



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:42 PM GMT

PDB ID : 4PNF  
Title : Glutathione S-Transferase from Drosophila melanogaster - isozyme E6  
Authors : Scian, M.; Le Trong, I.; Mannervik, B.; Atkins, W.M.; Stenkamp, R.E.  
Deposited on : 2014-05-23  
Resolution : 2.11 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

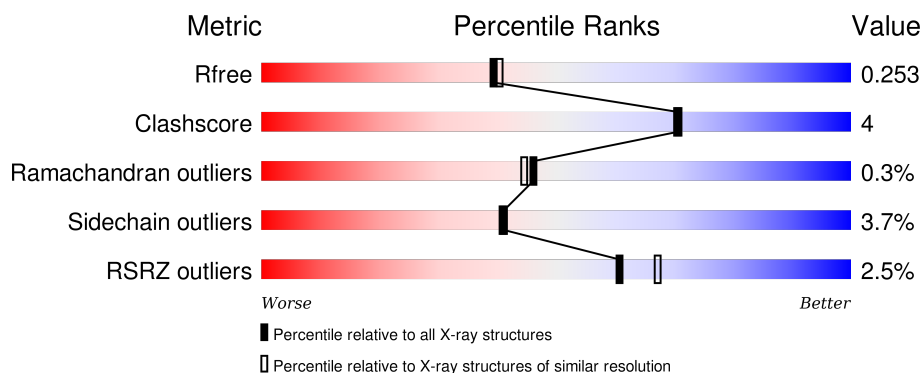
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.11 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	4587 (2.14-2.10)
Clashscore	102246	5132 (2.14-2.10)
Ramachandran outliers	100387	5080 (2.14-2.10)
Sidechain outliers	100360	5081 (2.14-2.10)
RSRZ outliers	91569	4597 (2.14-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	227	<div> <div>4%</div> <div>80% 15% . .</div> </div>
1	B	227	<div> <div>3%</div> <div>85% 11% . .</div> </div>
1	C	227	<div> <div>%</div> <div>89% 7% .</div> </div>
1	D	227	<div> <div></div> <div>85% 10% . .</div> </div>
1	E	227	<div> <div>3%</div> <div>82% 14% . .</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	227	<div><div></div><div>4%</div><div>83%</div><div>13%</div><div></div><div></div></div>
1	G	227	<div><div></div><div>2%</div><div>88%</div><div>8%</div><div></div><div></div></div>
1	H	227	<div><div></div><div>3%</div><div>84%</div><div>12%</div><div></div><div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14874 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called RE21095p.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	0	0	0
			1748	1139	283	326			
1	B	221	Total	C	N	O	0	0	0
			1752	1142	285	325			
1	C	219	Total	C	N	O	0	0	0
			1741	1134	281	326			
1	D	219	Total	C	N	O	0	0	0
			1747	1136	283	328			
1	E	220	Total	C	N	O	0	0	0
			1752	1141	282	329			
1	F	220	Total	C	N	O	0	0	0
			1756	1142	285	329			
1	G	219	Total	C	N	O	0	0	0
			1742	1133	281	328			
1	H	219	Total	C	N	O	0	0	0
			1747	1136	283	328			

There are 48 discrepancies between the modelled and reference sequences:

