418-8	101%	0.1	2%	114%	0.0	2%	0.1	KLLKLLK [SEQ ID NO: 353]	8	3.77		60 degrees K4-K1 100%	200 degrees L7-L8 100%
TAT	106%	0.1	1%	115%	0.0	2%	0.1	YGRKKRRRRR [SEQ ID NO: 368]	11	1.7		260 degrees K4-K5 88.9%	0 degrees 0%

Fig. 1 (cont'd)

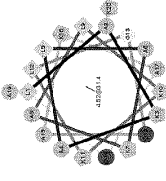
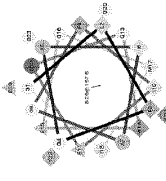
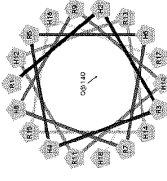
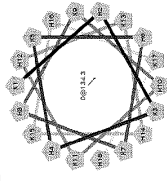
FSD439	109%	0.4	5%	99%	0.0	0%	0.2	LAKALAKLKL GOAKAQAK [SEQ ID NO: 358]	20	4.52		100 degrees K11-K10 83.3%	220 degrees A4-A17 28.6%
FSD442	172%	0.2	3%	97%	0.0	0%	0.2	GGGGGGLFGA IAGFIENGWEGMI DGWYGGGGGGG S [SEQ ID NO: 361]	37	8.41		-	-
FSD447	142%	0.2	4%	90%	0.0	1%	0.2	RHRHRHRHR HRHRHRH [SEQ ID NO: 371]	18	0		360 degrees 100%	0 degrees 0%
FSD444	98%	0.4	6%	90%	0.0	0%	0.2	KHKHKHKHKH HKHKHKH [SEQ ID NO: 364]	18	0		360 degrees 100%	0 degrees 0%
PTD4	124%	0.2	4%	111%	0.0	0%	0.2	YARAAARQARA [SEQ ID NO: 367]	11	2.44		60 degrees R7-R10 100%	220 degrees A11-A6 0%

Fig. 1 (cont'd)

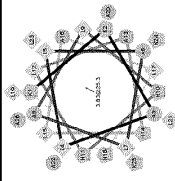
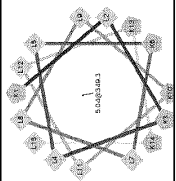
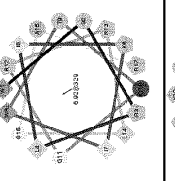
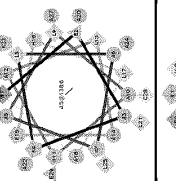
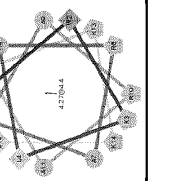
LAH4	126%	0.6	9%	79%	0.1	5%	0.4	KKALLALALHHL AHLALHLALALK KA [SEQ ID NO: 365]	26	3.83		-	-
FSD418-15	70%	1.4	14%	105%	0.3	10%	0.6	KLKLLKLLKLL KKL [SEQ ID NO: 356]	15	5.04		100 degrees K14-K13 100%	220 degrees L7-L2 90%
FSD205	135%	0.8	11%	97%	0.6	23%	0.8	WSRLIKIWTQGR RLGAR [SEQ ID NO: 131]	17	6.92		80 degrees R3-R13 80%	200 degrees L14-A16 60%
FSD443	249%	0.8	9%	99%	0.2	10%	1.1	GGSGGSWEAK LAKALAKALAK HLAKALAKALK ACEAGSGGGS [SEQ ID NO: 362]	44	4.76		-	-
FSD422	102%	1.1	13%	123%	0.9	41%	1.2	HHHHHHKWKLA RAFAKAIKLHH HHHH [SEQ ID NO: 329]	27	6.04		100 degrees K14-K13 100%	220 degrees A7-W2 50%

Fig. 1 (cont'd)

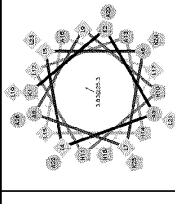
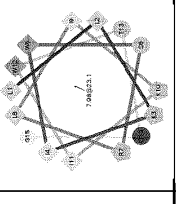
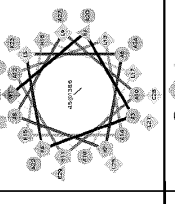
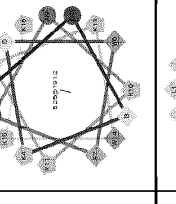
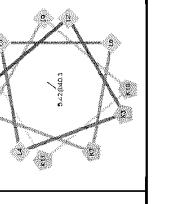
FSD441	106%	1.8	20%	99%	0.7	22%	1.3	GGSGGSKKALL ALALHHLAHLAL HLALAKKAGGS GGGS [SEQ ID NO: 360]	40	4.02		-	-
FSD92	129%	1.0	11%	80%	2.3	38%	1.5	LLKIWSRLKIWT OG [SEQ ID NO: 346]	15	7.99		60 degrees R7-K10 75%	180 degrees I11-L2 88.9%
KALA	120%	2.3	25%	97%	0.2	8%	1.5	WEAKLAKALAK ALAKHLAKALA KALKACEA [SEQ ID NO: 363]	30	4.5		-	-
Penetratin	106%	1.4	18%	104%	1.5	47%	1.5	RQIKIWFQNRRM KWKK [SEQ ID NO: 366]	16	5.25		80 degrees R11-R1 80%	200 degrees F7-I5 50%
FSD418-12-2	91%	3.1	20%	70%	1.2	20%	1.8	LLKLLKLLKLL [SEQ ID NO: 355]	12	5.42		100 degrees K11-K10 100%	200 degrees L4-L6 100%

Fig. 1 (cont'd)

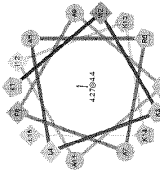
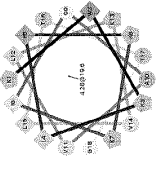
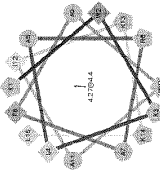
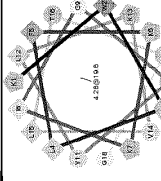
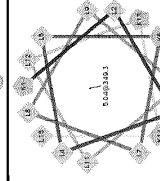
FSD10-15	92%	2.4	15%	128%	1.3	45%	1.9	KWKLARAFARAI KKL [SEQ ID NO: 352]	15	4.27		100 degrees K14-K13 100%	220 degrees A7-W2 50%
CM18	75%	4.4	29%	57%	1.3	18%	2.0	KWKLFFKKIGAVL KVLTTG [SEQ ID NO: 348]	18	4.28		120 degrees K7-K13 57.1%	200 degrees G18-W2 54.5%
FSD375	97%	2.8	19%	122%	1.4	28%	2.2	GGSGGSKWKL ARAFARAIKKLG SGSGGS [SEQ ID NO: 285]	29	4.4		100 degrees K14-K13 100%	220 degrees A7-W2 50%
FSD440	47%	5.8	26%	98%	2.9	33%	2.8	GGSGGSKWKL FKKIGAVLVL TGGSGGGS [SEQ ID NO: 359]	32	4.67		120 degrees K7-K13 57.1%	200 degrees G18-W2 54.5%
FSD418	108%	5.3	35%	79%	0.9	23%	3.2	GGSGGSKLKL KLLKLLKKLGG SGSGGS [SEQ ID NO: 326]	29	5.05		100 degrees K14-K13 100%	220 degrees L7-L2 90%

Fig. 1 (cont'd)

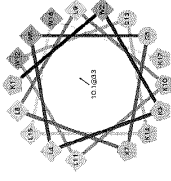
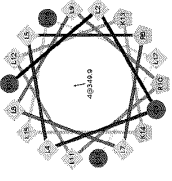
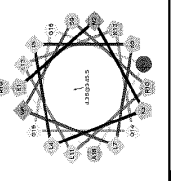
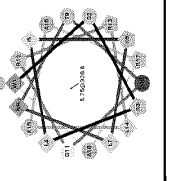
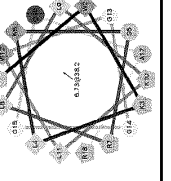
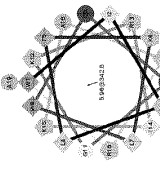
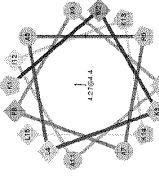
FSD390	112%	7.8	47%	14%	1.0	17%	4.4	KWKLWSKLLKL WSKLWK [SEQ ID NO: 299]	17	10.1		80 degrees K7-K17 100%	180 degrees L11-W2 90%
FSD387	89%	10.8	44%	70%	0.2	12%	4.9	QLQLRLRLRL KKLOLQ [SEQ ID NO: 296]	18	4		100 degrees K14-K13 66.7%	220 degrees L7-L2 75%
FSD367	111%	6.4	36%	85%	3.6	35%	5.1	KWKLLKLWSRL LKGGGQAR [SEQ ID NO: 277]	19	4.35		80 degrees K3-K13 80%	240 degrees G14-W2 50%
FSD201	129%	5.4	37%	48%	8.9	51%	5.6	WSRLIKLWTQGR RLKARAA [SEQ ID NO: 127]	19	5.75		80 degrees R3-R13 80%	180 degrees L14-A16 50% (including A19)
FSD366	146%	6.6	37%	83%	3.0	34%	6.1	KWKLWSRLKL WGGGQAR [SEQ ID NO: 276]	18	6.73		80 degrees R18-K10 80%	240 degrees L11-A17 53.8%

