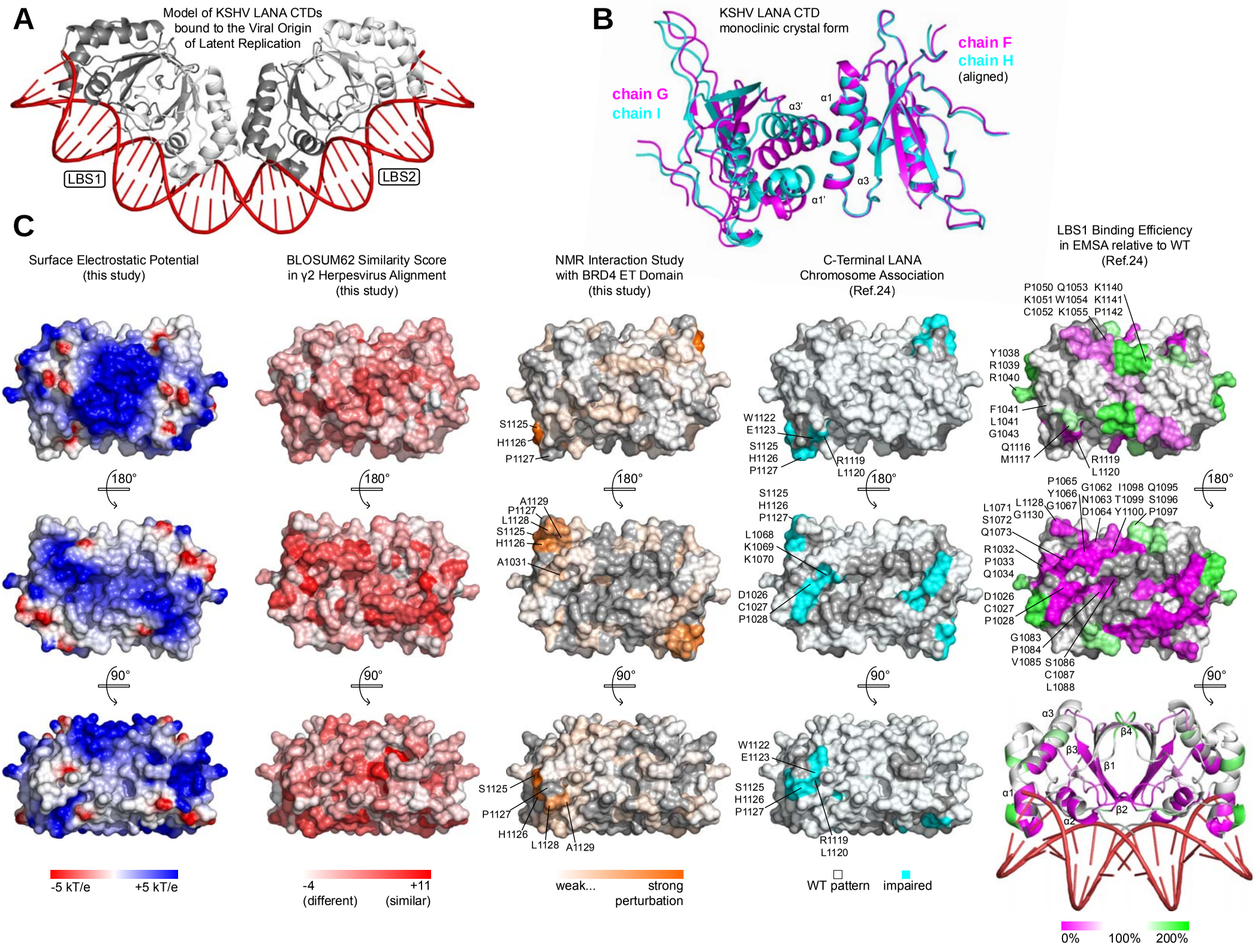
A
Model of KSHV LANA CTDs
bound to the Viral Origin
of Latent Replication
LBS1
LBS2
B
KSHV LANA CTD
monoclinic crystal form
chain F
chain H
(aligned)
chain G
chain I
α3'
α1
α3
α1'
C
Surface Electrostatic Potential
(this study)
BLOSUM62 Similarity Score
in γ2 Herpesvirus Alignment
(this study)
NMR Interaction Study
with BRD4 ET Domain
(this study)
C-Terminal LANA
Chromosome Association
(Ref.24)
LBS1 Binding Efficiency
in EMSA relative to WT
(Ref.24)
180°
90°
S1125
H1126
P1127
A1129
L1128
A1031
W1122
E1123
R1119
L1120
L1068
K1069
K1070
D1026
C1027
P1028
P1050 Q1053 K1140
K1051 W1054 K1141
C1052 K1055 P1142
Y1038
R1039
R1040
F1041
L1041
G1043
Q1116
M1117
P1065 G1062 I1098 Q1095
Y1066 N1063 T1099 S1096
L1071 L1128 G1067 D1064 Y1100 P1097
S1072 G1130
Q1073
R1032
P1033
Q1034
G1083
P1084
V1085 S1086
C1087
L1088
α3
β4
β3
β1
α1
α2
β2
-5 kT/e
+5 kT/e
-4
(different)
+11
(similar)
weak...
strong
perturbation
WT pattern
impaired
0%
100%
200%