



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:07 PM UTC

PDB ID : 3I69 / pdb_00003i69
Title : Apo Glutathione Transferase A1-1 GIMF-helix mutant
Authors : Balogh, L.M.; Le Trong, I.; Stenkamp, R.E.; Atkins, W.M.
Deposited on : 2009-07-06
Resolution : 2.38 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

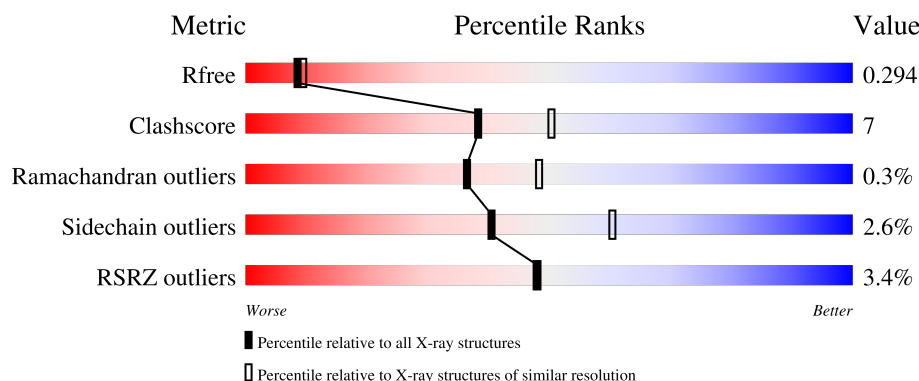
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	3% 79% 19% .
1	B	222	85% 14% .
1	C	222	2% 85% 13% ..
1	D	222	% 86% 12% ..
1	E	222	9% 80% 19% .

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Mol	Chain	Length	Quality of chain
1	F	222	7% 77% 20% • •
1	G	222	% 86% 12% •
1	H	222	3% 84% 14% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14543 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 A1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1781	1159	294	320	8			
1	B	221	Total	C	N	O	S	0	0	0
			1799	1170	299	322	8			
1	C	219	Total	C	N	O	S	0	2	0
			1796	1173	294	321	8			
1	D	219	Total	C	N	O	S	0	0	0
			1781	1159	294	320	8			
1	E	219	Total	C	N	O	S	0	1	0
			1787	1162	297	320	8			
1	F	216	Total	C	N	O	S	0	0	0
			1756	1142	291	315	8			
1	G	219	Total	C	N	O	S	0	0	0
			1781	1159	294	320	8			
1	H	219	Total	C	N	O	S	0	1	0
			1783	1160	294	321	8			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	GLY	ALA	engineered mutation	UNP P08263
A	107	ILE	LEU	engineered mutation	UNP P08263
A	108	MET	LEU	engineered mutation	UNP P08263
A	111	PHE	VAL	engineered mutation	UNP P08263
A	208	PRO	MET	engineered mutation	UNP P08263
A	211	ILE	LYS	engineered mutation	UNP P08263
A	212	TYR	SER	engineered mutation	UNP P08263
A	213	VAL	LEU	engineered mutation	UNP P08263
A	214	ARG	GLU	engineered mutation	UNP P08263
A	215	THR	GLU	engineered mutation	UNP P08263
A	216	VAL	ALA	engineered mutation	UNP P08263
A	217	TYR	ARG	engineered mutation	UNP P08263
A	218	ASN	LYS	engineered mutation	UNP P08263

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Chain	Residue	Modelled	Actual	Comment	Reference
A	222	PRO	PHE	engineered mutation	UNP P08263
B	12	GLY	ALA	engineered mutation	UNP P08263
B	107	ILE	LEU	engineered mutation	UNP P08263
B	108	MET	LEU	engineered mutation	UNP P08263
B	111	PHE	VAL	engineered mutation	UNP P08263
B	208	PRO	MET	engineered mutation	UNP P08263
B	211	ILE	LYS	engineered mutation	UNP P08263
B	212	TYR	SER	engineered mutation	UNP P08263
B	213	VAL	LEU	engineered mutation	UNP P08263
B	214	ARG	GLU	engineered mutation	UNP P08263
B	215	THR	GLU	engineered mutation	UNP P08263
B	216	VAL	ALA	engineered mutation	UNP P08263
B	217	TYR	ARG	engineered mutation	UNP P08263
B	218	ASN	LYS	engineered mutation	UNP P08263
B	222	PRO	PHE	engineered mutation	UNP P08263
C	12	GLY	ALA	engineered mutation	UNP P08263
C	107	ILE	LEU	engineered mutation	UNP P08263
C	108	MET	LEU	engineered mutation	UNP P08263
C	111	PHE	VAL	engineered mutation	UNP P08263
C	208	PRO	MET	engineered mutation	UNP P08263
C	211	ILE	LYS	engineered mutation	UNP P08263
C	212	TYR	SER	engineered mutation	UNP P08263
C	213	VAL	LEU	engineered mutation	UNP P08263
C	214	ARG	GLU	engineered mutation	UNP P08263
C	215	THR	GLU	engineered mutation	UNP P08263
C	216	VAL	ALA	engineered mutation	UNP P08263
C	217	TYR	ARG	engineered mutation	UNP P08263
C	218	ASN	LYS	engineered mutation	UNP P08263
C	222	PRO	PHE	engineered mutation	UNP P08263
D	12	GLY	ALA	engineered mutation	UNP P08263
D	107	ILE	LEU	engineered mutation	UNP P08263
D	108	MET	LEU	engineered mutation	UNP P08263
D	111	PHE	VAL	engineered mutation	UNP P08263
D	208	PRO	MET	engineered mutation	UNP P08263
D	211	ILE	LYS	engineered mutation	UNP P08263
D	212	TYR	SER	engineered mutation	UNP P08263
D	213	VAL	LEU	engineered mutation	UNP P08263
D	214	ARG	GLU	engineered mutation	UNP P08263
D	215	THR	GLU	engineered mutation	UNP P08263
D	216	VAL	ALA	engineered mutation	UNP P08263
D	217	TYR	ARG	engineered mutation	UNP P08263
D	218	ASN	LYS	engineered mutation	UNP P08263

