



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 20, 2016 – 11:28 AM EDT

PDB ID : 4ZDA
Title : Crystal structure of isocitrate dehydrogenase in complex with isocitrate and Mn from *M. smegmatis*
Authors : Pojer, F.; Murima, P.; McKinney, J.D.
Deposited on : 2015-04-17
Resolution : 2.80 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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) : rb-20027790

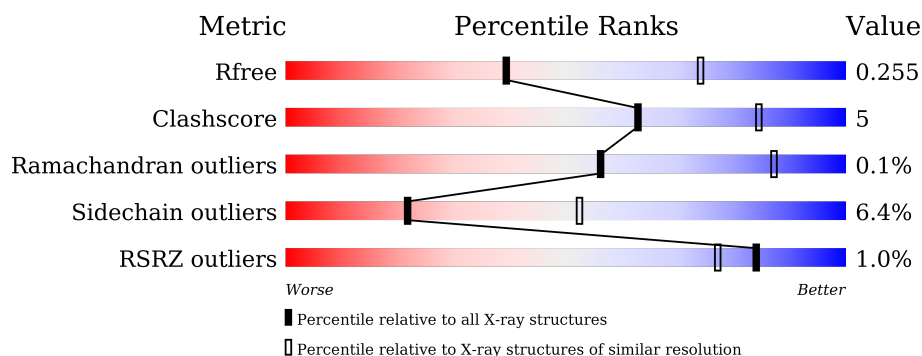
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	767	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>• •</div> </div> </div>
1	B	767	<div> <div></div> <div> <div>78%</div> <div>16%</div> <div>• •</div> </div> </div>
1	C	767	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>• •</div> </div> </div>
1	D	767	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>• •</div> </div> </div>
1	E	767	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>• •</div> </div> </div>
1	F	767	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34561 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 Isocitrate dehydrogenase (NADP) Icd2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	735	Total	C	N	O	S	0	1	0
			5752	3635	984	1106	27			
1	B	735	Total	C	N	O	S	0	0	0
			5745	3630	982	1106	27			
1	C	735	Total	C	N	O	S	0	0	0
			5745	3630	982	1106	27			
1	D	735	Total	C	N	O	S	0	0	0
			5745	3630	982	1106	27			
1	E	735	Total	C	N	O	S	0	0	0
			5745	3630	982	1106	27			
1	F	735	Total	C	N	O	S	0	0	0
			5745	3630	982	1106	27			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	744	PRO	-	expression tag	UNP A0QSZ3
A	745	ARG	-	expression tag	UNP A0QSZ3
A	746	TYR	-	expression tag	UNP A0QSZ3
A	747	PRO	-	expression tag	UNP A0QSZ3
A	748	TYR	-	expression tag	UNP A0QSZ3
A	749	ASP	-	expression tag	UNP A0QSZ3
A	750	VAL	-	expression tag	UNP A0QSZ3
A	751	PRO	-	expression tag	UNP A0QSZ3
A	752	ASP	-	expression tag	UNP A0QSZ3
A	753	TYR	-	expression tag	UNP A0QSZ3
A	754	ALA	-	expression tag	UNP A0QSZ3
A	755	LYS	-	expression tag	UNP A0QSZ3
A	756	LEU	-	expression tag	UNP A0QSZ3
A	757	ALA	-	expression tag	UNP A0QSZ3
A	758	ALA	-	expression tag	UNP A0QSZ3
A	759	ALA	-	expression tag	UNP A0QSZ3
A	760	LEU	-	expression tag	UNP A0QSZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	761	GLU	-	expression tag	UNP A0QSZ3
A	762	HIS	-	expression tag	UNP A0QSZ3
A	763	HIS	-	expression tag	UNP A0QSZ3
A	764	HIS	-	expression tag	UNP A0QSZ3
A	765	HIS	-	expression tag	UNP A0QSZ3
A	766	HIS	-	expression tag	UNP A0QSZ3
A	767	HIS	-	expression tag	UNP A0QSZ3
B	744	PRO	-	expression tag	UNP A0QSZ3
B	745	ARG	-	expression tag	UNP A0QSZ3
B	746	TYR	-	expression tag	UNP A0QSZ3
B	747	PRO	-	expression tag	UNP A0QSZ3
B	748	TYR	-	expression tag	UNP A0QSZ3
B	749	ASP	-	expression tag	UNP A0QSZ3
B	750	VAL	-	expression tag	UNP A0QSZ3
B	751	PRO	-	expression tag	UNP A0QSZ3
B	752	ASP	-	expression tag	UNP A0QSZ3
B	753	TYR	-	expression tag	UNP A0QSZ3
B	754	ALA	-	expression tag	UNP A0QSZ3
B	755	LYS	-	expression tag	UNP A0QSZ3
B	756	LEU	-	expression tag	UNP A0QSZ3
B	757	ALA	-	expression tag	UNP A0QSZ3
B	758	ALA	-	expression tag	UNP A0QSZ3
B	759	ALA	-	expression tag	UNP A0QSZ3
B	760	LEU	-	expression tag	UNP A0QSZ3
B	761	GLU	-	expression tag	UNP A0QSZ3
B	762	HIS	-	expression tag	UNP A0QSZ3
B	763	HIS	-	expression tag	UNP A0QSZ3
B	764	HIS	-	expression tag	UNP A0QSZ3
B	765	HIS	-	expression tag	UNP A0QSZ3
B	766	HIS	-	expression tag	UNP A0QSZ3
B	767	HIS	-	expression tag	UNP A0QSZ3
C	744	PRO	-	expression tag	UNP A0QSZ3
C	745	ARG	-	expression tag	UNP A0QSZ3
C	746	TYR	-	expression tag	UNP A0QSZ3
C	747	PRO	-	expression tag	UNP A0QSZ3
C	748	TYR	-	expression tag	UNP A0QSZ3
C	749	ASP	-	expression tag	UNP A0QSZ3
C	750	VAL	-	expression tag	UNP A0QSZ3
C	751	PRO	-	expression tag	UNP A0QSZ3
C	752	ASP	-	expression tag	UNP A0QSZ3
C	753	TYR	-	expression tag	UNP A0QSZ3
C	754	ALA	-	expression tag	UNP A0QSZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	755	LYS	-	expression tag	UNP A0QSZ3
C	756	LEU	-	expression tag	UNP A0QSZ3
C	757	ALA	-	expression tag	UNP A0QSZ3
C	758	ALA	-	expression tag	UNP A0QSZ3
C	759	ALA	-	expression tag	UNP A0QSZ3
C	760	LEU	-	expression tag	UNP A0QSZ3
C	761	GLU	-	expression tag	UNP A0QSZ3
C	762	HIS	-	expression tag	UNP A0QSZ3
C	763	HIS	-	expression tag	UNP A0QSZ3
C	764	HIS	-	expression tag	UNP A0QSZ3
C	765	HIS	-	expression tag	UNP A0QSZ3
C	766	HIS	-	expression tag	UNP A0QSZ3
C	767	HIS	-	expression tag	UNP A0QSZ3
D	744	PRO	-	expression tag	UNP A0QSZ3
D	745	ARG	-	expression tag	UNP A0QSZ3
D	746	TYR	-	expression tag	UNP A0QSZ3
D	747	PRO	-	expression tag	UNP A0QSZ3
D	748	TYR	-	expression tag	UNP A0QSZ3
D	749	ASP	-	expression tag	UNP A0QSZ3
D	750	VAL	-	expression tag	UNP A0QSZ3
D	751	PRO	-	expression tag	UNP A0QSZ3
D	752	ASP	-	expression tag	UNP A0QSZ3
D	753	TYR	-	expression tag	UNP A0QSZ3
D	754	ALA	-	expression tag	UNP A0QSZ3
D	755	LYS	-	expression tag	UNP A0QSZ3
D	756	LEU	-	expression tag	UNP A0QSZ3
D	757	ALA	-	expression tag	UNP A0QSZ3
D	758	ALA	-	expression tag	UNP A0QSZ3
D	759	ALA	-	expression tag	UNP A0QSZ3
D	760	LEU	-	expression tag	UNP A0QSZ3
D	761	GLU	-	expression tag	UNP A0QSZ3
D	762	HIS	-	expression tag	UNP A0QSZ3
D	763	HIS	-	expression tag	UNP A0QSZ3
D	764	HIS	-	expression tag	UNP A0QSZ3
D	765	HIS	-	expression tag	UNP A0QSZ3
D	766	HIS	-	expression tag	UNP A0QSZ3
D	767	HIS	-	expression tag	UNP A0QSZ3
E	744	PRO	-	expression tag	UNP A0QSZ3
E	745	ARG	-	expression tag	UNP A0QSZ3
E	746	TYR	-	expression tag	UNP A0QSZ3
E	747	PRO	-	expression tag	UNP A0QSZ3
E	748	TYR	-	expression tag	UNP A0QSZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	749	ASP	-	expression tag	UNP A0QSZ3
E	750	VAL	-	expression tag	UNP A0QSZ3
E	751	PRO	-	expression tag	UNP A0QSZ3
E	752	ASP	-	expression tag	UNP A0QSZ3
E	753	TYR	-	expression tag	UNP A0QSZ3
E	754	ALA	-	expression tag	UNP A0QSZ3
E	755	LYS	-	expression tag	UNP A0QSZ3
E	756	LEU	-	expression tag	UNP A0QSZ3
E	757	ALA	-	expression tag	UNP A0QSZ3
E	758	ALA	-	expression tag	UNP A0QSZ3
E	759	ALA	-	expression tag	UNP A0QSZ3
E	760	LEU	-	expression tag	UNP A0QSZ3
E	761	GLU	-	expression tag	UNP A0QSZ3
E	762	HIS	-	expression tag	UNP A0QSZ3
E	763	HIS	-	expression tag	UNP A0QSZ3
E	764	HIS	-	expression tag	UNP A0QSZ3
E	765	HIS	-	expression tag	UNP A0QSZ3
E	766	HIS	-	expression tag	UNP A0QSZ3
E	767	HIS	-	expression tag	UNP A0QSZ3
F	744	PRO	-	expression tag	UNP A0QSZ3
F	745	ARG	-	expression tag	UNP A0QSZ3
F	746	TYR	-	expression tag	UNP A0QSZ3
F	747	PRO	-	expression tag	UNP A0QSZ3
F	748	TYR	-	expression tag	UNP A0QSZ3
F	749	ASP	-	expression tag	UNP A0QSZ3
F	750	VAL	-	expression tag	UNP A0QSZ3
F	751	PRO	-	expression tag	UNP A0QSZ3
F	752	ASP	-	expression tag	UNP A0QSZ3
F	753	TYR	-	expression tag	UNP A0QSZ3
F	754	ALA	-	expression tag	UNP A0QSZ3
F	755	LYS	-	expression tag	UNP A0QSZ3
F	756	LEU	-	expression tag	UNP A0QSZ3
F	757	ALA	-	expression tag	UNP A0QSZ3
F	758	ALA	-	expression tag	UNP A0QSZ3
F	759	ALA	-	expression tag	UNP A0QSZ3
F	760	LEU	-	expression tag	UNP A0QSZ3
F	761	GLU	-	expression tag	UNP A0QSZ3
F	762	HIS	-	expression tag	UNP A0QSZ3
F	763	HIS	-	expression tag	UNP A0QSZ3
F	764	HIS	-	expression tag	UNP A0QSZ3
F	765	HIS	-	expression tag	UNP A0QSZ3
F	766	HIS	-	expression tag	UNP A0QSZ3

