

Molecular Insights in the Cleavage of Rubber by the Latex-Clearing-Protein (Lcp) of *Streptomyces* sp. strain K30

Supplementary material

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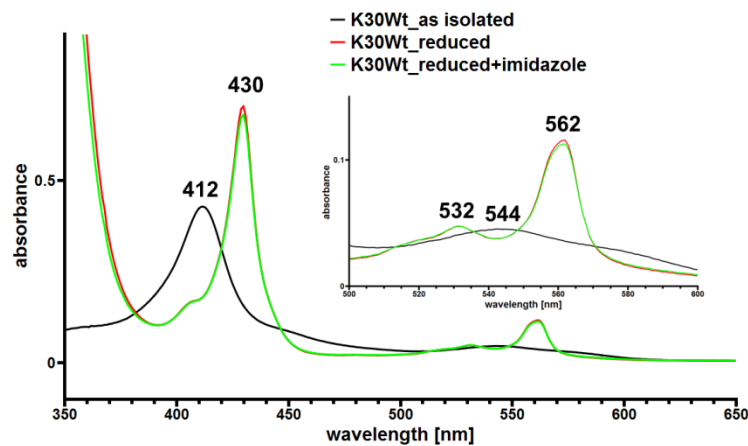
1. Alignment of 1280 DUF2236 amino acid sequences
2. UVvis spectra
3. Graphs of the oxygen consumption assays
4. HPLC chromatograms of separated polyisoprene cleavage products
5. List of amino acid sequence identifiers

1. Multi-sequence alignment of 1280 amino acid sequences containing the domain of unknown function DUF2236. 6598 sequences containing the DUF2236 were accessible with the identifier IPR018713 in the interpro database (June 2016). The first 1500 prokaryotic sequences were used and sequences shorter than 250 and longer than 450 residues were removed. This led to 1280 sequences that were used for a multiple sequence alignment (Clustal Omega). The sequences of Lcp_{K30}, Lcp_{Rf} and Lcp_{VH2} are provided for comparison, numbering refers to Lcp_{K30}. Values of conservation > 80 % were observed for residues R164, T168 and H198. The degree of conservation of each residue is represented by the height of the column.

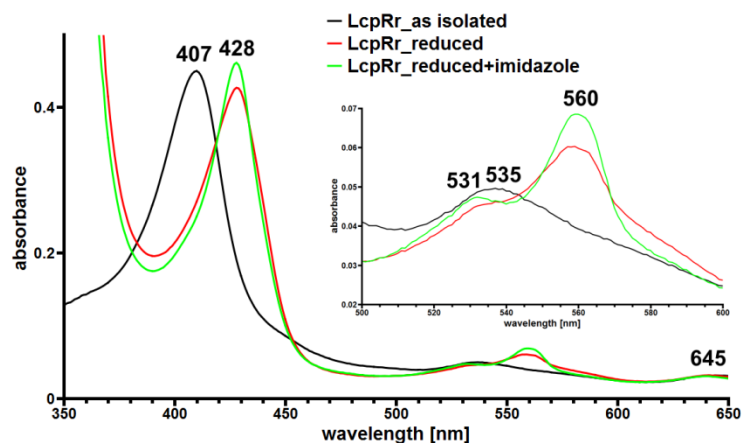


2. **UVvis spectra of Lcp_{K30} wild type (from *Streptomyces* sp. K30), Lcp_{Rr} (from *R. rhodochrous* PRK1) and the Lcp_{K30} mutants purified in this study.** Black lines refer to the *as isolated* states, red lines to the states after reduction with sodium dithionite and green lines to the spectra that were recorded after the addition of 10 mM imidazole to the reduced protein and incubation for 10 to 15 minutes at room temperature. The Q-band region is enlarged in the insets for the heme-containing mutants.

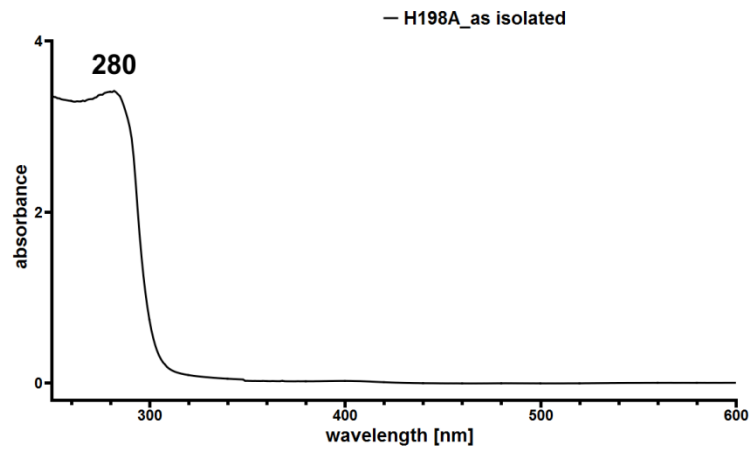
a. **Lcp_{K30} wild type.** In the *as isolated* state (black), a strong absorbance at 412 nm was observed (Soret band) as well as a 544 nm β -band. After chemical reduction (red line) a shift of the Soret band to 430 nm was detected and the Q-bands absorbed at 532 nm (β) and 562 nm (α). Addition of imidazole (green line) resulted in no increase of absorbance at 430 and 562 nm, indicating no accessibility for imidazole to the heme site and thereby suggesting a heme coordination by two axial amino acid heme ligands (closed state).



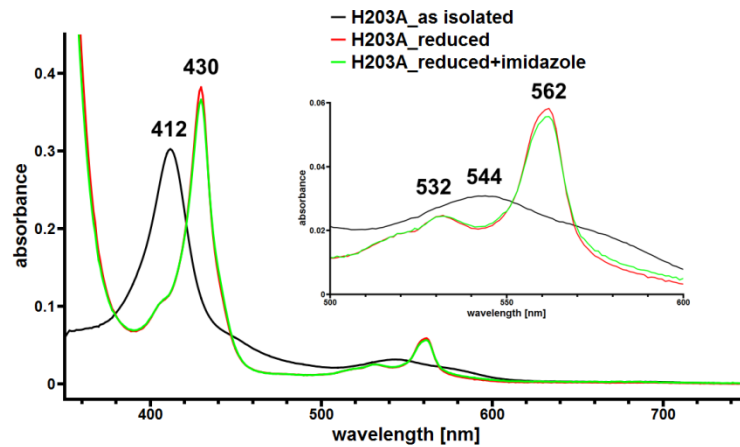
b. **Lcp_{Rr} wild type.** In the *as isolated* state (black) the Soret α band showed a maximum at 407 nm as well as a 535 nm band. After chemical reduction (red line) a shift to 428 nm occurs and the Q bands had maxima at 531 and 560 nm. A strong increase of absorbance at 430 and 560 nm after addition of imidazole (green line) was observed, indicating an open, accessible state suggesting the absence of an amino acid as a second heme ligand.



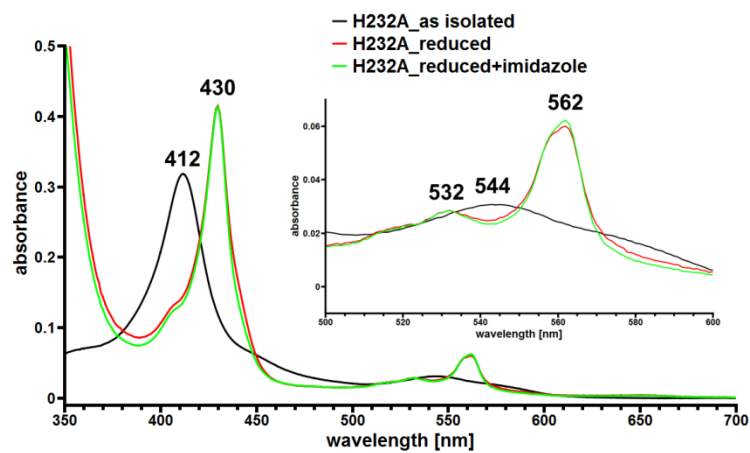
- c. **Lcp_{K30} mutain H198A**. In the *as isolated* state (black line) only a strong absorbance at 280 but no Soret band (absorbance around 400 nm) was observed, indicating the absence of heme.