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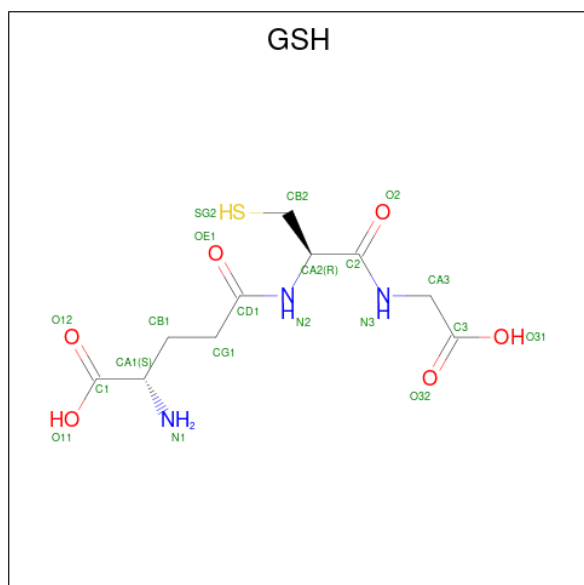
Chain	Residue	Modelled	Actual	Comment	Reference
D	222	PRO	PHE	engineered mutation	UNP P08263
E	12	GLY	ALA	engineered mutation	UNP P08263
E	107	ILE	LEU	engineered mutation	UNP P08263
E	108	MET	LEU	engineered mutation	UNP P08263
E	111	PHE	VAL	engineered mutation	UNP P08263
E	208	PRO	MET	engineered mutation	UNP P08263
E	211	ILE	LYS	engineered mutation	UNP P08263
E	212	TYR	SER	engineered mutation	UNP P08263
E	213	VAL	LEU	engineered mutation	UNP P08263
E	214	ARG	GLU	engineered mutation	UNP P08263
E	215	THR	GLU	engineered mutation	UNP P08263
E	216	VAL	ALA	engineered mutation	UNP P08263
E	217	TYR	ARG	engineered mutation	UNP P08263
E	218	ASN	LYS	engineered mutation	UNP P08263
E	222	PRO	PHE	engineered mutation	UNP P08263
F	12	GLY	ALA	engineered mutation	UNP P08263
F	107	ILE	LEU	engineered mutation	UNP P08263
F	108	MET	LEU	engineered mutation	UNP P08263
F	111	PHE	VAL	engineered mutation	UNP P08263
F	208	PRO	MET	engineered mutation	UNP P08263
F	211	ILE	LYS	engineered mutation	UNP P08263
F	212	TYR	SER	engineered mutation	UNP P08263
F	213	VAL	LEU	engineered mutation	UNP P08263
F	214	ARG	GLU	engineered mutation	UNP P08263
F	215	THR	GLU	engineered mutation	UNP P08263
F	216	VAL	ALA	engineered mutation	UNP P08263
F	217	TYR	ARG	engineered mutation	UNP P08263
F	218	ASN	LYS	engineered mutation	UNP P08263
F	222	PRO	PHE	engineered mutation	UNP P08263
G	12	GLY	ALA	engineered mutation	UNP P08263
G	107	ILE	LEU	engineered mutation	UNP P08263
G	108	MET	LEU	engineered mutation	UNP P08263
G	111	PHE	VAL	engineered mutation	UNP P08263
G	208	PRO	MET	engineered mutation	UNP P08263
G	211	ILE	LYS	engineered mutation	UNP P08263
G	212	TYR	SER	engineered mutation	UNP P08263
G	213	VAL	LEU	engineered mutation	UNP P08263
G	214	ARG	GLU	engineered mutation	UNP P08263
G	215	THR	GLU	engineered mutation	UNP P08263
G	216	VAL	ALA	engineered mutation	UNP P08263
G	217	TYR	ARG	engineered mutation	UNP P08263
G	218	ASN	LYS	engineered mutation	UNP P08263

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Chain	Residue	Modelled	Actual	Comment	Reference
G	222	PRO	PHE	engineered mutation	UNP P08263
H	12	GLY	ALA	engineered mutation	UNP P08263
H	107	ILE	LEU	engineered mutation	UNP P08263
H	108	MET	LEU	engineered mutation	UNP P08263
H	111	PHE	VAL	engineered mutation	UNP P08263
H	208	PRO	MET	engineered mutation	UNP P08263
H	211	ILE	LYS	engineered mutation	UNP P08263
H	212	TYR	SER	engineered mutation	UNP P08263
H	213	VAL	LEU	engineered mutation	UNP P08263
H	214	ARG	GLU	engineered mutation	UNP P08263
H	215	THR	GLU	engineered mutation	UNP P08263
H	216	VAL	ALA	engineered mutation	UNP P08263
H	217	TYR	ARG	engineered mutation	UNP P08263
H	218	ASN	LYS	engineered mutation	UNP P08263
H	222	PRO	PHE	engineered mutation	UNP P08263

- Molecule 2 is GLUTATHIONE (CCD ID: GSH) (formula: C₁₀H₁₇N₃O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	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		

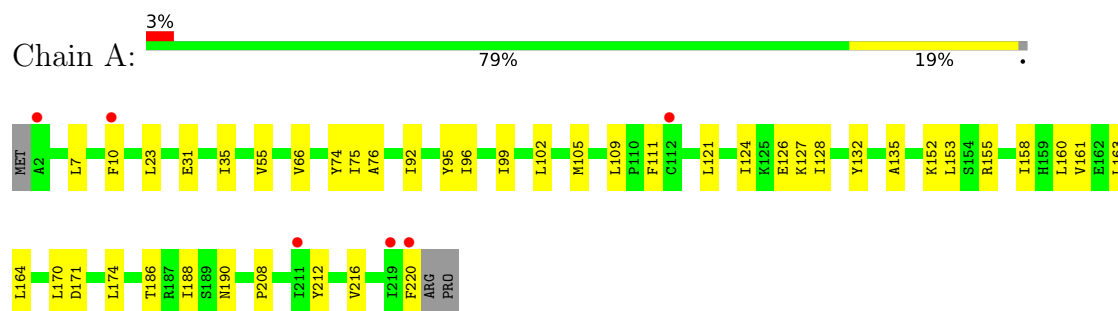
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	49	Total 49	O 49	0	0
3	B	45	Total 45	O 45	0	0
3	C	29	Total 29	O 29	0	0
3	D	38	Total 38	O 38	0	0
3	E	15	Total 15	O 15	0	0
3	F	18	Total 18	O 18	0	0
3	G	28	Total 28	O 28	0	0
3	H	17	Total 17	O 17	0	0

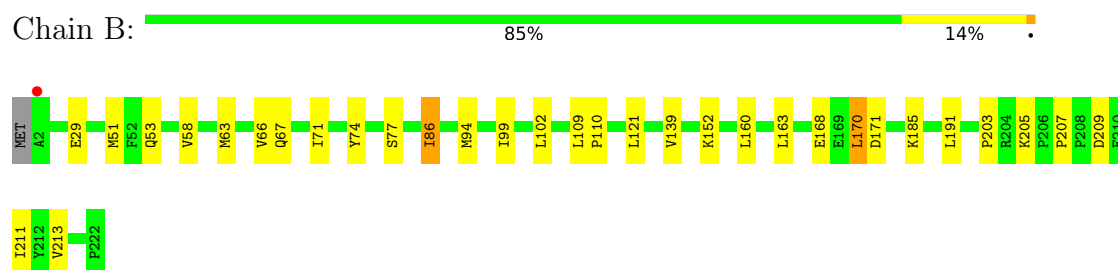
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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 ($RSRZ > 2$). 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.

