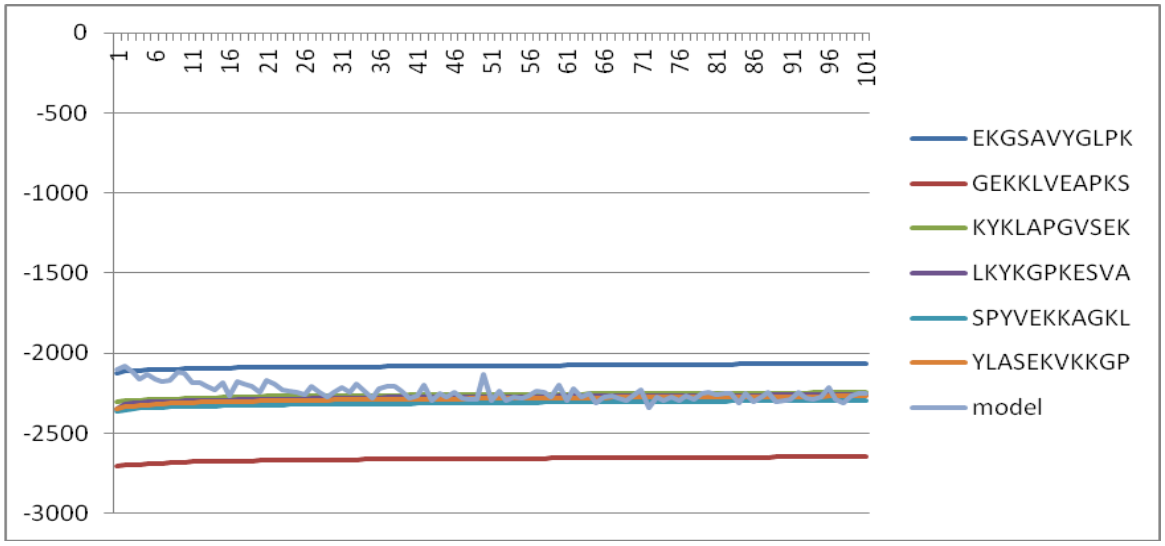
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61
66
71
76
81
86
91
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101
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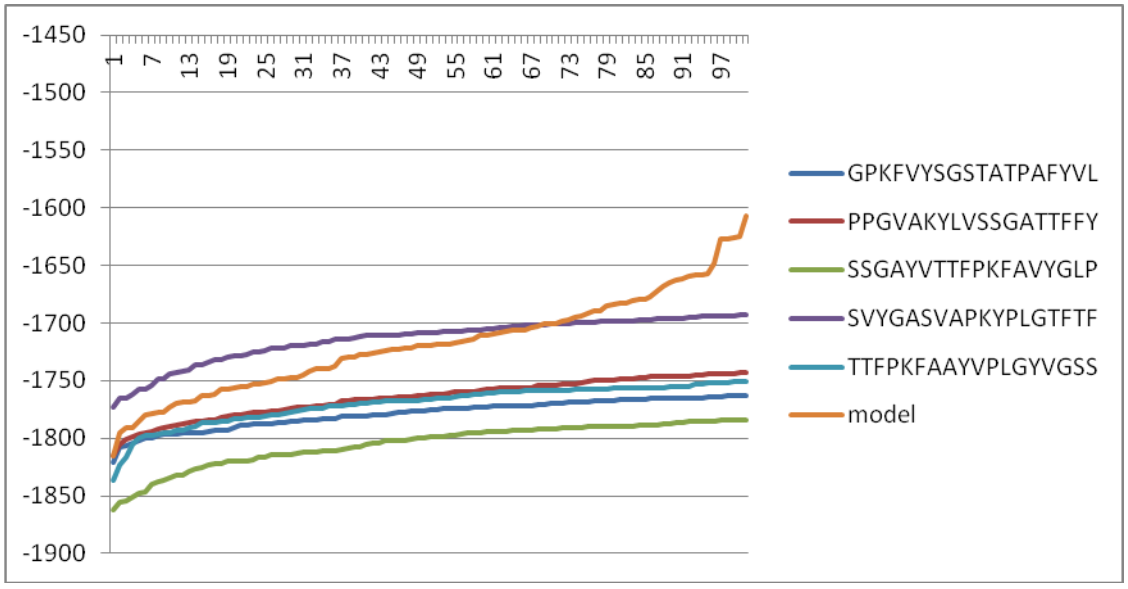
GEKKLVEAPKS
KYKLAPGVSEK
LKYKGPKESVA
SPYVEKKAGKL
YLASEKVKKGP
model