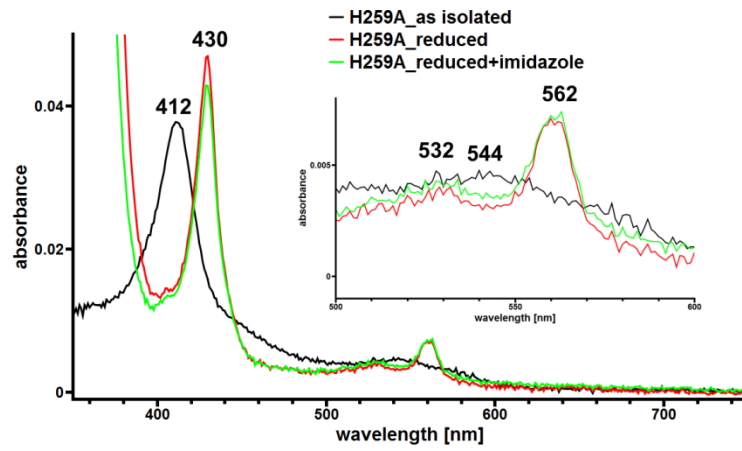
- d. **Lcp_{K30} mutain H203A**. Spectrum comparable to Lcp_{K30} wild type



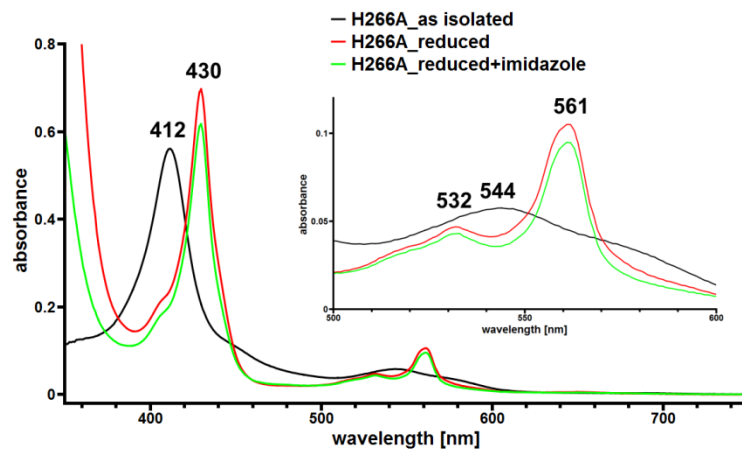
- Lcp_{K30} mutain H232A**. Spectrum comparable to Lcp_{K30} wild type.



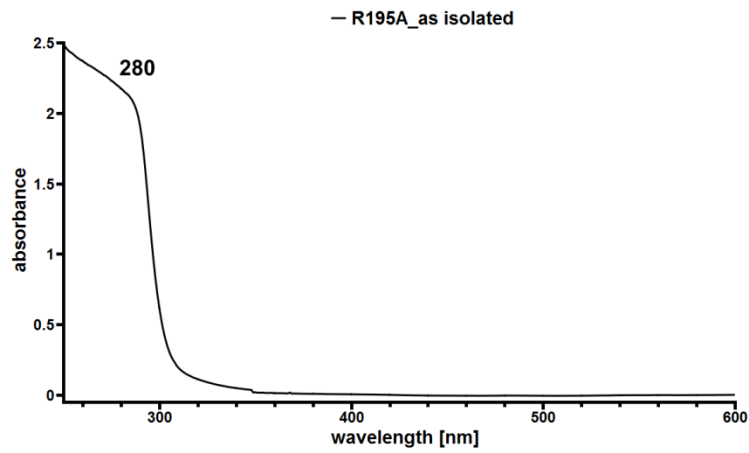
- e. **Lcp_{K30} mutain H259A**. Spectrum comparable to Lcp_{K30} wild type. Due to low yield, only a small amount of the protein was used for spectroscopic characterization.



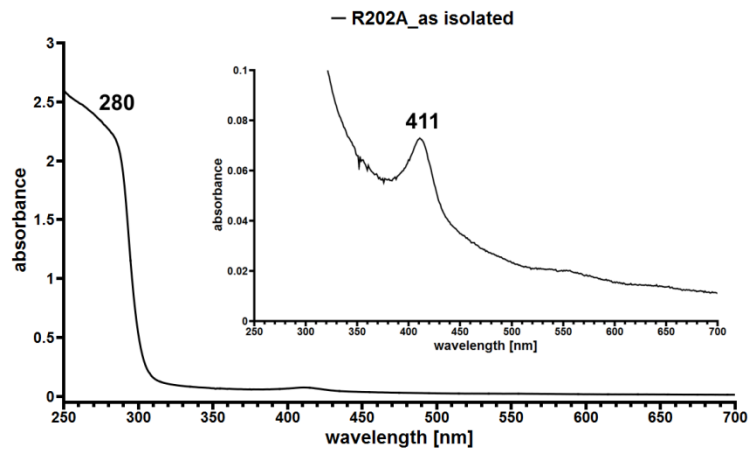
- f. **Lcp_{K30} mutain H266A**. Spectrum comparable to Lcp_{K30} wild type.



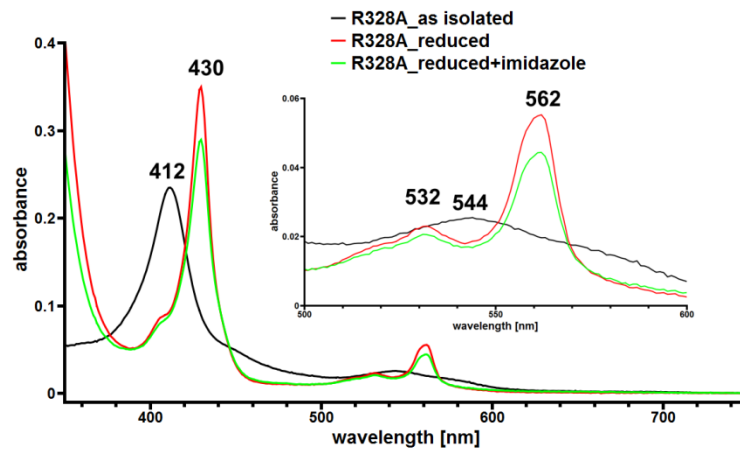
- g. **Lcp_{K30} mutein R195A**. In the *as isolated* state (black line) only a strong absorbance at 280 nm but no Soret band (absorbance around 400 nm) was observed, indicating the absence of heme.



- h. **Lcp_{K30} mutein R202A**. In the *as isolated* state (black line) a strong absorbance at 280 nm and a very weak Soret band (weak absorbance around 411 nm) was observed, indicating the presence of heme in only a minor fraction of mutein molecules. Due to instability of the Lcp_{K30} mutein R202A no spectra after reduction or with the potential heme ligand imidazole were recorded.

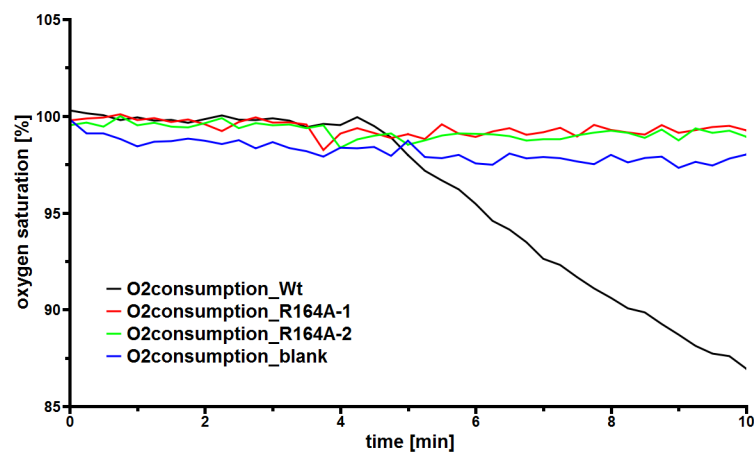


- i. **Lcp_{K30} mutain R328A**. Spectrum comparable to Lcp_{K30} wild type. The slight decrease in absorption after addition of imidazole can be explained by partial degradation of the protein upon the addition of dithionite.

