



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:30 AM GMT

PDB ID : 3B3D  
Title : B.subtilis YtbE  
Authors : Zhou, Y.F.; Li, L.F.; Liang, Y.H.; Su, X.-D.  
Deposited on : 2007-10-20  
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](mailto: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.

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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

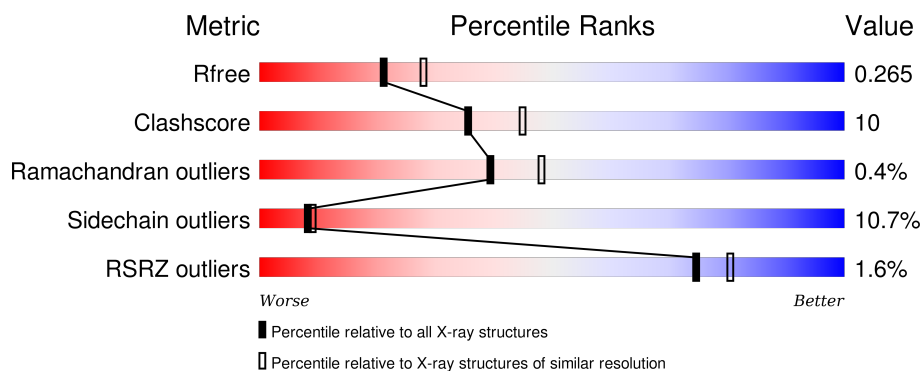
# 1 Overall quality at a glance

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  $\geq 3$ , 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	314	<div> <div>2%</div> <div>67% 16% 5% • 11%</div> </div>
1	B	314	<div> <div>%</div> <div>71% 13% • 12%</div> </div>
1	C	314	<div> <div>%</div> <div>71% 15% • • 11%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7067 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 Putative morphine dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	2	0
			2253	1432	382	431	8			
1	B	277	Total	C	N	O	S	0	6	0
			2271	1447	386	430	8			
1	C	280	Total	C	N	O	S	0	5	0
			2283	1454	387	433	9			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	EXPRESSION TAG	UNP O34678
A	-32	GLY	-	EXPRESSION TAG	UNP O34678
A	-31	SER	-	EXPRESSION TAG	UNP O34678
A	-30	SER	-	EXPRESSION TAG	UNP O34678
A	-29	HIS	-	EXPRESSION TAG	UNP O34678
A	-28	HIS	-	EXPRESSION TAG	UNP O34678
A	-27	HIS	-	EXPRESSION TAG	UNP O34678
A	-26	HIS	-	EXPRESSION TAG	UNP O34678
A	-25	HIS	-	EXPRESSION TAG	UNP O34678
A	-24	HIS	-	EXPRESSION TAG	UNP O34678
A	-23	SER	-	EXPRESSION TAG	UNP O34678
A	-22	SER	-	EXPRESSION TAG	UNP O34678
A	-21	GLY	-	EXPRESSION TAG	UNP O34678
A	-20	LEU	-	EXPRESSION TAG	UNP O34678
A	-19	VAL	-	EXPRESSION TAG	UNP O34678
A	-18	PRO	-	EXPRESSION TAG	UNP O34678
A	-17	ARG	-	EXPRESSION TAG	UNP O34678
A	-16	GLY	-	EXPRESSION TAG	UNP O34678
A	-15	SER	-	EXPRESSION TAG	UNP O34678
A	-14	HIS	-	EXPRESSION TAG	UNP O34678
A	-13	MET	-	EXPRESSION TAG	UNP O34678
A	-12	ALA	-	EXPRESSION TAG	UNP O34678
A	-11	SER	-	EXPRESSION TAG	UNP O34678

