



SUPPLEMENTARY MATERIAL TO
**A quantitative structure–activity relationship (QSAR) study of
peptide drugs based on a new descriptor of amino acids**

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TABLE S-I. The meanings of 99 WHIM descriptors

ID	Symbol	Meaning
1	L1u	1st component size directional WHIM index/unweighted
2	L2u	2nd component size directional WHIM index/unweighted
3	L3u	3rd component size directional WHIM index/unweighted
4	P1u	1st component shape directional WHIM index/unweighted
5	P2u	2nd component shape directional WHIM index/unweighted
6	G1u	1st component symmetry directional WHIM index/unweighted
7	G2u	2nd component symmetry directional WHIM index/unweighted
8	G3u	3rd component symmetry directional WHIM index/unweighted
9	E1u	1st component accessibility directional WHIM index/unweighted
10	E2u	2nd component accessibility directional WHIM index/unweighted
11	E3u	3rd component accessibility directional WHIM index/unweighted
12	L1m	1st component size directional WHIM index/weighted by atomic masses
13	L2m	2nd component size directional WHIM index/weighted by atomic masses
14	L3m	3rd component size directional WHIM index/weighted by atomic masses
15	P1m	1st component shape directional WHIM index/weighted by atomic masses
16	P2m	2nd component shape directional WHIM index/weighted by atomic masses
17	G1m	1st component symmetry directional WHIM index/weighted by atomic masses
18	G2m	2nd component symmetry directional WHIM index/weighted by atomic masses
19	G3m	3rd component symmetry directional WHIM index/weighted by atomic masses
20	E1m	1st component accessibility directional WHIM index/weighted by atomic masses
21	E2m	2nd component accessibility directional WHIM index/weighted by atomic masses
22	E3m	3rd component accessibility directional WHIM index/weighted by atomic masses

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TABLE S-I. Continued

ID	Symbol	Meaning
23	L1v	1st component size directional WHIM index/weighted by atomic van der Waals volumes
24	L2v	2nd component size directional WHIM index/weighted by atomic van der Waals volumes
25	L3v	3rd component size directional WHIM index/weighted by atomic van der Waals volumes
26	P1v	1st component shape directional WHIM index/weighted by atomic van der Waals volumes
27	P2v	2nd component shape directional WHIM index/weighted by atomic van der Waals volumes
28	G1v	1st component symmetry directional WHIM index/weighted by atomic van der Waals volumes
29	G2v	2nd component symmetry directional WHIM index/weighted by atomic van der Waals volumes
30	G3v	3rd component symmetry directional WHIM index/weighted by atomic van der Waals volumes
31	E1v	1st component accessibility directional WHIM index/weighted by atomic van der Waals volumes
32	E2v	2nd component accessibility directional WHIM index/weighted by atomic van der Waals volumes
33	E3v	3rd component accessibility directional WHIM index/weighted by atomic van der Waals volumes
34	L1e	1st component size directional WHIM index/weighted by atomic Sanderson electronegativities
35	L2e	2nd component size directional WHIM index/weighted by atomic Sanderson electronegativities
36	L3e	3rd component size directional WHIM index/weighted by atomic Sanderson electronegativities
37	P1e	1st component shape directional WHIM index/weighted by atomic Sanderson electronegativities
38	P2e	2nd component shape directional WHIM index/weighted by atomic Sanderson electronegativities
39	G1e	1st component symmetry directional WHIM index/weighted by atomic Sanderson electronegativities
40	G2e	2nd component symmetry directional WHIM index/weighted by atomic Sanderson electronegativities
41	G3e	3rd component symmetry directional WHIM index/weighted by atomic Sanderson electronegativities
42	E1e	1st component accessibility directional WHIM index/weighted by atomic Sanderson electronegativities
43	E2e	2nd component accessibility directional WHIM index/weighted by atomic Sanderson electronegativities
44	E3e	3rd component accessibility directional WHIM index/weighted by atomic Sanderson electronegativities

TABLE S-I. Continued

ID	Symbol	Meaning
45	L1p	1st component size directional WHIM index/weighted by atomic polarizabilities
46	L2p	2nd component size directional WHIM index/weighted by atomic polarizabilities
47	L3p	3rd component size directional WHIM index/weighted by atomic polarizabilities
48	P1p	1st component shape directional WHIM index/weighted by atomic polarizabilities
49	P2p	2nd component shape directional WHIM index/weighted by atomic polarizabilities
50	G1p	1st component symmetry directional WHIM index/weighted by atomic polarizabilities
51	G2p	2nd component symmetry directional WHIM index/weighted by atomic polarizabilities
52	G3p	3rd component symmetry directional WHIM index/weighted by atomic polarizabilities
53	E1p	1st component accessibility directional WHIM index/weighted by atomic polarizabilities
54	E2p	2nd component accessibility directional WHIM index/weighted by atomic polarizabilities
55	E3p	3rd component accessibility directional WHIM index/weighted by atomic polarizabilities
56	L1s	1st component size directional WHIM index/weighted by atomic electrotopological states
57	L2s	2nd component size directional WHIM index/weighted by atomic electrotopological states
58	L3s	3rd component size directional WHIM index/weighted by atomic electrotopological states
59	P1s	1st component shape directional WHIM index/weighted by atomic electrotopological states
60	P2s	2nd component shape directional WHIM index/weighted by atomic electrotopological states
61	G1s	1st component symmetry directional WHIM index/weighted by atomic electrotopological states
62	G2s	2nd component symmetry directional WHIM index/weighted by atomic electrotopological states
63	G3s	3rd component symmetry directional WHIM index/weighted by atomic electrotopological states
64	E1s	1st component accessibility directional WHIM index/weighted by atomic electrotopological states
65	E2s	2nd component accessibility directional WHIM index/weighted by atomic electrotopological states
66	E3s	3rd component accessibility directional WHIM index/weighted by atomic electrotopological states
67	Tu	T total size index/unweighted

TABLE S-I. Continued

ID	Symbol	Meaning
68	Tm	T total size index/weighted by atomic masses
69	Tv	T total size index/weighted by atomic van der Waals volumes
70	Te	T total size index/weighted by atomic Sanderson electronegativities
71	Tp	T total size index/weighted by atomic polarizabilities
72	Ts	T total size index/weighted by atomic electrotopological states
73	Au	A total size index/unweighted
74	Am	A total size index/weighted by atomic masses
75	Av	A total size index/weighted by atomic van der Waals volumes
76	Ae	A total size index/weighted by atomic Sanderson electronegativities
77	Ap	A total size index/weighted by atomic polarizabilities
78	As	A total size index/weighted by atomic electrotopological states
79	Gu	G total symmetry index/unweighted
80	Gm	G total symmetry index/weighted by atomic masses
81	Gs	G total symmetry index/weighted by atomic Sanderson electronegativities
82	Ku	K global shape index/unweighted
83	Km	K global shape index/weighted by atomic masses
84	Kv	K global shape index/weighted by atomic van der Waals volumes
85	Ke	K global shape index/weighted by atomic Sanderson electronegativities
86	Kp	K global shape index/weighted by atomic polarizabilities
87	Ks	K global shape index/weighted by atomic electrotopological states
88	Du	D total accessibility index/unweighted
89	Dm	D total accessibility index/weighted by atomic masses
90	Dv	D total accessibility index/weighted by atomic van der Waals volumes
91	De	D total accessibility index/weighted by atomic Sanderson electronegativities
92	Dp	D total accessibility index/weighted by atomic polarizabilities
93	Ds	D total accessibility index/weighted by atomic electrotopological states
94	Vu	V total size index/unweighted
95	Vm	V total size index/weighted by atomic masses
96	Vv	V total size index/weighted by atomic van der Waals volumes
97	Ve	V total size index/weighted by atomic Sanderson electronegativities
98	Vp	V total size index/weighted by atomic polarizabilities
99	Vs	V total size index/weighted by atomic electrotopological states

TABLE S-II. The meanings of 74 geometrical descriptors

ID	Symbol	Meaning
1	W3D	3D-Wener index
2	J3D	3D-Balaban index
3	H3D	3D-Harary index
4	AGDD	Average geometric distance degree
5	DDI	D/D index
6	ADDD	Average distance/ distance degree
7	G1	Gravitational index G1
8	G2	Gravitational index G2(bond-restricted)
9	RGyr	Radius of gyration (mass weighted)
10	SPAN	Span R

TABLE S-II. Continued

ID	Symbol	Meaning
11	SPAM	Average span R
12	MEcc	Average eccentricity
13	SPH	Spherosity
14	ASP	Asphericity
15	FDI	Folding degree index
16	PJI3	3D petitjean shape index
17	L/Bw	Length-to-breadth ratio by WHIM
18	SEig	Absolute eigenvalue sum on geometry matrix
19	HOMA	Harmonic Oscillator Model of Aromaticity index
20	RCI	Jug RG index
21	AROM	Aromaticity index
22	HOMT	HOMA total
23	DISPm	d COMMA2 value /weighted by atomic masses
24	QXXm	Qxx COMMA 2 value /weighted by atomic masses
25	QYYm	Qyy COMMA 2 value /weighted by atomic masses
26	QZZm	Qzz COMMA 2 value /weighted by atomic masses
27	DISPv	d COMMA2 value /weighted by atomic van der waals volumes
28	QXXv	Qxx COMMA 2 value /weighted by atomic van der Waals volumes
29	QYYv	Qyy COMMA 2 value /weighted by atomic van der Waals volumes
30	QZZv	Qzz COMMA 2 value /weighted by atomic van der Waals volumes
31	DISPe	d COMMA2 value /weighted by atomic Sanderson electronegativities
32	QXXe	Qxx COMMA 2 value /weighted by atomic Sanderson electronegativities
33	QYYe	Qyy COMMA 2 value /weighted by atomic Sanderson electronegativities
34	QZZe	Qzz COMMA 2 value /weighted by atomic Sanderson electronegativities
35	DISPp	d COMMA2 value /weighted by atomic polarizabilities
36	QXXp	Qxx COMMA 2 value /weighted by atomic polarizabilities
37	QYYp	Qyy COMMA 2 value /weighted by atomic polarizabilities
38	QZZp	Qzz COMMA 2 value /weighted by atomic polarizabilities
39	G(N..N)	Sum of geometrical distance between N..N
40	G(N..O)	Sum of geometrical distance between N..O
41	G(N..S)	Sum of geometrical distance between N..S
42	G(N..P)	Sum of geometrical distance between N..P
43	G(N..F)	Sum of geometrical distance between N..F
44	G(N..Cl)	Sum of geometrical distance between N..Cl
45	G(N..Br)	Sum of geometrical distance between N..Br
46	G(N..I)	Sum of geometrical distance between N..I
47	G(O..O)	Sum of geometrical distance between O..O
48	G(O..S)	Sum of geometrical distance between O..S
49	G(O..P)	Sum of geometrical distance between O..P
50	G(O..F)	Sum of geometrical distance between O..F
51	G(O..Cl)	Sum of geometrical distance between O..Cl
52	G(O..Br)	Sum of geometrical distance between O..Br
53	G(O..I)	Sum of geometrical distance between O..I
54	G(S..S)	Sum of geometrical distance between S..S
55	G(S..P)	Sum of geometrical distance between S..P

TABLE S-II. Continued

ID	Symbol	Meaning
56	G(S..F)	Sum of geometrical distance between S..F
57	G(S..Cl)	Sum of geometrical distance between S..Cl
58	G(S..Br)	Sum of geometrical distance between S..Br
59	G(S..I)	Sum of geometrical distance between S..I
60	G(P..P)	Sum of geometrical distance between P..P
61	G(P..F)	Sum of geometrical distance between P..F
62	G(P..Cl)	Sum of geometrical distance between P..Cl
63	G(P..Br)	Sum of geometrical distance between P..Br
64	G(P..I)	Sum of geometrical distance between P..I
65	G(F..F)	Sum of geometrical distance between F..F
66	G(F..Cl)	Sum of geometrical distance between F..Cl
67	G(F..Br)	Sum of geometrical distance between F..Br
68	G(F..I)	Sum of geometrical distance between F..I
69	G(Cl..Cl)	Sum of geometrical distance between Cl..Cl
70	G(Cl..Br)	Sum of geometrical distance between Cl..Br
71	G(Cl..I)	Sum of geometrical distance between Cl..I
72	G(Br..Br)	Sum of geometrical distance between Br..Br
73	G(Br..I)	Sum of geometrical distance between Br..I
74	G(I..I)	Sum of geometrical distance between I..I

TABLE S-III. The meanings of 160 3D-MORSE descriptors

ID	Symbol	Meaning
1	Mor01u	3D-MoRSE -signal 01/unweighted
2	Mor02u	3D-MoRSE -signal 02/unweighted
3	Mor03u	3D-MoRSE -signal 03/unweighted
4	Mor04u	3D-MoRSE -signal 04/unweighted
5	Mor05u	3D-MoRSE -signal 05/unweighted
6	Mor06u	3D-MoRSE -signal 06/unweighted
7	Mor07u	3D-MoRSE -signal 07/unweighted
8	Mor08u	3D-MoRSE -signal 08/unweighted
9	Mor09u	3D-MoRSE -signal 09/unweighted
10	Mor10u	3D-MoRSE -signal 10/unweighted
11	Mor11u	3D-MoRSE -signal 11/unweighted
12	Mor12u	3D-MoRSE -signal 12/unweighted
13	Mor13u	3D-MoRSE -signal 13/unweighted
14	Mor14u	3D-MoRSE -signal 14/unweighted
15	Mor15u	3D-MoRSE -signal 15/unweighted
16	Mor16u	3D-MoRSE -signal 16/unweighted
17	Mor17u	3D-MoRSE -signal 17/unweighted
18	Mor18u	3D-MoRSE -signal 18/unweighted
19	Mor19u	3D-MoRSE -signal 19/unweighted
20	Mor20u	3D-MoRSE -signal 20/unweighted
21	Mor21u	3D-MoRSE -signal 21/unweighted
22	Mor22u	3D-MoRSE -signal 22/unweighted
23	Mor23u	3D-MoRSE -signal 23/unweighted