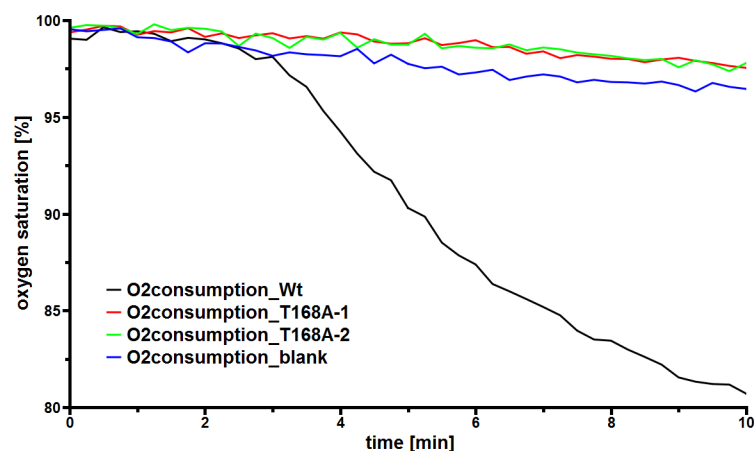


3. Oxygen consumption assays during polyisoprene cleavage. The degree of oxygen saturation of potassium phosphate buffer supplemented with 0.2% polyisoprene latex was recorded at 22°C in four cuvettes equipped with fluorescence sensor spots and the oxy-4-mini apparatus. After a constant oxygen concentration was recorded (3-5 min), 4 µg of the indicated purified protein (if not stated otherwise, blank without enzyme) was added. Assays with two cuvettes supplemented with the same mutein (A-1, A-2) were repeated at least three times; one representative data set is shown. Black line refers to activity of wild type Lcp_{K30} in all assays.

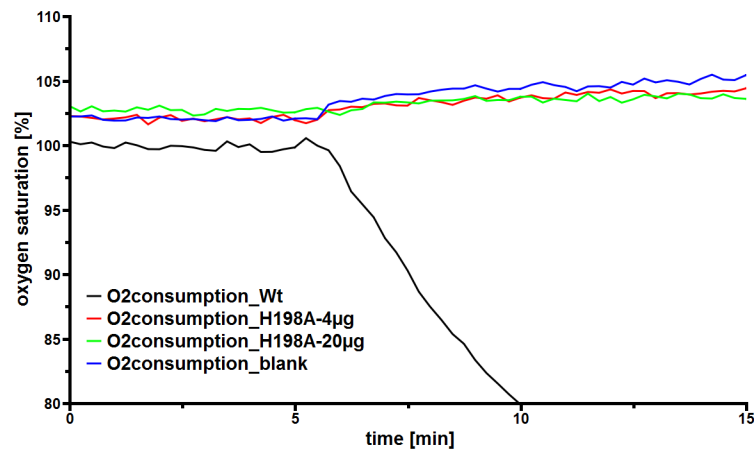
- a. **Lcp_{K30} R164A**, DUF 2236 residue, red, heme containing mutein albeit no consumption of oxygen was observed, indicating inactivity of the mutein and identifying Lcp_{K30} R164A as an essential residue for the catalytic mechanism. (Note: no residual activity could be shown by HPLC analysis).



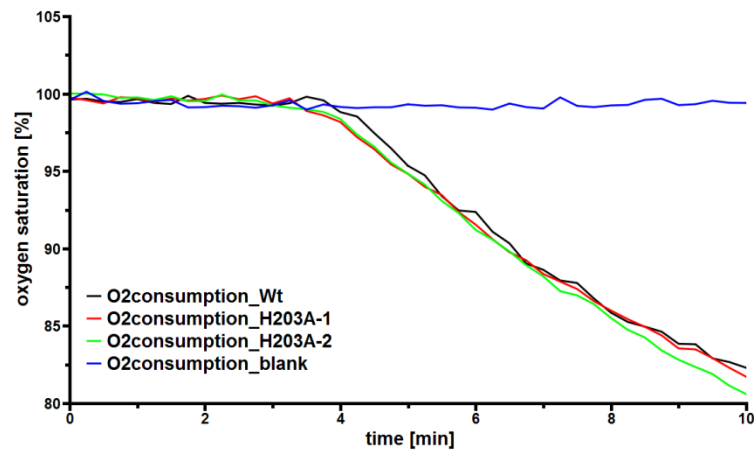
- b. **Lcp_{K30} T168A**, DUF 2236 residue, red, heme containing mutein albeit no consumption of oxygen was observed, indicating inactivity or very low activity of the mutein and identifying Lcp_{K30} T168A as an important residue for the catalytic mechanism. (Note: minor residual activity shown by HPLC analysis).



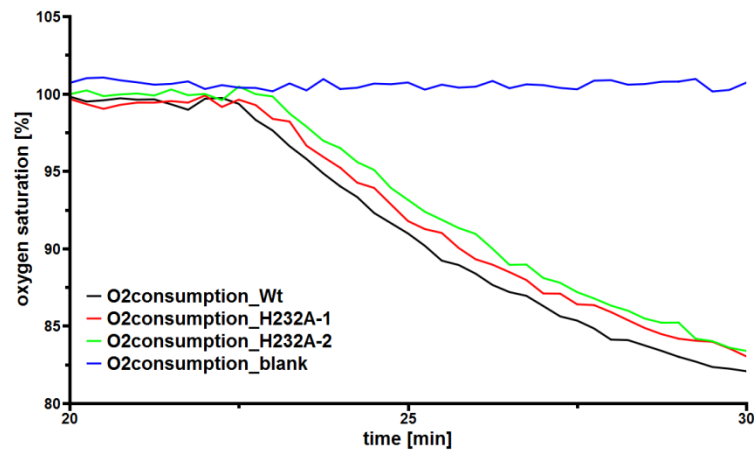
- c. **Lcp_{K30} H198A**, colorless mutain containing no heme group. No consumption of oxygen was observed for 4 and 20 μg enzyme, indicating inactivity of the mutain. (Note: no residual activity could be shown by HPLC analysis).



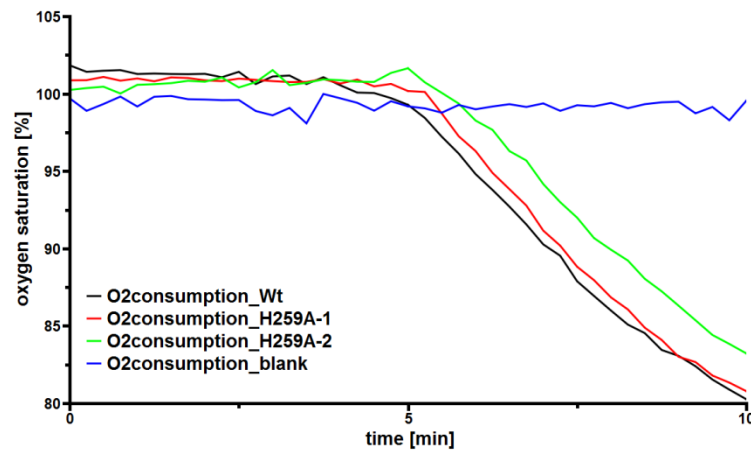
- d. **Lcp_{K30} H203A**, red, heme containing mutain showing consumption of oxygen comparable to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



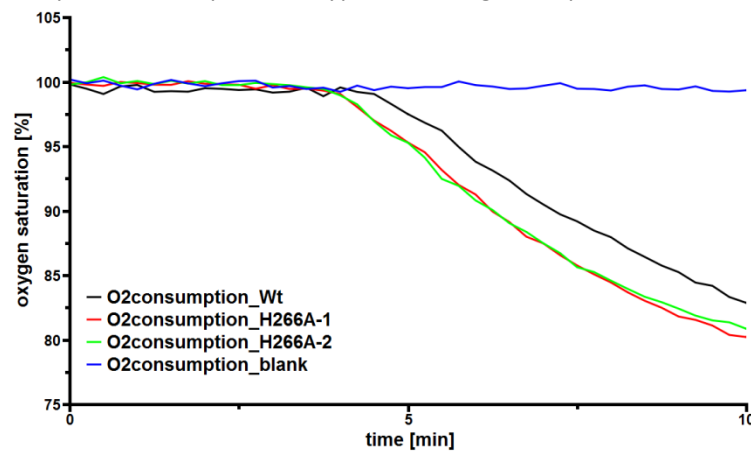
- e. **Lcp_{K30} H232A**, red, heme containing mutain showing consumption of oxygen comparable to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



