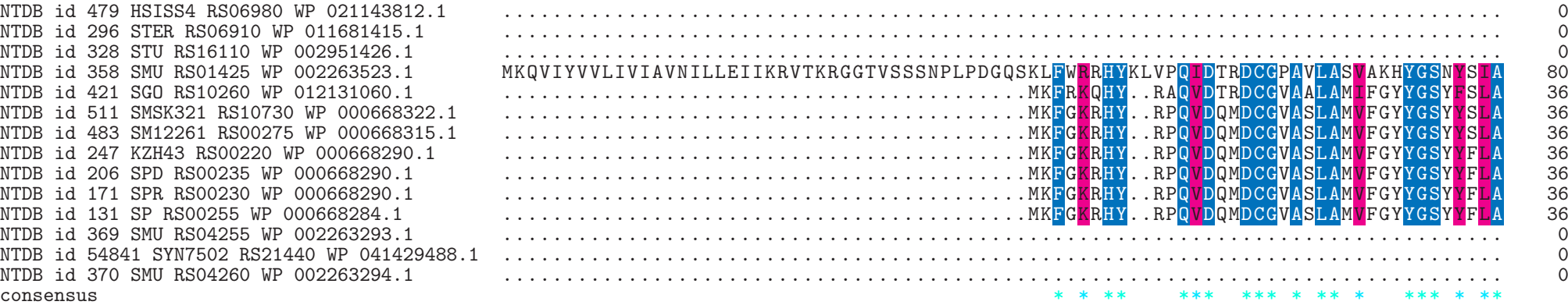
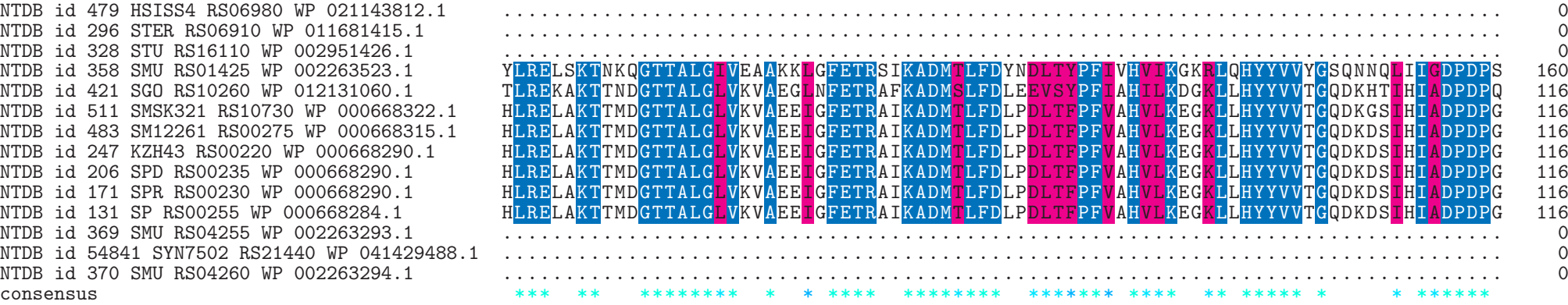


