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| Title | A review on viral metagenomics in extreme environments |
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| Publication date | 2019-10-18 |
| Original Citation | Dávila-Ramos, S., Castelán-Sánchez, H. G., Martínez-Ávila, L., Sánchez-Carbente, M. d. R., Peralta, R., Hernández-Mendoza, A., Dobson, A. D. W., Gonzalez, R. A., Pastor, N. and Batista-García, R. A. (2019) 'A Review on Viral Metagenomics in Extreme Environments', <i>Frontiers in Microbiology</i> , 10, 2403. (19pp.) DOI: 10.3389/fmicb.2019.02403 |
| Type of publication | Article (peer-reviewed) |
| Link to publisher's version | https://www.frontiersin.org/articles/10.3389/fmicb.2019.02403/full - 10.3389/fmicb.2019.02403 |
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| Download date | 2023-12-08 15:39:59 |
| Item downloaded from | https://hdl.handle.net/10468/8841 |



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A review on viral metagenomics in extreme environments

Running title: Viral metagenomics in extreme environments

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Keywords: metagenomic; virosphere; extreme environment; viral gene bioprospection; extremophile virome

Abstract

Viruses are the most abundant biological entities in the biosphere, and have the ability to infect Bacteria, Archaea and Eukaryotes. The virome is estimated to be at least ten times more abundant than the microbiome with 10^7 viruses per milliliter and 10^9 viral particles per gram in marine waters and sediments or soils, respectively. Viruses represent a largely unexplored genetic diversity, having an important role in the genomic plasticity of their hosts. Moreover, they also play a significant role in the dynamics of microbial populations. In recent years, metagenomic approaches have gained increasing popularity in the study of environmental viromes, offering the possibility of extending our knowledge related to both virus diversity and their functional characterization. Extreme environments represent an interesting source of both microbiota and their virome due to their particular physicochemical conditions, such as very high or very low temperatures and >1 atm hydrostatic pressures, among others. Despite the fact that some progress has been made in our understanding of the ecology of the microbiota in these habitats, few metagenomic studies have described the viromes present in extreme ecosystems. Thus, limited advances have been made in our understanding of the virus community structure in extremophilic ecosystems, as well as in their biotechnological potential. In this review, we critically analyse recent progress in metagenomic based approaches to explore the viromes in extreme environments and we discuss the potential for new discoveries, as well as methodological challenges and perspectives.

Table S1. Summary of studies metagenomics comparing to sequencing platforms, protocol extraction, and assembly and taxonomic tools

| ID | Name of sample | ID sample | Number of reads or contigs | Type of sample | Country or Region | Type of sequencing | Method of extraction | Assembly | Taxonomic |
|----------------|-------------------------|-------------------------------|-----------------------------------|---------------------------|----------------------------|---------------------------|-----------------------------|---------------------------------|------------------|
| SDEEP_ARCT_1a | EXPLODIVE | Arctic - Extra (2126) | 27037 | Sediment | Arctic Ocean | Pyrosequencing | CTAB/NaCl | CLC Genomics Workbench ver. 5.5 | Megan |
| SDEEP_ATL_1a | EXPLODIVE | Atlantic - Extra (2125) | 26826 | | Atlantic Ocean | | | | |
| SDEEP_ATL_1b | EXPLODIVE | Atl_Vir (1157) | 107090 | | Atlantic Ocean | | | | |
| SDEEP_ARCT_1b | EXPLODIVE | Arct_Vir (1159) | 63869 | | Arctic Ocean | | | | |
| SDEEP_BKSEA_1a | EXPLODIVE | Black sea (1155) | 784336 | | Black sea | | | | |
| SDEEP_MED_1a | EXPLODIVE | Mediterrano (1161) | 65340 | | Mediterraneo | | | | |
| SDEEP_ATL_1c | EXPLODIVE | NE Atlancic (1156) | 165517 | | Atlantic Ocean | | | | |
| SDEEP_ARCT_1c | EXPLODIVE | Arctic Ocean (1158) | 79646 | | Arctic Ocean | | | | |
| SDEEP_JAP_2a | (Hado)pelagic sediments | Izu-Ogasawara Trench (164) | 46458 | | Izu-Ogasawara Trench Japan | | | | |
| SDEEP_JAP_2b | (Hado)pelagic sediments | Mariana Trench (165) | 49584 | Mariana Trench Japan | | | | | |
| SDEEP_JAP_2c | (Hado)pelagic sediments | off Shimokita Peninsula (166) | 76498 | Shimokita Peninsula Japon | | | | | |
| WDEEP_ITA_3a | Marine viromes | KM3 Ioinan Sea (3814) | 9048 | Deep sea-Seawater | Italy | Pyrosequencing | formamide/CTAB extraction | WI | Blast |
| WDEEP_CAN_4a | POV LineP transect | LJ12O (1394) | 122565 | Deep sea-Seawater | Canada | Pyrosequencing | WI | WI | WI |
| WDEEP_CAN_4b | POV LineP transect | LJ12D (1395) | 49914 | | | | | | |
| WDEEP_CAN_4c | POV LineP transect | LA26O (1398) | 70596 | | | | | | |