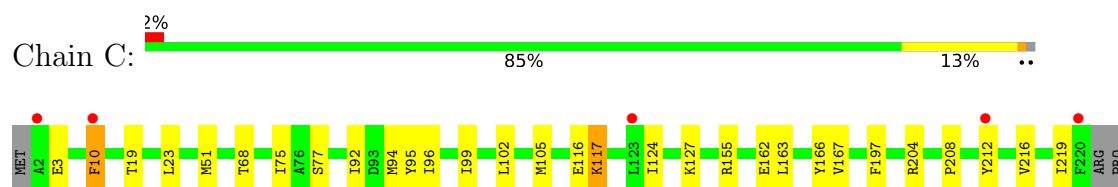
• Molecule 1: Glutathione S-transferase A1



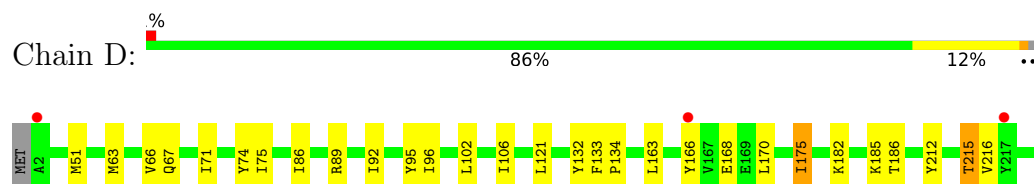
• Molecule 1: Glutathione S-transferase A1



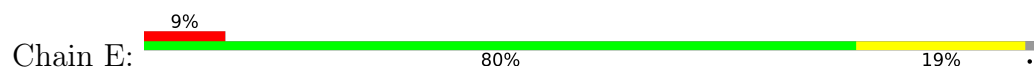
• Molecule 1: Glutathione S-transferase A1

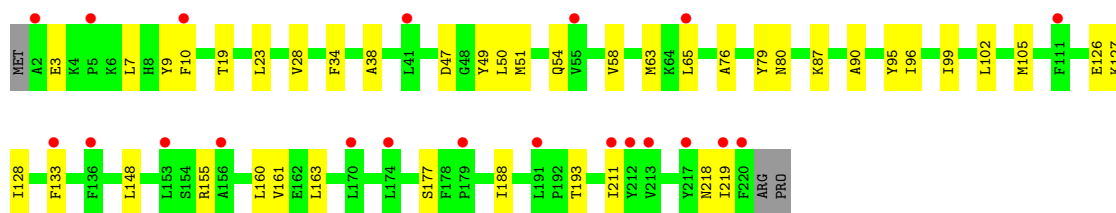


• Molecule 1: Glutathione S-transferase A1

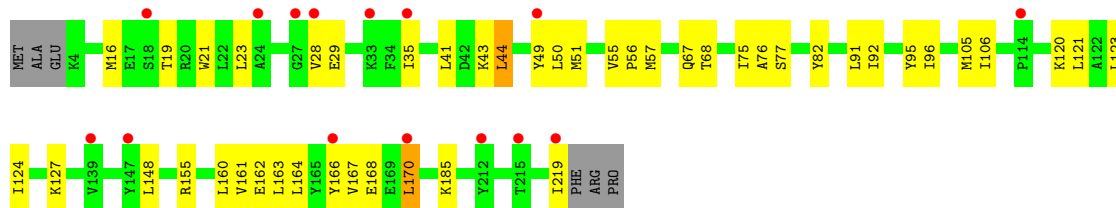
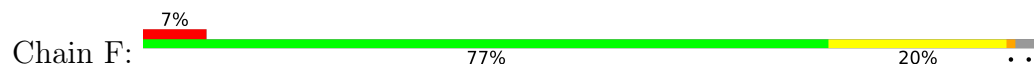


• Molecule 1: Glutathione S-transferase A1

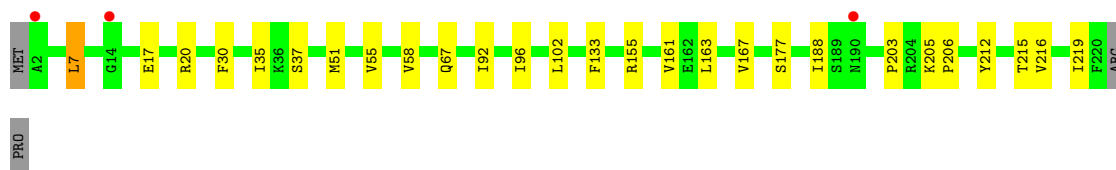
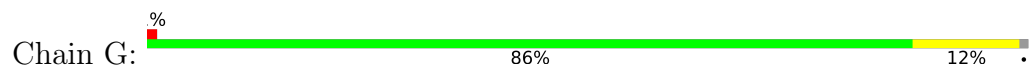




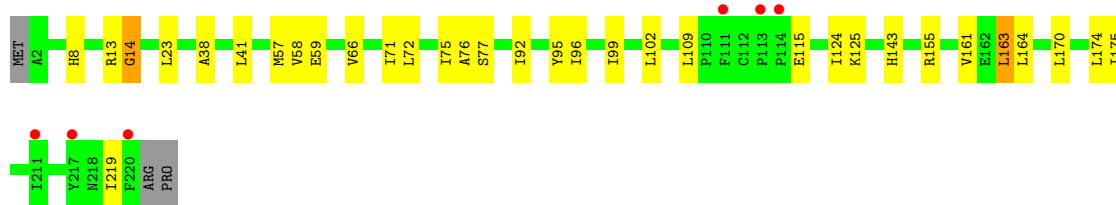
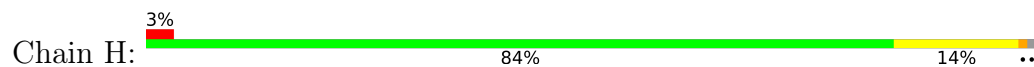
• Molecule 1: Glutathione S-transferase A1



