



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:59 PM UTC

PDB ID : 4ODI / pdb_00004odi
Title : 2.6 Angstrom Crystal Structure of Putative Phosphoglycerate Mutase 1 from *Toxoplasma gondii*
Authors : Minasov, G.; Ruan, J.; Ngo, H.; Shuvalova, L.; Dubrovskaya, I.; Flores, K.; Shanmugam, D.; Roos, D.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2014-01-10
Resolution : 2.60 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

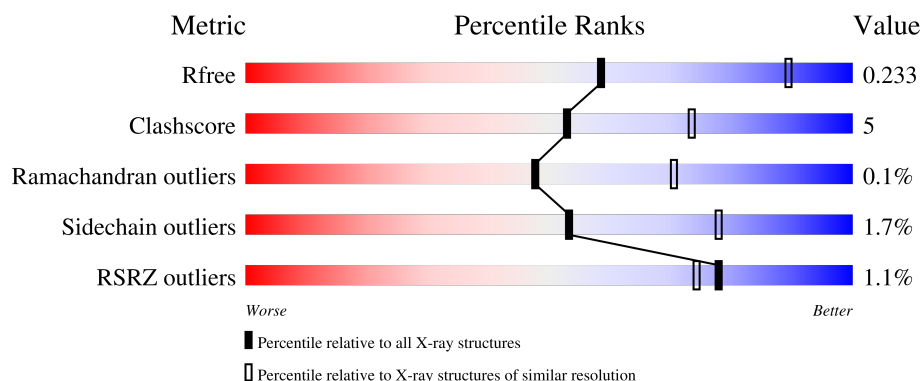
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	281	3% 75% 12% 12%
1	B	281	75% 11% • 13%
1	C	281	73% 13% 14%
1	D	281	3% 70% 11% • 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7909 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 Phosphoglycerate mutase PGMII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	2	0
			1982	1264	345	364	9			
1	B	245	Total	C	N	O	S	0	0	0
			1954	1249	337	360	8			
1	C	243	Total	C	N	O	S	0	0	0
			1942	1241	335	358	8			
1	D	232	Total	C	N	O	S	0	0	0
			1861	1190	321	343	7			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	266	GLY	-	expression tag	UNP S8GJT7
A	267	GLU	-	expression tag	UNP S8GJT7
A	268	ASN	-	expression tag	UNP S8GJT7
A	269	LEU	-	expression tag	UNP S8GJT7
A	270	TYR	-	expression tag	UNP S8GJT7
A	271	PHE	-	expression tag	UNP S8GJT7
A	272	GLN	-	expression tag	UNP S8GJT7
A	273	SER	-	expression tag	UNP S8GJT7
A	274	ALA	-	expression tag	UNP S8GJT7
A	275	GLY	-	expression tag	UNP S8GJT7
A	276	HIS	-	expression tag	UNP S8GJT7
A	277	HIS	-	expression tag	UNP S8GJT7
A	278	HIS	-	expression tag	UNP S8GJT7
A	279	HIS	-	expression tag	UNP S8GJT7
A	280	HIS	-	expression tag	UNP S8GJT7
A	281	HIS	-	expression tag	UNP S8GJT7
B	266	GLY	-	expression tag	UNP S8GJT7
B	267	GLU	-	expression tag	UNP S8GJT7
B	268	ASN	-	expression tag	UNP S8GJT7
B	269	LEU	-	expression tag	UNP S8GJT7
B	270	TYR	-	expression tag	UNP S8GJT7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	271	PHE	-	expression tag	UNP S8GJT7
B	272	GLN	-	expression tag	UNP S8GJT7
B	273	SER	-	expression tag	UNP S8GJT7
B	274	ALA	-	expression tag	UNP S8GJT7
B	275	GLY	-	expression tag	UNP S8GJT7
B	276	HIS	-	expression tag	UNP S8GJT7
B	277	HIS	-	expression tag	UNP S8GJT7
B	278	HIS	-	expression tag	UNP S8GJT7
B	279	HIS	-	expression tag	UNP S8GJT7
B	280	HIS	-	expression tag	UNP S8GJT7
B	281	HIS	-	expression tag	UNP S8GJT7
C	266	GLY	-	expression tag	UNP S8GJT7
C	267	GLU	-	expression tag	UNP S8GJT7
C	268	ASN	-	expression tag	UNP S8GJT7
C	269	LEU	-	expression tag	UNP S8GJT7
C	270	TYR	-	expression tag	UNP S8GJT7
C	271	PHE	-	expression tag	UNP S8GJT7
C	272	GLN	-	expression tag	UNP S8GJT7
C	273	SER	-	expression tag	UNP S8GJT7
C	274	ALA	-	expression tag	UNP S8GJT7
C	275	GLY	-	expression tag	UNP S8GJT7
C	276	HIS	-	expression tag	UNP S8GJT7
C	277	HIS	-	expression tag	UNP S8GJT7
C	278	HIS	-	expression tag	UNP S8GJT7
C	279	HIS	-	expression tag	UNP S8GJT7
C	280	HIS	-	expression tag	UNP S8GJT7
C	281	HIS	-	expression tag	UNP S8GJT7
D	266	GLY	-	expression tag	UNP S8GJT7
D	267	GLU	-	expression tag	UNP S8GJT7
D	268	ASN	-	expression tag	UNP S8GJT7
D	269	LEU	-	expression tag	UNP S8GJT7
D	270	TYR	-	expression tag	UNP S8GJT7
D	271	PHE	-	expression tag	UNP S8GJT7
D	272	GLN	-	expression tag	UNP S8GJT7
D	273	SER	-	expression tag	UNP S8GJT7
D	274	ALA	-	expression tag	UNP S8GJT7
D	275	GLY	-	expression tag	UNP S8GJT7
D	276	HIS	-	expression tag	UNP S8GJT7
D	277	HIS	-	expression tag	UNP S8GJT7
D	278	HIS	-	expression tag	UNP S8GJT7
D	279	HIS	-	expression tag	UNP S8GJT7
D	280	HIS	-	expression tag	UNP S8GJT7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	281	HIS	-	expression tag	UNP S8GJT7

