



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:23 AM UTC

PDB ID : 5ZG4 / pdb_00005zg4
Title : Crystal Structure of Triosephosphate isomerase SAD deletion mutant from *Opisthorchis viverrini*
Authors : Son, J.; Kim, S.; Kim, S.E.; Lee, H.; Lee, M.R.; Hwang, K.Y.
Deposited on : 2018-03-07
Resolution : 1.75 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

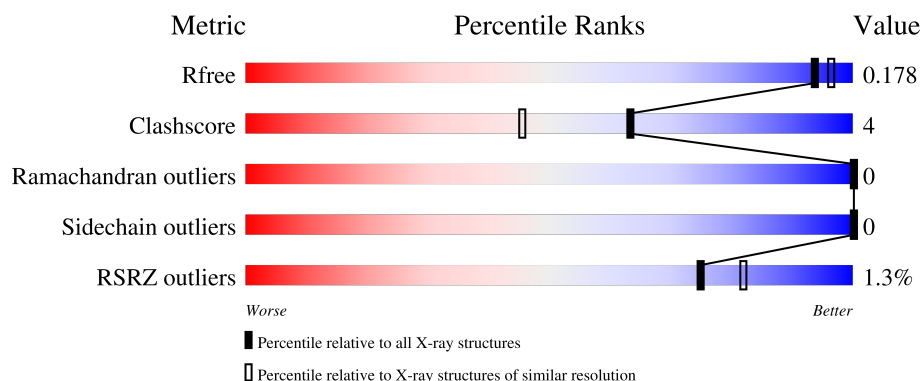
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	269	% 83% 8% 9%
1	B	269	% 83% 7% 10%
1	C	269	% 80% 9% 10%
1	D	269	% 81% 9% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8720 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 Triosephosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	0	0	0
			1900	1200	338	350	12			
1	B	243	Total	C	N	O	S	0	0	0
			1883	1189	334	349	11			
1	C	241	Total	C	N	O	S	0	0	0
			1877	1186	334	345	12			
1	D	242	Total	C	N	O	S	0	0	0
			1870	1180	332	347	11			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP A0A074Z863
A	-18	GLY	-	expression tag	UNP A0A074Z863
A	-17	SER	-	expression tag	UNP A0A074Z863
A	-16	SER	-	expression tag	UNP A0A074Z863
A	-15	HIS	-	expression tag	UNP A0A074Z863
A	-14	HIS	-	expression tag	UNP A0A074Z863
A	-13	HIS	-	expression tag	UNP A0A074Z863
A	-12	HIS	-	expression tag	UNP A0A074Z863
A	-11	HIS	-	expression tag	UNP A0A074Z863
A	-10	HIS	-	expression tag	UNP A0A074Z863
A	-9	SER	-	expression tag	UNP A0A074Z863
A	-8	SER	-	expression tag	UNP A0A074Z863
A	-7	GLY	-	expression tag	UNP A0A074Z863
A	-6	LEU	-	expression tag	UNP A0A074Z863
A	-5	VAL	-	expression tag	UNP A0A074Z863
A	-4	PRO	-	expression tag	UNP A0A074Z863
A	-3	ARG	-	expression tag	UNP A0A074Z863
A	-2	GLY	-	expression tag	UNP A0A074Z863
A	-1	SER	-	expression tag	UNP A0A074Z863
A	0	HIS	-	expression tag	UNP A0A074Z863
A	46	ALA	SER	conflict	UNP A0A074Z863

