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On the routine use of soft X-rays in macromolecular crystallography. Part IV. Efficient determination of anomalous substructures in biomacromolecules using longer X-ray wavelengths

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23 different crystal forms of 19 different biological macromolecules were examined with respect to their anomalously scattering substructures using diffraction data collected at a wavelength of 2.0 Å (6.2 keV). In more than 90% of the cases the substructure was found to contain more than just the protein S atoms. The data presented suggest that chloride, sulfate, phosphate or metal ions from the buffer or even from the purification protocol are frequently bound to the protein molecule and that these ions are often overlooked, especially if they are not bound at full occupancy. Thus, in order to fully describe the macromolecule under study, it seems desirable that any structure determination be complemented with a long-wavelength data set.

PDB References: anomalous substructures of apoferritin, 2g4h, r2g4hsf; concanavalin A, 2g4i, r2g4isf; glucose isomerase, 2g4j, r2g4jsf; human ADP-ribosylhydrolase 3, 2g4k, r2g4ksf; lysozyme, pH 4.5, 2g4p, r2g4psf; pH 8.0, 2g4q, r2g4qsf; hydroxynitrile lyase, 2g4l, r2g4lsf; insulin, 2g4m, r2g4msf; α-lactalbumin, 2g4n, r2g4nsf; 3-isopropylmalate dehydrogenase, 2g4o, r2g4osf; MogA, 2g4p, r2g4psf; NBR1 PB1, 2g4s, r2g4ssf; porcine pancreatic elastase, Na form, 2g4t, r2g4tsf; Ca form, 2g4u, r2g4usf; proteinase K, 2g4v, 2g4vsf; ribonuclease A, $C2$, 2g4w, r2g4wsf; $P3_221$, 2g4x, r2g4xsf; thaumatin, 2g4y, r2g4ysf; thermolysin, 2g4z, r2g4zsf; titin-(A168-A169), 2ill, r2illsf; trypsin, $P1$, 2g51, r2g51sf; $P2_1$, 2g52, r2g52sf; $P3_121$, 2g54, r2g55sf.

1. Introduction

The 1 August 2006 release of the Protein Data Bank (Berman *et al.*, 2000) contained 34 776 macromolecular crystal structures determined by X-ray crystallographic methods. A search for prosthetic groups/ligands in these structures yielded the result that 1066 of them (3.1%) were reported to contain one or more phosphate ions (PDB ID PO4), 4050 (11.6%) sulfate ions (PDB ID SO4), 1963 (5.6%) chloride ions (PDB ID CL), 848 (2.4%) potassium ions (PDB ID K) and 3295 (9.5%) calcium ions (PDB ID CA). These numbers are surprisingly low given the facts that NaCl or KCl are part of almost every buffer used in protein crystallization and that ammonium sulfate is one of the most widely used precipitants in protein crystallization. A possible explanation for this may be that partially occupied or partially disordered light-atom-containing ions are often mistakenly interpreted as water molecules. Since most protein structure refinements are based on a diffraction data set collected at a rather short wavelength of about 1.0 Å, additional information in the form of anomalous differences originating from these atoms is typically not available. Furthermore, diffraction data sets collected for refinement purposes are typically collected with the strategy of obtaining an as complete as possible set of structure-factor amplitudes to the diffraction limit of the crystal. Comparatively little effort is spent on collecting good and complete anomalous differences in such experiments.

As can be seen from Fig. 1, the anomalous scattering lengths of elements 11–20 are about three to four times larger at a wavelength of 2.0 Å than at 1.0 Å. Thus, it has recently been suggested that complementing a short-wavelength diffraction data set, which is usually used for refinement, with a long-wavelength data set can provide sufficient additional information to unequivocally identify the complete anomalously

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scattering substructure (Djinovic Carugo *et al.*, 2005; Mueller-Dieckmann *et al.*, 2005). The substructures of ten model systems, five of which were Xe derivatives, were described based on diffraction data sets collected at a wavelength of 1.5 Å by Mueller-Dieckmann *et al.* (2005). Further successful examples of the utilization of a longer wavelength data set include the identification of calcium ions in factor XIII (Weiss, Sicker, Djinović Carugo *et al.*, 2001; Weiss, Sicker & Hilgenfeld, 2001), in the oxygen-evolving centre of photosystem II (Ferreira *et al.*, 2004) and in furin (Than *et al.*, 2005), of chloride ions in alliinase (Kuettner *et al.*, 2002) and in phospholipase A_2 (Sekar *et al.*, 2004) and the distinction of Na^+ from Ca^{2+} in porcine pancreatic elastase (Weiss *et al.*, 2002).

Recently, it has been reported that the wavelength range at which the highest anomalous signal-to-noise ratio for light atoms can be obtained is around 2.0–2.1 Å (Mueller-Dieckmann *et al.*, 2005). Thus, diffraction data collected at such wavelengths should also be most suitable for the determination of anomalously scattering substructures. The power of this suggested approach is demonstrated in this study by identifying and describing the anomalously scattering atoms and ions in 23 protein crystal examples.

2. Materials and methods

2.1. Crystallization

13 of the 19 proteins used for crystallization are commercially available and 11 of these were used without further purification. Crystallization experiments using the hanging-drop vapour-diffusion technique were carried out at 293 K, except for the monoclinic crystal form of bovine ribonuclease A, which was crystallized at 277 K.

Crystallization of hen egg-white lysozyme (HEL), porcine pancreatic elastase (PPE), concanavalin A (ConA) from *Canavalia ensiformis*, thaumatin from *Thaumatococcus daniellii* and the trigonal form of bovine trypsin have been described previously in detail (Mueller-Dieckmann *et al.*, 2005). In brief, HEL was crystallized at pH 4.5 (HEL-45) in the presence of 50 m*M* sodium acetate buffer and 5%(*w*/*v*) NaCl as a precipitant and at pH 8.0 (HEL-80) in the presence of 50 m*M* tris(hydroxymethyl)aminoethane (Tris) buffer and 70%(*v*/*v*) 2-methyl-2,4-pentanediol (MPD) as a precipitant. The sodium-containing form of PPE (PPE-Na) was crystallized in the presence of 100 m*M* sodium acetate buffer pH 5.1 and 200 m*M* $Na_2(SO_4)$ as precipitant. The calcium-containing form (PPE-Ca) was obtained in 100 m*M* sodium acetate buffer pH 5.1, 10 m*M* $CaCl_2$ and 200 m*M* sodium citrate as precipitant. ConA was crystallized using 34%(*w*/*v*) polyethylene glycol (PEG) 1500 as the precipitant. Thaumatin was crystallized in the presence of 100 m*M* *N*-(2-acetamido)iminodiacetic acid (ADA) pH 6.5 and 1 *M* sodium/potassium tartrate as the precipitant and the trigonal form of bovine trypsin (trypsin-$P3_121$) was obtained in 200 m*M* Tris buffer pH 7.4 in the presence of 160 m*M* $(NH_4)_2SO_4$, 20%(*w*/*v*) PEG 6000 and 30%(*v*/*v*) ethylene glycol (Mueller-Dieckmann *et al.*, 2005). In the following, the crystallization experiments for the remaining 14 proteins are described in detail.

2.1.1. Apoferritin. Prior to crystallization, apoferritin from horse heart (Sigma, Lot No. 71K7101) was subjected to gel-filtration chromatography on a Superdex S200 column (Amersham-Pharmacia) in a buffer containing 50 m*M* Tris pH 8.0 and 150 m*M* NaCl. Protein fractions corresponding to the monomeric state were pooled and dialyzed against water. The protein concentration was determined by absorption at 280 nm and the protein solution was then diluted to a final concentration of 15 mg ml^{-1}. This solution was mixed in a 1:1 ratio with the reservoir solution, which consisted of 300 m*M* $(NH_4)_2SO_4$, 80 m*M* $CdSO_4$ and 3 m*M* NaN_3 (Granier *et al.*, 1997). Crystals grew within a few days and belonged to space group *F*432, with unit-cell parameter 182.2 Å. They were cryoprotected with 25%(*v*/*v*) ethylene glycol and diffracted X-rays to 2.0 Å resolution.

2.1.2. Glucose isomerase (GI). The supplied protein suspension (from *Streptomyces rubiinosus*; Hampton Research, Lot No. 022004) was, according to the manufacturer's specifications, extensively dialyzed against water and subsequently diluted to a final protein concentration of 20 mg ml^{-1}. Crystallization drops were made by mixing the protein solution with an equal volume of reservoir solution containing 19%(*w*/*v*) $(NH_4)_2SO_4$ in 100 m*M* *N*-(2-hydroxyethyl)-piperazine-*N*′-2-ethanesulfonic acid (HEPES) pH 7.2. Crystals belonging to space group *I*222 with unit-cell parameters a = 93.0, b = 97.6, c = 102.8 Å appeared after about two weeks. Prior to the diffraction experiment, the crystals were soaked in a solution of 4 *M* Tris methylaminooxide (TMAO) in reservoir solution for cryoprotection. X-ray diffraction was then observed to a resolution of better than 1.5 Å.

2.1.3. Human ADP-ribosylhydrolase 3. Crystals of human ADP-ribosylhydrolase 3 (hARH3) were obtained as described in Kernstock *et al.* (2006). In brief, a solution of 10 mg ml^{-1} protein in 20 m*M* Tris pH 8.0, 100 m*M* NaCl and 3 m*M* dithiothreitol (DTT) was mixed with the same volume of reservoir solution consisting of 100 m*M* 2-morpholinoethanesulfonic acid (MES) pH 6.0 and 10%(*w*/*v*) PEG 6000.

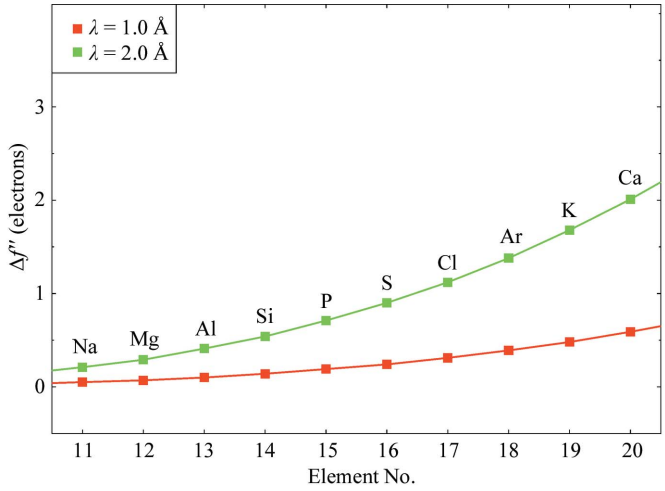

Figure 1
Anomalous scattering length ($\Delta f''$) values in units of electrons at λ = 1.0 Å (red) and λ = 2.0 Å (green) for elements 11–20 according to Cromer & Liberman (1970).

The crystals belong to the orthorhombic space group $P2_12_12_1$, with unit-cell parameters a = 57.3, b = 59.3, c = 98.7 Å. They were cryoprotected in dry paraffin oil (Riboldi-Tunnicliffe & Hilgenfeld, 1999) and diffracted X-rays to better than 1.7 Å.