• Molecule 1: Glutathione S-transferase A1



• Molecule 1: Glutathione S-transferase A1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	96.90Å 114.68Å 97.54Å 90.00° 117.76° 90.00°	Depositor
Resolution (Å)	47.22 – 2.38 47.22 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.22-2.38) 99.3 (47.22-2.38)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.5.0047	Depositor
R, R_{free}	0.225 , 0.289 0.229 , 0.294	Depositor DCC
R_{free} test set	3752 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 28.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.038 for -h-l,k,h 0.038 for l,k,-h-l 0.048 for h,-k,-h-l 0.090 for -h-l,-k,l 0.046 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14543	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.73% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.69	0/1820	0.83	0/2452
1	B	0.65	1/1839 (0.1%)	0.82	2/2478 (0.1%)
1	C	0.65	0/1845	0.84	0/2486
1	D	0.63	0/1820	0.85	0/2452
1	E	0.58	0/1831	0.81	0/2466
1	F	0.60	0/1794	0.83	0/2417
1	G	0.60	0/1820	0.84	0/2452
1	H	0.57	0/1826	0.79	0/2460
All	All	0.63	1/14595 (0.0%)	0.83	2/19663 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	207	PRO	CA-C	6.21	1.55	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	191	LEU	CA-C-N	5.21	124.66	119.24
1	B	191	LEU	C-N-CA	5.21	124.66	119.24

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1781	0	1836	31	0
1	B	1799	0	1856	20	0
1	C	1796	0	1846	41	0
1	D	1781	0	1836	21	0
1	E	1787	0	1845	25	0
1	F	1756	0	1816	33	0
1	G	1781	0	1836	21	0
1	H	1783	0	1837	22	0
2	B	20	0	15	0	0
2	D	20	0	15	0	0
3	A	49	0	0	1	0
3	B	45	0	0	0	0
3	C	29	0	0	0	0
3	D	38	0	0	1	0
3	E	15	0	0	0	0
3	F	18	0	0	1	0
3	G	28	0	0	0	0
3	H	17	0	0	0	0
All	All	14543	0	14738	200	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 7.