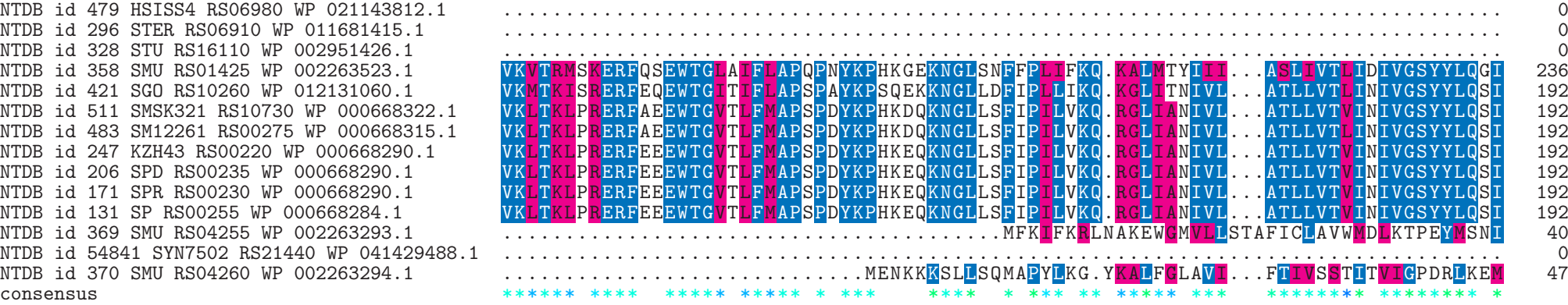
logo



logo



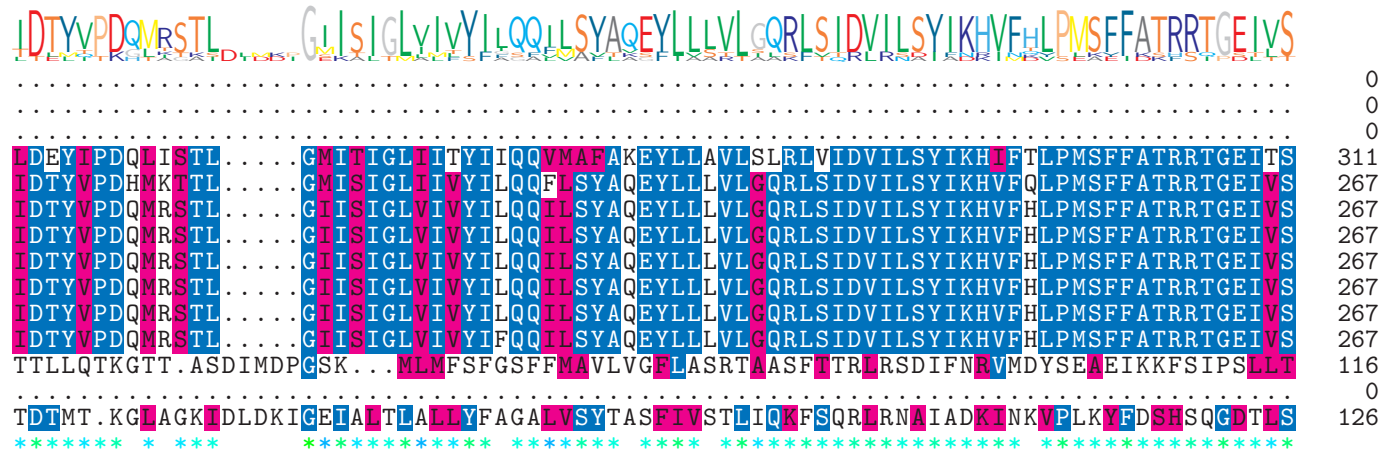
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consensus

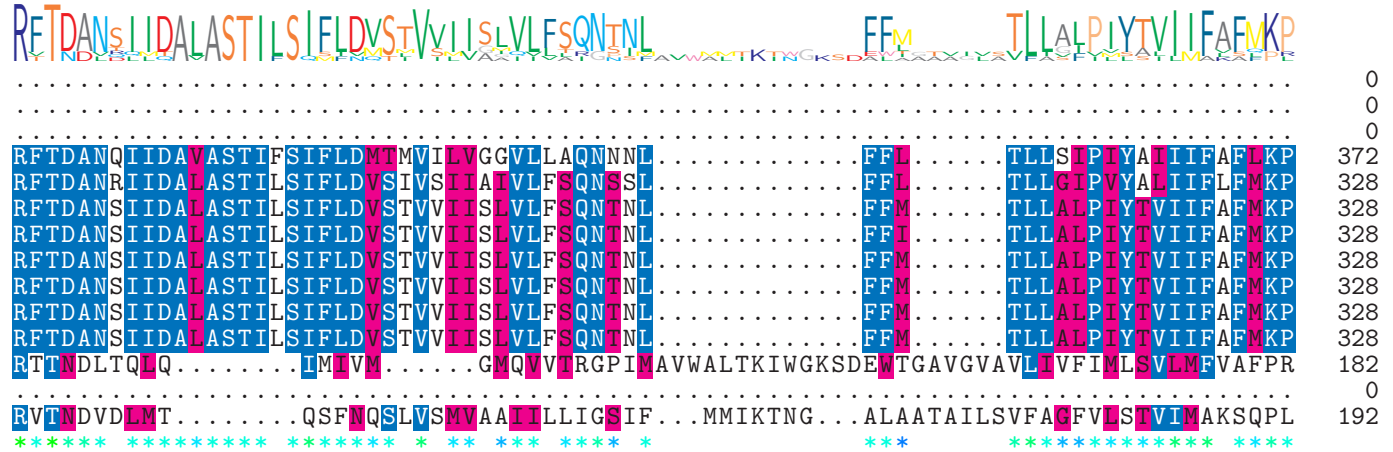
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consensus