(A)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49
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61
67
73
79
85
91
97
GPKFVYSGSTATPAFYVL
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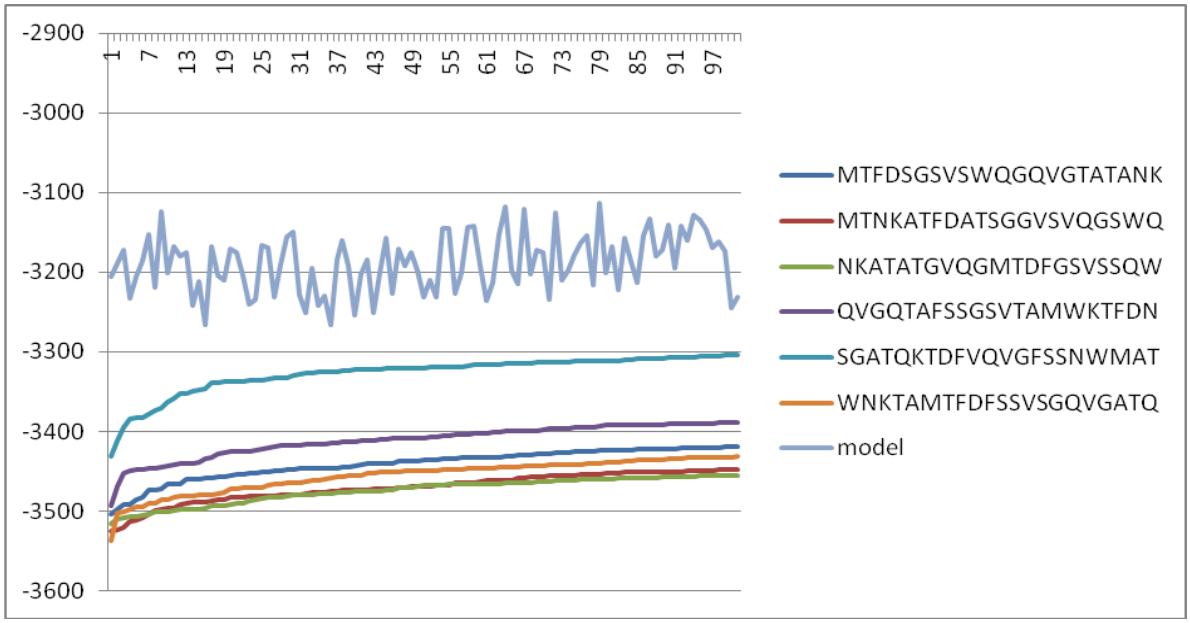
TTFPKFAAYVPLGYVGSS
model