| | | | | | | | | | | |
|--------------|-----------------------------------|------------------------------------|---------|----------------------|--------------------------|----------------|--------------------------------------|------------------|--------|---------------|
| WDEEP_CAN_4d | POV LineP transect | LA26D (1400) | 68516 | | | | | | | |
| WDEEP_CAN_4e | POV LineP transect | LF26O (1403) | 147537 | | | | | | | |
| WDEEP_CAN_4f | POV LineP transect | LF26D (1404) | 125896 | | | | | | | |
| WDEEP_CAN_4g | POV LineP transect | LJ26O (1407) | 101179 | | | | | | | |
| WDEEP_CAN_4h | POV LineP transect | LJ26D (1408) | 55332 | | | | | | | |
| WDEEP_CAN_4i | POV LineP transect | LJ4O (1414) | 97126 | | | | | | | |
| WDEEP_CAN_4j | POV LineP transect | LJ4D (1415) | 98478 | | | | | | | |
| WDEEP_EUA_4a | POV MBARI transect | M6O1K (1432) | 225833 | | | | | | | United States |
| WDEEP_EUA_4b | POV MBARI transect | M7O4K (1433) | 144588 | | | | | | | United States |
| OMZ_CAN_5a | Saanich Inlet | Saanich_200m_r200 (2915) | 1728968 | Oxygen minimum zones | Canada | Illumina | e Gentra Puregene Blood kit (Qiagen) | Geneious v7.1 | Blastx | |
| OMZ_CAN_5b | Saanich Inlet | Saanich_fosmids (3286) | 47 | | | Pyrosequencing | | | | |
| OMZ_CHL_6a | 2008OMZst3viral200m (898) | Pyrosequencing | 96706 | | Chile | Chile | CTAB/formamide | without assembly | Blastx | |
| OMZ_CHL_6b | 2008OMZst5viral200m (993) | Pyrosequencing | 163531 | | | Chile | | | | |
| ARID_ATA_7a | Antarctic soil metaviromes | Antarctic hypolith reads (2726) | 1057535 | Hyperarid | Miers Valley; Antarctica | Illumina | WI | WI | WI | |
| ARID_ATA_7b | Antarctic soil metaviromes | Antarctic open soil reads (2727) | 870687 | | Miers Valley; Antarctica | | | | | |
| ARID_ATA_7c | Antarctic soil metaviromes | Antarctic hypolith contigs (2472) | 32574 | | Miers Valley; Antarctica | | | | | |
| ARID_ATA_7d | Antarctic soil metaviromes | Antarctic open soil contigs (2473) | 8442 | | Miers Valley; Antarctica | | | | | |
| ARID_NAM_8a | Namib Desert transect metaviromes | NAM_130 (5775) | 3097 | | Namibia | Sanger | WI | WI | WI | |
| ARID_NAM_8b | Namib Desert transect metaviromes | NAM_100 (5774) | 2897 | | | Sanger | | | | |
| ARID_NAM_8c | Namib Desert transect metaviromes | NAM_70 (5773) | 545 | | | Sanger | | | | |
| ARID_NAM_8d | Namib Desert transect metaviromes | NAM_40 () | | | | | | | | |

| | | | | | | | | | |
|----------------|---------------------|---------------------------------------|--------|---------------|----------------|---|---------------------------------|---------|---------|
| ARID_NAM_8e | Namib hypolith 2012 | Namib_hypolith_2012_contigs (2186) | 4564 | | | Illumina | | | |
| ARID_NAM_8f | Namib hypolith 2012 | Namib_hypolith_2012_reads (2708) | 841458 | | | Illumina | | | |
| SALINE_NAM_9a | Archevir | P5_Ngallou (1700) | 3018 | Hypersaline | Namibia | Illumina | QIAamp DNA mini kit (Qiagen) | IDBA_UD | tBLASTx |
| SALINE_NAM_9b | Archevir | P2_Saloon(1701) | 7302 | | | Illumina | | | |
| SALINE_NAM_9c | Archevir | P6_Lake_Retba(1702) | 884 | | | Illumina | | | |
| SALINE_NAM_9d | Archevir | P7_Ngallou(1703) | 1312 | | | Illumina | | | |
| SALINE_NAM_9e | Archevir | P8_Ngallou(1704) | 3212 | | | Illumina | | | |
| SALINE_NAM_9f | Archevir | P9_Ngallou(1705) | 529 | | | Illumina | | | |
| SALINE_EUA_10a | Saltern ponds | Saltern medium - 112805 (23) | 39439 | | United_States | Pyrosequencing | Ultra Clean Soil DNA Kit | WI | tBLASTx |
| SALINE_EUA_10b | Saltern ponds | Saltern medium - 111605 (24) | 58319 | | | | | | |
| SALINE_EUA_10c | Saltern ponds | Saltern high - 111605 (25) | 151180 | | | | | | |
| SALINE_EUA_10d | Saltern ponds | Saltern low - 0704 (26) | 268049 | | | | | | |
| SALINE_EUA_10f | Saltern ponds | Saltern low - 111005 (27) | 109836 | | | | | | |
| SALINE_EUA_10g | Saltern ponds | Saltern medium - 111005 (28) | 39348 | | | | | | |
| SALINE_EUA_10h | Saltern ponds | Saltern medium - 112205 (29) | 55142 | | | | | | |
| SALINE_EUA_10i | Saltern ponds | Saltern high - 120705 (30) | 46628 | | | | | | |
| SALINE_EUA_10j | Saltern ponds | Saltern high - 112805 (31) | 4536 | | | | | | |
| SALINE_EUA_10k | Saltern ponds | Saltern low - 112805 (32) | 62363 | | | | | | |
| SALINE_EUA_11a | Freshwater | Tilapia Chanel 1105 (33) | 264844 | United_States | Pyrosequencing | CTAB/ formamide Ultra Clean Soil DNA kit | WI | tBLASTx | |
| SALINE_EUA_11b | Freshwater | Tilapia Channel 0406 (35) | 60135 | | | | | | |
| SALINE_EUA_11c | Freshwater | Tilapia Channel 0806 (36) | 56549 | | | | | | |
| SALINE_EUA_12a | Others | Tampa Bay induced(46) | 279129 | United_States | Pyrosequencing | WI | WI | WI | |

| | | | | | | | | | |
|----------------|---------------------------------------|-----------------------------------|--------|------------------|---|----------------|---|------------------------|--------|
| SALINE_EUA_12b | Others | Salton One (47) | 55467 | | | | | | |
| SALINE_EUA_12c | Others | Salton Sea (46) | 29814 | | | | | | |
| SALINE_EUA_12d | Others | Saltern Ponds fomids (1343) | 42 | | | | | | |
| COLD_GRL_13a | Supraglacial | Cryoconite_viruses_curated (4314) | 546 | Cold Freshwater | Greenland icesheet plus Svalbard cryoconite | Illumina | QIAamp MinElute Virus Spin Kit | CLC Genomics Workbench | Qiime |
| COLD_ATA_14a | Lake limnopolar | Antartic Lake Spring | 4132 | Cold Freshwater | Antartic | Sanger | phenol-chloroform and ethanol precipitated. | WI | BLASTX |
| COLD_ATA_14b | Lake limnopolar | Antartic Lake Summer | 387475 | Cold Freshwater | Antartic | Sanger | phenol-chloroform and ethanol precipitated. | WI | BLASTX |
| HOT_EUA_15a | Yellowstone Hot Springs | Hot Spring Octopus (52) | 22272 | Hyperthermophile | United_States | Sanger | phenol-chloroform and ethanol precipitated. | ManSeq | BLASTx |
| HOT_EUA_15b | Yellowstone Hot Springs | Hot Spring Bear Paw (53) | 8352 | Hyperthermophile | United_States | Sanger | | | |
| HOT_TBV_16a | Brazos-Trinity Basin (IODP site 1320) | Brazos-Trinity 8mbsf (3813) | 270730 | Hyperthermophile | Mexico | Pyrosequencing | WI | WI | WI |