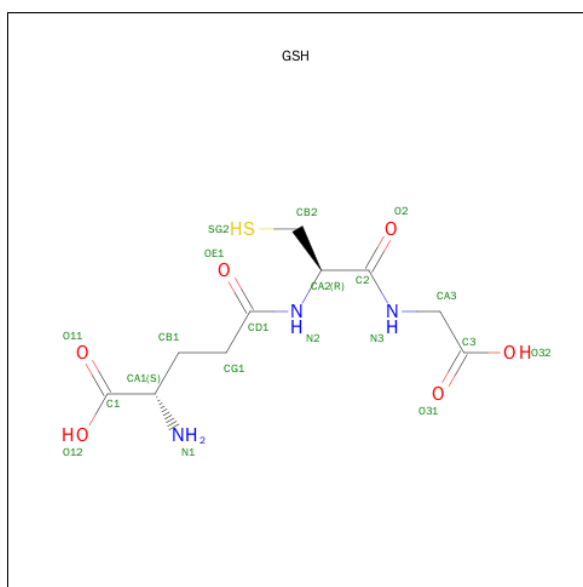
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	HIS	-	expression tag	UNP Q7JZM3
A	-3	HIS	-	expression tag	UNP Q7JZM3
A	-2	HIS	-	expression tag	UNP Q7JZM3
A	-1	HIS	-	expression tag	UNP Q7JZM3
A	0	HIS	-	expression tag	UNP Q7JZM3
A	1	HIS	-	expression tag	UNP Q7JZM3
B	-4	HIS	-	expression tag	UNP Q7JZM3
B	-3	HIS	-	expression tag	UNP Q7JZM3
B	-2	HIS	-	expression tag	UNP Q7JZM3
B	-1	HIS	-	expression tag	UNP Q7JZM3
B	0	HIS	-	expression tag	UNP Q7JZM3
B	1	HIS	-	expression tag	UNP Q7JZM3
C	-4	HIS	-	expression tag	UNP Q7JZM3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	HIS	-	expression tag	UNP Q7JZM3
C	-2	HIS	-	expression tag	UNP Q7JZM3
C	-1	HIS	-	expression tag	UNP Q7JZM3
C	0	HIS	-	expression tag	UNP Q7JZM3
C	1	HIS	-	expression tag	UNP Q7JZM3
D	-4	HIS	-	expression tag	UNP Q7JZM3
D	-3	HIS	-	expression tag	UNP Q7JZM3
D	-2	HIS	-	expression tag	UNP Q7JZM3
D	-1	HIS	-	expression tag	UNP Q7JZM3
D	0	HIS	-	expression tag	UNP Q7JZM3
D	1	HIS	-	expression tag	UNP Q7JZM3
E	-4	HIS	-	expression tag	UNP Q7JZM3
E	-3	HIS	-	expression tag	UNP Q7JZM3
E	-2	HIS	-	expression tag	UNP Q7JZM3
E	-1	HIS	-	expression tag	UNP Q7JZM3
E	0	HIS	-	expression tag	UNP Q7JZM3
E	1	HIS	-	expression tag	UNP Q7JZM3
F	-4	HIS	-	expression tag	UNP Q7JZM3
F	-3	HIS	-	expression tag	UNP Q7JZM3
F	-2	HIS	-	expression tag	UNP Q7JZM3
F	-1	HIS	-	expression tag	UNP Q7JZM3
F	0	HIS	-	expression tag	UNP Q7JZM3
F	1	HIS	-	expression tag	UNP Q7JZM3
G	-4	HIS	-	expression tag	UNP Q7JZM3
G	-3	HIS	-	expression tag	UNP Q7JZM3
G	-2	HIS	-	expression tag	UNP Q7JZM3
G	-1	HIS	-	expression tag	UNP Q7JZM3
G	0	HIS	-	expression tag	UNP Q7JZM3
G	1	HIS	-	expression tag	UNP Q7JZM3
H	-4	HIS	-	expression tag	UNP Q7JZM3
H	-3	HIS	-	expression tag	UNP Q7JZM3
H	-2	HIS	-	expression tag	UNP Q7JZM3
H	-1	HIS	-	expression tag	UNP Q7JZM3
H	0	HIS	-	expression tag	UNP Q7JZM3
H	1	HIS	-	expression tag	UNP Q7JZM3

- Molecule 2 is GLUTATHIONE (three-letter code: GSH) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>3</sub>O<sub>6</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	B	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	C	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	D	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	E	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	F	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	G	1	Total	C	N	O	S	0	0
			20	10	3	6	1		
2	H	1	Total	C	N	O	S	0	0
			20	10	3	6	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	82	Total	O	0	0
			82	82		
3	B	80	Total	O	0	0
			80	80		
3	C	122	Total	O	0	0
			122	122		
3	D	134	Total	O	0	0
			134	134		

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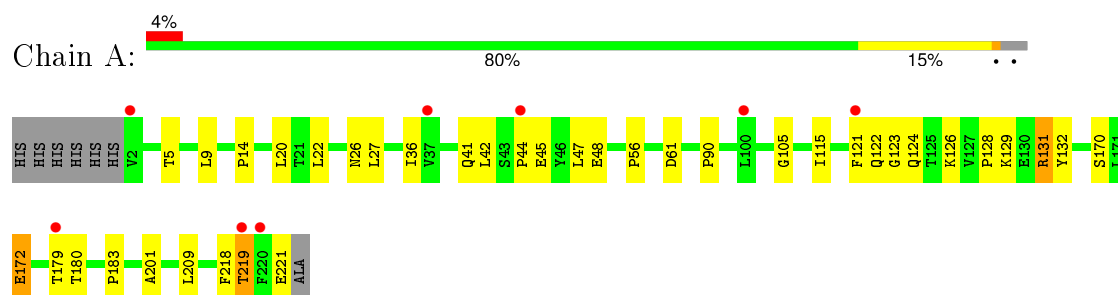
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	63	Total 63	O 63	0	0
3	F	78	Total 78	O 78	0	0
3	G	93	Total 93	O 93	0	0
3	H	77	Total 77	O 77	0	0