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	EXPRESSION TAG	UNP O34678
A	-9	THR	-	EXPRESSION TAG	UNP O34678
A	-8	GLY	-	EXPRESSION TAG	UNP O34678
A	-7	GLY	-	EXPRESSION TAG	UNP O34678
A	-6	GLN	-	EXPRESSION TAG	UNP O34678
A	-5	GLN	-	EXPRESSION TAG	UNP O34678
A	-4	MET	-	EXPRESSION TAG	UNP O34678
A	-3	GLY	-	EXPRESSION TAG	UNP O34678
A	-2	ARG	-	EXPRESSION TAG	UNP O34678
A	-1	GLY	-	EXPRESSION TAG	UNP O34678
A	0	SER	-	EXPRESSION TAG	UNP O34678
B	-33	MET	-	EXPRESSION TAG	UNP O34678
B	-32	GLY	-	EXPRESSION TAG	UNP O34678
B	-31	SER	-	EXPRESSION TAG	UNP O34678
B	-30	SER	-	EXPRESSION TAG	UNP O34678
B	-29	HIS	-	EXPRESSION TAG	UNP O34678
B	-28	HIS	-	EXPRESSION TAG	UNP O34678
B	-27	HIS	-	EXPRESSION TAG	UNP O34678
B	-26	HIS	-	EXPRESSION TAG	UNP O34678
B	-25	HIS	-	EXPRESSION TAG	UNP O34678
B	-24	HIS	-	EXPRESSION TAG	UNP O34678
B	-23	SER	-	EXPRESSION TAG	UNP O34678
B	-22	SER	-	EXPRESSION TAG	UNP O34678
B	-21	GLY	-	EXPRESSION TAG	UNP O34678
B	-20	LEU	-	EXPRESSION TAG	UNP O34678
B	-19	VAL	-	EXPRESSION TAG	UNP O34678
B	-18	PRO	-	EXPRESSION TAG	UNP O34678
B	-17	ARG	-	EXPRESSION TAG	UNP O34678
B	-16	GLY	-	EXPRESSION TAG	UNP O34678
B	-15	SER	-	EXPRESSION TAG	UNP O34678
B	-14	HIS	-	EXPRESSION TAG	UNP O34678
B	-13	MET	-	EXPRESSION TAG	UNP O34678
B	-12	ALA	-	EXPRESSION TAG	UNP O34678
B	-11	SER	-	EXPRESSION TAG	UNP O34678
B	-10	MET	-	EXPRESSION TAG	UNP O34678
B	-9	THR	-	EXPRESSION TAG	UNP O34678
B	-8	GLY	-	EXPRESSION TAG	UNP O34678
B	-7	GLY	-	EXPRESSION TAG	UNP O34678
B	-6	GLN	-	EXPRESSION TAG	UNP O34678
B	-5	GLN	-	EXPRESSION TAG	UNP O34678
B	-4	MET	-	EXPRESSION TAG	UNP O34678
B	-3	GLY	-	EXPRESSION TAG	UNP O34678

