



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:45 PM GMT

PDB ID : 4ACS
Title : Crystal structure of mutant GST A2-2 with enhanced catalytic efficiency with azathioprine
Authors : Zhang, W.; Moden, O.; Tars, K.; Mannervik, B.
Deposited on : 2011-12-19
Resolution : 2.10 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

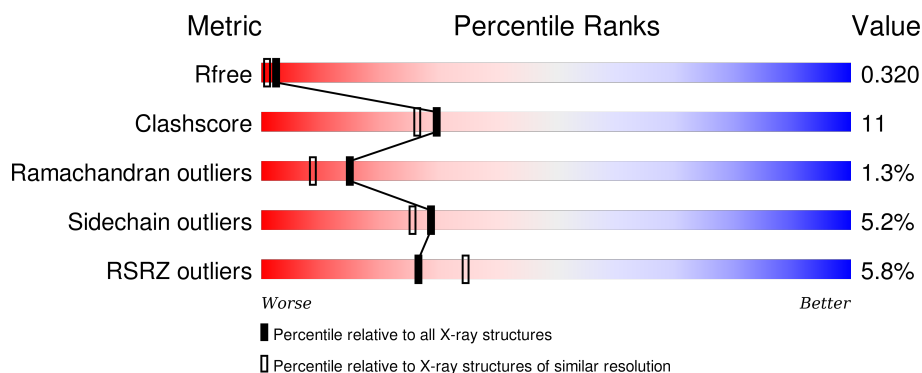
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 ≥ 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	222	<div> <div>2%</div> <div>75%</div> <div>22%</div> <div>..</div> </div>
1	B	222	<div> <div>4%</div> <div>69%</div> <div>27%</div> <div>..</div> </div>
1	C	222	<div> <div>6%</div> <div>64%</div> <div>31%</div> <div>..</div> </div>
1	D	222	<div> <div>10%</div> <div>70%</div> <div>26%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GSH	A	230	X	-	-	-
2	GSH	B	230	X	-	-	-
2	GSH	C	230	X	-	-	-
2	GSH	D	230	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7665 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.

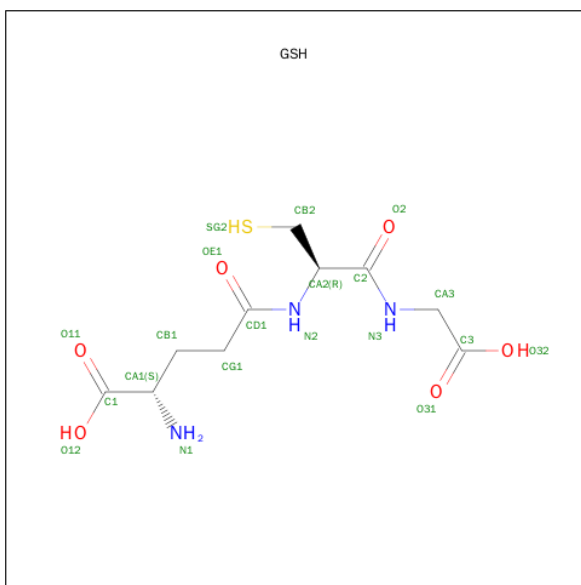
- Molecule 1 is a protein called GLUTATHIONE S-TRANSFERASE A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1778	1144	299	328	7			
1	B	217	Total	C	N	O	S	0	0	0
			1757	1132	292	326	7			
1	C	219	Total	C	N	O	S	0	0	0
			1778	1144	299	328	7			
1	D	217	Total	C	N	O	S	0	0	0
			1757	1132	292	326	7			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	GLY	LEU	ENGINEERED MUTATION	UNP P09210
A	108	ASP	LEU	ENGINEERED MUTATION	UNP P09210
A	110	SER	PRO	CONFLICT	UNP P09210
A	222	HIS	PHE	ENGINEERED MUTATION	UNP P09210
B	107	GLY	LEU	ENGINEERED MUTATION	UNP P09210
B	108	ASP	LEU	ENGINEERED MUTATION	UNP P09210
B	110	SER	PRO	CONFLICT	UNP P09210
B	222	HIS	PHE	ENGINEERED MUTATION	UNP P09210
C	107	GLY	LEU	ENGINEERED MUTATION	UNP P09210
C	108	ASP	LEU	ENGINEERED MUTATION	UNP P09210
C	110	SER	PRO	CONFLICT	UNP P09210
C	222	HIS	PHE	ENGINEERED MUTATION	UNP P09210
D	107	GLY	LEU	ENGINEERED MUTATION	UNP P09210
D	108	ASP	LEU	ENGINEERED MUTATION	UNP P09210
D	110	SER	PRO	CONFLICT	UNP P09210
D	222	HIS	PHE	ENGINEERED MUTATION	UNP P09210