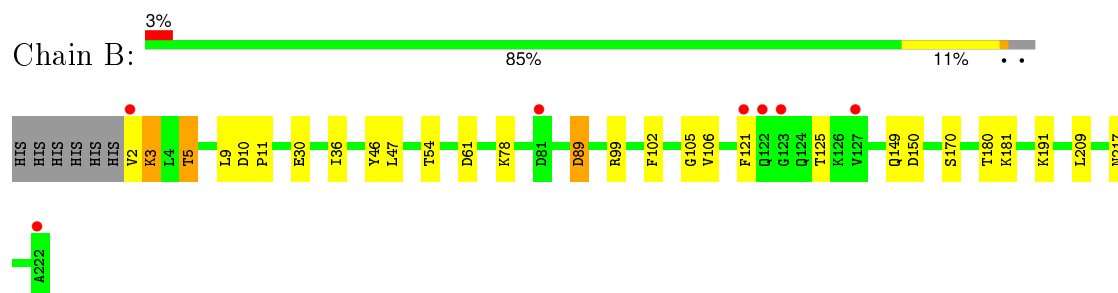
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

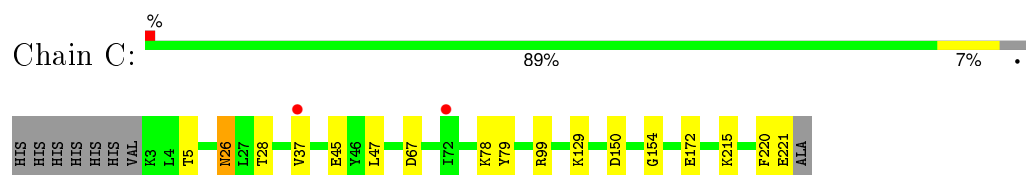
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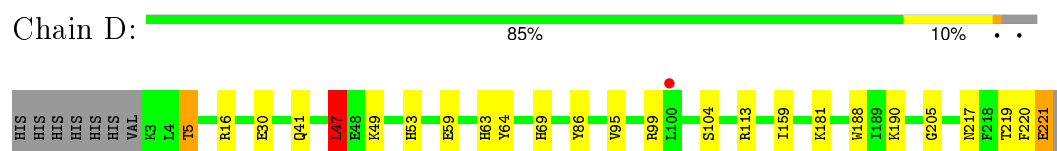
#### • Molecule 1: RE21095p



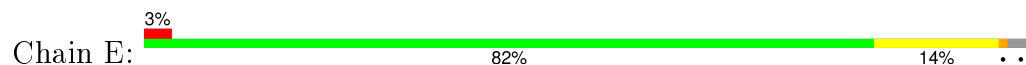
#### • Molecule 1: RE21095p



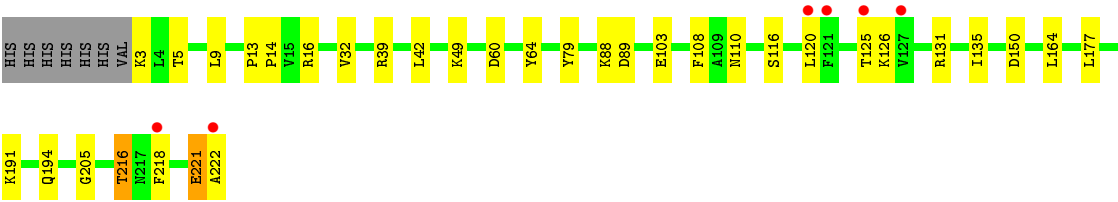
#### • Molecule 1: RE21095p



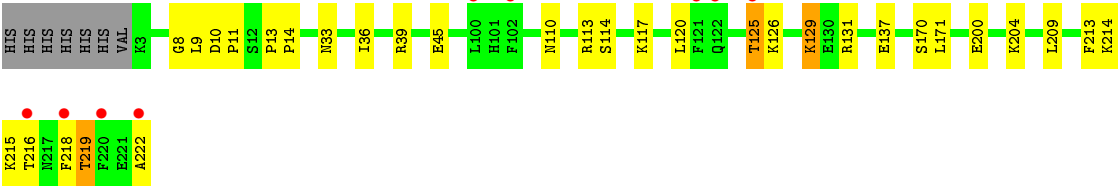
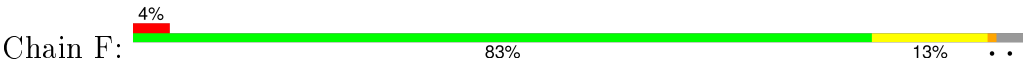
#### • Molecule 1: RE21095p