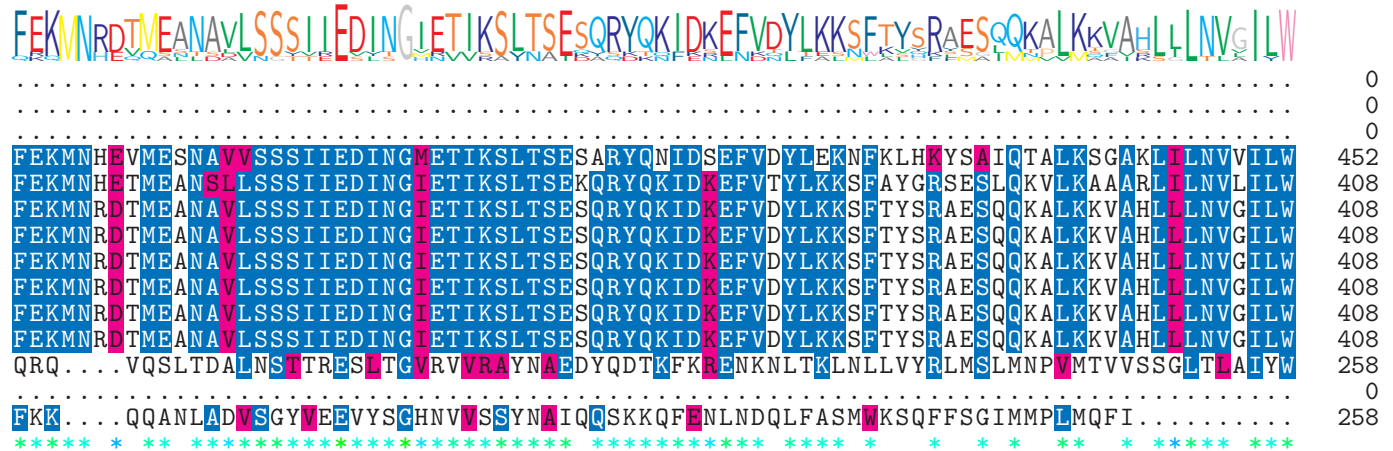
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consensus

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consensus

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[illegible]

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NTDB id 171 SPR RS00230 WP 000668290.1
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NTDB id 370 SMU RS04260 WP 002263294.1
consensus

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FLDEEEIEDENHKVKQLEKVEGCVNFDNV FFGYSPDK TLIHDFSAHAKA GQKIAIVGP TGAGKTTIVNLLMR FYEVD	62
VYLVESEFEKDGDLSENSFLDGDISFENL SYKYCYGR DTLSDINLSIKK GSKVSLVGASGSGKTTIGRAIIGLNDTS	62
VYLKSEFEKKLIKDL SHFQADIDFRGV SYKYCYGA NVLSEIDLHIPA GSKTSFVGVS GSGKTTLAKMMVHFYAPN	62
VYLVTSEFEKKTVEDLS LMK GDMTFKQV YKYCYGR DVLS DINLTIPQ GSKVAFVGI SSGKTTLAKMMVNFYDPS	537
VYLVA SEFEKKTVEDLS LMK GDMTFKQV SYKYCYGR DVLLDINLTIPQ GSKVAFVGI SSGKTTLAKMMVNFYDPS	537
VYLVA SEFEKKTVEDLS LMK GDMTFKQV HYKYCYGR DVLLDINLTVPQ GSKVAFVGI SSGKTTLAKMMVNFYDPS	537
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VYLVA SEFEKKTVEDLS LMK GDMTFKQV HYKYCYGR DVLS DINLTVPQ GSKVAFVGI SSGKTTLAKMMVNFYDPS	537
VLALN SSVHFKEYSKADNARKGEVEFHDV SFRYSKNSRAVIEHV SFSAKA GETVAFIGS TGSGKSTLVNLI PRFYDAT	405
FLDEEEIEDENHKVKQLEKVEGCVNFDNV FFGYSPDK TLIHDFSAHAKA GQKIAIVGP TGAGKTTIVNLLMR FYEVD	397