- Molecule 2 is GLUTATHIONE (three-letter code: GSH) (formula: C₁₀H₁₇N₃O₆S).



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

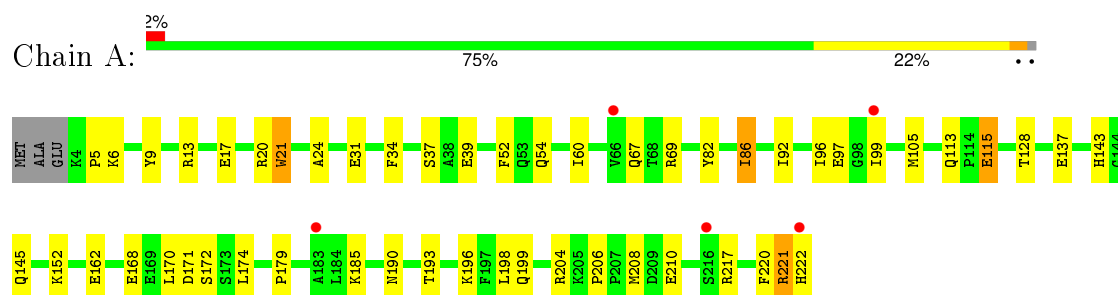
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	180	Total O 180 180	0	0
3	B	110	Total O 110 110	0	0
3	C	118	Total O 118 118	0	0
3	D	107	Total O 107 107	0	0

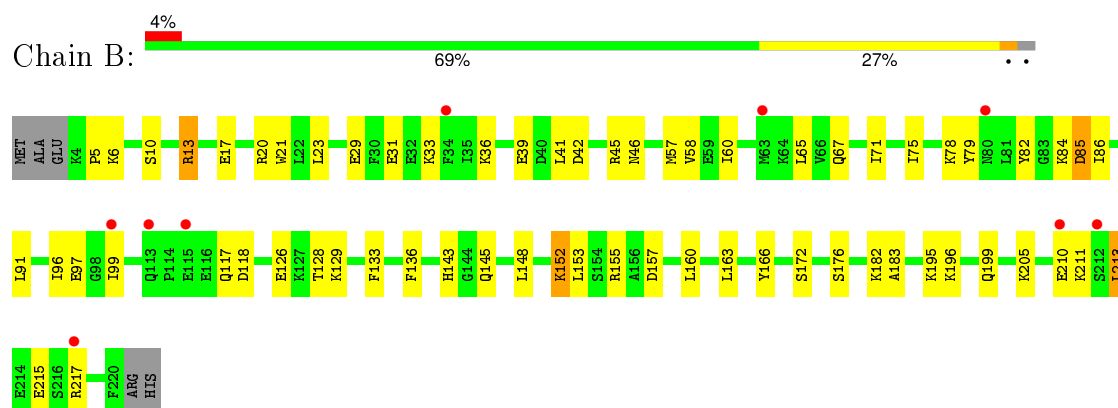
3 Residue-property plots [i](#)

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.