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	ARG	-	EXPRESSION TAG	UNP O34678
B	-1	GLY	-	EXPRESSION TAG	UNP O34678
B	0	SER	-	EXPRESSION TAG	UNP O34678
C	-33	MET	-	EXPRESSION TAG	UNP O34678
C	-32	GLY	-	EXPRESSION TAG	UNP O34678
C	-31	SER	-	EXPRESSION TAG	UNP O34678
C	-30	SER	-	EXPRESSION TAG	UNP O34678
C	-29	HIS	-	EXPRESSION TAG	UNP O34678
C	-28	HIS	-	EXPRESSION TAG	UNP O34678
C	-27	HIS	-	EXPRESSION TAG	UNP O34678
C	-26	HIS	-	EXPRESSION TAG	UNP O34678
C	-25	HIS	-	EXPRESSION TAG	UNP O34678
C	-24	HIS	-	EXPRESSION TAG	UNP O34678
C	-23	SER	-	EXPRESSION TAG	UNP O34678
C	-22	SER	-	EXPRESSION TAG	UNP O34678
C	-21	GLY	-	EXPRESSION TAG	UNP O34678
C	-20	LEU	-	EXPRESSION TAG	UNP O34678
C	-19	VAL	-	EXPRESSION TAG	UNP O34678
C	-18	PRO	-	EXPRESSION TAG	UNP O34678
C	-17	ARG	-	EXPRESSION TAG	UNP O34678
C	-16	GLY	-	EXPRESSION TAG	UNP O34678
C	-15	SER	-	EXPRESSION TAG	UNP O34678
C	-14	HIS	-	EXPRESSION TAG	UNP O34678
C	-13	MET	-	EXPRESSION TAG	UNP O34678
C	-12	ALA	-	EXPRESSION TAG	UNP O34678
C	-11	SER	-	EXPRESSION TAG	UNP O34678
C	-10	MET	-	EXPRESSION TAG	UNP O34678
C	-9	THR	-	EXPRESSION TAG	UNP O34678
C	-8	GLY	-	EXPRESSION TAG	UNP O34678
C	-7	GLY	-	EXPRESSION TAG	UNP O34678
C	-6	GLN	-	EXPRESSION TAG	UNP O34678
C	-5	GLN	-	EXPRESSION TAG	UNP O34678
C	-4	MET	-	EXPRESSION TAG	UNP O34678
C	-3	GLY	-	EXPRESSION TAG	UNP O34678
C	-2	ARG	-	EXPRESSION TAG	UNP O34678
C	-1	GLY	-	EXPRESSION TAG	UNP O34678
C	0	SER	-	EXPRESSION TAG	UNP O34678

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

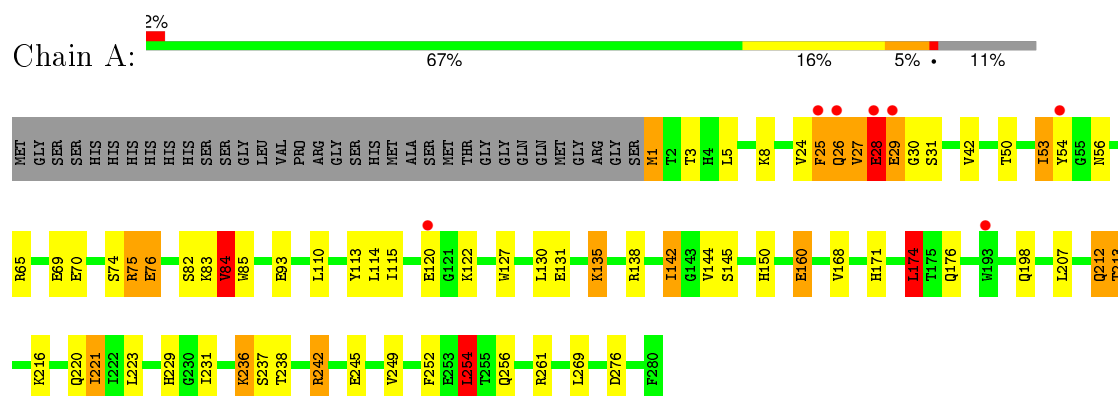
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	92	Total O 92 92	0	0
3	B	81	Total O 81 81	0	0
3	C	83	Total O 83 83	0	0

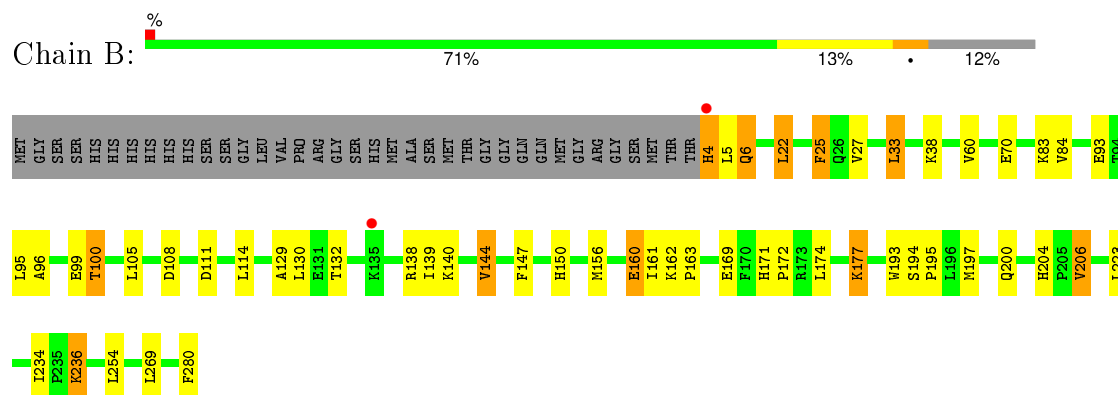
### 3 Residue-property plots [i](#)

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.