2.1.4. Hydroxynitrile lyase from *Hevea brasiliensis*. Hydroxynitrile lyase (HNL) was crystallized according to the method of Wagner and coworkers (Wagner, Hasslacher *et al.*, 1996; Wagner, Schall *et al.*, 1996) in the presence of Na HEPES pH 7.0 as a buffer and $(NH_4)_2SO_4$ and PEG 400 as precipitants. Crystals belonged to space group $C222_1$, with unit-cell parameters a = 47.1, b = 106.1, c = 128.2 Å. They were flash-cooled in a solution of 20%(v/v) PEG 200 in reservoir solution and diffracted X-rays to almost 1.0 Å resolution (Gruber *et al.*, 1999).

2.1.5. Insulin. Zn-free bovine pancreatic insulin (Sigma, Lot No. 033K1449) crystals were prepared by mixing protein dissolved at a concentration of 18 mg ml^{-1} in 50 m*M* Na_2HPO_4 pH 10.4 and 1 m*M* ethylenediaminetetraacetic acid (EDTA) and reservoir solution containing 400 m*M* Na_2HPO_4 pH 10.4 and 10 m*M* EDTA in a 1:1 ratio (Nanao *et al.*, 2005). Crystals belonging to the cubic space group $I2_13$ with unit-cell parameter a = 78.3 Å grew within a few days. They were cryoprotected in a 30%(v/v) solution of glycerol in water and usually diffracted X-rays to better then 1.5 Å resolution.

2.1.6. α-Lactalbumin. Crystals of bovine α-lactalbumin (Sigma, Lot No. 063K7009) were grown according to the method of Chrysina *et al.* (2000) by mixing equal amounts of a protein solution (20 mg ml^{-1} in water) and reservoir [50 m*M* KH_2PO_4 and 15%(w/v) PEG 8000]. Crystals grew within two weeks and belonged to space group $I222$, with unit-cell parameters a = 61.6, b = 86.1, c = 88.5 Å. They were cryoprotected in a solution of 30%(v/v) glycerol in water and diffracted X-rays to 2.4 Å resolution.

2.1.7. 3-Isopropylmalate dehydrogenase (LeuB). Crystallization of LeuB from *Mycobacterium tuberculosis* was performed as described in Singh *et al.* (2005). Briefly, a protein solution at a concentration of 10 mg ml^{-1} was mixed with reservoir solution [100 m*M* HEPES pH 8.0, 2.0 *M* $(NH_4)_2SO_4$ and 100 m*M* NaCl] in a 1.5:1 ratio. The crystals belong to space group $P2_12_12_1$, with unit-cell parameters a = 78.6, b = 98.6, c = 184.0 Å. After being cryoprotected in a solution of 2 *M* TMAO in reservoir solution, the crystals diffracted X-rays to about 2.0 Å resolution.

2.1.8. Probable molybdopterin-binding domain (MogA). Crystals of MogA from *M. tuberculosis* were obtained by mixing equal amounts of protein solution (10 mg ml^{-1} in Tris–HCl pH 7.5 and 50 m*M* NaCl) and reservoir solution (100 m*M* Tris pH 8.5 and 1 *M* trisodium citrate). Crystals appeared after 5 d and belonged to space group $P2_1$, with unit-cell parameters a = 31.6, b = 97.8, c = 57.7 Å, β = 105.0°. Crystals were flash-cooled directly from their crystallization drops and diffracted X-rays to about 1.9 Å resolution.

2.1.9. NBR1 PB1 domain. Crystallization of the PB1 domain of the human scaffold protein NBR1 was performed as described in Müller *et al.* (2006). In brief, crystals were obtained using 100 m*M* sodium acetate pH 4.1 as a buffer and 1.6–2.2 *M* $(NH_4)_2SO_4$ as the precipitant. Crystals belonging to space group $P6_322$ with unit-cell parameters a = 101.4, c = 42.6 Å diffracted X-rays to 2.15 Å resolution after being cryoprotected in dry paraffin oil.

2.1.10. Proteinase K. Proteinase K from *Tritirachium album* (Merck, Lot No. VL255368) was dissolved at a concentration of 20 mg ml^{-1} in 25 m*M* HEPES pH 7.0 with 1 m*M* phenylmethylsulfonylfluoride (PMSF) and mixed with an equal amount of reservoir solution consisting of 25 m*M* HEPES pH 7.0, 1 m*M* PMSF and 400 m*M* sodium/potassium tartrate. These crystallization conditions are somewhat different from those reported by Betzel *et al.* (2001), who crystallized the protein at pH 6.5 in the presence of $NaNO_3$ as a precipitant. Crystals belonging to space group $P4_32_12$ with unit-cell parameters a = 67.8, c = 101.9 Å were cryoprotected in a solution of 4 *M* TMAO in water. The diffraction limit was usually better than 1.5 Å resolution.

2.1.11. Ribonuclease A. Bovine ribonuclease A (RNase; Sigma, Lot No. 063K7677) was crystallized in a monoclinic and a trigonal crystal form. Monoclinic crystals were obtained according to McPherson *et al.* (1986) by mixing equal amounts of protein solution (20 mg ml^{-1} in water) with reservoir solution [16%(w/v) PEG 4000]. Crystals belonging to space group $C2$ with unit-cell parameters a = 100.1, b = 32.6, c = 72.5 Å, β = 90.6° grew within two months and could be flash-cooled directly from the crystallization drops. They diffracted X-rays to better than 1.5 Å resolution. Trigonal crystals were grown by mixing 10 mg ml^{-1} protein in 50 m*M* sodium acetate pH 5.5 with the same volume of reservoir solution consisting of 1.75 *M* $(NH_4)_2SO_4$, 2 *M* NaCl and 100 m*M* sodium acetate pH 5.5 (Schultz *et al.*, 1998). They grew within a few days in space group $P3_221$, with unit-cell parameters a = 64.3, c = 63.7 Å. They were flash-cooled in a solution of 30%(v/v) glycerol in water and diffracted X-rays to about 1.9 Å resolution.

2.1.12. Thermolysin (TLN). Thermolysin (Calbiochem, Lot No. B50060) from *Bacillus thermoproteolyticus* was dissolved at a concentration of 100 mg ml^{-1} in 50 m*M* MES pH 6.0 and 45%(v/v) dimethylsulfoxide (DMSO) by gently shaking the mixture for 1 h at room temperature. Undissolved particles were then removed by centrifugation for 10 min at 15 000*g*. Equal amounts of protein solution and a solution containing 50 m*M* MES, 1 *M* NaCl and 45%(v/v) DMSO were mixed and equilibrated over a well of 35%(v/v) saturated $(NH_4)_2SO_4$ solution. Crystals belonging to space group $P6_122$ with unit-cell parameters a = 92.5, c = 127.5 Å usually appeared within a few days. Prior to flash-cooling in a nitrogen stream at 100 K, they were transferred into a solution of dry paraffin oil. They typically diffract X-rays to better than 1.5 Å resolution.

2.1.13. Titin-(A168-A169). A construct consisting of the two immunoglobulin-like domains A168-A169 within the A-band segment of human cardiac titin was produced and crystallized as described in Mueller *et al.* (submitted). In brief, crystals belonging to the orthorhombic space group $I222$ with unit-cell parameters a = 69.3, b = 89.1, c = 103.6 Å grew from a cocktail containing 0.1 *M* bicine pH 9.2 and 1.4–1.6 *M* ammonium sulfate. For data collection, they were cryocooled

Table 1
Data-collection and processing statistics for the 23 data sets.

n.d., not determined. Values in parentheses are for the highest resolution shell.

Data set	Apoferritin	Concanavalin A	Glucose isomerase	hARH3	HEL-45	HEL-80	HNL	Insulin	α-Lactalbumin	LeuB	MogA	NBR1 PB1
No. of crystals	1	1	1	1	1	1	1	1	1	1	1	1
No. of images	1117	720	360	360	360	360	720	360	720	720	360	720
$\Delta\varphi$ (°)	0.3	0.5	1	1	1	1	0.5	1	0.5	0.5	1	0.5
Crystal-to-detector distance (mm)	65	80	50	50	50	50	50	50	80	60	50	80
Resolution limits (Å)	99–2.00 (2.05–2.00)	99–2.40 (2.46–2.40)	99–1.85 (1.90–1.85)	99–1.82 (1.87–1.82)	99–1.84 (1.89–1.84)	99–1.84 (1.89–1.84)	99–1.84 (1.89–1.84)	99–1.80 (1.85–1.80)	99–2.30 (2.36–2.30)	99–2.00 (2.05–2.00)	99–1.92 (1.97–1.92)	99–2.15 (2.00–2.15)
Space group	$F432$	$I222$	$I222$	$P2_12_12_1$	$P4_32_12$	$P4_32_12$	$C222_1$	$I2_13$	$P2_12_12$	$P2_12_12_1$	$P2_1$	$P6_322$
Unit-cell parameters												
a (Å)	182.16	61.64	93.02	57.03	78.66	77.17	47.09	78.27	68.43	78.57	31.59	101.31
b (Å)	182.16	86.05	97.59	59.34	78.66	77.17	106.05	78.27	104.80	98.58	97.84	101.31
c (Å)	182.16	88.45	102.77	98.71	37.12	37.05	128.18	78.27	119.11	184.03	57.71	42.57
α (°)	90	90	90	90	90	90	90	90	90	90	90	90
β (°)	90	90	90	90	90	90	90	90	90	90	105.02	90
γ (°)	90	90	90	90	90	90	90	90	90	90	90	120
Mosaicity (°)	0.53	1.44	0.39	0.59	0.38	0.49	0.62	0.19	1.02	0.45	0.87	0.69
Total No. of reflections	1318724	100146	500415	359216	253164	233948	329303	262194	429503	1168031	141449	253602
Unique reflections	18063	9511	40126	29384	10599	10192	28327	7553	37220	97128	25783	7403
Rejected reflections	166	9	60	27	9	2	32	6	468	38	1	17
Redundancy	73.0 (70.7)	10.5 (9.0)	12.5 (9.9)	12.2 (9.5)	23.9 (22.4)	23.0 (17.8)	11.6 (10.1)	34.7 (15.6)	11.5 (10.5)	12.0 (11.1)	5.5 (4.0)	34.3 (26.0)
Completeness (%)	99.9 (100)	99.9 (99.4)	99.8 (98.3)	95.7 (90.9)	99.9 (100)	99.9 (99.9)	100 (99.9)	99.9 (99.3)	96.4 (96.4)	99.9 (99.9)	99.6 (97.8)	99.9 (99.9)
$I/\sigma(I)$	81.9 (10.2)	28.4 (5.6)	19.5 (3.1)	30.7 (3.0)	59.0 (14.6)	49.8 (5.7)	26.9 (6.3)	52.3 (3.1)	15.0 (2.8)	24.3 (2.2)	17.4 (1.8)	50.4 (10.0)
R_{merge} (%)	6.2 (50.9)	6.7 (29.7)	14.1 (60.9)	6.0 (62.2)	5.0 (25.1)	5.3 (65.2)	7.0 (34.8)	6.3 (66.5)	10.4 (65.5)	6.9 (79.2)	7.1 (77.0)	6.4 (33.7)
$R_{r.i.m.}$ (%)	7.0 (51.1)	7.0 (31.5)	15.1 (66.5)	6.5 (68.7)	5.1 (25.7)	5.4 (67.2)	7.3 (36.6)	6.5 (70.8)	11.3 (77.2)	7.4 (86.8)	7.8 (82.4)	6.5 (34.3)
$R_{p.i.m.}$ (%)	n.d.	2.1 (10.3)	4.2 (21.1)	1.8 (24.3)	1.0 (5.4)	1.1 (15.7)	2.1 (11.3)	1.1 (18.9)	3.3 (23.8)	2.1 (27.1)	3.3 (42.8)	1.1 (6.6)
R_{anom} (%)	2.9 (1.7)	2.2 (11.2)	3.6 (21.3)	1.9 (22.9)	2.0 (4.9)	1.9 (12.0)	1.9 (9.9)	2.2 (27.6)	3.7 (21.5)	1.9 (25.9)	3.0 (39.6)	1.3 (5.9)
B factor from Wilson plot (Å^2)	30.0	48.7	19.6	32.5	22.9	30.9	27.3	27.5	53.2	40.2	32.7	46.2
Optical resolution (Å)	1.57	1.84	1.45	1.52	1.43	1.52	1.48	1.49	1.85	1.68	1.59	1.74

