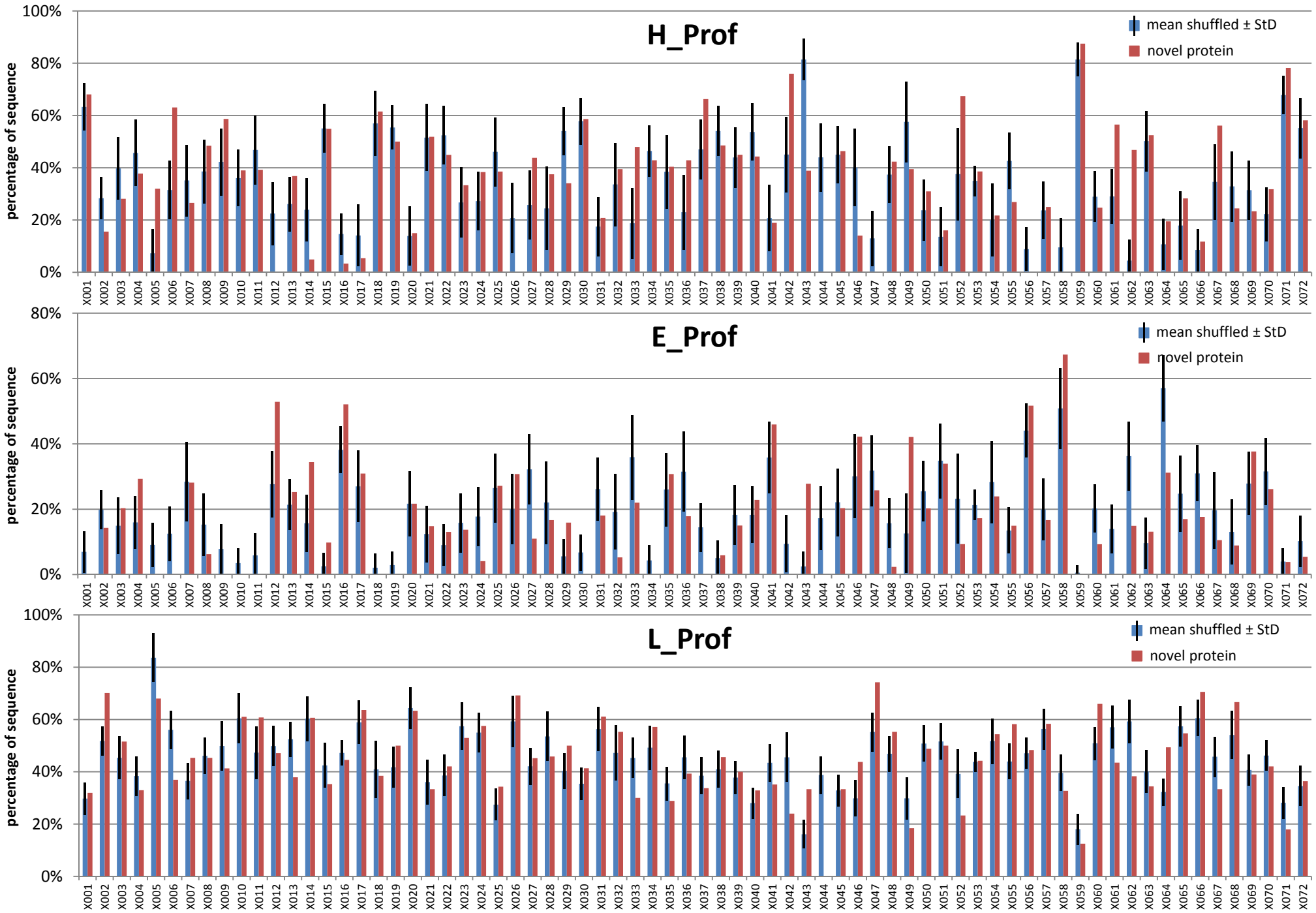