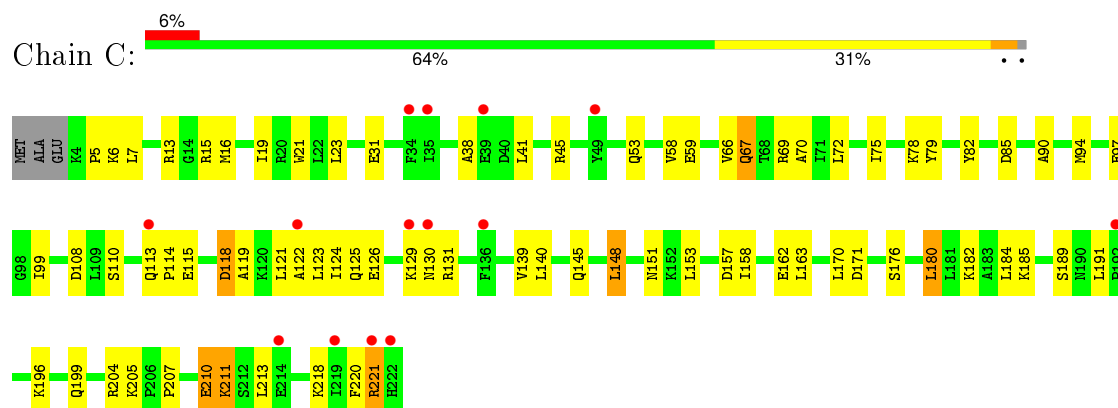
• Molecule 1: GLUTATHIONE S-TRANSFERASE A2



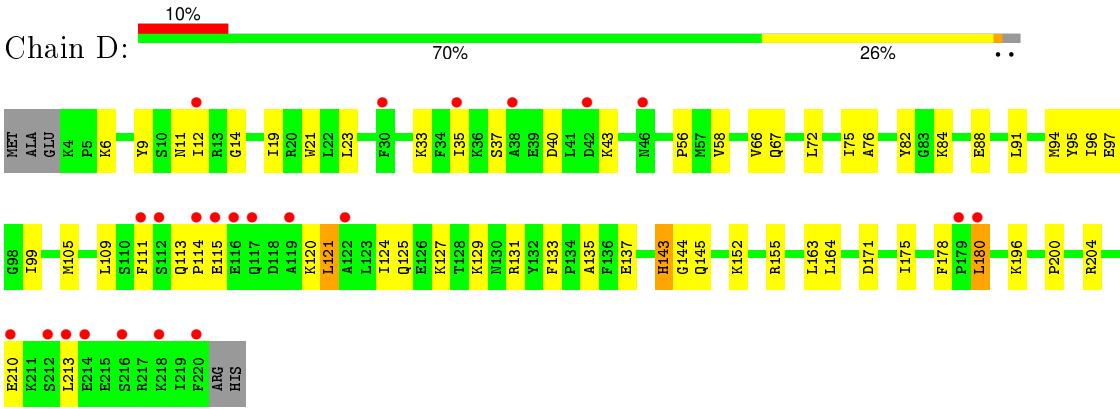
• Molecule 1: GLUTATHIONE S-TRANSFERASE A2



• Molecule 1: GLUTATHIONE S-TRANSFERASE A2



• Molecule 1: GLUTATHIONE S-TRANSFERASE A2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.66Å 94.80Å 113.72Å 90.00° 92.77° 90.00°	Depositor
Resolution (Å)	40.00 – 2.10 37.84 – 2.10	Depositor EDS
% Data completeness (in resolution range)	92.4 (40.00-2.10) 92.5 (37.84-2.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.26 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.261 , 0.321 0.261 , 0.320	Depositor DCC
R_{free} test set	2821 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	13.3	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 40.2	EDS
Estimated twinning fraction	0.229 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Outliers	0 of 55688 reflections	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	7665	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.60	1/1812 (0.1%)	0.77	0/2433
1	B	0.56	1/1790 (0.1%)	0.75	0/2404
1	C	0.56	0/1812	0.75	0/2433
1	D	0.53	1/1790 (0.1%)	0.71	0/2404
All	All	0.56	3/7204 (0.0%)	0.75	0/9674

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	21	TRP	CD2-CE2	5.44	1.47	1.41
1	B	21	TRP	CD2-CE2	5.22	1.47	1.41
1	A	21	TRP	CD2-CE2	5.09	1.47	1.41

There are no bond angle outliers.

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	1778	0	1826	34	0
1	B	1757	0	1806	40	0
1	C	1778	0	1826	53	0
1	D	1757	0	1806	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	20	0	15	2	0
2	B	20	0	15	0	0
2	C	20	0	15	0	0
2	D	20	0	15	1	0
3	A	180	0	0	7	0
3	B	110	0	0	6	0
3	C	118	0	0	9	0
3	D	107	0	0	8	0
All	All	7665	0	7324	162	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 11.