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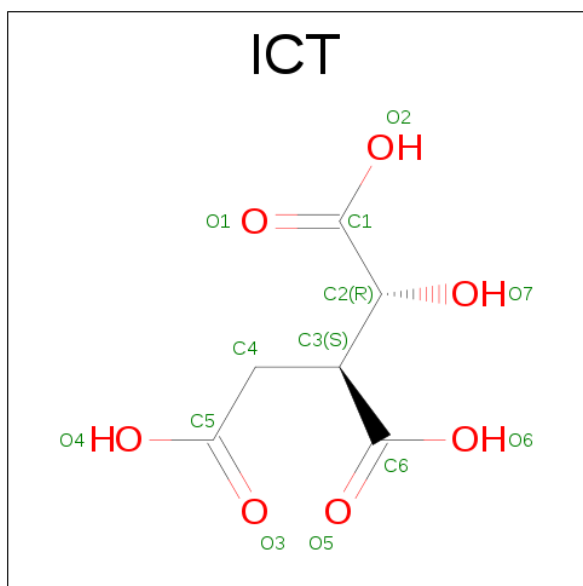
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Chain	Residue	Modelled	Actual	Comment	Reference
F	767	HIS	-	expression tag	UNP A0QSZ3

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Mn	0	0
			1	1		
2	E	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		
2	A	1	Total	Mn	0	0
			1	1		
2	F	1	Total	Mn	0	0
			1	1		

- Molecule 3 is ISOCITRIC ACID (three-letter code: ICT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		

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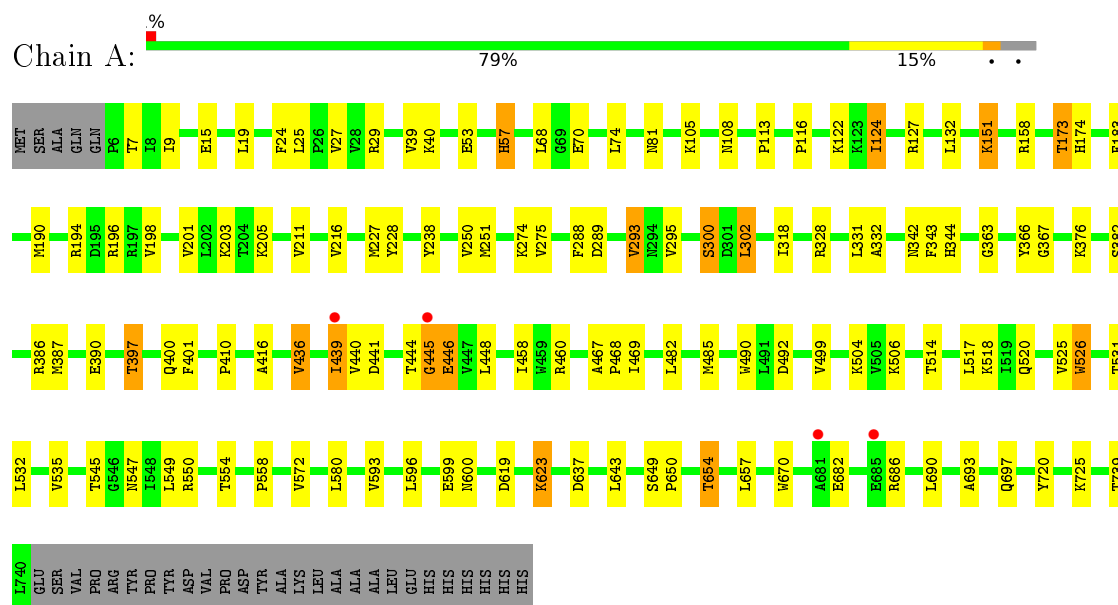
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			13	6	7		
3	E	1	Total	C	O	0	0
			13	6	7		
3	F	1	Total	C	O	0	0
			13	6	7		

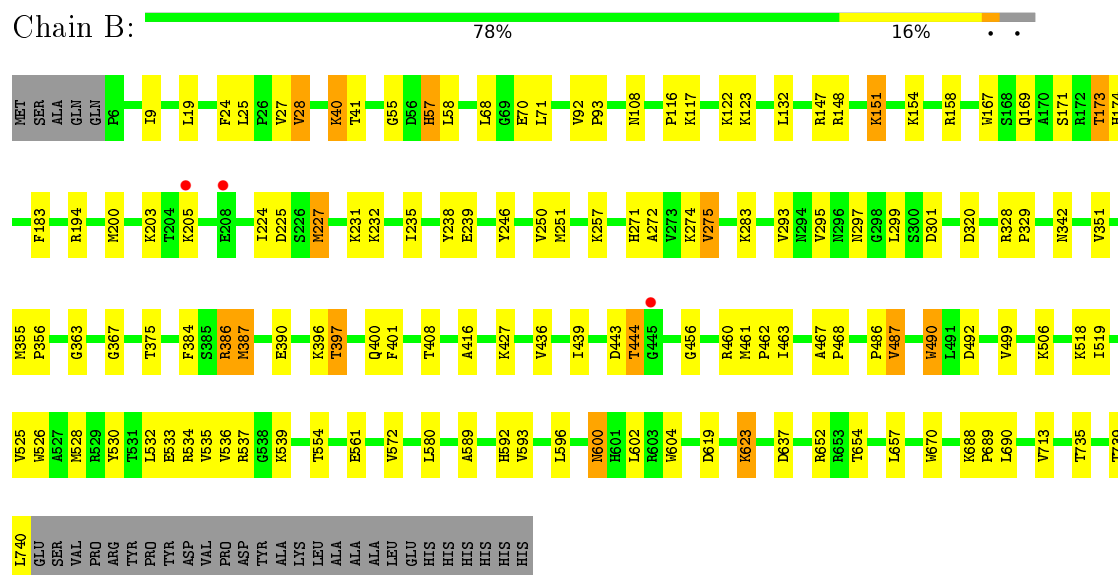
3 Residue-property plots

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.

