

TatC	b3839	-	0185, 0186	-	2586, 2585	-	-	-	1512, 1344	-	0254	2154,1	1059	-	-	-	0591	-	0774	-
	P69423	-	D4GZC9, D4GZD0	-	Q8PTX2, Q8PTX3	-	-	-	O28760, O28925	-	Q4JC08	Q9Y9Y5	G4RJF8	-	-	-	B1L4G5	-	A9A5F9	-
TatA	b3837, b0627	-	1027, 1162	-	2584, 2583	-	1201	-	2056	-	0256	2154a, 2139a	2052	-	-	-	1126	-	0773, 1318	-
	P69428, P0A843	-	D4GVK4, D4GWC8	-	Q8PTX4, Q8PTX5	-	Q8TW36	-	O28223	-	Q4JC06	Q05DY3, Q05DY4	G4RM70	-	-	-	B1L5Z3	-	A9A5F8, A9A2H5	-
TatB	b3838	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	P69425	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SPI	b2568	YIR022W	0002, 2603	0387	1344	2037, 1703	1031	1448	1791, 1655, 1657, 2078	0260	1795, 1380	1796.1	1710	04470	432	-	1465	0740	0208	-
	P00803	P15367	D4GYJ8, D4GUC5	Q6M084	Q8PX78	Q5JDG1, Q5JJ10	Q8TWK2	O27497	O28483, O28616, O28618, O28201	Q57708	Q4J7Y0, Q4J917	Q9YAZ9	G4RL86	A0A1L9GU74	Q74MX5	-	B1L6Y2	D6GW64	A9A2X6	-
sortase	EP54_00580 ⁴	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	Q9S446	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Xrt; archaeosortase ⁵ (ArtA, ArtC, ArtE)	NE1797 ⁶	-	0915(A)	1125(E)	1401(A), 2114(C)	-	-	-	2046(A)	O28233(E)	-	-	-	-	-	-	-	-	-	-
	Q82TS7	-	D4GUZ4	Q6LY66	Q8PX21, Q8PV60	-	-	-	O28233	Q60336	-	-	-	-	-	-	-	-	-	-
Lgt	b2828	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	P60955	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Lnt	b0657	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	P23930	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SPII ⁷	b0027	-	n.i.	n.i.	n.i.	n.i.	-	n.i.	n.i.	n.i.	-	-	n.i.	-	-	n.i.	-	-	-	n.i.
	P00804	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
AglB/PglB/STT3	CJE1267 ⁸	YGL022W	1530	1424	0646, 0647, 2210	0810, 1718	-	1623, 1898, 1906, 420	0380, 0329, 0040	1525	1274	-	0519	04060	155	02810	1056	0254	0075	28460
	Q5HTX8	P39005	D4GYH4	Q6LXC8	Q8PZ48, Q8PZ47, Q8PUW8	Q5JH70, Q5JJ26	-	O27660, O27920, O27928, O26520	O29867, O29918, O30195	Q58920	Q4J9B4	-	G4RNP0	A0A1L9GU13	Q74MN3	H0ADH6	B1L5S3	D6GUV6	A9A114	A0A0F8Y4P4
PiID/PiB/D/EppA	b0108	-	2993	0555, 0232	1678	0053	0703	421	0936	0902, 1282.1, 0835.2	-	-	-	-	-	00391	-	0088	-	-
	P36647	-	D4GY85	Q6LZR9, Q6M0N8	Q8PWB1	Q5JED9	Q8TXH1	O26521	O29326	Q58312, P81318, P81324	-	-	-	-	-	H0AD06	-	D6GUF4	-	-
AriH (FlaH)	-	-	1216	1674	0318, 0414	0047	-	-	1050	0899	1174	1898	-	-	-	-	-	-	-	-
	-	-	D4GWY9	Q6LWN5	Q8Q020, Q8PZS8	Q5JEE5	-	-	O29212	Q58309	Q4J9K9	Q9YAP5	-	-	-	-	-	-	-	-
AriI ⁹ (FlaI)	-	-	1217	1675	0317, 0413	0048	-	-	1049	0900	1173	1896.1	-	-	-	-	-	-	-	-
	-	-	D4GWZ0	Q6LWN4	Q8Q021, Q8PZS9	Q5JEE4	-	-	O29213	Q58310	Q4J9L0	Q9YAP7	-	-	-	-	-	-	-	-
AriJ ¹⁰ (FlaJ)	-	-	1218	1676	0316, 0412	0049	-	-	1048	0901	1172	1895.1	-	-	-	-	-	-	-	-
	-	-	D4GWZ2	Q6LWN3	Q8Q022, Q8PZT0	Q5JEE3	-	-	O29214	Q58311	Q4J9L1	Q9YAP8	-	-	-	-	-	-	-	-
PiIB ⁹	b0107, b3326	-	0620, 0748, 1034, 1160, 2385	0040	0938, 1516, 2298	1853	0707	1702	0659, 0996	0781, 1287, 1288	1494, 2317	2208.1	0895, 1134	02725	169, 425	01701, 03986	-	0031, 0601, 1030	-	-
	P36645, P45759	-	D4GSL6, D4GTC5,	Q6M177	Q8PYC5, Q8PWR0,	Q5JEN0	Q8TXG7	O27737	O29598, O29266	Q58191, Q58683,	Q4J8S4, Q4J6H9	Q9Y9T0	G4RPQ4, G4RJM9	A0A1L9GVK6	Q74NB8, Q74MY0	H0AA38, H0A9H4	-	D6GUA6, D6GVT4,	-	-

