



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:00 AM GMT

PDB ID : 3KHP
Title : Crystal structure of a possible dehydrogenase from Mycobacterium tuberculosis at 2.3Å resolution
Authors : Seattle Structural Genomics Center for Infections Disease (SSGCID)
Deposited on : 2009-10-30
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

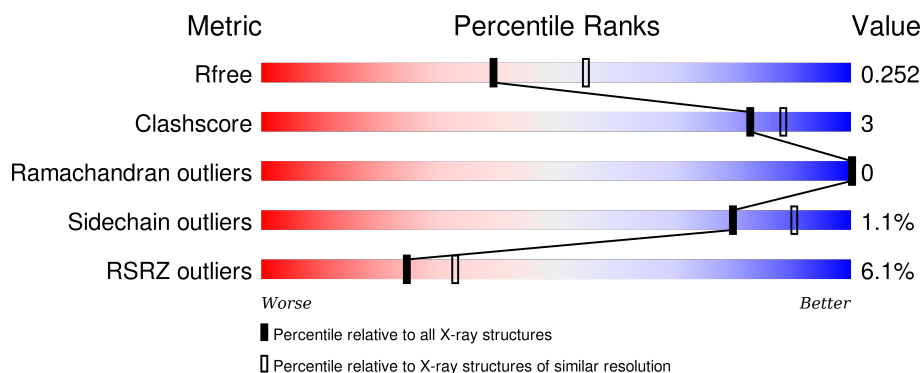
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	311	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 86%, yellow 86%, yellow 92%, grey 92%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> % 86% 6% 7% </div> </div>
1	B	311	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 87%, yellow 87%, yellow 92%, grey 92%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> % 87% 5% 8% </div> </div>
1	C	311	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 12%, green 12%, green 77%, yellow 77%, yellow 83%, grey 83%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 12% 77% 6% • 16% </div> </div>
1	D	311	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 8%, green 8%, green 77%, yellow 77%, yellow 84%, grey 84%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 8% 77% 7% • 14% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8708 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 MaoC family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	3	0
			2128	1347	376	398	7			
1	B	286	Total	C	N	O	S	0	2	0
			2117	1335	379	396	7			
1	C	261	Total	C	N	O	S	0	1	0
			1913	1214	335	358	6			
1	D	267	Total	C	N	O	S	0	3	0
			1977	1254	344	373	6			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP Q11198
A	-19	ALA	-	EXPRESSION TAG	UNP Q11198
A	-18	HIS	-	EXPRESSION TAG	UNP Q11198
A	-17	HIS	-	EXPRESSION TAG	UNP Q11198
A	-16	HIS	-	EXPRESSION TAG	UNP Q11198
A	-15	HIS	-	EXPRESSION TAG	UNP Q11198
A	-14	HIS	-	EXPRESSION TAG	UNP Q11198
A	-13	HIS	-	EXPRESSION TAG	UNP Q11198
A	-12	MET	-	EXPRESSION TAG	UNP Q11198
A	-11	GLY	-	EXPRESSION TAG	UNP Q11198
A	-10	THR	-	EXPRESSION TAG	UNP Q11198
A	-9	LEU	-	EXPRESSION TAG	UNP Q11198
A	-8	GLU	-	EXPRESSION TAG	UNP Q11198
A	-7	ALA	-	EXPRESSION TAG	UNP Q11198
A	-6	GLN	-	EXPRESSION TAG	UNP Q11198
A	-5	THR	-	EXPRESSION TAG	UNP Q11198
A	-4	GLN	-	EXPRESSION TAG	UNP Q11198
A	-3	GLY	-	EXPRESSION TAG	UNP Q11198
A	-2	PRO	-	EXPRESSION TAG	UNP Q11198
A	-1	GLY	-	EXPRESSION TAG	UNP Q11198
A	0	SER	-	EXPRESSION TAG	UNP Q11198

