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NTDB id 457	SSUD9	RS00080	WP 002936602.1	QEGMNTLFELEAQPWLVDDEQQVQLYCYFKVKFRNRITKDRIRKQESQKRKFDMPHEDIHESHATQSPGLINDELLMLR	111
NTDB id 461	GPW51	RS00080	WP 011921639.1	QEGMNTLFELEAQPWLVDDEQQVQLYCYFKVKFRNRITKDRIRKQESQKRKFDMPHEDIYELSHATQSPGLINDELLMLR	111
NTDB id 454	SSU	RS00080	WP 011921639.1	QEGMNTLFELEAQPWLVDDEQQVQLYCYFKVKFRNRITKDRIRKQESQKRKFDMPHEDIYELSHATQSPGLINDELLMLR	111
NTDB id 424	SGO	RS10430	WP 012130755.1	QEGMLVLYELIKSHPNLLEDQPRLYRYFKTKFRNRITHDLIIRKQESQKRKLDLDRQPYEEVSEIGHRIIRMKELYLDELVAFR	111
NTDB id 423	SGO	RS08370	WP 012130755.1	QEGMLVLYELIKSHPNLLEDQPRLYRYFKTKFRNRITHDLIIRKQESQKRKLDLDRQPYEEVSEIGHRIIRMKELYLDELVAFR	111
NTDB id 141	SP	RS10155	WP 000588925.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 140	SP	RS00070	WP 000588925.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 252	KZH43	RS09050	WP 000588897.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 251	KZH43	RS09050	WP 000588897.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 211	SPD	RS09675	WP 000588897.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 210	SPD	RS00065	WP 000588897.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 177	SPR	RS09210	WP 000588897.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 176	SPR	RS00065	WP 000588897.1	QEGMLCLHELISREEGLVDDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 489	SM12261	RS01070	WP 000471940.1	QEGMICLHELISREEEELVEDIPRLRKYFKTKFRNRILDHIRKQESQKRKYDKEPYEEVGEISHRISEGGLWLDEYYLFIH	110
NTDB id 517	SMSK321	RS10700	WP 000471945.1	QEGMICLHELISREEEELVEDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEAYEEVGEISHRISEGGLWLDDYYLFIH	110
NTDB id 516	SMSK321	RS09125	WP 000471944.1	QEGMICLHELISKEEELVEDIPRLRKYFKTKFRNRILDYIRKQESQKRKYDKEAYEEVGEISHRISEGGLWLDEYYLFIH	110
NTDB id 582	DLJ51	RS00505	WP 002962720.1	QEARIIILYQLIERFPDLANDEEKLRIFYFKTKFRSYVLDNIRKQESQKRAFDRMIYEEISELGHMIPSQQLDTADYCALK	159
NTDB id 554	STRINF	RS00370	WP 115283725.1	QEGRIVFFQLLEEHDPDLINNEGKCYSYFKTKFSNHVKDIIIRHQESFKRKFNRMPYEEISDISHCVQVFFFEVEDYVAIQ	112
NTDB id 44	SMU	RS09085	WP 002263585.1	QEGMILHLQILREHPELEEDDTKLYIYFKTRFSNYIKDVLIRKQESQKRKFNRMSYEEVGEIEHCLSSGMLQLDEYILFR	113
NTDB id 204344	BMF34	RS07745	WP 003101723.1	QEGRVVLHALLTEFPDLTENDKRLTYFKTKFSSYLKDVLRHQESYKRFNKMPLYEEI GEVSHK VASKGL VLDDYIAVQ	112
NTDB id 450	SPYM18	RS08475	WP 011018214.1	QEGHIIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEI GEVAHA I PSRGL VLDDYVAIQ	135
NTDB id 449	SPYM18	RS01395	WP 011018214.1	QEGHIIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEI GEVAHA I PSRGL VLDDYVAIQ	135
NTDB id 442	SPYM3	RS08515	WP 011106595.1	QEGHIIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEI GEVAHA I PSRGL VLDDYVAIQ	135
NTDB id 441	SPYM3	RS01385	WP 011106595.1	QEGHIIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEI GEVAHA I PSRGL VLDDYVAIQ	135
NTDB id 448	SpyM6JRS4	RS07800	WP 010921894.1	QEGHIIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEI GEVAHA I PSRGL VLDDYVAIQ	135
NTDB id 447	SpyM6JRS4	RS01370	WP 010921894.1	QEGHIIILLQLLERYPELIEEEERLYRYFKTKFSSYLKDLLRRQESQKRQFHKLAYEEI GEVAHA I PSRGL VLDDYVAIQ	135
consensus				!!*** * !* * !*** * * *!!!!** * ! *!*!!!!*!!*** *!***** *!***** * ! * ** **** *	