All (162) 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:D:105:MET:HG3	3:D:2056:HOH:O	1.65	0.96
1:C:15:ARG:HG2	1:C:15:ARG:HH11	1.42	0.84
1:D:121:LEU:O	1:D:125:GLN:HG3	1.78	0.83
1:A:217:ARG:HA	1:A:222:HIS:CE1	2.15	0.82
1:B:36:LYS:HD3	3:B:2032:HOH:O	1.80	0.81
1:C:140:LEU:HB3	1:C:180:LEU:HD12	1.63	0.80
1:B:46:ASN:ND2	3:B:2039:HOH:O	2.14	0.80
1:C:53:GLN:HB2	1:D:131:ARG:HE	1.50	0.76
1:C:145:GLN:OE1	1:C:151:ASN:HB2	1.87	0.74
1:B:143:HIS:CD2	1:B:145:GLN:HB2	2.25	0.71
1:D:196:LYS:HG3	3:D:2094:HOH:O	1.89	0.70
1:C:6:LYS:HE2	1:C:31:GLU:OE1	1.90	0.70
1:D:143:HIS:CE1	1:D:145:GLN:HB2	2.27	0.69
1:B:183:ALA:HA	3:B:2093:HOH:O	1.91	0.69
1:B:39:GLU:HA	1:B:42:ASP:HB2	1.77	0.66
1:A:96:ILE:HA	1:A:99:ILE:HD12	1.78	0.66
1:D:111:PHE:HA	1:D:213:LEU:HD21	1.79	0.64
1:B:143:HIS:HD2	1:B:145:GLN:H	1.45	0.64
1:A:69:ARG:HD2	1:B:97:GLU:OE1	1.99	0.63
1:A:198:LEU:O	1:A:204:ARG:NH2	2.30	0.63
1:A:96:ILE:HG21	3:A:2082:HOH:O	1.98	0.62
1:D:175:ILE:HG22	3:D:2080:HOH:O	1.99	0.62
1:A:152:LYS:HE2	3:A:2074:HOH:O	1.99	0.62
1:C:115:GLU:HA	3:C:2073:HOH:O	1.98	0.62
1:B:13:ARG:HG2	1:B:205:LYS:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:LYS:O	1:C:58:VAL:HA	2.01	0.61
1:D:19:ILE:HG13	1:D:72:LEU:HD21	1.83	0.61
1:A:6:LYS:HE2	1:A:31:GLU:OE2	2.02	0.60
1:C:21:TRP:NE1	1:C:162:GLU:HG3	2.17	0.60
1:C:7:LEU:HG	1:C:58:VAL:HG22	1.83	0.59
1:D:43:LYS:HD3	3:D:2032:HOH:O	2.02	0.59
1:D:113:GLN:O	1:D:115:GLU:N	2.36	0.59
1:A:92:ILE:O	1:A:96:ILE:HG23	2.03	0.58
1:A:96:ILE:HG13	1:A:97:GLU:N	2.19	0.57
1:C:23:LEU:HG	1:C:75:ILE:HD13	1.85	0.57
1:D:23:LEU:HD21	1:D:75:ILE:HD13	1.87	0.57
1:D:109:LEU:HD22	1:D:124:ILE:HD12	1.86	0.57
1:C:6:LYS:HG2	1:C:31:GLU:HB3	1.86	0.57
1:A:21:TRP:NE1	1:A:162:GLU:HG3	2.20	0.57
1:A:105:MET:HA	3:A:2093:HOH:O	2.06	0.56
1:B:118:ASP:HA	3:B:2069:HOH:O	2.06	0.55
1:B:143:HIS:CD2	1:B:145:GLN:H	2.25	0.54
1:D:19:ILE:HG13	1:D:72:LEU:CD2	2.38	0.54
1:B:57:MET:HA	1:B:65:LEU:O	2.08	0.54
1:A:24:ALA:O	1:A:193:THR:HB	2.08	0.54
1:D:33:LYS:HE3	3:D:2030:HOH:O	2.09	0.53
1:A:21:TRP:CD1	1:A:162:GLU:HG3	2.43	0.52
1:C:15:ARG:NH1	1:C:15:ARG:HG2	2.17	0.52
1:C:220:PHE:O	1:C:221:ARG:C	2.47	0.52
1:B:6:LYS:HG2	1:B:31:GLU:HB2	1.91	0.52
1:C:121:LEU:HG	1:C:125:GLN:OE1	2.10	0.52
1:C:210:GLU:HA	1:C:213:LEU:HD12	1.91	0.52
1:B:23:LEU:HG	1:B:75:ILE:HD13	1.91	0.52
1:D:204:ARG:NH1	3:D:2009:HOH:O	2.34	0.51
1:D:35:ILE:HG23	1:D:40:ASP:HB2	1.92	0.51
1:C:118:ASP:N	1:C:118:ASP:OD1	2.44	0.51