TABLE S-III. Continued

ID	Symbol	Meaning
24	Mor24u	3D-MoRSE -signal 24/unweighted
25	Mor25u	3D-MoRSE -signal 25/unweighted
26	Mor26u	3D-MoRSE -signal 26/unweighted
27	Mor27u	3D-MoRSE -signal 27/unweighted
28	Mor28u	3D-MoRSE -signal 28/unweighted
29	Mor29u	3D-MoRSE -signal 29/unweighted
30	Mor30u	3D-MoRSE -signal 30/unweighted
31	Mor31u	3D-MoRSE -signal 31/unweighted
32	Mor32u	3D-MoRSE -signal 32/unweighted
33	Mor01m	3D-MoRSE -signal 01/weighted by atomic masses
34	Mor02m	3D-MoRSE -signal 02/weighted by atomic masses
35	Mor03m	3D-MoRSE -signal 03/weighted by atomic masses
36	Mor04m	3D-MoRSE -signal 04/weighted by atomic masses
37	Mor05m	3D-MoRSE -signal 05/weighted by atomic masses
38	Mor06m	3D-MoRSE -signal 06/weighted by atomic masses
39	Mor07m	3D-MoRSE -signal 07/weighted by atomic masses
40	Mor08m	3D-MoRSE -signal 08/weighted by atomic masses
41	Mor09m	3D-MoRSE -signal 09/weighted by atomic masses
42	Mor10m	3D-MoRSE -signal 10/weighted by atomic masses
43	Mor11m	3D-MoRSE -signal 11/weighted by atomic masses
44	Mor12m	3D-MoRSE -signal 12/weighted by atomic masses
45	Mor13m	3D-MoRSE -signal 13/weighted by atomic masses
46	Mor14m	3D-MoRSE -signal 14/weighted by atomic masses
47	Mor15m	3D-MoRSE -signal 15/weighted by atomic masses
48	Mor16m	3D-MoRSE -signal 16/weighted by atomic masses
49	Mor17m	3D-MoRSE -signal 17/weighted by atomic masses
50	Mor18m	3D-MoRSE -signal 18/weighted by atomic masses
51	Mor19m	3D-MoRSE -signal 19/weighted by atomic masses
52	Mor20m	3D-MoRSE -signal 20/weighted by atomic masses
53	Mor21m	3D-MoRSE -signal 21/weighted by atomic masses
54	Mor22m	3D-MoRSE -signal 22/weighted by atomic masses
55	Mor23m	3D-MoRSE -signal 23/weighted by atomic masses
56	Mor24m	3D-MoRSE -signal 24/weighted by atomic masses
57	Mor25m	3D-MoRSE -signal 25/weighted by atomic masses
58	Mor26m	3D-MoRSE -signal 26/weighted by atomic masses
59	Mor27m	3D-MoRSE -signal 27/weighted by atomic masses
60	Mor28m	3D-MoRSE -signal 28/weighted by atomic masses
61	Mor29m	3D-MoRSE -signal 29/weighted by atomic masses
62	Mor30m	3D-MoRSE -signal 30/weighted by atomic masses
63	Mor31m	3D-MoRSE -signal 31/weighted by atomic masses
64	Mor32m	3D-MoRSE -signal 32/weighted by atomic masses
65	Mor01v	3D-MoRSE -signal 01/weighted by atomic van der Waals volumes
66	Mor02v	3D-MoRSE -signal 02/weighted by atomic van der Waals volumes
67	Mor03v	3D-MoRSE -signal 03/weighted by atomic van der Waals volumes
68	Mor04v	3D-MoRSE -signal 04/weighted by atomic van der Waals volumes

TABLE S-III. Continued

ID	Symbol	Meaning
69	Mor05v	3D-MoRSE -signal 05/weighted by atomic van der Waals volumes
70	Mor06v	3D-MoRSE -signal 06/weighted by atomic van der Waals volumes
71	Mor07v	3D-MoRSE -signal 07/weighted by atomic van der Waals volumes
72	Mor08v	3D-MoRSE -signal 08/weighted by atomic van der Waals volumes
73	Mor09v	3D-MoRSE -signal 09/weighted by atomic van der Waals volumes
74	Mor10v	3D-MoRSE -signal 10/weighted by atomic van der Waals volumes
75	Mor11v	3D-MoRSE -signal 11/weighted by atomic van der Waals volumes
76	Mor12v	3D-MoRSE -signal 12/weighted by atomic van der Waals volumes
77	Mor13v	3D-MoRSE -signal 13/weighted by atomic van der Waals volumes
78	Mor14v	3D-MoRSE -signal 14/weighted by atomic van der Waals volumes
79	Mor15v	3D-MoRSE -signal 15/weighted by atomic van der Waals volumes
80	Mor16v	3D-MoRSE -signal 16/weighted by atomic van der Waals volumes
81	Mor17v	3D-MoRSE -signal 17/weighted by atomic van der Waals volumes
82	Mor18v	3D-MoRSE -signal 18/weighted by atomic van der Waals volumes
83	Mor19v	3D-MoRSE -signal 19/weighted by atomic van der Waals volumes
84	Mor20v	3D-MoRSE -signal 20/weighted by atomic van der Waals volumes
85	Mor21v	3D-MoRSE -signal 21/weighted by atomic van der Waals volumes
86	Mor22v	3D-MoRSE -signal 22/weighted by atomic van der Waals volumes
87	Mor23v	3D-MoRSE -signal 23/weighted by atomic van der Waals volumes
88	Mor24v	3D-MoRSE -signal 24/weighted by atomic van der Waals volumes
89	Mor25v	3D-MoRSE -signal 25/weighted by atomic van der Waals volumes
90	Mor26v	3D-MoRSE -signal 26/weighted by atomic van der Waals volumes
91	Mor27v	3D-MoRSE -signal 27/weighted by atomic van der Waals volumes
92	Mor28v	3D-MoRSE -signal 28/weighted by atomic van der Waals volumes
93	Mor29v	3D-MoRSE -signal 29/weighted by atomic van der Waals volumes
94	Mor30v	3D-MoRSE -signal 30/weighted by atomic van der Waals volumes
95	Mor31v	3D-MoRSE -signal 31/weighted by atomic van der Waals volumes
96	Mor32v	3D-MoRSE -signal 32/weighted by atomic van der Waals volumes
97	Mor01e	3D-MoRSE -signal 01/weighted by atomic Sanderson electronegativities
98	Mor02e	3D-MoRSE -signal 02/weighted by atomic Sanderson electronegativities
99	Mor03e	3D-MoRSE -signal 03/weighted by atomic Sanderson electronegativities
100	Mor04e	3D-MoRSE -signal 04/weighted by atomic Sanderson electronegativities
101	Mor05e	3D-MoRSE -signal 05/weighted by atomic Sanderson electronegativities
102	Mor06e	3D-MoRSE -signal 06/weighted by atomic Sanderson electronegativities
103	Mor07e	3D-MoRSE -signal 07/weighted by atomic Sanderson electronegativities
104	Mor08e	3D-MoRSE -signal 08/weighted by atomic Sanderson electronegativities
105	Mor09e	3D-MoRSE -signal 09/weighted by atomic Sanderson electronegativities
106	Mor10e	3D-MoRSE -signal 10/weighted by atomic Sanderson electronegativities
107	Mor11e	3D-MoRSE -signal 11/weighted by atomic Sanderson electronegativities
108	Mor12e	3D-MoRSE -signal 12/weighted by atomic Sanderson electronegativities
109	Mor13e	3D-MoRSE -signal 13/weighted by atomic Sanderson electronegativities
110	Mor14e	3D-MoRSE -signal 14/weighted by atomic Sanderson electronegativities
111	Mor15e	3D-MoRSE -signal 15/weighted by atomic Sanderson electronegativities
112	Mor16e	3D-MoRSE -signal 16/weighted by atomic Sanderson electronegativities
113	Mor17e	3D-MoRSE -signal 17/weighted by atomic Sanderson electronegativities

TABLE S-III. Continued

ID	Symbol	Meaning
114	Mor18e	3D-MoRSE -signal 18/weighted by atomic Sanderson electronegativities
115	Mor19e	3D-MoRSE -signal 19/weighted by atomic Sanderson electronegativities
116	Mor20e	3D-MoRSE -signal 20/weighted by atomic Sanderson electronegativities
117	Mor21e	3D-MoRSE -signal 21/weighted by atomic Sanderson electronegativities
118	Mor22e	3D-MoRSE -signal 22/weighted by atomic Sanderson electronegativities
119	Mor23e	3D-MoRSE -signal 23/weighted by atomic Sanderson electronegativities
120	Mor24e	3D-MoRSE -signal 24/weighted by atomic Sanderson electronegativities
121	Mor25e	3D-MoRSE -signal 25/weighted by atomic Sanderson electronegativities
122	Mor26e	3D-MoRSE -signal 26/weighted by atomic Sanderson electronegativities
123	Mor27e	3D-MoRSE -signal 27/weighted by atomic Sanderson electronegativities
124	Mor28e	3D-MoRSE -signal 28/weighted by atomic Sanderson electronegativities
125	Mor29e	3D-MoRSE -signal 29/weighted by atomic Sanderson electronegativities
126	Mor30e	3D-MoRSE -signal 30/weighted by atomic Sanderson electronegativities
127	Mor31e	3D-MoRSE -signal 31/weighted by atomic Sanderson electronegativities
128	Mor32e	3D-MoRSE -signal 32/weighted by atomic Sanderson electronegativities
129	Mor01p	3D-MoRSE -signal 01/weighted by atomic polarizabilities
130	Mor02p	3D-MoRSE -signal 02/weighted by atomic polarizabilities
131	Mor03p	3D-MoRSE -signal 03/weighted by atomic polarizabilities
132	Mor04p	3D-MoRSE -signal 04/weighted by atomic polarizabilities
133	Mor05p	3D-MoRSE -signal 05/weighted by atomic polarizabilities
134	Mor06p	3D-MoRSE -signal 06/weighted by atomic polarizabilities
135	Mor07p	3D-MoRSE -signal 07/weighted by atomic polarizabilities
136	Mor08p	3D-MoRSE -signal 08/weighted by atomic polarizabilities
137	Mor09p	3D-MoRSE -signal 09/weighted by atomic polarizabilities
138	Mor10p	3D-MoRSE -signal 10/weighted by atomic polarizabilities
139	Mor11p	3D-MoRSE -signal 11/weighted by atomic polarizabilities
140	Mor12p	3D-MoRSE -signal 12/weighted by atomic polarizabilities
141	Mor13p	3D-MoRSE -signal 13/weighted by atomic polarizabilities
142	Mor14p	3D-MoRSE -signal 14/weighted by atomic polarizabilities
143	Mor15p	3D-MoRSE -signal 15/weighted by atomic polarizabilities
144	Mor16p	3D-MoRSE -signal 16/weighted by atomic polarizabilities
145	Mor17p	3D-MoRSE -signal 17/weighted by atomic polarizabilities
146	Mor18p	3D-MoRSE -signal 18/weighted by atomic polarizabilities
147	Mor19p	3D-MoRSE -signal 19/weighted by atomic polarizabilities
148	Mor20p	3D-MoRSE -signal 20/weighted by atomic polarizabilities
149	Mor21p	3D-MoRSE -signal 21/weighted by atomic polarizabilities
150	Mor22p	3D-MoRSE -signal 22/weighted by atomic polarizabilities
151	Mor23p	3D-MoRSE -signal 23/weighted by atomic polarizabilities
152	Mor24p	3D-MoRSE -signal 24/weighted by atomic polarizabilities
153	Mor25p	3D-MoRSE -signal 25/weighted by atomic polarizabilities
154	Mor26p	3D-MoRSE -signal 26/weighted by atomic polarizabilities
155	Mor27p	3D-MoRSE -signal 27/weighted by atomic polarizabilities
156	Mor28p	3D-MoRSE -signal 28/weighted by atomic polarizabilities
157	Mor29p	3D-MoRSE -signal 29/weighted by atomic polarizabilities
158	Mor30p	3D-MoRSE -signal 30/weighted by atomic polarizabilities
159	Mor31p	3D-MoRSE -signal 31/weighted by atomic polarizabilities
160	Mor32p	3D-MoRSE -signal 32/weighted by atomic polarizabilities

TABLE S-IV. The values of 99 WHIM descriptors of 20 amino acid

Amino acid	1	2	3	4	5	6	7	8	9	10
Ala A	2.076	1.214	0.482	0.55	0.322	0.213	0.213	0.213	0.427	0.51
Arg R	7.806	1.54	0.675	0.779	0.154	0.175	0.175	0.175	0.543	0.387
Asn N	2.115	1.541	0.908	0.463	0.338	0.197	0.236	0.197	0.579	0.503
Asp D	2.579	1.498	0.863	0.522	0.303	0.2	0.2	0.2	0.447	0.395
Cys C	2.627	1.089	0.638	0.603	0.25	0.208	0.208	0.208	0.43	0.424
Gln Q	4.74	1.209	0.66	0.717	0.183	0.188	0.219	0.188	0.509	0.448
Glu E	4.059	1.324	0.86	0.65	0.212	0.191	0.191	0.191	0.465	0.37
Gly G	2.36	0.727	0.168	0.725	0.223	0.231	0.231	0.231	0.482	0.446
His H	4.126	1.475	0.964	0.628	0.225	0.188	0.188	0.188	0.502	0.35
Ile I	3.163	1.692	1.022	0.538	0.288	0.183	0.183	0.183	0.49	0.461
Leu L	3.25	1.692	0.959	0.551	0.287	0.183	0.183	0.211	0.594	0.548
Lys K	6.389	1.219	0.862	0.754	0.144	0.179	0.179	0.179	0.55	0.35
Met M	5.175	1.355	0.866	0.7	0.183	0.188	0.188	0.188	0.491	0.367
Phe F	6.581	1.404	0.702	0.758	0.162	0.181	0.207	0.181	0.497	0.464
Pro P	2.17	1.347	0.775	0.506	0.314	0.197	0.197	0.197	0.497	0.553
Ser S	2.076	1.272	0.741	0.508	0.311	0.208	0.208	0.208	0.452	0.456
Thr T	2.884	1.397	0.624	0.588	0.285	0.197	0.197	0.197	0.471	0.36
Trp W	7.091	2.364	0.711	0.698	0.232	0.174	0.174	0.195	0.569	0.487
Tyr Y	6.392	1.859	0.716	0.713	0.207	0.179	0.179	0.179	0.523	0.448
Val V	3.033	1.424	0.784	0.579	0.272	0.191	0.191	0.191	0.433	0.527
	11	12	13	14	15	16	17	18	19	20
Ala A	0.306	1.835	0.891	0.292	0.608	0.295	0.213	0.213	0.213	0.352
Arg R	0.423	7.543	1.347	0.419	0.81	0.145	0.175	0.175	0.175	0.518
Asn N	0.455	2.38	1.404	0.428	0.565	0.333	0.197	0.197	0.197	0.791
Asp D	0.489	2.684	0.95	0.664	0.624	0.221	0.2	0.2	0.2	0.492
Cys C	0.428	3.449	0.708	0.323	0.77	0.158	0.208	0.208	0.208	0.767
Gln Q	0.408	4.594	1.12	0.304	0.777	0.176	0.188	0.188	0.188	0.637
Glu E	0.515	4.685	0.899	0.643	0.752	0.144	0.191	0.191	0.191	0.639
Gly G	0.202	1.814	0.661	0.045	0.72	0.262	0.231	0.231	0.231	0.29
His H	0.418	3.985	1.136	0.541	0.704	0.201	0.188	0.188	0.188	0.516
Ile I	0.549	3.146	1.111	0.712	0.633	0.224	0.183	0.211	0.183	0.502
Leu L	0.544	2.924	1.278	0.6	0.609	0.266	0.183	0.183	0.183	0.524
Lys K	0.508	6.63	0.917	0.556	0.818	0.113	0.179	0.179	0.179	0.598
Met M	0.428	4.902	0.849	0.646	0.766	0.133	0.188	0.188	0.188	0.489
Phe F	0.465	6.635	0.825	0.409	0.843	0.105	0.181	0.181	0.181	0.504
Pro P	0.451	2.747	0.862	0.325	0.698	0.219	0.197	0.197	0.197	0.774
Ser S	0.467	1.854	0.94	0.466	0.569	0.288	0.208	0.208	0.208	0.41
Thr T	0.428	2.703	1.067	0.418	0.646	0.255	0.197	0.197	0.197	0.421
Trp W	0.273	6.05	1.497	0.667	0.737	0.182	0.174	0.174	0.174	0.424
Tyr Y	0.349	6.215	1.161	0.577	0.782	0.146	0.179	0.179	0.204	0.53
Val V	0.526	2.932	0.983	0.402	0.679	0.228	0.191	0.191	0.191	0.405
	21	22	23	24	25	26	27	28	29	30
Ala A	0.272	0.102	1.672	0.982	0.347	0.557	0.327	0.213	0.213	0.213
Arg R	0.342	0.172	7.174	1.273	0.472	0.804	0.143	0.175	0.175	0.175
Asn N	0.357	0.08	1.985	1.204	0.68	0.513	0.311	0.197	0.197	0.217