		D4GVL0, D4GWC7, D4GWN3	Q8PUN4						Q58684									D6GX06		
PiIC ⁹	b0106, b3327	-	0619, 0749, 1033, 1159, 2386	0038, 0039	0937, 1515, 2297	1851, 1852	0705, 0706	1703	0658, 0995	0779, 0780, 1286	1495, 2318	2207.1, 2206.1	0894, 1133, 1135	02735, 02740	267, 268, 285	01696, 03976, 03981	-	0032, 0033, 0600, 1029	-	-
	P36646, P41441	-	D4GSL5, D4GTC7, D4GVK9, D4GWC6, D4GWN4	Q6M179, Q6M178	Q8PYC6, Q8PWR1, Q8PUN5	Q5JEN2, Q5JEN1	Q8TXG9, Q8TXG8	O27738	O29599, O29267	Q58189, Q58190, Q58682	Q4J8S3, Q4J6H8	Q9Y9T1, Q9Y9T2	G4RPQ3, G4RJM8, G4RJN0	A0A1L9GVF7, A0A1L9GVK2	Q74NG7, Q74NG6, Q74MT4	H0AA37, H0A9H2, H0A9H3	-	D6GUA7, D6GUA8, D6GVT3, D6GX05	-	-
SLG ¹¹	-	-	2072	0383	1976	0895	-	716	-	0822	2355 (SlaA) 2354 (SlaB)	0609.1	1887	-	300	-	-	-	-	-
	-	-	P25062 ¹²	Q6M088 ¹³	Q8Pv17 ¹²	Q5Ji58 ¹⁴	-	O26812 ¹⁵	-	Q58232 ¹²	Q4J6E5 ¹² Q4J6E6 ¹²	Q9YEG7 ¹⁴	G4RLQ9 ¹⁴	-	Q74MU7 ¹⁵	-	-	-	-	-

¹Components were identified by an iterative BLASTp analysis against a database consisting of the proteomes represented in this table. For each component, the analysis was initiated by sequences from *Escherichia coli*, *Saccharomyces cerevisiae*, and *Haloferax volcanii* (if applicable). BLASTp hits better than e-3 were inspected and homologs were manually selected. Identified homologs were then used for subsequent BLASTp analyses until no additional homologs were identified. For each homolog, the locus tag (upper value) and the UniProt accession (lower values) is provided. To confirm absence of components from archaea outside the phyla Euryarchaeota and Crenarchaeota, text searches were performed in UniProt with a limited set of spelling variants (Feb-2018). It should be noted that the seeming absence of a component might be due to the draft nature of the underlying genome sequence or to an incomplete annotation. In few cases, an annotation incompleteness could be resolved by tBLASTn analyses against the nonredundant database with restriction to the corresponding organism ("notAnno"). The absence of SRP components in *Nanoarchaeum equitans* was already reported (Podar, Makarova et al. 2013). The assignment of the locus tag NEQ375a to the secE gene was also taken from the same publication.

