



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:34 AM UTC

PDB ID : 2IL3 / pdb_00002il3
Title : Structures of an Insect Epsilon-class Glutathione S-transferase from the Malaria Vector Anopheles Gambiae: Evidence for High DDT-detoxifying Activity
Authors : Wang, Y.; Hemingway, J.; Ranson, H.; Meehan, E.J.; Chen, L.
Deposited on : 2006-10-02
Resolution : 2.20 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

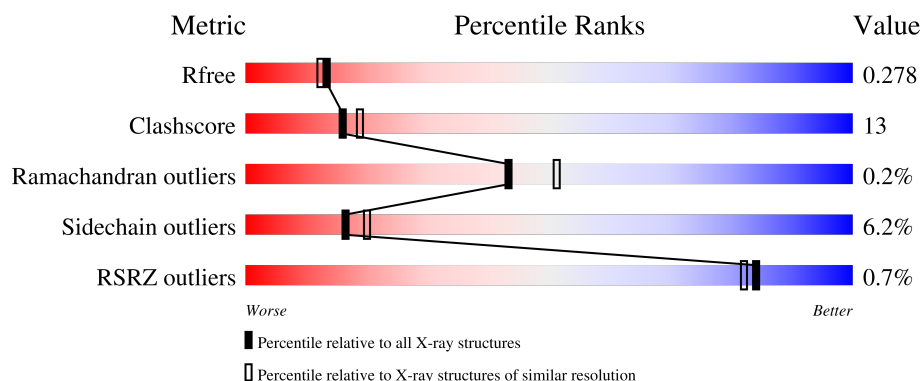
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	221	 63% 29% 7%
1	B	221	 60% 34% 6% 0%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3591 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 Epsilon-class Glutathione S-transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1742	1122	286	328	6			
1	B	218	Total	C	N	O	S	0	0	0
			1731	1115	283	326	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	220	LYS	-	insertion	UNP Q7PVS6
A	221	ALA	-	insertion	UNP Q7PVS6
B	220	LYS	-	insertion	UNP Q7PVS6
B	221	ALA	-	insertion	UNP Q7PVS6

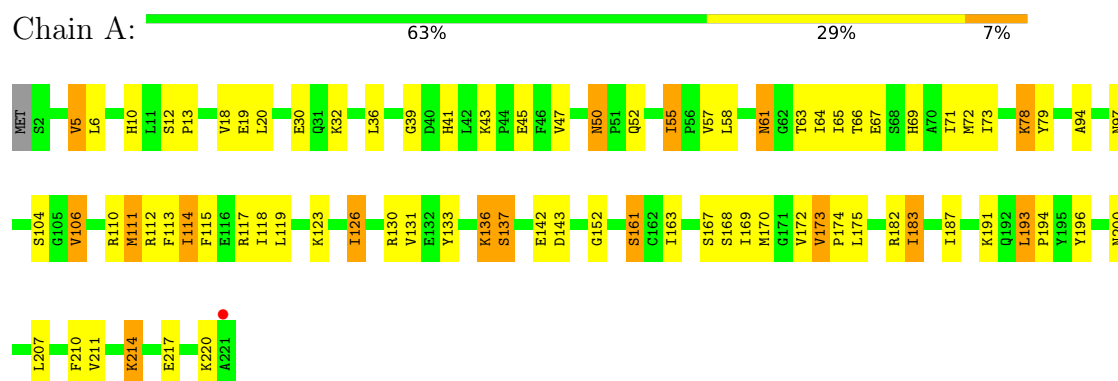
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	68	Total	O	0	0
			68	68		
2	B	50	Total	O	0	0
			50	50		

