
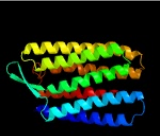

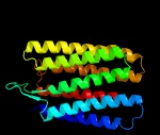









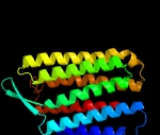





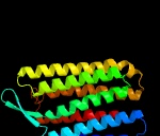



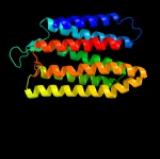

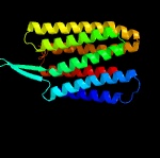

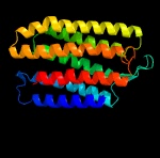

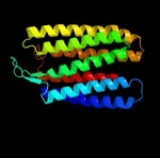

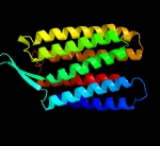

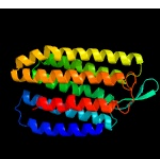

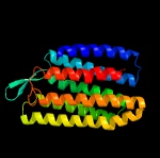
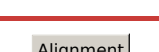
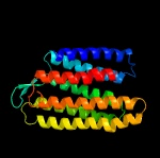
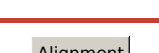
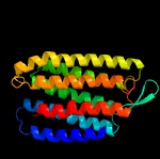

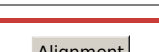
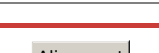
























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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4y9hA_</a>	 <a href="#">Alignment</a>		100.0	100	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> the 1.43 angstrom crystal structure of bacteriorhodopsin crystallized from bicelles <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
2	<a href="#">c5vn7B_</a>	 <a href="#">Alignment</a>		100.0	100	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> structure of bacteriorhodopsin from crystals grown at 20 deg celcius using glyncoc15+4 as an lcp host lipid <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
3	<a href="#">c7z09A_</a>	 <a href="#">Alignment</a>		100.0	100	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> crystal structure of the ground state of bacteriorhodopsin at 1.05 angstrom resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
4	<a href="#">c6guxA_</a>	 <a href="#">Alignment</a>		100.0	60	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> Archaelhodopsin-3 <b>PDBTitle:</b> dark-adapted structure of archaelhodopsin-3 at 100k <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
5	<a href="#">c1uazA_</a>	 <a href="#">Alignment</a>		100.0	59	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> archaelhodopsin-1 <b>PDBTitle:</b> crystal structure of archaelhodopsin-1 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
6	<a href="#">c2ei4A_</a>	 <a href="#">Alignment</a>		100.0	56	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> Archaelhodopsin-2 <b>PDBTitle:</b> trimeric complex of archaelhodopsin-2 <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
7	<a href="#">c4pxkA_</a>	 <a href="#">Alignment</a>		100.0	57	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> crystal structure of haloarcula marismortui bacteriorhodopsin i d94n mutant <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
8	<a href="#">c4fbzA_</a>	 <a href="#">Alignment</a>		100.0	56	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> deltarhodopsin <b>PDBTitle:</b> crystal structure of deltarhodopsin from haloterrigena thermotolerans <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
9	<a href="#">c4l35A_</a>	 <a href="#">Alignment</a>		100.0	57	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> Cruxrhodopsin-3 <b>PDBTitle:</b> crystal structure of cruxrhodopsin-3 at ph5 from haloarcula vallismortis at 2.1 angstrom resolution <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
10	<a href="#">c4wavA_</a>	 <a href="#">Alignment</a>		100.0	56	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> Bacteriorhodopsin-I <b>PDBTitle:</b> crystal structure of haloquadratum walsbyi bacteriorhodopsin mutant d93n <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>