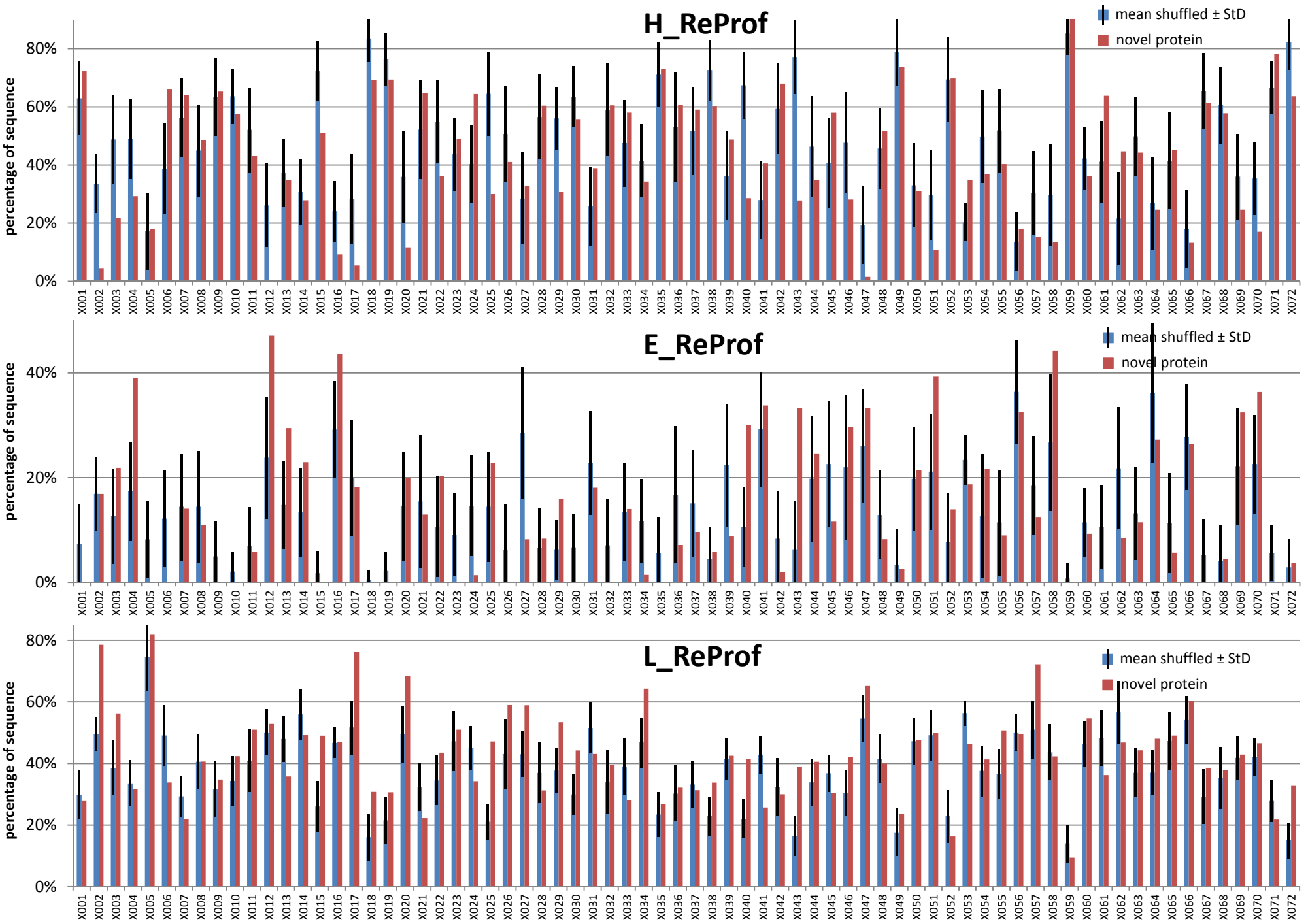
