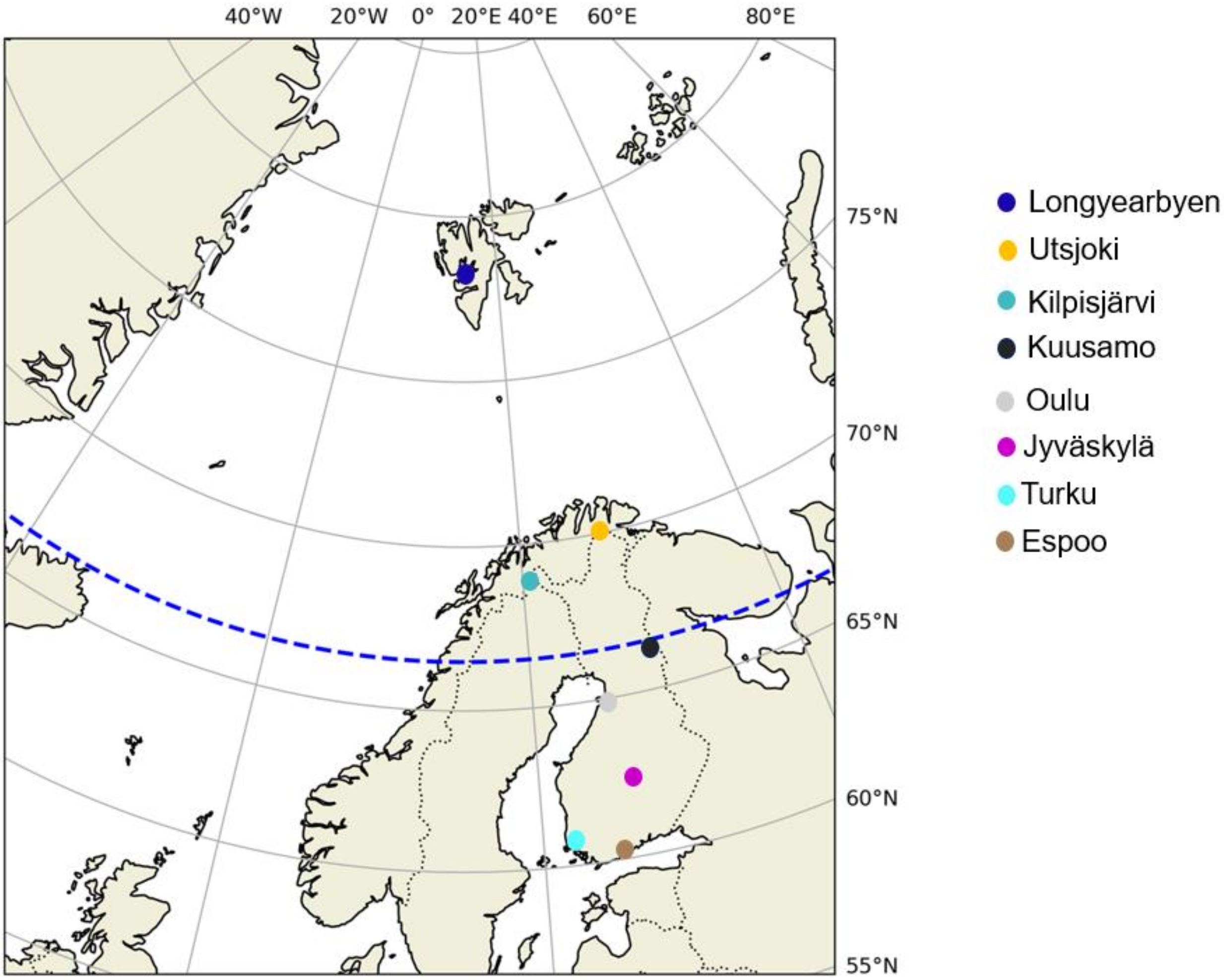
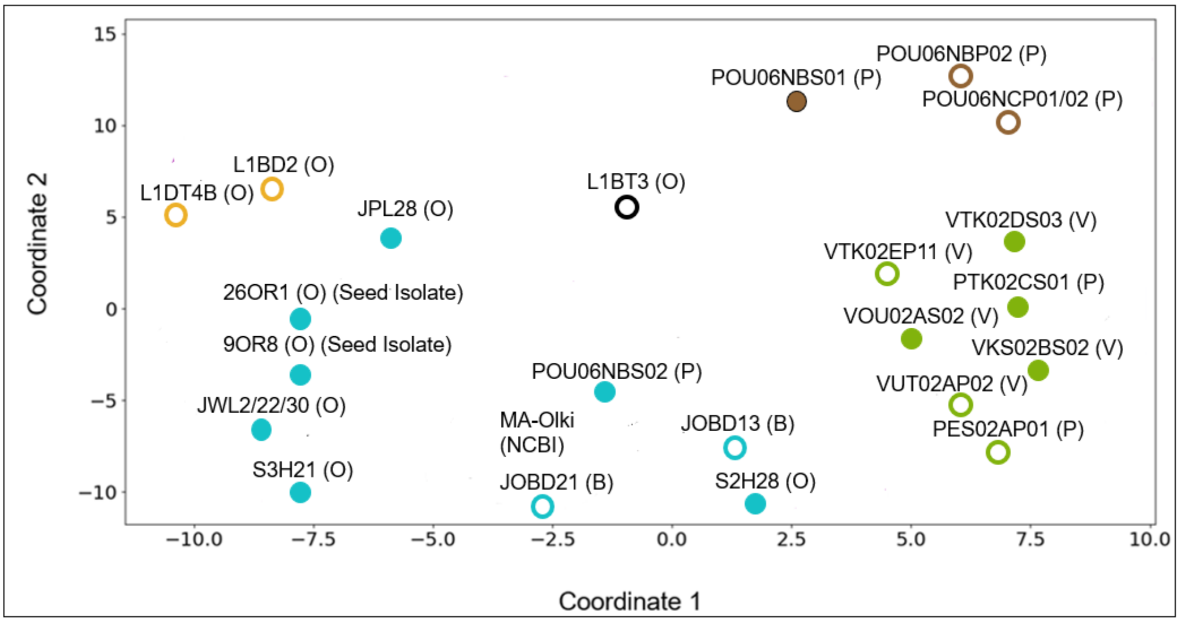
Supplementary Table 1. An overview of the genomic features and general characteristics of *S. faeni* strains. SR denotes sensory rhodopsin, as certain strains contain both sensory rhodopsin and xanthorhodopsin (XR).