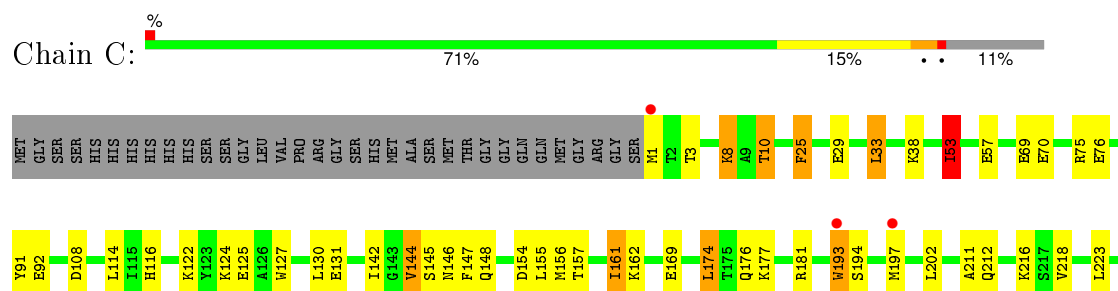
#### • Molecule 1: Putative morphine dehydrogenase

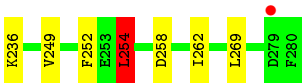


#### • Molecule 1: Putative morphine dehydrogenase



#### • Molecule 1: Putative morphine dehydrogenase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.11Å 89.17Å 115.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 41.55 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.2 (20.00-2.30) 97.2 (41.55-2.30)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.90 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.192 , 0.260 0.198 , 0.265	Depositor DCC
$R_{free}$ test set	1883 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.0	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 39.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 37935 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7067	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: CA

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	0/2302	0.91	7/3119 (0.2%)
1	B	0.86	1/2322 (0.0%)	0.86	3/3144 (0.1%)
1	C	0.79	0/2334	0.82	5/3162 (0.2%)
All	All	0.83	1/6958 (0.0%)	0.86	15/9425 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	3	1
1	B	1	0
1	C	1	0
All	All	5	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	280	PHE	C-OXT	-10.27	1.03	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	ARG	NE-CZ-NH2	-10.15	115.22	120.30
1	C	53	ILE	CB-CA-C	-7.67	96.26	111.60
1	A	65	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	B	84	VAL	CB-CA-C	-6.30	99.43	111.40
1	B	22	LEU	CA-CB-CG	6.17	129.50	115.30
1	C	174	LEU	CA-CB-CG	5.83	128.72	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	254	LEU	CA-CB-CG	5.58	128.14	115.30
1	C	108	ASP	CB-CG-OD2	5.57	123.31	118.30
1	B	108	ASP	CB-CG-OD1	5.47	123.23	118.30
1	A	138	ARG	NE-CZ-NH2	5.42	123.01	120.30
1	A	84	VAL	CB-CA-C	-5.40	101.13	111.40
1	C	130	LEU	CA-CB-CG	5.31	127.51	115.30
1	A	174	LEU	CA-CB-CG	5.11	127.06	115.30
1	C	254	LEU	CB-CG-CD1	5.01	119.52	111.00
1	A	65	ARG	CG-CD-NE	-5.01	101.28	111.80

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	26	GLN	CA
1	A	28	GLU	CA
1	A	142	ILE	CB
1	B	140[B]	LYS	CA
1	C	1	MET	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27	VAL	Peptide

## 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	2253	0	2203	48	1
1	B	2271	0	2218	47	0
1	C	2283	0	2228	36	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	92	0	0	4	0
3	B	81	0	0	3	1
3	C	83	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7067	0	6649	131	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 10.