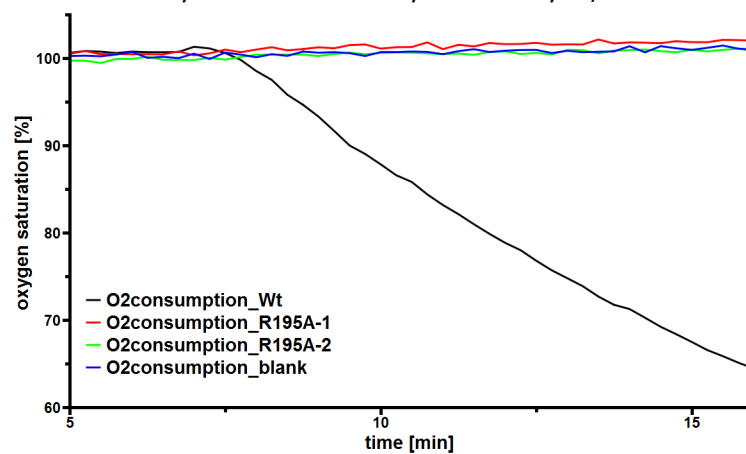
- f. **Lcp_{K30} H259A**, red, heme containing mutain showing consumption of oxygen comparable to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



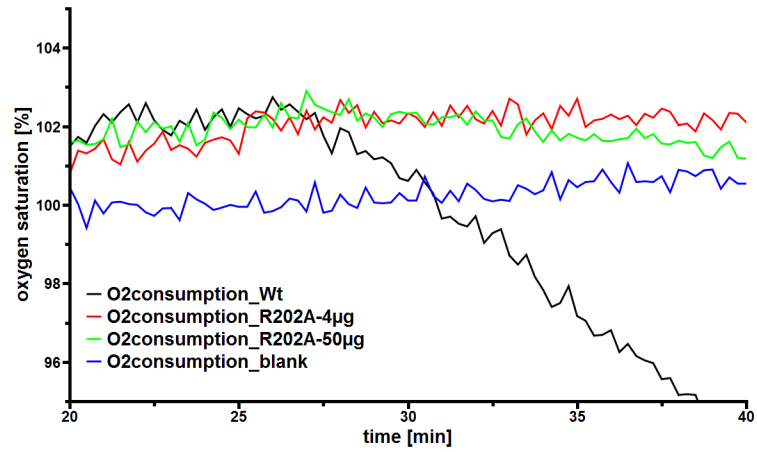
- g. **Lcp_{K30} H266A**, red, heme containing mutain showing consumption of oxygen comparable to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



- h. **Lcp_{K30} R195A**, instable, colorless mutain not containing a heme group and no consumption of oxygen was observed, indicating inactivity of the mutain. (Note: no residual activity could be shown by HPLC analysis).

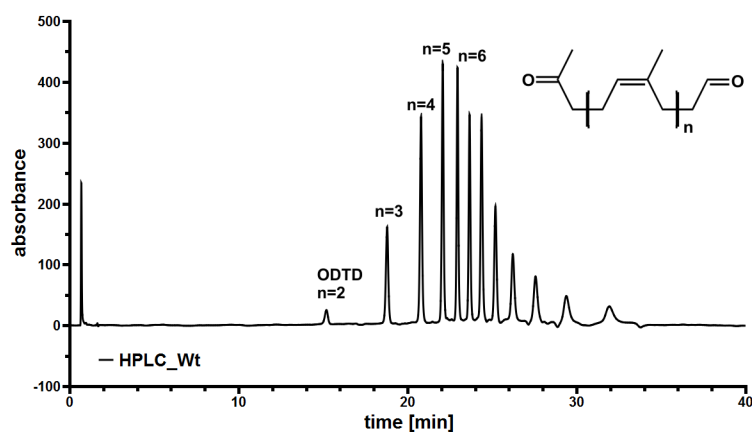


- i. **Lcp_{K30} R202A**, instable mutain. Only a few molecules of the mutain protein contained a heme group as revealed by a very weak Soret band. Only very low consumption of oxygen was observed even for 50µg enzyme. (Note: a minor residual activity could be shown by HPLC analysis for 50 µg enzyme).

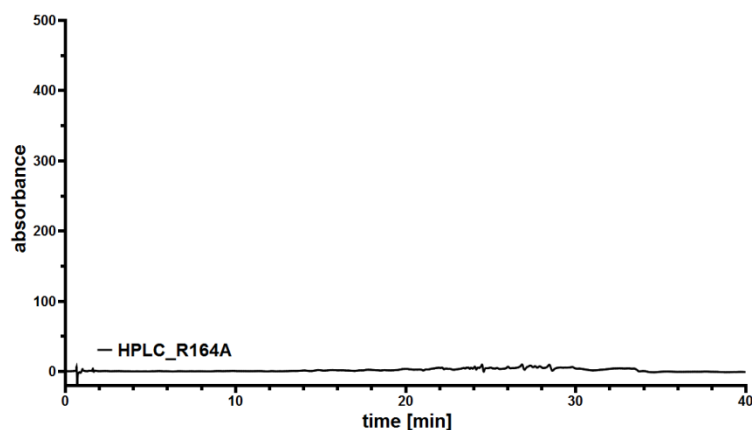


4. **HPLC chromatograms of Lcp_{K30}-generated cleavage products.** 4 µg of each enzyme was incubated in 1 ml potassium phosphate buffer supplemented with 0.2% latex for 2 hours at 22°C (for R164A and R195A, 25µg, for H198A 20 µg were incubated for 16 hours, in case of R202A, 50µg were used for 16 hours). The reaction mixtures were extracted with ethyl acetate after incubation and the solvent was evaporated. The formed cleavage products were dissolved in 100 µl methanol and analyzed by HPLC (RP8 column and methanol:water gradient from 50 to 100 % methanol, detection at 210nm). A blank without enzyme was prepared and was subtracted from the chromatogram with protein. Lcp_{K30} wild type served as positive control. For the wild type, the chemical formula of the formed oligo-isoprenoids with varying number (n=2 to 6) of isoprene units is shown.

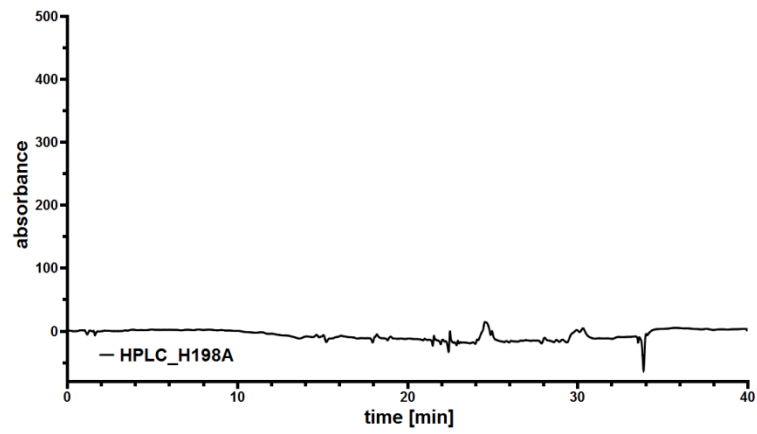
- a. **Lcp_{K30} wild type**, red, heme containing protein producing oligo-isoprenoids with varying number of isoprene units (n=2 to 6) resulting in a typical pattern that indicated a random (endo) cleavage mechanism.



