

logo

NTDB id 1015 ACIAD RS12005 WP 004928865.1

NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 1145151 B5474 RS14495 WP 079548891.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for motif 1. The logo shows the conservation of amino acids across four sequences. The consensus sequence is: **MFKIIILLGWIGGIALMGIDFPLIMQYEKVGEALLLLAFIFYLYKRPMFVDRPFLKAVFCLLCTTSLFMVGHYHAEKALIE**. The most conserved positions are the first 10 residues (MFKIIILLGWIGGIALMGIDFPLIMQYEKVGEALLLLAFIFYLYKRPMFVDRPFLKAVFCLLCTTSLFMVGHYHAEKALIE) and the last 10 residues (MFKIIILLGWIGGIALMGIDFPLIMQYEKVGEALLLLAFIFYLYKRPMFVDRPFLKAVFCLLCTTSLFMVGHYHAEKALIE).

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logo

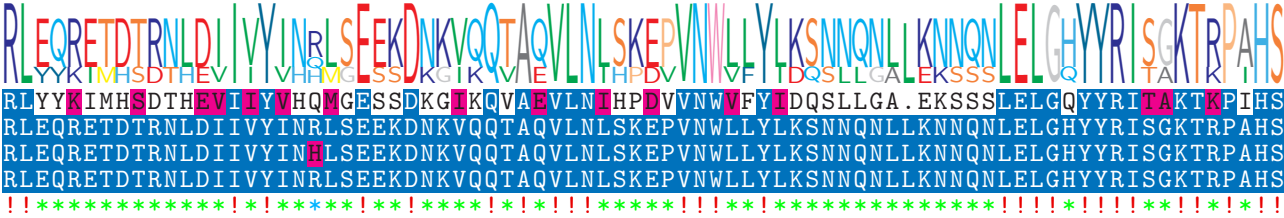
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NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 1145151 B5474 RS14495 WP 079548891.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for motif 2. The logo shows the conservation of amino acids across four sequences. The consensus sequence is: **RLEQRETDTRNLDIIVYNRLSEKDNKVQQTAAQVNLNSKEPVNWLLYLKSNQNLKNNQNLLELGHYYRISGKTRPAHS**. The most conserved positions are the first 10 residues (RLEQRETDTRNLDIIVYNRLSEKDNKVQQTAAQVNLNSKEPVNWLLYLKSNQNLKNNQNLLELGHYYRISGKTRPAHS) and the last 10 residues (RLEQRETDTRNLDIIVYNRLSEKDNKVQQTAAQVNLNSKEPVNWLLYLKSNQNLKNNQNLLELGHYYRISGKTRPAHS).

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logo

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consensus



Sequence logo for motif 3. The logo shows the conservation of amino acids across four sequences. The consensus sequence is: **YATPGAFDQEKFIQRNIMSGFNVRYLEPLSLDEIYRLGYQQHLKEQQSFSSSFRNLIEKLRLTFRQILNSSSLQQKGLI**. The most conserved positions are the first 10 residues (YATPGAFDQEKFIQRNIMSGFNVRYLEPLSLDEIYRLGYQQHLKEQQSFSSSFRNLIEKLRLTFRQILNSSSLQQKGLI) and the last 10 residues (YATPGAFDQEKFIQRNIMSGFNVRYLEPLSLDEIYRLGYQQHLKEQQSFSSSFRNLIEKLRLTFRQILNSSSLQQKGLI).

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logo

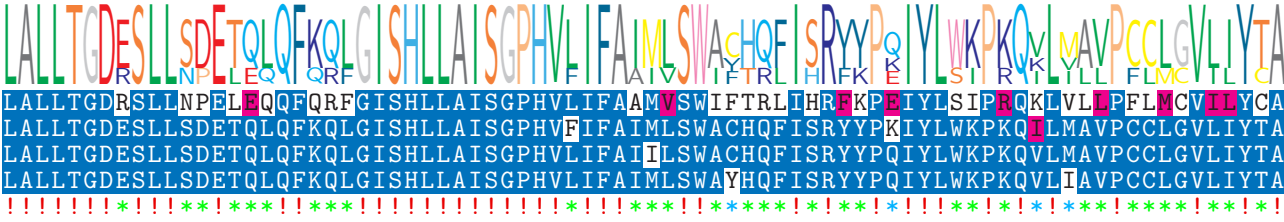
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NTDB id 1145151 B5474 RS14495 WP 079548891.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for motif 4. The logo shows the conservation of amino acids across four sequences. The consensus sequence is: **LALLTGDESLLSDETLQFQKLGISHLLAISGPHVLIFAAMVSWIFTRLTHRKPEIYLSIPQKIVLPEFLMCVILYCA**. The most conserved positions are the first 10 residues (LALLTGDESLLSDETLQFQKLGISHLLAISGPHVLIFAAMVSWIFTRLTHRKPEIYLSIPQKIVLPEFLMCVILYCA) and the last 10 residues (LALLTGDESLLSDETLQFQKLGISHLLAISGPHVLIFAAMVSWIFTRLTHRKPEIYLSIPQKIVLPEFLMCVILYCA).