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	EXPRESSION TAG	UNP Q11198
B	-19	ALA	-	EXPRESSION TAG	UNP Q11198
B	-18	HIS	-	EXPRESSION TAG	UNP Q11198
B	-17	HIS	-	EXPRESSION TAG	UNP Q11198
B	-16	HIS	-	EXPRESSION TAG	UNP Q11198
B	-15	HIS	-	EXPRESSION TAG	UNP Q11198
B	-14	HIS	-	EXPRESSION TAG	UNP Q11198
B	-13	HIS	-	EXPRESSION TAG	UNP Q11198
B	-12	MET	-	EXPRESSION TAG	UNP Q11198
B	-11	GLY	-	EXPRESSION TAG	UNP Q11198
B	-10	THR	-	EXPRESSION TAG	UNP Q11198
B	-9	LEU	-	EXPRESSION TAG	UNP Q11198
B	-8	GLU	-	EXPRESSION TAG	UNP Q11198
B	-7	ALA	-	EXPRESSION TAG	UNP Q11198
B	-6	GLN	-	EXPRESSION TAG	UNP Q11198
B	-5	THR	-	EXPRESSION TAG	UNP Q11198
B	-4	GLN	-	EXPRESSION TAG	UNP Q11198
B	-3	GLY	-	EXPRESSION TAG	UNP Q11198
B	-2	PRO	-	EXPRESSION TAG	UNP Q11198
B	-1	GLY	-	EXPRESSION TAG	UNP Q11198
B	0	SER	-	EXPRESSION TAG	UNP Q11198
C	-20	MET	-	EXPRESSION TAG	UNP Q11198
C	-19	ALA	-	EXPRESSION TAG	UNP Q11198
C	-18	HIS	-	EXPRESSION TAG	UNP Q11198
C	-17	HIS	-	EXPRESSION TAG	UNP Q11198
C	-16	HIS	-	EXPRESSION TAG	UNP Q11198
C	-15	HIS	-	EXPRESSION TAG	UNP Q11198
C	-14	HIS	-	EXPRESSION TAG	UNP Q11198
C	-13	HIS	-	EXPRESSION TAG	UNP Q11198
C	-12	MET	-	EXPRESSION TAG	UNP Q11198
C	-11	GLY	-	EXPRESSION TAG	UNP Q11198
C	-10	THR	-	EXPRESSION TAG	UNP Q11198
C	-9	LEU	-	EXPRESSION TAG	UNP Q11198
C	-8	GLU	-	EXPRESSION TAG	UNP Q11198
C	-7	ALA	-	EXPRESSION TAG	UNP Q11198
C	-6	GLN	-	EXPRESSION TAG	UNP Q11198
C	-5	THR	-	EXPRESSION TAG	UNP Q11198
C	-4	GLN	-	EXPRESSION TAG	UNP Q11198
C	-3	GLY	-	EXPRESSION TAG	UNP Q11198
C	-2	PRO	-	EXPRESSION TAG	UNP Q11198
C	-1	GLY	-	EXPRESSION TAG	UNP Q11198
C	0	SER	-	EXPRESSION TAG	UNP Q11198

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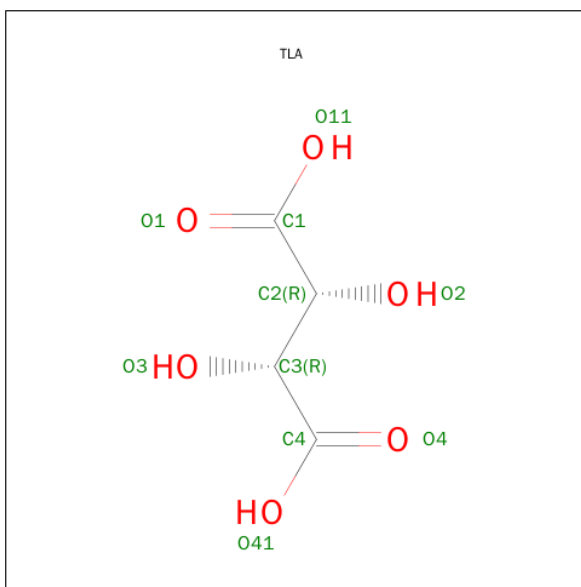
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	MET	-	EXPRESSION TAG	UNP Q11198
D	-19	ALA	-	EXPRESSION TAG	UNP Q11198
D	-18	HIS	-	EXPRESSION TAG	UNP Q11198
D	-17	HIS	-	EXPRESSION TAG	UNP Q11198
D	-16	HIS	-	EXPRESSION TAG	UNP Q11198
D	-15	HIS	-	EXPRESSION TAG	UNP Q11198
D	-14	HIS	-	EXPRESSION TAG	UNP Q11198
D	-13	HIS	-	EXPRESSION TAG	UNP Q11198
D	-12	MET	-	EXPRESSION TAG	UNP Q11198
D	-11	GLY	-	EXPRESSION TAG	UNP Q11198
D	-10	THR	-	EXPRESSION TAG	UNP Q11198
D	-9	LEU	-	EXPRESSION TAG	UNP Q11198
D	-8	GLU	-	EXPRESSION TAG	UNP Q11198
D	-7	ALA	-	EXPRESSION TAG	UNP Q11198
D	-6	GLN	-	EXPRESSION TAG	UNP Q11198
D	-5	THR	-	EXPRESSION TAG	UNP Q11198
D	-4	GLN	-	EXPRESSION TAG	UNP Q11198
D	-3	GLY	-	EXPRESSION TAG	UNP Q11198
D	-2	PRO	-	EXPRESSION TAG	UNP Q11198
D	-1	GLY	-	EXPRESSION TAG	UNP Q11198
D	0	SER	-	EXPRESSION TAG	UNP Q11198