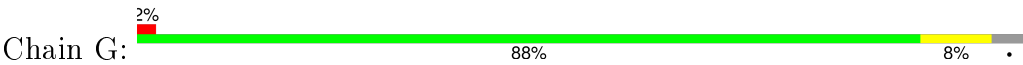




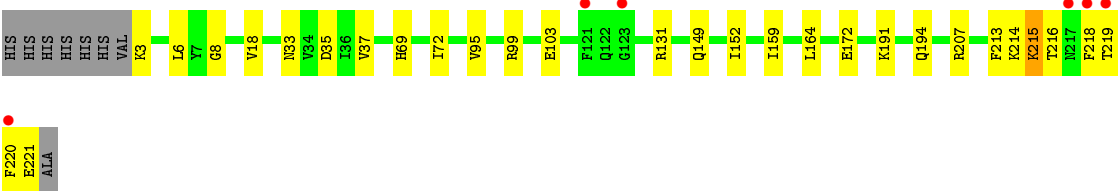
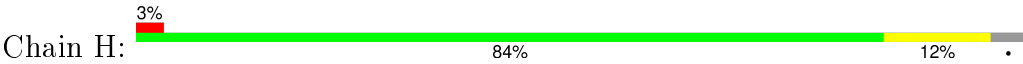
• Molecule 1: RE21095p



• Molecule 1: RE21095p



• Molecule 1: RE21095p



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.57Å 208.49Å 86.45Å 90.00° 92.45° 90.00°	Depositor
Resolution (Å)	39.90 – 2.11 39.90 – 2.11	Depositor EDS
% Data completeness (in resolution range)	96.2 (39.90-2.11) 96.2 (39.90-2.11)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.01 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.183 , 0.247 0.193 , 0.253	Depositor DCC
$R_{free}$ test set	5089 reflections (5.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.5	Xtriage
Anisotropy	0.727	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.1	EDS
Estimated twinning fraction	0.058 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 102222 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	14874	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GSH

