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**Supporting information for article:**

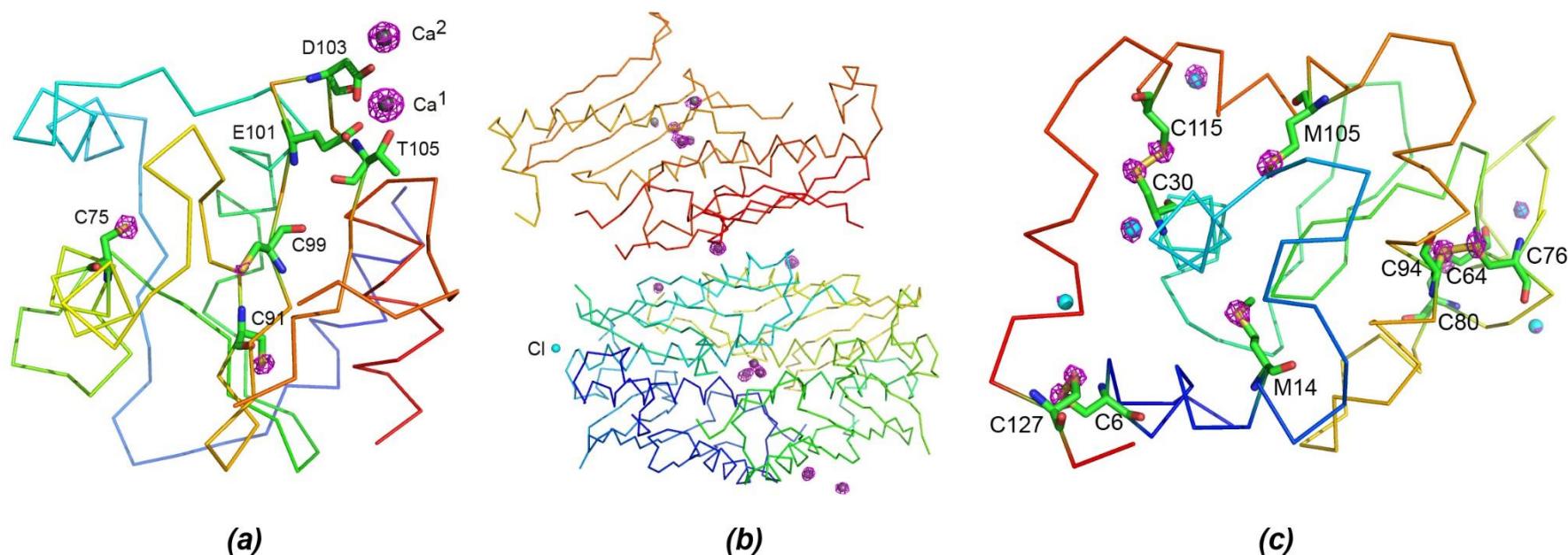
**The hidden treasure in your data: phasing with unexpected weak anomalous scatterers from routine data sets**

**Raghurama P. Hegde, Alexander A. Fedorov, J. Michael Sauder, Stephen K. Burley, Steven C. Almo and Udupi A. Ramagopal**

