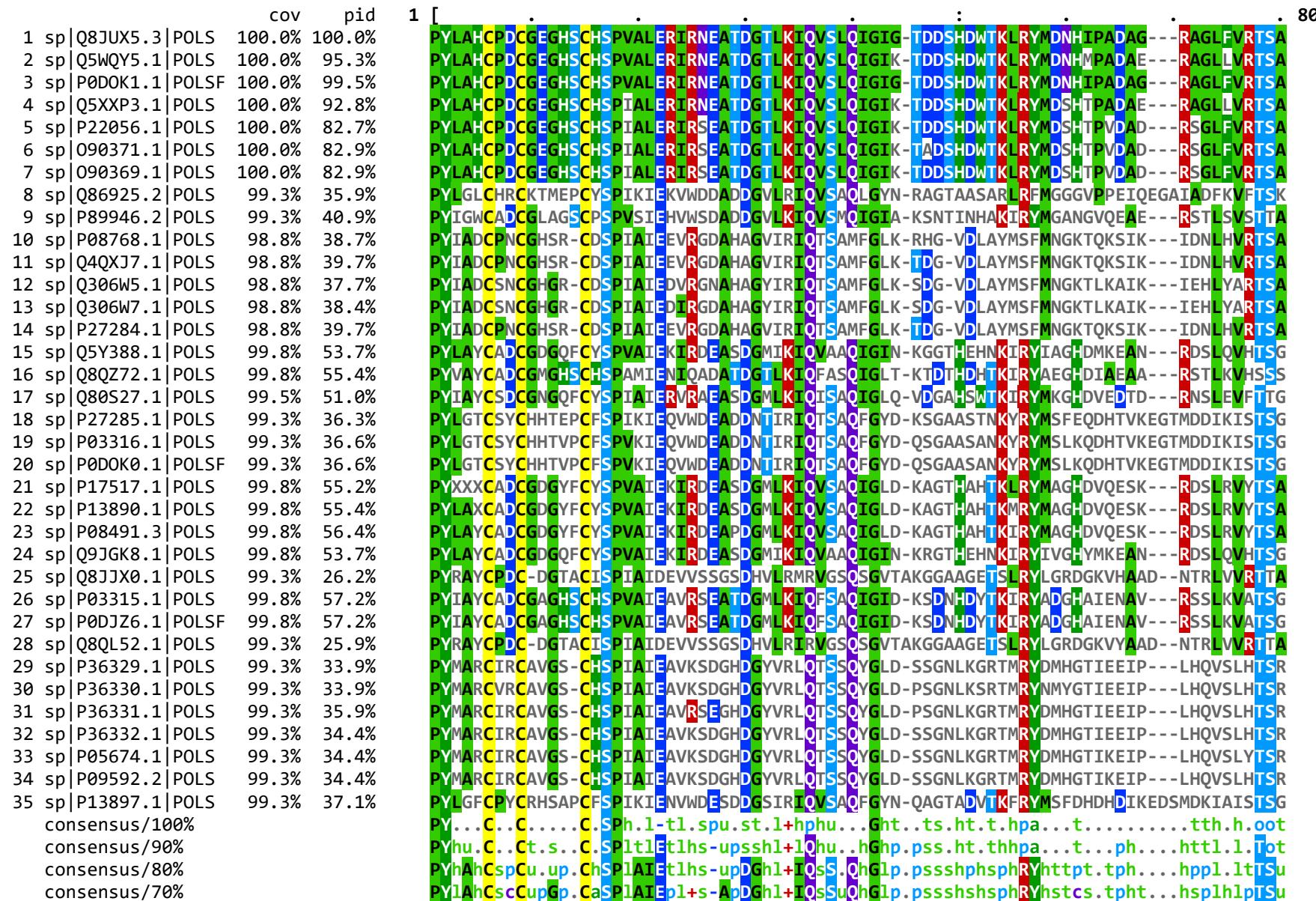
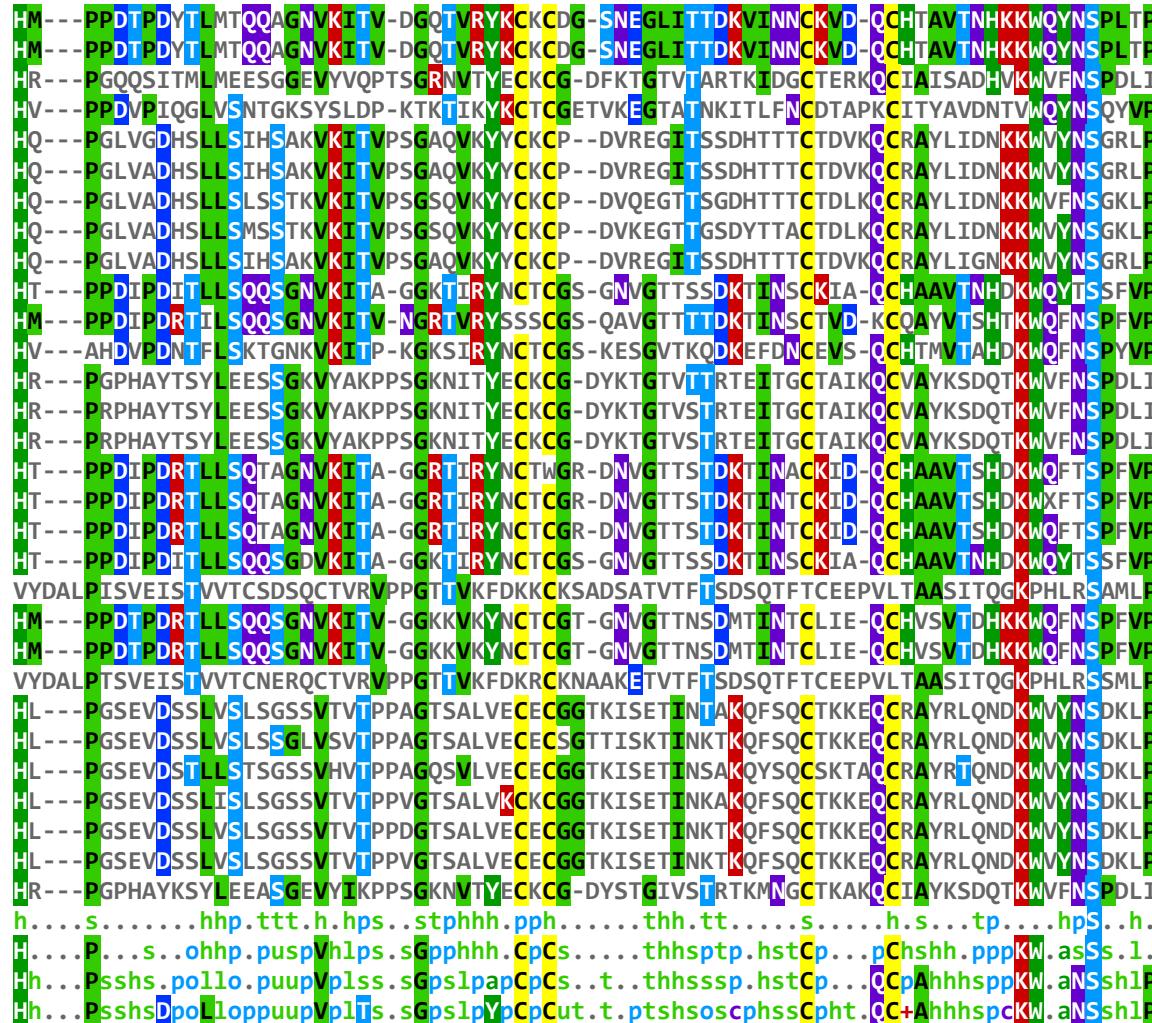


Reference sequence (1): sp|Q8JUX5.3|POLS  
 Identities normalised by aligned length.  
 Colored by: identity



		cov	pid	81	.	1	.	.	.	.	.	.	.	.	.	.	160	
1	sp Q8JUX5.3 POLS	100.0%	100.0%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
2	sp Q5WQY5.1 POLS	100.0%	95.3%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
3	sp P0DOK1.1 POLSF	100.0%	99.5%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
4	sp Q5XXP3.1 POLS	100.0%	92.8%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
5	sp P22056.1 POLS	100.0%	82.7%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
6	sp 090371.1 POLS	100.0%	82.9%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
7	sp 090369.1 POLS	100.0%	82.9%	PCTITGTMGHFILARCPKGETLTVGFTDSRKSHSCTHPFHHDPPVIGREKFHSRPQHGKELPCSTYVQSNAATAEEIEV	.	.	.	.	.	.	.	.	.	.	.	.		