Fig. 1 (cont'd)

FSD202	100%	14.6	51%	19%	4.1	43%	7.7	WIRLFKLWQQG KRIKAKRA [SEQ ID NO: 128]	19	5.96		80 degrees R3-R13 80%	240 degrees I14-I2 50% (including A19)
FSD10	83%	18.2	72%	103%	10.7	86%	13.1	KWKLARAFARAI KKLGSGGGSYA RALRRQARTG [SEQ ID NO: 13]	34	7.02		100 degrees K14-K13 100%	220 degrees A7-W2 50%
FSD395	105%	21.8	72%	101%	5.6	62%	14.3	KLKLLKLLKLL KKLGSGGGGQA KAQAKQAK [SEQ ID NO: 304]	32	5.15		100 degrees K14-K13 100%	220 degrees L7-L2 90%

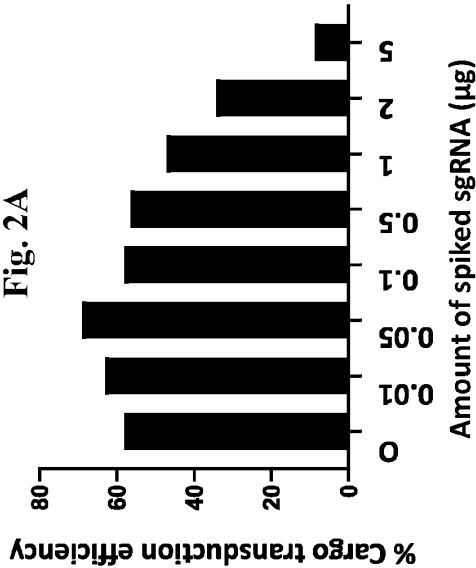


Fig. 2B

Shuttle Agent	Treatment	Concentration	Cas9-RNP (2.5µM/2.0µM)	Mean Viability	Mean GFP Delivery Score	Mean % cell GFP+
FSD250	1,3-Diaminoguanidine monohydrochloride	0	-	88%	4.7	56.1%
			+	93%	0.7	32.4%
		100 nM	-	76%	8.1	75.7%
			+	90%	0.6	32.8%
		1 µM	-	66%	8.5	78.7%
			+	79%	0.4	24.3%
		10 µM	-	74%	6.9	68.4%
			+	69%	0.3	16.6%
		100 µM	-	38%	6.2	66.7%
			+	62%	0.8	40.9%
		1 mM	-	91%	3.9	55.5%
			+	85%	0.8	33.4%
		10 mM	-	92%	3.0	44.1%
			+	117%	0.4	21.4%

Fig. 3

Shuttle Agent	Cas9/sgRNA (2.5µM/2.0µM)	Mean Viability	Mean GFP Delivery Score	Mean % cell GFP+	% inhibition (%GFP)	% inhibition (Delivery score)	Sequence [SEQ ID NO:]
GFP only	-	104%	0.0	1%	-	-	
NT	-	100%	0.0	0%	-	-	
LAH4	-	97%	0.3	17%	87%	78%	KKALLALALHHLAHLALALKKA [SEQ ID NO: 365]
	+	111%	0.1	2%			
FSD441	-	95%	1.6	33%	81%	94%	GGSGGSKKALLALHHLAHLALALKAGSGGGS [SEQ ID NO: 360]
	+	107%	0.1	6%			
CM18	-	82%	3.5	32%	12%	47%	KWKLFKKIGAVLKVLTTG [SEQ ID NO: 348]
	+	90%	1.8	28%			
FSD440	-	88%	4.4	30%	2%	19%	GGSGGSKWKLFKKIGAVLKVLTTGGSGGGS [SEQ ID NO: 359]
	+	98%	3.6	29%			
FSD268	-	90%	16.0	92%	68%	96%	KWKLLKLSRLLKLWGGSGGSGQARAQARQAR [SEQ ID NO: 43]
	+	99%	0.7	29%			
FSD268 cyclic disulfide	-	65%	6.1	52%	85%	98%	KWKLLKLSRLLKLWGGSGGSGQARAQARQAR [SEQ ID NO: 50]
	+	111%	0.1	8%			
FSD268 cyclic amide	-	96%	5.9	62%	91%	98%	KWKLLKLSRLLKLWGGSGGSGQARAQARQAR [SEQ ID NO: 49]
	+	103%	0.1	6%			

Fig. 3 (cont'd)

FSD293	-	108%	1.5	36%	80%	90%	KWKLLSLWSRLLSLWGGSGGSQARAQARQAR [SEQ ID NO: 204]
	+	104%	0.1	7%			
FSD294	-	109%	8.7	71%	69%	95%	KWKLLKLSLWSRLLSLWGGSGGSQARAQARQAR [SEQ ID NO: 205]
	+	112%	0.4	22%			
FSD250	-	85%	12.2	83%	84%	98%	KWKLLKLSLWSRLLSLWGGSGGSARAARQAR [SEQ ID NO: 35]
	+	102%	0.2	13%			
FSD356	-	96%	9.8	74%	31%	75%	KWKLLKLSLWSRLLSLWGGSGGSQAG [SEQ ID NO: 266]
	+	101%	2.5	51%			
FSD357	-	89%	6.6	59%	94%	99%	KWKLLKLSLWSRLLSLWGGSGGSRRR [SEQ ID NO: 267]
	+	105%	0.1	4%			
FSD359	-	81%	13.0	87%	64%	96%	KWKLLKLSLWSRLLSLWGGSGGGAAGAQAQAK [SEQ ID NO: 269]
	+	99%	0.6	32%			
FSD360	-	99%	0.8	28%	95%	97%	RWRLRLWSRLLSLWGGSGGGAARAARQAR [SEQ ID NO: 270]
	+	100%	0.0	1%			
FSD358	-	104%	4.7	57%	66%	93%	KWKLLHLSLWSRLLSLWGGSGGSARAARQAR [SEQ ID NO: 268]
	+	106%	0.4	19%			

Fig. 3 (cont'd)

FSD231	-	58%	7.4	67%	42%	83%	KWKLARAFARAIIKLGSGGSRRLKAKRALKA [SEQ ID NO: 156]
	+	99%	1.2	39%			
FSD229	-	53%	8.8	71%	35%	81%	KWKLARAFARAIIKLGSGGSRRLKAKRALKA [SEQ ID NO: 154]
	+	97%	1.7	46%			
FSD10	-	86%	6.6	76%	71%	94%	KWKLARAFARAIIKLGSGGSRRLKAKRALKA [SEQ ID NO: 13]
	+	107%	0.4	22%			
FSD174	-	75%	10.9	66%	84%	98%	LLKIWSRLIKWTQRRRLGSGGSRARAARQAR [SEQ ID NO: 32]
	+	103%	0.2	11%			
FSD445	-	95%	3.9	41%	80%	97%	GWGLLKLWSRLKLWGGSGGSRARAARQAR [SEQ ID NO: 369]
	+	101%	0.1	8%			
FSD385	-	29%	6.4	58%	98%	100%	LLKLLKLLKLLGSGGSRARAARQAR [SEQ ID NO: 294]
	+	97%	0.0	1%			
FSD446	-	100%	7.0	68%	49%	85%	KWKLKLWSRLKLWGGSGGSRHTSDQTN [SEQ ID NO: 370]
	+	98%	1.0	34%			
FSD375	-	94%	2.2	32%	-5%	21%	GGSGGSKWKLARAFARAIIKLGSGGGS [SEQ ID NO: 285]
	+	97%	1.8	34%			

Fig. 3 (cont'd)

FSD422	-	99%	0.5	27%	69%	87%	HHHHHKWKLARAFARAIIKKLHHHHHH [SEQ ID NO: 329]
	+	109%	0.1	9%			
FSD10-15	-	101%	0.4	21%	-12%	27%	KWKLARAFARAIIKL [SEQ ID NO: 352]
	+	97%	0.3	24%			
FSD395	-	82%	10.5	91%	81%	99%	KLKLLKLLKLLKLGSGGSQAQAQAQAQAK [SEQ ID NO: 304]
	+	98%	0.1	17%			
FSD418	-	96%	2.7	58%	77%	96%	GGSGGSKLKLKLLKLLKLLKLGSGGGS [SEQ ID NO: 326]
	+	118%	0.1	13%			
FSD418-15	-	10%	1.3	37%	66%	90%	KLKLLKLLKLLKLL [SEQ ID NO: 356]
	+	76%	0.1	12%			
Penetratin	-	102%	0.6	37%	26%	53%	RQIKIWFQNRMRMKWKK [SEQ ID NO: 366]
	+	88%	0.3	27%			