1:C:94:MET:SD	1:D:66:VAL:HG22	2.51	0.51
1:C:69:ARG:HB2	1:D:97:GLU:HG3	1.91	0.51
1:B:33:LYS:HD3	3:B:2006:HOH:O	2.09	0.51
3:A:2059:HOH:O	1:B:91:LEU:HG	2.10	0.50
1:C:41:LEU:HD21	1:C:45:ARG:NH2	2.27	0.50
1:A:190:ASN:ND2	3:A:2155:HOH:O	2.43	0.50
1:A:137:GLU:OE2	1:A:179:PRO:HD2	2.12	0.49
1:C:196:LYS:O	1:C:199:GLN:HG2	2.12	0.49
1:C:85:ASP:HB2	3:C:2056:HOH:O	2.12	0.49
1:C:7:LEU:HB3	1:C:16:MET:HE3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:SER:O	1:C:182:LYS:NZ	2.42	0.48
1:B:5:PRO:HB3	1:B:60:ILE:HG13	1.95	0.48
1:D:129:LYS:HG2	1:D:178:PHE:HE2	1.79	0.48
1:A:21:TRP:CE2	1:A:162:GLU:HG3	2.49	0.48
1:C:78:LYS:HE2	1:C:79:TYR:CZ	2.48	0.48
1:B:29:GLU:HB3	3:B:2021:HOH:O	2.14	0.48
1:D:127:LYS:NZ	1:D:131:ARG:NH1	2.62	0.48
1:C:53:GLN:HB2	1:D:131:ARG:NE	2.24	0.48
1:B:78:LYS:HD3	1:B:79:TYR:CE2	2.49	0.48
1:D:127:LYS:HZ2	1:D:131:ARG:NH1	2.12	0.47
1:C:158:ILE:HG22	3:C:2014:HOH:O	2.13	0.47
1:A:9:TYR:O	1:A:34:PHE:HA	2.14	0.47
1:C:21:TRP:CE2	1:C:162:GLU:HG3	2.49	0.47
1:D:33:LYS:CE	3:D:2030:HOH:O	2.62	0.47
1:B:211:LYS:HB2	1:B:211:LYS:HE2	1.40	0.47
1:B:143:HIS:HE1	1:B:148:LEU:O	1.97	0.47
1:A:220:PHE:O	1:A:221:ARG:C	2.53	0.47
1:D:109:LEU:HD13	1:D:120:LYS:HB2	1.97	0.47
1:C:140:LEU:HD11	1:C:184:LEU:HD22	1.96	0.47
1:A:5:PRO:HB3	1:A:60:ILE:HB	1.96	0.47
1:C:97:GLU:HB3	1:D:67:GLN:OE1	2.14	0.47
1:D:135:ALA:N	3:D:2065:HOH:O	2.47	0.47
1:C:13:ARG:NH2	1:C:207:PRO:HD3	2.29	0.47
1:B:84:LYS:HD2	1:B:85:ASP:OD2	2.15	0.46
1:B:17:GLU:HG2	1:B:166:TYR:OH	2.16	0.46
1:C:113:GLN:HB3	1:C:115:GLU:OE1	2.16	0.46
1:A:143:HIS:ND1	1:A:145:GLN:HB2	2.30	0.46
1:C:110:SER:HB3	3:C:2066:HOH:O	2.15	0.46
1:D:6:LYS:O	1:D:58:VAL:HA	2.16	0.46
1:B:153:LEU:HD12	1:B:157:ASP:HB2	1.98	0.46
1:A:196:LYS:O	1:A:199:GLN:HG2	2.16	0.46
1:C:45:ARG:HB3	1:C:53:GLN:OE1	2.16	0.45
1:C:21:TRP:CD1	1:C:162:GLU:HG3	2.52	0.45
1:C:70:ALA:HB2	1:D:94:MET:N	2.31	0.45
1:D:76:ALA:CB	1:D:155:ARG:HD2	2.46	0.45
1:C:131:ARG:HH12	2:D:230:GSH:C3	2.30	0.45
1:A:168:GLU:OE1	1:A:185:LYS:NZ	2.50	0.45
1:A:220:PHE:CE1	2:A:230:GSH:HB22	2.52	0.45
1:D:9:TYR:HE1	1:D:56:PRO:HD3	1.81	0.45
1:C:124:ILE:HG13	3:C:2075:HOH:O	2.16	0.45
1:C:139:VAL:HG11	1:C:148:LEU:HD23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:96:ILE:HA	1:D:99:ILE:HD12	1.99	0.45
1:D:143:HIS:O	1:D:145:GLN:N	2.50	0.45
1:C:148:LEU:HD12	1:C:157:ASP:OD1	2.17	0.45
1:B:195:LYS:O	1:B:199:GLN:HG2	2.17	0.44
1:C:205:LYS:HD3	3:C:2107:HOH:O	2.17	0.44