Data set	PPE-Na	PPE-Ca	Proteinase K	RNase A-$C2$	RNase A-$P3_221$	Thaumatin	Thermolysin	Titin-(A168-A169)	Trypsin-$P1$	Trypsin-$P2_1$	Trypsin-$P3_121$
No. of crystals	1	1	1	1	1	1	1	1	1	1	1
No. of images	360	360	360	360	360	720	720	360	360	360	360
$\Delta\varphi$ (°)	1	1	1	1	1	0.5	0.5	1	1	1	1
Crystal-to-detector distance (mm)	80	50	80	50	80	65	65	80	50	50	50
Resolution limits (Å)	99–2.15 (2.21–2.15)	99–1.84 (1.89–1.84)	99–2.14 (2.18–2.14)	99–1.84 (1.89–1.84)	99–1.95 (2.00–1.95)	99–1.98 (2.03–1.98)	99–1.98 (2.03–1.98)	99–2.20 (2.26–2.20)	99–1.84 (1.89–1.84)	99–1.84 (1.89–1.84)	99–1.82 (1.87–1.82)
Space group	$P2_12_12_1$	$P2_12_12_1$	$P4_32_12$	$C2$	$P3_221$	$P4_12_12$	$P6_122$	$I222$	$P1$	$P2_1$	$P3_121$
Unit-cell parameters											
a (Å)	49.92	50.09	67.78	100.12	64.32	57.90	92.49	69.26	32.90	33.10	54.59
b (Å)	57.66	57.79	67.78	32.60	64.32	57.90	92.49	89.12	36.80	66.69	54.59
c (Å)	74.380	74.40	101.88	72.47	63.74	150.39	127.84	103.55	39.63	39.25	107.09
α (°)	90	90	90	90	90	90	90	90	102.46	90	90
β (°)	90	90	90	90.56	90	90	90	90	104.97	108.23	90
γ (°)	90	90	90	90	120	90	120	90	102.16	90	120
Mosaicity (°)	0.22	0.38	0.52	0.48	0.93	0.89	0.41	0.38	0.36	0.46	0.21
Total No. of reflections	150747	233616	357530	115887	205614	465151	872807	194851	37406	77303	322233
Unique reflections	12194	18269	13741	20368	11476	18685	23130	16486	12841	13012	17178
Rejected reflections	11	1	21	22	56	266	51	3	0	3	13
Redundancy	12.4 (10.7)	12.8 (12.3)	26.0 (20.6)	5.7 (5.3)	17.9 (16.2)	24.9 (21.2)	37.7 (32.1)	11.8 (10.3)	2.9 (2.8)	5.9 (5.7)	18.8 (16.6)
Completeness (%)	99.9 (99.9)	94.8 (94.8)	100 (100)	98.4 (95.9)	99.9 (99.9)	99.9 (99.9)	99.9 (99.9)	99.0 (92.0)	88.0 (88.0)	92.5 (92.5)	99.9 (99.9)
$I/\sigma(I)$	60.6 (46.2)	44.7 (12.4)	71.3 (38.1)	21.6 (6.3)	24.5 (4.7)	34.8 (10.5)	51.7 (7.0)	34.1 (4.3)	28.2 (16.6)	32.1 (7.2)	44.8 (11.2)
R_{merge} (%)	4.3 (8.5)	4.5 (20.8)	5.3 (12.9)	7.6 (20.2)	12.3 (58.3)	8.6 (33.7)	6.7 (64.0)	5.7 (45.0)	3.1 (6.8)	4.0 (20.9)	5.7 (25.6)
$R_{r.i.m.}$ (%)	4.5 (9.0)	4.7 (21.8)	5.4 (13.3)	8.3 (22.3)	13.0 (61.2)	8.8 (34.5)	6.8 (65.1)	5.9 (47.3)	3.8 (8.4)	4.4 (23.1)	5.8 (26.5)
$R_{p.i.m.}$ (%)	1.3 (2.8)	1.3 (6.1)	1.1 (3.0)	3.4 (9.5)	3.0 (17.6)	1.7 (7.6)	1.1 (11.7)	1.7 (14.0)	2.2 (4.8)	1.8 (9.6)	1.3 (6.5)
R_{anom} (%)	1.5 (2.3)	1.8 (5.6)	1.3 (2.6)	3.3 (7.9)	3.3 (12.4)	1.9 (5.5)	1.8 (9.6)	1.9 (15.4)	2.4 (4.7)	2.2 (10.1)	1.9 (5.9)
B factor from Wilson plot (Å^2)	15.7	19.5	15.7	28.3	24.2	28.2	32.4	47.5	19.4	27.5	21.6
Optical resolution (Å)	1.55	1.43	1.56	1.51	1.52	1.55	1.58	1.75	1.43	1.49	1.46

in the presence of glycerol. They diffract X-rays to a resolution of about 2.2 Å.

2.1.14. Trypsin from *Fusarium oxysporum*. The crystallization conditions for the monoclinic and triclinic crystal

Table 2
Refinement statistics and PDB codes for the 23 structures described.

Data set	Apoferritin	Concanavalin A	Glucose isomerase	hARH3	HEL-45	HEL-80	HNL	Insulin	α-Lactalbumin	LeuB	MogA	NBR1 PB1
Resolution limits (Å)	30–2.00	30–2.40	30–1.85	30–1.82	30–1.84	30–1.84	30–1.84	30–1.80	30–2.30	30–2.00	30–1.92	30–2.15
Total No. of reflections												
In working set	17652	9332	39312	28683	10347	9949	27695	7364	34659	94983	25275	7223
In test set	373	178	796	523	213	206	587	169	707	2002	474	164
R_{cryst} (%)	19.5	19.2	15.2	19.1	16.6	16.7	17.7	16.7	29.6	20.9	17.9	21.4
R_{free} (%)	21.8	26.0	17.7	24.7	21.4	20.6	19.7	22.3	35.9	26.0	24.1	32.3
No. of protein atoms	1364	1809	3049	2607	1000	1001	2118	411	5856	10038	3180	691
No. of water molecules	101	26	238	125	140	77	181	61	74	535	151	52
No. of ions and other atoms	13	6	3	4	7	5	6	0	9	8	1	1
Average B factor (Å^2)												
All atoms	29.2	43.6	14.4	33.2	31.0	30.8	17.0	30.3	39.4	47.0	38.9	58.1
Protein atoms	28.7	43.6	14.2	33.1	25.2	30.1	26.6	28.6	39.4	47.1	38.7	57.9
Ions/other atoms	40.0	51.0	6.0	23.6	20.2	30.7	19.6	—	31.8	45.0	36.8	39.4
R.m.s.d. bond lengths (Å)	0.017	0.018	0.019	0.025	0.025	0.020	0.018	0.025	0.029	0.020	0.019	0.016
R.m.s.d. bond angles (°)	1.51	1.58	1.65	1.97	1.85	1.73	1.60	1.78	2.05	1.70	1.76	1.52
PDB code	2g4h	2g4i	2g4j	2g4k	2g4p	2g4q	2g4l	2g4m	2g4n	2g4o	2g4r	2g4s

Data set	PPE-Na	PPE-Ca	Proteinase K	RNase A-$C2$	RNase A-$P3_221$	Thaumatin	Thermolysin	Titin-(A168-A169)	Trypsin-$P1$	Trypsin-$P2_1$	Trypsin-$P3_121$
Resolution limits (Å)	30–2.15	30–1.84	30–2.14	30–1.84	30–1.95	30–1.98	30–1.98	30–2.20	30–1.84	30–1.84	30–1.82
Total No. of reflections											
In working set	11927	17854	13399	19941	11206	18237	22604	16151	12570	12729	16825
In test set	225	378	279	400	236	377	461	317	264	262	311
R_{cryst} (%)	15.6	14.3	16.3	21.3	17.5	19.4	19.0	21.2	16.0	15.4	15.8
R_{free} (%)	23.9	17.7	20.4	27.4	22.4	24.3	23.7	24.3	21.6	22.3	20.9
No. of protein atoms	1831	1845	2031	1902	951	1557	2437	1532	1553	1551	1626
No. of water molecules	146	200	131	87	88	100	92	95	139	153	130
No. of ions and other atoms	3	2	5	2	5	1	12	2	3	2	4
Average B factor (Å^2)											
All atoms	8.2	27.2	6.8	31.2	27.4	34.3	39.7	47.4	23.0	26.9	26.1
Protein atoms	8.0	26.7	6.6	31.2	27.1	33.4	39.6	47.2	22.8	26.5	25.7
Ions/other atoms	2.5	38.4	8.2	19.6	28.5	29.0	45.7	48.6	16.2	27.4	27.9
R.m.s.d. bond lengths (Å)	0.023	0.019	0.025	0.027	0.027	0.026	0.025	0.028	0.022	0.027	0.019
R.m.s.d. bond angles (°)	1.79	1.59	1.79	2.31	2.13	1.97	1.90	2.22	1.81	2.16	1.68
PDB code	2g4t	2g4u	2g4v	2g4w	2g4x	2g4y	2g4z	2ill	2g51	2g52	2g55

forms of trypsin from *F. oxysporum* were as described in Rypniewski *et al.* (1993). Crystals belonging to space groups $P2_1$ and $P1$ grew under identical conditions in the presence of citrate as the buffering agent at pH 5.0 and of Na_2SO_4 as the precipitant, with unit-cell parameters a = 33.1, b = 66.7, c = 39.3 Å, β = 108.2° and a = 32.9, b = 36.8, c = 39.6 Å, α = 102.5, β = 105.0, γ = 102.2°, respectively. Both crystal forms were cryoprotected in dry paraffin oil and diffracted X-rays to better than 1.7 Å resolution.

2.2. Diffraction data collection

Diffraction data sets were collected at the new energy-tunable beamline X12 at the EMBL Hamburg Outstation using a wavelength of 2.0 Å (E = 6.199 keV) and a 225 mm MAR Mosaic CCD detector. The relevant data-collection parameters are given in Table 1. No special data-collection strategy was employed. Since the plan was to collect 360° in either 1, 0.5 or 0.3° images for each data set, the starting spindle angle for the first data set was chosen randomly. For all data sets, the 2θ angle was kept at 0°. Together with the minimum crystal-to-detector distance of 50 mm, this limited the maximum resolution of the data sets to 1.80 Å.