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	B	1	Total Na 1 1	0	0
2	C	1	Total Na 1 1	0	0
2	D	1	Total Na 1 1	0	0

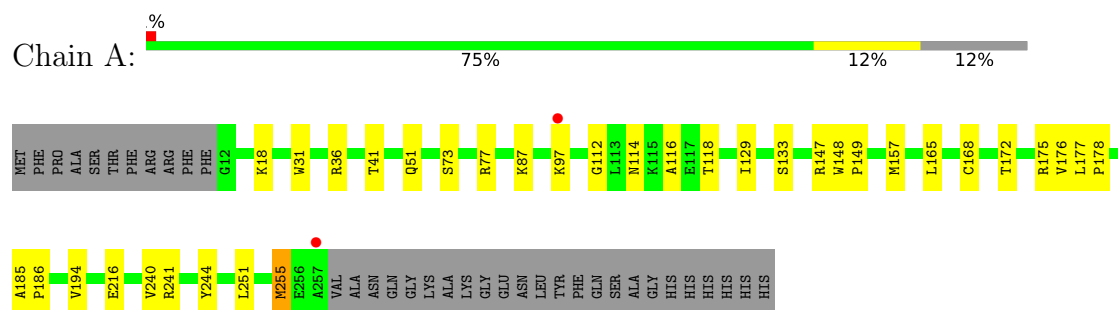
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	54	Total O 54 54	0	0
3	B	53	Total O 54 54	0	1
3	C	41	Total O 42 42	0	1
3	D	16	Total O 16 16	0	0