1:B:117:GLN:O	1:B:118:ASP:C	2.55	0.44
1:A:54:GLN:NE2	2:A:230:GSH:HB13	2.32	0.44
1:C:38:ALA:HB1	3:C:2025:HOH:O	2.17	0.44
1:C:99:ILE:HG23	1:C:163:LEU:HD22	2.00	0.44
1:B:176:SER:O	1:B:182:LYS:NZ	2.51	0.44
1:B:20:ARG:NE	1:B:205:LYS:HE2	2.32	0.44
1:C:129:LYS:HG3	1:C:130:ASN:OD1	2.17	0.44
1:A:96:ILE:HD13	3:A:2082:HOH:O	2.16	0.43
1:B:6:LYS:HB3	1:B:6:LYS:NZ	2.33	0.43
1:A:128:THR:HG21	1:A:174:LEU:HD13	1.99	0.43
1:A:52:PHE:HZ	1:B:136:PHE:CZ	2.36	0.43
1:D:40:ASP:O	1:D:43:LYS:HB3	2.18	0.43
1:D:12:ILE:HD12	1:D:14:GLY:CA	2.48	0.43
1:A:204:ARG:NH1	1:D:200:PRO:HG3	2.33	0.43
1:D:23:LEU:HD21	1:D:75:ILE:CD1	2.48	0.43
1:D:9:TYR:CE1	1:D:56:PRO:HD3	2.54	0.43
1:A:13:ARG:NH1	3:A:2011:HOH:O	2.50	0.43
1:A:206:PRO:HB3	1:D:200:PRO:O	2.19	0.43
1:D:12:ILE:HD12	1:D:14:GLY:HA3	2.00	0.43
1:D:6:LYS:HB3	1:D:6:LYS:HE2	1.86	0.43
1:C:185:LYS:O	1:C:189:SER:HB2	2.18	0.43
1:B:58:VAL:HG21	1:B:71:ILE:HG21	1.99	0.43
1:A:37:SER:HB2	1:A:39:GLU:OE1	2.19	0.43
1:D:84:LYS:HG2	1:D:88:GLU:OE1	2.19	0.43
1:D:95:TYR:O	1:D:99:ILE:HG13	2.18	0.43
1:C:66:VAL:O	1:C:67:GLN:HB2	2.18	0.43
1:D:137:GLU:CD	1:D:180:LEU:HB2	2.40	0.43
1:A:113:GLN:HB3	1:A:115:GLU:HG3	2.01	0.42
1:C:5:PRO:HA	1:C:59:GLU:O	2.19	0.42
1:B:96:ILE:HD12	1:B:155:ARG:CZ	2.49	0.42
1:C:90:ALA:HB2	3:C:2057:HOH:O	2.18	0.42
1:A:17:GLU:OE1	1:A:20:ARG:HD2	2.19	0.42
1:B:196:LYS:O	1:B:199:GLN:HB2	2.19	0.42
1:C:153:LEU:HD21	1:C:191:LEU:HD13	2.00	0.42
1:B:13:ARG:NE	1:B:205:LYS:O	2.47	0.42
1:C:204:ARG:NH1	3:C:2008:HOH:O	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:LEU:HD12	1:B:157:ASP:HA	2.02	0.42
1:D:143:HIS:ND1	1:D:145:GLN:HB2	2.34	0.42
1:C:119:ALA:O	1:C:122:ALA:HB3	2.20	0.41
1:C:113:GLN:HB3	1:C:114:PRO:HD2	2.02	0.41
1:D:133:PHE:CZ	1:D:164:LEU:HD23	2.55	0.41
1:B:152:LYS:HG2	1:B:153:LEU:N	2.35	0.41
1:D:23:LEU:CD2	1:D:75:ILE:HD13	2.50	0.41
1:B:99:ILE:HD11	1:B:160:LEU:HB2	2.02	0.41
1:B:128:THR:O	1:B:133:PHE:HB2	2.21	0.40
1:C:211:LYS:HB2	1:C:211:LYS:NZ	2.35	0.40
1:B:41:LEU:HD21	1:B:45:ARG:NH2	2.36	0.40
1:C:19:ILE:HA	1:C:72:LEU:HD21	2.02	0.40
1:A:86:ILE:HD11	1:B:78:LYS:N	2.36	0.40
1:B:213:LEU:O	1:B:217:ARG:HG3	2.21	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	217/222 (98%)	204 (94%)	10 (5%)	3 (1%)	14	7
1	B	215/222 (97%)	200 (93%)	13 (6%)	2 (1%)	21	15
1	C	217/222 (98%)	205 (94%)	9 (4%)	3 (1%)	14	7
1	D	215/222 (97%)	193 (90%)	19 (9%)	3 (1%)	14	7
All	All	864/888 (97%)	802 (93%)	51 (6%)	11 (1%)	15	9