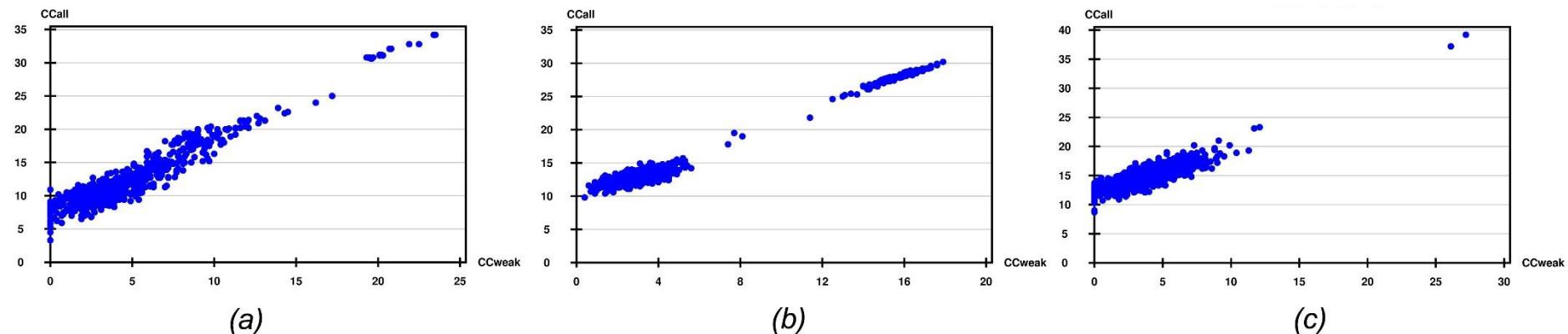
**Table S1** Anomalous peaks in final structure vs SHELXD peaks for HEWLAll data set.

Peaks were calculated by the program Anode (Thorn & Sheldrick, 2011). SHELXD was run using default parameters with three disulfide bonds resolved and an E-value cut off of 1.7

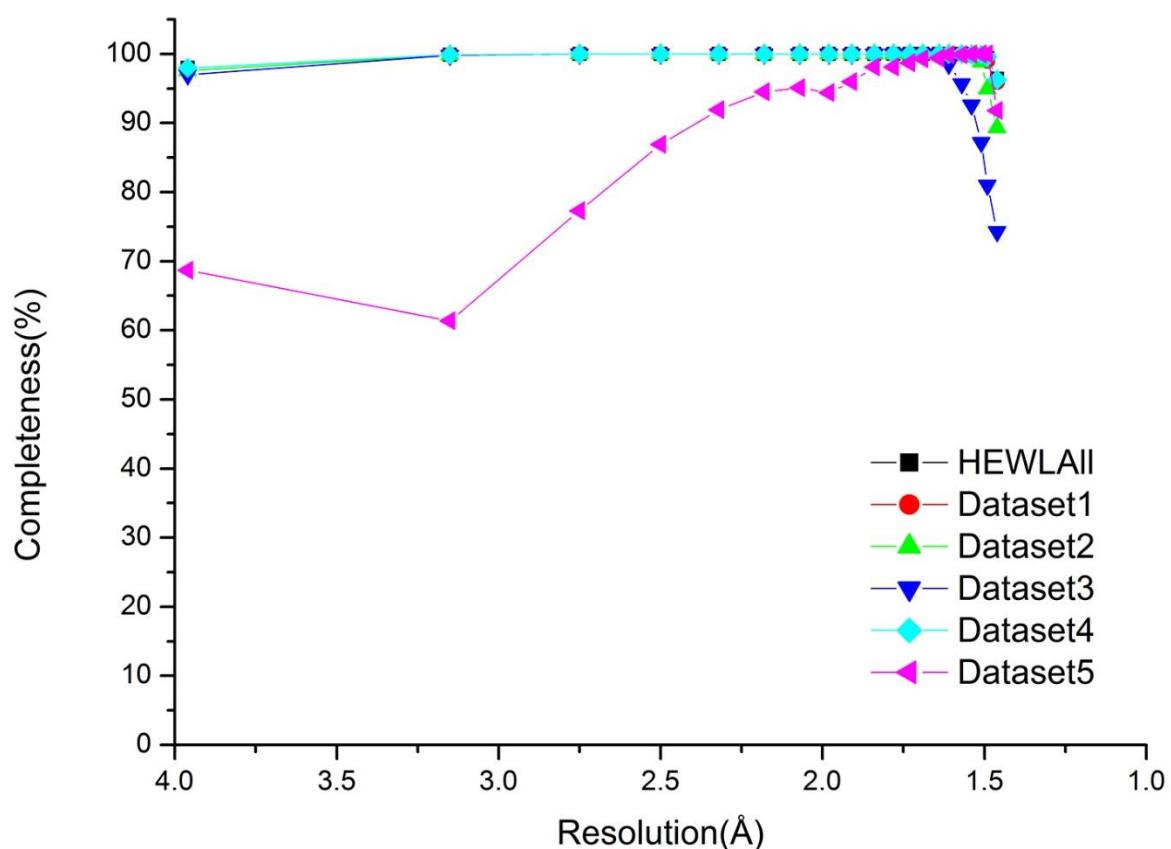
| Anomalous peak      | B-factor           | SHELXD peak no.                             |
|---------------------|--------------------|---|
| height ( $\sigma$ ) | ( $\text{\AA}^2$ ) |   |
| 19.59 (Met105)      | 11.43              | 5   |
| 18.81 (Cys80)       | 11.36              | 2   |
| 18.66 (Cys64)       | 11.96              | Not located (part of disulfide with Cys80)  |
| 18.17 (Cl5)         | 28.07              | 7   |
| 17.66 (Cys30)       | 12.2               | 4   |
| 16.73 (Met12)       | 12.97              | 1   |
| 15.77 (Cys115)      | 12.73              | 3 (disulfide with Cys30)                    |
| 15.49 (Cys6)        | 17.81              | Not located (part of disulfide with Cys127) |
| 15.36 (Cys94)       | 13.70              | 8 (part of disulfide with Cys76)            |
| 14.51 (Cys76)       | 14.47              | 6 (part of disulfide with Cys94)            |
| 13.78 (Cys127)      | 16.11              | 9 (part of a disulfide with Cys6)           |
| 12.60 (Cl1)         | 20.39              | Not located                                 |
| 12.13 (Cl3)         | 20.54              | 11  |
| 9.22 (Cl4)          | 26.73              | Not located                                 |
| 8.01 (Cl2)          | 28.92              | 10  |