Fig. 4A

SEQ ID NO:	Peptide	Sequence	Cas9-RNP		
			-	+	Change*
352	FSD10-15	KWKLARAFARA IKKL	21%	24%	+3%
285	FSD375	GGSGGSKWKLARAFARA IKKLGSGGGS	32%	34%	+2%
329	FSD422	HHHHHHKWKLARAFARA IKKLHHHHHH	27%	9%	-18%
331	FSD424	KWKLARAFARA IKKLGSGGSGSGGGS	37%	28%	-9%
339	FSD432	KWKLARAFARA IKKLGSGGSGQAQAKQAK	50%	34%	-16%
166	FSD241	KWKLARAFARA IKKLGSGGSGYARAAARQARA	69%	44%	-25%
156	FSD231	KWKLARAFARA IKKLGSGGSGSRRLKRLKRAIKAA	67%	39%	-28%
13	FSD10	KWKLARAFARA IKKLGSGGSGYARALRRQARTG	76%	22%	-54%
136	FSD210	KWKLARAFARA IKKLGSGGSGSRRLKRLKRAIKAA	75%	5%	-70%

*Change in GFP transduction efficiency in the presence (+) or absence (-) of Cas9-RNP

Fig. 4B

SEQ ID NO:	Peptide	Sequence	Cas9-RNP		
			-	+	Change*
348	CM18	KWKLFKKIGAVLKVLTGTG	32%	28%	-4%
359	FSD440	GGSGGSKWKLFKKIGAVLKVLTGTGSGSGGGS	30%	29%	-1%
374	CM18-L2-PTD4	KWKLFKKIGAVLKVLTGTGSGGSGSYARAAARQARA	34%	34%	0%
375	His-CM18-Transportan	HHHHHHKWKLFKKIGAVLKVLTGTGGWTLNSAGYLLIKINIKALAAALAKKLTLL	23%	27%	+4%
376	CM18-TAT	KWKLFKKIGAVLKVLTGTGYQRRRRQRRR	31%	1%	-30%
377	His-CM18-9Arg	HHHHHHKWKLFKKIGAVLKVLTGTGRRRRRRRRR	26%	1%	-25%
378	His-CM18-TAT	HHHHHHKWKLFKKIGAVLKVLTGTGYQRRRRQRRR	40%	2%	-38%

*Change in GFP transduction efficiency in the presence (+) or absence (-) of Cas9-RNP

Fig. 4C

SEQ ID NO:	Peptide	Sequence	Cas9-RNP		
			-	+	Change*
266	FSD356	KWLLKLWSRLIKLWGGSGGGGQAG	74%	51%	-23%
267	FSD357	KWLLKLWSRLIKLWGGSGGGGRRR	59%	4%	-55%
370	FSD446	KWLLKLWSRLIKLWGGSGGGGSHSDQTN	68%	34%	-34%
35	FSD250	KWLLKLWSRLIKLWGGSGGGGAAARQAR	73%	13%	-60%
207	FSD296	KWLLKLWSRLIKLWQQGGSGGGQAARQAR	80%	4%	-76%
169	FSD246	KWLLKLWSRLIKLWGGSGGGGYAARARAKRA	83%	1%	-82%
174	FSD251	KWLLKLWSRLIKLWGGSGGGGAEEAQAE	43%	36%	-7%

*Change in GFP transduction efficiency in the presence (+) or absence (-) of Cas9-RNP

Fig. 4D

SEQ ID NO:	Peptide	Sequence	Cas9-RNP		
			-	+	Change*
284	FSD374	GGSGGGSLIKIWSRLIKIWTQRRRLGGSGGGG	43%	42%	-1%
110	FSD183	LLKIWSRLIKIWTQRRRLGAR	52%	16%	-36%
30	FSD168	LLKIWSRLIKIWTQRRRLGARQAAR	64%	8%	-56%
101	FSD172	LLKIWSRLIKIWTQRRRLGGSGGGSAARQAAR	57%	15%	-42%
116	FSD189	LLKIWSRLIKIWTQRRRLGARQAAR	75%	2%	-73%
32	FSD174	LLKIWSRLIKIWTQRRRLGGSGGGSAARQAAR	52%	8%	-44%
114	FSD187	LLKIWSRLIKIWTQRRRLGARPRKPRQ	74%	1%	-73%

*Change in GFP transduction efficiency in the presence (+) or absence (-) of Cas9-RNP

Fig. 5

SEQ ID NO:	Peptide	Cas9-RNP		
		Sequence	-	+
13	FSD10	KWKLARAFARAIAKKLGGSGGSYAR IA LR QA RTG	33%	3%
285	FSD375	GGSGGGSKWKLARAFARAIAKKLGGSGGGS	10%	11%

Change* -30% +1%				

*Change in GFP transduction efficiency in the presence (+) or absence (-) of Cas9-RNP

Fig. 6A

HeLa cells	Cpfl-RNP		Cas9-RNP		SEQ ID NO:
	Mean Viability	Mean % cells KO B2M	Mean Viability	Mean % cells KO B2M	
Non-treated (unlabelled)	-	-	72%	100%	-
Non-treated (labelled)	-	-	100%	11%	-
FSD10	79%	80%	75%	43%	13
FSD375	92%	40%	65%	30%	285
FSD422	123%	30%	45%	18%	329
FSD250	95%	80%	45%	28%	35
FSD301	115%	37%	84%	22%	212
CM18	63%	30%	67%	19%	348
FSD440	38%	30%	73%	14%	359

*Residues highlighted in **black** represent “core” amphipathic cationic domains; **boxed** residues are C-terminal cationic residues.

Fig. 6D

HeLa cells	Cpf1-RNP		Cas9-RNP		Shuttle agent sequence*	SEQ ID NO:
	Mean Viability	Mean % cells KO B2M	Mean Viability	Mean % cells KO B2M		
Non-treated (unlabelled)	-	-	72%	100%	-	-
Non-treated (labelled)	-	-	100%	2%	-	-
FSD356	67%	40%	68%	3%	KWKLLKLSRLLKLLGGGGSSQAG	266
FSD357	69%	27%	50%	2%	KWKLLKLSRLLKLLGGGGSSRRR	267
FSD446	86%	13%	62%	2%	KWKLLKLSRLLKLLGGGGSSHTSDQTN	370
FSD296	75%	58%	72%	1%	KWKLLKLSRLLKLLGGGGSSQARQAAR	207
FSD246	72%	63%	68%	1%	KWKLLKLSRLLKLLGGGGSSYARAAAARQAAR	169
FSD251	71%	18%	65%	16%	KWKLLKLSRLLKLLGGGGSSAAEAQAE	174

*Residues highlighted in black represent "core" amphipathic cationic domains; boxed residues are C-terminal cationic residues.

Fig. 6E

HeLa cells	Cpf1-RNP		Cas9-RNP		Shuttle agent sequence*	SEQ ID NO:
	Mean Viability	Mean % cells KO B2M	Mean Viability	Mean % cells KO B2M		
Non-treated (unlabelled)	-	-	72%	100%	-	-
Non-treated (labelled)	-	-	100%	2%	-	-
FSD374	67%	18%	64%	20%	LLKIWSRLIKIWTQGRRLGGGGSS	284
FSD183	65%	26%	55%	2%	LLKIWSRLIKIWTQGRRLGAFA	110
FSD172	56%	39%	63%	5%	LLKIWSRLIKIWTQGRRLGGGGSSARQAAR	101
FSD174	56%	46%	56%	2%	LLKIWSRLIKIWTQGRRLGGGGSSARQAAR	32
FSD187	57%	41%	82%	5%	LLKIWSRLIKIWTQGRRLGAPKPKSBO	114

*Residues highlighted in black represent "core" amphipathic cationic domains; boxed residues are C-terminal cationic residues.

Fig. 7

CFF-16HBEge cells	Cpf1-RNP		Cas9-RNP		Shuttle agent sequence*	SEQ ID NO:
	Mean Viability	Mean % cells KO B2M	Mean Viability	Mean % cells KO B2M		
Non-treated (unlabelled)	-	-	104%	100%	-	-
Non-treated (labelled)	-	-	96%	3%	-	-
FSD374	97%	17%	87%	12%	GGSGGGSLLKINSRLIKITQRRRLGGSGGGS	284
FSD375	121%	21%	112%	9%	GGSGGGSKKKLAFARAFATKKLGGSGGGS	285
FSD10	118%	22%	122%	3%	KKKLAFARAFATKKLGGSGGGSYARALRRQAR ^{ETG}	13
FSD322	122%	11%	114%	3%	KKKLAKAWSRALKKLGGSGGGSARQARQA	233
FSD395	91%	11%	73%	4%	KKLKLKLLKLLKKLGGSGGGSQARQAR ^{QAR}	304
FSD397	122%	10%	115%	3%	KKKLAKAFARAKKKLGGSGGGSQARQAR ^{QAR}	306

*Residues highlighted in **black** represent “core” amphipathic cationic domains; **boxed** residues are C-terminal cationic residues.