TABLE S-IV. Continued

Amino acid	21	22	23	24	25	26	27	28	29	30
Asp D	0.166	0.296	2.274	1.094	0.656	0.565	0.272	0.2	0.2	0.2
Cys C	0.188	0.103	2.586	0.843	0.434	0.669	0.218	0.208	0.208	0.208
Gln Q	0.243	0.088	4.28	1.008	0.464	0.744	0.175	0.188	0.188	0.188
Glu E	0.224	0.27	3.762	0.967	0.639	0.701	0.18	0.191	0.191	0.224
Gly G	0.376	0.014	1.852	0.573	0.106	0.732	0.226	0.231	0.231	0.313
His H	0.221	0.135	3.912	1.084	0.691	0.688	0.191	0.188	0.188	0.188
Ile I	0.206	0.236	2.862	1.306	0.784	0.578	0.264	0.183	0.183	0.183
Leu L	0.284	0.211	2.86	1.362	0.703	0.581	0.277	0.183	0.183	0.183
Lys K	0.207	0.208	5.952	0.909	0.635	0.794	0.121	0.179	0.179	0.179
Met M	0.15	0.194	4.82	0.971	0.701	0.743	0.15	0.188	0.188	0.188
Phe F	0.178	0.143	5.965	1.035	0.486	0.797	0.138	0.181	0.181	0.181
Pro P	0.224	0.063	2.055	1.018	0.525	0.571	0.283	0.197	0.197	0.197
Ser S	0.266	0.181	1.726	1.014	0.539	0.526	0.309	0.208	0.208	0.208
Thr T	0.205	0.166	2.574	1.059	0.449	0.631	0.259	0.197	0.197	0.197
Trp W	0.198	0.262	6.203	1.762	0.562	0.727	0.207	0.174	0.174	0.174
Tyr Y	0.216	0.221	5.536	1.341	0.561	0.744	0.18	0.179	0.179	0.179
Val V	0.236	0.079	2.601	1.1	0.596	0.605	0.256	0.191	0.191	0.191
	31	32	33	34	35	36	37	38	39	40
Ala A	0.289	0.326	0.159	2.111	1.192	0.476	0.559	0.315	0.213	0.213
Arg R	0.459	0.267	0.213	7.869	1.562	0.669	0.779	0.155	0.175	0.175
Asn N	0.519	0.279	0.242	2.183	1.582	0.868	0.471	0.341	0.197	0.197
Asp D	0.348	0.208	0.286	2.673	1.445	0.861	0.537	0.29	0.2	0.2
Cys C	0.426	0.246	0.197	2.705	1.06	0.63	0.616	0.241	0.208	0.208
Gln Q	0.423	0.303	0.204	4.822	1.291	0.626	0.715	0.192	0.188	0.188
Glu E	0.402	0.209	0.294	4.264	1.297	0.867	0.663	0.202	0.191	0.191
Gly G	0.299	0.282	0.081	2.34	0.746	0.153	0.722	0.23	0.231	0.231
His H	0.467	0.193	0.223	4.12	1.501	0.932	0.629	0.229	0.188	0.188
Ile I	0.41	0.285	0.315	3.217	1.666	1.024	0.545	0.282	0.183	0.183
Leu L	0.465	0.367	0.291	3.255	1.701	0.949	0.551	0.288	0.183	0.183
Lys K	0.478	0.201	0.275	6.51	1.232	0.858	0.757	0.143	0.179	0.179
Met M	0.431	0.2	0.292	5.147	1.365	0.876	0.697	0.185	0.188	0.188
Phe F	0.408	0.25	0.221	6.751	1.36	0.695	0.767	0.154	0.181	0.181
Pro P	0.44	0.315	0.205	2.314	1.318	0.745	0.529	0.301	0.197	0.197
Ser S	0.319	0.291	0.249	2.089	1.251	0.73	0.513	0.307	0.208	0.208
Thr T	0.381	0.207	0.218	2.908	1.392	0.626	0.59	0.283	0.197	0.197
Trp W	0.436	0.27	0.172	7.065	2.311	0.749	0.698	0.228	0.174	0.174
Tyr Y	0.4	0.247	0.225	6.537	1.826	0.737	0.718	0.201	0.179	0.179
Val V	0.317	0.31	0.303	3.103	1.397	0.77	0.589	0.265	0.191	0.191
	41	42	43	44	45	46	47	48	49	50
Ala A	0.213	0.442	0.489	0.294	1.716	1.025	0.371	0.551	0.33	0.213
Arg R	0.175	0.554	0.411	0.419	7.174	1.305	0.507	0.798	0.145	0.175
Asn N	0.197	0.625	0.512	0.408	1.952	1.226	0.744	0.498	0.313	0.197
Asp D	0.2	0.482	0.371	0.488	2.265	1.164	0.686	0.551	0.283	0.2
Cys C	0.208	0.457	0.406	0.415	2.865	0.841	0.438	0.691	0.203	0.208
Gln Q	0.188	0.531	0.511	0.37	4.26	1.003	0.512	0.738	0.174	0.188

TABLE S-IV. Continued

Amino acid	41	42	43	44	45	46	47	48	49	50
Glu E	0.191	0.515	0.367	0.535	3.69	1.02	0.668	0.686	0.19	0.191
Gly G	0.231	0.474	0.469	0.167	1.929	0.587	0.123	0.731	0.222	0.231
His H	0.188	0.505	0.364	0.389	3.907	1.131	0.751	0.675	0.195	0.188
Ile I	0.183	0.505	0.447	0.555	2.885	1.376	0.818	0.568	0.271	0.183
Leu L	0.183	0.604	0.563	0.531	2.91	1.408	0.752	0.574	0.278	0.183
Lys K	0.179	0.571	0.364	0.505	5.917	0.948	0.676	0.785	0.126	0.179
Met M	0.188	0.487	0.384	0.445	4.922	0.967	0.74	0.742	0.146	0.188
Phe F	0.181	0.523	0.44	0.468	5.979	1.107	0.518	0.786	0.146	0.181
Pro P	0.197	0.557	0.528	0.397	2.005	1.081	0.577	0.547	0.295	0.197
Ser S	0.208	0.462	0.445	0.457	1.775	1.05	0.578	0.522	0.308	0.208
Thr T	0.197	0.478	0.353	0.431	2.614	1.1	0.477	0.624	0.263	0.197
Trp W	0.174	0.566	0.467	0.314	6.333	1.859	0.566	0.723	0.212	0.174
Tyr Y	0.179	0.551	0.446	0.385	5.555	1.433	0.573	0.735	0.189	0.179
Val V	0.191	0.45	0.499	0.49	2.638	1.167	0.63	0.595	0.263	0.191
	51	52	53	54	55	56	57	58	59	60
Ala A	0.213	0.213	0.302	0.358	0.182	2.032	0.955	0.268	0.624	0.293
Arg R	0.175	0.175	0.459	0.277	0.243	7.922	1.51	0.456	0.801	0.153
Asn N	0.197	0.197	0.496	0.296	0.3	2.73	1.628	0.336	0.582	0.347
Asp D	0.2	0.2	0.344	0.235	0.311	2.993	0.967	0.763	0.634	0.205
Cys C	0.208	0.208	0.531	0.241	0.201	3.181	0.818	0.361	0.73	0.188
Gln Q	0.188	0.188	0.415	0.309	0.247	5.576	1.22	0.243	0.792	0.173
Glu E	0.191	0.191	0.385	0.226	0.317	5.339	0.946	0.708	0.763	0.135
Gly G	0.231	0.231	0.324	0.296	0.11	1.891	0.779	0.027	0.701	0.289
His H	0.188	0.188	0.461	0.208	0.262	4.151	1.242	0.523	0.702	0.21
Ile I	0.183	0.183	0.415	0.313	0.339	3.509	1.111	0.688	0.661	0.209
Leu L	0.183	0.183	0.478	0.389	0.332	3.183	1.267	0.605	0.63	0.251
Lys K	0.179	0.179	0.472	0.216	0.31	7.233	0.975	0.565	0.824	0.111
Met M	0.188	0.188	0.451	0.198	0.325	4.939	0.995	0.68	0.747	0.15
Phe F	0.181	0.181	0.41	0.284	0.245	7.237	0.828	0.365	0.858	0.098
Pro P	0.197	0.197	0.423	0.356	0.254	3.391	0.846	0.222	0.761	0.19
Ser S	0.208	0.208	0.334	0.309	0.286	2.074	0.985	0.465	0.589	0.28
Thr T	0.197	0.197	0.392	0.225	0.25	2.992	1.177	0.438	0.649	0.255
Trp W	0.174	0.174	0.454	0.3	0.171	6.281	1.403	0.769	0.743	0.166
Tyr Y	0.179	0.179	0.4	0.277	0.229	6.809	1.199	0.593	0.792	0.139
Val V	0.191	0.191	0.327	0.353	0.34	3.29	1.063	0.286	0.709	0.229
	61	62	63	64	65	66	67	68	69	70
Ala A	0.279	0.279	0.279	0.445	0.323	0.081	3.773	3.017	3.001	3.778
Arg R	0.218	0.218	0.218	0.576	0.457	0.204	10.02	9.309	8.918	10.1
Asn N	0.24	0.24	0.24	1.063	0.483	0.046	4.564	4.212	3.869	4.633
Asp D	0.24	0.24	0.24	0.619	0.185	0.388	4.94	4.299	4.024	4.979
Cys C	0.263	0.263	0.263	0.639	0.299	0.122	4.354	4.48	3.863	4.395
Gln Q	0.231	0.231	0.231	0.872	0.23	0.054	6.61	6.378	5.751	6.739
Glu E	0.231	0.231	0.231	0.85	0.28	0.277	6.242	6.226	5.369	6.428
Gly G	0.301	0.301	0.218	0.6	0.196	0.082	8.686	7.868	7.487	8.806
His H	0.224	0.224	0.224	0.585	0.268	0.128	6.565	5.662	5.687	6.553