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Chain	Residue	Modelled	Actual	Comment	Reference
A	104	LEU	MET	conflict	UNP A0A074Z863
A	?	-	SER	deletion	UNP A0A074Z863
A	?	-	ALA	deletion	UNP A0A074Z863
A	?	-	ASP	deletion	UNP A0A074Z863
A	191	ARG	LYS	conflict	UNP A0A074Z863
A	203	LYS	ASN	conflict	UNP A0A074Z863
B	-19	MET	-	expression tag	UNP A0A074Z863
B	-18	GLY	-	expression tag	UNP A0A074Z863
B	-17	SER	-	expression tag	UNP A0A074Z863
B	-16	SER	-	expression tag	UNP A0A074Z863
B	-15	HIS	-	expression tag	UNP A0A074Z863
B	-14	HIS	-	expression tag	UNP A0A074Z863
B	-13	HIS	-	expression tag	UNP A0A074Z863
B	-12	HIS	-	expression tag	UNP A0A074Z863
B	-11	HIS	-	expression tag	UNP A0A074Z863
B	-10	HIS	-	expression tag	UNP A0A074Z863
B	-9	SER	-	expression tag	UNP A0A074Z863
B	-8	SER	-	expression tag	UNP A0A074Z863
B	-7	GLY	-	expression tag	UNP A0A074Z863
B	-6	LEU	-	expression tag	UNP A0A074Z863
B	-5	VAL	-	expression tag	UNP A0A074Z863
B	-4	PRO	-	expression tag	UNP A0A074Z863
B	-3	ARG	-	expression tag	UNP A0A074Z863
B	-2	GLY	-	expression tag	UNP A0A074Z863
B	-1	SER	-	expression tag	UNP A0A074Z863
B	0	HIS	-	expression tag	UNP A0A074Z863
B	46	ALA	SER	conflict	UNP A0A074Z863
B	104	LEU	MET	conflict	UNP A0A074Z863
B	?	-	SER	deletion	UNP A0A074Z863
B	?	-	ALA	deletion	UNP A0A074Z863
B	?	-	ASP	deletion	UNP A0A074Z863
B	191	ARG	LYS	conflict	UNP A0A074Z863
B	203	LYS	ASN	conflict	UNP A0A074Z863
C	-19	MET	-	expression tag	UNP A0A074Z863
C	-18	GLY	-	expression tag	UNP A0A074Z863
C	-17	SER	-	expression tag	UNP A0A074Z863
C	-16	SER	-	expression tag	UNP A0A074Z863
C	-15	HIS	-	expression tag	UNP A0A074Z863
C	-14	HIS	-	expression tag	UNP A0A074Z863
C	-13	HIS	-	expression tag	UNP A0A074Z863
C	-12	HIS	-	expression tag	UNP A0A074Z863
C	-11	HIS	-	expression tag	UNP A0A074Z863

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	HIS	-	expression tag	UNP A0A074Z863
C	-9	SER	-	expression tag	UNP A0A074Z863
C	-8	SER	-	expression tag	UNP A0A074Z863
C	-7	GLY	-	expression tag	UNP A0A074Z863
C	-6	LEU	-	expression tag	UNP A0A074Z863
C	-5	VAL	-	expression tag	UNP A0A074Z863
C	-4	PRO	-	expression tag	UNP A0A074Z863
C	-3	ARG	-	expression tag	UNP A0A074Z863
C	-2	GLY	-	expression tag	UNP A0A074Z863
C	-1	SER	-	expression tag	UNP A0A074Z863
C	0	HIS	-	expression tag	UNP A0A074Z863
C	46	ALA	SER	conflict	UNP A0A074Z863
C	104	LEU	MET	conflict	UNP A0A074Z863
C	?	-	SER	deletion	UNP A0A074Z863
C	?	-	ALA	deletion	UNP A0A074Z863
C	?	-	ASP	deletion	UNP A0A074Z863
C	191	ARG	LYS	conflict	UNP A0A074Z863
C	203	LYS	ASN	conflict	UNP A0A074Z863
D	-19	MET	-	expression tag	UNP A0A074Z863
D	-18	GLY	-	expression tag	UNP A0A074Z863
D	-17	SER	-	expression tag	UNP A0A074Z863
D	-16	SER	-	expression tag	UNP A0A074Z863
D	-15	HIS	-	expression tag	UNP A0A074Z863
D	-14	HIS	-	expression tag	UNP A0A074Z863
D	-13	HIS	-	expression tag	UNP A0A074Z863
D	-12	HIS	-	expression tag	UNP A0A074Z863
D	-11	HIS	-	expression tag	UNP A0A074Z863
D	-10	HIS	-	expression tag	UNP A0A074Z863
D	-9	SER	-	expression tag	UNP A0A074Z863
D	-8	SER	-	expression tag	UNP A0A074Z863
D	-7	GLY	-	expression tag	UNP A0A074Z863
D	-6	LEU	-	expression tag	UNP A0A074Z863
D	-5	VAL	-	expression tag	UNP A0A074Z863
D	-4	PRO	-	expression tag	UNP A0A074Z863
D	-3	ARG	-	expression tag	UNP A0A074Z863
D	-2	GLY	-	expression tag	UNP A0A074Z863
D	-1	SER	-	expression tag	UNP A0A074Z863
D	0	HIS	-	expression tag	UNP A0A074Z863
D	46	ALA	SER	conflict	UNP A0A074Z863
D	104	LEU	MET	conflict	UNP A0A074Z863
D	?	-	SER	deletion	UNP A0A074Z863
D	?	-	ALA	deletion	UNP A0A074Z863