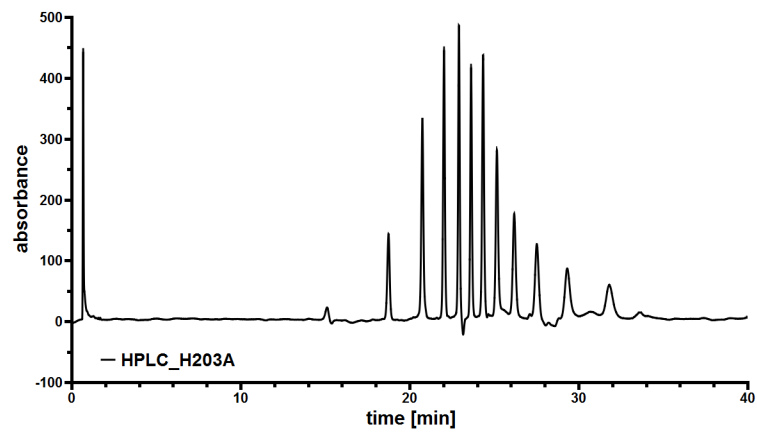
- b. **Lcp_{K30} R164A**, DUF2236 residue, red, heme containing. 25 µg were incubated for 16 hours but no cleavage products could be observed identifying R164A as an essential residue for the catalytic reaction.



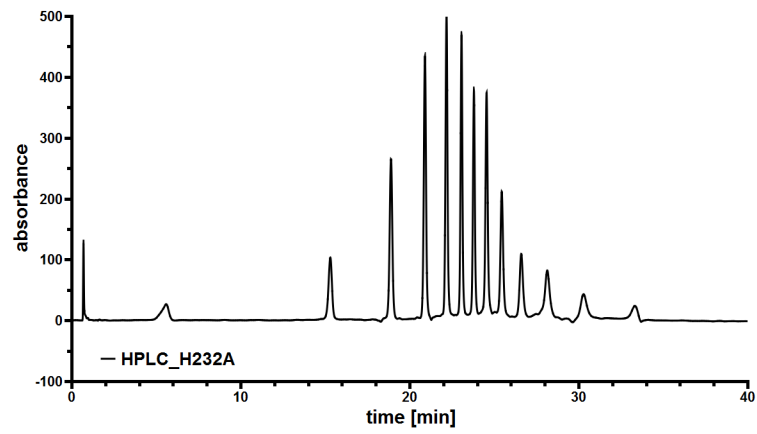
- c. **Lcp_{K30} H198A**, DUF2236 residue, colorless, containing no heme. 20 µg were incubated for 16 hours but no cleavage products could be observed identifying H198A as an essential residue for the catalytic reaction.



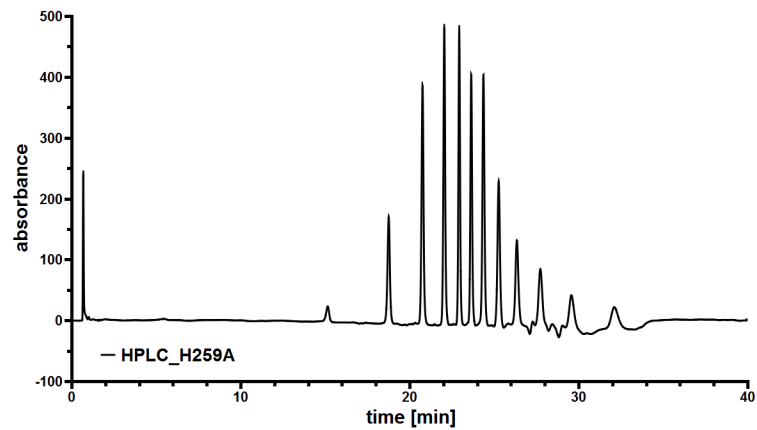
- d. **Lcp_{K30} H203A**, red, heme containing mutain showing a pattern of separated polyisoprene cleavage products similar to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



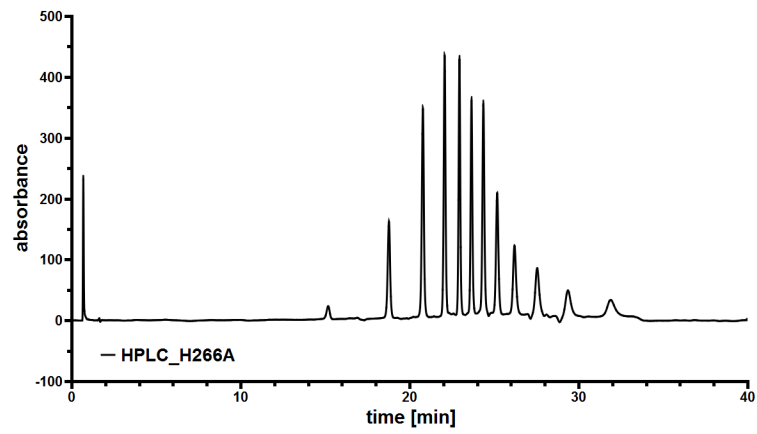
- e. **Lcp_{K30} H232A**, red, heme containing mutain showing a pattern of separated polyisoprene cleavage products similar to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



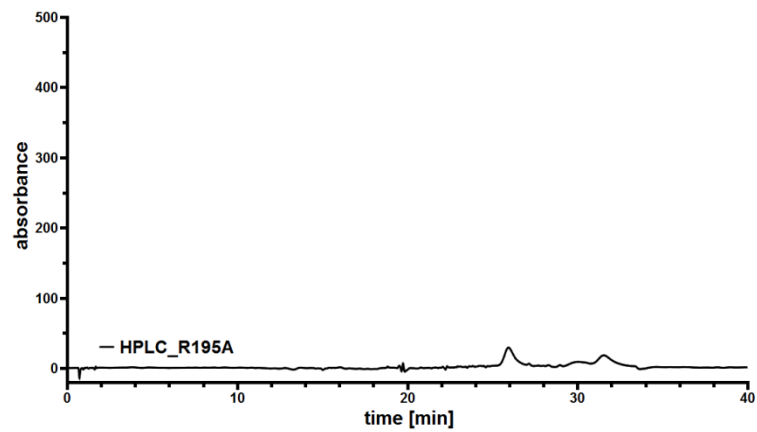
- f. **Lcp_{K30} H259A**, red, heme containing mutain showing a pattern of separated polyisoprene cleavage products similar to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



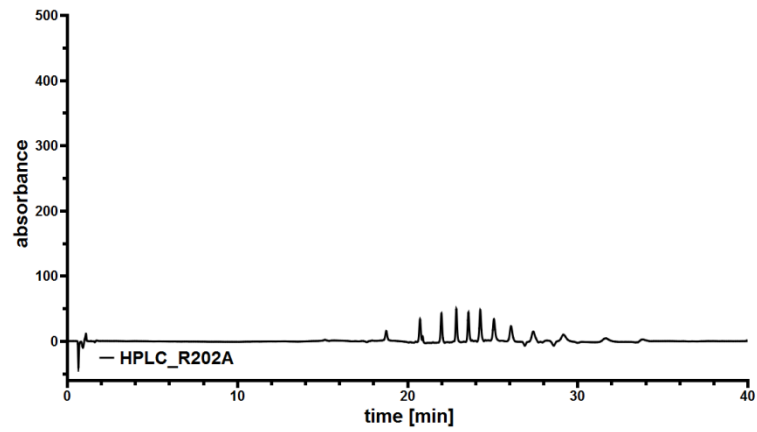
- g. **Lcp_{K30} H266A**, red, heme containing mutain showing a pattern of separated polyisoprene cleavage products similar to Lcp_{K30} wild type indicating no importance for the catalytic mechanism.



- h. **Lcp_{K30} R195A**, colorless, instable mutain containing no heme. 25 μ g were incubated for 16 hours but no cleavage products could be observed.



- i. **Lcp_{K30} R202A**, instable mutein. Only a few molecules of the mutein contained a heme group as revealed a very weak Soret band. 50 µg were incubated for 16 hours and a very low yield of cleavage products with the same pattern as observed for Lcp_{K30} wild type could be observed being in agreement with the observed instability of the mutein.



5. List of amino acid sequence identifiers used for the multiple sequence alignments.

1280 identifiers of the sequences containing the DUF2236 used for Figure S1.

