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Data in Brief



Data Article

Data from computational analysis of the peptide linkers in the MocR bacterial transcriptional regulators



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ABSTRACT

Detailed data from statistical analyses of the structural properties of the inter-domain linker peptides of the bacterial regulators of the family MocR are herein reported. MocR regulators are a recently discovered subfamily of bacterial regulators possessing an N-terminal domain, 60 residue long on average, folded as the winged-helix-turn-helix architecture responsible for DNA recognition and binding, and a large C-terminal domain (350 residue on average) that belongs to the fold type-I pyridoxal 5'-phosphate (PLP) dependent enzymes such aspartate aminotransferase. Data show the distribution of several structural characteristics of the linkers taken from bacterial species from five different phyla, namely Actinobacteria, Alpha-, Beta-, Gammaproteobacteria and Firmicutes.

Interpretation and discussion of reported data refer to the article "Structural properties of the linkers connecting the N- and C-terminal domains in the MocR bacterial transcriptional regulators"

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Specifications Table

Subject area More specific subject area	Biology Structural properties of linkers in the bacterial transcriptional regulators
Type of data	Table, graph, figure
How data was acquired	Databank searches. Computational analysis
Data format	Raw, filtered, analyzed
Experimental factors	Analyses were mostly carried out with Perl, Python and R scripts and software for structural bioinformatics
Experimental features	Linker sequences were extracted from multiple sequence alignments of MocR regulators. Computational analysis defined the residue and residue dyads propensities and the distribution of physicochemical properties in the linker sequences.
Data source location	UniProt, RefSeq
Data accessibility	Data is within this article. Linker sequence sets are available at https://sites.goo gle.com/a/uniroma1.it/pascarellalab/home/resources

Value of the data

- Data represent the description of the structural properties of the peptide linkers connecting the Nand C-terminal domains in the MocR bacterial regulators.
- Data provide researchers with a framework to select specific MocR for experimental characterization.
 Data provide a support to design experiments for the investigation of properties of specific MocR:
- for example, experiments of site-directed mutagenesis, deletions or insertions of linker regions.
- Data can help interpretation of experimental data obtained from MocR studies.
- Data provide a framework to derive rules for *de-novo* design of peptide linkers with desired properties.

1. Data

Results derived from computational analysis of the inter-domain sequences of the peptide linker connecting the N-terminal and the C-terminal domain of the bacterial transcriptional regulators of the subfamily MocR are herein reported. Data are shown as tables describing linker statistics such as residue and dyad composition propensities, predicted secondary structure frequency, and box-plots showing the distribution of several structural properties. Moreover, plots of length distributions of linkers from two specific MocR subgroups, namely PdxR and GabR, are also reported.

Table 1	
List of MocR regulators predicted to have linkers of length equal or greater to 60 residues	

UniProt code	Start ^a	End ^b	Length
A0A023C4T7_9PSED	88	148	60
A0A0B2AVS1_9ACTN	85	145	60
A0NP21_LABAI	80	140	60
I9W6R0_9RALS	87	147	60
W4CMK3_9BACL	121	181	60
A0A074LC92_PAEPO	82	143	61
I4N7I5_9PSED	87	148	61
A0A0D5NE20_9BACL	85	147	62
F8FPR4_PAEMK	106	168	62
G8QJ34_DECSP	85	147	62
V7DIJ8_9PSED	88	150	62
W4P2V0_9BURK	87	149	62
B9QZW6_LABAD	80	143	63
F3KUT6_9BURK	118	181	63
F7T5G0_9BURK	85	148	63
M2X958_9MICC	80	143	63
R9LS02_9BACL	83	146	63
S2WJB8_DELAC	89	152	63
A0A098SWK7 9PSED	88	152	64
A0A0[6]2M6_9PSED	88	152	64
A0A0F4KHT0 9ACTN	101	166	65
D5BN74 PUNMI	82	147	65
D7D074 METV0	90	156	66
KOYXF4 9ACTN	79	145	66
A0A077LFC1 9PSED	87	154	67
A0A095YLI49 9FIRM	78	145	67
HOBWG7 9BURK	75	142	67
A0A087DUC1 9BIFI	78	146	68
A0A0907CF9 PAFMA	83	152	69
	74	143	69
F3IFN8 PSFSX	88	157	69
WOHH53 DSECI	88	157	69
	80	157	70
	89	159	70
A0A088V9M0 BLIRPF	88	159	70
	62	135	73
	85	155	73
	105	101	74
	82	159	70
ASSUVO OFIDM	82	150	70
	75	155	70
ADADESIV25 OPLICE	24	155	77
	84	169	77
	90	162	78
ADADOILANO_9IVIICO	84	105	79
AUAUA8BLI7_9BUKK	89	108	/9
KOHHES_9ACIN	79	159	80
	84	164	80
AUAU89HPN9_PAEDU	78	162	84
D2PX75_KRIFD	93	1/8	85
D3F8U9_CUNWI	80	166	86
AUAUA4HID4_9PSED	88	1/9	91
F2RK57_STRVP	86	180	94
C/MPDU_CRYCD	79	1/4	95
F4QXL0_BREDI	83	179	96
AUAU87AB73_9BIFI	78	175	97
AUAU87E7D4_9BIFI	78	175	97
A0A0B4DPH0_KOCRH	85	183	98
F2RA50_STRVP	88	186	98
V6KRX5_STRRC	93	191	98
M8D4I1_9BACL	79	179	100

Table 1 (continued)

UniProt code	Start ^a	End ^b	Length
A0A0A3JRX6_BURPE	88	189	101
M8DED6_9BACL	80	183	103
A0A087BLK1_BIFLN	78	187	109
A0A087CXD8_9BIFI	78	187	109
S6CDU1_9ACTN	130	244	114
A0A0A6SYE7_9BURK	87	209	122
F5LR05_9BACL	82	209	127
A0A089IZ38_PAEDU	84	218	134
A0A0B6S8F7_BURGL	88	231	143
A0A087A119_9BIFI	78	222	144
A0A089MC10_9BACL	82	234	152
A0A089KZI8_9BACL	82	244	162

^a Linker N-terminal sequence position.

^b Linker C-terminal sequence position.

Table 2 Residue propensities in the linkers of length range 0-20.

	Actin	obacteria	A	Alpha		Beta	Fir	micutes	G	amma
AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}	P ^{b)}	AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}
Α	1.23	638	1.16	360	1.24	217	0.92	180	1.14	390
С	0.20	7	0.12	3	0.00	0	0.45	13	0.32	13
D	0.85	199	1.16	172	1.07	81	1.30	196	1.16	236
Е	1.00	208	1.37	190	1.44	104	1.40	264	1.35	285
F	0.36	39	0.35	33	0.20	10	0.43	52	0.55	82
G	1.10	387	1.20	254	1.43	161	0.74	132	1.21	307
Η	0.67	58	0.78	40	1.07	34	1.60	79	1.49	123
I	0.50	71	0.46	60	0.44	28	0.65	134	0.64	139
K	0.26	21	0.53	45	0.36	17	1.26	244	0.64	111
L	0.61	237	0.60	155	0.77	112	0.55	146	0.79	308
Μ	0.35	25	0.47	28	0.78	25	0.52	37	0.83	69
Ν	0.34	28	0.45	34	0.37	16	1.68	235	0.73	116
Р	2.90	697	2.69	354	2.13	155	1.71	160	1.80	287
Q	0.73	86	1.12	97	1.56	90	1.16	118	1.64	276
R	1.28	389	1.43	257	1.02	103	0.93	110	0.86	174
S	1.01	234	1.17	182	1.02	89	1.58	283	1.24	312
Т	1.18	288	0.96	135	1.12	85	1.21	188	0.94	191
V	0.79	257	0.66	117	0.71	70	0.69	125	0.90	216
W	0.41	25	0.28	10	0.43	9	0.27	8	0.31	16
Y	0.24	19	0.44	26	0.24	8	0.50	56	0.38	43

^aAmino acid one-letter code. ^bResidue propensity; cells containing values \geq 1.01 and \leq 1.19 and values \geq 1.20 are shaded with light and dark grey respectively. In the latter case, numbers are boldfaces.

^cNumber of residues in the sample.

Table 3		
Residue propensities in the lin	kers of length range 21–40).

	Actin	obacteria	I	Alpha		Beta	Fir	micutes	G	amma
AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}	P ^{b)}	AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}
Α	1.25	2020	1.08	1107	1.23	1593	0.89	1043	1.12	2186
С	0.16	18	0.10	8	0.28	32	0.37	65	0.54	123
D	0.88	638	1.17	574	1.04	585	1.05	948	0.99	1149
Ε	0.77	496	1.19	545	1.05	566	1.54	1740	1.09	1314
F	0.41	138	0.48	151	0.55	202	0.59	430	0.62	524
G	0.92	1004	0.75	520	0.72	606	0.51	546	0.60	862
Н	0.84	227	0.91	154	1.02	243	1.33	393	1.06	501
Ι	0.35	157	0.59	254	0.52	247	0.81	1001	0.63	782
K	0.44	112	0.60	166	0.48	168	1.19	1377	0.69	682
L	0.65	778	0.92	776	0.90	979	0.78	1237	0.92	2051
Μ	0.33	73	0.65	126	0.75	179	0.56	238	0.75	357
Ν	0.55	139	0.55	138	0.52	170	0.93	780	0.71	641
Р	2.77	2071	2.68	1163	2.39	1295	2.38	1339	2.67	2415
Q	0.89	322	1.25	356	1.11	474	1.61	981	1.36	1298
R	1.53	1447	1.17	691	1.33	997	1.15	810	1.22	1396
S	1.06	763	1.20	610	1.34	870	1.18	1267	1.22	1754
Т	1.08	818	0.82	378	0.88	498	0.91	845	0.97	1119
V	0.71	717	0.87	509	0.84	619	0.72	783	1.04	1421
W	0.60	114	0.92	106	0.82	127	0.67	119	0.58	167
Y	0.37	89	0.36	70	0.31	79	0.87	585	0.45	287

^aAmino acid one-letter code.

^bResidue propensity; cells containing values \geq 1.01 and \leq 1.19 and values \geq 1.20 are shaded with light and dark grey respectively. In the latter case, numbers are boldfaces.

^cNumber of residues in the sample.

2. Experimental design, materials and methods

Data was created from the analysis of MocR sequences taken from the most populated phyla Actinobacteria, Firmicutes, Alpha-, Beta- and Gammaproteobacteria. Sequences of the MocR regulators in each phylum were retrieved from the UniProt data bank [2] accessed on October, 2015 with the application of RPSBLAST of the BLAST suite [3] and the CDD data bank [4]. The protein sequences containing both the wHTH and AAT domains identified by RPSBLAST were conside-red genuine MocR regulators. Before further processing, retrieved sequences were filtered at 75% sequence identity with the program CD-HIT [5]. Multiple sequence alignments were calculated with the programs ClustalO [6] and processed with the software Jalview [7]. Linker sequences were manually extracted from the multiple sequence alignments according with the wHTH and AAT domain boundaries assigned by RPSBLAST. List of the MocR regulators possessing linkers longer than 60 residues is reported in Table 1. Residue frequency and propensities were calculated as described in [1] and are displayed in Tables 2–5 organized according to linker length and phylum class. Propensities for the entire linker set are reported in [1]. Dipeptide frequency and propensity

	Actin	obacteria	A	Alpha	J	Beta	Fir	micutes	G	amma
AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}	P ^{b)}	AA ^{a)}	P ^{b)}	Counts ^{c)}	$\mathbf{P}^{\mathbf{b})}$	Counts ^{c)}
Α	1.31	709	0.99	937	1.29	1636	0.83	775	1.10	871
С	0.22	8	0.30	22	0.23	25	0.37	52	0.53	49
D	1.03	250	1.03	463	0.94	516	1.01	732	0.90	424
Ε	0.85	184	0.95	401	0.93	488	1.10	997	0.89	437
F	0.62	71	0.64	183	0.45	163	0.61	356	0.47	160
G	0.94	346	0.74	475	0.86	708	0.73	623	0.68	400
Н	0.71	64	0.95	149	1.12	260	1.49	354	1.38	265
Ι	0.51	76	0.59	236	0.67	313	0.81	801	0.64	322
K	0.43	37	1.12	287	0.58	201	0.91	841	0.89	358
\mathbf{L}	0.64	257	0.73	572	0.76	805	0.74	936	0.83	752
Μ	0.61	45	0.53	95	0.75	176	0.81	278	0.57	111
Ν	0.63	54	0.83	191	0.57	181	1.54	1031	0.88	322
Р	2.20	550	2.41	965	2.30	1219	1.86	839	2.34	863
Q	0.97	118	1.22	322	1.20	502	1.53	748	1.44	559
R	1.08	343	1.54	843	1.37	1005	1.17	662	1.41	660
S	1.37	331	1.25	588	1.28	815	1.26	1086	1.39	812
Т	1.10	280	0.91	388	0.84	464	0.92	690	1.04	490
V	0.75	252	0.63	338	0.87	628	0.61	526	0.69	385
W	1.08	69	1.51	161	0.64	96	3.28	466	1.35	159

Table 4 Residue propensities in the linkers of length range 41-60.

0.32 ^aAmino acid one-letter code.

Y

^bResidue propensity; cells containing values \geq 1.01 and \leq 1.19 and values \geq 1.20 are shaded with light and dark grey respectively. In the latter case, numbers are boldfaces.

0.33

81

0.85

458

0.61

^cNumber of residues in the sample.

26

0.78

138

calculations relied on the software 'compseq' of the EMBOSS suite [8]. Table 6 reports the average number of residue dyads in each group. The highest the number, the highest the reliability of the dyad propensities reported in Figs. 1-5. Average content of predicted secondary structures (obtained with the program PREDATOR [9]) are displayed in Table 7. Physicochemical properties were assigned to the amino acid residues according to the indices provided by the AAindex data bank [10] incorporated in the Interpol package [11] of the R-project library [12]. Distribution of the properties are reported as box-plots in Figs. 6-10 limited to the phyla Alphaproteobacteria, Betaproteobacteria and Gammaproteobacteria and in Figs. 11 and 12 for all the phyla considered. Boxplots for Actinobacteria and Firmicutes missing in Figs. 6-10 are to be found in [1].

The linker length distribution were analyzed within two specific MocR subfamilies: GabR [13] and PdxR [14] involved in the regulation of the synthesis of acid γ -amino butyric and pyridoxal 5'-phosphate, respectively. Sequences assigned to each of the two subgroups were retrieved from the RegPrecise data bank [15] and aligned separately (Table 8); a HMM profile [16] was calculated for each one of the multiple alignment. The profile was utilized to search for other putative GabR or

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Table 5Residue propensities in the linkers of length range 61–200.

	Actin	obacteria	A	Alpha	E	Beta	Fir	micutes	G	amma
AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}	P ^{b)}	AA ^{a)}	P ^{b)}	Counts ^{c)}	P ^{b)}	Counts ^{c)}
Α	1.23	333	0.57	20	1.67	258	2.06	261	0.72	41
С	0.54	10	0.37	1	0.22	3	0.32	6	0.45	3
D	0.90	110	1.25	21	0.88	59	1.09	106	0.44	15
Е	0.67	73	0.51	8	0.69	44	1.11	136	0.82	29
F	0.77	44	0.19	2	0.27	12	0.33	26	0.20	5
G	1.44	267	0.54	13	1.54	154	2.08	239	0.87	37
Н	0.77	35	0.69	4	0.74	21	1.03	33	1.88	26
Ι	0.76	57	0.34	5	0.72	41	0.31	42	0.64	23
K	0.51	22	0.84	8	0.48	20	0.38	48	1.49	43
\mathbf{L}	0.40	81	0.34	10	0.47	61	0.55	94	1.46	95
Μ	0.27	10	0.60	4	0.49	14	0.48	22	0.36	5
Ν	1.03	44	0.82	7	0.83	32	0.62	56	0.57	15
Р	1.93	243	1.61	24	1.55	100	2.17	132	2.53	67
Q	0.77	47	1.23	12	1.04	53	1.04	69	0.61	17
R	1.13	180	0.54	11	1.35	121	1.62	124	0.80	27
S	1.74	211	0.97	17	1.54	119	1.45	169	2.11	89
Т	1.23	157	0.82	13	0.77	52	0.80	81	1.56	53
V	0.52	89	0.85	17	0.74	65	0.71	83	0.55	22
W	0.50	16	1.26	5	0.71	13	1.25	24	0.24	2
Y	0.44	18	0.61	4	0.40	12	0.49	36	0.11	2

^aAmino acid one-letter code.

^bResidue propensity; cells containing values \geq 1.01 and \leq 1.19 and values \geq 1.20 are shaded with light and dark grey respectively. In the latter case, numbers are boldfaces.

^cNumber of residues in the sample.

Table 6

Average number of residue pairs in each data set.

	Length interva	ls			
	All	0–20	21–40	41-60	61–200
Actinobacteria Alphaproteobacteria Betaproteobacteria Firmicutes Gammaproteobacteria	$53.5 \pm 93.1 \\ 45.7 \pm 56.7 \\ 57.1 \pm 78.2 \\ 83.0 \pm 63.5 \\ 82.0 \pm 81.9$	$\begin{array}{c} 9.2 \pm 17.6 \\ 6.0 \pm 9.0 \\ 3.2 \pm 5.1 \\ 6.4 \pm 6.8 \\ 8.7 \pm 9.4 \end{array}$	$\begin{array}{c} 29.2 \pm 53.8 \\ 20.3 \pm 28.5 \\ 25.5 \pm 35.1 \\ 39.9 \pm 34.8 \\ 50.8 \pm 54.1 \end{array}$	$\begin{array}{c} 10.0 \pm 16.4 \\ 18.9 \pm 22.4 \\ 25.1 \pm 34.8 \\ 32.4 \pm 25.0 \\ 20.9 \pm 20.6 \end{array}$	$5.0 \pm 8.5 \\ 0.5 \pm 0.8 \\ 3.0 \pm 5.8 \\ 4.4 \pm 6.4 \\ 1.5 \pm 3.5$

PdxR sequences in the reference proteomes data bank available at the Hmmer web server [17]. Sequences showing an E-value smaller than 10^{-120} , were retrieved and multiply aligned. Linker sequences were extracted as described above. Length distribution were plotted and compared for the GabR and PdxR sets (Fig. 13).

Perl and R-scripts were written for data analysis, processing and display.