8	sp Q86925.2 POLS	99.3%	35.9%	PCLHLHSHKGYFIVKCPGDSITSKL-VHGSQTCCTIPMRVGYKFVGREKYTLPPMHGTQIPCLTYERTREKSAGYVTM	.	.	.	.	.	.	.	.	.	.	.	.		
9	sp P89946.2 POLS	99.3%	40.9%	PCDTLATMGHFILARCRPGSQVEVSLSTDPKLLCRTPESIKPRFIGNEKSPAPTGHKTRIPCKTYSHQTDLTREEITM	.	.	.	.	.	.	.	.	.	.	.	.		
10	sp P08768.1 POLS	98.8%	38.7%	PCSLVSHHGGYYILAQCPCPGDITVTFH-DGPNRHTCRLAHKVEFRPVGREKRYRHPPEHGVELPCNRTHKRADQGHYVEM	.	.	.	.	.	.	.	.	.	.	.	.		
11	sp Q4QXJ7.1 POLS	98.8%	39.7%	PCSLVSHHGGYYILAQCPCPGDITVTFH-DGPNRHTCVAHKVEFRPVGREKRYRHPPEHGVELPCNRTHKRADQGHYVEM	.	.	.	.	.	.	.	.	.	.	.	.		
12	sp Q306W5.1 POLS	98.8%	37.7%	PCSLVSYHGGYYILAQCPCPGDITVTFH-DGANKHMCOTIAHKVEFRPVGREKRYRHPPEHGVELPCNRTHKRADQGHYVEM	.	.	.	.	.	.	.	.	.	.	.	.		
13	sp Q306W7.1 POLS	98.8%	38.4%	PCSLVSYHGGYYILAQCPCPGDITVTFH-DGAKTHMCOTIAHKVEFKPVGREKRYRHPPEHGVELPCNRTHKRADQGHYVEM	.	.	.	.	.	.	.	.	.	.	.	.		
14	sp P27284.1 POLS	98.8%	39.7%	PCSLVSHHGGYYILAQCPCPGDITVTFH-DGPNRHTCTVAHKVEFRPVGREKRYRHPPEHGVELPCNRTHKRADQGHYVEM	.	.	.	.	.	.	.	.	.	.	.	.		
15	sp Q5Y388.1 POLS	99.8%	53.7%	VCAIRGTMGHFIVAYCPCGDELKVQFDAESHTQACKVQYKHAAPAVGREKFTVRPHFGIEVPCTTYQLTTAPTEEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	
16	sp Q8QZ72.1 POLS	99.8%	55.4%	ECTVTGTMGHFILAKCPPGERISVSFVDSKNEHRTCRIAYHEQRLLIGRERFTVRPHHGIELPCTTYQLTTAETSEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	
17	sp Q80S27.1 POLS	99.5%	51.0%	ECTVHGTMGHFIVATCPEDGSLTVAFVDKHKVHACRIAYKHRVPVLGREGFTVRPHHGEVPCTTYAMRTSVTTEEEEM	.	.	.	.	.	.	.	.	.	.	.	.	.	
18	sp P27285.1 POLS	99.3%	36.3%	PCRRLSYKGYFLLAKCPPGDSVTVSIA-SSNSATSCMARKIKPKFVGREKYDLPPVHGKKIPCTVYDRLKETTAGYITM	.	.	.	.	.	.	.	.	.	.	.	.	.	
19	sp P03316.1 POLS	99.3%	36.6%	PCRRLSYKGYFLLAKCPPGDSVTVSIV-SSNSATSTLARKIKPKFVGREKYDLPPVHGKKIPCTVYDRLKETTAGYITM	.	.	.	.	.	.	.	.	.	.	.	.	.	
20	sp P0DOK0.1 POLSF	99.3%	36.6%	PCRRLSYKGYFLLAKCPPGDSVTVSIV-SSNSATSTLARKIKPKFVGREKYDLPPVHGKKIPCTVYDRLKETTAGYITM	.	.	.	.	.	.	.	.	.	.	.	.	.	