2.3. Data processing

All data sets were indexed and integrated using *DENZO* (Otwinowski & Minor, 1997). The post-refinement procedure in *SCALEPACK* (Otwinowski & Minor, 1997) was used to refine the unit-cell parameters and the mosaicity for each data set. Scaling and merging of the data was carried out using the program *SCALA* (Collaborative Computational Project, Number 4, 1994) and the scaling protocol *SCALA-Sec* as described in Mueller-Dieckmann *et al.* (2004). The redundancy-independent merging R factor $R_{r.i.m.}$ as well as the precision-indicating merging R factor $R_{p.i.m.}$ (Weiss, 2001) were calculated using the program *RMERGE* (available from http://www.embl-hamburg.de/~msweiss/projects/msw_qual.html or from MSW upon request).

2.4. Refinement

All 23 protein structures were refined using the program *REFMAC*5 (Collaborative Computational Project, Number 4, 1994). Relevant refinement statistics are given in Table 2. The refined coordinate files as well as the underlying structure-factor amplitudes including anomalous differences were deposited with the PDB (see Table 2 for PDB codes).

Table 3
Peak heights and ranks in the anomalous difference Fourier syntheses for the 23 structures described.

The maximum density ρ_{max} and the minimum density ρ_{min} are given in units of standard deviations $\sigma(\rho)$ above and below the mean value (set to 0.0) of the density map. The height of the lowest peak at which the analysis was stopped is also given. n.a., not assigned. The peak heights for the anomalously scattering atoms in α-lactalbumin were determined differently (see §2.5). Res. gives the resolution limits in Å.

Data set	Apoferritin	Concanavalin A	Glucose isomerase	hARH3	HEL-45	HEL-80	HNL	Insulin	α-Lactalbumin	LeuB	MogA	NBR1 PB1
Res.	30–2.00	30–2.40	30–1.85	30–1.82	30–1.84	30–1.84	30–1.84	30–1.80	30–2.30	30–2.00	30–1.92	30–2.15
ρ_{max}	2.64	0.76	1.75	1.00	1.51	1.06	1.04	0.97	1.06	0.37	0.92	0.47
ρ_{min}	−0.28	−0.16	−0.77	−0.30	−0.32	−0.33	−0.23	−0.22	−0.33	−0.17	−0.53	−0.11
$\sigma(\rho)$	0.037	0.035	0.165	0.063	0.074	0.063	0.045	0.048	0.060	0.032	0.113	0.024
Peak 1	71.5 (Cd)	21.4 (Ca)	10.6 (C305)	16.0 (C10)	20.5 (Cl)	16.8 (M12)	23.1 (C13)	20.3 (C19*B*)	17.0 (Ca)	12.3 (C245*C*)	8.1 (C117*C*)	20.1 (M80)
Peak 2	26.2 (Cd)	5.9 (Mn)	9.5 (M306)	15.3 (M305)	18.2 (M105)	16.3 (C115)	21.1 (M171)	17.0 (C6*A*)	16.7 (Ca)	11.2 (M289*A*)	8.1 (C117*A*)	16.4 (M34)
Peak 3	19.8 (Cd)	5.4 (Cl)	8.5 (M369)	15.2 (M84)	17.4 (C64)	15.8 (M105)	18.9 (C161)	16.5 (C11*A*)	15.1 (Ca)	10.1 (C245*D*)	7.5 (C117*B*)	14.3 (M70)
Peak 4	18.1 (Cd)	5.2 (M129)	8.2 (M83)	14.8 (C267)	17.1 (C80)	14.3 (C30)	16.3 (C81)	15.9 (C20*A*)	15.1 (Ca)	9.8 (C245*A*)	6.9 (C24*C*)	5.0 (M1)
Peak 5	16.9 (Cd)	4.7 (M42)	8.1 (M87)	14.4 (M139)	16.3 (M12)	14.3 (C80)	15.3 (SO4)	13.6 (C7*A*)	11.1 (Ca)	9.2 (M289*C*)	6.5 (C24*A*)	4.3 (Cl)
Peak 6	12.4 (M148)	4.7 (Na)	7.6 (M222)	14.3 (C327)	15.5 (C30)	14.3 (C76)	12.8 (SO4)	12.8 (C7*B*)	10.8 (Ca)	9.0 (M289*D*)	4.7 (n.a.)	3.9 (n.a.)
Peak 7	12.3 (Cl)	4.6 (Cl)	6.1 (M379)	14.0 (C19)	14.9 (Cl)	14.2 (C127)	12.2 (M122)	4.1 (n.a.)	8.3 (C73*F*)	8.1 (C245*B*)	4.7 (n.a.)	
Peak 8	11.0 (Cd)	4.5 (Cl)	5.8 (Ca)	12.6 (C271)	14.8 (C94)	14.0 (Cl)	9.6 (HEC)†		8.0 (C73*E*)	8.1 (C265*C*)	4.6 (C24*B*)	
Peak 9	10.6 (M72)	4.4 (n.a.)	5.4 (Cl)	12.6 (M203)	14.2 (Cl)	13.7 (C64)	7.2 (SO4)		8.0 (C77*A*)	8.0 (M265*D*)	4.5 (n.a.)	
Peak 10	9.4 (M100)		5.0 (M157)	12.4 (M65)	13.9 (C115)	12.3 (C94)	6.6 (HEC)†		7.8 (C91*A*)	7.8 (C217*C*)	4.5 (Cl)	
Peak 11	8.9 (C52)		5.0 (n.a.)	12.2 (M316)	13.8 (C76)	11.9 (Cl)	6.6 (HEC)†		7.7 (C61*A*)	7.8 (Cl)	4.4 (n.a.)	
Peak 12	8.5 (Cd)		4.6 (n.a.)	11.1 (M272)	13.3 (C6)	11.9 (C6)	6.4 (SO4)		7.3 (C77*B*)	7.3 (M217*D*)		
Peak 13	7.5 (Cl)		4.6 (n.a.)	10.8 (M1)	13.2 (Cl)	10.1 (Cl)	5.7 (Cl)		7.3 (C91*B*)	7.2 (C199*D*)		
Peak 14	7.1 (n.a.)		4.3 (Mg)	9.4 (C116)	13.1 (C127)	7.2 (Cl)	5.5 (SO4)		7.2 (C61*C*)	6.8 (M1*D*)		
Peak 15	7.1 (Cd)		4.3 (n.a.)	7.1 (Mg)	11.3 (Cl)	6.4 (Cl)	4.9 (C113)		7.2 (C91*D*)	6.5 (M217*A*)		
Peak 16	6.9 (C130)			6.4 (Cl)	7.7 (Cl)	5.0 (Cl)	4.8 (n.a.)		7.0 (C73*C*)	6.3 (SO4)		
Peak 17	6.8 (n.a.)			6.1 (Mg)	4.8 (Cl)	3.9 (n.a.)	4.8 (C113)		6.9 (C61*D*)	6.2 (M265*B*)		
Peak 18	6.7 (Cd)			5.3 (Cl)	4.6 (n.a.)		4.6 (n.a.)		6.9 (C73*B*)	6.2 (M265*A*)		
Peak 19	6.3 (n.a.)			5.3 (M221)					6.9 (C61*B*)	6.2 (M289*B*)		
Peak 20				4.8 (n.a.)					6.8 (C91*C*)	5.8 (M1*C*)		
Peak 21									6.8 (C111*D*)	5.8 (C199*C*)		
Peak 22									6.8 (C77*F*)	5.8 (SO4)		
Peak 23									6.7 (C77*E*)	5.7 (M265*B*)		
Peak 24									6.7 (C73*A*)	5.7 (Cl)		
Peak 25									6.6 (C111*A*)	5.7 (Cl)		
Peak 26									6.5 (C73*D*)	5.7 (C199*B*)		
Peak 27									6.4 (K)	5.4 (Cl)		
Peak 28									6.4 (C61*E*)	5.3 (Cl)		
Peak 29									6.4 (C61*F*)	5.2 (M265*A*)		
Peak 30									6.4 (C111*B*)	5.1 (n.a.)		
Peak 31									6.2 (C77*D*)	5.1 (n.a.)		
Peak 32									6.2 (C111*C*)	5.0 (n.a.)		
Peak 33									6.0 (C77*C*)	4.9 (n.a.)		
Peak 34									5.7 (K)	4.9 (n.a.)		
Peak 35									5.6 (C28*D*)	4.8 (Cl)		
Peak 36									5.5 (C6*C*)	4.8 (n.a.)		
Peak 37									5.4 (C111*F*)	4.8 (M217*B*)		
Peak 38									5.2 (C120*D*)	4.7 (n.a.)		
Peak 39									5.2 (C120*C*)	4.6 (C199*A*)		
Peak 40									5.2 (C91*F*)	4.6 (n.a.)		
Peak 41									5.1 (C111*E*)			
Peak 42									5.1 (C6*B*)			
Peak 43									4.9 (C6*A*)			
Peak 44									4.9 (C91*E*)			
Peak 45									4.8 (C28*E*)			
Peak 46									4.8 (C6*D*)			
Peak 47									4.8 (C28*C*)			
Peak 48									4.7 (C28*A*)			
Peak 49									4.7 (C28*B*)			
Peak 50									4.4 (C28*F*)			

2.5. Identification and quantification of the anomalous substructures

Anomalously scattering atoms were identified as peaks in anomalous difference Fourier syntheses (Table 3). In all cases, the anomalous electron-density maps were based on all data to the highest resolution collected without applying any cutoff to either structure-factor amplitudes or anomalous differences. Attempts to increase the signal in the maps by either limiting the resolution or by applying a σ-cutoff to the anomalous differences failed (data not shown). Since it is impossible to assign atom types based on anomalous differences collected at just one wavelength, in some cases the chemical environment was used to distinguish anions from cations. Occupancies of the anomalously scattering substructure atoms were estimated

Table 3 (continued)