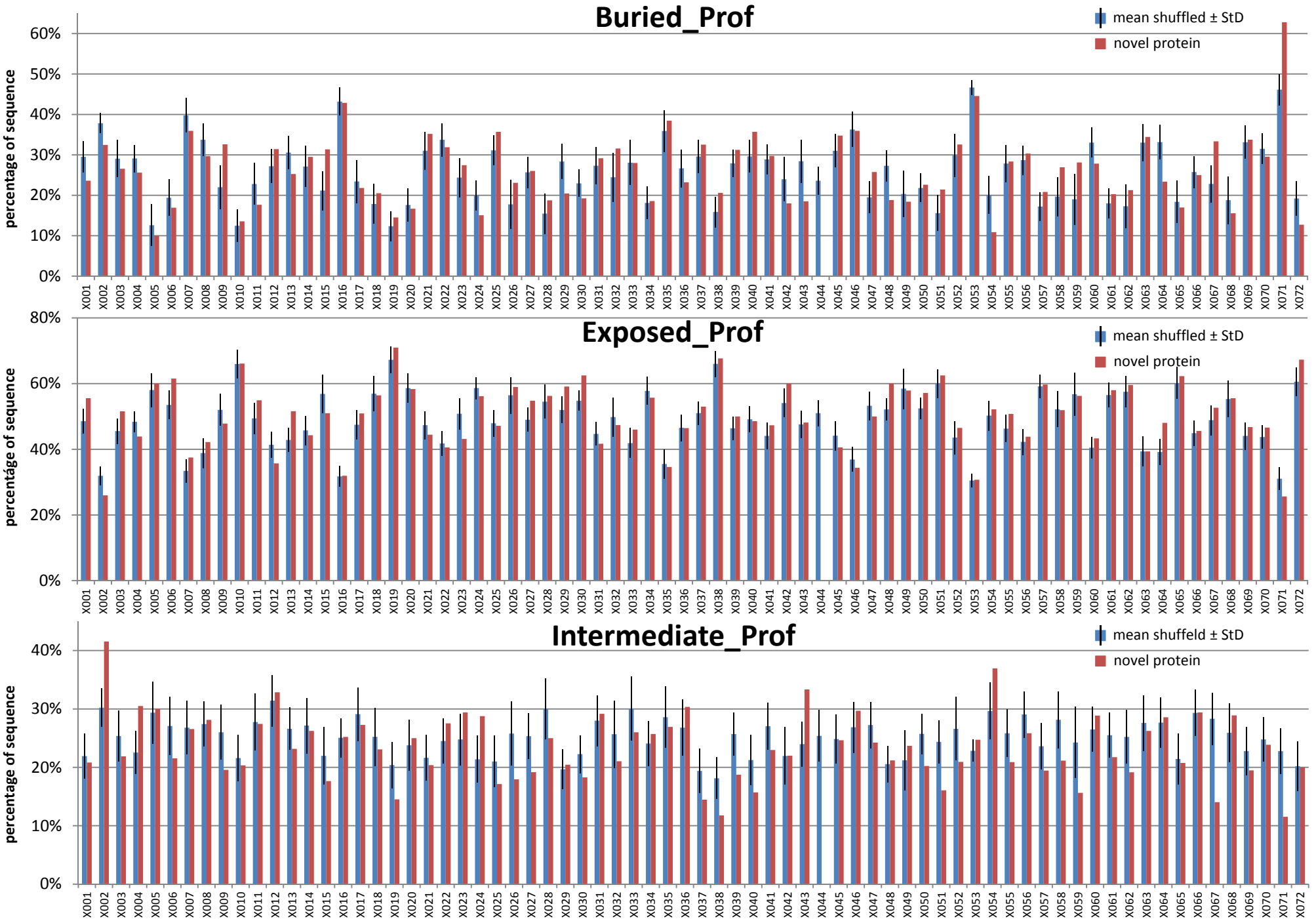
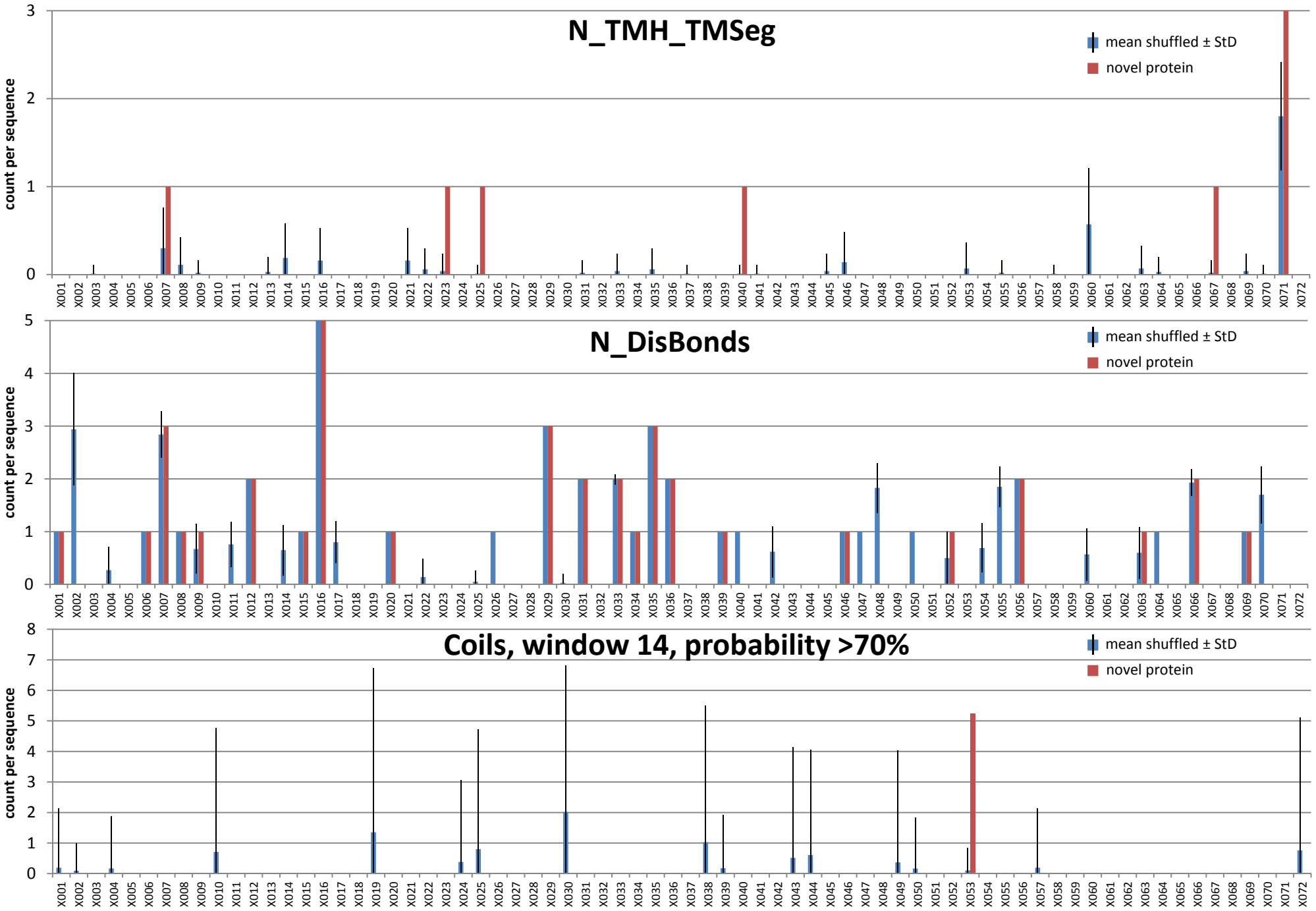