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NTDB id 479 HSISS4 RS06980 WP 021143812.1
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NTDB id 370 SMU RS04260 WP 002263294.1
consensus

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Sequence	Score
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NGEIIFDGKKINGYLSHSEKNDLIRRIQMIFQDPAASLNERATVDYILSEGTHNFHLYKDEEER.....KAKI	130
NGEIIFDGKKINGYLSHSEKNDLIRRIQMIFQDPAASLNERATVDYILSEGTHNFHLYKDEEER.....KAKI	130
KGIVRINGNDLKVIV...DKTALRRHISYLPQQAYV...FSGSIMDNLVLGAKEGT...SQEDITRACETIAEI	644
QGDICLGGVNLNQL...DKQALRQYINYPQQPYV...FNGTILENLLLGAREGT...TQEDILRAVELAEI	600
QGEISLGGVNLNQI...DKKALRQYINYPQQPYV...FNGTILENLLLGAREGT...TQEDILRAVELAEI	600
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QGEISLGSVNLNQI...DKKALRQYINYSQQPYV...FNGTILENLLLGAREGT...TQEDILRAVELAEI	600
EGWIKIDGIKVQDY...SHDDLNNKVGYPQRAVL...FSGTIRSNIAFGQSDQAPLDDAKIWEALELAQA	470
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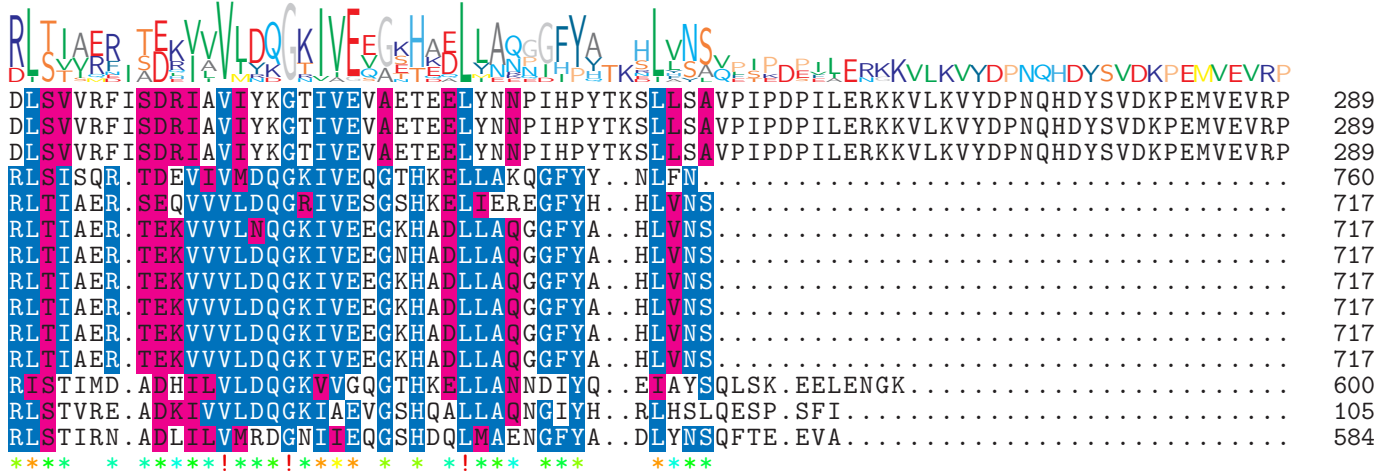
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consensus						



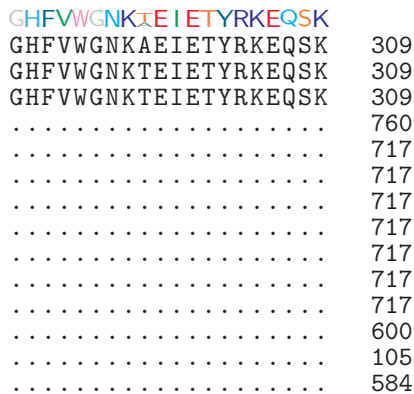
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consensus						



logo

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NTDB	id	370	SMU	RS04260	WP	002263294.1
consensus						



 non conserved
 similar
 $\geq 50\%$ conserved