Α	١.																			
<u>}</u>	1.3	0.4	1.1	1.0 0.2	0.5	1.4	0.7	0.4	0.3	0.9	0.4	0.7	4.2	1.0	1.9 0.4	1.5	1.4	0.9	0.7	0
D	1.2	0.1	0.7	0.6	0.5	1.0	0.5	0.7	0.1	0.7	0.9	0.3	1.1	0.8	1.2	0.8	1.5	1.1	1.3	1
	0.8	0.1	0.5	0.4	0.4	0.4	0.5	0.4	0.6	0.3	0.5	0.7	0.4	0.5	0.7	0.9	0.8	0.7	0.2	0
	1.5 0.9	0.4	0.9	0.9	0.5	1.1	0.9	0.5	0.3	0.6	0.4	0.5	2.2	0.5	1.4	1.1	1.1	1.0	1.0	0
	0.6	0.1	0.7	0.6	0.6	0.4	0.3	0.2	0.0	0.2	0.0	0.5	1.1	0.5	0.7	0.3	0.2	0.1	0.0	0
)	0.5	0.1	0.5	0.5	0.7	0.6	0.9	0.3	0.3	0.3	0.4	0.3	2.0	0.3	0.8	1.0	0.5	0.3	0.5	0
	0.3	0.0	0.4	0.3 0.4	0.4	0.2	0.3	0.1	0.0 0.4	0.4	0.3	0.2	0.9 0.9	0.5	0.6	0.4	0.2	0.2 0.4	0.2 0.6	0
	3.8	0.8	2.1	2.0	0.6	2.5	2.5	1.1	1.6	1.5	1.3	1.2	5.9	2.3	4.9	2.7	2.5	2.0	1.3	0
	1.7	0.1	1.1	0.9	0.5	1.3	0.8	0.8	0.6	0.7	0.5	0.6	4.1	1.1	1.4	1.7	2.0	1.0	0.5	0
	1.5	0.2	0.8	0.8	0.7	0.9	0.8	0.5	0.6	0.7	0.7	0.6	2.3	0.8	1.7	1.4	1.4	0.9	0.5	0
2	0.8	0.2 0.2	0.8	0.5	0.6	0.5	0.5	0.2	0.2	0.3	0.3	0.2 0.2	2.4 0.3	0.5 6.1	1.0 0.6	0.8	0.6 0.6	0.4	0.3	0
	0.5	0.0	0.1	0.3	0.0	0.5	1.3	0.0	0.1	0.1	0.0	0.4	0.6	0.3	0.5	1.1	0.1	0.2	0.0	0
ک	A	C 0.3	D	E	F	G 0.9	H	1	K	L 0.8	M	N 0.6	P 3.6	Q	R	S	T 0.9	V	W	0
	0.1	0.4	0.2	0.2	0.1	0.2	0.0	0.1	0.2	0.2	0.4	0.2	0.1	0.8	0.2	0.4	0.3	0.1	0.0	ŝ
	1.3	0.1	1.0	0.8	0.5	0.5	1.0	0.6	0.8	0.8	1.1	1.1	3.6	1.2	1.8	1.4	1.3	1.1	0.4	
	0.5	0.0 0.2	0.6	0.4	0.1	0.5	0.4	0.3 0.4	0.6 0.7	0.2	0.4 0.6	0.2	1.4	0.4	0.9	0.7	0.6	0.3	2.9 0.2	
J	1.0	0.0	0.8	0.7	0.4	0.2	0.9	0.6	0.8	1.0	1.4	0.9	1.5	0.9	1.4	1.2	0.9	0.9	0.8	ļ
	0.7	0.0	0.7	0.8	0.5	0.5	0.9	0.3	0.3	1.0	0.5	0.6	2.7	0.9	0.9	0.8	0.8	0.4	0.4	0
	0.9 0.5	0.2 0.0	1.2	1.0 0.5	0.3 0.4	0.5	0.8 0.4	0.3 0.4	0.6 0.4	0.5	0.5	0.5	2.3	0.9	0.8 0.6	1.2	0.6	0.4 0.3	1.7 0.3	0
ļ	0.8	0.4	0.6	0.5	0.4	0.4	0.7	0.9	0.5	0.8	0.6	0.1	1.1	0.7	0.7	0.7	0.7	0.4	3.1	0
ļ	1.3	0.2	1.3	0.9	0.4	0.8	1.3	0.8	1.1	1.2	0.6	1.1	2.6	0.9	1.8	2.4	1.4	0.8	0.4	0
	1.4 1.5	0.3 0.5	1.1	1.5 1.4	1.3	1.3	1.2	0.6	1.0	1.2	0.9	1.0	3.5 2.0	2.6	1.5	1.5	1.3	0.8 0.9	0.5	þ
	0.9	0.0	0.9	1.4	0.4 0.2	0.8	0.8	0.5	0.8	0.6	0.3	0.7	1.8	0.9	1.6	1.1	0.7	0.6	0.2	0
ļ	1.2	0.0	0.6	0.4	0.3	0.8	0.8	1.4	0.5	0.5	1.2	1.0	0.9	1.7	1.6	1.7	1.0	3.1 0.2	0.2	-
	•																			
	A 1.6	C 0.3	D	E	F 0.5	G 1.1	H 1.2	I 0.8	K 0.7	L 0.9	M	N 0.7	р 3.6	Q 1.5	R 1.9	S	T 1.2	V 0.9	W 0.7	(
	0.2	0.2	0.5	0.3 0.9	0.0	0.2 0.8	0.0	0.1	0.0 0.4	0.2 0.8	0.2	0.3	0.6	0.8	0.2	0.2	0.3	0.3	0.0	0
	1.0	0.1	0.8	0.7	0.5	0.9	1.0	0.7	0.5	0.7	0.9	0.5	3.3	1.3	1.3	1.4	1.2	0.9	0.7	0
	1.3	0.3	0.6	1.0	0.1	0.3	1.2	0.3	0.3	0.3	1.0	0.3	2.0	0.5	1.1	1.2	0.3	0.4	0.6	0
ļ	1.8 0.7	0.6 0.0	1.3	1.4 0.4	0.4	1.0 0.4	0.9	0.6	0.8	0.7	0.5	0.7	1.6 0.9	1.2 0.4	1.1 0.9	1.2	1.2 0.3	0.9	0.3	0
	0.5	0.6	0.4	0.4	0.1	0.3	1.0	0.2	0.2	0.3	0.3	0.2	1.7	0.6	0.9	0.7	0.6	0.6	0.1	0
	0.6	0.1	0.7	0.6	2.2	0.5	0.7	0.1	0.5	0.6	0.5	0.5	2.0	0.8	1.0	0.8	0.8	0.3	0.4	6
	0.8	0.9	0.6	0.6 2.3	0.4	0.3	0.5	0.9	0.1	0.6	1.4	0.4	0.5 4.4	0.3	0.6 3.6	0.6	0.6	0.4	1.1	0
	1.3	0.1	0.9	0.8	1.1	0.8	1.8	0.7	0.5	1.1	0.9	0.6	2.5	1.6	1.7	1.2	0.8	1.0	1.8	ļ
	1.7	0.4	1.3	1.6	0.4	1.2	1.3	1.0	1.0	1.2	1.5	0.8	2.3	1.4	2.0	1.3	1.5	0.9	0.5	0
	1.0	0.4	1.4	0.4	0.3	0.7	0.9	0.3	0.5	0.8	0.8	0.4	1.8	0.8	0.9	1.5	0.5	0.6	1.2	Ì
	0.1 0.4	0.0 0.2	0.1	1.1 0.5	0.1 0.2	0.3 0.2	0.3 0.4	0.4 0.2	0.3 0.1	1.4 0.4	0.7	0.9 0.1	0.3 0.8	1.3 0.6	0.6 0.2	1.2	0.2	0.5 0.6	0.0	0
))	с	D	Е	F	G	н	ī	к	L	м	N	р	0	R	s	т	v	w	
1	1.3	0.5	1.0	1.4	0.5	1.1	0.9	0.5	0.7	0.5	0.5	0.6	2.6	1.0	1.1	1.4	0.8	0.7	1.1	0
	0.3	1.0	0.0	1.1	0.2	0.1	1.2	1.6	0.3	1.0	1.0	0.9	1.4	1.1	1.0	1.4	1.0	0.9	5.2	
	1.3	0.3 0.2	1.3	1.8 0.8	1.3 0.2	1.5 0.2	1.7	1.2 0.4	1.5 0.7	1.0	0.8 0.3	1.3 0.6	3.1	1.8 1.5	1.3 0.9	1.6 0.7	1.2 0.6	0.8	1.2 0.4	1
	0.8	0.3	0.6	0.9	0.4	0.7	0.9	0.7	0.6	0.6	1.0	0.6	1.1	1.1	0.9	1.2	0.6	0.7	0.6	0
	0.5	0.3	0.7	1.1	0.3	0.2	1.7	0.4	0.9	0.4	0.4	1.7	1.4	2.0	1.2	0.9	0.6	0.4	1.1	0
	0.8 0.6	0.5 0.2	1.0	1.3	0.4 0.4	0.6 0.3	2.0	0.9 0.4	1.2 0.5	0.7	0.8	1.3	2.0 2.6	1.5	1.1 0.7	1.3	1.1 0.6	0.7	2.4 0.5	0
	0.4	0.3	0.7	0.9	0.2	0.3	1.1	0.5	0.6	0.4	0.5	0.7	1.4	0.7	0.6	0.7	0.5	0.4	0.7	
	2.6	0.7	2.2	1.8	1.2	1.6	1.6	1.3	1.8	2.0	1.2	3.7	5.9	2.4	2.7	2.6	1.8	2.2	2.5	ĥ
ļ	1.4 1.2	0.0 0.3	1.7	1.9 1.5	1.1 0.5	1.0 0.7	2.2	1.2	1.9 1.2	1.1	1.2 1.2	1.3	3.5 2.6	1.8 1.3	1.8	1.6 1.8	1.9 1.2	1.0	1.7 0.9	1
	1.4	0.9	1.4	1.5	0.9	1.0	1.8	0.9	1.2	1.0	1.2	1.4	2.7	1.7	1.6	1.5	1.2	0.8	2.4	ļ
	0.4	0.3	0.6	1.1	0.3	0.3	1.1	0.3	0.8	0.4	0.4	0.7	1.8	1.7	0.9	0.9	0.6	0.3	0.4	6
	0.5	0.5	1.3 0.6	1.9 0.9	0.6	4.5 0.4	3.5	0.3	1.5	0.4	0.3 0.7	4.3 0.6	1.0	4.1	2.6	3.4 0.9	1.1 0.6	0.2	0.0	0
		r	р	г	F	6	п		ĸ	T.	м	N	р	0	p	¢	т	v	w	,
1	1.2	0.7	0.8	1.0	0.6	0.9	1.3	0.7	0.8	0.9	1.0	0.7	3.5	1.6	1.7	1.6	1.1	1.0	0.4	(
	0.5	0.9 0.3	0.6 0.7	0.7	0.2	0.3 0.4	0.5	0.1	0.9 0.6	0.5	0.2	0.2	0.9	0.7	0.8	0.5	0.5	0.5	0.2	0
	0.9	0.4	0.7	0.6	0.6	1.0	1.7	1.0	0.8	1.1	0.9	0.8	2.6	1.4	1.3	1.4	1.3	1.1	0.7	(
	0.8	0.8	0.7	0.8	0.5	0.6	1.0	0.5	0.4	0.6	1.3	0.5	1.6	1.0	0.7	0.8	0.6	0.7	0.3	0
	1.7 0.5	0.3	1.0 0.8	1.2 0.8	0.9	0.9	1.4	0.9	0.9 0.6	1.3 0.5	1.0 0.9	1.0 1.0	1.9 1.3	1.3	1.1 0.5	1.7	1.0	1.3 0.4	0.8 0.4	1
	0.7	0.3	0.5	0.6	0.3	0.4	0.8	0.7	0.7	0.6	0.4	0.5	2.3	0.8	0.9	0.9	0.9	0.8	0.9	0
i	0.8	1.0	0.9	1.0	0.2	0.5	0.7	0.3	0.5	0.6	0.7	0.4	1.4	0.7	0.7	0.8	0.7	0.4	0.5	ć
	0.8	0.4	0.9	0.6	0.5	0.3	1.1 2.1	0.7	0.7	0.7	0.6	0.6	5.5	0.8	0.7	1.0 3.0	0.9	0.7	1.8 0.4	0
	1.4	0.6	1.2	1.3	1.0	0.8	1.6	1.0	1.0	1.0	1.3	1.1	3.3	1.6	1.7	1.4	1.7	1.6	3.2	1
	1.5	0.7	1.2	1.4	0.5	0.9	1.8	0.8	1.2	1.2	1.0	0.8	2.8	1.9	2.0	1.5	1.7	1.2	0.5	0
	1.2	0.6 0.4	0.8	1.1 0.9	0.5	0.7	1.1 0.9	0.6 0.6	0.7 0.7	0.9	0.5	0.7	2.2 2.0	1.5 1.4	1.5	1.3	1.1 0.9	0.8	0.6 0.4	0
6	0.6	0.3	1.6	1.3	0.3	0.6	0.5	0.9	0.4	0.4	1.2	0.5	0.5	1.1	1.1	0.9	0.4	0.7	0.0	0

Fig. 1. Dipeptide propensity for the entire set of linkers. Vertical and horizontal sides of each matrix indicate the N- and C-side residue of each dyad, respectively. Cells containing propensity values ≥ 1.1 and ≤ 1.99 or ≥ 2.0 and ≤ 3.99 or ≥ 4.0 are shaded with very light, light or dark grey respectively and numbers therein contained are boldfaced. A, B, C, D and E denote propensities for Actinobacteria, Alphaproteobacteria, Betaproteobacteria, Firmicutes and Gammaproteobacteria, respectively.