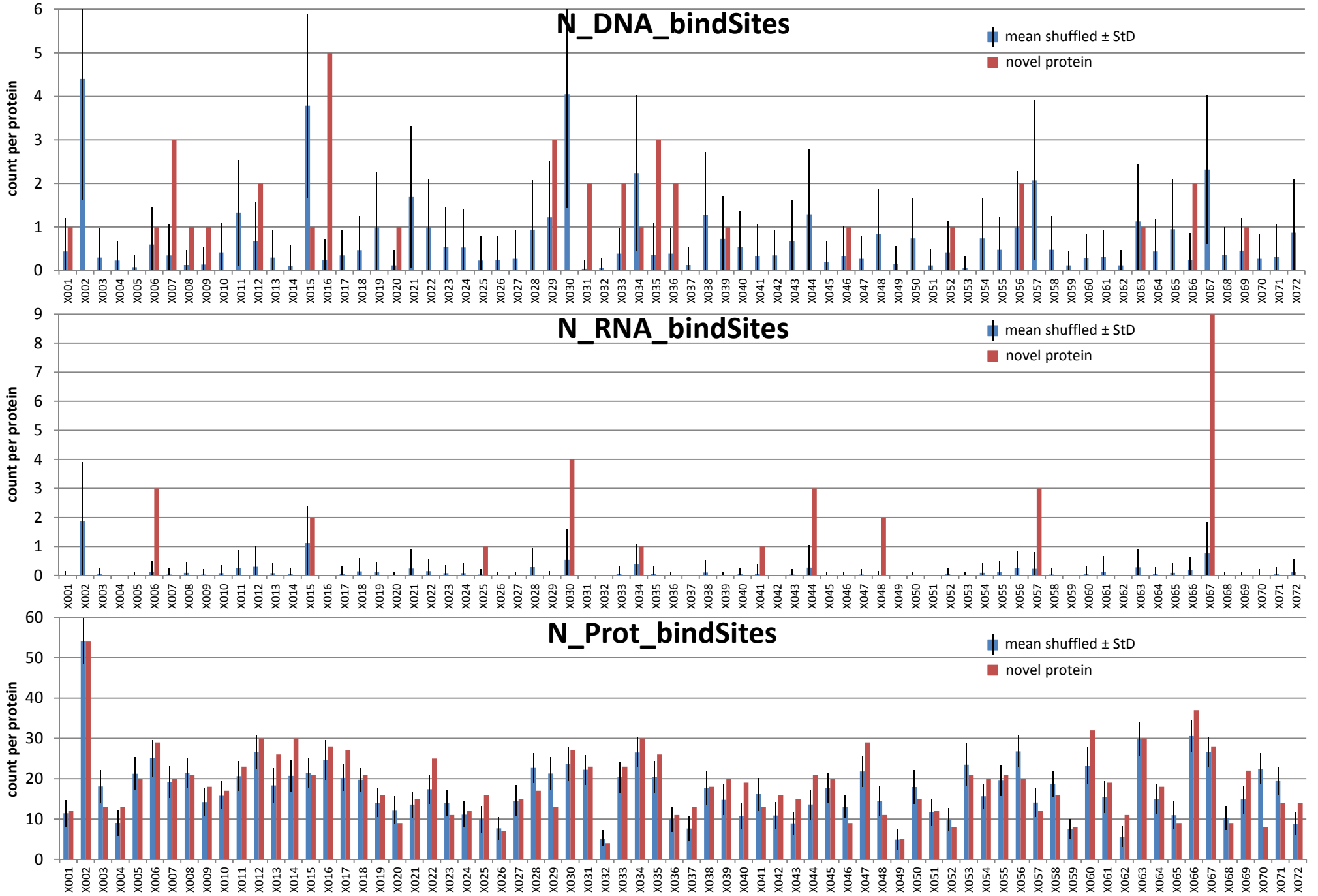