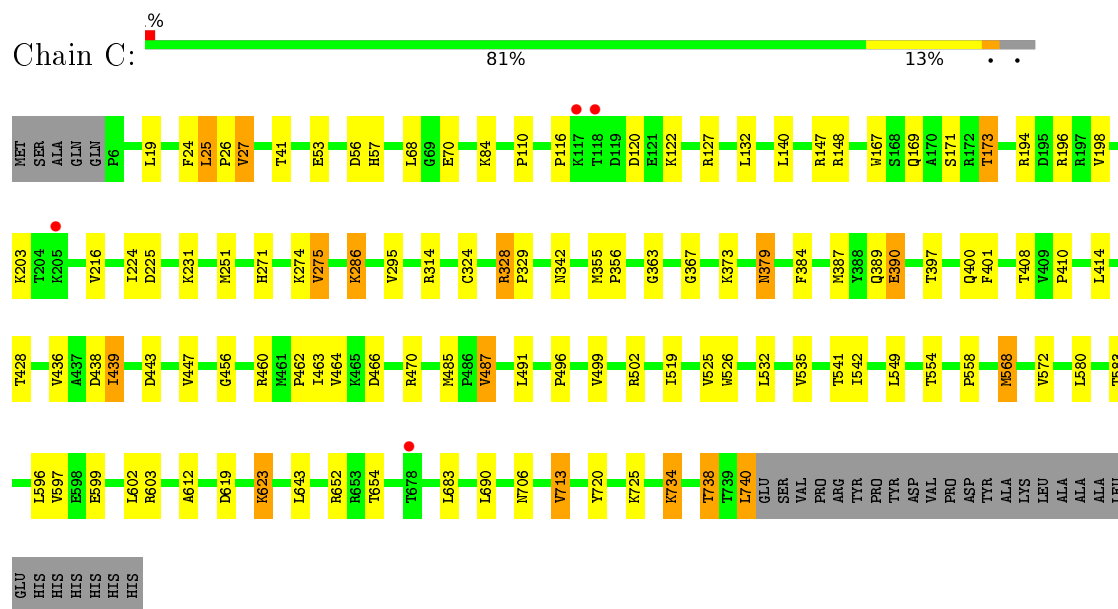
• Molecule 1: Isocitrate dehydrogenase (NADP) Icd2



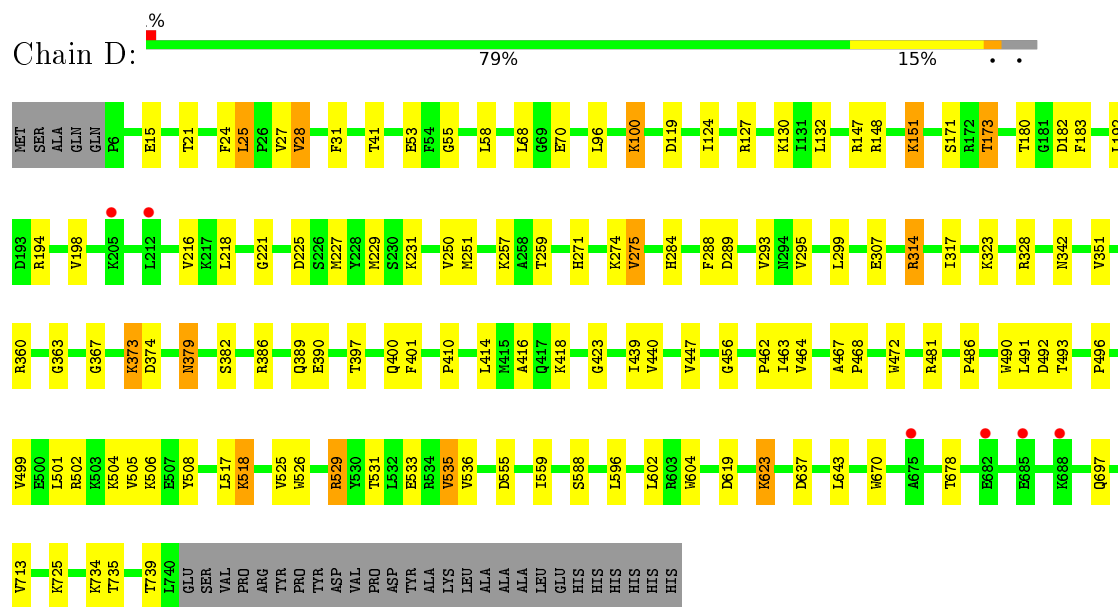
• Molecule 1: Isocitrate dehydrogenase (NADP) Icd2



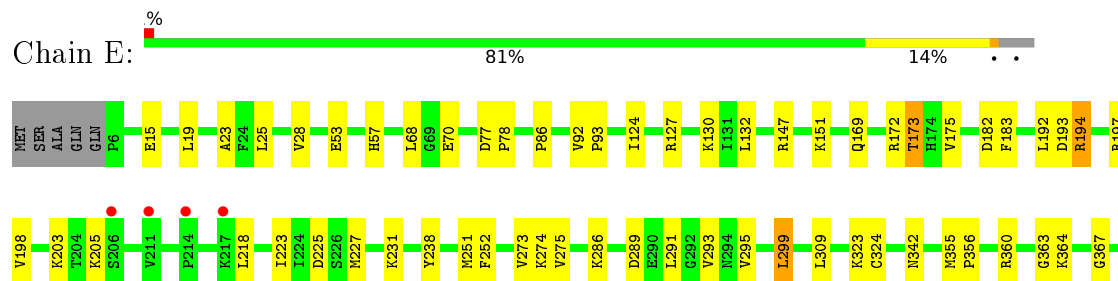
• Molecule 1: Isocitrate dehydrogenase (NADP) Icd2



• Molecule 1: Isocitrate dehydrogenase (NADP) Icd2



• Molecule 1: Isocitrate dehydrogenase (NADP) Icd2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	201.77Å 206.16Å 145.60Å 90.00° 90.97° 90.00°	Depositor
Resolution (Å)	48.59 – 2.80 48.59 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.59-2.80) 99.2 (48.59-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.214 , 0.257 0.211 , 0.255	Depositor DCC
R_{free} test set	7267 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	68.2	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 26.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for $-1/2^*h-1/2^*k-l, 1/2^*h+1/2^*k-l, 1/2^*h-1/2^*k$ 0.028 for $-1/2^*h-1/2^*k+l, 1/2^*h+1/2^*k+l, -1/2^*h+1/2^*k$ 0.023 for $-1/2^*h+1/2^*k+l, -1/2^*h+1/2^*k-l, -1/2^*h-1/2^*k$ 0.029 for $-1/2^*h+1/2^*k-l, -1/2^*h+1/2^*k+l, 1/2^*h+1/2^*k$ 0.013 for k,h,-l 0.014 for -k,-h,-l 0.017 for $-1/2^*h+1/2^*k-l, 1/2^*h-1/2^*k-l, -1/2^*h-1/2^*k$ 0.010 for $-1/2^*h-1/2^*k-l, -1/2^*h-1/2^*k+l, -1/2^*h+1/2^*k$ 0.011 for $-1/2^*h+1/2^*k+l, 1/2^*h-1/2^*k+l, 1/2^*h+1/2^*k$ 0.017 for $-1/2^*h-1/2^*k+l, -1/2^*h-1/2^*k-l, 1/2^*h-1/2^*k$ 0.021 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	34561	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

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.

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.00% of the height of the origin peak. No significant pseudotranslation is detected.*

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.41	2/5870 (0.0%)	0.52	0/7936
1	B	0.42	5/5859 (0.1%)	0.52	0/7921
1	C	0.41	2/5859 (0.0%)	0.55	1/7921 (0.0%)
1	D	0.42	4/5859 (0.1%)	0.51	0/7921
1	E	0.42	3/5859 (0.1%)	0.50	0/7921
1	F	0.42	3/5859 (0.1%)	0.50	0/7921
All	All	0.42	19/35165 (0.1%)	0.52	1/47541 (0.0%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	604	TRP	CD2-CE2	5.41	1.47	1.41
1	B	604	TRP	CD2-CE2	5.29	1.47	1.41
1	B	526	TRP	CD2-CE2	5.21	1.47	1.41
1	D	490	TRP	CD2-CE2	5.19	1.47	1.41
1	D	670	TRP	CD2-CE2	5.14	1.47	1.41
1	B	670	TRP	CD2-CE2	5.13	1.47	1.41
1	F	459	TRP	CD2-CE2	5.09	1.47	1.41
1	D	604	TRP	CD2-CE2	5.08	1.47	1.41
1	A	526	TRP	CD2-CE2	5.05	1.47	1.41
1	F	526	TRP	CD2-CE2	5.05	1.47	1.41
1	F	670	TRP	CD2-CE2	5.05	1.47	1.41
1	B	490	TRP	CD2-CE2	5.05	1.47	1.41
1	A	670	TRP	CD2-CE2	5.05	1.47	1.41
1	C	526	TRP	CD2-CE2	5.04	1.47	1.41
1	D	472	TRP	CD2-CE2	5.03	1.47	1.41
1	C	167	TRP	CD2-CE2	5.02	1.47	1.41
1	E	526	TRP	CD2-CE2	5.02	1.47	1.41
1	B	167	TRP	CD2-CE2	5.01	1.47	1.41
1	E	459	TRP	CD2-CE2	5.01	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	740	LEU	CA-C-O	-17.14	84.12	120.10