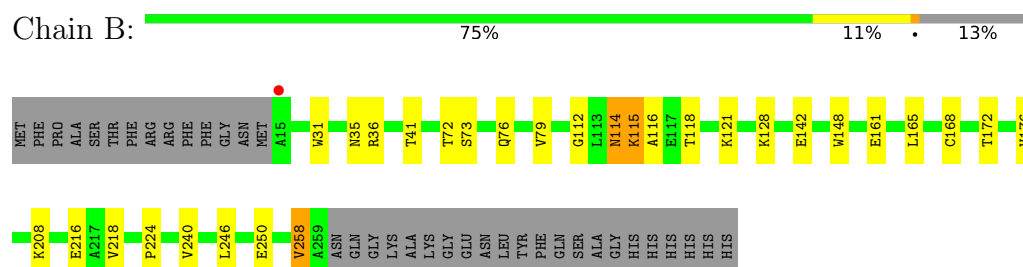
3 Residue-property plots [i](#)

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.

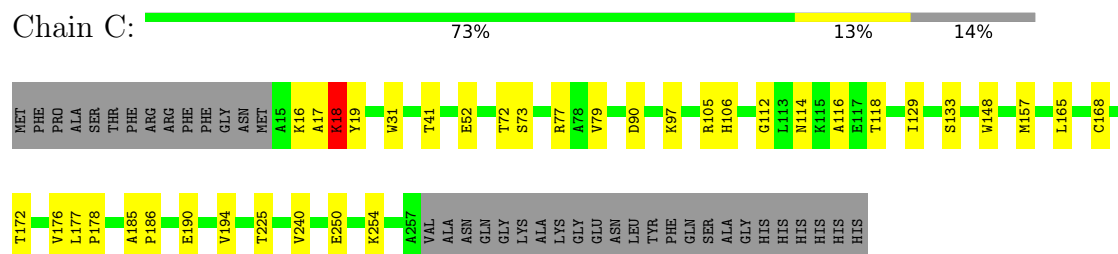
• Molecule 1: Phosphoglycerate mutase PGMII



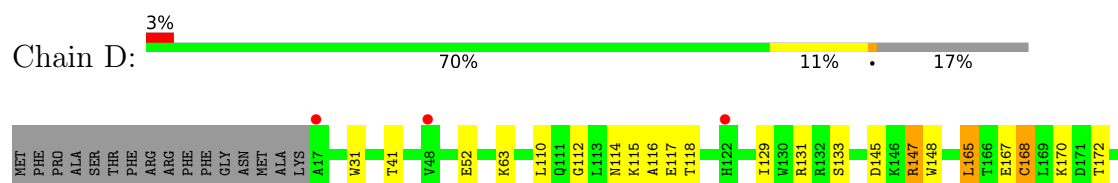
• Molecule 1: Phosphoglycerate mutase PGMII

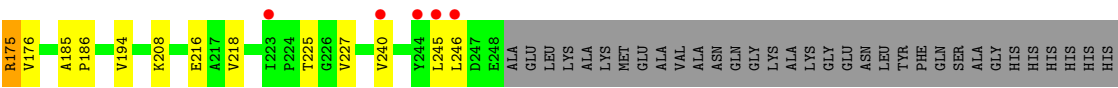


• Molecule 1: Phosphoglycerate mutase PGMII



• Molecule 1: Phosphoglycerate mutase PGMII





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	97.18Å 149.47Å 72.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.72 – 2.60 29.72 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.72-2.60) 99.8 (29.72-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.43 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.197 , 0.239 (Not available) , 0.233	Depositor DCC
R_{free} test set	1671 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 35.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7909	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: NA