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logo

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NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for motif 5. The logo shows the conservation of amino acids across four sequences. The consensus sequence is: **FVGFEIPALRTLFLSYLIFIGELLKQPIKPFILLVYSASILLLVMDPFSVLSAGFVLSYGACFILLRIYQTIQALPEQHFL**. The most conserved positions are the first 10 residues (FVGFEIPALRTLFLSYLIFIGELLKQPIKPFILLVYSASILLLVMDPFSVLSAGFVLSYGACFILLRIYQTIQALPEQHFL) and the last 10 residues (FVGFEIPALRTLFLSYLIFIGELLKQPIKPFILLVYSASILLLVMDPFSVLSAGFVLSYGACFILLRIYQTIQALPEQHFL).

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logo

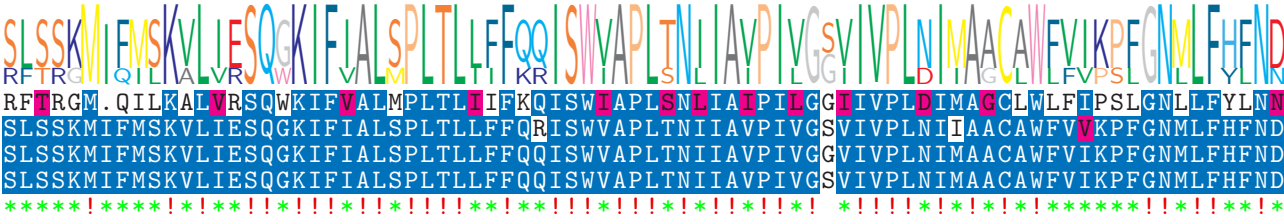
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NTDB id 1083 HON27 RS04190 WP 168726476.1

NTDB id 1145151 B5474 RS14495 WP 079548891.1

NTDB id 1070 ABD1 RS13145 WP 000472713.1

consensus



Sequence logo for motif 6. The logo shows the conservation of amino acids across four sequences. The consensus sequence is: **SLSSKMIFMSKVLIESQCKIFIALSPLTLLFFQQLSVIAPLTNIIAVPIVGSVIVPLNIIAACAWFVVKPFGNMLFHFND**. The most conserved positions are the first 10 residues (SLSSKMIFMSKVLIESQCKIFIALSPLTLLFFQQLSVIAPLTNIIAVPIVGSVIVPLNIIAACAWFVVKPFGNMLFHFND) and the last 10 residues (SLSSKMIFMSKVLIESQCKIFIALSPLTLLFFQQLSVIAPLTNIIAVPIVGSVIVPLNIIAACAWFVVKPFGNMLFHFND).

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logo

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NTDB id 1070 ABD1 RS13145 WP 000472713.1
consensus



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logo

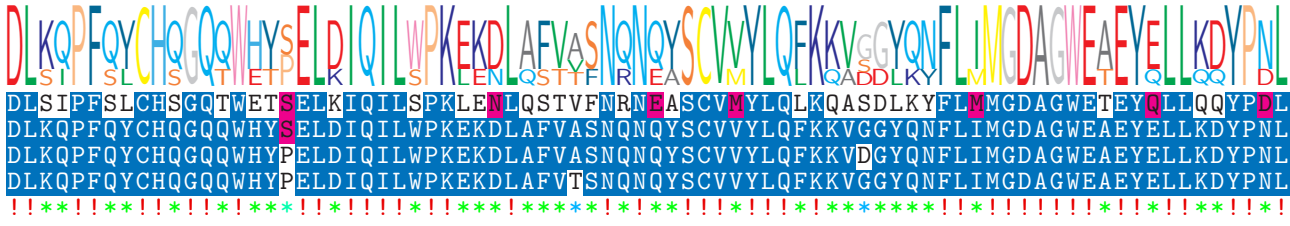
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consensus



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logo

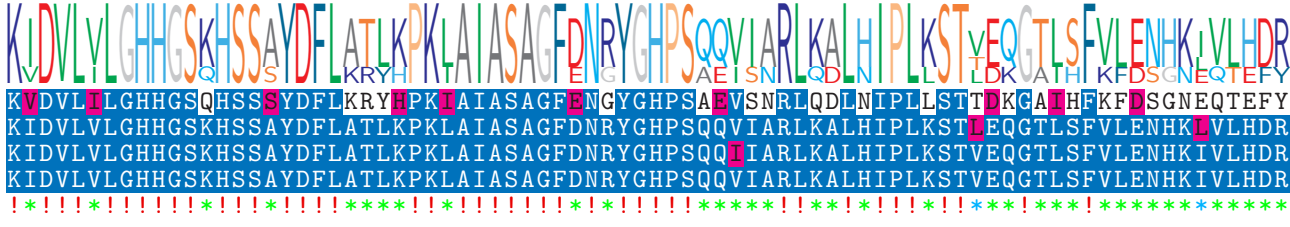
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NTDB id 1070 ABD1 RS13145 WP 000472713.1
consensus



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logo

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consensus



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logo

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NTDB id 1070 ABD1 RS13145 WP 000472713.1
consensus



806
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☒ non conserved
☒ similar
☒ ≥ 50% conserved