*WI without information

Table S2. Structures of viral proteins derived from structural proteomic approaches or from the analysis of functionally unannotated open reading frames.

| Family or order | Name | Extreme character | PDB ID | Molecule and function | Reference |
|-----------------------|---|-----------------------------|---|---|----------------------|
| <i>Mimiviridae</i> | <i>Megavirus chiliensis</i> | moderate salt | 4XUL (XRAY) | Mg662 (GTP binding protein) | to be published |
| <i>Mimiviridae</i> | <i>Acanthamoeba polyphaga mimivirus</i> | moderate salt | 4Z24, 5, 6 (XRAY) | R135 (outer layer protein, probably aryl alcohol oxidase) | Klose et al., 2015 |
| <i>Nimaviridae</i> | White spot syndrome virus | moderate salt | 2GJ2 (XRAY) 2GJI (NMR) | VP9 (hypothetical DNA binding protein) | Liu et al., 2006 |
| <i>Ligamenvirales</i> | <i>Sulfolobus islandicus</i> rod-shaped virus 1 | high temperature and low pH | 2X5T, G, H, (XRAY) 2X3G (XRAY) 2X48 (XRAY) 2X4I (XRAY) | ORF131 ORF119 ORF55 ORF114a (Scottish Structural Proteomics Facility) | Oke et al., 2010 |
| <i>Ligamenvirales</i> | <i>Acidianus filamentous</i> virus 1 | high temperature and low pH | 3II2, 3, 3ILD, E (XRAY) | ORF157 (nuclease) | Goulet et al., 2010 |
| <i>Ligamenvirales</i> | <i>Acidianus filamentous</i> virus 1 | high temperature and low pH | 3DF6, 3DJW (XRAY) | Afv1-99 (unknown) | Goulet et al., 2009a |
| <i>Ligamenvirales</i> | <i>Acidianus filamentous</i> virus 1 | high temperature and low pH | 2WB6 (XRAY) | Afv1-102 (unknown) | Keller et al., 2009 |
| <i>Ligamenvirales</i> | <i>Sulfolobus islandicus</i> filamentous virus | high temperature and low pH | 2H36 (XRAY) | ORF14 (putative structural protein) | Goulet et al., 2009b |
| <i>Ligamenvirales</i> | <i>Acidianus filamentous</i> virus 3 | high temperature and low pH | 2J6B, C (XRAY) | Afv3-109 (DNA binding protein) | Keller et al., 2007 |
| <i>Globuloviridae</i> | <i>Pyrobaculum spherical</i> virus | high temperature | 2X3M (XRAY) 2X5R (XRAY) 2X4J (XRAY) 2X5C (XRAY) 2VXZ (XRAY) | ORF239 ORF126 ORF137 ORF131 gp04 (Scottish Structural Proteomics Facility) | Oke et al., 2010 |
| <i>Fuselloviridae</i> | <i>Sulfolobus spindle-shape</i> virus 1 | high temperature and low pH | 2VQC (XRAY) | F112 (hypothetical DNA binding protein) | Menon et al., 2008 |
| <i>Fuselloviridae</i> | <i>Sulfolobus spindle-</i> | high temperature | 1SKV (XRAY) | D-63 (hypothetical | Kraft et al., 2004 |

| | | | | | |
|------------------------|------------------------------------|-----------------------------|----------------------------|---------------------------|-----------------------------------|
| | shape virus 1 | and low pH | | adaptor protein) | |
| <i>Bicaudaviridae</i> | Acidianus two-tailed virus | high temperature and low pH | 4ART (XRAY) 4ATS (XRAY) | ORF273 (novel fold) | Felisberto-Rodrigues et al., 2012 |
| <i>Bicaudaviridae</i> | Acidianus two-tailed virus | high temperature and low pH | 3FAJ (XRAY) | P131 (unknown) | to be published |
| <i>satellite virus</i> | <i>Sulfolobus islandicus</i> pSSVx | high temperature and low pH | 3O27 (XRAY) | C68 (DNA binding protein) | Contursi et al., 2011 |

XRAY: obtained by X-ray crystallography; NMR: obtained by Nuclear Magnetic Resonance

References

- Contursi, P., Farina, B., Pirone, L., Fusco, S., Russo, L., Bartolucci, S., Fattorusso, R., Pedone, E. (2014). Structural and functional studies of Stf76 from the *Sulfolobus islandicus* plasmid–virus pSSVx: a novel peculiar member of the winged helix–turn–helix transcription factor family. *Nucleic Acids Research*, 42(9), 5993-6011. doi:10.1093/nar/gku215
- Felisberto-Rodrigues, C., Blangy, S., Goulet, A., Vestergaard, G., Cambillau, C., Garrett, R., Ortiz-Lombardía, M. (2012). Crystal Structure of ATVORF273, a New Fold for a Thermo- and Acido-Stable Protein from the *Acidianus* Two-Tailed Virus. *PLoS ONE*, 7(10), p.e45847. doi:10.1371/journal.pone.0045847.
- Goulet, A., Lichiere, J., Prangishvili, D., van Tilbeurgh, H., Cambillau, C., Campanacci, V. (2010). Structure Of ORF157-K57A From *Acidianus filamentous* Virus 1. *Protein Data Bank, Rutgers University*. doi:10.2210/pdb3ild/pdb.
- Goulet, A., Spinelli, S., Blangy, S., van Tilbeurgh, H., Leulliot, N., Basta, T., Prangishvili, D., Cambillau, C., Campanacci, V. (2009). The thermo- and acido-stable ORF-99 from the archaeal virus AFV1. *Protein Science*, 18(6), 1316-1320. doi:10.1002/pro.122.
- Goulet, A., Spinelli, S., Blangy, S., van Tilbeurgh, H., Leulliot, N., Basta, T., Prangishvili, et al. (2009). The crystal structure of ORF14 from *Sulfolobus islandicus* filamentous virus. *Proteins: Structure, Function, and Bioinformatics*, 76(4), 1020-1022. doi:10.1002/prot.22448.