LcpK30/1-407	A0A0F5F7H9/1-291	A0A0E4AD53/1-305	A0A0E2CJ5/1-372
LcpRR/1-408	A0A0F5ADN0/1-311	A0A0E4ACI5/1-289	A0A0E2BS74/1-372
LcpVH2/1-407	A0A0F4Z2N9/1-330	A0A0E4A2K6/1-298	A0A0E2B030/1-372
Q3L8N0/1-407	A0A0F4YVV3/1-442	A0A0E4A1N6/1-285	A0A0E1WB16/1-318
P9WLH1/1-255	A0A0F4YNW3/1-478	A0A0E3ZKL6/1-289	A0A0E1UF60/1-318
P9WLH0/1-255	A0A0F4VF63/1-290	A0A0E3YQ18/1-317	A0A0E1U788/1-318
P64958/1-255	A0A0F4TIR6/1-290	A0A0E3YAK1/1-328	A0A0E1SB74/1-318
A0A0G2ZT22/1-375	A0A0F4T3B4/1-290	A0A0E3XTQ0/1-341	A0A0E1PVB1/1-404
A0A0G2ZSQ0/1-384	A0A0F4STK4/1-290	A0A0E3XTK1/1-393	A0A0E1JV39/1-404
A0A0G2ZL99/1-335	A0A0F4KBM2/1-297	A0A0E3XS80/1-452	A0A0E1EFV2/1-288
A0A0G2ZID7/1-446	A0A0F4K6B5/1-304	A0A0E3XRP7/1-449	A0A0E1CIB1/1-296
A0A0G2ZE11/1-380	A0A0F4JX08/1-458	A0A0E3XQL1/1-454	A0A0E1B570/1-293
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A0A0G2ENY3/1-425	A0A0F4J5T5/1-317	A0A0E3VG69/1-316	A0A0D9P545/1-301
A0A0G0A0W7/1-425	A0A0F4IZF3/1-293	A0A0E3VD89/1-291	A0A0D9NXA7/1-385
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A0A0F7T237/1-297	A0A0F3I7Q3/1-310	A0A0E3TRS7/1-348	A0A0D9ARQ5/1-291
A0A0F7TTD8/1-460	A0A0F3GG30/1-290	A0A0E3TRS3/1-405	A0A0D9A7G0/1-290
A0A0F7TLJ8/1-302	A0A0F2T673/1-416	A0A0E3TRQ2/1-369	A0A0D8I4Y2/1-416
A0A0F7THL6/1-400	A0A0F2SYL7/1-387	A0A0E3TR57/1-270	A0A0D8I4V0/1-305
A0A0F7NHH7/1-487	A0A0F2RMR0/1-303	A0A0E3TQ83/1-327	A0A0D8I3Z8/1-298
A0A0F7N124/1-304	A0A0F2QH58/1-441	A0A0E3TP53/1-366	A0A0D8I2X5/1-409
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A0A0F7FU02/1-480	A0A0F2GF99/1-351	A0A0E3BM07/1-372	A0A0D8HS83/1-298
A0A0F7EST6/1-291	A0A0F2GAK6/1-294	A0A0E2YYY7/1-308	A0A0D8HQH3/1-313
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A0A0F5N4D7/1-307	A0A0F0E9F9/1-298	A0A0E2WK04/1-334	A0A0D7CMX9/1-392
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A0A0F5N1V8/1-442	A0A0E9ZFS6/1-289	A0A0E2WF13/1-321	A0A0D7CI92/1-275
A0A0F5N0G4/1-262	A0A0E9NRE9/1-467	A0A0E2WDJ4/1-317	A0A0D7CGZ7/1-293
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A0A0F5MYT7/1-372	A0A0E9MMT4/1-289	A0A0E2WBD8/1-357	A0A0D6WLY9/1-301
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A0A0F5MWM1/1-402	A0A0E4GZA3/1-270	A0A0E2GG39/1-404	A0A0D6ULS8/1-297
A0A0F5MW64/1-318	A0A0E4GXR2/1-391	A0A0E2G7Z9/1-372	A0A0D6ULD4/1-320
A0A0F5MUQ6/1-304	A0A0E4GV91/1-302	A0A0E2E469/1-372	A0A0D6SY46/1-291
A0A0F5MSW4/1-277	A0A0E4FX2/1-316	A0A0E2D362/1-372	A0A0D6SR34/1-292
A0A0F5K5G4/1-296	A0A0E4CL89/1-322	A0A0E2DOC1/1-372	A0A0D6J3D1/1-299

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 AOA086W612/1-288
 AOA086THT5/1-433
 AOA086TDT0/1-471
 AOA086TD97/1-305
 AOA086TBJ3/1-479
 AOA086T536/1-301
 AOA086T2P9/1-373
 AOA086NEN4/1-299
 AOA086NB26/1-429
 AOA086N8E0/1-491
 AOA086N7F5/1-289
 AOA086N6P5/1-298
 AOA086MSR2/1-284
 AOA086H3U5/1-353
 AOA086H0D5/1-288
 AOA086G4A6/1-290
 AOA086E2B5/1-305
 AOA086D4C2/1-300
 AOA086D1R1/1-361
 AOA086BT72/1-293
 AOA086B533/1-395
 AOA086B212/1-395
 AOA086A0Q1/1-398
 AOA085ZWG4/1-398
 AOA085Z4V5/1-398
 AOA085VRN7/1-288
 AOA085UMN7/1-288
 AOA085JC61/1-294
 AOA085IE08/1-289
 AOA085HT34/1-290