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	221	ARG

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Mol	Chain	Res	Type
1	C	221	ARG
1	D	144	GLY
1	D	171	ASP
1	B	13	ARG
1	D	114	PRO
1	A	67	GLN
1	C	171	ASP
1	A	171	ASP
1	C	67	GLN
1	B	67	GLN

5.3.2 Protein sidechains [i](#)

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	195/197 (99%)	188 (96%)	7 (4%)	42	43
1	B	193/197 (98%)	181 (94%)	12 (6%)	23	19
1	C	195/197 (99%)	184 (94%)	11 (6%)	26	22
1	D	193/197 (98%)	183 (95%)	10 (5%)	29	25
All	All	776/788 (98%)	736 (95%)	40 (5%)	29	25

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	TYR
1	A	86	ILE
1	A	115	GLU
1	A	170	LEU
1	A	172	SER
1	A	208	MET
1	A	210	GLU
1	B	10	SER
1	B	82	TYR
1	B	85	ASP
1	B	86	ILE

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Mol	Chain	Res	Type
1	B	126	GLU
1	B	129	LYS
1	B	152	LYS
1	B	163	LEU
1	B	172	SER
1	B	210	GLU
1	B	213	LEU
1	B	215	GLU
1	C	82	TYR
1	C	108	ASP
1	C	118	ASP
1	C	123	LEU
1	C	126	GLU
1	C	148	LEU
1	C	170	LEU
1	C	180	LEU
1	C	210	GLU
1	C	211	LYS
1	C	218	LYS
1	D	11	ASN
1	D	37	SER
1	D	82	TYR
1	D	91	LEU
1	D	121	LEU
1	D	143	HIS
1	D	152	LYS
1	D	163	LEU
1	D	180	LEU
1	D	210	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	190	ASN
1	A	222	HIS
1	B	54	GLN
1	B	130	ASN
1	B	143	HIS
1	C	46	ASN
1	C	54	GLN
1	C	113	GLN