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	ASP	deletion	UNP A0A074Z863
D	191	ARG	LYS	conflict	UNP A0A074Z863
D	203	LYS	ASN	conflict	UNP A0A074Z863

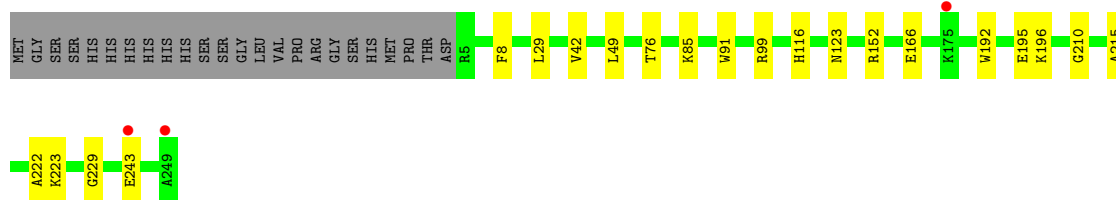
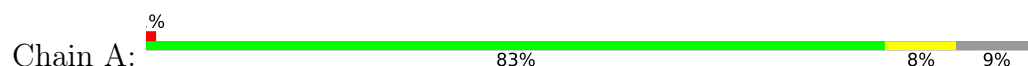
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	326	Total 326	O 326	0	0
2	B	292	Total 292	O 292	0	0
2	C	300	Total 300	O 300	0	0
2	D	272	Total 272	O 272	0	0

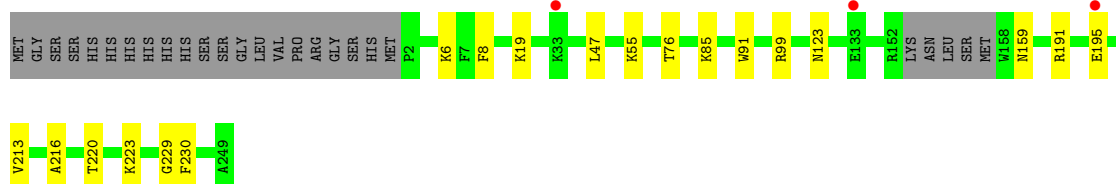
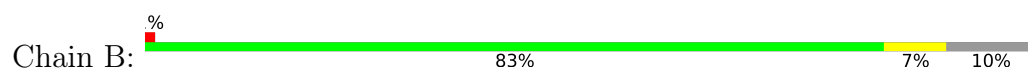
3 Residue-property plots [i](#)

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.

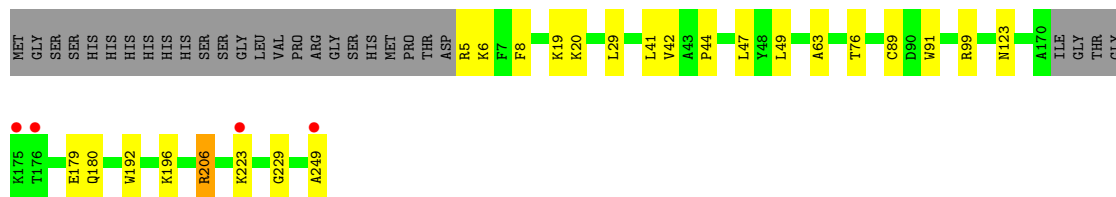
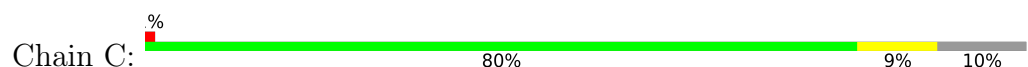
- Molecule 1: Triosephosphate isomerase