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	0.84	0/2031	1.08	10/2756 (0.4%)
1	B	0.83	0/2003	1.05	3/2722 (0.1%)
1	C	0.72	0/1991	1.02	5/2705 (0.2%)
1	D	0.72	0/1910	1.07	9/2599 (0.3%)
All	All	0.78	0/7935	1.05	27/10782 (0.3%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	175	ARG	NE-CZ-NH2	-10.43	109.81	119.20
1	A	77	ARG	N-CA-CB	-9.59	95.68	110.06
1	D	175	ARG	NE-CZ-NH1	9.49	130.99	121.50
1	A	18	LYS	N-CA-C	-9.26	100.37	112.68
1	C	18	LYS	N-CA-C	-8.11	103.22	113.43
1	C	77	ARG	CB-CA-C	-7.42	95.66	110.42
1	A	175	ARG	NE-CZ-NH2	6.84	125.36	119.20
1	B	168	CYS	N-CA-C	-6.68	100.32	110.14
1	A	77	ARG	CG-CD-NE	6.57	126.45	112.00
1	A	240	VAL	N-CA-C	-6.28	104.93	111.58
1	A	168	CYS	N-CA-C	-6.21	101.01	110.14
1	D	194	VAL	N-CA-C	6.18	117.92	108.71
1	B	194	VAL	N-CA-C	6.10	117.80	108.71
1	C	240	VAL	N-CA-C	-6.07	105.14	111.58
1	B	240	VAL	N-CA-C	-6.05	105.17	111.58
1	C	168	CYS	N-CA-C	-6.04	101.26	110.14
1	D	147	ARG	NE-CZ-NH2	-6.04	113.77	119.20
1	D	168	CYS	N-CA-C	-6.03	101.27	110.14
1	C	194	VAL	N-CA-C	6.00	117.64	108.71
1	A	175	ARG	NE-CZ-NH1	-5.75	115.75	121.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	240	VAL	N-CA-C	-5.72	105.51	111.58
1	A	194	VAL	N-CA-C	5.67	117.17	108.71
1	A	73	SER	N-CA-C	-5.29	101.55	109.79
1	A	147	ARG	NE-CZ-NH2	5.27	123.94	119.20
1	D	147	ARG	NE-CZ-NH1	5.22	126.72	121.50
1	D	175	ARG	CD-NE-CZ	5.20	131.68	124.40
1	D	165	LEU	N-CA-C	-5.08	106.92	113.23

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	1982	0	1980	17	0
1	B	1954	0	1952	23	0
1	C	1942	0	1938	21	0
1	D	1861	0	1847	19	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	54	0	0	0	0
3	B	54	0	0	3	0
3	C	42	0	0	2	0
3	D	16	0	0	0	0
All	All	7909	0	7717	78	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 5.