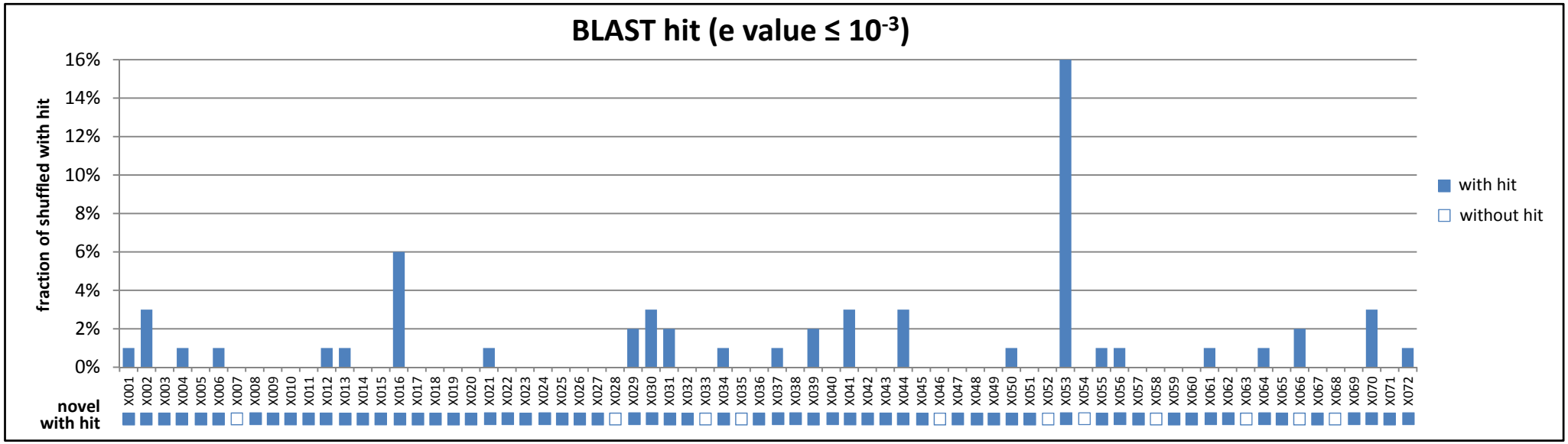