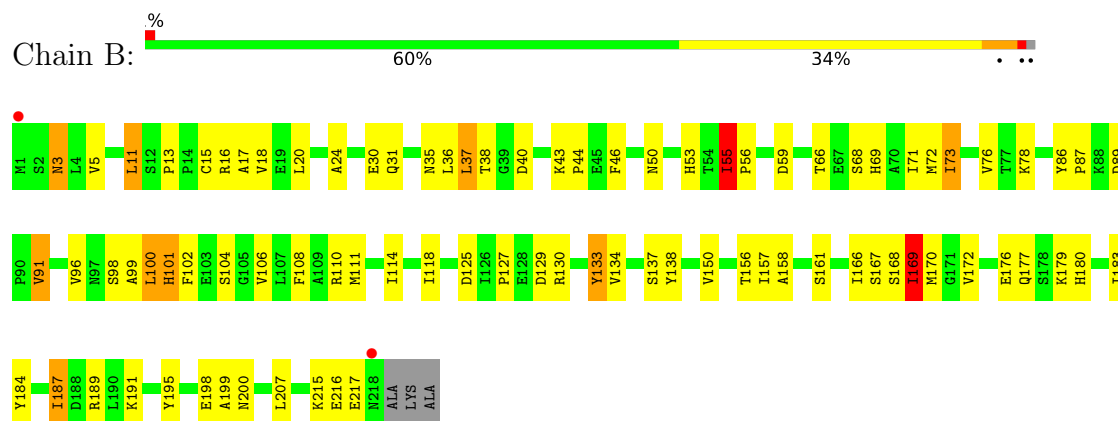
3 Residue-property plots

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: Epsilon-class Glutathione S-transferase



• Molecule 1: Epsilon-class Glutathione S-transferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	49.04Å 85.52Å 94.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	92.5 (50.00-2.20) 92.4 (50.00-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.195 , 0.288 0.189 , 0.278	Depositor DCC
R_{free} test set	998 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.268	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3591	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.01% 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

5.1 Standard geometry

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	1.61	11/1780 (0.6%)	1.53	28/2413 (1.2%)
1	B	1.51	12/1769 (0.7%)	1.51	15/2398 (0.6%)
All	All	1.56	23/3549 (0.6%)	1.52	43/4811 (0.9%)

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	126	ILE	CA-CB	10.52	1.67	1.54
1	A	66	THR	CA-CB	7.68	1.66	1.53
1	A	73	ILE	N-CA	7.12	1.54	1.46
1	B	86	TYR	N-CA	-6.58	1.40	1.46
1	B	55	ILE	CA-CB	6.46	1.62	1.55
1	A	94	ALA	CA-CB	6.25	1.63	1.53
1	B	150	VAL	C-O	6.21	1.32	1.24
1	B	138	TYR	N-CA	6.14	1.53	1.46
1	B	187	ILE	CA-CB	5.99	1.61	1.54
1	A	18	VAL	CA-CB	5.90	1.62	1.54
1	B	98	SER	C-O	-5.89	1.17	1.24
1	A	183	ILE	CA-CB	5.86	1.61	1.54
1	B	100	LEU	CG-CD2	5.82	1.71	1.52
1	B	156	THR	CA-CB	5.79	1.62	1.53
1	A	57	VAL	C-O	-5.69	1.18	1.24
1	A	55	ILE	CA-C	5.65	1.57	1.52
1	B	17	ALA	CA-CB	-5.36	1.44	1.53
1	B	189	ARG	N-CA	5.33	1.53	1.46
1	A	196	TYR	CA-C	5.21	1.59	1.52
1	A	136	LYS	CG-CD	5.15	1.68	1.52
1	B	169	ILE	CG1-CD1	-5.04	1.32	1.51
1	A	72	MET	SD-CE	-5.03	1.67	1.79
1	B	99	ALA	C-O	5.03	1.30	1.24