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	5752	0	5752	74	0
1	B	5745	0	5745	73	0
1	C	5745	0	5745	52	0
1	D	5745	0	5745	61	0
1	E	5745	0	5745	50	0
1	F	5745	0	5745	64	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
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	13	0	5	0	0
3	B	13	0	5	0	0
3	C	13	0	5	0	0
3	D	13	0	5	0	0
3	E	13	0	5	0	0
3	F	13	0	4	0	0
All	All	34561	0	34506	367	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 (367) 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:E:251:MET:HE1	1:E:367:GLY:HA2	1.45	0.98
1:A:251:MET:CE	1:A:367:GLY:HA2	1.93	0.98
1:C:485:MET:HE2	1:C:542:ILE:HG13	1.48	0.96
1:A:400:GLN:HE21	1:A:401:PHE:H	1.16	0.94
1:A:173:THR:HG21	1:A:363:GLY:O	1.69	0.92
1:E:251:MET:CE	1:E:367:GLY:HA2	2.02	0.89
1:B:386:ARG:HH11	1:B:386:ARG:HG3	1.38	0.88
1:A:251:MET:HE3	1:A:367:GLY:HA2	1.54	0.88
1:F:190:MET:HE1	1:F:448:LEU:HB3	1.56	0.84
1:A:390:GLU:HG3	1:A:525:VAL:HG13	1.62	0.82
1:E:173:THR:HG21	1:E:363:GLY:O	1.81	0.81
1:D:390:GLU:HG3	1:D:525:VAL:HG13	1.67	0.77
1:F:173:THR:HG21	1:F:363:GLY:O	1.85	0.77
1:B:173:THR:HG21	1:B:363:GLY:O	1.85	0.76
1:A:251:MET:HE1	1:A:367:GLY:HA2	1.67	0.76
1:C:400:GLN:HE21	1:C:401:PHE:H	1.35	0.74
1:C:173:THR:HG21	1:C:363:GLY:O	1.88	0.74
1:B:735:THR:O	1:B:739:THR:HG22	1.87	0.74
1:A:445:GLY:HA3	1:A:446:GLU:HB2	1.67	0.74
1:F:165:GLY:O	1:F:400:GLN:HG3	1.88	0.73
1:D:173:THR:HG21	1:D:363:GLY:O	1.88	0.73
1:D:529:ARG:HG2	1:D:529:ARG:HH11	1.51	0.72
1:D:386:ARG:HG3	1:D:386:ARG:HH11	1.55	0.71
1:F:326:GLU:HG3	1:F:327:HIS:HD2	1.55	0.71
1:A:386:ARG:HH11	1:A:386:ARG:HG3	1.56	0.70
1:D:529:ARG:CG	1:D:529:ARG:HH11	2.03	0.70
1:C:734:LYS:O	1:C:738:THR:HG22	1.92	0.69
1:A:158:ARG:HG2	1:A:158:ARG:HH11	1.56	0.69
1:B:400:GLN:HE21	1:B:401:PHE:H	1.40	0.69
1:F:400:GLN:HE21	1:F:401:PHE:H	1.38	0.68
1:A:251:MET:HE3	1:A:367:GLY:CA	2.24	0.68
1:D:400:GLN:HE21	1:D:401:PHE:H	1.40	0.68
1:A:410:PRO:HG2	1:A:485:MET:HE3	1.76	0.68
1:C:596:LEU:HD13	1:C:602:LEU:HB2	1.76	0.67
1:C:224:ILE:HG22	1:C:463:ILE:HG22	1.77	0.66
1:E:19:LEU:HD13	1:E:596:LEU:HD23	1.76	0.66
1:E:238:TYR:HB3	1:E:275:VAL:HG21	1.78	0.66
1:F:386:ARG:NH2	1:F:492:ASP:OD1	2.29	0.66
1:F:238:TYR:HB3	1:F:275:VAL:HG21	1.78	0.66
1:B:57:HIS:HB2	1:B:108:ASN:O	1.95	0.66
1:B:225:ASP:HB2	1:B:462:PRO:HD2	1.78	0.65
1:E:485:MET:HE2	1:E:542:ILE:HG13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:400:GLN:HE21	1:E:401:PHE:H	1.45	0.64
1:E:251:MET:CE	1:E:367:GLY:CA	2.76	0.63
1:F:596:LEU:HD12	1:F:602:LEU:HB2	1.81	0.63
1:B:251:MET:HE1	1:B:367:GLY:CA	2.29	0.63
1:A:198:VAL:HG23	1:A:216:VAL:HG13	1.79	0.62
1:F:248:THR:OG1	1:F:250:VAL:HG12	2.00	0.62
1:F:231:LYS:HD2	1:F:456:GLY:HA3	1.80	0.61
1:C:19:LEU:HD13	1:C:596:LEU:HD22	1.82	0.61
1:D:251:MET:HE2	1:D:367:GLY:HA2	1.83	0.61
1:D:251:MET:CE	1:D:367:GLY:HA2	2.31	0.60
1:F:167:TRP:HD1	1:F:400:GLN:HG2	1.66	0.60
1:C:619:ASP:HB3	1:C:623:LYS:HE2	1.83	0.60
1:F:30:LYS:HG3	1:F:740:LEU:HD23	1.84	0.59
1:F:652:ARG:HG2	1:F:652:ARG:HH11	1.67	0.59
1:B:227:MET:HE1	1:B:460:ARG:HE	1.68	0.59
1:A:390:GLU:CG	1:A:525:VAL:HG13	2.33	0.59
1:A:116:PRO:HB2	1:A:122:LYS:HG3	1.85	0.58
1:A:19:LEU:HD13	1:A:596:LEU:HD22	1.85	0.58
1:B:154:LYS:HD3	1:B:408:THR:HG22	1.86	0.57
1:C:603:ARG:HD2	1:C:652:ARG:HD2	1.86	0.57
1:E:25:LEU:HA	1:E:28:VAL:HG12	1.86	0.57
1:D:231:LYS:HD2	1:D:456:GLY:HA3	1.87	0.57
1:F:57:HIS:HB2	1:F:108:ASN:O	2.06	0.56
1:B:257:LYS:HB2	1:B:351:VAL:HG12	1.88	0.56
1:B:387:MET:HG3	1:B:490:TRP:HZ3	1.71	0.56
1:A:467:ALA:HB3	1:A:468:PRO:HD3	1.88	0.56
1:D:27:VAL:O	1:D:31:PHE:HD1	1.89	0.56
1:E:251:MET:HE3	1:E:367:GLY:CA	2.35	0.55
1:F:421:GLU:HB2	1:F:548:ILE:HD11	1.88	0.55
1:D:390:GLU:CG	1:D:525:VAL:HG13	2.34	0.55
1:B:235:ILE:O	1:B:239:GLU:HG2	2.06	0.55
1:C:271:HIS:O	1:C:275:VAL:HG13	2.06	0.55
1:F:147:ARG:HD2	1:F:554:THR:HB	1.89	0.54
1:F:400:GLN:HE21	1:F:401:PHE:N	2.02	0.54
1:B:443:ASP:O	1:B:444:THR:HB	2.07	0.54
1:D:198:VAL:HG23	1:D:216:VAL:HG13	1.87	0.54
1:B:408:THR:HG22	1:B:561:GLU:OE1	2.07	0.54
1:C:203:LYS:HB2	1:C:436:VAL:HG22	1.89	0.54
1:A:554:THR:O	1:A:558:PRO:HG2	2.07	0.54
1:D:619:ASP:HB3	1:D:623:LYS:HE2	1.90	0.54
1:D:491:LEU:O	1:D:502:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:MET:CE	1:B:367:GLY:HA2	2.38	0.53
1:A:293:VAL:HG21	1:A:302:LEU:HD12	1.90	0.53
1:B:386:ARG:HG3	1:B:386:ARG:NH1	2.15	0.53
1:B:227:MET:CE	1:B:460:ARG:HE	2.21	0.53
1:D:182:ASP:HA	1:D:229:MET:HG3	1.89	0.53
1:E:192:LEU:HD11	1:E:218:LEU:HD23	1.91	0.53
1:B:271:HIS:O	1:B:275:VAL:HG12	2.08	0.53
1:B:224:ILE:HG22	1:B:463:ILE:HG22	1.90	0.53
1:B:386:ARG:NH2	1:B:492:ASP:OD1	2.42	0.53
1:A:203:LYS:HB2	1:A:436:VAL:HG13	1.91	0.53
1:B:390:GLU:CG	1:B:525:VAL:HG13	2.39	0.53
1:E:183:PHE:HD1	1:E:227:MET:HB3	1.74	0.53
1:A:24:PHE:O	1:A:27:VAL:HG22	2.10	0.52
1:E:231:LYS:HD2	1:E:456:GLY:HA3	1.90	0.52
1:F:355:MET:HB2	1:F:356:PRO:HD3	1.90	0.52
1:D:440:VAL:HG22	1:D:447:VAL:HG12	1.91	0.52
1:B:596:LEU:HD13	1:B:602:LEU:HB2	1.91	0.52
1:A:113:PRO:HD3	1:A:124:ILE:HD11	1.91	0.52
1:C:599:GLU:OE2	1:C:654:THR:HG21	2.10	0.52
1:A:57:HIS:HB2	1:A:108:ASN:O	2.09	0.52
1:A:410:PRO:HG2	1:A:485:MET:CE	2.40	0.52
1:D:148:ARG:HB3	1:D:410:PRO:HB3	1.91	0.52
1:B:530:TYR:O	1:B:534:ARG:HG2	2.10	0.52
1:C:53:GLU:OE2	1:C:127:ARG:HD2	2.10	0.51
1:F:364:LYS:HB3	1:F:372:THR:HB	1.92	0.51
1:D:307:GLU:O	1:D:314:ARG:NH2	2.43	0.51
1:F:227:MET:HE1	1:F:460:ARG:HE	1.75	0.51
1:F:286:LYS:HD3	1:F:287:LEU:N	2.25	0.51
1:C:532:LEU:HA	1:C:535:VAL:HG22	1.93	0.51
1:F:203:LYS:HB3	1:F:436:VAL:HG22	1.93	0.51
1:B:386:ARG:HH11	1:B:386:ARG:CG	2.18	0.51
1:F:515:GLU:HG3	1:F:516:GLY:H	1.76	0.51
1:B:154:LYS:HD3	1:B:408:THR:CG2	2.41	0.51
1:B:24:PHE:O	1:B:28:VAL:HG12	2.11	0.51
1:B:40:LYS:HD3	1:B:41:THR:H	1.75	0.51
1:E:53:GLU:OE2	1:E:127:ARG:HD2	2.10	0.51
1:C:414:LEU:HD21	1:C:464:VAL:HG21	1.93	0.50
1:F:599:GLU:OE2	1:F:654:THR:HG21	2.11	0.50
1:D:529:ARG:CG	1:D:529:ARG:NH1	2.68	0.50
1:A:416:ALA:HB3	1:A:468:PRO:HB3	1.93	0.50
1:A:300:SER:HB3	1:A:344:HIS:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:ARG:HD2	1:C:554:THR:HB	1.92	0.50
1:C:355:MET:HB2	1:C:356:PRO:HD3	1.94	0.49
1:C:390:GLU:CG	1:C:525:VAL:HG13	2.42	0.49
1:D:171:SER:OG	1:D:173:THR:HG23	2.12	0.49
1:E:355:MET:HB2	1:E:356:PRO:HD3	1.94	0.49
1:F:607:LEU:HA	1:F:610:PHE:CD2	2.47	0.49
1:A:400:GLN:HE21	1:A:401:PHE:N	1.96	0.49
1:D:555:ASP:O	1:D:559:ILE:HG12	2.12	0.49
1:F:200:MET:HB2	1:F:213:LYS:HB3	1.93	0.49
1:D:531:THR:O	1:D:535:VAL:HG22	2.13	0.49
1:A:382:SER:O	1:A:386:ARG:HG3	2.11	0.49
1:B:116:PRO:HB2	1:B:122:LYS:HG3	1.94	0.49
1:A:251:MET:CE	1:A:332:ALA:HA	2.43	0.49
1:B:572:VAL:HB	1:B:580:LEU:HB3	1.94	0.49
1:B:355:MET:HB2	1:B:356:PRO:HD3	1.94	0.49
1:E:175:VAL:HG23	1:E:392:ILE:HD12	1.94	0.49
1:F:619:ASP:HB3	1:F:623:LYS:HE2	1.93	0.49
1:F:677:GLN:HE21	1:F:684:ALA:HB2	1.77	0.49
1:A:105:LYS:NZ	1:A:720:TYR:O	2.46	0.48
1:B:231:LYS:HD2	1:B:456:GLY:HA3	1.95	0.48
1:D:496:PRO:O	1:D:499:VAL:HG22	2.13	0.48
1:D:96:LEU:O	1:D:100:LYS:HE3	2.13	0.48
1:E:688:LYS:N	1:E:689:PRO:HD2	2.27	0.48
1:A:251:MET:HE1	1:A:366:TYR:O	2.13	0.48
1:A:386:ARG:NH2	1:A:492:ASP:OD1	2.45	0.48
1:C:328:ARG:HG3	1:C:329:PRO:HD2	1.94	0.48
1:F:514:THR:HA	1:F:517:LEU:HD12	1.95	0.48
1:A:53:GLU:OE2	1:A:127:ARG:HD2	2.13	0.48
1:B:203:LYS:HB3	1:B:436:VAL:HG13	1.95	0.48
1:B:92:VAL:HB	1:B:93:PRO:HD3	1.96	0.48
1:E:485:MET:CE	1:E:542:ILE:HG13	2.43	0.48
1:F:487:VAL:HG13	1:F:519:ILE:HG12	1.95	0.48
1:B:40:LYS:HD3	1:B:41:THR:N	2.28	0.48
1:B:532:LEU:HA	1:B:535:VAL:HG22	1.96	0.48
1:E:203:LYS:HB2	1:E:436:VAL:HG13	1.94	0.48
1:A:619:ASP:HB3	1:A:623:LYS:HE2	1.96	0.48
1:B:238:TYR:CZ	1:B:272:ALA:HB2	2.49	0.48
1:B:297:ASN:HB2	1:B:301:ASP:HB2	1.96	0.48
1:E:25:LEU:HA	1:E:28:VAL:CG1	2.43	0.48
1:B:400:GLN:NE2	1:B:401:PHE:H	2.09	0.48
1:D:288:PHE:HB3	1:D:293:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:MET:HE2	1:B:367:GLY:HA2	1.96	0.48
1:F:25:LEU:N	1:F:26:PRO:HD2	2.29	0.48
1:A:331:LEU:HD11	1:A:343:PHE:CD2	2.48	0.47
1:B:169:GLN:HG2	1:B:396:LYS:O	2.13	0.47
1:B:246:TYR:HB2	1:B:329:PRO:HD3	1.96	0.47
1:D:288:PHE:HB3	1:D:293:VAL:CG1	2.44	0.47
1:F:165:GLY:O	1:F:400:GLN:CG	2.61	0.47
1:B:158:ARG:HB3	1:D:678:THR:OG1	2.14	0.47
1:A:288:PHE:CZ	1:A:302:LEU:HD11	2.48	0.47
1:F:486:PRO:HB3	1:F:518:LYS:HB3	1.97	0.47
1:B:251:MET:CE	1:B:367:GLY:CA	2.93	0.47
1:A:251:MET:CE	1:A:367:GLY:CA	2.80	0.47
1:B:55:GLY:HA2	1:B:58:LEU:HD12	1.97	0.47
1:D:379:ASN:HD22	1:D:379:ASN:N	2.13	0.47
1:A:174:HIS:NE2	1:A:376:LYS:HE2	2.30	0.47
1:B:487:VAL:HG13	1:B:519:ILE:HG12	1.97	0.47
1:F:148:ARG:HB3	1:F:410:PRO:HB3	1.96	0.47