21	sp P17517.1 POLS	99.8%	55.2%	ACSIHGTMGHFIVAHCPGDPYLKVSEFADSHVKACKVQYKHNPLPVGREKFTVRPHFGIEVPCTSYQLTTAPTEEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	
22	sp P13890.1 POLS	99.8%	55.4%	ACSIHGTMGHFIVAHCPGDPYLKXSFEADSHVKACKVQYKHDPLPVGREKFTVRPHFGIEVPCTSYQLTTAPTEEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	
23	sp P08491.3 POLS	99.8%	56.4%	ACSIHGTMGHFIVAHCPGDPYLKVSFEADSHVKACKVQYKHDPLPVGREKFTVRPHFGIEVPCTSYQLTTAPTEEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	
24	sp Q9JGK8.1 POLS	99.8%	53.7%	VCAIRGTMGHFIVAYCPCGDELKVQFDAESHTQACKVQYKHDPLPVGREKFTVRPHFGIEVPCTSYQLTTAPTEEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	
25	sp Q8JJX0.1 POLS	99.3%	26.2%	KCDVLQATGHYILANCPVGQLSTVAATLDGTRHQCTTVFHVTEKTRERSKGHHLSDMTKKCTRFSTTPKKSALYLV	.	.	.	.	.	.	.	.	.	.	.	.	.	.
26	sp P03315.1 POLS	99.8%	57.2%	DCFVHGTMGHFILAKCPPGEFLQVSIQDTRNAVRACRIQYHHDQPVGREKFTIRPHYGKEIPCTTYQQTAAETVEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
27	sp P0DJZ6.1 POLSF	99.8%	57.2%	DCFVHGTMGHFILAKCPPGEFLQVSIQDTRNAVRACRIQYHHDQPVGREKFTIRPHYGKEIPCTTYQQTAAETVEEIDM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
28	sp Q8QL52.1 POLS	99.3%	25.9%	KCDVLQATGHYILANCPVGQLSTVAATLDGTRHQCTTVFHVTEKTRERSKGHHLSDLTKKCTRFSTTPKKSALYLV	.	.	.	.	.	.	.	.	.	.	.	.	.	.
29	sp P36329.1 POLS	99.3%	33.9%	PCHIVDGHGFFLLARCPAGDSITMEFK-KDAVTHSCSVPYEVKFNPVGRELYTHPPEHGAEQACQVYAHDAQNRRGAYVEM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
30	sp P36330.1 POLS	99.3%	33.9%	PCHIVDGHGFFLLARCPAGDSITMEFK-KDSVTHSCSVPYEVKFNPVGRELYTHPPEHGAEQACQVYAHDAQNRRGAYVEM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
31	sp P36331.1 POLS	99.3%	35.9%	PCHIVDGHGFFLLARCPAGDSITMEFK-KESVTHSCSVPYEVKFNPVGRELYTHPPEHGAEQACQVYAHDAQNRRGAYVEM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
32	sp P36332.1 POLS	99.3%	34.4%	PCHIVDGHGFFLLARCPAGDSITMEFK-KGSVTHSCSVPYEVKFNPVGRELYTHPPEHGAEQACQVYAHDAQNRRGAYVEM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
33	sp P05674.1 POLS	99.3%	34.4%	PCHIVDGHGFFLLARCPAGDSITMEFK-KDSVRHSCSVPYEVKFNPVGRELYTHPPEHGVQEACQVYAHDAQNRRGAYVEM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
34	sp P09592.2 POLS	99.3%	34.4%	PCHIVDGHGFFLLARCPAGDSITMEFK-KDSVTHSCSVPYEVKFNPVGRELYTHPPEHGVQEACQVYAHDAQNRRGAYVEM	.	.	.	.	.	.	.	.	.	.	.	.	.	.