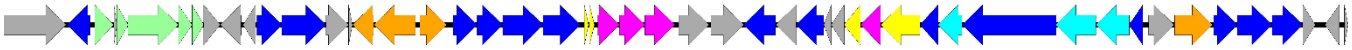
Strain	Size(Mbp)	No. Of Contigs	AAP	Rhodopsin	Completeness (%)	Contamination (%)
9OR8	4.4	17	-	XR	99.59	1.13
26OR1	4.2	26	-	SR+ XR	99.66	0.28
JOBD13	4.2	22	-	XR	99.20	0.82
JOBD21	5.1	128	-	-	99.66	0.86
JPL28	4.5	36	-	XR	99.66	0.28
JWL2	4.3	13	-	XR	99.66	0.77
JWL22	4.3	13	-	XR	99.66	0.77
JWL30	4.2	8	-	XR	99.66	0.77
L1BD2	5.0	84	-	XR	99.66	1.93
L1BT3	4.1	8	-	SR+ XR	99.57	1.02
L1DT4B	4.7	55	-	XR	99.54	0.62
PES02AP01	5.3	104	+	-	99.23	2.48
POU06NBP02	4.7	38	-	XR	99.32	1.19
POU06NBS01	4.3	69	-	XR	99.32	0.96
POU06NBS02	5.2	102	-	-	99.66	1.58
POU06NCP01	4.8	67	-	XR	99.32	0.54
POU06NCP02	4.9	69	-	XR	99.32	0.54
PTK02CS01	5.4	72	+	-	99.32	1.55
S2H28	4.6	42	-	XR	99.66	0.54
S3H21	4.7	62	-	XR	99.06	2.19
MA-Olki	4.4	31	-	-	99.19	1.33
VKS02BS02	5.1	60	+	-	99.15	1.70
VOU02AS02	4.7	63	+	SR	99.32	1.44
VTK02DS03	5.2	93	+	-	99.23	1.68
VTK02EP11	4.1	7	+	-	99.32	0.96
VUT02AP02	5.0	121	+	SR	99.15	2.07