Data set	PPE-Na	PPE-Ca	Proteinase K	RNase A-*C*2	RNase A-$P3_221$	Thaumatin	Thermolysin	Titin-(A168-A169)	Trypsin-*P*1	Trypsin-$P2_1$	Trypsin-$P3_121$
Res.	30–2.15	30–1.84	30–2.14	30–1.84	30–1.95	30–1.98	30–1.98	30–2.20	30–1.84	30–1.84	30–1.82
ρ_{max}	1.43	3.13	1.15	1.18	1.13	0.97	2.22	0.37	1.51	1.28	3.35
ρ_{min}	−0.32	−0.49	−0.27	−0.39	−0.57	−0.25	−0.26	−0.13	−0.46	−0.36	−0.46
$\sigma(\rho)$	0.060	0.075	0.045	0.075	0.102	0.051	0.053	0.027	0.093	0.080	0.081
Peak 1	23.7 (M172)	41.7 (Ca)	24.4 (Ca)	15.7 (C72*A*)	11.2 (M13)	19.0 (M112)	42.3 (Ca)	13.4 (M109)	16.2 (C57)	15.6 (C41)	42.7 (Ca)
Peak 2	21.5 (M41)	22.8 (M41)	20.4 (M55)	12.0 (C58*B*)	11.0 (C84)	17.5 (C149)	38.9 (Ca)	13.2 (C24)	14.3 (M178)	14.8 (C180)	21.0 (C31)
Peak 3	20.1 (C194)	20.5 (M172)	20.3 (M225)	12.0 (C110*B*)	10.6 (M30)	17.4 (C77)	30.9 (Ca)	10.5 (C177)	14.2 (C165)	13.9 (C57)	20.9 (M166)
Peak 4	20.0 (C30)	20.2 (C214)	20.2 (C34)	11.8 (C65*A*)	10.2 (C110)	17.4 (C145)	18.8 (Zn)	6.6 (M1)	14.2 (C180)	13.9 (C165)	20.1 (C47)
Peak 5	19.9 (C214)	20.1 (C194)	20.0 (C123)	10.9 (C110*A*)	10.1 (M79)	17.2 (C9)	14.2 (M205)	5.7 (Cl)	11.7 (C41)	13.8 (M178)	18.5 (C189)
Peak 6	18.6 (C127)	19.0 (C127)	19.5 (C178)	10.0 (C58*A*)	10.0 (Cl)	17.2 (C134)	12.2 (Cl)	4.7 (Cl)	11.3 (C216)	13.4 (C191)	17.1 (C216)
Peak 7	18.3 (C46)	17.3 (C184)	18.7 (C249)	9.5 (M30*A*)	9.9 (C26)	16.6 (C56)	8.7 (Cl)	4.4 (n.a.)	10.8 (Cl)	10.7 (C216)	17.1 (C168)
Peak 8	18.2 (C158)	17.2 (C30)	17.5 (M111)	9.4 (M30*A*)	9.7 (Cl)	16.5 (C204)	8.4 (Cl)		8.1 (C191)	5.7 (SO4)	16.9 (C13)
Peak 9	17.9 (C184)	17.2 (C46)	17.3 (C73)	9.3 (M79*B*)	9.4 (M29)	16.4 (C66)	8.0 (M120)		5.1 (Cl)	5.6 (SO4)	16.9 (M92)
Peak 10	17.2 (C174)	16.6 (C158)	17.1 (M154)	8.8 (C26*B*)	8.8 (Cl)	15.9 (C126)	7.7 (SO4)		5.0 (Cl)	5.4 (n.a.)	16.2 (C154)
Peak 11	16.0 (SO4)	16.5 (C174)	16.1 (Ca)	8.6 (C65*B*)	7.7 (C58)	15.8 (C158)	7.1 (M120)		4.2 (n.a.)		16.0 (C115)
Peak 12	9.5 (SO4)	4.2 (n.a.)	13.7 (M238)	8.5 (C84*B*)	7.7 (C40)	15.7 (C193)	6.4 (Cl)				15.3 (C143)
Peak 13	8.0 (Na)		9.6 (K)	8.4 (M13*B*)	7.5 (C72)	15.1 (C121)	6.1 (Cl)				15.3 (C203)
Peak 14	4.1 (n.a.)		8.3 (Cl)	8.3 (M79*A*)	6.6 (C95)	14.9 (C164)	5.0 (Cl)				15.0 (C122)
Peak 15			5.0 (K)	7.8 (C72*A*)	6.3 (Cl)	14.3 (C177)	4.8 (Cl)				13.2 (C179)
Peak 16			4.7 (n.a.)	7.5 (C40*A*)	6.2 (Cl)	12.1 (C71)	4.7 (n.a.)				8.3 (Cl)
Peak 17				7.2 (M13*A*)	6.1 (C65)	8.6 (C159)	4.4 (Cl)				6.4 (Cl)
Peak 18				7.1 (C26*A*)	6.0 (SO4)	4.2 (n.a.)	4.3 (n.a.)				5.4 (Cl)
Peak 19				6.7 (M29*B*)	5.0 (n.a.)						4.2 (n.a.)
Peak 20				6.5 (C84*A*)							
Peak 21				6.4 (SO4)							
Peak 22				6.4 (Cl)							
Peak 23				4.8 (M29*A*)							
Peak 24				4.5 (C95*A*)							
Peak 25				4.4 (n.a.)							
Peak 26				4.3 (n.a.)							
Peak 27				4.3 (C40*B*)							
Peak 28				4.2 (n.a.)							

† HEC is denoted MEC in the corresponding deposited PDB file.

as described by Weiss *et al.* (2002) based on the relative peak heights in the anomalous difference Fourier syntheses, with the sulfur peaks serving as a reference. In the case of α-lactalbumin, where the resolution of the data did not permit resolution of the two S atoms of a disulfide bridge, the anomalous electron-density height at the site of each anomalously scattering atom (Ca^{2+}, K^+, S) was calculated using the program *MAPMAN* (Kleywegt & Jones, 1996). Uncertainties in the occupancy values were estimated by comparing the relative peak heights of the protein S atoms in the anomalous difference Fourier syntheses and the corresponding peak heights from a previous study (Mueller-Dieckmann *et al.*, 2005). As a semi-quantitative measure of the reliability of the occupancy values, the correlation coefficients between the peak heights for HEL-45 (ten S atoms), PPE-Ca (ten S atoms), thaumatin (17 S-atoms) and trypsin-$P3_121$ (14 S atoms) were computed.

2.6. Phase-determination trials

In order to assess the usability of the anomalous signal for phase determination, we conducted phasing experiments by simply submitting all 23 data sets to the SAD protocol of the *AutoRickshaw* pipeline (Panjikar *et al.*, 2005). The quality of the anomalous differences was assessed by whether the anomalous substructure could be solved automatically and by the map correlation coefficient between the density-modified electron-density map and the $(2F_{obs} - F_{calc}, \alpha_{calc})$ map, where α_{calc} are the model phases after refinement.

3. Results

3.1. Diffraction data collection and processing

Based on common standards, such as resolution, merging statistics, completeness and redundancy values, all 23 diffraction data sets collected are of rather good quality (Table 1). The maximum resolution ranges from 1.80 Å for insulin to 2.40 Å for concanavalin A; 11 of the 23 data sets exhibit maximum resolutions of 1.80–1.90 Å and 20 of the 23 exhibit maximum resolutions equal or better than 2.15 Å. The only exceptions to this are the data sets for titin-(A168-A169), α-lactalbumin and concanavalin A, with 2.20, 2.30 and 2.40 Å resolution, respectively. Also, the completeness values for all but two of the data sets exceed 95% and in most cases (17 of 23) exceed 99%. The remaining two are the data sets of the triclinic and monoclinic forms of trypsin from *F. oxysporum*, which are only 89 and 93% complete, respectively. All data sets could also be integrated and scaled very well as evidenced by the merging statistics given in Table 1. The only exceptions

to this are the data sets of GI, α-lactalbumin and the trigonal form of RNAse A. The reason why these data sets exhibit somewhat poorer merging statistics is not clear, since the data were collected in the same way as for the other systems. Furthermore, all of the data sets exhibit a significant anomalous signal, which is manifested in the values of $R_{\rm anom}$ and the ratio $R_{\rm anom}/R_{\rm p.i.m.}$ (Table 1).

3.2. Refinement and anomalously scattering substructures

All model structures were well refined to good R and free R factors and good geometrical parameters (Table 2), except for α-lactalbumin, where the lower data quality probably prevented the refinement from proceeding as smoothly as for the other examples. Thus, the model phases derived from these refinements are reliable and the corresponding anomalously scattering substructures, which were derived based on the anomalous difference electron-density map using data collected at λ = 2.0 Å in all cases, are also reliable. The detailed compositions of the anomalously scattering substructures are described below and shown in Fig. 2. For the two model systems thaumatin (Fig. 2*p*) and insulin (Fig. 2*r*), only protein S atoms were found to constitute the anomalously scattering substructures. These two are thus not discussed any further. In the following, the anomalously scattering substructures of the remaining 21 systems are described in detail.

3.2.1. Apoferritin. The substructure of apoferritin (Fig. 2*a*) contains five S atoms, two partially occupied chloride ions (occupancies q = 0.85 and 0.50) and nine partially occupied cadmium ions (q = 0.50–0.05). Of the nine partially occupied cadmium ions, three were found at previously reported positions (Hempstead *et al.*, 1997), while the remaining six ion positions did not coincide with the remaining three reported Cd^{2+} positions. This also applies to the detected two Cl^- ions. None of them have been reported before.

3.2.2. Concanavalin A (ConA). In the case of ConA, the substructure (Fig. 2*d*) contained two protein S atoms, one manganese ion, one calcium ion, one sodium ion and three partially occupied chloride ions (q = 0.85–0.65). The sodium and the chloride ions constitute new features of this substructure, while the positions of the manganese and calcium ions are identical to those described previously (Mueller-Dieckmann *et al.*, 2005).

3.2.3. Glucose isomerase (GI). For GI, the substructure (Fig. 2*g*) is composed of eight S atoms, one magnesium ion, one calcium ion (q = 0.25) and one chloride ion (q = 0.40). Whereas the positions of the magnesium and the calcium ions are identical to those reported previously, the chloride position identified here does not correspond to either of the two chloride positions reported in PDB entry 1o1h (E. Nowak, S. Panjikar & P. A. Tucker, unpublished work). Furthermore, no anomalous signal could be detected for the two chloride ions reported previously.

3.2.4. Human ADP-ribosylhydrolase 3 (hARH3). The substructure for hARH3 (Fig. 2*b*) contains 15 protein S atoms, two magnesium ions and two partially occupied chloride ions (q = 0.45 and 0.35, respectively). The complete structure of hARH3 has been reported elsewhere (Mueller-Dieckmann *et al.*, 2006).

3.2.5. Lysozyme (HEL-45 and HEL-80). The substructure for HEL-45 (Fig. 2*c*), with ten protein S atoms and seven partially occupied Cl^- ions (q = 0.95–0.25), has been described previously (PDB code 2a7d, Mueller-Dieckmann *et al.*, 2005; PDB code 1lz8, Dauter *et al.*, 1999). The top four of the seven Cl^- ions found in our structure are identical to the previously described top four chlorides. The fifth chloride position has not been observed before, but the sixth and seventh chloride-ion positions are in close proximity to those previously described. In contrast, one of the previously reported positions could not be observed in our structure, probably owing to low occupancy. The substructure for HEL-80 (Fig. 2*f*) also contains all ten protein S atoms from the Cys and Met residues and five partially occupied chloride ions (q = 0.7–0.2). Of the two previously described chloride-ion positions (PDB code 1dpw; Weiss *et al.*, 2000), one is among those found, whilst the other was not found.

3.2.6. Hydroxynitrile lyase (HNL). The substructure (Fig. 2*h*) is composed of six protein S atoms; two alternative positions can be observed for Cys113 SG. In addition, the substructure comprises three alternative sites for the one S atom originating from an *S*,*S*-(2-hydroxyethyl)thiocysteine (HEC) molecule, five partially occupied sulfate ions (q = 0.70–0.25) and one partially occupied Cl^- ion (q = 0.20). In the 1.90 Å resolution structure of HNL (PDB code 1yas; Wagner, Hasslacher *et al.*, 1996; Wagner, Schall *et al.*, 1996) one of the sulfate ions was observed, whereas in a subsequent structure, which was refined at 1.1 Å resolution (Gruber *et al.*, 1999), three more sulfate ions were detected. Two of the four previously reported sulfate positions are also part of the anomalously scattering substructure reported here, while the other two could not be detected. In contrast, three additional sulfate positions as well as a Cl^--ion position were observed, none of which have been reported before.

3.2.7. α-Lactalbumin. In hexameric α-lactalbumin, 42 of the total 54 protein S atoms could be identified in the anomalous difference Fourier map at a threshold of 4.0σ above the mean value of the map. In addition, six partially occupied (q = 0.85–0.54) Ca^{2+} ions and two K^+ ions (q = 0.40 and 0.37) could be identified (Fig. 2*j*). While the Ca^{2+}-ion positions have been reported previously (Chrysina *et al.*, 2000), none of the K^+-ion positions have been reported to our knowledge.