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.68	0/1790	0.79	0/2438
1	B	0.70	0/1794	0.82	1/2443 (0.0%)
1	C	0.77	0/1783	0.82	3/2428 (0.1%)
1	D	0.78	1/1789 (0.1%)	0.85	3/2436 (0.1%)
1	E	0.75	0/1794	0.82	0/2443
1	F	0.71	0/1798	0.84	2/2447 (0.1%)
1	G	0.75	0/1784	0.85	4/2430 (0.2%)
1	H	0.67	0/1789	0.75	0/2435
All	All	0.72	1/14321 (0.0%)	0.82	13/19500 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	188	TRP	CB-CG	5.27	1.59	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	184	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	G	150	ASP	CB-CG-OD1	5.88	123.59	118.30
1	D	113	ARG	NE-CZ-NH1	5.65	123.13	120.30
1	C	150	ASP	CB-CG-OD1	-5.62	113.25	118.30
1	C	99	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	G	113	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	D	47	LEU	CB-CG-CD1	5.55	120.43	111.00
1	F	113	ARG	NE-CZ-NH1	5.31	122.96	120.30
1	C	150	ASP	CB-CG-OD2	5.31	123.08	118.30
1	F	113	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	B	99	ARG	NE-CZ-NH1	-5.17	117.72	120.30
1	G	184	ARG	NE-CZ-NH1	5.13	122.86	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	47	LEU	CA-CB-CG	5.04	126.90	115.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1748	0	1744	18	0
1	B	1752	0	1754	20	0
1	C	1741	0	1734	9	0
1	D	1747	0	1741	15	0
1	E	1752	0	1740	23	0
1	F	1756	0	1757	18	0
1	G	1742	0	1735	7	0
1	H	1747	0	1739	17	0
2	A	20	0	15	0	0
2	B	20	0	15	1	0
2	C	20	0	15	0	0
2	D	20	0	15	0	0
2	E	20	0	15	1	0
2	F	20	0	15	0	0
2	G	20	0	15	0	0
2	H	20	0	15	0	0
3	A	82	0	0	4	0
3	B	80	0	0	5	0
3	C	122	0	0	4	0
3	D	134	0	0	3	0
3	E	63	0	0	3	0
3	F	78	0	0	1	0
3	G	93	0	0	3	0
3	H	77	0	0	2	0
All	All	14874	0	14064	123	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (123) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:TYR:HB3	3:B:2165:HOH:O	1.66	0.96
1:F:110:ASN:O	1:F:131:ARG:NH2	1.99	0.96
1:H:131:ARG:NH2	3:H:2175:HOH:O	2.13	0.81
1:C:172:GLU:HG3	3:C:2145:HOH:O	1.87	0.74
1:E:3:LYS:NZ	3:E:2101:HOH:O	2.14	0.73
1:E:131:ARG:NH1	3:E:2129:HOH:O	2.19	0.73
1:A:22:LEU:O	3:A:2163:HOH:O	2.07	0.71
1:B:36:ILE:HD13	1:B:121:PHE:CZ	2.26	0.70
1:H:213:PHE:O	1:H:216:THR:HG22	1.92	0.67
1:E:3:LYS:CE	3:E:2101:HOH:O	2.44	0.65
1:E:191:LYS:HA	1:E:194:GLN:HE21	1.60	0.65
1:A:172:GLU:OE2	3:A:2167:HOH:O	2.14	0.65
1:H:3:LYS:N	3:H:2146:HOH:O	2.31	0.63
1:D:63:HIS:HD2	3:D:2217:HOH:O	1.82	0.62
1:H:95:VAL:O	1:H:99:ARG:HG2	2.02	0.60
1:G:156:GLN:CD	3:G:2191:HOH:O	2.40	0.60
1:B:9:LEU:HG	1:B:11:PRO:HD2	1.86	0.57
1:F:126:LYS:CD	1:F:219:THR:HG22	2.34	0.57
1:E:216:THR:CG2	1:E:218:PHE:HB3	2.35	0.57
1:F:215:LYS:C	1:F:216:THR:O	2.38	0.56
1:G:86:TYR:CD1	1:G:159:ILE:HD11	2.40	0.56
1:B:150:ASP:HB3	1:B:191:LYS:HE2	1.88	0.56
1:E:16:ARG:HD3	1:E:205:GLY:HA3	1.87	0.56
1:B:89:ASP:OD1	1:F:39:ARG:NH1	2.38	0.56
1:E:60:ASP:OD1	1:E:79:TYR:OH	2.23	0.55
1:D:47:LEU:HD13	1:D:53:HIS:HB3	1.88	0.55
1:B:2:VAL:O	1:B:3:LYS:CB	2.54	0.55
1:E:116:SER:HB2	1:E:120:LEU:HD12	1.89	0.55
1:F:9:LEU:HD21	1:F:36:ILE:HD12	1.88	0.54
1:B:36:ILE:HD13	1:B:121:PHE:HZ	1.70	0.54
1:E:108:PHE:HZ	2:E:2001:GSH:HSG	1.56	0.54
1:C:26:ASN:HA	3:C:2112:HOH:O	2.08	0.54
1:A:170:SER:HB3	1:A:209:LEU:HD23	1.90	0.53
1:D:219:THR:HG22	1:D:220:PHE:O	2.09	0.53
1:A:115:ILE:HG13	1:A:131:ARG:HG3	1.89	0.53
1:E:221:GLU:O	1:E:222:ALA:HB2	2.09	0.53
1:B:5:THR:HG22	3:B:2140:HOH:O	2.08	0.52
1:E:110:ASN:O	1:E:131:ARG:NH1	2.44	0.51
1:A:129:LYS:HB2	1:A:221:GLU:HG2	1.93	0.51
1:C:154:GLY:N	3:C:2201:HOH:O	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:N	3:A:2163:HOH:O	2.44	0.50
1:H:131:ARG:HA	1:H:131:ARG:NH2	2.27	0.50
1:E:9:LEU:N	1:E:9:LEU:HD23	2.27	0.50
1:C:78:LYS:HG2	1:C:79:TYR:CE1	2.47	0.50
1:C:129:LYS:HB2	1:C:221:GLU:HG2	1.93	0.49
1:E:39:ARG:HB3	1:E:42:LEU:HD12	1.94	0.49
1:A:14:PRO:HB2	1:A:56:PRO:HD3	1.95	0.49
1:F:170:SER:HB3	1:F:209:LEU:HD23	1.93	0.48
