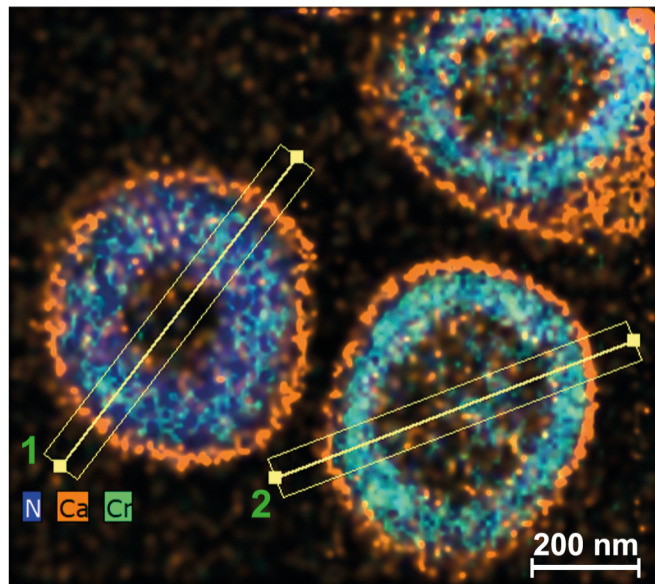
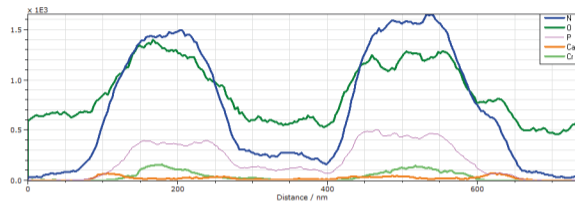


Fig. S1: Visualization of global eDNA mapping. eDNA reads generated via 454 sequencing were mapped against the draft genome of *L. chromiiresistens*. This graphical overview shows the coverage of reads against the longest scaffold of the draft genome (representing 97 % of the genome) with different read data aggregations. Reads mapped equally over the whole scaffold. Detailed coverage information can be obtained from Tab. S1. Dark blue, aggregation of 100 bp; blue, aggregation of 1 kb; light blue, aggregation of 10 kb.

a - EDS maps



b - path 1



c - path 2

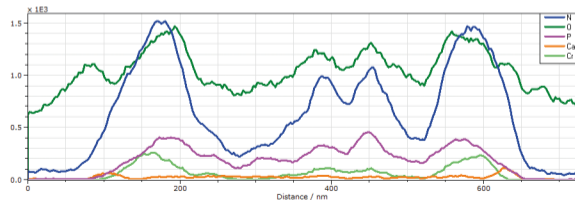


Fig. S2: Superimposed X-ray EDS element (N, Ca, Cr) maps (a) and profiles (b, c) in net counts of the elements along the paths 1 and 2.

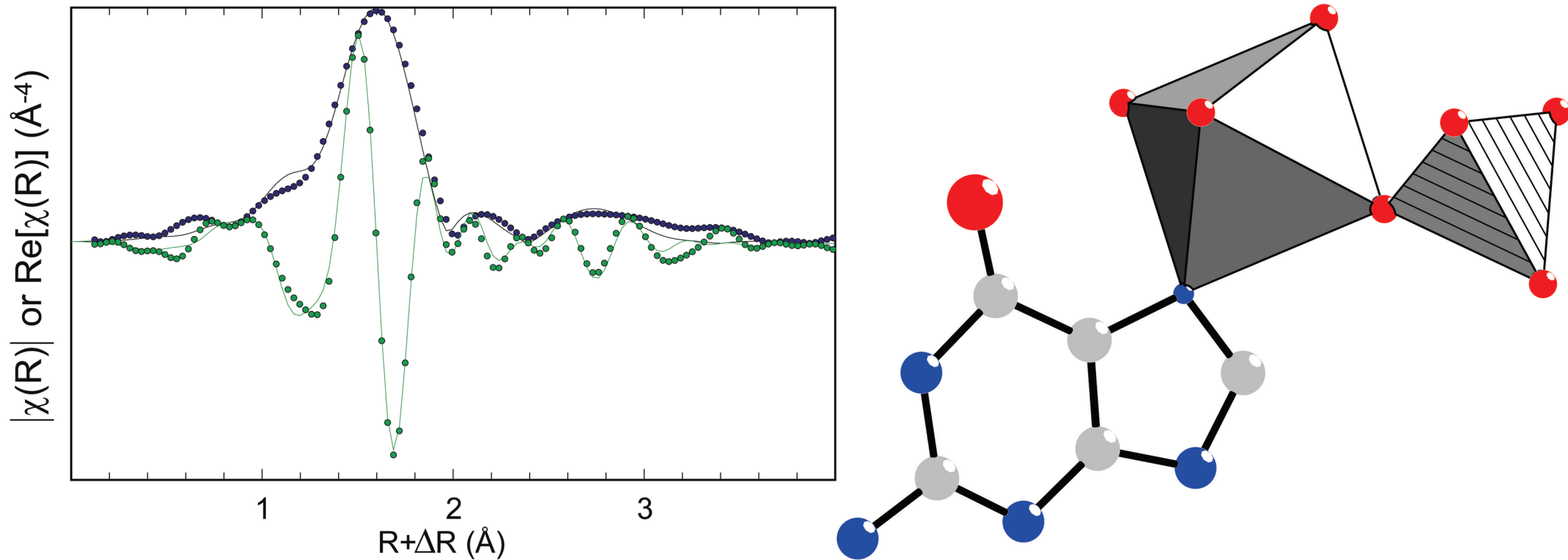


Fig. S3: Magnitude (blue) and real part (green) of the Fourier-transformed EXAFS spectrum. Circles represent the measured and reduced data, lines the fit. The fit is based on a configuration shown in the right panel. In this configuration that yielded the best agreement of the fit to the data, Cr^{3+} is octahedrally coordinated. The central Cr^{3+} is bonded via a bridging oxygen to a phosphate tetrahedron (hatched) and via a bridging nitrogen to a guanine molecule.