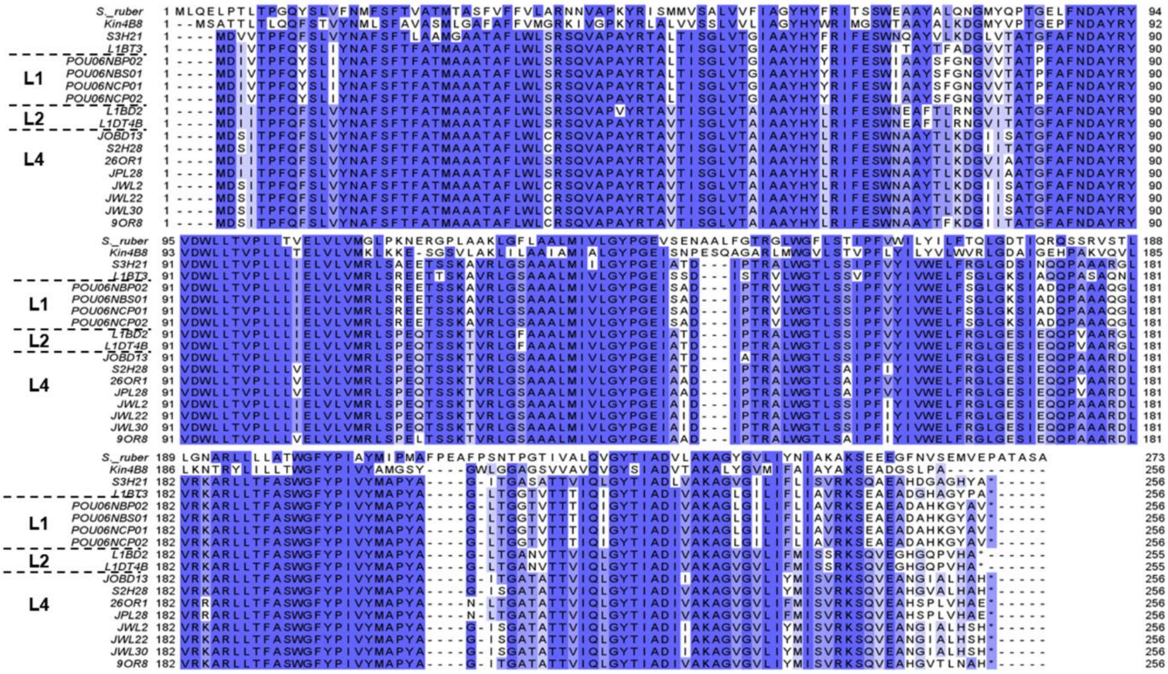
Supplementary Figure 1. Isolation locations of *S. faeni* strains. Blue line shows the arctic circle.



Supplementary Figure 2. Multidimensional Scaling (MDS) graph depicting the positioning of strains based on their ANIs, visualizing genomic similarities and differences among strains. Strains are distinguished by text formatting, with bold text representing endophytic strains and non-bold text for epiphytic strains. Isolation sources are indicated as: O for *O. digyna*, P for *V. vitis-idaea*, V for *V. myrtillus*, and B for *B. vivipara*.The lineages (L1-L4) used to categorize the strains in this study are color-coded as follows: L1 (brown), L2 (yellow), and L4 (cyan).



Supplementary Figure 3. Functional categories of gene products within the photosynthetic gene cluster (PGC) are color-coded as follows: Tetrapyrrole / (Bacterio)Chlorophyll Biosynthesis is shown in blue, Light-Independent Protochlorophyllide Reductase Complex (DPOR) in cyan, Reaction Center Core Proteins (Type II) in fuchsia, Light-Harvesting Complex Proteins & Assembly in yellow, Cytochrome c Maturation System in green, Carotenoid Biosynthesis in orange, Transcriptional Regulation in brown, and Hypothetical/Uncharacterized Function in gray.