4				~	-	2							~	6		~	~		11
П	A 1.0	0.2	1.0	E 1.3	F 0.4	G 1.4	H 0.6	0.4	6.4	L 1.0	M 0.3	0.2	4.3	1.2	R 1.4	S 1.5	1.7	V 0.9	W 0.6
	0.0	0.0	0.5	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.4	0.4	0.5	0.0	1.6
	1.2	0.0	0.9	0.5	0.3	0.8	0.0	0.4	0.0	0.7	0.8	0.0	1.0	2.3	1.1	0.8	2.2	0.8	0.6
P	1.0	0.0	0.6	0.5	0.2	2.7	0.7	0.1	0.2	0.3	0.0	0.5	4.8	0.2	0.8	0.7	1.1	1.1	0.0
1	0.7	0.0	0.6	0.6	0.0	0.2	0.0	0.3	0.0	0.1	0.0	0.0	0.4	0.4	0.5	0.6	0.7	0.1	0.0
P	1.0	0.0	0.7	1.1	1.1	1.3	1.3	0.4	0.3	0.8	0.7	0.0	1.7	0.6	1.2	1.4	1.0	1.4	0.5
1	0.7	0.0	0.9	0.6	0.0	0.5	0.0	0.2	0.0	0.1	0.0	0.0	1.9	0.3	0.7	0.2	0.2	0.2	0.0
6	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.1	0.0	0.0	2.0	0.4	0.4	0.0	0.4	0.3	0.0
1	0.5	0.0	0.4	0.6	0.0	0.5	0.5	0.2	0.0	0.2	0.6	0.1	3.4	0.0	0.6	0.6	0.6	0.2	0.0
19	0.2	0.0	0.3	0.8	0.0	0.0	0.7	0.0	0.0	0.2	0.0	0.0	1.1	0.0	0.4	0.4	0.0	0.6	0.0
Ľ	0.3	0.0	2.0	0.3	0.9	2.0	0.0	0.0	0.0	0.3	0.0	0.0	0.3	2.0	1.3	0.7	1.2	0.2	0.0
F	0.8	0.0	2.0	2.1	0.7	2.9	2.5	1.7	1.6	0.2	1.0	0.4	2.1	0.4	1.4	2.5	0.3	2.7	1.4
1	0.9	0.3	1.4	1.3	0.4	1.7	0.5	1.2	0.4	0.6	0.5	0.7	4.1	0.4	1.3	1.3	1.8	1.2	0.9
ĥ	1.2	0.0	0.8	1.1	0.5	1.1	1.2	0.5	0.2	0.7	1.7	0.4	1.8	0.5	2.2	0.7	1.9	0.7	0.5
D	1.7	1.0	0.5	1.4	0.6	1.1	0.7	0.4	0.2	0.4	0.3	0.2	3.3	0.9	1.4	1.0	1.6	1.2	0.0
	1.0	0.7	0.6	1.0	0.3	0.6	0.5	0.0	0.0	0.5	0.0	0.0	4.0	0.4	0.6	0.8	0.5	0.2	0.5
	0.2	0.0	0.0	0.8	0.5	0.5	0.0	0.0	0.0	0.3	0.0	0.0	0.3	0.9 0.0	1.2 0.0	1.7 0.5	0.0	0.0	0.0
3																			
Γ	A 1.3	C 0.0	D 1.5	E 1.4	F 0.2	G 1.5	H 0.8	0.3	K 0.6	L 0.7	M 0.8	N 0.8	P 3.5	Q 0.9	R 2.1	S	T 1.1	0.7	W 0.0
1	0.0	0.0	0.0	0.0	1.1	0.0	0.0	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7	0.0
	1.0	0.0	1.3	1.4	0.2	1.5	1.3	0.6	1.5	1.0	0.4	0.3	3.4	1.7	2.0	1.2	0.6	1.2	0.0
	1.6	1.1	0.9	1.4	0.7	1.4	0.4	0.8	0.6	0.2	0.4	0.9	4.9	1.7	1.9	1.2	2.1	2.1	0.0
1	0.3	0.0	0.3	0.0	0.0	0.0	0.6	0.5	1.1	0.0	1.3	0.0	0.8	0.4	0.7	0.5	0.2	0.3	0.0
	1.5	0.0	03	1.0	0.0	0.2	0.5	0.9	0.7	0.2	2.4	0.2	1.0	1.3	1.2	2.8	1.2	0.3	2.4
	0.3	0.0	0.1	0.5	0.2	0.4	0.5	0.4	0.0	0.2	0.0	0.5	2.1	0.6	0.9	0.6	0.2	0.2	0.0
1	0.8	0.0	0.2	0.7	0.0	0.7	2.0	0.2	0.0	0.1	0.7	0.7	2.0	0.0	0.6	1.0	0.6	0.2	0.0
	0.4	0.0	1.1	0.5	0.1	1.0	0.2	0.2	0.0	0.0	0.4	0.3	2.1	1.2	0.5	0.5	0.2	0.1	0.0
1	0.4	0.0	0.4	0.0	0.6	0.5	0.0	0.3	0.4	1.2	0.7	0.0	1.5	1.0	0.2	0.3	0.2	0.0	0.0
E	2.9	0.0	2.7	1.5	0.0	2.0	2.5	0.0	0.0	0.6	0.0	0.0	0.7	3.2	4.3	2.8	1.6	0.4	0.0
Į.	2.1	0.0	15	3.8	0.7	0.3	0.6	1.5	0.3	0.3	0.0	0.8	33	1.4	15	1.5	2.5	0.6	1.0
Fi i	1.8	0.6	1.4	1.6	0.3	1.5	1.6	0.7	0.7	1.1	1.2	0.6	4.0	1.2	2.4	1.8	1.7	1.1	0.8
[i	1.5	0.0	1.9	2.8	1.2	1.8	0.4	0.4	0.7	0.3	0.8	0.2	2.2	1.5	1.6	1.6	0.5	0.5	0.5
0	0.8	0.0	1.5	2.5	0.4	1.3	0.8	0.6	0.8	0.6	0.4	0.3	1.1	1.0	1.8	1.4	0.8	0.5	0.0
1	0.8	0.0	0.6	0.9	0.0	0.7	1.0	0.0	0.6	0.1	0.0	0.2	1.9	1.0	0.6	0.5	1.0	0.0	0.5
	0.0	0.0 0.0	0.0 0.0	0.0	1.6 0.4	0.5 0.4	0.0 0.9	0.0	0.9 0.0	0.0	0.0 0.0	0.0 0.0	0.6 0.4	0.7 1.0	1.0 0.5	0.4 0.0	0.0 0.0	0.0 0.5	0.0 0.0
;																			
Γ	A 1.1	C 0.0	D 1.7	E 1.1	F 0.2	G 1.5	H 1.8	1	K 0.2	L 1.0	M	N 0.5	P 3.5	Q 1.8	R 1.6	S	T	V 1.3	W 1.2
0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
[]	1.1	0.0	0.8	1.5	0.0	1.1	1.4	0.3	0.4	1.3	2.4	0.0	1.6	5.2	1.3	0.8	3.0	0.2	0.0
1	1.7	0.0	0.0	0.3	0.0	3.5	1.1	1.1	0.4	1.9	2.2	0.5	3.1	4.3	0.7	0.8	3.1	0.4	3.1
0	0.6	0.0	0.3	0.4	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.7	0.0	0.3	0.0	0.0	0.0
	1.0	0.0	1.1	3.4	0.5	3.1	11	1.8	0.7	1.0	2.1	0.3	1.9	0.7	0.8	1.5	1.2	2.4	0.0
6	0.4	0.0	1.9	0.5	0.0	0.2	0.8	0.0	0.0	0.4	0.0	0.0	1.1	0.5	0.5	0.8	0.3	0.0	0.0
10	0.6	0.0	0.5	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.0	1.3	0.0	0.7	1.7	0.0
	1.0	0.0	0.7	0.6	0.0	0.9	1.0	0.0	0.0	0.0	0.0	0.0	2.8	0.6	0.8	0.8	0.7	0.1	0.6
0	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	0.0	0.0	2.0	2.1	0.4	1.4	0.0	0.0	0.0
0	0.6	0.0	0.9	0.0	0.0	0.3	0.0	0.0	0.0	0.5	0.0	0.0	0.4	0.0	0.0	0.4	0.4	0.4	0.0
2	2.5	0.0	1.2	1.2	0.4	4.0	1.4	0.8	3.6	2.0	0.8	1.6	3.9	2.6	7.2	2.7	1.2	0.9	0.0
Lí	1.2	0.0	0.2	2.0	0.0	2.7	0.4	0.2	0.7	0.7	0.5	0.0	3.7	1.4	0.6	0.9	1.3	1.0	0.0
1	1.6	0.0	0.7	0.5	0.3	2.0	0.6	0.3	0.0	0.9	0.6	0.8	2.9	1.4	0.4	1.4	1.1	0.5	0.0
1	1.8	0.0	0.3	2.5	0.8	0.6	1.3	0.0	0.0	0.9	0.8	0.5	1.8	3.4	0.5	0.7	1.7	0.7	0.0
1	1.1 0.0	0.0 0.0	1.7	1.4 0.0	0.6	0.3	0.0 0.0	0.0	0.0	0.2	0.0	0.0 4.7	1.3	0.3	0.5	0.3	0.9 1.0	0.1	0.0
L	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	4.1	0.0	1.3	0.0	0.0	1.1	0.0	0.0	0.0
ר	A	с	D	E	F	G	Н	1	К	L	M	N	Р	Q	R	s	T	V	W
	0.6	2.0	0.7	0.0	0.8	0.4	0.0	0.0	0.0	0.0	1.6	0.0	0.0	0.0	0.7	0.5	0.0	0.0	0.0
0	0.6	1.4	1.1	0.8	1.0	1.4	4.3	0.7	1.4	0.7	1.6	2.4	0.9	0.7	1.3	3.1	2.7	1.8	1.7
0	0.7	0.0	2.1	2.9	0.3	2.0	2.3	0.6	2.0	0.5	0.3	2.6	2.1	1.4	LI	2.2	1.2	1.5	0.5
19	0.4	0.0	0.8	0.3	0.5	0.1	0.9	0.3	0.6	0.3	0.4	0.7	1.6	1.1	0.5	0.0	0.5	0.3	0.0
Ľ	1.0	0.5	2.1	2.9	0.7	0.5	1.7	0.5	1.5	0.6	0.0	2.0	1.7	4.3	0.7	1.0	0.9	2.2	0.0
1	0.5	0.4	0.5	0.5	0.6	0.1	0.0	0.3	0.5	0.2	0.3	0.3	0.7	0.8	0.4	2.1	1.5	0.0	0.0
b	1.3	0.0	1.6	1.8	0.0	0.6	3.1	1.0	1.7	0.6	1.1	2.4	2.8	1.9	1.2	1.8	1.4	0.5	0.0
0	0.3	0.7	0.2	0.6	0.2	0.2	0.9	0.2	0.2	0.8	0.2	0.7	1.5	0.6	0.3	0.8	0.7	0.3	0.0
1	0.0	0.0	0.6	0.9	0.0	0.5	0.9	0.4	0.2	0.0	0.6	1.3	1.2	0.0	0.7	0.2	0.3	0.0	0.0
1	5.1	0.8	1.9	1.9	0.2	2.0	3.6	1.5	2.0	1.6	2.8	2.5	1.7	1.7	1.4	2.4	2.3	1.8	0.0
E	1.1	0.0	2.5	2.2	0.0	1.3	1.2	0.3	1.7	0.2	0.0	2.1	2.2	1.5	0.7	1.2	1.6	1.6	1.9
	0.9	0.0	1.1	1.4	0.2	0.5	1.4	0.4	0.9	0.4	0.8	1.7	2.3	0.2	0.7	3.9	1.3	0.5	0.0
1	2.1	0.6	3.0	2.1	0.6	1.0	3.1	1.3	2.1	0.4	2.5	2.6	2.4	2.0	1.5	1.8	2.3	1.2	0.0
10	0.9	0.8	1.6	1.7	0.5	0.9	2.6	1.7	1.5	0.6	1.0	2.4	1.8	0.4	0.8	2.8	0.8	0.4	0.7
19	0.4	0.5	0.2	0.9	0.7	0.2	1.4	0.3	0.7	0.2	0.0	1.6	1.3	0.9	0.9	1.0	0.7	0.2	0.0
1.0	0.0	0.0	0.0	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4 0.0	0.8	1.5	0.0	0.0	0.0	0.0
L																			
L		с	D	E	F	G	Н	1	K	L	M	N	P	Q	R	s	T	V	W
	A	0.2	1.3	0.8	0.8	1.5	1.5	1.1	0.3	1.1	0.9	1.2	2.3	1.7	0.9	2.1	1.6	1.0	0.2
	A 1.1	0.3		0.0	0.0	0.5	13	1.1	0.7	0.5	2.9	0.0	1.4	5.0	1.5	1.5	0.0	2.0	0.0
	A 1.1 0.3	0.3	1.5		- M.C.	2.4	1.2	1.0	0.9	0.9	0.5	0.9	1.6	2.0	1.2	1.5	3.2	1.0	0.8
	A 1.1 0.3 1.0 1.3	0.3 0.0 0.0 0.6	1.5	1.7	0.1	2.4		0.2	0.2	0.2	0.4	0.6	0.4	1.6	2.1	0.7	0.5	0.3	0.0
	A 1.1 0.3 1.0 1.3 0.2	0.3 0.0 0.0 0.6 0.5	1.5 1.2 1.0 0.7	1.7	0.1	0.2	4.1		1.4	1.3	3.8	0.6	1.8	1.4	0.2	1.6	0.8	1.0	
	A 1.1 0.3 1.0 1.3 0.2 0.8	0.3 0.0 0.0 0.6 0.5 0.0	1.5 1.2 1.0 0.7 1.0	1.7 0.9 1.0	0.1 0.0 1.1	0.2	3.0	2.0			0.0	14	33						0.8
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9	0.3 0.0 0.6 0.5 0.0 0.9	1.5 1.2 1.0 0.7 1.0 2.2	1.0 1.7 0.9 1.0 1.5	0.1 0.0 1.1 0.5	0.2 1.0 3.6	2.1 3.0 1.6	2.0 0.5	0.7	1.7	0.0		0.00	1.5	0.6	2.0	0.8	1.6	0.8
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5	0.3 0.0 0.0 0.6 0.5 0.0 0.9 1.3	1.5 1.2 1.0 0.7 1.0 2.2 1.7	1.0 1.7 0.9 1.0 1.5 0.7	0.1 0.0 1.1 0.5 0.0	0.2 1.0 3.6 0.2	2.1 3.0 1.6 1.2	2.0 0.5 0.5	0.7	1.7 0.5	0.7	0.3	0.5	1.5	0.6	2.0 1.0	0.8	1.6	0.8
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 0.7	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7	1.0 1.7 0.9 1.0 1.5 0.7 1.0	0.1 0.0 1.1 0.5 0.0 0.4	0.2 1.0 3.6 0.2 0.8	2.1 3.0 1.6 1.2 0.8	2.0 0.5 0.5 0.0	0.7 0.7 0.2	1.7 0.5 0.7	0.7	0.3	0.5	1.5 2.0 2.2	0.6 0.7 0.2	2.0 1.0 1.3	0.8 0.5 0.4	1.6 0.3 0.8	0.8 0.0 0.0 0.0 0.5
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 0.7 1.0	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4	0.2 1.0 3.6 0.2 0.8 1.1	2.1 3.0 1.6 1.2 0.8 0.4 0.2	2.0 0.5 0.5 0.0 0.4 0.2	0.7 0.7 0.2 0.8	1.7 0.5 0.7 0.3	0.7 0.0 0.1	0.3 0.5 0.6	0.5 0.9 2.8	1.5 2.0 2.2 0.8 0.3	0.6 0.7 0.2 0.2	2.0 1.0 1.3 0.7	0.8 0.5 0.4 0.4	1.6 0.3 0.8 0.1	0.8 0.0 0.0 0.5 0.0
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 0.7 1.0 0.6	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0 0.0	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.5	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0	2.0 0.5 0.5 0.0 0.4 0.2 0.2	0.7 0.7 0.2 0.8 0.0 0.6	1.7 0.5 0.7 0.3 0.9 0.6	0.0 0.7 0.0 0.1 0.5 0.4	0.3 0.5 0.6 0.0	0.5 0.9 2.8 0.5 0.6	1.5 2.0 2.2 0.8 0.3 1.0	0.6 0.7 0.2 0.2 0.2 0.2	2.0 1.0 1.3 0.7 1.0 1.0	0.8 0.5 0.4 0.4 0.4 0.4 0.4	1.6 0.3 0.8 0.1 0.4 1.0	0.8 0.0 0.0 0.5 0.0 1.5
	A 1.1 1.3 0.2 0.8 1.9 0.5 0.7 1.0 0.6 2.2	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0 0.0 0.0 0.0	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.5 0.3	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3	2.0 0.5 0.5 0.0 0.4 0.2 0.2 0.3	0.7 0.7 0.2 0.8 0.0 0.6 1.3	1.7 0.5 0.7 0.3 0.9 0.6 1.7	0.0 0.7 0.0 0.1 0.5 0.4	0.3 0.5 0.6 0.0 1.1 1.4	0.5 0.9 2.8 0.5 0.6 6-1	1.5 2.0 2.2 0.8 0.3 1.0 2.0	0.6 0.7 0.2 0.2 0.2 0.9 1.6	2.0 1.0 1.3 0.7 1.0 1.0 1.0 2.0	0.8 0.5 0.4 0.4 0.4 0.4 0.6 1.0	1.6 0.3 0.8 0.1 0.4 1.0 1.5	0.8 0.0 0.0 0.5 0.0 1.5 0.0
	A 1.1 0.3 1.0 0.2 0.8 1.9 0.5 0.7 1.0 0.6 2.2 2.6	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0 0.0 0.0 0.0 0.0 0.7	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5 1.6	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2 2.3	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.5 0.3 0.7	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9 1.8	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3 3.6	2.0 0.5 0.0 0.4 0.2 0.2 0.3 0.6	0.7 0.7 0.2 0.8 0.0 0.6 1.3 0.9	1.7 0.5 0.7 0.3 0.9 0.6 1.7 0.8	0.0 0.7 0.0 0.1 0.5 0.4 1.5 1.4	0.3 0.5 0.6 0.0 1.1 1.4 1.2	0.5 0.9 2.8 0.5 0.6 6.1 3.6	1.5 2.0 2.2 0.8 0.3 1.0 2.0 3.1	0.6 0.7 0.2 0.2 0.2 0.9 1.6 0.8	2.0 1.0 1.3 0.7 1.0 1.0 2.0 1.4	0.8 0.5 0.4 0.4 0.4 0.4 0.6 1.0 2.4	1.6 0.3 0.8 0.1 0.4 1.0 1.5 2.0	0.8 0.0 0.0 0.5 0.0 1.5 0.0 0.0
	A 1.1 0.3 1.0 0.2 0.8 1.9 0.5 0.7 0.7 1.0 0.6 2.2 2.6 1.1	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0 0.0 0.0 0.0 0.0 0.7 0.5	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5 1.6 0.6	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2 2.3 1.5	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.3 0.3 0.7 0.6	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9 1.8 0.9	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3 3.6 1.1	2.0 0.5 0.0 0.4 0.2 0.2 0.3 0.6 0.4	0.7 0.2 0.8 0.0 0.6 1.3 0.9 0.0	1.7 0.5 0.7 0.3 0.9 0.6 1.7 0.8 0.8	0.7 0.0 0.1 0.5 0.4 1.5 1.4 1.1	0.3 0.5 0.6 0.0 1.1 1.4 1.2 0.3	0.5 0.9 2.8 0.5 0.6 6.1 3.6 1.7	1.5 2.0 2.2 0.8 0.3 1.0 2.0 3.1 1.6	0.6 0.7 0.2 0.2 0.9 1.6 0.8 1.3	2.0 1.0 1.3 0.7 1.0 1.0 1.0 2.0 1.4 0.9	0.8 0.5 0.4 0.4 0.4 0.6 1.0 2.4 1.0	1.5 1.6 0.3 0.8 0.1 0.4 1.0 1.5 2.0 0.5	0.8 0.0 0.0 0.5 0.0 1.5 0.0 0.0 0.0 0.0
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 0.7 1.0 0.6 2.2 2.6 1.1 1.5	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0 0.0 0.0 0.7 0.5 0.8	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5 1.6 0.6 2.1	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2 2.3 1.5 1.6	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.5 0.3 0.7 0.6 0.2	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9 1.8 0.9 1.0	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3 3.6 1.1 2.5	2.0 0.5 0.5 0.4 0.2 0.2 0.3 0.6 0.4 0.4	0.7 0.2 0.8 0.0 0.6 1.3 0.9 0.0 1.4	1.7 0.5 0.7 0.3 0.9 0.6 1.7 0.8 0.8 0.8 1.4	0.0 0.7 0.0 0.1 0.5 0.4 1.5 1.4 1.1 1.2	0.3 0.5 0.6 0.0 1.1 1.4 1.2 0.3 0.7	0.5 0.9 2.8 0.5 0.6 6.1 3.6 1.7 1.4	1.5 2.0 2.2 0.8 0.3 1.0 2.0 3.1 1.6 1.7	0.6 0.7 0.2 0.2 0.9 1.6 0.8 1.3 2.0	2.0 1.0 1.3 0.7 1.0 1.0 2.0 1.4 0.9 1.6	0.8 0.5 0.4 0.4 0.4 0.6 1.0 2.4 1.0 1.1	1.6 0.3 0.8 0.1 0.4 1.0 1.5 2.0 0.5 0.9	0.8 0.0 0.0 0.5 0.0 1.5 0.0 0.0 0.0 0.0 0.0
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 0.7 1.0 0.6 2.2 2.6 1.1 1.5 1.2	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5 1.6 0.6 2.1 0.8	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2 2.3 1.5 1.6 1.6	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.4 0.5 0.3 0.7 0.6 0.2 1.1	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9 1.8 0.9 1.0 0.7	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3 3.6 1.1 2.5 1.0	2.0 0.5 0.0 0.4 0.2 0.2 0.3 0.6 0.4 0.4 0.4 0.4	0.7 0.7 0.2 0.8 0.0 0.6 1.3 0.9 0.0 1.4 0.4	1.7 0.5 0.7 0.3 0.9 0.6 1.7 0.8 0.8 1.4 1.1	0.0 0.7 0.0 0.1 0.5 0.4 1.5 1.4 1.1 1.2 0.7	0.3 0.5 0.6 0.0 1.1 1.4 1.2 0.3 0.7 0.8	0.5 0.9 2.8 0.5 0.6 6.1 3.6 1.7 1.4 1.6	1.5 2.0 2.2 0.8 0.3 1.0 2.0 3.1 1.6 1.7 1.3	0.6 0.7 0.2 0.2 0.9 1.6 0.8 1.3 2.0 0.4	2.0 1.0 1.3 0.7 1.0 1.0 2.0 1.4 0.9 1.6 1.6	0.8 0.5 0.4 0.4 0.4 0.6 1.0 2.4 1.0 1.1 1.0	1.6 0.3 0.8 0.1 0.4 1.0 1.5 2.0 0.5 0.9 0.7	0.8 0.0 0.0 0.5 0.0 1.5 0.0 0.0 0.0 0.0 0.0 0.0
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 1.0 0.6 2.2 2.6 1.1 1.5 1.2 1.6	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5 1.6 0.6 2.1 0.8 1.5 1.6	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2 2.3 1.5 1.6 1.6 0.7 0.9	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.5 0.3 0.7 0.6 0.2 1.1 0.6 0.2	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9 1.8 0.9 1.0 0.7 0.5 0.5	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3 3.6 1.1 2.5 1.0 0.9 0.7	2.0 0.5 0.0 0.4 0.2 0.3 0.6 0.4 0.4 0.4 0.4 1.1	0.7 0.7 0.2 0.8 0.0 0.6 1.3 0.9 0.0 1.4 0.4 0.3	1.7 0.5 0.7 0.3 0.9 0.6 1.7 0.8 0.8 1.4 1.1 0.3 0.3	0.0 0.7 0.0 0.1 0.5 0.4 1.5 1.4 1.1 1.2 0.7 0.6	0.3 0.5 0.6 0.0 1.1 1.4 1.2 0.3 0.7 0.8 0.6	0.5 0.9 2.8 0.5 0.6 6.1 3.6 1.7 1.4 1.6 1.7	1.5 2.0 2.2 0.8 0.3 1.0 2.0 3.1 1.6 1.7 1.3 0.5 0.3	0.6 0.7 0.2 0.2 0.9 1.6 0.8 1.3 2.0 0.4 1.0	2.0 1.0 1.3 0.7 1.0 1.0 2.0 1.4 0.9 1.6 1.6 1.0	0.8 0.5 0.4 0.4 0.4 0.6 1.0 2.4 1.0 1.1 1.0 0.7 0.7	1.6 0.3 0.8 0.1 0.4 1.0 1.5 2.0 0.5 0.9 0.7 0.6	0.8 0.0 0.0 0.5 0.0 1.5 0.0 0.0 0.0 0.0 0.6 0.0 0.4 0.4
	A 1.1 0.3 1.0 1.3 0.2 0.8 1.9 0.5 0.7 0.7 1.0 0.6 2.2 2.6 1.1 1.5 1.2 1.6 0.3 0.4	0.3 0.0 0.6 0.5 0.0 0.9 1.3 0.0 0.9 0.2 0.0 0.0 0.0 0.0 0.0 0.5 0.8 0.6 0.0 0.0 0.0 0.0	1.5 1.2 1.0 0.7 1.0 2.2 1.7 0.5 0.7 1.1 0.2 1.5 1.6 0.6 2.1 0.8 1.5 0.9 0.2	1.0 1.7 0.9 1.0 1.5 0.7 1.0 1.1 1.7 1.4 2.2 2.3 1.5 1.6 1.6 0.7 0.0 0.2	0.1 0.0 1.1 0.5 0.0 0.4 1.4 0.4 0.4 0.5 0.3 0.7 0.6 0.2 1.1 0.6 0.0 0.0	0.2 1.0 3.6 0.2 0.8 1.1 0.8 0.6 3.9 1.8 0.9 1.0 0.7 0.5 0.0 0.1	2.1 3.0 1.6 1.2 0.8 0.4 0.0 3.0 1.3 3.6 1.1 2.5 1.0 0.9 0.7 2.4	2.0 0.5 0.0 0.4 0.2 0.2 0.3 0.6 0.4 0.4 0.4 1.1 0.4 0.4	0.7 0.7 0.2 0.8 0.0 0.6 1.3 0.9 0.0 1.4 0.4 0.4 0.3 0.0 0.4	1.7 0.5 0.7 0.3 0.9 0.6 1.7 0.8 0.8 1.4 1.1 0.3 0.2 0.3	0.0 0.7 0.0 0.1 0.5 0.4 1.5 1.4 1.1 1.2 0.7 0.6 0.0 0.6	0.3 0.5 0.6 0.0 1.1 1.4 1.2 0.3 0.7 0.8 0.6 0.0	0.5 0.9 2.8 0.5 0.6 6.1 3.6 1.7 1.4 1.6 1.7 0.5 0.4	1.5 2.0 2.2 0.8 0.3 1.0 2.0 3.1 1.6 1.7 1.3 0.5 0.3 1.0	0.6 0.7 0.2 0.2 0.9 1.6 0.8 1.3 2.0 0.4 1.0 0.3 0.0	2.0 1.0 1.3 0.7 1.0 1.0 1.0 2.0 1.4 0.9 1.6 1.6 1.0 0.3 0.3	0.8 0.5 0.4 0.4 0.4 0.6 1.0 2.4 1.0 1.1 1.0 0.7 0.0 0.4	1.6 0.3 0.8 0.1 0.4 1.0 1.5 2.0 0.5 0.9 0.7 0.6 1.6 0.3	0.8 0.0 0.0 0.5 0.0 1.5 0.0 0.0 0.0 0.6 0.0 0.4 0.0 0.4 0.0