35	sp P13897.1 POLS	99.3%	37.1%	PCRRLGHKGYFLLAQCPGDSVTVSIT-SGASENSCTVEKKIRRKFVGREREYLFPVHGKLVKCHVYDHLKETSAGYITM .C.hhhhGaalls.C..Gp.1p.th.....s.h.p....hspe.....th...C.a....t.p....1.. .CthhhshGaallApCP.G.-1phth..ttt..psCph.hcht..1GREha...P.aGhp.sCphY...tt.pst.1ph scplhsthGaflLaCP.G-p1pstht.stt.tpsCph.a+hc...1GRE+aph.PtaGhchsCpsYtppttspst.1ph scplhushGaflLaCPsG-olTvuFp.sps.p+sCplsa+hc...1GRE+aph.PpHghe1PCssYsppstspst.1-M	.	.	.	.	.	.	.	.	.	.	.	.	.	.
	consensus/100%																	
	consensus/90%																	
	consensus/80%																	
	consensus/70%																	

6	sp 090371.1 POLS	100.0%	82.9%
7	sp 090369.1 POLS	100.0%	82.9%
8	sp Q86925.2 POLS	99.3%	35.9%
9	sp P89946.2 POLS	99.3%	40.9%
10	sp P08768.1 POLS	98.8%	38.7%
11	sp Q4QXJ7.1 POLS	98.8%	39.7%
12	sp Q306W5.1 POLS	98.8%	37.7%
13	sp Q306W7.1 POLS	98.8%	38.4%
14	sp P27284.1 POLS	98.8%	39.7%
15	sp Q5Y388.1 POLS	99.8%	53.7%
16	sp Q8QZ72.1 POLS	99.8%	55.4%
17	sp Q80S27.1 POLS	99.5%	51.0%
18	sp P27285.1 POLS	99.3%	36.3%
19	sp P03316.1 POLS	99.3%	36.6%
20	sp P0DOK0.1 POLSF	99.3%	36.6%
21	sp P17517.1 POLS	99.8%	55.2%
22	sp P13890.1 POLS	99.8%	55.4%
23	sp P08491.3 POLS	99.8%	56.4%
24	sp Q9JGK8.1 POLS	99.8%	53.7%
25	sp Q8JJX0.1 POLS	99.3%	26.2%
26	sp P03315.1 POLS	99.8%	57.2%
27	sp P0DJZ6.1 POLSF	99.8%	57.2%
28	sp Q8QL52.1 POLS	99.3%	25.9%
29	sp P36329.1 POLS	99.3%	33.9%
30	sp P36330.1 POLS	99.3%	33.9%
31	sp P36331.1 POLS	99.3%	35.9%
32	sp P36332.1 POLS	99.3%	34.4%
33	sp P05674.1 POLS	99.3%	34.4%
34	sp P09592.2 POLS	99.3%	34.4%