(B)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97
MTFDSGSVSWQGQVGTATANK
MTNKATFDATSGGVSVQGSWQ
NKATATGVQGMTDFGSVSSQW
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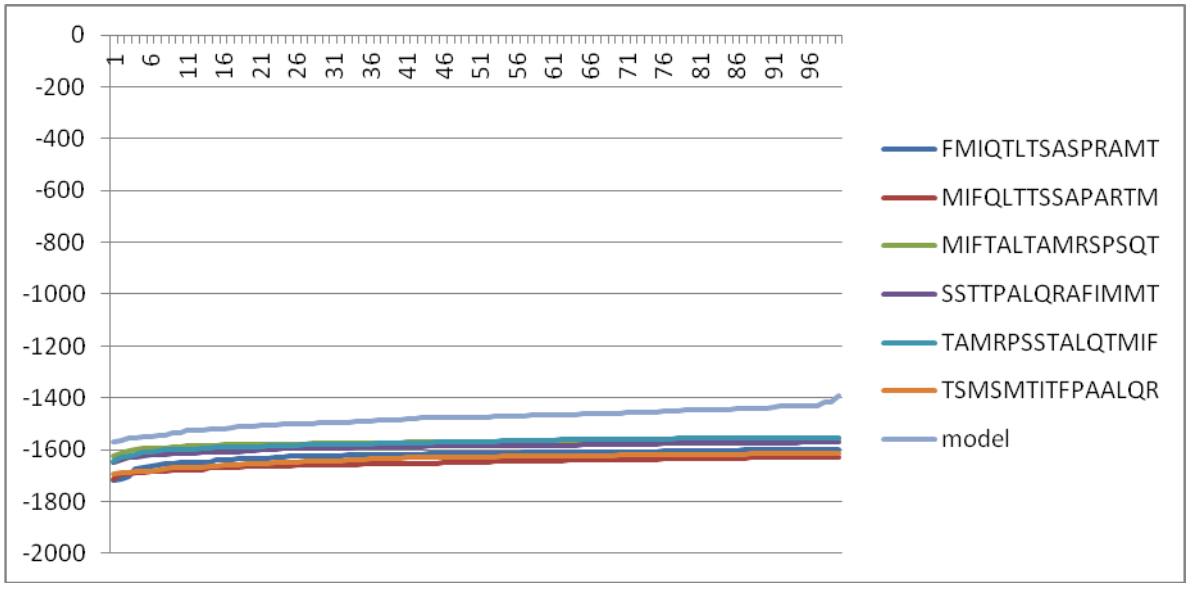
model

(C)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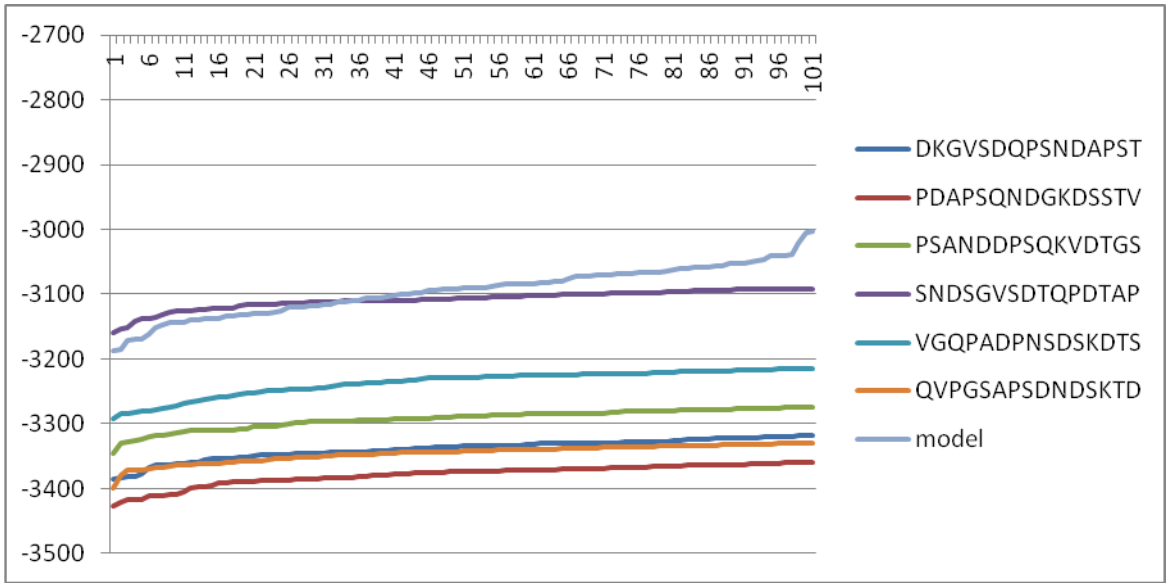
76
81
86
91
96
FMIQTLTSASPRAMT
MIFQLTTSSAPARTM
MIFTALTAMRSPSQT
SSTTPALQRAFIMMT
TAMRPSSTALQTMIF
TSMSMTITFPAALQR
model