1:B:78:LYS:NZ	3:B:2101:HOH:O	2.43	0.48
1:H:6:LEU:HD13	1:H:18:VAL:HG11	1.95	0.48
1:A:122:GLN:O	1:A:124:GLN:N	2.47	0.48
1:A:105:GLY:HA2	1:B:105:GLY:HA2	1.96	0.48
1:H:35:ASP:OD1	1:H:37:VAL:HG22	2.14	0.48
1:B:2:VAL:O	1:B:3:LYS:HB2	2.13	0.47
1:H:131:ARG:HA	1:H:131:ARG:CZ	2.45	0.47
1:A:44:PRO:HA	1:A:47:LEU:HB2	1.95	0.47
1:E:49:LYS:HG2	1:E:64:TYR:CZ	2.49	0.47
1:E:103:GLU:HG2	1:E:164:LEU:HD13	1.96	0.47
1:D:220:PHE:O	1:D:221:GLU:HB3	2.15	0.47
1:E:216:THR:HG22	1:E:218:PHE:H	1.80	0.46
1:F:200:GLU:OE1	1:F:204:LYS:HD2	2.15	0.46
1:F:200:GLU:HG2	3:F:2101:HOH:O	2.16	0.46
1:F:10:ASP:N	1:F:11:PRO:CD	2.78	0.46
1:F:126:LYS:HD3	1:F:219:THR:HG22	1.98	0.46
1:H:220:PHE:O	1:H:221:GLU:HB3	2.16	0.45
1:D:86:TYR:CD1	1:D:159:ILE:HD11	2.51	0.45
1:F:129:LYS:HG3	1:F:222:ALA:HA	1.99	0.45
1:A:126:LYS:HD3	1:A:219:THR:HB	1.98	0.45
1:B:180:THR:HG21	1:C:215:LYS:CD	2.46	0.45
1:F:120:LEU:HD11	1:F:213:PHE:CZ	2.52	0.45
1:G:10:ASP:N	1:G:11:PRO:CD	2.80	0.45
1:G:194:GLN:HG3	3:G:2150:HOH:O	2.17	0.45
1:H:220:PHE:O	1:H:221:GLU:CB	2.65	0.45
1:D:16:ARG:HD3	1:D:205:GLY:HA3	1.98	0.45
1:D:49:LYS:HG2	1:D:64:TYR:CE1	2.52	0.44
1:A:183:PRO:O	3:A:2155:HOH:O	2.21	0.44
1:B:10:ASP:N	1:B:11:PRO:CD	2.81	0.44
1:D:5:THR:HA	1:D:30:GLU:O	2.17	0.44
1:D:181:LYS:HE2	3:D:2117:HOH:O	2.17	0.44
1:B:102:PHE:CE1	1:B:106:VAL:HG11	2.52	0.44
1:G:152:ILE:HG22	1:G:161:ASP:OD1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:152:ILE:HG12	1:H:164:LEU:HD13	2.01	0.43
1:F:9:LEU:CD2	1:F:36:ILE:HD12	2.48	0.43
1:E:13:PRO:HB2	1:E:14:PRO:HD3	2.00	0.43
1:E:103:GLU:CG	1:E:164:LEU:HD13	2.49	0.43
1:A:36:ILE:HG22	1:A:121:PHE:HZ	1.83	0.43
1:E:216:THR:HG23	1:E:218:PHE:HB3	2.00	0.43
1:D:69:HIS:CE1	1:D:104:SER:OG	2.71	0.43
1:D:95:VAL:O	1:D:99:ARG:HG2	2.19	0.43
1:A:115:ILE:CG1	1:A:131:ARG:HG3	2.49	0.43
1:E:126:LYS:HB3	1:E:222:ALA:CB	2.48	0.43
1:F:214:LYS:O	1:F:216:THR:O	2.36	0.43
1:E:221:GLU:O	1:E:222:ALA:CB	2.67	0.43
1:B:61:ASP:HA	3:B:2103:HOH:O	2.17	0.43
1:A:20:LEU:HD23	1:A:201:ALA:HB3	2.00	0.43
1:H:191:LYS:HA	1:H:194:GLN:HE21	1.84	0.42
1:H:214:LYS:O	1:H:216:THR:N	2.51	0.42
1:E:191:LYS:HA	1:E:194:GLN:NE2	2.33	0.42
1:F:13:PRO:N	1:F:14:PRO:HD2	2.34	0.42
1:D:181:LYS:CE	3:D:2117:HOH:O	2.67	0.42
1:F:125:THR:O	1:F:218:PHE:HA	2.20	0.42
1:D:220:PHE:O	1:D:221:GLU:CB	2.66	0.42
1:B:5:THR:CG2	3:B:2140:HOH:O	2.67	0.42
1:D:41:GLN:OE1	1:D:41:GLN:N	2.49	0.42
1:B:54:THR:HA	2:B:2001:GSH:O2	2.20	0.41
1:H:8:GLY:O	1:H:33:ASN:HA	2.20	0.41
1:G:143:GLU:OE2	1:G:184:ARG:HB2	2.21	0.41
1:F:8:GLY:O	1:F:33:ASN:HA	2.21	0.41
1:B:170:SER:HB3	1:B:209:LEU:HD23	2.02	0.41
1:H:72:ILE:HD12	1:H:159:ILE:HB	2.03	0.41
1:B:30:GLU:HB2	3:G:2126:HOH:O	2.21	0.41
1:H:3:LYS:HB3	1:H:3:LYS:NZ	2.36	0.41
1:C:172:GLU:CG	3:C:2162:HOH:O	2.68	0.41
1:F:171:LEU:HA	1:F:171:LEU:HD23	1.90	0.41
1:C:220:PHE:O	1:C:221:GLU:HB2	2.22	0.40
1:D:5:THR:HG23	1:D:59:GLU:HB3	2.03	0.40
1:H:69:HIS:NE2	1:H:103:GLU:OE1	2.50	0.40
1:A:129:LYS:O	1:A:132:TYR:HB3	2.21	0.40
1:A:9:LEU:N	1:A:9:LEU:HD23	2.37	0.40
1:B:180:THR:HG21	1:C:215:LYS:HD2	2.02	0.40
1:A:41:GLN:HG2	1:A:42:LEU:HD23	2.03	0.40
1:G:87:PRO:CB	1:G:92:LYS:HE3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:88:LYS:O	1:E:89:ASP:C	2.60	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	218/227 (96%)	207 (95%)	10 (5%)	1 (0%)	34	29
1	B	219/227 (96%)	206 (94%)	11 (5%)	2 (1%)	21	14
1	C	217/227 (96%)	213 (98%)	3 (1%)	1 (0%)	34	29
1	D	217/227 (96%)	213 (98%)	4 (2%)	0	100	100
1	E	218/227 (96%)	213 (98%)	4 (2%)	1 (0%)	34	29
1	F	218/227 (96%)	209 (96%)	9 (4%)	0	100	100
1	G	217/227 (96%)	207 (95%)	10 (5%)	0	100	100
1	H	217/227 (96%)	209 (96%)	7 (3%)	1 (0%)	34	29
All	All	1741/1816 (96%)	1677 (96%)	58 (3%)	6 (0%)	46	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	3	LYS
1	E	221	GLU
1	A	123	GLY
1	H	215	LYS
1	C	67	ASP
1	B	217	ASN



### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	186/196 (95%)	173 (93%)	13 (7%)	19	14
1	B	186/196 (95%)	180 (97%)	6 (3%)	46	48
1	C	185/196 (94%)	179 (97%)	6 (3%)	46	48
1	D	187/196 (95%)	182 (97%)	5 (3%)	52	55
1	E	185/196 (94%)	178 (96%)	7 (4%)	40	39
1	F	188/196 (96%)	181 (96%)	7 (4%)	41	41
1	G	186/196 (95%)	181 (97%)	5 (3%)	52	55
1	H	187/196 (95%)	181 (97%)	6 (3%)	46	48
All	All	1490/1568 (95%)	1435 (96%)	55 (4%)	41	41

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	26	ASN
1	A	45	GLU
1	A	48	GLU
1	A	61	ASP
1	A	90	PRO
1	A	128	PRO
1	A	131	ARG
1	A	172	GLU
1	A	179	THR
1	A	180	THR
1	A	218	PHE
1	A	219	THR
1	B	5	THR
1	B	47	LEU
1	B	89	ASP
1	B	125	THR
1	B	149	GLN
1	B	181	LYS

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Mol	Chain	Res	Type
1	C	5	THR
1	C	26	ASN
1	C	28	THR
1	C	37	VAL
1	C	45	GLU
1	C	47	LEU
1	D	5	THR
1	D	47	LEU
1	D	190	LYS
1	D	217	ASN
1	D	221	GLU
1	E	5	THR
1	E	32	VAL
1	E	125	THR
1	E	135	ILE
1	E	150	ASP
1	E	177	LEU
1	E	216	THR
1	F	45	GLU
1	F	114	SER
1	F	117	LYS
1	F	125	THR
1	F	129	LYS
1	F	137	GLU
1	F	219	THR
1	G	117	LYS
1	G	122	GLN
1	G	125	THR
1	G	217	ASN
1	G	218	PHE
1	H	149	GLN
1	H	172	GLU
1	H	207	ARG
1	H	215	LYS
1	H	218	PHE
1	H	219	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	HIS
1	A	149	GLN

