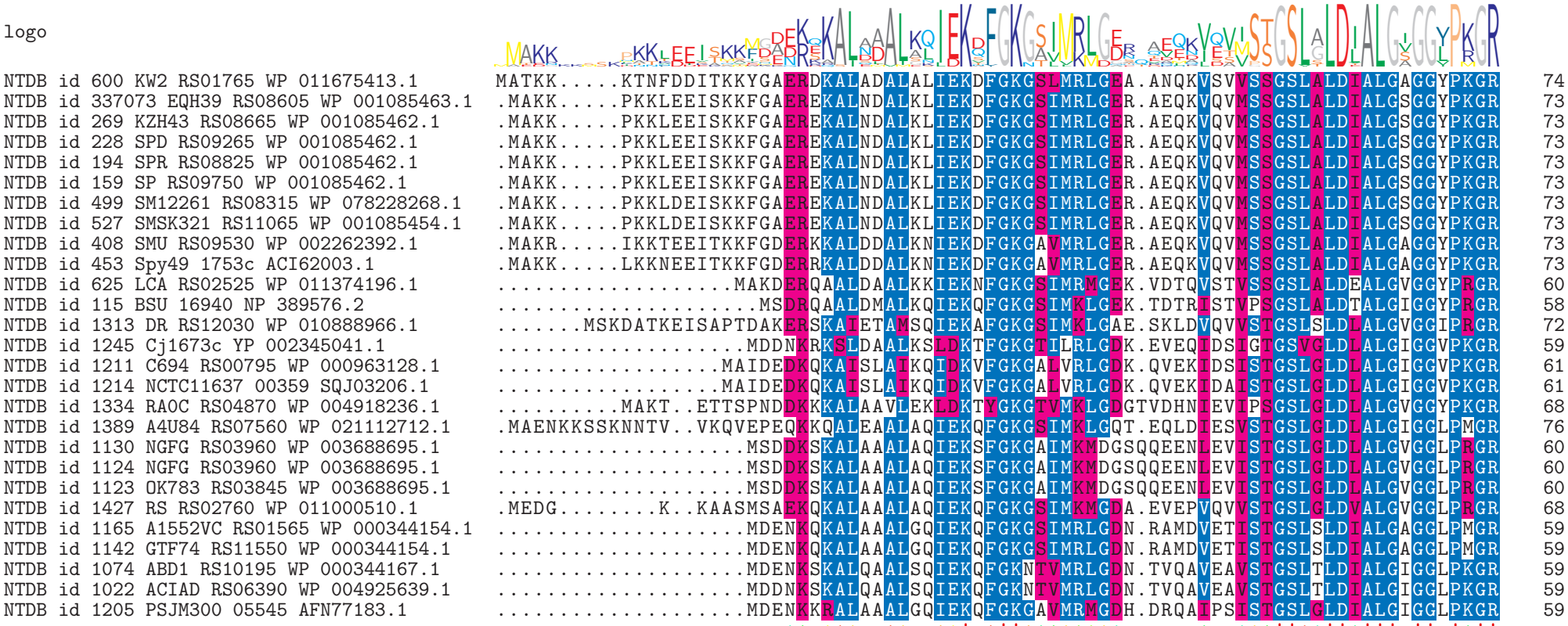
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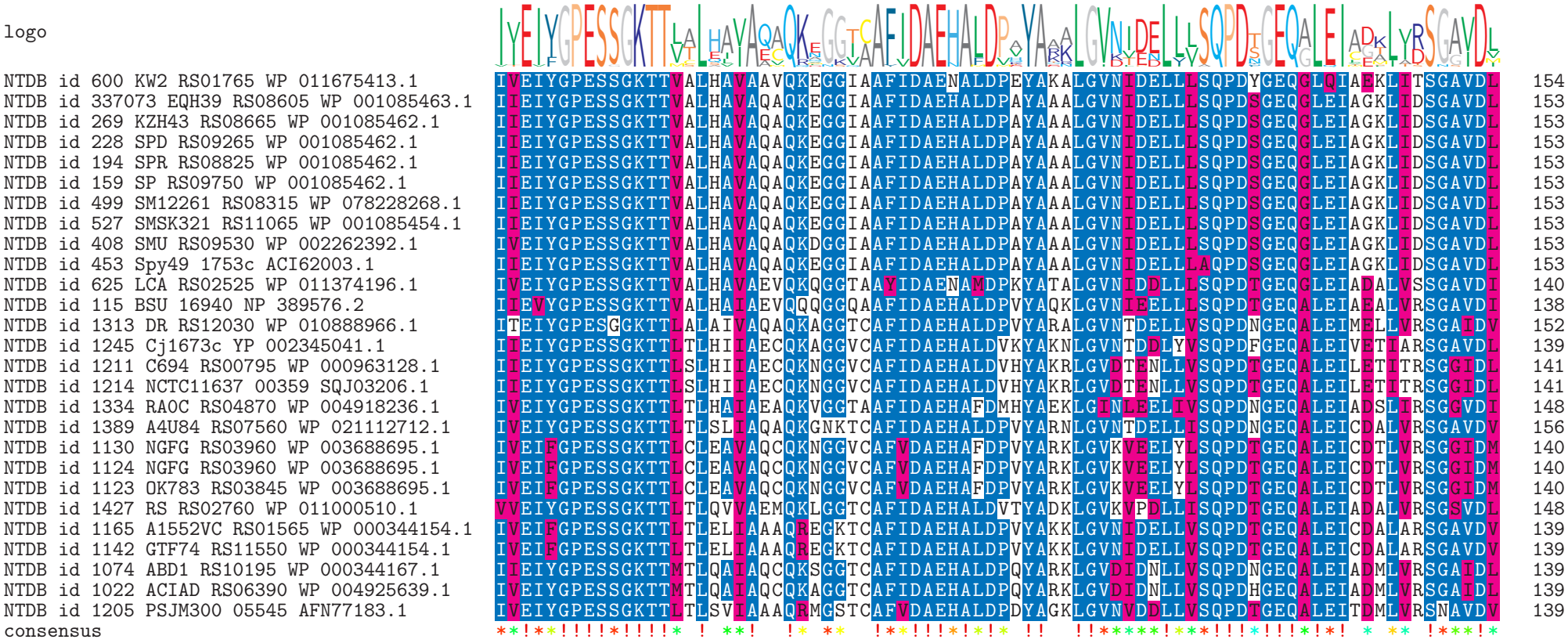
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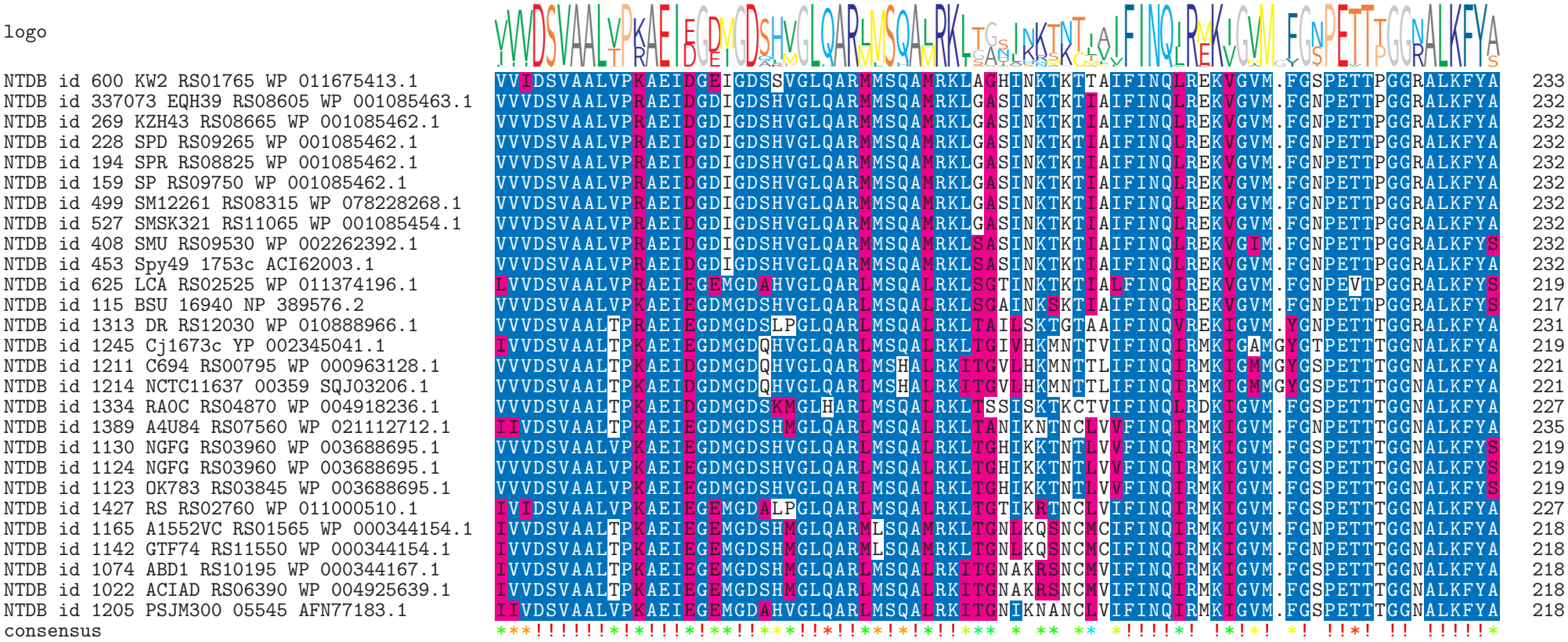
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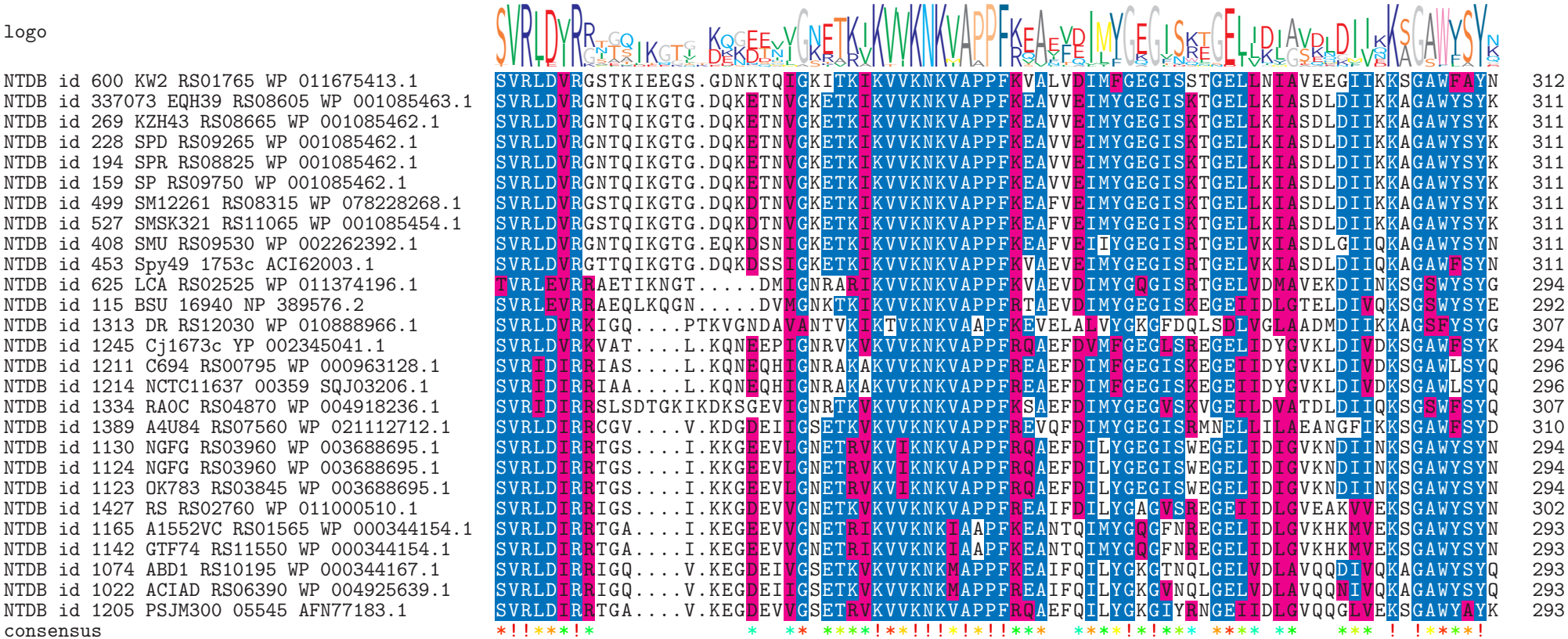
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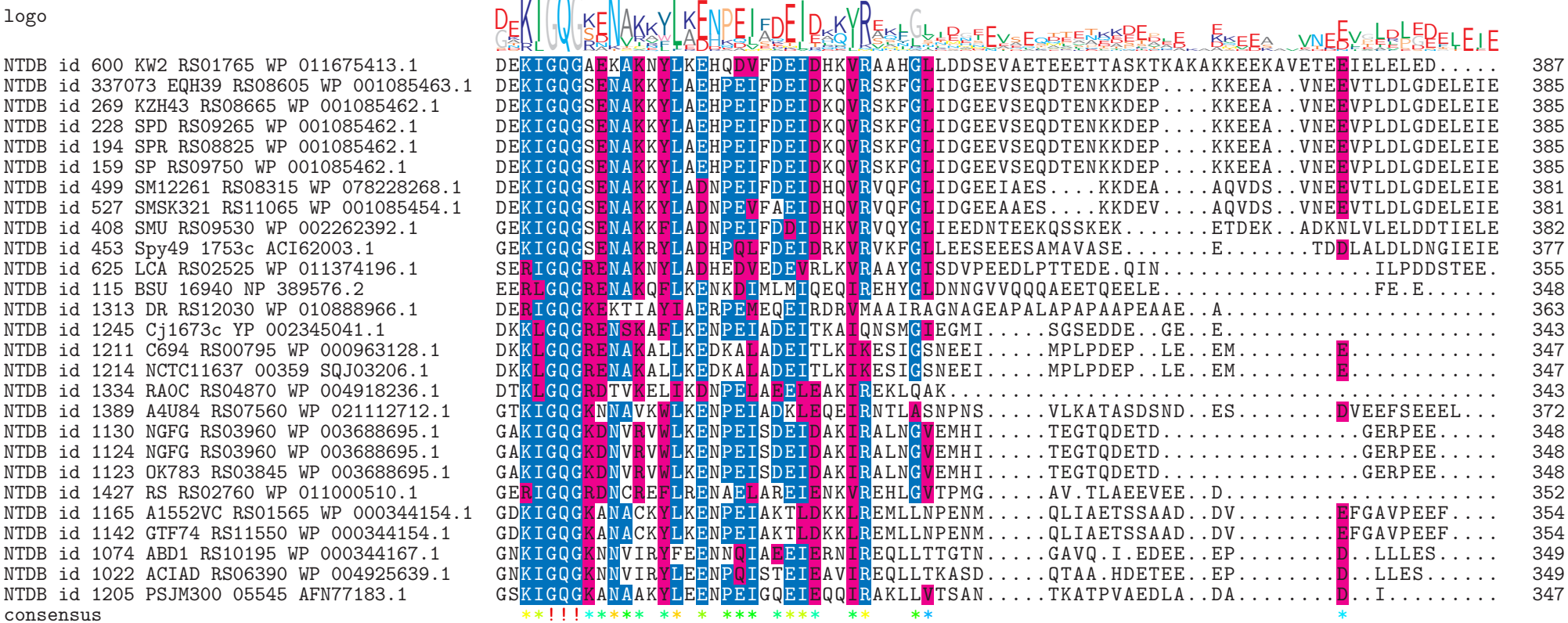
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NTDB id 527 SMSK321 RS11065 WP 001085454.1 DEKIGQGSENAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAES....KKDEV....AQVDS..VNEEVTLDLGDELEIE 381