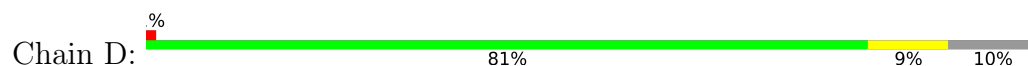
- Molecule 1: Triosephosphate isomerase



- Molecule 1: Triosephosphate isomerase



- Molecule 1: Triosephosphate isomerase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.74Å 91.92Å 75.78Å 90.00° 109.13° 90.00°	Depositor
Resolution (Å)	36.36 – 1.75 36.36 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.36-1.75) 99.8 (36.36-1.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.160 , 0.193 (Not available) , 0.178	Depositor DCC
R_{free} test set	4779 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.647	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8720	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.22 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.8696e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.34	0/1937	0.61	1/2619 (0.0%)
1	B	0.31	0/1920	0.62	1/2597 (0.0%)
1	C	0.36	0/1913	0.72	6/2585 (0.2%)
1	D	0.31	0/1905	0.59	1/2574 (0.0%)
All	All	0.33	0/7675	0.64	9/10375 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	223	LYS	CA-CB-CG	10.84	135.78	114.10
1	C	223	LYS	CB-CA-C	-9.69	90.06	110.31
1	C	223	LYS	N-CA-CB	7.98	123.63	110.39
1	C	223	LYS	CB-CG-CD	7.65	128.89	111.30
1	C	206	ARG	CA-CB-CG	-7.45	99.19	114.10
1	C	223	LYS	CG-CD-CE	-7.40	94.28	111.30
1	B	195	GLU	CA-CB-CG	-6.91	100.27	114.10
1	D	133	GLU	CA-CB-CG	5.14	124.39	114.10
1	A	85	LYS	CG-CD-CE	-5.05	99.69	111.30

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	1900	0	1916	17	0
1	B	1883	0	1890	17	0
1	C	1877	0	1891	18	0
1	D	1870	0	1887	19	0
2	A	326	0	0	4	1
2	B	292	0	0	5	1
2	C	300	0	0	2	0
2	D	272	0	0	5	0
All	All	8720	0	7584	61	1

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 (61) 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:A:223:LYS:NZ	2:A:303:HOH:O	2.20	0.75
1:A:166:GLU:HG2	1:A:210:GLY:HA3	1.74	0.69
1:D:90:ASP:OD2	2:D:301:HOH:O	2.11	0.69
1:D:203:LYS:NZ	2:D:302:HOH:O	2.26	0.67
1:B:55:LYS:NZ	2:B:303:HOH:O	2.30	0.64
1:A:215:ALA:HB1	1:A:243:GLU:OE1	1.98	0.64
1:D:191:ARG:NH1	2:D:304:HOH:O	2.32	0.62
1:B:223:LYS:NZ	2:B:302:HOH:O	2.30	0.61
1:B:216:ALA:HB3	2:B:312:HOH:O	2.00	0.60
1:B:220:THR:HA	1:B:223:LYS:HE2	1.85	0.59
1:C:6:LYS:NZ	2:C:304:HOH:O	2.31	0.59
1:C:5:ARG:N	2:C:306:HOH:O	2.36	0.58
1:A:195:GLU:OE2	2:A:301:HOH:O	2.18	0.56
1:A:49:LEU:HD12	1:B:47:LEU:CD2	2.36	0.56
1:C:49:LEU:HG	1:C:89:CYS:SG	2.48	0.54
1:A:222:ALA:O	2:A:302:HOH:O	2.18	0.53
1:D:220:THR:HG23	1:D:223:LYS:HE2	1.90	0.53
1:D:153:LYS:HE2	2:D:432:HOH:O	2.08	0.52
1:C:99:ARG:HD2	1:D:76:THR:O	2.09	0.51
1:B:85:LYS:NZ	2:B:308:HOH:O	2.44	0.51
1:C:91:TRP:CD2	1:C:123:ASN:HB2	2.47	0.50
1:D:213:VAL:HG21	1:D:230:PHE:CD1	2.47	0.50
1:A:49:LEU:HD12	1:B:47:LEU:HD21	1.94	0.50
1:A:166:GLU:HG2	1:A:210:GLY:CA	2.40	0.49
1:A:76:THR:O	1:B:99:ARG:HD2	2.11	0.49
1:D:137:ALA:HB3	1:D:139:LYS:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:PHE:O	1:C:229:GLY:HA3	2.14	0.47
1:A:99:ARG:HD2	1:B:76:THR:O	2.15	0.47
1:D:153:LYS:HD2	1:D:153:LYS:C	2.40	0.46
1:A:29:LEU:HD11	1:A:42:VAL:HG11	1.97	0.46
1:A:116:HIS:HD2	2:A:534:HOH:O	1.99	0.46
1:B:6:LYS:NZ	2:B:309:HOH:O	2.44	0.46
1:A:91:TRP:CD2	1:A:123:ASN:HB2	2.51	0.45
1:B:19:LYS:HA	1:B:19:LYS:HD2	1.82	0.45
1:B:191:ARG:HH21	1:C:249:ALA:HB2	1.82	0.45
1:D:150:ALA:O	1:D:153:LYS:HG3	2.16	0.45
1:C:41:LEU:HD11	1:C:63:ALA:HB2	1.98	0.45
1:C:6:LYS:O	1:C:206:ARG:HD2	2.17	0.44
1:C:20:LYS:N	1:C:20:LYS:HD3	2.32	0.44
1:B:213:VAL:HG21	1:B:230:PHE:CD1	2.53	0.43
1:C:47:LEU:HD21	1:D:49:LEU:HD12	2.00	0.43
1:C:47:LEU:CD2	1:D:49:LEU:HD12	2.48	0.43
1:D:91:TRP:CD2	1:D:123:ASN:HB2	2.53	0.43
1:D:99:ARG:NH1	1:D:103:LEU:HD13	2.34	0.43
1:C:29:LEU:HD11	1:C:42:VAL:HG11	2.00	0.43
1:A:152:ARG:O	1:A:152:ARG:HG2	2.19	0.43
1:A:8:PHE:O	1:A:229:GLY:HA3	2.19	0.42
1:C:76:THR:O	1:D:99:ARG:HD2	2.19	0.42
1:C:192:TRP:CE2	1:C:196:LYS:HG3	2.54	0.42
1:C:19:LYS:HE2	1:D:86:ASP:O	2.20	0.42
1:D:27:GLU:HG2	2:D:344:HOH:O	2.20	0.42
1:B:8:PHE:O	1:B:229:GLY:HA3	2.20	0.41
1:B:99:ARG:HD2	1:B:99:ARG:HH11	1.63	0.41
1:A:192:TRP:CE2	1:A:196:LYS:HG3	2.55	0.41
1:B:159:ASN:OD1	1:B:159:ASN:N	2.53	0.41
1:C:179:GLU:HG2	1:C:180:GLN:N	2.35	0.41
1:C:44:PRO:HG2	1:C:49:LEU:HD12	2.02	0.41
1:D:8:PHE:O	1:D:229:GLY:HA3	2.20	0.41
1:D:165:TYR:CE1	1:D:185:VAL:HG11	2.57	0.40
1:A:99:ARG:HD2	1:A:99:ARG:HH11	1.64	0.40
1:B:91:TRP:CD2	1:B:123:ASN:HB2	2.57	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:455:HOH:O	2:B:511:HOH:O[1_556]	2.10	0.10