All (131) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156[B]:MET:CE	1:B:163:PRO:HD3	1.97	0.94
1:A:1:MET:O	3:A:359:HOH:O	1.88	0.90
1:C:8:LYS:NZ	3:C:426:HOH:O	2.07	0.88
1:B:156[B]:MET:HE1	1:B:163:PRO:HD3	1.56	0.85
1:A:135:LYS:HE3	1:A:160:GLU:OE1	1.84	0.78
1:A:24:VAL:O	1:A:54:TYR:OH	2.01	0.78
1:A:50:THR:HA	1:A:54:TYR:CE2	2.21	0.76
1:C:169:GLU:HG3	1:C:197[A]:MET:HE3	1.68	0.74
1:B:83:LYS:HG2	1:B:114:LEU:HB2	1.71	0.72
1:A:245:GLU:OE2	3:A:367:HOH:O	2.08	0.72
1:C:38:LYS:HD3	3:C:400:HOH:O	1.90	0.70
1:C:142:ILE:HD11	1:C:161:ILE:CD1	2.22	0.70
1:B:156[B]:MET:HE3	1:B:163:PRO:HD3	1.73	0.69
1:A:229:HIS:HB3	1:A:231:ILE:HD12	1.75	0.68
1:B:111:ASP:OD1	1:B:140[B]:LYS:HE3	1.92	0.68
1:B:140[B]:LYS:HB2	3:B:360:HOH:O	1.93	0.67
1:C:169:GLU:HG3	1:C:197[A]:MET:CE	2.25	0.67
1:A:150:HIS:HE1	1:A:276:ASP:OD1	1.77	0.67
1:B:156[B]:MET:HE3	1:B:163:PRO:CD	2.26	0.65
1:C:142:ILE:HD11	1:C:161:ILE:HD12	1.80	0.64
1:B:177:LYS:HE3	3:B:344:HOH:O	1.98	0.63
1:C:75:ARG:HD3	1:C:75:ARG:O	1.98	0.62
1:B:156[B]:MET:CE	1:B:163:PRO:CD	2.75	0.62
1:C:10:THR:HG22	3:C:366:HOH:O	2.01	0.61
1:C:177:LYS:HE3	3:C:420:HOH:O	2.01	0.61
1:C:194:SER:O	1:C:197[A]:MET:HE2	2.01	0.60
1:C:91:TYR:HB2	1:C:125:GLU:HG3	1.83	0.60
1:B:5:LEU:HB3	1:B:6:GLN:HE21	1.65	0.60
1:C:177:LYS:CE	3:C:420:HOH:O	2.48	0.60
1:C:124:LYS:HE3	1:C:154:ASP:OD2	2.01	0.60
1:B:150:HIS:HD2	3:B:305:HOH:O	1.85	0.58
1:A:24:VAL:O	1:A:54:TYR:CZ	2.57	0.58
1:C:194:SER:HB2	1:C:197[A]:MET:CE	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ILE:HG13	1:A:85:TRP:CE2	2.39	0.57
1:B:193[A]:TRP:CE3	1:B:236[A]:LYS:NZ	2.73	0.56
1:A:83:LYS:HE3	1:A:114:LEU:HD12	1.87	0.56
1:C:148:GLN:NE2	3:C:382:HOH:O	2.38	0.56
1:B:156[B]:MET:HE1	1:B:162:LYS:HA	1.87	0.56
1:A:24:VAL:HB	1:A:54:TYR:CE2	2.41	0.56
1:A:261:ARG:HD2	3:A:370:HOH:O	2.06	0.56
1:C:57:GLU:HG3	3:C:359:HOH:O	2.06	0.56
1:A:42:VAL:CG2	1:A:70:GLU:HG2	2.36	0.55
1:A:24:VAL:HB	1:A:54:TYR:HE2	1.71	0.54