NTDB id 408 SMU RS09530 WP 002262392.1 GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.......ETDEK..ADKNLVLELDDTIELE 382
NTDB id 453 Spy49 1753c ACI62003.1 GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEESAMAVASE.......E.......TDDLALDLDNGIEIE 377
NTDB id 625 LCA RS02525 WP 011374196.1 SERIGQGRENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDLPTTEDE.QIN.....................ILPDDSTEE. 355
NTDB id 115 BSU 16940 NP 389576.2 EERLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQQAEETQEELE.....................FE.E..... 348
NTDB id 1313 DR RS12030 WP 010888966.1 DERIGQGKEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A..... 363
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NTDB id 1211 C694 RS00795 WP 000963128.1 DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDEP..LE..EM.....E..... 347
NTDB id 1214 NCTC11637 00359 SQJ03206.1 DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDEP..LE..EM.....E..... 347
NTDB id 1334 RAOC RS04870 WP 004918236.1 DTKLGQGRDTVKELIKDNPELAEELEAKIREKLQAK..... 343
NTDB id 1389 A4U84 RS07560 WP 021112712.1 GTKIGQGKNNAVKWLKENPEIADKLEQEIRNTLASNPNS.....VLKATASDSND..ES.....DVEEFSEEEL... 372
NTDB id 1130 NGFG RS03960 WP 003688695.1 GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETD.....GERPEE..... 348
NTDB id 1124 NGFG RS03960 WP 003688695.1 GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETD.....GERPEE..... 348
NTDB id 1123 OK783 RS03845 WP 003688695.1 GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETD.....GERPEE..... 348
NTDB id 1427 RS RS02760 WP 011000510.1 GERIGQGRDNCREFLRENAELAREIENKVREHLGVTPMG.....AV.TLAEEVEE..D..... 352
NTDB id 1165 A1552VC RS01565 WP 000344154.1 GDKIGQGKANACKYLKENPEIAKTLDKKLREMLLNPENM.....QLIAETSSAAD..DV.....EFGAVPEEF.... 354
