



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 4, 2026 – 11:34 PM UTC

PDB ID : 2WVH / pdb_00002wvh
Title : Structural insights into the pre-reaction state of pyruvate decarboxylase from
Zymomonas mobilis
Authors : Pei, X.Y.; Erixon, K.; Luisi, B.F.; Leeper, F.J.
Deposited on : 2009-10-16
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

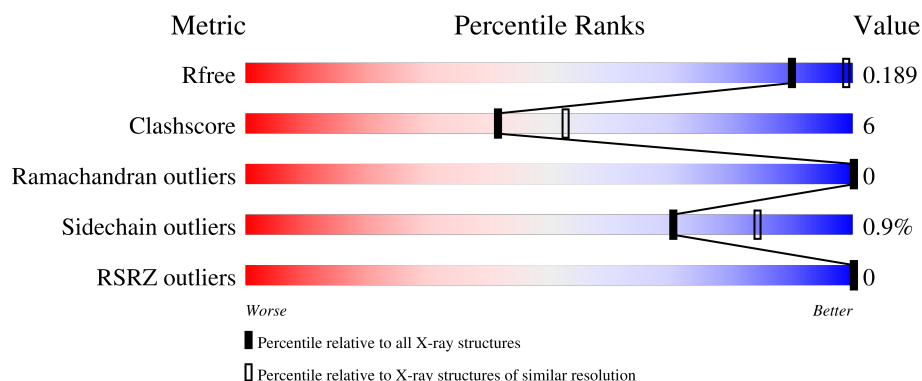
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	568	86% 13%
1	B	568	87% 12% .
1	E	568	87% 12% ..
1	F	568	85% 13% ..
1	V	568	87% 12% .

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Mol	Chain	Length	Quality of chain
1	X	568	 86% 13% .
1	Y	568	 88% 11% ..
1	Z	568	 87% 12% .

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 38331 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 PYRUVATE DECARBOXYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	566	Total	C	N	O	S	0	1	0
			4281	2724	730	808	19			
1	B	565	Total	C	N	O	S	0	1	0
			4276	2720	730	808	18			
1	E	565	Total	C	N	O	S	0	1	0
			4273	2719	729	807	18			
1	F	565	Total	C	N	O	S	0	1	0
			4273	2719	729	807	18			
1	V	565	Total	C	N	O	S	0	1	0
			4273	2719	729	807	18			
1	X	564	Total	C	N	O	S	0	1	0
			4264	2713	727	806	18			
1	Y	565	Total	C	N	O	S	0	1	0
			4273	2719	729	807	18			
1	Z	565	Total	C	N	O	S	0	1	0
			4273	2719	729	807	18			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	614	Total	O	0	0
			614	614		
2	B	479	Total	O	0	0
			479	479		
2	E	546	Total	O	0	0
			546	546		
2	F	522	Total	O	0	0
			522	522		
2	V	482	Total	O	0	0
			482	482		
2	X	486	Total	O	0	0
			486	486		

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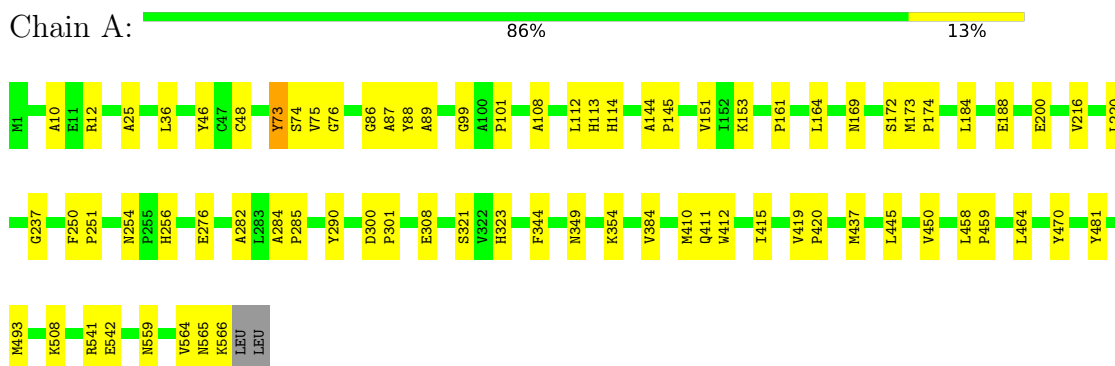
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	Y	503	Total 503	O 503	0	0
2	Z	513	Total 513	O 513	0	0