- Keller, J., Leulliot, N., Cambillau, C., Campanacci, V., Porciero, S., Prangishvilli, D., Forterre, P., et al. (2007). Crystal structure of AFV3-109, a highly conserved protein from crenarchaeal viruses. *Virology Journal*, 4(1), 12. doi:10.1186/1743-422x-4-12.
- Keller, J., Leulliot, N., Collinet, B., Campanacci, V., Cambillau, C., Pranghisvilli, D., van Tilbeurgh, H. (2009). Crystal structure of AFV1-102, a protein from the *Acidianus filamentous* Virus 1. *Protein Science*. NA-NA. doi:10.1002/pro.79.
- Klose, T., Herbst, D., Zhu, H., Max, J., Kenttämä, H., Rossmann, M. (2015). A Mimivirus Enzyme that Participates in Viral Entry. *Structure*, 23(6), 1058-1065. doi:10.1016/j.str.2015.03.023
- Kraft, P., Kummel, D., Oeckinghaus, A., Gauss, G., Wiedenheft, B., Young, M., Lawrence, C. (2004). Structure of D-63 from *Sulfolobus* Spindle-Shaped Virus 1: Surface Properties of the Dimeric Four-Helix Bundle Suggest an Adaptor Protein Function. *Journal of Virology*, 78(14), 7438-7442. doi:10.1128/jvi.78.14.7438-7442.2004.
- Liu, Y., Wu, J., Song, J., Sivaraman, J., Hew, C. (2006). Identification of a Novel Nonstructural Protein, VP9, from White Spot Syndrome Virus: Its Structure Reveals a Ferredoxin Fold with Specific Metal Binding Sites. *Journal of Virology*, 80(21), 10419-10427. doi:10.1128/jvi.00698-06.
- Menon, S., Maaty, W., Corn, G., Kwok, S., Eilers, B., Kraft, P., Gillitzer, E., Young, M., Bothner, B., Lawrence, C. (2008). Cysteine usage in *Sulfolobus* spindle-shaped virus 1 and extension to hyperthermophilic viruses in general. *Virology*, 376(2), 270-278. doi:10.1016/j.virol.2008.03.026.
- Oke, M., Carter, L., Johnson, K., Liu, H., McMahon, S., Yan, X., Kerou, M., et al. (2010). The Scottish Structural Proteomics Facility: targets, methods and outputs. *Journal of Structural and Functional Genomics*, 11(2), 167-180. doi:10.1007/s10969-010-9090-y.

Table S3. Structural proteins from extremophile viruses.

| <i>Family or order</i> | Name | Extreme character | PDB ID | Molecule | Reference |
|---------------------------|--|-----------------------------|----------------------------|---------------------------------------|-------------------------|
| <i>Siphoviridae</i> | marine siphovirus TW1 | moderate salt | 5WK1 (EM) | major capsid protein | Wang et al., 2018 |
| <i>Podoviridae</i> | Procholococcus cyanophage P-SSP7 | moderate salt | 2XD8 (EM) | capsid | Liu et al., 2010 |
| <i>Inoviridae</i> | Thermus phage PH75 | high temperature | 1HGV, Z, 1HH0 (FD) | capsid | Pederson et al., 2001 |
| <i>Sphaerolipoviridae</i> | Thermus virus P23-77 | high temperature | 3ZMN, O, 3ZN4, 5, 6 (XRAY) | VP16 and VP17 capsid proteins | Rissanen et al., 2013 |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 6BO3 (XRAY) | turret protein | to be published |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 3J31 (EM) 4IL7 (XRAY) | virus structural protein | Veesler et al., 2013 |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 4IND (XRAY) | turret | to be published |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 3RKL (XRAY) | structural protein | to be published |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 2BBD (XRAY) | major capsid protein | Khayat et al., 2005 |
| <i>Nimaviridae</i> | White spot syndrome virus | moderate salt | 5HLJ (XRAY) | envelope protein VP24 | Sun et al., 2016 |
| <i>Nimaviridae</i> | White spot syndrome virus | moderate salt | 2ED6, M (XRAY) | major envelope proteins VP26 and VP28 | Tang et al., 2007 |
| <i>Ligamenvirales</i> | Sulfolobus filamentous virus 1 | high temperature and low pH | 6D5F (EM) | virus | Liu et al., 2018 |
| <i>Ligamenvirales</i> | Acidianus filamentous virus 1 | high temperature and low pH | 5W7G (EM) | viral envelope with lipid monolayer | Kasson et al., 2017 |
| <i>Ligamenvirales</i> | Sulfolobus islandicus rod-shaped virus 2 | high temperature and low pH | 3J9X (EM) | virion | DiMaio et al., 2015 |
| <i>Ligamenvirales</i> | Acidianus filamentous virus 1 | high temperature and low pH | 3FBL, Z (XRAY) | coat protein | Goulet et al., 2009 |
| <i>Liigamenvirales</i> | Sulfolobus islandicus rod-shaped virus 1 | high temperature and low pH | 3F2E (XRAY) | coat protein | Szymczynna et al., 2009 |
| <i>Corticoviridae</i> | Pseudoalteromonas | moderate salt | 2W0C (XRAY) | virus | Abrescia et al., 2008 |

| | | | | | |
|-------------------------------|--|-----------------------------|---|---|------------------------|
| | phage PM2 | | 2VVD (XRAY) 2VVE (XRAY) 2VVF (XRAY) | spike protein P1 spike protein P1 capsid protein P2 | |
| <i>Bicaudaviridae</i> | Acidianus tailed spindle virus | high temperature and low pH | 5EQW (XRAY) | major capsid protein | Hochstein et al., 2018 |
| <i>Lavidaviridae</i> | Cafeteriavirus-dependent mavirus (virophage) | moderate salt | 6G41, 2, 3, 4, 5 (XRAY) | major capsid protein, full length and truncated, penton protein | Born et al., 2018 |
| <i>Lavidaviridae</i> | Sputnik virophage 3 | moderate salt | 3J26 (EM) | virus | Zhang et al., 2012 |
| <i>Satellite virus</i> | Sputnik virophage | moderate salt | 3KK5 (EM) | virus | Sun et al., 2009 |

XRAY: obtained by X-ray crystallography; NMR: obtained by Nuclear Magnetic Resonance; EM: obtained by cryo-electron microscopy; FD: obtained by fiber diffraction

References

Abrescia, N., Grimes, J., Kivelä, H., Assenberg, R., Sutton, G., Butcher, S., Bamford, J. et al. (2008). Insights into Virus Evolution and Membrane Biogenesis from the Structure of the Marine Lipid-Containing Bacteriophage PM2. *Molecular Cell*, 31(5), 749-761. doi:10.1016/j.molcel.2008.06.026.

Born, D., Reuter, L., Mersdorf, U., Mueller, M., Fischer, M., Meinhart, A., Reinstein, J. (2018). Capsid protein structure, self-assembly, and processing reveal morphogenesis of the marine virophage mavirus. *Proceedings of the National Academy of Sciences*, 115(28), 7332-7337. doi:10.1073/pnas.1805376115.