Supplementary Figure 4. Amino acid alignment and percentage identity based coloring of XR proteins from XR containing *S. faeni* strains, with *S. ruber* as the reference sequence.

Supplementary Table 2. The table presents amino acids categorized by their side chain properties and highlighted using a consistent color code. Non-polar, uncharged, hydrophobic amino acids Alanine (A), Valine (V), Leucine (L), Isoleucine (I), Methionine (M), Phenylalanine (F), and Proline (P) are shown in orange. Electrically charged amino acids Lysine (K) and Arginine (R) are marked in green. Polar, uncharged amino acids Serine (S), Threonine (T), Tyrosine (Y), Asparagine (N), and Glycine (G) are colored in blue.

Strain Residue

Position in *S. ruber*	**153**	**156**	**157**	**160**	**163**	**191**	**194**	**197**	**198**	**201**	**204**	**205**	**207**	**208**	**211**	**212**
Position in Kin4B8	150	153	154	157	160	188	191	194	195	198	201	202	204	205	208	209
Position in AAP5/*S. faeni*	146	149	150	153	156	184	187	190	191	194	197	198	200	201	204	205
S. ruber	G	G	F	T	F	N	L	L	A	G	P	I	Y	M	M	A
Kin4B8	L	G	V	T	F	N	Y	L	L	G	P	I	Y	A	S	Y
AAP5	R	G	T	A	F	K	L	F	A	G	P	I	Y	M	Y	A
POU06NCP01(L1)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
POU06NBS01(L1)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
POU06NBP02 (L1)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
POU06NCP02 (L1)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
L1DT4B (L2)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
L1BD2 (L2)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
S2H28 (L4)	R	G	T	A	F	K	L	F	A	G	P	I	Y	M	Y	A
JOBD13 (L4)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
JPL28 (L4)	R	G	T	A	F	R	L	F	A	G	P	I	Y	M	Y	A

26OR1 (L4)	R	G	T	A	F	R	L	F	A	G	P	I	Y	M	Y	A
9OR8 (L4)	R	G	T	A	F	K	L	F	A	G	P	I	Y	M	Y	A
JWL2 (L4)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A
JWL22 (L4)	R	G	T	S	F	K	L	F	A	G	P	I	Y	M	Y	A

Supplementary Table 3. 5′ and 3′ neighboring genes of photoreceptors in *S. faeni* strains, with strain names color-coded according to their phototrophic group: AAP: Dark blue, XR: Purple, None: Gray. Genes are arranged according to phylogenetic lineage, with homologous genes aligned vertically across lineages.

Photoreceptor-BLUF	**5' Neighbour**	**3' Neighbour**	**Lineage**
POU06NCP02 BLUF	Methyl-accepting chemotaxis protein	N5-carboxyaminoimidazole ribonucleotide synthase	1
POU06NCP01 BLUF	Methyl-accepting chemotaxis protein	N5-carboxyaminoimidazole ribonucleotide synthase	1
POU06NBS01 BLUF	Methyl-accepting chemotaxis protein	N5-carboxyaminoimidazole ribonucleotide synthase	1
POU06NBP02 BLUF	Methyl-accepting chemotaxis protein	N5-carboxyaminoimidazole ribonucleotide synthase	1
VUT02AP02 BLUF	Hypothetical Protein	EF-hand domain-containing protein	3
VOU02AS02 BLUF	Hypothetical Protein	EF-hand domain-containing protein	3
VKS02BS02 BLUF 1	Hypothetical Protein	EF-hand domain-containing protein	3
VKS02BS02 BLUF 2	Hypothetical Protein	EF-hand domain-containing protein	3
PTK02CS01 BLUF	Hypothetical Protein	EF-hand domain-containing protein	3
VTK02DS03 BLUF	Hypothetical Protein	EF-hand domain-containing protein	3
PES02AP01 BLUF	Hypothetical Protein	EF-hand domain-containing protein	3
9OR8 BLUF	Superoxide dismutase [Mn]	Energy transducer TonB	4
S2H28 BLUF	Hypothetical Protein	Hypothetical Protein	4