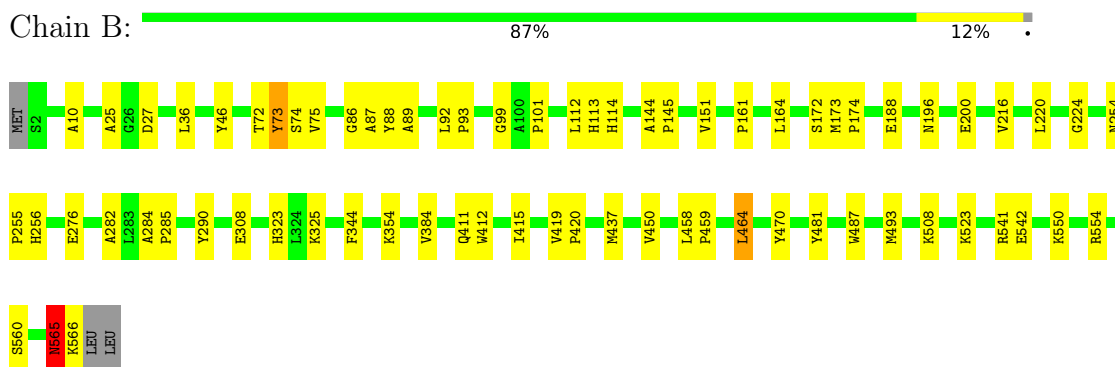
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