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	13	PRO	N-CA-C	7.42	119.75	110.70
1	B	101	HIS	N-CA-C	7.25	119.19	111.28
1	B	66	THR	N-CA-C	-7.23	99.51	110.14
1	A	193	LEU	CA-C-N	7.03	127.33	119.32
1	A	193	LEU	C-N-CA	7.03	127.33	119.32
1	A	196	TYR	N-CA-C	6.98	118.89	111.28
1	B	102	PHE	N-CA-C	-6.85	103.81	111.28
1	A	152	GLY	CA-C-N	6.70	126.41	119.64
1	A	152	GLY	C-N-CA	6.70	126.41	119.64
1	B	73	ILE	N-CA-CB	6.54	118.04	110.65
1	A	131	VAL	N-CA-C	6.47	117.16	110.36
1	B	11	LEU	N-CA-C	6.46	119.15	111.33
1	A	61	ASN	CB-CA-C	-6.38	102.79	112.11
1	A	113	PHE	N-CA-C	-6.37	104.77	112.54
1	A	43	LYS	CA-C-N	6.20	126.66	119.47
1	A	43	LYS	C-N-CA	6.20	126.66	119.47
1	A	97	ASN	N-CA-C	6.01	118.60	111.33
1	B	118	ILE	N-CA-C	5.99	116.46	110.23
1	A	173	VAL	CA-C-N	5.97	127.30	119.84
1	A	173	VAL	C-N-CA	5.97	127.30	119.84
1	A	66	THR	CB-CA-C	5.90	121.66	110.51
1	B	91	VAL	N-CA-C	5.82	116.00	110.53
1	B	167	SER	N-CA-C	5.80	119.61	112.54
1	A	71	ILE	N-CA-C	-5.73	104.93	110.72
1	B	172	VAL	N-CA-C	-5.73	107.09	111.62
1	A	112	ARG	N-CA-C	5.71	117.50	111.28
1	A	12	SER	CA-C-N	-5.69	114.52	120.38
1	A	12	SER	C-N-CA	-5.69	114.52	120.38
1	A	111	MET	N-CA-C	5.58	117.04	111.07
1	B	76	VAL	N-CA-C	5.46	115.67	110.42
1	A	217	GLU	N-CA-C	5.46	118.15	111.82
1	A	50	ASN	CA-C-N	5.38	125.09	119.82
1	A	50	ASN	C-N-CA	5.38	125.09	119.82
1	A	143	ASP	N-CA-C	5.36	119.08	112.54
1	B	101	HIS	CA-C-N	5.32	127.41	120.28
1	B	101	HIS	C-N-CA	5.32	127.41	120.28
1	A	161	SER	CB-CA-C	5.21	118.98	110.96
1	B	66	THR	CB-CA-C	5.16	119.54	110.36
1	A	47	VAL	N-CA-C	-5.11	105.40	112.50
1	A	172	VAL	O-C-N	-5.09	117.45	121.98
1	A	106	VAL	CB-CA-C	-5.09	107.39	111.71
1	B	89	ASP	CA-C-N	5.01	124.45	119.24
1	B	89	ASP	C-N-CA	5.01	124.45	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	1742	0	1757	39	0
1	B	1731	0	1746	55	0
2	A	68	0	0	0	0
2	B	50	0	0	2	0
All	All	3591	0	3503	92	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 13.