All (78) 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:145:ASP:OD1	1:D:147:ARG:HD3	1.77	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:245:LEU:O	1:D:246:LEU:HD12	1.86	0.75
1:C:97:LYS:NZ	3:C:439:HOH:O	2.26	0.66
1:B:246:LEU:HG	1:B:250:GLU:HB2	1.77	0.65
1:C:157:MET:HA	1:C:157:MET:HE2	1.79	0.65
1:D:227:VAL:HG13	1:D:246:LEU:HD13	1.78	0.65
1:C:148:TRP:CD1	1:C:165:LEU:HD23	2.31	0.64
1:B:148:TRP:CD1	1:B:165:LEU:HD23	2.33	0.63
1:B:35:ASN:OD1	1:B:115:LYS:HG2	1.98	0.63
1:D:148:TRP:CD1	1:D:165:LEU:HD23	2.33	0.63
1:A:36[B]:ARG:HH21	1:A:36[B]:ARG:HB2	1.62	0.63
1:B:224:PRO:HA	1:B:258:VAL:HG21	1.78	0.63
1:B:258:VAL:HG23	3:B:444:HOH:O	1.98	0.61
1:B:258:VAL:HG12	1:B:258:VAL:O	1.99	0.61
1:A:87:LYS:HE3	1:B:76:GLN:OE1	2.01	0.61
1:A:36[B]:ARG:HB2	1:A:36[B]:ARG:NH2	2.15	0.61
1:A:148:TRP:CD1	1:A:165:LEU:HD23	2.36	0.60
1:D:63:LYS:HG2	1:D:245:LEU:HD11	1.86	0.58
1:D:168:CYS:SG	1:D:170:LYS:HB3	2.44	0.58
1:C:72:THR:HG22	1:C:73:SER:N	2.18	0.57
1:C:250:GLU:O	1:C:254:LYS:HG3	2.05	0.56
1:C:72:THR:HG22	1:C:73:SER:O	2.05	0.56
1:B:72:THR:HG22	1:B:73:SER:O	2.07	0.55
1:B:72:THR:HG22	1:B:73:SER:N	2.21	0.55
1:B:31:TRP:CD2	1:B:36:ARG:HD2	2.42	0.54
1:A:114:ASN:O	1:A:118:THR:HG23	2.08	0.54
1:B:258:VAL:CG2	3:B:444:HOH:O	2.56	0.53
1:A:31:TRP:CZ3	1:A:112:GLY:HA2	2.43	0.53
1:B:31:TRP:CZ3	1:B:112:GLY:HA2	2.44	0.52
1:A:185:ALA:HB3	1:A:186:PRO:HD3	1.92	0.51
1:C:185:ALA:HB3	1:C:186:PRO:HD3	1.93	0.51
1:A:244:TYR:CE2	1:A:255:MET:HE1	2.46	0.50
1:D:31:TRP:CZ3	1:D:112:GLY:HA2	2.47	0.50
1:C:114:ASN:O	1:C:118:THR:HG23	2.12	0.50
1:B:185:ALA:HB3	1:B:186:PRO:HD3	1.94	0.50
1:D:185:ALA:HB3	1:D:186:PRO:HD3	1.93	0.49
1:D:115:LYS:HD3	1:D:131:ARG:HH12	1.78	0.49
1:B:114:ASN:OD1	1:B:116:ALA:N	2.42	0.48
1:B:31:TRP:CH2	1:B:41:THR:HG21	2.49	0.48
1:C:31:TRP:CH2	1:C:41:THR:HG21	2.49	0.48
1:A:157:MET:HE2	1:C:190:GLU:HG3	1.96	0.48
1:C:16:LYS:HG2	1:C:17:ALA:N	2.30	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:172:THR:O	1:D:176:VAL:HG23	2.15	0.47
1:C:52:GLU:OE1	1:C:225:THR:HG23	2.14	0.47
1:D:117:GLU:N	1:D:117:GLU:OE1	2.48	0.46
1:C:172:THR:O	1:C:176:VAL:HG23	2.15	0.46
1:A:31:TRP:CH2	1:A:41:THR:HG21	2.51	0.46
1:D:52:GLU:OE1	1:D:225:THR:HG23	2.15	0.46
1:B:114:ASN:O	1:B:118:THR:HG23	2.15	0.46
1:C:31:TRP:CZ3	1:C:112:GLY:HA2	2.50	0.46
1:C:90:ASP:C	3:C:403:HOH:O	2.59	0.46
1:A:172:THR:O	1:A:176:VAL:HG23	2.16	0.45
1:D:31:TRP:CH2	1:D:41:THR:HG21	2.51	0.45
1:D:167:GLU:OE2	1:D:175:ARG:HD3	2.16	0.45
1:D:110:LEU:HD22	1:D:118:THR:HG21	1.97	0.45
1:B:172:THR:O	1:B:176:VAL:HG23	2.17	0.44
1:B:208:LYS:HB2	1:B:218:VAL:HG11	1.99	0.44
1:A:114:ASN:OD1	1:A:116:ALA:N	2.47	0.43
1:C:18:LYS:HE2	1:C:19:TYR:CE1	2.53	0.43
1:C:72:THR:HG21	1:C:79:VAL:HA	2.00	0.43
1:C:114:ASN:OD1	1:C:116:ALA:N	2.50	0.43
1:A:216:GLU:N	1:A:216:GLU:OE1	2.52	0.43
1:A:251:LEU:C	1:A:251:LEU:HD23	2.43	0.43
1:D:114:ASN:OD1	1:D:116:ALA:N	2.50	0.43
1:D:129:ILE:O	1:D:133:SER:CB	2.67	0.43
1:C:105:ARG:HG2	1:C:106:HIS:N	2.32	0.43
1:B:72:THR:HG21	1:B:79:VAL:HA	2.02	0.42
1:C:177:LEU:HB2	1:C:178:PRO:HD3	2.02	0.42
1:B:216:GLU:OE1	1:B:216:GLU:N	2.53	0.42
1:D:216:GLU:OE1	1:D:216:GLU:N	2.51	0.41
1:A:177:LEU:HB2	1:A:178:PRO:HD3	2.01	0.41
1:D:208:LYS:HB2	1:D:218:VAL:HG11	2.02	0.41
1:A:148:TRP:CD1	1:A:149:PRO:HD2	2.55	0.41
1:C:129:ILE:O	1:C:133:SER:CB	2.69	0.41
1:A:129:ILE:O	1:A:133:SER:CB	2.69	0.41
1:B:114:ASN:OD1	1:B:114:ASN:C	2.64	0.41
1:B:114:ASN:OD1	1:B:115:LYS:N	2.54	0.41
1:B:161:GLU:HG2	3:B:439:HOH:O	2.20	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	246/281 (88%)	242 (98%)	4 (2%)	0	100	100
1	B	243/281 (86%)	238 (98%)	4 (2%)	1 (0%)	30	51
1	C	241/281 (86%)	237 (98%)	4 (2%)	0	100	100
1	D	230/281 (82%)	225 (98%)	5 (2%)	0	100	100
All	All	960/1124 (85%)	942 (98%)	17 (2%)	1 (0%)	48	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	258	VAL