1:D:53:GLU:OE2	1:D:127:ARG:HD2	2.15	0.47
1:F:421:GLU:HB2	1:F:548:ILE:CD1	2.44	0.47
1:C:491:LEU:O	1:C:502:ARG:NH2	2.48	0.46
1:F:496:PRO:O	1:F:499:VAL:HG22	2.15	0.46
1:A:19:LEU:HD13	1:A:596:LEU:CD2	2.46	0.46
1:A:227:MET:HE1	1:A:460:ARG:HH21	1.80	0.46
1:A:682:GLU:O	1:A:686:ARG:HB2	2.15	0.46
1:E:193:ASP:HB3	1:E:194:ARG:HD2	1.96	0.46
1:B:397:THR:HG22	1:C:389:GLN:HE21	1.78	0.46
1:D:221:GLY:O	1:D:504:LYS:NZ	2.49	0.46
1:D:504:LYS:HB3	1:D:508:TYR:CE2	2.50	0.46
1:A:151:LYS:CD	1:A:151:LYS:H	2.28	0.46
1:B:205:LYS:HD3	1:B:205:LYS:H	1.79	0.46
1:E:439:ILE:HG13	1:E:439:ILE:O	2.16	0.46
1:F:27:VAL:O	1:F:31:PHE:HD1	1.97	0.46
1:C:438:ASP:HB3	1:C:447:VAL:HG23	1.98	0.46
1:D:124:ILE:HG22	1:D:127:ARG:HH21	1.80	0.46
1:A:599:GLU:OE2	1:A:654:THR:HG21	2.15	0.46
1:E:469:ILE:HD13	1:E:504:LYS:HD2	1.97	0.46
1:C:148:ARG:HB2	1:C:410:PRO:HB3	1.97	0.46
1:B:467:ALA:HB3	1:B:468:PRO:HD3	1.98	0.46
1:C:379:ASN:N	1:C:379:ASN:HD22	2.14	0.46
1:C:390:GLU:HG3	1:C:525:VAL:HG13	1.98	0.46
1:A:397:THR:HG22	1:D:389:GLN:HE21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:416:ALA:HB3	1:D:468:PRO:HB3	1.97	0.46
1:E:599:GLU:OE2	1:E:654:THR:HG21	2.16	0.46
1:F:190:MET:HE1	1:F:448:LEU:HD23	1.98	0.46
1:A:190:MET:HE1	1:A:448:LEU:HB3	1.98	0.46
1:D:501:LEU:O	1:D:505:VAL:HG23	2.15	0.46
1:B:200:MET:HE1	1:B:461:MET:HB3	1.98	0.46
1:D:257:LYS:HB2	1:D:351:VAL:HG12	1.98	0.46
1:E:465:LYS:HB3	1:E:468:PRO:HD2	1.98	0.46
1:E:147:ARG:HD2	1:E:554:THR:HB	1.98	0.46
1:F:431:ILE:HA	1:F:432:PRO:HD3	1.80	0.46
1:B:200:MET:HE1	1:B:427:LYS:HB3	1.97	0.45
1:A:693:ALA:O	1:A:697:GLN:HG3	2.16	0.45
1:B:384:PHE:O	1:B:387:MET:HE3	2.16	0.45
1:E:692:LYS:O	1:E:696:GLU:HB2	2.16	0.45
1:C:428:THR:HG23	1:C:460:ARG:HB3	1.97	0.45
1:E:572:VAL:HB	1:E:580:LEU:HB3	1.98	0.45
1:A:532:LEU:HA	1:A:535:VAL:HG22	1.97	0.45
1:D:15:GLU:HB2	1:D:588:SER:HB2	1.97	0.45
1:D:386:ARG:NH1	1:D:386:ARG:HG3	2.29	0.45
1:E:23:ALA:HB2	1:E:730:MET:HB3	1.98	0.45
1:E:15:GLU:OE1	1:E:588:SER:HB2	2.16	0.45
1:D:24:PHE:O	1:D:28:VAL:HG12	2.16	0.45
1:D:251:MET:HE1	1:D:373:LYS:HE3	1.99	0.45
1:C:198:VAL:HG23	1:C:216:VAL:HG13	1.99	0.44
1:C:225:ASP:HB2	1:C:462:PRO:HD2	1.98	0.44
1:F:701:ILE:HG12	1:F:736:PHE:HB2	1.98	0.44
1:A:190:MET:CE	1:A:448:LEU:HB3	2.47	0.44
1:C:439:ILE:HG13	1:C:439:ILE:O	2.15	0.44
1:A:514:THR:HA	1:A:517:LEU:HD12	1.99	0.44
1:E:416:ALA:HB3	1:E:468:PRO:HB3	2.00	0.44
1:F:485:MET:CE	1:F:540:ASP:HB3	2.48	0.44
1:A:739:THR:HG22	1:A:739:THR:O	2.18	0.44
1:D:467:ALA:HB3	1:D:468:PRO:HD3	2.00	0.44
1:F:25:LEU:HA	1:F:28:VAL:HG12	1.98	0.44
1:C:466:ASP:OD2	1:C:470:ARG:NH1	2.50	0.44
1:D:481:ARG:HA	1:D:517:LEU:HD21	1.99	0.44
1:F:108:ASN:HD22	1:F:108:ASN:C	2.19	0.44
1:F:554:THR:O	1:F:558:PRO:HG2	2.17	0.44
1:B:151:LYS:H	1:B:151:LYS:NZ	2.16	0.44
1:D:192:LEU:HD11	1:D:218:LEU:HD23	1.99	0.44
1:A:526:TRP:HZ3	1:D:526:TRP:HE3	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:518:LYS:HE3	1:A:520:GLN:HE22	1.83	0.43
1:B:9:ILE:HG21	1:B:71:LEU:HD21	2.00	0.43
1:C:25:LEU:N	1:C:26:PRO:HD2	2.34	0.43
1:F:110:PRO:HB2	1:F:124:ILE:HD13	1.98	0.43
1:A:228:TYR:HA	1:A:458:ILE:O	2.18	0.43
1:C:597:VAL:HA	1:C:713:VAL:HG12	1.99	0.43
1:D:382:SER:O	1:D:386:ARG:HG3	2.19	0.43
1:F:439:ILE:O	1:F:439:ILE:HG13	2.18	0.43
1:A:29:ARG:HG2	1:A:39:VAL:HB	2.00	0.43
1:A:545:THR:HB	1:A:549:LEU:HB2	2.01	0.43
1:E:77:ASP:HA	1:E:78:PRO:HD2	1.87	0.43
1:B:251:MET:HE1	1:B:367:GLY:HA3	1.99	0.43
1:C:251:MET:CE	1:C:367:GLY:HA3	2.49	0.43
1:D:271:HIS:O	1:D:275:VAL:HG12	2.19	0.43
1:D:414:LEU:HD21	1:D:464:VAL:HG21	2.00	0.43
1:D:225:ASP:HB2	1:D:462:PRO:HD2	2.00	0.43
1:A:238:TYR:HB3	1:A:275:VAL:HG21	2.01	0.43
1:C:84:LYS:HD2	1:C:140:LEU:HD12	2.01	0.43
1:D:55:GLY:HA2	1:D:58:LEU:HD12	1.99	0.43
1:E:431:ILE:HA	1:E:432:PRO:HD3	1.80	0.43
1:A:440:VAL:HG13	1:A:446:GLU:H	1.83	0.43
1:C:116:PRO:HB2	1:C:122:LYS:HG3	2.00	0.43
1:E:364:LYS:HB3	1:E:372:THR:HB	2.00	0.43
1:A:300:SER:HB2	1:A:344:HIS:CE1	2.54	0.43
1:A:439:ILE:O	1:A:439:ILE:HG13	2.18	0.43
1:D:486:PRO:HB3	1:D:518:LYS:HB2	2.01	0.43
1:A:572:VAL:HB	1:A:580:LEU:HB3	2.00	0.43
1:C:384:PHE:HD2	1:C:549:LEU:HG	1.84	0.43
1:D:390:GLU:OE1	1:D:529:ARG:HG2	2.19	0.43
1:F:55:GLY:HA2	1:F:58:LEU:HD12	2.00	0.43
1:B:173:THR:HB	1:B:375:THR:H	1.84	0.42
1:F:692:LYS:O	1:F:696:GLU:HB2	2.19	0.42
1:A:15:GLU:HB3	1:A:593:VAL:HG21	2.01	0.42
1:B:171:SER:OG	1:B:173:THR:HG23	2.19	0.42
1:B:416:ALA:HB3	1:B:468:PRO:HB3	2.01	0.42
1:B:486:PRO:HB3	1:B:518:LYS:HE3	2.00	0.42
1:E:169:GLN:HB3	1:F:174:HIS:CD2	2.54	0.42
1:E:198:VAL:HG12	1:E:441:ASP:HA	2.01	0.42
1:A:444:THR:O	1:A:445:GLY:C	2.58	0.42
1:E:642:LYS:O	1:E:646:GLU:HB2	2.19	0.42
1:B:386:ARG:CG	1:B:386:ARG:NH1	2.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:PHE:O	1:C:27:VAL:HG13	2.19	0.42
1:C:496:PRO:O	1:C:499:VAL:HG22	2.19	0.42
1:E:223:ILE:HB	1:E:464:VAL:HG13	2.00	0.42
1:C:286:LYS:HD3	1:C:286:LYS:HA	1.81	0.42
1:C:390:GLU:HG2	1:C:525:VAL:HG13	2.02	0.42
1:A:9:ILE:HG13	1:A:74:LEU:HD21	2.01	0.42
1:D:183:PHE:HB3	1:D:227:MET:HE2	2.02	0.42
1:D:735:THR:O	1:D:739:THR:OG1	2.38	0.42
1:E:251:MET:HE3	1:E:367:GLY:HA3	2.01	0.42
1:E:589:ALA:HB1	1:E:592:HIS:CD2	2.55	0.42
1:B:174:HIS:CD2	1:C:169:GLN:HB3	2.55	0.42
1:B:534:ARG:HB2	1:B:539:LYS:HB2	2.01	0.42
1:C:324:CYS:O	1:C:328:ARG:HB2	2.20	0.42
1:D:418:LYS:HB3	1:D:423:GLY:HA3	2.01	0.42
1:F:382:SER:O	1:F:386:ARG:HD3	2.20	0.42
1:F:533:GLU:HG3	1:F:537:ARG:HH12	1.84	0.42
1:A:201:VAL:HG12	1:A:211:VAL:HA	2.01	0.42
1:B:390:GLU:HG2	1:B:525:VAL:HG13	2.00	0.42
1:B:589:ALA:HB1	1:B:592:HIS:CD2	2.55	0.42
1:D:151:LYS:H	1:D:151:LYS:NZ	2.18	0.42
1:C:231:LYS:HD2	1:C:456:GLY:HA3	2.02	0.41
1:E:567:LYS:HG2	1:E:607:LEU:HD23	2.02	0.41
1:A:469:ILE:HD13	1:A:504:LYS:HD2	2.02	0.41
1:A:531:THR:O	1:A:535:VAL:HG13	2.20	0.41
1:C:572:VAL:HB	1:C:580:LEU:HB3	2.01	0.41
1:D:596:LEU:HD13	1:D:602:LEU:HB2	2.02	0.41
1:E:183:PHE:CD1	1:E:227:MET:HB3	2.54	0.41
1:F:153:VAL:HG12	1:F:562:LEU:HD22	2.01	0.41
1:A:387:MET:HG3	1:A:490:TRP:HZ3	1.84	0.41
1:B:19:LEU:HD11	1:B:593:VAL:HG13	2.01	0.41
1:E:86:PRO:HD3	1:E:583:THR:OG1	2.21	0.41
1:F:224:ILE:HG22	1:F:463:ILE:HG22	2.02	0.41
1:A:547:ASN:O	1:A:550:ARG:HB3	2.19	0.41
1:B:688:LYS:N	1:B:689:PRO:HD2	2.35	0.41
1:E:389:GLN:HE21	1:F:397:THR:HG22	1.86	0.41
1:F:56:ASP:OD2	1:F:127:ARG:NH2	2.53	0.41
1:F:572:VAL:HB	1:F:580:LEU:HB3	2.02	0.41
1:B:183:PHE:HB3	1:B:227:MET:HE3	2.01	0.41
1:C:25:LEU:HD11	1:C:41:THR:CG2	2.50	0.41
1:C:558:PRO:HG3	1:C:568:MET:HE1	2.02	0.41
1:C:583:THR:HG22	1:C:612:ALA:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:MET:HE1	1:A:332:ALA:HA	2.02	0.41
1:B:283:LYS:HD3	1:B:320:ASP:OD2	2.20	0.41
1:B:400:GLN:HE21	1:B:401:PHE:N	2.14	0.41
1:B:387:MET:HG2	1:B:528:MET:CE	2.50	0.41
1:C:251:MET:HE2	1:C:367:GLY:HA3	2.03	0.41
1:D:314:ARG:HA	1:D:317:ILE:HD12	2.01	0.41
1:F:227:MET:CE	1:F:460:ARG:HE	2.33	0.41
1:F:416:ALA:HB3	1:F:468:PRO:HB3	2.01	0.41
1:A:183:PHE:HB3	1:A:227:MET:HE3	2.03	0.41
1:A:445:GLY:CA	1:A:446:GLU:HB2	2.44	0.41
1:A:596:LEU:O	1:A:600:ASN:HA	2.21	0.41
1:F:200:MET:HG2	1:F:459:TRP:CH2	2.55	0.41
1:C:487:VAL:HG13	1:C:519:ILE:HG12	2.03	0.41
1:C:554:THR:O	1:C:558:PRO:HG2	2.20	0.41
1:E:273:VAL:HG11	1:E:299:LEU:HD13	2.02	0.41
1:B:147:ARG:HD2	1:B:554:THR:HB	2.02	0.41
1:B:232:LYS:O	1:B:235:ILE:HG13	2.21	0.40
1:C:171:SER:OG	1:C:173:THR:HG23	2.20	0.40
1:D:386:ARG:NH2	1:D:492:ASP:OD1	2.54	0.40
1:B:533:GLU:HG3	1:B:537:ARG:HH12	1.85	0.40
1:D:21:THR:O	1:D:25:LEU:HB2	2.20	0.40
1:E:252:PHE:CE1	1:E:378:VAL:HG21	2.56	0.40
1:F:213:LYS:HA	1:F:214:PRO:HD2	1.88	0.40
1:A:649:SER:HB3	1:A:650:PRO:HD2	2.03	0.40
1:D:173:THR:HG22	1:D:374:ASP:CB	2.51	0.40
1:F:15:GLU:OE1	1:F:588:SER:HB2	2.20	0.40
1:F:652:ARG:CG	1:F:652:ARG:HH11	2.34	0.40
1:F:688:LYS:N	1:F:689:PRO:HD2	2.37	0.40
1:A:196:ARG:HD3	1:A:441:ASP:OD2	2.22	0.40
1:B:619:ASP:HB3	1:B:623:LYS:HE2	2.04	0.40
1:C:251:MET:HE3	1:C:373:LYS:HD2	2.02	0.40
1:D:284:HIS:HB2	1:D:288:PHE:CE2	2.56	0.40
1:E:291:LEU:HD11	1:E:309:LEU:HD11	2.04	0.40
1:A:400:GLN:NE2	1:A:401:PHE:H	1.99	0.40
1:E:182:ASP:HB2	1:E:381:GLU:OE1	2.21	0.40
1:E:619:ASP:O	1:E:623:LYS:HB2	2.21	0.40
1:E:92:VAL:HB	1:E:93:PRO:HD3	2.03	0.40
1:F:230:SER:HB3	1:F:233:ALA:HB3	2.02	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	734/767 (96%)	713 (97%)	19 (3%)	2 (0%)	46	79
1	B	733/767 (96%)	708 (97%)	23 (3%)	2 (0%)	46	79
1	C	733/767 (96%)	712 (97%)	21 (3%)	0	100	100
1	D	733/767 (96%)	707 (96%)	26 (4%)	0	100	100
1	E	733/767 (96%)	708 (97%)	24 (3%)	1 (0%)	56	87
1	F	733/767 (96%)	706 (96%)	26 (4%)	1 (0%)	56	87
All	All	4399/4602 (96%)	4254 (97%)	139 (3%)	6 (0%)	56	87