All (200) 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:C:10[B]:PHE:CZ	1:C:212[B]:TYR:CE1	2.19	1.29
1:C:10[B]:PHE:CE2	1:C:212[B]:TYR:CE1	2.21	1.28
1:C:10[B]:PHE:HE2	1:C:212[B]:TYR:CD1	1.69	1.08
1:C:10[B]:PHE:CZ	1:C:212[B]:TYR:HE1	1.64	1.06
1:A:121:LEU:HD11	1:A:170:LEU:HD21	1.41	1.02
1:C:10[B]:PHE:HZ	1:C:212[B]:TYR:CE1	1.72	0.95
1:B:121:LEU:HD11	1:B:170:LEU:HD21	1.48	0.94
1:F:106:ILE:HG23	1:F:166:TYR:CZ	2.08	0.89
1:C:10[B]:PHE:CE2	1:C:212[B]:TYR:CD1	2.52	0.86
1:A:102:LEU:HD23	1:A:163:LEU:HD21	1.58	0.85
1:C:95:TYR:CD1	1:D:51:MET:HE1	2.14	0.83
1:C:10[B]:PHE:CE2	1:C:212[B]:TYR:HE1	1.79	0.82
1:C:10[A]:PHE:CE1	1:C:219:ILE:HG21	2.21	0.76
1:C:10[B]:PHE:HZ	1:C:212[B]:TYR:CZ	2.04	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:212:TYR:O	1:G:216:VAL:HG23	1.86	0.75
1:A:95:TYR:CD1	1:B:51:MET:HE1	2.22	0.75
1:A:99:ILE:HG23	1:A:163:LEU:HD22	1.70	0.73
1:C:10[B]:PHE:HE2	1:C:212[B]:TYR:CE1	1.75	0.73
1:F:92:ILE:O	1:F:96:ILE:HG23	1.88	0.73
1:C:99:ILE:HG23	1:C:163:LEU:HD22	1.71	0.71
1:C:102:LEU:HD23	1:C:163:LEU:HD21	1.73	0.69
1:B:102:LEU:HD23	1:B:163:LEU:HD21	1.75	0.69
1:A:212:TYR:O	1:A:216:VAL:HG23	1.93	0.69
1:G:102:LEU:HD23	1:G:163:LEU:HD21	1.76	0.68
1:H:92:ILE:O	1:H:96:ILE:HG23	1.94	0.68
1:C:10[A]:PHE:HB2	1:C:212[A]:TYR:OH	1.94	0.67
1:A:23:LEU:HD21	1:A:75:ILE:HD13	1.74	0.67
1:C:105:MET:HE1	1:C:127:LYS:HD2	1.77	0.67
1:G:212:TYR:HA	1:G:215:THR:HG22	1.76	0.66
1:C:96:ILE:HD12	1:C:155:ARG:CZ	2.26	0.65
1:D:92:ILE:O	1:D:96:ILE:HG23	1.95	0.64
1:A:121:LEU:CD1	1:A:170:LEU:HD21	2.23	0.64
1:A:23:LEU:CD2	1:A:75:ILE:HD13	2.27	0.64
1:C:92:ILE:O	1:C:96:ILE:HG23	1.98	0.64
1:C:105:MET:HE2	1:C:124:ILE:HG12	1.80	0.64
1:F:106:ILE:CG2	1:F:166:TYR:CZ	2.82	0.62
1:D:212:TYR:O	1:D:215:THR:HG22	2.01	0.61
1:G:92:ILE:O	1:G:96:ILE:HG23	2.01	0.61
1:H:38:ALA:HA	1:H:219:ILE:HG23	1.80	0.61
1:H:41:LEU:HD23	1:H:219:ILE:HG22	1.83	0.60
1:A:121:LEU:HD11	1:A:170:LEU:CD2	2.25	0.59
1:E:28:VAL:HG21	1:E:79:TYR:CZ	2.38	0.59
1:H:164:LEU:HD22	1:H:175:ILE:HD12	1.84	0.59
1:C:94:MET:HE3	1:D:51:MET:SD	2.42	0.59
1:C:208:PRO:HB3	1:C:212[B]:TYR:CE2	2.38	0.59
1:C:10[B]:PHE:CZ	1:C:212[B]:TYR:CZ	2.82	0.58
1:C:163:LEU:O	1:C:167:VAL:HG23	2.03	0.57
1:F:106:ILE:HG23	1:F:166:TYR:OH	2.04	0.57
1:E:63:MET:HE3	1:E:65:LEU:HD11	1.87	0.56
1:G:35:ILE:HD11	1:G:55:VAL:HG11	1.87	0.56
1:C:95:TYR:CE1	1:D:51:MET:HE1	2.41	0.56
1:E:102:LEU:HD21	1:E:128:ILE:HG12	1.87	0.56
1:G:7:LEU:HD12	1:G:58:VAL:HG13	1.88	0.56
1:C:105:MET:HE2	1:C:124:ILE:CG1	2.35	0.55
1:G:37:SER:O	1:G:219:ILE:HG23	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:19:THR:HG22	1:C:23:LEU:HD12	1.89	0.55
1:C:23:LEU:HG	1:C:75:ILE:HD13	1.88	0.55
1:G:212:TYR:O	1:G:215:THR:HG22	2.07	0.54
1:F:35:ILE:CD1	1:F:55:VAL:HG11	2.37	0.54
1:E:10:PHE:CE2	1:E:219:ILE:HD13	2.42	0.54
1:E:51:MET:HE1	1:F:95:TYR:CD1	2.44	0.53
1:D:71:ILE:HG22	1:D:75:ILE:HD12	1.89	0.53
1:B:209:ASP:O	1:B:213:VAL:HG23	2.09	0.53
1:F:168:GLU:OE1	1:F:185:LYS:NZ	2.42	0.53
1:F:44:LEU:HB3	1:F:50:LEU:HD11	1.91	0.53
1:A:35:ILE:HD11	1:A:55:VAL:HG11	1.91	0.52
1:F:16:MET:HE2	1:F:56:PRO:HB3	1.92	0.52
1:D:102:LEU:HD23	1:D:163:LEU:HD21	1.90	0.52
1:B:109:LEU:HD21	1:B:121:LEU:HD13	1.92	0.52
1:C:10[B]:PHE:HE2	1:C:212[B]:TYR:HD1	1.45	0.51
1:F:166:TYR:CE1	1:F:170:LEU:HD12	2.45	0.51
1:G:7:LEU:HD22	1:G:30:PHE:CD1	2.46	0.51
1:H:58:VAL:HG23	1:H:71:ILE:HD13	1.91	0.51
1:D:63:MET:HE1	1:D:74:TYR:CE1	2.45	0.51
1:F:49:TYR:HB3	1:F:57:MET:HE2	1.93	0.51
1:F:76:ALA:HB1	1:F:155:ARG:HD2	1.93	0.51
1:B:66:VAL:O	1:B:67:GLN:HB2	2.10	0.51
1:F:28:VAL:HG12	1:F:29:GLU:O	2.12	0.50
1:A:74:TYR:CE1	1:B:86:ILE:HD13	2.46	0.50
1:C:116:GLU:O	1:C:117:LYS:C	2.55	0.50
1:E:105:MET:HE1	1:E:127:LYS:CD	2.42	0.50
1:D:106:ILE:HD13	1:D:166:TYR:CD1	2.47	0.50
1:F:148:LEU:HD11	1:F:160:LEU:HD22	1.93	0.49
1:G:161:VAL:HG21	1:G:188:ILE:HB	1.94	0.49
1:B:102:LEU:CD2	1:B:163:LEU:HD21	2.43	0.49
1:E:50:LEU:HD13	1:E:54:GLN:C	2.38	0.49
1:G:212:TYR:HA	1:G:215:THR:CG2	2.43	0.49
1:A:171:ASP:HB3	1:A:174:LEU:HD12	1.95	0.49
1:C:19:THR:O	1:C:23:LEU:HD12	2.12	0.49
1:E:99:ILE:HG23	1:E:163:LEU:HD22	1.95	0.49
1:F:105:MET:HE2	1:F:124:ILE:HG12	1.94	0.49
1:F:91:LEU:HD22	3:F:6144:HOH:O	2.12	0.48
1:E:96:ILE:HD12	1:E:155:ARG:NH2	2.29	0.48
1:E:105:MET:HE1	1:E:127:LYS:HD2	1.95	0.48
1:E:19:THR:HG22	1:E:23:LEU:HD12	1.94	0.48
3:A:6108:HOH:O	1:B:53:GLN:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:LEU:CD1	1:B:170:LEU:HD21	2.32	0.48
1:C:96:ILE:CD1	1:C:155:ARG:CZ	2.91	0.48
1:F:163:LEU:O	1:F:167:VAL:HG23	2.13	0.48
1:H:109:LEU:HD13	1:H:124:ILE:HD11	1.96	0.48
1:D:63:MET:HE1	1:D:74:TYR:CZ	2.49	0.47
1:A:76:ALA:CB	1:A:155:ARG:HD2	2.44	0.47