1:B:25:PHE:HB2	1:B:236[B]:LYS:NZ	2.22	0.54
1:B:156[A]:MET:CE	1:B:162:LYS:HD3	2.37	0.54
1:A:150:HIS:CE1	1:A:276:ASP:OD1	2.60	0.54
1:A:53:ILE:HG13	1:A:85:TRP:CD2	2.42	0.54
1:A:207:LEU:CD2	1:A:221:ILE:HD11	2.38	0.54
1:B:194:SER:N	1:B:236[A]:LYS:HE2	2.23	0.53
1:B:156[A]:MET:HE2	1:B:162:LYS:CD	2.39	0.53
1:A:50:THR:HA	1:A:54:TYR:HE2	1.73	0.52
1:A:28:GLU:O	1:A:29:GLU:HB3	2.09	0.52
1:C:211:ALA:HB1	1:C:216:LYS:O	2.10	0.52
1:C:53:ILE:HD11	1:C:116:HIS:CE1	2.45	0.52
1:B:234:ILE:O	1:B:236[A]:LYS:HD2	2.10	0.52
1:A:27:VAL:HG12	1:A:28:GLU:HA	1.92	0.52
1:A:114:LEU:HD13	1:A:145[B]:SER:OG	2.10	0.51
1:A:75:ARG:C	1:A:75:ARG:HD3	2.29	0.51
1:A:237:SER:OG	1:A:242:ARG:HG2	2.10	0.51
1:A:50:THR:OG1	1:A:54:TYR:CD2	2.55	0.51
1:B:195:PRO:HD2	1:B:236[A]:LYS:HE2	1.94	0.50
1:A:28:GLU:O	1:A:29:GLU:CB	2.58	0.50
1:B:25:PHE:HB2	1:B:236[B]:LYS:HZ2	1.77	0.50
1:B:236[A]:LYS:CD	1:B:236[A]:LYS:N	2.75	0.50
1:A:127:TRP:CH2	1:A:142:ILE:HG13	2.46	0.50
1:B:96:ALA:O	1:B:100:THR:HG23	2.12	0.49
1:C:202:LEU:HA	1:C:218:VAL:HG11	1.93	0.49
1:B:38:LYS:HD2	1:B:70:GLU:OE2	2.13	0.48
1:B:4:HIS:N	1:B:4:HIS:CD2	2.81	0.48
1:A:130:LEU:HD13	1:A:142:ILE:HG22	1.95	0.48
1:A:252:PHE:HE1	1:A:254:LEU:HD13	1.79	0.48
1:A:30:GLY:O	1:A:31:SER:C	2.51	0.48
1:C:193[B]:TRP:HE3	3:C:423:HOH:O	1.95	0.48
1:A:236:LYS:O	1:A:237:SER:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:ARG:HD3	1:C:75:ARG:C	2.34	0.47
1:C:146:ASN:ND2	3:C:368:HOH:O	2.45	0.47
1:A:50:THR:CA	1:A:54:TYR:CE2	2.95	0.47
1:A:42:VAL:HG22	1:A:70:GLU:HG2	1.97	0.47
1:C:194:SER:HB2	1:C:197[A]:MET:HE2	1.96	0.47
1:B:204:HIS:CE1	1:B:206:VAL:HG13	2.50	0.47
1:C:114:LEU:HD13	1:C:145[B]:SER:OG	2.15	0.46
1:A:242:ARG:HH11	1:A:242:ARG:HG3	1.79	0.46
1:A:207:LEU:HD22	1:A:221:ILE:HD11	1.97	0.46
1:B:60:VAL:HG22	1:B:105:LEU:CD2	2.46	0.46
1:B:160:GLU:HG2	1:B:161:ILE:HG13	1.98	0.46
1:C:38:LYS:HE2	1:C:70:GLU:OE2	2.16	0.45
1:C:252:PHE:HE1	1:C:254:LEU:HD13	1.81	0.45