Fig. 2. Dipeptide propensity for the 0–20 residue length linker set. Interpretation of figure refers to legend to Fig. 1.

4																		
A C	C D 1.3 1.0	E 0.9	F 0.5	G 1.1	H 0.8	0.2	0.3	L 0.8	0.5	0.5	P 4.6	Q 1.0	R 2.2	S 1.3	T 1.1	0.9	0.7	- Y 0.0
0.3 0.	0.0 0.2	0.4	0.0	0.2	0.0	0.0	0.6	0.0	0.0	0.5	0.0	0.0	0.3	0.1	0.2	0.1	0.0	0.0
0.9 0.	0.0 0.8	0.6	0.4	1.0	0.9	0.5	0.2	1.0	0.8	0.4	1.1	0.4	1.4	0.8	1.1	1.1	0.6	1.4
0.4 0.	0.0 0.4	0.5	0.2	0.5	0.3	0.0	0.0	0.3	0.0	0.3	0.4	0.7	0.8	0.7	0.5	0.3	0.6	0.
1.4 0.	.5 0.7	0.8	0.3	0.7	0.7	0.4	0.3	0.6	0.2	0.4	2.6	0.5	1.4	1.1	1.2	0.7	1.5	0.3
0.9 0.	0.0 1.2	0.7	0.3	0.7	0.4	0.5	0.0	1.0	0.0	0.6	1.9	0.9	1.1	1.1	0.8	0.6	0.0	0.4
0.4 1.	.2 0.2	0.6	0.0	0.1	0.8	0.4	0.5	0.3	0.0	0.6	2.1	0.1	0.5	0.1	0.3	0.4	0.0	0.0
0.4 0.	0.0 0.6	0.5	0.7	0.7	1.2	0.3	0.5	0.4	0.2	0.3	2.2	0.3	0.8	0.9	0.4	0.3	0.4	0.3
0.3 0.	0.0 0.2	0.1	0.7	0.1	0.0	0.0	0.0	0.2	0.5	0.2	0.8	0.7	0.6	0.4	0.2	0.1	0.4	0.
4.0 1.	.0 2.3	2.1	0.4	2.5	2.9	1.2	2.1	1.8	1.4	1.6	6.2	2.5	5.6	2.4	2.7	2.2	0.7	0.
1.0 0.	0.0 0.6	0.4	0.1	0.8	0.8	0.3	0.6	0.6	0.0	0.3	2.2	0.7	1.3	1.0	3.1	0.5	0.0	0.
2.0 0.	0.1 1.0	0.7	0.4	1.2	0.8	0.7	0.6	0.8	0.4	0.7	5.0	1.2	1.6	2.1	2.0	0.9	0.5	1.
1.6 0.	0.0 0.9	0.8	0.3	0.8	0.9	0.2	0.4	0.5	0.6	0.7	3.1	1.0	1.9	1.3	1.2	0.7	0.3	0.
0.9 0.	0.0 0.7	0.4	0.6	0.5	0.4	0.1	0.2	0.2	0.4	0.4	2.2	0.4	1.2	0.7	0.7	0.5	0.3	0.
0.2 0. 0.4 0.	0.0 0.4	0.4 0.5	0.0 0.0	0.1 0.8	0.2 0.7	0.3	0.2 0.2	0.7 0.1	0.3 0.0	0.2 0.2	0.2	7.2 0.5	0.4 0.9	0.5	0.8 0.1	0.0 0.1	0.0 0.0	0. 0.
3																		
A C	C D	E 1.4	F 0.2	G 0.9	H 0.9	1	K 0.7	L 0.8	M 0.9	N 0.5	P 4.1	Q 1.0	R 1.0	S 1.3	T 0.8	V 1.4	W 0.6	9 0.
0.0 0.	0 0.0	0.3	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.3	0.9	2.4	0.2	0.3	0.0	0.0	0.
1.6 0.	.0 1.0	0.9	0.3	0.7	0.8	1.2	0.4	0.8	1.9	0.6	3.7	1.5	1.5	1.2	1.4	1.3	0.2	0.
0.5 0.	.0 0.6	0.4	0.2	0.5	0.5	0.4	0.3	0.2	0.6	0.1	0.9	0.6	0.1	0.7	0.2	0.4	6.5	0.
0.7 0.	0.0	1.3	0.1	0.8	1.1	0.4	0.6	0.3	0.7	0.6	3.4	0.9	0.8	0.6	0.9	0.6	0.1	0.
0.5 0.	.0 1.5	0.9	0.1	0.8	0.4	0.2	0.3	0.3	0.5	0.4	1.0	0.7	0.4	0.8	0.4	0.4	0.4	0.
0.6 0.	.0 0.4	0.9	0.0	0.3	0.6	0.1	0.2	1.0	0.2	0.5	1.2	1.0	0.7	0.4	1.0	0.6	0.0	0.
1.2 0.	1.4 1.8	1.5	0.4	0.4	1.0	0.2	0.6	0.8	0.5	0.4	2.3	1.0	0.7	1.0	0.7	0.4	3.7	0.
0.6 0.	.4 0.5	0.3	0.7	0.4	0.7	0.5	0.5	0.5	0.3	0.0	1.2	0.4	0.8	0.8	0.7	0.4	0.5	1.
2.5 0.	.6 2.3	2.4	3.3	1.6	2.7	1.6	2.4	4.5	1.6	0.9	6.6	3.0	3.8	2.4	2.0	2.0	0.7	0.
1.3 0.	5 1.2	0.8	0.4	0.9	2.3	0.6	0.6	1.5	0.7	1.0	2.2	0.8	1.5	3.8	1.1	0.8	0.0	0.
1.4 0.	0 0.8	1.3	0.0	0.8	1.0	0.5	0.5	2.5	1.0	0.8	2.2	4.0	2.7	1.2	0.6	1.1	0.2	0.
0.9 0.	.0 0.7	1.1	0.3	0.8	0.6	0.5	0.4	0.6	0.5	0.6	2.0	1.0	1.5	1.1	0.6	0.5	0.4	0.
1.0 0.	.0 2.2	0.8	0.1	0.5	0.7	0.4	0.4	0.3	0.4	0.2	2.0	0.9	0.5	2.0	0.5	0.4	1.4	0.
0.2 0.	0.0 0.0	0.0	0.0 0.1	0.3	0.0	2.9 0.3	0.0	0.8	1.2	0.5	0.9	1.2	0.3	0.5	0.2	6.7 0.1	0.0	0.
•																		
	C D	E	F	G	н	1	K	L	M	N	P	Q	R	5	T	V	W	1
0.4 0.	0.5 0.7	1.2	0.0	0.8	0.0	0.5	0.7	0.9	0.0	0.4	0.6	0.9	0.1	0.3	0.5	0.9	0.0	0.
1.0 0.	0.0 0.8	1.0	1.0	0.6	1.9	1.0	0.4	0.8	0.8	0.8	2.1	0.8	1.4	1.7	1.1	1.7	1.0	0.
0.9 0.	0.2 1.2	0.9	0.5	0.7	1.3	0.7	0.4	0.7	1.1	0.7	3.0	1.5	1.2	1.6	1.4	1.1	0.7	0.
0.8 0.	0.1 0.6	1.0	0.1	0.5	1.2	0.4	0.2	0.5	0.9	0.5	2.3	0.4	1.1	0.7	0.5	0.2	0.6	0.
1.9 1.	1.0 1.4	0.9	0.3	0.4	0.7	0.9	0.9	0.8	0.6	0.4	1.6	0.9	1.2	1.7	1.2	0.8	0.2	0.
0.4 0.	0.0 1.0	0.5	1.1	0.3	0.3	0.1	0.2	0.6	0.2	0.4	0.9	0.3	1.0	0.7	0.2	0.4	0.7	0.
0.5 0.	0.0 0.5	0.3	0.1	0.4	0.7	0.3	0.2	0.4	0.0	0.3	1.5	0.7	0.6	0.8	0.4	0.5	0.0	0.
0.4 0.	0.0 1.4	0.6	2.6	0.7	0.9	0.0	0.3	0.4	0.2	0.1	1.8	0.4	1.3	0.9	1.0	0.3	0.5	0.
0.8 1.	1.6 0.4	0.6	0.3	0.1	0.9	0.4	0.1	0.7	1.6	0.3	0.6	0.4	0.8	0.5	0.5	0.3	0.6	0.
1.3 0.	0.8 2.1	0.7	1.1	0.7	1.8	0.8	0.3	1.3	0.4	0.7	4.9	1.2	3.9	2.6	0.9	1.2	0.4	0.
1.7 0.	0.2 1.0	1.6	0.4	1.3	1.1	0.6	0.7	1.2	1.1	1.3	3.5	1.7	1.5	1.7	1.2	1.3	1.0	0.
1.6 0.	0.6 1.8	1.4	0.6	1.0	1.7	1.1	0.6	1.5	1.8	0.7	2.4	1.1	2.2	1.5	1.5	0.9	0.9	0.
1.3 0.	0.6 0.5	0.8	0.3	0.6	0.8	0.3	0.6	0.8	0.6	0.4	1.8	1.2	1.5	1.1	0.6	0.7	0.8	0.
0.2 0.	0.0 1.1	1.0	0.2	0.2	0.2	0.9	0.0	2.4	1.4	1.0	0.4	0.7	0.5	1.0	0.1	0.8	0.0	1.
0.3 0.	0.3 0.1	0.7	0.1	0.2	0.2	0.0	0.0	0.4	0.5	0.0	0.5	0.6	0.3	0.8	0.1	0.2	0.2	0.
),	СЪ	E	F	G	н	I	к	L	М	N	Р	Q	R	s	т	v	W	Y
1.2 0.	.6 0.8	1.2	0.6	0.5	0.9	0.5	0.7	0.6	0.5	0.4	3.5	1.2	1.0	1.3	0.7	0.7	0.6	1.
0.4 0.	0 0.5	0.7	0.4	0.1	0.3	0.3	0.4	0.6	0.3	0.4	0.3	1.0	0.4	0.2	0.4	0.1	1.1	0.
1.2 0.	13 1.4	2.3	0.9	1.5	2.1	1.4	1.7	1.1	1.0	1.5	4.1	2.2	1.4	1.7	1.5	1.0	1.5	1.
0.5 0.	.2 0.6	1.2	0.2	0.1	0.9	0.5	1.0	0.4	0.2	0.6	1.2	1.4	1.1	0.7	0.5	0.2	0.0	0.
0.6 0.	0.5	0.8	0.3	0.3	0.9	0.4	0.5	0.6	0.3	0.3	1.0	1.0	0.6	0.8	0.5	0.4	0.4	0.
0.6 0.	.2 0.9	1.4	0.3	0.2	1.8	0.4	1.1	0.5	0.1	1.4	1.8	1.9	1.1	1.0	0.6	0.6	0.1	0.
0.6 0.	.6 0.9	1.8	0.5	0.6	1.6	1.0	1.7	0.9	0.8	1.2	2.4	1.9	1.2	1.2	1.5	0.8	0.8	0.
0.5 0.	0.2 0.9	1.4	0.4	0.3	1.3	0.4	0.7	0.4	0.3	0.9	2.8	1.2	0.8	1.0	0.6	0.2	0.6	0.
0.3 0.	.3 0.6	0.8	0.4 1.1	0.3	0.6	0.3	0.5	0.6	0.6	0.6	1.7	0.7	0.7	0.7	0.4	0.2	0.3	0.
3.7 1.	.3 1.7	2.5	1.3	1.4	1.3	2.0	2.6	2.5	1.5	1.5	6.0	3.4	3.0	3.2	2.1	3.0	0.7	1.
1.4 0.	.0 1.8	1.9	1.2	1.1	2.9	1.5	2.1	1.2	1.1	1.0	3.8	1.8	1.9	2.0	1.8	1.2	0.9	1.
0.9 0.	3 1.4	1.9	0.4	0.4	1.3	0.7	1.4	0.7	1.1	0.9	2.9	1.6	1.2	1.5	1.0	0.7	0.4	0.
0.7 0.		1.5	0.7	0.5	0.8	0.7	1.2	0.7	0.5	0.9	2.0	1.4	0.6	1.4	0.7	0.5	0.9	1.
0.5 0.	.5 0.5	1.3	0.2	0.3	1.3	0.5	0.8	0.5	0.5	0.5	2.1	1.7	1.0	0.9	0.8	0.5	0.5	0.
0.3 0.	0.5 0.6 0.1 0.7	0.6 1.0	0.6 0.7	0.6 0.2	0.8 1.5	0.1 0.5	0.9	0.5	0.0 0.5	0.3 0.6	0.9 1.3	2.6 1.7	1.2 1.4	1.1 1.0	0.2 0.8	0.3 1.0	0.0 0.4	0. 0.
=																		
A C	C D	E	F 0.6	G 0.8	H	1	K 0 9	L	M	N 0.5	P	Q 14	R	S	T	V	W 0.4	0
0.5 1	.2 0.7	0.7	0.2	0.3	0.6	0.2	1.3	0.3	0.3	0.3	0.6	0.8	1.0	0.5	0.6	0.7	0.0	0.
	.4 0.7	1.1	0.9	0.4	1.0	1.2	0.5	1.6	0.9	0.7	1.5	1.0	1.2	1.1	1.6	1.5	0.1	0.
0.9 0.	.4 0.6	0.6	0.6	0.7	2.0	1.1	0.7	1.1	1.0	0.7	3.2	1.5	1.4	1.3	1.2	1.3	0.6	0.
0.9 0.	0 1.2	0.9	0.3	0.3	0.7	0.5	0.5	0.6	0.5	0.8	1.1	1.1	0.7	0.8	0.5	0.6	0.2	0.
0.9 0.		0.7	0.4	0.5	0.6	0.3	0.2	0.4	1.3	0.0	1.7	0.9	0.7	0.7	0.5	0.5	0.2	0.
0.9 0. 0.8 0. 0.6 0. 0.7 1.	2 0.8	0.9	0.8	0.3	0.8	0.1	0.5	0.5	1.2	1.1	1.1	1.0	0.5	1.1	0.5	0.3	0.3	0.
0.9 0. 0.8 0. 0.6 0. 0.7 1. 1.6 0. 0.5 0.	.0 0.8 0.2 0.8 0.5 0.8		0.4	0.3	0.8	0.8	0.6	0.5	0.4	0.5	2.3	0.6	0.9	0.7	0.7	0.7	0.8	0.
0.9 0. 0.8 0. 0.6 0. 0.7 1. 1.6 0. 0.5 0. 0.7 0.	0 0.8 0.2 0.8 0.5 0.8 0.0 0.4	0.6		0.4	1.1	0.6	0.7	0.7	0.5	0.7	3.0	1.4	0.6	1.2	0.7	0.7	1.3	0.
0.9 0, 0.8 0, 0.6 0, 0.7 1, 1.6 0, 0.5 0, 0.7 0, 1.0 0,	0 0.8 0.2 0.8 0.5 0.8 0.0 0.4 0.3 1.2	0.6	0.5		0.7	0.3	0.4	0.6	0.9	0.3	1.7	0.7	0.7	0.9	0.7	0.5	0.7	0
0.9 0. 0.8 0. 0.6 0. 0.7 1. 1.6 0. 0.5 0. 0.7 0. 1.0 0. 0.8 1. 0.8 1.	0 0.8 0.2 0.8 0.5 0.8 0.0 0.4 0.3 1.2 0.8 0.8	0.6 1.2 1.1	0.5	0.3	0.7	0 1	0.4	0.4	n •		1 1	0.0	0.7	10	0.9	0.0	0.7	
0.9 0, 0.8 0, 0.6 0, 0.7 1, 1.6 0, 0.5 0, 0.5 0, 0.5 0, 1.0 0, 1.0 0, 1.0 0, 1.0 0, 1.0 0, 1.0 0, 1.0 0, 1.0 0, 0.8 1, 0.9 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0	0 0.8 0.2 0.8 0.5 0.8 0.0 0.4 0.3 1.2 0.3 0.8 0.6 1.2 0.3 2.2	0.6 1.2 1.1 0.6 2.6	0.5 0.2 0.5 1.0	0.3 0.3 1.9	0.6	0.6	0.6	0.6	0.6	0.4	5.6	0.8 3.8	0.7	1.0	0.8	0.8	0.5	0.
0.9 0, 0.8 0, 0.6 0, 0.7 1, 1.6 0, 0.5 0, 0.7 0, 1.0 0, 0.8 1, 0.9 0, 3.8 2, 1.2 0,	.0 0.8 0.2 0.8 0.5 0.8 0.0 0.4 0.3 1.2 .3 0.8 0.6 1.2 0.3 2.2 0.8 1.2	0.6 1.2 1.1 0.6 2.6 1.3	0.5 0.2 0.5 1.0 1.2	0.3 0.3 1.9 0.6	0.6 1.9 1.1	0.6 1.3 1.3	0.6 2.3 0.8	0.6 2.4 0.9	0.6 1.7 1.2	0.4 1.0 0.8	1.0 5.6 3.6	0.8 3.8 1.3	0.7 3.9 1.8	1.0 3.0 1.4	0.8 2.7 1.4	0.8 3.6 1.7	0.5 0.2 3.1	0. 0. 1.
0.9 0. 0.8 0. 0.6 0. 0.7 1. 1.6 0. 0.5 0. 0.7 0. 1.0 0. 0.8 1. 0.9 0. 3.8 2. 1.2 0. 1.4 0.	10 0.8 1.2 0.8 1.5 0.8 1.0 0.4 1.3 1.2 1.3 0.8 1.6 1.2 1.3 2.2 1.8 1.2 1.3 1.2 1.3 2.2 1.8 1.2 1.2 1.0	0.6 1.2 1.1 0.6 2.6 1.3 1.2	0.5 0.2 0.5 1.0 1.2 0.7	0.3 0.3 1.9 0.6 0.9	0.6 1.9 1.1 1.1	0.6 1.3 1.3 0.4	0.6 2.3 0.8 0.7	0.6 2.4 0.9 1.0	0.6 1.7 1.2 1.0	0.4 1.0 0.8 0.8	1.0 5.6 3.6 5.3	0.8 3.8 1.3 2.0	0.7 3.9 1.8 1.5	1.0 3.0 1.4 1.6	0.8 2.7 1.4 1.1	0.8 3.6 1.7 0.9	0.5 0.2 3.1 0.7	0. 0. 1. 0.
0.9 0. 0.8 0. 0.6 0. 0.7 1. 1.6 0. 0.7 0. 0.7 0. 0.7 0. 0.7 0. 0.8 1. 0.9 0. 3.8 2. 1.2 0. 1.4 0. 1.4 0. 1.4 0.	0.0 0.8 0.2 0.8 0.5 0.8 0.0 0.4 0.3 1.2 1.3 0.8 0.6 1.2 1.3 2.2 0.8 1.2 1.3 1.8 1.6 1.2 1.3 2.2 1.8 1.2 1.5 1.0 1.5 1.0 1.7 0.8	0.6 1.2 1.1 0.6 2.6 1.3 1.2 1.5 1.2	0.5 0.2 0.5 1.0 1.2 0.7 0.6 0.4	0.3 0.3 1.9 0.6 0.9 0.8 0.7	0.6 1.9 1.1 1.1 1.3	0.6 1.3 1.3 0.4 0.9 0.5	0.6 2.3 0.8 0.7 1.0 0.6	0.6 2.4 0.9 1.0 1.2 0.8	0.6 1.7 1.2 1.0 1.2 0.5	0.4 1.0 0.8 0.8 0.8 0.8	1.0 5.6 3.6 5.3 2.7 2.4	0.8 3.8 1.3 2.0 1.7	0.7 3.9 1.8 1.5 2.0	1.0 3.0 1.4 1.6 1.2 1.2	0.8 2.7 1.4 1.1 1.5	0.8 3.6 1.7 0.9 1.4	0.5 0.2 3.1 0.7 0.3 0.3	0. 0. 1. 0. 0.
	.0 0.8 1.2 0.8 1.5 0.8 1.5 0.8 1.3 1.2 1.3 0.8 1.6 1.2 1.3 2.2 1.8 1.2 1.8 1.2 1.5 1.0 1.5 1.0 1.7 0.8 1.6 1.6	0.6 1.2 1.1 0.6 2.6 1.3 1.2 1.5 1.2 0.9	0.5 0.2 0.5 1.0 1.2 0.7 0.6 0.4 1.3	0.3 0.3 1.9 0.6 0.9 0.8 0.7 0.5	0.6 1.9 1.1 1.1 1.3 1.0 0.9	0.6 1.3 1.3 0.4 0.9 0.5 0.4	0.6 2.3 0.8 0.7 1.0 0.6 0.7	0.6 2.4 0.9 1.0 1.2 0.8 1.2	0.6 1.7 1.2 1.0 1.2 0.5 1.0	0.4 1.0 0.8 0.8 0.8 0.5 1.0	1.0 5.6 3.6 5.3 2.7 2.4 2.2	0.8 3.8 1.3 2.0 1.7 1.6 1.5	0.7 3.9 1.8 1.5 2.0 1.6	1.0 3.0 1.4 1.6 1.2 1.2 1.2 1.8	0.8 2.7 1.4 1.1 1.5 0.9 1.0	0.8 3.6 1.7 0.9 1.4 0.9 0.6	0.5 0.2 3.1 0.7 0.3 0.3 0.5	0.: 0.2 0.2 1. 0.2 0.2 0.2 0.2 0.2
1.9 0.0 0.9 0.0 0.8 0.0 0.7 1.1 1.6 0.0 0.7 1.1 1.6 0.0 0.7 0.1 1.0 0.0 0.7 0.1 1.0 0.0 1.4 0.1 1.2 0.1 1.4 0.1 0.5 0.0	.0 0.8 .0 0.8 .12 0.8 .15 0.8 .10 0.4 .13 1.2 .3 0.8 .12 1.3 .13 0.8 .12 1.3 .13 0.8 .12 1.3 .13 0.8 .12 1.3 .13 0.8 .12 1.0 .15 1.0 .17 0.8 .16 1.6 .16 1.4	0.6 1.2 1.1 0.6 2.6 1.3 1.2 1.5 1.2 0.9 1.4	0.5 0.2 1.0 1.2 0.7 0.6 0.4 1.3 0.3	0.3 0.3 1.9 0.6 0.9 0.8 0.7 0.5 0.7	0.7 0.6 1.9 1.1 1.1 1.3 1.0 0.9 0.3	0.6 1.3 1.3 0.4 0.9 0.5 0.4 1.0	0.6 2.3 0.8 0.7 1.0 0.6 0.7 0.1	0.6 2.4 0.9 1.0 1.2 0.8 1.2 0.4	0.6 1.7 1.2 1.0 1.2 0.5 1.0 1.0	0.4 1.0 0.8 0.8 0.5 1.0 0.6	1.0 5.6 3.6 5.3 2.7 2.4 2.2 0.5	0.8 3.8 1.3 2.0 1.7 1.6 1.5 0.5	0.7 3.9 1.8 1.5 2.0 1.6 1.1 0.8	1.0 3.0 1.4 1.6 1.2 1.2 1.8 0.4	0.8 2.7 1.4 1.1 1.5 0.9 1.0 0.3	0.8 3.6 1.7 0.9 1.4 0.9 0.6 0.6	0.7 0.5 0.2 3.1 0.7 0.3 0.3 0.3 0.5 0.0	0. 0. 1. 0. 0. 0. 0. 0.