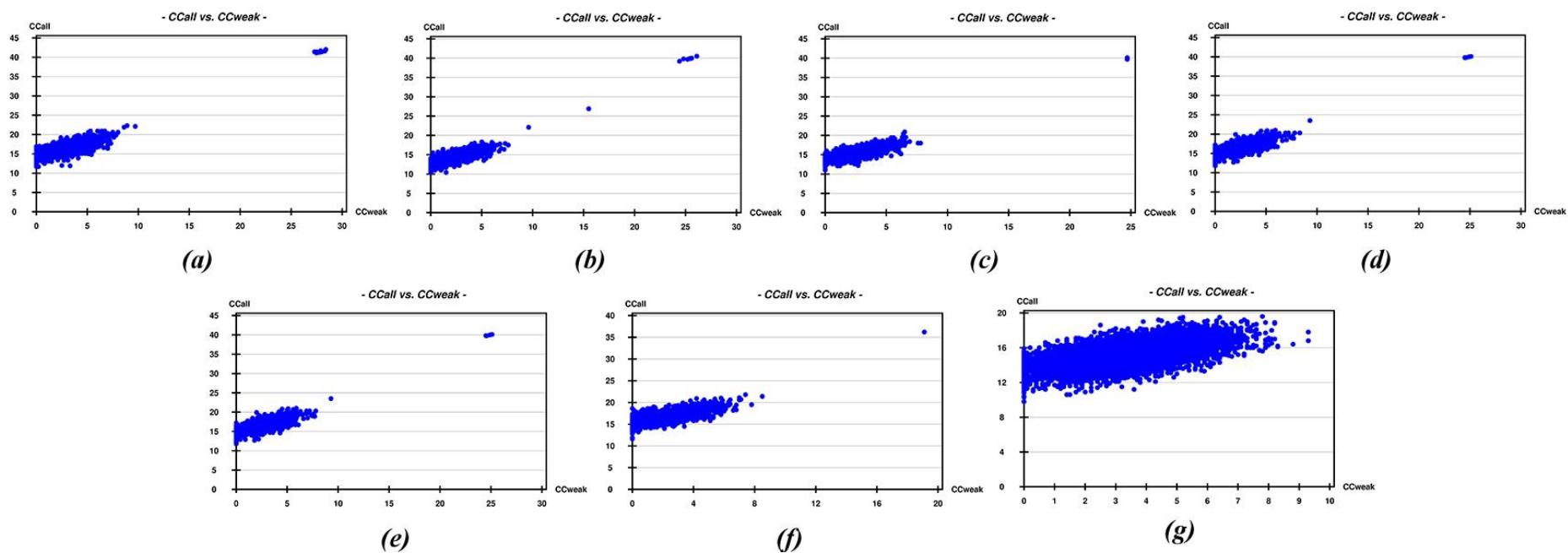
**Figure S1** Representation of the structures of the three proteins with anomalous maps displayed around the anomalous scatterers in the proteins. The protein chains are shown as  $C^\alpha$  traces and the anomalous maps are shown as purple meshes contoured at  $5\sigma$  level. (a) PSPTO, the two calcium atoms are shown as grey spheres, the residues coordinating with the calcium atoms and the cysteines in the protein chain are shown and labelled; (b) PTO, the calcium atoms are shown as grey spheres and the chlorine atom as a cyan sphere. Each of the six chains in the asymmetric unit are colored differently; (c) HEWL, the cysteines and methionines in the protein chain are shown and labelled, the chlorine atoms are shown as cyan spheres. Made using PyMOL (Schrodinger, 2010).