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			10	4	6		

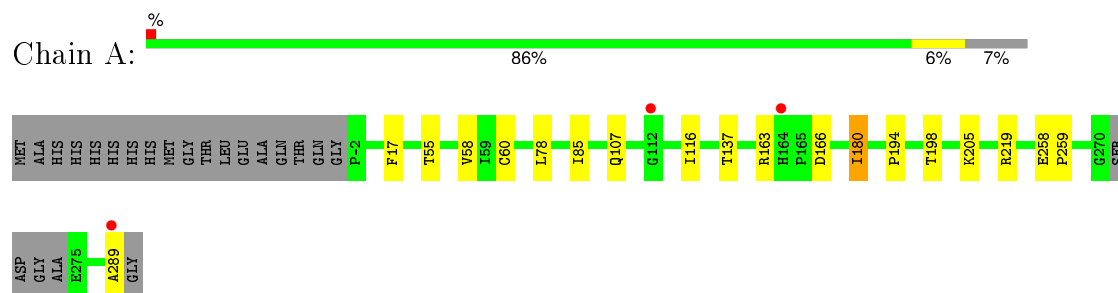
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	159	Total	O	0	0
			159	159		
4	B	168	Total	O	0	0
			168	168		
4	C	109	Total	O	0	0
			109	109		
4	D	120	Total	O	0	0
			120	120		

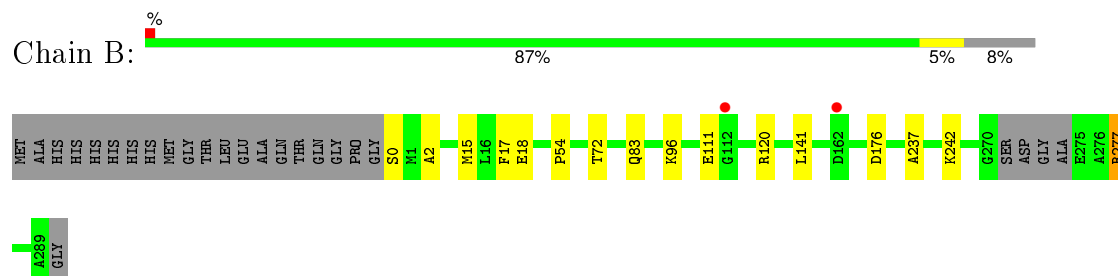
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