POU06NBS02 BLUF	Calcium-binding protein	Hypothetical Protein	4
MA-Olki BLUF	Calcium-binding protein	Hypothetical Protein	4
JOBD21 BLUF	Calcium-binding protein	Hypothetical Protein	4
L1BT3 BLUF 1	Superoxide dismutase [Mn]	Energy transducer TonB	Outlier
L1BT3 BLUF 2	Hypothetical Protein	EF-hand domain-containing protein	Outlier

Photoreceptor-BphP	**5' Neighbour**	**3' Neighbour**	**Lineage**
POU06NCP02 BphP 1	camP-binding proteins - catabolite gene activator	Hypothetical Protein	1
POU06NCP01 BphP 3	camP-binding proteins - catabolite gene activator	Hypothetical Protein	1
POU06NBP02 BphP 2	camP-binding proteins - catabolite gene activator	Hypothetical Protein	1
POU06NCP02 BphP 2	Sodium/bile acid symporter	Hypothetical Protein	1
POU06NCP01 BphP 2	Sodium/bile acid symporter	Hypothetical Protein	1
POU06NBS01 BphP	Sodium/bile acid symporter	Protoporphyrinogen/coproporphyrinogen oxidase	1
POU06NBP02 BphP 1	Sodium/bile acid symporter	Hypothetical Protein	1
POU06NCP02 BphP 3	Transposase	Protoporphyrinogen/coproporphyrinogen oxidase	1
POU06NCP01 BphP 1	Transposase	Protoporphyrinogen/coproporphyrinogen oxidase	1
L1DT4B BphP 1	Sodium/bile acid symporter	Esterase/lipase	2
L1BD2 Bphp 2	Sodium/bile acid symporter	Esterase/lipase	2
L1DT4B BphP 2	Mannonate dehydratase	Helix-turn-helix transcriptional regulator	2

L1BD2 Bphp 1	Mannonate dehydratase	Helix-turn-helix transcriptional regulator	2
VUT02AP02 BpHp 1	Sodium/bile acid symporter	Hypothetical Protein	3
VTK02EP11 BphP 1	Sodium/bile acid symporter	Hypothetical Protein	3
VOU02AS02 BphP 1	Sodium/bile acid symporter	M38 (beta-aspartyl dipeptidase)	3
VKS02BS02 BphP 1	Sodium/bile acid symporter	M38 (beta-aspartyl dipeptidase)	3
PTK02CS01 BphP 1	Sodium/bile acid symporter	M38 (beta-aspartyl dipeptidase)	3
VTK02DS03 BphP 2	Sodium/bile acid symporter	M38 (beta-aspartyl dipeptidase)	3
PES02AP01 BphP 3	Sodium/bile acid symporter	Hypothetical Protein	3
VTK02DS03 BphP 3	cAMP-binding proteins - catabolite gene activator	Transcriptional regulator, LysR family	3
PES02AP01 BphP 2	cAMP-binding proteins - catabolite gene activator	Transcriptional regulator, LysR family	3
VKS02BS02 BphP 3	Transposase related hp	Mobile element protein	3
VUT02AP02 BphP 2	Hypothetical Protein	Hypothetical Protein	3
VTK02EP11 BphP 2	Hypothetical Protein	Hypothetical Protein	3
VOU02AS02 BphP 2	Hypothetical Protein	Hypothetical Protein	3
VKS02BS02 BphP 2	Hypothetical Protein	Hypothetical Protein	3