Fig. S4: Enhanced pigment production by *L. chromiiresistens* during chromate stress. Membrane fractions of cells grown with 0 mM, 2 mM, 4 mM and 6 mM K_2CrO_4 (left to right).

Tab. S1: Global mapping of obtained 454 reads of eDNA sequencing. The average coverage over all contigs is 27-fold. Scaffold00001, representing 97% of the whole *L. chromiiresistens* genome shows a 28-fold coverage. The read coverage throughout all 29 scaffolds suggests a cell lysis-based origin of the eDNA.

Name	Consensus length (bp)	Total read count	Average coverage (x-fold)
scaffold00001_mapping	2990096	154937	28.21
scaffold00002_mapping	5572	277	25.71
scaffold00003_mapping	5378	1393	138.07
scaffold00004_mapping	4923	223	22.68
scaffold00005_mapping	4340	163	20.43
scaffold00006_mapping	4227	178	21.43
scaffold00007_mapping	4201	209	26.27
scaffold00008_mapping	4032	156	20.66
scaffold00009_mapping	3944	200	25.12
scaffold00010_mapping	3911	209	27.99
scaffold00011_mapping	3519	123	17.23
scaffold00012_mapping	3407	125	19.46
scaffold00013_mapping	3380	125	18.84
scaffold00014_mapping	3343	163	25.62
scaffold00015_mapping	3303	150	23.89
scaffold00016_mapping	3212	125	19.99
scaffold00017_mapping	3100	162	27.8
scaffold00018_mapping	3006	128	22.18
scaffold00019_mapping	2992	194	34.22
scaffold00020_mapping	2904	158	28.55
scaffold00021_mapping	2788	91	17.63
scaffold00022_mapping	2718	97	16.37
scaffold00023_mapping	2675	135	26.39
scaffold00024_mapping	2592	67	14.13
scaffold00025_mapping	2569	139	28.86
scaffold00026_mapping	2192	91	20.87
scaffold00027_mapping	2106	61	14.37
scaffold00028_mapping	2102	81	19.8
scaffold00029_mapping	2018	104	20.03

Tab. S2: Potential factors conferring resistance to chromate and/or other heavy metals. Besides *Leucobacter* common features, the genome of *L. chromiirestiens* harbors unique factors within the *Leucobacter* genus that potentially facilitate chromate resistance.

Possible resistance factors	Position on NZ_JH370377.1	Locus tag <i>L. chromiirestiens</i>	NCBI RefSeq
Common			
Arsenate reductase ArsC	2478357..2478761	KIE_RS0111130	WP_010157043.1
Arsenate reductase ArsC (EC_1.20.4.1)	711662..712066	KIE_RS0103040	WP_010155309.1
Arsenical-resistance protein ACR3	2476251..2477339	KIE_RS0111120	WP_010157040.1
Cobalt-zinc-cadmium resistance protein CzcD	725817..726758	KIE_RS0103120	WP_010155327.1
Cobalt-zinc-cadmium resistance protein CzcD	1018812..1019834	KIE_RS0104545	WP_010155643.1
Copper resistance protein D	1077644..1079644	KIE_RS0104765	WP_010155691.1
Heavy metal translocating P-type ATPase	2479764..2481713	KIE_RS0111145	WP_029608311.1
Heavy metal translocating P-type ATPase	3191458..3193668	KIE_RS0114300	WP_081473401.1
Heavy metal translocating P-type ATPase	719156..721345	KIE_RS0103085	WP_050803159.1
Heavy metal translocating P-type ATPase	767529..769499	KIE_RS0103395	WP_010155381.1
Copper resistance protein CopC	2440342..2440983	KIE_RS18150	WP_081473334.1
Arsenical resistance operon repressor ArsR	2483494..2483835	KIE_RS0111160	WP_010157049.1
Lycopene cyclase domain-containing protein	631188..631535	KIE_RS0102685	WP_010155226.1
Lycopene cyclase domain-containing protein	631532..631891	KIE_RS15680	WP_010155228.1
Chromate transport protein ChrA	2689182..2690411	KIE_RS0112145	WP_010157242.1
Copper chaperone PCu(A)C	2441030..2441587	KIE_RS0110955	WP_010157004.1
Cobald transporter	641245..642243	KIE_RS0102760	WP_010155245.1

Unique

Cadmium transporter CadD	745799..746401	KIE_RS0103250	WP_010155353.1
Mercuric ion reductase	755159..756583	KIE_RS0103325	WP_010155368.1
Heavy metal-responsive transcriptional regulator HTH-HMRTR	754665..755054	KIE_RS0103320	WP_010155367.1
Mercury transporter TauE	758102..759022	KIE_RS0103345	WP_006947554.1
Organomercurial lyase MerB	756604..757254	KIE_RS0103330	WP_010155369.1
Copper resistance protein CopZ	703929..704285	KIE_RS17935	WP_081473297.1