Fig. 3. Dipeptide propensity for the 21–40 residue length linker set. Interpretation of figure refers to legend to Fig. 1.

A 0.6 0.9 1.0 0.6 1.0 2.1 0.6 0.7 0.8	A 1.1 0.7 1.4 0.5 0.7 1.6 0.3 0.7 0.6 0.5 1.3 1.5 1.3 1.1 0.7 0.3 0.6 0.5 1.3 1.5 1.3 1.1 0.7 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	A 1.6 0.2 1.3 1.0 0.6 1.4 1.8 1.0 0.5 0.9 0.8 3.4 1.2 1.6 1.6 1.0 0.1 0.4 1.0 0.4	A 0.8 0.1 0.9 0.7 0.7 1.1 0.5 0.9 0.7 0.5 1.1 2.7 1.2 1.4 1.8 1.1 0.5 2.6 1.1	A 1.5 0.6 2.1 0.9 0.8 1.3 1.2 0.6 0.9 0.3 0.7 2.8 1.2 1.6 1.8 1.3 0.7 1.4 0.3
C 0.8 0.2 0.2 0.4 0.4 0.7 1.0 0.3	C 0.5 0.8 1.0 0.3 0.3 0.1 0.3 0.3 0.4 0.1 0.4 0.5 0.3 0.0 0.5 1.3 0.8 0.0 0.6 0.0	C 0.3 0.0 0.0 0.2 0.2 0.3 0.0 1.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C 0.7 0.8 0.3 0.0 0.3 0.0 0.2 0.0 0.1 0.0 0.5 0.3 0.0 0.4 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C 0.2 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
D 0.8 0.2 0.6 0.8 0.5 0.4 0.8 0.6 0.9 0.9	D 0.9 0.7 0.6 1.0 0.8 0.5 1.3 0.5 1.0 1.2 1.0 1.2 3.1 1.5 0.7 1.2 0.9 0.8 2.5 0.4	D 0.9 0.4 0.5 0.4 0.6 1.3 0.8 0.2 0.6 0.3 0.8 0.3 0.8 0.3 0.0 3.3 0.7 1.0 1.1 0.5 1.4 0.5 0.1	D 1.0 0.5 0.9 0.7 0.6 1.1 0.6 1.0 0.7 2.1 1.4 1.2 1.0 1.4 1.2 1.0 0.4	D 1.2 0.0 0.6 0.5 1.8 1.5 0.9 0.8 0.0 0.4 0.9 0.2 2.0 1.0 1.0 0.8 1.1 1.3 0.3 0.0 0.3 0.0 0.4 0.5 0.9 0.2 0.0 0.5 0.9 0.0 0.5 0.9 0.0 0.5 0.9 0.8 0.9 0.2 0.9 0.0 0.5 0.9 0.8 0.9 0.8 0.9 0.2 0.9 0.0 0.0 0.0 0.5 0.9 0.8 0.9 0.8 0.9 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0
E 0.9 0.8 0.5 0.5 0.7 1.5 0.7 0.6 0.6	E 1.3 1.4 0.9 1.0 0.6 0.8 1.4 0.9 0.7 0.8 1.1 1.9 1.3 2.0 1.1 1.1 1.4 1.0 1.0 0.9	E 0.9 0.6 0.7 0.8 2.0 0.4 0.4 0.4 0.4 0.4 0.4 0.5 0.6 0.5 0.8 2.1 0.9 0.2 1.2 0.3	E 0.7 0.3 0.7 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.4 3.1 0.9 0.8 1.0 1.4 0.6 0.9 0.3	E 1.0 0.0 0.5 0.3 0.7 0.6 0.2 0.9 0.0 0.5 0.4 0.3 1.9 4.2 0.9 0.6 0.5 1.4 0.5 1.4
F 0.6 0.0 0.5 0.6 0.3 0.2 1.3 0.3 0.2 0.2 0.0	F 0.3 0.1 0.5 2.0 0.2 0.3 1.1 0.3 0.3 0.5 0.0 0.7 1.4 1.3 0.5 1.1 0.5 0.4 0.5 0.4 0.3	F 0.4 0.0 0.6 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	F 0.7 0.0 1.0 0.7 0.1 0.3 0.3 0.3 0.3 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.3 0.6 0.5 0.3 0.3 0.3 0.3 0.3 0.5	F 0.7 0.0 0.3 1.5 1.6 0.0 0.0 0.1 1.0 0.9 1.0 0.0 0.4 0.3 0.0 0.2 0.6 0.4 1.0 0.0 0.2 0.6 0.4
G 0.9 0.3 0.4 0.7 0.2 0.8 0.8 0.3 0.4 0.4 0.4	G 1.1 0.2 0.6 1.1 0.3 0.8 0.2 0.2 0.3 1.2 0.3 1.2 0.7 1.0 1.1 0.5 0.2 9.9 0.5	G 1.2 0.1 0.9 0.6 0.3 0.7 1.1 0.3 0.2 0.4 0.4 0.4 0.4 0.4 2.0 0.7 0.7 2.2 1.0 0.7 0.9 0.5 0.4	G 0.7 0.4 0.3 0.8 0.6 0.5 0.8 0.6 0.5 0.4 0.3 1.5 0.8 1.9 0.9 0.7 0.4 1.3 0.6	G 1.6 0.0 0.8 0.7 0.3 0.7 0.3 0.7 0.1 0.3 0.4 0.4 2.6 1.1 9 0.3 0.9 0.3 0.0 0.3 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4
H 1.2 0.4 1.9 1.1 0.4 1.2 1.3 0.8 0.5 0.5 0.5	H 0.8 1.0 1.2 1.2 0.7 0.5 1.5 2.2 2.4 1.1 1.7 2.1 1.7 2.1 1.8 1.7 1.8 0.0 1.4 0.8 8.0 1.0	H 1.2 0.0 0.9 0.8 1.3 0.9 1.0 2.2 1.2 0.8 0.4 0.2 1.7 1.9 1.5 1.0 1.1 1.1 0.5 0.4	H 0.9 0.5 1.4 0.4 0.6 0.9 0.7 1.0 0.7 1.0 0.7 0.3 0.9 2.8 0.6 1.3 1.6 0.8 0.6 1.9 0.3	H 0.6 0.0 0.4 0.7 0.0 1.3 0.7 0.4 0.0 0.8 0.7 0.6 1.7 0.9 0.9 0.9 0.9 0.9 0.4 0.4 0.4 0.9 0.9 0.9 0.9 0.4 0.9 0.9 0.9 0.9 0.9 0.4 0.7 0.0 0.4 0.7 0.0 0.4 0.7 0.0 0.1 0.7 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
I 0.7 0.0 1.0 0.6 0.3 0.4 1.5 0.3 0.7 0.3 0.7	1 0.5 0.3 1.8 1.2 0.3 1.0 0.8 0.4 0.4 0.4 0.4 0.7 1.3 0.8 1.0 0.8 1.0 0.8 1.0 0.4 0.4 0.7 1.3 0.8 1.2 0.3 1.3 0.4 0.4 0.5 1.3 0.4 0.4 0.5 0.4 0.5 0.3 1.8 0.4 0.5 0.3 1.8 0.4 0.4 0.4 0.4 0.5 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	1 0.9 0.2 1.0 0.7 0.4 0.3 0.1 0.4 0.3 1.3 1.5 0.7 0.9 1.0 0.4 0.3 0.1 0.2	1 1.0 0.3 0.4 0.5 0.2 0.3 1.0 0.1 0.1 0.1 0.1 0.1 1.7 1.5 1.1 0.7 0.5 0.6 0.4 0.2 0.1 0.7 0.5 0.2 0.3 0.1 0.1 0.1 0.5 0.2 0.3 0.1 0.1 0.1 0.1 0.5 0.2 0.3 0.1 0.1 0.1 0.5 0.2 0.3 0.1 0.1 0.1 0.1 0.5 0.2 0.3 0.1 0.1 0.1 0.5 0.2 0.3 0.1 0.5 0.1 0.5 0.1 0.5 0.1 0.5 0.1 0.5 0.1 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	1 0.6 0.0 0.8 0.9 0.0 0.5 1.4 0.0 0.3 0.1 0.3 0.3 0.3 0.4 0.4 0.8 0.5 0.7 7 1.2 0.4 0.0 0.0
K 0.9 0.3 0.8 0.8 0.6 0.4 0.8 0.7 0.9 0.7 0.9	K 0.7 0.1 0.7 1.3 0.5 0.5 2.6 0.8 0.7 0.4 1.0 1.2 0.7 1.9 1.1 1.0 1.0 0.9 0.9 0.7	K 0.7 0.0 0.3 0.6 0.4 0.5 0.7 0.4 0.2 0.5 0.2 0.2 0.2 1.3 0.7 0.8 1.4 0.5 0.6 0.2 0.0 1.4	K 0.9 0.5 0.9 1.1 0.8 0.8 1.2 0.6 0.4 0.4 0.8 0.7 0.8 2.1 1.7 1.7 2.6 1.0 0.8 0.9 2.4	K 0.4 0.0 0.9 1.4 0.2 0.0 0.0 0.0 0.0 0.1 0.0 0.5 0.6 0.0 5 1.0 0.5 1.0 0.5 0.0 5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
L 0.7 0.7 1.1 0.4 0.5 1.3 0.4 0.6 0.6	L 0.5 0.8 1.1 0.7 0.5 1.0 0.3 0.3 0.6 0.7 0.3 1.6 1.4 1.3 0.9 0.0 0.6 0.3 0.5 1.0	L 0.8 0.7 0.7 0.7 0.7 0.5 0.3 0.4 0.7 0.5 1.9 1.0 1.1 1.0 0.9 0.8 0.7 0.4	L 0.8 0.1 0.7 0.5 0.3 0.7 0.8 0.4 1.1 0.3 0.4 1.0 1.3 1.1 1.6 0.9 0.7 0.5 0.4 0.3	L 1.1 0.3 0.6 0.2 0.7 0.4 0.3 0.3 0.2 1.4 0.5 1.2 0.5 1.2 0.5 0.8 1.1 0.6 0.1 0.4 0.4 0.4 0.5 0.5 0.4 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
M 1.0 0.0 0.7 0.6 0.3 0.2 1.5 0.3 0.6 0.3 0.6 0.5 0.5	M 0.5 0.0 1.0 0.6 0.4 1.8 2.7 0.7 0.9 1.1 0.6 1.5 0.7 1.7 1.7 1.7 1.7 1.7 1.0 5 0.4 0.9 1.0	M 1.3 0.5 0.2 1.2 0.3 0.5 0.5 1.0 1.6 2.0 1.6 2.0 1.1 1.4 1.1 0.4 0.0 0.0	M 0.9 0.7 0.5 0.0 0.5 1.1 0.7 0.5 0.0 0.5 1.1 0.7 0.6 0.0 1.1 1.4 4 0.7 0.9 0.5 0.1 0.2 1.7 0.4	M 0.3 0.0 1.4 1.0 0.7 1.9 0.0 0.0 0.0 0.0 0.0 0.0 3.5 1.9 2.2 1.1 1.1 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
N 0.9 0.3 0.6 0.9 0.4 0.4 0.9 1.0 0.6 1.3	N 0.9 0.2 0.8 0.9 0.6 0.8 1.7 2.6 1.3 0.6 0.7 3.0 6.2 1.5 0.8 1.7 1.1 0.9 10.4 0.6	N 0.9 0.4 0.6 0.3 0.1 0.5 0.1 0.5 0.1 0.3 1.0 0.4 1.0 0.9 0.3 0.5 0.4 0.0	N 0.8 0.5 1.0 1.7 0.4 0.4 1.3 0.3 0.6 0.6 0.4 0.1 1.8 1.1 1.3 0.9 0.9 0.9 0.9 1.7 0.2	N 1.2 0.0 0.2 0.4 0.0 0.3 0.6 1.6 1.1 0.5 0.0 2.0 0.4 1.1 1.3 0.2 0.2 0.2 0.2 0.2 0.5
P 2.9 1.8 1.0 1.5 0.9 1.1 2.1 2.2 3.1 3.2	P 1.7 0.4 1.7 1.9 0.9 0.8 1.3 1.2 1.6 2.4 1.3 1.3 6.4 3.4 2.1 2.2 2.1 1.6 1.1 1.5	P 3.5 0.8 1.4 3.8 1.0 1.8 1.7 1.0 2.2 2.3 2.2 0.4 4.3 3.1 2.9 2.1 1.9 2.0 0.3 0.9	P 3.1 0.0 1.1 3.2 2.1 1.5 1.9 1.5 4.4 2.5 1.3 1.0 5.4 2.9 3.4 1.8 1.5 1.1 3.1	P 3.8 0.0 1.0 2.7 0.6 1.8 1.5 0.7 1.3 1.2 1.3 0.3 5.8 1.8 2.4 2.7 2.3 2.2 0.6 1.6
Q 0.8 0.8 1.1 1.1 1.3 2.0 0.9 0.9 0.8	Q 0.6 0.2 0.8 1.4 1.7 1.1 2.0 2.6 1.2 0.9 0.8 2.4 1.6 1.9 1.1 1.1 8 1.4 1.8 1.4 1.8 1.4	Q 1.8 0.9 0.7 0.6 1.0 1.6 0.5 0.7 0.8 1.2 0.2 0.2 0.2 1.7 1.9 1.5 1.8 1.5 0.9 1.9 0.4	Q 1.3 0.9 1.2 0.8 0.2 1.7 0.8 0.8 1.3 0.7 0.9 1.0 3.0 0.8 1.6 1.8 0.7 0.7 2.7 1.1	Q 0.4 0.0 0.1 1.1 0.4 0.7 0.7 0.3 0.6 1.0 0.4 1.1 0.7 1.4 1.4 0.8 0.7 11.1 0.0
R 1.8 0.5 1.3 1.1 0.9 1.0 1.7 0.6 1.3 1.2 1.2	R 1.0 0.7 0.7 1.1 1.9 1.5 1.1 0.8 0.6 1.9 2.4 1.8 0.6 1.9 2.4 1.2 1.8 0.9 0.7 4.7 0.4	R 1.9 0.2 0.9 1.6 0.8 1.5 1.3 0.9 1.1 0.9 1.1 0.9 0.5 3.1 1.9 1.6 2.1 1.4 0.9 0.7 0.2	R 1.5 0.5 1.2 1.6 1.8 1.3 2.1 0.8 1.4 0.9 0.7 0.7 0.8 3.6 2.3 1.7 2.2 1.6 1.1 3.1 1.8	R 1.7 0.3 0.9 0.7 1.2 0.5 0.6 0.7 0.9 0.9 1.0 2.9 0.8 1.1 1.4 1.4 1.4 0.8 0.4 0.0
S 1.9 0.6 1.6 0.6 0.7 2.0 0.9 0.9 0.9 1.5	S 1.2 0.1 1.2 1.3 0.8 1.3 1.4 0.6 1.4 1.0 1.0 2.0 2.0 2.3 1.4 1.7 1.6 1.0 0.8 7.0 0.9	S 1.7 0.1 0.8 1.1 0.4 1.0 0.8 1.5 0.6 1.5 0.6 1.5 0.8 0.5 2.4 1.0 0.9 1.8 1.2 0.9 1.8 1.2 0.9 1.8 1.2 0.9 1.8 1.2 0.9 1.8 1.2 0.9 1.8 1.2 0.9 1.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0	\$ 1.2 0.5 1.2 0.8 0.8 0.6 1.4 0.8 1.1 1.6 0.7 0.8 3.3 1.2 1.8 1.3 1.0 0.7 3.3 0.7	S 1.4 0.8 0.9 0.9 0.7 0.4 0.4 0.4 1.6 0.5 0.8 3.2 0.8 3.2 0.8 1.6 2.4 1.9 1.0 2.5 0.7
T 1.2 0.7 1.2 0.9 0.3 0.9 0.6 0.5 1.2 0.7	T 0.7 0.3 0.8 1.0 0.7 0.6 0.8 0.6 0.5 2.2 0.6 0.5 2.4 1.5 1.3 1.3 1.3 1.4 0.5 0.4 2.4 0.4	T 1.4 0.2 1.3 0.8 0.3 0.7 1.2 0.4 0.7 0.5 0.7 1.2 0.4 0.5 0.5 1.3 1.5 0.8 0.4 0.1 0.0 0.0 0.5 0.5 0.5 0.5 0.5 0.5	T 1.0 0.3 1.6 1.0 1.2 0.6 0.5 0.7 0.6 0.4 1.9 1.4 1.3 1.0 0.8 0.5 2.1 0.7	T 1.9 0.0 2.6 0.7 1.4 0.8 1.2 0.4 0.4 0.2 1.7 2.2 0.8 1.7 0.6 1.3 0.6 0.7 0.2
V 0.6 0.2 0.7 0.5 0.2 0.8 1.1 0.7 1.0 0.4	V 0.6 0.0 0.7 0.4 0.3 0.7 1.2 0.2 0.6 0.3 0.7 0.7 1.4 0.6 1.0 0.7 0.5 0.1 1.0.1 2.3	V 0.9 0.0 1.4 0.9 1.0 0.6 0.6 0.8 0.4 1.9 0.8 1.4 1.0 0.6 0.4 1.1	V 0.6 0.0 0.4 0.5 0.3 0.6 0.3 0.6 0.3 0.6 0.4 0.4 0.5 1.9 0.8 1.1 0.9 0.7 0.4 0.2 0.3	V 0.9 0.4 1.1 1.1 1.4 0.0 0.1 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.9 9 1.2 0.5 0.4 0.0 0.0 8 0.9 0.9 0.9 0.4
W 0.4 0.7 4.3 1.0 1.1 0.2 1.7 0.9 1.6 1.2	W 1.4 0.0 11.0 0.7 0.9 1.1 3.7 2.6 5.1 0.4 1.5 12.2 4.8 2.8 2.8 1.9 4.5 7.3 0.5 0.0 0.0	W 0.4 0.0 2.3 0.8 0.1 0.5 0.6 0.2 0.6 0.5 1.3 0.8 0.2 9 0.6 0.1 0.1 0.1 0.5 0.0 0.0	W 0.8 0.0 0.8 0.0 0.4 1.1 0.2 1.0 0.1 0.0 0.1 0.0 0.1 0.0 6.3 0.2 0.2 0.2 0.6 0.4	W 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.1 0.0 0.0
Y 0. 1. 0. 0. 0. 0. 0. 0. 0. 0.	Y 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.	0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