1:E:95:TYR:CD1	1:F:51:MET:HE1	2.49	0.47
1:G:35:ILE:CD1	1:G:55:VAL:HG11	2.44	0.47
1:A:186:THR:O	1:A:190:ASN:ND2	2.48	0.47
1:C:94:MET:CE	1:D:51:MET:SD	3.03	0.47
1:B:168:GLU:OE1	1:B:185:LYS:NZ	2.46	0.47
1:E:38:ALA:HA	1:E:219:ILE:HG23	1.97	0.46
1:B:99:ILE:HD13	1:B:160:LEU:HA	1.97	0.46
1:F:106:ILE:HD13	1:F:166:TYR:CE1	2.51	0.46
1:H:76:ALA:CB	1:H:155:ARG:HD2	2.44	0.46
1:C:95:TYR:HD1	1:D:51:MET:HE1	1.77	0.46
1:E:148:LEU:HD11	1:E:160:LEU:HD22	1.96	0.46
1:G:17:GLU:OE1	1:G:20:ARG:NH1	2.47	0.46
1:H:13:ARG:O	1:H:14:GLY:C	2.58	0.46
1:D:66:VAL:O	1:D:67:GLN:HB2	2.15	0.46
1:H:109:LEU:HD13	1:H:124:ILE:CD1	2.44	0.46
1:A:111:PHE:CZ	1:A:216:VAL:HG11	2.51	0.46
1:A:7:LEU:CD1	1:A:7:LEU:N	2.79	0.46
1:C:10[A]:PHE:CD1	1:C:219:ILE:HD13	2.50	0.46
1:G:212:TYR:CA	1:G:215:THR:HG22	2.46	0.46
1:F:121:LEU:HD11	1:F:170:LEU:HD21	1.97	0.46
1:F:41:LEU:HD22	1:F:219:ILE:HG22	1.98	0.45
1:H:41:LEU:HD23	1:H:219:ILE:CG2	2.46	0.45
1:H:102:LEU:HD23	1:H:163:LEU:CD2	2.46	0.45
1:F:106:ILE:HD13	1:F:166:TYR:CD1	2.51	0.45
1:F:161:VAL:HA	1:F:164:LEU:HD12	1.98	0.45
1:C:19:THR:HG22	1:C:23:LEU:CD1	2.46	0.45
1:E:161:VAL:HG21	1:E:188:ILE:HB	1.98	0.45
1:G:203:PRO:O	1:G:205:LYS:NZ	2.45	0.45
1:D:89:ARG:NH1	3:D:6098:HOH:O	2.45	0.45
1:G:212:TYR:C	1:G:215:THR:HG22	2.42	0.45
1:A:153:LEU:HD11	1:A:158:ILE:HD11	1.98	0.45
1:A:105:MET:HE1	1:A:127:LYS:HD2	1.98	0.45
1:F:50:LEU:HD23	1:F:57:MET:HG3	1.99	0.45
1:E:76:ALA:CB	1:E:155:ARG:HD2	2.47	0.45
1:E:87:LYS:O	1:E:90:ALA:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:23:LEU:HG	1:H:75:ILE:HD13	1.99	0.44
1:C:10[B]:PHE:HZ	1:C:212[B]:TYR:OH	2.00	0.44
1:D:175:ILE:HD13	1:D:182:LYS:HG2	1.98	0.44
1:E:7:LEU:HG	1:E:58:VAL:HG22	2.00	0.44
1:A:95:TYR:CE1	1:B:51:MET:HE1	2.52	0.44
1:A:208:PRO:HB3	1:A:212:TYR:CE2	2.53	0.44
1:E:128:ILE:HG23	1:E:133:PHE:CE1	2.52	0.44
1:C:162:GLU:HG2	1:C:166:TYR:CE2	2.54	0.43
1:F:76:ALA:CB	1:F:155:ARG:HD2	2.48	0.43
1:E:9:TYR:O	1:E:34:PHE:HA	2.18	0.43
1:A:7:LEU:N	1:A:7:LEU:HD12	2.34	0.43
1:F:148:LEU:HD11	1:F:160:LEU:CD2	2.49	0.43
1:D:121:LEU:CD1	1:D:170:LEU:HD11	2.49	0.43
1:F:67:GLN:O	1:F:68:THR:C	2.61	0.43
1:E:28:VAL:HG21	1:E:79:TYR:CE2	2.53	0.43
1:A:92:ILE:O	1:A:96:ILE:HG23	2.19	0.43
1:A:161:VAL:HG21	1:A:188:ILE:HB	2.01	0.43
1:E:148:LEU:HD11	1:E:160:LEU:CD2	2.48	0.43
1:H:102:LEU:HD23	1:H:163:LEU:HD21	2.01	0.43
1:B:203:PRO:O	1:B:205:LYS:NZ	2.52	0.42
1:D:102:LEU:HD22	1:D:132:TYR:CD2	2.54	0.42
1:H:125:LYS:HG2	1:H:174:LEU:HD11	2.01	0.42
1:B:211:ILE:HD12	1:B:211:ILE:N	2.34	0.42
1:H:57:MET:HB2	1:H:66:VAL:HG12	2.00	0.42
1:D:168:GLU:OE1	1:D:185:LYS:NZ	2.48	0.42
1:E:63:MET:CE	1:E:65:LEU:HD11	2.50	0.42
1:B:58:VAL:HG21	1:B:71:ILE:HG21	2.02	0.42
1:F:35:ILE:HD11	1:F:55:VAL:HG11	2.00	0.42
1:G:51:MET:HE1	1:H:95:TYR:CD1	2.55	0.42
1:D:166:TYR:CD1	1:D:166:TYR:C	2.96	0.42
1:F:21:TRP:CD1	1:F:162:GLU:HG3	2.55	0.42
1:E:79:TYR:O	1:E:80:ASN:C	2.63	0.42
1:A:160:LEU:O	1:A:164:LEU:HG	2.20	0.42
1:G:7:LEU:N	1:G:7:LEU:CD1	2.83	0.42
1:H:96:ILE:HA	1:H:99:ILE:HD12	2.02	0.42
1:H:161:VAL:HA	1:H:164:LEU:HD12	2.01	0.41
1:A:95:TYR:HD1	1:B:51:MET:HE1	1.76	0.41
1:C:51:MET:HE1	1:D:95:TYR:CD1	2.56	0.41
1:F:23:LEU:CD2	1:F:75:ILE:HD13	2.50	0.41
1:F:41:LEU:HD22	1:F:219:ILE:CG2	2.50	0.41
1:G:205:LYS:HB3	1:G:206:PRO:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:LEU:HD13	1:A:124:ILE:HD12	2.02	0.41
1:B:109:LEU:HB3	1:B:110:PRO:HD3	2.02	0.41
1:G:96:ILE:CD1	1:G:155:ARG:CZ	2.99	0.41
1:H:8:HIS:NE2	1:H:59:GLU:OE2	2.43	0.41
1:A:66:VAL:HG22	1:B:94:MET:SD	2.60	0.41
1:A:171:ASP:HB3	1:A:174:LEU:CD1	2.51	0.41
1:A:208:PRO:HB3	1:A:212:TYR:CD2	2.55	0.41
1:A:102:LEU:HD21	1:A:128:ILE:HG12	2.01	0.41
1:A:132:TYR:O	1:A:135:ALA:HB3	2.21	0.41
1:B:63:MET:HE1	1:B:74:TYR:CZ	2.56	0.41
1:C:96:ILE:HD12	1:C:155:ARG:NH2	2.35	0.41
1:H:72:LEU:HB3	1:H:155:ARG:NH2	2.35	0.41
1:H:99:ILE:HG23	1:H:163:LEU:HD22	2.01	0.41
1:E:47:ASP:HB3	1:E:49:TYR:CE1	2.56	0.41
1:F:105:MET:HE1	1:F:127:LYS:HD2	2.03	0.41
1:F:166:TYR:CD1	1:F:166:TYR:C	2.98	0.41
1:C:197:PHE:CE2	1:C:204:ARG:HD3	2.56	0.41
1:G:133:PHE:CZ	1:G:167:VAL:HG11	2.56	0.41
1:H:57:MET:CB	1:H:66:VAL:HG12	2.52	0.41
1:D:133:PHE:N	1:D:134:PRO:CD	2.85	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%)	207 (95%)	10 (5%)	0	100	100
1	B	219/222 (99%)	213 (97%)	5 (2%)	1 (0%)	24	34
1	C	219/222 (99%)	203 (93%)	14 (6%)	2 (1%)	14	20
1	D	217/222 (98%)	213 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	218/222 (98%)	204 (94%)	14 (6%)	0	100	100
1	F	214/222 (96%)	204 (95%)	10 (5%)	0	100	100
1	G	217/222 (98%)	207 (95%)	9 (4%)	1 (0%)	24	34
1	H	218/222 (98%)	207 (95%)	10 (5%)	1 (0%)	24	34
All	All	1739/1776 (98%)	1658 (95%)	76 (4%)	5 (0%)	36	48

