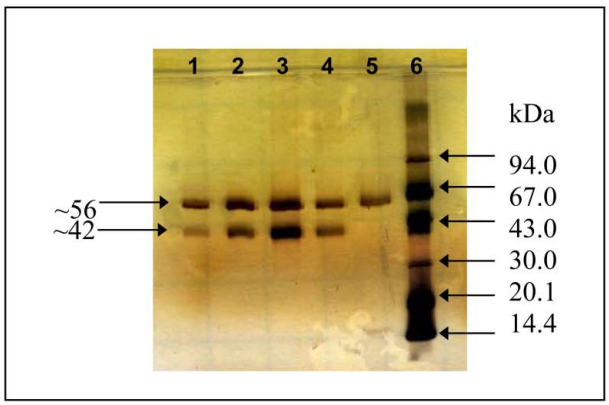
Supplemental Material

S1. SDS-silver stained gel. Lanes 1 –5, successive fractions from the pAMBS resin purification (lane 1-5 pooled and used for crystallization); Lane 6, Low molecular weight standards. Arrows indicate the position of HSA (56 kDa) and HCA VI (42 kDa).



S2. DENZO (Otwinowski & Minor, 1997) output listing the 14 possible Bravais lattices in decreasing order of symmetry and % distortion index. Cell dimensions given are not refined.

Lattice	Metric tensor distortion index	Best cell (symmetrized) Best cell (without symmetry restrains)					
primitive cubic	14.40%	71.61	83.28	90.97	78.30	90.28	115.35
		81.95	81.95	81.95	90.00	90.00	90.00
I centred cubic	14.02%	83.28	110.56	115.50	70.97	96.06	108.00
		103.11	103.11	103.11	90.00	90.00	90.00
F centred cubic	13.59%	157.64	115.50	116.05	76.42	73.20	73.47
		129.73	129.73	129.73	90.00	90.00	90.00
primitive rhombohedral	8.86%	90.97	110.56	110.17	37.86	47.75	47.69
		103.90	103.90	103.90	44.43	44.43	44.43
		83.35	83.35	280.88	90.00	90.00	120.00
primitive hexagonal	6.89%	71.61	83.41	90.97	101.44	90.28	115.54
		77.51	77.51	90.97	90.00	90.00	120.00
primitive tetragonal	13.05%	83.28	90.97	71.61	89.72	115.35	101.70
		87.13	87.13	71.61	90.00	90.00	90.00
I centred tetragonal	10.43%	71.61	90.97	157.64	68.59	90.27	90.28
		81.29	81.29	157.64	90.00	90.00	90.00
primitive orthorhombic	12.64%	71.61	83.28	90.97	78.30	90.28	115.35
		71.61	83.28	90.97	90.00	90.00	90.00
C centred orthorhombic	5.37%	71.61	150.52	90.97	77.17	90.28	89.88
		71.61	150.52	90.97	90.00	90.00	90.00
I centred orthorhombic	9.24%	71.61	90.97	157.64	68.59	90.27	90.28
		71.61	90.97	157.64	90.00	90.00	90.00
F centred orthorhombic	7.82%	83.28	131.29	184.10	87.35	75.41	99.63
		83.28	131.29	184.10	90.00	90.00	90.00
primitive monoclinic	5.37%	71.61	90.97	83.28	101.70	115.35	89.72
		71.61	90.97	83.28	90.00	115.35	90.00
C centred monoclinic	0.14%	150.52	71.61	90.97	90.28	102.83	90.12
		150.52	71.61	90.97	90.00	102.83	90.00
primitive triclinic	0.00%	71.61	83.28	90.97	78.30	89.72	64.65

S3. HSA X-ray diffraction data collection statistics.

Resolution shell (Å)	No. reflections	% Completeness	*R_{sym}
20.00 - 6.40	1809	90.8	0.096
6.40 - 5.11	1857	95.4	0.138
5.11 - 4.47	1872	97.7	0.121
4.47 - 4.06	1878	97.0	0.123
4.06 - 3.78	1848	97.5	0.139
3.78 - 3.55	1897	97.0	0.153
3.55 - 3.38	1859	97.4	0.201
3.38 - 3.23	1871	97.4	0.238
3.23 - 3.11	1862	97.3	0.274
3.11 - 3.00	1828	95.6	0.331
Total 20.00-3.00	18581	96.2	0.166

*R_{sym} – Σ |I-<I>)| / Σ I, where I is the intensity of a reflection and <I> is the average intensity.

S4. Ramachandran plot of refined HSA model. Generated by PROCHECK (Laskowski *et al.*, 1993). Black filled triangles represent glycines.