TABLE S-IV. Continued

Amino acid	61	62	63	64	65	66	67	68	69	70
Ile I	0.24	0.24	0.24	0.646	0.207	0.183	5.877	4.969	4.952	5.907
Leu L	0.24	0.24	0.24	0.638	0.239	0.215	5.901	4.802	4.925	5.904
Lys K	0.231	0.231	0.231	0.723	0.225	0.197	8.47	8.103	7.496	8.599
Met M	0.24	0.24	0.24	0.508	0.196	0.214	7.396	6.398	6.492	7.389
Phe F	0.218	0.251	0.218	0.6	0.196	0.082	8.686	7.868	7.487	8.806
Pro P	0.25	0.25	0.25	1.18	0.215	0.026	4.292	3.935	3.598	4.377
Ser S	0.263	0.263	0.263	0.559	0.298	0.173	4.088	3.261	3.279	4.07
Thr T	0.25	0.25	0.25	0.552	0.251	0.169	4.904	4.188	4.082	4.925
Trp W	0.204	0.204	0.204	0.469	0.177	0.334	10.17	8.214	8.527	10.13
Tyr Y	0.213	0.213	0.213	0.654	0.264	0.169	8.968	7.953	7.438	9.101
Val V	0.25	0.25	0.25	0.522	0.273	0.033	5.241	4.316	4.296	5.269
	71	72	73	74	75	76	77	78	79	80
Ala A	3.112	3.255	4.108	2.429	2.563	4.085	2.776	2.741	0.213	0.213
Arg R	8.986	9.888	18.34	13.89	13.12	18.61	13.66	16.27	0.175	0.175
Asn N	3.922	4.694	6.578	4.961	4.56	6.721	4.757	5.909	0.209	0.197
Asp D	4.115	4.723	7.381	4.966	4.697	7.409	4.988	5.917	0.2	0.2
Cys C	4.144	4.36	5.231	3.784	3.668	5.238	4.032	4.047	0.208	0.208
Gln Q	5.774	7.039	9.662	7.393	6.764	10.05	6.965	8.455	0.198	0.188
Glu E	5.378	6.993	10	7.798	6.664	10.35	6.912	9.504	0.191	0.191
Gly G	7.604	8.431	14.84	1.309	1.318	2.218	1.443	1.545	0.231	0.231
His H	5.788	5.917	11.48	7.296	7.693	11.42	8.199	7.979	0.188	0.188
Ile I	5.079	5.309	10.31	6.528	7.005	10.36	7.454	7.079	0.183	0.192
Leu L	5.069	5.054	10.24	6.258	6.864	10.24	7.342	6.723	0.192	0.183
Lys K	7.541	8.774	14.35	10.27	9.77	14.66	10.25	11.7	0.179	0.179
Met M	6.63	6.615	12.67	7.88	8.736	12.73	9.12	8.952	0.188	0.188
Phe F	7.604	8.431	14.84	8.522	9.581	14.82	10.29	8.94	0.189	0.181
Pro P	3.664	4.459	5.647	3.544	3.706	5.756	3.949	3.808	0.197	0.197
Ser S	3.403	3.524	5.12	3.046	3.227	5.052	3.497	3.465	0.208	0.208
Thr T	4.191	4.607	6.698	4.459	4.356	6.737	4.648	5.348	0.197	0.197
Trp W	8.758	8.453	23.48	14.09	15.41	23.36	16.41	14.72	0.181	0.174
Tyr Y	7.561	8.6	17.8	11.47	11.28	18.1	11.97	12.91	0.179	0.187
Val V	4.434	4.639	7.813	4.453	5.066	7.796	5.473	4.742	0.191	0.191
	81	82	83	84	85	86	87	88	89	90
Ala A	0.279	0.326	0.412	0.336	0.338	0.327	0.436	0.414	0.242	0.258
Arg R	0.218	0.668	0.715	0.707	0.669	0.698	0.702	0.451	0.344	0.313
Asn N	0.24	0.201	0.348	0.269	0.219	0.247	0.393	0.512	0.41	0.347
Asp D	0.24	0.283	0.437	0.348	0.305	0.326	0.45	0.444	0.318	0.28
Cys C	0.263	0.405	0.655	0.504	0.423	0.537	0.594	0.427	0.353	0.29
Gln Q	0.231	0.576	0.665	0.616	0.573	0.607	0.688	0.455	0.322	0.31
Glu E	0.231	0.475	0.629	0.551	0.495	0.529	0.645	0.45	0.378	0.301
Gly G	0.301	0.588	0.58	0.598	0.584	0.596	0.552	0.377	0.227	0.221
His H	0.224	0.443	0.556	0.532	0.443	0.512	0.552	0.423	0.291	0.294
Ile I	0.24	0.307	0.45	0.367	0.317	0.352	0.492	0.5	0.315	0.337
Leu L	0.24	0.326	0.413	0.371	0.327	0.361	0.445	0.562	0.34	0.375
Lys K	0.231	0.631	0.727	0.691	0.636	0.677	0.737	0.469	0.337	0.318

TABLE S-IV. Continued

Amino acid	81	82	83	84	85	86	87	88	89	90
Met M	0.24	0.55	0.649	0.614	0.545	0.614	0.62	0.429	0.277	0.308
Phe F	0.228	0.636	0.765	0.695	0.65	0.679	0.788	0.475	0.275	0.293
Pro P	0.25	0.259	0.547	0.357	0.293	0.321	0.641	0.5	0.354	0.32
Ser S	0.263	0.262	0.353	0.29	0.27	0.283	0.383	0.459	0.286	0.286
Thr T	0.25	0.382	0.468	0.446	0.386	0.435	0.474	0.42	0.264	0.269
Trp W	0.204	0.546	0.605	0.591	0.547	0.585	0.615	0.443	0.295	0.292
Tyr Y	0.213	0.569	0.672	0.616	0.577	0.602	0.688	0.44	0.322	0.291
Val V	0.25	0.368	0.519	0.408	0.383	0.392	0.564	0.495	0.24	0.31
	91	92	93	94	95	96	97	98	99	
Ala A	0.408	0.281	0.283	9.096	5.923	6.134	9.058	6.541	6.516	
Arg R	0.461	0.326	0.412	36.48	27.45	26.35	36.93	27.4	31.61	
Asn N	0.515	0.364	0.531	14.1	10.6	10.06	14.35	10.46	12.1	
Asp D	0.447	0.297	0.397	15.66	10.96	10.35	15.71	10.91	12.85	
Cys C	0.426	0.325	0.353	11.41	9.053	8.477	11.44	9.23	9.347	
Gln Q	0.47	0.323	0.385	20.06	15.46	14.51	20.69	14.93	17.15	
Glu E	0.472	0.309	0.469	20.86	16.73	14.36	21.57	14.81	20.08	
Gly G	0.37	0.243	0.284	5.777	3.882	3.961	5.725	4.222	4.281	
His H	0.419	0.31	0.327	23.92	15.41	16.31	23.74	17.3	16.59	
Ile I	0.503	0.356	0.345	21.66	13.99	14.89	21.76	15.78	15.07	
Leu L	0.566	0.4	0.364	21.41	13.3	14.53	21.39	15.49	14.22	
Lys K	0.48	0.333	0.382	29.54	21.75	20.7	30.14	21.59	24.46	
Met M	0.438	0.325	0.306	26.14	16.97	18.51	26.28	19.27	18.91	
Phe F	0.477	0.313	0.293	30.01	18.63	20.07	30.01	21.32	19.56	
Pro P	0.494	0.344	0.474	12.2	8.25	8.402	12.41	8.864	8.903	
Ser S	0.455	0.31	0.344	11.16	7.12	7.448	11.03	7.977	7.938	
Thr T	0.421	0.289	0.314	14.12	9.851	9.661	14.2	10.21	11.5	
Trp W	0.449	0.308	0.327	45.57	28.35	30.08	45.72	31.83	29.95	
Tyr Y	0.461	0.302	0.363	35.28	23.58	22.88	36.01	24.09	26.35	
Val V	0.48	0.34	0.276	16.44	9.926	11.07	16.4	11.85	10.38	

TABLE S-V. The values of 74 geometrical descriptors of 20 amino acid

Amino acid	1	2	3	4	5	6	7	8	9	10
Ala A	209.85	4.831	34.08	32.285	77.895	11.984	6.024	3.62	1.808	2.969
Arg R	1340.1	6.439	103.07	103.08	313.6	24.123	14.186	7.503	4.49	5.056
Asn N	400.83	5.79	54.002	47.156	129.08	15.186	10.862	5.677	2.442	2.965
Asp D	365.24	5.311	47.078	45.655	118.97	14.871	10.904	5.738	2.393	3.453
Cys C	261.67	4.892	37.263	38.381	93.191	13.313	8.069	4.449	2.285	3.051
Gln Q	651.02	5.934	68.797	65.102	185.19	18.519	11.626	6.239	3.259	4.285
Glu E	573	5.786	62.691	60.316	168.64	17.751	11.777	1.297	3.139	4.257
Gly G	112.57	3.913	21.436	22.514	45.863	9.173	4.721	3.077	1.448	2.741
His H	656.44	3.238	67.416	65.644	189.66	18.966	13.618	7.28	3.07	4.027
Ile I	760.03	6.831	83.806	69.094	222.15	20.196	10.101	5.299	3.018	3.586
Leu L	762.04	6.797	83.553	69.278	220.61	20.055	10.026	5.28	2.967	3.356
Lys K	1054.4	6.418	42.492	87.866	269.59	22.466	10.965	5.971	4.025	4.804
Met M	686.07	5.621	66.375	68.607	191.27	19.127	10.824	5.91	3.264	4.536

TABLE S-V. Continued

Amino acid	1	2	3	4	5	6	7	8	9	10
Phe F	981.29	3.314	83.241	85.3	256.27	22.284	13.931	7.395	3.883	4.898
Pro P	388.62	3.401	55.181	45.72	136.69	16.081	9.051	5.088	2.361	2.981
Ser S	254.55	5.031	38.337	36.357	90.225	12.889	7.715	4.33	1.949	3.066
Thr T	411.16	5.71	53.554	48.372	133.74	15.734	9.08	4.865	2.434	3.35
Trp W	1476.1	2.543	107.02	109.34	356.38	26.399	19.432	9.707	4.299	4.982
Tyr Y	1092.5	3.374	88.813	91.041	276.38	23.031	15.917	8.158	3.987	4.85
Val V	532.76	6.231	65.34	56.08	167.45	17.627	8.74	4.725	2.612	3.685
	11	12	13	14	15	16	17	18	19	20
Ala A	0.478	0.987	0.617	0.199	0.93	0.598	2.1	24.192	0	0
Arg R	0.441	0.998	0.798	0.519	0.937	0.967	5.6	50.44	0	0
Asn N	0.418	0.984	0.403	0.161	0.905	0.349	1.7	32.509	0	0
Asp D	0.465	0.969	0.476	0.194	0.938	0.499	2.8	30.58	0	0
Cys C	0.467	0.996	0.56	0.434	0.963	0.77	4.9	26.962	0	0
Gln Q	0.463	0.998	0.7	0.455	0.936	0.824	4.4	38.085	0	0
Glu E	0.473	0.991	0.587	0.396	0.943	0.818	5.2	36.537	0	0
Gly G	0.524	1	0.845	0.381	0.925	0.601	2.7	18.495	0	0
His H	0.449	0.991	0.56	0.317	0.956	0.73	3.5	39.695	0	0
Ile I	0.404	0.974	0.478	0.207	0.927	0.656	2.8	42.26	0	0
Leu L	0.391	0.979	0.512	0.186	0.921	0.488	2.3	42.613	0	0
Lys K	0.447	0.996	0.695	0.531	0.945	0.807	7.2	16.121	0	0
Met M	0.476	0.991	0.649	0.422	0.968	0.924	5.8	39.621	0	0
Phe F	0.461	0.998	0.758	0.587	0.977	0.766	8	46.298	0.969	1.4
Pro P	0.419	0.993	0.458	0.313	0.957	0.566	3.2	33.063	0	0
Ser S	0.463	0.968	0.456	0.14	0.929	0.591	2	26.024	0	0
Thr T	0.444	0.988	0.618	0.237	0.935	0.681	2.5	31.864	0	0
Trp W	0.43	0.994	0.79	0.373	0.984	0.689	4	55.378	0.908	1.42
Tyr Y	0.45	0.996	0.76	0.456	0.967	0.933	5.4	48.317	0.969	1.4
Val V	0.44	0.991	0.551	0.283	0.936	0.863	3	36.127	0	0
	21	22	23	24	25	26	27	28	29	30
Ala A	0	0	9.52	8.94	15.818	20.016	3.203	9.126	13.683	18.066
Arg R	0	0	5.07	25.892	115.41	128.82	0.889	24.416	106.95	118.11
Asn N	0	0	6.65	25.521	30.948	40.219	3.075	17.774	24.768	29.55
Asp D	0	0	5.398	17.96	37.146	40.194	1.729	15.481	25.878	29.735
Cys C	0	0	4.95	11.063	37.658	41.691	6.063	10.297	23.655	27.065
Gln Q	0	0	3.755	21.315	60.137	73.784	2.057	16.368	51.478	57.674
Glu E	0	0	3.762	19.35	65.428	67.79	0.806	16.788	45.949	49.278
Gly G	0	0	7.527	4.455	11.594	15.499	2.694	3.55	10.198	12.634
His H	0	0	5.286	22.59	57.811	65.904	6.272	21.096	54.274	58.816
Ile I	0	0	11.813	20.65	42.088	45.836	3.066	24.279	42.299	48.339
Leu L	0	0	8.735	21.601	37.431	45.877	1.356	23.985	41.33	48.979
Lys K	0	0	10.49	18.551	87.172	91.572	4.062	19.465	82.997	86.389
Met M	0	0	4.673	21.268	68.445	69.282	3.065	18.711	61.299	64.021
Phe F	0.992	5.813	5.748	17.032	97.253	102.19	5.382	21.317	90.361	98.039
Pro P	0	0	9.057	11.857	29.494	34.106	3.304	14.529	24.259	28.91
Ser S	0	0	6.939	12.891	20.124	24.059	4.034	11.395	16.587	20.034

TABLE S-V. Continued

Amino acid	21	22	23	24	25	26	27	28	29	30
Thr T	0	0	10.611	15.099	31.106	36.883	4.392	13.513	26.964	32.336
Trp W	0.977	5.447	3.784	37.626	114.21	127.55	6.332	39.537	115	135.38
Tyr Y	0.992	5.813	4.54	27.607	102.19	110.19	3.83	27.763	88.396	99.797
Val V	0	0	8.755	13.959	33.239	37.012	3.116	16.986	31.98	37.008
	31	32	33	34	35	36	37	38	39	40
Ala A	0.37	22.353	34.687	44.253	0.069	10.115	14.97	19.721	0	6.33
Arg R	0.245	59.118	226.07	249.74	0.061	26.72	113.22	124.96	21.46	43.73
Asn N	0.322	43.754	54.465	67.051	0.192	19.139	25.986	30.633	3.03	19.05
Asp D	0.302	39.354	60.293	70.259	0.085	16.859	26.877	31.219	0	13.84
Cys C	0.35	24.471	48.318	54.515	0.957	11.792	28.741	32.782	0	6.22
Gln Q	0.148	39.923	112.7	126.65	0.131	17.421	54.397	60.074	5.64	22.29
Glu E	0.206	43.192	102.33	110.89	0.087	18.362	47.383	51.172	0	16.7
Gly G	0.336	9.463	26.238	32.496	0.087	3.87	11.154	13.68	0	6.37
His H	0.243	50.194	104.09	115.84	0.385	23.064	56.819	61.426	10.69	24.35
Ile I	0.414	59.397	93.552	107.65	0.034	27.41	46.235	53.148	0	6.31
Leu L	0.357	58.499	92.662	109.3	0.106	26.961	45.72	53.881	0	6.39
Lys K	0.363	50.531	177.96	187.03	0.162	21.915	88.958	92.572	6.86	20.57
Met M	0.405	45.462	121.93	131.86	0.634	21.372	70.101	72.539	0	6.33
Phe F	0.439	47.633	172.58	187.93	0.479	23.922	95.659	104.3	0	6.22
Pro P	0.385	35.72	52.9	62.738	0.144	16.524	25.718	30.738	0	6.22
Ser S	0.329	29.217	41.531	49.199	0.243	12.462	18.014	21.615	0	9.15
Thr T	0.411	35.555	62.266	75.733	0.152	14.887	29.099	34.93	0	9.91
Trp W	0.365	83.527	213.16	255.71	0.479	42.999	122.31	145.21	5.95	15.99
Tyr Y	0.27	62.87	178.21	204.88	0.344	30.514	92.946	106.03	0	14.09
Val V	0.311	41.562	74.292	86.206	0.149	19.263	35.049	40.779	0	6.24
	41	42	43	44	45	46	47	48	49	50
Ala A	0	0	0	0	0	0	0	0	0	0
Arg R	0	0	0	0	0	0	0	0	0	0
Asn N	0	0	0	0	0	0	7.32	0	0	0
Asp D	0	0	0	0	0	0	16.5	0	0	0
Cys C	3.33	0	0	0	0	0	0	9.71	0	0
Gln Q	0	0	0	0	0	0	11.79	0	0	0
Glu E	0	0	0	0	0	0	22.57	0	0	0
Gly G	0	0	0	0	0	0	0	0	0	0
His H	0	0	0	0	0	0	0	0	0	0
Ile I	0	0	0	0	0	0	0	0	0	0
Leu L	0	0	0	0	0	0	0	0	0	0
Lys K	0	0	0	0	0	0	0	0	0	0
Met M	4.8	0	0	0	0	0	0	10.42	0	0
Phe F	0	0	0	0	0	0	0	0	0	0
Pro P	0	0	0	0	0	0	0	0	0	0
Ser S	0	0	0	0	0	0	6.91	0	0	0
Thr T	0	0	0	0	0	0	6.66	0	0	0
Trp W	0	0	0	0	0	0	0	0	0	0
Tyr Y	0	0	0	0	0	0	0	0	0	0