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Mol	Chain	Res	Type
1	C	190	ASN
1	D	113	GLN
1	D	190	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 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	230	-	13,19,19	0.43	0	15,24,24	0.76	1 (6%)
2	GSH	B	230	-	13,19,19	0.48	0	15,24,24	2.04	4 (26%)
2	GSH	C	230	-	13,19,19	0.61	0	15,24,24	1.63	2 (13%)
2	GSH	D	230	-	13,19,19	0.58	0	15,24,24	0.55	0

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	230	-	1/1/6/8	0/18/24/24	0/0/0/0
2	GSH	B	230	-	1/1/6/8	0/18/24/24	0/0/0/0
2	GSH	C	230	-	1/1/6/8	0/18/24/24	0/0/0/0
2	GSH	D	230	-	1/1/6/8	0/18/24/24	0/0/0/0

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	230	GSH	CB2-CA2-N2	-4.90	104.52	111.40
2	B	230	GSH	CA2-CB2-SG2	-3.20	110.22	114.16
2	B	230	GSH	CG1-CD1-N2	-3.09	110.79	115.83
2	C	230	GSH	O2-C2-N3	-2.67	117.72	123.08
2	A	230	GSH	CA2-CB2-SG2	2.02	116.64	114.16
2	B	230	GSH	CB2-CA2-C2	2.65	115.64	109.66
2	C	230	GSH	CA2-CB2-SG2	4.22	119.34	114.16

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	230	GSH	CA1
2	B	230	GSH	CA1
2	C	230	GSH	CA1
2	D	230	GSH	CA1

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	230	GSH	2	0
2	D	230	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, 95th 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 ²)	Q<0.9
1	A	219/222 (98%)	0.40	5 (2%) 64 70	4, 10, 22, 38	0
1	B	217/222 (97%)	0.67	9 (4%) 41 50	7, 14, 28, 37	0
1	C	219/222 (98%)	0.80	14 (6%) 23 30	8, 17, 29, 55	0
1	D	217/222 (97%)	0.84	23 (10%) 8 11	8, 18, 39, 45	0
All	All	872/888 (98%)	0.67	51 (5%) 26 34	4, 14, 30, 55	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	222	HIS	5.8
1	A	222	HIS	3.8
1	D	46	ASN	3.4
1	B	210	GLU	3.2
1	D	210	GLU	3.1
1	D	114	PRO	3.0
1	D	216	SER	2.9
1	D	214	GLU	2.9
1	B	115	GLU	2.9
1	D	119	ALA	2.8
1	D	115	GLU	2.8
1	C	122	ALA	2.8
1	D	30	PHE	2.7
1	D	111	PHE	2.6
1	B	34	PHE	2.6
1	D	220	PHE	2.6
1	D	180	LEU	2.5
1	C	221	ARG	2.4
1	D	38	ALA	2.4
1	D	213	LEU	2.4
1	D	212	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	129	LYS	2.4
1	C	192	PRO	2.3
1	C	49	TYR	2.3
1	C	113	GLN	2.3
1	D	42	ASP	2.3
1	D	116	GLU	2.2
1	D	218	LYS	2.2
1	C	219	ILE	2.2
1	C	39	GLU	2.2
1	A	183	ALA	2.2
1	A	99	ILE	2.2
1	B	99	ILE	2.2
1	C	214	GLU	2.1
1	C	130	ASN	2.1
1	B	217	ARG	2.1
1	D	12	ILE	2.1
1	C	136	PHE	2.1
1	C	34	PHE	2.1
1	B	63	MET	2.1
1	D	112	SER	2.1
1	D	179	PRO	2.1
1	B	212	SER	2.1
1	A	66	VAL	2.1
1	B	113	GLN	2.1
1	A	216	SER	2.1
1	C	35	ILE	2.0
1	D	122	ALA	2.0
1	D	117	GLN	2.0
1	B	80	ASN	2.0
1	D	35	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

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, 95th 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(Å ²)	Q<0.9
2	GSH	D	230	20/20	0.78	0.20	0.93	16,21,23,23	0
2	GSH	C	230	20/20	0.90	0.16	-0.40	13,15,16,16	0
2	GSH	A	230	20/20	0.91	0.14	-0.46	8,10,13,15	0
2	GSH	B	230	20/20	0.90	0.14	-0.77	11,14,15,16	0

6.5 Other polymers

There are no such residues in this entry.