1:B:156[A]:MET:HE2	1:B:162:LYS:HE2	1.98	0.45
1:A:42:VAL:HG21	1:A:70:GLU:HG2	1.98	0.45
1:C:177:LYS:HD3	1:C:181:ARG:NH2	2.32	0.45
1:A:29:GLU:OE2	1:A:56:ASN:HA	2.17	0.45
1:B:6:GLN:H	1:B:6:GLN:HG2	1.62	0.44
1:C:127:TRP:CG	1:C:155:LEU:HD11	2.53	0.44
1:C:258:ASP:O	1:C:262:ILE:HG13	2.18	0.44
1:A:113:TYR:HD2	1:A:130:LEU:HD22	1.81	0.44
1:B:129:ALA:O	1:B:132:THR:HG22	2.18	0.44
1:A:171:HIS:CE1	1:A:174:LEU:HB2	2.52	0.44
1:C:144:VAL:HG22	1:C:147:PHE:CE2	2.52	0.44
1:A:131:GLU:O	1:A:135:LYS:HD3	2.17	0.44
1:A:207:LEU:HD23	1:A:221:ILE:HD11	1.99	0.44
1:C:25:PHE:HB3	1:C:236[B]:LYS:HD3	1.99	0.44
1:A:93:GLU:HG2	3:A:368:HOH:O	2.18	0.43
1:B:144:VAL:HG22	1:B:147:PHE:CE2	2.53	0.43
1:A:212:GLN:HG3	1:A:213:THR:N	2.33	0.43
1:A:74:SER:HB3	1:A:76:GLU:HG2	2.01	0.43
1:B:156[A]:MET:HE2	1:B:162:LYS:HD3	2.00	0.43
1:A:216:LYS:HD2	1:A:252:PHE:CD2	2.54	0.43
1:C:131:GLU:HG2	1:C:161:ILE:HG23	2.00	0.43
1:C:169:GLU:CG	1:C:197[A]:MET:HE3	2.43	0.42
1:B:140[B]:LYS:HA	1:B:140[B]:LYS:HD2	1.50	0.42
1:B:144:VAL:HG13	1:B:147:PHE:HB2	2.01	0.42
1:B:171:HIS:HB2	1:B:172:PRO:HD2	2.00	0.42
1:A:84:VAL:HG23	1:A:115:ILE:HA	2.01	0.42
1:C:29:GLU:HA	1:C:33:LEU:HD12	2.01	0.42
1:B:99:GLU:OE2	1:B:138:ARG:NH2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:LEU:HD21	1:B:132:THR:CG2	2.49	0.42
1:B:197:MET:O	1:B:200:GLN:HG3	2.20	0.41
1:C:169:GLU:HB2	1:C:193[A]:TRP:HZ3	1.84	0.41
1:A:25:PHE:CD1	1:A:236:LYS:HE3	2.55	0.41
1:B:171:HIS:HB2	1:B:172:PRO:CD	2.50	0.41
1:B:156[A]:MET:HE2	1:B:162:LYS:CE	2.51	0.41
1:B:156[B]:MET:HE3	1:B:163:PRO:HD2	2.02	0.41
1:A:220:GLN:NE2	1:A:245:GLU:HG2	2.36	0.41
1:B:169:GLU:HB2	1:B:193[B]:TRP:CE3	2.56	0.41
1:A:24:VAL:HG12	1:A:25:PHE:H	1.86	0.41
1:C:127:TRP:CD1	1:C:155:LEU:HD11	2.55	0.40
1:B:5:LEU:HB3	1:B:6:GLN:NE2	2.34	0.40
1:B:27:VAL:HG23	1:B:33:LEU:HG	2.03	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)
1:A:122:LYS:NZ	3:B:333:HOH:O[2_455]	1.79	0.41

