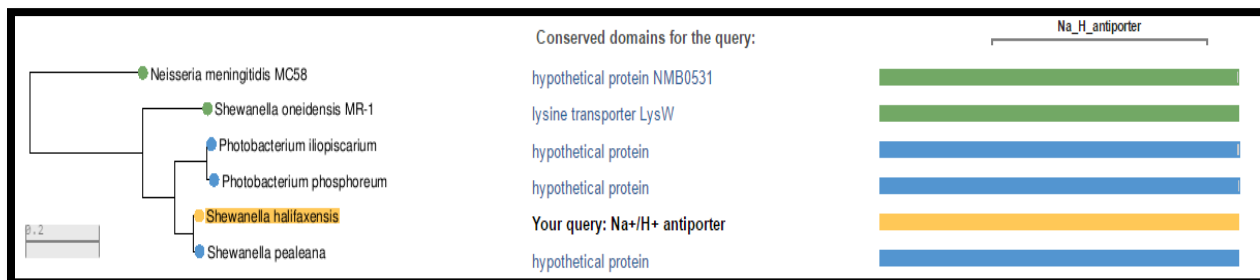


SMART BLAST

Query: *Shewanella halifaxensis* HAW-EB4 (*nhaC*-4071980-4073564)



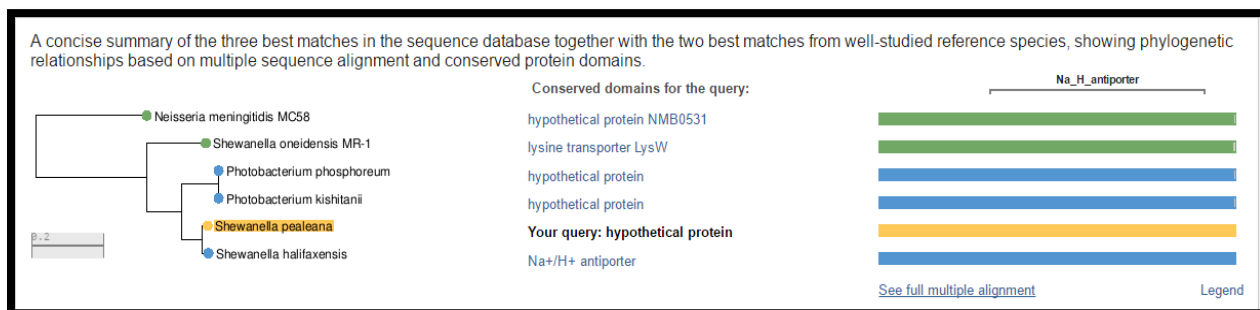
Best hits

Select: [All](#) [None](#) Selected: 0

Alignments [GenPept](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
	hypothetical protein [Shewanella pealeana]	1025	1025	100%	0.0	97%	WP_012156474.1
	hypothetical protein [Photobacterium illopiscarium]	892	892	99%	0.0	85%	WP_045037034.1
	hypothetical protein [Photobacterium phosphoreum]	891	891	99%	0.0	84%	WP_036794242.1
	lysine transporter LysW [Shewanella oneidensis MR-1]	744	744	100%	0.0	72%	NP_716635.1
	hypothetical protein NMB0531 [Neisseria meningitidis MC58]	466	466	98%	1e-157	48%	NP_273576.1

Query: *Shewanella pealeana* ATCC 700345 (*nhaC*-3996612-3998196)



Best hits

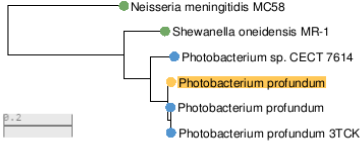
Select: [All](#) [None](#) Selected: 0

Alignments [GenPept](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
	Na⁺/H⁺ antiporter [Shewanella halifaxensis]	1025	1025	100%	0.0	97%	WP_012278401.1
	hypothetical protein [Photobacterium phosphoreum]	895	895	99%	0.0	85%	WP_036794242.1
	hypothetical protein [Photobacterium kishitani]	895	895	99%	0.0	85%	WP_045041850.1
	lysine transporter LysW [Shewanella oneidensis MR-1]	748	748	99%	0.0	72%	NP_716635.1
	hypothetical protein NMB0531 [Neisseria meningitidis MC58]	462	462	98%	6e-156	48%	NP_273576.1

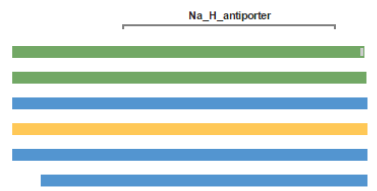
Query: *Photobacterium profundum* SS9 (*nhaC*-3172989-3174573)

A concise summary of the three best matches in the sequence database together with the two best matches from well-studied reference species, showing phylogenetic relationships based on multiple sequence alignment and conserved protein domains.