3.2.8. 3-Isopropylmalate dehydrogenase (LeuB). The substructure of the protein, which can be described as a dimer of dimers, consists of 22 of the totally occurring 24 protein S atoms from the Cys and Met residues. In addition, Met165 SD in both subunits *A* and *B* occurs in two alternative positions (Fig. 2*q*). No anomalous signal was observed for the S atom of Met1 SD of the two subunits *A* and *B*. Two partially occupied SO_4^{2-} ions (q = 0.50) and six partially occupied Cl^--ion positions (q = 0.50–0.35) were observed. Interestingly, the one sulfate reported earlier (PDB code 1w0d; Singh *et al.*, 2005) was not observed in our substructure, although the crystals were grown under identical conditions. However, the treat-

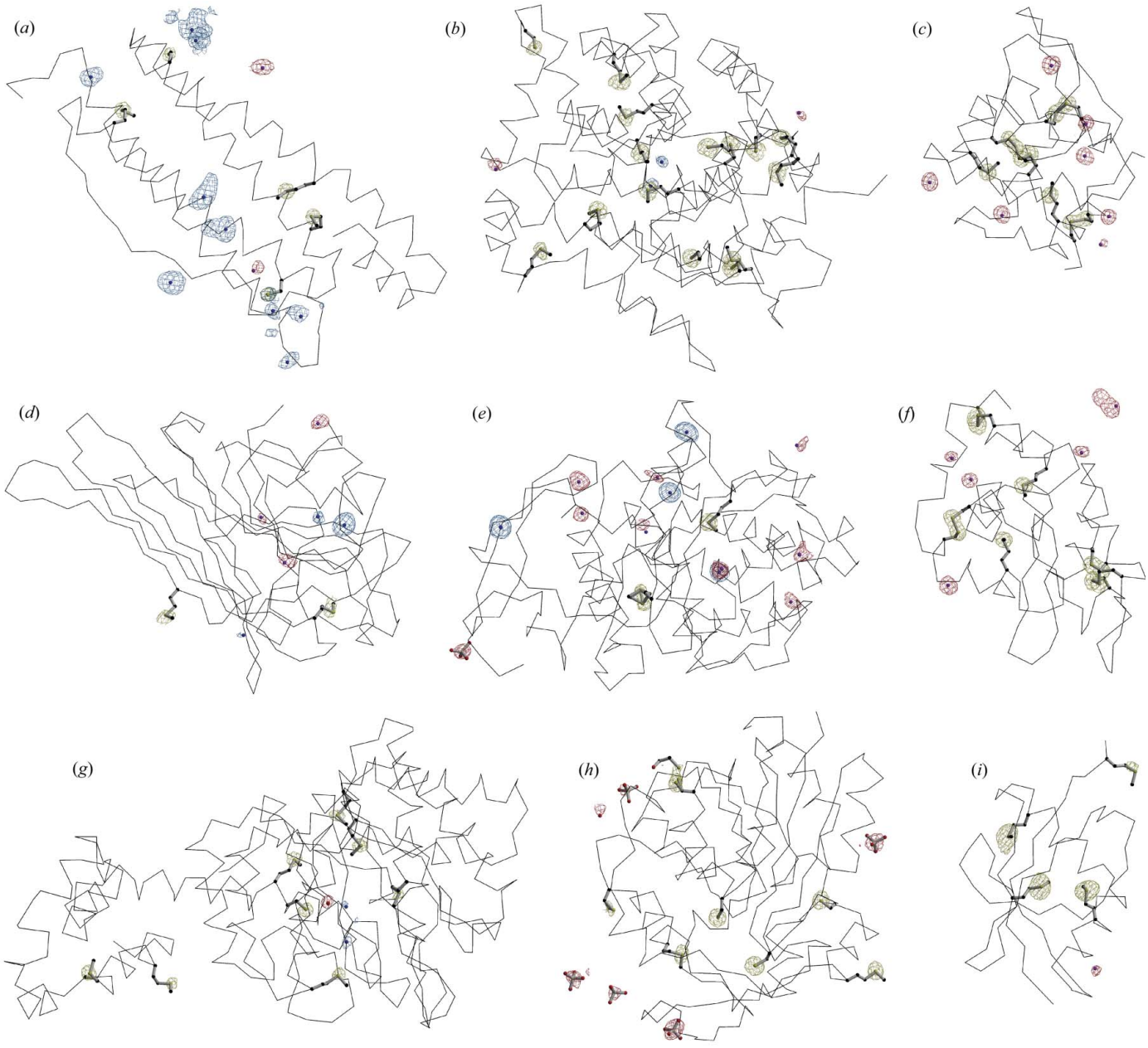

Figure 2
Anomalously scattering substructures for the 23 crystal systems. The proteins are depicted as C^{α} representations with the respective Cys and Met residues as ball-and-stick models. S atoms are shown in yellow, cations (Na^+, K^+, Mg^{2+}, Ca^{2+}, Cd^{2+}, Zn^{2+}, Mn^{2+}) as blue spheres and anions (Cl^-, SO_4^{2-}) as red spheres. All displayed anomalous electron-density maps are shown at a 3.0σ level and coloured yellow, red and blue according to the identity of the corresponding anomalous scatterers. The views are chosen for best visibility of all substructure atoms and electron-density peaks. (*a*) Apoferritin. All five sulfur positions (Cys52 SG, Met72 SD, Met100 SD, Cys130 SG and Met148 SD), two chloride and nine cadmium ions are shown with their anomalous electron densities. (*b*) Human ADP-ribosylhydrolase 3 (hARH3). All 15 inherent sulfur positions (Met1 SD, Cys10 SG, Cys19 SG, Met65 SD, Met84 SD, Cys116 SG, Cys271 SG, Met139 SD, Met203 SD, Met221 SD, Cys267 SG, Met272 SD, Met305 SD, Met316 SD and Cys327 SG) along with two magnesium and two chloride sites were identified within the anomalous substructure of the protein. (*c*) Hen egg-white lysozyme crystallized at pH 4.5 (HEL-4.5). All ten inherent S atoms (Cys6 SG, Met12 SD, Cys30 SG, Cys64 SG, Cys76 SG, Cys80 SG, Cys94 SG, Met105 SD, Cys115 SG and Cys127 SG) could be identified plus seven chloride ions. (*d*) Concanavalin A. The two S atoms from the inherent methionine residues (Met42 SD and Met129 SD) along with one Mn^{2+}, one Ca^{2+}, one Na^+ and three Cl^- are represented with the corresponding anomalous electron densities. (*e*) Thermolysin. In addition to the two sulfur positions Met120 SD (which exists in two alternative positions) and Met205 SD, an anomalous signal was found for one Zn^{2+} ion, three Ca^{2+} ions, one sulfate ion and eight chloride ions. (*f*) Hen egg-white lysozyme crystallized at pH 8.0 (HEL-8.0). All ten inherent S atoms (Cys6 SG, Met12 SD, Cys30 SG, Cys64 SG, Cys76 SG, Cys80 SG, Cys94 SG, Met105 SD, Cys115 SG and Cys127 SG) were identified plus five chloride ions. (*g*) Glucose isomerase. Eight sulfur positions representing the seven methionine (Met83 SD, Met87 SD, Met157 SD, Met222 SD, Met306 SD, Met369 SD and Met379 SD) and the one cysteine (Cys305 SG) residues as well as one calcium, one magnesium and one chloride ion were identified as part of the anomalous substructure. (*h*) Hydroxynitrile lyase (HNL). The substructure consists of 12 S atoms (six inherent sulfurs from Cys13 SG, Cys81 SG, Cys113 SG, Met122 SD, Cys161 SG and Met171 SD, five sulfate ions and one HEC molecule) and one chloride ion. For Cys113 SG two alternative positions can be observed. (*i*) NBR1 PB1 domain. All of the four sulfur positions from Met1 SD, Met34 SD, Met70 SD and Met80 SD as well as one chloride-ion position constitute the anomalous substructure.