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	3	GLU
1	C	117	LYS
1	B	171	ASP
1	G	67	GLN
1	H	14	GLY

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	194/197 (98%)	189 (97%)	5 (3%)	40	60
1	B	196/197 (100%)	190 (97%)	6 (3%)	35	54
1	C	196/197 (100%)	192 (98%)	4 (2%)	48	68
1	D	194/197 (98%)	189 (97%)	5 (3%)	40	60
1	E	195/197 (99%)	189 (97%)	6 (3%)	35	54
1	F	192/197 (98%)	184 (96%)	8 (4%)	26	42
1	G	194/197 (98%)	192 (99%)	2 (1%)	68	82
1	H	195/197 (99%)	189 (97%)	6 (3%)	35	54
All	All	1556/1576 (99%)	1514 (97%)	42 (3%)	40	59

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	PHE
1	A	31	GLU
1	A	126	GLU
1	A	152	LYS
1	A	220	PHE
1	B	29	GLU
1	B	77	SER
1	B	86	ILE
1	B	139	VAL
1	B	152	LYS
1	B	170	LEU
1	C	10[A]	PHE
1	C	10[B]	PHE
1	C	68	THR
1	C	77	SER
1	D	86	ILE
1	D	175	ILE
1	D	186	THR
1	D	215	THR
1	D	216	VAL
1	E	3	GLU
1	E	126	GLU
1	E	177	SER
1	E	193	THR
1	E	211	ILE
1	E	218	ASN
1	F	19	THR
1	F	43	LYS
1	F	44	LEU
1	F	77	SER
1	F	82	TYR
1	F	120	LYS
1	F	123	LEU
1	F	170	LEU
1	G	7	LEU
1	G	177	SER
1	H	77[A]	SER
1	H	77[B]	SER
1	H	115	GLU
1	H	143	HIS
1	H	163	LEU
1	H	170	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	C	54	GLN
1	D	53	GLN
1	D	54	GLN
1	E	11	ASN
1	E	53	GLN
1	E	54	GLN
1	F	145	GLN
1	G	53	GLN
1	H	46	ASN
1	H	130	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	B	5102	-	18,19,19	0.73	0	21,24,24	0.66	0
2	GSH	D	5104	-	18,19,19	0.76	0	21,24,24	0.79	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	B	5102	-	-	1/24/24/24	-
2	GSH	D	5104	-	-	1/24/24/24	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

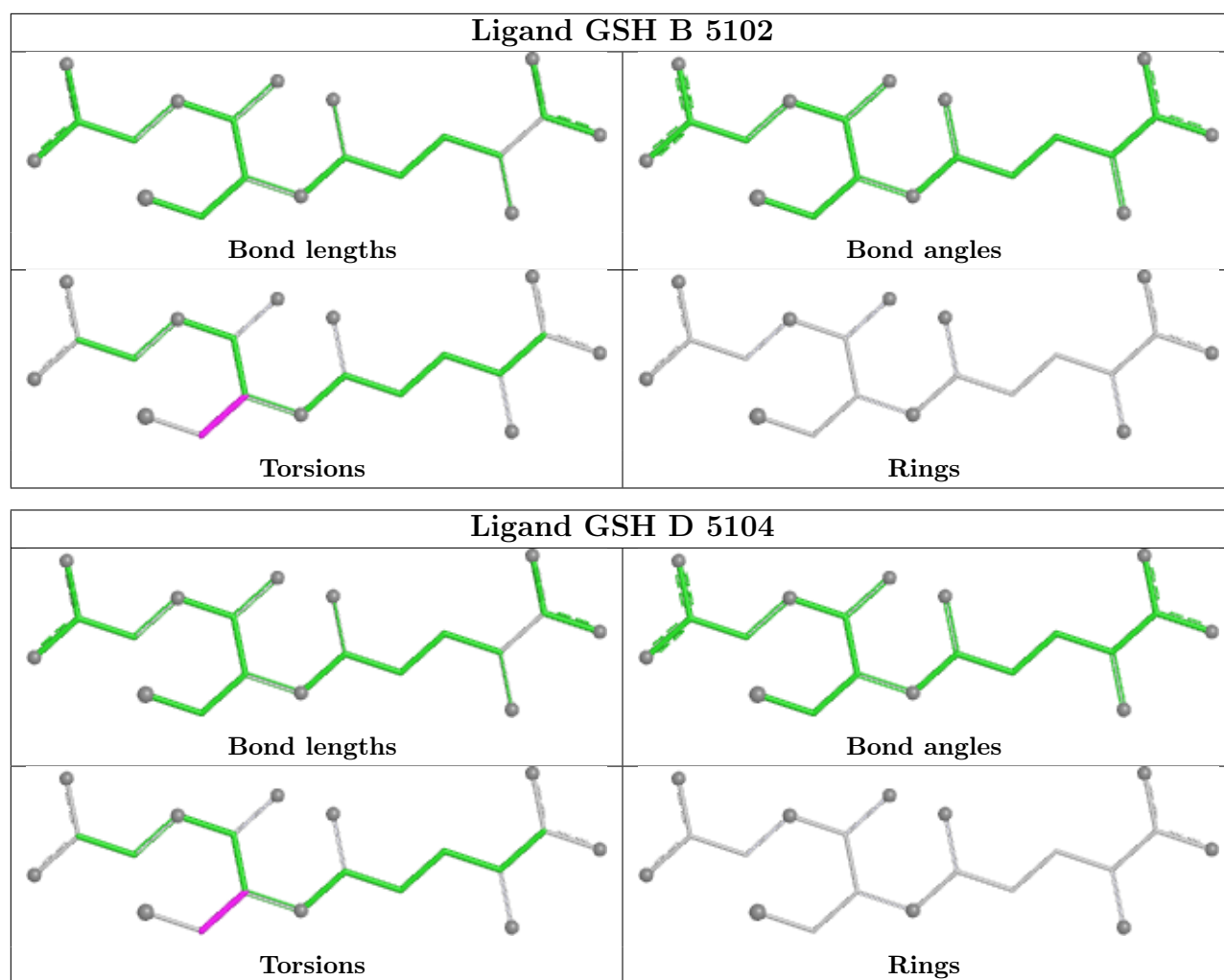
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	5102	GSH	N2-CA2-CB2-SG2
2	D	5104	GSH	C2-CA2-CB2-SG2