Fig. 8A

Peptide	Sequence	SEQ ID NO:
FSD10	KWKLARAFARA IKKL GGSGGGS YAPALRRQARTG	13
FSD375	GGSGGGS KWKLARAFARA IKKL GGSGGGS	285
FSD10-15	KWKLARAFARA IKKL	352
FSD448	KWKLARAFARA IKKL GGSGGGS	379
Linker-(FSD10-Cter)-Linker	GGSGGGS YAPALRRQARTG GGSGGGS	380
FSD10-Cter	YAPALRRQARTG	381

Fig. 8B

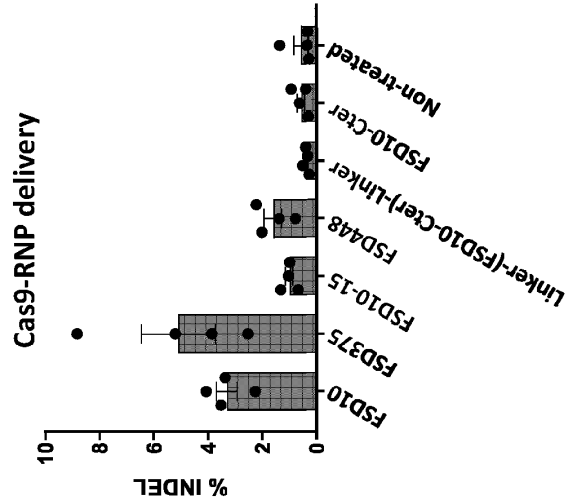


Fig. 8C

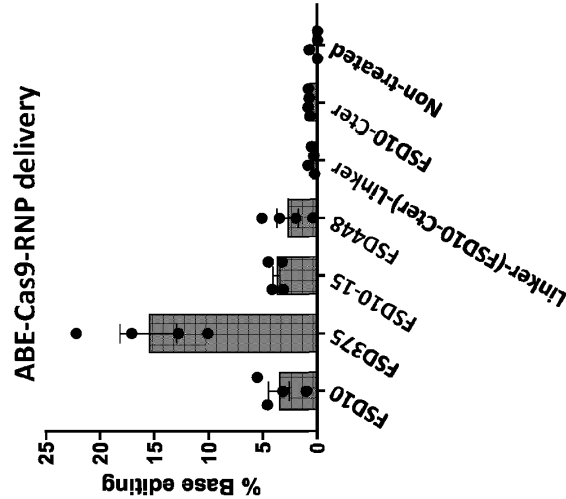


Fig. 9

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
1	CM18-Penetratin-cys	52%	12.1	12%	58%	25.5	18%
2	TAT-KALA	105%	8.4	12%	102%	4.6	9%
3	His-CM18-PTD4	66%	21.3	19%	71%	61.2	25%
4	His-LAH4-PTD4	109%	11.4	13%	102%	7	12%
5	PTD4-KALA	103%	7.8	10%	105%	29.9	22%
6	EB1-PTD4	70%	48.6	38%	77%	87.8	47%
12	FSD5	63%	39.2	37%	65%	57.2	30%
13	FSD10	100%	13.9	67%	104%	119.7	72%
15	FSD18	70%	65.2	30%	77%	129.2	42%
16	FSD19	89%	65.4	38%	96%	92	44%
17	FSD21	95%	43.3	35%	87%	87.8	41%
19	FSD120	80%	46.4	43%	109%	119.5	42%
21	FSD129	96%	69.8	40%	89%	195.6	49%
21	FSD129	104%	13.4	47%	117%	61.2	43%
22	FSD131	85%	35.5	43%	100%	92	42%
23	FSD134	83%	53.9	44%	83%	126.3	64%
23	FSD134	66%	11.8	55%	64%	154.7	65%
24	FSD146	98%	97.4	61%	98%	220.2	58%
26	FSD156	40%	53.8	30%	44%	107.7	36%
26	FSD156	31%	14.5	49%	55%	80	42%
27	FSD157	30%	98.9	58%	76%	285.2	57%
28	FSD159	80%	77.6	54%	56%	233	53%
29	FSD162	61%	85.2	54%	92%	344.2	66%
30	FSD168	88%	61.5	55%	86%	269.6	53%
31	FSD173	109%	27.8	30%	95%	232.4	63%
32	FSD174	93%	74.9	35%	85%	246.5	51%
33	FSD194	77%	22.6	37%	62%	292.4	78%
34	FSD220	102%	54.6	28%	102%	232.9	49%
35	FSD250	119%	33.6	37%	114%	284.8	70%
36	FSD250D	100%	5.4	14%	91%	12.9	19%
37	FSD253	73%	98.3	65%	65%	185.8	73%
38	FSD258	76%	106.2	69%	113%	178.6	62%
39	FSD262	81%	75.6	65%	88%	376.1	77%
40	FSD263	81%	88.7	68%	100%	279.3	75%
42	FSD265	86%	102	72%	80%	404.9	82%
43	FSD268	96%	52.1	33%	106%	131	51%
44	FSD286	87%	74.2	52%	90%	165.5	61%
45	FSD271	77%	73.8	63%	89%	279.5	73%
46	FSD272	85%	99.3	71%	97%	332.5	78%
47	FSD273	88%	91.9	66%	98%	321	74%
49	FSD268 Cyclic Amide	97%	52.1	29%	87%	155.4	50%

Fig. 9 (cont'd)

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
50	FSD268 Cyclic Disulfide	91%	30.1	21%	88%	119	48%
58	FSD117	99%	5.8	33%	122%	46.3	42%
59	FSD118	96%	12.9	41%	104%	73.6	45%
60	FSD119	71%	7	30%	109%	36.4	29%
61	FSD121	81%	19	46%	104%	76.2	44%
62	FSD122	80%	14.5	42%	99%	76	47%
63	FSD123	85%	13.5	32%	96%	86	36%
64	FSD124	88%	15.3	46%	98%	79.8	51%
65	FSD125	91%	14.3	46%	104%	87.6	51%
66	FSD126	93%	1.6	13%	107%	7.9	14%
67	FSD127	98%	3.5	22%	94%	16.6	16%
68	FSD128	97%	10.6	39%	87%	31.7	33%
69	FSD130	94%	2.5	16%	114%	25.1	40%
70	FSD132	80%	2.9	21%	110%	8.2	17%
71	FSD133	90%	10.4	37%	122%	56.2	46%
72	FSD135	105%	48.4	62%	99%	103.2	52%
73	FSD137	81%	1.5	10%	113%	0.7	7%*
74	FSD239	81%	9.7	40%	121%	41.1	44%
75	FSD139	82%	7.7	35%	97%	4	11%
76	FSD140	81%	6.9	31%	96%	13.1	19%
77	FSD141	91%	9.8	34%	95%	15.2	27%
78	FSD142	75%	4.3	26%	110%	4.9	10%*
80	FSD144	96%	1	10%	108%	3.8	11%
81	FSD145	103%	2.8	27%	107%	2.6	7%*
82	FSD147	84%	7.6	39%	90%	119.2	70%
83	FSD148	80%	1.1	11%	113%	5.4	5%
84	FSD149	70%	3.9	23%	107%	31	29%
85	FSD150	82%	17.4	49%	109%	88.3	54%
86	FSD151	79%	9.9	38%	105%	47.4	32%
87	FSD152	73%	13.7	45%	98%	69.6	41%
88	FSD153	41%	13.7	44%	89%	96.7	51%
89	FSD154	79%	18.7	49%	102%	44.5	30%
90	FSD158	57%	14.6	56%	43%	51.7	37%
91	FSD160	69%	14	38%	73%	147.9	53%
92	FSD161	78%	15.1	42%	102%	92.6	48%
93	FSD163	58%	16.8	47%	92%	115.5	59%
94	FSD164	24%	25.4	49%	101%	115.7	55%
95	FSD165	13%	18.3	51%	72%	95.3	55%
96	FSD166	61%	10.7	38%	29%	87.9	48%
97	FSD167	103%	5.9	29%	59%	81.4	45%
98	FSD169	105%	2.4	14%	89%	75.2	43%
99	FSD170	91%	15.4	35%	87%	166.4	61%
100	FSD171	108%	6.6	30%	107%	140.5	65%
101	FSD172	90%	4.6	20%	112%	87.3	47%

Fig. 9 (cont'd)

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
102	FSD175	113%	8.8	29%	106%	152.5	58%
103	FSD176	80%	6.2	24%	99%	148.5	59%
104	FSD177	99%	1.9	11%	101%	44.6	47%
105	FSD178	95%	1.7	10%	105%	18.4	37%
106	FSD179	108%	5.6	29%	91%	77.1	53%
107	FSD180	92%	5.2	26%	57%	69.8	51%
109	FSD182	108%	1.8	11%	102%	2.5	10%
110	FSD183	85%	4.1	17%	102%	132	54%
111	FSD184	93%	11.1	28%	99%	154.3	62%
112	FSD185	82%	10.6	33%	73%	159.1	61%
113	FSD186	88%	2	12%	107%	83.1	51%
114	FSD187	97%	9.3	41%	78%	123.5	66%
115	FSD188	95%	3.1	16%	94%	76.1	56%
116	FSD189	100%	7.1	29%	86%	185.1	71%
117	FSD190	107%	3.7	18%	110%	81.2	45%
118	FSD191	93%	2.2	14%	114%	31	38%
119	FSD192	96%	4.4	22%	104%	69.5	46%
120	FSD193	82%	7.6	37%	51%	154.5	73%
121	FSD195	85%	13.9	45%	83%	177.6	69%
122	FSD196	98%	12.3	40%	60%	140.2	54%
123	FSD197	48%	10.8	39%	73%	174.5	69%
124	FSD198	93%	2.2	13%	106%	3	6%
125	FSD199	90%	15.5	60%	14%	28.7	25%
126	FSD200	88%	13.2	42%	48%	137.3	56%
127	FSD201	98%	2	12%	110%	5.7	13%
128	FSD202	82%	2.8	16%	114%	18.2	39%
129	FSD203	87%	1.9	11%	112%	2.5	9%
130	FSD204	79%	3.2	18%	111%	23.4	32%
131	FSD205	96%	2.6	15%	112%	0.4	1%
132	FSD206	89%	3.6	20%	96%	49.2	37%
133	FSD207	105%	2.6	17%	111%	16.2	28%
134	FSD208	95%	6.3	33%	99%	132.2	68%
135	FSD209	66%	4.9	27%	112%	77.2	61%
136	FSD210	57%	7.3	36%	93%	129.5	74%
137	FSD211	63%	5.9	29%	89%	122.7	66%
138	FSD212	92%	2.1	11%	95%	11	30%
139	FSD213	56%	16.4	41%	104%	161.2	62%
141	FSD215	71%	6.6	30%	107%	80.8	54%
142	FSD216	64%	11.7	43%	111%	97.1	60%
143	FSD217	61%	1.6	10%	115%	8	26%
144	FSD218	111%	3	17%	115%	8.6	35%
145	FSD219	131%	9	27%	109%	74.2	45%
146	FSD221	58%	6.1	26%	69%	71.5	46%
149	FSD224	62%	8.1	38%	81%	93.7	66%
150	FSD225	128%	12.4	43%	82%	122.5	62%