Fig. 4. Dipeptide propensity for the 41–60 residue length linker set. Interpretation of figure refers to legend to Fig. 1.

1.1 0.0 1.2	С	D	Е	F	G	н	I	к	L	М	N	Р	Q	R	s	т	v	w
1.2	1.7	1.7	0.8	0.6	1.9	0.7	0.5	0.4	0.3	0.2	1.7	2.8	1.9	1.4	2.8	1.2	0.6	1.0
	0.0	0.5	0.4	1.8	1.4	0.0	2.0	0.0	0.3	0.0	0.0	1.8	0.9	LI	0.5	0.3	1.0	0.5
0.6	1.2	0.4	0.3	0.0	1.8	0.7	0.4	1.1	0.2	0.7	0.4	1.9	0.0	0.8	3.1	2.0	0.4	0.0
2.6	0.0	1.1	1.6	0.4	3.1	0.5	0.6	0.7	0.5	0.0	2.0	1.9	0.7	2.5	1.3	1.5	0.9	0.0
0.8	0.0	3.2 0.6	0.4	0.0	0.2	0.0	0.4	0.0	0.4	0.0	0.0	1.4	0.0	2.2	2.2	0.2	0.3	0.0
0.2	0.0	1.2	0.0	0.0	1.0	0.0	0.5	0.0	0.5	1.6	0.7	1.1	0.0	0.0	1.2	0.4	0.0	1.5
0.4	0.0	0.6	0.0	0.0	0.5	0.2	0.0	0.0	0.2	0.0	0.5	0.0	0.0	1.0	0.8	0.5	0.0	0.0
1.6	0.0	0.8	0.5	0.9	0.7	0.0	0.6	0.0	1.0	0.0	1.6	0.9	0.0	2.3	2.4	1.1	0.7	1.5
1.7	0.0	0.9	0.3	0.6	1.5	2.3	0.0	0.9	0.7	0.6	1.5	3.9	0.7	0.9	4.0	0.3	0.7	0.0
1.7	0.0	1.0	1.1	1.7	2.1	0.7	1.1	1.3	0.2	0.0	0.0	2.1	0.6	0.7	1.1	2.7	0.5	0.0
1.2	0.0	0.8	0.3	0.0	1.6	1.7	1.7	0.8	1.0	0.5	1.2	1.9	0.6	0.6	1.6	2.5	0.9	0.3
0.4	0.0	0.5	0.2	0.8	0.5	0.9	0.5	0.9	0.3	1.2	0.0	1.2	0.7	0.6	0.9	0.4	0.2	0.0
0.2	0.0	0.0	0.0	0.0	0.3	7.5	0.0	0.0	0.0	0.0	2.1	0.0	0.0	0.0	3.5	0.0	0.0	0.0
3																		
A 0.0	C 0.0	D 0.5	E 0.5	F 1.7	G 0.7	H 0.0	1	K 1.0	L 0.3	M 2.7	N 0.0	P 2.4	Q 1.7	R 0.0	S 0.5	T 0.0	V 0.9	0.0
0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.0	0.0	0.0	0.0
1.5	0.0	1.3	1.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	2.8	0.0	0.0	0.0
0.8	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
0.8	0.0	0.8	3.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	10.6	0.0	0.0	0.0	2.5	0.0
0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.6	1.1	2.1	0.0	0.0	0.0
0.0	0.0	1.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.6	1.2	0.0	0.0	0.0	1.0	0.0
0.0	0.0	3.3	0.0	0.0	0.0	8.2	0.0	0.0	0.0	0.0	0.0	0.0	4.1	0.0	0.0	0.0	2.3	0.0
1.6	0.0	1.9	1.0	0.0	0.8	3.4	3.1	6.6	0.7	0.0	2.5	1.2	0.0	0.0	2.2	2.7	2.6	0.0
0.0	0.0	0.0	2.1	0.0	2.8	0.0	0.0	2.8	1.1	0.0	6.4	1.9	0.0	1.4	1.6	1.8	1.5	0.0
1.5	6.1	0.9	0.9	0.0	0.0	0.0	0.9	0.0	0.0	0.0	0.0	2.3	0.0	0.0	0.0	2.3	0.8	8,
0.0	0.0	0.0	0.0	0.0	0.7	3.5	0.0	4.5	0.6	0.0	2.3	1.1	4.2	2.1	1.1	0.0	0.0	0.0
0.8	0.0	2.7 5.4	0.0	0.0	0.0 3.9	2.8	1.0	0.0	0.0	2.5	1.7	3.0 0.0	4.9 0.0	1.5	0.0	4.4	4.3	0.0
0.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	4.9	0.0	0.0	0.0	3.4	0.0	0.0	0.0	0.0	2.3	0.0
)	c	P	F	F	C	р		V		м	N	р	C	Р	¢	т	v	10-
2.9	1.6	1.4	0.7	0.8	2.4	1.0	1.1	0.5	0.4	0.3	1.2	3.0	2.0	2.5	2.7	1.4	1.3	0.4
0.0	0.0	0.0	0.0	0.0	1.8	0.0	0.0	0.0	0.8	0.0	0.0	0.0	1.4	1.6	1.4	2.1	1.1	2,0
0.3	0.0	0.4	0.0	0.0	1.5	0.6	1.2	0.0	0.3	0.0	0.5	2.7	0.9	0.5	1.7	0.9	0.2	1.
0.8	0.0	0.7	0.4	0.0	0.3	1.1	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.4	0.3	0.0	0.0	0.0
1.1	0.0	0.6	2.1	0.0	2.0	1.2	0.0	1.4	0.0	2.4	2.9	0.6	1.0	0.0	0.0	0.8	0.0	0.
1.2	0.0	0.5	0.3	0.0	1.4	0.0	0.5	0.5	0.5	1.3	0.0	0.0	0.6	1.1	0.5	0.0	2.2	0.0
0.5	0.0	0.4	0.5	0.0	0.2	0.4	0.6	0.2	0.2	0.4	0.5	1.4	0.2	0.5	1.6	0.0	0.4	0.
0.6	0.0	0.0	0.8	1.2	0.6	1.5	0.0	0.0	0.3	0.0	0.9	1.1	0.0	0.9	0.0	0.5	0.6	0.0
2.7	0.0	2.5	0.8	0.5	2.1	0.0	1.6	0.0	1.0	1.7	1.7	1.1	0.0	2.4	2.8	0.9	1.0	1.
1.5	0.0	1.0	0.5	0.0	1.4	0.8	0.0	1.3	0.2	0.0	0.7	1.8	1.4	2.2	1.4	0.8	0.3	1.
3.7	0.0	0.3	0.3	0.0	2.9	1.3	1.1	2.1	0.9	0.7	0.8	3.3	0.0	2.2	0.4	1.6	0.9	0.
1.9	0.0	0.6	1.0	0.0	0.8	0.7 2.3	1.0	0.0	0.3	0.9	0.5	0.9	0.8	1.7	0.5	0.0	0.6	1.
0.0 0.3	0.0 0.0	0.0 0.0	1.4 0.0	0.0 0.8	0.9 0.0	0.0 1.6	0.0 0.9	3.2 0.0	0.4 0.0	0.0	0.0	0.0 0.7	2.9 2.4	0.6 0.4	1.8 0.0	0.0 0.0	0.9 0.5	0.0 0.0
`																		
, 	с	D	E	F	G	Н	1	K	L	M	N	Р	Q	R	s	T	V	W
0.9	0.0	1.0	0.0	0.0	0.0	2.4	0.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	1.1	0.8	1000
1.6	1.0	1.2	1.1	0.0	2.1	1.9	0.9	0.5	0.4	0.5	0.2	0.6	1.0	3.2	25		0.0	5.
28	0.0	0.4	0.0	0.5	0.2	0.0	0.0	0.2	0.4	0.0			0.9	26	1.4	0.6	0.0	5.0 5.0 0.0
2.8 0.6								0.4	0.4	0.0	0.3	4.0	0.9	2.6 0.3	1.4	0.6 1.0 0.4	0.0 0.8 0.1 0.2	5.0 5.0 0.0 2.0 0.0
2.8 0.6 3.0	1.5	2.6	2.3	0.6	3.8	2.0	0.6	1.0	1.0	0.0	0.3	4.0 1.2 3.7	0.9 0.4 3.3 2.3	2.6 0.3 3.6 0.7	1.4 0.3 4.0	0.6 1.0 0.4 2.1 2.4	0.0 0.8 0.1 0.2 2.1 1.6	5. 5. 0. 2. 0. 0.
2.8 0.6 3.0 4.0 0.4	1.5 0.0 0.6	2.6 0.6 0.4	2.3 0.5 0.1	0.6 0.0 0.0	3.8 0.5 0.5	2.0 0.0 0.4	0.6 0.4 0.1	1.0 0.6 0.1	0.4 1.0 0.3 0.2	0.0 2.4 0.0 0.4	0.3 0.3 1.8 0.0 0.4	4.0 1.2 3.7 1.3 1.0	0.9 0.4 3.3 2.3 0.2	2.6 0.3 3.6 0.7 1.3	1.4 0.3 4.0 1.5 0.3	0.6 1.0 0.4 2.1 2.4 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1	5. 0. 2. 0. 2. 0. 2. 0.
2.8 0.6 3.0 4.0 0.4 1.2 0.6	1.5 0.0 0.6 0.0 0.0	2.6 0.6 0.4 0.6 0.2	2.3 0.5 0.1 0.4 0.7	0.6 0.0 0.5 0.1	3.8 0.5 0.5 0.2 0.2	2.0 0.0 0.4 1.5	0.6 0.4 0.1 0.0	1.0 0.6 0.1 0.2 0.2	0.4 1.0 0.3 0.2 0.3 0.4	0.0 2.4 0.0 0.4 0.0 1.7	0.3 0.3 1.8 0.0 0.4 0.8 0.1	4.0 1.2 3.7 1.3 1.0 0.5 2.5	0.9 0.4 3.3 2.3 0.2 0.4 0.2	2.6 0.3 3.6 0.7 1.3 0.4 0.4	1.4 0.3 4.0 1.5 0.3 0.6	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1	5.3 5.3 0.0 2.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
2.8 0.6 3.0 0.4 1.2 0.6 1.8	1.5 0.0 0.6 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4	2.3 0.5 0.1 0.4 0.7 1.3	0.6 0.0 0.5 0.1 0.0	3.8 0.5 0.2 0.2 0.4	2.0 0.0 0.4 1.5 1.7 1.4	0.6 0.4 0.1 0.0 0.0 0.3	1.0 0.6 0.1 0.2 0.2 0.3	0.4 1.0 0.3 0.2 0.3 0.4 0.2	0.0 2.4 0.0 0.4 0.0 1.7 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.0	5.: 5.: 0.: 0.: 0.: 0.: 0.: 0.: 0.: 0.: 0.: 0
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1	2.3 0.5 0.1 0.4 0.7 1.3 0.5	0.6 0.0 0.5 0.1 0.0 0.8 0.4	3.8 0.5 0.2 0.2 0.4 0.8	2.0 0.0 0.4 1.5 1.7 1.4 0.6	0.6 0.4 0.1 0.0 0.0 0.3 0.3 0.3	1.0 0.6 0.1 0.2 0.2 0.3 0.3 0.3	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2	1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.0 0.4	5.: 5.0 0.0 2.: 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0	0.6 0.4 0.1 0.0 0.0 0.3 0.3 0.5 0.6	1.0 0.6 0.1 0.2 0.2 0.3 0.3 0.6 0.4	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 2.2 0.6	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.6	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.4 2.7 1.0	5.: 5.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3 1.9	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 1.2	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3	0.6 0.4 0.1 0.0 0.3 0.3 0.5 0.6 0.5	1.0 0.6 0.1 0.2 0.3 0.3 0.6 0.4 0.5	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 2.2 0.6 1.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.6 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.4 2.7 1.0 1.3	5. 5. 0. 2. 0. 0. 2. 0. 0. 1. 0. 2. 4. 0. 2.
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 1.1 1.3 1.9 1.9 0.7	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 1.2 0.7 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.5 0.6 0.5 0.3 0.3	1.0 0.6 0.1 0.2 0.3 0.3 0.3 0.6 0.4 0.5 0.3 0.3	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 2.2 0.6 1.4 0.8 1.0	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.6 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1 2.1 1.7 0.6	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6	5.: 5.3 0.1 2.: 0.1 2.: 0.1 2.: 0.1 2.: 0.1 0.1 2.: 0.1 0.1 2.: 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 0.4	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 1.1 1.3 1.9 1.9 0.7 0.2	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7	0.6 0.0 0.5 0.1 0.8 0.4 0.0 1.2 0.7 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.3 0.2	1.0 0.6 0.1 0.2 0.3 0.3 0.6 0.4 0.5 0.3 0.3 0.3 0.7	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 2.2 0.6 1.4 0.8 1.0 0.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0 0.7	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.5	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1 1.7 0.6 0.8	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 0.5 0.5	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6 0.6	5.: 5.3 0.1 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.9 1.2 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 1.1 1.3 1.9 1.9 0.7 0.2 2.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 1.2 0.7 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5 6.7 1.8	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.3 0.3 0.2 0.0 0.0	1.0 0.6 0.1 0.2 0.3 0.3 0.3 0.6 0.4 0.5 0.3 0.3 0.7 0.0 0.4	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 2.2 0.6 1.4 0.8 1.0 0.4 0.0 0.6	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.6 0.0 0.0 0.0 1.2 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.0 1.2	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5	5.3 5.0 0.0 2.3 0.0 0.0 2.4 0.0 0.0 1.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3 1.9 1.9 0.7 0.2 2.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9	0.6 0.0 0.5 0.1 0.8 0.4 0.0 1.2 0.7 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5 6.7 1.8	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.3 0.2 0.0 0.0	1.0 0.6 0.1 0.2 0.3 0.3 0.6 0.4 0.5 0.3 0.3 0.7 0.0 0.4	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 2.2 0.6 1.4 0.8 1.0 0.4 0.0 0.4 0.0	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 1.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.3 0.3 1.8 0.0 0.4 0.4 0.4 0.4 0.4 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.0 1.2	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.6 8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 1.7 0.6 0.8 2.2 1.4	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5	5.: 5.1 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9 0.9	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5 6.7 1.8	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 H	0.6 0.4 0.1 0.0 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	0.2 1.0 0.6 0.1 0.2 0.3 0.3 0.4 0.3 0.3 0.3 0.3 0.7 0.0 0.4 K	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.0 1.2 P	0.9 0.4 3.3 2.3 0.2 0.4 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0 0 2	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 R	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.6 1.3 0.0 0.7 1.6 1.3 1.1 1.7 0.2 S	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.0 T	0.0 0.8 0.1 0.2 1.6 0.1 0.1 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 0.4 2.7 1.0 0.4 2.7 1.0 0.5 V	5.: 5.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9 0.9	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5 6.7 1.8 G 0.2 0.0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.3 0.5 0.3 0.3 0.3 0.3 0.2 0.0 0.0 0.0 0.0	1.0 0.6 0.1 0.2 0.2 0.3 0.3 0.4 0.5 0.3 0.3 0.7 0.0 0.4 K 1.7 0.0	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 2.4 0.0 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3 N 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.0 1.2 P 3.5 0.0	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0 0 0.0 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.0 0.0 1.8 3.0 2.1 1.7 0.6 0.8 2.2 1.4 R 0.3 0.0	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 S 0.8 0.0	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 1.2 2.1 1.6 0.1 0.1 0.1 0.1 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 V V 0.5	S.: S.: S.: S.: 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 1.7 2.9 1.7 2.9 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 2.0 1.4 1.6 0.7 0.9 0.9 0.9 E E 1.2 2.8 0.0	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 6.7 1.8 6.7 1.8 6.2 0.2 0.0 0.0 0.0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.2 0.0 0.0 0.0 1 0.0 0.0 0.0 0.0	1.0 0.6 0.1 0.2 0.2 0.3 0.3 0.4 0.5 0.3 0.7 0.0 0.4 K 1.7 0.0 1.2	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 2.4 0.0 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 2.2 2.2 1.9 0.5 0.0 0.7 2.8 0.3 0.3 N 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.7	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.0 1.2 P 3.5 0.0 0.7	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 R 0.3 0.0 0.0 0.6	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 S 0.8 0.0 0.0 0.0	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 1.6 0.8 2.4 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 1.6 0.1 0.1 0.1 0.1 0.1 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 V V	S.3 S.3 S.3 O.1 O.1 O.1 O.1 O.1 O.1 O.1 O.1
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9 4.2 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9 0.9 E E 1.2 2.8 0.0 0.0 0.0	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5 1.5 6.7 1.8 6.7 0.2 0.0 0.0 0.0 0.0 0.0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.3 0.5 0.5 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.0 0.6 0.1 0.2 0.2 0.3 0.6 0.4 0.5 0.3 0.7 0.0 0.4 K 1.7 0.0 1.2 2.0 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.2 2.2 2.2 1.9 0.5 0.0 0.7 2.8 0.3 0.0 0.7 2.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 0.9 0.0 1.2 P 3.5 0.0 0.7 3.0 1.1 1.2 1.3 1.0 1.0 1.1 1.1 1.0 1.1 1.1 1.1	0.9 0.4 3.3 2.2 0.4 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 R 0.3 0.0 0.6 0.0 0.0 0.8 0.8 2.2 1.4	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 S 0.8 0.0 0.0 0.5 1.5	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 1.0 6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.0 1.0 1.0 1.0 0.4 2.7 0.6 0.0 0.5 0.5 0.0 0.0 0.9 0.9	S.3 S.3 S.3 S.3 S.3 S.3 S.3 S.3
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.4 0.6 0.4 0.4 0.6 1.1 1.3 1.9 0.7 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 0.5 1.2 1.4 1.4 1.6 0.7 0.9 0.9 0.9 E 1.2 2.8 0.0 0.0 0.0 0.0 0.0	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 6.7 1.8 6.7 1.8 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	0.1 0.6 0.1 0.2 0.2 0.3 0.3 0.3 0.6 0.4 0.5 0.3 0.6 0.4 0.7 0.0 0.4 0.5 1.7 0.0 1.2 0.0 0.0 0.0	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.3 0.4 0.2 0.3 0.4 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 1.2 0.0 0.0 1.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.3 0.3 1.8 0.0 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3 0.0 0.0 0.7 2.8 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.5 0.0 0.0 0.5 0.0 0.0 0.5 0.0 0.5 0.0 0.5 0.5	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 1.7 0.9 0.0 1.2 P 3.5 0.0 0.7 3.5 0.0 1.1 3.5 0.0 1.1 3.5 0.0 1.1 3.5 0.0 1.1 3.5 0.0 1.1 1.2 1.3 1.0 1.0 1.0 1.0 1.1 1.1 1.0 1.1 1.1	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 2.1 1.7 0.6 0.8 2.2 1.4	2 1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 2.9 1.6 1.3 2.9 1.6 1.3 2.9 1.5 0.4	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 1.0 6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6 6 0.6 0.0 0.5 V V V 0.5 0.0 0.0 0.3	S.3 S.3 S.3 O.1 O.3 O.3 O.3 O.3 O.3 O.3 O.3 O.3
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 1.7 2.9 4.2 1.7 2.9 4.2 1.7 0.9 4.2 0.6 0.6 1.8 1.3 1.7 0.9 4.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 1.3 0.5 1.2 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9 0.9 E E 1.2 2.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 9 0.0 9	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 1.5 1.5 6.7 1.8 G 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	0.1 0.6 0.1 0.2 0.2 0.3 0.3 0.3 0.6 0.4 0.5 0.3 0.3 0.3 0.6 0.4 0.5 0.3 0.7 0.0 0.4 0.7 0.0 0.4	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.4 0.0 0.4 0.4 0.0 0.4 0.4	0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.3 0.3 1.8 0.0 0.4 0.4 0.4 0.4 0.4 0.8 0.2 2.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3 0.0 0.0 0.7 7 2.8 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 0.9 0.0 1.2 P 3.5 0.0 0.7 3.0 1.1 3.5 1.2 1.3 1.0 1.1 1.3 1.0 1.1 1.1 1.1 1.1 1.1 1.1 1.1	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.1 0.3 0.2 0.3 0.2 0.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 1.4 R 0.3 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 5 0.8 0.0 0.0 5 1.5 0.4 4 6.8	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0	S.3 S.3 S.3 S.3 S.3 S.3 S.3 S.3