²The following species were analyzed (data in parenthesis are the locus tag prefix and UniProt proteome code): *Haloferax volcanii* ("HVO_", UP000008243); *Methanococcus maripaludis* ("MMP", UP000000590); *Methanosarcina mazei* ("MM_", UP000000595); *Thermococcus kodakarensis* ("TK", UP000000536); *Methanopyrus kandleri* ("MK", UP000001826); *Methanothermobacter thermoautotrophicus* ("MTH_", UP000005223); *Archaeoglobus fulgidus* ("AF_", UP000002199); *Methanocaldococcus jannaschii* ("MJ", UP000000805); *Sulfolobus acidocaldarius* ("Saci_", UP000001018); *Aeropyrum pernix* ("APE_", UP000002518); *Thermoproteus tenax* ("TTX_", UP000002654); *Nitrosopumilus maritimus* ("Nmar_", UP000000792); *Candidatus Korarchaeum cryptofilum* ("Kcr_", UP000001686); *Nanoarchaeum equitans* ("NEQ", UP000000578); *Lokiarchaeum sp.* strain GC14_75 ("Lokiarch_", UP000034722); *Micrarchaeum acidophilum* ("BK997_", UP000184208); *Haloredivivus sp.* strain G17 ("HRED_", UP000003484); *Parvarchaeum acidophilus* ARMAN-5 ("BJBARM5_", UP000009376). "Bacteria" refers to *E.coli* (UP000000625); "Eukaryotes" refers to yeast (*Saccharomyces cerevisiae*) (UP000002311).

³*S. cerevisiae* SRP19 homolog (SRP65, YML105C) is significantly longer than human SRP19 homolog.

⁴Sortase, ⁶exosortase (Xrt) and ⁸PglB were not identified in *E. coli* but are present in bacteria like *S. aureus*, *Nitrosomonas europaea*, and *Campylobacter jejuni*, respectively.

⁵The subtype of archaeosortase is indicated in parenthesis after the locus tag (A for artA, C for artC, E for artE).

⁷Species which have lipobox proteins require signal peptidase II, which has not yet been identified ("n.i."); species lacking lipobox proteins are indicated as not having this enzyme; in case of very few lipobox predictions (up to 2), these are assumed to be false positives and the species is considered devoid of SPII.

⁹ArII (Flal) and ArIJ (FlaJ) are PilB and PilC homologs, respectively, which are genomically co-located with ArIH (FlaH) homologs.

¹⁰Only those PilB and PilC homologs are reported, which are genomic neighbors; an exception are those from *Nanoarchaeum equitans*; PilB homologs are those reported in the genome publication (Waters, Hohn et al. 2003); all PilC homologs are reported, independent of genomic vicinity.

¹¹SLGs are important cell surface components but lack a specific biosynthesis machinery. Therefore, the structural units themselves have been included here. However, since SLGs lack global sequence similarity, assignments are based on ¹²experimental characterization; ¹³sequence similarity to characterized SLGs from related species, taken from ¹⁴species-specific literature sources or from the ¹⁵review by Claus *et al.* (Claus, Akca et al. 2005).

¹²Experimentally characterized SLGs are from *H.volcanii* (Sumper, Berg et al. 1990) *M. mazei* (Francoleon, Boontheung et al. 2009), *M. jannaschii* (Akca, Claus et al. 2002), *S. acidocaldarius* (Grogan 1996, Veith, Klingl et al. 2009, Peyfoon, Meyer et al. 2010)

¹³SLGs assigned by sequence similarity are from *M. maripaludis* (based on UniProt:Q8X235 (Akca, Claus et al. 2002).

¹⁴The SLG from *T. kodakarensis* is the 3rd listed for this species in Claus et al. (Claus, Akca et al. 2005) but its correct GenBank accession is BAD85084. This identification, *csg*, TK0895, was taken from Takemasa (Takemasa, Yokooji et al. 2011). The *T. tenax* SLG assignment is taken from Siebers et al. (Siebers, Zaparty et al. 2011) as the structural analysis of this species (Wildhaber and Baumeister 1987) did not identify the SLG. The *A. pernix* assignment is taken from Palmieri et al. (Palmieri, Cannio et al. 2009).

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