PTK02CS01 BphP 2	Hypothetical Protein	Hypothetical Protein	3
VTK02DS03 BphP 1	Hypothetical Protein	Hypothetical Protein	3
PES02AP01 BphP 1	Hypothetical Protein	Hypothetical Protein	3
JPL28 BphP 1	Sodium/bile acid symporter	Uncharacterized MFS-type transporter	4
26OR1 BphP 1	Sodium/bile acid symporter	Uncharacterized MFS-type transporter	4
9OR8 BphP 3	Sodium/bile acid symporter	Hypothetical Protein	4
S3H21 BphP	Sodium/bile acid symporter	Uncharacterized MFS-type transporter	4
JWL30 BphP	Sodium/bile acid symporter	Uncharacterized MFS-type transporter	4
JWL22 BphP	Sodium/bile acid symporter	Uncharacterized MFS-type transporter	4
JWL2 BphP	Sodium/bile acid symporter	Uncharacterized MFS-type transporter	4
S2H28 BphP 1	Sodium/bile acid symporter	Ferrichrome-iron receptor	4
POU06NBS02 BphP 1	Sodium/bile acid symporter	Ferrichrome-iron receptor	4
MA-Olki BphP 2	Sodium/bile acid symporter	Ferrichrome-iron receptor	4
JOBD13 BphP 1	Sodium/bile acid symporter	Hypothetical Protein	4
JOBD21 BphP 2	Sodium/bile acid symporter	M38 (beta-aspartyl dipeptidase)	4
26OR1 BphP 2	cAMP-binding proteins - catabolite gene activator	Hypothetical Protein	4
S2H28 BphP 4	cAMP-binding proteins - catabolite gene activator	Transposase	4
JOBD13 BphP 5	camP-binding proteins - catabolite gene activator	Hypothetical Protein	4
S2H28 BphP 3	Mobile element protein	Hypothetical Protein	4
JOBD13 BphP 2	Imidazolonepropionase-like amidohydrolase	Helix-turn-helix transcriptional regulator	4
JOBD21 BphP 1	putative phospholipase D	Sphingolipid (S)-alpha-hydroxylase	4
JPL28 BphP 2	Sigma factor, ECF subfamily	Hypothetical Protein	4

9OR8 BphP 1	Hypothetical Protein	Oxidoreductase, short-chain dehydrogenase/reductase	4
9OR8 BphP 2	Hypothetical Protein	Alpha-galactosidase	4
S2H28 BphP 2	Hypothetical Protein	tRNA-Gln-TTG	4
POU06NBS02 BphP 2	Hypothetical Protein	Helix-turn-helix transcriptional regulator	4
POU06NBS02 BphP 3	Hypothetical Protein	Hypothetical Protein	4
MA-Olki BphP 1	Hypothetical Protein	Hypothetical Protein	4
JOBD13 BphP 3	Hypothetical Protein	Hypothetical Protein	4
JOBD13 BphP 4	Hypothetical Protein	Oxidoreductase, short-chain dehydrogenase/reductase	4
L1BT3 BphP	Sodium/bile acid symporter	Ferrichrome-iron receptor	Outlier

Photoreceptor-PYP	**5' Neighbour**	**3' Neighbour**	**Lineage**
L1DT4B PYP 1	Chloride channel protein	Sensor domain-containing diguanylate cyclase	2
L1BD2 PYP 3	Chloride channel protein	Sensor domain-containing diguanylate cyclase	2
L1DT4B PYP 2	ParD-like family protein	Sensor domain-containing diguanylate cyclase	2
L1BD2 PYP 2	Resolvase/integrase	Sensor domain-containing diguanylate cyclase	2
L1BD2 PYP 1	Hypothetical Protein	Sensor domain-containing diguanylate cyclase	2
VUT02AP02 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3
VTK02EP11 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3
VOU02AS02 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3
VKS02BS02 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3

PTK02CS01 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3
VTK02DS03 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3
PES02AP01 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	3
JWL30 PYP	Chloride channel protein	Sensor domain-containing diguanylate cyclase	4
JWL22 PYP	Chloride channel protein	Sensor domain-containing diguanylate cyclase	4
JWL2 PYP	Chloride channel protein	Sensor domain-containing diguanylate cyclase	4
9OR8 PYP 1	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	4
S2H28 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	4
JOBD13 PYP	GAF domain/GGDEF domain/EAL domain protein	Sensor domain-containing diguanylate cyclase	4
JOBD21 PYP	PaaI family thioesterase	Sensor domain-containing diguanylate cyclase	4
JPL28 PYP	Hypothetical Protein	Sensor domain-containing diguanylate cyclase	4
26OR1 PYP	Hypothetical Protein	Sensor domain-containing diguanylate cyclase	4
9OR8 PYP 2	Hypothetical Protein	Sensor domain-containing diguanylate cyclase	4
S3H21 PYP	Hypothetical Protein	Sensor domain-containing diguanylate cyclase	4
L1BT3 PYP	Epoxide hydrolase	Sensor domain-containing diguanylate cyclase	Outlier