(D)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66
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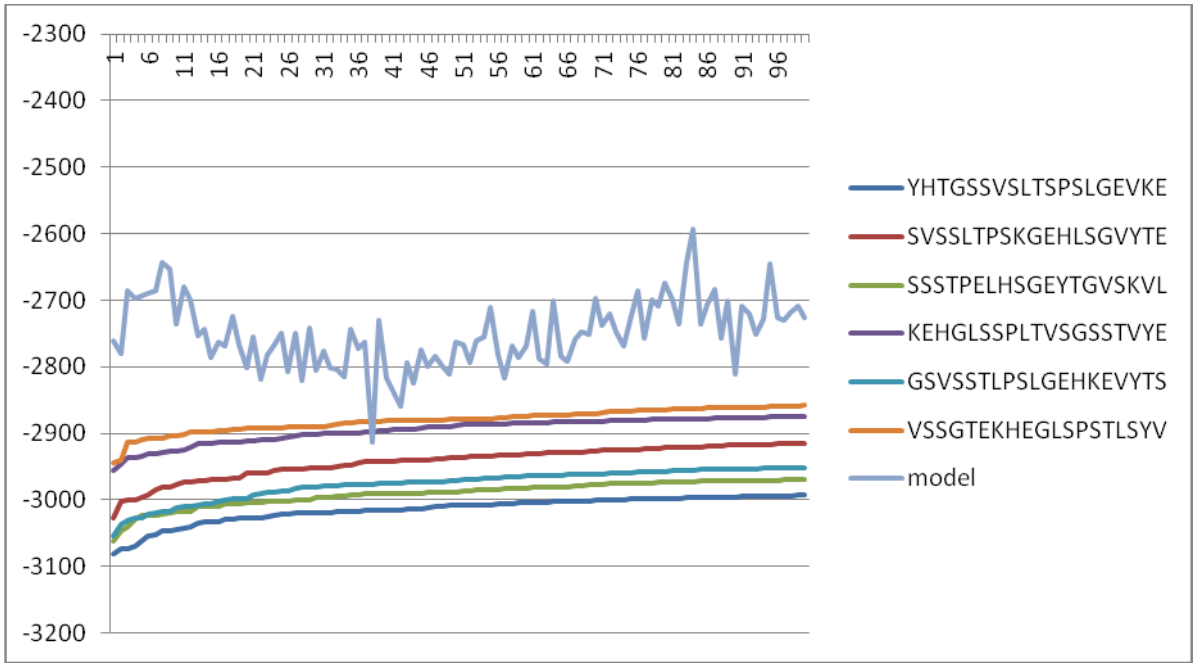
76
81
86
91
96
101
DKGVSDQPSNDAPST
PDAPSQNDGKDSSTV
PSANDDPSQKVDTGS
SNDSGVSDTQPDTAP
VGQPADPNSDSKDTS
QVPGSAPSDNDSKTD
model