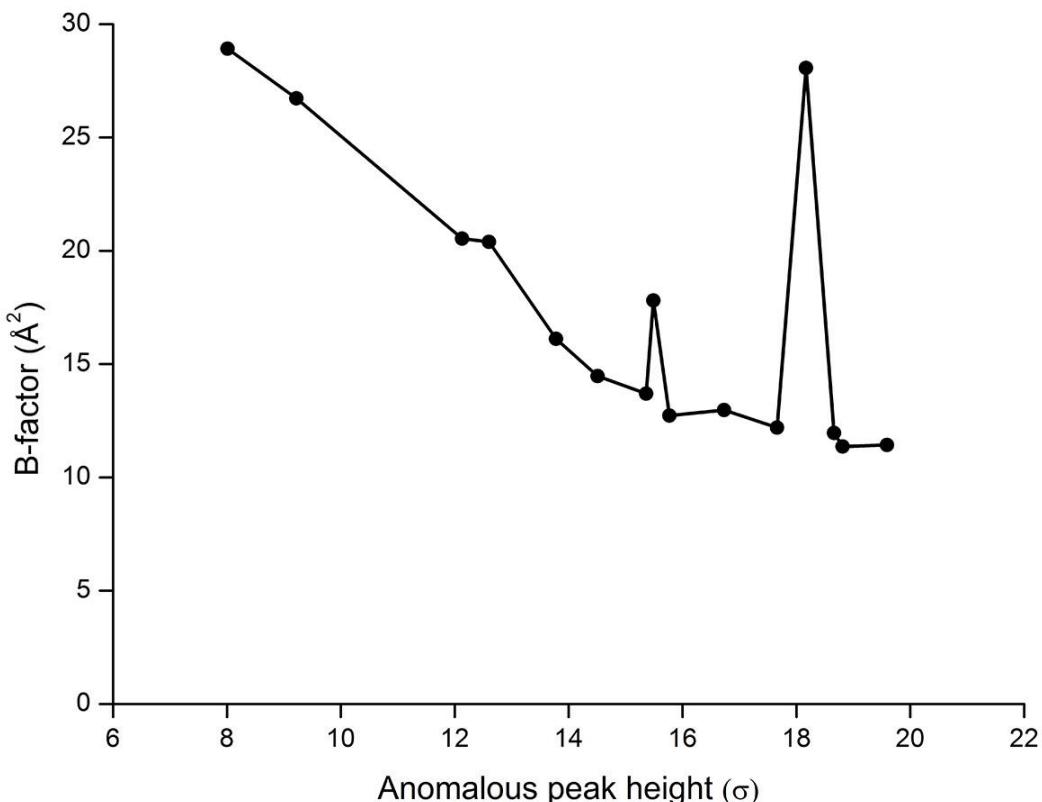
**Figure S2**  $\text{CC}_{\text{all}}$  vs  $\text{CC}_{\text{weak}}$  from SHELXD run of 1000 cycles for each of the three cases: (a) PSPTO, (b) PTO and (c) HEWL (corresponding to data set HEWLAll) showing a clear bimodal distribution of solutions, separating the correct and incorrect substructure solutions.