11	<a href="#">c5itcA_</a>	 Alignment		100.0	56	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> Bacteriorhodopsin-I <b>PDBTitle:</b> :2.2-angstrom in meso crystal structure of haloquadratum walsbyi bacteriorhodopsin (hwbr) from styrene maleic acid (sma) polymer nanodiscs; <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
12	<a href="#">c8wewA_</a>	 Alignment		100.0	46	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> Bacteriorhodopsin-II-like protein <b>PDBTitle:</b> haloquadratum walsbyi middle rhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
13	<a href="#">c8xhwD_</a>	 Alignment		100.0	48	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> Bacteriorhodopsin-II-like protein <b>PDBTitle:</b> haloquadratum walsbyi middle rhodopsin mutant - d84n <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
14	<a href="#">c6kfqA_</a>	 Alignment		100.0	46	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> Rhodopsin <b>PDBTitle:</b> crystal structure of thermophilic rhodopsin from rubrobacter xylanophilus <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
15	<a href="#">c6lm1A_</a>	 Alignment		100.0	37	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> Rhodopsin <b>PDBTitle:</b> the crystal structure of cyanorhodopsin (cyr) n4075r from cyanobacteria tolyporthrix sp. nies-4075 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
16	<a href="#">c6lm0C_</a>	 Alignment		100.0	37	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> Rhodopsin <b>PDBTitle:</b> the crystal structure of cyanorhodopsin (cyr) n2098r from cyanobacteria calothrix sp. nies-2098 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
17	<a href="#">c1e12A_</a>	 Alignment		100.0	35	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> HALORHODOPSIN <b>PDBTitle:</b> halorhodopsin, a light-driven chloride pump <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
18	<a href="#">c5ahyA_</a>	 Alignment		100.0	35	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> HALORHODOPSIN <b>PDBTitle:</b> halorhodopsin from halobacterium salinarum in a new rhombohedral crystal form <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
19	<a href="#">c6gyhA_</a>	 Alignment		100.0	34	<b>PDB header:</b> proton transport <b>Chain:</b> A; <b>PDB Molecule:</b> Family A G protein-coupled receptor-like protein <b>PDBTitle:</b> crystal structure of the light-driven proton pump coccomyxa subellipsoidea rhodopsin csr <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
20	<a href="#">c3qbgA_</a>	 Alignment		100.0	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> Halorhodopsin <b>PDBTitle:</b> anion-free blue form of pharaonis halorhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
21	<a href="#">c8anqD_</a>	 Alignment	not modelled	100.0	33	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> crystal structure of the microbial rhodopsin from sphingomonas paucimobilis (spar) <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
22	<a href="#">c8xx8F_</a>	 Alignment	not modelled	100.0	32	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> Rhodopsin <b>PDBTitle:</b> structure of glycihalorhodopsin from salinarimonas soli <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
23	<a href="#">c7bmhA_</a>	 Alignment	not modelled	100.0	31	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> Opsin <b>PDBTitle:</b> crystal structure of a light-driven proton pump lr (mac) from leptosphaeria maculans <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
24	<a href="#">c3am6A_</a>	 Alignment	not modelled	100.0	31	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> rhodopsin-2 <b>PDBTitle:</b> crystal structure of the proton pumping rhodopsin ar2 from marine alga acetabularia acetabulum <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>