35	sp P13897.1 POLS	99.3%	37.1%
	consensus/100%		
	consensus/90%		
	consensus/80%		
	consensus/70%		



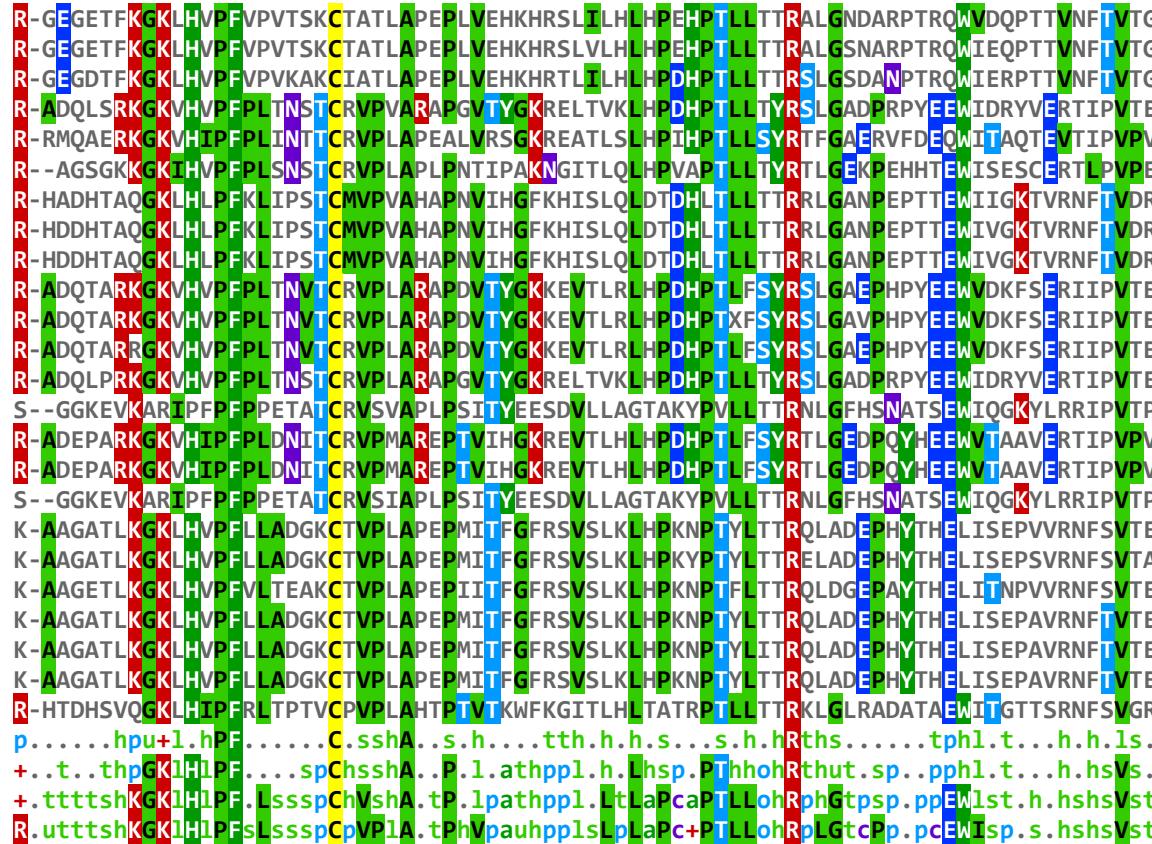
		cov	pid	241
1	sp Q8JUX5.3 POLS	100.0%	100.0%	
2	sp Q5WQY5.1 POLS	100.0%	95.3%	
3	sp P0DOK1.1 POLSF	100.0%	99.5%	
4	sp Q5XXP3.1 POLS	100.0%	92.8%	
5	sp P22056.1 POLS	100.0%	82.7%	
6	sp 090371.1 POLS	100.0%	82.9%	
7	sp 090369.1 POLS	100.0%	82.9%	
8	sp Q86925.2 POLS	99.3%	35.9%	
9	sp P89946.2 POLS	99.3%	40.9%	
10	sp P08768.1 POLS	98.8%	38.7%	
11	sp Q4QXJ7.1 POLS	98.8%	39.7%	

Sequence alignment showing 35 homologous protein sequences. The sequences are color-coded by residue type: green for hydrophobic, blue for polar, red for acidic, purple for basic, yellow for aromatic, and cyan for polar with partial charge.

Top section (positions 1-241):

Bottom section (positions 241-320):

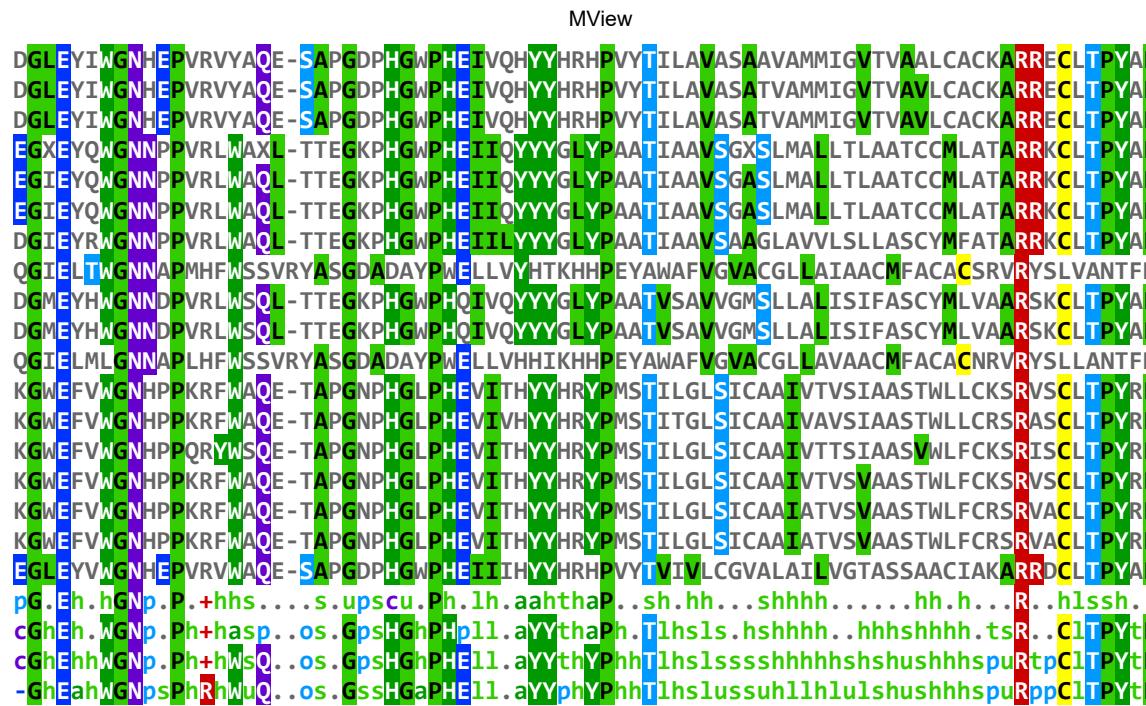
12	sp Q306W5.1 POLS	98.8%	37.7%
13	sp Q306W7.1 POLS	98.8%	38.4%
14	sp P27284.1 POLS	98.8%	39.7%
15	sp Q5Y388.1 POLS	99.8%	53.7%
16	sp Q8QZ72.1 POLS	99.8%	55.4%
17	sp Q80S27.1 POLS	99.5%	51.0%
18	sp P27285.1 POLS	99.3%	36.3%
19	sp P03316.1 POLS	99.3%	36.6%
20	sp P0DOK0.1 POLSF	99.3%	36.6%
21	sp P17517.1 POLS	99.8%	55.2%
22	sp P13890.1 POLS	99.8%	55.4%
23	sp P08491.3 POLS	99.8%	56.4%
24	sp Q9JGK8.1 POLS	99.8%	53.7%
25	sp Q8JJX0.1 POLS	99.3%	26.2%
26	sp P03315.1 POLS	99.8%	57.2%
27	sp P0DJZ6.1 POLSF	99.8%	57.2%
28	sp Q8QL52.1 POLS	99.3%	25.9%
29	sp P36329.1 POLS	99.3%	33.9%
30	sp P36330.1 POLS	99.3%	33.9%
31	sp P36331.1 POLS	99.3%	35.9%