H_Prof
E_Prof
L_Prof
mean shuffled ± StD
novel protein
percentage of sequence
100%
80%
60%
40%
20%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072

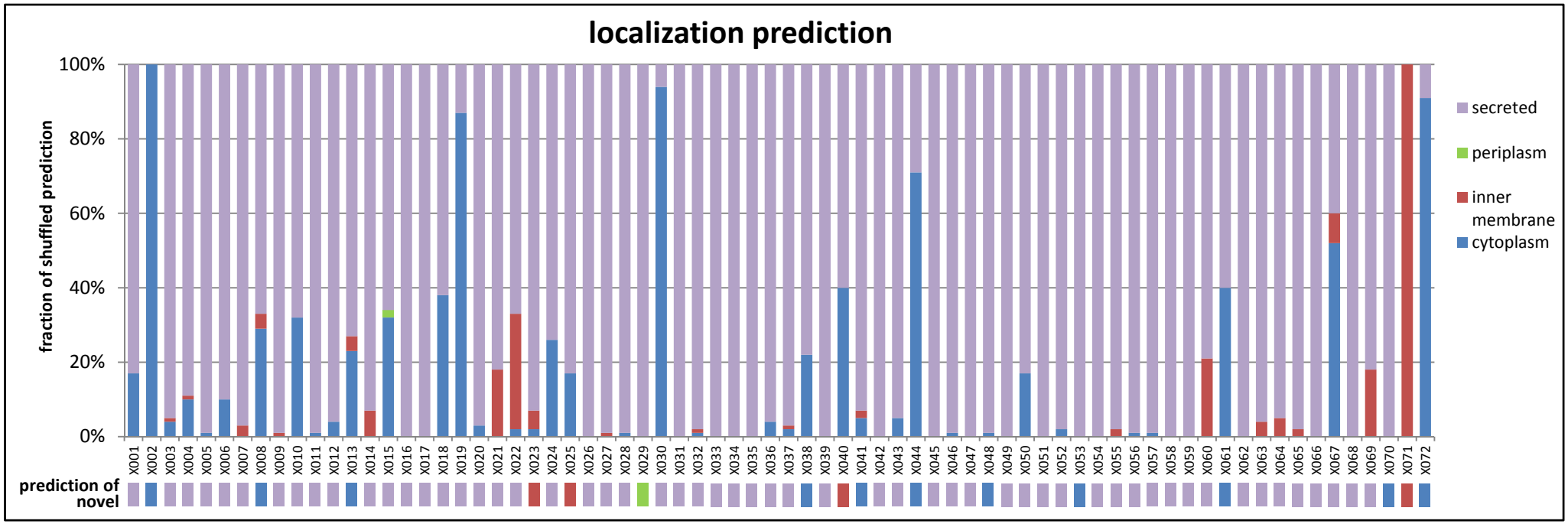

H_ReProf
E_ReProf
L_ReProf
mean shuffled ± StD
novel protein
percentage of sequence
0%
20%
40%
60%
80%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072

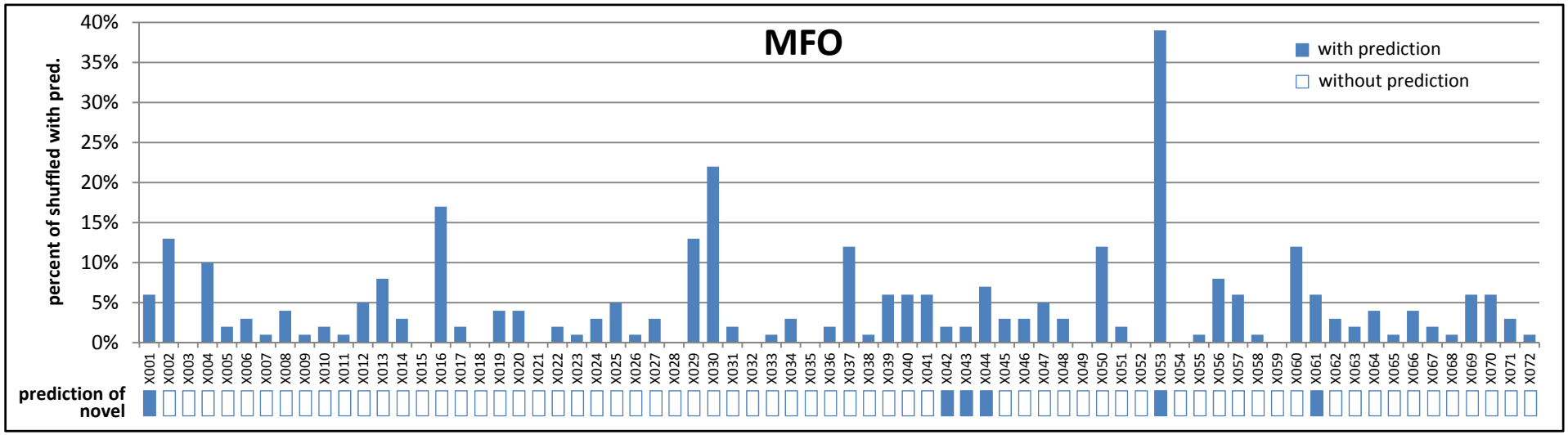

Buried_Prof
mean shuffled ± StD
novel protein
percentage of sequence
60%
50%
40%
30%
20%
10%
0%
Exposed_Prof
mean shuffled ± StD
novel protein
percentage of sequence
80%
60%
40%
20%
0%
Intermediate_Prof
mean shuffeld ± StD
novel protein
percentage of sequence
40%
30%
20%
10%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072