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	444	THR
1	B	600	ASN
1	E	444	THR
1	F	515	GLU
1	A	445	GLY
1	A	446	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	620/646 (96%)	584 (94%)	36 (6%)	25	57
1	B	619/646 (96%)	579 (94%)	40 (6%)	21	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	619/646 (96%)	579 (94%)	40 (6%)	21	52
1	D	619/646 (96%)	574 (93%)	45 (7%)	17	44
1	E	619/646 (96%)	578 (93%)	41 (7%)	21	51
1	F	619/646 (96%)	584 (94%)	35 (6%)	25	58
All	All	3715/3876 (96%)	3478 (94%)	237 (6%)	22	52

All (237) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	25	LEU
1	A	40	LYS
1	A	57	HIS
1	A	68	LEU
1	A	70	GLU
1	A	81	ASN
1	A	124	ILE
1	A	132	LEU
1	A	151	LYS
1	A	173	THR
1	A	194	ARG
1	A	205	LYS
1	A	250	VAL
1	A	274	LYS
1	A	289	ASP
1	A	293	VAL
1	A	295	VAL
1	A	300	SER
1	A	302	LEU
1	A	318	ILE
1	A	328	ARG
1	A	342	ASN
1	A	397	THR
1	A	436	VAL
1	A	439	ILE
1	A	482	LEU
1	A	499	VAL
1	A	506	LYS
1	A	623	LYS
1	A	637	ASP
1	A	643	LEU