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 4.9 1.7 2.9 4.2 1.8 1.0 2.7 0.9 2.7 0.9 0.6 0.3 0.0 1.7 0.0 0.6 0.3 0.0 0.4	1.5 0.0 0.6 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 2.0 1.4 1.6 0.7 0.9 0.9 0.9 E E 2.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.5 1.5 6.7 1.8 6.7 1.8 6.7 1.8 6.7 1.8 6.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.2	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 1.1 0.0 0.0 0.0 1.1 3.5 1.2 4.6	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.1 0.6 0.1 0.2 0.3 0.3 0.4 0.5 0.3 0.3 0.4 0.5 0.3 0.3 0.4 0.5 0.3 0.3 0.4 0.5 0.3 0.3 0.4 0.5 0.0 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.0 0.0 0.11 3.3	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.5 0.4 0.5 0.4 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	0.0 0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 0.0 1.2 0.0 0.0 0.0 0.0 1.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.3 0.3 1.8 0.0 0.4 0.4 0.4 0.4 0.4 0.8 0.2 2.2 2.2 1.2 1.9 0.5 0.0 0.7 7 2.8 0.3 N 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 7.3 6 4.1 4.0 9 0.0 1.2 7.5 0.0 1.1 1.2 7.5 0.0 1.1 1.3 1.0 1.2 7.5 0.0 1.1 1.1 1.2 1.3 1.0 1.1 1.1 1.2 1.2 1.2 1.3 1.0 1.1 1.1 1.1 1.1 1.1 1.2 1.2 1.1 1.1	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 2.1 1.7 1.7 0.6 0.8 2.2 1.4 0.3 0.0 0.6 0.8 2.2 1.4 R 0.3 0.0 0.0 1.9 0.0 0.0 1.9 0.0 0.0 1.9 0.0 1.3 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.7 1.3 0.7 1.3 0.4 0.7 1.3 0.7 0.7 1.3 0.7 0.7 1.4 0.7 0.7 0.7 1.4 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 5 0.8 0.0 0.0 5 1.5 0.4 4 6.8 0.0	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.6 1.5 0.8 2.4 1.0 0.3 1.0 0.3 1.0 0.0 0.0 0.0 0.0 0.0 0.0 1.1 1.0 0.0 0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 0.0 0.5 0.0 0.0 0.0 0.0 0.0 0.0	S.3. S.3.
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 1.0 2.9 4.2 1.8 1.0 0.7 0.9 2.7 0.9 2.7 0.9 2.7 0.9 0.6 0.3 0.0 1.7 0.0 0.6 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.4 0.7 0.9 0.9 0.9 0.9 0.9 0.9 E 1.2 2.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.2 1.2 1.2 2.8 0.0 0.0 1.2 1.2 2.0 0.1 1.3 0.5 1.2 0.5 1.2 0.5 1.2 0.5 1.2 0.5 0.5 1.2 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.8 6.3 1.3 1.7 2.9 1.5 1.5 6.7 1.8 6.7 1.8 6.7 1.8 6.7 1.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.2 0.2	2.0 0.0 0.4 1.5 1.7 1.4 0.6 8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.6 0.4 0.1 0.0 0.0 0.3 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.3 0.3 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.0 0.6 0.1 0.2 0.3 0.3 0.4 0.5 0.3 0.3 0.6 0.4 0.5 0.3 0.3 0.3 0.4 0.5 0.3 0.3 0.4 0.5 0.3 0.3 0.4 0.5 0.0 0.0 0.4 0.0 0.4 0.0 0.4 0.4 1.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.11 3.3 1.3 1.3	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.4 0.2 0.6 0.4 0.6 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.0	0.0 0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 2.2 1.9 0.5 0.0 0.7 2.8 0.3 N 0.0 0.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.7 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 4.1 4.0 1.7 7.3 6 4.1 4.0 9 0.0 1.2 7.5 0.0 1.1 1.3 0.5 2.5 0.0 1.1 1.3 0.5 2.5 0.0 1.1 1.1 1.3 0.5 2.5 0.0 1.1 1.1 1.2 1.3 0.5 2.5 0.0 1.1 1.1 1.2 1.3 0.5 2.5 0.0 1.1 1.1 1.2 1.2 1.2 1.2 1.2 1.2	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.6 0.2 0.6 0.8 1.4 1.3 2.2 0.7 0.3 2.1 2.3 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 R 0.3 0.0 0.6 0.8 2.2 1.4 1.4 0.6 0.7 1.2 1.4	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 5 0.8 0.0 0.0 5 1.5 0.4 4 6.8 0.0 0.5 1.5 0.4	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 1.0 0.2 0.7 1.1 1.0 0.2 0.7 1.5 0.8 2.4 1.0 0.3 0.5 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.4 2.7 1.0 1.3 0.4 2.7 1.0 0.4 2.7 1.0 0.5 0.6 0.5 0.0 0.5 0.0 0.0 0.5 0.0 0.0 0.0 0.2 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	S.3. S.3.
2.8 0.6 3.0 0.4 1.2 0.6 1.8 1.3 1.0 2.9 4.2 1.8 1.0 2.7 0.9 4.2 1.8 1.0 0.6 0.7 0.0 0.6 0.3 0.0 1.7 0.0 0.6 0.4 0.0 0.0	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 1.1 1.3 1.9 0.7 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 1.3 2.0 1.4 1.6 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.0 0.0	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.4 0.4 0.4 0.4 1.3 1.7 1.5 6.7 1.8 6.7 1.8 6.7 1.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.5 0.0 0.0 0.0 0.0 1.1 0.0 0.0 0.0 0.0 1.1 5.1 5.1 5.1	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.5 0.5 0.3 0.3 0.3 0.3 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.1 1.0 0.6 0.1 0.2 0.3 0.3 0.3 0.4 0.5 0.3 0.7 0.0 0.4 0.4 0.5 0.3 0.7 0.0 0.4 0.4 0.5 0.7 0.0 0.4 0.0 0.0 0.0 1.1 1.3 0.0 0.0	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 0.0 2.4 0.0 0.4 0.0 0.4 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3 N 0.0 0.0 0.0 0.7 0.0 0.0 0.0 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 3.6 4.1 1.7 1.3 4.0 1.7 0.9 0.0 1.2 3.5 0.0 0.7 1.2 1.3 1.0 1.1 3.6 4.1 1.7 1.3 0.5 1.1 3.6 4.1 1.7 1.3 0.5 1.1 1.1 3.6 4.1 1.7 1.7 1.3 1.0 1.1 1.7 1.7 1.3 1.1 3.6 1.1 1.7 1.7 1.7 1.7 1.1 3.6 1.1 1.7 1.7 1.7 1.7 1.7 1.7 1.7	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.3 2.1 2.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.6 0.3 3.6 0.7 1.3 0.4 0.0 1.8 3.0 2.1 1.7 0.6 0.8 2.2 1.4 1.7 0.6 0.3 0.0 0.6 0.9 0.0 0.0 0.9 0.0 0.7 1.2 1.3 0.0 7 1.4 0.7 7 1.4 0.6 8 2.1 1.7 1.7 0.7 7 1.3 0.4 0.7 7 1.3 0.4 1.7 1.3 0.4 0.7 7 1.3 0.4 1.7 0.7 1.3 0.4 1.7 0.7 1.3 0.4 1.7 0.7 1.3 0.4 1.7 0.7 1.3 0.4 1.7 0.7 1.3 0.4 1.7 0.7 1.3 0.4 1.7 0.7 1.7 0.6 1.7 1.7 0.7 1.7 1.7 0.7 1.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	1.4 0.3 4.0 1.5 0.3 0.6 1.3 0.6 1.3 0.0 0.7 1.6 1.3 1.1 1.7 1.6 1.3 1.1 1.7 1.6 1.3 0.2 0.2 0.8 0.0 0.0 0.5 1.5 0.4 8 0.5 1.5 0.2 0.0 0.0 0.5 1.5 0.2 0.0 0.0 0.5 1.5 0.2 0.0 0.7 1.5 0.2 0.7 1.5 0.2 0.7 0.7 1.6 0.3 0.7 1.5 0.7 0.7 1.6 0.7 0.7 1.6 0.7 0.7 1.6 0.7 0.7 0.7 1.6 0.7 0.7 1.6 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	0.6 1.0 0.4 2.1 2.4 0.0 0.2 0.7 1.1 0.0 0.2 0.7 1.1 0.8 2.4 1.5 0.8 2.4 1.5 0.8 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.3 0.0 0.0 0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 V V V V 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	S.3. S.3.
2.8 0.6 3.0 4.0 0.4 1.2 0.6 1.8 1.3 4.9 4.2 9 4.2 0.9 4.2 0.9 4.2 0.9 4.2 0.9 4.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.6 0.2 0.4 1.1 1.9 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 2.0 0.5 1.2 1.3 2.0 0.5 1.2 1.3 2.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.0 0.0	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.4 0.4 0.8 6.3 1.7 2.9 1.5 6.7 1.8 6.7 1.8 6.7 1.8 6.7 1.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.2 0.2 0.2 0.2 0.4 0.4 0.5 0.5 0.2 0.2 0.2 0.4 0.4 0.5 0.5 0.5 0.2 0.2 0.4 0.4 0.5 0.5 0.5 0.2 0.2 0.4 0.4 0.5 0.5 0.5 0.5 0.5 0.5 0.2 0.2 0.4 0.4 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	2.0 0.0 0.4 1.5 1.7 1.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 0.0 0.0 0.0 0.0 0.0 0.0 1.1 1.0 0.0 0.0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	6.2 1.0 0.6 0.1 0.2 0.2 0.3 0.3 0.3 0.3 0.3 0.3 0.7 0.0 0.4 1.7 0.0 1.2 2.0 0.0 0.4 1.7 0.0 1.2 0.0 0.3 0.3 0.3 0.3 0.4 0.4 0.4 0.5 0.3 0.4 0.4 0.5 0.3 0.4 0.4 0.5 0.4 0.5 0.4 0.5 0.4 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	0.4 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.6 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.4 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.4 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	0.0 0.0 2.4 0.0 0.4 0.0 0.4 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 1.8 0.0 0.4 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3 0.0 0.0 0.7 2.8 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 3.6 4.1 1.7 1.3 4.0 1.7 0.9 0.0 1.2 3.5 0.0 0.7 1.2 1.3 1.0 1.1 3.6 4.1 1.7 1.3 0.5 1.1 3.6 1.1 1.7 1.3 1.0 1.1 3.6 1.1 1.7 1.3 1.0 1.1 1.7 1.3 1.1 3.6 1.1 1.7 1.7 1.1 3.6 1.1 1.7 1.7 1.7 1.7 1.7 1.7 1.7	0.9 0.4 3.3 2.3 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.3 2.1 2.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.6 0.3 3.6 0.7 1.3 0.4 0.0 1.8 3.0 2.1 1.7 0.6 0.8 2.2 1.4 0.3 0.0 0.6 0.9 0.0 0.9 0.0 0.9 0.0 0.7 1.2 1.3 0.0 1.4 0.6 8 0.7 1.4 0.6 1.7 1.5 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.0 1.7 1.3 0.4 0.0 1.8 0.2 1.1 0.7 1.5 1.5 0.7 1.5 1.5 0.7 1.5 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	1.4 0.3 4.0 0.3 1.5 0.3 0.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 5 0.8 0.0 0.0 0.5 1.5 0.8 0.0 0.0 0.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1	0.6 1.0 0.4 2.1 2.4 2.1 2.4 0.0 0.2 0.7 1.1 1.0 6 1.5 0.8 1.0 0.3 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.1 0.1 0.0 0.4 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 V V V 0.5 0.0 0.0 0.0 0.3 0.0 0.0 0.3 0.0 0.0 0.3 0.0 0.0	S.3. S.3.
2.8 0.6 3.0 4.0 0.4 1.2 2.9 4.2 1.7 2.9 4.2 1.8 1.0 2.7 0.9 2.7 0.9 2.7 0.9 2.7 0.9 2.7 0.9 2.7 0.9 2.7 0.9 2.7 0.0 0.6 0.6 0.6 0.0 0.0 0.0 0.0 0.0 0.0	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 0.6 0.2 0.4 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 2.0 0.5 1.2 1.3 2.0 0.5 1.2 1.4 1.4 1.6 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.0 0.0 0.0	0.6 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.2 0.4 1.3 1.7 1.5 6.7 1.5 6.7 1.8 6 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.0 0.0 0.4 1.5 1.7 1.4 1.5 1.7 1.4 1.5 1.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	0.6 0.4 0.1 0.0 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.3	L0 0.6 0.1 0.2 0.2 0.3 0.6 0.4 0.3 0.3 0.3 0.3 0.3 0.3 0.3 0.0 0.4 K L2 2.0 0.0 0.4 1.2 2.0 0.0 0.4 1.2 2.0 0.0 0.2 0.3 0.3 0.3 0.3 0.4 0.4 0.3 0.3 0.4 0.4 0.4 0.4 0.3 0.3 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.4 0.3 0.2 0.3 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.4 0.4 0.2 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.4 0.6 0.4 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.6 0.4 0.6 0.4 0.6 0.4 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	0.0 0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 0.3 1.8 0.0 0.4 0.4 0.8 0.1 0.8 0.2 2.2 1.2 1.9 0.5 0.0 0.7 2.8 0.3 0.0 0.7 2.8 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 1.1 7.1 3.6 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.6 0.0 1.1 7.1 3.5 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2	0.9 0.4 3.3 2.3 0.2 0.6 0.4 0.2 0.6 0.8 1.4 1.3 2.2 2.3 0.7 0.3 2.1 2.3 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 1.8 3.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 R R 0.3 0.0 0.6 0.9 0.0 0.0 0.9 1.2 1.3 0.0 0.7 1.3 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.3 0.4 1.4 0.6 0.0 1.8 0.4 0.4 0.6 0.0 1.8 0.4 0.4 0.6 0.8 0.4 0.4 0.6 0.8 0.4 0.4 0.4 0.6 0.0 0.8 0.4 0.4 0.6 0.0 0.8 0.4 0.4 0.4 0.6 0.0 0.8 0.4 0.4 0.6 0.0 0.8 0.8 0.0 0.0 0.8 0.0 0.0 0.0 0.0	1.4 0.3 4.0 0.3 4.0 0.3 0.6 1.5 0.3 0.0 0.7 1.6 1.3 0.0 0.7 1.6 1.3 2.9 1.6 1.3 1.1 1.7 0.2 5 0.8 0.0 0.0 0.5 1.5 0.2 9 1.6 5 0.8 0.0 0.0 0.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1	0.6 1.0 0.4 2.1 2.4 2.1 2.4 0.0 0.2 0.7 1.1 1.0 6 1.5 0.8 2.4 1.0 0.3 0.5 2.4 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.0 0.4 1.3 1.2 2.7 1.0 1.3 1.2 0.6 0.6 0.5 0.0 0.5 0.0 0.0 0.5 0.0 0.0 0.0 0.0	5.5 5.6 6.0 2.2 0.0 2.2 0.0 0.0 2.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
2.8 0.6 0.6 1.8 1.3 1.3 1.7 2.9 1.7 2.9 1.8 1.0 2.7 0.9 1.7 2.7 0.9 1.8 1.0 0.6 1.8 1.3 1.3 1.4.9 1.7 2.9 0.9 1.7 0.9 0.9 0.6 0.6 0.6 0.6 1.8 1.3 0.6 0.6 1.8 1.3 0.6 0.6 1.8 1.3 0.6 0.6 1.7 2.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0	1.5 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.6 0.4 0.2 0.4 1.1 1.3 1.9 0.7 0.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.3 0.5 0.1 0.4 0.7 1.3 0.5 1.2 2.0 1.4 1.6 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.0 0.0 0.0	0.6 0.0 0.0 0.5 0.1 0.0 0.8 0.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	3.8 0.5 0.2 0.2 0.2 0.4 1.3 1.7 1.5 1.5 6.7 1.8 6.7 1.8 6.7 1.8 6.7 1.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	2.0 0.0 0.4 1.5 1.7 1.4 0.6 1.8 0.0 1.3 1.5 1.2 0.3 0.0 0.0 0.0 0.0 1.1 1.5 1.2 0.0 0.0 0.0 0.0 1.1 1.5 1.5 0.0 0.0 0.0 0.0 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5	0.6 0.4 0.4 0.0 0.0 0.3 0.3 0.5 0.6 0.5 0.3 0.3 0.3 0.3 0.3 0.3 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.0 0.6 0.1 0.2 0.2 0.3 0.6 0.4 0.3 0.6 0.4 0.3 0.7 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.0 0.0 0.1 1.2 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.4 1.0 0.3 0.2 0.3 0.4 0.2 0.6 1.4 1.0 0.4 0.2 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4	0.0 0.0 2.4 0.0 0.4 0.0 1.7 0.0 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.3 0.3 0.3 1.8 0.0 0.4 0.4 0.8 0.1 0.2 2.2 2.2 1.2 0.5 0.0 0.7 2.8 0.3 0.0 0.0 0.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0	4.0 1.2 3.7 1.3 1.0 0.5 2.5 0.0 1.1 7.1 3.6 1.1 7.1 3.6 1.1 7.1 3.6 0.0 0.5 1.1 7.1 3.6 0.0 0.5 1.1 7.1 3.6 0.0 0.5 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.6 0.0 0.0 1.1 7.1 3.5 0.0 0.0 1.2 7.5 0.0 0.0 1.1 7.1 3.5 0.0 0.0 1.2 7.1 3.5 0.0 0.0 1.1 1.2 7.1 3.5 1.1 0.0 0.0 1.1 1.2 7.1 3.5 1.4 1.3 5.5 1.4 1.3 5.5 1.4 1.3 5.5 1.4 1.3 5.5 1.4 1.3 5.5 1.4 1.3 5.5 1.4 1.3 5.5 1.4 1.4 1.3 5.5 1.4 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.4 1.5 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4	0.9 0.4 3.3 2.3 0.2 0.6 0.4 0.2 0.6 0.8 1.4 1.3 2.2 2.3 0.7 0.7 0.3 2.1 2.3 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.6 0.3 3.6 0.7 1.3 0.4 0.6 0.0 2.1 2.1 1.7 0.6 0.8 2.2 1.4 R R 0.3 0.0 0.6 0.8 2.2 1.4 R 0.3 0.0 0.9 0.0 0.7 1.2 1.3 0.0 0.8 2.2 1.4 1.4 0.6 0.7 1.3 0.4 1.5 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.7 1.3 0.4 0.6 0.7 1.3 0.4 0.7 1.4 0.6 0.7 1.4 0.6 0.7 1.4 0.7 0.7 1.4 0.7 0.7 1.4 0.6 0.7 1.4 0.7 0.7 1.4 0.6 0.7 1.4 0.7 1.4 0.6 0.7 1.4 0.7 1.4 0.6 0.0 0.7 1.4 0.7 0.7 1.4 0.6 0.0 0.7 1.4 0.6 0.7 1.4 0.6 0.7 1.4 0.6 0.7 1.4 0.6 0.0 0.8 0.7 1.4 0.6 0.0 0.8 0.7 1.4 0.6 0.0 0.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	2.1.4 0.3 4.0 0.3 0.6 1.5 0.3 0.0 0.7 1.5 0.3 0.0 0.7 1.3 0.0 0.7 1.3 1.3 1.3 1.1 1.7 0.2 5 5 0.8 0.0 0.0 0.5 1.5 0.2 7 7.2 0.0 6 6 8 8 0.4 0.0 0.0 0.0 0.0 0.7 6 1.3 1.3 1.5 0.6 0.0 0.0 0.7 6 1.3 1.5 0.6 0.0 0.0 0.0 0.7 6 1.3 1.5 0.6 0.0 0.0 0.0 0.7 6 1.3 1.3 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.6 1.0 0.4 2.1 2.4 2.4 1.0 0.0 0.2 0.7 1.1 0.6 1.5 1.0 0.3 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.5 1.0 0.0 0.0 0.0 0.5 1.0 0.0 0.0 0.0 0.0 0.5 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	0.0 0.8 0.1 0.2 2.1 1.6 0.1 0.1 0.1 0.0 0.4 1.3 1.2 2.7 1.0 1.3 1.2 0.6 0.6 0.0 0.5 0.0 0.0 0.5 0.0 0.0 0.5 0.0 0.0	5.5 5.6 5.6 0.0 2.3 0.0 0.0 2.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
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Fig. 5. Dipeptide propensity for the 61-200 residue length linker set. Interpretation of figure refers to legend to Fig. 1.