Fig. 9 (cont'd)

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
151	FSD226	137%	9.3	39%	95%	85.8	61%
152	FSD227	60%	6.3	27%	91%	116.7	58%
153	FSD228	86%	6.3	32%	80%	118.7	67%
154	FSD229	88%	11	44%	79%	111.2	63%
155	FSD230	96%	13	56%	121%	72.5	61%
156	FSD231	80%	20.5	67%	99%	181.3	75%
157	FSD232	98%	18.2	71%	108%	76.2	69%
158	FSD233	75%	14.2	58%	122%	97.3	62%
159	FSD234	99%	7.5	38%	77%	48.7	31%
160	FSD235	95%	13.1	56%	104%	79.5	59%
161	FSD236	62%	2.7	20%	117%	14.3	23%
163	FSD238	89%	30.5	67%	107%	189.9	80%
164	FSD138	83%	22.9	40%	95%	66.9	64%
165	FSD240	93%	1.7	14%	116%	4.9	18%
166	FSD241	94%	9.4	43%	107%	119.3	60%
167	FSD243	77%	10.6	40%	114%	107.6	61%
168	FSD244	56%	20.5	60%	111%	128.5	69%
169	FSD246	58%	30.5	74%	91%	142.8	66%
171	FSD248	132%	12.3	46%	96%	148.3	56%
174	FSD251	93%	6.9	31%	85%	149.7	58%
175	FSD254	85%	10.8	38%	92%	111.3	49%
176	FSD255	85%	18.2	63%	105%	81.6	59%
177	FSD256	83%	3.8	25%	98%	26.1	41%
178	FSD257	89%	20.3	57%	103%	24.5	37%
179	FSD259	95%	26.1	65%	82%	141.1	67%
180	FSD260	89%	21.3	55%	88%	183	69%
181	FSD261	88%	17.1	46%	95%	168.3	60%
182	FSD266	92%	14.5	56%	95%	77.6	55%
183	FSD267	89%	6.7	39%	76%	44.1	38%
184	FSD269	89%	12	52%	68%	105.7	63%
185	FSD270	79%	16.6	54%	103%	172.4	72%
186	FSD274	76%	14.4	51%	91%	134.5	68%
187	FSD275	94%	16.9	55%	118%	30.3	42%
188	FSD276	109%	16.9	56%	100%	144.1	76%
189	FSD277	104%	47.1	70%	95%	188.3	72%
190	FSD278	101%	3.5	26%	103%	39.1	42%
191	FSD279	89%	6.3	34%	103%	17.6	31%
192	FSD280	100%	26	74%	104%	86.1	73%
193	FSD281	107%	54.6	68%	85%	201.7	76%
194	FSD282	116%	18.5	66%	86%	80.1	61%
195	FSD283	110%	3	28%	99%	5.7	27%
196	FSD284	116%	2.9	21%	95%	10.3	20%
197	FSD285	113%	3.3	26%	93%	4.9	19%
198	FSD287	105%	9.8	48%	90%	102.6	57%
199	FSD288	82%	19.9	67%	96%	89.2	72%

Fig. 9 (cont'd)

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
200	FSD289	89%	39.8	82%	85%	131.1	75%
201	FSD290	101%	30.5	57%	69%	229.1	73%
202	FSD291	102%	44.6	84%	77%	234.4	85%
203	FSD292	101%	2	19%	98%	2.2	5%
204	FSD293	100%	13.3	43%	90%	8.9	18%
205	FSD294	81%	16.2	43%	86%	167.3	61%
206	FSD295	84%	18.8	43%	97%	40	34%
207	FSD296	40%	45.7	74%	84%	247.4	82%
208	FSD297	102%	42.1	72%	79%	247.2	81%
209	FSD298	101%	62.3	74%	90%	219.3	76%
210	FSD299	94%	3.8	30%	94%	16.5	32%
211	FSD300	89%	3.5	28%	108%	3.9	11%
212	FSD301	84%	24.2	48%	95%	87.8	51%
213	FSD302	89%	54.2	80%	94%	228.4	83%
214	FSD303	91%	50.2	77%	86%	198	77%
215	FSD304	83%	37.7	72%	96%	160.2	73%
216	FSD305	94%	50.1	78%	97%	254.5	86%
217	FSD306	81%	55.3	76%	96%	209.4	82%
218	FSD307	61%	26.1	60%	97%	107.6	62%
219	FSD308	85%	54	78%	85%	247.4	86%
220	FSD309	62%	25	56%	64%	221.5	69%
221	FSD310	90%	51.4	81%	92%	217.3	81%
222	FSD311	43%	47.6	80%	74%	211.3	79%
223	FSD312	90%	1.7	17%	98%	1.8	5%*
224	FSD313	66%	49.1	71%	57%	210.1	71%
225	FSD314	87%	36.1	70%	90%	119.8	69%
226	FSD315	93%	67.4	63%	89%	210.8	66%
227	FSD316	73%	36.5	69%	82%	202.2	74%
228	FSD317	58%	1.9	17%	107%	2.6	6%*
229	FSD318	65%	63.6	60%	74%	227.2	65%
230	FSD319	85%	43.3	73%	73%	250.6	75%
231	FSD320	109%	42.9	67%	76%	220.4	72%
232	FSD321	46%	13.9	32%	65%	156.5	53%
233	FSD322	55%	25.7	37%	132%	117.5	54%
234	FSD323	90%	27.9	54%	38%	90.7	53%
236	FSD325	56%	25.1	51%	141%	70.6	50%
237	FSD326	89%	1.7	10%	145%	9.5	27%
238	FSD327	98%	12.4	35%	95%	73.4	48%
239	FSD328	83%	14.1	33%	132%	81.9	53%
240	FSD330	87%	26.1	47%	124%	71.6	51%
242	FSD332	73%	2	13%	123%	0.9	5%
243	FSD333	39%	30.9	60%	69%	197.1	86%
244	FSD334	68%	12.8	47%	75%	87	80%
245	FSD335	37%	32.9	53%	76%	124.5	68%
246	FSD336	63%	42.4	78%	84%	164.5	90%

Fig. 9 (cont'd)

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
247	FSD337	92%	57.8	76%	66%	186.2	87%
248	FSD338	52%	40.9	69%	65%	169.3	89%
249	FSD339	86%	23.2	55%	92%	95.6	65%
250	FSD340	51%	60	77%	85%	169.9	83%
251	FSD341	104%	29.4	59%	66%	106.8	65%
252	FSD342	83%	59.2	86%	37%	92.2	70%
253	FSD343	38%	8.6	31%	115%	25.7	38%
254	FSD344	31%	35	51%	99%	188.1	68%
255	FSD345	51%	50.8	69%	86%	181.2	78%
256	FSD346	84%	58.4	81%	70%	193.2	84%
257	FSD347	44%	55.1	77%	75%	130.6	74%
258	FSD348	76%	38.3	70%	108%	68.2	68%
259	FSD349	104%	64.3	84%	90%	202.4	82%
260	FSD350	70%	50.7	70%	111%	100.6	65%
262	FSD352	58%	57.8	69%	105%	154.9	71%
263	FSD353	66%	2.1	13%	123%	1.1	5%
264	FSD354	61%	45.7	62%	102%	123.5	64%
265	FSD355	62%	41.7	60%	98%	124.7	61%
266	FSD356	97%	33.9	60%	102%	147.8	71%
267	FSD357	36%	27.9	69%	108%	42.1	44%
268	FSD358	77%	26.2	50%	120%	94.3	59%
269	FSD359	74%	52.3	79%	83%	213.1	82%
270	FSD360	78%	98.5	84%	105%	89.4	75%
271	FSD361	67%	13.6	29%	95%	97.3	39%
272	FSD362	89%	22.2	44%	114%	53.6	38%
273	FSD363	89%	13.3	28%	104%	49.7	31%
274	FSD364	74%	5.3	21%	165%	6.7	17%
275	FSD365	77%	18.3	44%	152%	96.3	58%
276	FSD366	74%	9.1	28%	140%	89.8	44%
277	FSD367	69%	4.5	20%	150%	31.9	28%
278	FSD368	68%	14.3	40%	130%	139.4	58%
279	FSD369	75%	13.6	42%	161%	116.8	58%
280	FSD370	72%	18.2	58%	161%	80	61%
281	FSD371	72%	30.6	61%	139%	119.7	53%
282	FSD372	67%	13.3	49%	140%	63.9	53%
283	FSD373	77%	11	29%	144%	93.2	48%
284	FSD374	73%	16.3	35%	152%	111	49%
285	FSD375	57%	8.7	23%	150%	62.7	32%
287	FSD377	63%	10.7	30%	159%	36.6	34%
288	FSD378	65%	18.1	33%	144%	35.1	31%
289	FSD379	47%	10.1	33%	76%	87.9	54%
290	FSD381	72%	16.3	37%	66%	115.2	44%
291	FSD382	94%	11	31%	44%	93.5	45%
292	FSD383	74%	30.5	52%	21%	91.6	55%
293	FSD384	81%	2.4	13%	106%	15.3	23%