A0A085FGW2/1-288	A0A076EEP3/1-319	A0A066TXA5/1-289	A0A059LAB6/1-288
A0A085BHF7/1-398	A0A076E2C2/1-341	A0A066TX87/1-397	A0A059KD36/1-419
A0A085BGE9/1-398	A0A076E0D6/1-271	A0A066TSD8/1-385	A0A059K8R4/1-450
A0A084YNW7/1-290	A0A076CX96/1-351	A0A066TR43/1-326	A0A059JW1/1-419
A0A084WJM8/1-468	A0A075V9N5/1-400	A0A066RWQ6/1-271	A0A059IXM8/1-450
A0A084W2A5/1-362	A0A075V796/1-283	A0A066PKM0/1-276	A0A059IDM6/1-290
A0A084SUL3/1-292	A0A075U203/1-396	A0A064CP13/1-291	A0A059GB93/1-444
A0A084STV6/1-379	A0A075UX79/1-306	A0A064CN91/1-299	A0A059G5S2/1-306
A0A084RF2/1-495	A0A075USY3/1-283	A0A064CN20/1-340	A0A059FXR2/1-307
A0A084R3B0/1-442	A0A075USE4/1-406	A0A064CMB0/1-271	A0A059FHU5/1-306
A0A084QYJ2/1-370	A0A075PGA0/1-289	A0A064CM21/1-462	A0A059FEL9/1-441
A0A084QXG6/1-495	A0A075K4G5/1-307	A0A064CJ85/1-287	A0A059F6I6/1-306
A0A084PJH9/1-495	A0A075JIV1/1-320	A0A064CHK9/1-343	A0A059ED20/1-440
A0A084PC73/1-442	A0A074Z280/1-483	A0A064BTD9/1-309	A0A059E7Z1/1-422
A0A084IPH3/1-311	A0A074XDQ2/1-485	A0A064BE53/1-292	A0A059E2G8/1-440
A0A084EIG5/1-302	A0A074WJ04/1-483	A0A064BBA6/1-467	A0A059DN78/1-305
A0A084DLE3/1-317	A0A074VQH6/1-484	A0A064BAM9/1-267	A0A059DLT1/1-461
A0A084C7A7/1-289	A0A074UHF6/1-310	A0A064AYA8/1-286	A0A058Z7V2/1-304
A0A084BXJ9/1-292	A0A074T1A7/1-515	A0A064AUR1/1-449	A0A051UH40/1-316
A0A084BM93/1-456	A0A074RU71/1-407	A0A064ARU6/1-305	A0A051UGH8/1-302
A0A084BJ13/1-290	A0A074NOG1/1-277	A0A063CAW9/1-412	A0A051U5X3/1-334
A0A084AZH5/1-495	A0A074MBK4/1-286	A0A063BNQ6/1-317	A0A051U1D3/1-359
A0A083WS53/1-399	A0A074M4Q0/1-279	A0A062VQ22/1-446	A0A051U0A0/1-321
A0A083WIN3/1-306	A0A074L0D5/1-368	A0A062VMQ5/1-287	A0A051TYG1/1-305
A0A083WBI8/1-351	A0A073B3F3/1-258	A0A062VBL4/1-307	A0A051TV99/1-271
A0A083UT38/1-289	A0A072SN15/1-485	A0A062US42/1-306	A0A051TS67/1-354
A0A081YDH5/1-292	A0A072SM86/1-289	A0A062UG17/1-444	A0A049ECL5/1-271
A0A081XQK4/1-293	A0A072S6N0/1-468	A0A062UE45/1-441	A0A049DW54/1-357
A0A081XK26/1-290	A0A072S6L3/1-306	A0A062U8G2/1-441	A0A049DS35/1-317
A0A081W362/1-308	A0A072S6F6/1-409	A0A062TZ65/1-294	A0A049DNE7/1-314
A0A081UZY3/1-317	A0A072PET6/1-479	A0A062TVC7/1-295	A0A049DKN9/1-334
A0A081R9X8/1-380	A0A072CSQ6/1-402	A0A062SM71/1-402	A0A049D9R0/1-355
A0A081I783/1-334	A0A071MFG3/1-317	A0A062MPS9/1-402	A0A049D562/1-369
A0A081I4S6/1-324	A0A070SC16/1-283	A0A062M253/1-404	A0A049D2R5/1-325
A0A081I413/1-302	A0A070HJA9/1-283	A0A062L6G8/1-404	A0A045KBU2/1-351
A0A081I261/1-350	A0A069Q2D6/1-293	A0A062IL57/1-402	A0A045JWK5/1-306
A0A081HWV4/1-327	A0A069PFT0/1-299	A0A062IHJ4/1-404	A0A045HJX5/1-351
A0A081HWV3/1-296	A0A069KKBK3/1-301	A0A062GVX0/1-404	A0A038CV17/1-289
A0A081HVA7/1-355	A0A069K9Z0/1-304	A0A062GHJ2/1-402	A0A037UZ79/1-318
A0A081GK86/1-294	A0A069K1E5/1-292	A0A062G3V1/1-404	A0A034VU34/1-379
A0A081FWV3/1-324	A0A069JIS17/1-298	A0A062FNF9/1-404	A0A034UMZ3/1-319
A0A081ENT2/1-297	A0A069JQT3/1-270	A0A062FDY0/1-404	A0A034UMX0/1-319
A0A081EGZ9/1-433	A0A069JMF6/1-310	A0A062EQZ5/1-404	A0A034UMC2/1-416
A0A081EBF3/1-314	A0A069JKZ3/1-295	A0A062DT04/1-404	A0A034ULU0/1-404
A0A081CTM5/1-440	A0A069JJO1/1-301	A0A062D905/1-404	A0A034UIW5/1-318
A0A081BA21/1-311	A0A069JE48/1-313	A0A062A1X1/1-404	A0A034UBT1/1-302
A0A080M8S5/1-275	A0A069J9P5/1-297	A0A061YW54/1-308	A0A034U9Y9/1-295
A0A078MHU4/1-304	A0A069E9A1/1-454	A0A061LXF9/1-319	A0A034U8C6/1-445
A0A078MG16/1-282	A0A069E7U8/1-306	A0A061JLS3/1-291	A0A034U745/1-301
A0A078LUG5/1-294	A0A069B4K5/1-318	A0A061H1Z4/1-407	A0A034U441/1-339
A0A077XX15/1-400	A0A068RRC5/1-349	A0A061CNZ9/1-290	A0A034U1U9/1-284
A0A077SFA2/1-289	A0A068RQS8/1-368	A0A061ARQ9/1-545	A0A034TZL5/1-290
A0A077R1X0/1-460	A0A068HBE7/1-289	A0A061AA25/1-257	A0A031LJ55/1-402
A0A077LFD0/1-289	A0A067TKT5/1-499	A0A061A9U4/1-323	A0A031FW5/1-322
A0A077L441/1-402	A0A067T351/1-505	A0A061A186/1-485	A0A031J848/1-289
A0A077KQC5/1-394	A0A067SSB4/1-369	A0A060ZQN9/1-286	A0A03111U6/1-286
A0A077HLD0/1-358	A0A067SNU7/1-406	A0A060V1H5/1-289	A0A031HW73/1-290
A0A077HJF3/1-459	A0A067R687/1-595	A0A060JEJ6/1-326	A0A031H644/1-309
A0A077HJ39/1-297	A0A067QHU4/1-321	A0A059ZQV4/1-301	A0A031GES7/1-290
A0A077F9C3/1-289	A0A067PSV2/1-422	A0A059ZKR9/1-404	A0A031GEL4/1-290
A0A076NQA3/1-399	A0A067P6C1/1-401	A0A059WJA2/1-478	A0A031G169/1-290
A0A076NLI5/1-436	A0A067N721/1-395	A0A059WHP0/1-305	A0A031FT35/1-292
A0A076NK24/1-305	A0A067MH68/1-394	A0A059WHD2/1-305	A0A028VAM3/1-290
A0A076N9W1/1-405	A0A067LME2/1-259	A0A059WH80/1-296	A0A028JW68/1-450
A0A076MWD7/1-307	A0A067LIU8/1-325	A0A059WH76/1-293	A0A026WNV6/1-388
A0A076MUD7/1-272	A0A067A4L6/1-289	A0A059W338/1-304	A0A026WML0/1-379
A0A076MTW2/1-295	A0A066YN67/1-283	A0A059VZA0/1-388	A0A026WKF5/1-338
A0A076HL55/1-288	A0A066YI39/1-285	A0A059V266/1-289	A0A026WJA4/1-264
A0A076ES36/1-410	A0A066YI26/1-466	A0A059ML34/1-273	A0A026WBV7/1-284
A0A076EMP1/1-301	A0A066Y2I9/1-471	A0A059MKH0/1-310	A0A024YXH3/1-395
A0A076EKD4/1-274	A0A066Y2I2/1-300	A0A059MJ37/1-276	A0A024YXA7/1-300
A0A076EIL6/1-310	A0A066XUJ9/1-464	A0A059MGH1/1-413	A0A024YV78/1-271
A0A076E172/1-437	A0A066TZB6/1-393	A0A059MG93/1-336	A0A024YUS2/1-304

A0A024YP78/1-307	A0A023Y7Y8/1-307	A0A022L7F8/1-303	A0A013M5V5/1-404
A0A024SCY6/1-453	A0A023XJQ8/1-308	A0A022KJ99/1-404	A0A013JNS5/1-404
A0A024SA94/1-424	A0A023WVG2/1-291	A0A022IPH2/1-408	A0A011P4U9/1-296
A0A024QY62/1-327	A0A023NNN7/1-313	A0A022IE52/1-402	A0A011MSU8/1-303
A0A024QXJ3/1-318	A0A023EUG4/1-437	A0A022I9F8/1-402	A0A011JSQ3/1-404
A0A024QTS1/1-289	A0A023EPG7/1-360	A0A022FX4/1-318	A0A01026T3/1-326
A0A024QSQ5/1-321	A0A023CIK3/1-289	A0A021VRR4/1-315	A0A010UM68/1-404
A0A024QMT6/1-294	A0A023AST6/1-419	A0A017T642/1-409	A0A010SX44/1-290
A0A024QMQ27/1-291	A0A023ANG2/1-450	A0A017SVH1/1-447	A0A010S3T6/1-472
A0A024QKJ5/1-404	A0A022ZY47/1-419	A0A017SGD2/1-420	A0A010QV24/1-511
A0A024M948/1-340	A0A022ZRS2/1-450	A0A017S3R7/1-421	A0A010QQJ5/1-404
A0A024M6P0/1-275	A0A022ZOY5/1-419	A0A017S3P3/1-299	A0A010M4V8/1-404
A0A024M5W9/1-319	A0A022YWN5/1-450	A0A017H9T4/1-293	A0A010L142/1-404
A0A024M469/1-326	A0A022Y5T8/1-419	A0A016PXF9/1-463	A0A010KZL8/1-404
A0A024M3C2/1-357	A0A022Y257/1-450	A0A016PRR0/1-433	A0A010J7V6/1-404
A0A024M1S4/1-314	A0A022XA13/1-419	A0A016PNG1/1-458	A0A010H6H4/1-404
A0A024M0R9/1-300	A0A022X6C6/1-450	A0A014NES8/1-299	A0A010G1B5/1-404
A0A024LZ38/1-332	A0A022WEPO/1-419	A0A014MSE8/1-316	A0A009ZMH1/1-401
A0A024LYQ9/1-284	A0A022WB92/1-450	A0A014L1E9/1-286	A0A009S0P3/1-404
A0A024LYJ2/1-301	A0A022VK15/1-419	A0A014E800/1-402	A0A009R9T2/1-404
A0A024LU56/1-288	A0A022VFD4/1-450	A0A014DME8/1-402	A0A009QKW2/1-404
A0A024LTX0/1-404	A0A022UMH7/1-419	A0A014CG19/1-402	A0A009PBA1/1-406
A0A024K4A3/1-360	A0A022UJP0/1-450	A0A014C2M7/1-402	A0A009MGU5/1-404
A0A024K1H5/1-270	A0A022U029/1-419	A0A014BXY6/1-402	A0A009LVS1/1-408
A0A024K091/1-369	A0A022TVX8/1-450	A0A014BGT3/1-402	A0A009L116/1-402
A0A024JXE0/1-343	A0A022SSN4/1-372	A0A014BD98/1-402	A0A009KKR8/1-402
A0A024JX98/1-391	A0A022MC72/1-302	A0A014AN09/1-402	A0A009K7Q0/1-402
A0A024JSW7/1-316	A0A022LSF5/1-335	A0A013UQ12/1-402	A0A009I2R8/1-404
A0A024JSH1/1-302	A0A022LNU1/1-289	A0A013U245/1-404	A0A009HYP7/1-300
A0A024HNN3/1-292	A0A022LMV2/1-409	A0A013TOL9/1-404	A0A009GVQ4/1-404
A0A024H776/1-308	A0A022LIJ1/1-290	A0A013SL55/1-404	A0A009GB05/1-402
A0A024GY94/1-272	A0A022LB97/1-274	A0A013RM47/1-404	A0A009FXS5/1-404