25	<a href="#">c3am6D_</a>		not modelled	100.0	31	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> rhodopsin-2 <b>PDBTitle:</b> crystal structure of the proton pumping rhodopsin ar2 from marine alga acetabularia acetabulum <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
26	<a href="#">c4hyjA_</a>		not modelled	100.0	30	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> Rhodopsin <b>PDBTitle:</b> crystal structure of exiguobacterium sibiricum rhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
27	<a href="#">c5jjnA_</a>		not modelled	100.0	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> Sensory rhodopsin-2 <b>PDBTitle:</b> ;structure of the srii/htrii(g83f) complex in p212121 space group ("v" shape); <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
28	<a href="#">c5uk6A_</a>		not modelled	100.0	29	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> structure of anabaena sensory rhodopsin determined by solid state nmr spectroscopy and deer <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
29	<a href="#">c5uk6C_</a>		not modelled	100.0	29	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> structure of anabaena sensory rhodopsin determined by solid state nmr spectroscopy and deer <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
30	<a href="#">c1xioA_</a>		not modelled	100.0	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ANABAENA SENSORY RHODOPSIN <b>PDBTitle:</b> anabaena sensory rhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
31	<a href="#">c5azdA_</a>		not modelled	100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> crystal structure of thermophilic rhodopsin. <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
32	<a href="#">c8i2zA_</a>		not modelled	100.0	27	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> Xanthorhodopsin <b>PDBTitle:</b> cryo-em structure of the zeaxanthin-bound kin4b8 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
33	<a href="#">c5awzA_</a>		not modelled	100.0	27	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> Rhodopsin I <b>PDBTitle:</b> crystal structure of the cell-free synthesized membrane protein, acetabularia rhodopsin i, at 1.57 angstrom <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
34	<a href="#">c4jq6B_</a>		not modelled	100.0	28	<b>PDB header:</b> proton transport <b>Chain:</b> B: <b>PDB Molecule:</b> Proteorhodopsin <b>PDBTitle:</b> crystal structure of blue light-absorbing proteorhodopsin from med12 at 2.3 angstrom <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
35	<a href="#">c2l6xA_</a>		not modelled	100.0	26	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> Green-light absorbing proteorhodopsin <b>PDBTitle:</b> solution nmr structure of proteorhodopsin. <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
36	<a href="#">c8cl7A_</a>		not modelled	100.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Sodium pumping rhodopsin <b>PDBTitle:</b> karkinobacter eikastus rhodopsin 2 (kr2) in dark state <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
37	<a href="#">c7b03D_</a>		not modelled	100.0	27	<b>PDB header:</b> proton transport <b>Chain:</b> D: <b>PDB Molecule:</b> Proteorhodopsin <b>PDBTitle:</b> cryo-em structure of the green-light absorbing proteorhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
38	<a href="#">c4klyB_</a>		not modelled	100.0	27	<b>PDB header:</b> proton transport <b>Chain:</b> B: <b>PDB Molecule:</b> Blue-light absorbing proteorhodopsin <b>PDBTitle:</b> crystal structure of a blue-light absorbing proteorhodopsin mutant d97n from hot75 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
39	<a href="#">c8cnkA_</a>		not modelled	100.0	26	<b>PDB header:</b> proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> Green-light absorbing proteorhodopsin <b>PDBTitle:</b> cryo-em structure of retinal-free proteopsin bound to decanoate <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
40	<a href="#">c8cnkD_</a>		not modelled	100.0	26	<b>PDB header:</b> proton transport <b>Chain:</b> D: <b>PDB Molecule:</b> Green-light absorbing proteorhodopsin <b>PDBTitle:</b> cryo-em structure of retinal-free proteopsin bound to decanoate <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
41	<a href="#">c6tk7A_</a>		not modelled	100.0	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Sodium pumping rhodopsin <b>PDBTitle:</b> femtosecond to millisecond structural changes in a light-driven sodium pump: dark structure in acidic conditions <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
42	<a href="#">c7o8fA_</a>		not modelled	100.0	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Chloride pumping rhodopsin <b>PDBTitle:</b> nmhr dark state structure determined by serial femtosecond crystallography <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
43	<a href="#">c6nwdA_</a>		not modelled	100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> Gll0198 protein <b>PDBTitle:</b> x-ray crystallographic structure of gloeobacter rhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
44	<a href="#">c8qleA_</a>		not modelled	100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Bacteriorhodopsin-like protein <b>PDBTitle:</b> crystal structure of the light-driven sodium pump ernar in the monomeric form at ph 4.6 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
45	<a href="#">c3ddlA_</a>		not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> Xanthorhodopsin <b>PDBTitle:</b> crystallographic structure of xanthorhodopsin, a light-driven ion pump with dual chromophore <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>