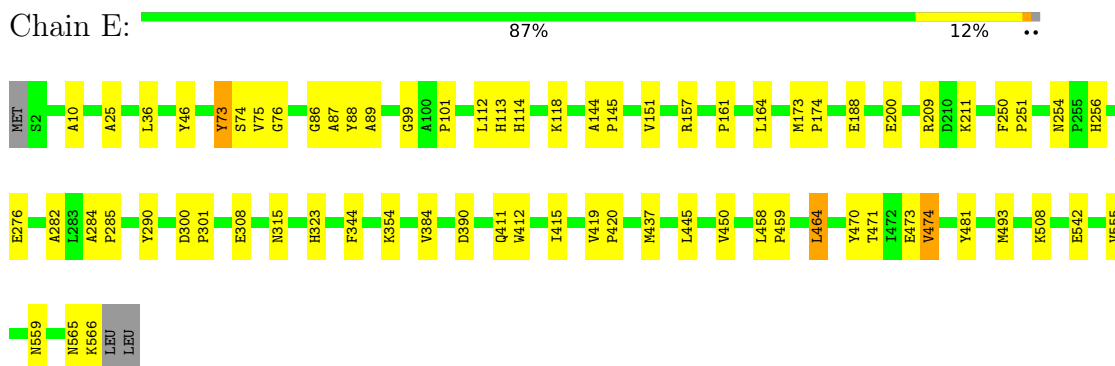
• Molecule 1: PYRUVATE DECARBOXYLASE



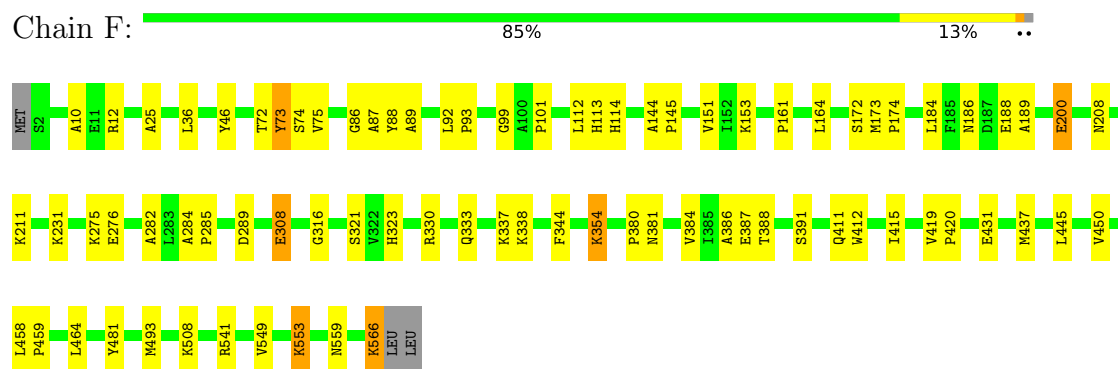
• Molecule 1: PYRUVATE DECARBOXYLASE



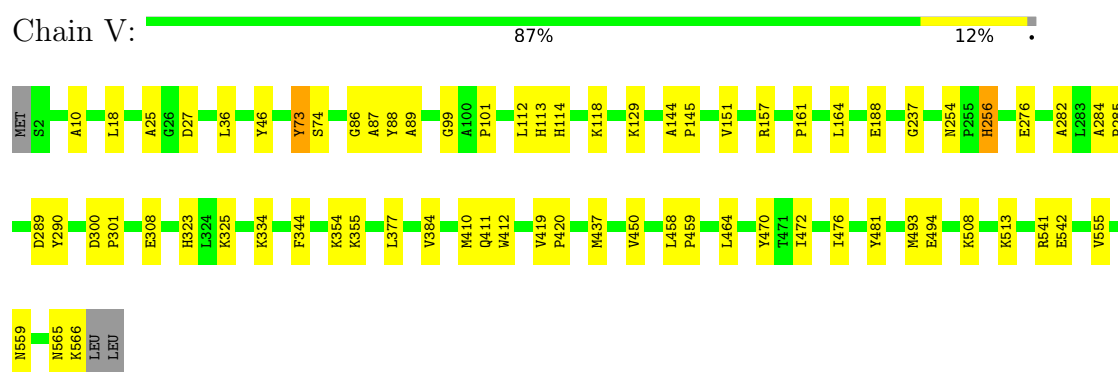
• Molecule 1: PYRUVATE DECARBOXYLASE



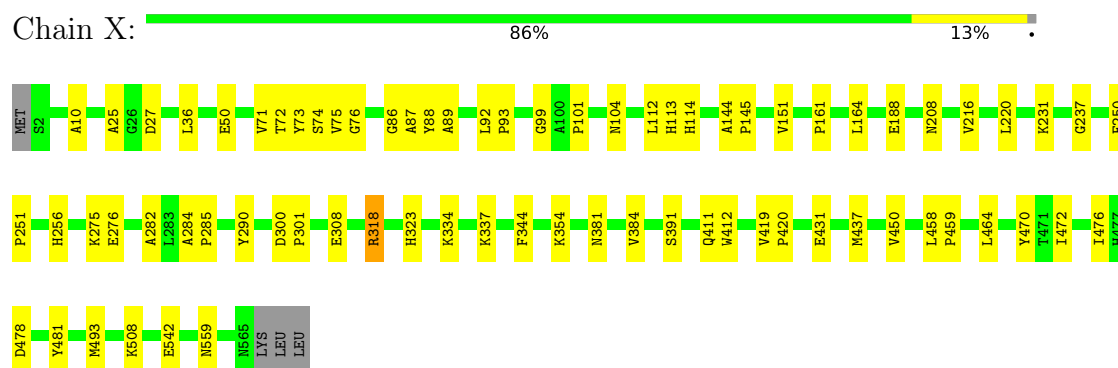
● Molecule 1: PYRUVATE DECARBOXYLASE



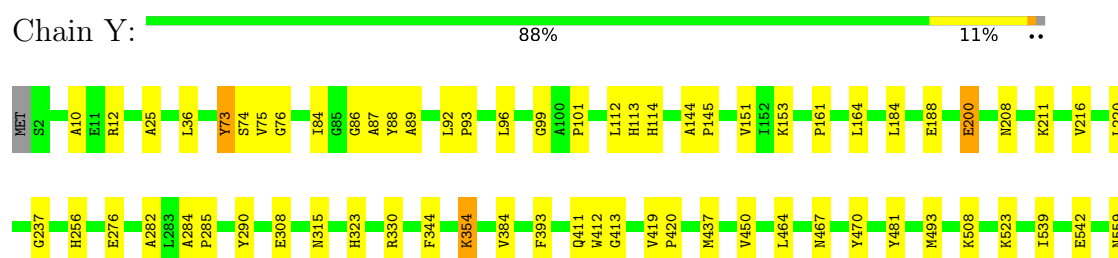
● Molecule 1: PYRUVATE DECARBOXYLASE



● Molecule 1: PYRUVATE DECARBOXYLASE

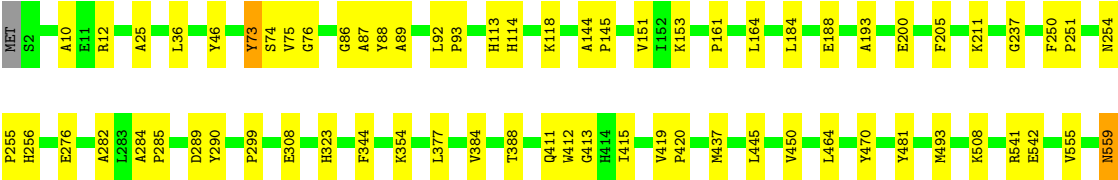
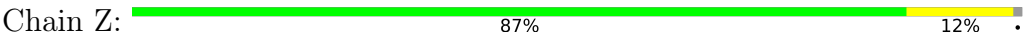


● Molecule 1: PYRUVATE DECARBOXYLASE





● Molecule 1: PYRUVATE DECARBOXYLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	70.90Å 111.17Å 167.12Å 89.89° 90.87° 101.27°	Depositor
Resolution (Å)	16.97 – 2.30 16.97 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.6 (16.97-2.30) 93.8 (16.97-2.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.29Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.171 , 0.194 0.168 , 0.189	Depositor DCC
R_{free} test set	10948 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	22.8	Xtriage
Anisotropy	0.424	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 20.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.337 for -h,-k,l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	38331	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.47	2/4377 (0.0%)	0.71	1/5950 (0.0%)
1	B	0.46	1/4369 (0.0%)	0.74	2/5940 (0.0%)
1	E	0.50	3/4369 (0.1%)	0.72	2/5940 (0.0%)
1	F	0.51	3/4369 (0.1%)	0.73	1/5940 (0.0%)
1	V	0.43	1/4369 (0.0%)	0.72	1/5940 (0.0%)
1	X	0.44	1/4360 (0.0%)	0.72	0/5929
1	Y	0.45	0/4369	0.71	1/5940 (0.0%)
1	Z	0.46	3/4369 (0.1%)	0.72	1/5940 (0.0%)
All	All	0.47	14/34951 (0.0%)	0.72	9/47519 (0.0%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	559	ASN	CA-C	-7.76	1.42	1.52
1	Z	559	ASN	C-O	-7.22	1.15	1.24
1	A	200	GLU	C-O	-7.13	1.15	1.24
1	B	560	SER	C-O	-6.36	1.15	1.24
1	F	553	LYS	C-O	-6.02	1.17	1.24