495 sequences homologue to Lcp_{K30} used for Figure 1

LcpK30/1-407
 LcpRr/1-408
 LcpVH2/1-407
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 gi|1001209655|gb|KXO96733.1|/1-418
 gi|1001212592|gb|KXO99636.1|/1-353
 gi|1001217188|gb|KXP04156.1|/1-353
 gi|1001225646|gb|KXP12521.1|/1-415
 gi|1002996378|ref|WP_061440650.1|/1-386
 gi|1011024729|ref|WP_061981012.1|/1-387
 gi|1011031315|ref|WP_061987588.1|/1-399
 gi|1011124826|ref|WP_062046683.1|/1-384
 gi|1011656815|ref|WP_062505992.1|/1-417
 gi|1011831196|ref|WP_062650159.1|/1-401
 gi|1011831775|ref|WP_062650738.1|/1-407
 gi|1011963691|ref|WP_062770100.1|/1-387
 gi|1011997432|ref|WP_062795088.1|/1-407
 gi|1016278947|ref|WP_062963305.1|/1-407
 gi|1016293073|ref|WP_062977206.1|/1-414
 gi|1016308244|ref|WP_062980248.1|/1-416
 gi|1016310210|ref|WP_062981848.1|/1-413
 gi|1016310488|ref|WP_062982080.1|/1-413
 gi|1016325893|ref|WP_062996681.1|/1-413
 gi|1016331483|ref|WP_063001876.1|/1-407
 gi|1016333737|ref|WP_063003752.1|/1-413
 gi|1016333822|ref|WP_063003837.1|/1-413
 gi|1016342323|ref|WP_063012276.1|/1-407
 gi|1016347704|ref|WP_063017553.1|/1-407
 gi|1016353625|ref|WP_063023207.1|/1-407
 gi|1016353920|ref|WP_063023502.1|/1-413
 gi|1016364826|ref|WP_063034184.1|/1-413
 gi|1016383054|ref|WP_063051239.1|/1-414
 gi|1016417186|ref|WP_063056674.1|/1-413
 gi|1016418827|ref|WP_063058203.1|/1-413
 gi|157734202|gb|ABV68924.1|/1-407
 gi|170180374|gb|ABV68923.1|/1-407
 gi|306756318|sp|Q3L8N0.2|/1-407
 gi|320012208|gb|ADW07058.1|/1-408
 gi|326197583|gb|EGD54772.1|/1-404
 gi|340545041|dbj|BAK52801.1|/1-407
 gi|358243017|dbj|GAB11151.1|/1-353
 gi|365817994|gb|EHN12936.1|/1-389
 gi|374846398|emb|CCF63468.1|/1-404
 gi|375755257|gb|AFA76036.1|/1-388
 gi|387846498|emb|CCH52581.1|/1-376
 gi|403206604|dbj|GAB89391.1|/1-345
 gi|407307034|gb|AFU00935.1|/1-404
 gi|443889260|dbj|GAC67155.1|/1-399
 gi|446890110|ref|WP_000967366.1|/1-377
 gi|455650289|gb|EMF29072.1|/1-397
 gi|478744316|gb|AGJ52896.1|/1-361
 gi|486081790|gb|EOD64895.1|/1-374
 gi|488788336|ref|WP_002700743.1|/1-368
 gi|490019951|ref|WP_003922454.1|/1-373
 gi|490055025|ref|WP_003957330.1|/1-404
 gi|490069076|ref|WP_003971251.1|/1-394
 gi|490070043|ref|WP_003972218.1|/1-401
 gi|490076123|ref|WP_003978298.1|/1-386
 gi|490119608|ref|WP_004020123.1|/1-407
 gi|491074837|ref|WP_004936459.1|/1-399
 gi|491309277|ref|WP_005167261.1|/1-399
 gi|491326241|ref|WP_005184204.1|/1-408
 gi|491342946|ref|WP_005200885.1|/1-407
 gi|491450158|ref|WP_005307945.1|/1-386
 gi|493115572|ref|WP_006144271.1|/1-386
 gi|493392537|ref|WP_006348693.1|/1-388
 gi|493412800|ref|WP_006368739.1|/1-407
 gi|493426072|ref|WP_006381778.1|/1-387
 gi|493481229|ref|WP_006436107.1|/1-407
 gi|493588158|ref|WP_006541094.1|/1-400
 gi|493589923|ref|WP_006542830.1|/1-408
 gi|493923362|ref|WP_006868302.1|/1-407
 gi|493955090|ref|WP_006898821.1|/1-407
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gi|494081187|ref|WP_007023227.1|/1-406
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gi|494621449|ref|WP_007373939.1|/1-386
gi|494771430|ref|WP_007506838.1|/1-403
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gi|496364252|ref|WP_009073242.1|/1-403
gi|496443941|ref|WP_009152786.1|/1-404
gi|496447928|ref|WP_009156773.1|/1-407
gi|498325812|ref|WP_010639968.1|/1-402
gi|498813298|ref|WP_010843589.1|/1-407
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gi|501350690|ref|WP_012382325.1|/1-394
gi|502441549|ref|WP_012787513.1|/1-393
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gi|502655470|ref|WP_012891671.1|/1-407
gi|502919509|ref|WP_013154485.1|/1-387
gi|502986999|ref|WP_013221975.1|/1-393
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gi|503050335|ref|WP_013285311.1|/1-407
gi|503050339|ref|WP_013285315.1|/1-405
gi|503240107|ref|WP_013474768.1|/1-407
gi|503570755|ref|WP_013804831.1|/1-409
gi|503811777|ref|WP_014045771.1|/1-386
gi|503815878|ref|WP_014049872.1|/1-399
gi|503825139|ref|WP_014059133.1|/1-387
gi|503918520|ref|WP_014152514.1|/1-392
gi|504256667|ref|WP_014443769.1|/1-404
gi|504257577|ref|WP_014444679.1|/1-406
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gi|504842985|ref|WP_015030087.1|/1-430
gi|504844162|ref|WP_015031264.1|/1-388
gi|505389052|ref|WP_015576154.1|/1-402
gi|505392891|ref|WP_015579993.1|/1-392
gi|505422443|ref|WP_015609545.1|/1-397
gi|506283335|ref|WP_015803110.1|/1-409
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