NTDB id 1142 GTF74 RS11550 WP 000344154.1 GDKIGQGKANACKYLKENPEIAKTLDKKLREMLLNPENM.....QLIAETSSAAD..DV.....EFGAVPEEF.... 354
NTDB id 1074 ABD1 RS10195 WP 000344167.1 GNKIGQGKNNVIRYFEENNQIAEEIERNIREQLLTTGTN.....GAVQ.I.EDEE..EP.....D..LLLES..... 349
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NTDB id 1205 PSJM300 05545 AFN77183.1 GSKIGQGKANAAKYLEENPEIGQEIEQQIRAKLLVTSAN.....TKATPVAEDLA..DA.....D..I..... 347
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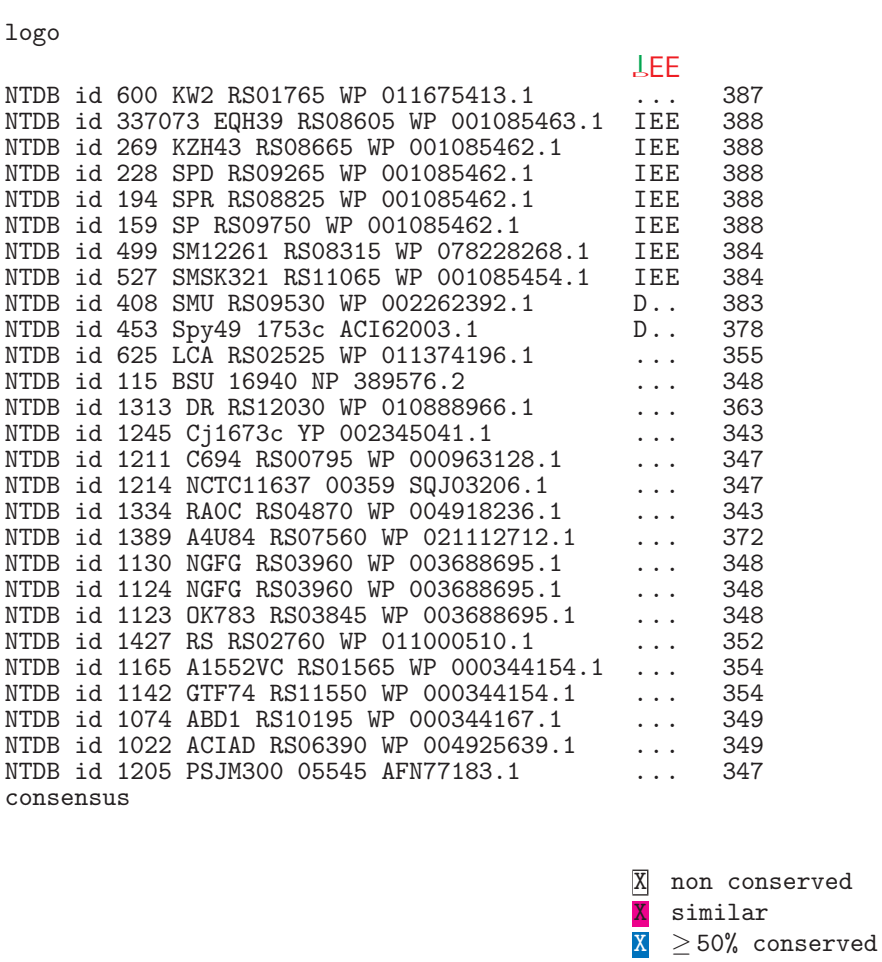
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consensus
X non conserved
X similar
X ≥ 50% conserved