

logo

NTDB id 92590 QMN04 RS16615 WP 000156646.1
NTDB id 1072 ABD1 RS01805 WP 000156662.1
consensus

85
85

logo

NTDB id 92590 QMN04 RS16615 WP 000156646.1
NTDB id 1072 ABD1 RS01805 WP 000156662.1
consensus

170
170

logo

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consensus

GVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQHVLNAQHQQYQAFLLDGLTGSCKTEVYLHIMHEVLKQG
GVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQHVLNAQHQQYQAFLLDGLTGSCKTEVYLHIMHEVLKQG
GVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQ*V*NAQHQQYQAFLLDGLTGSCKTEVYLHIMHEVLKQG

255
255

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consensus

KQVLVLVPEIGLTPQTSRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIIIGTRSAIYTPLPRLGLIILDEEHDLSYKQQ
KQVLVLVPEIGLTPQTSRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIIIGTRSAIYTPLPRLGLIILDEEHDLSYKQQ
KQVLVLVPEIGLTPQTSRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIIIGTRSAIYTPLPRLGLIILDEEHDLSYKQQ

340
340

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EGFR_{YHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMHLIDLKIVKKQHGISQPLIEQIKNTL}

425
425

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ARKEQVLIFLNRRGYAPVLVCECGWQANCPHCDAHFTLHTQPYSYLCHHCGTVHRLPDHCPECQQKSLKTLGAGTAKVEEHLQ
ARKEQVLIFLNRRGYAPVLVCECGWQANCPHCDAHFTLHTQPYSYLCHHCGTVHRLPDHCPECQQKSLKTLGAGTAKVEEHLQ
ARKEQVLIFLNRRGYAPVLVCECGWQANCPHCDAHFTLHTQPYSYLCHHCGTVHRLPDHCPECQQKSLKTLGAGTAKVEEHLQ

510
510

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ELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFPHVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGR
ELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFPHVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGR
ELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFPHVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGR

595
595

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680
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consensus



742
742

- ☐ non conserved
- ☒ similar
- ☒ ≥ 50% conserved