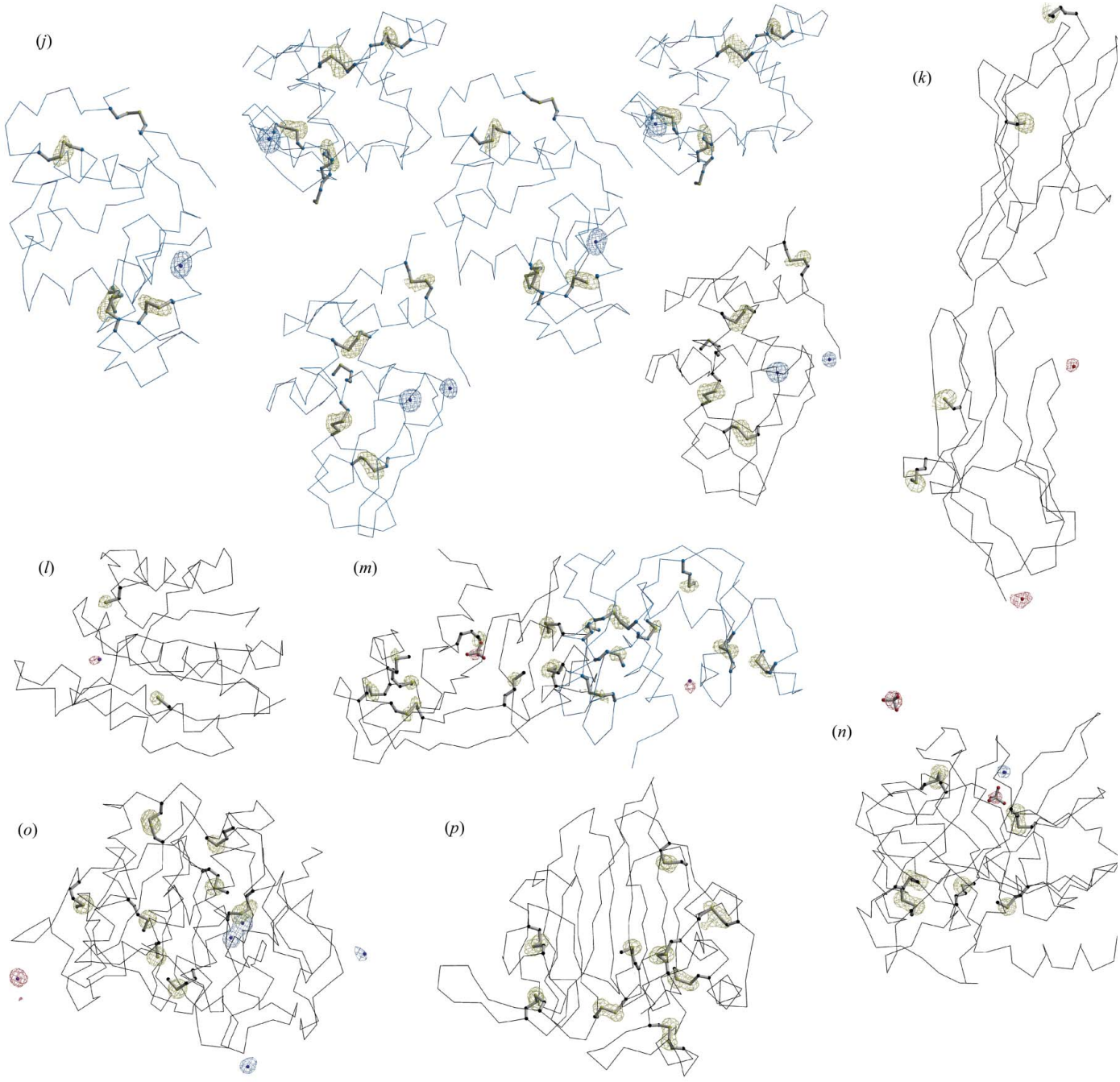

Figure 2 (continued)
(*j*) α-Lactalbumin. One protomer (chain *A*) C^{α} backbone is depicted in black and the other five protomer backbones (chains *B*–*F*) in blue. 42 of the 54 protein S atoms (Cys6*A*/*B*/*C*/*D* SG, Cys28*A*/*B*/*C*/*D*/*E*/*F* SG, Cys61*A*/*B*/*C*/*D*/*E*/*F* SG, Cys73*A*/*B*/*C*/*D*/*E*/*F* SG, Cys77*A*/*B*/*C*/*D*/*E*/*F* SG, Cys91*A*/*B*/*C*/*D*/*E*/*F* SG, Cys111*A*/*B*/*C*/*D*/*E*/*F* SG and Cys120*C*/*D* SG) were identified along with six calcium and two potassium ions. (*k*) Titin-(A168-A169). The anomalous substructure consists of the four S atoms from the inherent cysteine and methionine residues (Met1 SD, Cys24 SG, Met109 SD and Cys177 SG) and two Cl^{-} ions. (*l*) Probable molybdopterin-binding domain (MogA). In addition to the two inherent S atoms derived from Cys24 SG and Cys117 SG, one additional chloride-ion position was identified to reside in the active site of the protein. (*m*) Ribonuclease A in the monoclinic crystal form (RNAse A-C2). In the two protomers (chains *A* and *B*) per asymmetric unit, 23 of the expected 24 inherent sulfur positions (Met13*A*/*B* SD, Cys26*A*/*B* SG, Met29*A*/*B* SD, Met30*A*/*B* SD, Cys40*A*/*B* SG, Cys58*A*/*B* SG, Cys65*A*/*B* SG, Cys72*A*/*B* SG, Met79*A*/*B* SD, Cys84*A*/*B* SG, Cys95*A* SG and Cys110*A*/*B* SG) are above the noise level. Only the atom Cys95*B* SG exhibits an anomalous signal that is too low. One sulfate and one chloride ion were also found. (*n*) Porcine pancreatic elastase in its sodium form (PPE-Na). All ten inherent S atoms (Cys30 SG, Met41 SD, Cys46 SG, Cys127 SG, Cys158 SG, Met172 SD, Cys174 SG, Cys184 SG, Cys194 SG and Cys214 SG) were present. Two sulfate ions and one sodium ion were also found. (*o*) Proteinase K. The anomalous substructure comprises the ten expected protein S atoms (Cys34 SG, Met55 SD, Cys73 SG, Met111 SD, Cys123 SG, Met154 SD, Cys178 SG, Met225 SD, Met238 SD and Cys249 SG), two potassium ions, two calcium ions and one chloride ion. (*p*) Thaumatin. All of the 17 expected inherent sulfur positions (Cys9 SG, Cys56 SG, Cys66 SG, Cys71 SG, Cys77 SG, Met112 SD, Cys121 SG, Cys126 SG, Cys134 SG, Cys145 SG, Cys149 SG, Cys158 SG, Cys164 SG, Cys177 SG, Cys193 SG and Cys204 SG) could be found in the anomalous substructure and no additional ions were found.

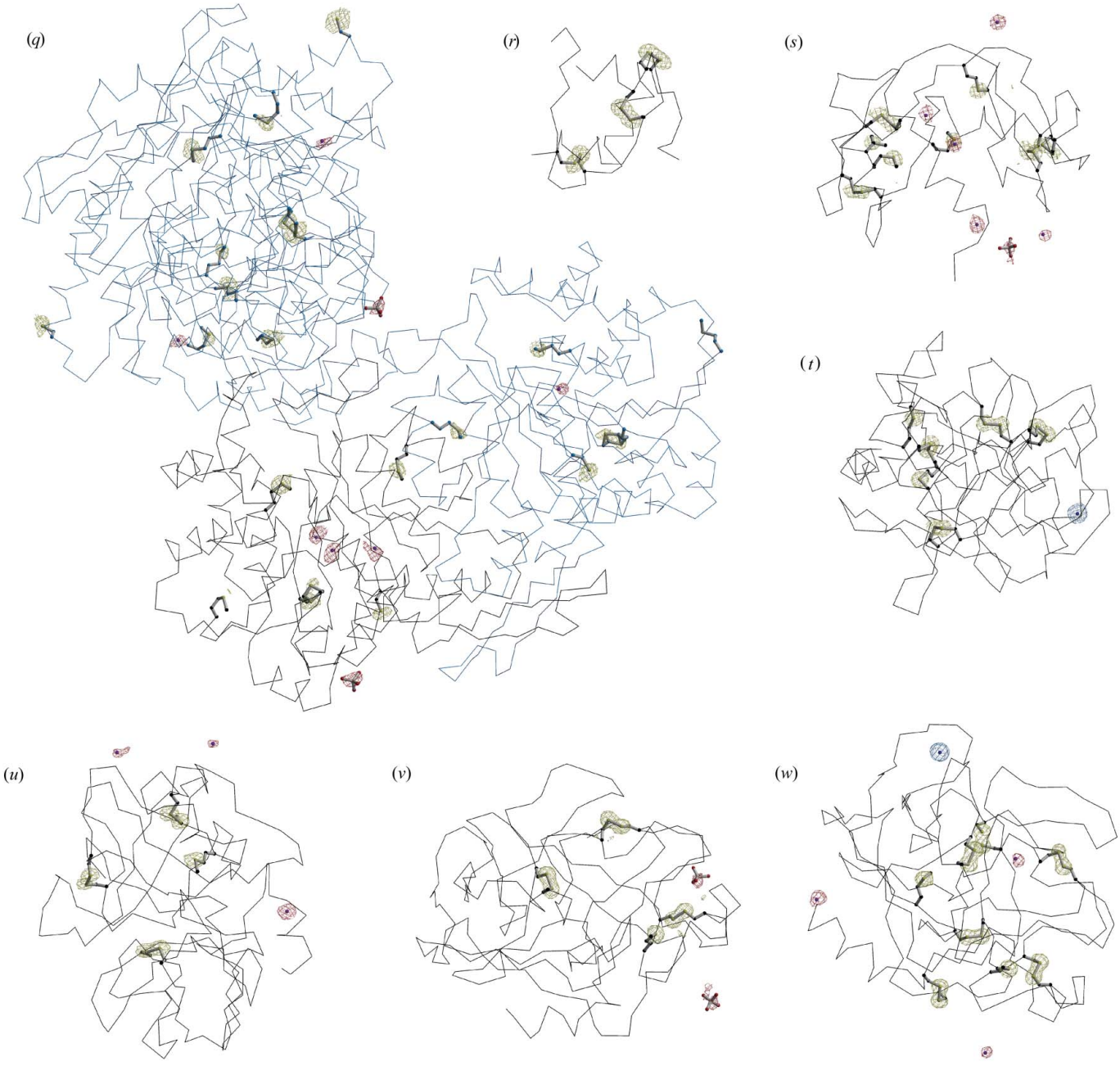

Figure 2 (continued)
(*q*) 3-Isopropylmalate dehydrogenase (LeuB). One protomer of the protein that can be seen as a dimer of dimers is shown in black (chain *A*), whereas the other three protomers (chains *B*–*D*) are in blue. 24 S atoms (the 22 protein S atoms from Met1*C*/*D* SD, Cys199*A*/*B*/*C*/*D* SG, Met217*A*/*B*/*C*/*D* SD, Cys245*A*/*B*/*C*/*D* SG, Met265*A*/*B*/*C*/*D* SD and Met289*A*/*B*/*C*/*D* SD and two sulfate ions) as well as six chloride-ion positions can be observed in the anomalous substructure. The Met165 SD atoms in both subunits *A* and *B* exist in two alternative positions. (*r*) Insulin. This substructure constitutes only the six S atoms from the inherent three disulfide bridges present in the two chains *A* and *B* (Cys6*A* SG, Cys7*A* SG, Cys7*B* SG, Cys11*A* SG, Cys19*B* SG, Cys20*A* SG). (*s*) Ribonuclease A in its trigonal crystal form (RNAse A-$P3_221$). All 12 naturally occurring S atoms (Met13 SD, Cys26 SG, Met29 SD, Met30 SD, Cys40 SG, Cys58 SG, Cys65 SG, Cys72 SG, Met79 SD, Cys84 SG, Cys95 SG and Cys110 SG), one sulfate and five chloride ions constitute the anomalous substructure. (*t*) Porcine pancreatic elastase in its calcium form (PPE-Ca). All ten inherent S atoms (Cys30 SG, Met41 SD, Cys46 SG, Cys127 SG, Cys158 SG, Met172 SD, Cys174 SG, Cys184 SG, Cys194 SG and Cys214 SG) were present. In addition, one calcium ion was found in the metal-binding site of the protein. (*u*) and (*v*) Trypsin from *F. oxysprum*. The anomalous substructure of the triclinic crystal form consists of all seven naturally occurring sulfur positions (Cys41 SG, Cys57 SG, Cys165 SG, Met178 SD, Cys180 SG, Cys191 SG and Cys216 SG) plus three chloride ions (*u*), whereas the substructure of the monoclinic crystal form (*v*) comprises the seven protein sulfur positions and two additional sulfate ions. For Cys41 SG, a second position can be observed approximately 1.2 Å away from its main position. (*w*) Bovine trypsin. Here, the anomalous substructure shows all of the 14 protein sulfur positions (Cys13 SG, Cys31 SG, Cys47 SG, Met92 SD, Cys115 SG, Cys122 SG, Cys143 SG, Cys154 SG, Met166 SD, Met168 SD, Cys179 SG, Cys189 SG, Cys203 SG and Cys216 SG) and in addition one Ca^{2+} and three Cl^- ions.

ment of the crystal for cryoprotection was different, which may have led to the different substructure.

3.2.9. Probable molybdopterin-binding domain (MogA). All of the six protein S atoms of this homotrimeric protein were visible in the anomalous difference Fourier synthesis. In addition, a partially occupied Cl^- ion ($q = 0.5$) was found to be bound in the presumed phosphate-binding site of the protein (Fig. 2*l*).

3.2.10. NBR1 PB1 domain. The substructure of the NBR1 PB1 domain (Fig. 2*i*) contains all four protein sulfur positions expected as well as one partially occupied Cl^- ion ($q = 0.2$) which has not been observed before (Müller *et al.*, 2006).

3.2.11. Porcine pancreatic elastase (PPE-Na and PPE-Ca). The substructures of PPE-Na with two partially occupied SO_4^{2-} ions ($q = 0.7$ and 0.4, respectively) and one fully occupied Na^+ ion (Fig. 2*n*) as well as of that of PPE-Ca (Fig. 2*t*) with a partially occupied Ca^{2+} position ($q = 0.85$) have been described previously (PDB codes 1lka and 1lkb; Weiss *et al.*, 2002). While a Cl^- position was previously reported for PPE-Na and PPE-Ca near the side chain of Ser14, this is not the case here. The explanation of this may be a too low an occupancy of the chloride in the case of PPE-Ca and the careful omission of any chloride during buffer equilibration in the case of PPE-Na.