DiMaio, F., Yu, X., Rensen, E., Krupovic, M., Prangishvili, D., Egelman, E. (2015). A virus that infects a hyperthermophile encapsidates A-form DNA. *Science*, 348(6237), 914-917. doi:10.1126/science.aaa4181.

Goulet, A., Blangy, S., Redder, P., Prangishvili, D., Felisberto-Rodrigues, C., Forterre, P., Campanacci, V., Cambillau, C. (2009). *Acidianus filamentous virus 1* coat proteins display a helical fold spanning the filamentous archaeal viruses lineage. *Proceedings of the National Academy of Sciences*, 106(50), 21155-21160. doi:10.1073/pnas.0909893106.

- Hochstein, R., Bollschweiler, D., Dharmavaram, S., Lintner, N., Plitzko, J., Bruinsma, R., Engelhardt, H., Young, M., et al. (2018). Structural studies of *Acidianus* tailed spindle virus reveal a structural paradigm used in the assembly of spindle-shaped viruses. *Proceedings of the National Academy of Sciences*, 115(9), 2120-2125. doi:10.1073/pnas.1719180115.
- Kasson, P., DiMaio, F., Yu, X., Lucas-Staat, S., Krupovic, M., Schouten, S., Prangishvili, D., Egelman, E. (2017). Model for a novel membrane envelope in a filamentous hyperthermophilic virus. *eLife*, 6. doi:10.7554/elife.26268.
- Khayat, R., Tang, L., Larson, E., Lawrence, C., Young, M., Johnson, J. (2005). Structure of an archaeal virus capsid protein reveals a common ancestry to eukaryotic and bacterial viruses. *Proceedings of the National Academy of Sciences*, 102(52), 18944-18949. doi:10.1073/pnas.0506383102.
- Liu, X., Zhang, Q., Murata, K., Baker, M., Sullivan, M., Fu, C., Dougherty, M., et al. (2010). Structural changes in a marine podovirus associated with release of its genome into *Prochlorococcus*. *Nature Structural & Molecular Biology*, 17(7), 830-836. doi:10.1038/nsmb.1823.
- Liu, Y., Osinski, T., Wang, F., Krupovic, M., Schouten, S., Kasson, P., et al. (2018). Structural conservation in a membrane-enveloped filamentous virus infecting a hyperthermophilic acidophile. *Nature Communications*, 9(1). doi:10.1038/s41467-018-05684-6.
- Pederson, D., Welsh, L., Marvin, D., Sampson, M., Perham, R., Yu, M., Slater, M. (2001). The protein capsid of filamentous bacteriophage PH75 from *Thermus thermophilus*. *Journal of Molecular Biology*, 309(2), 401-421. doi:10.1006/jmbi.2001.4685.
- Rissanen, I., Grimes, J., Pawlowski, A., Mäntynen, S., Harlos, K., Bamford, J., Stuart, D. (2013). Bacteriophage P23-77 Capsid Protein Structures Reveal the Archetype of an Ancient Branch from a Major Virus Lineage. *Structure*, 21(5), 718-726. doi:10.1016/j.str.2013.02.026.
- Sun, L., Su, Y., Zhao, Y., Fu, Z., Wu, Y. (2016). Crystal Structure of Major Envelope Protein VP24 from White Spot Syndrome Virus. *Scientific Reports*, 6(1). doi:10.1038/srep32309.

Sun, S., La Scola, B., Bowman, V., Ryan, C., Whitelegge, J., Raoult, D., Rossmann, M. (2009). Structural Studies of the Sputnik Virophage. *Journal of Virology*, 84(2), 894-897. doi: 10.1128/JVI.01957-09

Szymczyzna, B., Taurog, R., Young, M., Snyder, J., Johnson, J. and Williamson, J. (2009). Synergy of NMR, Computation, and X-Ray Crystallography for Structural Biology. *Structure*, 17(4), 499-507. doi:10.1016/j.str.2009.03.001.

Tang, X., Wu, J., Sivaraman, J., Hew, C. (2007). Crystal Structures of Major Envelope Proteins VP26 and VP28 from White Spot Syndrome Virus Shed Light on Their Evolutionary Relationship. *Journal of Virology*, 81(12), 6709-6717. doi:10.1128/jvi.02505-06.

Veesler, D., Ng, T., Sendamarai, A., Eilers, B., Lawrence, C., Lok, S., Young, M., Johnson, J., Fu, C. (2013). Atomic structure of the 75 MDa extremophile *Sulfolobus turreted* icosahedral virus determined by CryoEM and X-ray crystallography. *Proceedings of the National Academy of Sciences*, 110(14), 504-5509. doi:10.1073/pnas.1300601110.

Wang, Z., Hardies, S., Fokine, A., Klose, T., Jiang, W., Cho, B., Rossmann, M. (2018). Structure of the Marine Siphovirus TW1: Evolution of Capsid-Stabilizing Proteins and Tail Spikes. *Structure*, 26(2), 238-248.e3. doi:10.1016/j.str.2017.12.001.

Table S4. DNA binding proteins and proteins that bind histones from extremophilic viruses.

| Family or order | Name | Extreme character | PDB ID | molecule | Reference |
|-----------------------|---|-----------------------------|-------------|----------------------------------|------------------------|
| <i>Iridoviridae</i> | Singapore grouper iridovirus | moderate salt | 3RJ2 (XRAY) | H3 binding protein | Tran et al., 2011 |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 2J85 (XRAY) | DNA binding protein | Larson et al., 2007 |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 2CO5 (XRAY) | DNA binding protein | Larson et al., 2007a |
| <i>Nimaviridae</i> | White spot syndrome virus | moderate salt | 2ZUG (XRAY) | histone-binding DNA-like protein | Wang et al., 2008 |
| <i>Ligamenvirales</i> | Acidianus filamentous virus 1 | high temperature and low pH | 2LVH (NMR) | DNA binding protein (Zn finger) | Guilliere et al., 2013 |
| <i>Ligamenvirales</i> | Acidianus filamentous virus 6 | high temperature and low pH | 4HV0 (XRAY) | transcription regulator | Peixeiro et al., 2013 |
| <i>Ligamenvirales</i> | Sulfolobus islandicus rod-shaped virus 1 | high temperature and low pH | 2KEL (NMR) | transcriptional regulator SvtR | Guilliere et al., 2009 |
| <i>Fuselloviridae</i> | Sulfolobus spindle-shape virus 1 | high temperature and low pH | 4LID (XRAY) | DNA binding protein | to be published |
| <i>Fuselloviridae</i> | Sulfolobus islandicus plasmid-virus pSSVx | high temperature and low pH | 2MLG (NMR) | transcription factor Stf76 | Contursi et al., 2014 |
| <i>Fuselloviridae</i> | Sulfolobus virus Ragged Hills | high temperature and low pH | 4AAI (NMR) | DNA binding protein E73 | Schlenker et al., 2012 |
| <i>Fuselloviridae</i> | Sulfolobus spindle-shape virus 1 | high temperature and low pH | 2WBT (XRAY) | zinc finger protein | to be published |
| <i>Fuselloviridae</i> | Sulfolobus spindle-shape virus 1 | high temperature and low pH | 1TBX (XRAY) | DNA binding protein F-93 | Kraft et al., 2004 |