**Figure S3** A plot of completeness vs resolution for the lysozyme (HEWL) data sets.



**Figure S4** CC<sub>all</sub> vs CC<sub>weak</sub> from SHELDXL run for HEWLAll data set with (a) top 5% intense reflections removed (b) top 10% intense reflections removed (c) top 15% intense reflections removed (d) top 20% intense reflections removed (e) top 25% intense reflections removed (f) top 30% intense reflections removed (g) top 35% intense reflections removed. All the above are for 1000 runs in SHELDXL, except in (g) which represents the results after 10,000 runs.



**Figure S5** A scatter plot of the distribution of B-factor vs anomalous peak height in HEWL structure (generated from Table S1). The large spike around  $18\sigma$  corresponds to a surface bound chlorine which is expected to have a high B-factor and the smaller spike around  $15.5\sigma$  corresponds to the sulfur of Cys6. Other than these outliers the general trend observed for the intrinsic sulfurs is a decrease in anomalous peak height with increase in B-factor.

## References

- Thorn, A. & Sheldrick, G. M. (2011). J. Appl. Crystallogr. 44, 1285-1287.  
Schrodinger, LLC (2010). The PyMOL Molecular Graphics System, Version 1.5.0.3.

**PSPTO\_fa.res file**

```

REM Best SHELXD solution: CC 34.24 CC(weak) 23.47 CFOM 57.70
REM
TITL 10412i_S_fa.ins SAD in P41212
CELL 0.98000 47.43 47.43 122.49 90.00 90.00 90.00
LATI -1
SYMM 1/2-Y, 1/2+X, 1/4+Z
SYMM -X, -Y, 1/2+Z
SYMM 1/2+Y, 1/2-X, 3/4+Z
SYMM 1/2-X, 1/2+Y, 1/4-Z
SYMM Y, X, -Z
SYMM 1/2+X, 1/2-Y, 3/4-Z
SYMM -Y, -X, 1/2-Z
SFAC S
UNIT 256
S001 1 0.003403 0.426918 0.022643 1.0000 0.2
S002 1 0.117233 0.408012 -0.059802 0.8380 0.2
S003 1 0.080734 0.395813 0.103959 0.6848 0.2
S004 1 0.105286 0.356133 -0.035196 0.5262 0.2
S005 1 0.330635 0.424683 0.135382 0.3388 0.2
S006 1 0.532372 0.296120 0.192777 0.3233 0.2
S007 1 0.046387 0.391068 -0.095932 0.1191 0.2
HKLF 3
END

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**PTO\_fa.res file**