TABLE S-V. Continued

Amino acid	41	42	43	44	45	46	47	48	49	50
Val V	0	0	0	0	0	0	0	0	0	0
	51	52	53	54	55	56	57	58	59	60
Ala A	0	0	0	0	0	0	0	0	0	0
Arg R	0	0	0	0	0	0	0	0	0	0
Asn N	0	0	0	0	0	0	0	0	0	0
Asp D	0	0	0	0	0	0	0	0	0	0
Cys C	0	0	0	0	0	0	0	0	0	0
Gln Q	0	0	0	0	0	0	0	0	0	0
Glu E	0	0	0	0	0	0	0	0	0	0
Gly G	0	0	0	0	0	0	0	0	0	0
His H	0	0	0	0	0	0	0	0	0	0
Ile I	0	0	0	0	0	0	0	0	0	0
Leu L	0	0	0	0	0	0	0	0	0	0
Lys K	0	0	0	0	0	0	0	0	0	0
Met M	0	0	0	0	0	0	0	0	0	0
Phe F	0	0	0	0	0	0	0	0	0	0
Pro P	0	0	0	0	0	0	0	0	0	0
Ser S	0	0	0	0	0	0	0	0	0	0
Thr T	0	0	0	0	0	0	0	0	0	0
Trp W	0	0	0	0	0	0	0	0	0	0
Tyr Y	0	0	0	0	0	0	0	0	0	0
Val V	0	0	0	0	0	0	0	0	0	0
	61	62	63	64	65	66	67	68	69	70
Ala A	0	0	0	0	0	0	0	0	0	0
Arg R	0	0	0	0	0	0	0	0	0	0
Asn N	0	0	0	0	0	0	0	0	0	0
Asp D	0	0	0	0	0	0	0	0	0	0
Cys C	0	0	0	0	0	0	0	0	0	0
Gln Q	0	0	0	0	0	0	0	0	0	0
Glu E	0	0	0	0	0	0	0	0	0	0
Gly G	0	0	0	0	0	0	0	0	0	0
His H	0	0	0	0	0	0	0	0	0	0
Ile I	0	0	0	0	0	0	0	0	0	0
Leu L	0	0	0	0	0	0	0	0	0	0
Lys K	0	0	0	0	0	0	0	0	0	0
Met M	0	0	0	0	0	0	0	0	0	0
Phe F	0	0	0	0	0	0	0	0	0	0
Pro P	0	0	0	0	0	0	0	0	0	0
Ser S	0	0	0	0	0	0	0	0	0	0
Thr T	0	0	0	0	0	0	0	0	0	0
Trp W	0	0	0	0	0	0	0	0	0	0
Tyr Y	0	0	0	0	0	0	0	0	0	0
Val V	0	0	0	0	0	0	0	0	0	0
	71	72	73	74						
Ala A	0	0	0	0						

TABLE S-V. Continued

Amino acid	61	62	63	64	65	66	67	68	69	70
Asn N	0	0	0	0						
Asp D	0	0	0	0						
Cys C	0	0	0	0						
Gln Q	0	0	0	0						
Glu E	0	0	0	0						
Gly G	0	0	0	0						
His H	0	0	0	0						
Ile I	0	0	0	0						
Leu L	0	0	0	0						
Lys K	0	0	0	0						
Met M	0	0	0	0						
Phe F	0	0	0	0						
Pro P	0	0	0	0						
Ser S	0	0	0	0						
Thr T	0	0	0	0						
Trp W	0	0	0	0						
Tyr Y	0	0	0	0						
Val V	0	0	0	0						

TABLE S-VI. The values of 160 3D-MORSE descriptors of 20 amino acid

Amino acid	1	2	3	4	5	6	7	8	9	10
Ala A	78	16.945	-0.943	-0.031	-1.478	-1.004	0.556	0.387	0.569	0.135
Arg R	325	27.716	-3.756	3.192	-4.551	-1.631	1.132	0.944	0.563	-0.323
Asn N	136	18.987	-0.236	0.051	-1.883	-1.672	1.042	0.623	0.238	0.419
Asp D	120	16.214	-0.831	0.233	-1.719	-1.436	1.27	0.206	0.373	0.133
Cys C	91	15.743	-1.442	0.12	-1.55	-1.034	0.743	0.473	0.406	0.064
Gln Q	190	21.665	-2.455	0.811	-3.009	-1.294	0.416	1.492	0.12	0.456
Glu E	171	19.606	-2.639	0.744	-2.419	-1.696	1.199	0.408	0.266	0.343
Gly G	45	13.001	-0.719	-0.047	-0.908	-1.159	0.752	0.228	0.255	0.179
His H	190	15.678	-0.496	0.655	-2.74	-1.134	1.222	1.82	-0.219	0.035
Ile I	231	20.727	-2.519	1.631	-3.19	-1.295	0.711	0.579	1.166	0.12
Leu L	231	20.07	-1.863	0.765	-2.925	-1.92	0.88	0.972	1.144	-0.069
Lys K	276	27.074	-5.673	2.853	-3.553	-1.577	1.072	0.899	0.675	0.229
Met M	190	19.917	-3.055	0.82	-2.259	-1.028	0.705	1.109	0.908	0.099
Phe F	253	20.049	-2.17	0.998	-3.235	-2.403	2.762	0.172	0.235	-0.258
Pro P	136	22.565	-2.379	0.157	-1.578	-1.901	1.621	0.287	0.318	0.311
Ser S	91	16.798	-0.475	-0.093	-1.333	-1.4	0.777	0.337	0.527	-0.029
Thr T	136	19.421	-1.768	0.69	-2.436	-1.11	0.444	0.762	0.742	-0.145
Trp W	351	20.721	-1.789	0.169	-2.74	-2.385	3.609	0.628	-0.417	0.027
Tyr Y	276	19.38	-1.418	1.528	-2.606	-2.614	2.676	0.186	0.532	-0.611
Val V	171	20.914	-1.088	0.131	-2.712	-0.97	0.228	0.852	0.964	0.136
	11	12	13	14	15	16	17	18	19	20
Ala A	-0.648	-0.414	0.161	0.308	0.316	-0.181	-0.036	-0.513	0.338	0.172
Arg R	-0.338	-0.857	-0.429	1.284	0.218	0.002	-0.243	-0.905	0.301	0.585
Asn N	-0.685	-0.413	-0.266	0.663	0.321	-0.112	-0.189	-0.246	-0.073	0.198

TABLE S-VI. Continued

Amino acid	11	12	13	14	15	16	17	18	19	20
Asp D	-0.281	-0.573	-0.163	0.666	-0.062	0.143	-0.081	-0.321	0.114	0.056
Cys C	-0.449	-0.228	-0.089	0.265	0.349	-0.136	-0.051	-0.345	0.042	0.33
Gln Q	-0.26	-1.281	0.312	0.931	0.097	-0.186	-0.165	-0.633	0.478	0.131
Glu E	-0.334	-0.934	0.147	0.661	-0.068	-0.022	-0.143	-0.529	0.4	0.189
Gly G	-0.353	-0.299	-0.044	0.255	0.207	-0.037	-0.008	-0.323	-0.035	0.187
His H	0.155	-1.109	0.309	0.076	0.535	0.279	-0.107	-0.922	0.345	0.433
Ile I	-0.986	-1.047	0.756	0.847	0.054	0.044	-0.391	-0.958	0.985	0.213
Leu L	-0.849	-1.531	0.89	1.038	-0.148	0.216	-0.842	-0.704	0.98	0.428
Lys K	-0.816	-1.444	0.291	1.297	-0.252	0.237	-0.395	-0.937	0.621	0.501
Met M	-1.089	-0.576	0.399	0.661	0.275	-0.153	-0.302	-0.616	0.649	0.571
Phe F	0.165	-1.165	0.249	0.817	0.097	0.327	-0.619	-0.826	0.325	1.094
Pro P	-0.685	-0.959	0.731	0.359	0.219	0.034	-0.756	-0.146	0.466	0.443
Ser S	-0.107	-0.572	-0.255	0.553	0.228	-0.008	-0.084	-0.348	-0.02	0.287
Thr T	-0.221	-0.849	0.11	0.541	0.253	0.079	-0.364	-0.391	0.295	0.227
Trp W	0.455	-1.198	-0.248	0.726	0.263	0.634	-0.698	-1.053	0.82	0.645
Tyr Y	0.275	-1.007	-0.058	0.564	0.375	0.093	-0.364	-0.77	0.221	0.617
Val V	-0.802	-0.934	0.47	0.768	0.108	-0.057	-0.47	-0.562	0.601	0.445
	21	22	23	24	25	26	27	28	29	30
Ala A	-0.106	0.158	-0.18	-0.056	-0.032	0.087	0.17	-0.14	-0.056	0.019
Arg R	-0.041	0.191	-0.3	-0.006	-0.018	0.106	0.441	-0.078	-0.061	-0.251
Asn N	0.167	0.122	-0.16	-0.126	-0.171	0.158	0.157	0.07	-0.14	-0.052
Asp D	0.169	0.051	0.037	-0.212	-0.024	0.079	0.009	0.089	-0.032	-0.015
Cys C	-0.105	0.208	-0.199	-0.128	0	0.104	0.045	-0.028	-0.026	0.055
Gln Q	-0.079	0.153	-0.053	-0.28	-0.091	0.215	0.137	0.012	0.133	-0.006
Glu E	-0.278	0.309	-0.242	-0.152	-0.04	0.06	0.097	0.017	-0.143	-0.069
Gly G	0.01	0.009	0.052	-0.177	0.01	0.017	0.058	0.019	0.063	-0.131
His H	-0.101	0.24	-0.316	-0.171	0.202	0.229	-0.086	-0.003	-0.11	-0.053
Ile I	-0.065	-0.177	-0.132	-0.312	0.281	0.191	0.193	-0.225	-0.357	0.188
Leu L	-0.29	-0.072	-0.041	-0.204	0.231	0.245	-0.002	-0.118	-0.465	0.313
Lys K	-0.476	0.488	-0.665	0.136	-0.034	0.41	0.127	-0.031	-0.326	-0.205
Met M	-0.282	0.198	-0.225	-0.215	0.21	0.065	0.186	-0.281	-0.165	0.098
Phe F	-0.803	0.468	-0.769	-0.053	0.631	-0.108	-0.057	-0.214	0.052	-0.062
Pro P	-0.579	0.403	-0.356	-0.14	0.193	0.138	0.152	-0.155	-0.381	0.185
Ser S	-0.036	0.019	0.151	-0.32	0.058	0.012	0.107	-0.071	0.093	-0.042
Thr T	-0.159	0.085	-0.151	0.008	-0.082	-0.203	-0.005	0.008	-0.101	-0.033
Trp W	0.069	-0.088	-0.639	-0.148	0.437	-0.003	-0.029	-0.097	-0.004	-0.151
Tyr Y	-0.25	0.369	-0.529	-0.211	0.462	0.109	-0.302	-0.086	0.136	-0.131
Val V	-0.374	0.098	-0.191	-0.066	-0.131	0.379	0.067	-0.153	-0.277	0.107
	31	32	33	34	35	36	37	38	39	40
Ala A	0.017	0.042	23.545	7.14	-0.808	-0.249	-0.826	-0.015	0.883	-0.365
Arg R	0.378	-0.057	97.692	11.139	-1.326	-0.784	-1.636	0.389	1.813	-0.635
Asn N	-0.015	-0.061	54.475	9.434	-0.585	-0.181	-1.776	0.293	1.137	-0.209
Asp D	-0.085	0.05	55.173	9.337	-0.665	-0.398	-1.395	-0.026	1.495	-0.465
Cys C	-0.115	0.003	43.358	6.797	-1.352	-0.042	-0.568	0.035	0.507	-0.348
Gln Q	-0.085	0.107	67.503	8.786	-1.697	-0.176	-1.57	0.264	1.427	-0.42