46	<a href="#">c8jh0B_</a>		not modelled	100.0	22	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> Xanthorhodopsin <b>PDBTitle:</b> crystal structure of the light-driven sodium pump ianar <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
47	<a href="#">c6edqB_</a>		not modelled	100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> Anion channelrhodopsin 1 <b>PDBTitle:</b> crystal structure of the light-gated anion channelrhodopsin gtacr1 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
48	<a href="#">c6eyuA_</a>		not modelled	100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> crystal structure of the inward h(+) pump xenorhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
49	<a href="#">c7e4gA_</a>		not modelled	100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> schizorhodopsin 4 <b>PDBTitle:</b> crystal structure of schizorhodopsin 4 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
50	<a href="#">c7avpA_</a>		not modelled	100.0	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Bacteriorhodopsin <b>PDBTitle:</b> crystal structure of marine actinobacteria clade rhodopsin (mar) in the o state <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
51	<a href="#">c8yelA_</a>		not modelled	100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Cation channel rhodopsin 4 <b>PDBTitle:</b> cryo-em structure of the channelrhodopsin gtccr4 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
52	<a href="#">c7e6zA_</a>		not modelled	100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Archaeal-type opsin 1, Archaeal-type opsin 2 <b>PDBTitle:</b> time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin: 50 microsecond structure <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
53	<a href="#">c7c86A_</a>		not modelled	100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Sensory opsin A, Channelrhodopsin (ChR) chimera between ChR1 & ChR2 <b>PDBTitle:</b> time-resolved serial femtosecond crystallography reveals early structural changes in channelrhodopsin: dark state structure <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
54	<a href="#">c9go1A_</a>		not modelled	100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Archaeal-type opsin 1, Archaeal-type opsin 2 <b>PDBTitle:</b> c1c2 channelrhodopsin - smx dark structure <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
55	<a href="#">c8yekA_</a>		not modelled	100.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> GtCCR2 <b>PDBTitle:</b> cryo-em structure of the channelrhodopsin gtccr2 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
56	<a href="#">c6sqgE_</a>		not modelled	100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> viral rhodopsin OLPVR1I <b>PDBTitle:</b> crystal structure of viral rhodopsin olpvrii <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
57	<a href="#">c6sqgD_</a>		not modelled	100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> viral rhodopsin OLPVR1I <b>PDBTitle:</b> crystal structure of viral rhodopsin olpvrii <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
58	<a href="#">c6jo0A_</a>		not modelled	100.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> VirRDTs <b>PDBTitle:</b> crystal structure of the dts-motif rhodopsin from phaeocystis globosa virus 12t <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
59	<a href="#">c6eidB_</a>		not modelled	100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> Archaeal-type opsin 2 <b>PDBTitle:</b> crystal structure of wild-type channelrhodopsin 2 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
60	<a href="#">c7akxA_</a>		not modelled	100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> viral rhodopsin OLPVR1 <b>PDBTitle:</b> crystal structure of the viral rhodopsin olpvri1 in p1 space group <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
61	<a href="#">c7u55A_</a>		not modelled	96.1	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Heliorhodopsin <b>PDBTitle:</b> crystal structure of thermoplasmatales archaeon heliorhodopsin at ph 4.5 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
62	<a href="#">c9ljjA_</a>		not modelled	98.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> Heliorhodopsin <b>PDBTitle:</b> cryo-em structure of a nanobody bound heliorhodopsin <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
63	<a href="#">c6su3A_</a>		not modelled	98.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 48C12 heliorhodopsin <b>PDBTitle:</b> crystal structure of the 48c12 heliorhodopsin in the violet form at ph 8.8 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
64	<a href="#">c5abbC_</a>		not modelled	98.5	30	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> GREEN-LIGHT ABSORBING PROTEORHODOPSIN <b>PDBTitle:</b> visualization of a polytopic membrane protein during secy-mediated membrane insertion <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
65	<a href="#">c8wjhA_</a>		not modelled	13.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> Solute carrier family 22 member 11 <b>PDBTitle:</b> cryo-em structure of oat4 <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>
66	<a href="#">c6od7A_</a>		not modelled	40.1	36	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> Portal protein <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) pul6 portal protein, dodecameric complex <b>PDB Entry:</b> <a href="#">PDBe RCSB PDBj</a>

67	<a href="#">c6od7D_</a>	 <a href="#">Alignment</a>	not modelled	40.1	36	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> Portal protein <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) pul6 portal protein, dodecameric complex <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
68	<a href="#">c9je0A_</a>	 <a href="#">Alignment</a>	not modelled	7.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> Solute carrier family 22 member 12 <b>PDBTitle:</b> human urat1 bound to benzbromarone <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>
69	<a href="#">c6m20B_</a>	 <a href="#">Alignment</a>	not modelled	6.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> Hexose transporter 1 <b>PDBTitle:</b> crystal structure of plasmodium falciparum hexose transporter pfht1 bound with glucose <b>PDB Entry:</b> <a href="#">PDBe</a> <a href="#">RCSB</a> <a href="#">PDBj</a>