All (92) 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:114:ILE:HD11	1:B:134:VAL:CG2	1.82	1.09
1:B:114:ILE:CD1	1:B:134:VAL:HG21	1.91	0.99
1:B:114:ILE:CD1	1:B:134:VAL:CG2	2.44	0.96
1:B:114:ILE:HD11	1:B:134:VAL:HG23	1.54	0.88
1:B:108:PHE:HD1	2:B:253:HOH:O	1.59	0.86
1:B:169:ILE:O	1:B:169:ILE:HD13	1.78	0.83
1:A:118:ILE:HD11	1:A:126:ILE:CD1	2.07	0.82
1:B:40:ASP:HA	1:B:43:LYS:HE3	1.60	0.82
1:A:114:ILE:HD13	1:A:130:ARG:HB3	1.65	0.78
1:B:215:LYS:O	1:B:217:GLU:N	2.18	0.75
1:B:114:ILE:HD13	1:B:134:VAL:HG21	1.67	0.74
1:A:10:HIS:HD2	1:A:19:GLU:OE1	1.70	0.74
1:A:67:GLU:OE1	1:A:69:HIS:HD2	1.70	0.74
1:A:111:MET:HG3	1:A:169:ILE:HB	1.72	0.71
1:A:118:ILE:HD11	1:A:126:ILE:HD11	1.76	0.67
1:A:114:ILE:CD1	1:A:130:ARG:HB3	2.25	0.67
1:A:78:LYS:HE3	1:A:79:TYR:OH	1.98	0.63
1:B:72:MET:HE1	1:B:161:SER:OG	1.98	0.62
1:B:176:GLU:O	1:B:180:HIS:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:PHE:CE1	1:A:169:ILE:HD12	2.37	0.60
1:B:55:ILE:HB	1:B:56:PRO:HA	1.84	0.59
1:A:167:SER:HA	1:A:170:MET:HE2	1.85	0.58
1:B:73:ILE:CD1	1:B:157:ILE:HD11	2.33	0.58
1:A:119:LEU:HD21	1:A:211:VAL:HG22	1.85	0.58
1:A:167:SER:HA	1:A:170:MET:CE	2.35	0.57
1:A:210:PHE:O	1:A:214:LYS:HB2	2.05	0.56
1:B:73:ILE:HD13	1:B:157:ILE:CD1	2.36	0.56
1:B:18:VAL:HG23	1:B:68:SER:HB2	1.89	0.55
1:B:217:GLU:OE2	1:B:217:GLU:HA	2.07	0.54
1:B:127:PRO:HG2	1:B:130:ARG:HG2	1.90	0.54
1:B:110:ARG:O	1:B:114:ILE:HD12	2.08	0.54
1:A:142:GLU:CD	1:A:182:ARG:HB2	2.34	0.53
1:A:118:ILE:CD1	1:A:126:ILE:HD11	2.38	0.52
1:B:187:ILE:HG22	1:B:191:LYS:HE3	1.91	0.52
1:B:108:PHE:CE2	1:B:111:MET:HE1	2.45	0.52
1:B:114:ILE:HD11	1:B:134:VAL:HG21	1.61	0.52
1:A:118:ILE:HD11	1:A:126:ILE:HD13	1.92	0.52
1:B:73:ILE:CD1	1:B:157:ILE:CD1	2.87	0.51
1:B:15:CYS:SG	1:B:55:ILE:HG12	2.51	0.51
1:B:100:LEU:HD23	1:B:158:ALA:HA	1.92	0.51
1:B:3:ASN:HD22	1:B:3:ASN:N	2.10	0.50
1:B:13:PRO:HD3	1:B:207:LEU:HD22	1.93	0.50
1:A:30:GLU:OE1	1:A:32:LYS:NZ	2.45	0.49
1:A:114:ILE:HG23	1:A:126:ILE:HG23	1.94	0.48
1:A:36:LEU:HD21	1:A:55:ILE:HG12	1.95	0.48
1:A:63:THR:HG23	1:B:91:VAL:HG13	1.95	0.48
1:B:114:ILE:HG12	1:B:130:ARG:HB3	1.96	0.48
1:A:175:LEU:HD21	1:A:183:ILE:HG21	1.96	0.47
1:A:110:ARG:HD3	1:A:133:TYR:O	2.14	0.47
1:B:56:PRO:HG2	1:B:71:ILE:HD12	1.96	0.47
1:B:106:VAL:HG12	1:B:137:SER:HB2	1.97	0.47
1:A:106:VAL:HG12	1:A:137:SER:HB2	1.96	0.46
1:B:36:LEU:HD21	1:B:55:ILE:HD12	1.97	0.46
1:A:193:LEU:HA	1:A:194:PRO:HD3	1.84	0.46
1:B:35:ASN:OD1	1:B:38:THR:HG23	2.16	0.46
1:B:169:ILE:HD13	1:B:169:ILE:C	2.40	0.46
1:B:50:ASN:HD22	1:B:50:ASN:C	2.23	0.45
1:B:69:HIS:HA	1:B:72:MET:HE3	1.97	0.45
1:A:168:SER:HB3	1:A:207:LEU:HD23	1.98	0.45
1:A:58:LEU:HD23	1:A:65:ILE:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:HIS:CE1	1:A:161:SER:OG	2.69	0.45
1:B:215:LYS:C	1:B:217:GLU:N	2.74	0.45
1:A:20:LEU:HD11	1:A:200:ASN:HB2	2.00	0.44
1:A:187:ILE:HG22	1:A:191:LYS:HE3	1.98	0.44
1:B:110:ARG:HG2	1:B:133:TYR:CD1	2.53	0.44
1:A:50:ASN:ND2	1:A:52:GLN:H	2.16	0.43
1:B:5:VAL:HB	1:B:59:ASP:HB3	2.00	0.43
1:A:111:MET:HA	1:A:169:ILE:HD13	1.99	0.43
1:A:173:VAL:HA	1:A:174:PRO:HD2	1.62	0.43
1:B:87:PRO:HD2	1:B:96:VAL:HG21	2.01	0.42
1:A:104:SER:OG	1:B:101:HIS:ND1	2.48	0.42
1:B:125:ASP:OD2	1:B:125:ASP:N	2.51	0.42
1:B:168:SER:HB3	1:B:207:LEU:HD23	2.02	0.42
1:B:37:LEU:H	1:B:37:LEU:HG	1.63	0.42
1:A:5:VAL:HG22	1:A:30:GLU:HB3	2.01	0.42
1:B:72:MET:HE1	1:B:161:SER:HG	1.81	0.42
1:B:16:ARG:HG2	1:B:199:ALA:O	2.20	0.42
1:B:43:LYS:HA	1:B:44:PRO:HD3	1.90	0.42
1:B:20:LEU:HD21	1:B:200:ASN:HB2	2.02	0.41
1:B:50:ASN:C	1:B:50:ASN:ND2	2.78	0.41
1:B:108:PHE:CE2	1:B:111:MET:CE	3.03	0.41
1:A:117:ARG:HB2	1:A:123:LYS:HG3	2.02	0.41
1:B:180:HIS:HB3	1:B:183:ILE:HD12	2.02	0.41
1:B:46:PHE:CZ	1:B:55:ILE:HG22	2.56	0.41
1:B:78:LYS:NZ	2:B:266:HOH:O	2.53	0.41
1:A:39:GLY:HA2	1:A:41:HIS:CE1	2.56	0.41
1:B:166:ILE:O	1:B:170:MET:HG3	2.21	0.41
1:B:177:GLN:HA	1:B:184:TYR:CE2	2.56	0.40
1:B:24:ALA:HB2	1:B:195:TYR:OH	2.22	0.40
1:A:6:LEU:HD12	1:A:6:LEU:HA	1.90	0.40
1:A:78:LYS:HG2	1:A:79:TYR:CZ	2.56	0.40
1:A:142:GLU:OE2	1:A:182:ARG:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	218/221 (99%)	210 (96%)	8 (4%)	0	100	100
1	B	216/221 (98%)	207 (96%)	8 (4%)	1 (0%)	24	27
All	All	434/442 (98%)	417 (96%)	16 (4%)	1 (0%)	43	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	216	GLU