TABLE S-VI. Continued

Amino acid	31	32	33	34	35	36	37	38	39	40
Glu E	0.163	-0.035	68.296	8.636	-2.156	-0.486	-1.398	0.147	1.438	-0.559
Gly G	0.003	-0.013	16.067	5.861	0.466	-0.285	-0.684	-0.102	0.764	-0.14
His H	0.106	-0.075	76.626	9.474	-0.185	-1.376	-1.243	-0.281	1.841	-0.292
Ile I	0.284	-0.01	54.168	8.141	-0.794	-0.413	-1.316	0.473	0.979	0.708
Leu L	0.397	-0.193	54.168	7.653	-0.22	-0.778	-0.991	0.194	1.066	-0.736
Lys K	0.445	-0.107	67.928	9.252	-1.038	-0.535	-1.109	0.488	1.015	-0.681
Met M	0.244	-0.068	68.647	7.665	-2.776	-0.355	-0.545	0.599	0.292	-0.245
Phe F	0.267	-0.054	87.62	11.38	-1.573	-0.056	-2.002	0.54	1.834	0.974
Pro P	0.268	-0.099	40.976	9.56	-1.014	-0.807	-0.729	-0.057	1.377	-0.833
Ser S	-0.08	0.036	33.43	8.436	-0.884	-0.406	-0.965	0.056	1.061	-0.484
Thr T	0.158	-0.117	43.829	8.793	-1.035	-0.315	-1.103	0.12	1.157	-0.674
Trp W	-0.02	-0.015	135.935	11.872	-1.073	-1.115	-1.896	-0.197	2.571	-1.007
Tyr Y	0.159	-0.173	105.945	11.075	-1.371	-0.531	-2.208	0.448	2.385	-0.976
Val V	0.276	-0.051	42.596	8.325	-1.061	-0.131	-1.324	0.47	0.776	-0.548
	41	42	43	44	45	46	47	48	49	50
Ala A	-0.137	0.103	-0.051	0.077	-0.093	0.013	0.144	-0.151	0.028	-0.98
Arg R	-0.445	0.177	0.171	0.117	-0.517	0.261	0.377	-0.089	-0.097	-0.179
Asn N	-0.479	0.185	-0.14	0.323	-0.284	0.102	0.108	-0.198	0.037	0.135
Asp D	-0.533	0.318	-0.098	0.168	-0.104	-0.026	0.065	-0.068	0.026	0.029
Cys C	0.283	-0.145	-0.16	0.198	-0.014	-0.17	0.249	-0.124	-0.053	0.01
Gln Q	-0.231	0.132	-0.031	0.072	-0.202	0.283	0.057	-0.293	0.113	0.046
Glu E	-0.412	0.303	0.047	0.046	-0.055	0.056	0.043	-0.206	-0.025	0.117
Gly G	-0.28	0.115	-0.065	0.13	-0.047	-0.109	0.167	-0.099	0.027	-0.022
His H	-1.083	0.179	0.445	-0.01	-0.056	-0.984	0.247	0.296	-0.083	-0.254
Ile I	-1.083	0.179	0.445	-0.01	-0.056	-0.984	0.247	0.296	-0.083	-0.254
Leu L	0.063	0.134	0.07	-0.179	-0.218	0.434	-0.055	-0.083	-0.176	0.039
Lys K	-0.163	0.19	0.177	-0.365	-0.299	0.425	0.181	-0.056	-0.203	0.075
Met M	0.296	-0.141	-0.161	0.355	0.025	-0.366	0.188	0.017	-0.166	0.102
Phe F	-0.471	0.148	0.463	0.143	-0.505	-0.096	0.398	-0.021	-0.063	-0.284
Pro P	-0.18	0.389	-0.167	0.112	-0.31	0.234	0.232	-0.333	-0.035	0.108
Ser S	-0.22	0.164	-0.034	0.214	-0.356	0.155	0.071	-0.017	-0.048	-0.053
Thr T	-0.076	0.097	0.128	-0.089	-0.109	0.012	0.239	-0.171	-0.021	-0.018
Trp W	-1.183	0.272	0.479	0.438	-0.867	-0.327	0.577	0.315	-0.36	-0.337
Tyr Y	-0.587	0.157	0.348	0.347	-0.563	-0.316	0.636	-0.251	0.087	-0.378
Val V	-0.04	0.206	-0.046	-0.031	-0.236	0.34	0.005	-0.137	-0.076	0.015
	51	52	53	54	55	56	57	58	59	60
Ala A	0.082	-0.017	-0.111	0.097	-0.009	0.029	-0.059	-0.011	0.039	0.018
Arg R	0.172	-0.052	-0.059	0.033	0.083	0.063	-0.054	-0.1	0.162	-0.08
Asn N	-0.054	-0.014	-0.179	0.257	-0.062	0.022	-0.11	-0.008	0.104	0
Asp D	0.052	-0.098	-0.051	0.072	0.057	0.024	-0.124	0.024	-0.01	0.067
Cys C	0.125	-0.038	-0.152	0.151	-0.041	0.038	-0.064	0.027	-0.038	0.045
Gln Q	0.303	-0.28	-0.047	0.11	0.094	-0.064	-0.098	0.041	0.097	0.003
Glu E	0.11	-0.036	-0.172	0.117	-0.052	0.077	-0.167	0.038	0.014	0.088
Gly G	0.018	0.048	-0.098	0.04	0.016	0.03	-0.024	-0.059	0.029	0.038
His H	0.043	0.119	-0.021	0.05	-0.096	0.084	0.002	0.04	-0.053	0.023

TABLE S-VI. Continued

Amino acid	51	52	53	54	55	56	57	58	59	60
Ile I	0.043	0.119	-0.021	0.05	-0.096	0.084	0.002	0.04	-0.053	0.023
Leu L	0.324	-0.227	-0.092	0.092	0.093	-0.051	-0.099	0.032	0.119	-0.061
Lys K	0.193	-0.123	-0.222	0.206	0.016	0.085	-0.163	0.087	0.074	0.013
Met M	0.182	0.013	-0.214	0.314	-0.116	-0.048	-0.082	0.174	-0.057	-0.048
Phe F	0.152	0.4	-0.315	0.057	-0.142	0.141	0.139	-0.084	-0.099	0.009
Pro P	0.117	-0.02	-0.268	0.192	0.114	-0.15	-0.024	0.02	0.073	0.04
Ser S	0.103	-0.012	-0.045	-0.04	0.114	-0.06	0.06	-0.139	0.094	-0.014
Thr T	0.079	0.069	-0.2	0.108	-0.01	0.072	-0.098	0.012	-0.002	0.053
Trp W	0.19	0.248	0.032	-0.185	-0.286	0.254	0.048	-0.147	-0.157	-0.006
Tyr Y	0.003	0.325	-0.077	0.068	-0.207	0.069	0.161	-0.023	-0.169	0.047
Val V	0.222	-0.119	-0.151	0.144	0.009	0.045	-0.164	0.065	0.089	-0.047
	61	62	63	64	65	66	67	68	69	70
Ala A	-0.048	0.047	-0.021	-0.024	20.873	6.303	-0.446	-0.239	-0.614	0.113
Arg R	0.101	-0.041	0.057	0.045	92.957	10.834	-1.227	-0.069	-1.718	0.034
Asn N	-0.07	0.073	-0.048	-0.048	40.157	8.201	-0.456	-0.39	-0.877	-0.074
Asp D	-0.022	0.041	-0.049	-0.077	35.939	7.424	-0.517	-0.335	-0.855	0.009
Cys C	-0.02	0.127	-0.208	0.065	28.284	6.41	-0.77	-0.203	-0.615	0.028
Gln Q	-0.03	0.11	-0.09	-0.036	55.727	8.7	-1.05	-0.22	-1.179	0.042
Glu E	-0.082	0.113	-0.03	-0.071	50.739	8.289	-1.044	-0.217	-1.097	0.015
Gly G	-0.002	-0.007	-0.014	-0.043	11.858	4.46	-0.148	-0.289	-0.368	-0.183
His H	-0.057	0.151	-0.048	-0.11	65.203	8.596	-0.204	-0.779	-1.067	-0.237
Ile I	-0.107	0.06	0.097	-0.123	63.23	9.217	-0.779	-0.034	-1.449	0.154
Leu L	-0.109	0.091	0.061	-0.062	63.23	9.026	-0.547	-0.291	-1.189	-0.099
Lys K	-0.088	-0.004	0.114	-0.069	74.967	10.245	-1.451	-0.049	-1.314	0.196
Met M	0.049	0.075	-0.004	-0.09	57.446	8.017	-1.531	-0.099	-1.017	0.161
Phe F	0.058	0.103	-0.107	-0.137	92.58	11.443	-1.185	-0.197	-1.824	-0.087
Pro P	-0.202	0.13	0.042	-0.058	40.847	9.749	-1.02	-0.566	-0.554	-0.387
Ser S	0.015	0.037	-0.08	0.012	24.358	6.569	-0.448	-0.322	-0.604	-0.072
Thr T	-0.061	0.077	-0.052	-0.039	36.743	7.754	-0.713	0.176	-0.94	0.069
Trp W	0.134	0.065	-0.333	-0.075	137.702	12.289	-1.027	-1.072	-1.798	-0.389
Tyr Y	0.059	0.153	-0.116	0.21	99.748	10.75	-1.066	-0.356	-1.706	-0.061
Val V	0.073	0.088	-0.038	0.037	46.559	8.842	-0.718	-0.168	-1.212	0.141
	71	72	73	74	75	76	77	78	79	80
Ala A	0.432	-0.093	0.056	0.061	-0.063	-0.148	-0.043	0.176	0.119	0.119
Arg R	0.864	-0.079	-0.087	0.019	0.247	-0.327	-0.32	0.499	0.192	-0.106
Asn N	0.607	-0.091	-0.097	0.158	-0.07	-0.076	-0.228	0.315	0.073	-0.113
Asp D	0.61	-0.168	-0.072	0.112	0.007	-0.141	-0.146	0.27	0.025	-0.068
Cys C	0.316	-0.081	0.106	0.021	-0.079	-0.052	-0.087	-0.087	0.179	-0.129
Gln Q	0.562	0.009	-0.078	0.158	0.096	-0.382	-0.133	0.451	0.041	-0.209
Glu E	0.695	-0.203	-0.111	0.181	0.075	-0.328	-0.102	0.363	-0.001	-0.134
Gly G	0.369	-0.008	-0.048	0.044	-0.021	-0.054	-0.068	0.073	0.114	0.077
His H	1.045	0.019	-0.562	0.094	0.338	-0.305	-0.057	0.005	0.186	0.153
Ile I	0.546	-0.18	0.175	0.06	0.039	-0.522	0.014	0.574	-0.026	-0.138
Leu L	0.679	-0.239	0.283	0.027	0.035	-0.615	0.065	0.555	0.008	-0.147
Lys K	0.652	-0.108	-0.016	0.152	0.128	-0.688	-0.087	0.597	0.062	-0.079

TABLE S-VI. Continued

Amino acid	71	72	73	74	75	76	77	78	79	80
Met M	0.315	0.154	0.238	0.036	-0.293	-0.119	0.009	0.204	0.142	-0.126
Phe F	1.65	-0.562	-0.294	-0.073	0.527	-0.279	-0.322	0.158	0.296	0.094
Pro P	1.006	-0.456	0.022	0.309	-0.163	-0.306	0.003	0.298	0.188	-0.248
Ser S	0.447	-0.131	0.031	0.038	0.041	-0.128	-0.173	0.225	0.108	-0.099
Thr T	0.425	-0.107	0.063	0.048	0.069	-0.31	-0.058	0.263	0.124	-0.125
Trp W	2.291	-0.523	-0.856	0.148	0.572	-0.092	-0.563	-0.001	0.47	0.293
Tyr Y	1.737	-0.592	-0.298	-0.138	0.48	-0.123	-0.379	0.034	0.459	-0.042
Val V	0.403	-0.1	0.16	0.096	-0.042	-0.368	-0.072	0.501	-0.008	-0.127
	81	82	83	84	85	86	87	88	89	90
Ala A	-0.042	-0.078	0.141	0.02	-0.089	0.068	-0.027	-0.025	-0.007	0.022
Arg R	-0.177	-0.248	0.269	0.041	-0.085	0.109	-0.051	0.005	-0.05	0.04
Asn N	-0.074	0.018	0.018	0.038	-0.083	0.119	-0.011	-0.065	-0.065	0.062
Asp D	-0.065	-0.03	0.125	-0.05	-0.051	0.044	0.059	-0.057	-0.065	0.072
Cys C	-0.042	-0.06	0.103	0.037	-0.107	0.113	-0.044	-0.047	-0.01	0.051
Gln Q	-0.058	-0.084	0.279	-0.108	0.101	0.107	0.022	-0.109	0.066	0.122
Glu E	-0.1	-0.049	0.211	-0.081	-0.162	0.13	-0.029	-0.031	-0.059	0.058
Gly G	0.016	-0.065	0.047	0.065	-0.066	0.007	0.034	-0.032	0	-0.014
His H	-0.118	-0.303	0.177	0.134	-0.067	0.068	-0.124	0	0.051	0.085
Ile I	-0.208	-0.121	0.42	-0.133	-0.026	0.004	0.003	-0.132	0.045	0.085
Leu L	-0.273	-0.1	0.462	-0.102	-0.109	0.048	0.026	-0.129	0.035	0.12
Lys K	-0.236	-0.103	0.342	-0.019	-0.239	0.201	-0.093	0.007	-0.049	0.134
Met M	-0.206	-0.054	0.263	0.105	-0.148	0.149	-0.088	-0.09	0.028	0.104
Phe F	-0.228	-0.394	0.196	0.514	-0.351	0.107	-0.274	0.068	0.214	-0.011
Pro P	-0.178	0.017	0.231	0.039	-0.251	0.174	-0.002	-0.149	0.053	0.075
Ser S	-0.045	-0.068	0.087	0.045	-0.071	0.028	0.044	-0.069	0.016	-0.022
Thr T	-0.114	-0.065	0.186	0.011	-0.116	0.069	-0.024	-0.006	-0.045	0.071
Trp W	-0.413	-0.434	0.34	0.347	-0.002	-0.145	-0.297	0.102	0.174	-0.054
Tyr Y	-0.086	-0.434	0.152	0.356	-0.126	0.025	-0.203	-0.018	0.205	0.044
Val V	-0.188	-0.082	-0.313	-0.008	-0.168	0.125	-0.073	0.008	-0.101	0.154
	91	92	93	94	95	96	97	98	99	100
Ala A	0.055	-0.035	-0.056	0.027	0.031	0.005	82.837	17.763	-0.833	0.048
Arg R	0.162	-0.071	-0.036	-0.046	0.164	0.001	336.929	28.849	-3.378	3.075
Asn N	0.072	-0.003	-0.103	0.05	0.017	-0.029	149.531	20.016	-0.021	0.35
Asp D	-0.002	0.022	-0.048	0.002	0.043	-0.027	136.252	17.582	-0.698	0.462
Cys C	0.02	-0.022	-0.041	0.058	-0.039	0.027	97.269	16.618	-1.469	0.24
Gln Q	0.048	-0.036	-0.071	0.031	0.032	-0.006	203.734	22.159	-2.48	1.033
Glu E	0.033	0.013	-0.102	0.011	0.102	-0.031	188.222	20.43	-3.045	0.878
Gly G	0.023	0.019	-0.012	-0.023	0.008	0.006	49.721	14.26	-0.768	0.091
His H	-0.035	-0.012	-0.059	0.023	0.086	-0.073	201.631	16.419	-0.163	0.525
Ile I	-0.035	-0.012	-0.059	0.023	0.086	-0.073	201.631	16.419	-0.163	0.525
Leu L	0.054	-0.096	-0.181	0.1	0.192	-0.067	232.078	19.713	-1.482	0.796
Lys K	0.058	-0.029	-0.157	-0.019	0.223	-0.061	279.532	27.373	-5.107	2.638
Met M	0.022	-0.078	-0.066	0.05	0.106	-0.056	194.655	20.285	-2.995	0.836
Phe F	-0.117	-0.044	0.05	0.019	0.077	-0.155	256.714	20.944	-2.253	1.086
Pro P	0.052	-0.018	-0.222	0.118	0.127	-0.068	140.56	22.745	-2.214	0.1