```

REM Best SHELXD solution: CC 30.19 CC(weak) 17.94 CFOM 48.13
REM
TITL 10163d_360_fa.ins SAD in C2221
CELL 0.98000 90.76 143.49 129.80 90.00 90.00 90.00
LATI -7
SYMM -X, -Y, 1/2+Z
SYMM -X, Y, 1/2-Z
SYMM X, -Y, -Z
SFAC S
UNIT 256
S001 1 0.286736 0.135002 0.057452 1.0000 0.2
S002 1 0.416985 0.240723 0.127700 0.7908 0.2
S003 1 0.349785 0.005997 0.007505 0.5983 0.2
S004 1 0.180847 0.282982 0.107185 0.5293 0.2
S005 1 -0.012398 0.258965 0.233591 0.5050 0.2
S006 1 0.296280 0.315948 0.067201 0.4804 0.2
S007 1 0.467339 -0.012825 0.203872 0.4767 0.2
S008 1 -0.046928 0.337044 0.231282 0.4726 0.2
S009 1 0.030632 0.380539 0.060239 0.4725 0.2
S010 1 -0.134888 0.380630 0.103190 0.4388 0.2
S011 1 0.322906 0.001480 0.104827 0.4371 0.2
S012 1 0.183197 0.151321 0.143926 0.4284 0.2

```

|      |   |           |           |           |        |     |
|------|---|-----------|-----------|-----------|--------|-----|
| S013 | 1 | 0.570572  | 0.235069  | 0.079985  | 0.4273 | 0.2 |
| S014 | 1 | 0.458809  | -0.008781 | 0.099924  | 0.4164 | 0.2 |
| S015 | 1 | 0.149506  | 0.239586  | 0.136381  | 0.4105 | 0.2 |
| S016 | 1 | 0.161339  | 0.364388  | 0.098257  | 0.4092 | 0.2 |
| S017 | 1 | 0.238289  | 0.051743  | 0.004251  | 0.4066 | 0.2 |
| S018 | 1 | 0.265968  | 0.314857  | 0.195208  | 0.4042 | 0.2 |
| S019 | 1 | 0.041702  | 0.448143  | -0.002794 | 0.4004 | 0.2 |
| S020 | 1 | 0.516685  | 0.324188  | 0.039774  | 0.3964 | 0.2 |
| S021 | 1 | 0.048965  | 0.205032  | 0.178017  | 0.3922 | 0.2 |
| S022 | 1 | 0.122383  | 0.277672  | 0.016079  | 0.3907 | 0.2 |
| S023 | 1 | 0.342438  | 0.201790  | 0.061948  | 0.3877 | 0.2 |
| S024 | 1 | 0.327911  | 0.338631  | 0.286071  | 0.3762 | 0.2 |
| S025 | 1 | 0.261909  | 0.254570  | 0.325043  | 0.3759 | 0.2 |
| S026 | 1 | 0.203514  | 0.242760  | 0.231148  | 0.3618 | 0.2 |
| S027 | 1 | 0.318268  | -0.005173 | 0.208022  | 0.3564 | 0.2 |
| S028 | 1 | 0.281044  | 0.233078  | -0.032458 | 0.3347 | 0.2 |
| S029 | 1 | 0.088036  | 0.201172  | 0.048840  | 0.3297 | 0.2 |
| S030 | 1 | -0.212364 | 0.386841  | 0.117061  | 0.3273 | 0.2 |
| S031 | 1 | 0.018074  | 0.370079  | 0.034250  | 0.2872 | 0.2 |
| S032 | 1 | 0.385262  | 0.214951  | 0.188541  | 0.2840 | 0.2 |
| S033 | 1 | 0.317459  | 0.308258  | 0.346873  | 0.2829 | 0.2 |
| S034 | 1 | 0.575638  | 0.283142  | 0.126433  | 0.2727 | 0.2 |
| S035 | 1 | -0.096169 | 0.348991  | 0.252597  | 0.2707 | 0.2 |
| S036 | 1 | -0.125580 | 0.314468  | 0.233224  | 0.2310 | 0.2 |
| S037 | 1 | 0.346344  | -0.021973 | 0.311114  | 0.1765 | 0.2 |
| S038 | 1 | -0.085876 | 0.175034  | 0.127747  | 0.1701 | 0.2 |
| S039 | 1 | 0.170486  | 0.216293  | 0.103913  | 0.1521 | 0.2 |
| S040 | 1 | 0.222885  | 0.313072  | 0.114861  | 0.1233 | 0.2 |
| S041 | 1 | 0.357903  | 0.175400  | 0.200828  | 0.1228 | 0.2 |
| S042 | 1 | -0.124092 | 0.367493  | 0.194925  | 0.1187 | 0.2 |

HKLF 3

END