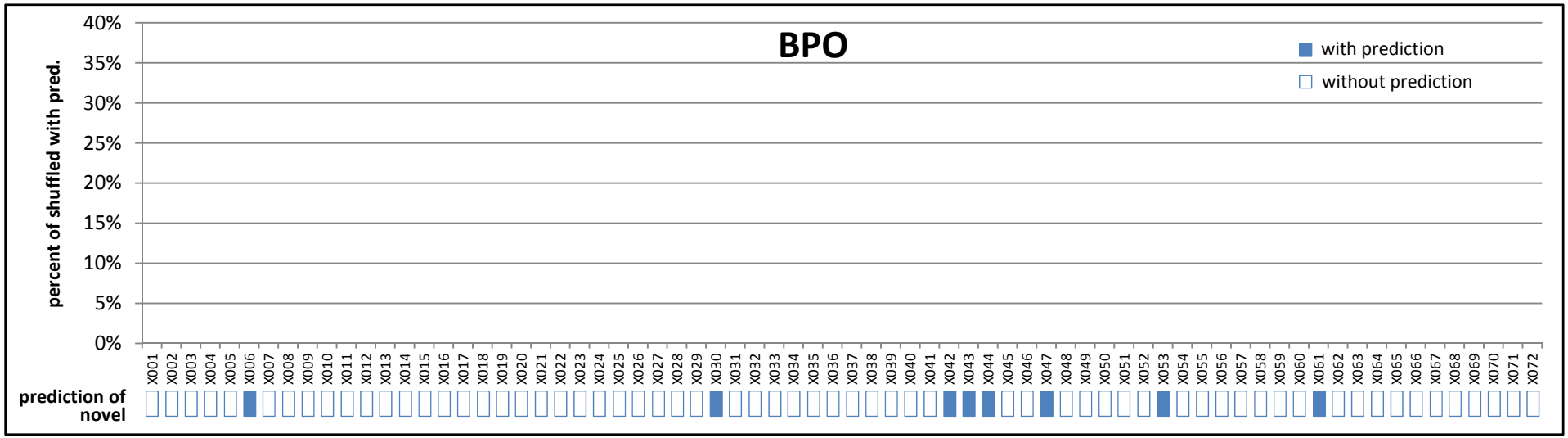

N_TMH_TMSeg
mean shuffled ± StD
novel protein
count per sequence
N_DisBonds
mean shuffled ± StD
novel protein
count per sequence
Coils, window 14, probability >70%
mean shuffled ± StD
novel protein
count per sequence

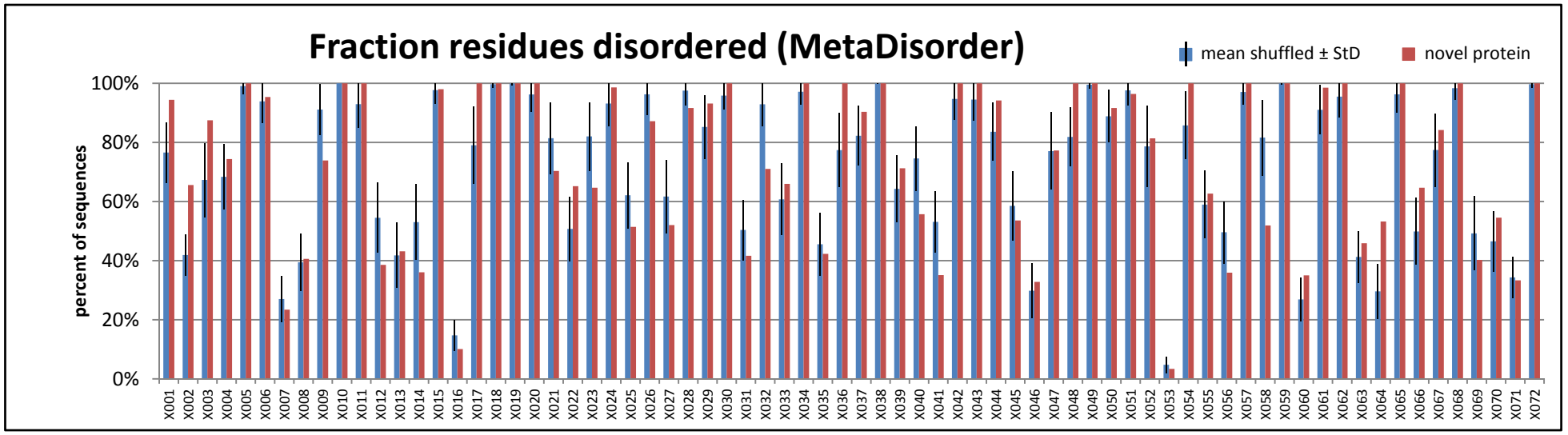

N_DNA_bindSites
mean shuffled ± StD
novel protein
count per protein
0
1
2
3
4
5
6
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
N_RNA_bindSites
mean shuffled ± StD
novel protein
count per protein
0
1
2
3
4
5
6
7
8
9
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
N_Prot_bindSites
mean shuffled ± StD
novel protein
count per protein
0
10
20
30
40
50
60
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072