Fig. 9 (cont'd)

SEQ ID NO	Candidate shuttle agent (10 μ M)	Propidium iodide (10 μ g/mL)			GFP-NLS (10 μ M)		
		Mean Viability	Norm. Mean Delivery Score ¹	Mean % of PI+ cells	Mean Viability	Norm. Mean Delivery Score ¹	Mean % of GFP+ cells
294	FSD385	88%	37.5	62%	31%	105.5	60%
296	FSD387	58%	3.4	18%	94%	74.5	50%
297	FSD388	84%	22.5	56%	70%	56.9	54%
298	FSD389	83%	8	29%	50%	72.5	41%
299	FSD390	93%	3.7	19%	98%	38.5	45%
300	FSD391	81%	25.1	57%	55%	94.7	59%
302	FSD393	52%	24.3	58%	61%	59.5	54%
303	FSD394	69%	4.7	23%	23%	17	25%
304	FSD395	98%	34.1	67%	74%	303	87%
305	FSD396	79%	8.1	29%	85%	105.1	50%
306	FSD397	74%	1.6	11%	99%	10.4	30%
307	FSD398	88%	6.8	26%	87%	70.5	53%
308	FSD399	73%	7.9	27%	94%	66.3	49%
310	FSD401	99%	28.4	55%	93%	144.9	68%
311	FSD402	79%	20.6	34%	64%	108.2	41%
313	FSD404	72%	8.4	29%	85%	72	54%
314	FSD406	65%	28	64%	75%	174.7	74%
315	FSD407	110%	28.9	66%	62%	203.3	80%
316	FSD408	72%	14.6	45%	72%	102.1	58%
317	FSD409	82%	1.1	10%	89%	5.2	10%
318	FSD410	88%	3.1	19%	45%	14.5	20%
319	FSD411	110%	27.6	66%	65%	200.4	81%
320	FSD412	118%	10.9	40%	71%	63.9	47%
321	FSD413	45%	1.6	13%	82%	5.1	15%
322	FSD414	97%	2.8	19%	106%	14.8	26%
323	FSD415	110%	14.8	43%	78%	124	56%
324	FSD416	106%	8.2	28%	101%	48.1	32%
326	FSD418	107%	5.3	26%	91%	70.3	55%
327	FSD419	99%	1.7	13%	102%	8	19%
328	FSD421	103%	3.7	21%	106%	38.9	33%
329	FSD422	96%	4.1	22%	94%	8.1	31%
330	FSD423	79%	1	10%	106%	4	17%
331	FSD424	78%	7.7	24%	90%	75.5	37%
332	FSD425	126%	22.9	12%	94%	111.4	27%
338	FSD431	107%	98.9	26%	88%	407	50%
339	FSD432	110%	31.3	12%	87%	266.3	39%
340	FSD433	104%	45	26%	90%	247.5	54%
341	FSD434	108%	38.1	13%	82%	282.5	43%
342	FSD435	41%	119.5	47%	55%	339.1	67%
344	FSD438	59%	397.5	81%	69%	686.2	84%

¹ Normalized Mean Delivery Scores were normalized to that of the "cargo alone" control for each experimental batch.

Fig. 10

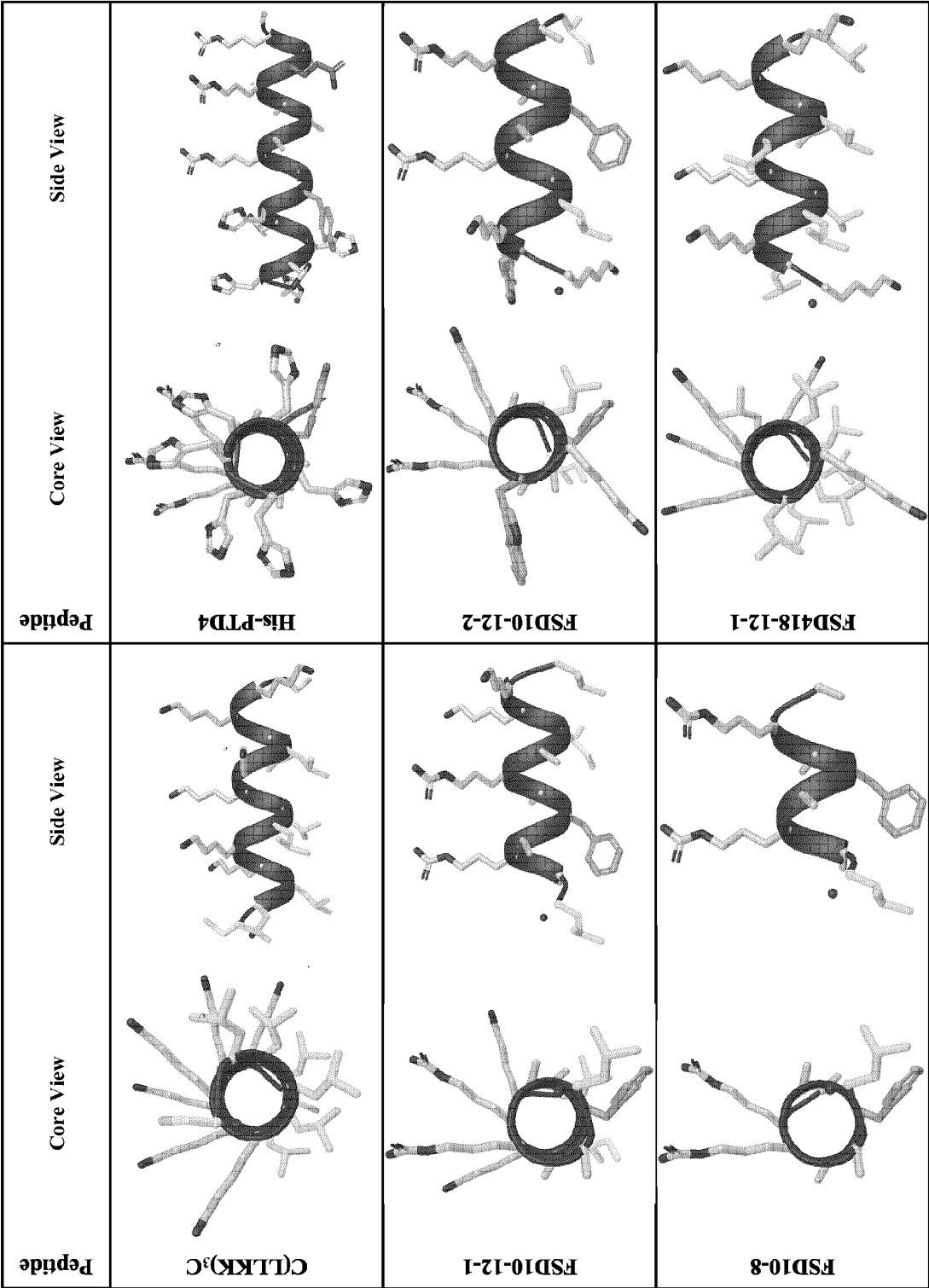


Fig. 10 (cont'd)