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Mol	Chain	Res	Type
1	A	208	GLN
1	B	33	ASN
1	B	149	GLN
1	C	149	GLN
1	D	63	HIS
1	D	149	GLN
1	E	194	GLN
1	F	26	ASN
1	H	26	ASN
1	H	149	GLN
1	H	194	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	GSH	A	2001	-	13,19,19	0.53	0	15,24,24	0.87	0
2	GSH	B	2001	-	13,19,19	0.48	0	15,24,24	1.04	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GSH	C	2001	-	13,19,19	1.02	1 (7%)	15,24,24	1.37	3 (20%)
2	GSH	D	2001	-	13,19,19	1.23	2 (15%)	15,24,24	1.31	2 (13%)
2	GSH	E	2001	-	13,19,19	0.79	0	15,24,24	1.68	2 (13%)
2	GSH	F	2001	-	13,19,19	0.80	0	15,24,24	1.18	2 (13%)
2	GSH	G	2001	-	13,19,19	0.57	0	15,24,24	1.52	1 (6%)
2	GSH	H	2001	-	13,19,19	0.84	1 (7%)	15,24,24	1.54	4 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GSH	A	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	B	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	C	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	D	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	E	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	F	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	G	2001	-	-	0/18/24/24	0/0/0/0
2	GSH	H	2001	-	-	0/18/24/24	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	2001	GSH	CA3-N3	-2.15	1.41	1.46
2	D	2001	GSH	CB2-SG2	2.13	1.86	1.81
2	C	2001	GSH	C2-N3	2.16	1.38	1.33
2	D	2001	GSH	CB2-CA2	3.06	1.56	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2001	GSH	OE1-CD1-CG1	-3.06	116.71	121.98
2	C	2001	GSH	CB1-CG1-CD1	-2.78	106.66	113.27
2	B	2001	GSH	CB2-CA2-N2	-2.40	108.03	111.40
2	D	2001	GSH	OE1-CD1-CG1	-2.36	117.91	121.98
2	H	2001	GSH	CB2-CA2-N2	-2.26	108.22	111.40
2	H	2001	GSH	CB1-CG1-CD1	-2.15	108.15	113.27
2	C	2001	GSH	CB1-CA1-N1	-2.11	104.52	110.52
2	F	2001	GSH	OE1-CD1-CG1	-2.06	118.44	121.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2001	GSH	CB1-CG1-CD1	-2.02	108.47	113.27
2	C	2001	GSH	C3-CA3-N3	2.01	116.92	111.74
2	F	2001	GSH	CB2-CA2-N2	2.45	114.84	111.40
2	H	2001	GSH	CA2-CB2-SG2	2.69	117.46	114.16
2	H	2001	GSH	CA3-N3-C2	2.87	126.28	122.34
2	E	2001	GSH	CA2-CB2-SG2	4.42	119.59	114.16
2	G	2001	GSH	CA2-CB2-SG2	4.59	119.79	114.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2001	GSH	1	0
2	E	2001	GSH	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	220/227 (96%)	0.20	8 (3%)	46	55	24, 36, 55, 81	0
1	B	221/227 (97%)	0.21	7 (3%)	51	60	24, 35, 57, 86	0
1	C	219/227 (96%)	0.09	2 (0%)	85	88	20, 30, 43, 54	0
1	D	219/227 (96%)	0.01	1 (0%)	91	93	20, 28, 45, 52	0
1	E	220/227 (96%)	0.13	6 (2%)	58	65	23, 32, 52, 75	0
1	F	220/227 (96%)	0.15	9 (4%)	41	49	22, 33, 59, 80	0
1	G	219/227 (96%)	0.08	5 (2%)	64	70	22, 32, 47, 62	0
1	H	219/227 (96%)	0.29	6 (2%)	58	65	24, 35, 62, 76	0
All	All	1757/1816 (96%)	0.14	44 (2%)	61	67	20, 32, 54, 86	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	VAL	5.5
1	H	121	PHE	4.0
1	B	121	PHE	3.9
1	E	121	PHE	3.9
1	A	121	PHE	3.5
1	B	123	GLY	3.4
1	E	218	PHE	3.3
1	E	222	ALA	3.2
1	D	100	LEU	3.0
1	H	218	PHE	2.9
1	F	218	PHE	2.9
1	F	216	THR	2.8
1	H	217	ASN	2.8
1	F	220	PHE	2.8
1	G	44	PRO	2.7
1	A	100	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	37	VAL	2.5
1	B	127	VAL	2.5
1	E	120	LEU	2.4
1	A	44	PRO	2.4
1	A	179	THR	2.4
1	B	222	ALA	2.3
1	G	100	LEU	2.3
1	A	2	VAL	2.3
1	F	222	ALA	2.3
1	F	100	LEU	2.3
1	G	38	ALA	2.3
1	F	121	PHE	2.3
1	H	220	PHE	2.3
1	A	219	THR	2.3
1	F	122	GLN	2.2
1	E	125	THR	2.2
1	F	102	PHE	2.2
1	C	72	ILE	2.2
1	B	122	GLN	2.2
1	B	81	ASP	2.2
1	F	125	THR	2.1
1	C	37	VAL	2.1
1	H	123	GLY	2.1
1	E	127	VAL	2.1
1	G	45	GLU	2.0
1	A	220	PHE	2.0
1	H	219	THR	2.0
1	G	101	HIS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GSH	H	2001	20/20	0.94	0.16	0.42	26,31,36,42	0
2	GSH	E	2001	20/20	0.93	0.15	0.23	22,27,36,37	0
2	GSH	A	2001	20/20	0.93	0.14	0.18	25,32,42,43	0
2	GSH	B	2001	20/20	0.93	0.16	0.11	31,34,38,48	0
2	GSH	F	2001	20/20	0.94	0.14	0.07	26,29,34,37	0
2	GSH	C	2001	20/20	0.94	0.13	-0.29	23,26,30,35	0
2	GSH	D	2001	20/20	0.95	0.12	-0.48	22,26,31,36	0
2	GSH	G	2001	20/20	0.93	0.12	-0.61	27,31,35,39	0

## 6.5 Other polymers

There are no such residues in this entry.