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	243/269 (90%)	236 (97%)	7 (3%)	0	100	100
1	B	239/269 (89%)	233 (98%)	6 (2%)	0	100	100
1	C	237/269 (88%)	230 (97%)	7 (3%)	0	100	100
1	D	238/269 (88%)	231 (97%)	7 (3%)	0	100	100
All	All	957/1076 (89%)	930 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	202/223 (91%)	202 (100%)	0	100	100
1	B	200/223 (90%)	200 (100%)	0	100	100
1	C	200/223 (90%)	200 (100%)	0	100	100
1	D	199/223 (89%)	199 (100%)	0	100	100
All	All	801/892 (90%)	801 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	HIS
1	D	115	ASN
1	D	116	HIS

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](#)

There are no ligands in this entry.

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 [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	245/269 (91%)	-0.42	3 (1%) 76 83	9, 15, 27, 43	0
1	B	243/269 (90%)	-0.36	3 (1%) 76 83	9, 16, 28, 41	0
1	C	241/269 (89%)	-0.38	4 (1%) 69 76	9, 15, 30, 61	0
1	D	242/269 (89%)	-0.32	3 (1%) 76 83	9, 17, 31, 47	0
All	All	971/1076 (90%)	-0.37	13 (1%) 75 82	9, 15, 30, 61	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	249	ALA	5.6
1	A	249	ALA	3.5
1	C	175	LYS	3.3
1	C	176	THR	2.9
1	B	133	GLU	2.7
1	D	151	ILE	2.6
1	B	195	GLU	2.5
1	D	3	THR	2.5
1	A	243	GLU	2.3
1	D	153	LYS	2.3
1	A	175	LYS	2.1
1	B	33	LYS	2.1
1	C	223	LYS	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.