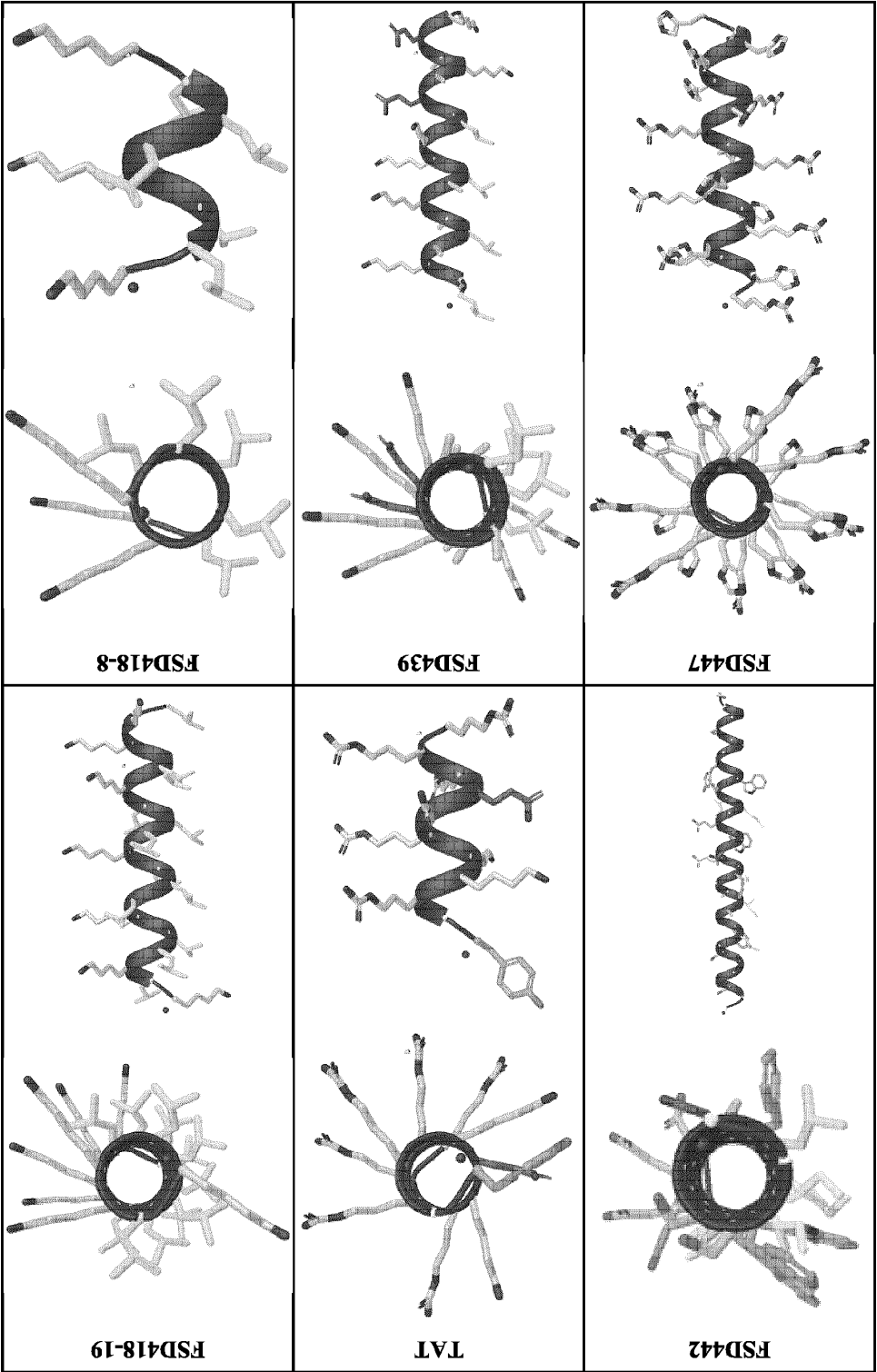


Fig. 10 (cont'd)

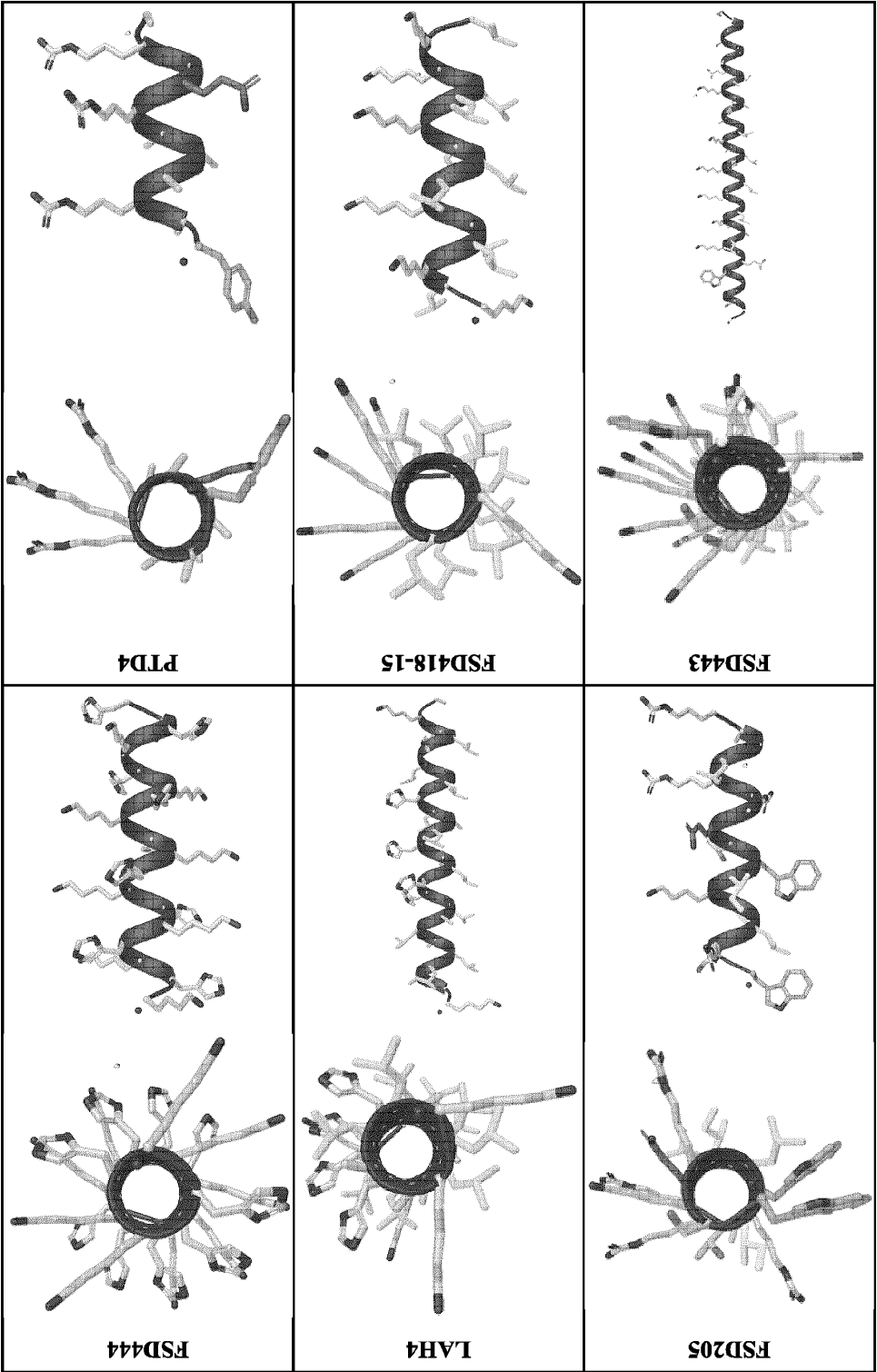


Fig. 10 (cont'd)