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Mol	Chain	Res	Type
1	A	654	THR
1	A	657	LEU
1	A	690	LEU
1	A	725	LYS
1	B	25	LEU
1	B	27	VAL
1	B	28	VAL
1	B	40	LYS
1	B	57	HIS
1	B	68	LEU
1	B	70	GLU
1	B	117	LYS
1	B	123	LYS
1	B	132	LEU
1	B	148	ARG
1	B	151	LYS
1	B	173	THR
1	B	194	ARG
1	B	227	MET
1	B	250	VAL
1	B	274	LYS
1	B	275	VAL
1	B	293	VAL
1	B	295	VAL
1	B	299	LEU
1	B	328	ARG
1	B	342	ASN
1	B	386	ARG
1	B	387	MET
1	B	397	THR
1	B	439	ILE
1	B	487	VAL
1	B	499	VAL
1	B	506	LYS
1	B	536	VAL
1	B	600	ASN
1	B	623	LYS
1	B	637	ASP
1	B	652	ARG
1	B	654	THR
1	B	657	LEU
1	B	690	LEU

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Mol	Chain	Res	Type
1	B	713	VAL
1	B	740	LEU
1	C	25	LEU
1	C	27	VAL
1	C	56	ASP
1	C	57	HIS
1	C	68	LEU
1	C	70	GLU
1	C	110	PRO
1	C	120	ASP
1	C	132	LEU
1	C	173	THR
1	C	194	ARG
1	C	196	ARG
1	C	274	LYS
1	C	275	VAL
1	C	286	LYS
1	C	295	VAL
1	C	314	ARG
1	C	328	ARG
1	C	342	ASN
1	C	379	ASN
1	C	387	MET
1	C	390	GLU
1	C	397	THR
1	C	408	THR
1	C	439	ILE
1	C	443	ASP
1	C	487	VAL
1	C	541	THR
1	C	568	MET
1	C	623	LYS
1	C	643	LEU
1	C	683	LEU
1	C	690	LEU
1	C	706	ASN
1	C	713	VAL
1	C	720	TYR
1	C	725	LYS
1	C	734	LYS
1	C	738	THR
1	C	740	LEU