32	sp P36332.1 POLS	99.3%	34.4%
33	sp P05674.1 POLS	99.3%	34.4%
34	sp P09592.2 POLS	99.3%	34.4%
35	sp P13897.1 POLS	99.3%	37.1%
consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			



		cov	pid	321
1	sp Q8JUX5.3 POLS	100.0%	100.0%	
2	sp Q5WQY5.1 POLS	100.0%	95.3%	
3	sp P0DOK1.1 POLSF	100.0%	99.5%	
4	sp Q5XXP3.1 POLS	100.0%	92.8%	
5	sp P22056.1 POLS	100.0%	82.7%	
6	sp 090371.1 POLS	100.0%	82.9%	
7	sp 090369.1 POLS	100.0%	82.9%	
8	sp Q86925.2 POLS	99.3%	35.9%	
9	sp P89946.2 POLS	99.3%	40.9%	
10	sp P08768.1 POLS	98.8%	38.7%	
11	sp Q4QXJ7.1 POLS	98.8%	39.7%	
12	sp Q306W5.1 POLS	98.8%	37.7%	
13	sp Q306W7.1 POLS	98.8%	38.4%	
14	sp P27284.1 POLS	98.8%	39.7%	
15	sp Q5Y388.1 POLS	99.8%	53.7%	
16	sp Q8QZ72.1 POLS	99.8%	55.4%	
17	sp Q80S27.1 POLS	99.5%	51.0%	



18	sp P27285.1 POLS	99.3%	36.3%
19	sp P03316.1 POLS	99.3%	36.6%
20	sp P0DOK0.1 POLSF	99.3%	36.6%
21	sp P17517.1 POLS	99.8%	55.2%
22	sp P13890.1 POLS	99.8%	55.4%
23	sp P08491.3 POLS	99.8%	56.4%
24	sp Q9JGK8.1 POLS	99.8%	53.7%
25	sp Q8JJX0.1 POLS	99.3%	26.2%
26	sp P03315.1 POLS	99.8%	57.2%
27	sp P0DJZ6.1 POLSF	99.8%	57.2%
28	sp Q8QL52.1 POLS	99.3%	25.9%
29	sp P36329.1 POLS	99.3%	33.9%
30	sp P36330.1 POLS	99.3%	33.9%
31	sp P36331.1 POLS	99.3%	35.9%
32	sp P36332.1 POLS	99.3%	34.4%
33	sp P05674.1 POLS	99.3%	34.4%
34	sp P09592.2 POLS	99.3%	34.4%
35	sp P13897.1 POLS	99.3%	37.1%
consensus/100%			
consensus/90%			
consensus/80%			
consensus/70%			



Index	Sequence Name	Cov (%)	pid
1	Q8JUX5.3 POLS	100.0%	100.0%
2	Q5WQY5.1 POLS	100.0%	95.3%