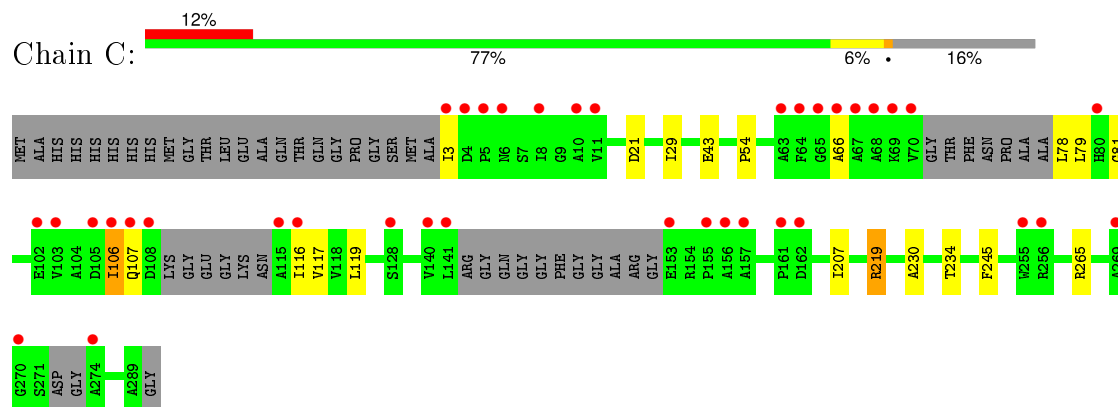
- Molecule 1: MaoC family protein



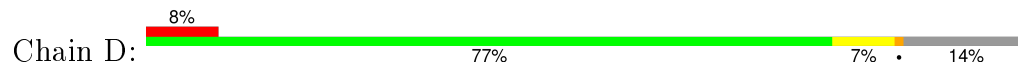
- Molecule 1: MaoC family protein

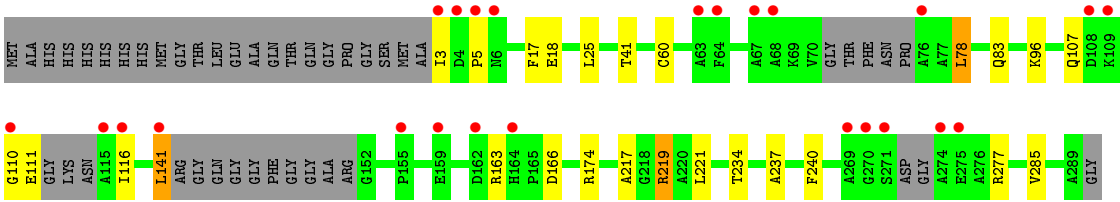


- Molecule 1: MaoC family protein



- Molecule 1: MaoC family protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.29Å 135.17Å 162.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 35.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.9 (40.00-2.30) 97.9 (35.98-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.10 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0104	Depositor
R, R_{free}	0.206 , 0.263 0.200 , 0.252	Depositor DCC
R_{free} test set	3167 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 36.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 62400 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8708	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TLA, CL

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	0.76	0/2185	0.78	1/2979 (0.0%)
1	B	0.78	0/2169	0.80	3/2957 (0.1%)
1	C	0.76	0/1954	0.80	3/2670 (0.1%)
1	D	0.73	0/2027	0.79	3/2768 (0.1%)
All	All	0.76	0/8335	0.79	10/11374 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	219	ARG	NE-CZ-NH1	-8.43	116.08	120.30
1	D	219	ARG	NE-CZ-NH2	7.69	124.15	120.30
1	D	277	ARG	NE-CZ-NH1	-6.33	117.13	120.30
1	C	21	ASP	CB-CG-OD1	6.26	123.93	118.30
1	A	219	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	C	219	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	B	277	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	B	120	ARG	NE-CZ-NH1	-5.15	117.72	120.30
1	B	277	ARG	NE-CZ-NH2	5.14	122.87	120.30
1	C	219	ARG	NE-CZ-NH1	5.05	122.83	120.30

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	2128	0	2108	12	0
1	B	2117	0	2100	11	0
1	C	1913	0	1894	14	0
1	D	1977	0	1946	16	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
3	B	10	0	4	0	0
4	A	159	0	0	1	0
4	B	168	0	0	1	0
4	C	109	0	0	2	0
4	D	120	0	0	1	0
All	All	8708	0	8052	50	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 3.