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	193/194 (100%)	182 (94%)	11 (6%)	18	23
1	B	193/194 (100%)	180 (93%)	13 (7%)	15	17
All	All	386/388 (100%)	362 (94%)	24 (6%)	16	20

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	45	GLU
1	A	61	ASN
1	A	64	ILE
1	A	78	LYS
1	A	114	ILE
1	A	136	LYS
1	A	137	SER
1	A	163	ILE
1	A	214	LYS
1	A	220	LYS

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Mol	Chain	Res	Type
1	B	3	ASN
1	B	11	LEU
1	B	30	GLU
1	B	31	GLN
1	B	37	LEU
1	B	53	HIS
1	B	55	ILE
1	B	104	SER
1	B	129	ASP
1	B	133	TYR
1	B	169	ILE
1	B	179	LYS
1	B	198	GLU

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	10	HIS
1	A	31	GLN
1	A	50	ASN
1	A	69	HIS
1	A	135	GLN
1	B	3	ASN
1	B	31	GLN
1	B	52	GLN
1	B	61	ASN
1	B	97	ASN
1	B	180	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	220/221 (99%)	-0.38	1 (0%) 87 85	16, 25, 43, 52	0
1	B	218/221 (98%)	-0.08	2 (0%) 81 79	15, 34, 53, 68	0
All	All	438/442 (99%)	-0.23	3 (0%) 84 82	15, 31, 51, 68	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	3.3
1	A	221	ALA	2.1
1	B	218	ASN	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.