3	P0DOK1.1 POLSF	100.0%	99.5%
4	Q5XXP3.1 POLS	100.0%	92.8%
5	P22056.1 POLS	100.0%	82.7%
6	O90371.1 POLS	100.0%	82.9%
7	O90369.1 POLS	100.0%	82.9%
8	Q86925.2 POLS	99.3%	35.9%
9	P89946.2 POLS	99.3%	40.9%
10	P08768.1 POLS	98.8%	38.7%
11	Q4QXJ7.1 POLS	98.8%	39.7%
12	Q306W5.1 POLS	98.8%	37.7%
13	Q306W7.1 POLS	98.8%	38.4%
14	P27284.1 POLS	98.8%	39.7%
15	Q5Y388.1 POLS	99.8%	53.7%
16	Q8QZ72.1 POLS	99.8%	55.4%
17	Q80S27.1 POLS	99.5%	51.0%
18	P27285.1 POLS	99.3%	36.3%
19	P03316.1 POLS	99.3%	36.6%
20	P0DOK0.1 POLSF	99.3%	36.6%
21	P17517.1 POLS	99.8%	55.2%
22	P13890.1 POLS	99.8%	55.4%
23	P08491.3 POLS	99.8%	56.4%



24	sp Q9JGK8.1 POLS	99.8%	53.7%	TPGA <b>VVPVTLGVLCC</b>
25	sp Q8JJX0.1 POLS	99.3%	26.2%	SNPPPLTALTAAAL <b>CC</b>
26	sp P03315.1 POLS	99.8%	57.2%	TPGA <b>AVPWTLGILCC</b>
27	sp P0DJZ6.1 POLSF	99.8%	57.2%	TPGA <b>AVPWTLGILCC</b>
28	sp Q8QL52.1 POLS	99.3%	25.9%	PNPPPLTALTAAAL <b>CC</b>
29	sp P36329.1 POLS	99.3%	33.9%	TPNARMPLCLAVL <b>CC</b>
30	sp P36330.1 POLS	99.3%	33.9%	TPNAKMPPLCLAVL <b>CC</b>
31	sp P36331.1 POLS	99.3%	35.9%	TPNARMPLCLAVL <b>CC</b>
32	sp P36332.1 POLS	99.3%	34.4%	TPNARMPLCLAVL <b>CC</b>
33	sp P05674.1 POLS	99.3%	34.4%	TPNARIPFCLAVL <b>CC</b>
34	sp P09592.2 POLS	99.3%	34.4%	TPNARIPFCLAVL <b>CC</b>
35	sp P13897.1 POLS	99.3%	37.1%	APNAT <b>VPTALAVLCC</b>
	consensus/100%			ssss.hsh.hsh..C
	consensus/90%			sPsA.hPhh <u>lull</u> <b>CC</b>
	consensus/80%			sPsA.1Phh <u>lull</u> <b>CC</b>
	consensus/70%			sPsAh <u>lPhhLull</u> <b>CC</b>

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