All (50) 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:180:ILE:HD12	1:C:29:ILE:HG21	1.53	0.90
1:D:219:ARG:HD2	4:D:315:HOH:O	1.72	0.87
1:C:219:ARG:HD2	4:C:304:HOH:O	1.84	0.76
1:D:78:LEU:HD13	1:D:240:PHE:CE2	2.24	0.73
1:C:106:ILE:HD13	1:C:117:VAL:HG22	1.76	0.68
1:B:54:PRO:HD2	4:B:393:HOH:O	1.94	0.67
1:C:66:ALA:HB3	1:C:119:LEU:HD22	1.81	0.62
1:A:258:GLU:O	1:A:259:PRO:C	2.39	0.61
1:B:111:GLU:OE1	1:B:111:GLU:HA	2.03	0.59
1:A:194:PRO:O	1:A:198:THR:HG22	2.04	0.58
1:D:163:ARG:HH12	1:D:166:ASP:CG	2.08	0.56
1:B:242:LYS:HD3	1:B:277:ARG:CG	2.37	0.54
1:B:141:LEU:N	1:B:141:LEU:HD12	2.23	0.54
1:D:163:ARG:NH1	1:D:166:ASP:OD2	2.39	0.53
1:A:180:ILE:HD13	1:A:180:ILE:N	2.23	0.53
1:C:78:LEU:O	1:C:81:GLY:N	2.39	0.52
1:D:110:GLY:HA2	1:D:111:GLU:C	2.30	0.52
1:B:15:MET:HG2	1:B:17:PHE:CE1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:141:LEU:H	1:D:141:LEU:HD12	1.77	0.50
1:C:54:PRO:HD3	1:C:230:ALA:HB1	1.94	0.49
1:A:17[B]:PHE:CD2	1:A:60:CYS:HA	2.47	0.49
1:D:107:GLN:HB2	1:D:116:ILE:HB	1.95	0.48
1:A:163:ARG:NH2	1:A:166:ASP:OD1	2.46	0.46
1:B:18:GLU:HG2	1:B:96:LYS:HG2	1.97	0.46
1:D:3:ILE:O	1:D:5:PRO:HD3	2.15	0.46
1:D:141:LEU:N	1:D:141:LEU:HD12	2.30	0.46
1:A:107:GLN:HB2	1:A:116:ILE:HB	1.98	0.46
1:B:83:GLN:O	1:B:237:ALA:HA	2.16	0.46
1:B:242:LYS:HD3	1:B:277:ARG:HG3	1.97	0.46
1:D:17[A]:PHE:CD2	1:D:60:CYS:HA	2.51	0.46
1:B:2:ALA:HA	1:B:72:THR:OG1	2.16	0.45
1:B:176:ASP:OD2	1:D:174:ARG:NH1	2.49	0.45
1:D:110:GLY:CA	1:D:111:GLU:C	2.85	0.45
1:C:3:ILE:O	1:C:3:ILE:HG22	2.17	0.45
1:D:83:GLN:O	1:D:237:ALA:HA	2.18	0.44
1:C:207:ILE:HG22	1:C:245:PHE:CE1	2.52	0.44
1:A:289:ALA:HB2	4:A:390:HOH:O	2.17	0.43
1:B:141:LEU:CD1	1:B:141:LEU:N	2.81	0.43
1:C:265:ARG:NH2	4:C:504:HOH:O	2.52	0.43
1:A:55:THR:HA	1:A:85:ILE:HD13	2.01	0.42
1:A:78:LEU:HD21	1:A:137:THR:HG23	2.02	0.42
1:D:18:GLU:HG2	1:D:96:LYS:HB3	2.02	0.42
1:C:43:GLU:OE1	1:C:43:GLU:N	2.49	0.41
1:C:107:GLN:HB2	1:C:116:ILE:HB	2.02	0.41
1:A:55:THR:O	1:A:58:VAL:HG22	2.20	0.41
1:C:78:LEU:HA	1:C:78:LEU:HD23	1.94	0.41
1:C:78:LEU:O	1:C:79:LEU:C	2.59	0.41
1:D:217:ALA:O	1:D:221:LEU:HG	2.20	0.40
1:D:25:LEU:HD22	1:D:41:THR:O	2.21	0.40
1:A:180:ILE:HD12	1:C:29:ILE:CG2	2.37	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	287/311 (92%)	283 (99%)	4 (1%)	0	100	100
1	B	284/311 (91%)	276 (97%)	8 (3%)	0	100	100
1	C	252/311 (81%)	244 (97%)	8 (3%)	0	100	100
1	D	260/311 (84%)	253 (97%)	7 (3%)	0	100	100
All	All	1083/1244 (87%)	1056 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	215/232 (93%)	213 (99%)	2 (1%)	84	93
1	B	214/232 (92%)	213 (100%)	1 (0%)	92	97
1	C	194/232 (84%)	192 (99%)	2 (1%)	82	91
1	D	201/232 (87%)	197 (98%)	4 (2%)	63	79
All	All	824/928 (89%)	815 (99%)	9 (1%)	80	90