XRAY: obtained by X-ray crystallography; NMR: obtained by Nuclear Magnetic Resonance

References

- Contursi, P., Farina, B., Pirone, L., Fusco, S., Russo, L., Bartolucci, S., Fattorusso, R., Pedone, E. (2014). Structural and functional studies of Stf76 from the *Sulfolobus islandicus* plasmid–virus pSSVx: a novel peculiar member of the winged helix–turn–helix transcription factor family. *Nucleic Acids Research*, 42(9), 5993-6011 doi:10.1093/nar/gku215.
- Guillière, F., Danioux, C., Jaubert, C., Desnoues, N., Delepierre, M., Prangishvili, D., Sezonov, G., Guijarro, J. (2013). Solution Structure of an Archaeal DNA Binding Protein with an Eukaryotic Zinc Finger Fold. *PLoS ONE*, 8(1), p.e52908. doi:10.1371/journal.pone.0052908.
- Guillière, F., Peixeiro, N., Kessler, A., Raynal, B., Desnoues, N., Keller, J., Delepierre, M., Prangishvili, D., et al. (2009). Structure, Function, and Targets of the Transcriptional Regulator SvtR from the Hyperthermophilic Archaeal Virus SIRV1. *Journal of Biological Chemistry*, 284(33), 22222-22237. doi: 10.1074/jbc.M109.029850
- Kraft, P., Oeckinghaus, A., Kummel, D., Gauss, G., Gilmore, J., Wiedenheft, B., Young, M., Lawrence, C. (2004). Crystal Structure of F-93 from *Sulfolobus* Spindle-Shaped Virus 1, a Winged-Helix DNA Binding Protein. *Journal of Virology*, 78(21), 11544-11550. doi:10.1128/jvi.78.21.11544-11550.2004.
- Larson, E., Eilers, B., Menon, S., Reiter, D., Ortmann, A., Young, M., Lawrence, C. (2007). A winged-helix protein from *Sulfolobus turreted* icosahedral virus points toward stabilizing disulfide bonds in the intracellular proteins of a hyperthermophilic virus. *Virology*, 368(2), 249-261. doi.org/10.1016/j.virol.2007.06.040
- Larson, E., Eilers, B., Reiter, D., Ortmann, A., Young, M., Lawrence, C. (2007). A new DNA binding protein highly conserved in diverse crenarchaeal viruses. *Virology*, 363(2), 387-396 doi:10.1016/j.virol.2007.01.027.
- Peixeiro, N., Keller, J., Collinet, B., Leulliot, N., Campanacci, V., Cortez, D., Cambillau, C., Nitta, K., et al. (2012). Structure and Function of AvtR, a Novel Transcriptional Regulator from a Hyperthermophilic Archaeal Lipothrixvirus. *Journal of Virology*, 87(1), 124-136. doi:10.1128/jvi.01306-12.

Schlenker, C., Goel, A., Tripet, B., Menon, S., Willi, T., Dlakić, M., et al. (2012). Structural Studies of E73 from a Hyperthermophilic Archaeal Virus Identify the “RH3” Domain, an Elaborated Ribbon–Helix–Helix Motif Involved in DNA Recognition. *Biochemistry*, 51(13), 2899-2910. doi:10.1021/bi201791s.

Tran, B., Chen, L., Liu, Y., Wu, J., Velazquez-Campoy, A., Sivaraman, J. Hew, C. (2011). Novel Histone H3 Binding Protein ORF158L from the Singapore Grouper Iridovirus. *Journal of Virology*, 85(17), 9159-9166. doi:10.1128/jvi.02219-10.

Wang, H., Wang, H., Ko, T., Lee, Y., Leu, J., Ho, C., Huang, W., Lo, C. and Wang, A. (2008). White spot syndrome virus protein ICP11: A histone-binding DNA mimic that disrupts nucleosome assembly. *Proceedings of the National Academy of Sciences*, 105(52), 20758-20763. doi:10.1073/pnas.0811233106.

Table S5. Enzymes from extremophilic viruses.

| Family or order | Name | Environment | PDB ID | Molecule | Reference |
|------------------------|----------------------------------|----------------------------|-------------------|--|-----------------------|
| <i>Caudovirales</i> | Thermus phage G20c | high temperature | 6IBG (XRAY) | portal protein | Bayfield et al., 2019 |
| <i>Myoviridae</i> | Prochlorococcus phage P-HM1 | moderate salt | 5HI8 (XRAY) | phycobiliprotein lyase | Gasper et al., 2017 |
| <i>Myoviridae</i> | cyanophage S-TIM5 | moderate salt | 4P9C, D, E (XRAY) | deoxycytidylate deaminase | Marx and Alian 2014 |
| <i>Myoviridae</i> | Synechococcus phage S-SSM7 | moderate salt | 3UWA, B (XRAY) | peptide deformylase | Frank et al., 2013 |
| <i>Phycodnaviridae</i> | Ostreococcus tauri virus 2 | moderate salt, high copper | 4B8N (XRAY) | cytochrome b5 | Reid et al., 2013 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 5YEU, T (XRAY) | Cas4-like protein | Dou et al., 2018 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 6AX6, 7 (XRAY) | lysyl hydroxylase | Guo et al., 2018 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 5XC3, 5 (XRAY) | Rab GTPase | Ku et al., 2017 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 5X55 (XRAY) | uracil-DNA glycosylase | Kwon et al., 2017 |
| <i>Mimiviridae</i> | Megavirus chiliensis | moderate salt | 4P37, 4WSE (XRAY) | polyadenylate synthase | Priet et al., 2015 |
| <i>Mimiviridae</i> | Megavirus chiliensis | moderate salt | 4U4I (XRAY) | superoxide dismutase | Lartigue et al., 2014 |
| <i>Mimiviridae</i> | Megavirus chiliensis | moderate salt | 4TQG (XRAY) | UDP-GlcNac 4,6-dehydratase 5-epimerase | Piacente et al., 2014 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 4NRW (XRAY) | DNA glycosylase Nei1-G86D | Prakash et al., 2014 |
| <i>Mimiviridae</i> | Acanthamoeba | moderate salt | 4MB7 (XRAY) | DNA glycosylase | Prakash et al., 2013 |