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	565	ASN	O-C-N	7.19	131.12	123.42
1	Y	73	TYR	N-CA-C	5.59	118.34	109.96
1	V	73	TYR	N-CA-C	5.51	118.22	109.96
1	F	73	TYR	N-CA-C	5.48	118.18	109.96
1	E	73	TYR	N-CA-C	5.44	118.13	109.96

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	4281	0	4255	58	0
1	B	4276	0	4242	58	0
1	E	4273	0	4243	53	0
1	F	4273	0	4243	69	0
1	V	4273	0	4243	61	0
1	X	4264	0	4230	70	0
1	Y	4273	0	4243	54	0
1	Z	4273	0	4243	58	0
2	A	614	0	0	13	0
2	B	479	0	0	13	0
2	E	546	0	0	12	0
2	F	522	0	0	26	0
2	V	482	0	0	15	0
2	X	486	0	0	12	0
2	Y	503	0	0	12	0
2	Z	513	0	0	12	0
All	All	38331	0	33942	434	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 6.

The worst 5 of 434 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:X:72:THR:CG2	1:X:75:VAL:HG23	1.69	1.23
1:X:72:THR:HG23	1:X:75:VAL:CG2	1.77	1.14
1:X:72:THR:CG2	1:X:75:VAL:CG2	2.26	1.12
1:F:308:GLU:HG3	2:F:2343:HOH:O	1.52	1.07
1:Y:450:VAL:HG11	1:Y:493:MET:HE1	1.39	1.03

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	565/568 (100%)	553 (98%)	12 (2%)	0	100	100
1	B	564/568 (99%)	554 (98%)	10 (2%)	0	100	100
1	E	564/568 (99%)	554 (98%)	10 (2%)	0	100	100
1	F	564/568 (99%)	553 (98%)	11 (2%)	0	100	100
1	V	564/568 (99%)	555 (98%)	9 (2%)	0	100	100
1	X	563/568 (99%)	553 (98%)	10 (2%)	0	100	100
1	Y	564/568 (99%)	554 (98%)	10 (2%)	0	100	100
1	Z	564/568 (99%)	555 (98%)	9 (2%)	0	100	100
All	All	4512/4544 (99%)	4431 (98%)	81 (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	436/437 (100%)	433 (99%)	3 (1%)	76	87
1	B	435/437 (100%)	429 (99%)	6 (1%)	59	76
1	E	435/437 (100%)	431 (99%)	4 (1%)	70	84
1	F	435/437 (100%)	430 (99%)	5 (1%)	65	81
1	V	435/437 (100%)	432 (99%)	3 (1%)	76	87
1	X	434/437 (99%)	431 (99%)	3 (1%)	76	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	435/437 (100%)	431 (99%)	4 (1%)	70	84
1	Z	435/437 (100%)	432 (99%)	3 (1%)	76	87
All	All	3480/3496 (100%)	3449 (99%)	31 (1%)	70	84

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	354	LYS
1	Y	464	LEU
1	F	566	LYS
1	Z	354	LYS
1	Y	200	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
1	V	323	HIS
1	X	396	GLN
1	Z	434	ASN
1	V	396	GLN
1	X	208	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	566/568 (99%)	-1.69	0 100 100	15, 21, 39, 65	2 (0%)
1	B	565/568 (99%)	-1.63	0 100 100	8, 27, 49, 73	2 (0%)
1	E	565/568 (99%)	-1.69	0 100 100	15, 23, 41, 73	2 (0%)
1	F	565/568 (99%)	-1.69	0 100 100	12, 22, 42, 71	2 (0%)
1	V	565/568 (99%)	-1.62	0 100 100	15, 27, 48, 66	2 (0%)
1	X	564/568 (99%)	-1.65	0 100 100	15, 27, 48, 67	2 (0%)
1	Y	565/568 (99%)	-1.65	0 100 100	16, 27, 45, 67	2 (0%)
1	Z	565/568 (99%)	-1.65	0 100 100	16, 26, 45, 63	2 (0%)
All	All	4520/4544 (99%)	-1.66	0 100 100	8, 25, 47, 73	16 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.