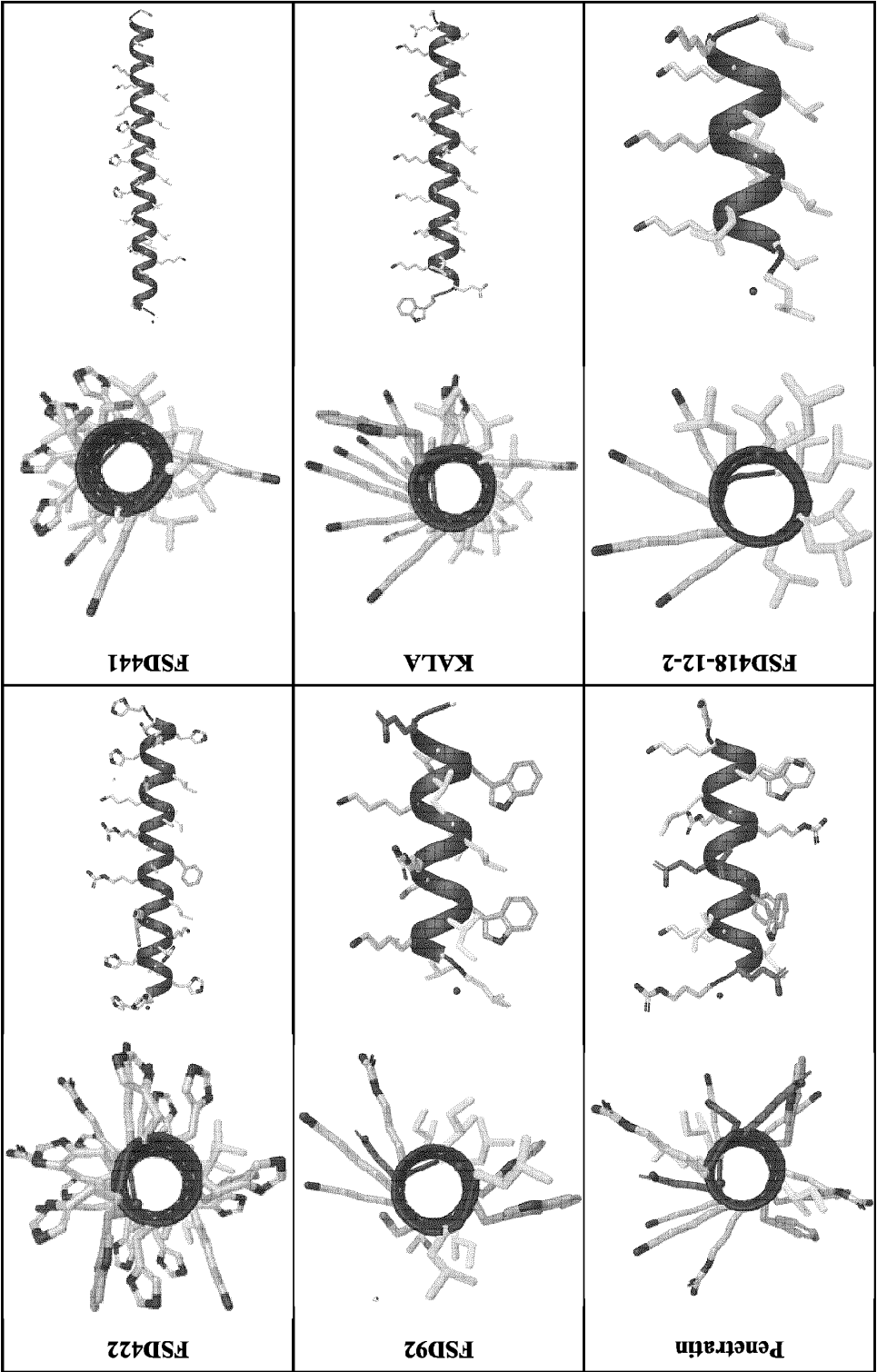


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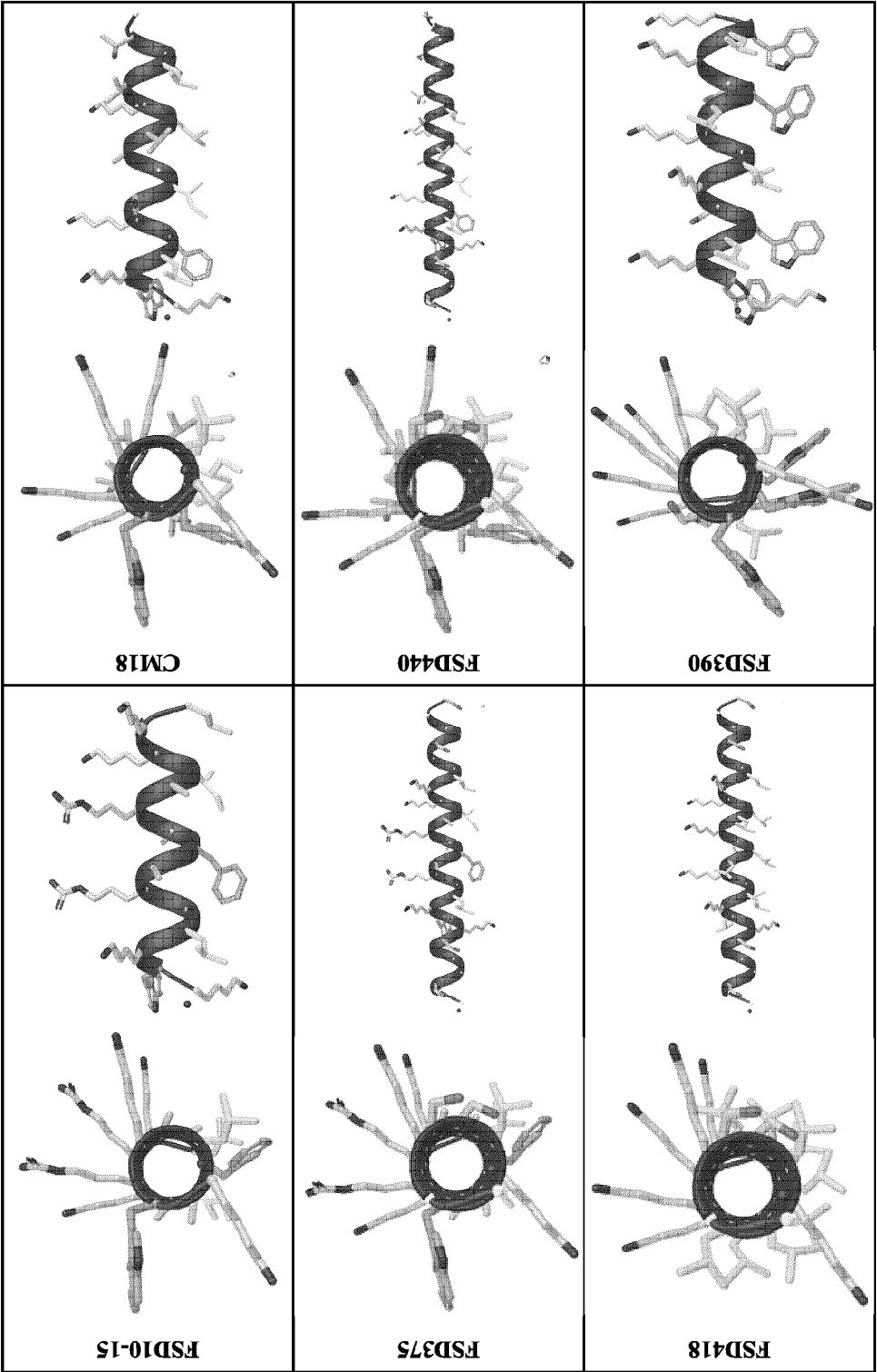


Fig. 10 (cont'd)

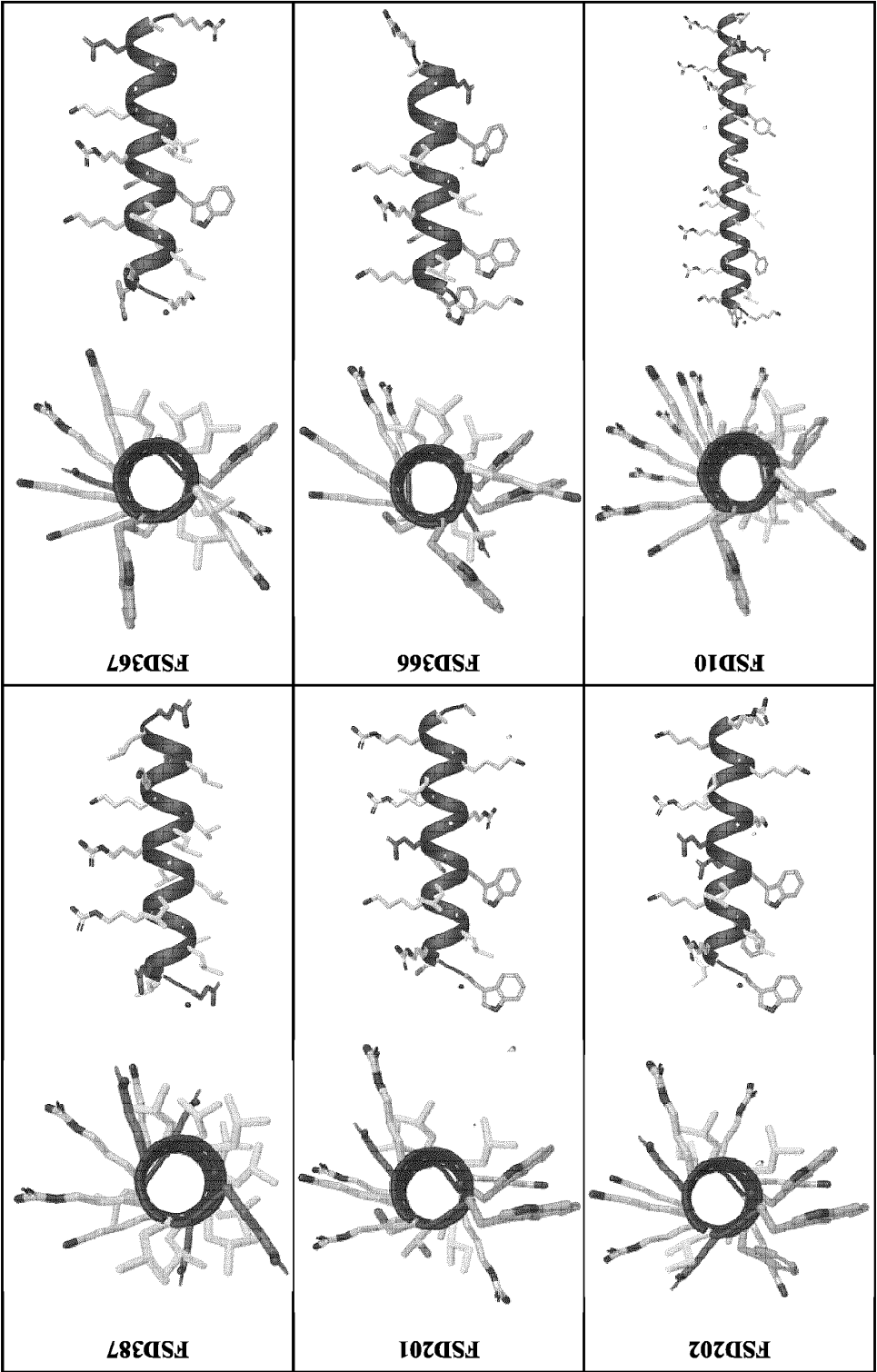


Fig. 10 (cont'd)