3.2.12. Proteinase K. The anomalous substructure of proteinase K (Fig. 2*o*) consists of all ten expected protein sulfur positions, two calcium ions ($q = 0.65$ and 0.35), two potassium ions ($q = 0.30$ and 0.15) and one chloride ion ($q = 0.40$). Except for the calcium positions, none of the other ions of the anomalous substructure have been reported in the 0.98 Å resolution structure of proteinase K (PDB code 1ic6; Betzel *et al.*, 2001). This can be explained by the fact that the crystal on which the 1ic6 structure is based was grown at pH 6.5 in the presence of $NaNO_3$ as a precipitant, while the crystals described here were grown at pH 7.0 using sodium/potassium tartrate as the precipitant.

3.2.13. Ribonuclease A (RNase A). Of the 12 expected sulfur positions per protomer derived from Cys and Met residues, all 12 were observed in the trigonal crystal form, which contains one protomer per asymmetric unit (Fig. 2*s*). In addition to this, one partially occupied SO_4^{2-} ion ($q = 0.5$) and five chloride ions ($q = 0.75$ and 0.45) were detected. None of these ions has been described in the published structure of RNAse A in the trigonal form (PDB code 1fs3; Chatani *et al.*, 2002). In the case of the monoclinic crystal form, which contains two protomers per asymmetric unit, only the anomalous signal of the S atoms of Cys95 SG in subunit *B* was at 3.7σ below the set threshold (Fig. 2*m*). In addition to the protein S atoms, one partially occupied SO_4^{2-} ion ($q = 0.4$; not at the same position as in the trigonal form) and one partially occupied chloride ion ($q = 0.3$; corresponding to one Cl^- position in the trigonal form) were identified within the monoclinic form of RNase. None of them had been described previously (PDB code 1w4o; Jenkins *et al.*, 2005). This is interesting in so far as neither SO_4^{2-} nor Cl^- ions were present in the crystallization cocktail. This can only be explained by the fact that these ions must have remained bound to the protein during protein preparation.

3.2.14. Thermolysin (TLN). In TLN (Fig. 2*e*), one Zn^{2+} ion and three Ca^{2+} ions were found in addition to the two protein S atoms (where Met120 SD occurs in two alternative positions), as well as one SO_4^{2-} ion and eight partially occupied chloride ions ($q = 0.70$–0.20). This substructure differs from that previously reported (PDB code 2a7g; Mueller-Dieckmann *et al.*, 2005). For the two DMSO molecules that had been reported to bind to the surface of the protein, the explanation may be that although DMSO was used during the crystallization, it has been replaced by dry paraffin oil as cryoprotectant. As a consequence, the two DMSO molecules may have simply been washed off by the dry paraffin oil. The three Ca^{2+} ions and the Zn^{2+} ion identified are located on identical positions as reported previously. The other Ca^{2+} ions reported previously are missing, but eight chloride ions have been identified that had not been reported previously. One of the chlorides occupies the position where an acetate ion has previously been reported to bind. It is likely that the different crystallization conditions caused this difference in the substructure.

3.2.15. Titin-(A168-A169). The substructure of the two immunoglobulin-like domains A168-A169 of human cardiac titin (Fig. 2*k*) consists of all four protein S atoms and two additional chloride ions ($q = 0.35$ and 0.30, respectively). The complete structure of titin-(A168-A169) will be described elsewhere (Müller *et al.*, manuscript in preparation).

3.2.16. Trypsin from *F. oxysporum*. In the case of the triclinic form of trypsin (Fig. 2*u*), all seven protein sulfur positions could be detected in the anomalous difference Fourier map. In addition, three partially occupied chloride ions ($q = 0.50$–0.25) were found, one occupying the position where a sulfate ion was reported to bind (PDB code 1pq5; Schmidt *et al.*, 2003). Because of the nearly spherical shape of the corresponding peak in the ($2F_{\rm obs} - F_{\rm calc}$, $\alpha_{\rm calc}$) electron-density map, as well as the distances to the surrounding protein atoms of 2.6–3.9 Å, the assignment of this ion as a chloride seems to be most plausible. The other two sulfate ions reported in PDB entry 1pq5 did not exhibit a detectable anomalous signal, probably owing to occupancies that were too low. The anomalous substructure of the monoclinic form of trypsin (Fig. 2*v*) contains all seven protein sulfur positions derived from Cys and Met residues and two partially occupied sulfate ions ($q = 0.35$). A peak was detected in the anomalous difference Fourier map approximately 1.2 Å distant from the SG atom of Cys41, indicating that the disulfide bridge Cys41–Cys57 has been partially reduced during data collection. However, owing to the extra peak being below the threshold of 4.0σ, a second conformation for Cys41 was not modelled. Neither of the two sulfate positions coincided with the one sulfate position previously described (PDB code 1ppz; Schmidt *et al.*, 2003).

3.2.17. Bovine trypsin. In the trigonal form of bovine trypsin the substructure contains all 14 sulfurs from the protein Cys and Met residues (Fig. 2*w*). Additionally, one fully occupied Ca^{2+} ion as well as three partially occupied Cl^- ions

(q = 0.40–0.25) complement the protein part. Interestingly, none of these three chloride positions coincide with the two described previously (PDB code 2a7h; Mueller-Dieckmann *et al.*, 2005).

3.3. Uncertainties in occupancy values

The correlation coefficients between the peak heights of the protein S atoms for the systems HEL-45, PPE-Ca, thaumatin and trypsin-$P3_121$ were 0.91, 0.83, 0.92 and 0.75, respectively, when compared with data collected at a wavelength of 1.5 Å (8.26 keV) as reported in Mueller-Dieckmann *et al.* (2005). Consequently, a safe estimate of the uncertainty in the occupancy values is approximately 25% of the peak height of an S atom. Expressed in units of electrons, this would be 0.23 e at the wavelength used for collecting the diffraction data for this study.

3.4. Usability of the anomalous signal for phase determination

11 of the 23 structures could be solved automatically using the SAD protocol of the *AutoRickshaw* pipeline (Panjikar *et al.*, 2005). These include all high-symmetry examples (cubic, hexagonal and tetragonal) except apoferritin. 50% of the trigonal systems and 33% of the orthorhombic systems could be solved, but none of the monoclinic and triclinic systems.

4. Discussion

4.1. Reliability of the substructures

The reliability of the presented anomalously scattering substructures can best be gauged by looking at how many of the protein S atoms that are known to be present show a detectable signal in the anomalous difference Fourier map. In nearly all of the presented cases practically all protein S atoms could be observed, which lends a high degree of reliability to the remainder of the substructure. The only real exception to this was the case of α-lactalbumin, where only about 78% of all protein S atoms show a strong enough signal ($\geq 4.0\sigma$) in the anomalous difference Fourier synthesis. The reason for this may be the relatively low resolution of the data set (2.30 Å), the relatively high overall temperature factor ($\sim$40 Å^2) and/or the comparatively lower data quality. Other examples of protein S atoms not being detected were the N-terminal Met SDs in LeuB in two of the four subunits present in the asymmetric unit. However, N-terminal Met residues are notoriously flexible, so this observation is not surprising. A second measure of the reliability of the substructure is the noise in the anomalous electron-density map as expressed by the peak height of the first spurious or unassigned peak in the anomalous difference Fourier syntheses. With the sole exception being apoferritin, all peaks above 5.0σ could be unambiguously assigned to a protein S atom or an ion bound to the surface of the protein. Peaks between 4.0σ and 5.0σ could sometimes be assigned with the help of the known protein structure or if the chemical environment permitted a meaningful assignment. A more quantitative analysis of the uncertainties in the occupancy values based on the correlation coefficient between peak heights in two different data sets from the same crystal system revealed that the error in the peak heights is at most one quarter of the peak height of an S atom. Consequently, the assignment of peaks to weakly bound light-atom ions (phosphate, sulfate or chloride) with occupancy values significantly below 0.25 has to be treated with caution.

4.2. Alternative positions

In some of the cases, alternative positions could be clearly observed for individual substructure atoms. In the case of Cys residues which are involved in a disulfide bond, such as Cys41 in the monoclinic form of trypsin from *F. oxysporum*, this can be attributed to the advent of radiation damage during data collection. In the case of Met residues, for instance Met165 in LeuB or Met120 in TLN, or of free Cys residues, such as Cys113 in HNL, these alternative positions probably indicate generic alternate side-chain conformations of the amino-acid residues.

4.3. New features in substructures

In only two of the 23 cases studied (insulin and thaumatin) does the anomalous substructure consist of protein S atoms alone. This means that in more than 90% of all cases the protein molecule binds light-atom ions such as chloride, phosphate, sulfate, potassium calcium or others. This number is in stark contrast to the findings in the PDB, where only about 15% of all protein structures have other ions bound to them. In our opinion, this can only mean that in most of the macromolecular structures deposited in the PDB the anomalously scattering substructures are not completely defined. We would therefore like to propose the collection of a long-wavelength data set to complement and to complete any macromolecular structure determination.

4.4. Malleability of the substructures

In some of the described cases, it was observed that substructures may differ slightly even between crystals of the same protein grown under identical conditions. In particular, the ions bound to the macromolecule at low occupancy values appear to be detectable in one experiment but not in another. The reason for this may be that slight differences in crystal handling may cause some alterations in the substructures. In particular, the choice of the cryoprotectant may be crucial in this respect. For instance, the use of paraffin oil to cryoprotect TLN crystals may have led to the removal of surface-bound DMSO molecules, whereas the surface-bound chloride ions remained bound to the protein. In contrast, the use of DMSO/glycerol as cryoprotectant apparently leads to the removal of the surface-bound chloride ions (Mueller-Dieckmann *et al.*, 2005). It is typically the case, however, that the only parts of the substructures that are affected by this are the weakly bound compounds and ions, which exhibit low occupancy values. Nevertheless, they are still capable of delivering some information about the binding properties of the protein

surface, although they may just be bound to the protein serendipitously.

4.5. Inferring function from ion binding

In some favourable cases it may be that bound ions identify functionally important sites in the protein. For instance, the bound chloride ion in MogA pinpoints the presumed phosphate-binding site and thus the active site of the protein. At the least, careful examination of the substructure provides additional information towards the analysis of the function of the protein.

4.6. Usability of the anomalous signal for phase determination

The most obvious use of collecting good anomalous differences in macromolecular crystallography is of course phase determination. Although none of the data sets described here were collected with this aim, it turned out that 11 of the 23 structures could be solved automatically based on the anomalous differences collected. For all of the successful cases the data redundancy was 18 or above, except for the three successful examples belonging to the orthorhombic crystal system [PPE-Na, PPE-Ca and titin-(A168-A169)]. It must of course be expected that if higher redundancy data for the lower symmetry systems were available, these structures could also be solved. The only unsuccessful case at such high data redundancy is apoferritin, but the reason for this example failing in the automated structure determination is presently not clear to us.

5. Summary and conclusions

From the results presented, it is clear that longer wavelength data carefully collected to high redundancy and properly processed and scaled can be very useful in establishing which ions from the buffer or even from the purification protocol might be bound to the protein molecule of interest. In particular, the positions and occupancies of phosphate, sulfate, chloride, calcium *etc*. can be established reliably. In many cases this information may turn out to be very important for elucidating the function of a molecule. Thus, it would be desirable that any macromolecular structure determination be complemented with a long-wavelength data set.

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