Conserved domains for the query:

- hypothetical protein NMB0531
- lysine transporter LysW
- hypothetical protein
- Your query: Na⁺/H⁺ antiporter**
- hypothetical protein
- putative Na⁺/H⁺ antiporter



[See full multiple alignment](#) Legend

Best hits

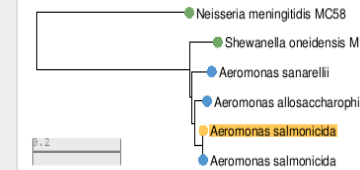
Select: [All](#) [None](#) Selected: 0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
	hypothetical protein [Photobacterium profundum]	1047	1047	100%	0.0	98%	WP_036804011.1
	putative Na⁺/H⁺ antiporter [Photobacterium profundum 3TCK]	966	966	92%	0.0	98%	EAS42662.1
	hypothetical protein [Photobacterium aphoticum]	922	922	100%	0.0	87%	WP_047873042.1
	lysine transporter LysW [Shewanella oneidensis MR-1]	815	815	99%	0.0	77%	NP_716635.1
	hypothetical protein NMB0531 [Neisseria meningitidis MC58]	454	454	98%	6e-153	47%	NP_273576.1

Query: *Aeromonas salmonicida* subsp. *salmonicida* A449

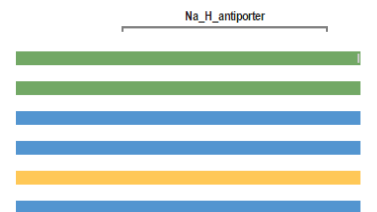
Summary [Please let us know what you think](#)

A concise summary of the three best matches in the sequence database together with the two best matches from well-studied reference species, showing phylogenetic relationships based on multiple sequence alignment and conserved protein domains.



Conserved domains for the query:

- hypothetical protein NMB0531
- lysine transporter LysW
- hypothetical protein
- hypothetical protein
- Your query: hypothetical protein**
- Na⁺/H⁺ antiporter



[See full multiple alignment](#) Legend

Best hits

Select: [All](#) [None](#) Selected: 0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
	Na⁺/H⁺ antiporter [Aeromonas salmonicida]	1053	1053	100%	0.0	99%	WP_058394088.1
	hypothetical protein [Aeromonas allosaccharophila]	1015	1015	100%	0.0	95%	WP_042057294.1
	hypothetical protein [Aeromonas sanarellii]	991	991	100%	0.0	93%	WP_042076508.1
	lysine transporter LysW [Shewanella oneidensis MR-1]	939	939	100%	0.0	90%	NP_716635.1
	hypothetical protein NMB0531 [Neisseria meningitidis MC58]	468	468	98%	1e-158	50%	NP_273576.1

Query: *Aeromonas veronii* B565

A concise summary of the three best matches in the sequence database together with the two best matches from well-studied reference species, showing phylogenetic relationships based on multiple sequence alignment and conserved protein domains.

Conserved domains for the query:

- hypothetical protein NMB0531
- lysine transporter LysW
- Na+/H+ antiporter
- Your query: Na+/H+ antiporter**
- Na+/H+ antiporter
- Na+/H+ antiporter

[See full multiple alignment](#) Legend

Best hits

Select: [All](#) [None](#) Selected: 0

Alignments [GenPept](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
	Na+/H+ antiporter [Aeromonas veronii]	1049	1049	100%	0.0	99%	WP_005359896.1
	Na+/H+ antiporter [Aeromonas sp. 159]	1048	1048	100%	0.0	99%	WP_019444693.1
	Na+/H+ antiporter [Aeromonas allosaccharophila]	1045	1045	100%	0.0	99%	WP_058051766.1
	lysine transporter LysW [Shewanella oneidensis MR-1]	946	946	100%	0.0	91%	NP_716635.1
	hypothetical protein NMB0531 [Neisseria meningitidis MC58]	450	450	98%	2e-151	48%	NP_273576.1

Query: *Oceanimonas sp. GK1*

A concise summary of the three best matches in the sequence database together with the two best matches from well-studied reference species, showing phylogenetic relationships based on multiple sequence alignment and conserved protein domains.

Conserved domains for the query:

- hypothetical protein NMB0531
- Na+/H+ antiporter NhaC
- lysine transporter LysW
- Na+/H+ antiporter
- Your query: Na+/H+ antiporter**
- hypothetical protein

[See full multiple alignment](#) Legend

Best hits

Select: [All](#) [None](#) Selected: 0

Alignments [GenPept](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
	hypothetical protein [Oceanimonas sp. GK1]	985	985	100%	0.0	99%	WP_041543184.1
	Na+/H+ antiporter [Oceanimonas smirnovii]	875	875	100%	0.0	88%	WP_019934824.1
	Na+/H+ antiporter NhaC [Shewanella frigidimarina NCIMB 400]	543	543	99%	0.0	56%	ABI72586.1
	lysine transporter LysW [Shewanella oneidensis MR-1]	542	542	98%	0.0	58%	NP_716635.1
	hypothetical protein NMB0531 [Neisseria meningitidis MC58]	452	452	99%	1e-152	48%	NP_273576.1

■ Query sequence ■ Best matches ■ Reference species

■ Not aligned to query □ Gap