TABLE S-VI. Continued

Amino acid	91	92	93	94	95	96	97	98	99	100
Ser S	0.075	-0.047	-0.003	0.005	0.004	0.012	100.633	18.38	-0.323	-0.044
Thr T	0.026	-0.024	-0.066	0.009	0.089	-0.04	145.892	20.31	-1.579	0.816
Trp W	-0.158	-0.022	0.077	0.028	-0.127	-0.088	358.067	21.217	-1.518	0.218
Tyr Y	-0.186	0.011	0.066	0.009	0.034	-0.174	287.473	20.412	-1.225	1.738
Val V	0.054	-0.095	-0.102	0.036	0.131	-0.002	174.016	20.95	-1.043	0.334
	101	102	103	104	105	106	107	108	109	110
Ala A	-1.678	-1.164	0.777	0.366	0.499	0.219	-0.694	-0.39	-0.147	0.238
Arg R	-4.895	-1.662	1.434	0.889	0.524	-0.24	-0.379	-0.823	-0.556	1.245
Asn N	-2.445	-1.747	1.241	0.696	0.161	0.472	-0.774	-0.331	-0.316	0.616
Asp D	-2.176	-1.617	1.61	0.164	0.272	0.25	-0.318	-0.584	-0.171	0.598
Cys C	-1.698	-1.21	0.932	0.444	0.413	0.089	-0.506	-0.26	-0.096	0.221
Gln Q	-3.454	-1.366	0.638	1.512	0.142	0.448	-0.299	-1.227	0.24	0.95
Glu E	-2.76	-1.855	1.496	1.376	0.178	0.487	-0.395	-0.888	0.159	0.526
Gly G	-1.143	-1.31	0.93	0.258	0.179	0.264	-0.408	-0.296	-0.027	0.18
His H	-2.887	-1.356	1.528	0.809	-0.377	0.118	0.174	-1.086	0.328	-0.086
Ile I	-3.356	-1.364	0.948	0.469	1.061	0.136	-0.918	-1.047	0.747	0.743
Leu L	-3.018	-2.089	1.126	0.908	1.093	-0.033	-0.79	-1.522	0.815	0.996
Lys K	-3.641	-1.706	1.28	0.888	0.607	0.33	-0.788	-1.476	0.26	1.194
Met M	-2.399	-1.17	0.944	1.046	0.825	0.178	-1.115	-0.547	0.363	0.541
Phe F	-3.407	-2.351	2.833	0.187	0.151	-0.157	0.144	-1.125	0.214	0.72
Pro P	-1.656	-1.952	1.755	0.274	0.229	0.338	-0.653	-0.915	0.659	0.352
Ser S	-1.62	-1.571	1.001	1.301	0.518	0.016	-0.09	-0.597	-0.335	0.575
Thr T	-2.693	-1.249	0.666	0.651	0.821	-0.177	-0.119	-0.965	0.12	0.449
Trp W	-2.897	-2.54	3.768	0.541	-0.505	0.036	0.459	-1.17	-0.333	0.605
Tyr Y	-3.045	-2.627	2.863	0.174	0.493	-0.529	0.283	-1.017	-0.14	0.471
Val V	-2.905	-1.019	0.354	0.805	0.886	0.212	-0.764	-0.937	0.424	0.717
	111	112	113	114	115	116	117	118	119	120
Ala A	0.397	-0.195	-0.011	-0.52	0.3	0.16	-0.086	0.179	-0.173	-0.058
Arg R	0.408	-0.018	-0.213	-0.94	0.235	0.546	0.043	0.173	-0.233	-0.035
Asn N	0.399	-0.122	-0.18	-0.237	-0.118	0.178	0.166	0.225	-0.22	-0.111
Asp D	-0.026	0.233	-0.108	-0.317	0.056	-0.116	0.24	0.081	0.036	-0.187
Cys C	0.389	-0.103	-0.055	-0.358	0.015	0.317	-0.089	0.235	-0.203	-0.113
Gln Q	0.165	-0.213	-0.123	-0.631	0.475	0.054	-0.01	0.178	-0.042	-0.297
Glu E	0.014	-0.028	-0.132	-0.514	0.334	0.187	-0.256	0.325	-0.237	-0.15
Gly G	0.279	-0.032	-0.004	-0.332	0.001	0.191	0.015	0.041	0.047	-0.173
His H	0.631	0.34	-0.082	-0.947	0.262	0.46	-0.067	0.261	-0.296	-0.188
Ile I	0.178	-0.01	-0.346	-0.921	0.909	0.178	-0.013	-0.155	-0.115	-0.328
Leu L	-0.085	0.211	-0.833	-0.665	0.925	0.37	-0.254	-0.032	-0.024	-0.208
Lys K	-0.103	0.237	-0.39	-0.898	0.541	0.465	-0.452	0.503	-0.611	0.111
Met M	0.338	-0.158	-0.273	-0.58	0.582	0.568	-0.249	0.242	-0.226	-0.216
Phe F	0.148	0.352	-0.605	-0.801	0.285	1.062	-0.763	0.453	-0.716	-0.05
Pro P	0.242	0.027	-0.73	-0.138	0.443	0.411	-0.575	0.439	-0.339	-0.16
Ser S	0.221	0.087	-0.095	-0.396	-0.036	0.264	0.013	0.005	0.197	-0.334
Thr T	0.356	0.096	-0.355	-0.388	0.223	0.246	-0.167	0.129	-0.142	0.021
Trp W	0.343	0.698	-0.717	-1.059	0.747	0.61	0.102	-0.095	-0.637	-0.11

TABLE S-VI. Continued

	111	112	113	114	115	116	117	118	119	120
Tyr Y	0.469	0.06	-0.341	-0.793	0.159	0.583	-0.191	0.412	-0.541	-0.198
Val V	0.168	-0.049	-0.0453	-0.556	0.561	0.388	-0.339	0.143	-0.185	-0.056
	121	122	123	124	125	126	127	128	129	130
Ala A	-0.059	0.073	0.168	-0.097	-0.055	0.02	-0.015	0.026	23.503	6.852
Arg R	-0.024	0.118	0.499	-0.064	0.007	-0.264	0.297	-0.034	103.614	11.716
Asn N	-0.197	0.111	0.21	0.089	-0.129	-0.058	-0.07	-0.06	43.369	8.672
Asp D	-0.098	0.071	0.005	0.138	-0.012	-0.008	-0.145	0.024	38.361	7.734
Cys C	-0.031	0.082	0.06	0.016	0.002	0.062	-0.182	0.135	35.365	7.289
Gln Q	-0.134	0.18	0.178	0.047	-0.098	-0.005	-0.166	0.113	61.289	9.482
Glu E	-0.103	0.042	0.112	0.06	-0.125	-0.043	0.098	-0.069	55.31	8.968
Gly G	-0.012	-0.009	0.085	0.024	0.085	-0.142	-0.014	-0.036	13.019	4.754
His H	0.182	0.197	-0.078	0.035	-0.111	-0.011	0.028	-0.091	70.101	8.839
Ile I	0.262	0.152	0.198	-0.188	-0.328	0.182	0.228	-0.032	73.57	10.225
Leu L	0.197	0.183	0.043	-0.106	-0.435	0.31	0.321	-0.167	73.57	10.049
Lys K	-0.069	0.376	0.165	0.006	-0.303	-0.221	0.392	-0.109	86.362	11.419
Met M	0.165	0.066	0.176	-0.226	-0.149	0.095	0.213	-0.078	71.445	9.327
Phe F	0.595	-0.132	-0.041	-0.189	0.062	-0.053	0.21	-0.072	102.665	12.055
Pro P	0.181	0.111	0.164	-0.124	-0.371	0.176	0.235	-0.101	46.05	10.611
Ser S	0.031	-0.026	0.123	-0.047	0.133	-0.052	-0.131	0.035	26.775	6.929
Thr T	-0.127	0.177	-0.013	0.065	-0.094	-0.007	0.08	0.124	41.162	8.368
Trp W	0.37	-0.028	-0.01	-0.068	0.021	-0.175	-0.099	-0.021	150.163	12.814
Tyr Y	0.429	0.082	-0.297	-0.054	0.157	-0.094	0.097	-0.213	109.356	11.268
Val V	-0.168	0.344	0.092	-0.105	-0.277	0.113	0.2	-0.044	53.778	9.748
	131	132	133	134	135	136	137	138	139	140
Ala A	-0.479	-0.227	-0.623	-0.184	0.395	-0.022	0.095	0.049	-0.091	-0.191
Arg R	-1.459	0.197	-1.882	-0.126	0.767	0.079	-0.031	-0.028	0.227	-0.421
Asn N	-0.516	-0.387	-0.795	-0.211	0.576	-0.022	-0.062	0.16	-0.084	-0.142
Asp D	-0.573	-0.323	-0.791	-0.092	0.567	-0.105	-0.021	0.089	0.004	-0.195
Cys C	-0.97	-0.198	-0.676	0.023	0.26	0.013	0.134	0.617	-0.146	-0.015
Gln Q	-1.15	-0.166	-1.187	-0.083	0.476	0.157	-0.075	0.175	0.086	-0.486
Glu E	-1.11	-0.16	-1.112	-0.116	0.657	-0.105	-0.079	0.17	0.058	-0.407
Gly G	-0.175	-0.287	-0.34	-0.246	0.347	0.026	-0.013	0.033	-0.03	-0.082
His H	-0.262	-0.635	-1.108	-0.29	0.955	0.109	-0.479	0.07	0.306	-0.386
Ile I	-0.901	0.103	-1.564	0.001	0.517	-0.033	0.226	0.072	-0.054	-0.589
Leu L	-0.687	-0.183	-1.3	-0.265	0.655	-0.081	0.333	0.011	-0.033	-0.718
Lys K	-1.791	0.177	-1.455	0.036	0.638	0.048	0.013	0.139	0.071	-0.756
Met M	-2.146	0.189	-1.096	0.08	0.205	0.289	0.377	-0.015	-0.426	-0.053
Phe F	-1.22	-0.157	-1.856	-0.332	1.713	-0.446	-0.252	-0.128	0.526	-0.399
Pro P	-1.108	-0.498	-0.585	-0.554	1.022	-0.353	0.054	0.298	-0.203	-0.397
Ser S	-0.451	-0.319	-0.57	-0.166	0.409	-0.062	0.073	0.013	0.038	-0.181
Thr T	-0.78	-0.133	-0.974	-0.024	0.367	0.015	0.095	0.026	0.045	-0.364
Trp W	-1.103	-1.028	-1.804	-0.554	2.353	-0.372	-0.805	0.115	0.574	-0.222
Tyr Y	-1.077	-0.276	-1.654	-0.292	1.739	-0.484	-0.237	-0.207	0.486	-0.23
Val V	-0.731	-0.154	-1.284	0.01	0.372	0.032	0.215	0.072	-0.086	-0.447

TABLE S-VI. Continued

Amino acid	141	142	143	144	145	146	147	148	149	150
Ala A	-0.012	0.203	0.118	-0.141	-0.055	-0.102	0.164	0.032	-0.09	0.067
Arg R	-0.265	0.565	0.157	-0.107	-0.195	-0.278	0.299	0.076	-0.101	0.122
Asn N	-0.208	0.358	0.072	-0.114	-0.086	-0.006	0.031	0.048	-0.062	0.097
Asp D	-0.133	0.315	0.013	-0.068	-0.073	-0.048	0.14	-0.045	-0.043	0.038
Cys C	-0.089	0.051	0.226	-0.138	-0.044	-0.087	0.116	0.059	-0.112	0.127
Gln Q	-0.072	0.494	0.029	-0.2	-0.087	-0.121	0.297	-0.073	-0.112	0.103
Glu E	-0.069	0.411	-0.021	-0.124	-0.117	-0.088	0.247	-0.004	-0.172	0.135
Gly G	-0.061	0.103	0.107	-0.078	-0.019	-0.079	0.055	0.071	-0.059	0.001
His H	-0.021	0.063	0.188	0.129	-0.123	-0.332	0.208	0.152	-0.081	0.076
Ile I	0.087	0.632	-0.043	-0.125	-0.244	-0.186	0.487	-0.104	-0.032	-0.016
Leu L	0.161	0.607	-0.007	-0.133	-0.329	-0.146	0.522	-0.059	-0.124	0.032
Lys K	-0.01	0.656	0.02	-0.072	-0.254	-0.165	0.39	0.024	-0.263	0.215
Met M	0.047	0.2	0.187	-0.14	-0.231	-0.121	0.325	0.145	-0.2	0.183
Phe F	-0.24	0.228	0.259	0.123	-0.283	-0.426	0.217	0.568	-0.387	0.132
Pro P	0.099	0.31	0.177	-0.223	-0.232	-0.005	0.267	0.065	-0.262	0.18
Ser S	-0.145	0.246	0.114	-0.109	-0.053	-0.073	0.082	0.066	-0.081	0.03
Thr T	-0.02	0.298	0.118	-0.121	-0.138	-0.087	0.214	0.021	-0.114	0.063
Trp W	-0.486	0.085	0.429	0.302	-0.445	-0.471	0.397	0.38	-0.01	-0.138
Tyr Y	-0.318	0.105	0.425	-0.012	-0.127	-0.452	0.181	0.382	-0.149	0.038
Val V	-0.001	0.537	-0.01	-0.128	-0.222	-0.118	0.352	0.032	-0.183	0.113
	151	152	153	154	155	156	157	158	159	160
Ala A	-0.043	-0.029	0.004	0.03	0.062	-0.054	-0.058	0.029	0.039	0.011
Arg R	-0.088	0.002	-0.036	0.064	0.167	-0.076	-0.062	-0.049	0.202	-0.01
Asn N	-0.013	-0.072	-0.064	0.079	0.066	-0.004	-0.11	0.046	0.029	-0.03
Asp D	0.054	-0.073	-0.049	0.079	-0.002	0.014	-0.052	0.002	0.049	-0.013
Cys C	-0.072	-0.065	0.004	0.081	0.002	-0.029	-0.045	0.074	-0.043	0.025
Gln Q	0.011	-0.121	-0.056	0.142	0.041	-0.04	-0.084	-0.049	0.046	0.003
Glu E	-0.046	-0.046	-0.035	0.062	0.036	-0.002	-0.108	0.002	0.125	-0.024
Gly G	0.033	-0.042	0.005	-0.004	0.021	0.011	-0.01	-0.026	0.011	0.011
His H	-0.139	-0.016	0.07	0.102	-0.038	-0.02	-0.066	0.006	0.109	-0.065
Ile I	-0.018	-0.15	0.088	0.154	0.025	-0.082	-0.2	0.082	0.21	-0.068
Leu L	0.002	-0.141	0.077	0.142	0.037	-0.107	-0.211	0.116	0.23	-0.076
Lys K	-0.149	0.012	-0.022	0.156	0.052	-0.043	-0.178	-0.024	0.261	-0.068
Met M	-0.104	-0.139	0.099	0.105	0.03	-0.125	-0.068	0.067	0.102	-0.057
Phe F	-0.325	0.051	0.251	-0.005	-0.119	-0.067	0.046	0.005	0.119	-0.151
Pro P	-0.044	-0.143	0.075	0.089	0.052	-0.039	-0.236	0.127	0.149	-0.072
Ser S	0.039	-0.083	0.025	-0.01	0.075	-0.059	-0.004	0.005	0.013	0.013
Thr T	-0.042	-0.009	-0.033	0.089	0.022	-0.036	-0.074	0.004	0.114	-0.044
Trp W	-0.322	0.068	0.216	-0.04	-0.154	-0.03	0.061	0.016	-0.086	-0.085
Tyr Y	-0.228	-0.037	0.236	0.059	-0.197	-0.007	0.065	-0.014	0.068	-0.167
Val V	-0.094	0	-0.083	0.18	0.045	-0.111	-0.119	0.04	0.165	-0.007