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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%)	0.27	6 (2%) 56 56	34, 47, 72, 86	0
1	B	221/222 (99%)	0.13	1 (0%) 87 86	37, 48, 70, 84	0
1	C	219/222 (98%)	0.35	5 (2%) 61 60	29, 51, 78, 84	3 (1%)
1	D	219/222 (98%)	0.23	3 (1%) 73 72	35, 50, 75, 81	0
1	E	219/222 (98%)	0.92	21 (9%) 13 12	40, 69, 91, 96	3 (1%)
1	F	216/222 (97%)	0.82	15 (6%) 23 21	47, 64, 89, 94	1 (0%)
1	G	219/222 (98%)	0.33	3 (1%) 73 72	41, 54, 71, 84	0
1	H	219/222 (98%)	0.53	6 (2%) 56 56	38, 59, 88, 102	1 (0%)
All	All	1751/1776 (98%)	0.45	60 (3%) 48 48	29, 54, 81, 102	8 (0%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	49	TYR	6.0
1	E	2	ALA	5.0
1	E	212	TYR	4.8
1	C	220	PHE	4.8
1	D	2	ALA	4.2
1	F	166	TYR	4.2
1	F	24	ALA	4.0
1	A	220	PHE	3.9
1	E	219	ILE	3.9
1	E	136	PHE	3.9
1	A	10	PHE	3.6
1	E	55	VAL	3.4
1	E	41	LEU	3.4
1	D	166	TYR	3.4
1	F	170	LEU	3.3
1	A	211	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	E	220	PHE	3.2
1	F	212	TYR	3.1
1	C	2	ALA	3.1
1	E	217	TYR	3.1
1	H	220	PHE	3.1
1	A	219	ILE	3.0
1	F	219	ILE	3.0
1	F	27	GLY	2.9
1	E	133	PHE	2.8
1	E	156	ALA	2.8
1	F	35	ILE	2.8
1	E	153	LEU	2.7
1	G	2	ALA	2.6
1	F	114	PRO	2.6
1	E	174	LEU	2.5
1	A	2	ALA	2.5
1	G	14	GLY	2.5
1	H	113	PRO	2.4
1	H	114	PRO	2.4
1	H	211	ILE	2.4
1	E	65	LEU	2.4
1	A	112	CYS	2.3
1	E	213	VAL	2.3
1	F	18	SER	2.3
1	H	111	PHE	2.3
1	E	5	PRO	2.3
1	D	217	TYR	2.3
1	B	2	ALA	2.3
1	F	139	VAL	2.3
1	F	28	VAL	2.3
1	E	179	PRO	2.2
1	F	33	LYS	2.2
1	E	191	LEU	2.2
1	C	123	LEU	2.1
1	E	111	PHE	2.1
1	C	212[A]	TYR	2.1
1	G	190	ASN	2.1
1	E	10	PHE	2.1
1	E	170	LEU	2.1
1	H	217	TYR	2.1
1	F	147	TYR	2.1
1	C	10[A]	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	215	THR	2.0
1	E	211	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

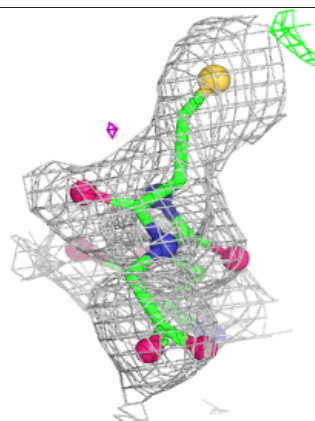
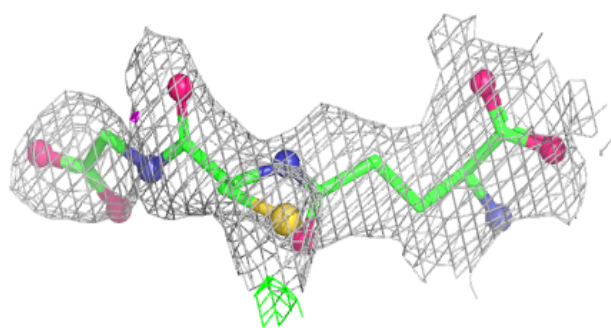
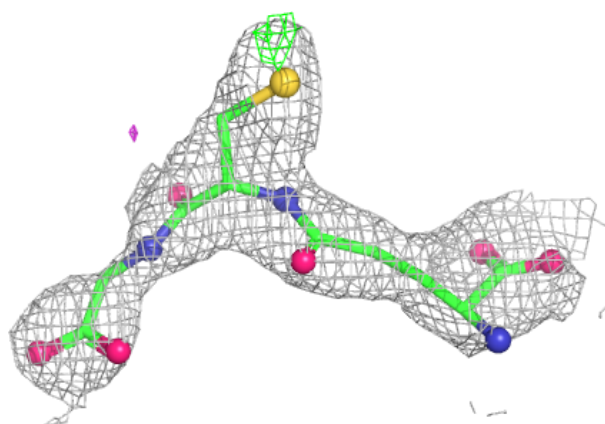
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GSH	B	5102	20/20	0.83	0.14	73,78,80,81	0
2	GSH	D	5104	20/20	0.83	0.14	68,73,74,76	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

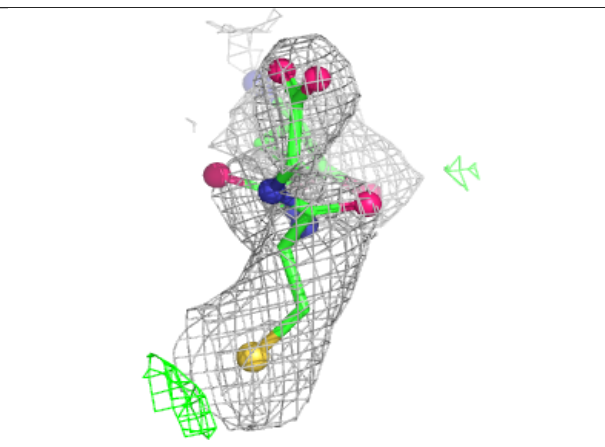
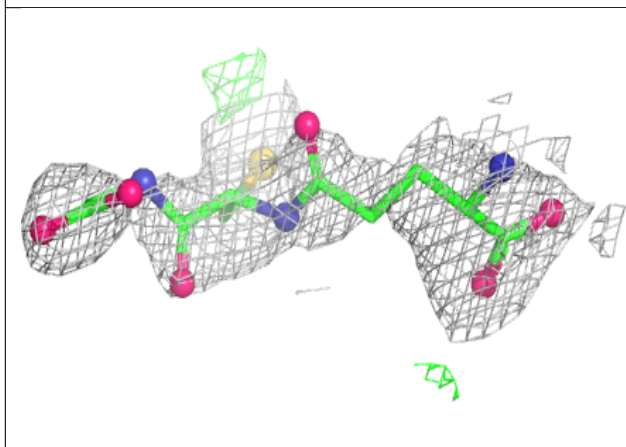
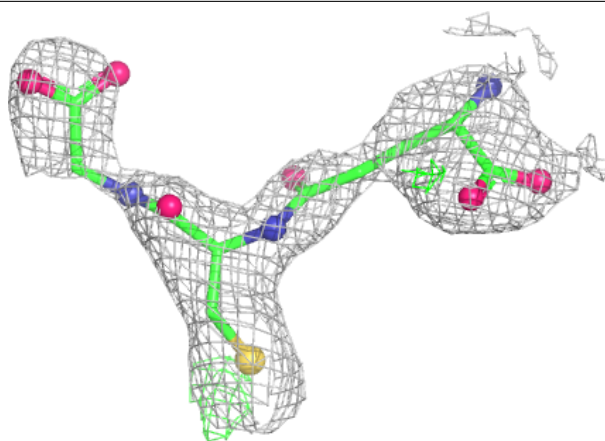
Electron density around GSH B 5102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GSH D 5104:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.