

[illegible]

NTDB	id	1184	GTF74	RS02335	WP	000649326.1	..AAGFTT...RLGTVEDMGDCKI	VIAPTASGALGGTIKYTFDAGVVSSSKIQLARDANGLWTCSTTT.VTSEIAPKG.CTA	148					
NTDB	id	1167	A1552VC	RS11065	WP	000649326.1	..AAGFTT...RLGTVEDMGDCKI	VIAPTASGALGGTIKYTFDAGVVSSSKIQLARDANGLWTCSTTT.VTSEIAPKG.CTA	148					
NTDB	id	1160	ABDM36	RS02330	WP	000649326.1	..AAGFTT...RLGTVEDMGDCKI	VIAPTASGALGGTIKYTFDAGVVSSSKIQLARDANGLWTCSTTT.VTSEIAPKG.CTA	148					
NTDB	id	1383	A4U84	RS08530	WP	005711781.1	GVRADKSDVPDAKYLKSISV	SGVITVAGKGNIDG.YGYTMTPK.FA.....NNNITWATSCQGDADISLFPAFNCQG	150					
NTDB	id	180733	A4205	RS02755	WP	005741096.1	GIRADAA..ASKKYLKAITVKA	GVITVTGQGSLEG..ISYTLTASGNA.....AQGVSWTVNCG.AQSDIFPAGFCA.	144					
NTDB	id	1365	NTHI	RS01955	WP	011271973.1	GIAADIIT..TAKGYVKSVTTSNG	IATVKGNDGTLAN.MEYILQATGNA.....ATGVTWTTTCKGTDASLFPANFCGS	146					
NTDB	id	1354	HI	O299	AAC21963.1	GIAADIK..TAKGYVASVITQS	GGITVKGNDGTLAN.MEYILQAKGNA.....AAGVTWTTTCKGTDASLFPANFCGS	146						
consensus							***!***	* * * * *	! * * * *	* * * ! * * *	* * * * *	*****!	****!	*****!

NTDB id 1184	GTF74	RS02335	WP 000649326.1	GATIN	153
NTDB id 1167	A1552VC	RS11065	WP 000649326.1	GATIN	153
NTDB id 1160	ABDM36	RS02330	WP 000649326.1	GATIN	153
NTDB id 1383	A4U84	RS08530	WP 005711781.1	KATP.	154
NTDB id 180733	A4205	RS02755	WP 005741096.1		144
NTDB id 1365	NTHI	RS01955	WP 011271973.1	VTQ..	149
NTDB id 1354	HI 0299	AAC21963.1		VTK..	149
consensus				**	

Sequence	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
2	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
3	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
4	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
5	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
6	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
7	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D	Y	I	A	T	E	G	S	F	P	A	T	I	..	A	G	T	..																						
8	M	K	K	A	Y	K	N	K	Q	Q	K	G	F	T	L	I	E	L	M	I	V	V	A	V	I	G	V	L	A	A	I	A	I	P	Q	Y	Q	N	Y	V	K	K	S	A	I	G	V	G	L	A	N	I	T	A	L	K	T	N	I	E	D																																							



 GATIN 153

 GATIN 153

 GATIN 153

 KATP. 154

 144

 VTQ.. 149

 VTK.. 149

 **

[X] non conserved

 [X] similar

 [X] > 50% conserved