## 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	280/314 (89%)	266 (95%)	11 (4%)	3 (1%)	17	18
1	B	281/314 (90%)	273 (97%)	8 (3%)	0	100	100
1	C	283/314 (90%)	275 (97%)	8 (3%)	0	100	100
All	All	844/942 (90%)	814 (96%)	27 (3%)	3 (0%)	39	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	29	GLU
1	A	28	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	240/264 (91%)	206 (86%)	34 (14%)	4	4
1	B	241/264 (91%)	222 (92%)	19 (8%)	15	19
1	C	242/264 (92%)	217 (90%)	25 (10%)	9	10
All	All	723/792 (91%)	645 (89%)	78 (11%)	8	9

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	THR
1	A	5	LEU
1	A	8	LYS
1	A	25	PHE
1	A	26	GLN
1	A	28	GLU
1	A	53	ILE
1	A	69	GLU
1	A	75	ARG
1	A	76	GLU
1	A	82	SER
1	A	84	VAL
1	A	110	LEU
1	A	120	GLU
1	A	135	LYS
1	A	142	ILE
1	A	144	VAL
1	A	160	GLU
1	A	168	VAL

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Mol	Chain	Res	Type
1	A	174	LEU
1	A	176	GLN
1	A	198	GLN
1	A	212	GLN
1	A	213	THR
1	A	221	ILE
1	A	223	LEU
1	A	236	LYS
1	A	238	THR
1	A	242	ARG
1	A	249	VAL
1	A	254	LEU
1	A	256	GLN
1	A	269	LEU
1	B	4	HIS
1	B	6	GLN
1	B	22	LEU
1	B	25	PHE
1	B	33	LEU
1	B	93	GLU
1	B	100	THR
1	B	130	LEU
1	B	139	ILE
1	B	144	VAL
1	B	160	GLU
1	B	174	LEU
1	B	177	LYS
1	B	206	VAL
1	B	223	LEU
1	B	236[A]	LYS
1	B	236[B]	LYS
1	B	254	LEU
1	B	269	LEU
1	C	1	MET
1	C	3	THR
1	C	8	LYS
1	C	10	THR
1	C	25	PHE
1	C	33	LEU
1	C	53	ILE
1	C	69	GLU
1	C	76	GLU

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Mol	Chain	Res	Type
1	C	92	GLU
1	C	122	LYS
1	C	144	VAL
1	C	156	MET
1	C	157	THR
1	C	161	ILE
1	C	162	LYS
1	C	174	LEU
1	C	176	GLN
1	C	193[A]	TRP
1	C	193[B]	TRP
1	C	212	GLN
1	C	223	LEU
1	C	249	VAL
1	C	254	LEU
1	C	269	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	26	GLN
1	A	150	HIS
1	A	166	ASN
1	A	176	GLN
1	A	200	GLN
1	B	6	GLN
1	B	146	ASN
1	B	166	ASN
1	B	198	GLN
1	C	6	GLN
1	C	12	HIS
1	C	146	ASN
1	C	148	GLN
1	C	166	ASN
1	C	176	GLN
1	C	215	ASN
1	C	229	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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	280/314 (89%)	-0.13	7 (2%) 61 70	17, 24, 36, 49	3 (1%)
1	B	277/314 (88%)	-0.26	2 (0%) 89 92	18, 24, 34, 46	0
1	C	280/314 (89%)	-0.13	4 (1%) 78 83	18, 24, 33, 41	0
All	All	837/942 (88%)	-0.17	13 (1%) 74 80	17, 24, 34, 49	3 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	GLU	10.7
1	A	54	TYR	5.4
1	A	193	TRP	3.9
1	A	25	PHE	3.5
1	C	1	MET	3.3
1	A	26	GLN	3.0
1	A	29	GLU	2.8
1	C	279	ASP	2.5
1	C	193[A]	TRP	2.5
1	C	197[A]	MET	2.3
1	B	4	HIS	2.1
1	A	120	GLU	2.1
1	B	135	LYS	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	CA	B	281	1/1	0.98	0.16	0.36	31,31,31,31	0
2	CA	C	281	1/1	0.99	0.14	-0.24	25,25,25,25	0
2	CA	A	281	1/1	0.98	0.06	-3.22	23,23,23,23	0
2	CA	A	282	1/1	0.92	0.08	-	51,51,51,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.