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	180	ILE
1	A	205	LYS
1	B	0	SER
1	C	106	ILE
1	C	234	THR
1	D	78	LEU
1	D	141	LEU
1	D	234	THR

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Mol	Chain	Res	Type
1	D	285	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

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
3	TLA	B	300	-	3,9,9	2.50	1 (33%)	6,12,12	4.42	4 (66%)

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
3	TLA	B	300	-	-	0/4/12/12	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	300	TLA	O2-C2	4.24	1.51	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	300	TLA	O3-C3-C2	-6.98	88.95	108.61
3	B	300	TLA	O2-C2-C3	-4.35	96.36	108.61
3	B	300	TLA	C4-C3-C2	4.81	123.20	113.35
3	B	300	TLA	C1-C2-C3	5.08	123.75	113.35

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 ⓘ

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	288/311 (92%)	-0.13	3 (1%) 84 88	12, 25, 43, 54	0
1	B	286/311 (91%)	-0.12	2 (0%) 89 92	11, 23, 42, 55	0
1	C	261/311 (83%)	0.29	38 (14%) 3 5	13, 26, 50, 65	0
1	D	267/311 (85%)	0.12	24 (8%) 12 17	12, 25, 49, 66	0
All	All	1102/1244 (88%)	0.03	67 (6%) 25 33	11, 24, 47, 66	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	3	ILE	5.2
1	C	68	ALA	5.2
1	C	106	ILE	4.9
1	D	115	ALA	4.6
1	C	69	LYS	4.4
1	C	66	ALA	4.3
1	C	156	ALA	4.2
1	C	141	LEU	4.1
1	D	141	LEU	4.0
1	C	70	VAL	4.0
1	C	67	ALA	4.0
1	D	64	PHE	3.9
1	D	270	GLY	3.7
1	D	67	ALA	3.7
1	C	11	VAL	3.5
1	C	115	ALA	3.5
1	C	63	ALA	3.4
1	C	64	PHE	3.3
1	C	65	GLY	3.3
1	D	271	SER	3.2
1	C	116	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	108	ASP	3.2
1	C	274	ALA	3.1
1	C	157	ALA	3.1
1	D	6	ASN	3.1
1	D	3	ILE	3.0
1	C	6	ASN	3.0
1	C	5	PRO	2.9
1	A	289	ALA	2.9
1	D	116	ILE	2.8
1	C	269	ALA	2.8
1	D	162	ASP	2.7
1	D	110	GLY	2.7
1	D	5	PRO	2.6
1	C	80	HIS	2.6
1	D	164[A]	HIS	2.6
1	C	162	ASP	2.5
1	B	112	GLY	2.5
1	C	161	PRO	2.5
1	C	107	GLN	2.5
1	D	76	ALA	2.4
1	D	275	GLU	2.4
1	D	274	ALA	2.4
1	C	102	GLU	2.4
1	A	164	HIS	2.3
1	D	109	LYS	2.3
1	C	270	GLY	2.3
1	C	256[A]	ARG	2.3
1	D	4	ASP	2.3
1	C	105	ASP	2.3
1	C	155	PRO	2.2
1	C	103	VAL	2.2
1	C	153	GLU	2.2
1	C	128	SER	2.2
1	D	269	ALA	2.2
1	C	10	ALA	2.2
1	C	4	ASP	2.1
1	C	8	ILE	2.1
1	C	140	VAL	2.1
1	B	162	ASP	2.1
1	A	112	GLY	2.1
1	C	255	TRP	2.1
1	C	108	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	159	GLU	2.0
1	D	63	ALA	2.0
1	D	68	ALA	2.0
1	D	155	PRO	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CL	D	303	1/1	0.97	0.22	1.86	44,44,44,44	0
3	TLA	B	300	10/10	0.86	0.18	0.87	11,15,18,19	0
2	CL	A	302	1/1	0.95	0.11	-0.65	33,33,33,33	0
2	CL	A	301	1/1	1.00	0.10	-1.08	18,18,18,18	0
2	CL	C	301	1/1	0.99	0.07	-2.38	24,24,24,24	0
2	CL	B	302	1/1	0.98	0.07	-3.17	25,25,25,25	0
2	CL	D	301	1/1	0.99	0.07	-3.62	21,21,21,21	0
2	CL	B	301	1/1	1.00	0.10	-3.83	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.