(E)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76
81
86
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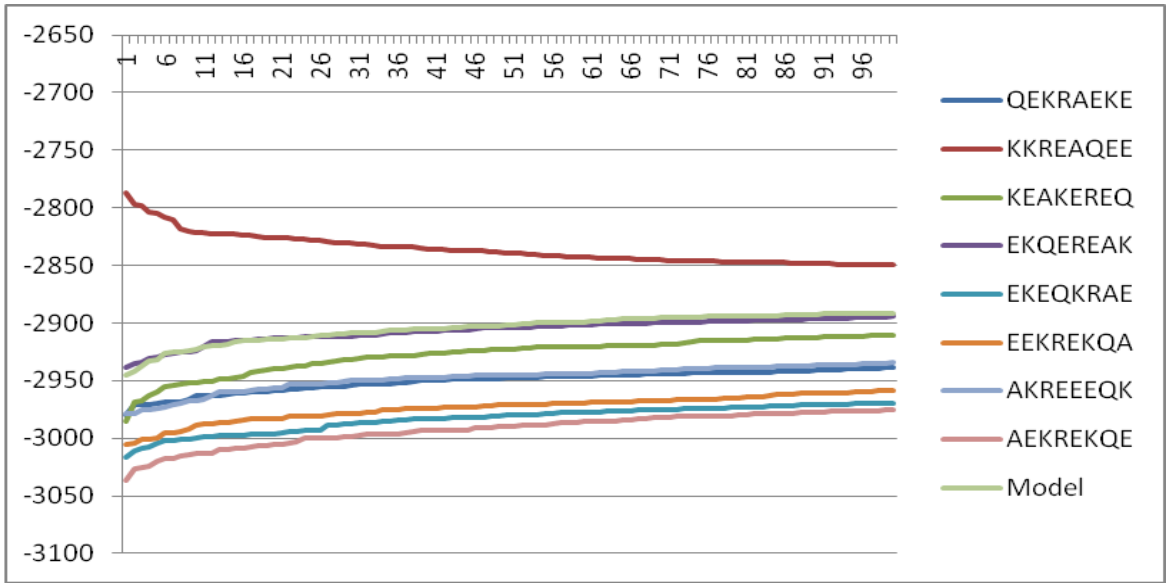
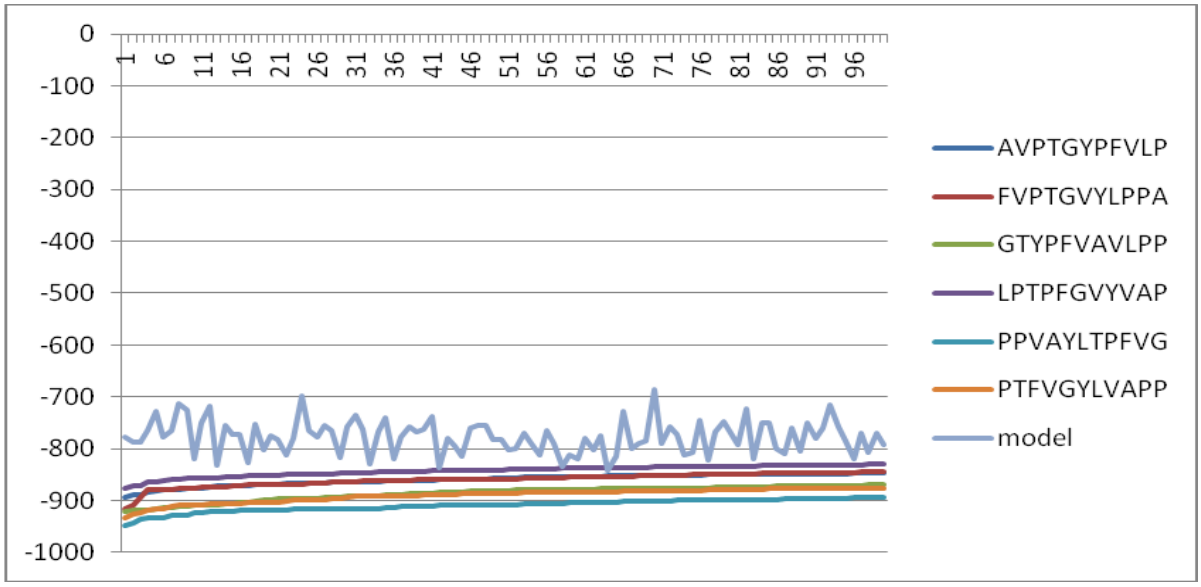
96
YHTGSSVSLTSPSLGEVKE
SVSSLTPSKGEHLSGVYTE
SSSTPELHSGEYTGVSKVL
KEHGLSSPLTVSGSSTVYE
GSVSSTLPSLGEHKEVYTS
VSSGTEKHEGLSPSTLSYV
model

(F)



(G)



(H)

Graphical representation of potential energies of designed oligopeptides and original oligopeptide represented as model in each graph

(a) **PGKYKLAVSEK (b) PGKFYVSSGATTFPAVYL**
(c)QVGFSSTAMWNKTFDVSGATQ (d) QTAMRMIFTALTSPS
(e) SGVQPDAPSNDSKDT (f) PSTLSVSSGTVYEKHEGLS
(g) KREAKQEE (h) PGPTVFPAVLY

Peptides are differentially coloured and represented at the right side of the graph which helps in identifying the most stable oligopeptide in terms of their potential energy.