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Mol	Chain	Res	Type
1	D	25	LEU
1	D	28	VAL
1	D	41	THR
1	D	68	LEU
1	D	70	GLU
1	D	100	LYS
1	D	119	ASP
1	D	130	LYS
1	D	132	LEU
1	D	147	ARG
1	D	151	LYS
1	D	173	THR
1	D	180	THR
1	D	194	ARG
1	D	250	VAL
1	D	259	THR
1	D	274	LYS
1	D	275	VAL
1	D	289	ASP
1	D	295	VAL
1	D	299	LEU
1	D	314	ARG
1	D	323	LYS
1	D	328	ARG
1	D	342	ASN
1	D	360	ARG
1	D	373	LYS
1	D	379	ASN
1	D	397	THR
1	D	439	ILE
1	D	463	ILE
1	D	493	THR
1	D	506	LYS
1	D	518	LYS
1	D	529	ARG
1	D	533	GLU
1	D	535	VAL
1	D	536	VAL
1	D	623	LYS
1	D	637	ASP
1	D	643	LEU
1	D	697	GLN

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Mol	Chain	Res	Type
1	D	713	VAL
1	D	725	LYS
1	D	734	LYS
1	E	57	HIS
1	E	68	LEU
1	E	70	GLU
1	E	124	ILE
1	E	130	LYS
1	E	132	LEU
1	E	151	LYS
1	E	172	ARG
1	E	173	THR
1	E	194	ARG
1	E	197	ARG
1	E	205	LYS
1	E	225	ASP
1	E	274	LYS
1	E	286	LYS
1	E	289	ASP
1	E	293	VAL
1	E	295	VAL
1	E	299	LEU
1	E	323	LYS
1	E	324	CYS
1	E	342	ASN
1	E	360	ARG
1	E	397	THR
1	E	436	VAL
1	E	439	ILE
1	E	442	ILE
1	E	463	ILE
1	E	487	VAL
1	E	506	LYS
1	E	588	SER
1	E	623	LYS
1	E	637	ASP
1	E	652	ARG
1	E	654	THR
1	E	657	LEU
1	E	688	LYS
1	E	690	LEU
1	E	696	GLU

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Mol	Chain	Res	Type
1	E	725	LYS
1	E	739	THR
1	F	56	ASP
1	F	57	HIS
1	F	68	LEU
1	F	70	GLU
1	F	108	ASN
1	F	132	LEU
1	F	159	LYS
1	F	173	THR
1	F	193	ASP
1	F	194	ARG
1	F	197	ARG
1	F	205	LYS
1	F	227	MET
1	F	286	LYS
1	F	289	ASP
1	F	293	VAL
1	F	295	VAL
1	F	299	LEU
1	F	324	CYS
1	F	325	HIS
1	F	328	ARG
1	F	342	ASN
1	F	360	ARG
1	F	397	THR
1	F	400	GLN
1	F	439	ILE
1	F	443	ASP
1	F	487	VAL
1	F	588	SER
1	F	619	ASP
1	F	623	LYS
1	F	652	ARG
1	F	657	LEU
1	F	666	LEU
1	F	725	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN

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Mol	Chain	Res	Type
1	A	108	ASN
1	A	325	HIS
1	A	344	HIS
1	A	379	ASN
1	A	400	GLN
1	A	451	GLN
1	A	520	GLN
1	A	672	GLN
1	A	706	ASN
1	B	325	HIS
1	B	393	ASN
1	B	400	GLN
1	B	451	GLN
1	B	592	HIS
1	B	594	HIS
1	B	672	GLN
1	B	706	ASN
1	C	108	ASN
1	C	325	HIS
1	C	379	ASN
1	C	400	GLN
1	C	592	HIS
1	C	672	GLN
1	C	706	ASN
1	D	108	ASN
1	D	379	ASN
1	D	393	ASN
1	D	400	GLN
1	D	592	HIS
1	D	672	GLN
1	D	697	GLN
1	E	108	ASN
1	E	325	HIS
1	E	379	ASN
1	E	400	GLN
1	E	451	GLN
1	E	672	GLN
1	F	108	ASN
1	F	325	HIS
1	F	327	HIS
1	F	379	ASN
1	F	393	ASN

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Mol	Chain	Res	Type
1	F	400	GLN
1	F	592	HIS
1	F	672	GLN
1	F	677	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	ICT	A	802	2	2,12,12	0.53	0	2,16,16	0.84	0
3	ICT	B	802	2	2,12,12	0.50	0	2,16,16	0.44	0
3	ICT	C	802	2	2,12,12	0.53	0	2,16,16	0.68	0
3	ICT	D	802	2	2,12,12	0.49	0	2,16,16	0.62	0
3	ICT	E	802	2	2,12,12	0.53	0	2,16,16	0.37	0
3	ICT	F	802	2	2,12,12	0.39	0	2,16,16	0.66	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
3	ICT	A	802	2	-	0/6/16/16	0/0/0/0
3	ICT	B	802	2	-	0/6/16/16	0/0/0/0
3	ICT	C	802	2	-	0/6/16/16	0/0/0/0
3	ICT	D	802	2	-	0/6/16/16	0/0/0/0
3	ICT	E	802	2	-	0/6/16/16	0/0/0/0
3	ICT	F	802	2	-	0/6/16/16	0/0/0/0

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 ⓘ

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	735/767 (95%)	-0.16	4 (0%)	91 88	37, 57, 86, 116	0
1	B	735/767 (95%)	-0.14	3 (0%)	93 90	41, 61, 91, 112	0
1	C	735/767 (95%)	-0.14	4 (0%)	91 88	42, 64, 95, 127	0
1	D	735/767 (95%)	-0.07	6 (0%)	87 81	39, 68, 102, 118	0
1	E	735/767 (95%)	0.05	8 (1%)	82 74	49, 71, 97, 126	0
1	F	735/767 (95%)	0.07	18 (2%)	62 50	48, 73, 105, 135	0
All	All	4410/4602 (95%)	-0.06	43 (0%)	84 77	37, 66, 98, 135	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	690	LEU	5.1
1	B	445	GLY	3.2
1	E	206	SER	3.1
1	D	205	LYS	3.1
1	E	734	LYS	3.1
1	F	444	THR	3.0
1	F	515	GLU	3.0
1	F	697	GLN	3.0
1	F	698	GLU	2.9
1	F	694	LEU	2.8
1	A	685	GLU	2.7
1	D	212	LEU	2.7
1	F	117	LYS	2.7
1	D	685	GLU	2.7
1	E	442	ILE	2.7
1	A	681	ALA	2.6
1	F	212	LEU	2.6
1	F	689	PRO	2.6
1	F	632	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	205	LYS	2.6
1	F	687	PHE	2.6
1	D	675	ALA	2.5
1	B	205	LYS	2.5
1	F	206	SER	2.5
1	D	682	GLU	2.5
1	F	696	GLU	2.4
1	E	217	LYS	2.4
1	E	681	ALA	2.4
1	E	439	ILE	2.3
1	E	211	VAL	2.3
1	C	117	LYS	2.2
1	F	31	PHE	2.1
1	F	678	THR	2.1
1	B	208	GLU	2.1
1	C	678	THR	2.1
1	D	688	LYS	2.1
1	C	118	THR	2.1
1	F	688	LYS	2.1
1	E	214	PRO	2.1
1	A	439	ILE	2.0
1	F	202	LEU	2.0
1	A	445	GLY	2.0
1	F	702	VAL	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(\AA^2)	Q<0.9
3	ICT	F	802	13/13	0.93	0.24	1.89	70,75,79,80	0
3	ICT	B	802	13/13	0.95	0.22	0.85	57,58,61,61	0
3	ICT	E	802	13/13	0.95	0.22	0.72	64,68,72,74	0
2	MN	F	801	1/1	0.98	0.22	0.69	80,80,80,80	0
3	ICT	A	802	13/13	0.96	0.20	0.25	57,59,60,61	0
2	MN	E	801	1/1	0.96	0.20	0.02	86,86,86,86	0
3	ICT	C	802	13/13	0.95	0.20	-0.08	58,59,63,63	0
3	ICT	D	802	13/13	0.94	0.17	-0.46	60,64,71,73	0
2	MN	C	801	1/1	0.96	0.19	-0.87	68,68,68,68	0
2	MN	B	801	1/1	0.96	0.17	-1.70	65,65,65,65	0
2	MN	A	801	1/1	0.98	0.23	-	66,66,66,66	0
2	MN	D	801	1/1	0.98	0.22	-	70,70,70,70	0

6.5 Other polymers ⓘ

There are no such residues in this entry.