| | polyphaga mimivirus | | | Nei2 | |
|---------------------|--|---------------|--|--|----------------------|
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 4AMQ (XRAY) | nucleotidyl transferase | to be published |
| <i>Mimiviridae</i> | Megavirus chiliensis | moderate salt | 4AMS (XRAY) | nucleotidyl transferase | to be published |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 3TD7 (XRAY) | sulfhydryl oxidase | Hakim et al., 2012 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 3VK7, 8 (XRAY) | DNA glycosylase Nei1 | Imamura et al., 2012 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 3DKD, 3GPA, 3GP9, 3G2X, 3FCW, 3FCV, 3FC9, 3FBF, 3FBE, 3FBC, 3FBB, 3EVW, 3EVO, 3EVM, 3ETM, 3ENA, 3EMT, 3EM1, 3ELH, 3EJM, 3EIC, 3EE3, 3DDI, 3B6B, 2B8Q, 2B8P (XRAY) | nucleoside diphosphate kinase, wild type and mutants | Jeudy et al., 2009 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 3A42, 5, 6 (XRAY) | DNA glycosylase Nei1 | Imamura et al., 2009 |
| <i>Mimiviridae</i> | Acanthamoeba polyphaga mimivirus | moderate salt | 3GWN (XRAY) | sulfhydryl oxidase | Hakim and Fass, 2009 |
| <i>Iridoviridae</i> | grouper iridovirus | moderate salt | 5VMN, O (XRAY) | Bcl-2 protein apoptosis inhibitor | Banjara et al., 2018 |
| <i>Iridoviridae</i> | grouper iridovirus | moderate salt | 3KHS (XRAY) | purine nucleoside | Kang et al., 2010 |

| | | | | | |
|---------------------|---|-----------------------------|-------------------------|-------------------------|-----------------------|
| | | | | phosphorylase | |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 4R2H, I (XRAY) | DNA packing ATPase B204 | Dellas et al., 2015 |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 2 | high temperature and low pH | 4KFR, S, T, U (XRAY) | DNA packing ATPase B204 | Happonen et al., 2013 |
| <i>Turriviridae</i> | Sulfolobus turreted icosahedral virus 1 | high temperature and low pH | 2C0N (XRAY) | glycosyltransferase | Larson et al., 2006 |
| nimaviridae | White spot syndrome virus | moderate salt | 5Y5O, P, Q (XRAY) | dUTPase | Zang et al., 2018 |
| ligamenvirales | Sulfolobus islandicus rudivirus 3 | high temperature and low pH | 6EXP (XRAY) | anti-CRISPR protein | He et al., 2018 |
| ligamenvirales | Acidianus filamentous virus 1 | high temperature and low pH | 3II2, 3, 3ILD, E (XRAY) | nuclease ORF157 | Goulet et al., 2010 |
| fuselloviridae | Sulfolobus spindle-shape virus 1 | high temperature and low pH | 3VCF, 4DKS (XRAY) | integrase | Zhan et al., 2012 |
| fuselloviridae | Sulfolobus spindle-shape virus 1 | high temperature and low pH | 3UXU (XRAY) | integrase | Eilers et al., 2012 |
| fuselloviridae | Sulfolobus virus Ragged Hills | high temperature and low pH | 2W8M (XRAY) | PD-(D/E)XK nuclease | Menon et al., 2010 |

XRAY: obtained by X-ray crystallography

References

- Banjara, S., Mao, J., Ryan, T., Caria, S., Kvensakul, M. (2018). Grouper iridovirus GIV66 is a Bcl-2 protein that inhibits apoptosis by exclusively sequestering Bim. *Journal of Biological Chemistry*, 293(15), 5464-5477. doi:10.1074/jbc.ra117.000591.
- Bayfield, O., Klimuk, E., Winkler, D., Hesketh, E., Chechik, M., Cheng, N., Dykeman, E., et al. (2019). Cryo-EM structure and in vitro DNA packaging of a thermophilic virus with supersized T=7 capsids. *Proceedings of the National Academy of Sciences*, 116(9), 3556-3561 doi: 10.1073/pnas.1813204116

Dellas, N., Snyder, J., Dills, M., Nicolay, S., Kerchner, K., Brumfield, S., Lawrence, C., Young, M. (2015). Structure-Based Mutagenesis of Sulfolobus Turreted Icosahedral Virus B204 Reveals Essential Residues in the Virion-Associated DNA-Packaging ATPase. *Journal of Virology*, 90(6), 2729-2739. doi:10.1128/jvi.02435-15.

Dou, C., Yu, M., Gu, Y., Wang, J., Yin, K., Nie, C., Zhu, X., Qi, S., Wei, Y., Cheng, W. (2018). Structural and Mechanistic Analyses Reveal a Unique Cas4-like Protein in the Mimivirus Virophage Resistance Element System. *Science*, 3, 1-10. doi:10.1016/j.isci.2018.04.001.

Eilers, B., Young, M., Lawrence, C. (2012). The Structure of an Archaeal Viral Integrase Reveals an Evolutionarily Conserved Catalytic Core yet Supports a Mechanism of DNA Cleavage in trans. *Journal of Virology*, 86(15), 8309-8313. doi:10.1128/jvi.00547-12.

Frank, J., Lorimer, D., Youle, M., Witte, P., Craig, T., Abendroth, J., Rohwer, F., Edwards, R., Segall, A., Burgin, A. (2013). Structure and function of a cyanophage-encoded peptide deformylase. *The ISME Journal*, 7(6), 1150-1160. doi:10.1038/ismej.2013.4.

Frank, J., Lorimer, D., Youle, M., Witte, P., Craig, T., Abendroth, J., Rohwer, F., et al. (2013). Structure and function of a cyanophage-encoded peptide deformylase. *The ISME Journal*, 7(6), 1150-1160. doi: 10.1007/s00705-017-3510-2

Gasper, R., Schwach, J., Hartmann, J., Holtkamp, A., Wiethaus, J., Riedel, N., Hofmann, E., Frankenberg-Dinkel, N. (2017). Distinct Features of Cyanophage-encoded T-type Phycobiliprotein Lyase Φ CpeT. *Journal of Biological Chemistry*, 292(8), 3089-3098. doi:10.1074/jbc.m116.769703

Goulet, A., Pina, M., Redder, P., Prangishvili, D., Vera, L., Lichiere, J., Leulliot, N., et al. (2010). ORF157 from the Archaeal Virus Acidianus Filamentous Virus 1 Defines a New Class of Nuclease. *Journal of Virology*, 84(10), 5025-5031. doi:10.1128/jvi.01664-09.