TABLE S-VII. The prominent principal component score and the corresponding eigenvalue of 99 WHIM, 74 geometrical and 160 3D-MORSE descriptors

No.	WHIM descriptors		Geometrical descriptors			3D-MORSE descriptors		
	Eigenvalue	%	No.	Eigenvalue	%	No.	Eigenvalue	%
1	50.53231	51.04274	1	24.0685	55.9734	1	51.4977	32.186
2	21.8993	22.1205	2	5.3808	12.5134	2	33.1044	20.6902
3	7.79161	7.87031	3	4.2917	9.9808	3	13.9686	8.7304
4	6.45442	6.51961	4	2.6995	6.2779	4	12.3945	7.7466
5	3.857	3.89596	5	2.1097	4.9062	5	9.3042	5.8151
6	2.10476	2.12602	6	1.4465	3.364	6	6.4255	4.0159
7	1.90928	1.92857	7	0.7745	1.8012	7	6.1609	3.8505
8	1.28317	1.29613	8	0.5868	1.3648	8	5.1864	3.2415
9	1.00451	1.01465	9	0.4141	0.9629	9	4.2146	2.6341
10	0.49921	0.50425	10	0.3348	0.7786	10	3.7662	2.3539
11	0.40984	0.41398	11	0.3145	0.7313	11	3.2758	2.0474
12	0.31501	0.31819	12	0.201	0.4675	12	2.7476	1.7173
13	0.29745	0.30046	13	0.144	0.3349	13	2.0126	1.2579
14	0.20545	0.20753	14	0.1035	0.2406	14	1.673	1.0456
15	0.18188	0.18372	15	0.0674	0.1567	15	1.2115	0.7572
16	0.12194	0.12317	16	0.0304	0.0706	16	1.0376	0.6485
17	0.08147	0.0823	17	0.015	0.0349	17	0.7839	0.4899
18	0.03159	0.03191	18	0.0101	0.0234	18	0.696	0.435
19	0.0198	0.02	19	0.0073	0.017	19	0.5391	0.337

TABLE S-VIII. SVWGM descriptors for amino acid

Amino acid	4 PCs of 99 WHIM descriptors				5 PCs of 74 GEOMETRICAL descriptors				
	1	2	3	4	5	6	7	8	9
Ala A	-11.6344	-1.89677	1.97792	-2.60584	-4.8673	4.8567	0.2935	-1.1984	-1.7882
Arg R	11.87107	-2.87032	2.74823	1.25733	2.8074	-5.7328	-10.0304	0.1795	-1.8715
Asn N	-5.34951	7.68317	4.11656	4.1737	-4.2352	4.4868	-1.581	-0.5684	2.9533
Asp D	-4.02676	2.99296	-3.35851	-3.77013	-3.675	5.6066	-1.3744	2.375	2.2126
Cys C	-5.65032	-2.87927	-2.99048	2.3435	-4.8303	6.3381	0.7404	-3.6652	-1.4237
Gln Q	2.17649	-2.40014	0.84542	3.57161	-4.7011	-0.8588	-3.5331	2.8551	0.7795
Glu E	2.36689	0.15236	-4.04847	0.80392	-2.5167	-0.6925	-1.4272	-0.5017	3.8605
Gly G	-11.7823	-13.6975	3.47023	0.20083	-4.6947	9.543	-0.1147	-0.1988	-0.4047
His H	2.33867	0.36099	-1.56522	-1.07602	4.3481	3.6123	1.8679	3.8021	0.8011
Ile I	0.41167	6.40422	-1.24429	-1.62207	-2.213	-5.2	3.6825	5.6186	-5.5525
Leu L	0.26884	8.11636	2.89694	0.98231	-3.1883	-9.1722	5.8668	4.8209	-0.3621
Lys K	9.00644	-2.09657	-3.35485	2.39215	-0.5855	-11.934	-4.8895	-1.5481	3.8189
Met M	4.36305	-1.66543	-3.97675	-1.02332	-3.9573	-4.0717	2.3255	-4.3088	-5.9397
Phe F	7.26373	-4.36604	-1.09058	1.62148	13.8796	-2.8069	2.0969	-6.5485	-0.7813
Pro P	-5.3069	3.18399	0.59462	4.27735	-2.7762	-3.1282	7.5571	-2.5701	7.0349
Ser S	-9.15545	2.32007	-0.49944	-2.26929	-3.3416	6.8606	-0.9756	0.8169	-1.6716
Thr T	-4.22009	-0.27234	-1.39095	-2.53752	-2.7966	0.8798	-1.07	-1.2773	-0.1541
Trp W	11.70248	0.16164	5.62047	-4.91875	19.2063	3.7382	-0.0853	6.6477	1.0446
Tyr Y	8.54042	-1.52583	1.74131	-1.28473	13.2974	2.2367	0.8869	-4.4618	-1.3706
Val V	-3.18401	2.29446	-0.49218	-0.51649	-5.1598	-4.5618	-0.2362	-0.2687	-1.1856

TABLE S-VIII. Continued

Amino acid	9 PCs of 160 3D-MORSE descriptors								
	10	11	12	13	14	15	16	17	18
Ala A	0.1084	-0.9456	2.594	-0.4204	-5.9082	0.7197	-0.4996	1.1106	1.2405
Arg R	-2.2739	1.9078	1.1935	-2.4422	7.4386	-3.1167	4.6443	-0.2724	0.8752
Asn N	-1.0546	0.4217	-0.9058	-0.1832	-3.2495	-2.6099	-1.4085	-0.0991	-1.3005
Asp D	1.3277	2.1233	-0.3749	2.3417	-3.4151	-1.5233	-0.4735	0.8486	-2.1593
Cys C	-1.5163	-2.8869	-1.281	-0.17	-3.4528	4.8887	0.7554	-2.7832	-1.1356
Gln Q	-1.1897	0.1375	-5.7141	1.1501	0.7412	-0.9023	3.0675	1.2869	-1.4086
Glu E	1.0923	-0.405	-1.4034	3.1204	-0.6074	-0.935	2.76	1.4287	-2.2504
Gly G	1.5034	0.8204	3.4931	0.5227	-6.8679	2.8835	1.4014	2.882	1.5407
His H	5.1879	-5.1697	-0.707	-3.4635	1.2963	-0.2267	0.2235	0.0099	-1.0526
Ile I	2.8169	1.2975	-0.3499	3.6691	-0.6107	-3.1206	-2.2368	-1.9152	1.3986
Leu L	-0.8706	3.2602	1.0827	-2.473	-0.7406	-3.4737	-1.9935	-1.5138	0.4502
Lys K	2.5185	-2.3203	1.6602	1.1263	3.019	-0.349	2.4237	-0.6669	3.2261
Met M	-3.4378	-3.8467	-2.0643	0.6833	1.3496	3.1447	1.4995	-4.1297	-0.9596
Phe F	0.7353	0.795	2.6529	2.9515	6.3729	3.7134	-1.7188	1.5139	1.1937
Pro P	-3.0942	0.809	-0.1377	-0.9751	-3.2208	0.2478	-1.5559	-0.0085	0.8157
Ser S	-2.4715	3.4412	1.2993	-0.512	-5.334	-0.3277	-1.1852	0.4623	-0.9085
Thr T	2.2859	0.1757	1.2979	-0.8649	-3.2382	-0.3181	-0.8146	-0.0062	1.1008
Trp W	-4.6764	-2.6452	0.9322	0.8924	11.0178	0.4087	-3.3601	0.4752	-0.9542
Tyr Y	3.1242	4.2243	-4.419	-2.4006	7.4664	1.5601	-1.4356	1.7758	-0.5768
Val V	-0.1157	-1.1943	1.1514	-2.5526	-2.0567	-0.6638	-0.0932	-0.399	0.8648

TABLE S-IX. Statistics of PLS on variables selected by SMR (OT analogues)

No.	Variable	t^a	R^2_{cum}	Q^2_{LOO}
1	v_{24}	1	0.516	0.501
2	v_{24}, v_{17}	2	0.855	0.596
3	v_{24}, v_{17}, v_{36}	2	0.909	0.777
4	$v_{24}, v_{17}, v_{36}, v_{51}$	2	0.950	0.843
5	$v_{24}, v_{17}, v_{36}, v_{51}, v_{23}$	2	0.944	0.864
6	$v_{24}, v_{17}, v_{36}, v_{51}, v_{23}, v_{14}$	3	0.955	0.647
7	$v_{24}, v_{17}, v_{36}, v_{51}, v_{23}, v_{14}, v_{46}$	3	0.948	0.657
8	$v_{24}, v_{17}, v_{36}, v_{51}, v_{23}, v_{14}, v_{46}, v_{40}$	2	0.954	0.668
9	$v_{24}, v_{17}, v_{36}, v_{51}, v_{23}, v_{14}, v_{46}, v_{40}, v_{27}$	2	0.953	0.601
10	$v_{24}, v_{17}, v_{36}, v_{51}, v_{23}, v_{14}, v_{46}, v_{40}, v_{27}, v_{19}$	2	0.952	0.747

^aPrincipal components

TABLE S-X. Statistics of PLS on variables selected by SMR (BTT)

No.	Variable	t^a	R^2_{cum}	Q^2_{LOO}
1	v_{32}	1	0.462	0.421
2	v_{32}, v_1	1	0.692	0.646
3	v_{32}, v_1, v_{34}	2	0.709	0.644
4	$v_{32}, v_1, v_{34}, v_{36}$	2	0.882	0.825
5	$v_{32}, v_1, v_{34}, v_{36}, v_{25}$	2	0.887	0.799
6	$v_{32}, v_1, v_{34}, v_{36}, v_{25}, v_6$	2	0.891	0.812

TABLE S-X. Continued

No.	Variable	l^a	R^2_{cum}	Q^2_{LOO}
7	v 32, v 1, v 34, v 36, v 25, v 6, v 12	2	0.911	0.818
8	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29	2	0.913	0.812
9	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27	3	0.926	0.795
10	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20	3	0.927	0.812
11	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23	3	0.92	0.814
12	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7	3	0.926	0.772
13	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18	3	0.921	0.659
14	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28	3	0.920	0.672
15	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22	3	0.921	0.641
16	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22 v 21	3	0.926	0.606
17	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22, v 21, v 24	3	0.919	0.623
18	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22, v 21, v 24, v 35	3	0.930	0.589
19	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22, v 21, v 24, v 35, v 30	3	0.917	0.553
20	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22, v 21, v 24, v 35, v 30, v 5	3	0.927	0.607
21	v 32, v 1, v 34, v 36, v 25, v 6, v 12, v 29, v 27, v 20, v 23, v 7, v 18, v 28, v 22, v 21, v 24, v 35, v 30, v 5, v 9	3	0.931	0.564

^aPrincipal components

TABLE S-XI. Statistics of PLS on variables selected by SMR (ace)

No.	Variable	l^a	R^2_{cum}	Q^2_{LOO}
1	v23	1	0.637	0.633
2	v23, v34	1	0.703	0.691
3	v23, v34, v6	1	0.756	0.734
4	v23, v34, v6, v30	1	0.786	0.768
5	v23, v34, v6, v30, v28	2	0.835	0.795
6	v23, v34, v6, v30, v28, v9	2	0.852	0.786
7	v23, v34, v6, v30, v28, v9, v21	2	0.865	0.799
8	v23, v34, v6, v30, v28, v9, v21, v29	2	0.852	0.777
9	v23, v34, v6, v30, v28, v9, v21, v29, v36	3	0.862	0.748
10	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17	3	0.858	0.757
11	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4	3	0.874	0.708
12	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18	3	0.873	0.694
13	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12	3	0.882	0.719
14	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31	3	0.883	0.710
15	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11	3	0.884	0.711
16	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25	3	0.883	0.709
17	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26	3	0.883	0.702

TABLE S-XI. Continued

No.	Variable	l^a	R^2_{cum}	Q^2_{LOO}
18	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13	3	0.876	0.686
19	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20,	3	0.875	0.696
20	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19	3	0.876	0.692
21	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2	3	0.873	0.692
22	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3	3	0.787	0.629
23	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10	3	0.87	0.685
24	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8	3	0.873	0.664
25	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5	3	0.871	0.655
26	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7	3	0.871	0.642
27	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7, v14	3	0.878	0.625
28	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7, v14, v16	3	0.879	0.62
29	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7, v14, v16, v15	3	0.883	0.619
30	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7, v14, v16, v15, v33	3	0.879	0.614
31	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7, v14, v16, v15, v33, v27	3	0.88	0.613
32	v23, v34, v6, v30, v28, v9, v21, v29, v36, v17, v4, v18, v12, v31, v11, v25, v26, v13, v20, v19, v2, v3, v10, v8, v5, v7, v14, v16, v15, v33, v27, v32	3	0.88	0.629

^aPrincipal components