Table 7	Table	7
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Fraction of predicted secondary structure in linker regions.

	Secondary structure						
	α-helix	β-strand	coil				
Actinobacteria	0.14	0.02	0.86				
Alphaproteobacteria	0.19	0.03	0.78				
Betaproteobacteria	0.30	0.01	0.69				
Firmicutes	0.02	0.06	0.92				
Gammaproteobacteria	0.26	0.02	0.72				



Fig. 6. Box-plots of the distribution of the average linker flexibility (index #425 of Table 2 in [1] and code VINM940101 in AAindex [10]). Horizontal axis indicates the average flexibility distribution in the wHTH, AAT domains, in all linkers, and in linkers belonging to different length intervals: 0–20, 21–40, 41–60 and > 60 residues. Y-axis reports the flexibility scale (label AI stands for Average Index). A, B, and C, denote Alphaproteobacteria, Betaproteobacteria, and Gammaproteobacteria, respectively.



Fig. 7. Box plots of the distribution of average linker hydrophobicity (index #58 of Table 2 in [1] and code CIDH920105 in AAindex [10]). For interpretation of plots, refer to Fig. 6 caption.



Fig. 8. Box plots of the distribution of average Linker propensity index (#491 of Table 2 in [1] and code GEOR03010 in AAindex [10]). For interpretation of plots, refer to Fig. 6 caption.



Fig. 9. Box plots of the distribution of the average normalized β -turn propensity (index #37 Table 2 in [1] and code CHOP780101 in AAindex [10]). For interpretation of plots, refer to Fig. 6 caption.



Fig. 10. Box plots of the distribution of the average Chou–Fasman coil propensity (#24 of Table 2 in [1] and code CHAM830101 in AAindex [10]). For interpretation of plots, refer to Fig. 6 caption.



Fig. 11. Box plots of the distribution of average normalized α -helix propensity (index #38 of Table 2 in [1] and code CHOP780102 in AAindex [10]). A, B, C, D and E denote Actinobacteria, Alphaproteobacteria, Betaproteobacteria, Firmicutes and Gammaproteobacteria, respectively.



Fig. 12. Box plots of the distribution of average normalized β -sheet propensity (index #39 of Table 2 in [1] and code CHOP780103 in AAindex [10]). Letter interpretation is as in Fig. 11 caption.



Fig. 13. Histogram of the linker length distribution in the MocR subgroups GabR and PdxR. Horizontal axis labels indicate length intervals: 20 corresponds to 0–20, 30 (21–30), 40 (31–40), 50 (41–50), 60 (51–60) and > 60 (longer than 60 residues). Percentage (%) on the vertical axis indicates the fraction of linkers in the length interval. Sequences were retrieved from the reference proteomes data bank available at the Hmmer web server [17] using a significance E-value thresholds equal to 10⁻¹²⁰. With this threshold, 885 and 334 sequences were retrieved for GabR and PdxR, respectively.

Table 8

GabR and PdxR sequences retrieved from RegPrecise data bank.

GabR

UniProt code	Specie	Phylum
A0A098SFD5	Acinetobacter baumannii AB0057	Gammaproteobacteria
Q6F766	Acinetobacter sp. AD	Gammaproteobacteria
A7Z1D7	Bacillus amyloliquefaciens FZB42	Firmicutes
A8F9Y9	Bacillus pumilus SAFR 032	Firmicutes
P94426	Bacillus subtilis subsp. subtilis str. 168	Firmicutes
O2KX56	Bordetella avium 197N	Betaproteobacteria
A0A0H3LKN1	Bordetella bronchiseptica RB50	Betaproteobacteria
O0B6G3	Burkholderia cepacia AMMD	Betaproteobacteria
C5ALU9	Burkholderia glumae BGR1	Betaproteobacteria
A0A0H2XDM4	Burkholderia mallei ATCC 23344	Betaproteobacteria
B2JSD8	Burkholderia phymatum STM815	Betaproteobacteria
B2JR38	Burkholderia phymatum STM815	Betaproteobacteria
063NL7	Burkholderia pseudomallei K96243	Betaproteobacteria
A4JIX2	Burkholderia vietnamiensis G4	Betaproteobacteria
013LC0	Burkholderia xenovorans LB400	Betaproteobacteria
A9BMY2	Delfia acidovorans SPH-1	Betaproteobacteria
D4HXE9	Erwinia amylovora ATCC 49946	Gammaproteobacteria
O6D5I8	Erwinia carotovora subsp.atroseptica	Gammaproteobacteria
	SCRI1043	1
A6TF79	Klebsiella pneumonia subsp. pneumo-	Gammaproteobacteria
	niae MGH 78578	1
B2U7Y5	Ralstonia pickettii 121	Betaproteobacteria
A8GJW1	Serratia proteamaculans 568	Gammaproteobacteria
O4A0R1	Staphylococcus saprophyticus subsp.	Firmicutes
0	saprophyticus ATCC 15305	
C4ZIR5	Thauera sp.MZ1T	Betaproteobacteria
07CIK7	Yersinia pestis KIM	Gammaproteobacteria
A1VQK3	Polaromonas naphthalenivorans CJ2	Betaproteobacteria
0129G7	Polaromonas sp. IS666	Betaproteobacteria
0221G1	Rhodoferax ferrireducens DSM 15236	Betaproteobacteria
C5CM40	Variovorax paradoxus S110	Betaproteobacteria
D.L.D.		
PUXK	An ann callum thannan bilum DCMC725	Finneisutes
B9INIKZU	Anderocellum thermophilum DSM6725	Firmicutes
Α4ΧΙΒ4	DSM 8903	Firmicutes
Q929S0	Listeria innocua Clip11262	Firmicutes
Q8Y5G3	Listeria monocytogenes EGD e	Firmicutes
A0AKK7	Listeria welshimeri serovar 6b str.	Firmicutes
	SLCC5334	
C7MF20	Brachybacterium faecium DSM 4810	Actinobacteria
Q6AFC0	Leifsonia xyli subsp.xyli str. CTCB07	Actinobacteria
B3GXB5	Actinobacillus pleuropneumoniae servar 7 str. AP76	Gammaproteobacteria
O5WKW3	Bacillus clausii KSM K16	Firmicutes
C3PLB2	Corvnebacterium aurimucosum ATCC	Actinobacteria
0000000	700975	
Q6NK11	Corynebacterium diphtheriae NCIC 13129	Actinobacteria
Q8NS92	Corynebacterium glutamicum ATCC 13032	Actinobacteria
B2GK63	Kocuria rhizophila DC2201	Actinobacteria
B9E8T3	Macrococcus caseolyticus JCSC5402	Firmicutes
W8TRW2	Staphylococcus aureus subsp. aureus	Firmicutes
	N325	
B9DKX6	Staphylococcus aureus subsp.carnosus TM300	Firmicutes

GabR		
UniProt code	Specie	Phylum
A0A0H2VKR4 A0A0Q1AKJ7 Q49V27	Staphylococcus epidermidis ATCC 12228 Staphylococcus haemolyticus JCSC1435 Staphylococcus saprophyticus subsp. saprophyticus ATCC15035	Firmicutes Firmicutes Firmicutes

Table 8 (continued)

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Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at http://dx.doi. org/10.1016/j.dib.2016.08.064.

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