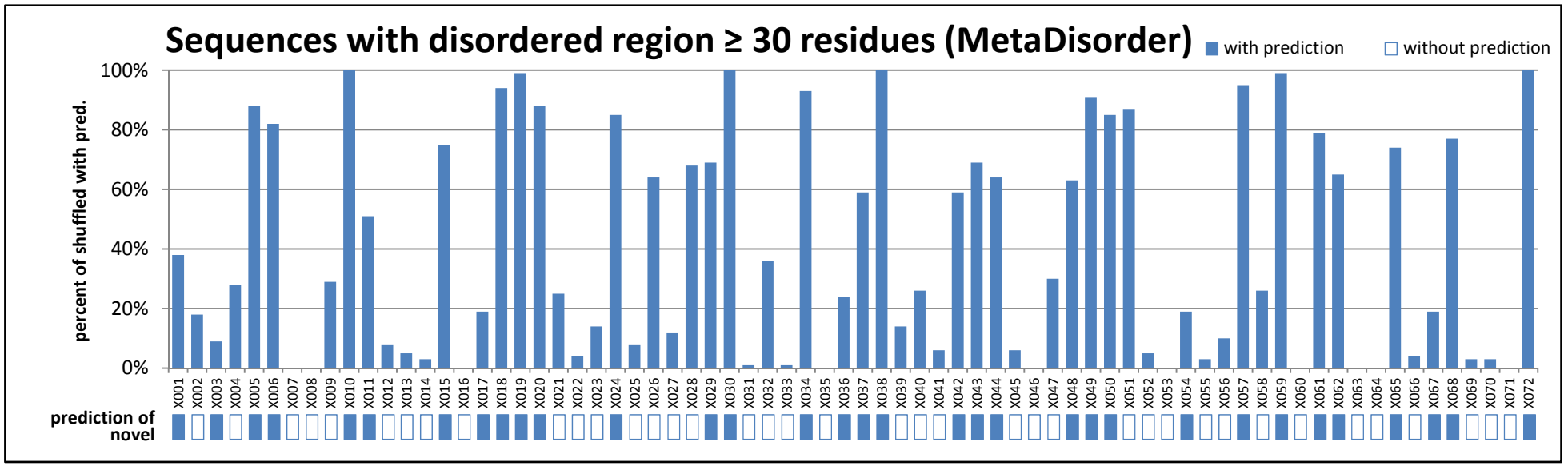

BLAST hit (e value ≤ 10-3)
fraction of shuffled with hit
16%
14%
12%
10%
8%
6%
4%
2%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
novel with hit
with hit
without hit


localization prediction
fraction of shuffled prediction
100%
80%
60%
40%
20%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
prediction of novel
secreted
periplasm
inner membrane
cytoplasm


MFO
with prediction
without prediction
percent of shuffled with pred.
40%
35%
30%
25%
20%
15%
10%
5%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
prediction of novel


BPO
with prediction
without prediction
percent of shuffled with pred.
40%
35%
30%
25%
20%
15%
10%
5%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
prediction of novel


Fraction residues disordered (MetaDisorder)
mean shuffled ± StD
novel protein
percent of sequences
100%
80%
60%
40%
20%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072


Sequences with disordered region ≥ 30 residues (MetaDisorder)
with prediction
without prediction
percent of shuffled with pred.
100%
80%
60%
40%
20%
0%
X001 X002 X003 X004 X005 X006 X007 X008 X009 X010 X011 X012 X013 X014 X015 X016 X017 X018 X019 X020 X021 X022 X023 X024 X025 X026 X027 X028 X029 X030 X031 X032 X033 X034 X035 X036 X037 X038 X039 X040 X041 X042 X043 X044 X045 X046 X047 X048 X049 X050 X051 X052 X053 X054 X055 X056 X057 X058 X059 X060 X061 X062 X063 X064 X065 X066 X067 X068 X069 X070 X071 X072
prediction of novel