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	207/239 (87%)	202 (98%)	5 (2%)	43	70
1	B	179/239 (75%)	174 (97%)	5 (3%)	38	66
1	C	173/239 (72%)	172 (99%)	1 (1%)	78	91
1	D	36/239 (15%)	36 (100%)	0	100	100
All	All	595/956 (62%)	584 (98%)	11 (2%)	53	76

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	GLN
1	A	97[A]	LYS
1	A	97[B]	LYS
1	A	241	ARG
1	A	255	MET
1	B	114	ASN
1	B	115	LYS
1	B	121	LYS
1	B	128	LYS
1	B	142	GLU
1	C	18	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	GLN
1	A	76	GLN
1	A	122	HIS
1	A	126	GLN

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 ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	246/281 (87%)	-0.41	2 (0%) 82 80	20, 38, 86, 110	2 (0%)
1	B	245/281 (87%)	-0.38	1 (0%) 88 86	23, 39, 80, 96	0
1	C	243/281 (86%)	-0.12	0 100 100	28, 61, 99, 127	0
1	D	232/281 (82%)	0.13	8 (3%) 48 42	30, 74, 126, 150	0
All	All	966/1124 (85%)	-0.20	11 (1%) 78 74	20, 49, 106, 150	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	17	ALA	4.4
1	B	15	ALA	3.4
1	A	97[A]	LYS	3.4
1	D	246	LEU	2.9
1	D	245	LEU	2.8
1	D	122	HIS	2.3
1	D	240	VAL	2.3
1	D	244	TYR	2.2
1	A	257	ALA	2.2
1	D	48	VAL	2.1
1	D	223	ILE	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](#)

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	NA	D	301	1/1	0.78	0.10	64,64,64,64	0
2	NA	C	301	1/1	0.93	0.04	52,52,52,52	0
2	NA	B	301	1/1	0.96	0.05	52,52,52,52	0
2	NA	A	301	1/1	0.98	0.03	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.