Guo, H., Tsai, C., Terajima, M., Tan, X., Banerjee, P., Miller, M., Liu, X., Yu, J., Byemerwa, J., et al. (2018). Pro-metastatic collagen lysyl hydroxylase dimer assemblies stabilized by Fe²⁺-binding. *Nature Communications*, 9(1). doi:10.1038/s41467-018-02859-z.

Hakim, M., Ezerina, D., Alon, A., Vonshak, O., Fass, D. (2012). Exploring ORFan Domains in Giant Viruses: Structure of Mimivirus Sulfhydryl Oxidase R596. *PLoS ONE*, 7(11), p.e50649. doi:10.1371/journal.pone.0050649.

- Happonen, L., Oksanen, E., Liljeroos, L., Goldman, A., Kajander, T., Butcher, S. (2013). The Structure of the NTPase That Powers DNA Packaging into Sulfolobus Turreted Icosahedral Virus 2. *Journal of Virology*, 87(15). 8388-8398. doi:10.1128/jvi.00831-13.
- He, F., Bhoobalan-Chitty, Y., Van, L., Kjeldsen, A., Dedola, M., Makarova, K., Koonin, E., Brodersen, D. et al, (2018). Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. *Nature Microbiology*, 3(4), 461-469. doi:10.1038/s41564-018-0120-z.
- Imamura, K., Averill, A., Wallace, S., Doublé, S. (2011). Structural Characterization of Viral Ortholog of Human DNA Glycosylase NEIL1 Bound to Thymine Glycol or 5-Hydroxyuracil-containing DNA. *Journal of Biological Chemistry*, 287(6).4288-4298. doi:10.1074/jbc.m111.315309.
- Jeudy, S., Lartigue, A., Claverie, J., Abergel, C. (2009). Dissecting the Unique Nucleotide Specificity of Mimivirus Nucleoside Diphosphate Kinase. *Journal of Virology*, 83(14). 7142-7150. doi:10.1128/jvi.00511-09
- Kang, Y., Zhang, Y., Allan, P., Parker, W., Ting, J., Chang, C., Ealick, S. (2010). Structure of grouper iridovirus purine nucleoside phosphorylase. *Acta Crystallographica Section D Biological Crystallography*, 66(2).155-162. doi:10.1107/s0907444909048276.
- Ku, B., You, J., Oh, K., Yun, H., Lee, H., Shin, H., Jung, J., Shin, Y., Kim, S. (2017). Crystal structures of two forms of the Acanthamoeba polyphaga mimivirus Rab GTPase. *Archives of Virology*, 162(11). 3407-3416. doi:10.1007/s00705-017-3510-2.
- Ku, B., You, J., Oh, K., Yun, H., Lee, H., Shin, H., Jung, J., Shin, Y., Kim, S. (2017). Crystal structures of two forms of the Acanthamoeba polyphaga mimivirus Rab GTPase. *Archives of Virology*, 162(11), 3407-3416.
- Kwon, E., Pathak, D., Chang, H. and Kim, D. (2017). Crystal structure of mimivirus uracil-DNA glycosylase. *PLOS ONE*, 12(8),0182382. doi:10.1371/journal.pone.0182382.
- Larson, E., Reiter, D., Young, M., Lawrence, C. (2006). Structure of A197 from Sulfolobus Turreted Icosahedral Virus: a Crenarchaeal Viral Glycosyltransferase Exhibiting the GT-A Fold. *Journal of Virology*, 80(15).7636-7644. doi:10.1128/jvi.00567-06.

- Lartigue, A., Burlat, B., Coutard, B., Chaspoul, F., Claverie, J., Abergel, C. (2014). The Megavirus Chilensis Cu,Zn-Superoxide Dismutase: the First Viral Structure of a Typical Cellular Copper Chaperone-Independent Hyperstable Dimeric Enzyme. *Journal of Virology*, 89(1),824-832. doi:10.1128/jvi.02588-14.
- Marx, A., Alian, A. (2014). The First Crystal Structure of a dTTP-bound Deoxycytidylate Deaminase Validates and Details the Allosteric-Inhibitor Binding Site. *Journal of Biological Chemistry*, 290(1). 682-690. doi:10.1074/jbc.m114.617720.
- Menon, S., Eilers, B., Young, M., Lawrence, C. (2010). The Crystal Structure of D212 from Sulfolobus Spindle-Shaped Virus Ragged Hills Reveals a New Member of the PD-(D/E)XK Nuclease Superfamily. *Journal of Virology*, 84(12). 5890-5897. doi:10.1128/jvi.01663-09.
- Piacente, F., De Castro, C., Jeudy, S., Molinaro, A., Salis, A., Damonte, G., Bernardi, C., et al. (2014). Giant Virus Megavirus chilensis Encodes the Biosynthetic Pathway for Uncommon Acetamido Sugars. *Journal of Biological Chemistry*, 289(35), 24428-24439. doi:10.1074/jbc.m114.588947.
- Prakash, A., Carroll, B., Sweasy, J., Wallace, S., Doublé, S. (2014). Genome and cancer single nucleotide polymorphisms of the human NEIL1 DNA glycosylase: Activity, structure, and the effect of editing. *DNA Repair*, 14,17-26. doi:10.1016/j.dnarep.2013.12.003.
- Priet, S., Lartigue, A., Debart, F., Claverie, J., Abergel, C. (2015). mRNA maturation in giant viruses: variation on a theme. *Nucleic Acids Research*, 43(7). 3776-3788. doi:10.1093/nar/gkv224.
- Reid, E., Weynberg, K., Love, J., Isupov, M., Littlechild, J., Wilson, W., Kelly, S., Lamb, D., Allen, M. (2013). Functional and structural characterisation of a viral cytochrome b5. *FEBS Letters*, 587(22),3633-3639. doi:10.1016/j.febslet.2013.09.035.
- Zang, K., Li, F., Ma, Q. (2017). The dUTPase of white spot syndrome virus assembles its active sites in a noncanonical manner. *Journal of Biological Chemistry*, 293(3),1088-1099. doi:10.1074/jbc.m117.815266.
- Zhan, Z., Ouyang, S., Liang, W., Zhang, Z., Liu, Z., Huang, L. (2012). Structural and functional characterization of the C-terminal catalytic domain of SSV1 integrase. *Acta Crystallographica Section D Biological Crystallography*, 68(6),659-670. doi:10.1107/s0907444912007202.